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Evolution of plant-specific Snf2 proteins and RNA polymerases and their function in maintaining paramutations in *Zea mays*

by

Jennifer Lynn Stonaker

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Committee in charge:

Professor Jay B. Hollick, Chair
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Abstract

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Professor Jay B. Hollick, Chair

Paramutation describes an interaction between specific alleles which results in heritable epigenetic changes in gene expression. To study the mechanisms underlying paramutation, genetic screens were performed to identify factors required to maintain repression (rmr) of paramutant states. For my thesis research I mapped and identified rmr1 as encoding a novel, plant-specific Rad54-like Snf2 protein. Additionally, I have participated in the identification of rmr6 as encoding RPD1, the largest subunit of the plant specific RNA polymerase IV (Pol IV), and rmr7 as encoding RPD2a, the second largest subunit of either Pol IV and / or an additional plant-specific RNA polymerase, Pol V. Pol IV and Pol V, along with RMR1 and related Snf2 proteins, have evolved exclusively in plants to mediate RNA-based epigenetic repression. While the epigenetic changes mediated by rmr1, rmr6, and rmr7 appear to indirectly affect the paramutation mechanism, the identification of these factors has facilitated cross-species comparisons of the RNA-based repression mechanisms and provided new evidence for the role of these types of regulatory mechanisms in plant development and evolution.

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Chapter 1 -- Introduction

Since the early 20th century, when scientists combined Mendel's rules of inheritance with knowledge of DNA as the molecule of heredity, genetics has been a powerful tool for analyzing the function, development, and evolution of organisms. However, as the study of genetics progressed it became clear that the basic gene concept was not sufficient to explain higher organism complexity. Information was encoded, not just by DNA, but by modifications which altered phenotype through chromatin changes instead of DNA sequence modification. The field of epigenetics formed to study this additional level of biological information.

Paramutation: a rare but general feature of eukaryotes

Paramutation is an epigenetic behavior in which heritable changes in gene regulation occur as a result of allelic interactions [Brink 1958]. Typically, only specific alleles of a given locus participate in paramutation. Paramutagenic alleles facilitate gene regulation changes in paramutable, or responding, alleles. Neutral alleles do not participate in paramutation. The directed interaction between paramutagenic and paramutable alleles represents the hallmark of paramutation and results in a violation of Mendel's law that alleles segregate away from the heterozygote unchanged [Brink 1973].

The first report of a paramutation-like transmission phenotype was the "Rabbit Ear" rogue phenotype of garden peas, *Pisum sativum* [Bateson and Pellew 1915]. These rogues were produced at variable rates by commercial pea lines, and exhibited weedy traits such as narrow leaves, curved pods, and smaller seeds. Crossing rogues by normal types resulted in intermediate F1 generations in which only the upper portion of the plant developed rogue characteristics [Bateson and Pellew 1915; Bateson and Pellew 1916]. Selfing these intermediate F1 plants resulted in true breeding rogue types [Bateson and Pellew 1915] suggesting that the normal, commercial traits were altered in the F1 generation [Brotherton 1923]. Specific loci required for the rogue phenotype were never identified.

Similar non-Mendelian inheritance patterns were independently discovered in other plant species. Examples include the cruciata character in *Oenothera* [Renner 1959] and the *sulfurea* locus of tomato [Hagemann and Snoad 1971]. With the production of genetically modified plants in the 1980s, additional examples resembling paramutation were identified at several transgenes including the bacterial herbicide resistance genes *nptII, hpt*, and *spt* in tobacco and the maize *a1* color gene in Petunia [reviewed in Chandler and Stam 2004]. Paramutation-like phenomena have also been observed in fungi and animals [reviewed in Chandler and Stam 2004] including humans, where interactions between specific alleles of the *IDDM2* locus in males appear to reduce risk of type 1 diabetes in their children [Bennett *et al.* 1997]. These examples highlight the diversity of alleles which participate in paramutation or paramutation-like behaviors.

Paramutation in maize

Historically, models for paramutation research have been developed at the *colored1* (*r1*), *colored plant1 / booster1* (*b1*), and *purple plant1* (*pl1*) loci in maize [Hollick *et al.* 1997]. These loci encode transcriptional activators of the maize anthocyanin biosynthesis pathway with distinct but overlapping functions [reviewed in Dooner *et al.* 1991]. These model loci are ideal for studying paramutation because modifications of the anthocyanin pathway do not affect plant fitness, and changes in gene activity due to paramutation are easily observed by visual changes in plant pigmentation. The three loci each exhibit distinct behaviors during paramutation that facilitate study of different aspects of the complex paramutation mechanism.

1. *purple plant1* (*pl1*)

Our lab has focused on paramutation occurring at *Pl1-Rhoades,* the only allele of *pl1* known to participate in paramutation. *Pl1-Rhoades* can exist in distinct regulatory states, termed *Pl* and *Pl'*, that are distinguished by their pigmentation differences [Hollick *et al.* 1995]. The *Pl* state produces intense and complete coloration of plant tissues, most notably in the seedling leaf sheath, anthers, and roots. The *Pl'* state is identified by reduced pigmentation that takes on a variegated or mottled appearance in the anthers and is sunlight dependent in other plant tissues.

The *Pl* state can spontaneously change to *Pl'*, and this happens at different frequencies in different stocks [Hollick *et al.* 1995; Hollick *et al.* 2000; Gross and Hollick 2007]. When *Pl* and *Pl'* are brought together in the heterozygote *Pl'* types are exclusively transmitted. This non-Mendelian inheritance pattern is not due to a chromosome segregation disorder because genetic markers linked to the *pl1* locus segregate equally in F2 progeny [Hollick *et al.* 1995]. Backcrossing F1 progeny from the cross above to a *Pl* tester also produces all *Pl'*-like progeny illustrating that *Pl* acquires the expression levels and paramutagenicity of *Pl'* [Hollick *et al.* 1995]. The *Pl'* state is highly stable, but reversion to *Pl* can occur when the allele is kept in hemizygous state or with certain neutral alleles [Hollick and Chandler 1998; Gross and Hollick 2007].

A precise measurement of pigmentation can be achieved using the Anther Color Score (ACS), a standardized scale providing seven categories for anther color [Hollick *et al.* 1995]. Plants having anthers with an ACS1 through 4 have a *Pl'* genotype; they only transmit paramutagenic *Pl'*-type states. They produce little pigmentation, and are highly stable, only producing progeny with equal or lower ACS scores. Plants having ACS7 anthers represent completely colored *Pl* types which are moderately stable. Plants with ACS5 and ACS6 are considered to be metastable and can produce progeny with anther color scores that are either higher or lower.

Anther color directly correlates with the amount of *pl1* RNA produced [Hollick *et al.* 2000]. As measured by RNase protection assays, there is 18.6-fold more *pl1* RNA in *Pl/Pl* types than in *Pl'/Pl'* types [Hollick *et al.* 2000]. However, nuclear run-on transcription assays detect only a 3-fold difference in transcription from the *pl1* locus in the two states, suggesting that both transcriptional and post-transcriptional repression mechanisms are required to maintain the *Pl'* state [Hollick *et al.* 2000]. Additionally, expression from the *Pl1-Rhoades* allele correlates with paramutagenicity--weakly expressed alleles are more paramutagenic [Hollick *et al.* 1995].

The *cis*-acting sequence features responsible for mediating paramutation of *Pl1-Rhoades* have not been identified. Mutational analysis of *pl1* indicates that PL protein is not required for paramutation although either *pl1* transcription or *pl1* RNA are required [Gross and Hollick 2007]. *Pl1-Rhoades*, like all *pl1* alleles, contains a 3' duplication that includes a portion of the coding sequence [Cone *et al.* 1993]. The 5' proximal region, which appears to have undergone rearrangement relative to other neutral *pl1* alleles, contains a CpG island and *doppia*, a fragment of a CACTA-like transposon found in *Pl1-Rhoades* and a related neutral allele *Pl1-Blotched* [Gross 2007]. No DNA methylation changes have been observed between *Pl* and *Pl'* [Hollick *et al.* 2000; Gross 2007]. Recombinational analysis indicates that the elements which facilitate paramutation are located 3' distal to the coding sequence, but their molecular nature has not been identified [Gross 2007].

2. *colored plant1* (*b1*)

Paramutation at *b1* is observed through changes in pigmentation in the plant body. *B1-Intense* is the only allele of *b1* which participates in paramutation. It exists in two epigenetic states, a paramutable and highly expressed state referred to as *B-I* and a paramutagenic and weakly expressed state referred to as *B'* [Patterson *et al.* 1993]. Like *Pl, B-I* is unstable and can spontaneously change to *B'*, and *B-I* is always converted to *B'* when the two states are combined in the heterozygote [Coe 1959; Coe 1966]. However, unlike *Pl'*, the *B'* state is extremely stable with no reversion of *B'* to *B-I* being observed in any background [Coe 1966; Dorweiler *et al.* 2000].

The cis-acting elements required for paramutation at the *b1* locus have been identified. Both the ability to induce and respond to paramutation is localized to a tandem array of seven 853-bp repeats located 100-kb upstream of the *b1* promoter [Stam *et al.* 2002]. The repeats are identical in sequence between *B'* and *B-I*, but *B-I* is highly methylated and contains a more open chromatin structure relative to *B'* [Stam *et al.* 2002]. Long distance interactions are detected between the repeats, the *b1* promoter, and addition regulatory elements between the repeats and the *b1* locus in highly expressing *B-I* alleles while less frequent interactions are detected only between the repeats and the *b1* promoter in weakly expressed *B'* alleles [Louwers *et al.* 2009]. Reduction in the number of repeats decreases the paramutagenicity of *B'* [Stam *et al.* 2002] and prevents long distance interactions with the *b1* promoter [Louwers *et al.* 2009]. The repeats and additional regulatory elements acts as functional enhancers of *b1* transcription and highlight the emerging role of transcription in paramutation.

3. *colored1* (*r1*)

The *r1* locus controls pigmentation in both the plant body and aleurone layer of the seed. Paramutation of *r1* is typically observed only in the aleurone and is somewhat distinct from paramutation at either *pl1* or *b1*. Namely, the paramutable and paramutagenic haplotypes of *r1* are structurally distinct, and paramutation of a paramutable allele is only measurable upon testcrossing from the F1 heterozygote [Brink 1956]. Paramutant alleles (*R-r'*) are not highly paramutagenic [Brown and Brink 1960] or stable, with reversion from *R-r'* to *R-r* occurring at high frequency [Brink *et al.* 1968]. Spontaneous conversion of *R-r* to *R-r'* can occur, but the subsequent *R-r'* state is not heritable [Brink *et al.* 1968].

Paramutable haplotype *R-r* contains two components, P, a single *r1* gene necessary for pigment production in the plant body, and the S subcomplex, an inverted duplication of the *r1* coding sequence required for pigment production in the aleurone layer of the seed. [Walker *et al.* 1995]. Additionally, the S subcomplex contains *doppia* elements, also found in *Pl1-Rhoades* and *Pl1-Blotched* alleles, which may have contributed to the formation of the complex *R-r* haplotype structure [Walker *et al.* 1995]. Paramutagenic alleles *R-st* and *R-mb* contain multiple direct repeats of the coding sequence [Eggleston *et al.* 1995; Panavas *et al.* 1999]. Regions responsible for paramutation localize to the *r1* locus, rather than at distal elements as in *b1* and potentially *pl1*, but similarly depend on repetitive features and transcription. Deletion derivatives of *R-st* and *R-mb* which have fewer *r1* copies are less paramutagenic, and haplotypes or deletion derivatives with a single *r1* coding sequence are neutral with regard to paramutation [Kermicle 1995; Panavas *et al.* 1999]. Acquisition of paramutation at *R-r* depends on a large region including the inverted duplication [Brown 1966]. Small deletion derivatives of *R-r* which remove only *doppia* can still acquire paramutagenic activity, but larger derivatives which remove portions of the coding region cannot [Kermicle *et al.* 1996]. As with *b1*, changes in methylation are observed between *R-r* and *R-r'* alleles (increased in *R-r'* [Walker 1998]), but the causative relationship between methylation and paramutation remains unclear.

Trans-acting Factors

In addition to research into *cis*-acting elements required for paramutation, genetic screens were performed to identify loci required to maintain heritable repression of paramutant states in *trans*. Mutant individuals were identified by *Pl*-like seedling and anther phenotypes in a *Pl'* background. To date, 12 loci have been identified by recessive, ethyl methanesulfonate (EMS)-induced mutations and given the name *required to maintain repression* (*rmr*) [Hollick and Chandler 2001; Hollick *et al.* 2005; Stonaker *et al.* 2009; J. Hollick unpublished]. Mutant alleles identifying an additional factor, *mediator of paramutation1* (*mop1*), were also isolated in this screen [Hollick and Chandler 2001].

Homozygous mutants of *rmr1*, *rmr2*, *rmr6*, and *mop1* show varying increases in *pl1* RNA levels compared to wild-type siblings [Dorweiler *et al.* 2000; Hollick and Chandler 2001; Hollick *et al.* 2005]. Additional analysis shows that *rmr6* mutants have increased transcription from the *pl1* and *b1* loci indicating that *rmr6* is involved in transcriptional gene regulation [Hollick *et al.* 2005]. Individual *rmr1, rmr2*, *rmr6*, and *mop1* mutants allow *Pl'* alleles to heritably revert to *Pl* at different frequencies [Dorweiler *et al.* 2000; Hollick and Chandler 2001; Hollick *et al.* 2005], but *rmr7* mutants do not allow reversion except after several generations in the mutant background [Stonaker *et al.* 2009]. While normal function from all the rmr and mop loci are required for maintenance of *Pl'*, genetic tests indicate that *rmr6* and *mop1* are also necessary for maintenance of *B'* and acquisition of paramutant states at *b1*, *r1* ,and *pl1* (*rmr6* only) [Dorweiler *et al.* 2000; Hollick *et al.* 2005].

Several *rmr* factors are also important for normal maize plant development. Homozygous *rmr6* mutants exhibit severe defects in development including delayed flowering time, leaf polarity reversals, ectopic outgrowths, and improper sex determination [Parkinson *et al.* 2007]. Similar developmental phenotypes are observed sporadically in *mop1* mutants [Dorweiler *et al.* 2000]. Homozygous *rmr12* mutants show severe developmental defects which make plant propagation extremely difficult, and in certain field conditions, *rmr3* mutants exhibit stunted growth and localized regions of necrosis [J. Hollick, unpublished information]. These results indicate that there is some overlap between the mechanisms underlying paramutation and normal plant development. It is therefore thought that elucidation of the paramutation mechanism may have a broader impact on understanding of general organism function and evolution.

Paramutation and RNA-directed DNA Methylation

mop1 encodes the maize ortholog of RNA-DEPENDENT RNA POLYMERASE2 (RDR2) from *Arabidopsis* [Alleman *et al.* 2006; Woodhouse *et al.* 2006]. RDR2 is involved in a so-called RNA-directed DNA methylation (RdDM) pathway [Xie *et al.* 2004] which uses 24 nt small interfering RNAs (siRNAs) to direct DNA methylation and subsequent repression of target sequences [Matzke *et al.* 2009; Pikaard *et al.* 2008]. RdDM is well studied in *Arabidopsis* where forward and reverse genetics screens have identified the major pathway components and targets.

RdDM depends on the function of two plant-specific DNA-dependent RNA polymerases (RNAPs) named Pol IV and Pol V [Herr *et al.* 2005; Onodera *et al.* 2005; Kanno *et al.* 2005a; Pontier *et al.* 2005]. Pol IV is required for the accumulation of 24 nt RNAs, but the substrate for Pol IV activity is unknown [Pikaard *et al.* 2008]. CLASSY1 (CLSY1), a novel, plant-specific Snf2 protein is also required for 24 nt siRNA accumulation [Smith *et al.* 2007], and, while the precise function of CLSY1 is unknown, it is hypothesized to facilitate Pol IV action [Matzke *et al.* 2009]. Downstream of Pol IV activity, RDR2 generates double stranded RNA (dsRNA) molecules from single stranded RNA transcripts [Pontes *et al.* 2006; Xie *et al.* 2004]. dsRNAs are processed by DICER-LIKE3 (DCL3) into 24 nt siRNAs [Xie *et al.* 2004] and a single-stranded guide siRNA is bound to ARGONAUTE4 (AGO4) [Zilberman *et al.* 2003].

Pol V functions downstream of siRNA accumulation [Pontes *et al.* 2006] and produces low levels of non-coding RNA transcripts from target loci [Wierzbicki *et al.* 2008]. Homology-mediated interaction of AGO4 bound siRNAs to nascent Pol V transcripts could direct *de novo* DNA methylation at target loci through recruitment of DOMAINS REARRANGED METHYLASE1 and 2 (DRM1 and DRM2) and CHROMOMETHYLASE3 (CMT3) [Wierzbicki *et al.* 2008; Cao *et al.* 2003]. DRM1, DRM2, and CMT3 specifically methylate cytosine residues in CNG and CHH sites (where N is A or T and where H is A, T or C) facilitated by chromatin proteins SUVH9, SUVH2 [Johnson *et al.* 2008] and DEFECTIVE IN RNA-DIRECTED DNA METHYLATION1 (DRD1) [Kanno *et al.* 2004]. DRD1 is a Snf2 protein related to CLSY1 [Hale *et al.* 2007; Chapter 2, this work], but unlike CLSY1 it is not required for the accumulation of 24nt siRNAs [Kanno *et al.* 2004]. DRD1 is instead required for *de novo* acquisition and removal of RNA-directed cytosine methylation which facilitates dynamic control of RdDM targets [Kanno *et al.* 2005b].

The RdDM pathway functions to maintain heterochromatic regions and regulate a set of genes important for control of flowering time and stress responses [Matzke *et al.* 2007]. RdDM targets are mostly repetitive elements, such as the 5S rDNA repeat arrays, and transposable elements, such as AtSN1 retroelements, localized to heterochromatic regions of the genome [Onodera *et al.* 2005; Herr *et al.* 2005; Pontier *et al.* 2005; Tran *et al.* 2005]. The RdDM pathway also targets repetitive elements in euchromatic regions [Huettel *et al.* 2006] and can regulate expression of genes with attendant transposons, such as flowering regulators FWA and FLC [Chan *et al.* 2006; Kinoshita *et al.* 2007; Liu *et al.* 2004]. RdDM components are also required for the production of natural antisense siRNAs (nat-siRNAs) in response to abiotic and biotic stresses [Borsani *et al.* 2005; Henz *et al.* 2007; Pikaard *et al.* 2008] demonstrating that the RdDM pathway plays an important role in *Arabidopsis* genome function.

The identification of *mop1* as a RDR2 ortholog indicates that the RdDM pathway may play a similarly important role in maize genome functions, including paramutation. The *trans*-interactions observed in paramutation could be mediated by siRNAs produced from paramutagenic alleles that induce heterochromatin formation in paramutable alleles. Tandem repeats, like those at *b1* and *r1*, allow for sustainable production of siRNA silencing signals [Martienssen *et al.* 2003], and heterochromatin states of paramutant alleles could then be maintained by the RdDM machinery. Identification and characterization of additional *cis*- and *trans*-acting components of the paramutation mechanism will clarify the role of RdDM in paramutation.

Alternative Paramutation Mechanisms

siRNAs are not the only RNA molecules which affect epigenetic processes. Interactions between sense and antisense long non-coding RNAs (ncRNAs) can direct chromatin changes and are required for X-inactivation and imprinting at some loci [Yang and Kuroda 2007]. Other models of paramutation postulate direct physical interaction between paramutagenic and paramutable alleles via a mechanism similar to transvection or *trans*-inactivation in *Drosophila* [Hollick *et al.* 1997; Chandler and Stam 2004]. Upon the identification of RdDM components as necessary for paramutation [Alleman *et al.* 2006; Hale *et al.* 2007; Erhard *et al.* 2009; Stonaker *et al.* 2009], these models had largely fallen out of favor because physical pairing is not a requirement of RNA-based mechanisms. However, identification of long distance interactions at the *b1* locus [Louwers *et al.* 2009] has reactivated interest in physical interaction mechanisms.

Expression rate differences between *B-I* and *B'* are directly related to the amount and frequency of interactions between the *b1* promoter and upstream repeat / enhancer elements. *B-I* has more interactions, and the repeat / enhancers have a more open chromatin state, relative to *B'* [Louwers *et al.* 2009; Stam *et al.* 2002]. To date, only *cis*-interactions have been identified, but it is tempting to speculate that *trans*-interactions are also occurring. *Trans*-interaction of *B'* repeat / enhancer elements with the *B-I* promoter could result in decreased transcription from *B-I* and heterochromatin formation at *B-I* repeat / enhancer elements through spreading of repressive factors in a transvection-like mechanism. This would convert *B-I* to *B'* and allow for stable transmission of the *B'* state upon segregation of the paramutagenic allele.

Alternatively, paramutant states could be established by pairing-dependent interactions between alleles and subsequently maintained by RNA-mediated chromatin modifications. This would support the identified roles of both the repeat / enhancer elements and *mop1 / rdr2* in mediating paramutation at *b1* [Stam *et al.* 2002; Louwers *et al.* 2009; Alleman *et al.* 2006]. *Trans*-interactions between the *B'* enhancer and *B-I* promoter could cause RNA-mediated heterochromatin formation through a transcription-dependent process, examples of which are well-documented in both yeast and *Arabidopsis* [Buhler *et al.* 2007; Wierzbicki *et al.* 2008]. Further analysis of the *cis*- and *trans*-acting components of paramutation will help determine the relative contributions of pairing and RNA-based mechanisms.

Paramutation was once thought to be a rare and unusual feature of plants. Now, models highlight a role for critical nuclear processes, such as RNA-mediated chromatin changes, long-distance enhancer function, and transcription, in paramutation. Species- and genome context-dependent applications of these processes could produce the diversity of paramutation phenotypes observed in different organisms and at different loci. This current view indicates that paramutation is not a single, unusual mechanism but an emergent property of the systems required for normal genome function and homeostasis.

Research Directions

The goal of my graduate research was to better understand the molecular mechanisms of paramutation through analysis of the *trans*-acting factors involved in maintenance of *pl1* paramutation. To this end, I have mapped several *rmr* loci and identified *rmr1* as a novel Snf2-domain containing protein involved in a maize RdDM-type pathway (Chapter 2). Phylogenetic analysis classify RMR1, CLSY1 and DRD1 as members of a plant specific subfamily of a Rad54-like Snf2 proteins which contain novel sequence features predicted to mediate DNA-protein or protein-protein interactions (Chapter 2). I also participated in the identification of *rmr6* as encoding the largest subunit of Pol IV and *rmr7* as encoding the second largest subunit of Pol IV and / or Pol V (Chapter 3). Phylogenetic analysis of different polymerase components provided an updated look at the evolution of the Pol IV and Pol V complexes and the difference in their composition between grasses and eudicots (Chapter 3). Finally, genetic analyses of the *rmr1* allelic series support the function of *rmr1* in mediating interactions with other *rmr* factors, namely *rmr6* and *rmr7* (Chapter 4). However, unlike typical Snf2 protein function, *rmr1* is not required for transcriptional repression of *Pl'* but rather stability of *pl1* RNA (Chapter 4). The work I present in this dissertation supports the role of a RdDM pathway in maintenance of *Pl'* and contributes to an increased understanding of the evolution and function of RdDM components in land plants.

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Chapter 2 -- Mapping *rmr* loci and identification and phylogenetic analysis of the novel Snf2 protein RMR1

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Introduction

Genetic screens have identified multiple loci *required to maintain repression* (*rmr*) of the *Pl'* state [Dorweiler *et al.* 2000; Hollick and Chandler 2001; Hollick *et al*. 2005; Stonaker *et al.* 2009, see also Chapter 1, this work]. Plants homozygous for these EMS-induced *rmr*-type mutations have dark, *Pl*-like pigmentation patterns despite being homozygous for *Pl'*. Projects to map and characterize these loci were initiated to better understand their role in the paramutation mechanism. Here I detail my efforts to positionally clone *rmr2*, *rmr6*, and *rmr11* / *rmr1* and the subsequent phylogenetic analysis upon identification of *rmr1* as a Snf2 protein. Phylogenetic analysis of *rmr6* is presented in Chapter 3, and genetic and molecular characterization of *rmr1* is provided in Chapter 4.

Previous positional information for *rmr1*, *rmr2*, and *rmr6* was determined using a combination of 2-point linkage analyses and B-A mapping, a process in which supernumerary chromosome translocations are used to generate specific segmental aneuploids and uncover recessive mutations [Beckett 1978]. Linkage to the *T6-9 (043-1)* translocation breakpoint placed *rmr1* on either the long arm of chromosome 6 (6L) or the short arm of chromosome 9 (9S) [Hale *et al.* 2007]. *rmr2* was located on 2S through linkage to *b1* and confirmed with B-A mapping. B-A mapping was also used to position *rmr6* on the long arm of chromosome 1 [Hollick *et al.* 2005]. Neither B-A mapping or genetic linkage was successful in determining the location of *rmr11*.

The maize genome had not been sequenced when mapping projects were initiated, but refinements of positional information were facilitated by a high resolution genetic map onto which over 1500 simple sequence repeat (SSR) markers have been mapped [Sharopova *et al.* 2002]. SSR markers are size polymorphisms that can be detected by PCR making high throughput screening of mapping populations relatively straightforward. SSR markers were used to determine the location of *rmr11* and refine the map position of *rmr1*, *rmr2*, and *rmr6*.

Synteny between maize and rice [Ahn and Tanksley 1993] facilitated candidate gene selection using rice gene order as a proxy. When sequence information was available, Cleaved Amplified Polymorphic Sequences (CAPS) [Konieczny and Ausubel 1993] and derived CAPS (dCAPS) markers [Neff *et al.* 1998] were generated. These PCR-based markers identify specific single nucleotide polymorphisms (SNPs) between samples. While not as amenable to high-throughput screening due to an additional restriction enzyme digest step, CAPS and dCAPS markers are useful for refining mapping position and verifying potential mutant lesions.

Using the general strategy indicated above, I generated two new markers in an attempt to refine the map position of *rmr2* and *rmr*6, sequenced a candidate gene for *rmr2*, and initiated a screen to identify new *rmr2* alleles. I successfully mapped *rmr11* and determined that it was not a separate locus but rather that *rmr11-1* represented a mutant allele of *rmr1*. Subsequently, we identified *rmr1* as encoding a Snf2 protein related to *Arabidopsis* RNA-directed DNA methylation (RdDM) component DEFECTIVE IN RNA-DIRECTED DNA METHYLATION1 (DRD1) [Hale *et al.* 2007, this work]. Phylogenetic analyses identify RMR1 and related DRD1 subfamily proteins as ATP-hydrolysis dependent DNA translocases with the potential to form multiple interactions with DNA and chromatin proteins through their variable amino-terminal domains. This identification, along with the cloning of additional *trans*-acting factors, supports a role for the RdDM pathway in maintaining paramutant states and provides new evidence for the roles of DRD1 subfamily proteins in RdDM.

Results

rmr2 marker development hindered by breakdown of maize / rice microsynteny.

Using an A632 *Pl'* / *rmr2-1* F2 mapping population, *rmr2* had been previously mapped to an ~8 cM region between simple sequence repeat (SSR) markers *umc1845* and *bnlg1064* in bin *2.03* (Figure 1A). As no publicly available SSR markers in this interval were polymorphic in our mapping population, we undertook a strategy to refine the position of *rmr2* through the creation of new molecular markers. Primers were designed to available maize expressed sequence tags (EST) predicted to be in the *umc1845 - bnlg1064* interval by rice synteny (Table 1). 22 genomic regions were successfully amplified from parental genomic DNA and sequenced to identify 6 SNPS and 2 indels. A derived cleaved amplified polymorphic sequence (dCAPS) marker based on the SNP identified in 2map14, proved to be unlinked when tested against the *rmr2-1* F2 mapping population. dCAPs primers generated to the other SNPs did not successfully amplify. The PCR size polymorphism at 2map23 (Figure 1C) showed 8.86 cM (39 / 440 recombinant chromosomes) linkage to *rmr2*. However, linkage of *rmr2* to *bnlg1064* was only 6.00 cM (36 / 600 recombinant chromosomes), suggesting that 2map23 was more distal to *rmr2* than *bnlg1064*, and therefore unhelpful in refining the position of *rmr2*.

Given the linkage results with 2map14 and 2map23, an analysis of microsynteny between maize and rice was undertaken for this region (Figure 1A, B). While a framework of syntenic features can be identified, several features have undergone rearrangement, most notably, maize EST AY107034 and marker *ivr1*. AY107034 is located at ~230 cM, outside of the mapping interval created between *umc1845* and *bnlg1064* (Figure 1A). However, the rice homolog to AY107034 is located in the syntenic mapping interval adjacent to the rice homolog of 2map14 (Os2map14) (Figure 1B). If this region has undergone rearrangements between maize and rice it could explain the observed non-linkage of the 2map14 marker. 2map23 also appears to be in a region with loss of microsynteny, as the gene order of *ivr1*, predicted to be adjacent to 2map23, is not conserved (Figure 1A, B). In total, these results highlight a breakdown of microsynteny between maize and rice in the vicinity of *rmr2*, and indicate that using synteny with rice may not be a successful approach to positional cloning *rmr2*. Fortunately, current assemblies of the B73 reference genome now make this synteny strategy obsolete.

rmr2 does not encode SET domain protein SDG104.

Concurrent with new marker development described in the previous section, we undertook a search for potential candidate genes in the *rmr2* mapping interval. The *sdg104* gene model, encoding a putative histone methlytransferase related to *Su(var)3-9*, had been localized to this region by Springer *et al.* [2003] (Figure 1A). SET domain proteins such as those encoded by *sdg104* are involved in numerous epigenetic processes and transcriptionally regulate gene expression through methylation of histone tails [Dillon *et al.* 2005], making *sdg104* a likely candidate for *rmr2*. If *rmr2* turned out to not be *sdg104*, sequencing of the parental alleles could identify polymorphisms which could be used to generate new mapping markers.

Three polymorphisms were identified in the *sdg104* sequence between *rmr2-1* and the B73 genomic DNA (Figure 2A): INS1, a small 14 nucleotide indel in the 5' UTR intron, SNP1, a G to C conversion at base 521 generating a non-conserved substitution in protein sequence (Figure 2B), and SNP2, a silent T to C conversion at base 1149. None of these polymorphisms occurred in the conserved YGD, Pre-SET or SET domains characteristic of SET domain proteins (Figure 2B), and the apparent transversion at SNP1 was not indicative of an EMS-generated lesion. Subsequent sequencing of other non-mutant Rmr2 alleles found the polymorphisms were not unique to *rmr2-1* (Figure 2C).

Primer sets were also used to evaluate structural polymorphisms in DNA isolated from mutants homozygous for a putative transposon-tagged allele *rmr2-m1*, although *rmr2-m1* had not been fully-vetted as a stable allele of *rmr2*. A transposon insertion into the *sdg104* coding sequence would predict a failure to amplify or an increase in amplicon size with certain primer sets. Neither of these predictions was observed (Figure 2D), suggesting that either the transposon had jumped out of *sdg104* or that *sdg104* was not *rmr2*. Partial sequencing of *sdg104* in *rmr2-m1* homozygotes revealed no evidence of transposon insertion (See Appendix 2 for DNA sequences). Given the failure to identify unique polymorphisms in either *rmr2-1* and *rmr2-m1* backgrounds, *sdg104* was abandoned as a both a candidate and a source of marker development for *rmr2* mapping.

Screen identifies two putative new *rmr2* alleles.

The mapping efforts described above failed to identify the *rmr2* gene. The mapping interval could not be further refined due to the lack of linked, polymorphic markers, and the most obvious candidate in the region had been excluded. Without either conserved microsynteny or a maize genome sequence over the region new candidates would be difficult to identify. Therefore, mapping efforts for *rmr2* were halted until the genome information was sufficient to either generate new markers or select new candidate genes. In the meantime, an allele screen was initiated to identify new *rmr2* alleles. Additional alleles would facilitate vetting of new candidate genes once they were available.

Pollen from A619 *Pl'* plants was treated with the chemical mutagen EMS and crossed to *rmr2-1* heterozygotes in an A632 background (Figure 3A). Dark anthered M1 plants represent potential non-complementation between the new EMS-generated and existing *rmr2-1* allele. The alleles can be distinguished from each other by SSR genotyping because each was generated in a unique genetic background. For the initial growout of M1 material, ears were pooled into four groups based on maternal family number and pollination date (Figure 3A). Approximately 2000 M1 plants were grown out, and one dark plant was identified in Series D, family 04-1601. This putative new allele was given the temporary designation *ems041601*. An additional 2288 M1 plants were grown out during the following field season, but series information for individual families was not recorded. One dark plant was also identified in this growout with the putative new allele given the designation *ems05446*.

The *ems041601* / *rmr2-1* heterozygote was crossed to an A632 *Pl'* tester and by a plant that was heterozygous for the TB-2Sb chromosome (Figure 3B). TB-2Sb was chosen because it contains a break point along the 2S chromosome which could potentially uncover the *rmr2* locus and facilitate isolation of the new allele. However, subsequent growouts showed that the TB-2Sb stock did not uncover the *rmr2* locus as 8 out of 8 putative segmental monoploid hypoploid plants were *Pl'*. Plants from the cross with A632 were selfed to generate families segregating 1:3 from either *rmr2-1* or *ems041601*. These families were grown out in the winter 2005 season, but no ears were returned. The *ems05446* / *rmr2-1* heterozygote was also crossed to A632 *Pl'* (Figure 3C), and the resulting plants were selfed to generate families segregating 1:3 for either *rmr2-1* or *ems05446*. *Pl*-types from these families were selfed and await SSR genotyping to distinguish *rmr2-1* homozygotes from *ems05446* homozygotes (Table 2).

Mapping efforts for *rmr6* generate a new molecular marker.

Using publicly available markers, *rmr6* had been previously localized to an ~450 kb region on the long arm of chromosome 1 (1L) [Parkinson 2007]. The syntenic region in rice contained 51 putative genes [Parkinson 2007]. Several strategies were undertaken to develop new markers to refine the position of *rmr6* and aid candidate gene selection, including sequencing of BAC subclones and genes predicted to be in the region based on rice synteny. I selected one such gene model, *Os08g39880*, to look for polymorphisms which could be used to generate CAPS or dCAPS markers. Sequencing an ~500 bp region identified 4 SNPs (Figure 4A), and dCAPS primers were generated for each polymorphism. Of these only one, SNP2ApaI, produced a digestion product that was easily scored on agarose gels (Figure 4B). This new marker was tested against a set of *rmr6-1* F2 mutant DNA samples and determined to be linked to *rmr6* (0 / 26 recombinant chromosomes). However, additional development identified a more proximal marker, SBP [Parkinson 2007], and the SNP2ApaI marker was no longer needed.

Mapping *rmr11* identifies linkage to 6L and *rmr1*.

In addition to *rmr2* and *rmr6* a mapping project was also initiated for *rmr11*, but, unlike the other two loci, the general genome position of *rmr11* had not been determined. Initial mapping efforts and stock construction had excluded various regions (Figure 5) but not positively identified the location of *rmr11*. A genome wide approach to identify linkage between *rmr11* and specific SSR markers was undertaken to determine the position of *rmr11*.

SSR markers were selected on chromosomes 2L, 3S, 4S, 5L, 7S, 8, 9L and 10L. To verify the selected markers were polymorphic in the F2 mapping population they were initially tested on DNA samples from the A632 and *rmr11-1* parents and the F1 hybrid. If necessary, additional selections were made until a polymorphic marker was found. In total, 48 SSR markers were tested covering 33 bins on 8 chromosomes (Table 3). Of these, 26 were polymorphic in the mapping population, 20 were not polymorphic, and 2 failed to amplify. None of the markers tested were found to be linked to *rmr11*.

Next, regions previously eliminated from analysis were reconsidered. One marker on 6L, *bnlg2249*, amplified well with a clear polymorphism and showed potential linkage with the *rmr11* mutant phenotype by bulked segregant analysis. The marker was then tested on 20 individual mutant samples of which 15 were homozygous for the *rmr11-1* parental polymorphism, 4 were heterozygous, and 1 had only an A632-like polymorphism, demonstrating highly statistically significant linkage (χ^2=25.600, P=0.0001). Further screening with *bnlg2249* identified 47 recombinants out of 370 total chromosomes resulting in a recombination frequency of 12.7%. Flanking markers *umc2141* (11/90 recombinant chromosomes, 12.2%) and *umc2165* (65/200 recombinant chromosomes, 32.5%) were subsequently identified distal to *bnlg2249*. Within this region, tightly linked *bnlg1174a* (0/178 recombinant chromosomes) narrowed down the possible location of *rmr11* to a less than 0.56 cM interval around the marker.

Markers *bnlg2249*, *bnlg1174a*, and *umc2165* were also found to be linked to *rmr1* at similar frequencies as *rmr11* (Table 4). These results suggested the two loci were either in a similar genomic location on *6L* or alleles of the same gene. This second scenario seemed unlikely given the unusual genetic complementation results observed for *rmr11-1*. *rmr11-1*, the only allele of *rmr11*, non-complements both *rmr1-1* and mutations at *rmr6* (See Chapter 4 for data). The *rmr11-1* allele was originally designated as defining a unique locus because plants homozygous for *rmr11-1* are phenotypically distinct from plants homozygous for mutations identifying *rmr1* and *rmr6*, and it did map to the known location of *rmr6*. However, in light of this molecular linkage data, *rmr11* was tentatively re-assigned as an allele of *rmr1*, hereafter referred to as *rmr1-3*.

***rmr11-1* is an allele of *rmr1*, *rmr1-3*, and encodes a Snf2 protein.**

Similar to mapping efforts for *rmr2* and *rmr6*, little maize genome sequence information was available for the *rmr1* mapping interval, but, fortunately, microsynteny with rice seemed to be well conserved (Figure 6A). Within this syntenic region rice gene model *Os05g32610*, a Snf2 protein, was identified as a possible candidate for *rmr1* because of the known role of Snf2 proteins in chromatin remodeling and other nuclear processes [Flaus *et al*. 2006]. BLAST searches with *Os05g32610* as a query identified similar maize and sorghum GSS sequences, but no maize ESTs were identified. Oligonucleotide primers to a maize *Os05g32610*-like locus were designed from the collected rice, maize, and sorghum sequence and used to amplify sequence from maize BAC c0007N19 (Figure 6A). Marker *bnlg1174a* was also amplified from this BAC verifying that an *Os05g32610* homolog was present in the mapping interval (Figure 6A).

Genomic DNA PCR amplicons spanning the *Os05g32610* homolog were sequenced from *Rmr* progenitor alleles and mutant derivatives. In each allele of *rmr1*, unique, transition-type lesions indicative of EMS mutagenesis were identified (Figure 6B). The *rmr1-1*, *rmr1-2,* and *rmr1-4* alleles encode missense mutations predicted to disrupt protein function (Figure 6C). The *rmr1-3* allele contains a nonsense mutation in the 5' portion of the gene resulting in a potentially truncated protein (Figure 6B, 6C). CAPS markers generated to the *rmr1-1* and *rmr1-3* lesions verified invariant cosegregation of the lesion and mutant phenotype for both *rmr1-1* (876 chromosomes tested) and *rmr1-3* (268 chromosomes tested). This result, combined with the disruptive nature of the mutant-specific lesions, confirm that *rmr11-1* is an allele of *rmr1*, *rmr1-3,* and that *rmr1* encodes a Snf2 protein homologous to *Os05g32610*.

cDNA sequencing confirmed that *rmr1* had a gene structure similar to *Os05g32610* but with an additional intron early in the coding sequence (Figure 6B). Upstream from this intron was an extremely GC rich region (initial 500 bp at an average 71% GC, 64% - 76% GC over 50bp windows) with 6 potential translational start sites. Using a modified 5' RACE protocol optimized for high GC content, I identified the same transcriptional start site (85 bp upstream of the first translational start site) in 6 separate amplicons (see Appendix 2 for sequences). While it is still unclear which of the 6 potential translational start sites is used *in vivo*, I have used the first start site for subsequent *in silico* analysis.

The *rmr1* locus is predicted to encode a 1435 amino acid protein and contains a nuclear localization signal from amino acids 151 to 174 (Figure 6C). Pfam [Bateman *et al.* 2004] identified a SNF2_N domain from amino acids 851 to 1211 (PF00176, E value = 7.4e-30) and a Helicase_C domain from amino acids 1255 to 1334 (PF00271, E value = 1.1e-11) (Figure 6C) which together comprise the bipartite domain characteristic of proteins in the Snf2 family [Flaus *et al*. 2006]. Snf2 proteins are part of the SF2 helicase superfamily, but instead of separating DNA they use the energy from ATP hydrolysis to translocate along the DNA duplex. The seven helicase motifs found in all helicase-like proteins are highly conserved in RMR1 (Figure 6D). Motifs I and II contain the Walker A and Walker B boxes involved in ATP hydrolysis [Thomä *et al*. 2005]. Motifs III and VI are required for sensing ATP hydrolysis while motifs Ia, IV, and V interact with the DNA molecule [Thomä *et al*. 2005]. The *rmr1-4* allele has a missense mutation affecting an invariantly conserved glycine residue (G→R) in motif III (Figures 6D, 9). The *rmr1-1* and *rmr1-2* alleles do not have mutations in the helicase motifs, but instead encode amino acid substitutions (A→V and S→N respectively) near regions involved in DNA binding and sensing ATP hydrolysis (Figure 6D). These results predict that RMR1 is a nuclear-localized and functional ATP-hydrolysis dependent translocase.

In contrast to the conserved carboxy (C)-terminal half of RMR1, no conserved sequence domains or motifs could be identified in the the amino (N)-terminal half of RMR1 (RMR1n) apart from the nuclear localization signal. Submission of the RMR1n sequence to structural prediction program PHYRE (Protein Homology/analogY/Recognition Engine http://www.sbg.bio.ic.ac.uk/phyre/html) did not identify any conserved structural motifs with significant E values, but the program PONDR [Xue *et al*. 2010] identified regions of intrinsic disorder (ID) in RMR1n. ID refers to proteins or protein regions that lack a stable secondary and / or tertiary structures under physiological conditions [Uversky and Dunker 2010] and can be predicted based on amino acid composition [He *et al*. 2009]. Figure 6C shows the four regions of intrinsic disorder in RMR1: A (amino acids 1-322, avg. PONDR score=0.8476), B (aa 352-426, 0.8258), C (aa 448-528, 0.7579), and D (aa 551-675, 0.7502). PONDR scores range from 0 to 1 and scores above 0.5 are considered to represent intrinsic disordered regions. Larger PONDR scores represent regions with greater support for the ID prediction. The nuclear localization signal is found in the first region of ID, and the nonsense mutation in the *rmr1-3* allele produces a stop between the second and third regions. Two regions of ID were identified in the C-terminal half of RMR1, but they were small (aa 1089-1097 and aa 1374-1401) and not as well supported (0.5185 and 0.5054, respectively) as the ID regions in RMR1n. Intrinsically disordered regions often mediate protein-protein interactions [Dunker *et al.* 2005]. Protein interactions mediated by the RMR1 ID regions could couple the presumed translocase function of the RMR1 Snf2 domain to other nuclear processes, such as chromatin remodeling, transcription, or targeted recruitment of DNA modifying enzymes.

***rmr1*, including the *rmr1-3* allele, is expressed in rapidly dividing tissues.**

Rmr1 cDNA has been successfully amplified from seedling leaves, immature ears and tassels, shoot apical meristems, and root tips but not cDNAs made from adult leaves suggesting that *rmr1* is primarily expressed from rapidly dividing tissues [Hale *et al*. 2007]. *rmr1-3* cDNA could be amplified by RT-PCR from seedling leaves (Figure 7A) indicating that the allele is expressed despite an early nonsense mutation that might be predicted to lead to nonsense-mediated decay [Hori and Watanabe 2007]. However, no *rmr1* mRNAs were observed in Northern blots of both total and poly(A)+ enriched RNA samples from tassels, ears, and seedlings (Figure 7D, 7E). This result is not due to RNA degradation as clear rRNA bands were observed by methylene blue staining (Figure 7B). Additionally, probe #1 hybridized with the linearized plasmid control demonstrating that there were no problems with probe hybridization. The failure of the Northern blot but the success of the RT-PCR indicates that *rmr1* may be expressed at very low levels. This idea is consistent with our finding that no existing maize EST collection or trace archive contains signatures of the *rmr1* gene.

RMR1 belongs to the DRD1 subfamily of Rad54-like Snf2 proteins.

The Snf2 protein family is large, but it is divisible into subfamilies based on sequence similarity within the SNF2 domain, and subfamily assignments are typically good predictors of protein function [Flaus *et al*. 2006]. To determine the subfamily to which RMR1 belonged, protein sequences with similarity to the RMR1 SNF2 domain (amino acids 851-1435; RMR1cd) were gathered from BLAST searches and aligned with MAFFT (Appendix 3). A phylogenetic tree generated from the alignment places RMR1 in the DRD1 subfamily (Figure 8) which is part of the larger Rad54-like group including subfamilies Rad54, ATRX, ARIP4, and JBP2. Members of the Rad54-like group use their ATP-hydrolysis dependent translocase activity to mediate DNA-protein interactions required for DNA or chromatin modifications [Mazin *et al*. 2010; Xue *et al*. 2003; Rouleau *et al*. 2002; Domanskyi *et al*. 2006]. Regulation of pyrimidine ring modifications, such as cytosine methylation, is a specific conserved function of the ATRX, DRD1, and JBP2 subfamilies [Gibbons *et al*. 2000; Kanno *et al*. 2004; Smith *et al*. 2007; Hale *et al*. 2007; Vainio *et al*. 2008; Cliffe *et al*. 2009].

The DRD1 subfamily is most closely related to the JBP2 subfamily, found exclusively in trypanosomes, with the ATRX / ARIP4 and Rad54 subfamilies more distant, respectively (Figure 8). In a previous analysis [Flaus *et al*. 2006], ATRX and ARIP4 were identified as distinct subfamilies, but in this analysis the ARIP4 sequences clustered within the larger ATRX subfamily. This is likely due to the small number of ARIP4 sequences in the multiple sequence alignment (two). Outside of the Rad54-like group the remaining sequences clustered into two main groups, here annotated as SSO1653-like and Snf2-like. The group annotated as Snf2-like in Figure 8 also contains members of the Swr1-like and Rad5/16-like groups, but was annotated as Snf2-like for clarity in the figure. The gross phylogenetic relationships identified in this analysis follow the same pattern as that identified by Flaus *et al*. [2006].

To examine the relationship of RMR1 to the DRD1 subfamily in more detail, proteins were excerpted from the large alignment, realigned (Figure 9), and used to generate a DRD1 subfamily specific tree (Figure 10). Unlike Rad54 and ATRX subfamilies, which show wide distribution in eukaryotes, the DRD1 subfamily is found exclusively in plants (Figure 9). Cr13231 from the green algae *Chlamydomonas reinhardtii* was used to root the tree as it is the closest non-plant sequence, but it groups with the ATRX subfamily in the larger tree (Figure 8, Figure 10).

In addition to RMR1, the only members of the DRD1 subfamily which have been identified by mutation are *Arabidopsis* proteins CLASSY1 (CLSY1) [Smith *et al.* 2007] and DRD1, the founding member of the subfamily [Kanno *et al*. 2004; Flaus *et al*. 2006]. DRD1 is a component of the RNA-directed DNA methylation (RdDM) pathway where it functions with the largest subunit of Pol V to direct DNA methylation at target loci [Matzke *et al.* 2009]. CLSY1 is required for the systemic spread of silencing signals [Smith *et al.* 2007] and is necessary for siRNA production in the RdDM pathway along with Pol IV [Matzke *et al.* 2009].

RMR1, DRD1, and CLSY1 each define distinct monophyletic clades within the subfamily (Figure 10). Predicted maize proteins ZM064574 and ZM093940 are more similar to DRD1 while ZM000342 and ZM108166 are more similar to CLSY1. *Arabidopsis* proteins At3g24340 and At1g05490 are more similar to RMR1, but neither has been identified in RdDM mutant screens or tested for a role in RdDM. They were tested for DNA repair function due to the similarity between the DRD1 subfamily and Rad54, but RNAi knockdowns of the loci had no effect on DNA damage responses [Shaked *et al.* 2006]. The position of RMR1 in the DRD1 subfamily indicates that it functions in RdDM but likely in a distinct role from DRD1 and CLSY1. However, the larger grouping of the RMR and CLSY clades indicate that the function of RMR1 and CLSY1 may be related while the function of DRD1 is more divergent.

The DRD1 subfamily is characterized by gene expansion.

The total number of DRD1 subfamily members and their distribution within the three clades is not conserved between different plant species (Figure 10, Table 5). Basal grass *Brachypodium dystachion* is predicted to contain the largest number of subfamily members at nine while rice and sorghum contain seven and five, respectively. Maize and *Arabidopsis* genomes are each predicted to encode six DRD1 subfamily members, and poplar and grape are predicted to contain four, although with differing distributions. Papaya and basal vascular plant *Selaginella* are only predicted to contain two subfamily members and are the only species which do not contain a representative in each clade.

The current papaya genome release lacks a DRD1 ortholog. As related species grape, poplar, and *Arabidopsis* each contain DRD1 orthologs this could represent gene loss or, more likely, incomplete sequence information in the draft release of the papaya genome. *Selaginella* contains two DRD1 subfamily members, one of which clusters in the CLSY clade and one which roots the CLSY and RMR clades. This topology indicates that the duplication giving rise to the DRD clade and the subfunctionalization of the RMR1 and CLSY1 clades occurred sometime after divergence of *Selaginella* from the angiosperm ancestor. This evolutionary history is similar to that of the largest subunits of plant specific RNA polymerases Pol IV and Pol V which function in *Arabidopsis* RdDM. The duplication which gave rise to Pol IV occurred in the ancestor of land plants while the duplication which gave rise to Pol V occurred in the ancestor of the angiosperms [Luo and Hall 2007]. This pattern correlates with the proposed functional interactions between DRD1 subfamily members and the RNA polymerase subunits in RdDM [Matzke *et al*. 2009].

Branch topologies within each angiosperm clade highlight a history of both ancient and recent sequence duplications. The CLSY clade is the smallest with relatively recent duplications only in maize, *Arabidopsis*, and poplar. These duplications correspond to tetraploidy events which occurred in these lineages after they diverged from other plants [Gaut and Doebley 1997; Swigonová *et al*. 2004; Lyons *et al.* 2008]. The RMR clade shows evidence of gene retention after a duplication which corresponds to the whole genome duplication that occurred in the grass ancestor [Paterson *et al.* 2004] combined with more recent duplications in *Brachypodium* and *Arabidopsis*. The DRD clade is the largest with evidence of gene retention after duplication in the grass ancestor and multiple additional duplications in the grass lineage. Low branch support makes the relative timing of these duplications difficult to determine. Surprisingly grape, without a recent history of whole genome duplication [Jaillon *et al*. 2007], also contains two DRD1-like proteins. The functional significance of the species-specific expansion of the DRD1 subfamily remains unclear.

Proposed RNA-binding activity of CLSY1 is not supported by phylogenetic analysis

Smith *et al*. [2007] suggested that CLSY1 may preferentially bind RNA as opposed to DNA due to alterations in the DNA binding residues from several large insertions in the DNA binding region. However, in our alignment, the specific residues they indicated are often not conserved amongst CLSY1 clade members (Table 6, Figure 9), and only one moderate-sized insertion, conserved in CLSY1 and to a lesser extent in RMR1 clade members, is observed (Figure 9). The multiple sequence alignment shows that the majority of predicted subfamily members have conserved helicase-like motifs I through VI. The only exceptions are Vv29366, missing half of motif I, Cp19.123, containing a large gap from just past motif II through the end of motif IV, and Bg3g18910, missing motifs 1a and IV. These proteins could be non-functional or the gaps could be due to protein model prediction errors or poor genome sequence quality. As additional genome sequence information becomes available these proteins will need to be reanalyzed. However, the strong conservation of helicase motifs for both ATP binding and hydrolysis and DNA binding indicates that the majority of DRD1 subfamily members are functional ATP-hydrolysis dependent DNA translocases.

Phylogenetic analysis of the N-terminal region of DRD1 subfamily proteins highlights both variability and strictly conserved residues.

Rad54-like group members ARIP4, ATRX, and JBP2 all contain functional important N-terminal domains in addition to the SNF2 domain [Rouleau *et al.* 2002; Wong *et al.* 2010; McDowell *et al*. 1999; Tang *et al*. 2004; Vainio *et al*. 2008; Cliffe *et al*. 2009]. Initial analysis of the RMR1 protein showed no conserved domains in the N-terminus, only regions of intrinsic disorder (Figure 6C), and attempts to identify sequences with similarity to the RMR1 N-terminal region (amino acids 1-850; RMR1n) only identified Sb09g19410 and Os05g32610, the RMR1 homologs from sorghum and rice, respectively. Using the sequences identified from analysis of the RMR1cd I created new multiple sequence alignments of the N-terminal regions of all DRD1 subfamily members (Appendix 5, Figure 11) and specific RMR-, DRD-, and CLSY-clade members (Figures 12, 13, 14). These alignments were then scanned for conserved regions or motifs which could provide additional information about the function of the DRD1 subfamily proteins.

All DRD1 subfamily members were aligned over the N-terminal region using alignment programs MAFFT, MUSCLE, SATCHMO, and TCOFFEE. Each program identified a single region of sequence conservation approximately 100 amino acids N-terminal to the SNF2 domain containing invariantly conserved glycine, histidine, and cysteine residues which I have annotated as the cysteine-rich motif (Figure 11A, 11C). The non-conserved region outside of this motif corresponds with the regions of intrinsic disorder identified in RMR1. The cysteine-rich motif shows no homology with the thymidine hydroxylase domain of JBP2 indicating that, unlike JBP2, DRD1 subfamily members are not involved in the catalysis of pyrimidine base modifications. The arrangement of residues within the motif (Cys-His, Cys_2) is predicted to form a secondary structure of loop - β sheet - β sheet and is flanked by two α helices (Figure 11B). This motif and structure does not match any known protein folds, but it is similar to zinc-finger motifs involved in DNA and protein interactions (Cys_2His_2 or Cys_{4-6}; β β α) [Krishna *et al.* 2003]. ATRX proteins contain a modified zinc-finger domain called ADD (ATRX-DNMT3-DNMT3L) which binds to histone H3 and recognizes its methylation status [Otani *et al.* 2009]. The DRD1 subfamily cysteine-rich motif shows no sequence or structural similarity to the ADD domain, but these results indicate that DRD1 subfamily proteins may have a modified zinc-finger-like motif which might be used for DNA or histone binding.

As with the DRD1 subfamily alignment, specific N-terminal alignments of RMR (Figure 12), CLSY (Figure 13), and DRD (Figure 14) clade members show the main region of amino acid similarity occurring in the last 100-150 amino acids before the SNF2 domain. The CLSY clade is distinct from the RMR and DRD clades in that much higher levels of sequence conservation are observed outside of the cysteine-rich region. Submission of CLSY1 and maize orthologs ZM000342 and ZM108166 to Phyre did not identify any statistically significant structural motifs (all E values >19), and thus the specific functions of these conserved regions remain unclear.

The RMR and DRD clades show relatively less sequence conservation, but many of the conserved residues scattered throughout the sequence alignment are positively or negatively charged. The CLSY clade members also have conserved positive or negative charged residues, but they are not as distinct because of the generally high levels of conservation within the CLSY clade. The conserved residues could function in DNA (positively charged) or histone (negatively charged) binding interactions. In particular, the RMR clade has an aspartic acid and glutamic acid-rich region around position 885 in the alignment (Figure 12). Similarly, human ARTX has a low-complexity polyglutamic acid string in the N-terminal region predicted to function in protein-protein interactions [Picketts *et al.* 1996] and a variable N-terminal region required for interactions with heterochromatin protein HP1 [Cardoso *et al.* 1998], the SET domain of polygroup protein EZH2 [McDowell *et al.* 1999], and transcriptional regulator Daxx [Tang *et al.* 2004].

In total, these results suggest that the N-terminal region of DRD1 subfamily members contains subfamily and clade-specific conserved regions which potentially function in unique protein-DNA or protein-protein interactions. The failure to identify similar motifs in proteins outside of the DRD1 subfamily may represent specialization of the motifs or, alternatively, low-complexity, intrinsically disordered regions involved in meditating protein-protein interactions.

Discussion

In this chapter I describe my efforts to map *rmr2* and *rmr6* and the identification of *rmr1* as encoding a member of the DRD1 subfamily of Rad54-like Snf2 proteins involved in RdDM. The phylogenetic analysis presented here is the most up-to-date survey of DRD1 subfamily diversity and the relationship of the subfamily to other Snf2 domain containing proteins. Additionally, this work is the first analysis of the regions outside of the Snf2 domain and has provided new insight as to the function of DRD1 subfamily members in RdDM.

Mapping efforts in our lab have been greatly facilitated by the release of the draft sequence of the maize genome [Schnable *et al.* 2009]. We are no longer dependent on synteny with rice, which proved so problematic for both *rmr2* and, ultimately, *rmr6* [Erhard *et al*. 2009], for candidate gene selection. Using this genome sequence information we have identified *rmr6* as encoding RPD1, the largest subunit of Pol IV [Erhard *et al*. 2009]. An additional *rmr* factor, *rmr7*, has been identified as encoding RPD2a, the second largest subunit of either Pol IV and or / Pol V [Stonaker *et al.* 2009]. Very recently, the *rmr2* gene has been identified, and it encodes a completely novel protein of 366 amino acids [Jay Hollick, unpublished]. This will be the first *rmr* factor not predicted to encode a component of the RdDM mechanism, and it could introduce a promising new avenue of research. Interesting, like the RMR1 N-terminal region, RMR2 is predicted to contain large regions of intrinsic disorder [Jay Hollick, unpublished]. The two putative new alleles from the *rmr2* allele screen should facilitate characterization of this new protein.

We were able to map and identify *rmr1* prior to the draft release of the maize genome because synteny with rice was conserved over the mapping interval. In fact, assembly of BAC c0007N19 sequence was facilitated by the *rmr1* sequence information deposited in Genbank. The *rmr1* locus encodes the founding member of the DRD1 subfamily of Rad54-like Snf2 proteins in maize. The phylogenetic analysis presented in this chapter predicts that RMR1 functions in a RdDM-like pathway, and, as expected, mutations in *rmr1* reduce 24 nt siRNA accumulation and asymmetric cytosine methylation at *doppia*, a transposable element fragment ~100 bp upstream of the *Pl1-Rhoades* coding sequence [Hale *et al*. 2007]. Additionally, RMR1 is required for 24 nt siRNA accumulation globally and both siRNA and non-polyadenylated transcript accumulation at long terminal repeat (LTR) retroelements which are abundant in the highly repetitive maize genome [Hale *et al*. 2009]. This analysis confirms the identification of RMR1 as a component of a RdDM-like pathway in maize.

While the identifications of *mop1*, *rmr1*, *rmr6*, and *rmr7* as encoding components of a RdDM-like pathway have begun to describe RdDM in maize, the effect of RdDM on paramutation is not clear. Mutations in *mop1* specifically reduce 24 nt siRNA accumulation at the *b1* repeat / enhancer sequences ~100 kb upstream of the *b1* coding sequence [Arteaga-Vazquez and Chandler 2010], but *b1* repeat / enhancer siRNAs are produced in all *b1* alleles, even those which do not participate in paramutation [Arteaga-Vazquez and Chandler 2010]. Like *rmr1*, mutations in *rmr6* reduce 24 nt siRNA accumulation and cytosine methylation at the *doppia* transposable element fragment upstream of *Pl1-Rhoades*, but *doppia* is methylated to the same extent in both the *Pl'* and *Pl* states [Hale *et al*. 2007; Erhard *et al*. 2009]. These results suggest that RdDM-mediated epigenetic changes at proximal repetitive elements can alter regulation of *Pl1-Rhoades* but may only indirectly affect paramutation. Analysis of RMR6/RPD1 and RMR7/RPD2a in Chapter 3 will highlight a new model for RNAP function in RdDM and in Chapter 4 I will present additional characterization of the effect of *rmr1* on *pl1*.

Previous phylogenetic analyses of the DRD1 subfamily were limited by a lack of plant genome sequence information [Flaus *et al.* 2006; Hale *et al.* 2007], but since those initial analyses, draft sequences for several plant genomes, including the draft maize genome, have been released [www.phytozome.net]. This additional sequence information facilitated the phylogenetic analysis presented here and highlights several important features of the DRD1 subfamily: (1) The DRD1 subfamily is found exclusively in plants and has expanded as plant evolution progressed; (2) DRD1 subfamily members contain highly conserved Rad54-like Snf2 domains and putatively function as ATP-hydrolysis dependent DNA translocases; (3) The N-terminal region of DRD1 subfamily members is generally variable but also contains a novel, subfamily specific cysteine-rich motif. The N-terminal domains putatively functions to mediate protein-protein or protein-nucleic acid interactions based on the function of similar domains in related Rad54-like Snf2 proteins.

Rad54 proteins are the founding members and best characterized representatives of the Rad54-like Snf2 proteins. Rad54 functions during multiple steps of the homologous recombination (HR) DNA repair pathway including mediating Rad51-bound single stranded DNA invasion of the DNA duplex, branch migration, and resolution of the Holliday junction through interaction with endonuclease Mus81/Mms4 [Mazin *et al.* 2010]. Rad54 activity during HR depends both on an unstructured N-terminal domain which interactions with Rad51 and Mus81/Mms4 and the ATP-hydrolysis dependent DNA translocase activity of the Snf2 domain that generates torsional strain to open the DNA duplex and increase the accessibility of the DNA to modifying enzymes [Mazin *et al.* 2010]. I propose a model for DRD1 subfamily members where similar translocase functions of the Snf2 domain could facilitate DNA accessibility while the variable N-terminal region could recruit additional RdDM components.

Pol IV and Pol V complexes are RdDM components with the potential to interact with the DRD1 subfamily N-terminal region. As described in the text, the DRD1 subfamily and the largest subunits of Pol IV and Pol V show similar patterns of gene duplication. Additionally, mutations in *DRD1* disrupt the localization and function of Pol V [Wierzbicki *et al.* 2008] while subcellular localization analysis indicate that CLSY1 is not required for Pol IV localization but may be required for Pol IV function [Smith *et al.* 2007]. Analysis of different *mop* and *rmr* mutants on LTR transcript accumulation also places RMR1 downstream of Pol IV and upstream of RDR2 [Hale *et al.* 2009]. Together, the molecular, localization, and phylogenetic results support the function of DRD1 with Pol V while RMR1 and CLSY1 are predicted to function with Pol IV and RDR2. The proposed functional interactions could be direct or indirect.

The intrinsic disorder regions identified in the RMR1 variable N-terminal regions could facilitate direct interactions with the Pol IV complex and / or other RdDM components. Intrinsic disorder describes proteins or protein regions which do not form a specific 3-D structures and can be predicted based on amino acid content and charge-hydrophobicity plots [He *et al.* 2009]. Intrinsic disorder is a common but often overlooked feature of eukaryotic proteomes. Greater than 50% of eukaryotic proteins are predicted to have long regions of intrinsic disorder, and these proteins disproportionately function in protein interaction networks [Uversky and Dunker 2010]. Disordered regions act as molecular scaffolds to bind multiple protein or nucleic acid partners and facilitate the activity of ordered proteins [Uversky and Dunker 2010]. RMR1 is interesting because it contains both ordered (Snf2 domain) and intrinsically disordered (N-terminus) regions within the same protein. Intrinsic disorder regions in the variable N-terminus of RMR1 could scaffold the ATP-hydrolysis dependent DNA translocase activity of the C-terminal Snf2 domain to other RdDM components.

The *rmr1-3* allele may provide a way to test this previously stated protein interaction hypothesis. The *rmr1-3* allele contains a nonsense mutation, but RT-PCR analysis indicates that the *rmr1-3* mRNA is still expressed. If this mutant *rmr1-3* mRNA was translated it would encode a truncated peptide lacking a Snf2 domain but retaining a nuclear localization signal and intrinsically disordered regions with the potential to form protein-protein interactions. Interestingly, as described in this chapter, *rmr1-3* was originally characterized as an allele of a separate locus, *rmr11-1* because unlike other *rmr1* alleles it non-complemented alleles of *rmr6*, which has since been identified as encoding the largest subunit of Pol IV. Non-allelic non-complementation is often a sign of protein interactions [Yook 2005], and perhaps the truncated protein produced by *rmr1-3* can still interact with RPD1 or the Pol IV complex but cannot function due to lack of the Snf2 domain. Further genetic analysis of *rmr1-3* is presented in Chapter 4.

Unlike the multifunctional Rad54 and ATRX proteins [Mazin *et al.* 2010; De Sario 2009], the DRD1 subfamily members appear to be highly specialized for different parts of the RdDM pathway. RMR1, CLSY1, and DRD1 are not structural orthologs. Proteins in clades defined by RMR1 and CLSY1 function in the Pol IV / RDR2 portion of the pathway while proteins in clade defined by DRD1 function in the Pol V portion of the pathway. However, these functional distinctions do not fully account for the diversity of subfamily members. Many plant species, including *Arabidopsis* and maize, contain multiple proteins in each clade, but as DRD1, CLSY1, and RMR1 were each identified by recessive, loss-of-function mutations [Kanno *et al.* 2004; Smith *et al*. 2007; Hale *et al*. 2007] duplicate proteins At2g21450, At5g20429, and ZM178435, respectively, cannot be functionally redundant. As these proteins differ mainly in their N-terminal regions, the diversity could provide a mechanism for fine tuning the RdDM response to different physiological conditions or genomic contexts via different protein interactions. Further characterization of the current DRD1 subfamily mutants and identification of additional mutants will help determine the extent of potential subfunctionalization within the DRD1 subfamily.

The data presented in this chapter supports a proposed in which the DRD1 subfamily functions to mediate interactions between RdDM components and target DNA sequences depending on predicted functions of the Snf2 and N-terminal domains. In the next chapter, I will study the phylogenetics and biochemistry of additional RdDM components identified in the *rmr* genetic screens. This information will further refine the model of the maize RdDM-like pathway.

Materials and Methods

Genetic Stocks

Elite inbred lines B73, A619, and A632 were provided by the North Central Plant Introduction Station (http://www.ars-grin.gov/ars/MidWest/Ames/). Color-converted versions of A619 and A632 inbred lines were created by introgression of the *Pl1-Rhoades* allele. *rmr2-1, rmr6-1, rmr1-1*, *rmr1-2*, and *rmr1-3* were derived from EMS-treated pollen obtained from stock accession no. 661A (*Pl-Rh sm1*; *R-r*; Maize Cooperative Stock Center, http://maizecoop.cropsci.uiuc.edu/) applied to a *Pl'* pistillate parent. *rmr1-4* was derived from EMS-treated color-converted A619 applied to color-converted A632. EMS-derived mutant plants were identified from M2 growouts by their dark seedling and anther phenotypes. Mutant individuals were crossed to *Pl'* and *Pl-Rh* testers, and individuals from these crosses were either sib crossed or selfed to generate working lines. Mutant plants were also crossed to the T6-9 translocation line carrying the *Pl1-Rhoades* allele which has been described by Hollick *et al*. [2005]. The *rmr2-m1* allele was identified in progeny of a cross between a *rmr2-1* homozygote and a line containing active *Mutator* (*Mu*) elements (J. Hollick, unpublished).

Genetic mapping of *rmr* mutants

F2 mapping populations for *rmr* mutants were created by crossing inbred *rmr* / *rmr*, *Pl'*/ *Pl'* to color-converted A632 (>93% A632). Seeds from F2 populations, mapping parents, and F1 hybrids were grown in sand bench flats under high light in the greenhouse, and sheath pigmentation was assessed between 10 and 14 days. For questionable seedlings, presence of root pigmentation was used as an additional mutant phenotypic characteristic. 1cm square leaf clippings were taken from parents, F1 hybrids, and F2 mutant plants, and DNA was isolated using the DNeasy 96 plant kit (Qiagen, http://www1.qiagen.com). Selected seedlings were grown to maturity in the greenhouse to assess anther pigmentation and verify mutant status.

SSR markers primer sequences for the markers were retrieved from MaizeGDB (http://www.maizegdb.org) and ordered from Sigma-Genosys (http://www.sigmaaldrich.com/Brands/Sigma_Genosys.html). Using resources provided by the Maize Mapping Project (MMP), markers were chosen that appeared to be highly polymorphic in A632 and A619 inbred lines to enrich for polymorphism in our mapping population. SSR markers were amplified from DNA samples using the following PCR reaction: 9.4µL PCR master mix (1.87mM $MgCl_2$, 12.5 mM Tris-HCl pH 8.3, 62.5 mM KCl, 0.00125% gelatin, 0.0125% BSA, 125µM each dNTP), 0.25µL SSR forward primer (20µM), 0.25µL SSR reverse primer (20µM), 0.1µL Taq DNA polymerase. Reactions were run in either 8 well strips or 96 well plates on a thermocycler using the following touchdown program: 1 cycle of [95˚C, 60 sec; 65˚C, 60 sec; 72˚C, 90sec], n cycles of [95˚C, 60 sec; (65-n)˚C, 60 sec; 72˚C, 90sec] until annealing temperature reaches 55˚C, and finally 30 cycles of [95˚C, 60 sec; 55˚C, 60 sec; 72˚C, 90sec]. PCR products were screened on 3-4% agarose TBE gels containing ethidium bromide. Gels were melted down and reused until background made it difficult to interpret banding patterns.

rmr2 mapping and candidate gene sequencing

Maize EST sequences predicted to be in the mapping interval were identified by querying Genbank with sequences from genes in the syntenic rice region. Primers were designed to these sequences with specific attention given to predicted non-coding regions such as introns and untranslated regions (UTR) to increase probability of finding polymorphisms. The reaction mix was identical to that used for SSR markers but run on the following PCR program: 95˚C, 5min; 35 cycles of [95˚C, 30 sec; 60˚C, 30 sec; 72˚C, 1 minute / kb]; 72˚C, 10 minutes. PCR products were run out on 1% agarose TBE gels containing ethidium bromide, and amplicons were excised from the gel, purified using the QIAquick gel extraction kit (Qiagen), and resuspended in autoclaved dH_2O. Sequencing reactions were set up with 100ng/1000bp PCR product and 0.8pmol primer and dideoxy sequencing was performed at the UC Berkeley Sequencing Facility (http://mcb.berkeley.edu/barker/dnaseq/). Resulting sequencing reads were aligned with Sequencher (Gene Codes, http://www.genecodes.com/).

dCAPS primers for 2map14 were designed using the dCAPS Finder online program [Neff *et al.* 1998] and used to amplify DNA of *rmr2-1* F2 mapping population mutants (see Appendix 1 for primer sequences and Appendix 2 for DNA sequences) using the same reaction conditions used for the initial primer amplification. The subsequent PCR amplicons were digested with DraIII (NEB, http://www.neb.com) under the following conditions: 3uL 10X NEB3, 0.5 uL Dra III, 0.3 uL 100X BSA, 16.2 uL H2O, and incubated at 37˚C for 3 hours to overnight. Digest products were run out on a 1.5% agarose TBE gel containing ethidium bromide. The 2map23 marker was amplified and run using the SSR protocol described above.

Oligonucleotide primers (Sigma-Genosys) were designed from the B73 genomic *sdg104* sequences either manually or with Primer3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). Primer sequences are available in Appendix 1. Primers were used to amplify DNA from individuals homozygous for either *rmr2-1*, *rmr2-m1*, and from A632 inbreds and sequenced using the methods described above. DNA sequences are available in Appendix 2.

rmr2 allele screen

The pistillate parent was generated by crossing 7th generation *rmr2-1* to 94% A632 *Pl'*. Pollen from 98.5% A619 *Pl'* plants was treated with EMS following the method outlined by Neuffer and Coe [1978] and applied to the heterozygous *rmr2-1* ears. Dark anthered M1 plants were crossed to A632 and the resulting plants were selfed. New *rmr2* alleles can be identified from these selfed ears by looking for A619-like polymorphisms with SSR markers *umc1845* and *bnlg1064*.

dCAPS marker analysis of *rmr6*

Primers designed to rice locus *Os08g39880* were used to amplify gDNA from maize using similar reaction and thermocycler conditions as described for *rmr2* primers above. Sequencing of these amplicons revealed 4 SNPs. DNA sequences are available in Appendix 2. dCAPS primers were designed as for *rmr2* and used to amplify DNA of 12 mutant individuals from the *rmr6-1* F2 mapping population to verify linkage (see Appendix 1 for primer sequences). The subsequent PCR amplicons were digested with *Apa1* (NEB, http://www.neb.com) and run out on a 1.5% agarose TBE gel. Digested samples represent individuals with the non-mutant polymorphism.

Candidate gene selection and sequencing of *rmr1*

The syntenous rice region was identified through identification of homologous sequence features between maize and rice. A BLAST search using the *Os05g32610* ORF as a query identified maize GSS (CG886593, BZ668661, BZ681915, CZ392826, BH878936, CG882444) and sorghum EST sequences (AW287235, BG322766, AW285838, BG323020) that were used to generate a pseudo contig representing the putative maize gene. Oligonucleotide primers (Sigma-Genosys) were designed from these sequences either manually or with Primer3 (http://frodo.wi.mit.edu/cgi-bin/primer3/primer3_www.cgi). Primer sequences are available in Appendix 1.

Genomic DNA from three separate individuals homozygous for each *rmr1* allele, *Pl1-Rhoades* converted A632 and A619 inbreds, and the progenitor line used in the EMS mutagenesis screen was amplified by PCR and sequenced as described for *rmr2*. *rmr1* sequences can be accessed from GenBank (EU154999, progenitor sequence; EU155000, A632 color converted; EU155001, A619 color converted; EU155002, *rmr1-1*; EU155003, *rmr1-2*; EU155004, *rmr1-3*; EU155005, *rmr1-4*).

CAPS marker analysis of *rmr1*

CAPS markers were used to test cosegregation of *rmr1-1* and *rmr1-3* associated lesions with *rmr1* mutant phenotypes. DNA of 438 mutant individuals from the *rmr1-1* F2 mapping population, representing 876 potential recombinant chromosomes, was amplified with primers 1CAPS6F and 1CAPS6R using the same reaction mix as described for *rmr2* (see Appendix 1 for primer sequences). The subsequent PCR amplicons were digested with *Pvu*II (NEB, http://www.neb.com) and run out on a 1.5% agarose TBE gel. Digested samples represent individuals with the non-mutant polymorphism. For the *rmr1-3* F2 population, (134 mutant individuals, 268 chromosomes tested) the primers were 1CAPS10F and 1CAPS10R, the restriction enzyme was *Bcl*I (NEB), and digested samples represent mutant individuals.

Physical mapping of *rmr1*

Using overgo markers CL27352_1_ov (homologous to rice locus *Os05g32530*) and CL6571_1_ov (homologous to rice locus *Os05g32630*) I identified a 120kb region on the maize FPC map which contained *rmr1*. Two BACs were selected from this region (CH201-007N19 and CH201-137L12) to form a minimum tiling path and ordered from the CHORI BACPAC Resources Center (BPRC, http://bacpac.chori.org/). BAC cultures were propagated according to instructions from the BPRC, and BAC DNA was isolated in small-scale cultures using the alkaline lysis protocol from Sambrook and Russell [2001]. To determine which BAC contained *rmr1*, PCR amplification with primers identifying *rmr1* and *bnlg1174a* was performed on the BAC DNA using the sequencing and SSR protocols respectively.

Verification of the *rmr1* gene model

For the following protocols, RNA was isolated from 14-day old seedlings using Trizol (Invitrogen, www.invitrogen.com). Intron-exon boundaries were confirmed by sequencing *rmr1* cDNA amplified by reverse transcriptase (RT)-PCR using the SuperScript One-Step RT-PCR with Platinum *Taq* kit from (Invitrogen cat. no. 10928-034) and primer sets 11F-15R and 19F-19R. Primer set 11F-15R was also used to confirm expression of *rmr1-3*.

The 5' start site was confirmed using 5' RACE. 5' adapter ligated 1st strand cDNA was generated using the FirstChoice RLM-RACE Kit (Ambion cat. no. AM1700, www.ambion.com). The PCR reaction was set up as follows: 10µL GC buffer (Finnzymes, www.finnzymes.us), 1µL 10mM dNTPs, 1µL 10µM Gene-specific primer, 1µL 10µM Outer adapter primer (Ambion), 2.5µL DMSO, 10µL 5M Betaine, 1µL Adapter-ligated 1st strand cDNA, 0.5µL Phusion DNA polymerase (Finnzymes), 23µL Nuclease-free water. Primary PCR amplification was done in 8-well strips using the following touchdown program: 3 min, 98˚C; 5 cycles of [30 sec, 98˚C; 15 sec, 68˚C; 15 sec, 72˚C; 20 sec, 75˚C; 25 sec, 78˚C]; 5 cycles of [30 sec, 98˚C; 15 sec, 63˚C; 15

sec, 72˚C; 20 sec, 75˚C; 25 sec, 78˚C]; 5 cycles of [30 sec, 98˚C; 15 sec, 56˚C; 15 sec, 72˚C; 20 sec, 75˚C; 25 sec, 78˚C]; 30 cycles of [30 sec, 98˚C; 15 sec, 50˚C; 15 sec, 72˚C; 20 sec, 75˚C; 25 sec, 78˚C]. A secondary PCR amplification was then performed using 1µL of the primary PCR reaction and nested primers using the following program: 3min, 98˚C; 30 cycles of [30 sec, 98˚C; 15 sec, 64˚C; 15 sec, 72˚C; 20 sec, 75˚C; 25 sec, 78˚C]. Products from the secondary PCR amplification were phosphorylated with T4 polynucleotide kinase (NEB), purified (QIAquick PCR purification kit, Qiagen), and ligated into pSMART vectors according to the provided protocol. Ligated vectors were transformed into *E.coli* and grown for 18-24 hours on Kan$^+$ plates. Plasmid DNA from eight colonies was isolated using a Qiagen plasmid miniprep kit and sent for sequencing with plasmid specific primers. For RACE and cloning primers please see Appendix 1.

Northern Blotting

RNA was isolated from 14-day old seedlings, immature tassels, and immature ears using Trizol (Invitrogen, www.invitrogen.com). Poly(A)+ RNA was selected using batch chromatography on oligo(dT)-cellulose following the protocol outlined in Sambrook and Russell [2001]. 10 ug of each sample was run on 1.2% agarose formaldehyde gel in MOPS buffer at 50V for ~15 hours. RNA was transferred to nylon membrane by the capillary transfer method overnight then UV crosslinked at maximum setting. Membrane was stained with methylene blue to check RNA and then probed as described [Hale *et al*. 2007] for genomic Southern blots with random primed DNA probes from either the pJS1 plasmid or the Os6F/R PCR product. pJS1 contains nucleotides 1921 to 2775 of the *rmr1* cDNA in a pGEM T-Easy (Promega, www.promega.com) vector.

Phylogenetic analyses

Sequences were gathered through blastp searches of the NCBI nr database and tblastn searches of Phytozome [www.phytozome.net] using either full length (Accession ABV80238) or truncated RMR1 (RMR1cd; amino acids 851-1435) as the query. Default values were used for all parameters except for the NCBI search where "Max target sequences" was increased to 500. Gene model predictions for some plant loci were refined using FGENESH+ [www.softberry.com]. Plant sequences are identified by their Phytozome locus identifier. Non-plant species are identified by their NCBI GI number. Some proteins with known functions, such as DRD1 or Rad54, are identified by species abbreviation and protein name. Species abbreviations are as follows: Sso, *Sulfolobus solfataricus*; Sc, *Saccharomyces cerevisiae*; Dr, *Danio rerio*; Mm, *Mus musculus*; Hs, *Homo sapiens*; Tb, *Trypanosoma brucei*; Tce, *Trypanosoma cruzi* strain *Esmeraldo*; Lb, *Leishmania braziliensis*; Li, *Leishmania infantum*; Cr, *Chlamydomonas reinhardtii*; Sm, *Selaginella moellendorffii*; At, *Arabidopsis thaliana*; Pt, *Populus trichocarpa*; Vv, *Vitis vinifera*; Cp, *Carica papaya*; Os, *Oryza sativa*; Bd, *Brachypodium distachyon*; Sb, *Sorghum bicolor*; Zm, *Zea mays*. Protein sequence and prediction information can be found in Appendix 4.

The hits from NCBI and Phytozome were aligned using the web-based alignment program MAFFT under default conditions. The resulting multiple sequence alignment was edited in Jalview [Waterhouse *et al*. 2009] for length (alignment was restricted to the RMR1cd limits) and sequence composition. Duplicate hits were removed using the Remove Redundancy tool at 99% identity level, and incomplete or partial sequences were removed manually. This edited alignment containing 285 sequences was used to create a maximum likelihood tree with PhyML under default conditions. Using this tree, additional manual editing of the alignment was performed to remove remaining redundancy in the Rad54 and outgroup subfamilies. The resulting edited alignment contained 194 sequences. The GeneDoc [http://www.psc.edu/biomed/genedoc] shaded alignment can be found in Appendix 3. This alignment was used to create maximum likelihood trees with six different substitution models in PhyML [Guindon and Gascuel, 2003]: LG, WAG, Dayhoff, BLOSUM62, JTT, and DCMut. The resulting trees were viewed and edited with Dendroscope [Huson *et al*. 2007].

Additional DRD1 subfamily and clade alignments were generated with MAFFT. Alignments were edited for length using JalView, and alignment figure was prepared with GeneDoc. The lightest level of shading represents conserved residues in at least 60% of the sequences, the middle level is conserved residues is at least 80% of the sequences, and the darkest level is amino acid identity in all sequences. The tree was generated with PhyML under default conditions using the JTT model and edited with Dendroscope as above. SNF2 motifs were annotated as in Thomä *et al.* [2005]. Secondary structure predictions were performed using Phyre [Kelley and Sternberg 2009], and intrinsic disorder predictions were performed using PONDR [Xue et al. 2010].

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Figures

Figure 1. *rmr2* is found on chromosome 2S. (A) Maize IBM frame 2 map (cM). This high resolution map was created from intermated recombinant inbred lines and genetic distances are ~3-fold those observed for F2 populations [Sharopova *et al*. 2002]. Therefore the ~24 cM distance between markers *umc1845* and *bnlg1064* on the IBM map represents ~8 cM distance in our F2 mapping population. (B) Rice chromosome 4 (Mb). Features with conserved gene order are illustrated as black boxes. Gray boxes represent features which are out of order. Unfilled boxes represent features where homology between maize and rice could not be established. (C) Agarose gel image showing 2map23 polymorphism.

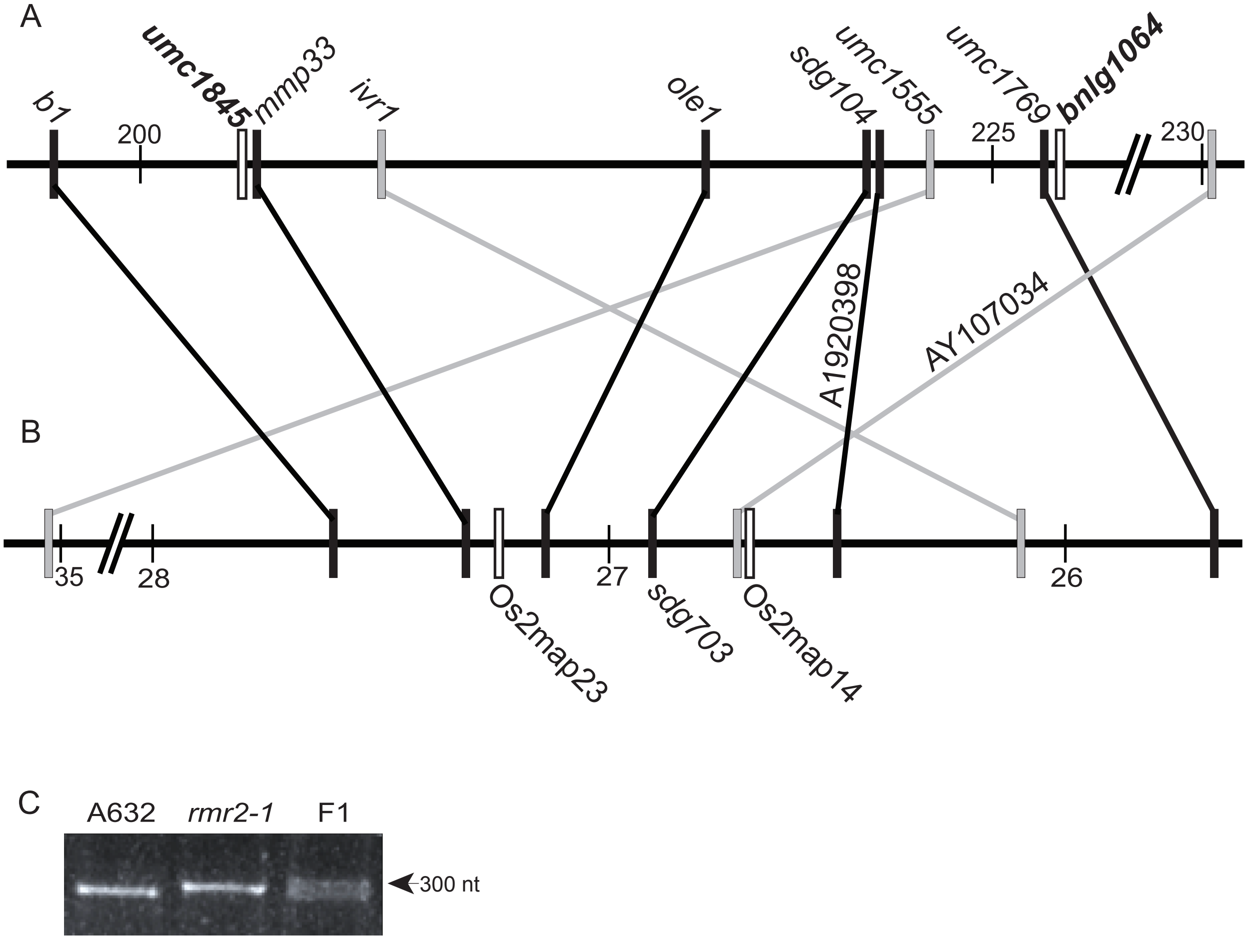
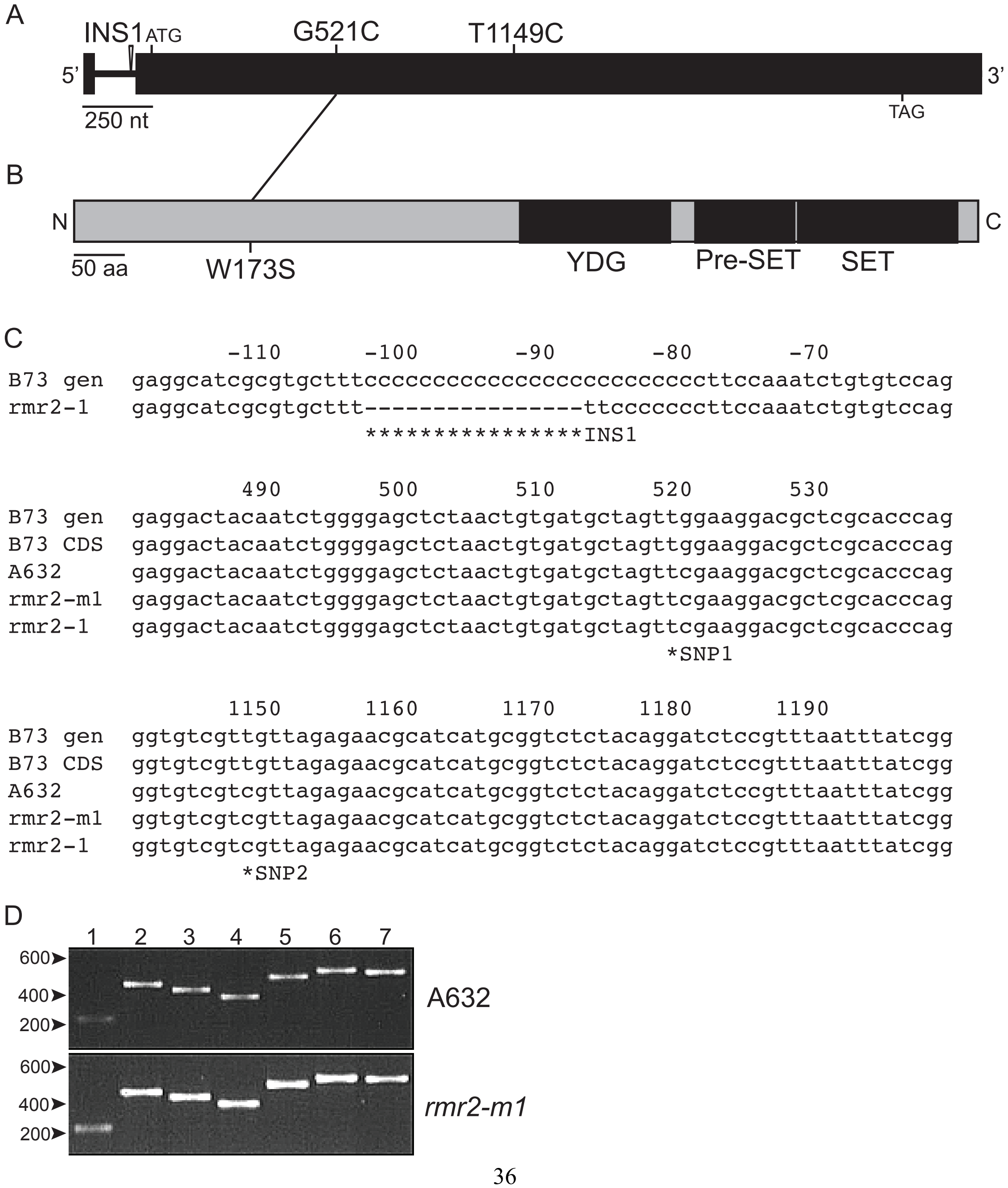


Figure 2. *rmr2* does not encode SET domain protein SDG104. (A) Gene structure showing SNPs relative to B73 reference sequence. Heavier bar represent exonic sequence while thinner bar represents intron. (B) Protein structure showing amino acid polymorphism relative to B73 and conserved functional domains (black boxes) predicted by Pfam (YDG, E value= 3.4 e-72; Pre-SET, E value= 4.7 e-32; SET, E value= 4.5 e-43). (C) Alignment of *sdg104* DNA sequence from B73 inbred, color converted A632 inbred, and *rmr2* homozygous mutants with DNA polymorphisms indicated with an asterisk. (D) No size polymorphisms exist between A632 and *rmr2-m1* over the *sdg104* coding sequence. Scale is shown at left. Genomic DNA regions amplified by each primer set are as follows: 1. nucleotides (nt) 170-382; 2. nt 419-874; 3. nt 747-1158; 4. nt 1023-1383; 5. nt 1322-1863; 6. nt 1648-2217; 7. nt 1900-2455.



```
                -110      -100       -90       -80       -70
B73 gen  gaggcatcgcgtgctttcccccccccccccccccccccccccttccaaatctgtgtccag
rmr2-1   gaggcatcgcgtgcttt----------------ttcccccccttccaaatctgtgtccag
                          ****************INS1

                 490       500       510       520       530
B73 gen  gaggactacaatctggggagctctaactgtgatgctagttggaaggacgctcgcacccag
B73 CDS  gaggactacaatctggggagctctaactgtgatgctagttggaaggacgctcgcacccag
A632     gaggactacaatctggggagctctaactgtgatgctagttcgaaggacgctcgcacccag
rmr2-m1  gaggactacaatctggggagctctaactgtgatgctagttcgaaggacgctcgcacccag
rmr2-1   gaggactacaatctggggagctctaactgtgatgctagttcgaaggacgctcgcacccag
                                                *SNP1

                1150      1160      1170      1180      1190
B73 gen  ggtgtcgttgttagagaacgcatcatgcggtctctacaggatctccgtttaatttatcgg
B73 CDS  ggtgtcgttgttagagaacgcatcatgcggtctctacaggatctccgtttaatttatcgg
A632     ggtgtcgtcgttagagaacgcatcatgcggtctctacaggatctccgtttaatttatcgg
rmr2-m1  ggtgtcgtcgttagagaacgcatcatgcggtctctacaggatctccgtttaatttatcgg
rmr2-1   ggtgtcgtcgttagagaacgcatcatgcggtctctacaggatctccgtttaatttatcgg
                 *SNP2
```

Figure 3. *rmr2* allele screen pedigrees. For each entry, upper line denotes family number, middle number denotes ear number, and bottom line describes genotype. (A) New alleles were generated in an A619 background to distinguish them from the *rmr2-1* parent. Ears segregating for new mutations were pooled into four different series. Series A: pollinated on 9/01/2004, 20 ears pooled; Series B: pollinated 9/01/2004, 36 pooled ears; Series C: pollinated 8/29/2004, 53 pooled ears; Series D: pollinated 8/29/2004, 74 pooled ears. Crosses with new alleles *ems041601* (B) and *ems05446* (C) are described. Description of families 06-679 - 06-683 found in Table 2.

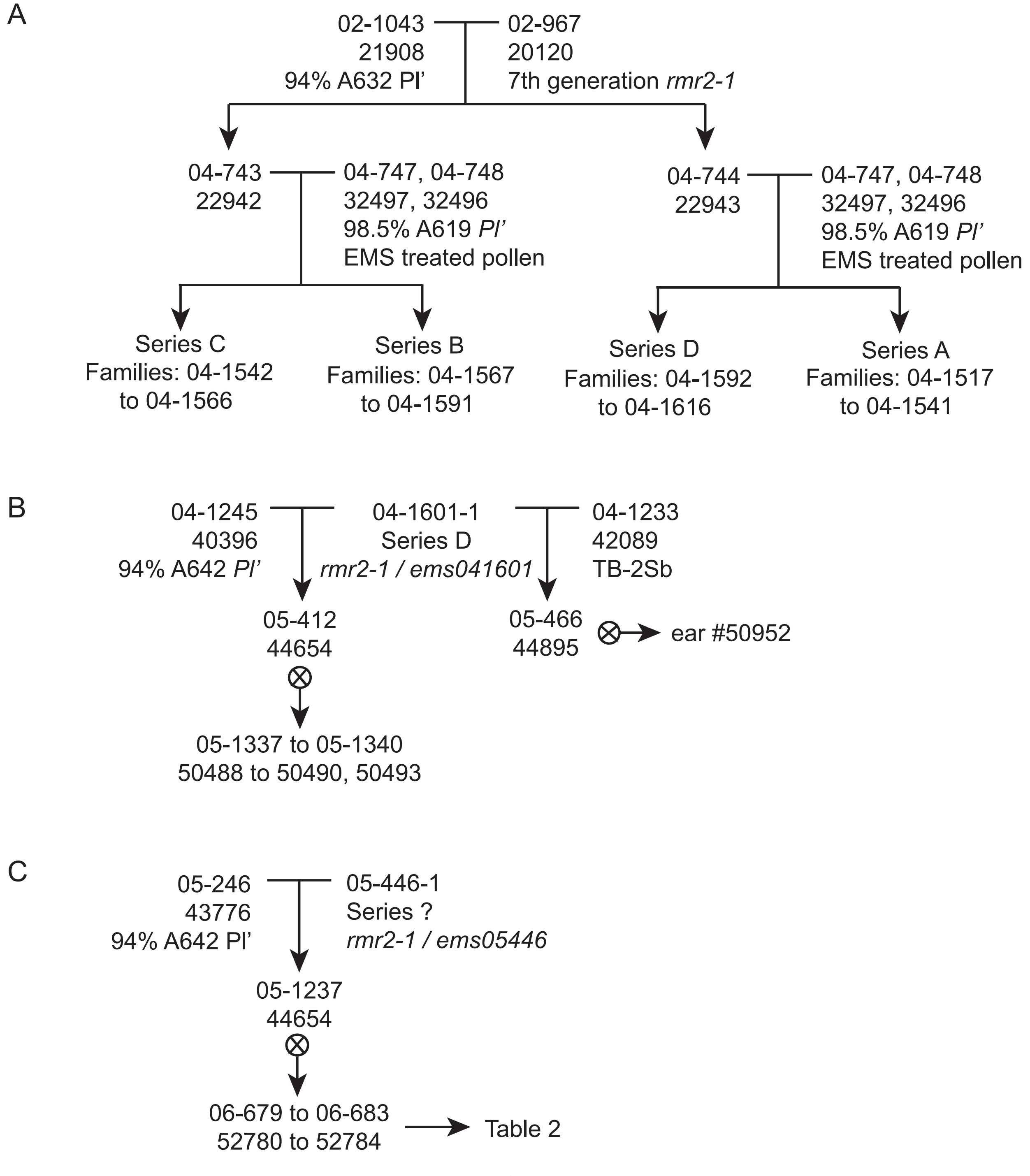


Figure 4. *rmr6* marker development using *Os08g39880* homology. (A) Alignment of maize *Os08g39880* homolog sequence from color converted A632 and *rmr6-1* homozygotes with asterisks indicating polymorphisms. (B) dCAPS marker developed from the SNP2 polymorphism. PCR amplicons from individuals homozygous for an *rmr6-1* chromosome (r) are not cleaved by *Apa*I while those from homozygous A632 individuals (A) are cleaved.

A

```
               190                 210                 230
A632   cccattgtttaggatcacagactcacagggccaatgtgattgtgctatgngttatgattt
rmr6-1 cccgttgtttaggatcacagactcaca-ggccaatgtgattgtgctatgcgttatgattt
          *SNP1                   *SNP2

               310                 330                 350
A632   gtcaacacaaaactgatcatggtgttaaatcaggaacattactgttcaaccatattaaca
rmr6-1 gtcaacacaaaactgatcatggtgttaaattaggaacattactgttcagccatattaaca
                                     *SNP3             *SNP4
```

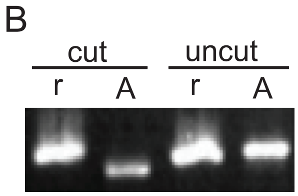


Figure 5. Regions excluded as possible location of *rmr11*. Diagrams of ten maize chromosomes showing chromosomal regions excluded as potential locations for *rmr11*. Darkest gray represents regions conclusively excluded by B-A mapping, while lightest gray represents regions where preliminary B-A mapping excluded *rmr11*. Medium gray represents regions subsequently excluded by SSR mapping. Unshaded regions were not tested. Hashed region on 6L was initially excluded because *rmr11* did not appear to segregate with the *T6-9* translocation breakpoint but which was ultimately shown to contain *rmr11* / *rmr1* by SSR mapping.

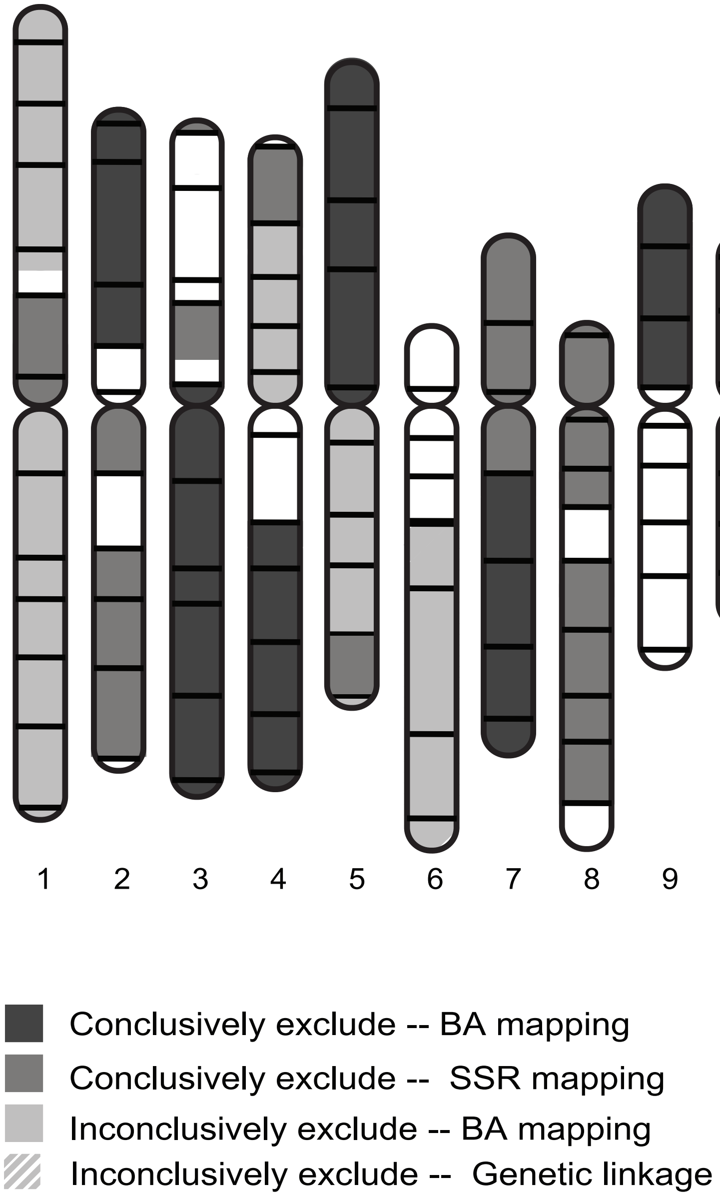


Figure 6. Genetic mapping and molecular characterization of *rmr1*. (A) Synteny between maize chromosome 6 and rice chromosome 5 is highlighted. Connecting gray lines indicate correspondence between rice ORFs and maize markers, genes, or BACs. (B) Gene structure of *rmr1* showing intron-exon boundaries. Hashed box represents GC rich region. Genomic sequencing identified unique transition-type single base pair changes characteristic of EMS-induced mutations in each of the *rmr1* mutant DNA samples as indicated. CAPS analysis of the *rmr1-1* and *rmr1-3* lesions demonstrated invariant cosegregation between base pair changes and mutant phenotype. (C) RMR1 is predicted to encode a 1435 amino acid protein. White box represents a nuclear localization signal (NLS). Black boxes highlight conserved SNF2_N and Helicase_C Pfam domains. Missense or nonsense mutations encoded by each transition lesion found with the known *rmr1* mutant alleles are indicated. Regions of intrinsic disorder are noted by black bars under the protein. (D) SNF2 helicase motifs annotated according to Thomä *et al.* [2005].

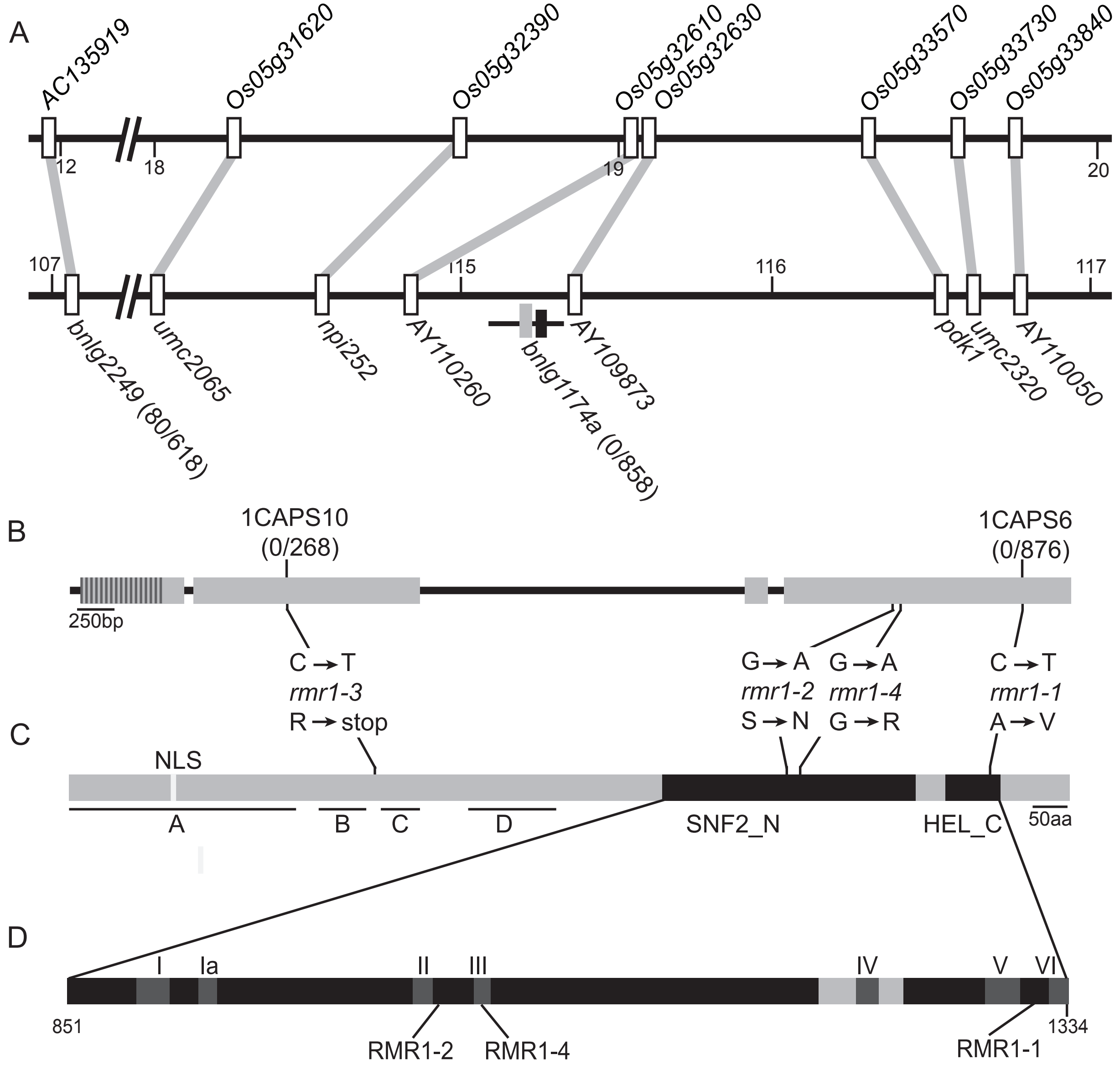


Figure 7. The *rmr1-3* allele is expressed. (A) RT-PCR of seedling cDNA from indicated genotypes using primers 11F and 15R (exact same region as probe #1). DNA control is blank because the expected product size is large (~2.6 kb) and would not be preferentially amplified by the RT-PCR program. (B) Model of *rmr1* cDNA showing splice junctions (black lines), SNF2 domain (black boxes), and location of probe 1 and 2 (black bars under gene model). Note: exact 3' UTR length is not known. (C) Methylene blue stained blot showing rRNA bands. RNA was isolated from the following tissues as indicated: t, immature tassel; e, immature ear; s, 2 week old seedling. (D) Blot hybridized with probe #1. The only bands observed were in the linearized plasmid positive control lane. (E) Blot stripped and re-probed with probe #2.

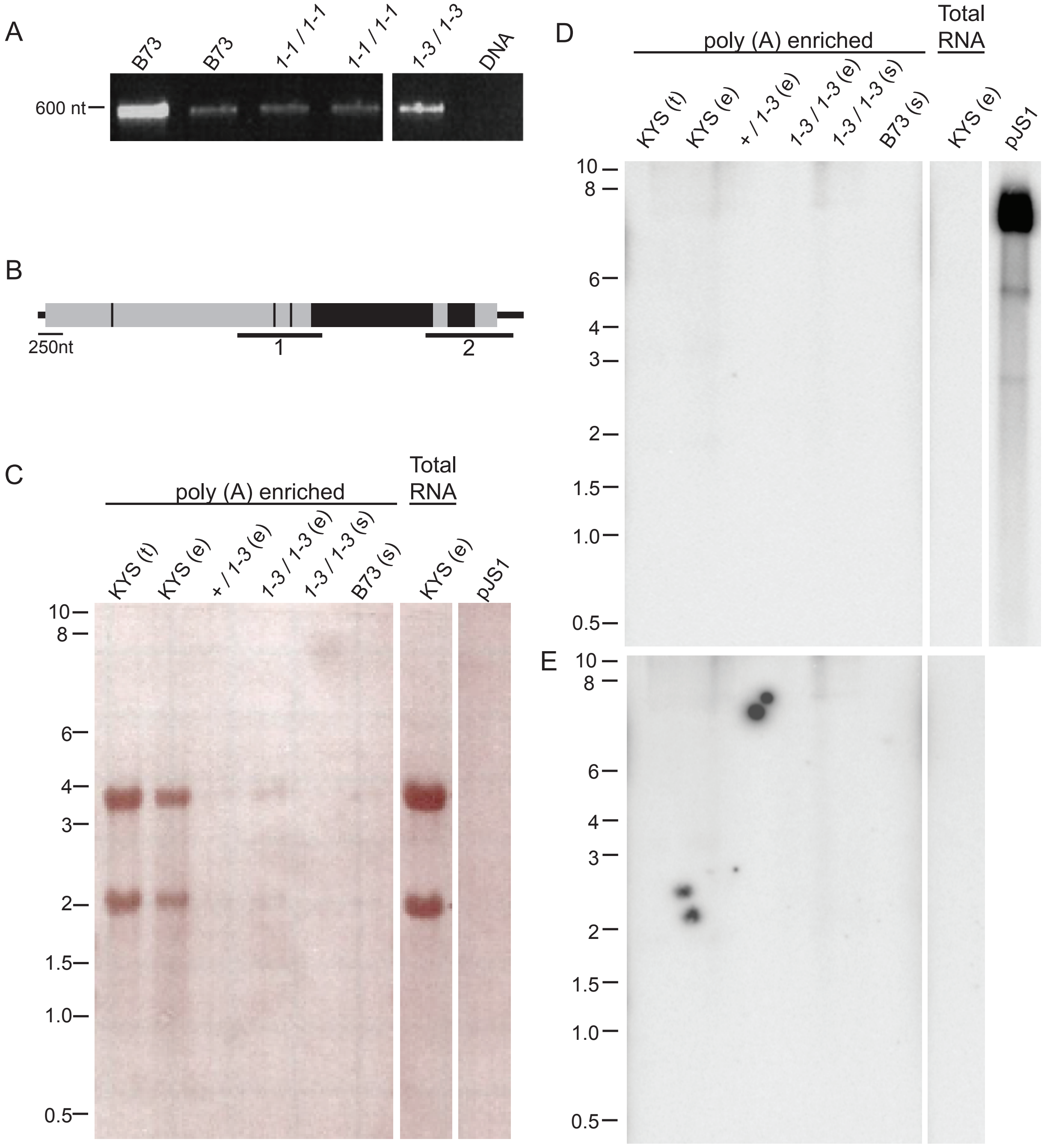


Figure 8. Phylogenetic relationship of DRD1 subfamily to other Snf2 proteins. Maximum likelihood trees were generated from the MAFFT protein alignment in Appendix 3 using six different amino acid substitution models. The JTT model tree (A) and Dayhoff model tree (B) are representative of the two tree topologies produced in the analysis. Both trees firmly place the DRD1 subfamily, including RMR1, as part of the Rad54-like group (gray shaded area). The main difference between the two models is the relationship of the DRD1 subfamily to the ATRX/ARIP4 and JBP2 subfamilies. In the JTT model (A) DRD1 is most closely related to JBP2 while in the Dayhoff model (B) DRD1 and ATRX/ARIP4 are more closely related. The implications for these relationships is discussed in the text.

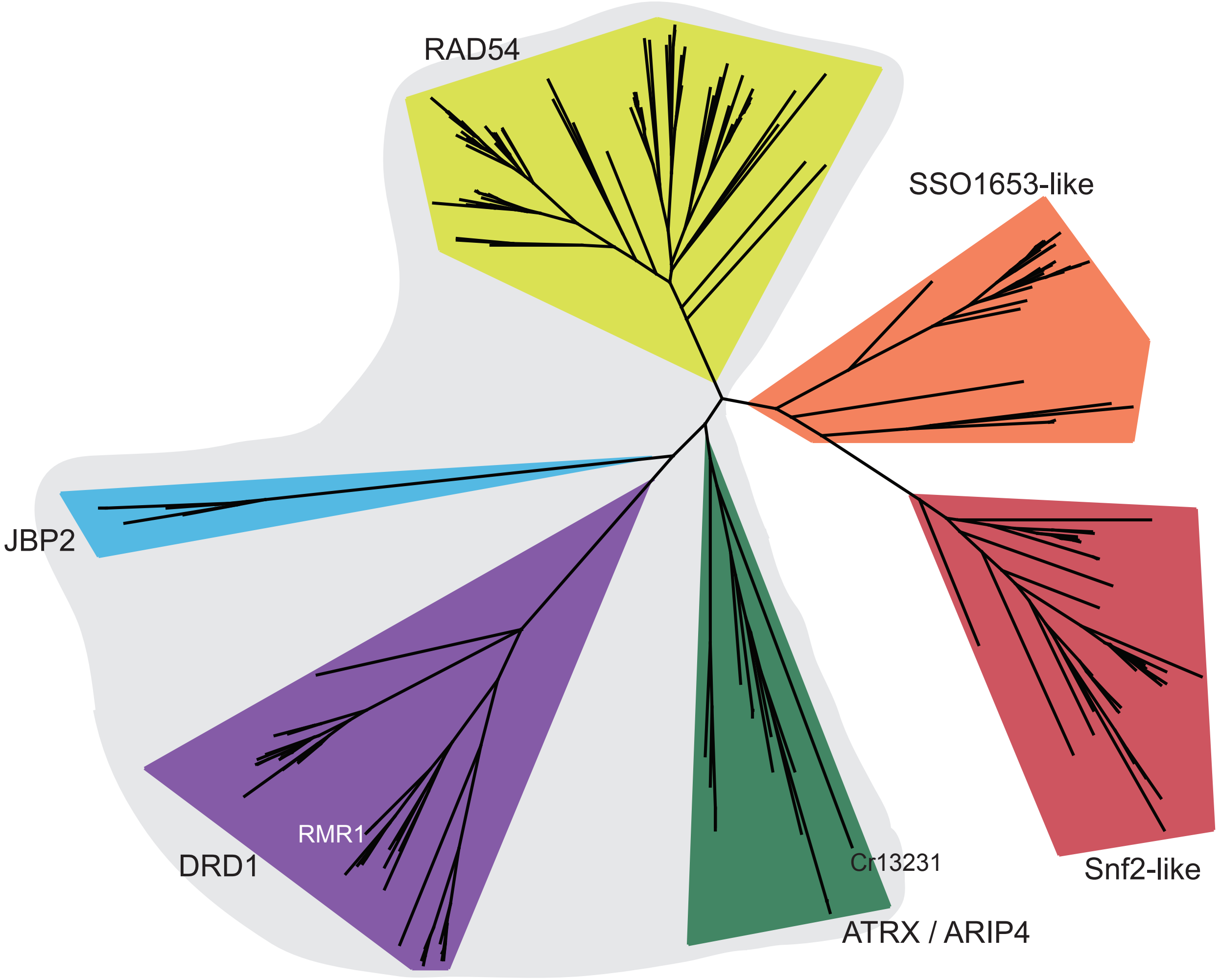


Figure 9. MAFFT alignment of DRD1 subfamily members over SNF2 conserved domain. Conserved motifs are denoted by black boxes below the text. Mutations are indicated in RMR1 by bold, red text and residues potentially involved in RNA binding are indicated by bold, red text in the CLSY1 sequence.

```
                                  20                  40                  60
ScSNF2        TLKDYQIKGLQWMVSLFNNHL---------------------------------------
ScRAD54       ILRPHQVEGVRFLYRCVTGLVMKDYLEAEAFNTSSEDPLKSDEKALTESQKTEQNNRGAY
Sm441121      SLHAHQRRAVRFMKRNIV--------------------------------------DEEG
Bd1g16720     KLLPHQKEAFEFIWKNIAGSLQ-------------------------LEEMDNPTASSTG
Os07g49210    KLLPHQRKALDFLWKNIAGSIQ--------------------------VEGMDNSNVSTG
Sb02g043870   KLLAHQRKAFEFIWKNIAGSLQ---------------------------LEEMDDSTSRG
ZM108166      KLLAHQRKAFEFIWKNIAGSLQ---------------------------LEEMDGSTSRG
ZM000342      KLLAHQRKAFEFIWKNIAGSLQ---------------------------LEEMDGSTSRG
Vv29366       -----------FVIK------------------------------------------RRG
Pt832603      KLHMHQKKAFEFLWKNTAGSLV--------------------------PAHMEKTSKKIG
Pt567214      KLHMHRKKAFECLWRNIAGSLV--------------------------PALMEKASKKIG
Cp19.123      KLHLHQKRAYEFLWRNIAGDLV--------------------------PAQMESKSDNIG
AtCLSY1       KLHLHQKKAFEFLWKNIAGSVV--------------------------PAMMDPSSDKIG
At5g20420     KLHVHQRRAFEFLWRNVAGSVE--------------------------PSLMDPTSGNIG
Bd2g26500     TMYQHQREAFEFMWTNLVGDIR------------------------LDELKHGAKPDVVG
Os05g32610    DMYQHQREAFEFMWTNLVGDIR------------------------LNEIKHGAKPDVVG
Sb09g019410   TMYEHQREAFEFMWTNLVGGIR------------------------LDELKHGAKPDVVG
RMR1          TMYEHQREAFEFMWTNLVGDIR------------------------LDEIKHGAKPDVVG
Bd2g43500     HMFPHQREGFEFMWKKLAGGID------------------------IQQVKHTVNTDSTS
Os02g43460    DMFPHQQEGFEFMWRKLAGGTS------------------------IEQLRNNANT-IEG
Bd3g50300     GLFTYQAAAVEFMWKNLAGGTK------------------------IQDVKNNINSDDLR
Sb04g033300   TMFPHQQDAFEFLWTKLAGGTT------------------------IEQLKQTVKSDVGG
ZM178435      TMFPHQQDAFEFMWTKLAGGTT------------------------IEQLKHTIKSDAGG
Vv15867       SMYRHQCEGFEFIWKNVAGGIY------------------------LDELKRSSFSDGGS
Pt286483      GMHGHQREGFEFLWKNIAGGIY------------------------LDKLKENANLNGGT
Cp76.2        SMYPHQREGFEFIWKNIAGGII------------------------LDKMKVPPQFDGGN
At1g05490     QMYPHQQEGFEFIWKNLAGTIM------------------------LNELKDFENSDETG
At3g24340     TLYPHQQEGFEFIWKNLAGTTK------------------------INEL-NSVGVKGSG
Bd3g18910     EIRLHQFEGFKFLVKNIMST------------------------------------SDPG
Bd1g74070     QMKPHQLEGFNFLVKNIADE------------------------------------KNPG
Os03g06920    HMKPHQVEGFNFLVKNIADE------------------------------------NNPG
Sb01g046180   QMKPHQVEGFNFLIKNIADE------------------------------------DNPG
Bd3g19890     QIRSHQLEGFHFLVKNLVS-------------------------------------DKPG
Os06g14440    QMRPHQLEGFSFLVKNLVG-------------------------------------DKPG
Os07g25390    QMRPHQLEGFSFLVKNLVG-------------------------------------DKPG
Sb07g002945   TMKPHQLEGFNFLVKNLIG-------------------------------------DKPG
ZM093940      AMKPHQVEGFNFLVKNLIG-------------------------------------DKPG
ZM064574      IMKPHQLEGFNFLVKNLIG-------------------------------------DKPG
Bd2g21430     HIRPHQLEGFHFLVKNLVC-------------------------------------DKPG
Bd2g21450     HIKPHQLEGFEFLVKNLVS-------------------------------------DKPG
Os08g14610    NIRPHQLEGFKFLVNNLVT-------------------------------------DEPG
Vv35918       QMKPHQVEGFNFLVSNLVA-------------------------------------ENPG
Vv23895       QMKPHQVEGFNFLVSNLVA-------------------------------------DNPG
Pt195587      QMKPHQVEGFNFLRNNLVA-------------------------------------DNPG
AtDRD1        EMKPHQIEGFQFLCSNLVA-------------------------------------DDPG
At2g21450     EMRPHQTEGFRFLCNNLAA-------------------------------------DEPG
Sm84719       RMYPHQREAFIFISRNLLS-------------------------------------KEPG
Cr13231       AIKPHQLDGLRFMWENLVERHR------------------------LQAQDPDNSCLDAG
```

Motif I

```
                                80                 100                 120
ScSNF2        NGILADEMGLGKTIQTISLLTYLYEMKNIRGPY---------------------------
ScRAD54       GCIMADEMGLGKTLQCIALMWTLLRQ------GPQGKRLI-------------------D
Sm441121      GCILAHAPGTGKTFATVYFYLKYKEI------MAGCRL----------------------
Bd1g16720     GCVVAHTPGSGKTLLLISFLVSYLKV------HPRSRP----------------------
Os07g49210    GCVIAHTPGSGKTLLLISFLVSYMKA------HPRSRP----------------------
Sb02g043870   GCVVAHTPGAGKTLLLISFLVSYLKV------HPRSRP----------------------
ZM108166      GCVVAHTPGAGKTLLLISFLVSYLKV------HPRSRP----------------------
ZM000342      GCVVAHTPGAGKTLLLISFLVSYLKV------HPRSRP----------------------
Vv29366       GCVISHSPGAGKTFLVISFLVSYLKL------FPGKRP----------------------
Pt832603      GCVVSHTPGAGKTFLIIAFLVSYLKL------FPGKRP----------------------
Pt567214      GCVISHTPGAGKTFLKIAFLVSYLKL------FPGKRP----------------------
Cp19.123      GCVVSHSPGAGKTFLIIAFLVSYLKL------FPGKRP----------------------
AtCLSY1       GCVVSHTPGAGKTFLIIAFLASYLKI------FPGKRP----------------------
At5g20420     GCVISHSPGAGKTFLIIAFLTSYLKL------FPGKRP----------------------
Bd2g26500     GCVICHAPGTGKTRLAIVFIQTYMKV------FPDCRP----------------------
Os05g32610    GCVICHAPGTGKTRLAIVFIQTYMKV------FPDCRP----------------------
Sb09g019410   GCVICHAPGTGKTRLAIVFIQTYMKV------FPDCRP----------------------
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Bd2g43500     GCVISHAPGTGKTRLAITFVQSYLEL------FPWCRP----------------------
Os02g43460    GCVISHAPGTGKTRLAITFVQSYFAF------FPECCP----------------------
Bd3g50300     GCWISHAPGTGKTRSTIAFLQSYRVL------FPRSCV----------------------
Sb04g033300   GCVISHAPGTGKTRLAITFVQSYLEV------FPRCRP----------------------
ZM178435      GCVISHAPGTGKTRLAITFVQSYLEV------FPHCSP----------------------
Vv15867       GCIISHAPGTGKTRLTIVFLQTYMEL------YPACRP----------------------
Pt286483      GCIISHAPGTGKTRLTIVFLQTYMQL------YPTSRP----------------------
Cp76.2        GCIISHAPGTGKTRLTIVFLQSYMML------YPRCRP----------------------
At1g05490     GCIMSHAPGTGKTRLTIIFLQAYLQC------FPDCKP----------------------
At3g24340     GCIISHKAGTGKTRLTVVFLQSYLKR------FPNSHP----------------------
Bd3g18910     GCIIAHAPGSGKTFMVISFIQSFLAK------HSSARW----------------------
Bd1g74070     GCILAHAPGSGKTFMLISFVQSYLTK------YPEGRP----------------------
Os03g06920    GCILAHAPGSGKTFLIISFVHSFLAK------YPAGRP----------------------
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Os07g25390    GCILAHAPGSGKTFMLISFIQSFLAK------YPSARP----------------------
Sb07g002945   GCILAHAPGSGKTFMLISFIQSFMAR------YPSARP----------------------
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Bd2g21430     GCILAHAAGSGKTFMIICFIQSFLAK------HPSARP----------------------
Bd2g21450     GCILAHAPGSGKTFMIICFIQSFLAK------DPSARP----------------------
Os08g14610    GCILVHAPGSGEIFMLISFIQGFMAR------HFTARP----------------------
Vv35918       GCILAHAPGSGKTFMIISFMQSFLAK------YPQARP----------------------
Vv23895       GCILAHAPGSGKTFMIISFMQSFLAK------YPQARP----------------------
Pt195587      GCILAHAPGSGKTFMIISFMQSFLAK------YPHAKS----------------------
AtDRD1        GCIMAHAPGSGKTFMIISFMQSFLAK------YPQAKP----------------------
At2g21450     GCILAHAPGSGKTFLLISFLQSFMAM------DPQARP----------------------
Sm84719       GVILHHAPGTGKTFLVISFLTSFFAN------FQSARA----------------------
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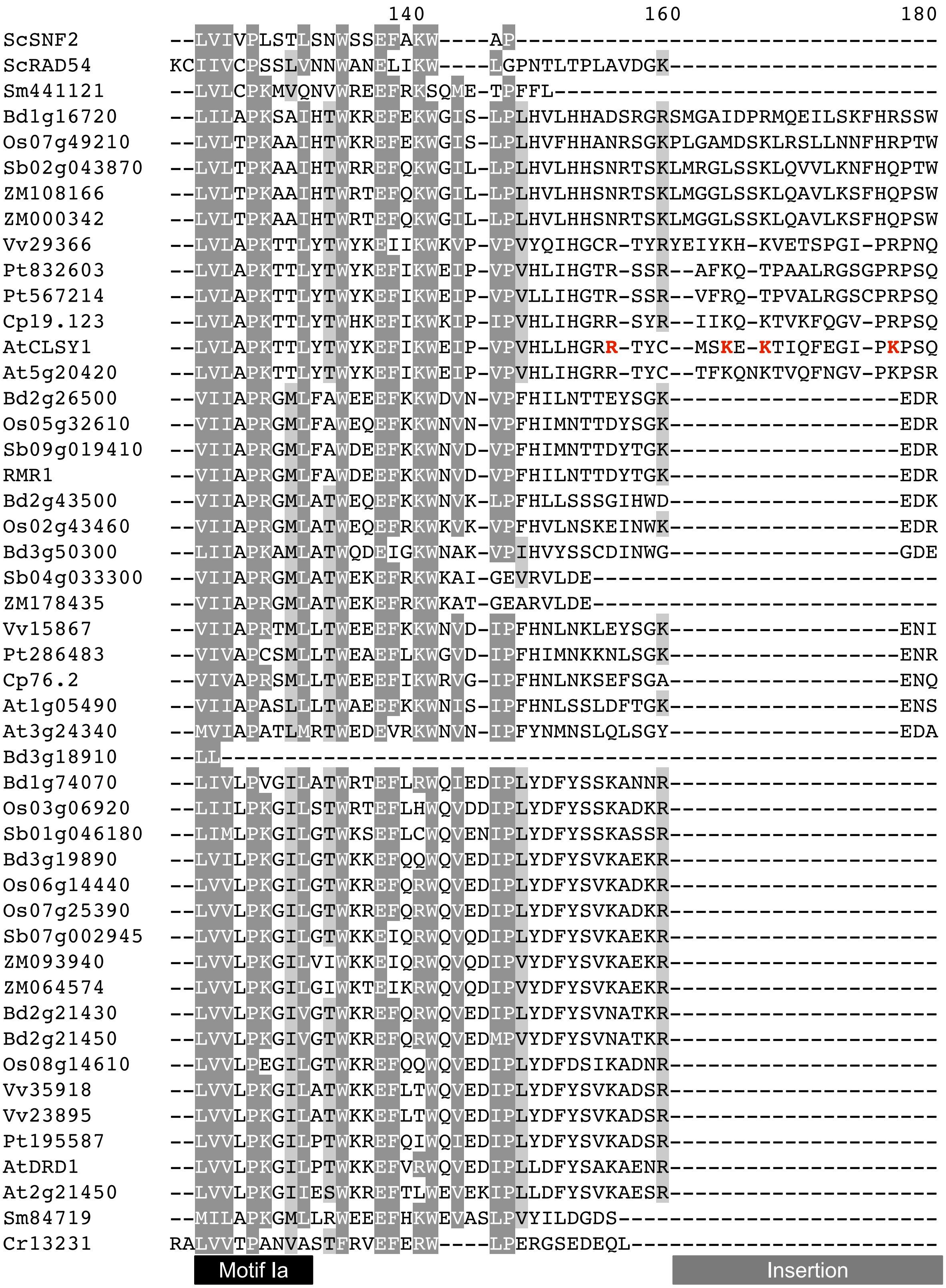

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Bd1g16720    --LILAPKSAIHTWKREFEKWGIS-LPLHVLHHADSRGRSMGAIDPRMQEILSKFHRSSW
Os07g49210   --LVLTPKAAIHTWKREFEKWGIS-LPLHVFHHANRSGKPLGAMDSKLRSLLNNFHRPTW
Sb02g043870  --LVLTPKAAIHTWRREFQKWGIL-LPLHVLHHSNRTSKLMRGLSSKLQVVLKNFHQPTW
ZM108166     --LVLTPKAAIHTWRTEFQKWGIL-LPLHVLHHSNRTSKLMGGLSSKLQAVLKSFHQPSW
ZM000342     --LVLTPKAAIHTWRTEFQKWGIL-LPLHVLHHSNRTSKLMGGLSSKLQAVLKSFHQPSW
Vv29366      --LVLAPKTTLYTWYKEIIKWKVP-VPVYQIHGCR-TYRYEIYKH-KVETSPGI-PRPNQ
Pt832603     --LVLAPKTTLYTWYKEFIKWEIP-VPVHLIHGTR-SSR--AFKQ-TPAALRGSGPRPSQ
Pt567214     --LVLAPKTTLYTWYKEFIKWEIP-VPVLLIHGTR-SSR--VFRQ-TPVALRGSCPRPSQ
Cp19.123     --LVLAPKTTLYTWHKEFIKWKIP-IPVHLIHGRR-SYR--IIKQ-KTVKFQGV-PRPSQ
AtCLSY1      --LVLAPKTTLYTWYKEFIKWEIP-VPVHLLHGRR-TYC--MSKE-KTIQFEGI-PKPSQ
At5g20420    --LVLAPKTTLYTWYKEFIKWEIP-VPVHLIHGRR-TYC--TFKQNKTVQFNGV-PKPSR
Bd2g26500    --VIIAPRGMLFAWEEEFKKWDVN-VPFHILNTTEYSGK------------------EDR
Os05g32610   --VIIAPRGMLFAWEQEFKKWNVN-VPFHIMNTTDYSGK------------------EDR
Sb09g019410  --VIIAPRGMLFAWDEEFKKWNVD-VPFHIMNTTDYTGK------------------EDR
RMR1         --VIIAPRGMLFAWDEEFKKWNVD-VPFHILNTTDYTGK------------------EDR
Bd2g43500    --VIIAPRGMLATWEQEFKKWNVK-LPFHLLSSSGIHWD------------------EDK
Os02g43460   --VIIAPRGMLATWEQEFRKWKVK-VPFHVLNSKEINWK------------------EDR
Bd3g50300    --LIIAPKAMLATWQDEIGKWNAK-VPIHVYSSCDINWG------------------GDE
Sb04g033300  --VIIAPRGMLATWEKEFRKWKAI-GEVRVLDE---------------------------
ZM178435     --VIIAPRGMLATWEKEFRKWKAT-GEARVLDE---------------------------
Vv15867      --VIIAPRTMLLTWEEEFKKWNVD-IPFHNLNKLEYSGK------------------ENI
Pt286483     --VIVAPCSMLLTWEAEFLKWGVD-IPFHIMNKKNLSGK------------------ENR
Cp76.2       --VIVAPRSMLLTWEEEFIKWRVG-IPFHNLNKSEFSGA------------------ENQ
At1g05490    --VIIAPASLLLTWAEEFKKWNIS-IPFHNLSSLDFTGK------------------ENS
At3g24340    --MVIAPATLMRTWEDEVRKWNVN-IPFYNMNSLQLSGY------------------EDA
Bd3g18910    --LL--------------------------------------------------------
Bd1g74070    --LIVLPVGILATWRTEFLRWQIEDIPLYDFYSSKANNR---------------------
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Sb01g046180  --LIMLPKGILGTWKSEFLCWQVENIPLYDFYSSKASSR---------------------
Bd3g19890    --LVILPKGILGTWKKEFQQWQVEDIPLYDFYSVKAEKR---------------------
Os06g14440   --LVVLPKGILGTWKREFQRWQVEDIPLYDFYSVKADKR---------------------
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Sb07g002945  --LVVLPKGILGTWKKEIQRWQVQDIPLYDFYSVKAEKR---------------------
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Bd2g21430    --LVVLPKGIVGTWKREFQRWQVEDIPLYDFYSVNATKR---------------------
Bd2g21450    --LVVLPKGIVGTWKREFQRWQVEDMPVYDFYSVNATKR---------------------
Os08g14610   --LVVLPEGILGTWKREFQQWQVEDIPLYDFDSIKADNR---------------------
Vv35918      --LVVLPKGILATWKKEFLTWQVEDIPLYDFYSVKADSR---------------------
Vv23895      --LVVLPKGILATWKKEFLTWQVEDIPLYDFYSVKADSR---------------------
Pt195587     --LVVLPKGILPTWKREFQIWQIEDIPLYDFYSVKADSR---------------------
AtDRD1       --LVVLPKGILPTWKKEFVRWQVEDIPLLDFYSAKAENR---------------------
At2g21450    --LVVLPKGIIESWKREFTLWEVEKIPLLDFYSVKAESR---------------------
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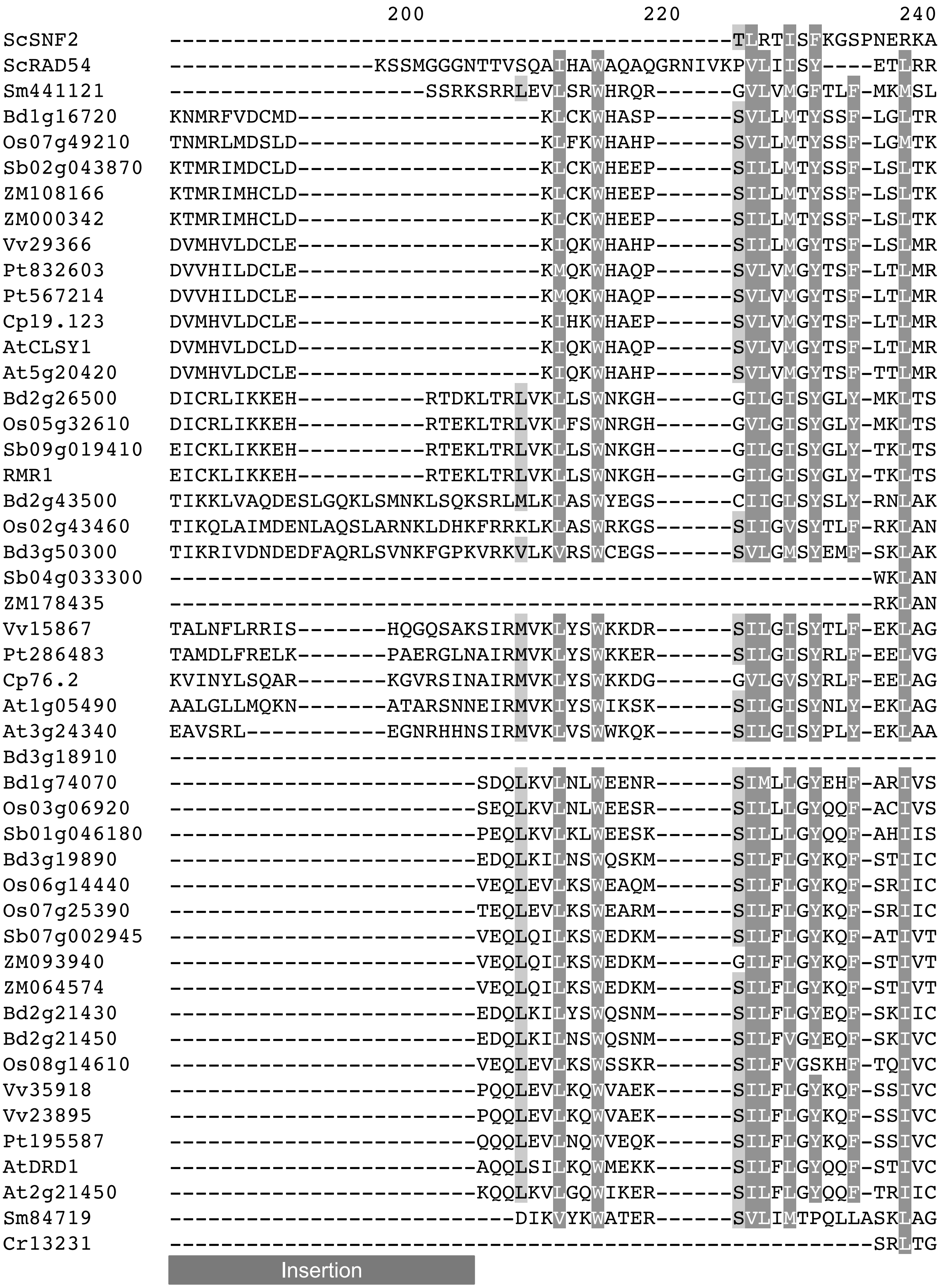

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Bd1g16720    KNMRFVDCMD-------------------KLCKWHASP------SVLLMTYSSF-LGLTR
Os07g49210   TNMRLMDSLD-------------------KLFKWHAHP------SVLLMTYSSF-LGMTK
Sb02g043870  KTMRIMDCLD-------------------KLCKWHEEP------SILLMTYSSF-LSLTK
ZM108166     KTMRIMHCLD-------------------KLCKWHEEP------SILLMTYSSF-LSLTK
ZM000342     KTMRIMHCLD-------------------KLCKWHEEP------SILLMTYSSF-LSLTK
Vv29366      DVMHVLDCLE-------------------KIQKWHAHP------SILLMGYTSF-LSLMR
Pt832603     DVVHILDCLE-------------------KMQKWHAQP------SVLVMGYTSF-LTLMR
Pt567214     DVVHILDCLE-------------------KMQKWHAQP------SVLVMGYTSF-LTLMR
Cp19.123     DVMHVLDCLE-------------------KIHKWHAEP------SVLVMGYTSF-LTLMR
AtCLSY1      DVMHVLDCLD-------------------KIQKWHAQP------SVLVMGYTSF-LTLMR
At5g20420    DVMHVLDCLE-------------------KIQKWHAHP------SVLVMGYTSF-TTLMR
Bd2g26500    DICRLIKKEH----------RTDKLTRLVKLLSWNKGH------GILGISYGLY-MKLTS
Os05g32610   DICRLIKKEH----------RTEKLTRLVKLFSWNRGH------GVLGISYGLY-MKLTS
Sb09g019410  EICKLIKKEH----------RTEKLTRLVKLLSWNKGH------GILGISYGLY-TKLTS
RMR1         EICKLIKKEH----------RTEKLTRLVKLLSWNKGH------GILGISYGLY-TKLTS
Bd2g43500    TIKKLVAQDESLGQKLSMNKLSQKSRLMLKLASWYEGS------CIIGLSYSLY-RNLAK
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Bd3g50300    TIKRIVDNDEDFAQRLSVNKFGPKVRKVLKVRSWCEGS------SVLGMSYEMF-SKLAK
Sb04g033300  -------------------------------------------------------WKLAN
ZM178435     -------------------------------------------------------RKLAN
Vv15867      TALNFLRRIS-------HQGQSAKSIRMVKLYSWKKDR------SILGISYTLF-EKLAG
Pt286483     TAMDLFRELK-------PAERGLNAIRMVKLYSWKKER------SILGISYRLF-EELVG
Cp76.2       KVINYLSQAR-------KGVRSINAIRMVKLYSWKKDG------GVLGVSYRLF-EELAG
At1g05490    AALGLLMQKN-------ATARSNNEIRMVKIYSWIKSK------SILGISYNLY-EKLAG
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Bd3g18910    ------------------------------------------------------------
Bd1g74070    ------------------------SDQLKVLNLWEENR------SIMLLGYEHF-ARIVS
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Sb01g046180  ------------------------PEQLKVLKLWEESK------SILLLGYQQF-AHIIS
Bd3g19890    ------------------------EDQLKILNSWQSKM------SILFLGYKQF-STIIC
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Os08g14610   ------------------------VEQLEVLKSWSSKR------SILFVGSKHF-TQIVC
Vv35918      ------------------------PQQLEVLKQWVAEK------SILFLGYKQF-SSIVC
Vv23895      ------------------------PQQLEVLKQWVAEK------SILFLGYKQF-SSIVC
Pt195587     ------------------------QQQLEVLNQWVEQK------SILFLGYKQF-SSIVC
AtDRD1       ------------------------AQQLSILKQWMEKK------SILFLGYQQF-STIVC
At2g21450    ------------------------KQQLKVLGQWIKER------SILFLGYQQF-TRIIC
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Cr13231      -------------------------------------------------------SRLTG
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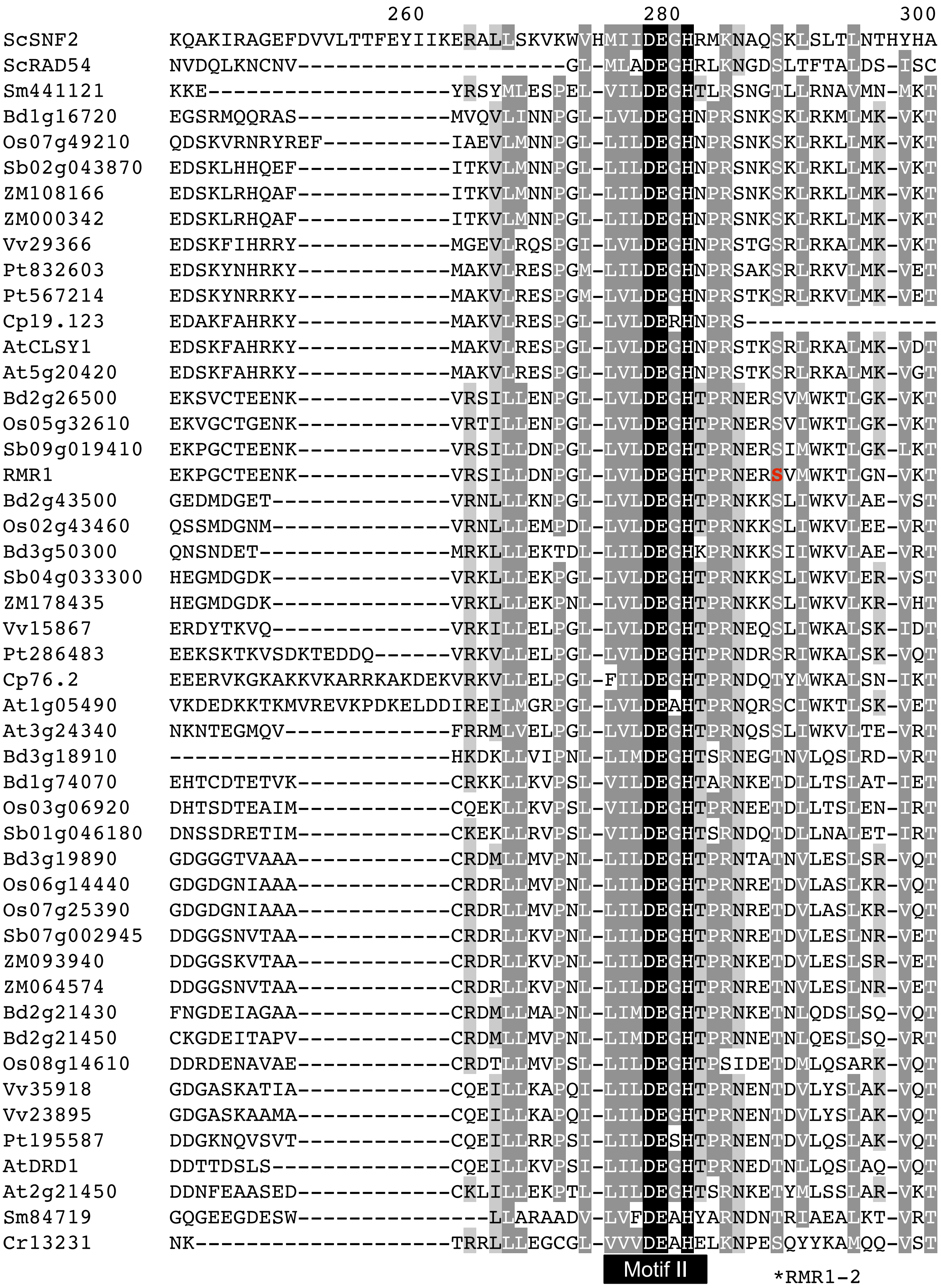

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Sm441121     KKE-------------------YRSYMLESPEL-VILDEGHTLRSNGTLLRNAVMN-MKT
Bd1g16720    EGSRMQQRAS------------MVQVLINNPGL-LVLDEGHNPRSNKSKLRKMLMK-VKT
Os07g49210   QDSKVRNRYREF----------IAEVLMNNPGL-LILDEGHNPRSNKSKLRKLLMK-VKT
Sb02g043870  EDSKLHHQEF------------ITKVLMNNPGL-LILDEGHNPRSNKSKLRKLLMK-VKT
ZM108166     EDSKLRHQAF------------ITKVLMNNPGL-LILDEGHNPRSNKSKLRKLLMK-VKT
ZM000342     EDSKLRHQAF------------ITKVLMNNPGL-LILDEGHNPRSNKSKLRKLLMK-VKT
Vv29366      EDSKFIHRRY------------MGEVLRQSPGI-LVLDEGHNPRSTGSRLRKALMK-VKT
Pt832603     EDSKYNHRKY------------MAKVLRESPGM-LILDEGHNPRSAKSRLRKVLMK-VET
Pt567214     EDSKYNRRKY------------MAKVLRESPGM-LVLDEGHNPRSTKSRLRKVLMK-VET
Cp19.123     EDAKFAHRKY------------MAKVLRESPGL-LVLDERHNPRS---------------
AtCLSY1      EDSKFAHRKY------------MAKVLRESPGL-LVLDEGHNPRSTKSRLRKALMK-VDT
At5g20420    EDSKFAHRKY------------MAKVLRESPGL-LVLDEGHNPRSTKSRLRKALMK-VGT
Bd2g26500    EKSVCTEENK------------VRSILLENPGL-LVLDEGHTPRNERSVMWKTLGK-VKT
Os05g32610   EKVGCTGENK------------VRTILLENPGL-LVLDEGHTPRNERSVIWKTLGK-VKT
Sb09g019410  EKPGCTEENK------------VRSILLDNPGL-LVLDEGHTPRNERSIMWKTLGK-LKT
RMR1         EKPGCTEENK------------VRSILLDNPGL-LVLDEGHTPRNERSVMWKTLGN-VKT
Bd2g43500    GEDMDGET--------------VRNLLLKNPGL-LVLDEGHTPRNKKSLIWKVLAE-VST
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Vv15867      ERDYTKVQ--------------VRKILLELPGL-LVLDEGHTPRNEQSLIWKALSK-IDT
Pt286483     EEKSKTKVSDKTEDDQ------VRKVLLELPGL-LVLDEGHTPRNDRSRIWKALSK-VQT
Cp76.2       EEERVKGKAKKVKARRKAKDEKVRKVLLELPGL-FILDEGHTPRNDQTYMWKALSN-IKT
At1g05490    VKDEDKKTKMVREVKPDKELDDIREILMGRPGL-LVLDEAHTPRNQRSCIWKTLSK-VET
At3g24340    NKNTEGMQV-------------FRRMLVELPGL-LVLDEGHTPRNQSSLIWKVLTE-VRT
Bd3g18910    ----------------------HKDKLLVIPNL-LIMDEGHTSRNEGTNVLQSLRD-VRT
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Os03g06920   DHTSDTEAIM------------CQEKLLKVPSL-VILDEGHTPRNEETDLLTSLEN-IRT
Sb01g046180  DNSSDRETIM------------CKEKLLRVPSL-VILDEGHTSRNDQTDLLNALET-IRT
Bd3g19890    GDGGGTVAAA------------CRDMLLMVPNL-LILDEGHTPRNTATNVLESLSR-VQT
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Vv35918      GDGASKATIA------------CQEILLKAPQI-LILDEGHTPRNENTDVLYSLAK-VQT
Vv23895      GDGASKAAMA------------CQEILLKAPQI-LILDEGHTPRNENTDVLYSLAK-VQT
Pt195587     DDGKNQVSVT------------CQEILLRRPSI-LILDESHTPRNENTDVLQSLAK-VQT
AtDRD1       DDTTDSLS--------------CQEILLKVPSI-LILDEGHTPRNEDTNLLQSLAQ-VQT
At2g21450    DDNFEAASED------------CKLILLEKPTL-LILDEGHTSRNKETYMLSSLAR-VKT
Sm84719      GQGEEGDESW---------------LLARAADV-LVFDEAHYARNDNTRIAEALKT-VRT
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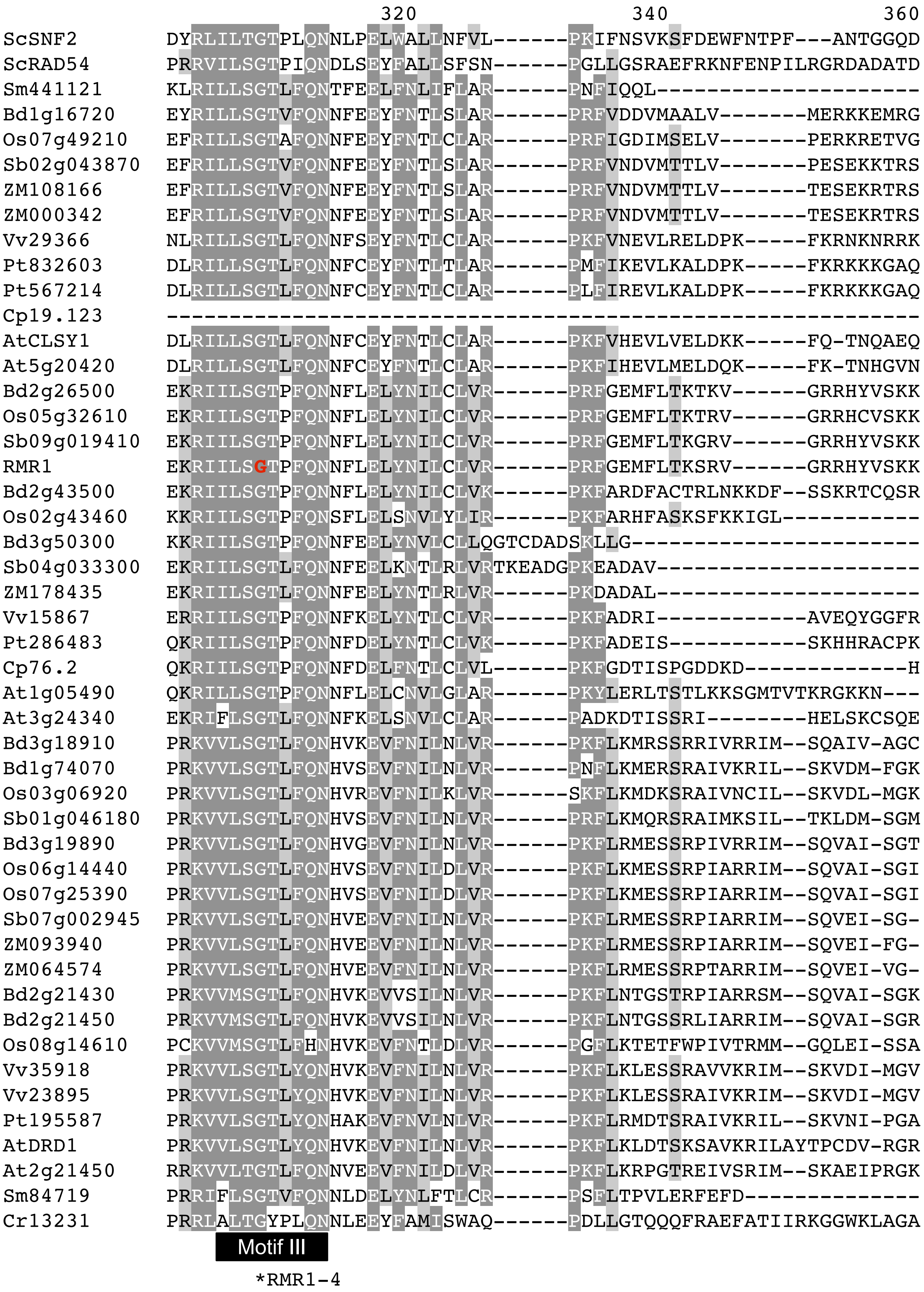

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ScRAD54      PRRVILSGTPIQNDLSEYFALLSFSN------PGLLGSRAEFRKNFENPILRGRDADATD
Sm441121     KLRILLSGTLFQNTFEELFNLIFLAR------PNFIQQL---------------------
Bd1g16720    EYRILLSGTVFQNNFEEYFNTLSLAR------PRFVDDVMAALV-------MERKKEMRG
Os07g49210   EFRILLSGTAFQNNFEEYFNTLCLAR------PRFIGDIMSELV-------PERKRETVG
Sb02g043870  EFRILLSGTVFQNNFEEYFNTLSLAR------PRFVNDVMTTLV-------PESEKKTRS
ZM108166     EFRILLSGTVFQNNFEEYFNTLSLAR------PRFVNDVMTTLV-------TESEKRTRS
ZM000342     EFRILLSGTVFQNNFEEYFNTLSLAR------PRFVNDVMTTLV-------TESEKRTRS
Vv29366      NLRILLSGTLFQNNFSEYFNTLCLAR------PKFVNEVLRELDPK-----FKRNKNRRK
Pt832603     DLRILLSGTLFQNNFCEYFNTLTLAR------PMFIKEVLKALDPK-----FKRKKKGAQ
Pt567214     DLRILLSGTLFQNNFCEYFNTLCLAR------PLFIREVLKALDPK-----FKRKKKGAQ
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Vv15867      ERRIILSGTPFQNNFKELYNTLCLVR------PKFADRI------------AVEQYGGFR
Pt286483     QKRIILSGTPFQNNFDELYNTLCLVK------PKFADEIS-----------SKHHRACPK
Cp76.2       QKRIILSGTPFQNNFDELFNTLCLVL------PKFGDTISPGDDKD-------------H
At1g05490    QKRILLSGTPFQNNFLELCNVLGLAR------PKYLERLTSTLKKSGMTVTKRGKKN---
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Bd3g18910    PRKVVLSGTLFQNHVKEVFNILNLVR------PKFLKMRSSRRIVRRIM--SQAIV-AGC
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Pt195587     PRKVVLSGTLYQNHAKEVFNVLNLVR------PKFLRMDTSRAIVKRIL--SKVNI-PGA
AtDRD1       PRKVVLSGTLYQNHVKEVFNILNLVR------PKFLKLDTSKSAVKRILAYTPCDV-RGR
At2g21450    RRKVVLTGTLFQNNVEEVFNILDLVR------PKFLKRPGTREIVSRIM--SKAEIPRGK
Sm84719      PRRIFLSGTVFQNNLDELYNLFTLCR------PSFLTPVLERFEFD--------------
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ScRAD54      KEI---------------------------------------------------------
Sm441121     ----QMEDRARRWFIKEIGRKFDD------------------------------------
Bd1g16720    RRAKHREAVARRIFVERVAQKMES------------------------------------
Os07g49210   RRAKHQEAVARRAFVEKVGQKIES------------------------------------
Sb02g043870  RTGKHQEALARRIFVERVGQKIES------------------------------------
ZM108166     RTGKHQEALARHVFVERVGHKIES------------------------------------
ZM000342     RTGKHQEALARHVFVERVGHKIES------------------------------------
Vv29366      RRYSSTESRARKFFTDEIAKRINS------------------------------------
Pt832603     KARHLLESRARKFFIDNIASKINS------------------------------------
Pt567214     KARHFLESRARKFFIDNIASKINL------------------------------------
Cp19.123     ------------------------------------------------------------
AtCLSY1      KAPHLLENRARKFFLDIIAKKIDT------------------------------------
At5g20420    KAPHLLENRARKLFLDIIAKKIDA------------------------------------
Bd2g26500    QRDKFSDKYEKGVWASLTSNVTDD------------------------------------
Os05g32610   QRDKFSDKYEKGVWASLTSNVTDD------------------------------------
Sb09g019410  QKDKFSDKYEKGVWASLTSNVTDD------------------------------------
RMR1         QKDKFSDKYEKGVWASLTSNVTDD------------------------------------
Bd2g43500    ATHHLEEDEGKEFWKSL--RMSNI------------------------------------
Os02g43460   ----------EDYWTSL--TLNNI------------------------------------
Bd3g50300    ------KDEDKGFWTSM--SVDNI------------------------------------
Sb04g033300  ---HLETDEGKDFWSSL--RLNDI------------------------------------
ZM178435     ---HLETDESKDFWSSL--RLNDI------------------------------------
Vv15867      GKRGRKSNAARGKWDLLTSSIGKI------------------------------------
Pt286483     RRRCKRNTDARRNWASLTTAIGKV------------------------------------
Cp76.2       KRHARKRSEAKGKWTSLTSSMGKF------------------------------------
At1g05490    ------------------------------------------------------------
At3g24340    GEHGRVNEENR-------------------------------------------------
Bd3g18910    SSSKK---ADEVFAESVEATLLAD------------------------------------
Bd1g74070    SAWSKNT-SDKCFYDMVEENLQKD------------------------------------
Os03g06920   SARSKNI-SDKDFFDLVQEHLQKD------------------------------------
Sb01g046180  AIRSKMI-SEKVFFELIEENLQKD------------------------------------
Bd3g19890    RVSKGVP--DNVFTESVEETLLHD------------------------------------
Os06g14440   RSLKGVH--DSAFTESVEDTLLND------------------------------------
Os07g25390   RSLKGVH--DSAFTESVEDTLLND------------------------------------
Sb07g002945  RGSKGFA--DSAFTEAVEGTLLND------------------------------------
ZM093940     RSSKGLA--DGAFTEAVEGTLLND------------------------------------
ZM064574     RSSKGLA--DGAFTKAVEETLLND------------------------------------
Bd2g21430    KIPKDPRKFDKVFAESVEETLLHD------------------------------------
Bd2g21450    RIPKDPRKFDKAFAESVEETLLHD------------------------------------
Os08g14610   RSITEIS-------ESMEDTLLND------------------------------------
Vv35918      RKQLKSN-AADAFYDLVENTLQKD------------------------------------
Vv23895      RKQLKSN-AADAFYDLVENTLQKD------------------------------------
Pt195587     RKQFKAG-ADAAFYDLVEQTIQKD------------------------------------
AtDRD1       LTGSNSD-MASMFNETVEHTLQKS------------------------------------
At2g21450    QVNQSSSSIEGTFFAAVELTLQRS------------------------------------
Sm84719      ---ASKDDAERHFFKEMIENRLEN------------------------------------
Cr13231      GGAGSTEGAGEGVRTGAGGRLGGDGWGRGARGGADSAPLQLITYTHTCIYTPLLRITRTG
```

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                              440                 460                 480
ScSNF2       -------LSEEETLLVIRR-LHKVLRPFLLRRLKKDV--EKELPDKVEKVVKCKMSALQQ
ScRAD54      -------TKGEAQ---LQK-LSTIVSKFIIRRTNDIL--AKYLPCKYEHVIFVNLKPLQN
Sm441121     -------GHGHREMQAAQMKLVKMTQGFTDHYTGAIL--TEVLPGLRDYEITTAMTELQH
Bd1g16720    -------SSSRDRIDGLNL-LNKLTCGFIDSFEGAKL---SNLPGIHVYTVFMKPGKIQE
Os07g49210   -------DNKHIRSDGISL-LNKLTRGFIDSFEGAKL---INLPGIHVYTVFMKPTDIQE
Sb02g043870  -------SSKHDRMDGISL-LNDLTHGFIDSFEGTKL---NILPGIHVYTLFMKPTDVQE
ZM108166     -------SSKHDRMDGISL-LNELTQGFIDSFEGTKL---NILPGIRVYTLFMKPTDVQE
ZM000342     -------SSKHDRMDGISL-LNELTQGFIDSFEGTKL---NILPGIRVYTLFMKPTDVQE
Vv29366      -------NVPEEQIEGLNM-LRNLTSKFIDVYEGGSS---DNLPGLQVYTLLMKSTTIQQ
Pt832603     -------DEAEEKMQGLNM-LRNMTNGFIDVYEGTAS---DTLPGIQIYTILMNPTDIQH
Pt567214     -------DEAEEKMQGLNM-LRNMTNGFIDVYEGTAS---DTLPGLQIYTIMINPTDIQH
Cp19.123     ------------------------------------------------------------
AtCLSY1      -------KVGDERLQGLNM-LRNMTSGFIDNYEGSGSGSGDVLPGLQIYTLLMNSTDVQH
At5g20420    -------SVGDERLQGLNM-LKNMTNGFIDNYEGSGSGSGDALPGLQIYTLVMNSTDIQH
Bd2g26500    -------NAEK---------VRSILKPFVHIHNGTIL---RTLPGLRESVIVLKPPPLQK
Os05g32610   -------NAEK---------VRSILKPFVHIHNGTIL---RTLPGLRECVIVLKPLPLQK
Sb09g019410  -------NAEK---------VRSILKPFVHIHNGNIL---RTLPGLRESVIILKPLPLQK
RMR1         -------NAEK---------VRSILKPFVHIHNGNIL---RTLPGLRESVIILKPLPLQK
Bd2g43500    -------TDDH-----LSE-IREKLDPFVHIHNGDIL--QKSLPGLKESVVILNPLPHQK
Os02g43460   -------TEKK-----IDE-IRQILDPIVHIHNGDIL--QKSLPGLRESVVILNPLPHQK
Bd3g50300    -------TDER-----VNE-IRDKLKPFLHIYNGEFL--QKSLPGLRESVVILNPFPHQK
Sb04g033300  -------TEAD-----INE-VRKKLDPIVHIHSGKFL--QKSLPGLGESVVILNPLPYQK
ZM178435     -------TKAN-----INE-VRKKLDPIVHIHSGRFL--QKSLPGLRESVVILNPLLYQK
Vv15867      -------ADDK-----VEE-LRAMIEPFVHIHKGTIL--QENLPGLKDSVVVLQPSDLQR
Pt286483     -------TDDKLEAQRVEE-LRKMIWQFVHVHKGGVL--RERLPGLRDSVVILQPVHLQK
Cp76.2       -------LDVKADNLKV---IRDVIAPFVHVHKGKIL--KDSLPGLRHSVVVLRPVDLQK
At1g05490    -------LGNEINNRGIEE-LKAVMLPFVHVHKGSIL--QSSLPGLRECVVVLNPPELQR
At3g24340    ----------------IVD-LKAMIAHFVHVHEGTIL--QESLPGLRDCVVVLNPPFQQK
Bd3g18910    -------DNFERKSHVISG-LRELTEDVLHYYKGDVL---DKLLGLVDFSVFLKLTQKQK
Bd1g74070    -------ANDKIREMIIEN-LRELTANVLHYYQGELS---EELPGLVDFTVFLNMTTKQE
Os03g06920   -------GNDKMRAVIIQN-LRELTADVLHYYQGKLL---DELPGIVDFTVFLNMSSKQE
Sb01g046180  -------SK-TMRVMIIQN-LRKLTENILHYYQGEIL---KELPGLVDFTVLLNMSSKQE
Bd3g19890    -------ENFTRKAHIIRS-LRELTNDVLHYYKGDIL---DELPGLVDFSVFLKLSPRQK
Os06g14440   -------DNFTRKAHVIRS-LRELTKDVLHYYKGDIL---DELPGLVDFSVFLKLSTKQK
Os07g25390   -------DNFTRKSHVIRS-LRELTKDVLHYYKGDIL---DELPGLVDFSVFLKLSTKQK
Sb07g002945  -------ENFKRKAHVIRG-LRELTKDVLHYYKGDIL---DELPGLVDFSVFLKLTPKQK
ZM093940     -------ENFKRKVHVIRG-LRELTRDVLHYYKGAIL---DELPGLVDFSVFLKLTPKQK
ZM064574     -------ENFKRKAHVIRG-LRELTKDVLHYYKGDIL---DELPGLVDFSVFLKLTPKQK
Bd2g21430    -------VNFTRKKHVIRS-LRELTEGVIHYYKGDIL---HELPGLIDFSVFLKLSPMQK
Bd2g21450    -------ENFTRKKHVIRS-LKELTEDVIHYYKGDIL---HELPGLIDFSVFLKLSPRQN
Os08g14610   -------DNFTRKVNVIRS-LGELTKDVLHYCKGEDL---NEFPVLLDFSVFLELSPKQK
Vv35918      -------DNFRRKITVIQD-LREMTSKVLHYYKGDFL---DELPGLVDFTVLLNLSARQK
Vv23895      -------DNFRRKITVIQD-LREMTSKVLHYYKGDFL---DELPGLVDFTVLLNLSARQK
Pt195587     -------QDFKRKVTVIRD-LHEMTSKVLHYYKGDFL---DELPGLVDFTLMLNLSSRQK
AtDRD1       -------EDFTVKIKVIQD-LREMTKKVLHYYKGDFL---DELPGLADFTVVLNLSPKQL
At2g21450    -------TNFSAKASLIKD-LREMTRNILHYHKADFS---GLLPGLSEFTVMLNLSSIQR
Sm84719      -------NLGA----AVRF-FRKLTAPFLHWHGGKVL---DSLPGIEEVLVTLNLTEAHK
Cr13231      QQPDASRADREACAKKLYLLTERLTKDCIH---------RPMLPPKSDVVLFLDMTPRQR
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                               500                 520                 540
ScSNF2        IMY-QQMLKYRRLFIGDQNNKKMV-GLRGFNNQIMQ----LKKICNHP--FVFE------
ScRAD54       ELY-NKLIKSREV-------KKVVKGVGGS--QPLRAIGILKKLCNHPNLLNFEDEFDDE
Sm441121      KLV-AAVA------------------------GTLEMDITRTRISIHPLL----------
Bd1g16720     EIL-AKVSMSTSC--------------TGR--YPLEIELLITVGSIHPWLI-----KTTN
Os07g49210    EML-AKVTMPKLG--------------SSR--FPLEVELLITIGSIHPWLI-----KTTK
Sb02g043870   EVL-AKLSMPLAD--------------NAR--YLLEIELLITIASIHPWLI-----NTTR
ZM108166      EVL-AKLLMPLSG--------------NAR--YPLEYELLITIASIHPWLI-----NTTK
ZM000342      EVL-AKLLMPLSG--------------NAR--YPLEYELLITIASIHPWLI-----NTTK
Vv29366       QFL-SKLQKKKDE--------------YKG--YPLELELLVTLGSIHPWLI-----TTAA
Pt832603      QIL-VKLHKIMEK--------------CPG--YPLEVELLITLASIHPSLV-----NSSV
Pt567214      EIL-VKLHKIMEK--------------CPG--YPLEVELLITLASIHPSII-----NSSV
Cp19.123      ------------------------------------------------------------
AtCLSY1       KSL-TKLQNIMST--------------YHG--YPLELELLITLAAIHPWLV-----KTTT
At5g20420     KIL-TKLQDVIKT--------------YFG--YPLEVELQITLAAIHPWLV-----TSSN
Bd2g26500     SII-RKVENIGSG-------------------NNFEHEYVISLASTHPSLVTAI--NMSD
Os05g32610    SII-RKVENVGSG-------------------NNFEHEYVISLASTHPSLVNAI--NMTE
Sb09g019410   SII-RKVENIGSG-------------------NNFEHEYVISLASTHPSLVTAI--NMSE
RMR1          SII-KKVENIGSG-------------------NNFEHEYVISLASTHPSLVTAI--NMSE
Bd2g43500     EII-TMM-----E--------------KSAGKGFLDAEYKISLASIHPFLLTSV--KLSD
Os02g43460    EII-TAM-----E--------------NTVTMGTLDAEYKISLASIHPFLVTCA--KLSE
Bd3g50300     KII--KMLEDSRT--------------KSGTNGHLDFEYKISLASVHPSLITSTQ-KLPY
Sb04g033300   EVI-ATM-----E--------------KTVATTGLDEEYKISIASIHPSLLASA--KLSE
ZM178435      EVI-ASM-----E--------------KTVA-MGLDAEYKISLASIHPSLLASA--KLSM
Vv15867       RLL-ESIREKK---------------------NPLELGYLVSLISVHPSLLPSDERKL--
Pt286483      TLL-ENVKQINGL-------------------DHFEMEYLLSVLSVHPSLLPEK--SVGT
Cp76.2        SLL-DGLQGTR---------------------NTILLDFRVSLVSVHPSLLIDCH-----
At1g05490     RVL-ESIEVTHNR--------------KTK--NVFETEHKLSLVSVHPSLVSRC--KISE
At3g24340     KIL-DRIDTSQ---------------------NTFEFEHKLSAVSVHPSLYLCCNPTKK-
Bd3g18910     DIL-DTLEA-Y---------------------GSLKRAAVETAVYIHPCLKDISEADSNE
Bd1g74070     ESI-KSFVG-Q---------------------NKFSKRSNCNAVSLHPCLKDIKNICEKN
Os03g06920    HII-KGLDG-I---------------------NKFAKRSRCNAVSLHPCLKNANKADADD
Sb01g046180   DII-KGLAG-L---------------------KRFEAHAKCNAVSLHPCLKDVKIVDKKN
Bd3g19890     EIV-HKLEA-Y---------------------EKFKRSAVGTALYMHPCLSEMSEGDATD
Os06g14440    EIV-HKIEA-Y---------------------EKFKRSAVGTALYIHPCLSEISEGDAAD
Os07g25390    EIV-HKIEA-Y---------------------EKFKRSAVGTALYIHPCLSEISEGDAAD
Sb07g002945   DIIRNKLES-H---------------------DRFKRSAVGTALYIHPCLSQLSEVNAEN
ZM093940      DIV-HKLEM-H---------------------DRFKRSAVGSALYIHPCLSGLSEVNAEN
ZM064574      DII-YKLEA-H---------------------DRFKRNAVGSALYIHPCLSELSEVNAEH
Bd2g21430     ESI-QKLEA-Y---------------------EYLKSSAVGTALYVHPCLFEMSEAGAAD
Bd2g21450     ELV-QKLEG-Y---------------------EYLKRSAVGTALYMHPCLSEMSEAGAAD
Os08g14610    DIL-CKLEEDH---------------------GMLKTSAVGAALYVHPCLSEISEANDVD
Vv35918       KEV-GNLNKFE---------------------RKFKKNSVGSAVYLHPQLKYFAEKLAAN
Vv23895       KEV-GNLNKFE---------------------RKFKKNSVGSAVYLHPQLKYFAEKLAAN
Pt195587      HEV-KKLKKLA---------------------MKFKRSSVGSAVYLHPKLNSFSKNSAIT
AtDRD1        NEV-KKLRREK---------------------RKFKVSAVGSAIYLHPKLKVFSDKSDDV
At2g21450     DEV-KGLRK-M---------------------ELFKQISLGAALYIHPKLKSFLEENPSN
Sm84719       ALVLNAGKSYTKE--------------KKK--GFLAEDSRLARACVHPCFAVDV------
Cr13231       AMY---------------------------------------------------------
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                                560                 580                 600
ScSNF2       ---EVE--------DQI-----N-PTRETNDDIWRVAG----------------------
ScRAD54      DDLELP--------DDY-----NMPGSKARDVQTKYSA----------------------
Sm441121     --------------RSAEAAGGDFSAVAAEVVDVRASM----------------------
Bd1g16720    CASTFF--------TSA-----ELDKVDKYKKDFAAGC----------------------
Os07g49210   AVSTFF--------SPA-----EVKKVERYKRDFAAGC----------------------
Sb02g043870  CASTYF--------TPA-----EVARVGKYKRNFAVGC----------------------
ZM108166     CASTYF--------TPA-----EVASVDKYKRNFAAGC----------------------
ZM000342     CASTYF--------TPA-----EVASVDKYKRNFAAGC----------------------
Vv29366      CADKYF--------SRE-----ELLELKKHKDDVKKGS----------------------
Pt832603     CVKKFY--------NLE-----ELMELEKLRFDCKKGS----------------------
Pt567214     CVKKFY--------EQE-----ELMELEKLRFDCKKGS----------------------
Cp19.123     ------------------------------------------------------------
AtCLSY1      CCAKFF--------NPQ-----ELLEIEKLKHDAKKGS----------------------
At5g20420    CCTKFF--------NPQ-----ELSEIGKLKHDAKKGS----------------------
Bd2g26500    EEASLI--------DK--------PMLERLRSNPYEGV----------------------
Os05g32610   EEASLI--------DK--------PMLERLRSNPYEGV----------------------
Sb09g019410  EEASLI--------DK--------HMLGKLRSNPYEGV----------------------
RMR1         EEASLI--------DK--------PMLAKVRSNPYEGV----------------------
Bd2g43500    EEASIV--------NK----------LKSSRLDPCEGV----------------------
Os02g43460   KETSSV--------DV--------SLLKSLRPNPCVGV----------------------
Bd3g50300    QLTSVM--------DK--------PLLESLRLNPCEGV----------------------
Sb04g033300  QEESIL--------DI--------PKLESLRSRPSEGV----------------------
ZM178435     KEESIL--------DK--------PKLESLRSNPSGGV----------------------
Vv15867      ----FF--------DQ--------TKLEKIKLNPDIGV----------------------
Pt286483     LEFKFV--------DR--------MELEMLRSKPEAGV----------------------
Cp76.2       --------------PEMDHGYIDWKKLEKCRMIPNAGV----------------------
At1g05490    KERLSI--------DEA-----LLAQLKKVRLDPNQSV----------------------
At3g24340    --------------EDLVIGPATLGTLKRLRLKYEEGV----------------------
Bd3g18910    K--NWT--------DAE-----IDSLIESI--NIRDGV----------------------
Bd1g74070    E--NTTYQKIFLRNHEK-----ISSVMSGI--DINDGA----------------------
Os03g06920   G--NVT--------NRK-----IGSIISGI--DINDGV----------------------
Sb01g046180  R--NIN--------KRM-----MDSIVCGI--DISDGV----------------------
Bd3g19890    RANNLT--------DAA-----VDSMVQSI--NVRDGV----------------------
Os06g14440   RASNLT--------DAT-----VDSLIESI--IIKDGV----------------------
Os07g25390   RATNLT--------DAT-----VDSLIESI--IIKDGV----------------------
Sb07g002945  RANTLR--------DDL-----VDSLLDSI--NVKDGV----------------------
ZM093940     RAHTLR--------DDS-----VDSLMDSI--NVRDGV----------------------
ZM064574     RANTFR--------DDL-----VDSLVDSI--TVRDGV----------------------
Bd2g21430    RAKNLT--------DAT-----VDTLVESV--QLSDGV----------------------
Bd2g21450    KANILT--------DAT-----VDTLFESV--HVGDGV----------------------
Os08g14610   R-------------DDR-----VDSLVNSI--NLGDGV----------------------
Vv35918      E--SKT--------DEMTCQKKMDEILEQL--DVRDGV----------------------
Vv23895      E--SKT--------DEMTYQKKMDEILEQL--DVREGV----------------------
Pt195587     --------------DDM-----MDDLLETV--DVRDGV----------------------
AtDRD1       S-------------DTT-----MDEMVEKL--DLNEGV----------------------
At2g21450    GEKGFS--------DNNTTVMKLDKMLKKI--NVRDGV----------------------
Sm84719      ----------------------ESPELEQQ--DPKAGA----------------------
Cr13231      -----------------------TAYLRALQGRPPPGAAGGTGTSGEGAEGGGGGSGGVL
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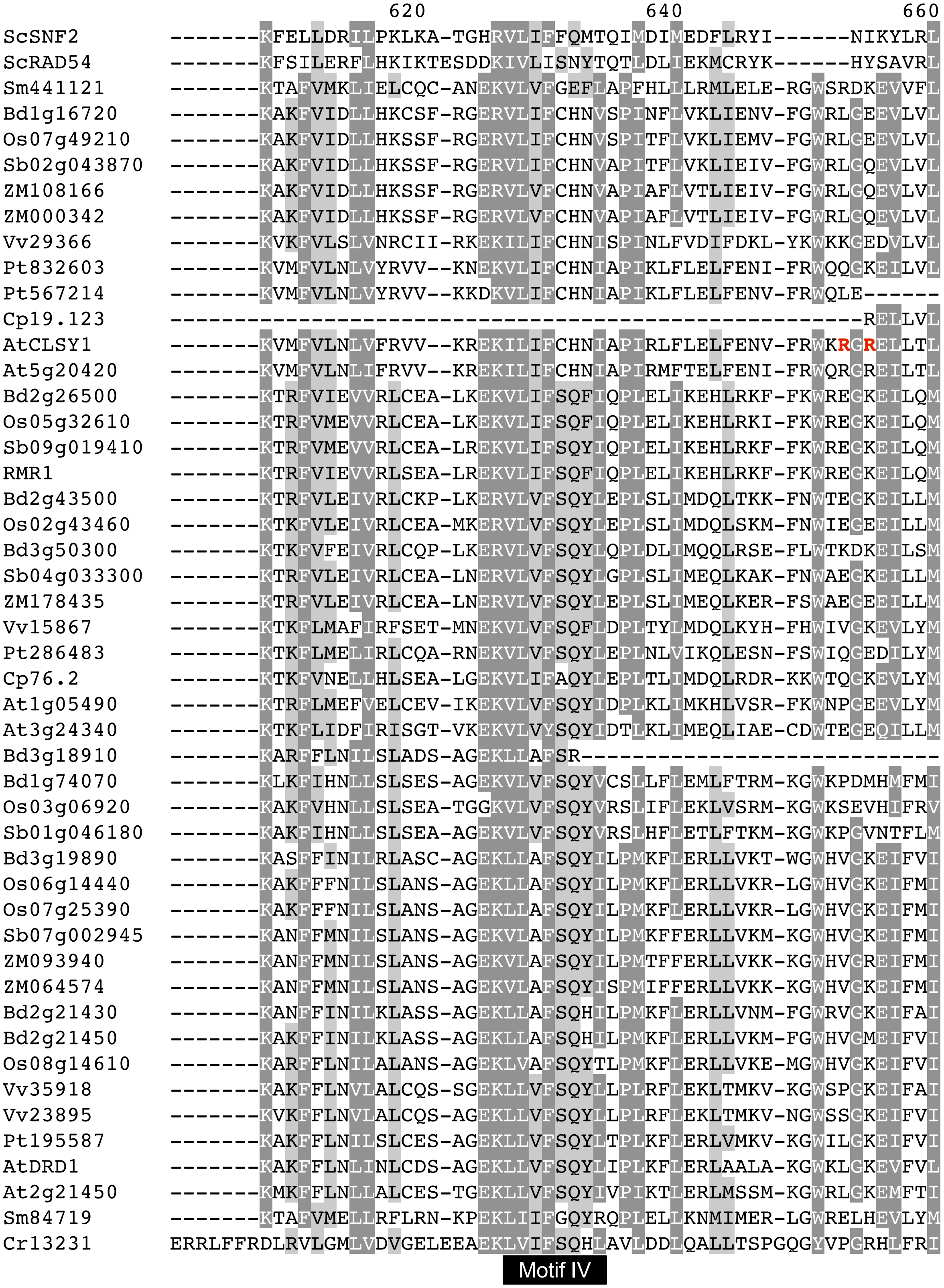

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ScSNF2            -------KFELLDRILPKLKA-TGHRVLIFFQMTQIMDIMEDFLRYI------NIKYLRL
ScRAD54           -------KFSILERFLHKIKTESDDKIVLISNYTQTLDLIEKMCRYK------HYSAVRL
Sm441121          -------KTAFVMKLIELCQC-ANEKVLVFGEFLAPFHLLLRMLELE-RGWSRDKEVVFL
Bd1g16720         -------KAKFVIDLLHKCSF-RGERVLIFCHNVSPINFLVKLIENV-FGWRLGEEVLVL
Os07g49210        -------KAKFVIDLLHKSSF-RGERVLIFCHNVSPITFLVKLIEMV-FGWRLGEEVLVL
Sb02g043870       -------KAKFVIDLLHKSSF-RGERVLIFCHNVAPITFLVKLIEIV-FGWRLGQEVLVL
ZM108166          -------KAKFVIDLLHKSSF-RGERVLVFCHNVAPIAFLVTLIEIV-FGWRLGQEVLVL
ZM000342          -------KAKFVIDLLHKSSF-RGERVLVFCHNVAPIAFLVTLIEIV-FGWRLGQEVLVL
Vv29366           -------KVKFVLSLVNRCII-RKEKILIFCHNISPINLFVDIFDKL-YKWKKGEDVLVL
Pt832603          -------KVMFVLNLVYRVV--KNEKVLIFCHNIAPIKLFLELFENI-FRWQQGKEILVL
Pt567214          -------KVMFVLNLVYRVV--KKDKVLIFCHNIAPIKLFLELFENV-FRWQLE------
Cp19.123          -------------------------------------------------------RELVL
AtCLSY1           -------KVMFVLNLVFRVV--KREKILIFCHNIAPIRLFLELFENV-FRWKRGRELLTL
At5g20420         -------KVMFVLNLIFRVV--KREKILIFCHNIAPIRMFTELFENI-FRWQRGREILTL
Bd2g26500         -------KTRFVIEVVRLCEA-LKEKVLIFSQFIQPLELIKEHLRKF-FKWREGKEILQM
Os05g32610        -------KTRFVMEVVRLCEA-LKEKVLIFSQFIQPLELIKEHLRKI-FKWREGKEILQM
Sb09g019410       -------KTRFVMEVVRLCEA-LREKVLIFSQYIQPLELIKEHLRKF-FKWREGKEILQM
RMR1              -------KTRFVIEVVRLSEA-LREKVLIFSQFIQPLELIKEHLRKF-FKWREGKEILQM
Bd2g43500         -------KTRFVLEIVRLCKP-LKERVLVFSQYLEPLSLIMDQLTKK-FNWTEGKEILLM
Os02g43460        -------KTKFVLEIVRLCEA-MKERVLVFSQYLEPLSLIMDQLSKM-FNWIEGEEILLM
Bd3g50300         -------KTKFVFEIVRLCQP-LKERVLVFSQYLQPLDLIMQQLRSE-FLWTKDKEILSM
Sb04g033300       -------KTRFVLEIVRLCEA-LNERVLVFSQYLGPLSLIMEQLKAK-FNWAEGKEILLM
ZM178435          -------KTRFVLEIVRLCEA-LNERVLVFSQYLEPLSLIMEQLKER-FSWAEGEEILLM
Vv15867           -------KTKFLMAFIRFSET-MNEKVLVFSQFLDPLTYLMDQLKYH-FHWIVGKEVLYM
Pt286483          -------KTKFLMELIRLCQA-RNEKVLVFSQYLEPLNLVIKQLESN-FSWIQGEDILYM
Cp76.2            -------KTKFVNELLHLSEA-LGEKVLIFAQYLEPLTLIMDQLRDR-KKWTQGKEVLYM
At1g05490         -------KTRFLMEFVELCEV-IKEKVLVFSQYIDPLKLIMKHLVSR-FKWNPGEEVLYM
At3g24340         -------KTKFLIDFIRISGT-VKEKVLVYSQYIDTLKLIMEQLIAE-CDWTEGEQILLM
Bd3g18910         -------KARFFLNILSLADS-AGEKLLAFSR----------------------------
Bd1g74070         -------KLKFIHNLLSLSES-AGEKVLVFSQYVCSLLFLEMLFTRM-KGWKPDMHMFMI
Os03g06920        -------KAKFVHNLLSLSEA-TGGKVLVFSQYVRSLIFLEKLVSRM-KGWKSEVHIFRV
Sb01g046180       -------KAKFIHNLLSLSEA-AGEKVLVFSQYVRSLHFLETLFTKM-KGWKPGVNTFLM
Bd3g19890         -------KASFFINILRLASC-AGEKLLAFSQYILPMKFLERLLVKT-WGWHVGKEIFVI
Os06g14440        -------KAKFFFNILSLANS-AGEKLLAFSQYILPMKFLERLLVKR-LGWHVGKEIFMI
Os07g25390        -------KAKFFFNILSLANS-AGEKLLAFSQYILPMKFLERLLVKR-LGWHVGKEIFMI
Sb07g002945       -------KANFFMNILSLANS-AGEKVLAFSQYILPMKFFERLLVKM-KGWHVGKEIFMI
ZM093940          -------KANFFMNILSLANS-AGEKVLAFSQYILPMTFFERLLVKK-KGWHVGREIFMI
ZM064574          -------KANFFMNILSLANS-AGEKVLAFSQYISPMIFFERLLVKK-KGWHVGKEIFMI
Bd2g21430         -------KANFFINILKLASS-AGEKLLAFSQHILPMKFLERLLVNM-FGWRVGKEIFAI
Bd2g21450         -------KAKFFINILKLASS-AGEKLLAFSQHILPMKFLERLLVKM-FGWHVGMEIFVI
Os08g14610        -------KARFFLNILALANS-AGEKLVAFSQYTLPMKFLERLLVKE-MGWHVGKEIFVI
Vv35918           -------KAKFFLNVLALCQS-SGEKLLVFSQYLLPLRFLEKLTMKV-KGWSPGKEIFAI
Vv23895           -------KVKFFLNVLALCQS-AGEKLLVFSQYLLPLRFLEKLTMKV-NGWSSGKEIFVI
Pt195587          -------KAKFFLNILSLCES-AGEKLLVFSQYLTPLKFLERLVMKV-KGWILGKEIFVI
AtDRD1            -------KAKFFLNLINLCDS-AGEKLLVFSQYLIPLKFLERLAALA-KGWKLGKEVFVL
At2g21450         -------KMKFFLNLLALCES-TGEKLLVFSQYIVPIKTLERLMSSM-KGWRLGKEMFTI
Sm84719           -------KTAFVMELLRFLRN-KPEKLIIFGQYRQPLELLKNMIMER-LGWRELHEVLYM
Cr13231           ERRLFFRDLRVLGMLVDVGELEEAEKLVIFSQHLAVLDDLQALLTSPGQGYVPGRHLFRI
                                            Motif IV
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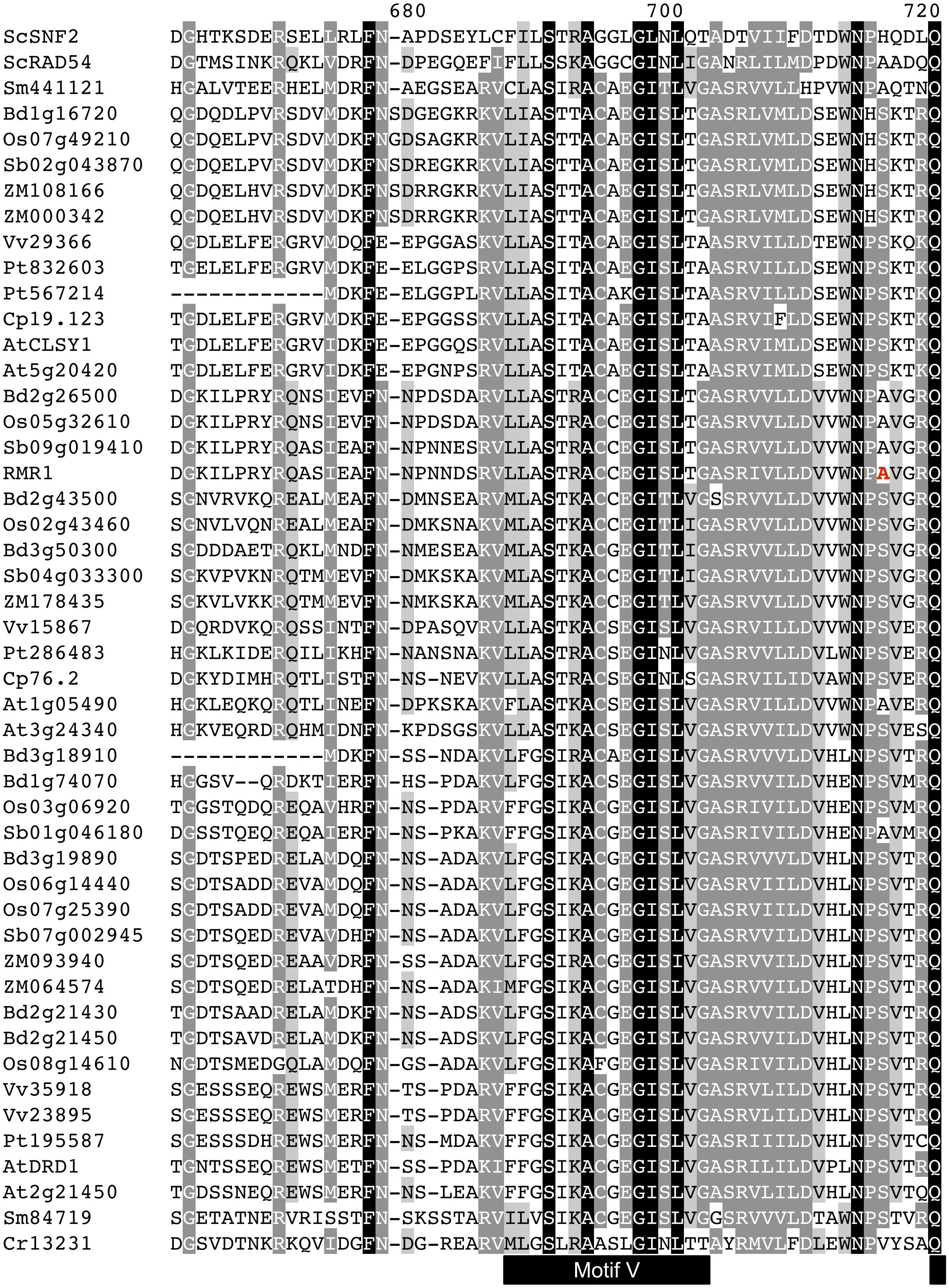

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                                         680                                     700                                       720
ScSNF2        DGHTKSDERSELLRLFN-APDSEYLCFILSTRAGGLGINLQTADTVIIFDTDWNPHQDLQ
ScRAD54       DGTMSINKRQKLVDRFN-DPEGQEFIFLLSSKAGGCGINLIGANRLILMDPDWNPAADQQ
Sm441121      HGALVTEERHELMDRFN-AEGSEARVCLASIRACAEGITLVGASRVVLLHPVWNPAQTNQ
Bd1g16720     QGDQDLPVRSDVMDKFNSDGEGKRKVLIASTTACAEGISLTGASRLVMLDSEWNHSKTRQ
Os07g49210    QGDQELPVRSDVMDKFNGDSAGKRKVLIASTTACAEGISLTGASRLVMLDSEWNHSKTRQ
Sb02g043870   QGDQELPVRSDVMDKFNSDREGKRKVLIASTTACAEGISLTGASRLVMLDSEWNHSKTRQ
ZM108166      QGDQELHVRSDVMDKFNSDRRGKRKVLIASTTACAEGISLTGASRLVMLDSEWNHSKTRQ
ZM000342      QGDQELHVRSDVMDKFNSDRRGKRKVLIASTTACAEGISLTGASRLVMLDSEWNHSKTRQ
Vv29366       QGDLELFERGRVMDQFE-EPGGASKVLLASITACAEGISLTAASRVILLDTEWNPSKQKQ
Pt832603      TGELELFERGRVMDKFE-ELGGPSRVLLASITACAEGISLTAASRVILLDSEWNPSKTKQ
Pt567214      ------------MDKFE-ELGGPLRVLLASITACAKGISLTAASRVILLDSEWNPSKTKQ
Cp19.123      TGDLELFERGRVMDKFE-EPGGSSKVLLASITACAEGISLTAASRVIFLDSEWNPSKTKQ
AtCLSY1       TGDLELFERGRVIDKFE-EPGGQSRVLLASITACAEGISLTAASRVIMLDSEWNPSKTKQ
At5g20420     TGDLELFERGRVIDKFE-EPGNPSRVLLASITACAEGISLTAASRVIMLDSEWNPSKTKQ
Bd2g26500     DGKILPRYRQNSIEVFN-NPDSDARVLLASTRACCEGISLTGASRVVLLDVVWNPAVGRQ
Os05g32610    DGKILPRYRQNSIEVFN-NPDSDARVLLASTRACCEGISLTGASRVVLLDVVWNPAVGRQ
Sb09g019410   DGKILPRYRQASIEAFN-NPNNESRVLLASTRACCEGISLTGASRVVLLDVVWNPAVGRQ
RMR1          DGKILPRYRQASIEAFN-NPNNDSRVLLASTRACCEGISLTGASRIVLLDVVWNPAVGRQ
Bd2g43500     SGNVRVKQREALMEAFN-DMNSEARVMLASTKACCEGITLVGSSRVVLLDVVWNPSVGRQ
Os02g43460    SGNVLVQNREALMEAFN-DMKSNAKVMLASTKACCEGITLIGASRVVLLDVVWNPSVGRQ
Bd3g50300     SGDDDAETRQKLMNDFN-NMESEAKVMLASTKACGEGITLIGASRVVLLDVVWNPSVGRQ
Sb04g033300   SGKVPVKNRQTMMEVFN-DMKSKAKVMLASTKACCEGITLIGASRVVLLDVVWNPSVGRQ
ZM178435      SGKVLVKKRQTMMEVFN-NMKSKAKVMLASTKACCEGITLVGASRVVLLDVVWNPSVGRQ
Vv15867       DGQRDVKQRQSSINTFN-DPASQVRVLLASTKACSEGISLVGASRVILLDVVWNPSVERQ
Pt286483      HGKLKIDERQILIKHFN-NANSNAKVLLASTRACSEGINLVGASRVVLLDVLWNPSVERQ
Cp76.2        DGKYDIMHRQTLISTFN-NS-NEVKVLLASTRACSEGINLSGASRVILIDVAWNPSVERQ
At1g05490     HGKLEQKQRQTLINEFN-DPKSKAKVFLASTKACSEGISLVGASRVILLDVVWNPAVERQ
At3g24340     HGKVEQRDRQHMIDNFN-KPDSGSKVLLASTKACSEGISLVGASRVVILDVVWNPSVESQ
Bd3g18910     ------------MDKFN-SS-NDAKVLFGSIRACAEGISLVGASRVVVLDVHLNPSVTRQ
Bd1g74070     HGGSV--QRDKTIERFN-HS-PDAKVLFGSIKACSEGISLVGASRVVILDVHENPSVMRQ
Os03g06920    TGGSTQDQREQAVHRFN-NS-PDARVFFGSIKACGEGISLVGASRIVILDVHENPSVMRQ
Sb01g046180   DGSSTQEQREQAIERFN-NS-PKAKVFFGSIKACGEGISLVGASRIVILDVHENPAVMRQ
Bd3g19890     SGDTSPEDRELAMDQFN-NS-ADAKVLFGSIKACGEGISLVGASRVVVLDVHLNPSVTRQ
Os06g14440    SGDTSADDREVAMDQFN-NS-ADAKVLFGSIKACGEGISLVGASRVIILDVHLNPSVTRQ
Os07g25390    SGDTSADDREVAMDQFN-NS-ADAKVLFGSIKACGEGISLVGASRVIILDVHLNPSVTRQ
Sb07g002945   SGDTSQEDREVAVDHFN-NS-ADAKVLFGSIKACGEGISLVGASRVVILDVHLNPSVTRQ
ZM093940      SGDTSQEDREAAVDRFN-SS-ADAKVLFGSIRACGEGISIVGASRVVILDVHLNPSVTRQ
ZM064574      SGDTSQEDRELATDHFN-NS-ADAKIMFGSIKACGEGISLVGASRVVILDVHLNPSVTRQ
Bd2g21430     TGDTSAADRELAMDKFN-NS-ADSKVLFGSIKACGEGISLVGASRVVILDVHLNPSVTRQ
Bd2g21450     TGDTSAVDRELAMDKFN-NS-ADSKVLFGSIKACGEGISLVGASRVVILDVHLNPSVTRQ
Os08g14610    NGDTSMEDGQLAMDQFN-GS-ADAKVLFGSIKAFGEGISLVGASRIVILDVHLNPSVTRQ
Vv35918       SGESSSEQREWSMERFN-TS-PDARVFFGSIKACGEGISLVGASRVLILDVHLNPSVTRQ
Vv23895       SGESSSEQREWSMERFN-TS-PDARVFFGSIKACGEGISLVGASRVLILDVHLNPSVTRQ
Pt195587      SGESSSDHREWSMERFN-NS-MDAKVFFGSIKACGEGISLVGASRIIILDVHLNPSVTCQ
AtDRD1        TGNTSSEQREWSMETFN-SS-PDAKIFFGSIKACGEGISLVGASRILILDVPLNPSVTRQ
At2g21450     TGDSSNEQREWSMERFN-NS-LEAKVFFGSIKACGEGISLVGASRVLILDVHLNPSVTQQ
Sm84719       SGETATNERVRISSTFN-SKSSTARVILVSIKACGEGISLVGGSRVVVLDTAWNPSTVRQ
Cr13231       DGSVDTNKRKQVIDGFN-DG-REARVMLGSLRAASLGINLTTAYRMVLFDLEWNPVYSAQ
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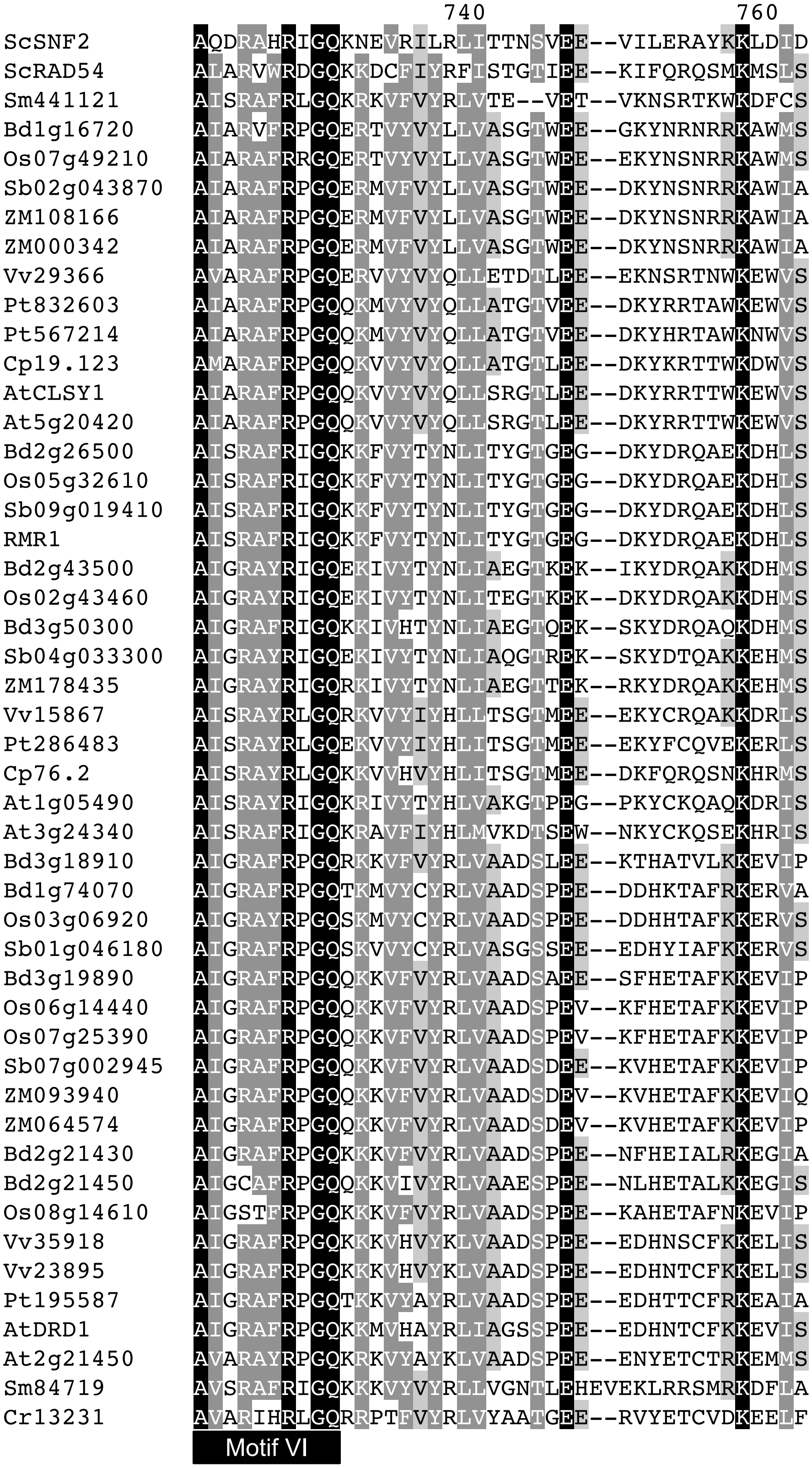


```
                                 740                 760
ScSNF2          AQDRAHRIGQKNEVRILRLITTNSVEE--VILERAYKKLDID
ScRAD54         ALARVWRDGQKKDCFIYRFISTGTIEE--KIFQRQSMKMSLS
Sm441121        AISRAFRLGQKRKVFVYRLVTE--VET--VKNSRTKWKDFCS
Bd1g16720       AIARVFRPGQERTVYVYLLVASGTWEE--GKYNRNRRKAWMS
Os07g49210      AIARAFRRGQERTVYVYLLVASGTWEE--EKYNSNRRKAWMS
Sb02g043870     AIARAFRPGQERMVFVYLLVASGTWEE--DKYNSNRRKAWIA
ZM108166        AIARAFRPGQERMVFVYLLVASGTWEE--DKYNSNRRKAWIA
ZM000342        AIARAFRPGQERMVFVYLLVASGTWEE--DKYNSNRRKAWIA
Vv29366         AVARAFRPGQERVVYVYQLLETDTLEE--EKNSRTNWKEWVS
Pt832603        AIARAFRPGQQKMVYVYQLLATGTVEE--DKYRRTAWKEWVS
Pt567214        AIARAFRPGQQKMVYVYQLLATGTVEE--DKYHRTAWKNWVS
Cp19.123        AMARAFRPGQQKVVYVYQLLATGTLEE--DKYKRTTWKDWVS
AtCLSY1         AIARAFRPGQQKVVYVYQLLSRGTLEE--DKYRRTTWKEWVS
At5g20420       AIARAFRPGQQKVVYVYQLLSRGTLEE--DKYRRTTWKEWVS
Bd2g26500       AISRAFRIGQKKFVYTYNLITYGTGEG--DKYDRQAEKDHLS
Os05g32610      AISRAFRIGQKKFVYTYNLITYGTGEG--DKYDRQAEKDHLS
Sb09g019410     AISRAFRIGQKKFVYTYNLITYGTGEG--DKYDRQAEKDHLS
RMR1            AISRAFRIGQKKFVYTYNLITYGTGEG--DKYDRQAEKDHLS
Bd2g43500       AIGRAYRIGQEKIVYTYNLIAEGTKEK--IKYDRQAKKDHMS
Os02g43460      AIGRAYRIGQEKIVYTYNLITEGTKEK--DKYDRQAKKDHMS
Bd3g50300       AIGRAFRIGQKKIVHTYNLIAEGTQEK--SKYDRQAQKDHMS
Sb04g033300     AIGRAYRIGQEKIVYTYNLIAQGTREK--SKYDTQAKKEHMS
ZM178435        AIGRAYRIGQRKIVYTYNLIAEGTTEK--RKYDRQAKKEHMS
Vv15867         AISRAYRLGQRKVVYIYHLLTSGTMEE--EKYCRQAKKDRLS
Pt286483        AISRAYRLGQEKVVYIYHLITSGTMEE--EKYFCQVEKERLS
Cp76.2          AISRAYRLGQKKVVHVYHLITSGTMEE--DKFQRQSNKHRMS
At1g05490       AISRAYRIGQKRIVYTYHLVAKGTPEG--PKYCKQAQKDRIS
At3g24340       AISRAFRIGQKRAVFIYHLMVKDTSEW--NKYCKQSEKHRIS
Bd3g18910       AIGRAFRPGQRKKVFVYRLVAADSLEE--KTHATVLKKEVIP
Bd1g74070       AIGRAFRPGQTKMVYCYRLVAADSPEE--DDHKTAFRKERVA
Os03g06920      AIGRAYRPGQSKMVYCYRLVAADSPEE--DDHHTAFKKERVS
Sb01g046180     AIGRAFRPGQSKVVYCYRLVASGSSEE--EDHYIAFKKERVS
Bd3g19890       AIGRAFRPGQQKKVFVYRLVAADSAEE--SFHETAFKKEVIP
Os06g14440      AIGRAFRPGQQKKVFVYRLVAADSPEV--KFHETAFKKEVIP
Os07g25390      AIGRAFRPGQQKKVFVYRLVAADSPEV--KFHETAFKKEVIP
Sb07g002945     AIGRAFRPGQQKKVFVYRLVAADSDEE--KVHETAFKKEVIP
ZM093940        AIGRAFRPGQQKKVFVYRLVAADSDEV--KVHETAFKKEVIQ
ZM064574        AIGRAFRPGQQKKVFVYRLVAADSDEV--KVHETAFKKEVIP
Bd2g21430       AIGRAFRPGQKKKVFVYRLVAADSPEE--NFHEIALRKEGIA
Bd2g21450       AIGCAFRPGQQKKVIVYRLVAAESPEE--NLHETALKKEGIS
Os08g14610      AIGSTFRPGQKKKVFVYRLVAADSPEE--KAHETAFNKEVIP
Vv35918         AIGRAFRPGQKKKVHVYKLVAADSPEE--EDHNSCFKKELIS
Vv23895         AIGRAFRPGQKKKVHVYKLVAADSPEE--EDHNTCFKKELIS
Pt195587        AIGRAFRPGQTKKVYAYRLVAADSPEE--EDHTTCFRKEAIA
AtDRD1          AIGRAFRPGQKKMVHAYRLIAGSSPEE--EDHNTCFKKEVIS
At2g21450       AVARAYRPGQKRKVYAYKLVAADSPEE--ENYETCTRKEMMS
Sm84719         AVSRAFRIGQKKKVYVYRLLVGNTLEHEVEKLRRSMRKDFLA
Cr13231         AVARIHRLGQRRPTFVYRLVYAATGEE--RVYETCVDKEELF
                Motif VI
```

Figure 10. Phylogenetic relationships within the DRD1 subfamily. Maximum likelihood tree of DRD1 subfamily members from various plant species. The tree is based on the MAFFT protein alignment in Figure 9 and rooted using Cr13231, ScRad54 and ScSNF2.

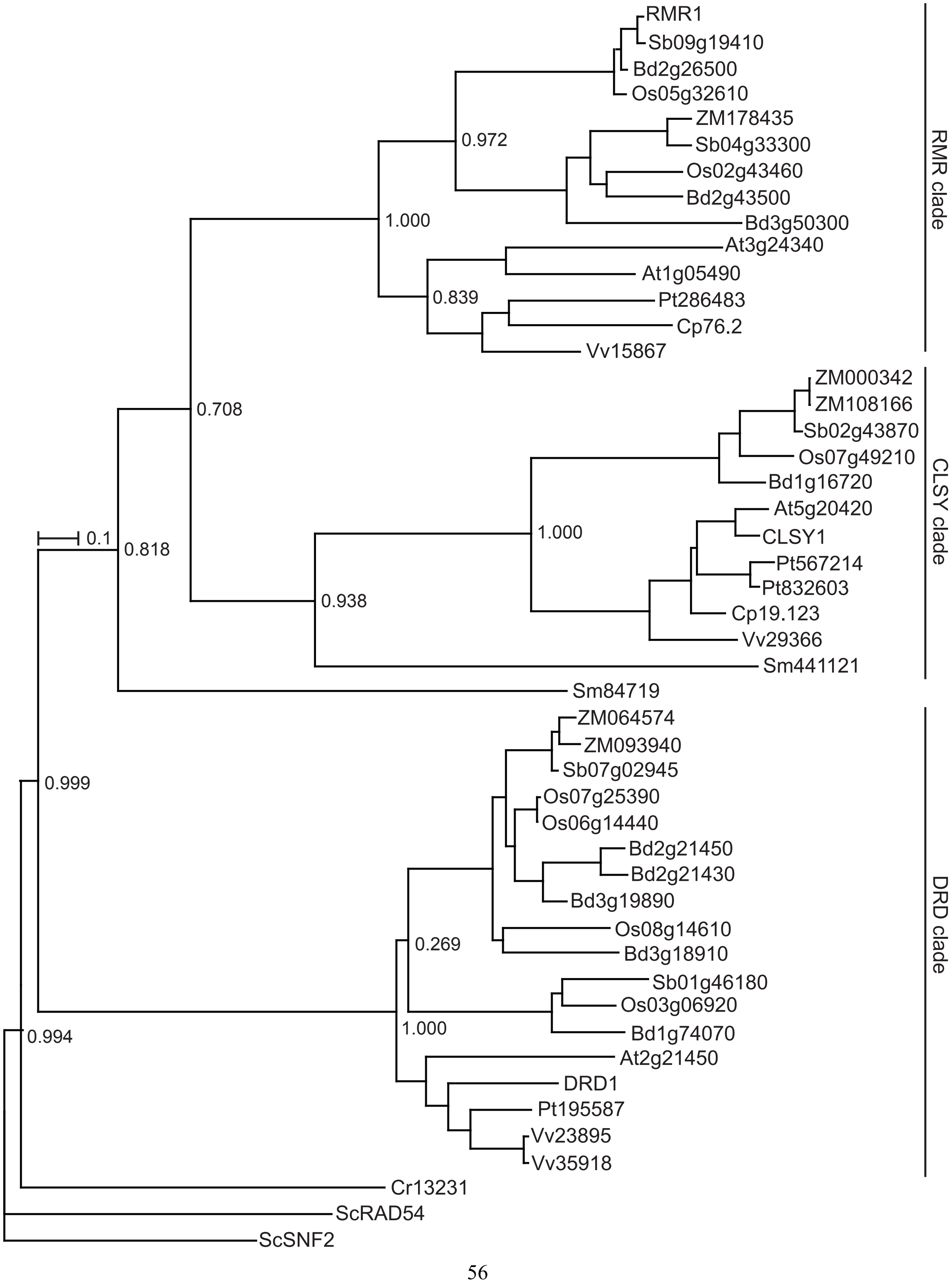
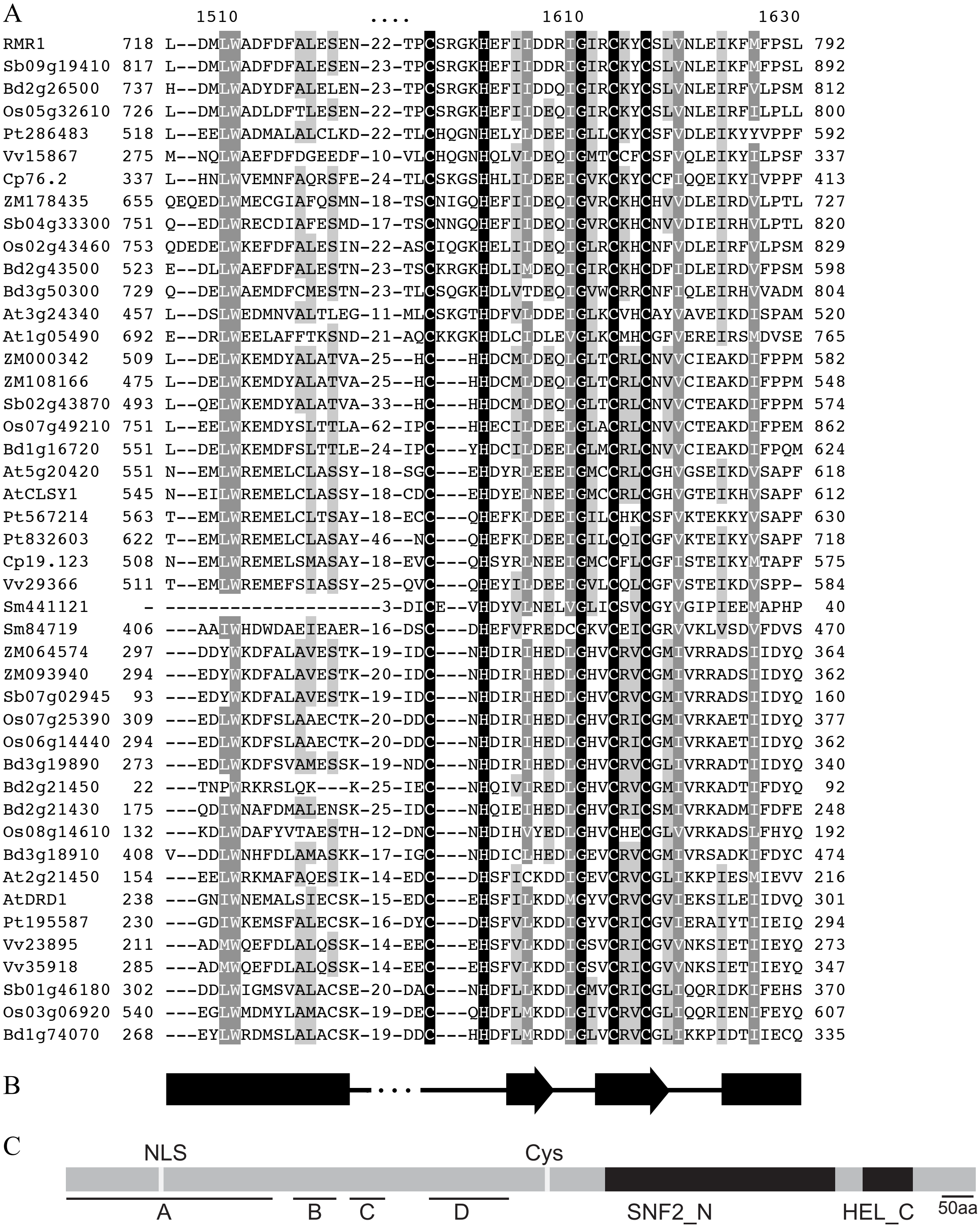


Figure 11. DRD1 subfamily members contain an additional N-terminal conserved motif. (A) Excerpt of DRD1 subfamily N-terminal MAFFT alignment (Appendix 5) over the cysteine-rich motif. (B) Predicted secondary structure of region. (C) Relative position of cysteine-rice motif (Cys) in comparison to other RMR1 sequence features including the nuclear localization signal (NLS), intrinsic disorder regions (underlined regions A, B, C, D), and SNF2 domains (black boxes marked SNF2_N and HEL_C).



```
A                   1510           ....                1610                 1630
RMR1        718 L--DMLWADFDFALESEN-22-TPCSRGKHEFIIDDRIGIRCKYCSLVNLEIKFMFPSL 792
Sb09g19410  817 L--DMLWADFDFALESEN-23-TPCSRGKHEFIIDDRIGIRCKYCSLVNLEIKFMFPSL 892
Bd2g26500   737 H--DMLWADYDFALELEN-23-TPCSRGKHEFIIDDQIGIRCKYCSLVNLEIRFVLPSM 812
Os05g32610  726 L--DMLWADLDFTLESEN-22-TPCSRGKHEFIIDEQIGIRCKYCSLVNLEIRFILPLL 800
Pt286483    518 L--EELWADMALALCLKD-22-TLCHQGNHELYLDEEIGLLCKYCSFVDLEIKYYVPPF 592
Vv15867     275 M--NQLWAEFDFDGEEDF-10-VLCHQGNHQLVLDEQIGMTCCFCSFVQLEIKYILPSF 337
Cp76.2      337 L--HNLWVEMNFAQRSFE-24-TLCSKGSHHLILDEEIGVKCKYCCFIQQEIKYIVPPF 413
ZM178435    655 QEQEDLWMECGIAFQSMN-18-TSCNIGQHEFIIDEQIGVRCKHCHVVDLEIRDVLPTL 727
Sb04g33300  751 Q--EDLWRECDIAFESMD-17-TSCNNGQHEFIIDEQIGVRCKHCNVVDIEIRHVLPTL 820
Os02g43460  753 QDEDELWKEFDFALESIN-22-ASCIQGKHELIIDEQIGLRCKHCNFVDLEIRFVLPSM 829
Bd2g43500   523 E--DLLWAEFDFALESTN-23-TSCKRGKHDLIMDEQIGIRCKHCDFIDLEIRDVFPSM 598
Bd3g50300   729 Q--DELWAEMDFCMESTN-23-TLCSQGKHDLVTDEQIGVWCRRCNFIQLEIRHVVADM 804
At3g24340   457 L--DSLWEDMNVALTLEG-11-MLCSKGTHDFVLDDEIGLKCVHCAYVAVEIKDISPAM 520
At1g05490   692 E--DRLWEELAFFTKSND-21-AQCKKGKHDLCIDLEVGLKCMHCGFVEREIRSMDVSE 765
ZM000342    509 L--DELWKEMDYALATVA-25--HC---HHDCMLDEQLGLTCRLCNVVCIEAKDIFPPM 582
ZM108166    475 L--DELWKEMDYALATVA-25--HC---HHDCMLDEQLGLTCRLCNVVCIEAKDIFPPM 548
Sb02g43870  493 L--QELWKEMDYALATVA-33--HC---HHDCMLDEQLGLTCRLCNVVCTEAKDIFPPM 574
Os07g49210  751 L--EELWKEMDYSLTTLA-62-IPC---HHECILDEELGLACRLCNVVCTEAKDIFPEM 862
Bd1g16720   551 L--DELWKEMDFSLTTLE-24-IPC---YHDCILDEELGLMCRLCNVVCIEAKDIFPQM 624
At5g20420   551 N--EMLWREMELCLASSY-18-SGC---EHDYRLEEEIGMCCRLCGHVGSEIKDVSAPF 618
AtCLSY1     545 N--EILWREMELCLASSY-18-CDC---EHDYELNEEIGMCCRLCGHVGTEIKHVSAPF 612
Pt567214    563 T--EMLWREMELCLTSAY-18-ECC---QHEFKLDEEIGILCHKCSFVKTEKKYVSAPF 630
Pt832603    622 T--EMLWREMELCLASAY-46--NC---QHEFKLDEEIGILCQICGFVKTEIKYVSAPF 718
Cp19.123    508 N--EMLWREMELSMASAY-18-EVC---QHSYRLNEEIGMCCFLCGFISTEIKYMTAPF 575
Vv29366     511 T--EMLWREMEFSIASSY-25-QVC---QHEYILDEEIGVLCQLCGFVSTEIKDVSPP- 584
Sm441121      - --------------------3-DICE--VHDYVLNELVGLICSVCGYVGIPIEEMAPHP  40
Sm84719     406 ---AAIWHDWDAEIEAER-16-DSC---DHEFVFREDCGKVCEICGRVVKLVSDVFDVS 470
ZM064574    297 ---DDYWKDFALAVESTK-19-IDC---NHDIRIHEDLGHVCRVCGMIVRRADSIIDYQ 364
ZM093940    294 ---EDYWKDFALAVESTK-20-IDC---NHDIRIHEDLGHVCRVCGMIVRRADSIIDYQ 362
Sb07g02945   93 ---EDYWKDFALAVESTK-19-IDC---NHDIRIHEDLGHVCRVCGMIVRRADSIIDYQ 160
Os07g25390  309 ---EDLWKDFSLAAECTK-20-DDC---NHDIRIHEDLGHVCRICGMIVRKAETIIDYQ 377
Os06g14440  294 ---EDLWKDFSLAAECTK-20-DDC---NHDIRIHEDLGHVCRICGMIVRKAETIIDYQ 362
Bd3g19890   273 ---EDLWKDFSVAMESSK-19-NDC---NHDIRIHEDLGHVCRVCGLIVRRADTIIDYQ 340
Bd2g21450    22 ---TNPWRKRSLQK---K-25-IEC---NHQIVIREDLGHVCRVCGMIVRKADTIFDYQ  92
Bd2g21430   175 ---QDIWNAFDMALENSK-25-IDC---NHQIEIHEDLGHVCRICSMIVRKADMIFDFE 248
Os08g14610  132 ---KDLWDAFYVTAESTH-12-DNC---NHDIHVYEDLGHVCHECGLVVRKADSLFHYQ 192
Bd3g18910   408 V--DDLWNHFDLAMASKK-17-IGC---NHDICLHEDLGEVCRVCGMIVRSADKIFDYC 474
At2g21450   154 ---EELWRKMAFAQESIK-14-EDC---DHSFICKDDIGEVCRVCGLIKKPIESMIEVV 216
AtDRD1      238 ---GNIWNEMALSIECSK-15-EDC---EHSFILKDDMGYVCRVCGVIEKSILEIIDVQ 301
Pt195587    230 ---GDIWKEMSFALECSK-16-DYC---DHSFVLKDDIGYVCRICGVIERAIYTIIEIQ 294
Vv23895     211 ---ADMWQEFDLALQSSK-14-EEC---EHSFVLKDDIGSVCRICGVVNKSIETIIEYQ 273
Vv35918     285 ---ADMWQEFDLALQSSK-14-EEC---EHSFVLKDDIGSVCRICGVVNKSIETIIEYQ 347
Sb01g46180  302 ---DDLWIGMSVALACSE-20-DAC---NHDFLLKDDLGMVCRICGLIQQRIDKIFEHS 370
Os03g06920  540 ---EGLWMDMYLAMACSK-19-DEC---QHDFLMKDDLGIVCRVCGLIQQRIENIFEYQ 607
Bd1g74070   268 ---EYLWRDMSLALACSK-19-DDC---HHDFLMRDDLGLVCRVCGLIKKPIDTIIECQ 335
```

Figure 12. MAFFT alignment of RMR clade over N terminal region. Specific sequence features are noted below the alignment.

```
                             20                  40                  60
RMR1       MDRATPRVCG--RRGVSQAAVEAAPSSSRARRRDKAPAVVMDLGDD--------------
Sb09g19410 MDRAAPRARGRRRRGVSQ----AAPSSSRARRRDKAPVVVVDLGDD------------ED
Os05g32610 MDRAARLAR----RGGGVTVAEYRMVRGRRRGGDAGPVVVIDVEDD-------------G
Bd2g26500  MDRSGRRGRA---RGRGETLAEAS-PRTRRRHAE---TIVIDL--D-------------S
ZM178435   MP------------------APPSTEAGRSRTMTRVIILLDSDKED-------------D
Sb04g33300 MP------------------APPSAVPGKGRTKPREIIVIDSDEEG------------VG
Os02g43460 MP---------RRKGKGKGVEDEVEVYEPASPPERVLIILDSSEDDLDLQEVRRSLMITG
Bd2g43500  MP----------------------------------------------------------
Bd3g50300  MP----------------------PAADFPASKRKSRIEIPDSDDDADRRRESRSSVGTG
At3g24340  MD----------------------------------------------------------
At1g05490  ME----------------------------------------------------------
Pt286483   MSKSPIGHRK--------------------------------------------------
Vv15867    MD----------------------------------------------------------
Cp76.2     ME----------------------------------------------------------
                        Intrinsic disorder region A

                             80                 100                 120
RMR1       -DC-GGGGARKTVGGAAGRCEG--------------------------------------
Sb09g19410 EDCGGGGGARKTVGGAAGGRGG--------------------------------------
Os05g32610 ED--AADDSAGGGGGAAAAVKR--------------------------------------
Bd2g26500  ED--GGGGSSTAAAAASSSSSR--------------------------------------
ZM178435   GTGRQAGRELG-GAAIASAGEASKLVKPEVVDDVGSNPVRPGA-----------------
Sb04g33300 GGGRQAGRDLGSGAAIGAAGEAVKLVKPEPVDDAGFHPVLPGAPRLGAVPVPPRAQNPRA
Os02g43460 RGRARAAERVGEEAPRGSGRRAAPVVASRRRRR---------------------------
Bd2g43500  ------------------------------------------------------------
Bd3g50300  GQRERSAEAGRSGG----------------------------------------------
At3g24340  ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Pt286483   --------------------------------------------------PTPYQTR---
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
                        Intrinsic disorder region A

                            140                 160                 180
RMR1       ---------------------------------------------STKAPLPLLPPMMVP
Sb09g19410 ---------------------------------------------STEASPPPPPPMMVP
Os05g32610 ---------------------------------------------RVVV-----P-----
Bd2g26500  ---------------------------------------------RSSA-----PLTLVT
ZM178435   ---------------------------------------------LPTSLRVQGHRAPSS
Sb04g33300 PSSPRAQAQNPRAPSSPRTPSPRAPSLPSLVAAHPLGPGAPRLGVVPVPPRAQNPRAPSS
Os02g43460 -----------------------------------------RSRSRSRSPRAARPRAESS
Bd2g43500  ------------------------------------------------------------
Bd3g50300  --------------------------------------------------------LERR
At3g24340  -----------------------------------------------------------M
At1g05490  ------------------------------------------------------------
Pt286483   -----------------------------------------EANSNVPVTKDNIYSTHRS
Vv15867    -----------------------------------------------------------F
Cp76.2     -----------------------------------------------------GKRLKLD
                        Intrinsic disorder region A
```

```
                            200                 220                 240
RMR1       AGAVALRTRSRRRAM---------------------------------------------
Sb09g19410 AGAVAMRTRSRRRAM---------------------------------------------
Os05g32610 -GAVATRTRSRRMAM---------------------------------------------
Bd2g26500  SGSVATRTRSRSLAM---------------------------------------------
ZM178435   PSPVPAAVRKQPEIIAISDEDNDGSRF-------------RRVRRVKDEA-----SDWVL
Sb04g33300 PSPVAPEDRHQPEIIAISDDDG-GSRFRGAVPLDMIEESGRRVRPVKEEALDDLDCDWVR
Os02g43460 RRPTARRARARARSPSLEIIDVDSGSD-------------RGVVRVKEEPRSGSDSDYNG
Bd2g43500  ------------------------------------------------------------
Bd3g50300  LAAAIARRRTRAAAASRPEVVNLTGDDDDDIRDEEAAGRREVLGRVKEEPLDDRGLDPEA
At3g24340  TSCVARRTRSRTESYLNSILNKSKGISGEEEDQSLGCVNSR-------------------
At1g05490  --CIGKRVKSRSWQRLQAV-----------------------------------------
Pt286483   PSPSLQWTRLREAEVYKKLHD---------------------------------------
Vv15867    SSPVAKRTRLQEALV---------------------------------------------
Cp76.2     NQPVARRTRLKEAQFFKEYY----------------------------------------
```

Intrinsic disorder region A

```
                            260                 280                 300
RMR1       ----------LAAAVVEEAPTKKKKKEGA-IPDAAEAPRGHG------------------
Sb09g19410 ----------QAAAVVEETPTTKRRKRGATTPDAAEASRGRG------------------
Os05g32610 ----AQQAPVTPPAAAEEAPSRRRKRKGA----ASAEAGGGG------------------
Bd2g26500  ----K-----SPVAEAEAAPRAKRRRKGT----SAEADGGGG------------------
ZM178435   S---AKAKRAMVSGVPPGSSDVKRKRKRGSSGA--------GDFHALDRNLSASGAGRRT
Sb04g33300 S---AEAKRALVAVLPPGSSHAKRKRKRASSGRAKPDKRADGGVHALDRNSSASGAGHPT
Os02g43460 A---RGRARARARAPVAATAAKKKKRKRGKEAPSRAQESREV------------------
Bd2g43500  ----------KNKSPLVETPRRRIRR----------------------------------
Bd3g50300  SVARRGRGRGRARAAAASAPVASRKRRREDDSGSRGRGGRRA------------------
At3g24340  ----TEKRRVNMRDACSPSPRKKKRRRRKDDDDDVVFVRTEY------------------
At1g05490  ----NKRKKMETVAPVTSPPKKRRQKKPKNYDSDIEDITPTC------------------
Pt286483   --------------------EIRKGRNQGKESNAAATGSTNG------------------
Vv15867    ------------------------------------------------------------
Cp76.2     --------------------ERRRKEDGKNVARPSGQSEDRG------------------
```

Intrinsic disorder region A

```
                            320                 340                 360
RMR1       -----SKAAATSMATSSHKRRAGTSRSTSRD-----KRRARSGRASEPAR-------VGR
Sb09g19410 -----SKAAAASRATSRDKRRAGASRSTSRD-----KRRARSGRASEPAR-------AAR
Os05g32610 -----PSKRRVRSSGSAGGRG---------------ARKRKEAEADEEEA-------EAE
Bd2g26500  -----SKGAEASESASKGNRR-GRSRTASEPPDRALARKSKDADA-EEEA-------EAE
ZM178435   SWMAEDAGSSRNVSSSELSRGGVGDRSGSTKKA-------RGAPGKTRRGGGTRRERSTS
Sb04g33300 AWMSDDARSSRGVKSRESSRGVAGDRPGSAKKALVSSEESRGAPGKARSGGGARRERSTS
Os02g43460 ----------------------VRVKEEPNSDGNGAGGRAR-ARSPVAAAAKQRKRGGRE
Bd2g43500  ----------------------LLIDDDDDDDDSGDGGRAREAISPSVAAGGSRRVGA--
Bd3g50300  -----TRSAKQCTRGRRGGLRSLPSRPSSSDEPLGDSGRAKRVRRGHAEGGGSGRHGAAP
At3g24340  -----PEGKR---------------------DDENVGSTSGNLQSKSFDFGDR-------
At1g05490  -----NDSVPPPQVSNMYSVPNNSVKESFSRIMRDLNVEKKSGPSSSRLTDGSEQNP---
Pt286483   -----LNGAQEESVG---------------------GLSYKGSKSPV-------------
Vv15867    ------------------------------------------------------------
Cp76.2     -----VNGSKLGRVGLKG----------TNMETRDLGLNCKGSAGLE-------------
```

Intrinsic disorder region A

Predicted NLS

```
                            380                 400                 420
RMR1       A-------------------------RKRK------RNELEAPARRERVKAPCVSESDD-
Sb09g19410 A-------------------------CKRKGIELGAETEVDAPARSERAKAPCVSESDD-
Os05g32610 A-------------------------EEEA------EAEAGTPARGESME---VSQVDGG
Bd2g26500  A-------------------------EEEA------EAEA--PACGKRVE---VSRVDGC
ZM178435   A-------------------------APANLVGGSATVGSRIRLRSR-------------
Sb04g33300 V-------------------------APANWIGTS--IGSRIRSRSR-------------
Os02g43460 APSRAQESRVPVQIKEEPYSGSDSDGNVAGGRAVVPAADAKQGKRGKKTPSRG-----KG
Bd2g43500  --------------------------EISGWLVRDPLAPSSSAQPGTLLRSRE---QEQP
Bd3g50300  S-------------------------KQAGSLVASSSRSRKGKQRAALPPKHQFPLVSQS
At3g24340  ------------------------------------------------------------
At1g05490  ------------------------------------------------CLKERSFRVSDL
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
```

Intrinsic disorder region A

```
                            440                 460                 480
RMR1       -NSGRGDDASHDGDAEPRVGVAIGTDLVNGD------------------HPAAK------
Sb09g19410 -DGGRGDDASDDGNAEPRAGVAIGADLVNGD------------------RRTAKGEDHIE
Os05g32610 GSSGRADDASHNGNGESRVCNADGIDQASEERPSVAGGDLIEEEHYGNGEASVAGGDRIE
Bd2g26500  ANSERGEDPLDDHNNGSNAREACGIGHGNEE------------------HHNAAGKNRIG
ZM178435   ------------------------------------------------------------
Sb04g33300 ------------------------------------------------------------
Os02g43460 RRVVVRETSTPAAPSNGAPSVGRGKGRGPGRGRQRSKGAVRGRATPVNRVSTGVGSRTRS
Bd2g43500  EIIVISDDDHEDEEEDGA----RGGEIRHGEIPARVKDEESEEGSSVDWDALMLSDDEST
Bd3g50300  ESSSESDDDDDDEEGDDGL----------DDVCSETSDESWQPRYNSEFQVAMKGEKKVE
At3g24340  ------------------------------------------------------------
At1g05490  GVEKKCSPEITDLDVGIPVPRFSKLKDVSEQKNTCLMQKSSPEIADLDLVISVPSSSVLK
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
```

Intrinsic disorder region A

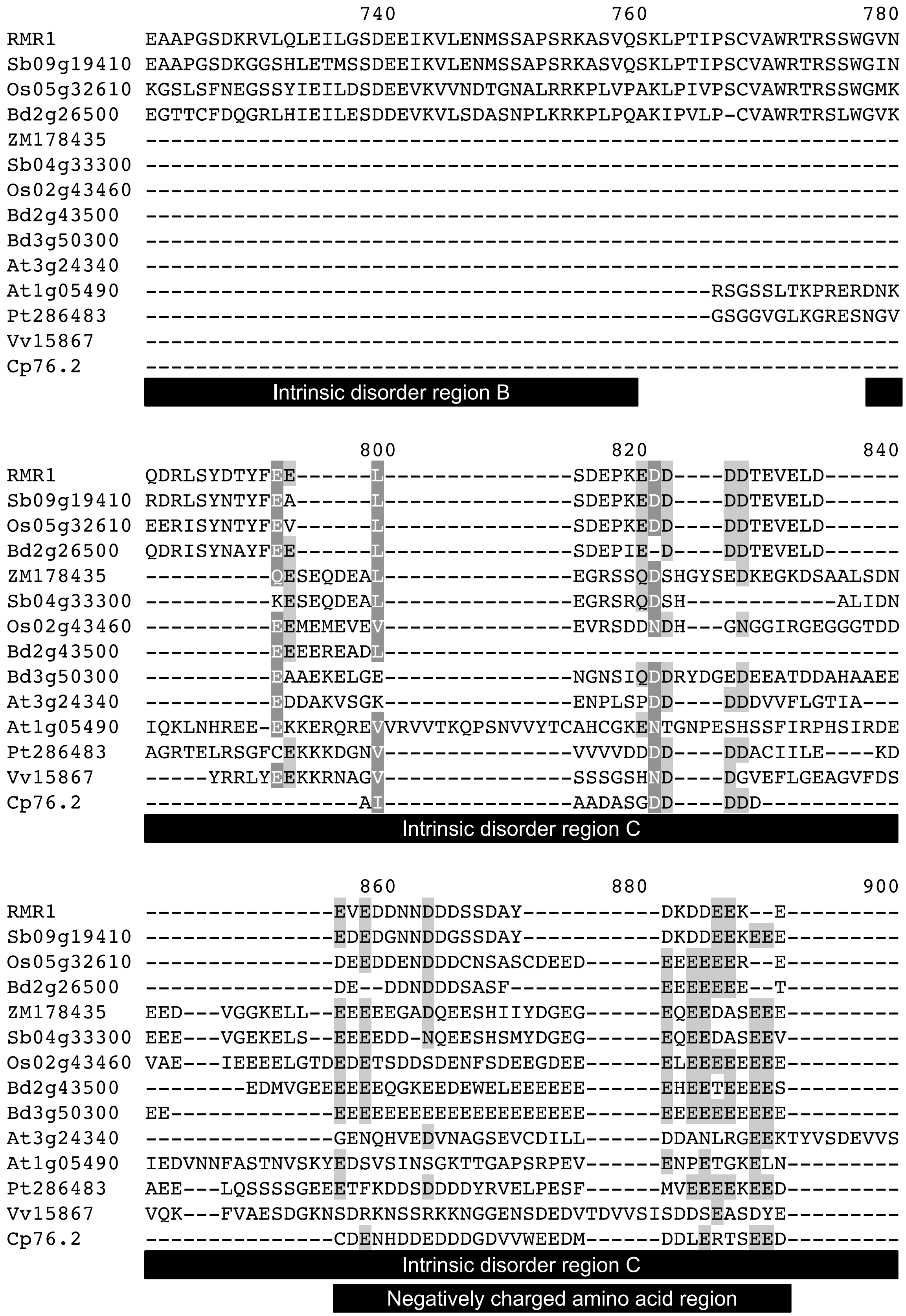
```
                            500                 520                 540
RMR1       ----------------------EVVEGAGDEDTGDGGNS--GLASTADVFAEEM------
Sb09g19410 EHGGDQENSAVNLNDDLVSGDAEAVEGAGDEDT--RGNS--GLASTADVVAEEM------
Os05g32610 EHCGNVEASVANSNRDG-----GEIIAG--EGTEDRGNT--EL-SVVDPVNEEL------
Bd2g26500  EPCGNGVASILNSSHGM-----NVVASGHAEGVKDWGNKGGEL-DDGFEVDEEY------
ZM178435   -----------------------------------------QQGRVQCATYSAR------
Sb04g33300 -----------------------------------------KQGTGQ---YSAR------
Os02g43460 RLA--------------------------------------EQGRAFAQEEEEQ------
Bd2g43500  AAAPP------------------------------------GTATGVPDEEEE-------
Bd3g50300  GRRNSVEEEATEKELG-------------------------ENGNGIPVLEEAAEKELRE
At3g24340  ------------------------------------------------------------
At1g05490  DVSEEIRFLKDKCSPEIRGLVLEKSVPGEIE-----------------------------
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     -----------------------------------------NRARRIKTREK--------
```

Intrinsic disorder region A

```
                                 560                 580                 600
RMR1        ------APFED-DY-DDEMLEEQLV------GD-------VIRAYSNGRNFDSDGVDWEA
Sb09g19410  ------APFED-DY-DDEMLEEQLV------GD-------VIRAYSNGRNFDADEADWEA
Os05g32610  ------ASDED-DY-DDEMLEEKLV------GD-------VIRAYSNGADLDTNGVDWEA
Bd2g26500   ------MNEEDTED-DDEMLEEKLV------GD-------LIRAYSNGDDLDADGVDWEA
ZM178435    ------VSSEDTGEDEKHMQEQTRV------ED-------VEFMEVDDDYDD-VNVAGNV
Sb04g33300  ------VSSEDTGEDEVQEQKQKRV------ED-------VESMDVDDDDDNNTNEAGNG
Os02g43460  ------VEEREEEE---EEEEQGRAFAQVKEEQ-------VEEQEEDEEEGE--------
Bd2g43500   ------AELEDKDNLEEEQEED----------------------EEDEWEEE--------
Bd3g50300   NGNSIPVQEEAAEK---ELGENGNSIPVLEEAA-------EKELRENGKSIPVEE-----
At3g24340   ------VCDFDADDRNLGCEEKASNFNPIDDDDDVVFVGTVQRENDHVEDDDNVGSASVI
At1g05490   ------ILSDSESETEARRRASAKKKLFEESSR-------IVESISDGEDSSSETDEEEE
Pt286483    ------VLDDSEDD---AFLDDCEKGGLEEGLD-------VVSLDDSDDDDQSEGVESKS
Vv15867     ------------------------------------------------------------
Cp76.2      ------VTDENKDRVREMNAKDCGDLNPEKCRD-------VIVIDDDDNE----------
                                  Intrinsic disorder region A

                                 620                 640                 660
RMR1        EDEMEFNDDADNSDFMDDADD-------------------SDFMDDAY------------
Sb09g19410  EDEMEFDDDADNSDFMDDAHDSDFVNDADEGGKSGDDAENSDFMDDAHD----SDFVNDA
Os05g32610  EDEMEFAD-----------LDTNVVDWEAEDEMEFDDDNDNDADDD--G----DNFGGDA
Bd2g26500   EDEMEF-----------------------------------DDDGD--D----DYFVHDA
ZM178435    ID----------------------------------------------------------
Sb04g33300  IQ----------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Bd2g43500   ------------------------------------------------------------
Bd3g50300   ------------------------------------------------------------
At3g24340   SPRVCDFD----------------------------------------------------
At1g05490   ENQDSEDNNTKDNVTVESLSSEDPSSSSSSSSSSSSSSSSSSSDDESYVKEVVGDNRDDD
Pt286483    FDV---GGKKSGGTDVGGSCSGVKSDGEESGRSKVPLPRWQRIVNESYNGDVFAHERNEG
Vv15867     ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
                      Intrinsic disorder region A

                                 680                 700                 720
RMR1        -EGGNSKPIQNHAKLEIQDWVNQKVVLSGGRCEARGEGDLEEELDVGKEA-DEEDVEPKS
Sb09g19410  DEGGKSEPIKSHAKMEIQDLVNQKVVLCGGGCEE--EGGEKEELGVGKEAGKKEDVEPKS
Os05g32610  DEGDKSVQMHDFSKVETQDLVSHNVNVSEVRPHE-------------DEEAIKDEMESKG
Bd2g26500   DECGMSEPMCDDYKVGTQYLSDHEVVVGEVSCQL-------------EEDVVKDEVDPKR
ZM178435    ------------------------------------------------------------
Sb04g33300  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Bd2g43500   ------------------------------------------------------------
Bd3g50300   ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
At1g05490   DLRKASSPIKRVSLVERKALVRYK------------------------------------
Pt286483    GVCFLSSGIGN-------------------------------------------------
Vv15867     ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
                                          Intrinsic disorder region B
```



```
                        740                 760                 780
RMR1        EAAPGSDKRVLQLEILGSDEEIKVLENMSSAPSRKASVQSKLPTIPSCVAWRTRSSWGVN
Sb09g19410  EAAPGSDKGGSHLETMSSDEEIKVLENMSSAPSRKASVQSKLPTIPSCVAWRTRSSWGIN
Os05g32610  KGSLSFNEGSSYIEILDSDEEVKVVNDTGNALRRKPLVPAKLPIVPSCVAWRTRSSWGMK
Bd2g26500   EGTTCFDQGRLHIEILESDDEVKVLSDASNPLKRKPLPQAKIPVLP-CVAWRTRSLWGVK
ZM178435    ------------------------------------------------------------
Sb04g33300  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Bd2g43500   ------------------------------------------------------------
Bd3g50300   ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
At1g05490   ---------------------------------------------RSGSSLTKPRERDNK
Pt286483    ---------------------------------------------GSGGVGLKGRESNGV
Vv15867     ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------

                        800                 820                 840
RMR1        QDRLSYDTYFEE------L---------------SDEPKEDD----DDTEVELD------
Sb09g19410  RDRLSYNTYFEA------L---------------SDEPKEDD----DDTEVELD------
Os05g32610  EERISYNTYFEV------L---------------SDEPKEDD----DDTEVELD------
Bd2g26500   QDRISYNAYFEE------L---------------SDEPIE-D----DDTEVELD------
ZM178435    ----------QESEQDEAL---------------EGRSSQDSHGYSEDKEGKDSAALSDN
Sb04g33300  ----------KESEQDEAL---------------EGRSRQDSH------------ALIDN
Os02g43460  ----------EEMEMEVEV---------------EVRSDDNDH---GNGGIRGEGGGTDD
Bd2g43500   ----------EEEEREADL-----------------------------------------
Bd3g50300   ----------EAAEKELGE---------------NGNSIQDDRYDGEDEEATDDAHAAEE
At3g24340   ----------EDDAKVSGK---------------ENPLSPDD----DDDVVFLGTIA---
At1g05490   IQKLNHREE-EKKERQREVVRVVTKQPSNVVYTCAHCGKENTGNPESHSSFIRPHSIRDE
Pt286483    AGRTELRSGFCEKKKDGNV---------------VVVVDDDD----DDACIILE----KD
Vv15867     -----YRRLYEEKKRNAGV---------------SSSGSHND----DGVEFLGEAGVFDS
Cp76.2      -----------------AI---------------AADASGDD----DDD-----------

                        860                 880                 900
RMR1        ---------------EVEDDNNDDDSSDAY-----------DKDDEEK--E---------
Sb09g19410  ---------------EDEDGNNDDGSSDAY-----------DKDDEEKEEE---------
Os05g32610  ---------------DEEDDENDDDCNSASCDEED------EEEEEER--E---------
Bd2g26500   ---------------DE--DDNDDDSASF------------EEEEEEE--T---------
ZM178435    EED---VGGKELL--EEEEEGADQEESHIIYDGEG------EQEEDASEEE---------
Sb04g33300  EEE---VGEKELS--EEEEDD-NQEESHSMYDGEG------EQEEDASEEV---------
Os02g43460  VAE---IEEEELGTDEDETSDDSDENFSDEEGDEE------ELEEEEEEEE---------
Bd2g43500   --------EDMVGEEEEEEQGKEEDEWELEEEEEE------EHEETEEEES---------
Bd3g50300   EE-------------EEEEEEEEEEEEEEEEEEEE------EEEEEEEEEE---------
At3g24340   ---------------GENQHVEDVNAGSEVCDILL------DDANLRGEEKTYVSDEVVS
At1g05490   IEDVNNFASTNVSKYEDSVSINSGKTTGAPSRPEV------ENPETGKELN---------
Pt286483    AEE---LQSSSSGEEETFKDDSDDDDYRVELPESF------MVEEEEKEED---------
Vv15867     VQK---FVAESDGKNSDRKNSSRKKNGGENSDEDVTDVVSISDDSEASDYE---------
Cp76.2      ---------------CDENHDDEDDDGDVVWEEDM------DDLERTSEED---------
```

```
                                920                 940                 960
RMR1          -EEEEEAERRKLNNRICTSDEDMINITVPTSRYDMFKKKN--------------------
Sb09g19410    -EEEEEAERRKLNNGIYTSDDDMINITVPTSRYDMFERKNISRYDMF--KRKNTSRYDIF
Os05g32610    -EEEEEAQRRKQKKGID-------------------------------------------
Bd2g26500     -KQEEVAEKSKHKKGIHSSFPEIRSRPMPL----FVNRERRMQTSIP--KWRGTSKK---
ZM178435      -TQELDETGE----------------------AQPFNPSNTMAGSTM--RSGGDGKQVFR
Sb04g33300    -EQEMDETGEEDEKELDGTGEEDEQELDGAGKAQPVTPSNTIAGSSM--RSGGDDTRVFR
Os02g43460    -EEEDDDDDDEEEEE-----------------PGDAPDQPGEAGEESPPRSRIMAMPLMG
Bd2g43500     -ESEQDEEAAEEPRR-------------------GGPRNSAAAGRYA---HRAEDGEIFA
Bd3g50300     -EEEQDDESDEAGEE-----------------LHPVPNSNADAGGNA--RSGGEGTP-IG
At3g24340     LSSSSDDE----------------------------------------------------
At1g05490     -TPEKPS-----------------------------------------------------
Pt286483      -GDREQGEMELKRNKVY-------------------------------------------
Vv15867       -EEEDDDD----------------------------------------------------
Cp76.2        -NDDSDDE----------------------------------------------------
```

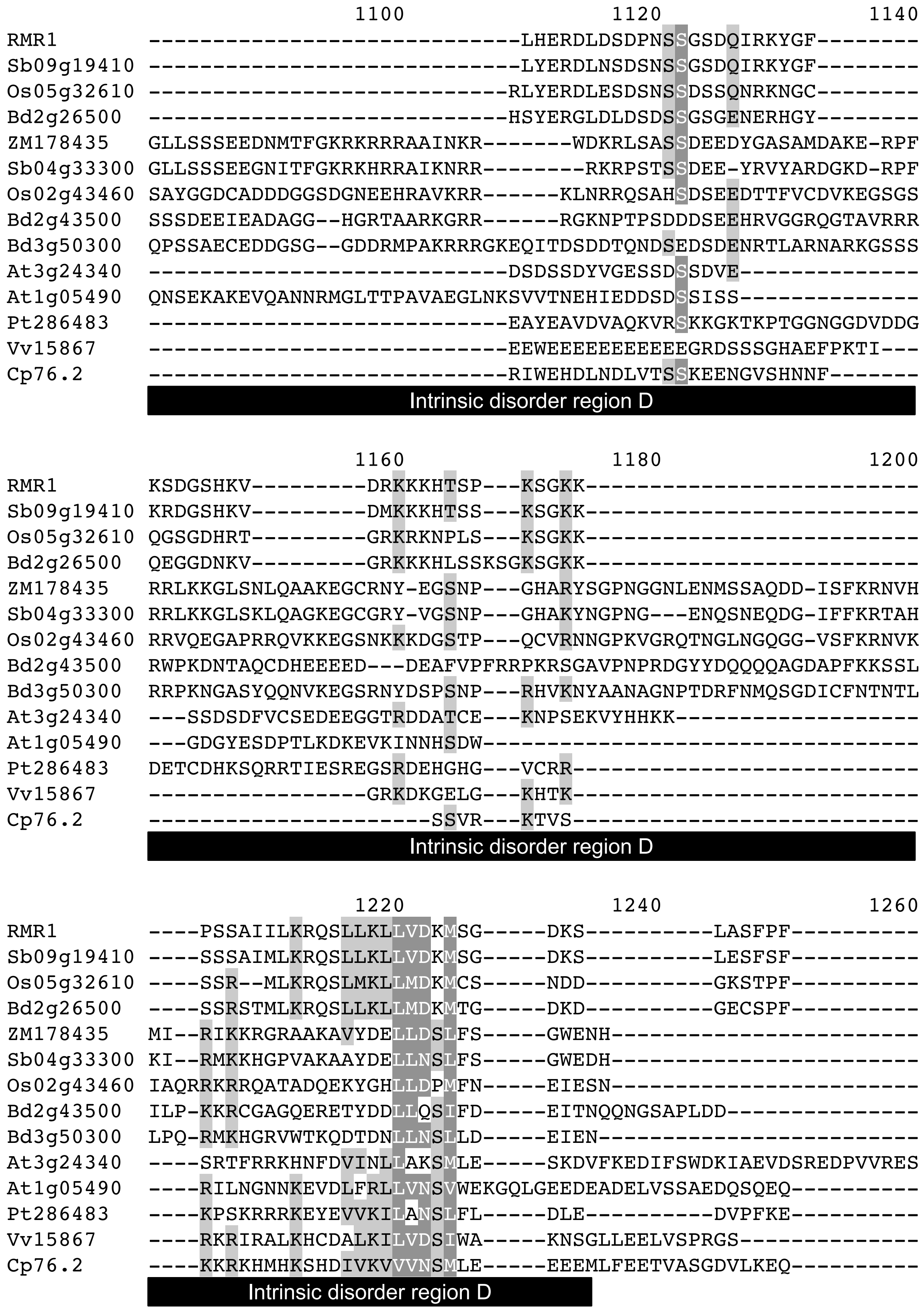
Intrinsic disorder region C

```
                                980                1000                1020
RMR1          --------------------SSRYDIEWVEDE--DASVDMLQPVSFKKDSSWKPVAVGND
Sb09g19410    KRKNTSRYDIFKR-----KKTSRYDIEWVEDEDKDANVDTLQPISLRKGSSWNPVAVGND
Os05g32610    -----------SSDDEMIDDAVDCGIDWEEDY---PEVDFTRPLTFQKDGSEAP--VGSE
Bd2g26500     ARQPETCHVIYSSDDEIIDDTAKDGLKCEVDE--DPRNNVFQPLNFEKVGSDGT--VGNG
ZM178435      RRVFEGIYLPENPHRT-VGKGIQ-------------------------------------
Sb04g33300    RRVFEGICLPQKPRKT-VGKGIG-------------------------------------
Os02g43460    KRMFEGFSFLQQVDTS-TGRDIR-------------------------------------
Bd2g43500     KRLFEGLCISKAADTSAAGKPVA-------------------------------------
Bd3g50300     KRVFEGLCLVDNADNAVTTKSIR-------------------------------------
At3g24340     ------------------------------------------------------------
At1g05490     ---------ISRPEIFTTEKAIDVQVPEEPSRPEI-------------------------
Pt286483      --------------------GIEVLCDSDIGKFENNDVDMDDSLCVA-------------
Vv15867       -------------DDYIVDPTID-------------------------------------
Cp76.2        --------------DYAVMKTMY---RKEKCKPKNHDVN---------------------
```

Intrinsic disorder region D

```
                               1040                1060                1080
RMR1          TFTEQQKRSRFT---WELE-RRKKLKLEMKTNP---------------------------
Sb09g19410    TFTEQQKQSRFT---WQLE-RRKKNKLEMKTNP---------------------------
Os05g32610    AFTEQQKRSRFT---WELE-RRKKLKLGMMTNH---------------------------
Bd2g26500     ITTEQQKGSRFT---WDLE-RRKKLKLGIIKSR---------------------------
ZM178435      ------GRTRSQ---RKCK-DKKLLKRGTFSKPYNIDIP--DSTSDSEEEIE--PPAPQQ
Sb04g33300    ------ARTRSQ---RKCK-DKKLLRRGTFSKPYNIDIP--DSTSDSEEDIE--PPAPQQ
Os02g43460    ------ARTRSNFKRKKLL-DKKLLKRGTFAKPYCIDVS----SSGSEEDV----PQPEQ
Bd2g43500     ------GRTRSR---RRCL-NTKLLRQGTYNKPYCLDTPSESGSSEAEEGVNKTPPAPAL
Bd3g50300     ------QRTRSNFKDRACL-DKKLLGQGTCSKPYCIDTE-------SEEDV---PPPPQP
At3g24340     --------------------EDPLEELGTDSREEVSGEDRDSGESDMDEDAN--------
At1g05490     ---------------YSSEKAKEVQAPEMPSRPEVFSSE-----KAKEIQVPEMPSIPEI
Pt286483      ------KRTRSH---YNLESAKKRMKLETVSRPLCVDEEKLDDNGDNDEDDT--------
Vv15867       ------RDERGN---QASKLGKKKVELGTSSHPFCVDVD--EGEGDGDGEGE--------
Cp76.2        --------GRDF---SSLE-GNKQSPATTFDHHDCDDND---------------------
```

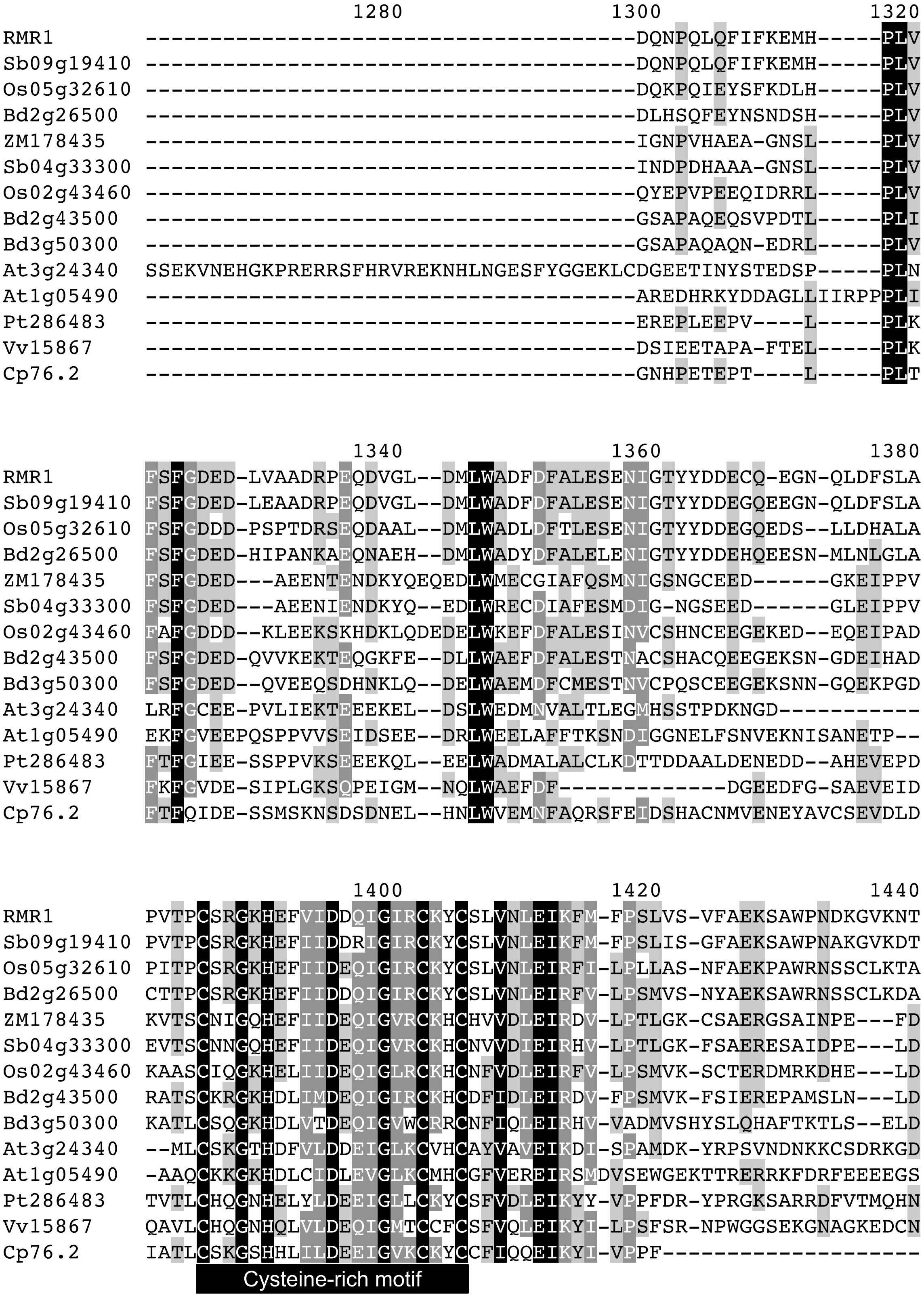
Intrinsic disorder region D



```
                           1100                1120                1140
RMR1       -----------------------------LHERDLDSDPNSSGSDQIRKYGF--------
Sb09g19410 -----------------------------LYERDLNSDSNSSGSDQIRKYGF--------
Os05g32610 ----------------------------RLYERDLESDSNSSDSSQNRKNGC--------
Bd2g26500  ----------------------------HSYERGLDLDSDSSGSGENERHGY--------
ZM178435   GLLSSSEEDNMTFGKRKRRRAAINKR-------WDKRLSASSDEEDYGASAMDAKE-RPF
Sb04g33300 GLLSSSEEGNITFGKRKHRRAIKNRR--------RKRPSTSSDEE-YRVYARDGKD-RPF
Os02g43460 SAYGGDCADDDGGSDGNEEHRAVKRR------KLNRRQSAHSDSEEDTTFVCDVKEGSGS
Bd2g43500  SSSDEEIEADAGG--HGRTAARKGRR------RGKNPTPSDDDSEEHRVGGRQGTAVRRR
Bd3g50300  QPSSAECEDDGSG--GDDRMPAKRRRGKEQITDSDDTQNDSEDSDENRTLARNARKGSSS
At3g24340  ----------------------------DSDSSDYVGESSDSSDVE--------------
At1g05490  QNSEKAKEVQANNRMGLTTPAVAEGLNKSVVTNEHIEDDSDSSISS--------------
Pt286483   ----------------------------EAYEAVDVAQKVRSKKGKTKPTGGNGGDVDDG
Vv15867    ----------------------------EEWEEEEEEEEEEEGRDSSSGHAEFPKTI---
Cp76.2     ----------------------------RIWEHDLNDLVTSSKEENGVSHNNF-------
                        Intrinsic disorder region D

                           1160                1180                1200
RMR1       KSDGSHKV---------DRKKKHTSP---KSGKK--------------------------
Sb09g19410 KRDGSHKV---------DMKKKHTSS---KSGKK--------------------------
Os05g32610 QGSGDHRT---------GRKRKNPLS---KSGKK--------------------------
Bd2g26500  QEGGDNKV---------GRKKKHLSSKSGKSGKK--------------------------
ZM178435   RRLKKGLSNLQAAKEGCRNY-EGSNP---GHARYSGPNGGNLENMSSAQDD-ISFKRNVH
Sb04g33300 RRLKKGLSKLQAGKEGCGRY-VGSNP---GHAKYNGPNG---ENQSNEQDG-IFFKRTAH
Os02g43460 RRVQEGAPRRQVKKEGSNKKKDGSTP---QCVRNNGPKVGRQTNGLNGQGG-VSFKRNVK
Bd2g43500  RWPKDNTAQCDHEEEED---DEAFVPFRRPKRSGAVPNPRDGYYDQQQQAGDAPFKKSSL
Bd3g50300  RRPKNGASYQQNVKEGSRNYDSPSNP---RHVKNYAANAGNPTDRFNMQSGDICFNTNTL
At3g24340  ---SSDSDFVCSEDEEGGTRDDATCE---KNPSEKVYHHKK-------------------
At1g05490  ---GDGYESDPTLKDKEVKINNHSDW----------------------------------
Pt286483   DETCDHKSQRRTIESREGSRDEHGHG---VCRR---------------------------
Vv15867    -----------------GRKDKGELG---KHTK---------------------------
Cp76.2     ----------------------SSVR---KTVS---------------------------
                        Intrinsic disorder region D

                           1220                1240                1260
RMR1       ----PSSAIILKRQSLLKLLVDKMSG-----DKS----------LASFPF----------
Sb09g19410 ----SSSAIMLKRQSLLKLLVDKMSG-----DKS----------LESFSF----------
Os05g32610 ----SSR--MLKRQSLMKLLMDKMCS-----NDD----------GKSTPF----------
Bd2g26500  ----SSRSTMLKRQSLLKLLMDKMTG-----DKD----------GECSPF----------
ZM178435   MI--RIKKRGRAAKAVYDELLDSLFS-----GWENH------------------------
Sb04g33300 KI--RMKKHGPVAKAAYDELLNSLFS-----GWEDH------------------------
Os02g43460 IAQRRKRRQATADQEKYGHLLDPMFN-----EIESN------------------------
Bd2g43500  ILP-KKRCGAGQERETYDDLLQSIFD-----EITNQQNGSAPLDD---------------
Bd3g50300  LPQ-RMKHGRVWTKQDTDNLLNSLLD-----EIEN-------------------------
At3g24340  ----SRTFRRKHNFDVINLLAKSMLE-----SKDVFKEDIFSWDKIAEVDSREDPVVRES
At1g05490  ----RILNGNNKEVDLFRLLVNSVWEKGQLGEEDEADELVSSAEDQSQEQ----------
Pt286483   ----KPSKRRRKEYEVVKILANSLFL-----DLE----------DVPFKE----------
Vv15867    ----RKRIRALKHCDALKILVDSIWA-----KNSGLLEELVSPRGS--------------
Cp76.2     ----KKRKHMHKSHDIVKVVVNSMLE-----EEEMLFEETVASGDVLKEQ----------
              Intrinsic disorder region D
```



```
                                    1280                1300                1320
RMR1        --------------------------------------DQNPQLQFIFKEMH-----PLV
Sb09g19410  --------------------------------------DQNPQLQFIFKEMH-----PLV
Os05g32610  --------------------------------------DQKPQIEYSFKDLH-----PLV
Bd2g26500   --------------------------------------DLHSQFEYNSNDSH-----PLV
ZM178435    --------------------------------------IGNPVHAEA-GNSL-----PLV
Sb04g33300  --------------------------------------INDPDHAAA-GNSL-----PLV
Os02g43460  --------------------------------------QYEPVPEEQIDRRL-----PLV
Bd2g43500   --------------------------------------GSAPAQEQSVPDTL-----PLI
Bd3g50300   --------------------------------------GSAPAQAQN-EDRL-----PLV
At3g24340   SSEKVNEHGKPRERRSFHRVREKNHLNGESFYGGEKLCDGEETINYSTEDSP-----PLN
At1g05490   --------------------------------------AREDHRKYDDAGLLIIRPPPLI
Pt286483    --------------------------------------EREPLEEPV----L-----PLK
Vv15867     --------------------------------------DSIEETAPA-FTEL-----PLK
Cp76.2      --------------------------------------GNHPETEPT----L-----PLT

                                    1340                1360                1380
RMR1        FSFGDED-LVAADRPEQDVGL--DMLWADFDFALESENIGTYYDDECQ-EGN-QLDFSLA
Sb09g19410  FSFGDED-LEAADRPEQDVGL--DMLWADFDFALESENIGTYYDDEGQEEGN-QLDFSLA
Os05g32610  FSFGDDD-PSPTDRSEQDAAL--DMLWADLDFTLESENIGTYYDDEGQEDS--LLDHALA
Bd2g26500   FSFGDED-HIPANKAEQNAEH--DMLWADYDFALELENIGTYYDDEHQEESN-MLNLGLA
ZM178435    FSFGDED---AEENTENDKYQEQEDLWMECGIAFQSMNIGSNGCEED------GKEIPPV
Sb04g33300  FSFGDED---AEENIENDKYQ--EDLWRECDIAFESMDIG-NGSEED------GLEIPPV
Os02g43460  FAFGDDD--KLEEKSKHDKLQDEDELWKEFDFALESINVCSHNCEEGEKED--EQEIPAD
Bd2g43500   FSFGDED-QVVKEKTEQGKFE--DLLWAEFDFALESTNACSHACQEEGEKSN-GDEIHAD
Bd3g50300   FSFGDED--QVEEQSDHNKLQ--DELWAEMDFCMESTNVCPQSCEEGEKSNN-GQEKPGD
At3g24340   LRFGCEE-PVLIEKTEEEKEL--DSLWEDMNVALTLEGMHSSTPDKNGD-----------
At1g05490   EKFGVEEPQSPPVVSEIDSEE--DRLWEELAFFTKSNDIGGNELFSNVEKNISANETP--
Pt286483    FTFGIEE-SSPPVKSEEEKQL--EELWADMALALCLKDTTDDAALDENEDD--AHEVEPD
Vv15867     FKFGVDE-SIPLGKSQPEIGM--NQLWAEFDF-------------DGEEDFG-SAEVEID
Cp76.2      FTFQIDE-SSMSKNSDSDNEL--HNLWVEMNFAQRSFEIDSHACNMVENEYAVCSEVDLD

                                    1400                1420                1440
RMR1        PVTPCSRGKHEFVIDDQIGIRCKYCSLVNLEIKFM-FPSLVS-VFAEKSAWPNDKGVKNT
Sb09g19410  PVTPCSRGKHEFIIDDRIGIRCKYCSLVNLEIKFM-FPSLIS-GFAEKSAWPNAKGVKDT
Os05g32610  PITPCSRGKHEFIIDEQIGIRCKYCSLVNLEIRFI-LPLLAS-NFAEKPAWRNSSCLKTA
Bd2g26500   CTTPCSRGKHEFIIDDQIGIRCKYCSLVNLEIRFV-LPSMVS-NYAEKSAWRNSSCLKDA
ZM178435    KVTSCNIGQHEFIIDEQIGVRCKHCHVVDLEIRDV-LPTLGK-CSAERGSAINPE---FD
Sb04g33300  EVTSCNNGQHEFIIDEQIGVRCKHCNVVDIEIRHV-LPTLGK-FSAERESAIDPE---LD
Os02g43460  KAASCIQGKHELIIDEQIGLRCKHCNFVDLEIRFV-LPSMVK-SCTERDMRKDHE---LD
Bd2g43500   RATSCKRGKHDLIMDEQIGIRCKHCDFIDLEIRDV-FPSMVK-FSIEREPAMSLN---LD
Bd3g50300   KATLCSQGKHDLVTDEQIGVWCRRCNFIQLEIRHV-VADMVSHYSLQHAFTKTLS--ELD
At3g24340   --MLCSKGTHDFVLDDEIGLKCVHCAYVAVEIKDI-SPAMDK-YRPSVNDNKKCSDRKGD
At1g05490   -AAQCKKGKHDLCIDLEVGLKCMHCGFVEREIRSMDVSEWGEKTTRERRKFDRFEEEEGS
Pt286483    TVTLCHQGNHELYLDEEIGLLCKYCSFVDLEIKYY-VPPFDR-YPRGKSARRDFVTMQHN
Vv15867     QAVLCHQGNHQLVLDEQIGMTCCFCSFVQLEIKYI-LPSFSR-NPWGGSEKGNAGKEDCN
Cp76.2      IATLCSKGSHHLILDEEIGVKCKYCCFIQQEIKYI-VPPF--------------------
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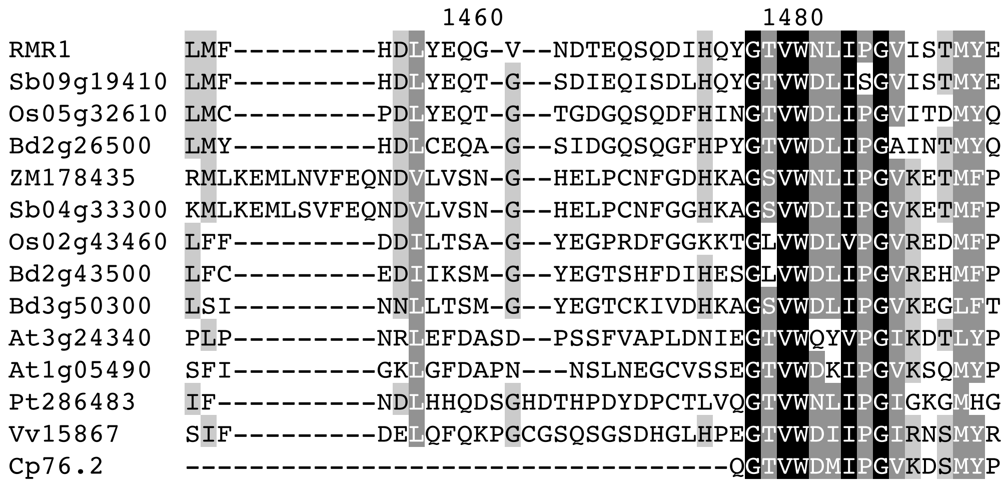


```
                            1460                1480
RMR1        LMF---------HDLYEQG-V--NDTEQSQDIHQYGTVWNLIPGVISTMYE
Sb09g19410  LMF---------HDLYEQT-G--SDIEQISDLHQYGTVWDLISGVISTMYE
Os05g32610  LMC---------PDLYEQT-G--TGDGQSQDFHINGTVWDLIPGVITDMYQ
Bd2g26500   LMY---------HDLCEQA-G--SIDGQSQGFHPYGTVWDLIPGAINTMYQ
ZM178435    RMLKEMLNVFEQNDVLVSN-G--HELPCNFGDHKAGSVWNLIPGVKETMFP
Sb04g33300  KMLKEMLSVFEQNDVLVSN-G--HELPCNFGGHKAGSVWDLIPGVKETMFP
Os02g43460  LFF---------DDILTSA-G--YEGPRDFGGKKTGLVWDLVPGVREDMFP
Bd2g43500   LFC---------EDIIKSM-G--YEGTSHFDIHESGLVWDLIPGVREHMFP
Bd3g50300   LSI---------NNLLTSM-G--YEGTCKIVDHKAGSVWDLIPGVKEGLFT
At3g24340   PLP---------NRLEFDASD--PSSFVAPLDNIEGTVWQYVPGIKDTLYP
At1g05490   SFI---------GKLGFDAPN---NSLNEGCVSSEGTVWDKIPGVKSQMYP
Pt286483    IF----------NDLHHQDSGHDTHPDYDPCTLVQGTVWNLIPGIGKGMHG
Vv15867     SIF---------DELQFQKPGCGSQSGSDHGLHPEGTVWDIIPGIRNSMYR
Cp76.2      ----------------------------------QGTVWDMIPGVKDSMYP
```

Figure 13. Multiple sequence alignment of CLSY clade over N terminal region. Specific sequence features are noted below the alignment.

```
                             20                  40                  60
ZM000342   MMIKKKSGRCHLLAGH--------------------------------------------
ZM108166   MV----------------------------------------------------------
Sb02g43870 MV----------------------------------------------------------
Os07g49210 MAGKKMSGEVRSVPAFDFAEWLKRTVSEQDYVVMKMDVEGTEFDLIPRLFDTGAICLIDE
Bd1g16720  MAGKTLKGPS--------------------------------------------------
At5g20420  MKKRGF------------------------------------------------------
AtCLSY1    MKRKHY------------------------------------------------------
Pt567214   MKRKHL------------------------------------------------------
Pt832603   MKRKRL------------------------------------------------------
Cp19.123   MRKRRL------------------------------------------------------
Vv29366    M-----------------------------------------------------------
Sm441121   M-----------------------------------------------------------

                             80                 100                 120
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 LFLECHYNRWQKCCPDRAEAFEMAKGVSCFYWSIQFPNFKDHLCFRNCSNASSTRHFSYR
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   ------------------------------------------------------------
Pt832603   ------------------------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------

                            140                 160                 180
ZM000342   ------------------------------------------------LELEDLTVDSTP
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 SLLIRTEKPVTTRNHAYAEVVVFVLDQNPMFFLFLRFFYPAIQRGPNCWSSANSTVMRQA
Bd1g16720  -------------------------------------------------RAAGHPICATP
At5g20420  -------------------------------------------------YNLKHPFDPCP
AtCLSY1    -------------------------------------------------FEFNHPFNPCP
Pt567214   -------------------------------------------------HQSKHPYNAHP
Pt832603   -------------------------------------------------HQSKHPFNAHP
Cp19.123   -------------------------------------------------YESRHPFGLHP
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------

                            200                 220                 240
ZM000342   LPFLPQGP----------NGQPIFFTVQRPVA--VQHDIDGSYLRVRSRKATCSDCSHVL
ZM108166   -----KGS----------TGHH-----SNPIAPVLQHDIDGSYLRVRSRKATCSDCSHVL
Sb02g43870 -----KGS----------TGHH-----NNPIGSVLQHDIDGSYLRIRSRKATCSDCSHVL
Os07g49210 FEVFYDGSWHGVNCIRIRNGNLFVKFIYS--GSTVEHNVDGDCLRLRSRRATCSDCSNVL
Bd1g16720  FEAFHHGSWHGVNCIRVQNSRLFVRFVYS--GSTVERNIDRDHLRLRSRRATCFDCSHVL
At5g20420  FEFFCSGTWKPVEYMRIEDGMMTIRLLEN--GYVLEDIRPFQRLRLRSRKAALSDCICFL
AtCLSY1    FEVFCWGTWKAVEYLRIENGTMTMRLLEN--GQVLDDIKPFQRLRIRSRKATLIDCTSFL
Pt567214   FEALYGGSWQSVELIEIRDGAMTLHFADS--HHRIEEKGPFSNIRVKSRKSTLSDCTCFL
```

```
Pt832603   FEALCCGSWQSVELIQIRDGAMTVHFVDS--HHRIEEKGPFSNVRVKSRKATSSDCTCFL
Cp19.123   FEAFSRGSWRMVDCIRIEDGTMSLRFVDG--RHVIKRKRPFSELRVRSRQANLTDCTCFL
Vv29366    ---------------RIEDGTVALHLAES--EYVIEEKSPIPNLRIRPRKATLSDCTCFL
Sm441121   ------------------------------------------------------------

                            260                 280                 300
ZM000342   KPGADVCVW-----QAVYRGETKDSVLLCCRDARLIKIKRNHQSDRCLCLFAVIFYKDQC
ZM108166   KPGADVCVW-----QAVYRGETKDSVLLCCRDARLIKIKRNHQSDRCLCLFAVIFYKDQC
Sb02g43870 KPGADVCVW-----QATYGGETKDSVPL-CRDARLIKIKRNHQLDRCLCLFAVIFYKDQC
Os07g49210 KPGVDVCVQSSHTPEASSQGGTNASVLL-RHDARLITIKKNHQEDKCLCLFVVILYKNQC
Bd1g16720  KPGVDVCVQSPHPLQACSTGDQKSSISL-CHDARIVTIKRNHNADQCLCLFLVILDDSQC
At5g20420  RPDIDVCVLY------RIHEDDLEPVWV---DARIVSIERKPHESECSCKINVRIYIDQG
AtCLSY1    RPGIDVCVLY------QRDEETPEPVWV---DARVLSIERKPHESECLCTFHVSVYIDQG
Pt567214   RPGIDVCVLSFSERAKSSEEGNSEPVWV---DARINSIKRKPHESQCSCQFFVNLYVNQG
Pt832603   RPGIDVCVLSSSERAKNTGEGNSEPVWV---DAKISSIKRKPHVSHCSCQFFVNLYVNQG
Cp19.123   RPGIDVCVLIPSKDLASSDEANLELVLI---DAKIRSIERKPHESQCSCQFYVNLYVNQG
Vv29366    RPGTEITVLWTLQQSESSDEENREPVWI---DAKISSIERRPHEPECSCQFFVNFYITQD
Sm441121   ------------------------------------------------------------

                            320                 340                 360
ZM000342   PGSKEK--VISGTIADVVTIDDICILQNLQPEELQD-------GSVRWNSAVDCFHHNRS
ZM108166   PGSKEK--VISGTIADVVTIDDICILQNLQPEELQD-------GSVRWNSAVDCFHHNRS
Sb02g43870 PGSKEK--VISGTIADVVTIDDVCILQNLQSEELQD-------GSVQWNSAVDCFHHNRS
Os07g49210 PGNAEK--VITDRRAEVVTINDIFLLQKLQP-EVHE-------GSMKWSFSKDRLSLNKG
Bd1g16720  PGNTEKGGKATDRRQEVVTLNNIFLLQKLQPKELQE-------GSVQWNSAEDCLYQNRS
At5g20420  CIGSEK--QRINRDSVVIGLNQISILQKFYKEQSTD-------QFYRWRFSEDCTSLMKT
AtCLSY1    CIGLEK--HRMNKVPVLVGLNEIAILQKFCKEQSLD-------RYYRWRYSEDCSSLVKT
Pt567214   PLGSER--ATLSKETEAVGIDQISILQKLDNDPCEADNNRHETQFYRWEFCEDCSLVQRT
Pt832603   PLGSER--ARLSKETEAVGINEISVLQKLDNDPCEADNNQQEAQFYRWEFCEDCSLVQRS
Cp19.123   PLGSEK--LELDKDTKVLGIDQILILQRLEKHPCEG-------QYYRWSLSEDCSSLSRT
Vv29366    PLGTEK--GTLSKDISVVELDQISILQKLGKYPCED-------EHYRWKFSEDCSLLQRT
Sm441121   ------------------------------------------------------------

                            380                 400                 420
ZM000342   KLLS-ARFSLEVAYLIVLSSLRRMEFNIKMVDGNIIYQIIKGDQARDSIDSMSIPPGFGK
ZM108166   KLLS-ARFSLEVAYLIVLSSLRRMEFNIKMVDGNIIYQIIKGDQARDSIDSMSIPPGFGK
Sb02g43870 KLLS-ARFSLEVAYLIVLSSLRGMEFSIKLVDGNIIYQIIKGDQARYSIDSMSIPPGFGK
Os07g49210 RLIS-ARFSSEITHLIVLSILRGMEFNIKLVEGQIVYQIIKGDQAQWNLDSMAIPPGFGN
Bd1g16720  RLLSAARFSSEISHLIVLSALRGMEFSIKLVEGNIIYRVIKGDQARRGVDCMSIPPGFGR
At5g20420  RLSL-GKFLPDLSWLTVTSTLKSIVFQIRTVQTKMVYQIVTDEEGSSST-----------
AtCLSY1    RLNL-GKFLPDLTWLLVTSVLKNIVFQIRTVHEKMVYQIVTDEDCEGSSSS---------
Pt567214   ------------------SIPKQVAFDVRSVQNKIAYQIFGGDDDHCSLKS-------NN
Pt832603   KLFL-GRFSADLTWLLVASVLKQVEFNVRSVQNKIVYQILGGENEHCSLKS-------NN
Cp19.123   KLFL-GKFSSDLSWLLVASVLKQVAFEVRTEQYKIVYQILADDDGSPSKS--------NN
Vv29366    KLFL-GKFSSDLSWLVVTSVLKQAVFDVRSVQNRIVYQIVGGDHDKVS------------
Sm441121   ------------------------------------------------------------

                            440                 460                 480
ZM000342   NMDIISFKPRGEALRPITRTVPVTQVEEGNLTEDGCIAVKGESDS---------------
ZM108166   NMDIISFKPRGEALRPITRTVPVTQVEEGNLTEDGCIAVKGESDS---------------
Sb02g43870 SMDIISFKPRAEALRPIIRTVLITQVKEDNLIEDGCTAVKHESDS---------------
Os07g49210 TMEIISFQLRDEALRPTITNIPITHVKKNNITEDMRFTVKSEMDS---------------
Bd1g16720  NMEIVSFQLHDKNLRPTIRNIPVTHAKKHNLTEDNRFTLKTELDDQLEYIRVAVKIELDD
At5g20420  -LSSMNITLEDGVSLSKV----VKFNPADILDDSQDLEIKQETDY---------------
```

```
AtCLSY1    -LSAMNITVEDGVVMSKV----VLFNPAE--DTCQDSDVKEEI-----------------
Pt567214   HINCVTFKVEDGISTPFV----VQLDPID-------------------------------
Pt832603   HINCVTFKVKDSISTPFV----VQLVPTDACSEAGHISDTNGTEQ---------------
Cp19.123   YISATMF-INGG------------------------------------------------
Vv29366    -LNAVNFRVDNGISTPVI----FPFVPADTI-EADPLNGTNEAGP---------------
Sm441121   ------------------------------------------------------------

                            500                 520                 540
ZM000342   ----AQDVEILYAHVDIRRSKRMKTQPDRFTSYDAR------------------NFNRTY
ZM108166   ----AQDVEILYAHVDIRRSKRMKTQPDRFTSYDAR------------------NFNRTY
Sb02g43870 ----AQDVEVLYEHVDIRRSKRMKTQPDRFTSYDAP------------------NFNRTY
Os07g49210 ELDRALDVEILYEHVDLRRSKRLKTQPDRFTSYDTP------------------RFLSGY
Bd1g16720  QLEDQFDVGLLYKHVDLRRSKRLKTQPERFTSYDAP------------------NFNRDT
At5g20420  -------YQEEDEVVELRRSKRRNVRPDIYTGCDYEPDTIDGWVRMMPYQFGKCAVNVES
AtCLSY1    ----------EEEVMELRRSKRRSGRPERYGDSEIQPDSKDGWVRMMPYRYNIWNVSSDD
Pt567214   -------------------------------TCNTPAETEIGWVRSLPYTPLKWK----E
Pt832603   --------SPCYDVMSLRRSKRRNVQPERFLACDAPAETEIGWVRSLPYTPLKWKAEEEE
Cp19.123   -------------WWELRRSKRRNVQPERFIGGQGLTESDSVWVRQMPIKTDKWK-----
Vv29366    --------LPFCDIVDLRRSKRRNVQPDRFFSLGGFSESDIGSVRAGIHKVDYWR-----
Sm441121   ------------------------------------------------------------

                            560                 580                 600
ZM000342   NKKEADGPSTKYEDSESGLSC---DSSEQRESSDEEAL----------------------
ZM108166   NKKEADGPSTKYEDSESGLSC---DSSEQRESSDEEAL----------------------
Sb02g43870 NKKEAYGPSNKNENSESDLSF---YSSEQTESSDEEVLGNPGVKKKVSRSFVVK------
Os07g49210 KKKEASSSPTKHVRGAVHCDSPVDDSKKEVESCCVEIPGNVTQKQTGVHSPMVDEKSNSP
Bd1g16720  KKKGASASSTMHYD-------HRRASQVKVESSCGEDP----VKITGASSFMFN------
At5g20420  DEDEDDNNEDGDTNDDLYIPLSRLFIKKKKTNSREAKP----KSRKG-------------
AtCLSY1    DDEEEDCEDDKDTDDDLYLPLSHLLRKK---GSKKGFS----KDKQR-------------
Pt567214   EEE-------------LHLPLAYLFGTHADASCAEEKP----GNEVRVNSPKLEFLEGPP
Pt832603   EEE-------------MHLPLAYLFGTHAGASCAEEQT----CNEVGASSPKLELLEGIP
Cp19.123   EKM-------------KCLPLSRLF--KMQPLYLKEQP----KNETR-------------
Vv29366    KEE---------------MPLALPDEGDVHSIFSEKHI---IDYEKGAHSLQIDSYE---
Sm441121   ------------------------------------------------------------

                            620                 640                 660
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 EGQHKNTTKRTTCSLVKEKASSPEGQHEKT------------------------------
Bd1g16720  ------------------------------------------------------------
At5g20420  ------EIVVIDK-----------------------------------------------
AtCLSY1    ------EIVLVDKTERK-------------------------------------------
Pt567214   VSRTKTNSRKIKSNVFNRREHQAELGEVESGIDNRRERQKSTVANRIKHQTRLGEAKSGM
Pt832603   VSRTKTYLKEIKSNVVNRRDHQTEPGEVRAGMAKRRECQKSTMADRIEHQTRLGDAESGM
Cp19.123   ------DLVVYKSNKYS-------------------------------------------
Vv29366    ------DFLVCKSKDRS-------------------------------------------
Sm441121   ------------------------------------------------------------

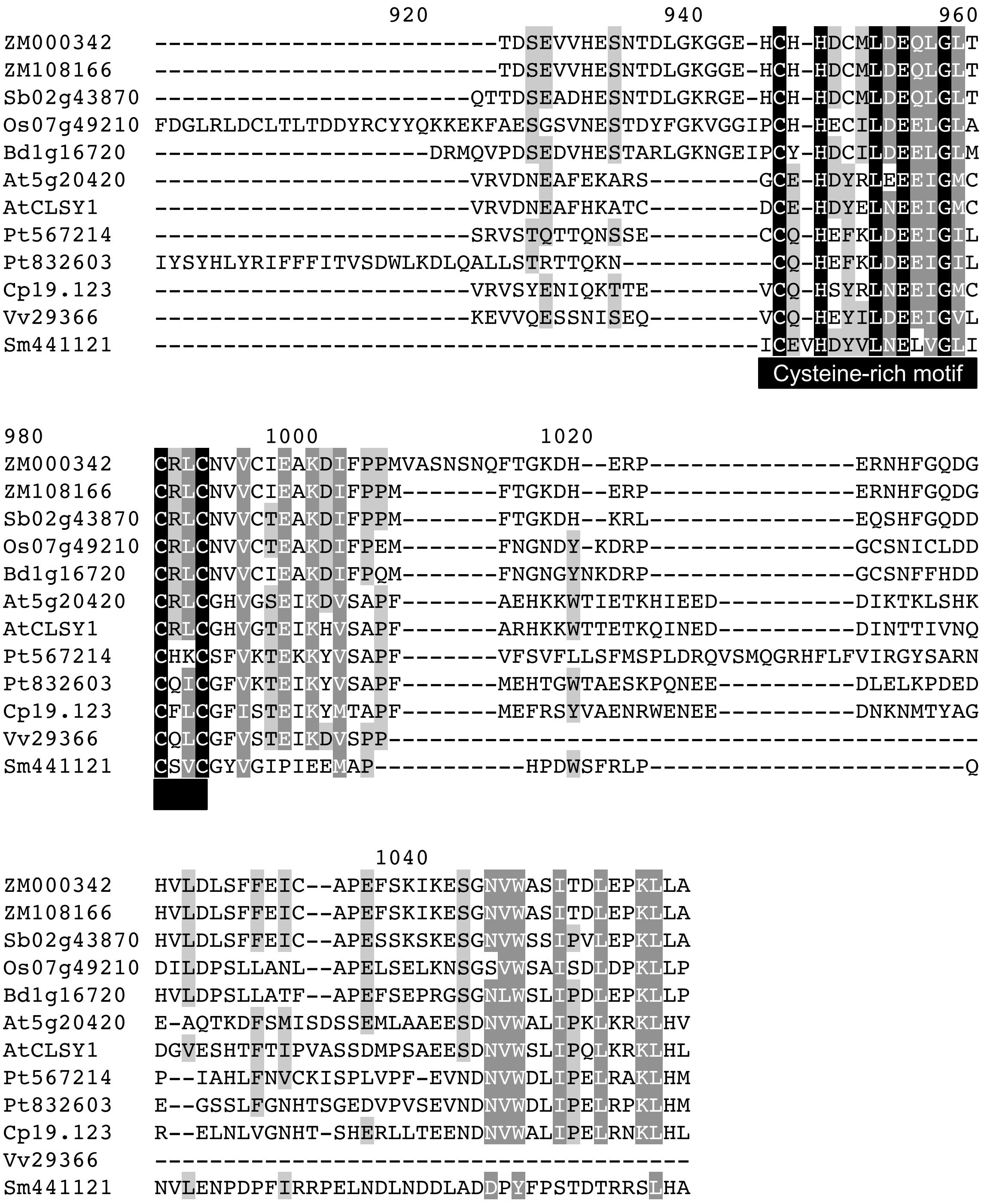
                            680                 700                 720
ZM000342   -----------ENPRSMAAEHKYPVKRNQCSLP----VKEKQISMEI-KKNTTD-----Q
ZM108166   -----------ENPRSMAAEHKYPVKRNQCSLP----VKEKQISMEI-KKNTTD-----Q
Sb02g43870 -----------EDPRSMKGQHKYPVKRNQCSLP----IKENQTSMET-KKNATD-----Q
Os07g49210 TKRTTCALPVKEKASSPEGQHKNTIKRTTCSLP----VKEEPSSVEIEEKSSKE-----Q
```

```
Bd1g16720  -----------ENPSTTKGQHKNTRRRTPCSLP----MKEKPSSVK--EESKTE-----E
At5g20420  ------------RRVHGFGRKERKSELSVIPFT----PVFEPIPLEQFGLNANSFGGGGS
AtCLSY1    ----------KRKKTEGF---SRSCELSVIPFT----PVFEPIPLEQFGLNANSLCGGVS
Pt567214   ANRKKHGTQIREVKLGVANRIEHQDQLAIVPVP----TEDDLVTFEQYDSPLKT-----P
Pt832603   ANRKKHGTQIREVKSGVANRREHQDQLAIVPVH----TEDVLATFEQFDSPVKT-----P
Cp19.123   ----------KDVKSGLADQVEHQNKLAIIPVPNVPELEPEPLASEHHDYHANL-----S
Vv29366    ----------REVKPILAAQNEDQHQFAIVPVP----LIIEPIAHGEDHLHDET-----P
Sm441121   ------------------------------------------------------------

                              740                 760                 780
ZM000342   GCSDSYIPHTPAKNTE---RPR------------------------FRLKPFASSRSL--
ZM108166   GCSDSYIPHTPAKNTE---RPR------------------------FRLKPFASSRSL--
Sb02g43870 GCSDSHIPHTPAKNIEKCNRPT------------------------FRLKSFASSRSL--
Os07g49210 SAPEFHIPRTPAQNKEKHNRPPFS----------------------CKPKLFTSSGTL--
Bd1g16720  RASDSHIPQTPAQNKEKNHRTPSS----------------------FHRKSGTSPCSL--
At5g20420  FSRSQYFDETE-KYRSKGMKYGKKMTEMEEM--MEADLCWKGP---NQVKSFQKRTSRSS
AtCLSY1    ---GNLMDEID-KYRSKAAKYGKKKKKKIEMEEMESDLGWNGPIG-NVVHKRNGPHSR-I
Pt567214   DNFPQECIEFPIRSYSKKGY-SVQRKNDFDE-DMMFGSGWGG---KSSRKKVQRARYQ--
Pt832603   EPYSQAFIEFPISYYRKKSSPAAHRKNDRDE-DLMFGNGWGG---KFSTKKVQRARYR--
Cp19.123   ANNSKRVEELSFRYNSLKCSRTSSRKKFSQIDDMDLVPRWEGIQGKGSNRKAQIRKHR--
Vv29366    WNESGEIGEISPKYYCTNGVPKLQRKNMSDL-YMEVESRWEG---KGPIRKLRRKRGF--
Sm441121   ------------------------------------------------------------

                              800                 820                 840
ZM000342   -DGNSEPAFCQKRGRKRKKHMCQIEYKRMIDQCIGNIQCEV-ERDSDFKFGDQILDGCVR
ZM108166   -DGNSEPAFCQKRGRKRKKHMCQIEYKRMIDQCIGNIQCEV-ERDSDFKFGDQILDGCVR
Sb02g43870 -DGNSEPAFCQKRGRKRKKGMCQREYKRMIEQCIGNIQCEV-ERDSDFKIDAQILNGCGH
Os07g49210 -GVNCEPAFCQKVGGKRKRHMCEREYKQMIDQCIGNIESEM-ERDSMFNFDANMMNYVQH
Bd1g16720  -GGNYEPAFCQKRGRKRKERMCDEEYEKIINQCIGNIQSEM-ERDYEFNLDVPMMHCCQG
At5g20420  RSVAPKTEDSDEPRVYKKVTLSAGAYNKLIDTYMNNIESTIAAKDEPTSVVDQWEELKKT
AtCLSY1    RSVSRETGVSEEPQIYKKRTLSAGAYNKLIDSYMSRIDSTIAAKDKATNVVEQWQGLKNP
Pt567214   -STHLKRDDSCKPKTYKQTALSAGAYDKLISFYMKNFDSTIKSKEVT-RIIDQWEEFKAK
Pt832603   -STHLKQDGSCAPMTYKRTALSAGAYNKLISSYMKNIDATIKSKEVP-RIIDQWEEFKAK
Cp19.123   -GISSKEDF-DEPITYKKKSLSAGAYDKLIHSYMKNIDSTM-IKEEP-HIIDQWQEFKKA
Vv29366    -TIRTKTESYGEVRPHKKRPFSEPGYKEVIEAYMKNIESTI-NKEQP-LVIDQWKELQVR
Sm441121   ------------------------------------------------------------

                              860                 880                 900
ZM000342   A---YQEVDFTWPSSADSQE-EKDELDELWKEMDYALATVAILEQKQM------------
ZM108166   A---YQEVDFTWPSSADSQE-EKDELDELWKEMDYALATVAILEQKQM------------
Sb02g43870 A---YQEEDFMWPSSADSQE-EKDELQELWKEMDYALATVAIDEQKQLIK------CLDF
Os07g49210 S---YREEDFTWPPSADNQEVEEDELEELWKEMDYSLTTLALLEQKQVMAQSRINMLVDN
Bd1g16720  A---YPEEDFTWPSLADSQEEKKDELDELWKEMDFSLTTLEL------------------
At5g20420  NFAFKLHGDMEKNLSEDGEG-ETSENEMLWREMELCLASSYILDDNE-------------
AtCLSY1    A-SFSIEAEERLSEEEEDDG-ETSENEILWREMELCLASSYILDDHE-------------
Pt567214   H--SSDQKETMEPSLVEDDG-ESSETEMLWREMELCLTSAYIFEDNE-------------
Pt832603   H--SSDQKEKMEPSSVKDDG-ESSETEMLWREMELCLASAYILEDNEVEL------CVVF
Cp19.123   S--FPEQRMEIEQSSSEDEG-ESSENEMLWREMELSMASAYFLEDNE-------------
Vv29366    N-DLNQRRDCNSPSSVGDQE-ESSETEMLWREMEFSIASSYLLEENEGSN------VEVL
Sm441121   -------------SSFDD------------------------------------------
```



```
                             920                 940                 960
ZM000342   -------------------------TDSEVVHESNTDLGKGGE-HCH-HDCMLDEQLGLT
ZM108166   -------------------------TDSEVVHESNTDLGKGGE-HCH-HDCMLDEQLGLT
Sb02g43870 -----------------------QTTDSEADHESNTDLGKRGE-HCH-HDCMLDEQLGLT
Os07g49210 FDGLRLDCLTLTDDYRCYYQKKEKFAESGSVNESTDYFGKVGGIPCH-HECILDEELGLA
Bd1g16720  --------------------DRMQVPDSEDVHESTARLGKNGEIPCY-HDCILDEELGLM
At5g20420  -----------------------VRVDNEAFEKARS--------GCE-HDYRLEEEIGMC
AtCLSY1    -----------------------VRVDNEAFHKATC--------DCE-HDYELNEEIGMC
Pt567214   -----------------------SRVSTQTTQNSSE--------CCQ-HEFKLDEEIGIL
Pt832603   IYSYHLYRIFFFITVSDWLKDLQALLSTRTTQKN-----------CQ-HEFKLDEEIGIL
Cp19.123   -----------------------VRVSYENIQKTTE--------VCQ-HSYRLNEEIGMC
Vv29366    -----------------------KEVVQESSNISEQ--------VCQ-HEYILDEEIGVL
Sm441121   --------------------------------------------ICEVHDYVLNELVGLI
                                                        Cysteine-rich motif

980                   1000                1020
ZM000342   CRLCNVVCIEAKDIFPPMVASNSNQFTGKDH--ERP---------------ERNHFGQDG
ZM108166   CRLCNVVCIEAKDIFPPM-------FTGKDH--ERP---------------ERNHFGQDG
Sb02g43870 CRLCNVVCTEAKDIFPPM-------FTGKDH--KRL---------------EQSHFGQDD
Os07g49210 CRLCNVVCTEAKDIFPEM-------FNGNDY-KDRP---------------GCSNICLDD
Bd1g16720  CRLCNVVCIEAKDIFPQM-------FNGNGYNKDRP---------------GCSNFFHDD
At5g20420  CRLCGHVGSEIKDVSAPF-------AEHKKWTIETKHIEED----------DIKTKLSHK
AtCLSY1    CRLCGHVGTEIKHVSAPF-------ARHKKWTTETKQINED----------DINTTIVNQ
Pt567214   CHKCSFVKTEKKYVSAPF-------VFSVFLLSFMSPLDRQVSMQGRHFLFVIRGYSARN
Pt832603   CQICGFVKTEIKYVSAPF-------MEHTGWTAESKPQNEE----------DLELKPDED
Cp19.123   CFLCGFISTEIKYMTAPF-------MEFRSYVAENRWENEE----------DNKNMTYAG
Vv29366    CQLCGFVSTEIKDVSPP-------------------------------------------
Sm441121   CSVCGYVGIPIEEMAP-----------HPDWSFRLP----------------------Q

                            1040
ZM000342   HVLDLSFFEIC--APEFSKIKESGNVWASITDLEPKLLA
ZM108166   HVLDLSFFEIC--APEFSKIKESGNVWASITDLEPKLLA
Sb02g43870 HVLDLSFFEIC--APESSKSKESGNVWSSIPVLEPKLLA
Os07g49210 DILDPSLLANL--APELSELKNSGSVWSAISDLDPKLLP
Bd1g16720  HVLDPSLLATF--APEFSEPRGSGNLWSLIPDLEPKLLP
At5g20420  E-AQTKDFSMISDSSEMLAAEESDNVWALIPKLKRKLHV
AtCLSY1    DGVESHTFTIPVASSDMPSAEESDNVWSLIPQLKRKLHL
Pt567214   P--IAHLFNVCKISPLVPF-EVNDNVWDLIPELRAKLHM
Pt832603   E--GSSLFGNHTSGEDVPVSEVNDNVWDLIPELRPKLHM
Cp19.123   R--ELNLVGNHT-SHERLLTEENDNVWALIPELRNKLHL
Vv29366    ---------------------------------------
Sm441121   NVLENPDPFIRRPELNDLNDDLADDPYFPSTDTRRSLHA
```

Figure 14. MAFFT alignment of DRD clade over N terminal region. Specific sequence features are noted below the alignment.

```
                              20                  40                  60
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Os03g06920  MARYPAPTSSRAIGAPIQPTEPHAPLPNTGGEGAPPPARTMPPPSSQAATSTPPAAATPL
Bd1g74070   ------------------------------------------------------------

                              80                 100                 120
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Os03g06920  QRPPAQATAQPSTQRYYVGVQRDKGTGKWAACVVDPSNPTKHRLVGAFPDEHAAALAHDR
Bd1g74070   ------------------------------------------------------------

                             140                 160                 180
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
```

```
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Os03g06920  LDLAFRGGGHRGAGDNFRPAFHAVELEFLRLCAATSSPGSHCGLVAGGDKYDEKYSEFLR
Bd1g74070   ------------------------------------------------------------

                             200                 220                 240
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ----------------------------------------------------MEPTNGGL
Sb01g46180  ------------------------------------------------------------
Os03g06920  KIYHGVMDNSPSYKKFFDVILDFFIARAREIGREALEDGGDMLVERFVAMHKNKAVTPRW
Bd1g74070   ------------------------------------------------------------

                             260                 280                 300
ZM064574    ----------------------------------M-------------------------
ZM093940    ----------------------------------M-------------------------
Sb07g02945  ------------------------------------------------------------
Os07g25390  ----------------------------------M-----------------------AA
Os06g14440  ----------------------------------M-------------------------
Bd3g19890   ----------------------------------M-------------------------
Bd2g21450   ----------------------------------M-------------------------
Bd2g21430   ----------------------------------M-------------------------
Os08g14610  ----------------------------------M-------------------------
Bd3g18910   ----------------------------------M-------------------------
At2g21450   ----------------------------------M-------------------FTAWNL
AtDRD1      ----------------------------------MGFVYIVMTGYYKNVHKRKQNQVDDG
Pt195587    ----------------------------------M-------------------------
Vv23895     ----------------------------------M----------------------HSE
Vv35918     SSNYGNPIPVNFEPYKLTEFNSTKHKRIWTFEENM----------------------HSE
Sb01g46180  --------------------MNLRGDYLSDKYTRM-----------GSAGQKRQKLGSEH
Os03g06920  RAWYRSDSRKVLQIPLSLRGGGGEIDHSTQKEARM-----------DSDSCKRRKHESGH
Bd1g74070   ----------------------------------M-----------DPSGCKRQKHEIEH

                             320                 340                 360
ZM064574    ---SQSPGGREGIYYSRQRK-P-ERNGSVFTPIAAMYSSGHALPVANRSHGLVFGSLSKD
ZM093940    ---SQSPGGREGIYYSRQRK-PSERNGSVFTPIAAMYPSGHALPDANRNHSLVFGGTSKD
Sb07g02945  ------------------------------------------------------------
Os07g25390  AGRDPPATPSSRMYYCRQRKASSEVNANVFVPGGQ---NGISFPASNRAHDWGYGGVREE
```

```
Os06g14440  --------DLISMYYRRQRKASSEANANVFMPGGP---NDISFPASNRDHDWGYGGVGKE
Bd3g19890   -------------YYRRKNRASDPI-------------SGLSLPAGSGVHSWGCGSVTKD
Bd2g21450   ------------------------------------------------------------
Bd2g21430   -----DAAAAATKIFRRNHRLPPVVQQKRFPPSGG---ASFLPPRCEALS----------
Os08g14610  ------------------------------------------------------------
Bd3g18910   --------------------------------GGEMPNANMTNCFMEQTEKKKY------
At2g21450   RSRSRSITQEELAKRPDPFCLPNNLL--------------------DGLEDGLYGRLADD
AtDRD1      PEAKRVKSSAKVIDYSNPFAVSNML---------------------EALDSGKFGSVSKE
Pt195587    -----KDTKEKVTDYAKPFAIRGLL---------------------ERLDSGRYGSVTDD
Vv23895     PKQKRQKAGSNVVDYSDPFAIPNLL---------------------EGLDAGKFGSMTKE
Vv35918     PKQKRQKAGPNVVDYSDPFAIPNLL---------------------EGLDAGRFGSVTKE
Sb01g46180  TSSPGTQSQSNIFLANKRLRLQFL----------------------EQVNELKAWSVTKD
Os03g06920  DSSSRVQSQSSILSRNRILCHQLL----------------------EQCDDLKYGSSTND
Bd1g74070   DSSPGNQSQATIISHNSSVRLRFL----------------------EQFDDLKYASATKD

                             380                 400                 420
ZM064574    WDDIRQRKDQLVNFLASLER-----------------------ASGDSAA-AGKIEDSKL
ZM093940    WDNIRQ-------FIASLER-----------------------ASENSSAIASKTGGGKS
Sb07g02945  ------------------------------------------------------------
Os07g25390  WEASYARKLQLINFLSSLHQ-----------------------RTANSLI-TTRMDANMD
Os06g14440  WEASYARKLQLMNFLSSLHQ-----------------------RTANPLV-TTRMDANMD
Bd3g19890   MEDIYARNVQLINFLSTLHE-----------------------PTRSSVP---MVETNVK
Bd2g21450   ------------------------------------------------------------
Bd2g21430   -----------VNFVATYFL----------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------NVLLILDS----------------------------------------
At2g21450   VKRLCKLRQEYLNGSISLED----------------------------------------
AtDRD1      LEEIADMRMDLVKRSIWLYP-SLAYTVFEAEKTMDNQQV-----------VEGVINLDDD
Pt195587    IRSLFYRRAQLIHPCLAMHP-TLSNEPRGRGMSFGEGKC-------------NVIDLDDD
Vv23895     IEALCARRMQMLHPYYVMYP-SLSYMSTDLGKQPSKKASKLVNRHASHLGHEDVIDLEDD
Vv35918     IEALCARRMQMLQPYYVMYP-SLSYMCTDLGKKQGKKASKLVNREASHLAHEDVIDLEDD
Sb01g46180  LKAITAKRRELFGIIERLRQVPIEQLYSSPFPKPSDARLDNFGKMESSYNPDNVINLDAD
Os03g06920  YKAISMKRLELISILQKLQEVPIQLPYASPLKSSETNRL---VQDGRNSSCRNIIDLDSD
Bd1g74070   YKAVNAKMHELLSTLEKLKEVPIKLPYVSPVLKTSDARLHSATQSGSNFSSDNIIDLDPD

                             440                 460                 480
ZM064574    AS------PVEPTEQKEKAAIIVLDSDDEDG--------NGSG--NSKLASETNKELGTS
ZM093940    TNH-----SVEPAEQKGKGDIIVLDSDDEDG--------DGNSPEHNKLASEMNKELGTS
Sb07g02945  ------------------------------------------------------------
Os07g25390  --------TPLEQKQKDSSAIIVLDSDDED-----------EAERCEQLASENNKQQAPS
Os06g14440  --------TPLEQKQKDSSAIIVLDSDDEDG----------YTEGCEQLTSENNKQQAPS
Bd3g19890   YCSIKQETKVTDCSVKQTEPILIPDSDDEDG-------------STAELAPEKNKELIPL
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Os08g14610  ---------SGSGNSLDTVALIVGGGSDSSGIVG--------------------------
Bd3g18910   ----------------PPKELIILDSDDEDGNSGKTQVPSYPTKELIILDSNDRKTLLPP
At2g21450   ------IEARQDNKRAKSSHNLIIDSDDELPQES--------------------------
AtDRD1      DDDDTDVEKKALCVVPSSSEIVLLDSDDEDNERQR-------------------------
Pt195587    --EIEGVGDSVGNVAVGRTPVVVIDSDDDESNENRMVG----------------------
Vv23895     --HIVYDVPTATAVADAALPVVIIDSDDEESGDQK-------------------------
Vv35918     --HVVDDALTATAVEDATLPVVIIDSDDEDCGDQKV------------------------
Sb01g46180  EENVEYHTQVNAGNTEADSTASADDSGDKDRVKS--------------------------
Os03g06920  --NDEDYTFANVDNIGANTTVVLVDSDDGDSVAS--------------------------
Bd1g74070   --NVGDHTHPNMENTGAHNTTYLVDSGDGDMIKS--------------------------
```

```
                             500                 520                 540
ZM064574    GLINNIA-----------------------------------ERMTFNGSQAFGTVHTY-
ZM093940    VLASNIA-----------------------------------ERMATNGSQTFETVHAYG
Sb07g02945  ------------------------------------------------------------
Os07g25390  GPTSPCT-----------------------------------TWIVSSAKDQVNGTLHVD
Os06g14440  GLTSPYT-----------------------------------TWIVSSAKDQVNGTLHVD
Bd3g19890   GLAGTLT-----------------------------------AHVTSKGKDQVNETRHY-
Bd2g21450   ------------------------------------------------------------
Bd2g21430   -------------------------------------------RCTCESKKLYTHNLFF-
Os08g14610  ------------------------------------------------------------
Bd3g18910   YPTKELIILDSYDEDRNPPCQRKRKISEVSSQVNRDASNDPRQKKLKNEPTYFGFDEPME
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------

                             560                 580                 600
ZM064574    GDKNTQIVP-YGQCSALVNQFPLQTSWQPSIQFERVVLQKRPEEQRMQD-----------
ZM093940    GSKNTQIVP-YGQGSALVNQFPLQTSWQPSIQFERVVLTKRPEEQRMQD-----------
Sb07g02945  ----------------------------------------------MQD-----------
Os07g25390  GVQSTQIVP-YGQNAPLINQSPLQTSWQPSIQYERVILQRRPEEQRVQD-----------
Os06g14440  GVQSTQIVPYYGQNAPLINQFPLQTSWQPSIQYERVILQKRPEEQRVQD-----------
Bd3g19890   GYQNSQIVP-YGQSAALINHHSLQTSWQPSIQYESVILQTRTEEERIKY-----------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   -------------VINVIDNVVNQGGQQP-VRFDRVILHTRTEENIFKI-----------
Os08g14610  ------------------------------------------------------------
Bd3g18910   KKKNPRKESDCHFNLAVPSKKLLLSNLWPSESLNKLIIQPKQSEEVANDEVFNDETQNES
At2g21450   ------------------------------------------------------------
AtDRD1      ----------------------------PMYQFQSTLVQHQKNQGDVTP-----------
Pt195587    -------------------------------HFQGIVLPKP-EGQFSTD-----------
Vv23895     ------------------------------------------------------------
Vv35918     -------------------SHPPQETAWPSFSYQEVVLRKPSVGLLANN-----------
Sb01g46180  ----------------FGDENSS-SNRNDNYIQQNPLLEHPVGHQE--------------
Os03g06920  ----------------FVDEKSSDSKQNANYIEESVLPEQHAQQQE--------------
Bd1g74070   ----------------IRDGNSSGCMQNVNFTQECSLAEQPGQYQD--------------

                             620                 640                 660
ZM064574    -----------------------------------------------LVAASIAEKRAET
ZM093940    -----------------------------------------------LVAATIAEKRAET
Sb07g02945  -----------------------------------------------LVAASIAEKRAET
Os07g25390  -----------------------------------------------LVAASHAEKIAET
Os06g14440  -----------------------------------------------LVAASHAEKIAET
Bd3g19890   -----------------------------------------------LAAASHAEKMAET
Bd2g21450   ------------------------------------------------------------
Bd2g21430   --------------------------------------------------WSDVEKIAET
Os08g14610  ------------------------------------------------------------
Bd3g18910   ECFMDAMCDHFDLAIASKKGSEEVANDEAQNESELFVDALCNHFDLAIASKNDSKKVAND
At2g21450   -----------------------------------------------VTQINPLEKR---
AtDRD1      -----------------------------------------------LIPQCSFEEV---
Pt195587    -----------------------------------------------VMVSDNVGRRIQG
```

```
Vv23895       -------------------------------------------------VRDYVESIAPK
Vv35918       -----------------------------------------------PVVRDYVGSIAPK
Sb01g46180    -----------------------------------------------ITRPDNCNSSTEP
Os03g06920    -----------------------------------------------ISMLDNENISSEA
Bd1g74070     -----------------------------------------------IIMLGNENINSED

                                680                 700                 720
ZM064574      QVFLSLPTE------------------KKRRR------------------S---------
ZM093940      QMFLSLPTE------------------RKRRR------------------T---------
Sb07g02945    QMFLSLPTE------------------KKRKR------------------S---------
Os07g25390    QVFLTLPTLPNE---------------RKRRK------------------S---------
Os06g14440    QVLLTLPTLPNE---------------RKRRK------------------T---------
Bd3g19890     QVFPDLPRE------------------RKQRK------------------L---------
Bd2g21450     ------------------------------------------------------------
Bd2g21430     QTSPALPGS---------------------------------------------------
Os08g14610    ---------------------------RKRRRCDLIRERWCCLCPVWCKEAQEVVVPGRG
Bd3g18910     EVAHDEPQKESECLVHDTWNHFDHAIASKNLK------------------ESEVVANDEV
At2g21450     ---------------------------LKKLK------------------EVIVVKNGD-
AtDRD1        ------------------------------------------------------------
Pt195587      EV-ASLTGEPD----------------SKKDK------------------GVYVGVEDD-
Vv23895       KEERSLTASSE----------------IRKDK----------------------------
Vv35918       VEEGSLMGATE----------------IRKDK----------------------------
Sb01g46180    QAL------------------------VKQVK----------------------------
Os03g06920    QA-------------------------VKKGK----------------------------
Bd1g74070     QAV------------------------AKQGN----------------------------

                                740                 760                 780
ZM064574      ------------------------------------------DPSLHASDDTATVPKQRK
ZM093940      ------------------------------------------DHSLLMLD--SFVPKQRR
Sb07g02945    ------------------------------------------DLSLLMLD--SFVPKQ-R
Os07g25390    ------------------------------------------EPTTLVDGDGGTNLGKGK
Os06g14440    ------------------------------------------EPTTLVDVDGGTNLGKRK
Bd3g19890     ------------------------------------------DPNSQVDGDAGTAPRKRK
Bd2g21450     --------------------------------------------------EMLKLPQEKE
Bd2g21430     ----------------------------------------------HVDGDAETAPRKRK
Os08g14610    RNGARQRDGGGCALGTTEVLGRICNSSVEKAEERETVIPAISNTEKMGEKQQKSIPRDRK
Bd3g18910     ANDEPQKE--------SEYLVDDMWNHFELAIASENLEESEEVTHDEQKKENEYLVRDRW
At2g21450     ------------------------------------------SSGSDSSPQGYDEEDSSR
AtDRD1        -----------------------------------------------DLGRGKEMPSAIK
Pt195587      ------------------------------------------EVDTEIKDDGLQVSDNVG
Vv23895       ------------------------------------------------------------
Vv35918       ------------------------------------------------------------
Sb01g46180    ------------------DAMDND----NVSAEAKKIVLFDCHSTSEQQPLMKQARGNIK
Os03g06920    ------------------DSMDINDVIYNKSGHEE-------IGEEEAQAENVQIKGNLK
Bd1g74070     ------------------DIMDID----NENHDEQ-------KGKREGEGEDVQSAGSIE

                                800                 820                 840
ZM064574      SKGATVVAAANLSLV-------SQQTATS----PEPDMVIEEEE--------KHK-NESD
ZM093940      RKGDTGLAPADLSLD-------LHQTATS----QEPDIAIEEEE--------KRK-NDGD
Sb07g02945    RKSDTGLAAADLSLD-------LQQPAKSPEPEPEPDMAIEEEE--------KCK-NESD
Os07g25390    RKNHQNQAAVDSILDLQQTVVPLQQNDVP----SQSYRTMIEEE--------KPV-KESD
Os06g14440    RKNHQNQAAVDSNLD-------LQQNDVP----SQSYRTMIEEE--------KPV-KESD
Bd3g19890     RKTGPDPAAVDLPSE-------TYNPVEE----EEP----AEED--------KPE-NKSD
Bd2g21450     REKTICPQ--------------------------------------------KPT-----
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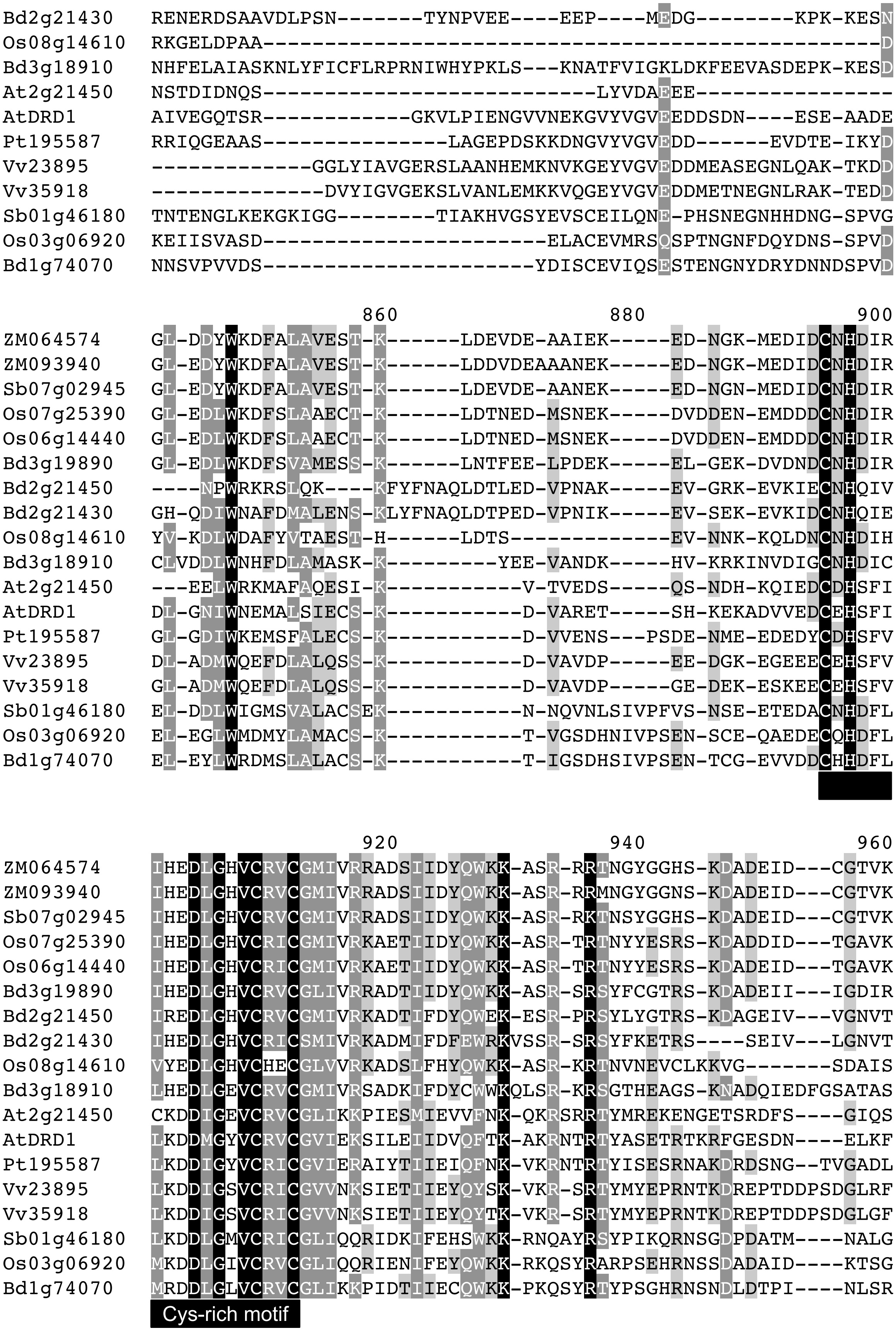

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Bd2g21430   RENERDSAAVDLPSN-------TYNPVEE----EEP----MEDG--------KPK-KESN
Os08g14610  RKGELDPAA--------------------------------------------------D
Bd3g18910   NHFELAIASKNLYFICFLRPRNIWHYPKLS---KNATFVIGKLDKFEEVASDEPK-KESD
At2g21450   NSTDIDNQS---------------------------LYVDAEEE----------------
AtDRD1      AIVEGQTSR------------GKVLPIENGVVNEKGVYVGVEEDDSDN----ESE-AADE
Pt195587    RRIQGEAAS---------------LAGEPDSKKDNGVYVGVEDD------EVDTE-IKYD
Vv23895     -------------GGLYIAVGERSLAANHEMKNVKGEYVGVEDDMEASEGNLQAK-TKDD
Vv35918     --------------DVYIGVGEKSLVANLEMKKVQGEYVGVEDDMETNEGNLRAK-TEDD
Sb01g46180  TNTENGLKEKGKIGG--------TIAKHVGSYEVSCEILQNE-PHSNEGNHHDNG-SPVG
Os03g06920  KEIISVASD-----------------------ELACEVMRSQSPTNGNFDQYDNS-SPVD
Bd1g74070   NNSVPVVDS----------------------YDISCEVIQSESTENGNYDRYDNNDSPVD

                              860                 880                 900
ZM064574    GL-DDYWKDFALAVEST-K------LDEVDE-AAIEK-----ED-NGK-MEDIDCNHDIR
ZM093940    GL-EDYWKDFALAVEST-K------LDDVDEAAANEK-----ED-NGK-MEDIDCNHDIR
Sb07g02945  GL-EDYWKDFALAVEST-K------LDEVDE-AANEK-----ED-NGN-MEDIDCNHDIR
Os07g25390  GL-EDLWKDFSLAAECT-K------LDTNED-MSNEK-----DVDDEN-EMDDDCNHDIR
Os06g14440  GL-EDLWKDFSLAAECT-K------LDTNED-MSNEK-----DVDDEN-EMDDDCNHDIR
Bd3g19890   GL-EDLWKDFSVAMESS-K------LNTFEE-LPDEK-----EL-GEK-DVDNDCNHDIR
Bd2g21450   ----NPWRKRSLQK----KFYFNAQLDTLED-VPNAK-----EV-GRK-EVKIECNHQIV
Bd2g21430   GH-QDIWNAFDMALENS-KLYFNAQLDTPED-VPNIK-----EV-SEK-EVKIDCNHQIE
Os08g14610  YV-KDLWDAFYVTAEST-H------LDTS-------------EV-NNK-KQLDNCNHDIH
Bd3g18910   CLVDDLWNHFDLAMASK-K---------YEE-VANDK-----HV-KRKINVDIGCNHDIC
At2g21450   ---EELWRKMAFAQESI-K-----------V-TVEDS-----QS-NDH-KQIEDCDHSFI
AtDRD1      DL-GNIWNEMALSIECS-K-----------D-VARET-----SH-KEKADVVEDCEHSFI
Pt195587    GL-GDIWKEMSFALECS-K-----------D-VVENS---PSDE-NME-EDEDYCDHSFV
Vv23895     DL-ADMWQEFDLALQSS-K-----------D-VAVDP-----EE-DGK-EGEEECEHSFV
Vv35918     GL-ADMWQEFDLALQSS-K-----------D-VAVDP-----GE-DEK-ESKEECEHSFV
Sb01g46180  EL-DDLWIGMSVALACSEK-----------N-NQVNLSIVPFVS-NSE-ETEDACNHDFL
Os03g06920  EL-EGLWMDMYLAMACS-K-----------T-VGSDHNIVPSEN-SCE-QAEDECQHDFL
Bd1g74070   EL-EYLWRDMSLALACS-K-----------T-IGSDHSIVPSEN-TCG-EVVDDCHHDFL

                              920                 940                 960
ZM064574    IHEDLGHVCRVCGMIVRRADSIIDYQWKK-ASR-RRTNGYGGHS-KDADEID---CGTVK
ZM093940    IHEDLGHVCRVCGMIVRRADSIIDYQWKK-ASR-RRMNGYGGNS-KDADEID---CGTVK
Sb07g02945  IHEDLGHVCRVCGMIVRRADSIIDYQWKK-ASR-RKTNSYGGHS-KDADEID---CGTVK
Os07g25390  IHEDLGHVCRICGMIVRKAETIIDYQWKK-ASR-TRTNYYESRS-KDADDID---TGAVK
Os06g14440  IHEDLGHVCRICGMIVRKAETIIDYQWKK-ASR-TRTNYYESRS-KDADEID---TGAVK
Bd3g19890   IHEDLGHVCRVCGLIVRRADTIIDYQWKK-ASR-SRSYFCGTRS-KDADEII---IGDIR
Bd2g21450   IREDLGHVCRVCGMIVRKADTIFDYQWEK-ESR-PRSYLYGTRS-KDAGEIV---VGNVT
Bd2g21430   IHEDLGHVCRICSMIVRKADMIFDFEWRKVSSR-SRSYFKETRS----SEIV---LGNVT
Os08g14610  VYEDLGHVCHECGLVVRKADSLFHYQWKK-ASR-KRTNVNEVCLKKVG-------SDAIS
Bd3g18910   LHEDLGEVCRVCGMIVRSADKIFDYCWWKQLSR-KRSGTHEAGS-KNADQIEDFGSATAS
At2g21450   CKDDIGEVCRVCGLIKKPIESMIEVVFNK-QKRSRRTYMREKENGETSRDFS----GIQS
AtDRD1      LKDDMGYVCRVCGVIEKSILEIIDVQFTK-AKRNTRTYASETRTKRFGESDN----ELKF
Pt195587    LKDDIGYVCRICGVIERAIYTIIEIQFNK-VKRNTRTYISESRNAKDRDSNG--TVGADL
Vv23895     LKDDIGSVCRICGVVNKSIETIIEYQYSK-VKR-SRTYMYEPRNTKDREPTDDPSDGLRF
Vv35918     LKDDIGSVCRICGVVNKSIETIIEYQYTK-VKR-SRTYMYEPRNTKDREPTDDPSDGLGF
Sb01g46180  LKDDLGMVCRICGLIQQRIDKIFEHSWKK-RNQAYRSYPIKQRNSGDPDATM----NALG
Os03g06920  MKDDLGIVCRVCGLIQQRIENIFEYQWKK-RKQSYRARPSEHRNSSDADAID----KTSG
Bd1g74070   MRDDLGLVCRVCGLIKKPIDTIIECQWKK-PKQSYRTYPSGHRNSNDLDTPI----NLSR
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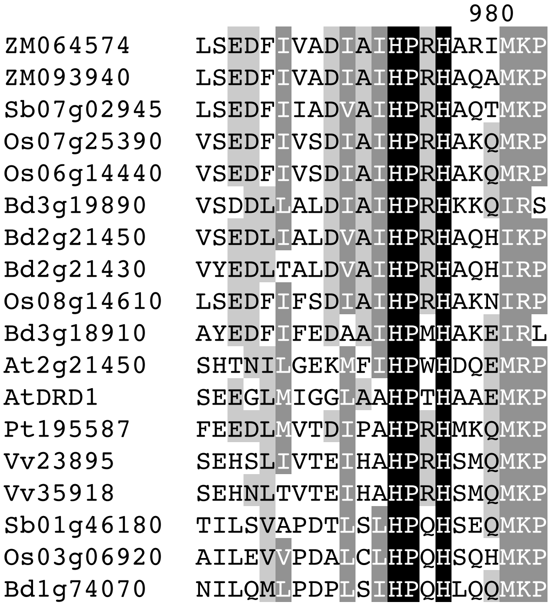

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                                980
ZM064574       LSEDFIVADIAIHPRHARIMKP
ZM093940       LSEDFIVADIAIHPRHAQAMKP
Sb07g02945     LSEDFIIADVAIHPRHAQTMKP
Os07g25390     VSEDFIVSDIAIHPRHAKQMRP
Os06g14440     VSEDFIVSDIAIHPRHAKQMRP
Bd3g19890      VSDDLLALDIAIHPRHKKQIRS
Bd2g21450      VSEDLIALDVAIHPRHAQHIKP
Bd2g21430      VYEDLTALDVAIHPRHAQHIRP
Os08g14610     LSEDFIFSDIAIHPRHAKNIRP
Bd3g18910      AYEDFIFEDAAIHPMHAKEIRL
At2g21450      SHTNILGEKMFIHPWHDQEMRP
AtDRD1         SEEGLMIGGLAAHPTHAAEMKP
Pt195587       FEEDLMVTDIPAHPRHMKQMKP
Vv23895        SEHSLIVTEIHAHPRHSMQMKP
Vv35918        SEHNLTVTEIHAHPRHSMQMKP
Sb01g46180     TILSVAPDTLSLHPQHSEQMKP
Os03g06920     AILEVVPDALCLHPQHSQHMKP
Bd1g74070      NILQMLPDPLSIHPQHLQQMKP
```

Tables

Table 1. New marker development for *rmr2.* Marker names are listed in their predicted order based on rice synteny from *umc1845* (top) to *bnlg1064* (bottom). The accession numbers represent the maize EST sequences used for primer design. SNP information is formatted so the first letter is the base in the non-mutant parent, the number refers to the position in the maize amplicon, and the last letter refers to the *rmr2-1* base. Primer sequences were designed by undergraduate student Clarissa Lee.

Name	Maize EST	Polymorphism	Marker development
2map13	BU499437	SNP: A199C	SNP not suitable for CAPS or dCAPS
2map14	BU499437	SNP: A74G	dCAPS with DraIII; not linked
2map1	CF637444	--	--
2map15	AW288927	--	--
2map2	CD650821	--	--
2map16	CF034137	--	--
2map4	CK370377	--	--
2map3	CK370377	--	--
2map17	CD440054	--	--
2map18	CD440054	--	--
2map5	CD440054	SNP: C224T	no amplification with dCAPS primers
2map6	BQ485194	--	--
2map19	BQ485194	--	--
2map7	AW066777	--	--
2map20	CD434384	--	--
2map8	BM498426	--	--
2map21	CF038398	SNPs: A108T, T162C, C246T	no amplification with dCAPS primers
2map9	CF647259	amplicon size difference in acrylamide	not carried forward
2map10	CA398302	--	--
2map11	CK347668	no amplification with primer set	--
2map12	CN070734	--	--
2map22	BE510846	--	--
2map23	BI134304	amplicon size difference in 3.5% agarose	PCR based marker, linked but not informative

Table 2. *rmr2* allele screen progeny. Families segregating 1:3 for either *rmr2-1* or *ems05446* homozygous mutants. See Figure 3 for pedigree information. Dark progeny plants were selfed as indicated with resulting ear numbers listed. 06-681 and 06-682 segregated runty plants in addition to Pl types. 7 (06-679), 12 (06-680), 5 (06-681), 9 (06-682), and 4 (06-683) Pl' types recorded.

Family Number	Plant Number	Anther Color	Notes
06-679	1	Pl	selfed, ear #61241
	6	Pl	selfed, ear #61242
	8	Pl	selfed, ear #61243
	12	Pl	selfed, ear #61244
06-680	3	Pl	selfed, ear #61245
	5	Pl	selfed, ear #61246
	11	Pl	selfed, ear #61247
06-681	1	ns	runt
	5	Pl	selfed, ear #61248
	6	ns	runt
	9	Pl	selfed, ear #61249
	11	ns	runt
06-682	2	Pl	selfed, ear #61250
	3	Pl	--
	6	ns	runt
06-683	--	ns	no Pl types

Table 3. SSR markers used for *rmr11 / rmr1* mapping. SSR markers polymorphic in the *rmr* / A632 F2 mapping population. Asterisks denote markers initially in the excluded region and not tested until the second round of mapping (see text).

Name	**Chromosome Bin**	**Polymorphic**	**Linked to** rmr1
*umc1395**	1.05	Y	N
*umc1281**	1.06	Y	N
*umc1197**	1.08	Y	N
bnlg1175	2.04	no amplification	-
umc1635	2.05	Y	N
umc2178	2.06	N	N
bnlg2077	2.07	Y	N
mmc0381	2.08	Y	N
umc1252	2.09	Y	N
umc2105	3.00	Y	N
umc2071	3.01	N	-
bnlg1523	3.02	N	-
umc1458	3.02	N	-
bnlg1144	3.02	N	-
umc1647	3.02	N	-
bnlg1447	3.03	N	-
umc2000	3.04	N	-
umc1223	3.04	no amplification	-
mmc0321	3.04	Y	N
umc1759	4.01	Y	N
umc1829	5.09	Y	N
*bnlg1154**	6.04	N	-
*bnlg2249**	6.05	Y	Y
*umc2141**	6.05	Y	Y
*bnlg1174a**	6.05	Y	Y
*bnlg1732**	6.05	Y	Y
*umc2165**	6.07	Y	Y
*umc2323**	6.07	N	-
*umc1248**	6.07	Y	Y
umc1695	7.00	Y	N
umc2160	7.01	N	-
umc1409	7.01	Y	N
bnlg1380	7.02	Y	N
umc1359	8.00	Y	N
umc1592	8.01	N	-
umc1786	8.01	N	-
bnlg1194	8.01	Y	N
bnlg2235	8.02	Y	N
umc1910	8.03	N	-
umc1778	8.03	Y	N
umc1149	8.05	N	-

Name	**Chromosome Bin**	**Polymorphic**	**Linked to** rmr1
bnlg2181	8.05	Y	N
umc1724	8.06	Y	N
umc1807	8.07	Y	N
bnlg1056	8.08	Y	N
phi233376	8.09	N	-
*umc1810**	9.01	Y	N
*umc1583**	9.01	Y	N
*umc1636**	9.02	Y	N
umc1366	9.06	N	-
umc1506	9.07	N	-
umc1137	9.07	N	-
umc2163	10.04	Y	N
phi323152	10.05	Y	N
umc1993	10.06	N	-
umc2122	10.06	Y	N
umc1084	10.07	N	-
umc1038	10.07	Y	N
umc1640	10.07	N	-

Table 4. Linkage results for *rmr11* and *rmr1* mapping populations on *6L*. *rmr11* and *rmr1* show similar linkage patterns to SSR markers on 6L suggesting the two loci are tightly linked or allelic. *rmr1-1* linkage data provided by Chris Hale and Jyothi Chandra.

	rmr11-1 **mapping population**		rmr1-1 **mapping population**	
Marker name	**rec / total chr**	**cM**	**rec / total chr**	**cM**
bnlg2249	47 / 370	12.7	33 / 248	13.3
umc2141	11 / 90	12.2	--	--
bnlg1174a	0 / 178	< 0.56	0 / 680	< 0.15
bnlg1732	--	--	2 / 60	3.3
umc2165	65 / 200	32.5	90 / 290	31.0

Table 5. Distribution of DRD1 subfamily members in RMR, CLSY, and DRD clades. [a]Contains minor gaps within SNF2 domain. [b]Contains large gaps within SNF2 domain.

Species	RMR	CLSY	DRD	Total
Maize	2	2	2	6
Sorghum	2	1	2	5
Rice	2	1	4	7
Brachypodium	3	1	5	9[a]
Arabidopsis	2	2	2	6
Poplar	1	2	1	4
Grape	1	1[a]	2	4
Papaya	1	1[b]	0	2
Selaginella	0	2	0	2
Total	14	13	18	45

Table 6. Putative RNA binding residues in CLSY1 are not conserved. Residues were identified in CLSY1 by Smith *et al*. [2007] as potentially involved in RNA binding. Based on the multiple sequence alignment in Figure 9, the conservation of these residues was determined as indicated. [a]Located in CLSY1 / RMR1 specific insertion in both this analysis and Smith *et al*. [b]Located in CLSY1 specific insertion only in Smith *et al*. [2007] [c]Conserved lysine at this position in DRD1 clade. [d]Partial conservation in DRD1 clade.

Residue-Location	Conserved in:		
	CLSY1 clade	RMR1 clade	DRD1 clade
Arg-770[a]	Yes	No	Yes[c]
Lys-776[a]	No	No	No
Lys-778[a]	Yes	No	No
Lys-787[a]	No	No	No
Lys-995[b]	No	No	No
Lys-999[b]	Yes	No	Yes[d]
Lys-1029	No	No	No
Lys-1048	Yes	No	No
Arg-1097	No	No	No
Lys-1099	No	Yes	Yes

Chapter 3 -- Phylogenetic analysis of plant-specific RNA polymerase subunits

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Introduction

Plants have two DNA-dependent RNA polymerases (RNAPs), Pol IV and Pol V, in addition to the ubiquitous eukaryotic polymerases I, II, and III. Derived from Pol II, Pol IV and Pol V are functionally distinct RNAPs defined by their largest subunits, RPD1 and RPE1, respectively [Luo and Hall 2007]. The catalytic cores of these respective polymerases are created by physical interaction between the largest and second largest subunits (RPD2 / RPE2). In *Arabidopsis*, Pol IV and V share a single second largest subunit, NRPD2a. Additional subunits are shared with Pol II, or exist in Pol IV and/or Pol V-specific forms [Ream *et al*. 2009].

Subunits for these plant-specific RNA polymerases were originally identified in the *Arabidopsis* genome [Arabidopsis Genome Initiative 2000] and subsequently in genetic screens for factors involved in small RNA-mediated transgene silencing [Herr *et al*. 2005; Kanno *et al*. 2005]. In *Arabidopsis*, mutations in the loci encoding the largest or shared second largest subunits of Pol IV and Pol V do not affect viability or development but do have distinct molecular effects on small RNA silencing pathways [Pikaard *et al*. 2008; Matzke *et al*. 2009]. Pol IV is required for the accumulation of 24 nt RNAs while Pol V produces non-coding RNA transcripts at low levels [Pikaard *et al*. 2008; Huettel *et al*. 2007; Wierzbicki *et al*. 2008].

In maize, *rmr6* has been identified as encoding the largest subunit of Pol IV [Erhard *et al.* 2009] while *rmr7* has been identified as encoding the second largest subunit of either Pol IV or Pol V [Stonaker *et al.* 2009]. In this chapter, I present bioinformatic and phylogenetic characterization of the two loci. This analysis provides new clues to Pol IV and Pol V function and indicates that polymerase evolution, and potentially RdDM function, have diverged along different plant lineages.

Results

RMR6 is a RNAP largest subunit with an altered G domain

The *rmr6* locus encodes the largest subunit of Pol IV in maize, ZmRPD1 [Erhard *et al.* 2009]. A diagram of ZmRPD1 is presented in Figure 1. Black boxes represent the highly conserved A-H polymerase domains [Cramer *et al.* 2001] and lesions encoded by maize *rpd1* mutants [Erhard *et al.* 2009] are indicated. The *rpd1-8* allele encodes a non-conservative substitution at an invariantly conserved cysteine residue likely involved in coordinating Zn^{2+} ions necessary for polymerase function [Cramer *et al*. 2001]. The *rpd1-1*, *rpd1-7*, and *rpd1-14* alleles all encode premature stop codons. The *rpd1-7* allele is most likely a loss-of-function type, truncating domains B-H, while the *rpd1-14* lesion occurs in domain C. The *rpd1-1* allele predicts truncation of the last third of the protein including domains G and H. These lesions are all predicted to seriously disrupt protein function.

I used phylogenetic analysis to identify clues regarding putative ZmRPD1 action. BLAST searches of databases at Phytozome identified RPD1 and RPE1 sequences from spikemoss *Selaginella moellendorffii*, eudicots *Arabidopsis*, poplar, grape, and papaya, and grasses maize, sorghum, rice, and *Brachypodium distachyon* which were aligned with MAFFT. Conserved RPB1 domains were identified on the multiple sequence alignment (Figure 2). Several predicted proteins have gaps over the conserved domains (BdRPD1, domains A and H; CpRPE1, domain A; VvRPD1, domain E; CpRPD1, domains F and G) likely due to incorrect gene model predictions. A new prediction was attempted for CpRPD1, which contains the largest gaps, but the model could not be improved upon due to lack of genome sequence information. These models will need to be refined as updated information becomes available.

Strong conservation with RPB1 was observed for both RPD1 and RPE1 over domains C and D which form the presumed RNAP active site along with domains E, F, H and I from RPD2. The three aspartic acid resides which comprise the metal A binding site are invariantly conserved (Figure 2). Strong conservations between RPB1, RPD1, and RPE1 was also observed for domains A, B which form the clamp that holds nucleic acids in place during transcription [Cramer *et al.* 2001] and domain E which is part of the pore below the active site that allows entry of nucleoside triphosphates [Cramer *et al.* 2001]. Weak conservation was observed between RPB1 and RPD1 and RPE1 over domain G, and previous alignments with AtRPD1 could not identify any conservation with RPB1 over this region [Herr *et al.* 2005]. Concerned that these results could be due to alignment algorithms, I created alignments with five unique programs and looked for a consensus (Appendix 6). Alignments created using MAFFT, T-COFFEE and MUSCLE algorithms identified a RPD1 region that contained a deeply conserved backbone relative to RPB1, but which also contained unique RPD1 and RPE1 specific sequences. I have annotated this region as domain G (Figure 1, Figure 2), but noted that it is not well conserved with the canonical RPB1 domain.

The most distinct differences between RPB1 and RPD1 and RPE1 in domain G occur in a region known as the Trigger Loop (TL). RPD1 proteins contain specific sequences near the carboxy terminus of the TL which differ significantly from either RPE1 or RPB1 but are conserved amongst the RPD1 proteins. Similar conservation is observed for RPE1 with regard to RPD1 and RPB1. The TL has recently been shown in *S. cerevisiae* to be both a binding site of the Pol II-specific inhibitor α-amanitin and the mediator of nucleotide selectivity during rapid transcript synthesis [Kaplan *et al.* 2008]. The altered Domain G within the plant-specific RPD1 and RPE1 proteins may therefore be of considerable significance regarding Pol IV and Pol V action.

RPD1 and RPE1 both diverge from RPB1 over a portion of the bridge helix region of domain F (Figure 2) which is involved in mediating nucleic acid-protein interactions during translocation [Cramer *et al.* 2001], although total conservation is much higher. However, this region is a site of α-amanitin inhibition in RPB1 [Bushnell *et al.* 2002]. Together with the divergence over the Trigger Loop in domain G, these results indicate that RPD1 and RPE1 should be insensitive to α-amanitin. Additionally, RPD1 and RPE1 contain a similar, conserved difference with RPB1 in the amino-terminal end of domain H which is involved in the conformation change to an actively transcribing complex [Cramer *et al.* 2001]. Near the middle of domain H, involved in binding with the second largest subunit [Cramer *et al.* 2001], there is another RPD1/RPE1 specific region which may represent adaptations to distinct second largest subunit proteins (RPB2 vs. RPD2). RPD1 and RPE1 proteins also lack the foot region which is exclusively found in RPB1 proteins and not other polymerases [Cramer *et al.* 2001].

Phylogenetic Analysis of RPD1 and RPE1 proteins.

A maximum likelihood tree was generated from the MAFFT alignment of plant RPD1, RPE1, and RPB1 proteins (Figure 3). This tree agrees with the evolutionary relationship of

RPD1 to RPE1 and RPB1 proposed by Luo and Hall [2007], but updates the tree with proteins from more recently sequenced genomes. *Selaginella* only contains RPD1, not RPE1, as the duplication which gave rise to RPE1 had not yet occurred. Rice is the only species with a duplicated RPD1 protein, but both rice, sorghum and poplar have retained duplicate RPE1 proteins. Based on the tree topology, it appears as though RPE1 was duplicated in the grass ancestor but then subsequently lost in the maize and *Brachypodium* lineages. The duplicate proteins are likely functional as they are full-length and contain the conserved polymerase domains, but the significance of the retention of these proteins in only certain species is unclear.

Maize contains three RPD2-type proteins.

The *rmr7* locus encodes ZmRPD2a, a protein with highest similarity to the second largest subunit of Pol IV and Pol V from *Arabidopsis* [Stonaker *et al*. 2009]. Figure 4 shows a model of ZmRPD2a with mutant lesions and conserved polymerase domains identified. The inferred peptide encoded by *rpd2a-1* lacks both conserved subunit domains C – I and the metal binding sites known to be critical for *Saccharomyces cerevisiae* RNAP catalysis and *Arabidopsis* Pol IV/V function [Cramer *et al*. 2001, Haag *et al*. 2009]. The inferred peptide encoded by the *rpd2a-3* allele lacks the conserved domains that are required for contacts with the largest subunit in *S. cerevisiae* Pol II [Cramer *et al*. 2001]. The lesion identified in *rpd2a-2* predicts an amino acid substitution of a glycine residue that is strictly conserved amongst all RNAP second largest subunits to glutamate.

While *rpd2a* is currently the only RPD2-type protein in maize to have been identified by mutation, BLAST searches identified two additional RPD2-encoding gene models in the genome, *rpd2c* on 10S and *rpd2b* on 10L. 2S and 10L contain duplicated regions retained from an ancient tetraploidy event in maize [Swigonová *et al*. 2005]. I identified synteny between the chromosomal regions around *rpd2a* and *rpd2b* (Figure 5) indicating these genes are homoeologs. No significant synteny was observed between the regions around *rpd2a* and *rpd2c*. Both *rpd2c* and *rpd2b* are predicted to encode full-length proteins with high amino acid sequence conservation to that encoded by *rpd2a* (67 and 94% identity, respectively) indicating that these loci likely produce functional RPD2-type proteins.

Grasses contain multiple RPD2-type proteins.

To determine if the expansion of genes encoding RPD2-type proteins was unique to maize, I identified full-length predicted proteins from other plant genomes including spikemoss *Selaginella moellendorffii*, eudicots grape, poplar, papaya, and *Arabidopsis* and the grasses *Brachypodium distachyon*, rice, and sorghum. These protein sequences were aligned (Figure 6), and a maximum likelihood tree was constructed (Figure 7) using the second largest subunit of Pol II, RPB2, from *Arabidopsis* and maize as outgroups. This analysis indicates that retention of duplicated genes encoding RPD2 proteins has occurred in the *Selaginella* and grass lineages but not eudicots. *Arabidopsis* is the only representative eudicot with evidence of a *rpd2* locus duplication, yet only one functional locus has been retained from this recent event [Herr *et al*. 2005; Kanno *et al*. 2005; Onodera *et al*. 2005; Pontier *et al*. 2005]. An *rpd2* locus duplication in the grass common ancestor resulted in two distinct and well-supported clades, A and B. Unlike *Arabidopsis*, all of these *rpd2*-encoding loci appear to be functional. The relative timing of this duplication corresponds with a whole genome duplication that occurred in the cereal genome prior to the divergence of rice, *Brachypodium*, sorghum, and maize [Paterson *et al*. 2004]. Accordingly, the rice clade A (Os04g54840) and clade B (Os08g07480) loci are located in the homoeologous r8-r4 chromosomal segments retained from this duplication [Bolot *et al*. 2009].

Within clade A, further *rpd2* duplications have been retained in individual species lineages. The two maize clade A loci, homoeologs *rpd2a* and *ZM2G128427*, are located in regions syntenic with sorghum chromosome 6 [Bolot *et al*. 2009], the location of clade A locus Sb06g030300. However, the additional sorghum clade A locus, Sb01g042100, is in an asyntenic region on chromosome 1 [Bolot *et al*. 2009] indicating that the duplication in sorghum occurred independently of that in maize. The maize clade A duplication is consistent with a tetraploidy event which occurred after the divergence of maize and sorghum [Gaut and Doebley 1997; Swigonová *et al*. 2004] while the sorghum clade A duplication corresponds to a small-scale event occurring post-divergence [Swigonová *et al*. 2004]. The origins of the *Brachypodium* duplications are unclear, as no large scale duplications have been proposed in that lineage, but the high degree of amino acid similarity (98.5%) between Bd_6.650 and Bd_2.4317 indicates that this duplication was relatively recent. This diversity of RPD2-type subunits implies that, in contrast to *Arabidopsis*, Pol IV and Pol V-type RNAPs in other lineages may not be defined by a single or shared second largest subunit.

Discussion

Genetic screens in maize have identified two RNA polymerase subunits as required to maintain repressed epigenetic states associated with paramutation in maize. The *rmr6/rpd1* locus encodes RPD1, the largest subunit of Pol IV [Erhard *et al*. 2009], and the *rmr7/rpd2a* locus encodes RPD2a, the second largest subunit of Pol IV and / or Pol V [Stonaker *et al*. 2009]. Mutations in both *rmr6/rpd1* and *rmr7/rpd2a* are predicted to disrupt protein function and reduce accumulation of 24 nt siRNAs, as expected from the function of Pol IV in the *Arabidopsis* RdDM pathway.

Previous phylogenetic analysis with limited sequence information concluded that RPD1 and RPD2 were derived from a single duplication of RPB1 and RPB2, respectively, in the ancestor of land plants while RPE1 was derived from a single duplication of RPD1 in the ancestor of the angiosperms [Luo and Hall 2007]. The phylogenetic analyses of RNAP subunit sequences from complete or near complete genomes presented here agree with this general trend but indicate that additional locus duplications have occurred in the angiosperms, particularly for RPD2. Although maize contains only single *rpd1* and *rpe1* loci, *rpd2a* is one of three maize loci predicted to encode a protein similar to the *Arabidopsis* second largest subunit, NRPD2a. Based on predicted protein alignments with *S. cerevisiae* RPB2, the additional maize RPD2-type proteins are predicted to be functional. Further, all three *rpd2*-type loci appear to express RNA more or less constitutively throughout growth and development [Sidorenko *et al*. 2009].

While both the eudicot and grass RPD2 lineages have undergone genome duplication events [Lyons *et al*. 2008; Swigonová *et al*. 2004], only the grasses have retained potentially functional RPD2-type duplicates. This general observation indicates that grasses have a fundamentally different type of polymerase biology relative to eudicots. One possibility is that the additional RPD2-type proteins interact with both Pol IV and Pol V, as in *Arabidopsis*, but in a semi-redundant fashion. Complete functional redundancy is inconsistent with recessive loss-of-function lesions at the *rpd2a* locus [Stonaker *et al*. 2009], but perhaps the individual RPD2-type subunits overlap only for certain RNAP functions. Alternatively, the A and B clades identified in the phylogenetic tree could represent a functional division between RPD2 proteins that participate in either Pol IV, Pol V or in RNAPs that are specific for different tissues or developmental time points. Regardless, the grasses clearly support a potentially greater diversity of RNAP complexes than the representative eudicots examined here.

RPD2 proteins have expanded in certain plant lineages, but they have not diverged greatly from the RPB2 proteins. All RPD2 proteins retain conserved RNAP second largest subunit domains A through I and presumably function in an analogous fashion to RPB2. That is, in binding with the largest subunit to form the active site core of the polymerase. Conversely, RPD1 and RPE1 proteins have diverged rather extensively from RPB1 over RNAP largest subunit domain G which contains the Trigger Loop (TL) [Cramer *et al.* 2001]. The TL mediates nucleotide selectivity during rapid transcript synthesis [Kaplan *et al.* 2008]. Both α-amanitin treatment and TL mutations dramatically decrease the rate of synthesis, and they allow *S. cerevisiae* Pol II to misincorporate both rNTP and dNTPs in *in vitro* assays [Kaplan *et al.* 2008]. The sequence divergence identified here corresponds to functional divergence of RPD1 and RPE1 away from a Pol II-like enzyme toward a less efficient and more error prone enzyme. Pol V has been shown to transcribe a DNA template in vivo, but it produces only low level, non-polyadenylated transcripts [Wierzbicki *et al.* 2008]. No Pol IV transcripts have been identified *in vitro* [Pikaard *et al.* 2008] or *in vivo* in either *Arabidopsis* [Wierzbicki *et al.* 2008] or maize [Erhard *et al.* 2009]. The main polymerase for repetitive regions, at least in maize but also likely in Arabidopsis, is Pol II [Erhard *et al.* 2009]. However, given the conservation of the active site among all RPD1 proteins and the requirement of the active site residues for RdDM [Haag *et al.* 2009], Pol IV is likely transcribing, just at very low levels.

The role of Pol II in transcription of repetitive regions and the predicted enzymatic characteristics of Pol IV is consistent with a model in which the main role of Pol IV is to interfere with Pol II transcription. In non-mutant conditions, Pol IV facilitates repression of *Pl1-Rhoades* by inhibition of Pol II either through direct competition for initiation sites or by titration of shared RNAP subunits. Evidence for both scenarios has been identified. First, 7 out of 12 Pol II subunits copurify with RPD1 in *Arabidopsis* [Ream *et al.* 2009]. Secondly, mutations in maize *rpd1* result in an increase in polyadenylated transcripts from *CRM2* long terminal repeat (LTR) retroelements indicating that removal of Pol IV allows increased access of Pol II to these repetitive sequences [Hale *et al.* 2009].

Like RPD1, RPD2a is required for somatic maintenance of *Pl'* states and approximately 85% of all 24 nt RNA accumulation, consistent with a Pol IV-type function [Stonaker *et al.* 2009]. However, loss of RPD2a function does not completely mimic the loss of RPD1 as *rpd2a* mutants have unique molecular, genetic, and morphological phenotypes [Stonaker *et al.* 2009]. Interestingly, mutations in *rpd2a* do not affect *CRM2* LTR transcript levels even though the same transcripts are increased in *rpd1* mutants [Stonaker *et al.* 2009]. This indicates that there are functionally distinct Pol IV-type RNAPs, those that require RPD2a (for 24 nt RNA accumulation) and those that do not (for inhibition of Pol II). Either one or the other RPD2-type proteins define these functionally distinct complexes or perhaps RPD1 can act independently of a RNAP holoenzyme.

A gain-of-function *rpd2a* mutation that could dominantly interfere with all RPD1-containing complexes would be predicted to have phenotypic overlap with *rpd1* mutants. While no such dominant alleles have been identified in our mutational screens (0/15,000 M_1 plants), Sidorenko *et al*. [2009] report on a semi-dominant mutant allele (*Mop2-1*) identifying the same locus as *rpd2a* that predicts a single amino acid change in the terminal domain presumably required for interaction with RPD1. Since our evaluation of 2S segmental aneuploids indicate that the *rpd2a* locus is haplosufficient [Stonaker *et al*. 2009], the dominant nature of the *Mop2-1* allele is unlikely to be simply due to a dosage effect. Homozygous *Mop2-1* mutants do have a developmental phenotype reported to be similar in some respects to that displayed by *rpd1* mutants [Sidorenko *et al*. 2009], and this may indicate that the RPD2a variant encoded by *Mop2-1* poisons multiple RNAP complexes.

From the analyses of maize and *Arabidopsis* mutants, it is clear that the evolution of Pol IV and Pol V-type RNAPs facilitated unique mechanisms for epigenetic repression in plants. While models for Pol IV and Pol V function have been generated in *Arabidopsis*, it will be important to determine how applicable they will be in the cereal crops. The inferred increased diversity of RNAPs combined with enormous expansion of repetitious sequences in large genome cereals provides a potential basis for the innovation of regulatory novelty. A further understanding of the mechanistic relationship between paramutation and maize RNAP diversity promises to illuminate how such features have been co-opted during evolution and domestication of the grasses.

Materials and Methods

Phylogenetic analysis

Polymerase conserved domains were annotated per Cramer *et al.* [2001]. Protein sequences were retrieved by BLAST searches of Phytozome plant genome databases (www.phytozome.net). When necessary, gene models were predicted or altered with FGENESH+ (www.softberry.com). Sequence information can be found in Appendix 4. Sequences were aligned using ClustalW [Larkin *et al.* 2007], SATCHMO [Edgar and Sjolander 2003], T-COFFEE [Notredame *et al*. 2000], MUSCLE [Edgar 2004], or MAFFT [Katoh *et al.* 2002] under default conditions as indicated in the text. Alignments were edited with Jalview 2 [Waterhouse *et al.* 2009] and used to generate maximum likelihood trees with Phyml [Guindon and Gascuel 2003] with substitution models and conditions described in the text. Trees were edited with Dendroscope 2.2.2 [Huson *et al*. 2007].

Homoeologous regions for RPD2 synteny analysis were identified using ESTs, simple sequence repeat markers, and genes to identify sequence similarity on chromosomes 2S and 10L. Features used and the corresponding BACs they identify are as follows: AY111545 (AC206980, AC190732), nrpd2a (AC191113), ZM2G128427 (AC199156), AY112227 (AC209428, AC197497), AY110965 (AC215994, AC204716), AY105682 (AC186195, AC183941), AY109473 (AC177886, AC214263), p-umc44b, p-umc44a, b1 (AC191025), r1 (AC199387).

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Figures

Figure 1. *rmr6* encodes an RPD1 protein. RMR6 / RPD1 gene model showing EMS-generated mutant lesions and conserved Pol II domains A to H (black boxes). Domain G, with <20% sequence similarity to Pol II, is identified with a dark gray box.

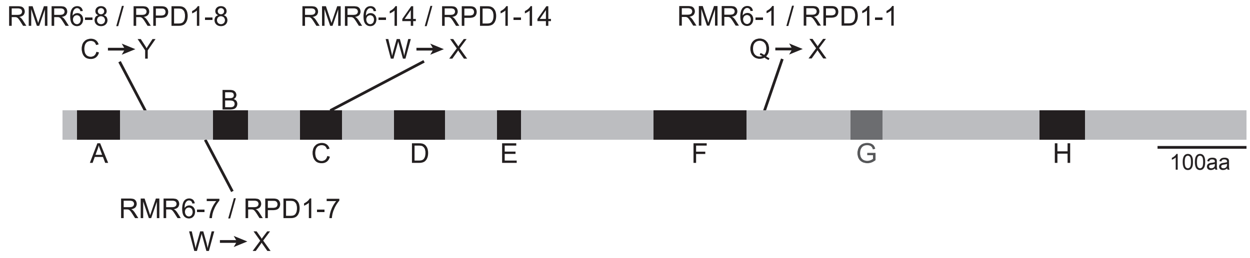
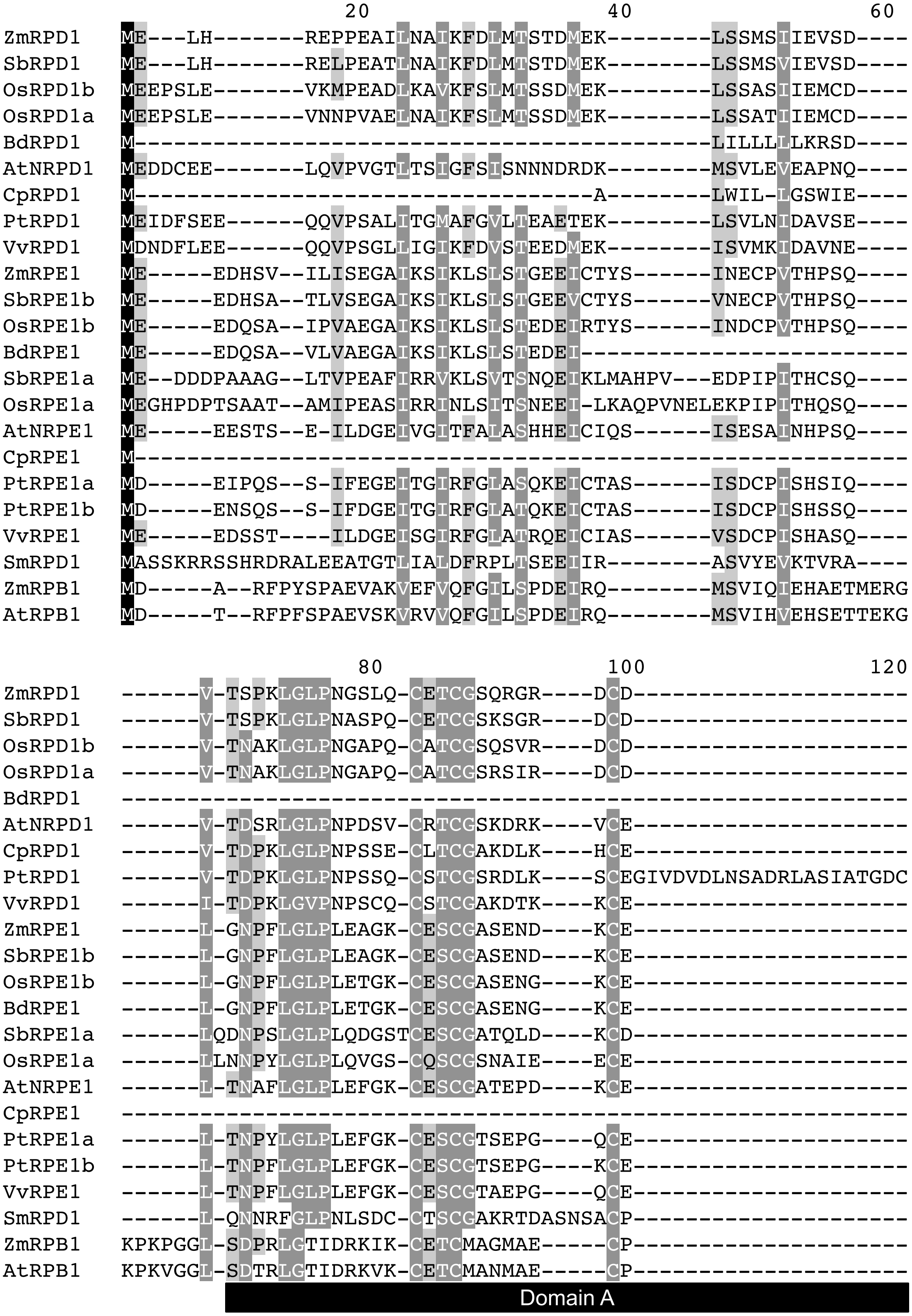


Figure 2. Alignment of full-length RNAP largest subunits from various plant species. Conserved polymerase domains are indicated by black boxes below the alignment. Mutant lesions in ZmRPD1 are indicated by red text in the alignment and an asterisk below.



```
                             20                  40                  60
ZmRPD1    ME---LH-------REPPEAILNAIKFDLMTSTDMEK--------LSSMSIIEVSD----
SbRPD1    ME---LH-------RELPEATLNAIKFDLMTSTDMEK--------LSSMSVIEVSD----
OsRPD1b   MEEPSLE-------VKMPEADLKAVKFSLMTSSDMEK--------LSSASIIEMCD----
OsRPD1a   MEEPSLE-------VNNPVAELNAIKFSLMTSSDMEK--------LSSATIIEMCD----
BdRPD1    M--------------------------------------------LILLLLKRSD----
AtNRPD1   MEDDCEE-------LQVPVGTLTSIGFSISNNNDRDK--------MSVLEVEAPNQ----
CpRPD1    M-----------------------------------A--------LWIL-LGSWIE----
PtRPD1    MEIDFSEE------QQVPSALITGMAFGVLTEAETEK--------LSVLNIDAVSE----
VvRPD1    MDNDFLEE------QQVPSGLLIGIKFDVSTEEDMEK--------ISVMKIDAVNE----
ZmRPE1    ME-----EDHSV--ILISEGAIKSIKLSLSTGEEICTYS------INECPVTHPSQ----
SbRPE1b   ME-----EDHSA--TLVSEGAIKSIKLSLSTGEEVCTYS------VNECPVTHPSQ----
OsRPE1b   ME-----EDQSA--IPVAEGAIKSIKLSLSTEDEIRTYS------INDCPVTHPSQ----
BdRPE1    ME-----EDQSA--VLVAEGAIKSIKLSLSTEDEI-------------------------
SbRPE1a   ME--DDDPAAAG--LTVPEAFIRRVKLSVTSNQEIKLMAHPV---EDPIPITHCSQ----
OsRPE1a   MEGHPDPTSAAT--AMIPEASIRRINLSITSNEEI-LKAQPVNELEKPIPITHQSQ----
AtNRPE1   ME-----EESTS--E-ILDGEIVGITFALASHHEICIQS------ISESAINHPSQ----
CpRPE1    M-----------------------------------------------------------
PtRPE1a   MD-----EIPQS--S-IFEGEITGIRFGLASQKEICTAS------ISDCPISHSIQ----
PtRPE1b   MD-----ENSQS--S-IFDGEITGIRFGLATQKEICTAS------ISDCPISHSSQ----
VvRPE1    ME-----EDSST----ILDGEISGIRFGLATRQEICIAS------VSDCPISHASQ----
SmRPD1    MASSKRRSSHRDRALEEATGTLIALDFRPLTSEEIIR--------ASVYEVKTVRA----
ZmRPB1    MD-----A--RFPYSPAEVAKVEFVQFGILSPDEIRQ--------MSVIQIEHAETMERG
AtRPB1    MD-----T--RFPFSPAEVSKVRVVQFGILSPDEIRQ--------MSVIHVEHSETTEKG

                             80                 100                 120
ZmRPD1    ------V-TSPKLGLPNGSLQ-CETCGSQRGR----DCD---------------------
SbRPD1    ------V-TSPKLGLPNASPQ-CETCGSKSGR----DCD---------------------
OsRPD1b   ------V-TNAKLGLPNGAPQ-CATCGSQSVR----DCD---------------------
OsRPD1a   ------V-TNAKLGLPNGAPQ-CATCGSRSIR----DCD---------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------V-TDSRLGLPNPDSV-CRTCGSKDRK----VCE---------------------
CpRPD1    ------V-TDPKLGLPNPSSE-CLTCGAKDLK----HCE---------------------
PtRPD1    ------V-TDPKLGLPNPSSQ-CSTCGSRDLK----SCEGIVDVDLNSADRLASIATGDC
VvRPD1    ------I-TDPKLGVPNPSCQ-CSTCGAKDTK----KCE---------------------
ZmRPE1    ------L-GNPFLGLPLEAGK-CESCGASEND----KCE---------------------
SbRPE1b   ------L-GNPFLGLPLEAGK-CESCGASEND----KCE---------------------
OsRPE1b   ------L-GNPFLGLPLETGK-CESCGASENG----KCE---------------------
BdRPE1    ------L-GNPFLGLPLETGK-CESCGASENG----KCE---------------------
SbRPE1a   ------LQDNPSLGLPLQDGSTCESCGATQLD----KCD---------------------
OsRPE1a   ------LLNNPYLGLPLQVGS-CQSCGSNAIE----ECE---------------------
AtNRPE1   ------L-TNAFLGLPLEFGK-CESCGATEPD----KCE---------------------
CpRPE1    ------------------------------------------------------------
PtRPE1a   ------L-TNPYLGLPLEFGK-CESCGTSEPG----QCE---------------------
PtRPE1b   ------L-TNPFLGLPLEFGK-CESCGTSEPG----KCE---------------------
VvRPE1    ------L-TNPFLGLPLEFGK-CESCGTAEPG----QCE---------------------
SmRPD1    ------L-QNNRFGLPNLSDC-CTSCGAKRTDASNSACP---------------------
ZmRPB1    KPKPGGL-SDPRLGTIDRKIK-CETCMAGMAE-----CP---------------------
AtRPB1    KPKVGGL-SDTRLGTIDRKVK-CETCMANMAE-----CP---------------------
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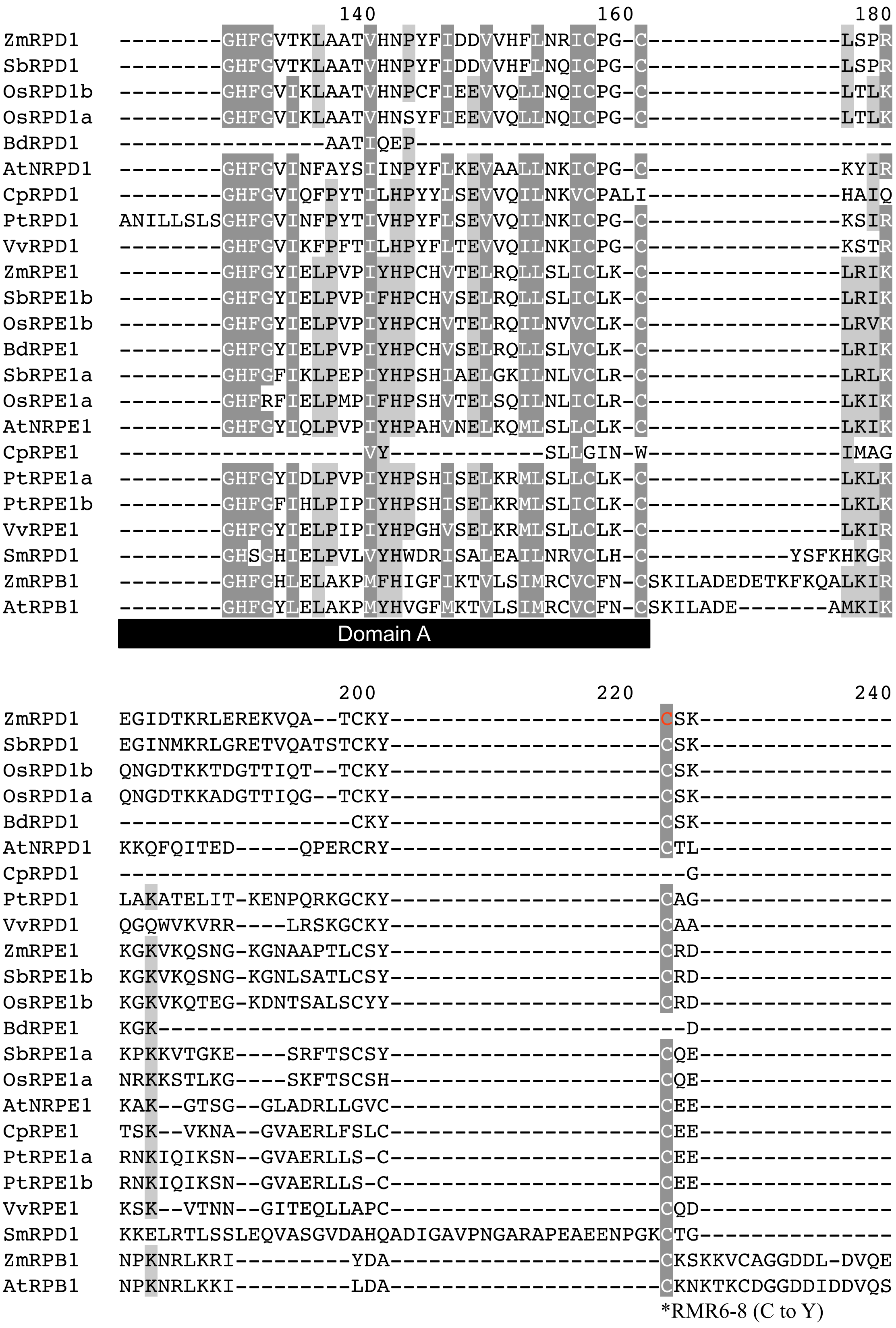

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                             140                 160                 180
ZmRPD1    --------GHFGVTKLAATVHNPYFIDDVVHFLNRICPG-C---------------LSPR
SbRPD1    --------GHFGVTKLAATVHNPYFIDDVVHFLNQICPG-C---------------LSPR
OsRPD1b   --------GHFGVIKLAATVHNPCFIEEVVQLLNQICPG-C---------------LTLK
OsRPD1a   --------GHFGVIKLAATVHNSYFIEEVVQLLNQICPG-C---------------LTLK
BdRPD1    ----------------AATIQEP-------------------------------------
AtNRPD1   --------GHFGVINFAYSIINPYFLKEVAALLNKICPG-C---------------KYIR
CpRPD1    --------GHFGVIQFPYTILHPYYLSEVVQILNKVCPALI---------------HAIQ
PtRPD1    ANILLSLSGHFGVINFPYTIVHPYFLSEVVQILNKICPG-C---------------KSIR
VvRPD1    --------GHFGVIKFPFTILHPYFLTEVVQILNKICPG-C---------------KSTR
ZmRPE1    --------GHFGYIELPVPIYHPCHVTELRQLLSLICLK-C---------------LRIK
SbRPE1b   --------GHFGYIELPVPIFHPCHVSELRQLLSLICLK-C---------------LRIK
OsRPE1b   --------GHFGYIELPVPIYHPCHVTELRQILNVVCLK-C---------------LRVK
BdRPE1    --------GHFGYIELPVPIYHPCHVSELRQLLSLVCLK-C---------------LRIK
SbRPE1a   --------GHFGFIKLPEPIYHPSHIAELGKILNLVCLR-C---------------LRLK
OsRPE1a   --------GHFRFIELPMPIFHPSHVTELSQILNLICLR-C---------------LKIK
AtNRPE1   --------GHFGYIQLPVPIYHPAHVNELKQMLSLLCLK-C---------------LKIK
CpRPE1    -------------------VY------------SLLGIN-W---------------IMAG
PtRPE1a   --------GHFGYIDLPVPIYHPSHISELKRMLSLLCLK-C---------------LKLK
PtRPE1b   --------GHFGFIHLPIPIYHPSHISELKRMLSLICLK-C---------------LKLK
VvRPE1    --------GHFGYIELPIPIYHPGHVSELKRMLSLLCLK-C---------------LKIR
SmRPD1    --------GHSGHIELPVLVYHWDRISALEAILNRVCLH-C-----------YSFKHKGR
ZmRPB1    --------GHFGHLELAKPMFHIGFIKTVLSIMRCVCFN-CSKILADEDETKFKQALKIR
AtRPB1    --------GHFGYLELAKPMYHVGFMKTVLSIMRCVCFN-CSKILADE-------AMKIK
                  Domain A

                             200                 220                 240
ZmRPD1    EGIDTKRLEREKVQA--TCKY---------------------CSK---------------
SbRPD1    EGINMKRLGRETVQATSTCKY---------------------CSK---------------
OsRPD1b   QNGDTKKTDGTTIQT--TCKY---------------------CSK---------------
OsRPD1a   QNGDTKKADGTTIQG--TCKY---------------------CSK---------------
BdRPD1    ------------------CKY---------------------CSK---------------
AtNRPD1   KKQFQITED-----QPERCRY---------------------CTL---------------
CpRPD1    --------------------------------------------G---------------
PtRPD1    LAKATELIT-KENPQRKGCKY---------------------CAG---------------
VvRPD1    QGQWVKVRR----LRSKGCKY---------------------CAA---------------
ZmRPE1    KGKVKQSNG-KGNAAPTLCSY---------------------CRD---------------
SbRPE1b   KGKVKQSNG-KGNLSATLCSY---------------------CRD---------------
OsRPE1b   KGKVKQTEG-KDNTSALSCYY---------------------CRD---------------
BdRPE1    KGK-----------------------------------------D---------------
SbRPE1a   KPKKVTGKE----SRFTSCSY---------------------CQE---------------
OsRPE1a   NRKKSTLKG----SKFTSCSH---------------------CQE---------------
AtNRPE1   KAK--GTSG--GLADRLLGVC---------------------CEE---------------
CpRPE1    TSK--VKNA--GVAERLFSLC---------------------CEE---------------
PtRPE1a   RNKIQIKSN--GVAERLLS-C---------------------CEE---------------
PtRPE1b   RNKIQIKSN--GVAERLLS-C---------------------CEE---------------
VvRPE1    KSK--VTNN--GITEQLLAPC---------------------CQD---------------
SmRPD1    KKELRTLSSLEQVASGVDAHQADIGAVPNGARAPEAEENPGKCTG---------------
ZmRPB1    NPKNRLKRI---------YDA---------------------CKSKKVCAGGDDL-DVQE
AtRPB1    NPKNRLKKI---------LDA---------------------CKNKTKCDGGDDIDDVQS
                                                  *RMR6-8 (C to Y)
```

```
                           260                 280                 300
ZmRPD1    ------------DGSKLYPSIVFKTLSSPRVLLFKSKLHRNASVMERISIVAEAADRMPN
SbRPD1    ------------DGSKLYPSVIFKTLSSPRVLLSKSKLHRSPSVMERISIVAEAAERVSN
OsRPD1b   ------------DGAKLYPSVIFKMLTSPRVTLSRSKLHRNTSVMDKISIIAEVAGGVTH
OsRPD1a   ------------DGSKLYPSIIFKMLTSPRVTLSRSKLHRNTSVMDKMSIIAEVAGGVAH
BdRPD1    ------------DGL--YPSVIFKVLTSPRITLSKSKLQRNTSVMDKVSVTAEV----IN
AtNRPD1   ------------NTG--YPLMKFRVTTK--------------EVFRRSGIVVEVNEESLM
CpRPD1    ------------NSLNWYPPMKFKVLSE--------------DIFRLSAIMVEVNENVLR
PtRPD1    ------------NSLGWYPPMKFKVSSK--------------EIFRKTAIIAEIRETLSK
VvRPD1    ------------NSNDWYPTMKFKVSSK--------------DLFRKTAIIVEMNEKLPK
ZmRPE1    -----------------IPALSLKEIKT------------TDG-----AIRLELR-----
SbRPE1b   -----------------IPALSVKEVKT------------ADG-----AIRLELS-----
OsRPE1b   -----------------LPALSLKEIKT------------ADG-----AFRLELK-----
BdRPE1    -----------------VPALSLKEVKT------------ADG-----AFRLELR-----
SbRPE1a   -----------------LSPLCVSQVKK------------SNG-----ARSLELK-----
OsRPE1a   -----------------LPPLCVAEVKK------------SNG-----ARGLELR-----
AtNRPE1   -----------------ASQISIKD-RA------------SDG-----ASYLELK-----
CpRPE1    -----------------VSQVSIKEGKT------------PDD-----ACYLQLK-----
PtRPE1a   -----------------CAQISIREVKN------------TDG-----ACFLELK-----
PtRPE1b   -----------------CAQISIREVKN------------TDG-----ACFLELK-----
VvRPE1    -----------------SPQVSVREFRP------------TEG-----ACFLELK-----
SmRPD1    ------------------PAAAVKKIFK------------KVGTANVPALLLEID-----
ZmRPB1    QDTDEPIKK-RGGCGAQQPNITVDGMKM----------------------VAEFK-----
AtRPB1    HSTDEPVKKSRGGCGAQQPKLTIEGMKM----------------------IAEYK-----


                           320                 340                 360
ZmRPD1    RSKGKGSL-EGLPLDFWDFVPSENKQVQSNMT----------------------------
SbRPD1    RSKGKGLL-EGLPQDYWDFVPSENKQVQSNMT----------------------------
OsRPD1b   NSKNKAPH-ETLPQDFWDFVPDDNQPPQSNVA----------------------------
OsRPD1a   KSKNKAPH-ETLPQDFWDFIPDDNQPPIFNVT----------------------------
BdRPD1    MSKNKSSL-EVLPHDYWNFVP-HNQPPQPNTT----------------------------
AtNRPD1   KLKKRGVL--TLPPDYWSFLPQDSNIDESCLK----------------------------
CpRPD1    KFQ-KRRK-EALPADYWDFLPKDSHQEESGTR----------------------------
PtRPD1    KPQ-KGFK-KILAADYWDIFPKDEQEEEEETN----------------------------
VvRPD1    KLQKKSFR-PVLPLDYWDFIPKDPQQEENCLN----------------------------
ZmRPE1    APH----N-KHMTERSWNFLDKYGF---------HH------------------------
SbRPE1b   APH----K-RHMTERSWNFLDKYGF---------HH------------------------
OsRPE1b   MPP----R-KFMTEGSWNFLDKYGF---------HH------------------------
BdRPE1    APP----R-RLMKDSSWNFLDKYGF---------HH------------------------
SbRPE1a   LPL----K-QEVADGFWSFLDQFGF---------HT------------------------
OsRPE1a   API----K-KELEEGFWSFLDQFGS---------CT------------------------
AtNRPE1   LPS----R-SRLQPGCWNFIERYGY---------RY------------------------
CpRPE1    LPS----M-SRLRESFWNFLEKYGFSLRLCGLGSQI------------------------
PtRPE1a   LPS----R-SRLRDGCWNFLERYGF---------RYVFVTFEKYSYIHMPKVYAFMSKGV
PtRPE1b   LPS----R-SRLRDGCWNFLERYGF---------RY------------------------
VvRPE1    IPS----R-SRPKDGFWDFLARYGY---------RY------------------------
SmRPD1    ---GKVRR-EDIPPGFQSLILKDEMTP---------------------------------
ZmRPB1    APKKKTDDQDQLPEP---------------------------------------------
AtRPB1    NSKEENDEPDQLPEP---------------------------------------------
                         *RMR6-7 (W to X)
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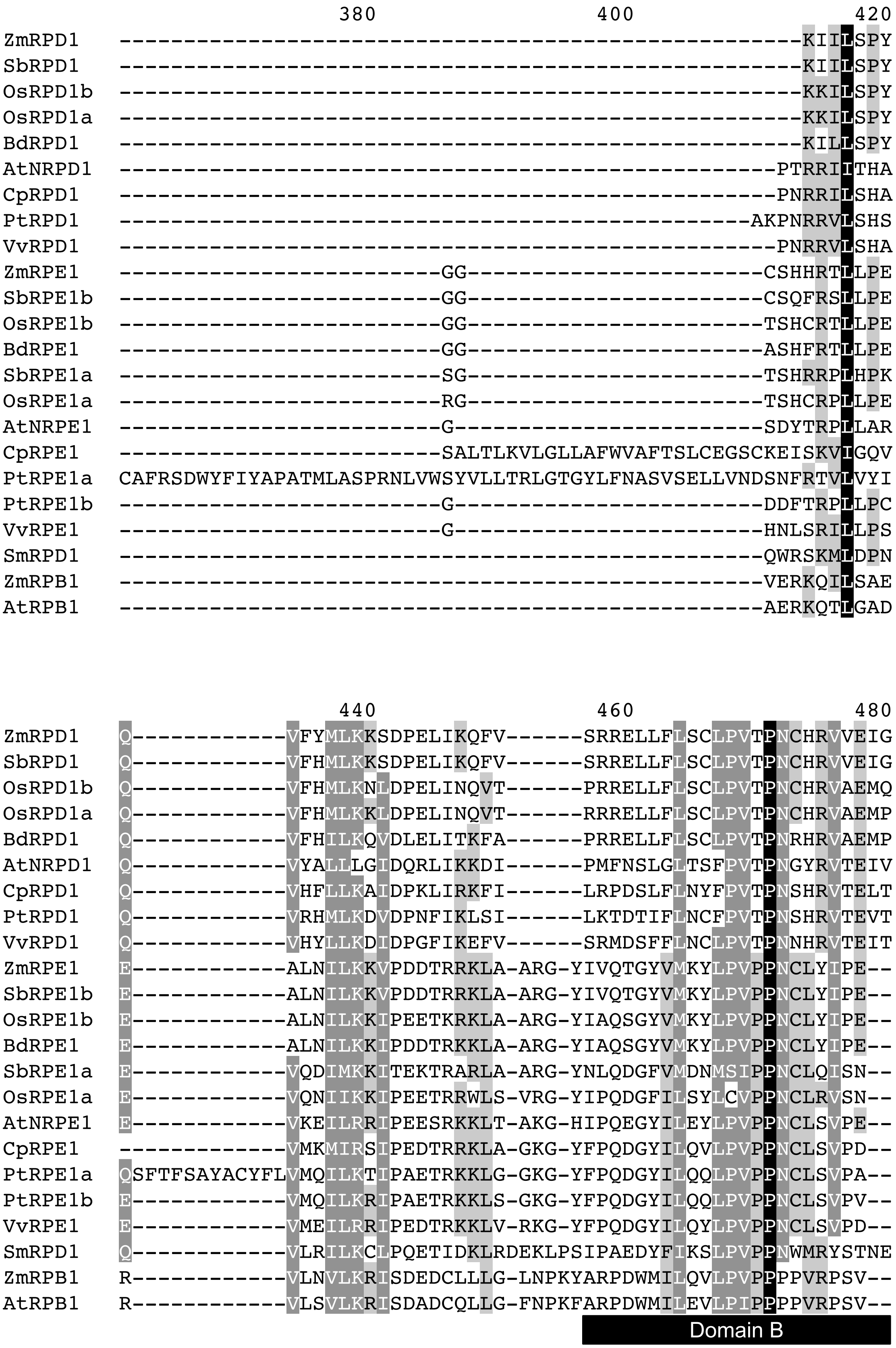

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                       380                 400                 420
ZmRPD1    -----------------------------------------------------KIILSPY
SbRPD1    -----------------------------------------------------KIILSPY
OsRPD1b   -----------------------------------------------------KKILSPY
OsRPD1a   -----------------------------------------------------KKILSPY
BdRPD1    -----------------------------------------------------KILLSPY
AtNRPD1   ---------------------------------------------------PTRRIITHA
CpRPD1    ---------------------------------------------------PNRRILSHA
PtRPD1    -------------------------------------------------AKPNRRVLSHS
VvRPD1    ---------------------------------------------------PNRRVLSHA
ZmRPE1    -------------------------GG-----------------------CSHHRTLLPE
SbRPE1b   -------------------------GG-----------------------CSQFRSLLPE
OsRPE1b   -------------------------GG-----------------------TSHCRTLLPE
BdRPE1    -------------------------GG-----------------------ASHFRTLLPE
SbRPE1a   -------------------------SG-----------------------TSHRRPLHPK
OsRPE1a   -------------------------RG-----------------------TSHCRPLLPE
AtNRPE1   -------------------------G------------------------SDYTRPLLAR
CpRPE1    -------------------------SALTLKVLGLLAFWVAFTSLCEGSCKEISKVIGQV
PtRPE1a   CAFRSDWYFIYAPATMLASPRNLVWSYVLLTRLGTGYLFNASVSELLVNDSNFRTVLVYI
PtRPE1b   -------------------------G------------------------DDFTRPLLPC
VvRPE1    -------------------------G------------------------HNLSRILLPS
SmRPD1    --------------------------------------------------QWRSKMLDPN
ZmRPB1    --------------------------------------------------VERKQILSAE
AtRPB1    --------------------------------------------------AERKQTLGAD

                       440                 460                 480
ZmRPD1    Q------------VFYMLKKSDPELIKQFV------SRRELLFLSCLPVTPNCHRVVEIG
SbRPD1    Q------------VFHMLKKSDPELIKQFV------SRRELLFLSCLPVTPNCHRVVEIG
OsRPD1b   Q------------VFHMLKNLDPELINQVT------PRRELLFLSCLPVTPNCHRVAEMQ
OsRPD1a   Q------------VFHMLKKLDPELINQVT------RRRELLFLSCLPVTPNCHRVAEMP
BdRPD1    Q------------VFHILKQVDLELITKFA------PRRELLFLSCLPVTPNRHRVAEMP
AtNRPD1   Q------------VYALLLGIDQRLIKKDI------PMFNSLGLTSFPVTPNGYRVTEIV
CpRPD1    Q------------VHFLLKAIDPKLIRKFI------LRPDSLFLNYFPVTPNSHRVTELT
PtRPD1    Q------------VRHMLKDVDPNFIKLSI------LKTDTIFLNCFPVTPNSHRVTEVT
VvRPD1    Q------------VHYLLKDIDPGFIKEFV------SRMDSFFLNCLPVTPNNHRVTEIT
ZmRPE1    E------------ALNILKKVPDDTRRKLA-ARG-YIVQTGYVMKYLPVPPNCLYIPE--
SbRPE1b   E------------ALNILKKVPDDTRRKLA-ARG-YIVQTGYVMKYLPVPPNCLYIPE--
OsRPE1b   E------------ALNILKKIPEETKRKLA-ARG-YIAQSGYVMKYLPVPPNCLYIPE--
BdRPE1    E------------ALNILKKIPDDTRKKLA-ARG-YIAQSGYVMKYLPVPPNCLYIPE--
SbRPE1a   E------------VQDIMKKITEKTRARLA-ARG-YNLQDGFVMDNMSIPPNCLQISN--
OsRPE1a   E------------VQNIIKKIPEETRRWLS-VRG-YIPQDGFILSYLCVPPNCLRVSN--
AtNRPE1   E------------VKEILRRIPEESRKKLT-AKG-HIPQEGYILEYLPVPPNCLSVPE--
CpRPE1    -------------VMKMIRSIPEDTRRKLA-GKG-YFPQDGYILQVLPVPPNCLSVPD--
PtRPE1a   QSFTFSAYACYFLVMQILKTIPAETRKKLG-GKG-YFPQDGYILQQLPVPPNCLSVPA--
PtRPE1b   E------------VMQILKRIPAETRKKLS-GKG-YFPQDGYILQQLPVPPNCLSVPV--
VvRPE1    E------------VMEILRRIPEDTRKKLV-RKG-YFPQDGYILQYLPVPPNCLSVPD--
SmRPD1    Q------------VLRILKCLPQETIDKLRDEKLPSIPAEDYFIKSLPVPPNWMRYSTNE
ZmRPB1    R------------VLNVLKRISDEDCLLLG-LNPKYARPDWMILQVLPVPPPPVRPSV--
AtRPB1    R------------VLSVLKRISDADCQLLG-FNPKFARPDWMILEVLPIPPPPVRPSV--
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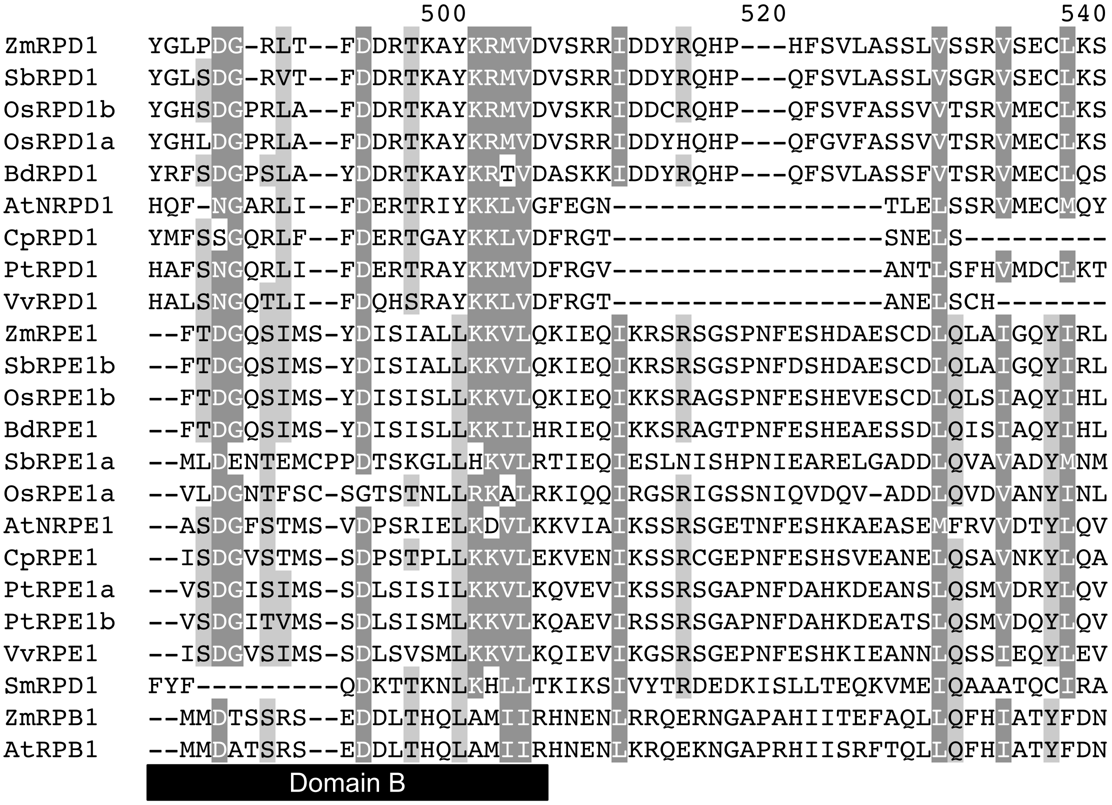

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                                  500             520                 540
ZmRPD1     YGLPDG-RLT--FDDRTKAYKRMVDVSRRIDDYRQHP---HFSVLASSLVSSRVSECLKS
SbRPD1     YGLSDG-RVT--FDDRTKAYKRMVDVSRRIDDYRQHP---QFSVLASSLVSGRVSECLKS
OsRPD1b    YGHSDGPRLA--FDDRTKAYKRMVDVSKRIDDCRQHP---QFSVFASSVVTSRVMECLKS
OsRPD1a    YGHLDGPRLA--FDDRTKAYKRMVDVSRRIDDYHQHP---QFGVFASSVVTSRVMECLKS
BdRPD1     YRFSDGPSLA--YDDRTKAYKRTVDASKKIDDYRQHP---QFSVLASSFVTSRVMECLQS
AtNRPD1    HQF-NGARLI--FDERTRIYKKLVGFEGN-----------------TLELSSRVMECMQY
CpRPD1     YMFSSGQRLF--FDERTGAYKKLVDFRGT-----------------SNELS---------
PtRPD1     HAFSNGQRLI--FDERTRAYKKMVDFRGV-----------------ANTLSFHVMDCLKT
VvRPD1     HALSNGQTLI--FDQHSRAYKKLVDFRGT-----------------ANELSCH-------
ZmRPE1     --FTDGQSIMS-YDISIALLKKVLQKIEQIKRSRSGSPNFESHDAESCDLQLAIGQYIRL
SbRPE1b    --FTDGQSIMS-YDISIALLKKVLQKIEQIKRSRSGSPNFDSHDAESCDLQLAIGQYIRL
OsRPE1b    --FTDGQSIMS-YDISISLLKKVLQKIEQIKKSRAGSPNFESHEVESCDLQLSIAQYIHL
BdRPE1     --FTDGQSIMS-YDISISLLKKILHRIEQIKKSRAGTPNFESHEAESSDLQISIAQYIHL
SbRPE1a    --MLDENTEMCPPDTSKGLLHKVLRTIEQIESLNISHPNIEARELGADDLQVAVADYMNM
OsRPE1a    --VLDGNTFSC-SGTSTNLLRKALRKIQQIRGSRIGSSNIQVDQV-ADDLQVDVANYINL
AtNRPE1    --ASDGFSTMS-VDPSRIELKDVLKKVIAIKSSRSGETNFESHKAEASEMFRVVDTYLQV
CpRPE1     --ISDGVSTMS-SDPSTPLLKKVLEKVENIKSSRCGEPNFESHSVEANELQSAVNKYLQA
PtRPE1a    --VSDGISIMS-SDLSISILKKVLKQVEVIKSSRSGAPNFDAHKDEANSLQSMVDRYLQV
PtRPE1b    --VSDGITVMS-SDLSISMLKKVLKQAEVIRSSRSGAPNFDAHKDEATSLQSMVDQYLQV
VvRPE1     --ISDGVSIMS-SDLSVSMLKKVLKQIEVIKGSRSGEPNFESHKIEANNLQSSIEQYLEV
SmRPD1     FYF---------QDKTTKNLKHLLTKIKSIVYTRDEDKISLLTEQKVMEIQAAATQCIRA
ZmRPB1     --MMDTSSRS--EDDLTHQLAMIIRHNENLRRQERNGAPAHIITEFAQLLQFHIATYFDN
AtRPB1     --MMDATSRS--EDDLTHQLAMIIRHNENLKRQEKNGAPRHIISRFTQLLQFHIATYFDN
```

```
                                  560             580                 600
ZmRPD1     SKLYSKKADGE-------------TSTDTYGMKWLKDVVLSKRSDNVFRSIMVGDPKIKL
SbRPD1     SKLYSKKTDGE-------------TSTDPSGMKWLKDAVLSKRSDNAFRSTMVGDPKIKL
OsRPD1b    SKLYSRKSDGE-----------DPTSPDTYGTKWLKDIILSKRSDNAFRSIMVGDPKINL
OsRPD1a    SKLYSKKSDDE-----------SSASTDTYGTKWLKDIILSKRSDNAFRSIMVGDPKINL
BdRPD1     SKLYSKKTDKE-------------SSTDSYGT---SDAILSKRSDYAFRSIMVGDPKIRL
AtNRPD1    SRLFSETVSSSKDSANPYQK--KSDTPKLCGLRFMKDVLLGKRSDHTFRTVVVGDPSLKL
CpRPD1     SRLHTFKSSSK-DATTALLK--NEDSSNMVGLRYMKDVLLGKRNDSSFRTVVIGDRSLKL
PtRPD1     SKLNPDKSGNI-DPWTAQPKKSNDYVNNASGLRWIKDVVLGKRNDHSFRMVIVGDPHLQL
VvRPD1     ------------------------SASKMSGLKWIKEVLLGKRTNHSFRMIVVGDPKLRL
ZmRPE1     RG--TTRGPQDNTKRFTVGSADSAALSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGL
SbRPE1b    RG--TTRGPQDNTKRFTVGSADSAALSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGL
OsRPE1b    RG--TTRGPQDNTKRFAI-STDPSALSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGV
BdRPE1     RG--TTK-------RFTI-STDSSHLSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGV
SbRPE1a    GG--AAKVSQH--------VTFTRQPAPKQWHKKMKTLFLSKSSSYTCRAVITGDPYIGL
OsRPE1a    GG--TTKGHGD--------DTFTSQPTAMQWKQKMKTLFISKSSSFSSRGVITGDPYIGL
AtNRPE1    RG--TAKAARNIDMRYGV-SKISDSSSSKAWTEKMRTLFIRKGSGFSSRSVITGDAYRHV
CpRPE1     RG--TAKASRE-DTRYGV-SKNSNDCSTKAWLEKMRTLFIRKGSGFSSRSVITGDPYKKV
PtRPE1a    RG--TTKTSRDVDVRYGV-KKDSSESSTKAWLEKMRTLFIRKGSGFSSRSVITGDAYTKV
PtRPE1b    RG--TTKTSRDVDTRYGV-KKESSESTTKAWLEKMRTLFIRKGSGFSSRSVITGDAYTLV
VvRPE1     RG--TAKTSRSLDTRFGS-SKEPNESSTKAWLEKMRTLFIRKGSGFSSRSVITGDAYKRV
SmRPD1     NPLYGNVSDEDPRY-----GNVSDESKPLSGLHFLRS-LTGKYCGSSARAVVIGDPALKL
ZmRPB1     DLPGQPRATQRSGRPI---KSICSRLKAKEG--RIRGNLMGKRVDFSARTVITPDPNINI
AtRPB1     ELPGQPRATQKSGRPI---KSICSRLKAKEG--RIRGNLMGKRVDFSARTVITPDPTINI
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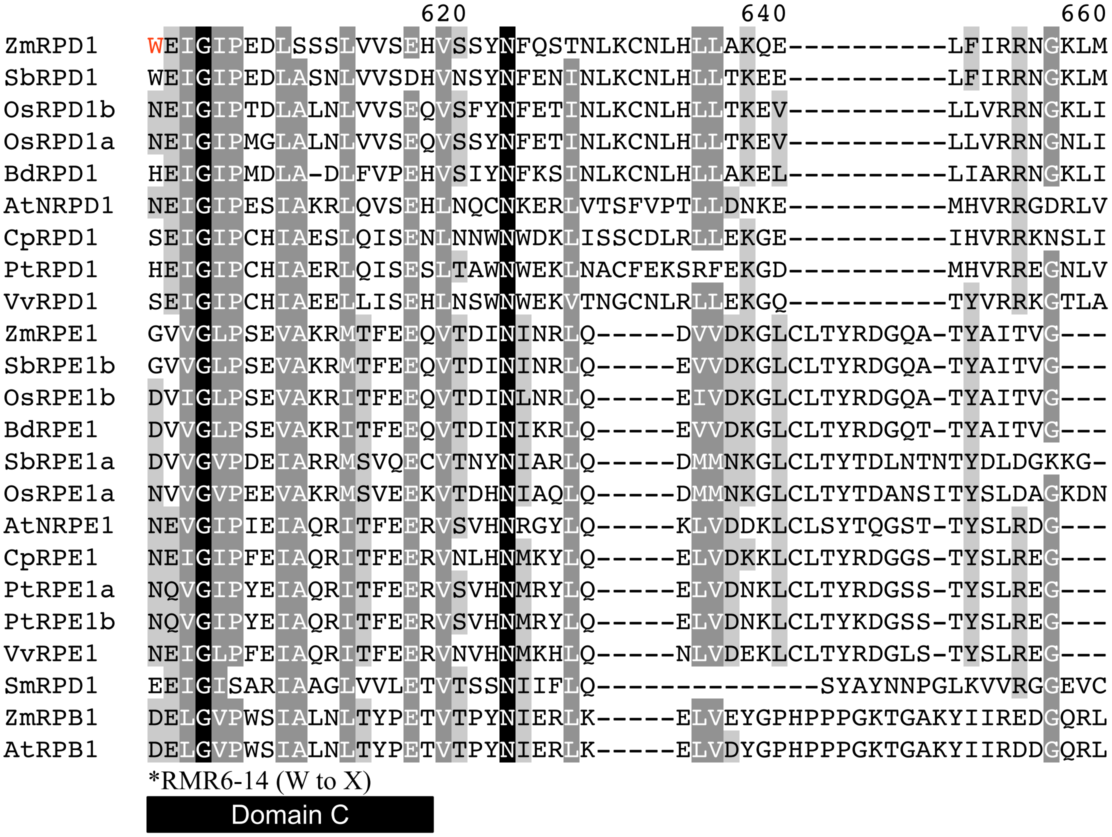

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                                   620                 640                 660
ZmRPD1   WEIGIPEDLSSSLVVSEHVSSYNFQSTNLKCNLHLLAKQE----------LFIRRNGKLM
SbRPD1   WEIGIPEDLASNLVVSDHVNSYNFENINLKCNLHLLTKEE----------LFIRRNGKLM
OsRPD1b  NEIGIPTDLALNLVVSEQVSFYNFETINLKCNLHLLTKEV----------LLVRRNGKLI
OsRPD1a  NEIGIPMGLALNLVVSEQVSSYNFETINLKCNLHLLTKEV----------LLVRRNGNLI
BdRPD1   HEIGIPMDLA-DLFVPEHVSIYNFKSINLKCNLHLIAKEL----------LIARRNGKLI
AtNRPD1  NEIGIPESIAKRLQVSEHLNQCNKERLVTSFVPTLLDNKE----------MHVRRGDRLV
CpRPD1   SEIGIPCHIAESLQISENLNNWNWDKLISSCDLRLLEKGE----------IHVRRKNSLI
PtRPD1   HEIGIPCHIAERLQISESLTAWNWEKLNACFEKSRFEKGD----------MHVRREGNLV
VvRPD1   SEIGIPCHIAEELLISEHLNSWNWEKVTNGCNLRLLEKGQ----------TYVRRKGTLA
ZmRPE1   GVVGLPSEVAKRMTFEEQVTDININRLQ-----DVVDKGLCLTYRDGQA-TYAITVG---
SbRPE1b  GVVGLPSEVAKRMTFEEQVTDININRLQ-----EVVDKGLCLTYRDGQA-TYAITVG---
OsRPE1b  DVIGLPSEVAKRITFEEQVTDINLNRLQ-----EIVDKGLCLTYRDGQA-TYAITVG---
BdRPE1   DVVGLPSEVAKRITFEEQVTDINIKRLQ-----EVVDKGLCLTYRDGQT-TYAITVG---
SbRPE1a  DVVGVPDEIARRMSVQECVTNYNIARLQ-----DMMNKGLCLTYTDLNTNTYDLDGKKG-
OsRPE1a  NVVGVPEEVAKRMSVEEKVTDHNIAQLQ-----DMMNKGLCLTYTDANSITYSLDAGKDN
AtNRPE1  NEVGIPIEIAQRITFEERVSVHNRGYLQ-----KLVDDKLCLSYTQGST-TYSLRDG---
CpRPE1   NEIGIPFEIAQRITFEERVNLHNMKYLQ-----ELVDKKLCLTYRDGGS-TYSLREG---
PtRPE1a  NQVGIPYEIAQRITFEERVSVHNMRYLQ-----ELVDNKLCLTYRDGSS-TYSLREG---
PtRPE1b  NQVGIPYEIAQRITFEERVSVHNMRYLQ-----ELVDNKLCLTYKDGSS-TYSLREG---
VvRPE1   NEIGLPFEIAQRITFEERVNVHNMKHLQ-----NLVDEKLCLTYRDGLS-TYSLREG---
SmRPD1   EEIGISARIAAGLVVLETVTSSNIIFLQ--------------SYAYNNPGLKVVRGGEVC
ZmRPB1   DELGVPWSIALNLTYPETVTPYNIERLK-----ELVEYGPHPPPGKTGAKYIIREDGQRL
AtRPB1   DELGVPWSIALNLTYPETVTPYNIERLK-----ELVDYGPHPPPGKTGAKYIIRDDGQRL
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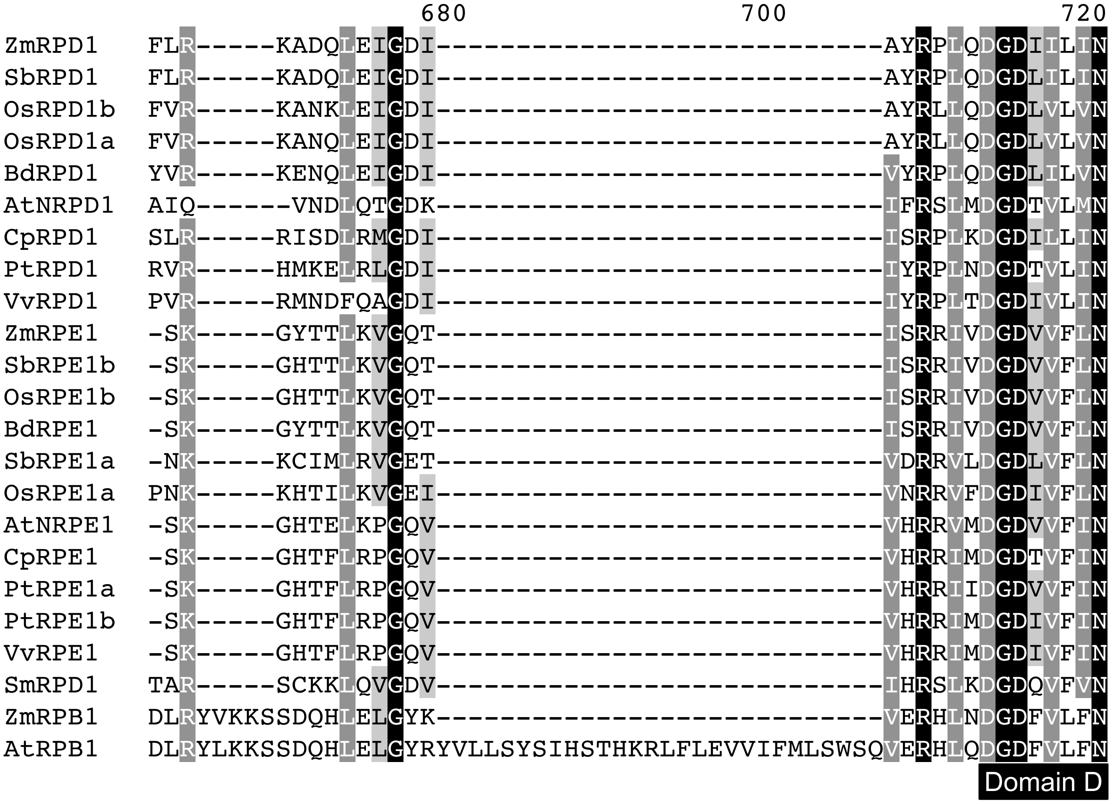

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                                   680                 700                 720
ZmRPD1   FLR-----KADQLEIGDI----------------------------AYRPLQDGDIILIN
SbRPD1   FLR-----KADQLEIGDI----------------------------AYRPLQDGDLILIN
OsRPD1b  FVR-----KANKLEIGDI----------------------------AYRLLQDGDLVLVN
OsRPD1a  FVR-----KANQLEIGDI----------------------------AYRLLQDGDLVLVN
BdRPD1   YVR-----KENQLEIGDI----------------------------VYRPLQDGDLILVN
AtNRPD1  AIQ------VNDLQTGDK----------------------------IFRSLMDGDTVLMN
CpRPD1   SLR-----RISDLRMGDI----------------------------ISRPLKDGDILLIN
PtRPD1   RVR-----HMKELRLGDI----------------------------IYRPLNDGDTVLIN
VvRPD1   PVR-----RMNDFQAGDI----------------------------IYRPLTDGDIVLIN
ZmRPE1   -SK-----GYTTLKVGQT----------------------------ISRRIVDGDVVFLN
SbRPE1b  -SK-----GHTTLKVGQT----------------------------ISRRIVDGDVVFLN
OsRPE1b  -SK-----GHTTLKVGQT----------------------------ISRRIVDGDVVFLN
BdRPE1   -SK-----GYTTLKVGQT----------------------------ISRRIVDGDVVFLN
SbRPE1a  -NK-----KCIMLRVGET----------------------------VDRRVLDGDLVFLN
OsRPE1a  PNK-----KHTILKVGEI----------------------------VNRRVFDGDIVFLN
AtNRPE1  -SK-----GHTELKPGQV----------------------------VHRRVMDGDVVFIN
CpRPE1   -SK-----GHTFLRPGQV----------------------------VHRRIMDGDTVFIN
PtRPE1a  -SK-----GHTFLRPGQV----------------------------VHRRIIDGDVVFIN
PtRPE1b  -SK-----GHTFLRPGQV----------------------------VHRRIMDGDIVFIN
VvRPE1   -SK-----GHTFLRPGQV----------------------------VHRRIMDGDIVFIN
SmRPD1   TAR-----SCKKLQVGDV----------------------------IHRSLKDGDQVFVN
ZmRPB1   DLRYVKKSSDQHLELGYK----------------------------VERHLNDGDFVLFN
AtRPB1   DLRYLKKSSDQHLELGYRYVLLSYSIHSTHKRLFLEVVIFMLSWSQVERHLQDGDFVLFN
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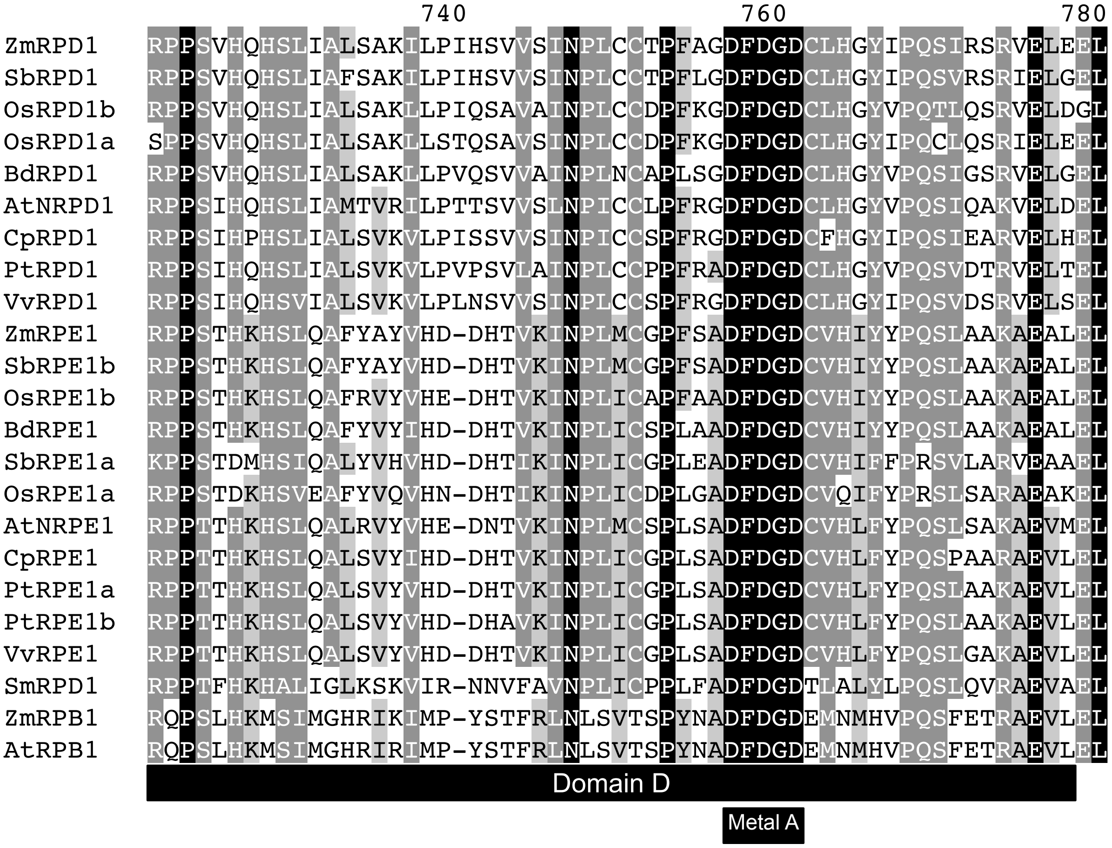

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OsRPD1b   RPPSVHQHSLIALSAKLLPIQSAVAINPLCCDPFKGDFDGDCLHGYVPQTLQSRVELDGL
OsRPD1a   SPPSVHQHSLIALSAKLLSTQSAVSINPLCCDPFKGDFDGDCLHGYIPQCLQSRIELEEL
BdRPD1    RPPSVHQHSLIALSAKLLPVQSVVAINPLNCAPLSGDFDGDCLHGYVPQSIGSRVELGEL
AtNRPD1   RPPSIHQHSLIAMTVRILPTTSVVSLNPICCLPFRGDFDGDCLHGYVPQSIQAKVELDEL
CpRPD1    RPPSIHPHSLIALSVKVLPISSVVSINPICCSPFRGDFDGDCFHGYIPQSIEARVELHEL
PtRPD1    RPPSIHQHSLIALSVKVLPVPSVLAINPLCCPPFRADFDGDCLHGYVPQSVDTRVELTEL
VvRPD1    RPPSIHQHSVIALSVKVLPLNSVVSINPLCCSPFRGDFDGDCLHGYIPQSVDSRVELSEL
ZmRPE1    RPPSTHKHSLQAFYAYVHD-DHTVKINPLMCGPFSADFDGDCVHIYYPQSLAAKAEALEL
SbRPE1b   RPPSTHKHSLQAFYAYVHD-DHTVKINPLMCGPFSADFDGDCVHIYYPQSLAAKAEALEL
OsRPE1b   RPPSTHKHSLQAFRVYVHE-DHTVKINPLICAPFAADFDGDCVHIYYPQSLAAKAEALEL
BdRPE1    RPPSTHKHSLQAFYVYIHD-DHTVKINPLICSPLAADFDGDCVHIYYPQSLAAKAEALEL
SbRPE1a   KPPSTDMHSIQALYVHVHD-DHTIKINPLICGPLEADFDGDCVHIFFPRSVLARVEAAEL
OsRPE1a   RPPSTDKHSVEAFYVQVHN-DHTIKINPLICDPLGADFDGDCVQIFYPRSLSARAEAKEL
AtNRPE1   RPPTTHKHSLQALRVYVHE-DNTVKINPLMCSPLSADFDGDCVHLFYPQSLSAKAEVMEL
CpRPE1    RPPTTHKHSLQALSVYIHD-DHTVKINPLICGPLSADFDGDCVHLFYPQSPAARAEVLEL
PtRPE1a   RPPTTHKHSLQALSVYVHD-DHTVKINPLICGPLSADFDGDCVHLFYPQSLAAKAEVLEL
PtRPE1b   RPPTTHKHSLQALSVYVHD-DHAVKINPLICGPLSADFDGDCVHLFYPQSLAAKAEVLEL
VvRPE1    RPPTTHKHSLQALSVYVHD-DHTVKINPLICGPLSADFDGDCVHLFYPQSLGAKAEVLEL
SmRPD1    RPPTFHKHALIGLKSKVIR-NNVFAVNPLICPPLFADFDGDTLALYLPQSLQVRAEVAEL
ZmRPB1    RQPSLHKMSIMGHRIKIMP-YSTFRLNLSVTSPYNADFDGDEMNMHVPQSFETRAEVLEL
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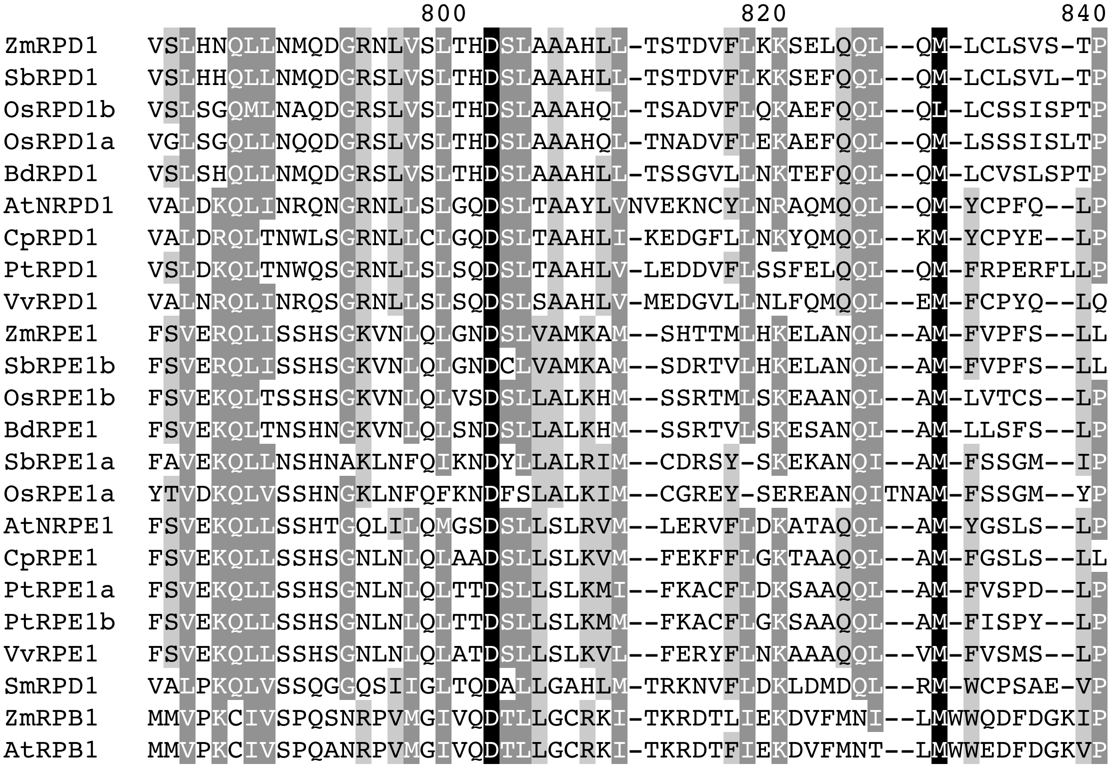

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OsRPD1b   VSLSGQMLNAQDGRSLVSLTHDSLAAAHQL-TSADVFLQKAEFQQL--QL-LCSSISPTP
OsRPD1a   VGLSGQLLNQQDGRSLVSLTHDSLAAAHQL-TNADVFLEKAEFQQL--QM-LSSSISLTP
BdRPD1    VSLSHQLLNMQDGRSLVSLTHDSLAAAHLL-TSSGVLLNKTEFQQL--QM-LCVSLSPTP
AtNRPD1   VALDKQLINRQNGRNLLSLGQDSLTAAYLVNVEKNCYLNRAQMQQL--QM-YCPFQ--LP
CpRPD1    VALDRQLTNWLSGRNLLCLGQDSLTAAHLI-KEDGFLLNKYQMQQL--KM-YCPYE--LP
PtRPD1    VSLDKQLTNWQSGRNLLSLSQDSLTAAHLV-LEDDVFLSSFELQQL--QM-FRPERFLLP
VvRPD1    VALNRQLINRQSGRNLLSLSQDSLSAAHLV-MEDGVLLNLFQMQQL--EM-FCPYQ--LQ
ZmRPE1    FSVERQLISSHSGKVNLQLGNDSLVAMKAM--SHTTMLHKELANQL--AM-FVPFS--LL
SbRPE1b   FSVERQLISSHSGKVNLQLGNDCLVAMKAM--SDRTVLHKELANQL--AM-FVPFS--LL
OsRPE1b   FSVEKQLTSSHSGKVNLQLVSDSLLALKHM--SSRTMLSKEAANQL--AM-LVTCS--LP
BdRPE1    FSVEKQLTNSHNGKVNLQLSNDSLLALKHM--SSRTVLSKESANQL--AM-LLSFS--LP
SbRPE1a   FAVEKQLLNSHNAKLNFQIKNDYLLALRIM--CDRSY-SKEKANQI--AM-FSSGM--IP
OsRPE1a   YTVDKQLVSSHNGKLNFQFKNDFSLALKIM--CGREY-SEREANQITNAM-FSSGM--YP
AtNRPE1   FSVEKQLLSSHTGQLILQMGSDSLLSLRVM--LERVFLDKATAQQL--AM-YGSLS--LP
CpRPE1    FSVEKQLLSSHSGNLNLQLAADSLLSLKVM--FEKFFLGKTAAQQL--AM-FGSLS--LL
PtRPE1a   FSVEKQLLSSHSGNLNLQLTTDSLLSLKMI--FKACFLDKSAAQQL--AM-FVSPD--LP
PtRPE1b   FSVEKQLLSSHSGNLNLQLTTDSLLSLKMM--FKACFLGKSAAQQL--AM-FISPY--LP
VvRPE1    FSVEKQLLSSHSGNLNLQLATDSLLSLKVL--FERYFLNKAAAQQL--VM-FVSMS--LP
SmRPD1    VALPKQLVSSQGGQSIIGLTQDALLGAHLM-TRKNVFLDKLDMDQL--RM-WCPSAE-VP
ZmRPB1    MMVPKCIVSPQSNRPVMGIVQDTLLGCRKI-TKRDTLIEKDVFMNI--LMWWQDFDGKIP
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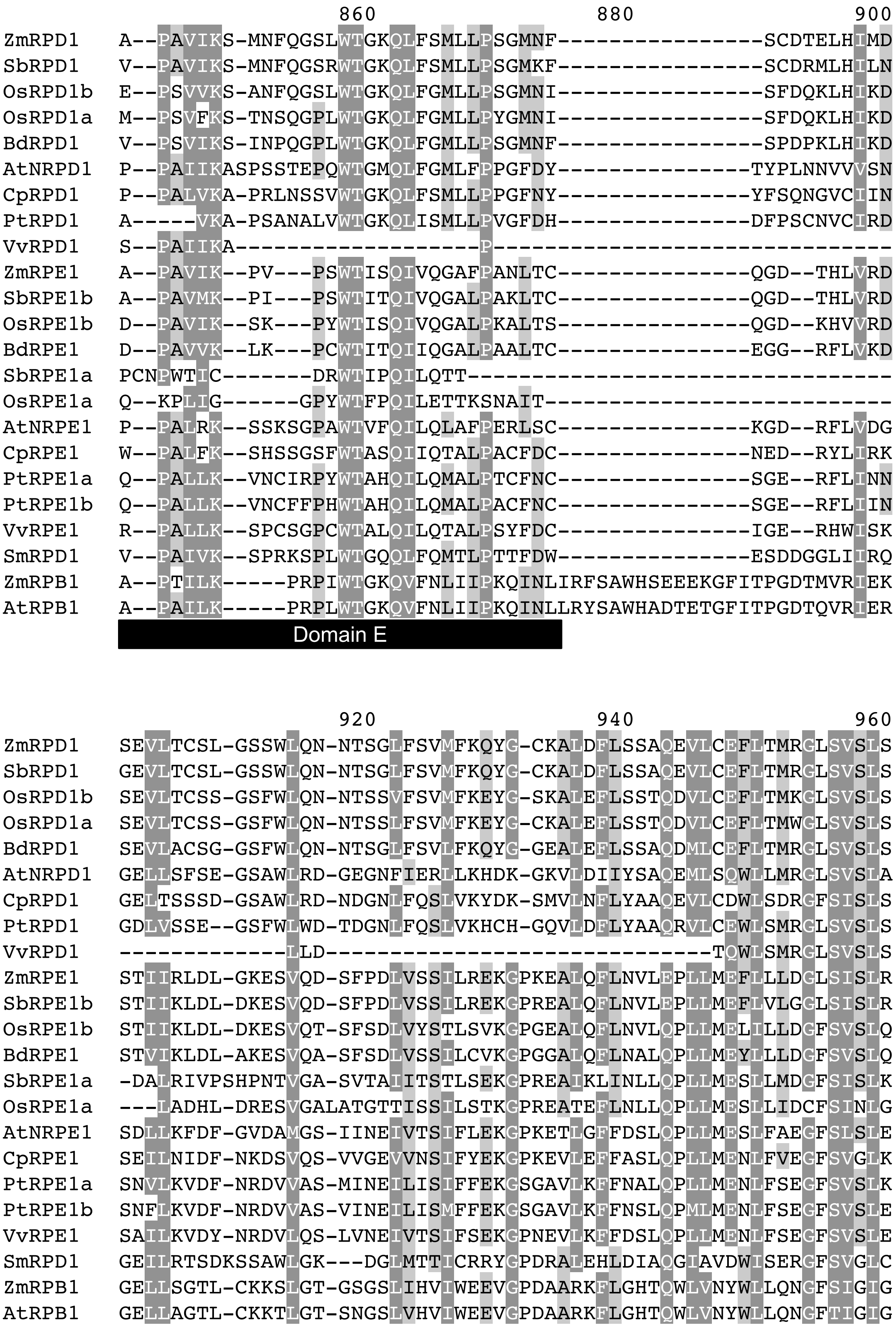

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OsRPD1b    E--PSVVKS-ANFQGSLWTGKQLFGMLLPSGMNI----------------SFDQKLHIKD
OsRPD1a    M--PSVFKS-TNSQGPLWTGKQLFGMLLPYGMNI----------------SFDQKLHIKD
BdRPD1     V--PSVIKS-INPQGPLWTGKQLFGMLLPSGMNF----------------SPDPKLHIKD
AtNRPD1    P--PAIIKASPSSTEPQWTGMQLFGMLFPPGFDY---------------TYPLNNVVVSN
CpRPD1     P--PALVKA-PRLNSSVWTGKQLFSMLLPPGFNY---------------YFSQNGVCIIN
PtRPD1     A-----VKA-PSANALVWTGKQLISMLLPVGFDH---------------DFPSCNVCIRD
VvRPD1     S--PAIIKA-------------------P-------------------------------
ZmRPE1     A--PAVIK--PV---PSWTISQIVQGAFPANLTC---------------QGD--THLVRD
SbRPE1b    A--PAVMK--PI---PSWTITQIVQGALPAKLTC---------------QGD--THLVRD
OsRPE1b    D--PAVIK--SK---PYWTISQIVQGALPKALTS---------------QGD--KHVVRD
BdRPE1     D--PAVVK--LK---PCWTITQIIQGALPAALTC---------------EGG--RFLVKD
SbRPE1a    PCNPWTIC-------DRWTIPQILQTT---------------------------------
OsRPE1a    Q--KPLIG------GPYWTFPQILETTKSNAIT---------------------------
AtNRPE1    P--PALRK--SSKSGPAWTVFQILQLAFPERLSC---------------KGD--RFLVDG
CpRPE1     W--PALFK--SHSSGSFWTASQIIQTALPACFDC---------------NED--RYLIRK
PtRPE1a    Q--PALLK--VNCIRPYWTAHQILQMALPTCFNC---------------SGE--RFLINN
PtRPE1b    Q--PALLK--VNCFFPHWTAHQILQMALPACFNC---------------SGE--RFLIIN
VvRPE1     R--PALLK--SPCSGPCWTALQILQTALPSYFDC---------------IGE--RHWISK
SmRPD1     V--PAIVK--SPRKSPLWTGQQLFQMTLPTTFDW---------------ESDDGGLIIRQ
ZmRPB1     A--PTILK-----PRPIWTGKQVFNLIIPKQINLIRFSAWHSEEEKGFITPGDTMVRIEK
AtRPB1     A--PAILK-----PRPLWTGKQVFNLIIPKQINLLRYSAWHADTETGFITPGDTQVRIER
           ------------- Domain E -----------

                              920                 940                 960
ZmRPD1     SEVLTCSL-GSSWLQN-NTSGLFSVMFKQYG-CKALDFLSSAQEVLCEFLTMRGLSVSLS
SbRPD1     GEVLTCSL-GSSWLQN-NTSGLFSVMFKQYG-CKALDFLSSAQEVLCEFLTMRGLSVSLS
OsRPD1b    SEVLTCSS-GSFWLQN-NTSSVFSVMFKEYG-SKALEFLSSTQDVLCEFLTMKGLSVSLS
OsRPD1a    SEVLTCSS-GSFWLQN-NTSSLFSVMFKEYG-CKALEFLSSTQDVLCEFLTMWGLSVSLS
BdRPD1     SEVLACSG-GSFWLQN-NTSGLFSVLFKQYG-GEALEFLSSAQDMLCEFLTMRGLSVSLS
AtNRPD1    GELLSFSE-GSAWLRD-GEGNFIERLLKHDK-GKVLDIIYSAQEMLSQWLLMRGLSVSLA
CpRPD1     GELTSSSD-GSAWLRD-NDGNLFQSLVKYDK-SMVLNFLYAAQEVLCDWLSDRGFSISLS
PtRPD1     GDLVSSE--GSFWLWD-TDGNLFQSLVKHCH-GQVLDFLYAAQRVLCEWLSMRGLSVSLS
VvRPD1     -------------LLD------------------------------TQWLSMRGLSVSLS
ZmRPE1     STIIRLDL-GKESVQD-SFPDLVSSILREKGPKEALQFLNVLEPLLMEFLLLDGLSISLR
SbRPE1b    STIIKLDL-DKESVQD-SFPDLVSSILREKGPREALQFLNVLEPLLMEFLVLGGLSISLR
OsRPE1b    STIIKLDL-DKESVQT-SFSDLVYSTLSVKGPGEALQFLNVLQPLLMELILLDGFSVSLQ
BdRPE1     STVIKLDL-AKESVQA-SFSDLVSSILCVKGPGGALQFLNALQPLLMEYLLLDGFSVSLQ
SbRPE1a    -DALRIVPSHPNTVGA-SVTAIITSTLSEKGPREAIKLINLLQPLLMESLLMDGFSISLK
OsRPE1a    ---LADHL-DRESVGALATGTTISSILSTKGPREATEFLNLLQPLLMESLLIDCFSINLG
AtNRPE1    SDLLKFDF-GVDAMGS-IINEIVTSIFLEKGPKETLGFFDSLQPLLMESLFAEGFSLSLE
CpRPE1     SEILNIDF-NKDSVQS-VVGEVVNSIFYEKGPKEVLEFFASLQPLLMENLFVEGFSVGLK
PtRPE1a    SNVLKVDF-NRDVVAS-MINEILISIFFEKGSGAVLKFFNALQPLLMENLFSEGFSVSLK
PtRPE1b    SNFLKVDF-NRDVVAS-VINEILISMFFEKGSGAVLKFFNSLQPMLMENLFSEGFSVSLE
VvRPE1     SAILKVDY-NRDVLQS-LVNEIVTSIFSEKGPNEVLKFFDSLQPLLMENLFSEGFSVSLE
SmRPD1     GEILRTSDKSSAWLGK---DGLMTTICRRYGPDRALEHLDIAQGIAVDWISERGFSVGLC
ZmRPB1     GELLSGTL-CKKSLGT-GSGSLIHVIWEEVGPDAARKFLGHTQWLVNYWLLQNGFSIGIG
AtRPB1     GELLAGTL-CKKTLGT-SNGSLVHVIWEEVGPDAARKFLGHTQWLVNYWLLQNGFTIGIG
```

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                           980                1000                1020
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SbRPD1    D--MFSDHYSR-RKLTEGVKLALDEAEEAFRIKQILLDPINIPVLKCQDETED-------
OsRPD1b   DFYLFSDHYSR-KKLSEEIHLALDEAEEAFQIKQILLNTVSIPNLKHYDGPDN-------
OsRPD1a   DLYLFSDHYSR-RKLSEEVHLALDEAEEAFQIKQILLNSVSIPNLKYYDGGDD-------
BdRPD1    DIYLFSDHYSR-RKFAEEVNLALDEAEEAFRVTQILLSPNFIPHLKCYDDCDD-------
AtNRPD1   DLYLSSDLQSR-KNLTEEISYGLREAEQVCNKQQLMVESWRDFLAVNGEDKEEDS-----
CpRPD1    DLYLSSDLHSR-ENLMDEISWGLLEAEQTCNFKQLMVDSCRDLLAGNDEESQNVI-----
PtRPD1    DLYLCPDSNSR-KNMMDEIWYGLQDADYACNLKHLMVDSCRDFLTGNNEEDQCNVERLRF
VvRPD1    DIYLSSDSISR-KNMIDEVFCGLLVAEQTCHFKQLLVDSSQNFLIGSGENNQNGV-----
ZmRPE1    DFNVPK----------------ALLEEAQKD-IRNQSL----------------------
SbRPE1b   DFNVPK----------------ALLEEAQKN-IQNQSL----------------------
OsRPE1b   DFNVPK----------------VLLEEAQKN-IEKQSL----------------------
BdRPE1    DFNVPK----------------VLLEEVHKS-IQEQSL----------------------
SbRPE1a   DLDGQS----------------AMQKANQSISLE--------------------------
OsRPE1a   DFTVPS----------------PILEAIQNNPLE--------------------------
AtNRPE1   DLSMSR----------------ADMDVIHNLIIREISP----------------------
CpRPE1    DFSMPK----------------SDMQAIQKL-IHDTSL----------------------
PtRPE1a   DFSISQ----------------AVKQSIQES-FKVISP----------------------
PtRPE1b   DFSISR----------------AVKQRIPES-FKAISP----------------------
VvRPE1    DFSIPS----------------EVTQNIQKN-VEDISS----------------------
SmRPD1    DFYMAADAVSR-RKLEEETLCAVEEAKISSLAHQIVSDPRFQVNSVSRPRC---------
ZmRPB1    DTIADASTMETINDTISKAKNAVKELIKKAHEKQLEAEPGRTMMES--------------
AtRPB1    DTIADSSTMEKINETISNAKTAVKDLIRQFQGKELDPEPGRTMRDT--------------

                          1040                1060                1080
ZmRPD1    --------------VTYRQSDCIQSNPSVIRSSIMAFKDVFRDLLKMVQQHV---SNDNS
SbRPD1    --------------VTYRQSDCIQNNPSVIRSSIMAFKDVFSDLLKMVQQHV---SNDNS
OsRPD1b   ------------LSNSHGQSDFTQVSLPIIKSSITGFKSVFNDLLKMVLQHV---SKDNS
OsRPD1a   ------------RSNTDEQSGFTQVSLPIIRSSMTSFKSVFNDLLKMVQQYV---SKDNS
BdRPD1    ------------LSDSYEQSDFVQSNLPIIKSSIMAFKSVFSDLLKMVQQHT---PKDNS
AtNRPD1   ------------VSDLARFCYERQKSATLSELAVSAFKDAYRDVQALAYRYG---DQSNS
CpRPD1    ------------TFDVERLCYEKQGSAVLSQASVDAFKQVFRDIQTLAFKYA---SKENS
PtRPD1    LSGCSEEDYCVMAFDGERLCYEKQRSAALSQSSVDAFRLVFRDIQSLVYKYA---SQDNS
VvRPD1    ------------VPDVQSLWYERQGSAALCQSSVCAFKQKFRDIQNLVYQYA---NKDNS
ZmRPE1    --------------------ILEQSRCSTSQFVEFRVENNLKNVKQQISDSV---GKFSD
SbRPE1b   --------------------VLEQSRCSTSQFVELRVENNLKSVKQQISDYV---GKFSG
OsRPE1b   --------------------ILEQSRFAENQVVEMRVDNNLKDIKQQISDFV---VKRSH
BdRPE1    --------------------VLEQSRCSKSQFVEMRVDNNLKDVKQQISDFV---VESSH
SbRPE1a   ----------------------------------------IDKFSKSIVDFI---ANSSA
OsRPE1a   ----------------------------------------LNKYREPIMDFI---THSSA
AtNRPE1   --------------------MVSRLRLSYRD--ELQLENSIHKVKEVAANFM---LKSYS
CpRPE1    --------------------FLSCLGSTYNE--ELQLENRIRCLKETAENFI---IKSS-
PtRPE1a   --------------------LLCNLRSTYNELVELQVENHIQDVKTPVLEFI---LTSSA
PtRPE1b   --------------------LLCNLRSTFNELVELQVENHIRDVKQPVREFI---LTSSA
VvRPE1    --------------------LLYNLRSMYNELLQLQAENHLRLTKVPVANFI---LNSSA
SmRPD1    ------------NSWNERVQPVTSVNEATQQAAISAFQSTMKAFERTIEEHVRENSRENS
ZmRPB1    --------------------FENRVNQVLNKARDDAGSSAQNSL-----------SESNN
AtRPB1    --------------------FENRVNQVLNKARDDAGSSAQKSL-----------AETNN
```

```
                                 1100                     1120                     1140
ZmRPD1    MMVMINAGSKGSMLKYAQQTACIGLQLP-ASKFPF-RIPSQLSCISWNGQKSLNYE-AES
SbRPD1    MMVMINAGSKGSMLKYAQQTACVGLQLP-ASKFPF-RVPSQLSCIRWNRQKSLNYE-AEG
OsRPD1b   MMAMINSGSKGSVLKFVQQTACVGLQLP-ASTFPF-RIPSELSCVSWNRQKSLNCEITNN
OsRPD1a   MMTMINSGSKGSVLKFVQQTACVGLQLP-ASKFPF-RIPSQLSCVSWNRHKSRNCEITDG
BdRPD1    MMAMINAGSKGSMLKFVQQAACVGLQLP-AGKFPF-RIPSELTCASWNRHKSLDCDISEG
AtNRPD1   FLIMSKAGSKGNIGKLVQHSMCIGLQNS-AVSLSF-GFPRELTCAAWNDPNSPLRGAKGK
CpRPD1    LLAMYKAGSKGSLPKLVQHSMCLGLQHS-LVPLSF-RFPHQLSCAAWNKQK---------
PtRPD1    FLAMFKAGSKGNLLKLVQHSMCLGLQHA-LASLSF-RIPHQLSCAGWNKQK------ADD
VvRPD1    LLAMLKAGSKGNLLKLVQQGLCLGLQHS-LVPLSF-KIPHQLSCAAWNKQK-VPGLIQND
ZmRPE1    LGLLIDPKKEASMSKVVQQVGFVGLQLYREGKLYSRRLVEDCFTNFVNKHL--------A
SbRPE1b   LGLLIDPKKEASMAKVVQQVGFVGLQLYREGKLYSRRLVEDCFSSFVNKHS--------A
OsRPE1b   LGLLIDPKSDSSVSKVVQQLGFVGLQLYREGKFYSRRLVEDCYYTFVNKHP--------A
BdRPE1    LGLLIDPKSEPSMSKVVQQLGFVGLQLYREGKFYSSRLVEDCFSSFVDKHP--------P
SbRPE1a   LGLLVDPKNDSALMNLVEQVGFLGYQLQSTDRLYSNNLVEDCYNFLEKRS---------G
OsRPE1a   IGLLVDPKSDSNMNKVVEQLGFLGPQLQHNGRLYSSRLVEDCLSKSLHRCC--------G
AtNRPE1   IRNLIDIKSNSAITKLVQQTGFLGLQLSDKKKFYTKTLVEDMAIFCKRKY----------
CpRPE1    LRNLIDFRSDSAVNKVVQQIGFLGLQLSDKGKFYSKNLVEDVAFLFRSKHP--------G
PtRPE1a   LGYLIDSKSDGAVAKLVQQIGFLGLQVSDRGKLYSKTLVEDLASHFQSKYP--------T
PtRPE1b   LGYLIDSKSDAAVTKVVQQIGFLGLQVSDRGKLYSKTLVEDLASHFLSKYP--------A
VvRPE1    LGNLIDSKSDSAINKVVQQIGFLGQQLSEKGKFYSRTLVEGMAYLFKSKYP--------F
SmRPD1    LLRMVEANSKGSFSKMMQQGGCLGLQLR-QGEFVYHRVKSLFPRAVENESR--------G
ZmRPB1    LKAMVTAGSKGSFINISQMTACVGQQNVEGKRIPFGFIDRTLPHFTKDDYG---------
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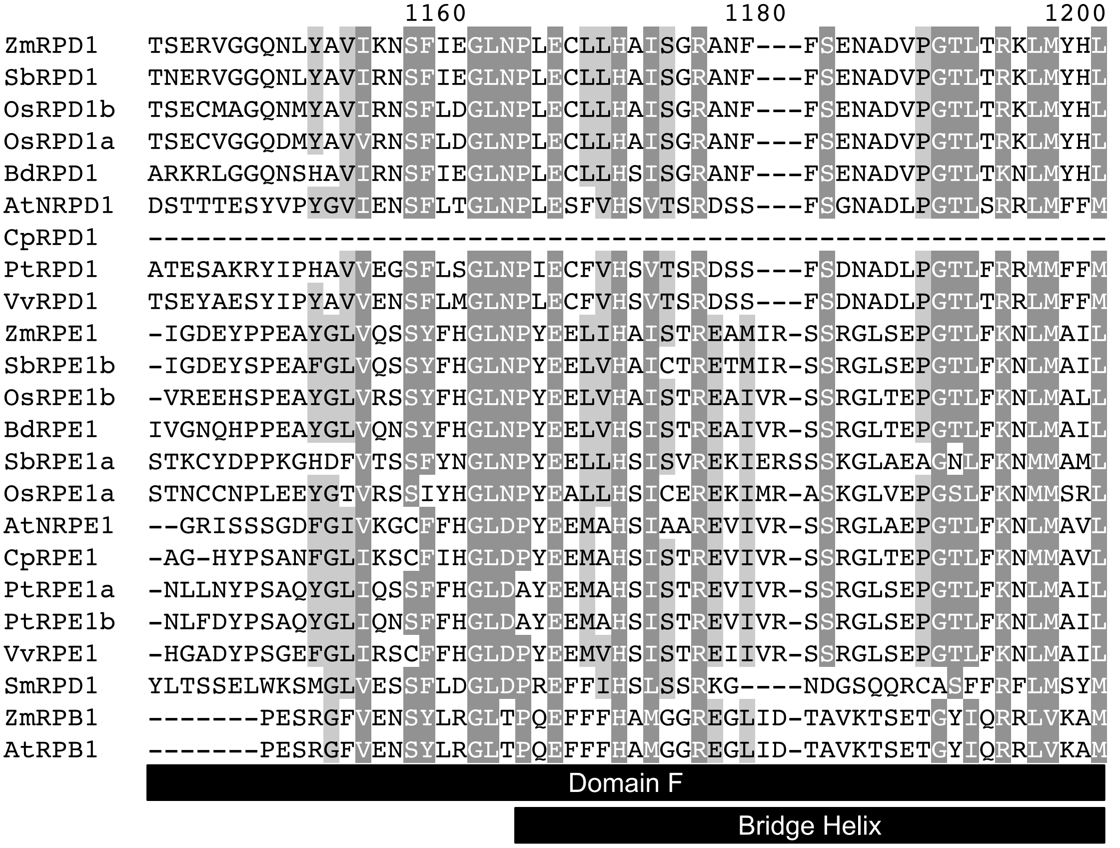

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SbRPD1    TNERVGGQNLYAVIRNSFIEGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHL
OsRPD1b   TSECMAGQNMYAVIRNSFLDGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHL
OsRPD1a   TSECVGGQDMYAVVRNSFLDGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHL
BdRPD1    ARKRLGGQNSHAVIRNSFIEGLNPLECLLHSISGRANF---FSENADVPGTLTKNLMYHL
AtNRPD1   DSTTTESYVPYGVIENSFLTGLNPLESFVHSVTSRDSS---FSGNADLPGTLSRRLMFFM
CpRPD1    ------------------------------------------------------------
PtRPD1    ATESAKRYIPHAVVEGSFLSGLNPIECFVHSVTSRDSS---FSDNADLPGTLFRRMMFFM
VvRPD1    TSEYAESYIPYAVVENSFLMGLNPLECFVHSVTSRDSS---FSDNADLPGTLTRRLMFFM
ZmRPE1    -IGDEYPPEAYGLVQSSYFHGLNPYEELIHAISTREAMIR-SSRGLSEPGTLFKNLMAIL
SbRPE1b   -IGDEYSPEAFGLVQSSYFHGLNPYEELVHAICTRETMIR-SSRGLSEPGTLFKNLMAIL
OsRPE1b   -VREEHSPEAYGLVRSSYFHGLNPYEELVHAISTREAIVR-SSRGLTEPGTLFKNLMALL
BdRPE1    IVGNQHPPEAYGLVQNSYFHGLNPYEELVHSISTREAIVR-SSRGLTEPGTLFKNLMAIL
SbRPE1a   STKCYDPPKGHDFVTSSFYNGLNPYEELLHSISVREKIERSSSKGLAEAGNLFKNMMAML
OsRPE1a   STNCCNPLEEYGTVRSSIYHGLNPYEALLHSICEREKIMR-ASKGLVEPGSLFKNMMSRL
AtNRPE1   --GRISSSGDFGIVKGCFFHGLDPYEEMAHSIAAREVIVR-SSRGLAEPGTLFKNLMAVL
CpRPE1    -AG-HYPSANFGLIKSCFIHGLDPYEEMAHSISTREVIVR-SSRGLTEPGTLFKNMMAVL
PtRPE1a   -NLLNYPSAQYGLIQSSFFHGLDAYEEMAHSISTREVIVR-SSRGLSEPGTLFKNLMAIL
PtRPE1b   -NLFDYPSAQYGLIQNSFFHGLDAYEEMAHSISTREVIVR-SSRGLSEPGTLFKNLMAIL
VvRPE1    -HGADYPSGEFGLIRSCFFHGLDPYEEMVHSISTREIIVR-SSRGLSEPGTLFKNLMAIL
SmRPD1    YLTSSELWKSMGLVESSFLDGLDPREFFIHSLSSRKG----NDGSQQRCASFFRFLMSYM
ZmRPB1    -------PESRGFVENSYLRGLTPQEFFFHAMGGREGLID-TAVKTSETGYIQRRLVKAM
AtRPB1    -------PESRGFVENSYLRGLTPQEFFFHAMGGREGLID-TAVKTSETGYIQRRLVKAM
```

```
                          1220                1240                1260
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SbRPD1    RDIHVAYDGTVRSSYGQQIVQFSYDS----------------------------------
OsRPD1b   RDTYVAYDGTVRSSYGRQIVQFSYDT----------------------------------
OsRPD1a   RDTYVAYDGTVRSSYGQQIVRFSYDT----------------------------------
BdRPD1    RDIYVAYDGTVRSSYGQQIVQFTYDT----------------------------------
AtNRPD1   RDIYAAYDGTVRNSFGNQLVQFTYETDGPVED----------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    RDLHGAYDGTVRNAYGNQLVQFSYNIDDMDP-----------------------------
VvRPD1    RDLYIAYDGTVRNAYGNQLVQFSYNIEHTSTP----------------------------
ZmRPE1    RDVVICYDGTVRNICSNSIIQLKYGEDDETDS----------------------------
SbRPE1b   RDVVICYDGTVRNICSNSIIQLKYGEDDEADS----------------------------
OsRPE1b   RDVVICYDGTVRNVCSKSIIQLNYTEDDALDF----------------------------
BdRPE1    RDVVICYDGTVRNICSNSIMQLKYNEDDATDI----------------------------
SbRPE1a   RDVTVCYDGTMRTSYNNSIVQF-----DSTNV----------------------------
OsRPE1a   RDVTACYDGSIRTSSGNLVLQF-----GSRDA----------------------------
AtNRPE1   RDIVITNDGTVRNTCSNSVIQFKYGVDSERGH----------------------------
CpRPE1    RDIIVCYDGTVRNICSNSVIQFKYGLKADNEP----------------------------
PtRPE1a   RDVVICYDGTVRNVCSNSIIQSEYGVKVGAES----------------------------
PtRPE1b   RDVVICYDGTVRNVSSNSIIQFEYGVKVGTES----------------------------
VvRPE1    RDVVICYDGTVRNVCSNSIIQFEYGVKARTKP----------------------------
SmRPD1    KDIRVEYDNTIRSTHGGHIFQFSYGATA--------------------------------
ZmRPB1    EDIMVKYDGTVRNSLGD-VIQFLYGEDGMDAVWIESQKLDSLKMKKPEFDNVFRYELDDE
AtRPB1    EDIMVKYDGTVRNSLGD-VIQFLYGEDGMDAVWIESQKLDSLKMKKSEFDRTFKYEIDDE
                              *RMR6-1 (Q to X)


                          1280                1300                1320
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    ------------------------------------------------------------
SbRPE1b   ------------------------------------------------------------
OsRPE1b   ------------------------------------------------------------
BdRPE1    ------------------------------------------------------------
SbRPE1a   ------------------------------------------------------------
OsRPE1a   ------------------------------------------------------------
AtNRPE1   ------------------------------------------------------------
CpRPE1    ------------------------------------------------------------
PtRPE1a   ------------------------------------------------------------
PtRPE1b   ------------------------------------------------------------
VvRPE1    ------------------------------------------------------------
SmRPD1    ------------------------------------------------------------
ZmRPB1    NWRPNYMLPEHVDDLKTIREFRNVFEAEVQKLEADRYQLGSEITTTGDNSWPMPVNLKRL
AtRPB1    NWNPTYLSDEHLEDLKGIRELRDVFDAEYSKLETDRFQLGTEIATNGDSTWPLPVNIKRH
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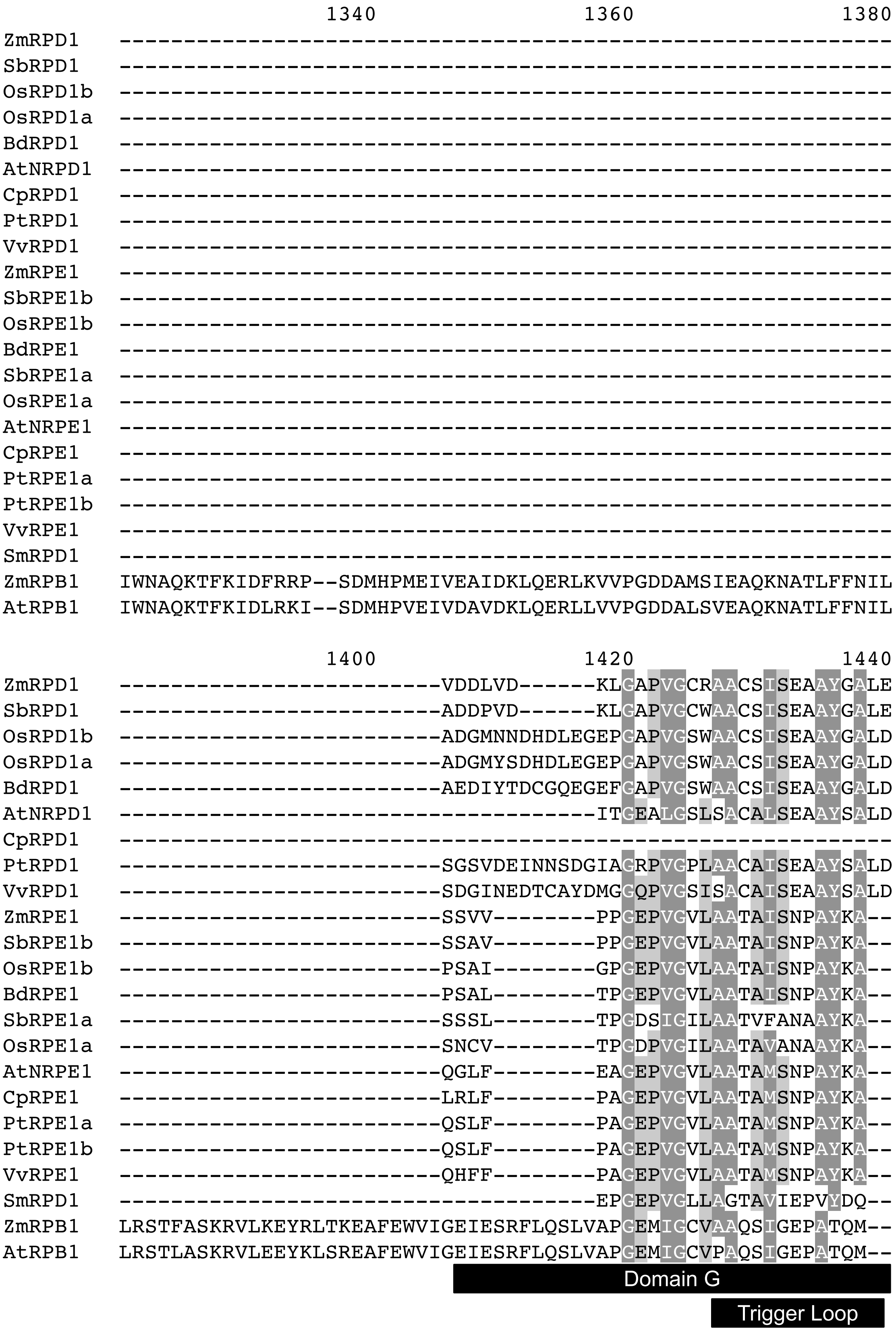

```
                          1340                1360                1380
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    ------------------------------------------------------------
SbRPE1b   ------------------------------------------------------------
OsRPE1b   ------------------------------------------------------------
BdRPE1    ------------------------------------------------------------
SbRPE1a   ------------------------------------------------------------
OsRPE1a   ------------------------------------------------------------
AtNRPE1   ------------------------------------------------------------
CpRPE1    ------------------------------------------------------------
PtRPE1a   ------------------------------------------------------------
PtRPE1b   ------------------------------------------------------------
VvRPE1    ------------------------------------------------------------
SmRPD1    ------------------------------------------------------------
ZmRPB1    IWNAQKTFKIDFRRP--SDMHPMEIVEAIDKLQERLKVVPGDDAMSIEAQKNATLFFNIL
AtRPB1    IWNAQKTFKIDLRKI--SDMHPVEIVDAVDKLQERLLVVPGDDALSVEAQKNATLFFNIL

                          1400                1420                1440
ZmRPD1    -------------------------VDDLVD------KLGAPVGCRAACSISEAAYGALE
SbRPD1    -------------------------ADDPVD------KLGAPVGCWAACSISEAAYGALE
OsRPD1b   -------------------------ADGMNNDHDLEGEPGAPVGSWAACSISEAAYGALD
OsRPD1a   -------------------------ADGMYSDHDLEGEPGAPVGSWAACSISEAAYGALD
BdRPD1    -------------------------AEDIYTDCGQEGEFGAPVGSWAACSISEAAYGALD
AtNRPD1   -------------------------------------ITGEALGSLSACALSEAAYSALD
CpRPD1    ------------------------------------------------------------
PtRPD1    -------------------------SGSVDEINNSDGIAGRPVGPLAACAISEAAYSALD
VvRPD1    -------------------------SDGINEDTCAYDMGGQPVGSISACAISEAAYSALD
ZmRPE1    -------------------------SSVV--------PPGEPVGVLAATAISNPAYKA--
SbRPE1b   -------------------------SSAV--------PPGEPVGVLAATAISNPAYKA--
OsRPE1b   -------------------------PSAI--------GPGEPVGVLAATAISNPAYKA--
BdRPE1    -------------------------PSAL--------TPGEPVGVLAATAISNPAYKA--
SbRPE1a   -------------------------SSSL--------TPGDSIGILAATVFANAAYKA--
OsRPE1a   -------------------------SNCV--------TPGDPVGILAATAVANAAYKA--
AtNRPE1   -------------------------QGLF--------EAGEPVGVLAATAMSNPAYKA--
CpRPE1    -------------------------LRLF--------PAGEPVGVLAATAMSNPAYKA--
PtRPE1a   -------------------------QSLF--------PAGEPVGVLAATAMSNPAYKA--
PtRPE1b   -------------------------QSLF--------PAGEPVGVLAATAMSNPAYKA--
VvRPE1    -------------------------QHFF--------PAGEPVGVLAATAMSNPAYKA--
SmRPD1    -------------------------------------EPGEPVGLLAGTAVIEPVYDQ--
ZmRPB1    LRSTFASKRVLKEYRLTKEAFEWVIGEIESRFLQSLVAPGEMIGCVAAQSIGEPATQM--
AtRPB1    LRSTLASKRVLEEYKLSREAFEWVIGEIESRFLQSLVAPGEMIGCVPAQSIGEPATQM--
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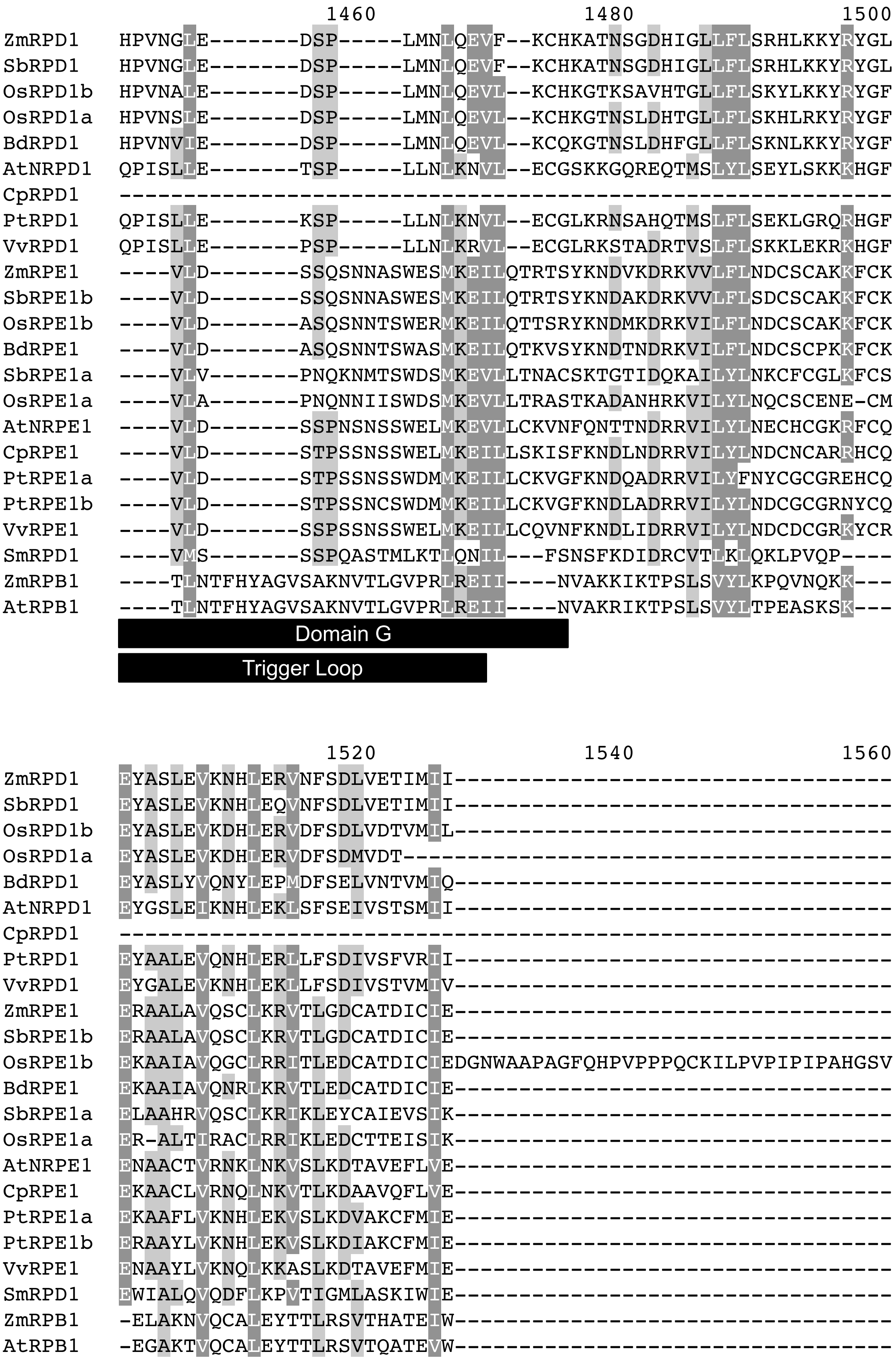

```
                           1460                1480                1500
ZmRPD1   HPVNGLE-------DSP-----LMNLQEVF--KCHKATNSGDHIGLLFLSRHLKKYRYGL
SbRPD1   HPVNGLE-------DSP-----LMNLQEVF--KCHKATNSGDHIGLLFLSRHLKKYRYGL
OsRPD1b  HPVNALE-------DSP-----LMNLQEVL--KCHKGTKSAVHTGLLFLSKYLKKYRYGF
OsRPD1a  HPVNSLE-------DSP-----LMNLQEVL--KCHKGTNSLDHTGLLFLSKHLRKYRYGF
BdRPD1   HPVNVIE-------DSP-----LMNLQEVL--KCQKGTNSLDHFGLLFLSKNLKKYRYGF
AtNRPD1  QPISLLE-------TSP-----LLNLKNVL--ECGSKKGQREQTMSLYLSEYLSKKKHGF
CpRPD1   ------------------------------------------------------------
PtRPD1   QPISLLE-------KSP-----LLNLKNVL--ECGLKRNSAHQTMSLFLSEKLGRQRHGF
VvRPD1   QPISLLE-------PSP-----LLNLKRVL--ECGLRKSTADRTVSLFLSKKLEKRKHGF
ZmRPE1   ----VLD-------SSQSNNASWESMKEILQTRTSYKNDVKDRKVVLFLNDCSCAKKFCK
SbRPE1b  ----VLD-------SSQSNNASWESMKEILQTRTSYKNDAKDRKVVLFLSDCSCAKKFCK
OsRPE1b  ----VLD-------ASQSNNTSWERMKEILQTTSRYKNDMKDRKVILFLNDCSCAKKFCK
BdRPE1   ----VLD-------ASQSNNTSWASMKEILQTKVSYKNDTNDRKVILFLNDCSCPKKFCK
SbRPE1a  ----VLV-------PNQKNMTSWDSMKEVLLTNACSKTGTIDQKAILYLNKCFCGLKFCS
OsRPE1a  ----VLA-------PNQNNIISWDSMKEVLLTRASTKADANHRKVILYLNQCSCENE-CM
AtNRPE1  ----VLD-------SSPNSNSSWELMKEVLLCKVNFQNTTNDRRVILYLNECHCGKRFCQ
CpRPE1   ----VLD-------STPSSNSSWELMKEILLSKISFKNDLNDRRVILYLNDCNCARRHCQ
PtRPE1a  ----VLD-------STPSSNSSWDMMKEILLCKVGFKNDQADRRVILYFNYCGCGREHCQ
PtRPE1b  ----VLD-------STPSSNCSWDMMKEILLCKVGFKNDLADRRVILYLNDCGCGRNYCQ
VvRPE1   ----VLD-------SSPSSNSSWELMKEILLCQVNFKNDLIDRRVILYLNDCDCGRKYCR
SmRPD1   ----VMS-------SSPQASTMLKTLQNIL---FSNSFKDIDRCVTLKLQKLPVQP----
ZmRPB1   ----TLNTFHYAGVSAKNVTLGVPRLREII----NVAKKIKTPSLSVYLKPQVNQKK---
AtRPB1   ----TLNTFHYAGVSAKNVTLGVPRLREII----NVAKRIKTPSLSVYLTPEASKSK---

                           1520                1540                1560
ZmRPD1   EYASLEVKNHLERVNFSDLVETIMII----------------------------------
SbRPD1   EYASLEVKNHLEQVNFSDLVETIMII----------------------------------
OsRPD1b  EYASLEVKDHLERVDFSDLVDTVMIL----------------------------------
OsRPD1a  EYASLEVKDHLERVDFSDMVDT--------------------------------------
BdRPD1   EYASLYVQNYLEPMDFSELVNTVMIQ----------------------------------
AtNRPD1  EYGSLEIKNHLEKLSFSEIVSTSMII----------------------------------
CpRPD1   ------------------------------------------------------------
PtRPD1   EYAALEVQNHLERILFSDIVSFVRII----------------------------------
VvRPD1   EYGALEVKNHLEKLLFSDIVSTVMIV----------------------------------
ZmRPE1   ERAALAVQSCLKRVTLGDCATDICIE----------------------------------
SbRPE1b  ERAALAVQSCLKRVTLGDCATDICIE----------------------------------
OsRPE1b  EKAAIAVQGCLRRITLEDCATDICIEDGNWAAPAGFQHPVPPPQCKILPVPIPIPAHGSV
BdRPE1   EKAAIAVQNRLKRVTLEDCATDICIE----------------------------------
SbRPE1a  ELAAHRVQSCLKRIKLEYCAIEVSIK----------------------------------
OsRPE1a  ER-ALTIRACLRRIKLEDCTTEISIK----------------------------------
AtNRPE1  ENAACTVRNKLNKVSLKDTAVEFLVE----------------------------------
CpRPE1   EKAACLVRNQLNKVTLKDAAVQFLVE----------------------------------
PtRPE1a  EKAAFLVKNHLEKVSLKDVAKCFMIE----------------------------------
PtRPE1b  ERAAYLVKNHLEKVSLKDIAKCFMIE----------------------------------
VvRPE1   ENAAYLVKNQLKKASLKDTAVEFMIE----------------------------------
SmRPD1   EWIALQVQDFLKPVTIGMLASKIWIE----------------------------------
ZmRPB1   -ELAKNVQCALEYTTLRSVTHATEIW----------------------------------
AtRPB1   -EGAKTVQCALEYTTLRSVTQATEVW----------------------------------
```

```
                          1580                1600                1620
ZmRPD1    ---------------------YDG-----------------------------HDKIRNE
SbRPD1    ---------------------YDG-----------------------------HDKIRKE
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ---------------------YDG----------------------------GGVQKTKG
AtNRPD1   ---------------------FSP----------------------------SSNTKVPL
CpRPD1    ------------------------------------------------------------
PtRPD1    ---------------------FSP----------------------------QSDGRMHF
VvRPD1    ---------------------FSP----------------------------QNGSKTHF
ZmRPE1    ---------------------HQK-------------------------QINLDGTSEAA
SbRPE1b   ---------------------HQK-------------------------QINLDGTSEAA
OsRPE1b   KFPPVPIPAPEHLKYNIHVVRYQK-------------------------QIGLDGTSEAA
BdRPE1    -----------------YI---------------------------------LDGSSEAT
SbRPE1a   ---------------------YQQ------------------------------EATQAA
OsRPE1a   ---------------------YQQ------------------------------QATQAA
AtNRPE1   ---------------------YRK-------------------------QPTISEIFGID
CpRPE1    ---------------------YKN-------------------------HRTVSEGLEID
PtRPE1a   ---------------------Y-K-------------------------NQQIPESFGSD
PtRPE1b   ---------------------Y-K-------------------------SQQIPESFGSD
VvRPE1    ---------------------YVK-------------------------QHAVSGSSEPG
SmRPD1    ---------------------YSP--------------------------CSEVGGQKKR
ZmRPB1    ---------------------YDP----DPLGTIIEEDTEFVQSYYEMPDEDID--PDKI
AtRPB1    ---------------------YDP----DPMSTIIEEDFEFVRSYYEMPDEDVS--PDKI


                          1640                1660                1680
ZmRPD1    GMWTTHFHINKAMMKKKRLGLRFVVDELAKEYDT------TRDQLNNAIPSIRISRRKCL
SbRPD1    GTWTTHFHISKEMMKKKRLGLRFVIEELTKEYNA------TRDQLKNAIPSICISRRKCV
OsRPD1b   ----------LETMKIKRLRLGFIVRELIDQYNA------LRKKLNNMIPSVCISYSKCS
OsRPD1a   -----------ETMKIKRLRLEFIVREIIDQYNT------LRKQLNNAIPSVSISNSKCS
BdRPD1    SPWITHFHISKEMMKRKRLGLRLLVEDLTEHYNA------KRDQLNNVIPKVYISKCKCS
AtNRPD1   SPWVCHFHISEKVLKRKQLSAESVVSSLNEQYKS------RNRELKLDIVDLDIQNTNHC
CpRPD1    --------------------------------------------------------RECP
PtRPD1    SPWVCHFHVYKEIVKKRSLKVHYIIDALEKQCKS-----------KTRFPKVQITSRYCT
VvRPD1    SPWVCHFHVCEEIAKKRSLKPHSIIDALYMKCNS------ARAESKINLPDLQITSKDCF
ZmRPE1    PTLVGHIHLDKGHLERINISTQDILQKCQEVSGRFG-K--KKGHLCHIFKKITFATCDCS
SbRPE1b   PTLVGHIHLDKGQLERINISIQDILQKCQEVSGRYG-K--KKGHLCHLLKKITFATC---
OsRPE1b   PALVGHIHLDRAHLERINISTEDILQKCQEVSGKYG-K--KKGHLSNLFKNITFSTCDCL
BdRPE1    PALVGHIHLEKARLDMINVSTEDILQKCQEVSLKHG-K--KKGHLGHLFKKITFSTCDCS
SbRPE1a   QCLVGHIHLDKEQLNWMEITMGNILQTCQKNVNKHV-M--KNRQLMQILKTTEIISSEYC
OsRPE1a   HHLVGHIHLDKKQLNQIETIMDSVLHKCQETFRNNI-K--KKGSMREILKTVTFISS-TS
AtNRPE1   SCLHGHIHLNKTLLQDWNISMQDIHQKCEDVINSLGQK--KKKKATDDFKRTSLSVSECC
CpRPE1    AGLAGHVHLNKTLLQVLNIDMQEILQQCRERISLF--R--KKKKVGHCFKKIILSVSKCC
PtRPE1a   AGLVGHVHLEKRILQELNISAQVILEKCQETVNSF--R--KKKKVGNLFKKTTLSISECC
PtRPE1b   AGLVGHVHLDKRKLQDLNITAQVILEKCQETVNTF--R--KKKKVGNLFKKTILLVSESC
VvRPE1    TGLVGHIHLNKLLLQDLNVSMQEVCQKCEETINSF--R--KKKNVGPFFKKIILSFRECC
SmRPD1    VPWIGCFQLRAEAMERCSLNIDTIVCHLRKLLPT------SLDDPDAFIQGLHFFSRDV-
ZmRPB1    SPWLLRIELNREMMVDKKLSMADIAEKINREFDDDLSCIFNDDNADKLILRIRITNDE--
AtRPB1    SPWLLRIELNREMMVDKKLSMADIAEKINLEFDDDLTCIFNDDNAQKLILRIRIMNDE--
```

```
                         1700                1720                1740
ZmRPD1   VGDE----GVKSSSCCIAVVAHA------ERNSISQLDTIKTRVI---PS---ILDTLLK
SbRPD1   VGDE----GVKISACCIAVVALA------EPNSMSQLDTIKKRVI---PI---ILDTLLK
OsRPD1b  VGNE----CVKNRSCCVTMVAQV------ESNSTSQLDIIKERVI---PS---ILATLLK
OsRPD1a  VGNE----CVKNQTCCVTMVVQV------EINSMSQLDVIKERVI---PS---ILATLLK
BdRPD1   DDDD----CINNQTCCITVVAQDES----NSTSTSQLDDLKKRAI---PV---LLATPVK
AtNRPD1  SSDD---QAMKDDNVCITVTVVEA-----SKHSVLELDAIRLVLI---PF---LLDSPVK
CpRPD1   IDDG----PRQEDSFCISVTVVKK-----SKDSSVQLDTVRGLVM---PF---LLRAVIK
PtRPD1   VADT---WKEKKETFCITVTIVET-----SKNEFIELETIQDLMI---PF---LLETVIK
VvRPD1   VDME----KEDSDCFCITVSIVN------SKKSCIQLDTVRDLVI---PF---LLGAVVK
ZmRPE1   FTQM-PIDGKLHKVPCVQFAFSDD--IVLSESIERAVNVIADSVC---SV---LLDTIIK
SbRPE1b  --------GKLHKVPCVQFSFSDE-STVLSESVERAVNVIADSVC---SV---LLDTIIK
OsRPE1b  FTQK-LVDGKLPKLPCLQFFVSDN-M-IVSESVERAVSVLADSLC---GV---LLNTIIK
BdRPE1   FTQKPMIDGKLPKVPCLQFSFSED-IPMLSESVERAVSVLANSLCDSATI---FWSICSA
SbRPE1a  LCGQDIGDERALQVSCLQCFIHASTTTVQPES--NVIQMMTNTIF---PI---LLDTVIK
OsRPE1a  LCDQHTDDDKKFQVSCLQFFLPGSITKNISESTERVIDFMTNAIF---PI---ILDTVIK
AtNRPE1  SFRD-PCGSKGSDMPCLTFSY-NA-T---DPDLERTLDVLCNTVY---PV---LLEIVIK
CpRPE1   SFQQ-SCEENSSDLPCLIFCWHDT-S---DIHLERTSYVLANMIY---PV---LLETVIK
PtRPE1a  SFEQ-CT----DELLCLMFFWQDA-N---DVHLERTSNILADMIC---PV---LLETTIK
PtRPE1b  SFQQ-CI----DESPCLMFFWQGA-D---DVHLERTSNILADMIC---PV---LLETIIK
VvRPE1   TFQH-SCQSKGSDMPCLLFFWQGN-R---DDNLEQILHILAHKIC---PV---LLQTIIK
SmRPD1   ------------EVLCF-FPITSSVSNYDSKQ------IHKHMIG---TMFGNLLQVVVK
ZmRPB1   ----------------------APKGEIQDESAE--DDVFLKKIE-----GNMLTEMALR
AtRPB1   ----------------------GPKGELQDESAE--DDVFLKKIE-----SNMLTEMALR
```

```
                         1760                1780                1800
ZmRPD1   GFLE-FKDVEIQ--------------CPHDGELLVKVCMSEHC--KGGRFWPTLQNAC--
SbRPD1   GFLE-FKDVEIQ--------------CQHDGELLVKVCMSHHC--KGGRFWATLQNAC--
OsRPD1b  GFLE-FENVKVE--------------CQQDSELVVKVGMSEHC--KTGKFWATLQNAC--
OsRPD1a  GFLE-FKNVKVQ--------------CQEDNELVLKVGMSEHC--KSGKFWATLQNAC--
BdRPD1   GFLE-FKDVEIQ--------------CQRDNELVVKVNMSKHC--KSGIFWTTLKKAC--
AtNRPD1  GDQG-IKKVNILWTDRP--KAPKRNGNHLAGELYLKVTMYGDR--GKRNCWTALLETC--
CpRPD1   GFPE-IKKVDILWKDRP--KLSKSYDS--RGELYLRVSMSEEH--GTRTSWNALMDGC--
PtRPD1   GFME-IQKVDILWNDKP--KIPKSH-NRLRGELFLRVHMSRGS--DKTRLWNQLMDDC--
VvRPD1   GLLD-VKKVDILWNDNPDSDVLKSS----SGRLYLRVYVSGDC--GKKNFWGVLMDAC--
ZmRPE1   GDPR-IQAAKVIWVESDAASWVKHTRKVSKGESALEIIVEKDDAVSNGDAWRTAIDAC--
SbRPE1b  GDPR-IQAAKVIWVESDATAWVKNTRKVSKGEPALEIIVEKDHAVSNGDAWRTTIDAC--
OsRPE1b  GDPR-IQEAKIVWVGSDATSWVKNTQKASKGEPAVEIIVEEEEALHIGDAWRTTMDAC--
BdRPE1   GDPR-IQEAKIMWVGSDAQSWVKNTRKVSKGEPTVEIVVEKNEASKQGDAWRIAMDAC--
SbRPE1a  GDPQ-VQEAKLIWVEPKLTRWVKNSSAEQKGELAVEITVEKIAAAENGGTWGVVMDAC--
OsRPE1a  GDPR-VEEANLVRIEPESTFWVQSSGAEQKGEAALEITVEEAAAAESGNAWGVAMNAC--
AtNRPE1  GDSR-ICSANIIWNSSDMTTWIRNRHASRRGEWVLDVTVEKSAVKQSGDAWRVVIDSC--
CpRPE1   GDPR-ICSANIIWASPDTMTWIRKPSRTRKGEWVLDVVVEKSMVKRSGDAWRIVMDSC--
PtRPE1a  GDHR-ISCANIIWASQETTTWIRNPSRTQKGELALDIVLEKSVVKQSGDAWRIVLDSC--
PtRPE1b  GDHR-ISCANIIWATPETNTWIRNPSRTQKGELALDIVLEKSVVKKSGDAWRIVLDSC--
VvRPE1   GDSR-VCTVNIIWISPDTTTWIRNPCKSRKGELALDIVLEKAAVKQRGDAWRIVLDAC--
SmRPD1   GCPRGIEFVNVKWED----------------ELCIEVAFLSRT---RGVPWTHALEAC--
ZmRPB1   GIPD-INKVFIK-------------------EGKVNTFYQDDG-FKAANEWMLDTEGVNL
AtRPB1   GIPD-INKVFIK-------------------QVRKSRFDEEGG-FKTSEEWMLDTEGVNL
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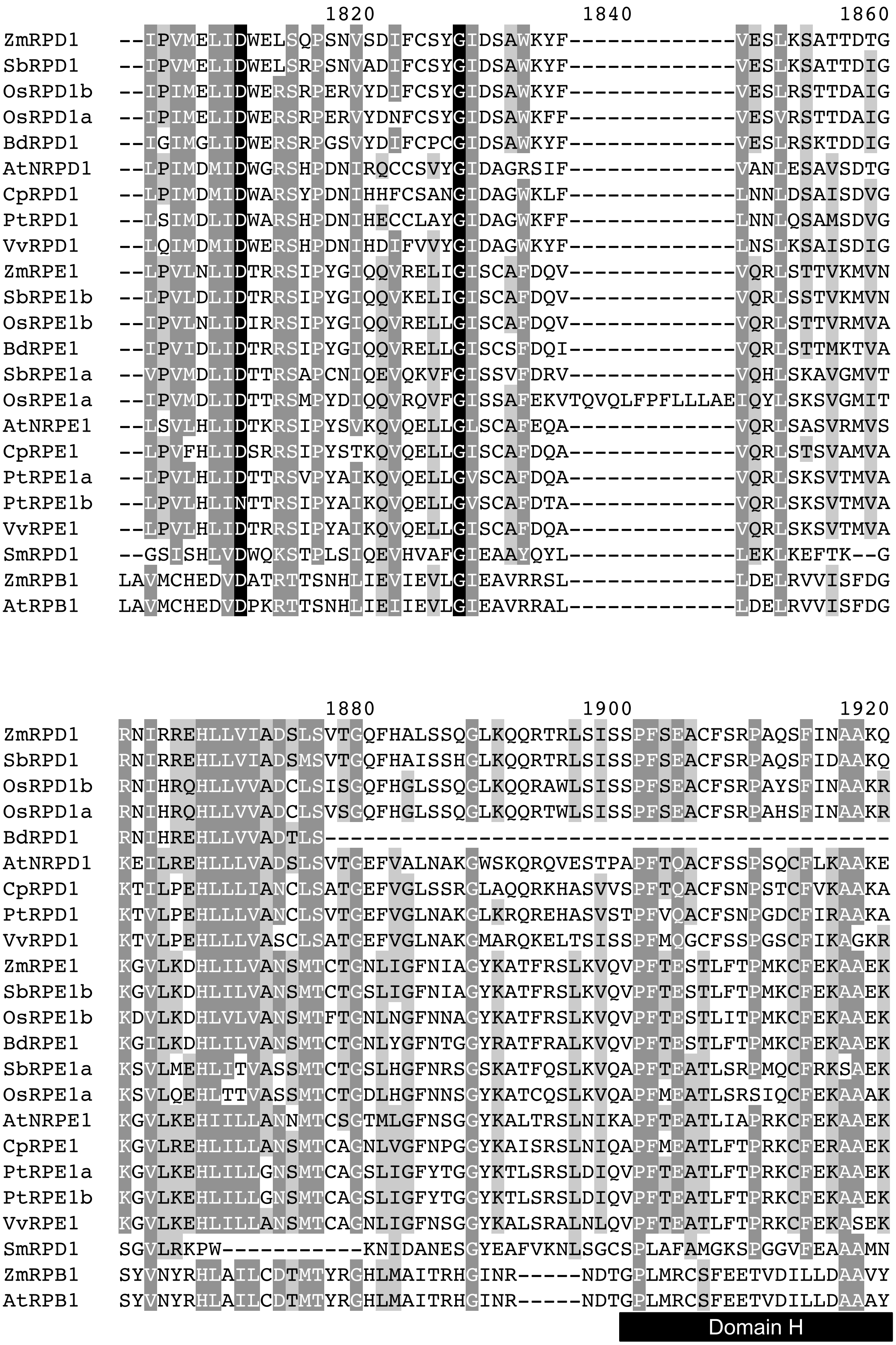

```
                               1820                1840                1860
ZmRPD1     --IPVMELIDWELSQPSNVSDIFCSYGIDSAWKYF-------------VESLKSATTDTG
SbRPD1     --IPVMELIDWELSRPSNVADIFCSYGIDSAWKYF-------------VESLKSATTDIG
OsRPD1b    --IPIMELIDWERSRPERVYDIFCSYGIDSAWKYF-------------VESLRSTTDAIG
OsRPD1a    --IPIMELIDWERSRPERVYDNFCSYGIDSAWKFF-------------VESVRSTTDAIG
BdRPD1     --IGIMGLIDWERSRPGSVYDIFCPCGIDSAWKYF-------------VESLRSKTDDIG
AtNRPD1    --LPIMDMIDWGRSHPDNIRQCCSVYGIDAGRSIF-------------VANLESAVSDTG
CpRPD1     --LPIMDMIDWARSYPDNIHHFCSANGIDAGWKLF-------------LNNLDSAISDVG
PtRPD1     --LSIMDLIDWARSHPDNIHECCLAYGIDAGWKFF-------------LNNLQSAMSDVG
VvRPD1     --LQIMDMIDWERSHPDNIHDIFVVYGIDAGWKYF-------------LNSLKSAISDIG
ZmRPE1     --LPVLNLIDTRRSIPYGIQQVRELIGISCAFDQV-------------VQRLSTTVKMVN
SbRPE1b    --LPVLDLIDTRRSIPYGIQQVKELIGISCAFDQV-------------VQRLSSTVKMVN
OsRPE1b    --IPVLNLIDIRRSIPYGIQQVRELLGISCAFDQV-------------VQRLSTTVRMVA
BdRPE1     --IPVIDLIDTRRSIPYGIQQVRELLGISCSFDQI-------------VQRLSTTMKTVA
SbRPE1a    --VPVMDLIDTTRSAPCNIQEVQKVFGISSVFDRV-------------VQHLSKAVGMVT
OsRPE1a    --IPVMDLIDTTRSMPYDIQQVRQVFGISSAFEKVTQVQLFPFLLLAEIQYLSKSVGMIT
AtNRPE1    --LSVLHLIDTKRSIPYSVKQVQELLGLSCAFEQA-------------VQRLSASVRMVS
CpRPE1     --LPVFHLIDSRRSIPYSTKQVQELLGISCAFDQA-------------VQRLSTSVAMVA
PtRPE1a    --LPVLHLIDTTRSVPYAIKQVQELLGVSCAFDQA-------------VQRLSKSVTMVA
PtRPE1b    --LPVLHLINTTRSIPYAIKQVQELLGVSCAFDTA-------------VQRLSKSVTMVA
VvRPE1     --LPVLHLIDTRRSIPYAIKQVQELLGISCAFDQA-------------VQRLSKSVTMVA
SmRPD1     --GSISHLVDWQKSTPLSIQEVHVAFGIEAAYQYL-------------LEKLKEFTK--G
ZmRPB1     LAVMCHEDVDATRTTSNHLIEVIEVLGIEAVRRSL-------------LDELRVVISFDG
AtRPB1     LAVMCHEDVDPKRTTSNHLIEIIEVLGIEAVRRAL-------------LDELRVVISFDG
```

```
                               1880                1900                1920
ZmRPD1     RNIRREHLLVIADSLSVTGQFHALSSQGLKQQRTRLSISSPFSEACFSRPAQSFINAAKQ
SbRPD1     RNIRREHLLVIADSMSVTGQFHAISSHGLKQQRTRLSISSPFSEACFSRPAQSFIDAAKQ
OsRPD1b    RNIHRQHLLVVADCLSISGQFHGLSSQGLKQQRAWLSISSPFSEACFSRPAYSFINAAKR
OsRPD1a    RNIHRQHLLVVADCLSVSGQFHGLSSQGLKQQRTWLSISSPFSEACFSRPAHSFINAAKR
BdRPD1     RNIHREHLLVVADTLS--------------------------------------------
AtNRPD1    KEILREHLLLVADSLSVTGEFVALNAKGWSKQRQVESTPAPFTQACFSSPSQCFLKAAKE
CpRPD1     KTILPEHLLLIANCLSATGEFVGLSSRGLAQQRKHASVVSPFTQACFSNPSTCFVKAAKA
PtRPD1     KTVLPEHLLLVANCLSVTGEFVGLNAKGLKRQREHASVSTPFVQACFSNPGDCFIRAAKA
VvRPD1     KTVLPEHLLLVASCLSATGEFVGLNAKGMARQKELTSISSPFMQGCFSSPGSCFIKAGKR
ZmRPE1     KGVLKDHLILVANSMTCTGNLIGFNIAGYKATFRSLKVQVPFTESTLFTPMKCFEKAAEK
SbRPE1b    KGVLKDHLILVANSMTCTGSLIGFNIAGYKATFRSLKVQVPFTESTLFTPMKCFEKAAEK
OsRPE1b    KDVLKDHLVLVANSMTFTGNLNGFNNAGYKATFRSLKVQVPFTESTLITPMKCFEKAAEK
BdRPE1     KGILKDHLILVANSMTCTGNLYGFNTGGYRATFRALKVQVPFTESTLFTPMKCFEKAAEK
SbRPE1a    KSVLMEHLITVASSMTCTGSLHGFNRSGSKATFQSLKVQAPFTEATLSRPMQCFRKSAEK
OsRPE1a    KSVLQEHLTTVASSMTCTGDLHGFNNSGYKATCQSLKVQAPFMEATLSRSIQCFEKAAAK
AtNRPE1    KGVLKEHIILLANNMTCSGTMLGFNSGGYKALTRSLNIKAPFTEATLIAPRKCFEKAAEK
CpRPE1     KGVLREHLILLANSMTCAGNLVGFNPGGYKAISRSLNIQAPFMEATLFTPRKCFERAAEK
PtRPE1a    KGVLKEHLILLGNSMTCAGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRKCFEKAAEK
PtRPE1b    KGVLKEHLILLGNSMTCAGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRKCFEKAAEK
VvRPE1     KGVLKEHLILLANSMTCAGNLIGFNSGGYKALSRALNLQVPFTEATLFTPRKCFEKASEK
SmRPD1     SGVLRKPW-----------KNIDANESGYEAFVKNLSGCSPLAFAMGKSPGGVFEAAAMN
ZmRPB1     SYVNYRHLAILCDTMTYRGHLMAITRHGINR-----NDTGPLMRCSFEETVDILLDAAVY
AtRPB1     SYVNYRHLAILCDTMTYRGHLMAITRHGINR-----NDTGPLMRCSFEETVDILLDAAAY
```

```
                         1940                1960                19
ZmRPD1   CSVDNLCGSLDAVAWGKEPFNGTSGPFEIMHSGKPHEPEQN----ESIYDFLCSSKV---
SbRPD1   CSVDNLCGSLDAIAWGKEPFNGTSGPFEIMHSGKPHEPEQD----ESIYDFLRSPKV---
OsRPD1b  DSVDNLSGALDAIAWGKEPCAGTSGPFKVLYSGKSQKTKQN----KNIYDFLHNPEV---
OsRPD1a  DSVDNLSGTLDAIAWGKEPCAGSSGPFKILYSGKSHETKQN----EHIYDFLHNPEV---
BdRPD1   ----------------------------------PHEPVQN----ENIYGFLHNPEV---
AtNRPD1  GVRDDLQGSIDALAWGKVPGFGTGDQFEIIISPKVHGFTTP----VDVYDLLSSTKT---
CpRPD1   GVTDDLQGSIDALAWGKPPCFGTGGQFDIIYSWRP----------VDVYDLLNSIVT---
PtRPD1   GVVDDLQGSIDALAWGKVPAIGTG-QFDIVYSGKGLEFSKP----VDVYNLLGSQMI---
VvRPD1   AVADNLHGSLDALAWGKIPSVGSGGHFDILYSAKGHELARP----EDIYKLLGSQTS---
ZmRPE1   CDSDSLGCVVSSSAWGKHAAVGTGSSFQILWNENQLKSNKE--YGDGLYDFLALVRTD--
SbRPE1b  CDSDSLGCVVSSSSWGKHAAVGTGSSFQILWNENQLKSNKD--YGDGLYDFLALVRTD--
OsRPE1b  CHSDSLGCVVSSCSWGKHAASGTGSSFQILWNESQLKSNKE--YGDGLYDYLALVRTD--
BdRPE1   CHSDALGCVVSSCSWGKHAALGTGSSFQILWNENQVNCNKE--YGDGLYDFLAMVRTD--
SbRPE1a  VDSDQLDSVVSTCSWGNHAAIGTGSAFKIHWNDENQSASNEILREYNLYDFLEAVGRIGA
OsRPE1a  AYSDQLGNVVSACSWGNNAEIGTGSAFEILWNDENMSSSKSILGGYGLYDFLEAVETTGA
AtNRPE1  CHTDSLSTVVGSCSWGKRVDVGTGSQFELLWNQKETGLDDK--EETDVYSFLQMVISTTN
CpRPE1   CHTDSLSSVVGSCSWGKNVAVGTGSRFDVLWDTKEARFNEG--GKLDVYTFLHMVRSSSH
PtRPE1a  CHTDYLSSIVASCSWGKHVTVGTGSRFDVLWDTKEACLNPE--GGIDAYSFLNMVRSTAG
PtRPE1b  CHTDSLSSIVASCAWGKHVTVGTGSHFDVLWDTKEACLNPE--GSMDVYSFLNMVRSTAG
VvRPE1   CHTDSLSSIVASCSWGKHVTVGTGSRFDVLWDTKEIGPAQD--GGIDIYSFLHLVRSGSY
SmRPD1   REVDYLAGANELAFCGKSPSLGTGANIELFFKEDKGPVSRF----PDFESLVFSRRV---
ZmRPB1   AESDHLRGVTENIMLGQLAPIGTGG-CALYLNDQMLQQAIE----LQLPSYVEGL-----
AtRPB1   AETDCLRGVTENIMLGQLAPIGTGD-CELYLNDEMLKNAIE----LQLPSYMDGL-----
```

```
                         2000                2020                2040
ZmRPD1   ------------------------------------------------------------
SbRPD1   ------------------------------------------------------------
OsRPD1b  ------------------------------------------------------------
OsRPD1a  ------------------------------------------------------------
BdRPD1   ------------------------------------------------------------
AtNRPD1  ------------------------------------------------------------
CpRPD1   ------------------------------------------------------------
PtRPD1   ------------------------------------------------------------
VvRPD1   ------------------------------------------------------------
ZmRPE1   -QEKTDY---MFLDDVDYLVEENAADDMCLSPEPDGTLGKPTFEDNFEEQNIQKGSSWEI
SbRPE1b  -QEKTGY---MFLDDVDYLLEENAIDDMCLSPEPDGTVGKPTFEDNFEEQNIQKGSSWEN
OsRPE1b  -EEKARY---TFFDDVDYLAEENEA-DVCLSPELDGTIGQPIFDDNLEEQDVQNNSSWDN
BdRPE1   -QEKARY---TFLDDVDYLVEDNAMDDICLSPELNGTHGVPTFEDNFEHQDTQNGNSWEN
SbRPE1a  TEQKTDAPHSLCLYDVGQLPEDEVQEDEVVCFGGTSPI----------------------
OsRPE1a  TKDKAIVPHNYCLYDVDCIPEDK------VCLEENNQI----------------------
AtNRPE1  A-DAFVS---SPGFDVT----EEEMAEWAESPERDSALGEPKFEDSADFQNL-----HDE
CpRPE1   GEDLSTA---CLGEEIDDLVPDEETFDWSPSPEHYSTSGKPVFEDGEDILEN-----LET
PtRPE1a  GEESVTA---CLGAEVDDLILEDEDWNL--SPEHHSSSDKPTFEDSAEFQDF-----LGN
PtRPE1b  GEESVTA---CLGAEVDDLMLEDEDWNL--SPEHNSSSDKPTFEDSAEFQDF-----LGN
VvRPE1   GKEPDTA---CLGAEVEDLILEDENLELGMSPEHSSNFEKPVFEDSAEFQNT-----WEN
SmRPD1   ------------------------------------------------------------
ZmRPB1   --------------------------DFGMTPARSPITGTPYHE-GMMSPSYLLSPNIRA
AtRPB1   --------------------------EFGMTPARSPVSGTPYHE-GMMSPNYLLSPNMRL
```

```
                         2060                2080                2100
ZmRPD1   ------------------------------------------------------------
SbRPD1   ------------------------------------------------------------
OsRPD1b  ------------------------------------------------------------
OsRPD1a  ------------------------------------------------------------
BdRPD1   ------------------------------------------------------------
AtNRPD1  ------------------------------------------------------------
CpRPD1   ------------------------------------------------------------
PtRPD1   ------------------------------------------------------------
VvRPD1   ------------------------------------------------------------
ZmRPE1   GITTNSSWEQNASVAN---DSGDWGGWSSGGGAA----------AKPADQDNS-WEVHAK
SbRPE1b  GITMKSSWEQDASAAN---DSGDWGGWSSGGGAS----------AKPADQDNS-WEVHAK
OsRPE1b  GTTTNASWEQNGSAGN---DSDKWGGWNDAAAGAD------TGVTKPANQGNSCWDVPAT
BdRPE1   GTKANASWEQNASAGN---DSDNWGGWSNAAAAAD------TGAAKPADQGNSSWDVPAT
SbRPE1a  ------------------------------------------------------------
OsRPE1a  ------------------------------------------------------------
AtNRPE1  GKPSGANWEKSSSWDNGCSGGSEWGVSKSTGGEAN---------------PESNWEKTTN
CpRPE1   Q-PTKPSWEHL--------NNGRADLQKQ-------------------------------
PtRPE1a  Q-PAESNWGKASSLKDGSWSAGNWDVDKNDSAGKEKPWSLGMSSAETNDV---GWDTAAT
PtRPE1b  Q-PAESNWEKISSLKDRSRSSGNWDVDKNDGAVKEKPWSLGMNTAEANDVASSGWDTAAA
VvRPE1   HVPG---------------SGGDWAVNQNK-------------------------ETTAS
SmRPD1   ------------------------------------------------------------
ZmRPB1   SPINTDASFSPYVGHMAFSPFPSPGGYSPSSGGYS--PSSPVFTPEKGYSPLSPSYSPAS
AtRPB1   SPMS-DAQFSPYVGGMAFSPSSSP-----------------------GYSPSSPGYSPTS


                         2120                2140                2160
ZmRPD1   -----------------------------------------------------------R
SbRPD1   -----------------------------------------------------------Q
OsRPD1b  -----------------------------------------------------------Q
OsRPD1a  -----------------------------------------------------------Q
BdRPD1   -----------------------------------------------------------W
AtNRPD1  ------------------------------------------------------------
CpRPD1   --------------------------------------------------------PLKQ
PtRPD1   --------------------------------------------------------STEQ
VvRPD1   --------------------------------------------------------CHEQ
ZmRPE1   VQDNST--------------------------------TDWGG------------WSVEK
SbRPE1b  VQDNSTDWGGWSSGVGAAAKPADQDNSWEVHAKAQDNCTDWGG------------WSTDK
OsRPE1b  VEKSS---------------------------------SDWGG------------WGTEK
BdRPE1   AENDS---------------------------------TDWGG------------WGNEK
SbRPE1a  ---------------------------------------SW----------------TDK
OsRPE1a  ---------------------------------------TW----------------TDK
AtNRPE1  VEKED----------------------------------AWSS------------WNTR-
CpRPE1   ----S----------------------------------SWSS------------WSTDR
PtRPE1a  RKINS----------------------------------SWNSENDVTQSNSLSGWATKK
PtRPE1b  RTTNN----------------------------------SWNSENNVAQSNSFSGWATKK
VvRPE1   TLKPS----------------------------------AWSS------------WGTDK
SmRPD1   ------------------------------------------------------------
ZmRPB1   PS-----------------------------------------------------YSPTS
AtRPB1   PG-----------------------------------------------------YSPTS
```

```
                          2180                2200                2220
ZmRPD1    NFEKNHLDTRRQSTENASIC----------------------------------------
SbRPD1    NVEKNHLDTRRQSTENASIC----------------------------------------
OsRPD1b   ALEKNFMDTYKQRTEKPSKQ----------------------------------------
OsRPD1a   ALEKNVMDTYRKRTEKTSKR----------------------------------------
BdRPD1    GPEKNHMETDSTRTKNASER----------------------------------------
AtNRPD1   ----MRRTNSAPKSDKATVQ----------------------------------------
CpRPD1    NVKSDLPNSMNIKSDKYGDR----------------------------------------
PtRPD1    NTEFGVLDAQIYKSDKCGAQ----------------------------------------
VvRPD1    NLKVKVPITCYQTTTKCGAQ----------------------------------------
ZmRPE1    PTGEATVSGEPAETDTWADK-----GAKMESDAGDGNWEK-SSTPEAS----KKNDS---
SbRPE1b   PTGEATVSGQPAEMDTWADK-----GTKMESGAGDANWEKKSSTPEAS----NKNDPWGK
OsRPE1b   AKEKEKISEEPAQHDAWSVQ-----GPKRATD-GGASWKKQSST-QNDGNSWKENKGRGS
BdRPE1    AKDNRTVSTEPAELDTWSDR-----GAKKGTDGGGGSWGKQTNTCEDSGTNLERN-----
SbRPE1a   PKGDSLLHDFMGRAGMWSTVQKHQEMQNKTKWNSVANWKNDKPMGPPRTAFAESTSTRGQ
OsRPE1a   PKAEFLMESEGRRAGMHSTGQKH---------PRKPNWHEGNTKSSPNSTAVEF------
AtNRPE1   ---------KDAQESSKS--------------DSGGAWGIKTKDADADTTPNWETSPAPK
CpRPE1    AHSQDVCSTKTLEECLNSAGGTGVIGSDKTNLDSQNTWANWNTKGSYPTKASEDSP----
PtRPE1a   SETHNGFATKVQEKPARSND-----------WDVGTAWG-RKAGDNKFA--N--------
PtRPE1b   PEPHNGFATKVQEEPTTSND-----------WDAGAAWG-RKDRDNKFAETN--------
VvRPE1    VTMKDTFSTREPDESSRSAG-----------WDDKGTWGTDKAQNTAFRRTHEDSPRSSG
SmRPD1    ------------------------------------------------------------
ZmRPB1    PSYTPGSPTYSPTSPNYSPTSPTYSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSP---
AtRPB1    PGYSPTSPGYSPTSPTYSPSSPGYSPTSPAYSPTSPSYSPTSPSYSPTSPSYSPTSP---
```

```
                          2240                2260                2280
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    ------------SENTWDKR------------------KGDGGDGAWGNRSD--------
SbRPE1b   ------------SENTWDKR---------------KGDGGDGGDGAWEKKSV--------
OsRPE1b   ------------NGGSWEK--DNAQKGSWGRGNDEAENNNDVQNKSWETVAA--------
BdRPE1    ---------------SWAKRPSSPSLSTW------AKKNSDGGDGTWDKQAN--------
SbRPE1a   NKRQF-------TGQVYARKQPKHS-----------------------------------
OsRPE1a   ------------TGQVFQRRQLKTKSN---------------------------------
AtNRPE1   DSIVPENNEP--TSDVW------GHKSVSDKSWDKKNWGTESAPAAWGSTDA-----AVW
CpRPE1    ------------KSCGWV-----ADKCGSGETNAK-------GEHNWSNWTA--------
PtRPE1a   ------------VTKSWWGKVTDGDESEQNKNK-QHQEDQELGTHGWDDKMSPDQLISGW
PtRPE1b   ------------ASKSWWGKVTDGDESGQNKSKNKRPEDQDVGTHGWDDKMSQDQSISGW
VvRPE1    RDETFRDGRPQFASSAWGKKIDEADKTGWNKNDGKPQMDKLRESYDWDCKVA--------
SmRPD1    ------------------------------------------------------------
ZmRPB1    ------------------------------------------------------------
AtRPB1    ------------------------------------------------------------
```

```
                              2300                2320                2340
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    --DGHGNWEHPSNWNGQSLDVDQDT----------------------WGNARGKKKADGN
SbRPE1b   --DGHGNWDHPGNWNGQSLNVDQDT----------------------WGNARGKKKADGN
OsRPE1b   --DAHASTEK-S-WGNVTASPSDNA----------------------W-SAAPVSQGNGS
BdRPE1    --SCKKNVEQDS-WKNMPVSPARNA----------------------W-NKKESSRGDAT
SbRPE1a   -----------------------------------------------W-SQAATHQNNKL
OsRPE1a   -----------------------------------------------W-NSDATQQDDKP
AtNRPE1   GSSDKKNSETES----DAAAWGSRDKNNSDVGSGAGVLGP-------WNKKSSETESNGA
CpRPE1    VKGGSQDFTATKTWEESSKAGG-------------------------WGSKKSGN-----
PtRPE1a   ASTTTQEATTESCSSKAASVWGTKNTNVDEQGSENHVLLNQAKESSDWNKKSNSNQTDAA
PtRPE1b   ASKTTQEATTESLG---------------------------------WDSKGNSNPGDAA
VvRPE1    -----QEKTTQSTYGGISSTTG------------------------DW--KKNELQMEVV
SmRPD1    ------------------------------------------------------------
ZmRPB1    ------------------------------------------------------------
AtRPB1    ------------------------------------------------------------

                              2360                2380                2400
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    YCQWEEQPSNYKQKKTNADHDSSYNNVMPSSEIAWNAGDGTGRPNAKSNA----ESSWGE
SbRPE1b   -CQWEEQPSTYRRKKTNADHNSSYNNVMPSSDNAWNAGERFGRSNAKSNA----GSSWGE
OsRPE1b   ---SDTK----------------------QSD-SWDGWKSAGVDKAINKD----KESLGN
BdRPE1    ---WEMRASTLEEKKTSESNEGSWEKSNAQKD-SWGNTQHGSSDKMAVKDNDMQQDPWGH
SbRPE1a   ---------------------------------SWCGENVAGAQDFANA-----------
OsRPE1a   ---------------------------------SWYSSNSAGTQNFTIAG----------
AtNRPE1   -----------------TWGSSDKTKSGAAAWNSWDKKNIETDSE---------PAAWGS
CpRPE1    ------------------GESNVGEGS------PWSNWKTNKGN------------SQGT
PtRPE1a   -----------------CGSKA---AS------SWGAKNTDADK------------RWGR
PtRPE1b   -----------------CGWKA---AS------TWGAENTDGDK------------LWGK
VvRPE1    -----------------QHDESPVNEH------SWDA-NLPED-----------------
SmRPD1    ------------------------------------------------------------
ZmRPB1    ------------------------------------------------------------
AtRPB1    ------------------------------------------------------------
```

```
                          2420                2440                2460
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    EDKMESDDHPKVPKESDTWNT-------------------------------------GR
SbRPE1b   KDKMESDEHPKVPKESDTWNT-------------------------------------GK
OsRPE1b   VPAS-----PSFSA----WNASP---------------------------------VSQG
BdRPE1    I-AT-----QNINAQDDLWGS-----------------------------------VAAK
SbRPE1a   ------------------------------------------------------------
OsRPE1a   ------------------------------------------------------------
AtNRPE1   QGKKNSETESGPAA----WGAWD----------------------------------KKK
CpRPE1    HPQKAQEESSDFGG----WGSNK------------------------------FSRCETN
PtRPE1a   KVDLNQADTS--CS----WGRSKTP---------------DRGWGLSNYGGSNGSEMENK
PtRPE1b   EVSSNQADTA--SG----WGKPKSPEISLGWGSTKESVKSDRGWGVSSSGGGR----DKK
VvRPE1    --PLAQATTS--VG----WDSST-----------------GKDWT------------KRK
SmRPD1    ------------------------------------------------------------
ZmRPB1    ------------------------------------------------------------
AtRPB1    ------------------------------------------------------------


                          2480                2500                2520
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    SNESPWDNTDALQDSW-VKSAARNNNTQDGSWDKVVSMKDLDSLQDSWSKATI-------
SbRPE1b   SNESPWDNTDALQDSWGVNSATHDNNTEDGSWDKVVAIKDPVSQQDSWSNVAI-------
OsRPE1b   NERSDAKQSDSW-DGWKSAGVDKAINKDKESLGNVPA----SPSFSAWNAAPVSQGN---
BdRPE1    AQTSTAENTDAQDDSWGAVAAKAQTSTAQESWGNVAA----SPSDNAWKAPPISQTS---
SbRPE1a   -----------------------------------------ESSKGGWNRKNSGFGRGGH
OsRPE1a   -----------------------------------------SSRPGEWNRKNNNRGQGGG
AtNRPE1   SETE------PGPAGWGMGD--------KKNSETELG----PAAMGNWDKKKSDTKS---
CpRPE1    LKEQSTWSK------WNSNKGDNQDAYATMLENNDND----TGKEKGW------------
PtRPE1a   TENQSLLDRGKESVGWGGKNTDADKPWSNKVNSNQAD----TA--SGWGKSKSLDRG---
PtRPE1b   TENQSLAGQGKESGGWG-----------NKVTSNQAD----TA--SGWGKPKSSENSQGW
VvRPE1    LQSPSEQQRDPAIKSWSSSHNV------MKEQSNQPA----ST--HGWDSP---------
SmRPD1    ------------------------------------------------------------
ZmRPB1    ------------------------------------------------------------
AtRPB1    ------------------------------------------------------------
```

```
                         2540                2560                2580
ZmRPD1   -----------------------------------------------------------R
SbRPD1   -----------------------------------------------------------R
OsRPD1b  ------------------------------------------------------------
OsRPD1a  ------------------------------------------------------------
BdRPD1   ------------------------------------------------------------
AtNRPD1  --------------------------------------------------------PFGL
CpRPD1   --------------------------------------------------------SIYV
PtRPD1   --------------------------------------------------------FLHK
VvRPD1   --------------------------------------------------------LVYA
ZmRPE1   ------------------------QTNDA-QNDS----------------------WDNV
SbRPE1b  ------------------------QKNDA-QNDS----------------------WDNV
OsRPE1b  ------------------------ERLDAKQSDS----------------------WDGW
BdRPE1   ----------------------AAEHTDA-HNDS----------------------W-GI
SbRPE1a  R-------------------------------------------------------GGGR
OsRPE1a  REV-----------------------------------------------------WKSE
AtNRPE1  ----------------------GPAAWGSTDAAA----------------------WGSS
CpRPE1   ----------------------SSWARDDSINGSVLPEGDSSKSNGLDAGTVGDGSWEQT
PtRPE1a  ------------WGVSNSGGGNGSEMEDKTENQSLLDRGKESGGWG-GKNTDADKPWSNK
PtRPE1b  GLSKESGKEVHEWGVPNSAGGNGSETNNNNENQSLVEQGKESG-------------WDNK
VvRPE1   ----------------------GAKGWNDVEEQSQ---------------------WNQR
SmRPD1   ------------------------------------------------------------
ZmRPB1   --------------------------------------------------------SYSP
AtRPB1   --------------------------------------------------------SYSP
```

```
                         2600                2620                2640
ZmRPD1   LACKSSKGSTTVNGVAITID----------------------------------------
SbRPD1   LACK-SKGSATVNGVAITSD----------------------------------------
OsRPD1b  RSAFSSKGNATINGGTISVN----------------------------------------
OsRPD1a  RSALNSEGNATINGGAISFN----------------------------------------
BdRPD1   ----WSSGNATFNGGTISVE----------------------------------------
AtNRPD1  LHSAFLKDIKVLDGKGIPMS----------------------------------------
CpRPD1   HSGSISLGLKKLE--GISRA----------------------------------------
PtRPD1   FGGCGPKGFKVKE--GIPRS----------------------------------------
VvRPD1   NGDSASKGCKSLE--KISKS----------------------------------------
ZmRPE1   --AKNAPDSAAEDSWGAATP----------------------------------------
SbRPE1b  --AEKALNSASQDSWGHLAA------------------------------TPVSNS----
OsRPE1b  KSAGVDDSVKDKESWGNVPA------------------------------SPSDSAWNAA
BdRPE1   VAAKAQTSTAQQESWGNATA------------------------------SPSDNAWNAA
SbRPE1a  GMAFANAESSSSGGWNRKNS----------------------------------------
OsRPE1a  GPHRGGSSSNRNQGGGRAV-----------------------------------------
AtNRPE1  -DKNNSETESDAAAWGSRNK----------------------------------------
CpRPE1   -------PTGTSDGWGVLSE----------------------------------------
PtRPE1a  ---VNSNQADTASGWGKSKSLDRGWGVSNSGGGNGSEMEDKTENQSLLDRGKESGGWGKP
PtRPE1b  ---ASSNQEGTASGWGKPKS----------------------------------------
VvRPE1   GSAVKNDQSESSHGWGPSNE----------------------------------------
SmRPD1   ----------VDDTVSATLS----------------------------------------
ZmRPB1   TSPSYSPTSPVYSPTSPAYS----------------------------------------
AtRPB1   TSPSYSPTSPSYSPTSPAYS----------------------------------------
```

```
                          2660                2680                2700
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    ------------------------------------------------------------
SbRPE1b   ---------DAKQSDSWDGWNAVP--AENSQGTA--------------------------
OsRPE1b   PVSQGNESSDAKQSDSWDGWKSAG--VDASTNKDKESWGNVPASPSDSAWNAAPVSQGDD
BdRPE1    PMDL-----DAKQPGSWDGWSSAL--AEDS------------------------------
SbRPE1a   -----------------------------------------------GFGRGGRRGGGRG
OsRPE1a   -------------------WK-----SEASHRGSGNNRNR---------------GGGRA
AtNRPE1   --------KTSEIESGAGAWGSWGQPSPTAEDKDTNEDDRNPWVSLKETKSREKDDKERS
CpRPE1    ----------STEPAGCHGWG-----LPNNEDITQNESQG------------------RR
PtRPE1a   KSISQGWGSSKDSVKAVDGWG-----VPNSA--GSNGSER------------------DQ
PtRPE1b   PALSEGWGSPREPVKAVHGWG-----VPNSG--GGNGSGR------------------DQ
VvRPE1    ----------QNQLPSSQGWG-----SPNAG--AGHESET------------------QS
SmRPD1    ------------------------------------------------------------
ZmRPB1    ------------------------------------------------------------
AtRPB1    ------------------------------------------------------------
```

```
                          2720                2740                2760
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    ----AETTDSGNKEWKSDGWGAKSG-NWSSQRNNPGRP---------PRRPDERGPP---
SbRPE1b   --QWKERTDSGNKDWKSDGWGAKSG-NWSSQRNNPGRP---------PRRPDERGPP---
OsRPE1b   VWNSAEANESRNKDWKSDGWGARGG-NWRGQRNNPGRPPRKPDGRGLPRRPDERG-----
BdRPE1    --NKADDSSNKNKGWKSDGWGAK-G-NRRDQRDNPSMP---------PMRPDER------
SbRPE1a   MW----------KSEGSHRGGSNST-NWRAQNNNSARQCGISY-----------------
OsRPE1a   VW----------KSEASRRGGSMRQ-----------------------------------
AtNRPE1   QWGNP-----AKKFPSSGGWSNGGGADWKGNRNHTPRP---------PRSED-NLAPMFT
CpRPE1    TWEFS----KKKRNEGSRGWSSNSG-DWKGKKNLPGKLAG-------NVKDDFGAGRLYT
PtRPE1a   QWGQQSGEFKKNRTEGSRGWGSNNG-HWK-KRNRPSKP-----------HEDSSSSGLFT
PtRPE1b   QWGQQSREFKKDRFEGSRGWGSNNG-DWKNKRNRPSKP-----------HEDLNASGIFT
VvRPE1    QWGQPSG--KKSRPEGSRGWGSNNT-EWKNKKNRPNKPQG-------PLNDDYSAGGIFT
SmRPD1    ------------------------------------------------------------
ZmRPB1    -----------------------------------------------------PTSPAYS
AtRPB1    -----------------------------------------------------PTSPAYS
```

```
                         2780                2800                2820
ZmRPD1   ------QDFLHAKVSIWDNIIDMRTSLQNMLREYP--LNGYVAEPDKSQLIE-ALKFHSR
SbRPD1   ------QDFLHAKVSIWDNIIDMRASLQNMLREYP--LNGYVMEPDKSKLIE-ALKFHPR
OsRPD1b  ------QKFLDSKVGIWENIIDMRTCLQNMLREYT--LNEVVTEQDKSCLIE-ALKFHPR
OsRPD1a  ------QKFLNAKVGIWENIIDMRTSLQNMLREYT--LNEVVTEQDKSCLME-ALKFHPR
BdRPD1   ------QNYLGAKVGVWDSIIDMRTCLQNMLREYQ--LDEYVVELDKSRVIE-ALRFHPR
AtNRPD1  ---------LLRTIFTWKNIELLSQSLKRILHSYE--INELLNERDEGLVKM-VLQLHPN
CpRPD1   ---------YLRTVLTWKDIQKLYHASKKILNKYP--IDHRLNEGEKKILMM-ALYFHPQ
PtRPD1   ---------FLRRLLTYDDIQRMSYTVRKILNKYS--VDQQLNESDKSVLMM-TLYFHPR
VvRPD1   ---------VLRSFLSLNDIQKLSRRLKFILQKYP--INHQLSEIDKTTLMM-ALYFHPR
ZmRPE1   PPRQRFEL-TVAEKNILLEVEPIKLRVRSIFREAC--DGVRLNPEDEKFILEKVLEHHPE
SbRPE1b  PPRQRFEL-TIEEKKILLEVEPLIFRVRRIFREAC--DGVRLKPEDEKFIQEKILEHHPE
OsRPE1b  PPRRHFDL-TAEEEKILGEIEPTVLSIRKIFRESI--DSIKLSPEDEKFIKENVLEHHPE
BdRPE1   PPRPRFEV-PAEAKKILREIEPIVSMVRKIFRESC--DGVRLPLEDEKFIKESILEHHPE
SbRPE1a  -------SFTPVEQQIYTQVEPIIKNVKRIIRESR--DGMKLSQDDEMFIMNKILMYHPE
OsRPE1a  ---VASCAFTPVEQQIFEQIEPITKNVKRIIRESR--DGIKLPPDDEKFIVTNVLMYHPE
AtNRPE1  ATRQRLDSFTSEEQELLSDVEPVMRTLRKIMHPSAYPDGDPISDDDKTFVLEKILNFHPQ
CpRPE1   HTRQRLDMFTSEEQDVLSDVEPLMQSIRRIMHQSGYNDGDPLSVDDQSFVIDKVFMYHPD
PtRPE1a  MTRQWLDIFTSQEQDILSDVEPLMLSIRRIMHQTGYSDGDPLSADDQSYVLDNVFNYHPD
PtRPE1b  TTRQRLDVFTSQEQDILSDIEPLMLSIRRIMHQTGYNDGDPLSADDQSYVLDNVFHYHPD
VvRPE1   ATRQRVDIFTSEEQDILLDVEPIMQSIRRIMHQAGYNDGDPLSADDQSYILDKVFNNHPD
SmRPD1   ---------AKDREIVWARIDQRSQKLHDILRKSL--TGTPVSAANEAVILD-TLKYHPM
ZmRPB1   PTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPSYS-PTSPSYSPTSPAYSPT-SPGYSPT
AtRPB1   PTSPAYSPTSPSYSPTSPSYSPTSPSYSPTSPSYS-PTSPSYSPTSPAYSPT-SPGYSPT
```

```
                         2840                2860                2880
ZmRPD1   GAEKIGVGVREIKIGLNPSHPGTRCFILLRNDDTTEDF---------------------S
SbRPD1   GAEKIGVGVREIKVGLNPNHPGTRCFILLRNDDTTEDF---------------------S
OsRPD1b  GYDKIGVGIREIKIGVNPGHPNSRCFIVQRSDDTSADF---------------------S
OsRPD1a  GYDKIGVGIREIKIGVNPGHPSSRCFIVLRNDDTTADF---------------------S
BdRPD1   GREKIGVGIRDIK-----------------------------------------------
AtNRPD1  SVEKIGPGVKGIRVAK-SKHGDSCCFEVVRIDGTFEDF---------------------S
CpRPD1   SYEKIGTGAQYIKVLKTE------------------------------------------
PtRPD1   RDEKIGIGAKDIKVINHPEYQDTRCFSLVRTDGTIEDF---------------------S
VvRPD1   RDEKIGPGAQNIKVRYHSKYHNTRCFSLVRTDGTEEDF---------------------S
ZmRPE1   KQSKVSGEIDYLTVNKHQTFQDTRCFFVVSTDGSQADF---------------------S
SbRPE1b  KQSKVSSEIDHIMVNKHHTFEDTRCFFVVSTDGSQADF---------------------S
OsRPE1b  KQSKVSGEIDHIMVDKHQVFQDSRCLFVVSSDGTRSDF---------------------S
BdRPE1   KERKVPGEIDHIMVNKHHIFQESRCFYVVLADGTHTDF---------------------S
SbRPE1a  KEKKMAGQGNYIMVNKHQTFPSSRCLYVASSDGSSSDF---------------------S
OsRPE1a  RKKKIAGNGNYITVDRHQVFHGSRCLYVMSSDGSRKDF---------------------S
AtNRPE1  KETKLGSGVDFITVDKHTIFSDSRCFFVVSTDGAKQDF---------------------S
CpRPE1   RAVKMGAGIDFVTVSRHSNFQDSRCFYIVSTDGRKQDF---------------------S
PtRPE1a  KAVKMGAGINHVTVSRHSNFQESRCFYIVSTDDCKQDIFPTANVWRTSSGENNLTWQMNS
PtRPE1b  KAVKMGAGIDHVTVSRHSNFQESRCFYIVSTDGCKQDF---------------------S
VvRPE1   KAVKMGTGIDYVMVSRHSSFLESRCFYVVSTDGHKEDF---------------------S
SmRPD1   MDSKVGCGVRHIRVDNHHSF-GGRCFHIVRLDGSVEDF---------------------S
ZmRPB1   SP---------------------------------------------------------S
AtRPB1   SP---------------------------------------------------------S
```

```
                          2900                2920                2940
ZmRPD1    YHKCVQGAADSIS---PQLGSYLKKLYYRA------------------------------
SbRPD1    YHKCVHGAANSIS---PQLGSYLKKLYHRA------------------------------
OsRPD1b   YNKCVLGAANSIS---PELGSYIEKILSNRAIRPHQL-----------------------
OsRPD1a   YNKCVLGAANSIS---PELG----------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   YHKCVLGATKIIA---PKKMNFYKSKYLKNGTLESGGFSENP------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    YRKCLHNALEIIA---PQRAKRYCEKYLTSKVSATDNSGCTDLPLDN-------------
VvRPD1    YHKCVHGALEIID---PRRARSYQSRWLPYSEV---------------------------
ZmRPE1    YLKCLENFVRKSY---TEDADTFCMKYLRP-------------------------PETEQ
SbRPE1b   YLKCLENFVRKNY---TEDVDSFCMKYLRPRRRQAPPPDVGTAPGTPAEVPPSTAAETEQ
OsRPE1b   YLKCMENFVRKTY---PEHGDSFCKKYFKRRRDQPPAADGGTAPGTPAGATQSTAVDTQE
BdRPE1    YNKCMDNYVRKTYTDAAEHADL--------------------------------------
SbRPE1a   YKKCLENFIRIHY---PHAAESFCRKYFK-------------------------------
OsRPE1a   YKKCLENYIRAQY---PDAADSFCRKYFK-------------------------------
AtNRPE1   YRKSLNNYLMKKY---PDRAEEFIDKYF-TKPRPSGNRDRNNQDATPPGEEQSQPPNQSI
CpRPE1    YRKCLDNFIKGKY---PDIAEQFIGKYF-RKPRSSGNQQKPVLEE---------------
PtRPE1a   SESILQEEAIGSA---PLLQRE-------PR----RNRPRD------------V------
PtRPE1b   YRKCLENFIKGKY---PDLADEFIAKYFARR----GNRQRTPAPEGTEEEKQAL------
VvRPE1    YRKCLENFIKEKY---PDNAETFIGKYF-RRPRAGGNRERSVIPEDGGNREQSVVP----
SmRPD1    YHKCLLERIKGNT---------VLVQRYKKKFMGGKNGRKEEVPVEIFSQKNDTGRMYDK
ZmRPB1    YSPTSPSYSPTSPSYNPSSAKYSPSHAYSPSSPRMSP---YSQTSPSYSPT---SPTYSP
AtRPB1    YSPTSPSYGPTSPSYNPQSAKYSPSIAYSPSNARLSPASPYSPTSPNYSPT---SPSYSP

                          2960                2980                3000
ZmRPD1    ------------------------------------------------------------
SbRPD1    ------------------------------------------------------------
OsRPD1b   ------------------------------------------------------------
OsRPD1a   ------------------------------------------------------------
BdRPD1    ------------------------------------------------------------
AtNRPD1   ------------------------------------------------------------
CpRPD1    ------------------------------------------------------------
PtRPD1    ------------------------------------------------------------
VvRPD1    ------------------------------------------------------------
ZmRPE1    GTPPAPQAEVPQETWGSPAVPLEGGTHIAGPDSTGDAVILGEQHDLTPASPAVAPQVASE
SbRPE1b   GT-PAPPAEVPQETLGSPAVALE-GTHNPRTDPTDDTELLGKDSDLTPASPAVAPQEAPK
OsRPE1b   GTSQQTQPDIATAPAATQQETLQ----------------------DTPAPPADDGLLGKG
BdRPE1    ------------------------------------------------------------
SbRPE1a   ------------------------------------------------------------
OsRPE1a   ------------------------------------------------------------
AtNRPE1   GNGGDDFQTQTQSQSPSQTRAQS--PSQAQAQSPSQTQSQSQSQSQSQSQSQSQSQSQSQ
CpRPE1    ------------------------------------------------------------
PtRPE1a   ------------------------------------------------------------
PtRPE1b   ------------------------------------------------------------
VvRPE1    ------------------------------------------------------------
SmRPD1    KTHGFLLVENHFVPVKTLKKT---------------------------------------
ZmRPB1    T----SPSYSQPSPSYSPTSPSGS--------------YSP--TAPGYSPSSTGQ----G
AtRPB1    T----SPSYSPSSPTYSPSSPYSSGASPDYSPSAG---YSP--TLPGYSPSSTGQYTPHE
```

```
                          3020                3040
ZmRPD1    ----------------------------------------
SbRPD1    ----------------------------------------
OsRPD1b   ----------------------------------------
OsRPD1a   ----------------------------------------
BdRPD1    ----------------------------------------
AtNRPD1   ----------------------------------------
CpRPD1    ----------------------------------------
PtRPD1    ----------------------------------------
VvRPD1    ----------------------------------------
ZmRPE1    PDTTDGTGLLGKAPQADWGPRFDAD---------------
SbRPE1b   PDPTDDTELLGNE-KPDLTPSSPGEALQATADPDSTLTDI
OsRPE1b   PSPSD-----------------------------------
BdRPE1    ----------------------------------------
SbRPE1a   ----------------------------------------
OsRPE1a   ----------------------------------------
AtNRPE1   SQSQSQSQSQSPSQTQTQSPSQTQAQAQSPSSQSPSQTQT
CpRPE1    -----------------------------------TENML
PtRPE1a   ----------------------------------------
PtRPE1b   ----------------------------------------
VvRPE1    -------------------------------EETGSENRQ
SmRPD1    ----------------------------------------
ZmRPB1    NDKDDKSAR-------------------------------
AtRPB1    GDKKDKTGKKDASKDDKGNP--------------------
```

Figure 3. Phylogenetic analysis of RPD1. Maximum likelihood tree generated from the MAFFT multiple sequence alignment (Figure 2) using the JTT substitution model. RPB1 from maize and *Arabidopsis* root the tree. Outgroup branch length is not to scale.

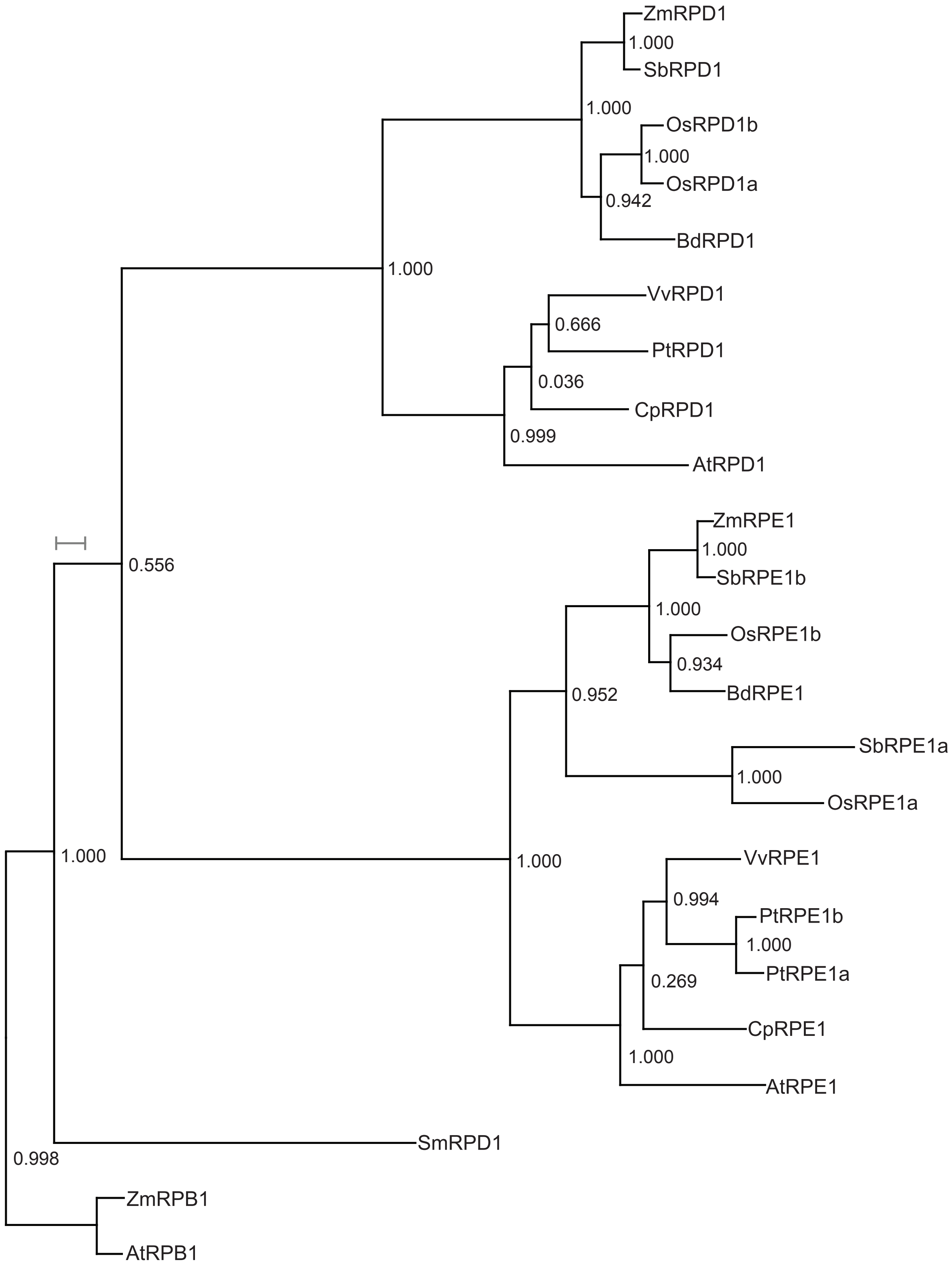

Figure 4. rmr7 encodes an RPD2-type protein and is renamed rpd2a. (A) Rmr7/Rpd2a gene model highlighting transition-type mutations in the respective mutant alleles. (B) Schematic of the predicted protein model highlighting domains (black boxes labeled A–I) that are highly conserved within all prokaryotic and eukaryotic RPB2 proteins [Cramer *et al*. 2001]. Predicted polypeptides inferred by three mutant alleles are indicated.

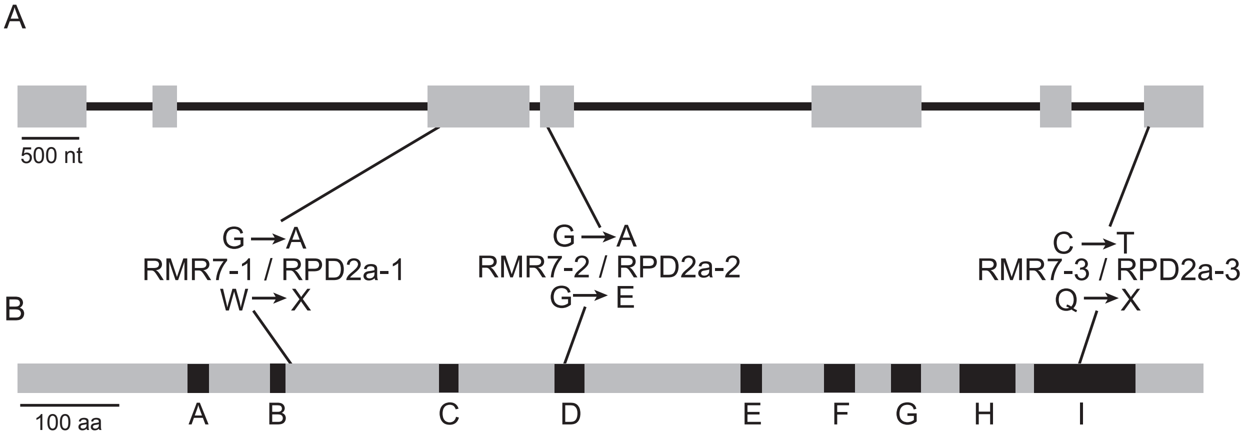

Figure 5. *rpd2a* and *rpd2b* are located on homoeologous regions of 2S and 10L. Gray boxes represent maize BACs, simple sequence repeat markers, or genes. Gray lines connect homoeologous features. Chromosomes are anchored on the right by known homoeologous gene pair of *b1* and *r1* [Swigonová *et al*. 2005].

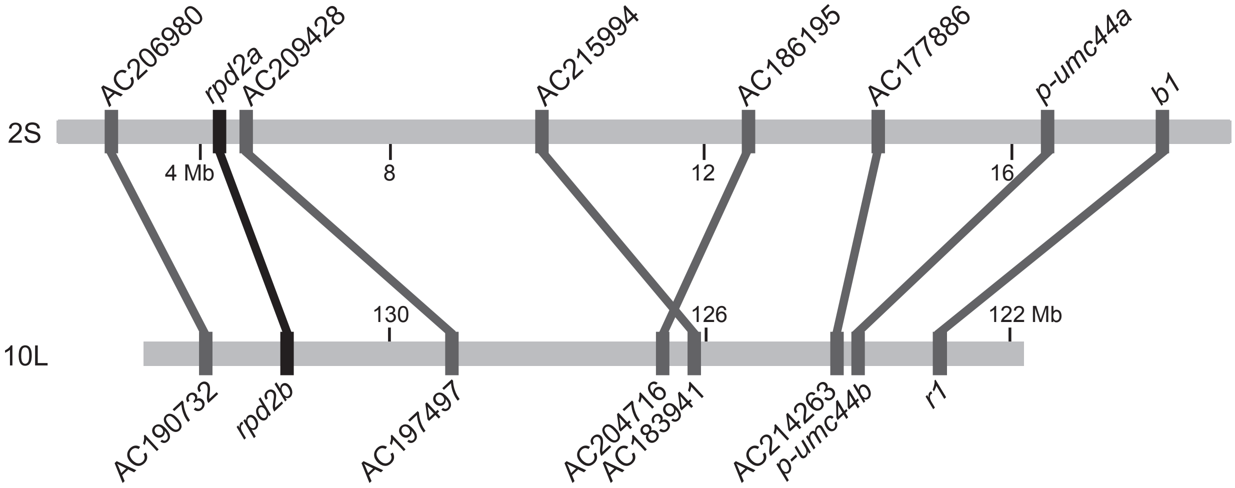

Figure 6. Alignment of full-length second largest polymerase subunits from various plant species. Conserved polymerase domains are indicated by black boxes below the alignment. Mutant lesions in ZmRPD2a are indicated by red text in the alignment and an asterisk below.

```
                            20                  40                  60
ZmRPD2a   ------------------------------------------------------------
SbRPD2a   ----------------------------------------MEELQKDGGQQSNGSDSEPE
SbRPD2b   ----------------------------------------MEELQKDSGQPSNGSDSEPE
ZmRPD2b   ------------------------------------------------------------
OsRPD2a   ----------------------------------------MEEPSKDNGQSSCVVDPELE
BdRPD2c   ----------------------------------------MEDIPRGSGHSTNGTEPELE
BdRPD2b   ----------------------------------------MEEPPRDNAHSKNGLEPELE
BdRPD2a   MYMTFLLSRLLVSYLMFFYDPFLNYRIAILDRVLAAVAGVMEEPPRDNAHSKNGPEPELE
ZmRPD2c   ----------------------------------------MGKPQTDGDQSPVNSD--TD
SbRPD2c   ---------------------------------------------MDGDQSTVVLD--TD
OsRPD2b   ---------------MWDEKERPRVFCLAPQDGEAVWWLAMEDPEITGQQSPNATSIVTD
BdRPD2d   ----------------------------------------MEEPQANDLQSPNGSDIELD
AtNRPD2a  ------------------------------------------------------------
CpRPD2    ------------------------------------------------------------
PtRPD2    ------------------------------------------------------------
VvRPD2    ------------------------------------------------------------
SmRPD2b   ------------------------------------------------------------
SmRPD2a   ------------------------------------------------------------
ZmRPB2a   ------------------------------------------------------------
ZmRPB2b   ------------------------------------------------------------
AtRPB2    ------------------------------------------------------------
```

```
                            80                 100                 120
ZmRPD2a   ------------------------------------------------------------
SbRPD2a   AMV---LDDNGAGKSHSMDG------------NRDSPVDVD-------------------
SbRPD2b   AMV---LDDNGAGKSRSMEG--NEDSPIDADVGKDSPIDVN-------------------
ZmRPD2b   ------------------------------------------------------------
OsRPD2a   PMM---LDDAREGVSHTLD-----------DANGHSSMDVD-------------------
BdRPD2c   PMI---LDDDGESRSRTID-----------DSNEQSSMGID-------------------
BdRPD2b   PMI---LDDNEESGSHTMD-----------DSNGQSSMDID-------------------
BdRPD2a   PMI---LDDNEESRSHTMD-----------DSNGQSSMDID-------------------
ZmRPD2c   VMDCLNFDGHGDVEDPHKEVAKGEQQPSGEVDEQQSVMDVDLTCITSVGDEGN-------
SbRPD2c   MMDCLNFDGYGDVEDPRKEGAKGERQPSGKVDELQSTMDVDLTCIAYVEDEGN-------
OsRPD2b   LMD---LDD-----------------IIVEGNEVQFAMDVDLRAIPSLKDGGHTDPLVQI
BdRPD2d   VVDFIALDYDGDAKCHIKQDAKGEQQPLADAD----------------------------
AtNRPD2a  ------------------------------------------------------------
CpRPD2    ------------------------------------------------------------
PtRPD2    ------------------------------------------------------------
VvRPD2    -----------------------------------------MGASDAKGDLGMSSSMGEK
SmRPD2b   ------------------------------------------------------------
SmRPD2a   ------------------------------------------------------------
ZmRPB2a   ----------------------------------------------MEDDEYEDGMDMGY
ZmRPB2b   ----------------------------------------------M-------------
AtRPB2    ----------------------------------------------M-------------
```

```
                                   140                 160                 180
ZmRPD2a   ------------------------------------MS------VESLEKFCKEASRSFF
SbRPD2a   -EGQSSMDVDTKGKPSLNDDVNGK-SSEPYSNAPIDLS------VESLEKFCKEASRSFF
SbRPD2b   -EGQSSMDVDIKAKSSLNDDVNGKSSSEPYSNAPIDMS------VESLEKFCKEASRSFF
ZmRPD2b   ------------------------------------MS------VESLEKFCKEASRSFF
OsRPD2a   -RGCHSMDT---TRSSLGDDGKGK--RDSYAQIPVDMS------IPSLEKFCKEASRSFF
BdRPD2c   -SDRSSMDVDMKGKSSLDGDGKGKYSSESHEEFPIDMS------LTSLEKFCKEASRSFF
BdRPD2b   -IEGSSMG-----------------------EQIPADMN------LTSLEKFCKEASRSFF
BdRPD2a   -IEGSSMG-----------------------EQIPADMN------LTSLEKFCKEASRSFF
ZmRPD2c   -EKQNAMDVDLKEILSEEDGGEGKASSDLPSQVPVDFN------VASLEKFCKEAARSFF
SbRPD2c   -EKQNAMDVDLKEILPEEDEGKGKASSDIPSHVPVDFD------VASLEKFCREASRSFF
OsRPD2b   PGDMSHMDVDLRVIPSLKDG----GHADPPVQVPVDKR------IASLEKLCKEASRSFF
BdRPD2d   -GGLSPMNVDLKGIPSLEDEREVMSSSDPCVQAPIDFN------VATLEKFCKEAARSFF
AtNRPD2a  ---MPDMDIDVKDLEEFEATTGEINLS--------ELG------EGFLQSFCKKAATSFF
CpRPD2    ------MN-D-------LDHIEQVNIH--------DLG------EDFLKKLCRNASISFF
PtRPD2    ----MDMDMD-------EDLMDTTNLN--------ELG------KETLQSFCKKAASLFF
VvRPD2    LSNGVQMEID-------DDLMGSIEID--------DLN------KEYLKTFCKKVAVSFF
SmRPD2b   --------------------------------------------------MEEEACDAWF
SmRPD2a   --------------------------------------------------MAEDVLAAFL
ZmRPB2a   GGHHQRGGGHAGYGAEEDDEMGYGEGGGDGDEMEEEADGDAEQQEDITQDDAWAVISAYF
ZmRPB2b   ------------------------------------------------------------
AtRPB2    ---------------------EYNEYEPEPQYVEDDDD------EEITQEDAWAVISAYF

                                   200                 220                 240
ZmRPD2a   DEVGLISHQINSYNEFVSHG---LQELFDSLGEVI----------VEPG--YDPSKKG-S
SbRPD2a   DEVGLISHQINSYNDFVSHG---LQELFDSLGEVI----------VEPG--YDPSKKG-S
SbRPD2b   DEVGLISHQINSYNEFVSHG---LQELFDSLGEVI----------VEPG--YDPSKKG-S
ZmRPD2b   DEVGLISHQINSYNEFVSHG---LQELFDSLGEVI----------VEPG--YDPSKKG-S
OsRPD2a   DEIGLISHQINSYNEFVSHG---LQELFDSLGEVT----------VEPS--YDPSNRG-P
BdRPD2c   DEIGLISHQINSYNDFISHG---LQELFDSLGEVT----------VEPS--YDPSKKG-P
BdRPD2b   EEIGLISHQINSYNEFISHG---LQELFDSLGEVT----------VEPG--YDPSKKG-P
BdRPD2a   EEIGLISHQINSYNEFVSHG---LQELFDSLGEVT----------VEPG--YDPSKKG-P
ZmRPD2c   SETGLVSHQINSYDHFVSHG---LQELFDSLGEIT----------VEPD--YDPSNK--H
SbRPD2c   SATGLVSHQINSYNQFVSHG---LQDLFDSLGEIT----------VEPD--YDPSNK--S
OsRPD2b   RETRLVSHQINSYNDFVSHG---LQKMFDSLDEVT----------VEPD--YDPSKK--V
BdRPD2d   SETGLVSHQINSYNDFISHG---LQELIDSVGEIT----------VEPD--YDPSKKAEA
AtNRPD2a  DKYGLISHQLNSYNYFIEHG---LQNVFQSFGEML----------VEPS--FDVVKKK-D
CpRPD2    KEYGLNSHQINSYNDFVKHG---LQKVFDSYGEMT----------IEPT--YDPSKKG-D
PtRPD2    DEYGLISHQINSYNSFINSG---LQRVFDSFGEVA----------VEPG--YDSSKQK-D
VvRPD2    NEYGLIQHQINSFNDFIKNG---IQRVFDSFGEIP----------VEPG--YDPSKRG-E
SmRPD2b   QARGLVAHQLDSFNRFCGAGAHSLALLFGSPAHFTDIKGEVRMAAMPPC--RDPV-----
SmRPD2a   RGRSPVAHLIDSFDDFCEA----LPSLFQQTEEIS----------VEKE-----------
ZmRPB2a   EEKGLVRQQLDSFDEFIQNT---MQEIVDESADIE----------IRPESQHNPGRQA-E
ZmRPB2b   ------------------------------------------------------------
AtRPB2    EEKGLVRQQLDSFDEFIQNT---MQEIVDESADIE----------IRPESQHNPGHQS-D
```

```
                           260                 280                 300
ZmRPD2a   GGWKHAIIKFGRVKLEKPVFWTGK----DEGSVDFKPWHARLQNMTYASRLIVEVTIQVL
SbRPD2a   GGWKHAIIKFGRVKLEKPVFWTGK----DEGSVDFKPWHARLQNMTYASRLIVEVNIQVY
SbRPD2b   GGWKHAIIKFGRVKLEKPVFWTGK----DEGSVDFKPWHARLQNMTYASRLKVEVTIQVY
ZmRPD2b   GSWKHAIIKFGRVKLEKPVFWTGK----DEVSVDFKPWHARLQNMTYASRLRVEVTIQ--
OsRPD2a   GGWRHAIIKFGRVQLEEPVFWSHGC-DIDEQSLKLKPRHARLQNMTYSSKMKVEVHFQVY
BdRPD2c   GGWRHAIIKFGKVKLQEPVFWSDKCEDKYEEALKLKPRHARLQNMTYSSKMEVEMNIQVY
BdRPD2b   GGWRHAIIKFGKVKLEEPVFWSGKI-DIDEESLKLKPRHARLQNMTYSSKMEVEVNIQVY
BdRPD2a   GGWRHAIIKFGKVKLEEPVFWSGKI-GIDEESLKLKPRHARLQNMTYSSKMEVEVNIQVY
ZmRPD2c   GAWKHATVKFGRVKLDEPVFMLENS-DLEEQDLKFKPRHARLQKMTYASRMNVEMTVQVY
SbRPD2c   GAWKHATIKFGRVELSEPVFMVDNL-DLEQQDLKFKPRHARLQRMTYASRMNVEMTAQVY
OsRPD2b   GPWRHATIKFGRVELEEPVFWVDNC-DLDVETLKLKPKHARLQKMTYSSKMKVEMTVQVY
BdRPD2d   GAWRHATIKFGRVKFEEPVFWVEDT-ELDEHTLKLKPKHARLQNMTYSSKMFVEMTVQVY
AtNRPD2a  NDWRYATVKFGEVTVEKPTFFSDD------KELEFLPWHARLQNMTYSARIKVNVQVEVF
CpRPD2    NDWRYASVRFGKVTVDQPTFVGGT--NCDEK--NMLPRHARLQNMTYASRMKVNVHVQV-
PtRPD2    GEWRRASVRFGKVTLDRPSFWGGT--SSDAEH-NMFPRHARLQNMTYSARMKIHVNVQVY
VvRPD2    GDWRYASVRFGKVTLERPRVWAGE--SDGKESLNFLPRHARLQNMTYSSRMKAQVHFQVY
SmRPD2b   --PALATIRIRNLVLHKPADATTGR--------PLFPREARLRGITYSARLCADVELQVG
SmRPD2a   --GSTASIKLLNASLRPPVVK--------------YPWEARLGDQSYSARLFADIHVRLS
ZmRPB2a   FAETLHKISFGQIYLSKPMMT-----EADGETATLFPKSARLRNLTYSAPLYVDVSYRVM
ZmRPB2b   ---TLHRISFGQIYLSKPMMT-----EADGETATLFPKSARLRNLTYSAPLYVDVSYRVM
AtRPB2    FAETIYKISFGQIYLSKPMMT-----ESDGETATLFPKAARLRNLTYSAPLYVDVTKRVI
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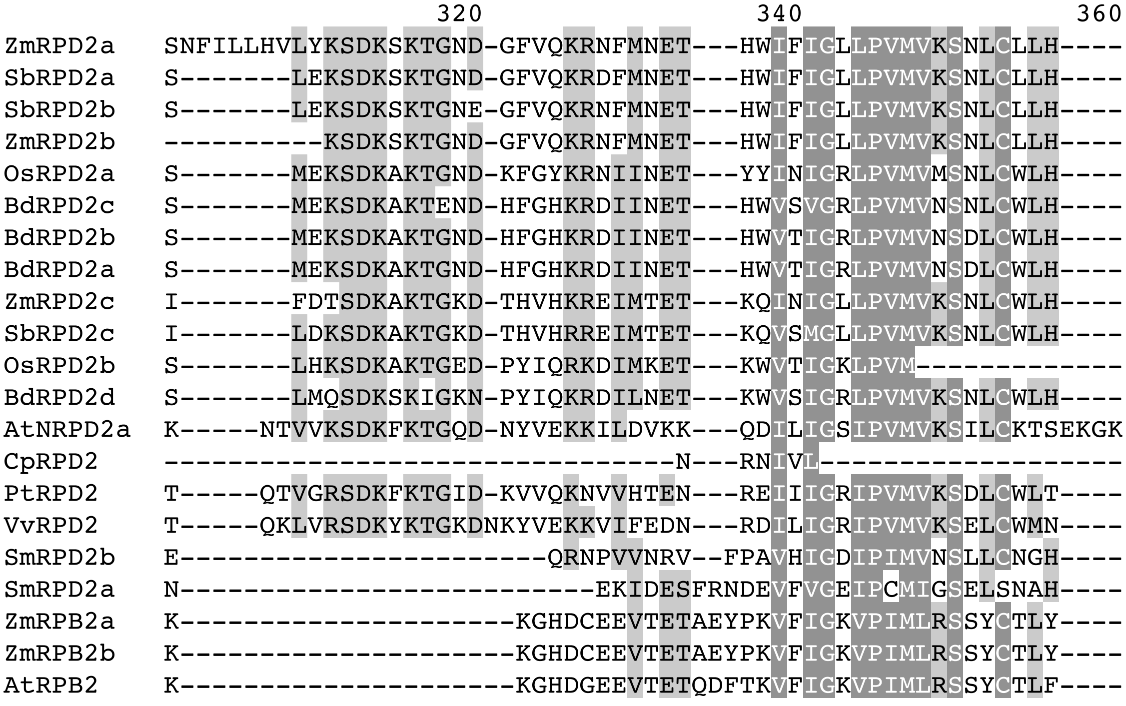

```
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SbRPD2a   S-------LEKSDKSKTGND-GFVQKRDFMNET---HWIFIGLLPVMVKSNLCLLH----
SbRPD2b   S-------LEKSDKSKTGNE-GFVQKRNFMNET---HWIFIGLLPVMVKSNLCLLH----
ZmRPD2b   ----------KSDKSKTGND-GFVQKRNFMNET---HWIFIGLLPVMVKSNLCLLH----
OsRPD2a   S-------MEKSDKAKTGND-KFGYKRNIINET---YYINIGRLPVMVMSNLCWLH----
BdRPD2c   S-------MEKSDKAKTEND-HFGHKRDIINET---HWVSVGRLPVMVNSNLCWLH----
BdRPD2b   S-------MEKSDKAKTGND-HFGHKRDIINET---HWVTIGRLPVMVNSDLCWLH----
BdRPD2a   S-------MEKSDKAKTGND-HFGHKRDIINET---HWVTIGRLPVMVNSDLCWLH----
ZmRPD2c   I-------FDTSDKAKTGKD-THVHKREIMTET---KQINIGLLPVMVKSNLCWLH----
SbRPD2c   I-------LDKSDKAKTGKD-THVHRREIMTET---KQVSMGLLPVMVKSNLCWLH----
OsRPD2b   S-------LHKSDKAKTGED-PYIQRKDIMKET---KWVTIGKLPVM-------------
BdRPD2d   S-------LMQSDKSKIGKN-PYIQKRDILNET---KWVSIGRLPVMVKSNLCWLH----
AtNRPD2a  K-----NTVVKSDKFKTGQD-NYVEKKILDVKK---QDILIGSIPVMVKSILCKTSEKGK
CpRPD2    -------------------------------N---RNIVL--------------------
PtRPD2    T-----QTVGRSDKFKTGID-KVVQKNVVHTEN---REIIIGRIPVMVKSDLCWLT----
VvRPD2    T-----QKLVRSDKYKTGKDNKYVEKKVIFEDN---RDILIGRIPVMVKSELCWMN----
SmRPD2b   E----------------------QRNPVVNRV--FPAVHIGDIPIMVNSLLCNGH----
SmRPD2a   N-------------------------EKIDESFRNDEVFVGEIPCMIGSELSNAH----
ZmRPB2a   K---------------------KGHDCEEVTETAEYPKVFIGKVPIMLRSSYCTLY----
ZmRPB2b   K---------------------KGHDCEEVTETAEYPKVFIGKVPIMLRSSYCTLY----
AtRPB2    K---------------------KGHDGEEVTETQDFTKVFIGKVPIMLRSSYCTLF----
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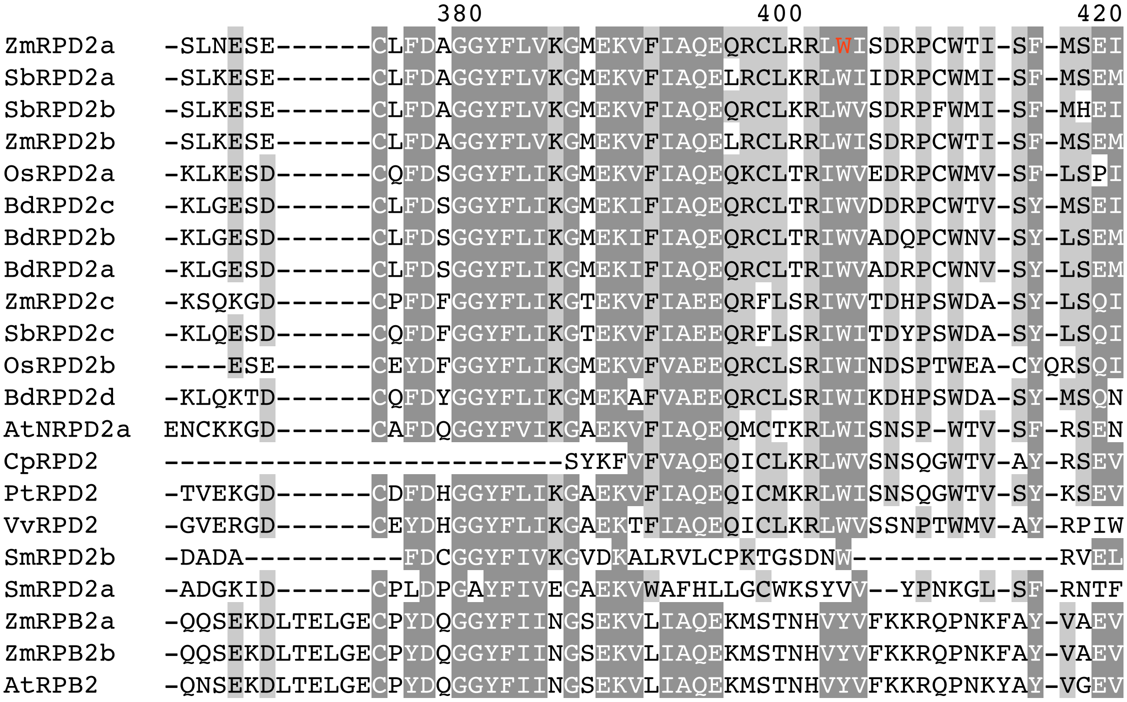

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                           380                 400                 420
ZmRPD2a   -SLNESE------CLFDAGGYFLVKGMEKVFIAQEQRCLRRLWISDRPCWTI-SF-MSEI
SbRPD2a   -SLKESE------CLFDAGGYFLVKGMEKVFIAQELRCLKRLWIIDRPCWMI-SF-MSEM
SbRPD2b   -SLKESE------CLFDAGGYFLVKGMEKVFIAQEQRCLKRLWVSDRPFWMI-SF-MHEI
ZmRPD2b   -SLKESE------CLFDAGGYFLVKGMEKVFIAQELRCLRRLWISDRPCWTI-SF-MSEM
OsRPD2a   -KLKESD------CQFDSGGYFLIKGMEKVFIAQEQKCLTRIWVEDRPCWMV-SF-LSPI
BdRPD2c   -KLGESD------CLFDSGGYFLIKGMEKIFIAQEQRCLTRIWVDDRPCWTV-SY-MSEI
BdRPD2b   -KLGESD------CLFDSGGYFLIKGMEKIFIAQEQRCLTRIWVADQPCWNV-SY-LSEM
BdRPD2a   -KLGESD------CLFDSGGYFLIKGMEKIFIAQEQRCLTRIWVADRPCWNV-SY-LSEM
ZmRPD2c   -KSQKGD------CPFDFGGYFLIKGTEKVFIAEEQRFLSRIWVTDHPSWDA-SY-LSQI
SbRPD2c   -KLQESD------CQFDFGGYFLIKGTEKVFIAEEQRFLSRIWITDYPSWDA-SY-LSQI
OsRPD2b   ----ESE------CEYDFGGYFLIKGMEKVFVAEEQRCLSRIWINDSPTWEA-CYQRSQI
BdRPD2d   -KLQKTD------CQFDYGGYFLIKGMEKAFVAEEQRCLSRIWIKDHPSWDA-SY-MSQN
AtNRPD2a  ENCKKGD------CAFDQGGYFVIKGAEKVFIAQEQMCTKRLWISNSP-WTV-SF-RSEN
CpRPD2    -------------------------SYKFVFVAQEQICLKRLWVSNSQGWTV-AY-RSEV
PtRPD2    -TVEKGD------CDFDHGGYFLIKGAEKVFIAQEQICMKRLWISNSQGWTV-SY-KSEV
VvRPD2    -GVERGD------CEYDHGGYFLIKGAEKTFIAQEQICLKRLWVSSNPTWMV-AY-RPIW
SmRPD2b   -DADA----------FDCGGYFIVKGVDKALRVLCPKTGSDNW-------------RVEL
SmRPD2a   -ADGKID------CPLDPGAYFIVEGAEKVWAFHLLGCWKSYVV--YPNKGL-SF-RNTF
ZmRPB2a   -QQSEKDLTELGECPYDQGGYFIINGSEKVLIAQEKMSTNHVYVFKKRQPNKFAY-VAEV
ZmRPB2b   -QQSEKDLTELGECPYDQGGYFIINGSEKVLIAQEKMSTNHVYVFKKRQPNKFAY-VAEV
AtRPB2    -QNSEKDLTELGECPYDQGGYFIINGSEKVLIAQEKMSTNHVYVFKKRQPNKYAY-VGEV
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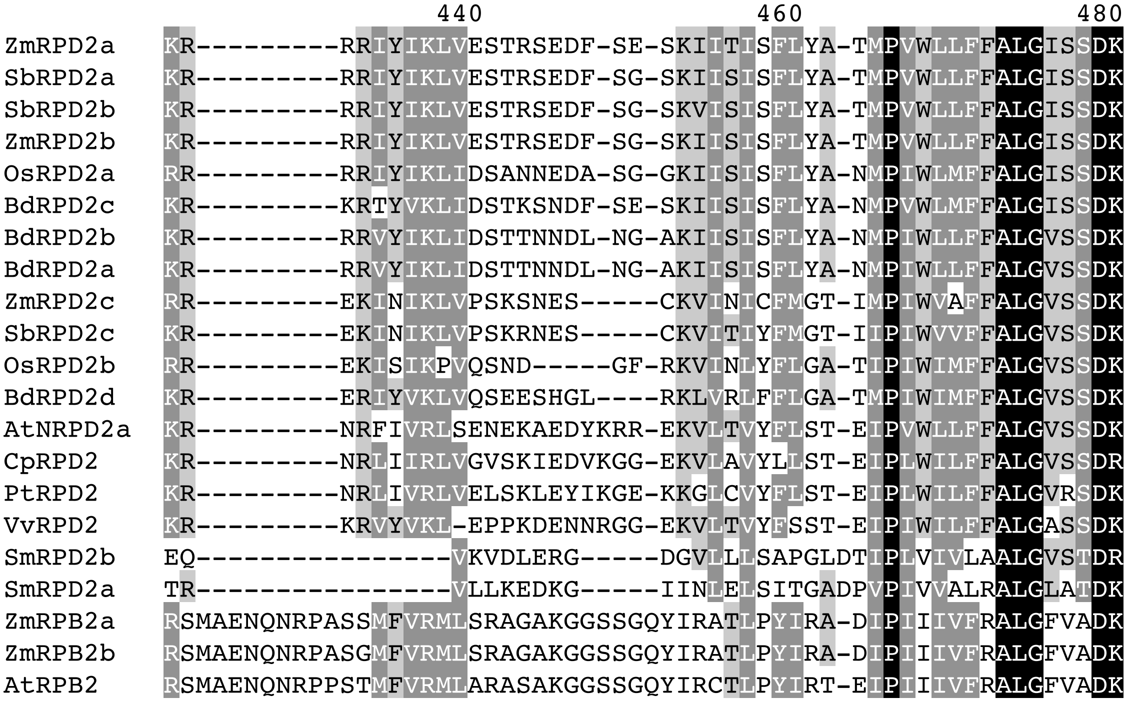
*RMR7-1 (W to X)



```
                           440                 460                 480
ZmRPD2a   KR---------RRIYIKLVESTRSEDF-SE-SKIITISFLYA-TMPVWLLFFALGISSDK
SbRPD2a   KR---------RRIYIKLVESTRSEDF-SG-SKIISISFLYA-TMPVWLLFFALGISSDK
SbRPD2b   KR---------RRIYIKLVESTRSEDF-SG-SKVISISFLYA-TMPVWLLFFALGISSDK
ZmRPD2b   KR---------RRIYIKLVESTRSEDF-SG-SKIISISFLYA-TMPVWLLFFALGISSDK
OsRPD2a   RR---------RRIYIKLIDSANNEDA-SG-GKIISISFLYA-NMPIWLMFFALGISSDK
BdRPD2c   KR---------KRTYVKLIDSTKSNDF-SE-SKIISISFLYA-NMPVWLMFFALGISSDK
BdRPD2b   KR---------RRVYIKLIDSTTNNDL-NG-AKIISISFLYA-NMPIWLLFFALGVSSDK
BdRPD2a   KR---------RRVYIKLIDSTTNNDL-NG-AKIISISFLYA-NMPIWLLFFALGVSSDK
ZmRPD2c   RR---------EKINIKLVPSKSNES-----CKVINICFMGT-IMPIWVAFFALGVSSDK
SbRPD2c   KR---------EKINIKLVPSKRNES-----CKVITIYFMGT-IIPIWVVFFALGVSSDK
OsRPD2b   RR---------EKISIKPVQSND-----GF-RKVINLYFLGA-TIPIWIMFFALGVSSDK
BdRPD2d   KR---------ERIYVKLVQSEESHGL----RKLVRLFFLGA-TMPIWIMFFALGVSSDK
AtNRPD2a  KR---------NRFIVRLSENEKAEDYKRR-EKVLTVYFLST-EIPVWLLFFALGVSSDK
CpRPD2    KR---------NRLIIRLVGVSKIEDVKGG-EKVIAVYLLST-EIPLWILFFALGVSSDR
PtRPD2    KR---------NRLIVRLVELSKLEYIKGE-KKGLCVYFIST-EIPLWILFFALGVRSDK
VvRPD2    KR---------KRVYVKL-EPPKDENNRGG-EKVLTVYFSST-EIPIWILFFALGASSDK
SmRPD2b   EQ----------------VKVDLERG-----DGVLLLSAPGLDTIPLVIVLAALGVSTDR
SmRPD2a   TR----------------VLLKEDKG-----IINLELSITGADPVPIVVALRALGLATDK
ZmRPB2a   RSMAENQNRPASSMFVRMLSRAGAKGGSSGQYIRATLPYIRA-DIPIIIVFRALGFVADK
ZmRPB2b   RSMAENQNRPASGMFVRMLSRAGAKGGSSGQYIRATLPYIRA-DIPIIIVFRALGFVADK
AtRPB2    RSMAENQNRPPSTMFVRMLARASAKGGSSGQYIRCTLPYIRT-EIPIIIVFRALGFVADK
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SbRPD2b    EAFDVIDMQDCDASVINTISATIKESDELCKG----FRKS------DKARQYVDE---LV
ZmRPD2b    EAFDVIDMQDCDASVINTISATIKESDELCGG----FRKS------DKARQYVDE---LV
OsRPD2a    DIFDVINMEDCDACVINTITATIKESDELCEG----FRKS------DKARQYVDE---LI
BdRPD2c    EVFDIIDFKDSDASVINMISATISESNELCEG----FRKS------DKARQYVDD---LV
BdRPD2b    EVFDMIDMKDCDASVINAIYATIRESDELCEG----FRQS------DKARKYVDD---LV
BdRPD2a    EVFDMIDMKDCDASVINAISATIRESDELCEG----FRQS------DKARKYVDD---LV
ZmRPD2c    EAFDMIDILDCDADIVNIISLTIKESHEEFEG----FRTP------GRARQYVDE---LI
SbRPD2c    EAFDMIDILDCDASIVNIISSTIKESHEEFEG----FRAP------GRACQYVDK---LI
OsRPD2b    EAFDIIDIQECDASMANIISATITESHEQCEG----FQRE------GRASEYIDK---LI
BdRPD2d    EAFDMIDIQDCDASLVNIISATIKESDEQCEG----FRRG------GRARQYVDE---FI
AtNRPD2a   EAMDLIAFDGDDASITNSLIASIHVADAVCEA----FRCG------NNALTYVEQ---QI
CpRPD2     EIIGLIDYDGDDANIINVLFASIHDADEKCEG----FRRG------KKALHYVGK---LI
PtRPD2     EVIDLIDYASNDASIVNIFFASIHDADEKCEH----FRRE------DRALDYVDK---LL
VvRPD2     EVVDLIDFNIDDAGISNILVASIHEADREAEKKGMYFRRQ------GNAISFVDK---LV
SmRPD2b    QLLEVMVHDTQDVELTELVRPSIVHAREQMQE----FVNSSGVHGGGRDVTSVAV---EL
SmRPD2a    SVLDVM-HATNDPELANMILPSLREAADQVSD----FFGDEDVN--HRDCAANQE---FL
ZmRPB2a    DILEHICYDFSDTQMMELLRPSLEEAFV--------IQNQ------QVALDYIGKRGATV
ZmRPB2b    DILEHICYDFSDTQMMELLRPSLEEAFV--------IQNQ------QVALDYIGKRGATV
AtRPB2     DILEHICYDFADTQMMELLRPSLEEAFV--------IQNQ------LVALDYIGKRGATV
```

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                           560                 580                 600
ZmRPD2a    KSSRFPPAESFDDYIARFLFP-DI----SGNRNKALFLGYMVKCLLMAFTGKRKCDNKDD
SbRPD2a    KSSRFPPAESFDDYIARFLFP-DI----SGNRNKALFLGYMVKCLLMAFTGKRKCDNKDD
SbRPD2b    KSSRFPPAESFDDYVARFLFP-DI----NGNRNKAFFLGYMVKCLLMAFTGKRKCDNKDD
ZmRPD2b    KSSKFPPVESFDDYIAKFLFP-GI----SGNRNKALFLGYMVKCLLMAFTGKRKCDNKDD
OsRPD2a    KNSKFPPAEPFDDYIAKYLFP-SI----SGNRNKALFLGYMVKCLLMAFTGKRKCDNKDD
BdRPD2c    KSSKFPPAESFDDYVARFLFP-GI----SGNRNKAFFLGYMVKYLLMAFTGKLKCDNRDA
BdRPD2b    KSSKFPPAEPFTDYVAKYLFP-GI----SGNRNKSFFLGYMVKCLLMAFTGKRKCDNKDD
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ZmRPD2c    RKSKFPPKESFDEYVCRYMFP-GV----NGFRSKALFLGYMVKCLLMAYSGNRKCDNKDD
SbRPD2c    RKSKFPPKESFDEYVCRYMFP-SV----NGVRSKALFLGYMVKCLLMAYSGNRKCDNKDD
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BdRPD2d    KKTKFPPEQSFDGYVGRYMFPGDV----SDNRSKAFFLGYMVKCLLMAYSGHRKCDDRAN
AtNRPD2a   KSTKFPPAESVDECLHLYLFP-GL----QSLKKKARFLGYMVKCLLNSYAGKRKCENRDS
CpRPD2     KDTRFPPGDSIEECLSLYLFP-TL----HGLKQKARFLGYMVKCLLIAYTGKRKCDNRDN
PtRPD2     KKTRFPPKESIEDAISAYLFP-RL----NSRRHKARFLGYMVKCLLEAYTGHRKCDNRDS
VvRPD2     KSCKFPPGESIQECISKYLFP-NF----SGVKQKARFLGYMVKCLLQAYTGRRKCDNRDD
SmRPD2b    VGSRIKPVTPLAGPAQEKLVSLLCNTSSSRPADKALLMGYMVRCLCLCVVGRSTADDIHS
SmRPD2a    ASKS----RKLKGSFVEALFP-AL----DSPKSKVIYLGYMVEFLCTSYLGRRQ-PRKNS
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ZmRPB2b    GVTREKRIKYAKEILQKEMLP-HVGVGEFCETKKAYYFGYIIHRLLMCALSRRAEDDRDH
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                               620                 640                 660
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SbRPD2a     FRNKRLDLPGELLGRELRAHLRLAEKRMVKAIQRDLNSDR-ELQDLERYIDASIVTNGLS
SbRPD2b     FRNKRLDLPGELLGRELRAQLRLLERRMVKAIQRDLNNDR-ELQDLERYIDASIVTNGLN
ZmRPD2b     FRNKRLDLPGELLGRELRAHLRQAERRMVKAIQRDLNSDR-ELQDLERYIDASIVTNGLN
OsRPD2a     FRNKRLDLAGELLGRELRAHIRHAERLMVKALQRDLNSER-ELQEFDHYLDASIITNGLN
BdRPD2c     FRNKRLELPGELLGRELRAHLRHAERLMVKAMQRDLNSDR-DLQFPLGYLDPTIITNGIN
BdRPD2b     FRNKRLELPGQLLGRELRAHLRHAERLMVKAMQRDLNSDR-DLQFPLRYLDASIITNGIN
BdRPD2a     FRNKRLELPGQLLGRELRAHLRHAERLMVKAMQRDLNSDR-DLQFPLRYLDASIITNGIN
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SbRPD2c     FRNKRLGLACQLLRRELWTHIKRAEWRMVKLMQRDLSNDG-NLQDLRRYVDASIITNGLN
OsRPD2b     FRNKRLDLACELLQRELWVHIMHAQKRMVKVMQRHLSGDG-DLQPLECYVHASIVTNGLN
BdRPD2d     FRNKRLDLACQLLRRELWVHLRHAQRRMVKIMQRHLSGDG-DLQVLDHYVDTSIVTNGLN
AtNRPD2a    FRNKRIELAGELLERELRVHLAHARRKMTRAMQKHLSGDG-DLKPIEHYLDASVITNGLS
CpRPD2      FRNKRLELAGELLERELKVHLAHARKSMTKAFQKNLNGD--DIKPIEHYLDASIITNGLQ
PtRPD2      FRNKRFELASELLERELKVHVSHALRRMTKALQRDLYGDR-DVHPIEHYLDASIVTNGLT
VvRPD2      FRNKRLELAGELLERELRVHIRHAERRMVKAMQRELYGDR-DLRPIENYLDASIITNGLS
SmRPD2b     LKNKRVDLAGDCMFKQMRHLSARFRKTTLKRVLKHVEAGGLDCLTDNLIVDKSVITNGLR
SmRPD2a     LVNKRILGVNELLALLLTKAMTRFMRETCKKMLLMKSVT-------DGIFNDKIVTCDFR
ZmRPB2a     YGNKRLDLAGPLLGGLFRMLFRKLTRDVRSYVQKCVDNG--KEVNLQFAIKAKTITSGLK
ZmRPB2b     YGNKRLDLAGPLLGGLFRM---------------CVDNG--KEVNLQFAIKAKTVTSGLK
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```

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                               680                 700                 720
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SbRPD2a     RAFSTGSWCHPYKRAERCSGIVAT------------------LRRTNP------------
SbRPD2b     RAFSTGSWCHPYKRAERCSGIVAT------------------LRRTNP------------
ZmRPD2b     RAFSTGSWCHPYKRAERCSGIVAT------------------LRRTNP------------
OsRPD2a     RAFSTGSWCHPYKRNERCAGIVAT------------------LRRTNP------------
BdRPD2c     RAFATGSWCHPYKRNERCSGVVAT------------------LRRTNP------------
BdRPD2b     RAFATGSWSHPYIRNERCSGIVAT------------------LRRTNP------------
BdRPD2a     RAFATGSWSHPYIRNERCSGIVAT------------------LRRTNP------------
ZmRPD2c     RAFSTGSWRHPYKK-ERCSGVVAT------------------LRRTNP------------
SbRPD2c     RAFSTGSWRHPYLK-ARCSGVVAT------------------LRRTNP------------
OsRPD2b     RAFSTGSWCHPFNKRERCSGIVAT------------------LRRTNP------------
BdRPD2d     RAFSTGSWCHPYK-YERCSGIVGN------------------LRRTNP------------
AtNRPD2a    RAFSTGAWSHPFRKMERVSGVVAN------------------LGRANP------------
CpRPD2      RAFSTGAWSHPFKRMERISGVVAN------------------LGRANP------------
PtRPD2      RAFSTGAWCHPFKWMERVSGVVGN------------------LGRANP------------
VvRPD2      RAFSTGQWSHPFKRMERISGVVAT------------------LRRTNP------------
SmRPD2b     AAFSTGIWSLNRYSSCT-SGVVAT------------------LQRDNP------------
SmRPD2a     DAFKRGVWAQPQTYG---SGVVEA------------------LKRQNV------------
ZmRPB2a     YSLATGNWGQANQAGTR-AGVSQV------------------LNRLTY------------
ZmRPB2b     YSLATGNWGQANQAGTR-AGVSQAKQAGSRKGVFQVPKNTFPLNTFGYCAVSVTSSQSCP
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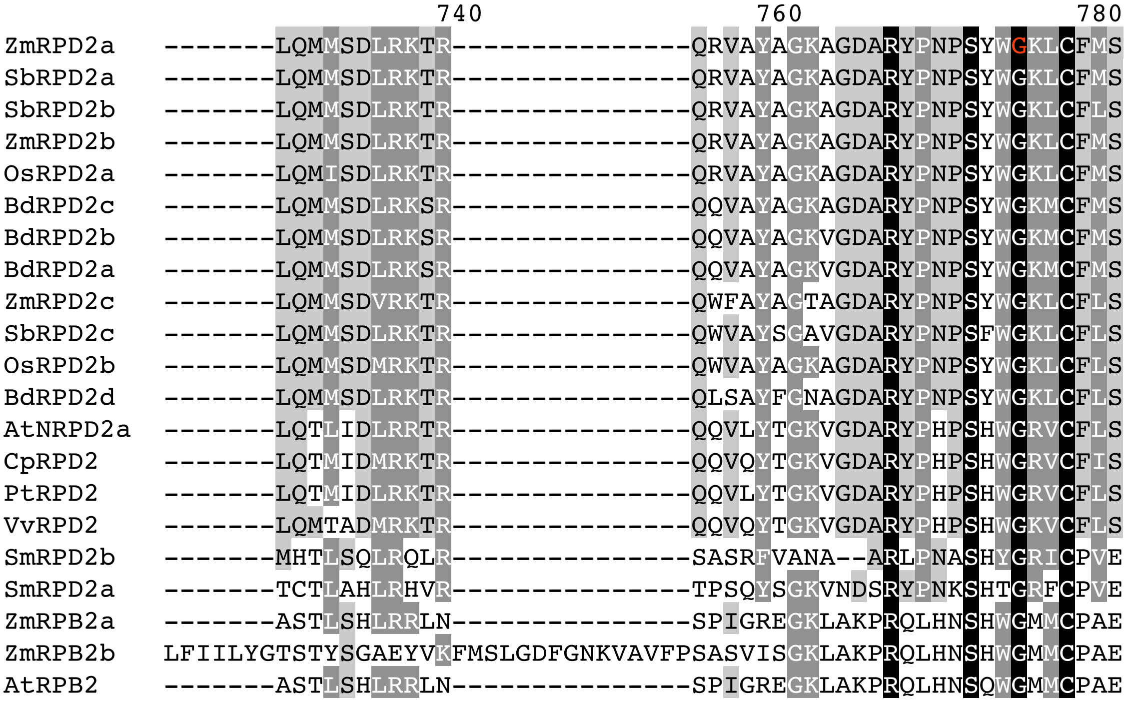

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OsRPD2a     -------LQMISDLRKTR---------------QRVAYAGKAGDARYPNPSYWGKLCFMS
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SbRPD2c     -------LQMMSDLRKTR---------------QWVAYSGAVGDARYPNPSFWGKLCFLS
OsRPD2b     -------LQMMSDMRKTR---------------QWVAYAGKAGDARYPNPSYWGKLCFLS
BdRPD2d     -------LQMMSDLRKTR---------------QLSAYFGNAGDARYPNPSYWGKLCFLS
AtNRPD2a    -------LQTLIDLRRTR---------------QQVLYTGKVGDARYPHPSHWGRVCFLS
CpRPD2      -------LQTMIDMRKTR---------------QQVQYTGKVGDARYPHPSHWGRVCFIS
PtRPD2      -------LQTMIDLRKTR---------------QQVLYTGKVGDARYPHPSHWGRVCFLS
VvRPD2      -------LQMTADMRKTR---------------QQVQYTGKVGDARYPHPSHWGKVCFLS
SmRPD2b     -------MHTLSQLRQLR---------------SASRFVANA--ARLPNASHYGRICPVE
SmRPD2a     -------TCTLAHLRHVR---------------TPSQYSGKVNDSRYPNKSHTGRFCPVE
ZmRPB2a     -------ASTLSHLRRLN---------------SPIGREGKLAKPRQLHNSHWGMMCPAE
ZmRPB2b     LFIILYGTSTYSGAEYVKFMSLGDFGNKVAVFPSASVISGKLAKPRQLHNSHWGMMCPAE
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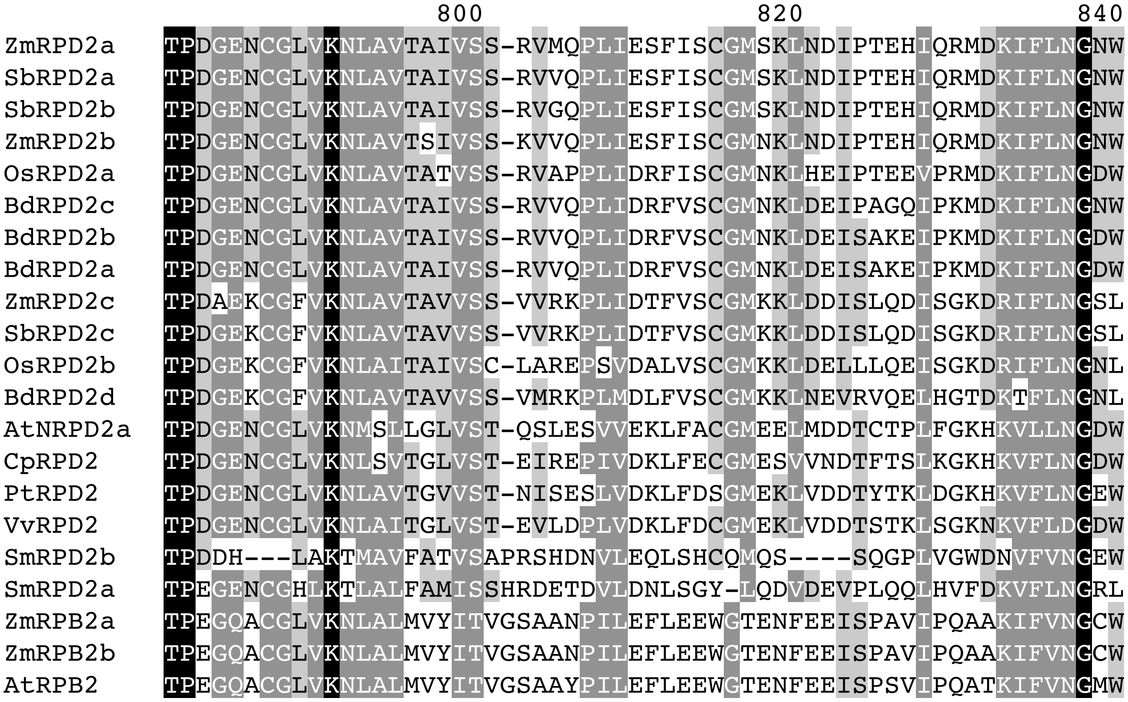
RMR7-2 * (G to E)



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SbRPD2b     TPDGENCGLVKNLAVTAIVSS-RVGQPLIESFISCGMSKLNDIPTEHIQRMDKIFLNGNW
ZmRPD2b     TPDGENCGLVKNLAVTSIVSS-KVVQPLIESFISCGMNKLNDIPTEHIQRMDKIFLNGNW
OsRPD2a     TPDGENCGLVKNLAVTATVSS-RVAPPLIDRFISCGMNKLHEIPTEEVPRMDKIFLNGDW
BdRPD2c     TPDGENCGLVKNLAVTAIVSS-RVVQPLIDRFVSCGMNKLDEIPAGQIPKMDKIFLNGNW
BdRPD2b     TPDGENCGLVKNLAVTAIVSS-RVVQPLIDRFVSCGMNKLDEISAKEIPKMDKIFLNGDW
BdRPD2a     TPDGENCGLVKNLAVTAIVSS-RVVQPLIDRFVSCGMNKLDEISAKEIPKMDKIFLNGDW
ZmRPD2c     TPDAEKCGFVKNLAVTAVVSS-VVRKPLIDTFVSCGMKKLDDISLQDISGKDRIFLNGSL
SbRPD2c     TPDGEKCGFVKNLAVTAVVSS-VVRKPLIDTFVSCGMKKLDDISLQDISGKDRIFLNGSL
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BdRPD2d     TPDGEKCGFVKNLAVTAVVSS-VMRKPLMDLFVSCGMKKLNEVRVQELHGTDKTFLNGNL
AtNRPD2a    TPDGENCGLVKNMSLLGLVST-QSLESVVEKLFACGMEELMDDTCTPLFGKHKVLLNGDW
CpRPD2      TPDGENCGLVKNLSVTGLVST-EIREPIVDKLFECGMESVVNDTFTSLKGKHKVFLNGDW
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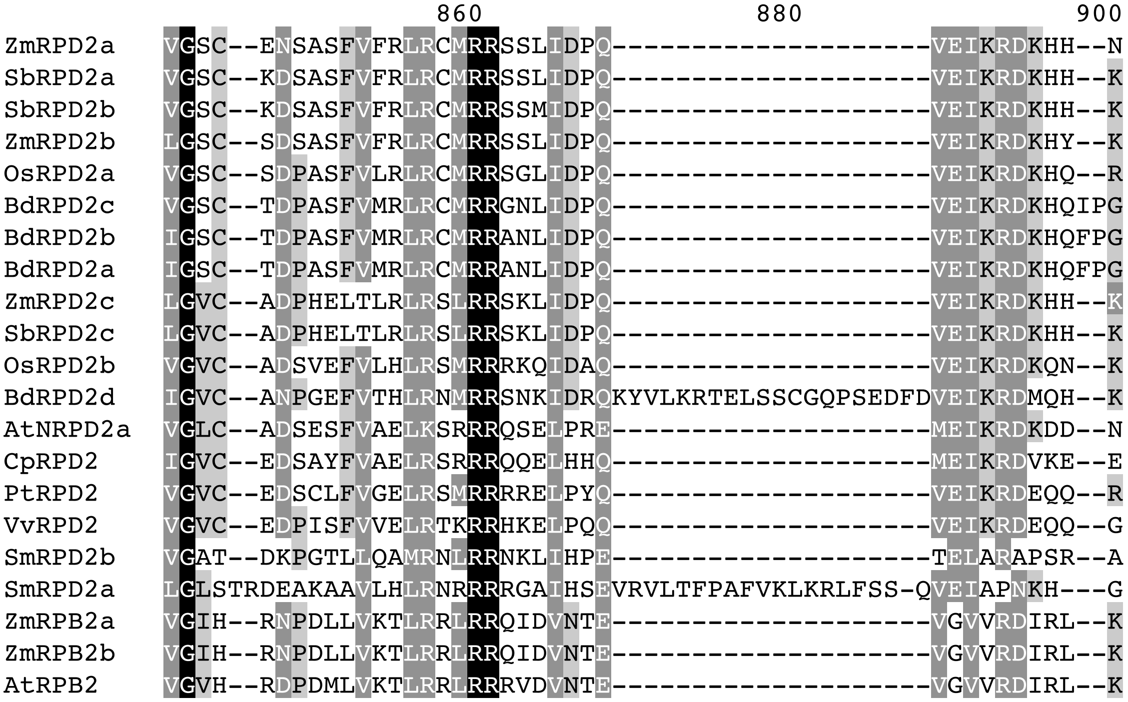

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OsRPD2a   VGSC--SDPASFVLRLRCMRRSGLIDPQ--------------------VEIKRDKHQ--R
BdRPD2c   VGSC--TDPASFVMRLRCMRRGNLIDPQ--------------------VEIKRDKHQIPG
BdRPD2b   IGSC--TDPASFVMRLRCMRRANLIDPQ--------------------VEIKRDKHQFPG
BdRPD2a   IGSC--TDPASFVMRLRCMRRANLIDPQ--------------------VEIKRDKHQFPG
ZmRPD2c   LGVC--ADPHELTLRLRSLRRSKLIDPQ--------------------VEIKRDKHH--K
SbRPD2c   LGVC--ADPHELTLRLRSLRRSKLIDPQ--------------------VEIKRDKHH--K
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BdRPD2d   IGVC--ANPGEFVTHLRNMRRSNKIDRQKYVLKRTELSSCGQPSEDFDVEIKRDMQH--K
AtNRPD2a  VGLC--ADSESFVAELKSRRRQSELPRE--------------------MEIKRDKDD--N
CpRPD2    IGVC--EDSAYFVAELRSRRRQQELHHQ--------------------MEIKRDVKE--E
PtRPD2    VGVC--EDSCLFVGELRSMRRRRELPYQ--------------------VEIKRDEQQ--R
VvRPD2    VGVC--EDPISFVVELRTKRRHKELPQQ--------------------VEIKRDEQQ--G
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ZmRPB2a   VGIH--RNPDLLVKTLRRLRRQIDVNTE--------------------VGVVRDIRL--K
ZmRPB2b   VGIH--RNPDLLVKTLRRLRRQIDVNTE--------------------VGVVRDIRL--K
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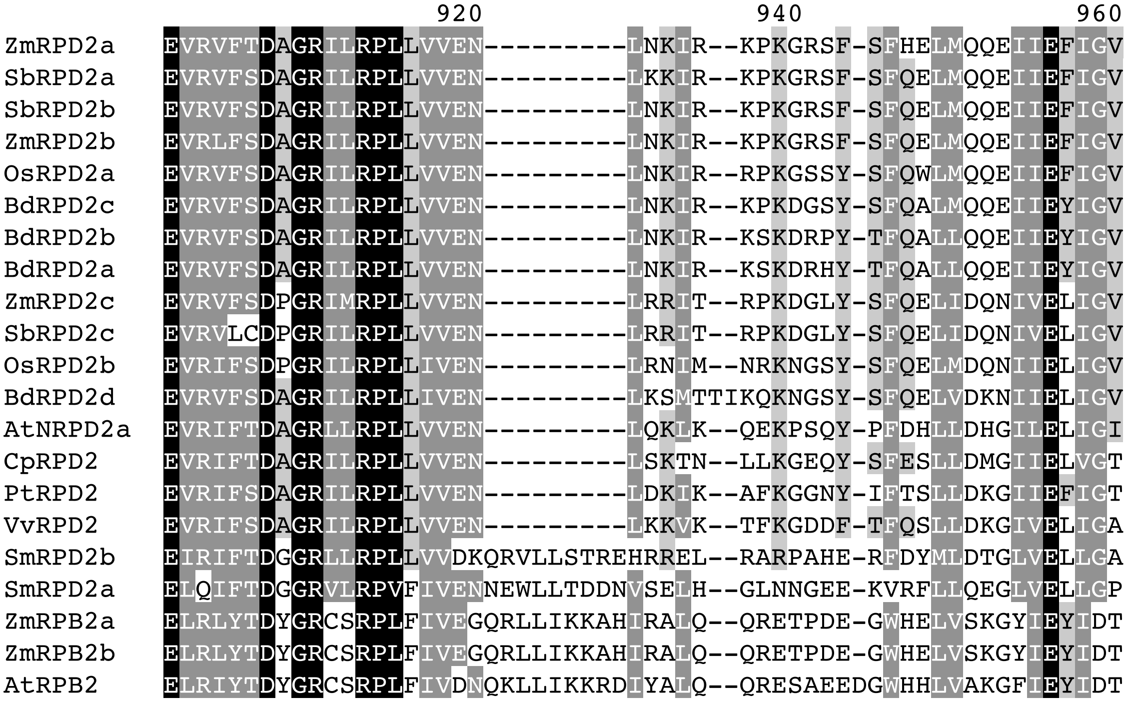

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BdRPD2c   EVRVFSDAGRILRPLLVVEN----------LNKIR--KPKDGSY-SFQALMQQEIIEYIGV
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SbRPD2c   EVRVLCDPGRILRPLLVVEN----------LRRIT--RPKDGLY-SFQELIDQNIVELIGV
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CpRPD2    EVRIFTDAGRILRPLLVVEN----------LSKTN--LLKGEQY-SFESLLDMGIIELVGT
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VvRPD2    EVRIFSDAGRILRPLLVVEN----------LKKVK--TFKGDDF-TFQSLLDKGIVELIGA
SmRPD2b   EIRIFTDGGRLLRPLLVVDKQRVLLSTREHRREL--RARPAHE-RFDYMLDTGLVELLGA
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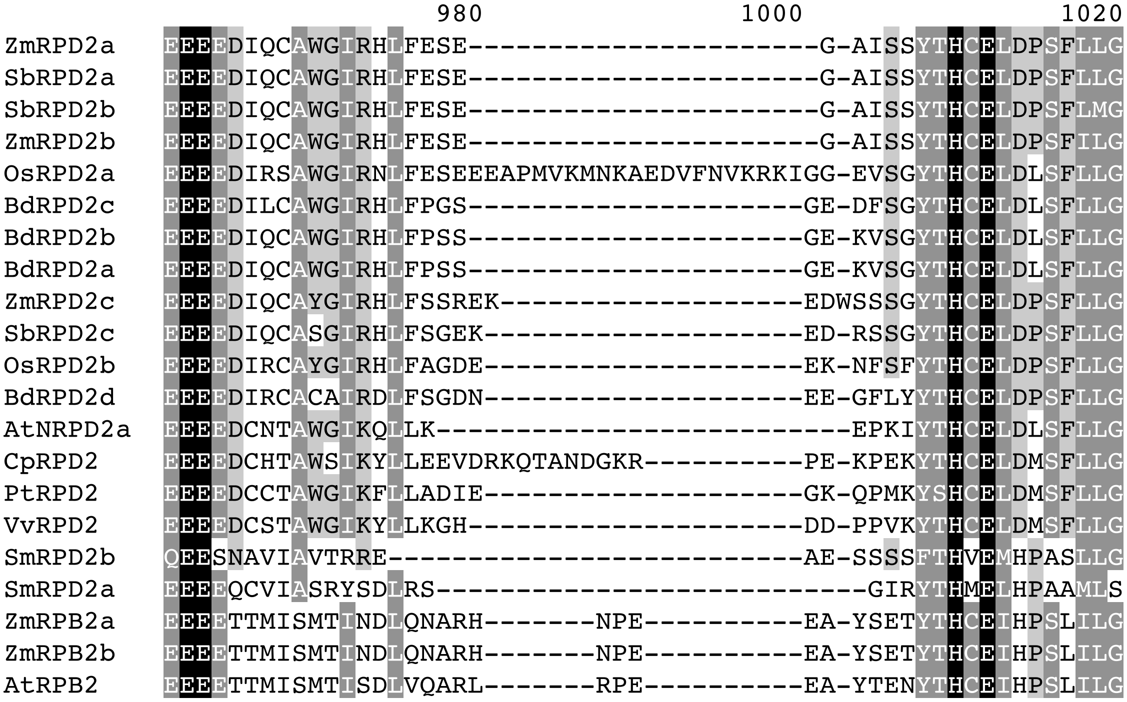

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CpRPD2    EEEEDCHTAWSIKYLLEEVDRKQTANDGKR----------PE-KPEKYTHCELDMSFLLG
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VvRPD2    EEEEDCSTAWGIKYLLKGH---------------------DD-PPVKYTHCELDMSFLLG
SmRPD2b   QEESNAVIAVTRRE--------------------------AE-SSSSFTHVEMHPASLLG
SmRPD2a   EEEEQCVIASRYSDLRS---------------------------GIRYTHMELHPAAMLS
ZmRPB2a   EEEETTMISMTINDLQNARH-------NPE----------EA-YSETYTHCEIHPSLILG
ZmRPB2b   EEEETTMISMTINDLQNARH-------NPE----------EA-YSETYTHCEIHPSLILG
AtRPB2    EEEETTMISMTISDLVQARL-------RPE----------EA-YTENYTHCEIHPSLILG
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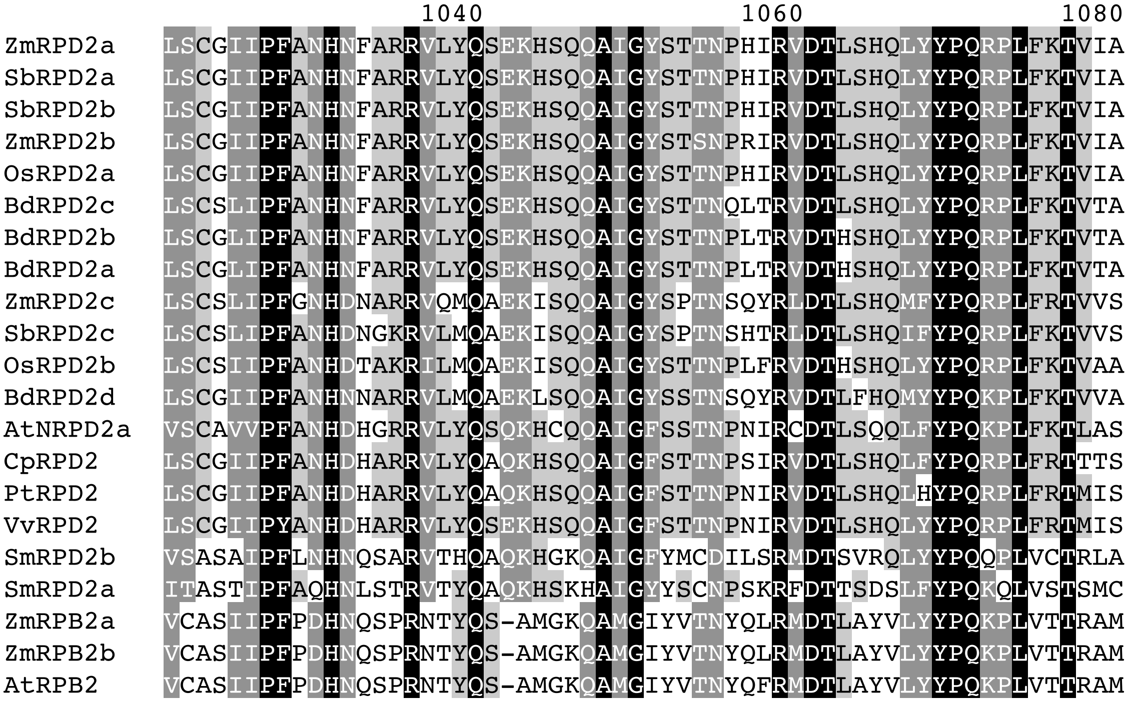

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SbRPD2a   LSCGIIPFANHNFARRVLYQSEKHSQQAIGYSTTNPHIRVDTLSHQLYYPQRPLFKTVIA
SbRPD2b   LSCGIIPFANHNFARRVLYQSEKHSQQAIGYSTTNPHIRVDTLSHQLYYPQRPLFKTVIA
ZmRPD2b   LSCGIIPFANHNFARRVLYQSEKHSQQAIGYSTSNPRIRVDTLSHQLYYPQRPLFKTVIA
OsRPD2a   LSCGIIPFANHNFARRVLYQSEKHSQQAIGYSTTNPHIRVDTLSHQLYYPQRPLFKTVIA
BdRPD2c   LSCSLIPFANHNFARRVLYQSEKHSQQAIGYSTTNQLTRVDTLSHQLYYPQRPLFKTVTA
BdRPD2b   LSCGLIPFANHNFARRVLYQSEKHSQQAIGYSTTNPLTRVDTHSHQLYYPQRPLFKTVTA
BdRPD2a   LSCGLIPFANHNFARRVLYQSEKHSQQAIGYSTTNPLTRVDTHSHQLYYPQRPLFKTVTA
ZmRPD2c   LSCSLIPFGNHDNARRVQMQAEKISQQAIGYSPTNSQYRLDTLSHQMFYPQRPLFRTVVS
SbRPD2c   LSCSLIPFANHDNGKRVLMQAEKISQQAIGYSPTNSHTRLDTLSHQIFYPQRPLFKTVVS
OsRPD2b   LSCSIIPFANHDTAKRILMQAEKISQQAIGYSTTNPLFRVDTHSHQLYYPQRPLFKTVAA
BdRPD2d   LSCGIIPFANHNNARRVLMQAEKLSQQAIGYSSTNSQYRVDTLFHQMYYPQKPLFKTVVA
AtNRPD2a  VSCAVVPFANHDHGRRVLYQSQKHCQQAIGFSSTNPNIRCDTLSQQLFYPQKPLFKTLAS
CpRPD2    LSCGIIPFANHDHARRVLYQAQKHSQQAIGFSTTNPSIRVDTLSHQLFYPQRPLFRTTTS
PtRPD2    LSCGIIPFANHDHARRVLYQAQKHSQQAIGFSTTNPNIRVDTLSHQLHYPQRPLFRTMIS
VvRPD2    LSCGIIPYANHDHARRVLYQSEKHSQQAIGFSTTNPNIRVDTLSHQLYYPQRPLFRTMIS
SmRPD2b   VSASAIPFLNHNQSARVTHQAQKHGKQAIGFYMCDILSRMDTSVRQLYYPQQPLVCTRLA
SmRPD2a   ITASTIPFAQHNLSTRVTYQAQKHSKHAIGYYSCNPSKRFDTTSDSLFYPQKQLVSTSMC
ZmRPB2a   VCASIIPFPDHNQSPRNTYQS-AMGKQAMGIYVTNYQLRMDTLAYVLYYPQKPLVTTRAM
ZmRPB2b   VCASIIPFPDHNQSPRNTYQS-AMGKQAMGIYVTNYQLRMDTLAYVLYYPQKPLVTTRAM
AtRPB2    VCASIIPFPDHNQSPRNTYQS-AMGKQAMGIYVTNYQFRMDTLAYVLYYPQKPLVTTRAM
```

```
                            1100                1120                1140
ZmRPD2a     DCLGRSD--YASFGRKNDFARPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
SbRPD2a     DCLGRSD--YTTFGRKDDFMRPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
SbRPD2b     DCLGRSD--YTAFGRKDDYTRPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
ZmRPD2b     DCLG----------------RPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
OsRPD2a     DCIGRSE--Y-TFGRKDDFARPE---YFNGQNAIVAVNVHQGFNQEDSVVMNRASLERGM
BdRPD2c     DCIGRSD--Y-TIGRTDDFARPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
BdRPD2b     DCIGRSD--Y-TIGRKDDFARPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
BdRPD2a     DCIGRSD--Y-TIGRKDDFARPE---YFNGQNAIVAVNVHQGFNQEDSLVMNRASLERGM
ZmRPD2c     YGLGEAKTDC-SSGRKDDFNTPE---YFNGQNAIVSVNVHQGFNQEDSLVMNRASLERGM
SbRPD2c     YGLGKAETAY-SFGRKDDFNTPE---YFNGQNAIVSINVHQGFNQEDSLVLNRASLERGM
OsRPD2b     DCLGKRD--Y-TSGSKHDFARPE---YFNGQNAIVSISVHQGFNQEDSLVLNRASLERGM
BdRPD2d     DCIGKSD--H-NFGEEDDFTRPENFPYFNGQNAIVSISVHQGFNQEDSLVFNRGSLERGM
AtNRPD2a    ECLKKEV-------------------LFNGQNAIVAVNVHLGYNQEDSIVMNKASLERGM
CpRPD2      DCLGKAG--Y-PLGHDGIVPRPE---LFNGQNAIVAVNVHLGYNQEDSLVMNQASLQRGM
PtRPD2      DCL--------------VLPKPE---LFNGQNAIVAVNVHLGYNQEDSLVMNRASLERGM
VvRPD2      DCLGKPG--Y-SEGHKGIVPRPE---YFNGQIAIVAVNVHLGYNQEDSLVMNRASLERGM
SmRPD2b     QLLARPE-------------------LANGVNCVVAVACYGGYNQEDSLILNQSSLDRGL
SmRPD2a     RLLSPND-------SAMMRGWPEK--LMHGQSCVVAVACYDGYNQEDSLIFNQAAIDRGL
ZmRPB2a     EHLHFRQ-------------------LPAGINAIVAIACYSGYNQEDSVIMNQSSIDRGF
ZmRPB2b     EHLHFRQ-------------------LPAGINAIVAIACYSGYNQEDSVIMNQSSIDRGF
AtRPB2      EHLHFRQ-------------------LPAGINAIVAISCYSGYNQEDSVIMNQSSIDRGF
```

```
                            1160                1180                1200
ZmRPD2a     FRTEHLRSYKADVENK---DG-TKRLKLKEKIDFGKT-----ESKRGRVDNLDDDGLPYV
SbRPD2a     FRTEHLRSYKADVENK---DG-TKRLKLKEKIDFGKT-----ESKRGRVDNLDDDGLPYI
SbRPD2b     FRTEHLRSYKTDVENK---DG-TKRLKLKEKIDFGKT-----ESKRGRVDNLDDDGLPYI
ZmRPD2b     FRTEHLRSYKADVENK---DG-TKRLKLKEKIDFGKT-----ESKRGRVDNLDDDGLPYI
OsRPD2a     FRTEHFRNYKAEVENKGGPGG-NKRLKMKDKIDFGKM-----QSKRGRVDNLDDDGLPYV
BdRPD2c     FRTELIRSYKADVETK---EP-AKRLKLKEKVDFGKM-----QSKRGRVDSLDDDGLPYV
BdRPD2b     FRTEHIRSYKAEVETK---EP-TKRLKLKEKVDFGKM-----QSKRGRVDNLDDDGLPYV
BdRPD2a     FRTEHIRSYKAEVETK---EP-IKRLKLKEKVDFGKM-----QSKRGRVDNLDDDGLPYV
ZmRPD2c     FRTLHFKSYKAQVENK---EI-TRRLKHRENINFGKV-----QSKRGKVDSLDSDGLPYV
SbRPD2c     FRTLHLKSYKAQVENK---EI-TRRLKHRESINFGKV-----QSKRGKVDSLDSEGLPYV
OsRPD2b     FRTQHFKSYKALIENK---EI-TKRLKHKENINFGKT-----PSKKGLVDSLDIDGLPYI
BdRPD2d     FRTQHFKSYKTQIENK---EV-TRRLKYREKIDFGKT-----QSKRGRVDSLDIDGLPYI
AtNRPD2a    FRSEQIRSYKAEVDAK---DS-EKRKKMDELVQFGKT-----HSKIGKVDSLEDDGFPFI
CpRPD2      FRTEHIRSYKAEVENK---ELMDKRRKFDDPVNFGKI-----QSKLGRVDSIDDDGFPFV
PtRPD2      FRSEHIRSYKAEVDNK---ELTDKRRKSEDSITFGKI-----QSKIGRVDSLDDDGFPFI
VvRPD2      FRSEHIRSYKSEVDNN---ESLDKKRKSEDSVHFGKM-----QSKIGRVDSLDDDGFPFI
SmRPD2b     FRSTHFRVHRATLDYS---SS-DIR---------FCRPETEVARSNTDGIDKLDSDGLPFI
SmRPD2a     FRSIHERTHRYNINLQ---SS-EES---------FGRP-VEEDGSPQQRYQHLDEDGFPEI
ZmRPB2a     FRSLFFRSYRDEEKKM---GT-LIKEEFGRPNRENTM-----GMRHGSYDKLDDDGLAPP
ZmRPB2b     FRSLFFRSYRDEEKKM---GT-LVKEEFGRPNRENTM-----GMRHGSYDKLDDDGLAPP
AtRPB2      FRSLFFRSYRDEEKKM---GT-LVKEDFGRPDRGSTM-----GMRHGSYDKLDDDGLAPP
```

```
                          1220                1240                1260
ZmRPD2a   GASLQTNDIVIGKVSE-------------SGEDHSIKLKHTEKGMVQKVL----------
SbRPD2a   GASLQTNDIVIGKVSE-------------SGEDHSIKLKHTEKGMVQKVL----------
SbRPD2b   GASLQTNDIVIGKVSE-------------SGEDHSIKLKHTEKGMVQKVL----------
ZmRPD2b   GASLQTNDIVIGKVSE-------------SGEDHSIKLKHTEKGMVQKVL----------
OsRPD2a   GASLQSGDIVIGKVSE-------------SGEDHSIKLKHTEKGMVQRVL----------
BdRPD2c   GASLQSGDIVIGKVSE-------------SGEDHSIKLKHTEKGMVQRVL----------
BdRPD2b   GASLQSGDIVIGKVSE-------------SGEDHSIKMKHTEKGMAQRVL----------
BdRPD2a   GASLQSGDIVIGKVSE-------------SGEDHSIKMKHTEKGMVQRVL----------
ZmRPD2c   GASLQSGDIVIGKVTE-------------SGEDHSAKLMHTEKGMVDKVV----------
SbRPD2c   GASLQSGDIVIGKVSE-------------SGEDHSAKLMHTEKGMVDKVV----------
OsRPD2b   GASLQSNDIIIGKVSD-------------SGEDHSIKLLHTEKGIVEKVV----------
BdRPD2d   GASLQSGDIVIGKVSE-------------SGEDHSMKLMHTEKGMVEKVV----------
AtNRPD2a  GANMSTGDIVIGRCTE-------------SGADHSIKLKHTERGIVQKVV----------
CpRPD2    GANLQSGDIVIGRCAE-------------SGADHSIKLKHTEKGMVQKVV----------
PtRPD2    GANMQSGDIVIGKCAE-------------SGADHSVKLKHTERGMVQKVV----------
VvRPD2    GANLQNGDIVIGRCAE-------------SGVDHSIKLKHTERGMVQKVV----------
SmRPD2b   GAEMKAADVVIGKAGRRPAS---------KLVDHSSKLRKLEQGWVDQVV----------
SmRPD2a   GARLQSSQAVIGKTRKLKEG---------TVSNSSIFLKNFEEGSVKEVVRLPKIAQGSH
ZmRPB2a   GTRVSGEDVIIGKTSPIPQDDAQGQASRYSKRDHSTALRHSESGMVDQVL----------
ZmRPB2b   GTRVSGEDVIIGKTSPIPQDDAQGQASRYSKRDHSTSLRHSESGMVDQVL----------
AtRPB2    GTRVSGEDVIIGKTTPISQDEAQGQSSRYTRRDHSISLRHSETGMVDQVL----------
```

```
                          1280                1300                1320
ZmRPD2a   -LSAND-EGKNF----AVVTLRQVRTPCLGDKFSSMHGQKGVVGFLESQENFPFTHEGIV
SbRPD2a   -LSAND-EGKNF----AVVTLRQVRTPCLGDKFSSMHGQKGVVGFLESQENFPFTHKGIV
SbRPD2b   -LSAND-EGKNF----AVVTLRQVRTPCLGDKFSSMHGQKGVVGFLESQENFPFTHEGIV
ZmRPD2b   -LSAND-EGKNF----AVVTLRQVRTPCLGDKFSSMHGQKGVVGFLESQENFPFTHDGIV
OsRPD2a   -LSAND-EGKNF----AVVTLRQVRSPCLGDKFSSMHGQKGVVGFLESQENFPFTYQGIV
BdRPD2c   -LSAND-EEKNF----AVVTLRQVRSPCVGDKFSSMHGQKGVIGFLESQENFPFTCQGIV
BdRPD2b   -LSAND-EGKNF----AVVTLRQVRSPCVGDKFSSMHGQKGVIGFLESQENFPFTCQGIV
BdRPD2a   -LSAND-EGKNF----AVVTLRQVRSPCVGDKFSSMHGQKGVIGFLESQENFPFTCQGIV
ZmRPD2c   -LSAND-DGVNF----ATVTLRQSRSPCVGDKFASMHGQKGVVGLLDSQENFPFTSQGIV
SbRPD2c   -LSAND-DGVNF----ATVTLRQSRSPCVGDKFASMHGQKGVVGLLDSQENFPFTCQGIV
OsRPD2b   -LSATD-DGTNS----AFVTLRQTRSPRIGDKFASMHGQKGVIGFLDSQENFPFTHQGIV
BdRPD2d   -LSAND-DGKNS----AVVTLRQVRSPCVGDKFASMHGQKGVVGLLDSQENFPFTFQGIV
AtNRPD2a  -LSSND-EGKNF----AAVSLRQVRSPCLGDKFSSMHGQKGVLGYLEEQQNFPFTIQGIV
CpRPD2    -LSSND-DGKNF----AVVSLRQVRSPCLGDKFSSMHGQKGVLGFLESQENFPFTRQGIV
PtRPD2    -LSSND-EGKNF----AVVSLRQVRSPCLGDKFSSMHGQKGVLGFLESQENFPFTIQGVV
VvRPD2    -VSAND-DGKNF----AVVSLRQVRTPCLGDKFSSMHGQKGVLGFLESQENFPFTIQGIV
SmRPD2b   -CSGGDEEGERH----VRVRLREARCPQVGDKFSSMHGQKGVVGMKLRQEELLFTQQGIV
SmRPD2a   DVNVKT-ASASFPHGGVKVKIASTRAPQAGDKFSSMHGQKGVIGCCLSQEDLPFTRQGIV
ZmRPB2a   -LTTNA-DGLRF----VKVRMRSVRIPQIGDKFSSRHGQKGTVGMTYTQEDMPWTIEGIT
ZmRPB2b   -LTTNA-DGLRF----VKVRMRSVRIPQIGDKFSSRHGQKGTVGMTYTQEDMPWTIEGIT
AtRPB2    -LTTNA-DGLRF----VKVRVRSVRIPQIGDKFSSRHGQKGTVGMTYTQEDMPWTIEGVT
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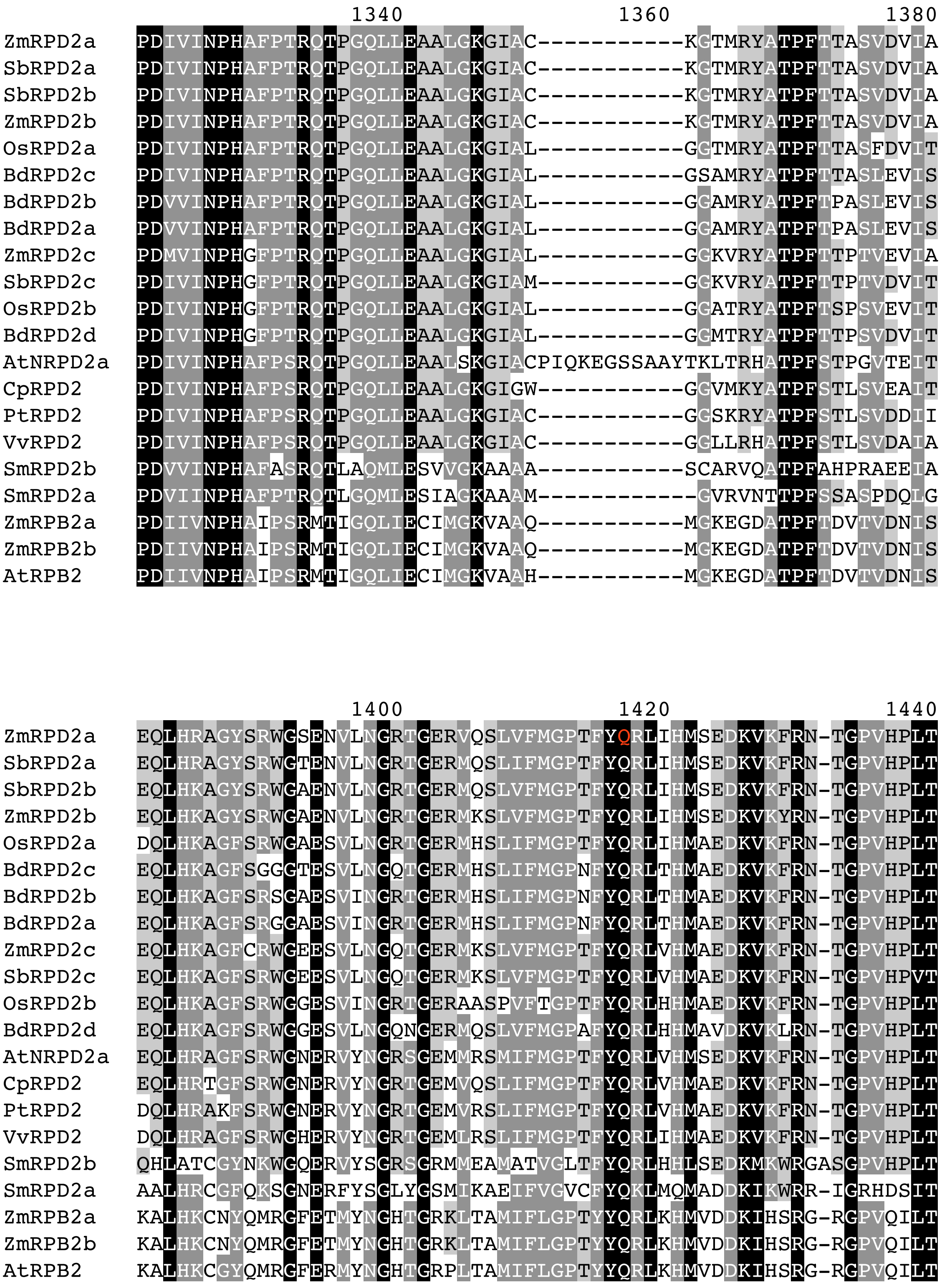

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                              1340                1360                1380
ZmRPD2a    PDIVINPHAFPTRQTPGQLLEAALGKGIAC-----------KGTMRYATPFTTASVDVIA
SbRPD2a    PDIVINPHAFPTRQTPGQLLEAALGKGIAC-----------KGTMRYATPFTTASVDVIA
SbRPD2b    PDIVINPHAFPTRQTPGQLLEAALGKGIAC-----------KGTMRYATPFTTASVDVIA
ZmRPD2b    PDIVINPHAFPTRQTPGQLLEAALGKGIAC-----------KGTMRYATPFTTASVDVIA
OsRPD2a    PDIVINPHAFPTRQTPGQLLEAALGKGIAL-----------GGTMRYATPFTTASFDVIT
BdRPD2c    PDIVINPHAFPTRQTPGQLLEAALGKGIAL-----------GSAMRYATPFTTASLEVIS
BdRPD2b    PDVVINPHAFPTRQTPGQLLEAALGKGIAL-----------GGAMRYATPFTPASLEVIS
BdRPD2a    PDVVINPHAFPTRQTPGQLLEAALGKGIAL-----------GGAMRYATPFTPASLEVIS
ZmRPD2c    PDMVINPHGFPTRQTPGQLLEAALGKGIAL-----------GGKVRYATPFTTPTVEVIA
SbRPD2c    PDIVINPHGFPTRQTPGQLLEAALGKGIAM-----------GGKVRYATPFTTPTVDVIT
OsRPD2b    PDIVINPHGFPTRQTPGQLLEAALGKGIAL-----------GGATRYATPFTSPSVEVIT
BdRPD2d    PDIVINPHGFPTRQTPGQLLEAALGKGIAL-----------GGMTRYATPFTTPSVDVIT
AtNRPD2a   PDIVINPHAFPSRQTPGQLLEAALSKGIACPIQKEGSSAAYTKLTRHATPFSTPGVTEIT
CpRPD2     PDIVINPHAFPSRQTPGQLLEAALGKGIGW-----------GGVMKYATPFSTLSVEAIT
PtRPD2     PDIVINPHAFPSRQTPGQLLEAALGKGIAC-----------GGSKRYATPFSTLSVDDII
VvRPD2     PDIVINPHAFPSRQTPGQLLEAALGKGIAC-----------GGLLRHATPFSTLSVDAIA
SmRPD2b    PDVVINPHAFASRQTLAQMLESVVGKAAAA-----------SCARVQATPFAHPRAEEIA
SmRPD2a    PDVIINPHAFPTRQTLGQMLESIAGKAAAM------------GVRVNTTPFSSASPDQLG
ZmRPB2a    PDIIVNPHAIPSRMTIGQLIECIMGKVAAQ-----------MGKEGDATPFTDVTVDNIS
ZmRPB2b    PDIIVNPHAIPSRMTIGQLIECIMGKVAAQ-----------MGKEGDATPFTDVTVDNIS
AtRPB2     PDIIVNPHAIPSRMTIGQLIECIMGKVAAH-----------MGKEGDATPFTDVTVDNIS
```

```
                              1400                1420                1440
ZmRPD2a    EQLHRAGYSRWGSENVLNGRTGERVQSLVFMGPTFYQRLIHMSEDKVKFRN-TGPVHPLT
SbRPD2a    EQLHRAGYSRWGTENVLNGRTGERMQSLIFMGPTFYQRLIHMSEDKVKFRN-TGPVHPLT
SbRPD2b    EQLHKAGYSRWGAENVLNGRTGERMQSLVFMGPTFYQRLIHMSEDKVKFRN-TGPVHPLT
ZmRPD2b    EQLHKAGYSRWGAENVLNGRTGERMKSLVFMGPTFYQRLIHMSEDKVKYRN-TGPVHPLT
OsRPD2a    DQLHKAGFSRWGAESVLNGRTGERMHSLIFMGPTFYQRLIHMAEDKVKFRN-TGPVHPLT
BdRPD2c    EQLHKAGFSGGGTESVLNGQTGERMHSLIFMGPNFYQRLTHMAEDKVKFRN-TGPVHPLT
BdRPD2b    EQLHKAGFSRSGAESVINGRTGERMHSLIFMGPNFYQRLTHMAEDKVKFRN-TGPVHPLT
BdRPD2a    EQLHKAGFSRGGAESVINGRTGERMHSLIFMGPNFYQRLTHMAEDKVKFRN-TGPVHPLT
ZmRPD2c    EQLHKAGFCRWGEESVLNGQTGERMKSLVFMGPTFYQRLVHMAEDKVKFRN-TGPVHPLT
SbRPD2c    EQLHKAGFSRWGEESVLNGQTGERMKSLVFMGPTFYQRLVHMAEDKVKFRN-TGPVHPVT
OsRPD2b    EQLHKAGFSRWGGESVINGRTGERAASPVFTGPTFYQRLHHMAEDKVKFRN-TGPVHPLT
BdRPD2d    EQLHKAGFSRWGGESVLNGQNGERMQSLVFMGPAFYQRLHHMAVDKVKLRN-TGPVHPLT
AtNRPD2a   EQLHRAGFSRWGNERVYNGRSGEMMRSMIFMGPTFYQRLVHMSEDKVKFRN-TGPVHPLT
CpRPD2     EQLHRTGFSRWGNERVYNGRTGEMVQSLIFMGPTFYQRLVHMAEDKVKFRN-TGPVHPLT
PtRPD2     DQLHRAKFSRWGNERVYNGRTGEMVRSLIFMGPTFYQRLVHMAEDKVKFRN-TGPVHPLT
VvRPD2     DQLHRAGFSRWGHERVYNGRTGEMLRSLIFMGPTFYQRLIHMAEDKVKFRN-TGPVHPLT
SmRPD2b    QHLATCGYNKWGQERVYSGRSGRMMEAMATVGLTFYQRLHHLSEDKMKWRGASGPVHPLT
SmRPD2a    AALHRCGFQKSGNERFYSGLYGSMIKAEIFVGVCFYQKLMQMADDKIKWRR-IGRHDSIT
ZmRPB2a    KALHKCNYQMRGFETMYNGHTGRKLTAMIFLGPTYYQRLKHMVDDKIHSRG-RGPVQILT
ZmRPB2b    KALHKCNYQMRGFETMYNGHTGRKLTAMIFLGPTYYQRLKHMVDDKIHSRG-RGPVQILT
AtRPB2     KALHKCGYQMRGFERMYNGHTGRPLTAMIFLGPTYYQRLKHMVDDKIHSRG-RGPVQILT
```

*RMR7-3 (Q to X)

```
                     1460                1480                1500
ZmRPD2a   RQPVADRKRFGGVKFGEMERDCLLAHGSAANLHERLFLLSDFSQMHICQTCERVANVVMR
SbRPD2a   RQPVADRKRFGGVKFGEMERDCLLAHGSAANLHERLFMLSDFSQMHICQTCERVANVVMR
SbRPD2b   RQPVADRKRFGGVKFGEMERDCLLAHGSAANLHERLFMLSDFSQMHICQTCERVANVVMR
ZmRPD2b   RQPVADRKRFGGVKFGEMERDCLLAHGSAANLHERLFMLSDFSQMHICQTCERVANVVMR
OsRPD2a   RQPVADRKRFGGVKFGEMERDCLLAHGAAANLHERLFMLSDFSQMHVCQTCERVANVIMR
BdRPD2c   RQPVADRKRFGGVKFGEMERDCLLAHGAAANLHERLFMLSDFAQMHICQTCQRAANVVMR
BdRPD2b   RQPVADRKRFGGVKFGEMERDCLLAHGAAANLHERLFMLSDFSQMHICRTCERVANVVMR
BdRPD2a   RQPVADRKRFGGVKFGEMERDCLLAHGAAANLHERLFMLSDFSQMHICRTCERVANVVMR
ZmRPD2c   RQPVEDKKRFGGVKFGEMERDCMLAHGAAANLHERLFTLSDFSRMHICQACERVANVIVR
SbRPD2c   RQPVEDKKRFGGVKFGEMERDCMLAHGAAANLHERLFTLSDFSQMHICQACQRVANVIMR
OsRPD2b   RQPVEDRRRYGGVKFGEMERDCLLAHGAAANLHERLFLLSDVSRLHVCRRCQRAAVVVSP
BdRPD2d   RQPVEDKKRFGGVKFGEMERDCLLAHGATANVHERLFRVSDLSEMHICQACQRVANVILR
AtNRPD2a  RQPVADRKRFGGIKFGEMERDCLIAHGASANLHERLFTLSDSSQMHICRKCKTYANVIER
CpRPD2    RQPVADRKRFGGVKFGEMERDCLIAHGASANLHERLFTLSDSSQMHVCQKCENVANVIQR
PtRPD2    RQPVADRKRFGGIKFGEMERDCLIAHGASANLHERLFTLSDSSEMHICQKCKNVANVIQR
VvRPD2    RQPVSDRKRFGGIKFGEMERDCLIAHGAAANLHERLFTLSDSAYMHICRRCKNISNVIQR
SmRPD2b   HQPVKDRKREGGTKFGEMERDCLISHGASATVKERLFFVSDRSLVPVCTNCHRLAILNCK
SmRPD2a   RQPIKDRQKYGGIKFSQMERSSLVAHGAAASIQERMFHLSDPHQVEVCTRCDRMASI---
ZmRPB2a   RQPAEGRSRDGGLRFGEMERDCMIAHGAAFFLKERLFDQSDAYRVHVCEKCGLIAIANLK
ZmRPB2b   RQPAEGRSRDGGLRFGEMERDCMIAHGAAFFLKERLFDQSDAYRVHVCEKCGLIAIANLK
AtRPB2    RQPAEGRSRDGGLRFGEMERDCMIAHGAAHFLKERLFDQSDAYRVHVCEVCGLIAIANLK
```

```
                          1520                1540                1560
ZmRPD2a   SVP----GGKKIRGPYCGFCKSS-ENIVRINVPYGAKLLYQELFSMGICLKFETQVC---
SbRPD2a   SVS----GGKKIRGPYCGFCKSS-ENIVRINVPYGAKLLYQELFSMGICLKFDTEVC---
SbRPD2b   SVP----GGKKIRGPYCGFCKSS-ENIVRINVPYGAKLLYQELFSMGICLKFDTEVC---
ZmRPD2b   SVP----GGKKIRGPYCGFCKSS-ENIVRINVPYGAKLLYQELFSMGICLKFETEVC---
OsRPD2a   PVP----GGKKIRGPYCGFCRSS-ENIVRINVPYGAKLLYQELFSMGICLRFETEVC---
BdRPD2c   AIP----GGKKIRGPYCGFCRSS-ENKVRIAVPYGAKLLYQELFSMGICLKFKTEVC---
BdRPD2b   SVP----GGKRIRGPYCGFCRSS-ENTVRIAVPYGAKLLYQELFCMGICLKFQTEIC---
BdRPD2a   GVP----GGKRIRGPYCGFCRSS-ENTVRIAVPYGAKLLYQELFCMGICLKFQTEIC---
ZmRPD2c   AAE--GGGGKKVRGPYCLFCRSA-ERVVRVDVPYGSKLLYQELFSMGICLKFETEVR---
SbRPD2c   PAE---GGSKKVHGPYCMFCRSA-ERIVRVNVPYGSKLLYQELFCMGICLKFDTEIR---
OsRPD2b   AVAADGGGGRKVRGPYCRFCRSA-EEVVRVSVPYGAKILYQELFSMGICLKFDTELI---
BdRPD2d   S-E----GGKKVHGPYCGFCKSA-ENILRVNVPYGASLLYKELFCMGICLKFETEVI---
AtNRPD2a  TPS----SGRKIRGPYCRVCVSS-DHVVRVYVPYGAKLLCQELFSMGITLNFDTKLC---
CpRPD2    AVP----GGRKVRGPYCHICETV-DHIVRVNVPYGAKLLCQELFSMGISLKFETRLC---
PtRPD2    GVP----GGRKIRGPYCRVCESV-DDLVKVSVPYGAKLLCQELFSMGISLKFDTRVS---
VvRPD2    SVA----GGRKVRGPYCRYCESS-EEIVKVNVPYGAKLLCQELFSMGISLKFETQLC---
SmRPD2b   ------------QHPRCLFCNPQ-QRIATLDMPHACKLLSMELRSMGVDMRFRVSQH---
SmRPD2a   ---------GRSRAPSCRFCKDKFPGFARLEIPYSCKLLVQELNSMGIDLRLVTDSSASL
ZmRPB2a   K-----------NSFECRGCKNK-TDIVQVHIPYACKLLFQELMAMAIAPRMLTHDMKTG
ZmRPB2b   K-----------NSFECRGCKNK-TDIVQVHIPYACKLLFQELMAMAIAPRMLTHDMKTG
AtRPB2    K-----------NSFECRGCKNK-TDIVQVYIPYACKLLFQELMSMAIAPRMLTKHLKSA
```

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                1570
ZmRPD2a   -------
SbRPD2a   -------
SbRPD2b   -------
ZmRPD2b   -------
OsRPD2a   -------
BdRPD2c   -------
BdRPD2b   -------
BdRPD2a   -------
ZmRPD2c   -------
SbRPD2c   -------
OsRPD2b   -------
BdRPD2d   -------
AtNRPD2a  -------
CpRPD2    -------
PtRPD2    -------
VvRPD2    -------
SmRPD2b   -------
SmRPD2a   RGREDKN
ZmRPB2a   KDQKKR-
ZmRPB2b   KDQKKR-
AtRPB2    KGRQ---
```
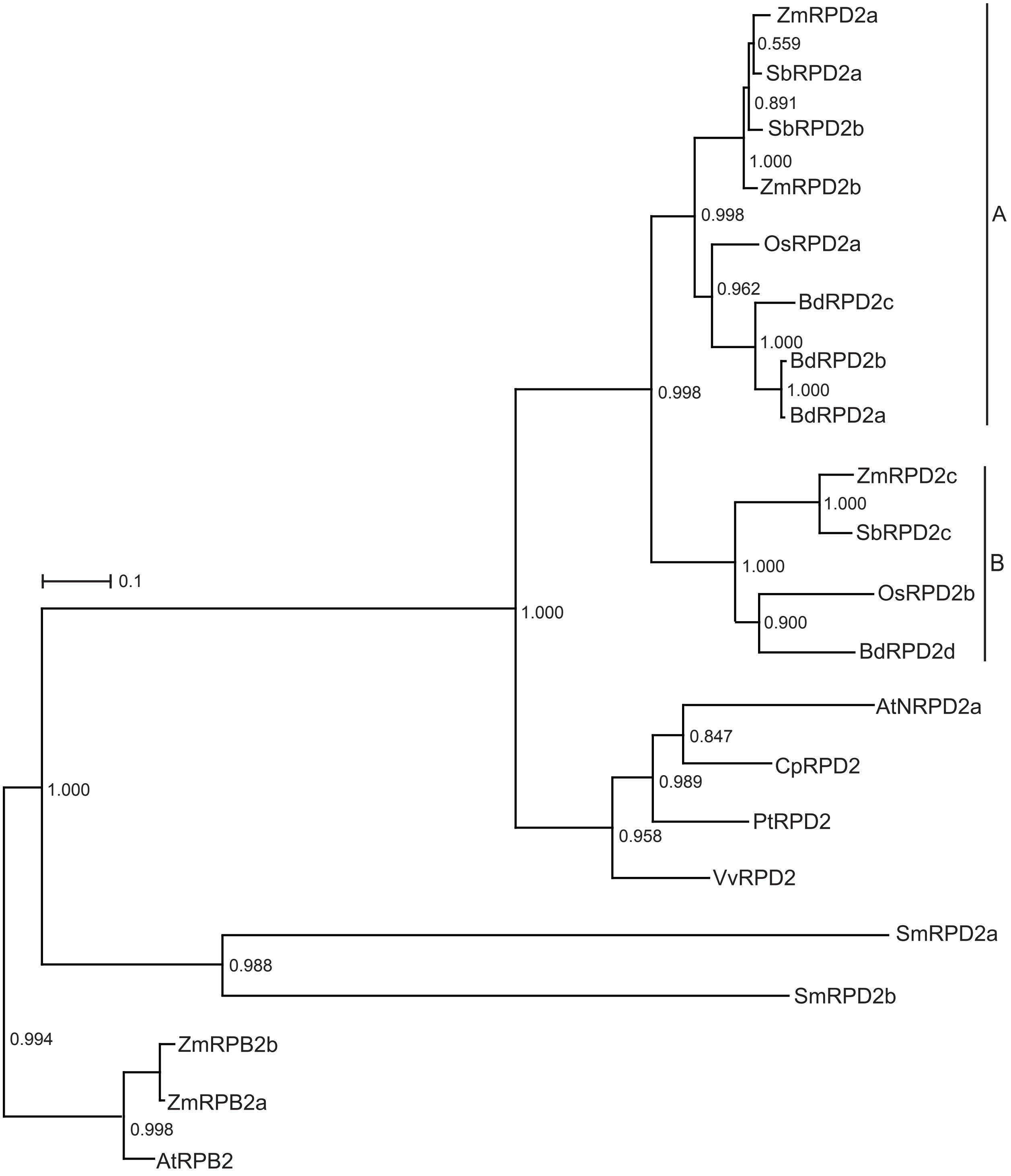

Figure 7. Grasses contain multiple RPD2-type proteins. Maximum likelihood tree produced from the alignment of RPD2a with other plant RPD2-type proteins. RPB2 proteins from maize and *Arabidopsis* root the tree. Outgroup branch length is not to scale.



Chapter 4 -- Genetic and molecular characterization of *rmr* factors

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Introduction

Concurrent with mapping efforts described in Chapter 2, we undertook projects to characterize effects of the *rmr* factors on *pl1* and normal functions of the maize plant. Due to the nature of the genetic screen in which they were identified, all *rmr* factors are required to maintain somatic repression of the *Pl'* state, but it was unknown if they were also required for maintenance of *Pl'* across generations and for establishment of *Pl'*. All *rmr* and *mop* mutants which have been analyzed show increased levels of *pl1* RNA [Dorweiler *et al.* 2000; Hollick and Chandler 2001; Hollick *et al*. 2005], but it was unclear if this increase in RNA was exclusively due to increases in transcription, as comparisons between run-on transcription assays and RNase protection measurements indicated that the *Pl'* state might be dependent on post-transcriptional mechanisms as well [Hollick *et al*. 2000].

In this chapter I present the genetic and molecular characterization of the *rmr1-3* allele. As described in Chapter 2, *rmr1-3* has the potential to encode a truncated peptide containing regions of intrinsic disorder but lacking the Snf2 domain. Initial crosses with the *rmr1-3* allele demonstrated non-allelic non complementation with alleles of *rmr6* / *rpd1*, encoding the largest subunit of Pol IV in maize, indicating that the protein products encoded by the two loci may be interacting. Further analysis of the non-allelic non-complementation results will be presented to help understand potential interactions between the alleles, and peptide antibodies will be raised against RMR1 in part to determine if a RMR1-3 peptide is produce. Additionally, *Pl'* reversion rates, *Pl'* establishment, and *pl1* expression are compared between *rmr1-3* and *rmr1-1* mutants to study the *rmr1* allelic series and to better understand the role of *rmr1*, and the RdDM pathway, in paramutation.

Results

Non-allelic non-complementation of *rmr1* alleles is background dependent.

Previously, dark plants from the original M2 family segregating for *rmr1-3* (99-45B) were crossed by both a *Pl'* tester for stock construction and a *Pl* tester to determine the rate of *Pl'* to *Pl* reversion in the new mutant (Figure 1). The resulting heterozygous *Pl* / *Pl; +* / *rmr1-3* revertants and *Pl'* / *Pl'; +* / *rmr1-3* plants were crossed with other *rmr* mutants to test potential complementation (Figure 1). Progeny from these crosses were grown out in two separate field seasons (years 2000 by J. Hollick and 2005 by J. Stonaker) and scored for Pl' and Pl types. Non-complementation would be indicated by finding Pl types in the progeny sets.

All progeny from the cross of *Pl'* / *Pl'*; + / *rmr1-3* X *Pl'* / *Pl'*; *rmr2-1* / *rmr2-1* were *Pl'* (26 / 26) demonstrating complementation between the two alleles (Table 1). When this same + / *rmr1-3* plant was used as a male and crossed to a *rpd1-1* homozygote 13 Pl types were observed out of 45 total plants suggesting partial non-complementation between *rmr1-3* and *rpd1-1* (Table 1). Non-complementation was also observed in progeny of the cross of *Pl* / *Pl*; *rmr1-3* / + X *Pl'* / *Pl'*; *rpd1-1* / +. Out of 48 plants, 8 were Pl types which is not significantly different from the null hypothesis of non-complementation (χ^2=1.778, p=0.1824; Table 1).

Results of the cross between *Pl* / *Pl*; *rmr1-3* / + and *Pl'* / *Pl'*; *rmr1-1* / *rmr1-1* are more difficult to interpret. Since the *rmr1-3* heterozygote used for this cross was carrying alleles in the *Pl* state, Pl types observed in the progeny set could result from reversion occurring in the *rmr1-1* homozygote or non-complementation between the two alleles. Thus, even if complementation occurred a certain number of Pl types could be expected due to reversion in the *rmr1-1* homozygote, but if non-complementation occurred we could expect a larger number of Pl types than expected due to the combination of non-complementation and reversion. Significantly more Pl types were observed than expected (χ^2=18.132, p=0.0001; Table 1) suggesting that non-complementation and ~30% reversion occurred. This reversion rate is consistent with other reported rates in *rmr1-1* mutants [Hollick and Chandler 2001].

These genetic results indicate that *rmr1-3* non-complements both *rmr1-1* and *rpd1-1* alleles. As *rmr1-3* and *rmr1-1* were determined to be allelic through mapping (Chapter 2), non-complementation is expected. However, it was not expected for *rpd1-1* as it defines a separate locus and *rmr1-1* and *rpd1-1* demonstrate complete complementation [Hollick *et al.* 2005]. To further explore the relationship between the two alleles I crossed a *rmr1-3* homozygote by a *rpd1-1* homozygote to generate double mutants (see below), but the progeny of this cross showed complete complementation (20 / 20 Pl' types; Table 2). In light of these results, I made new crosses between *Pl'* / *Pl'* ; *rmr1-3* / *rmr1-3* mutants and *Pl'* / *Pl'* + / *rmr1-1* and *Pl'* / *Pl'* + / *rpd1-1* heterozygotes, and grew out progeny sets segregating for *rmr1-3* / *rmr1-1* mutants and *rmr1-3* ; *rpd1-1* double heterozygotes. *rmr1-1* and *rmr1-3* showed non-complementation as expected, but two individual crosses of *Pl'* / *Pl'* ; + / *rpd1-1* X *Pl'* / *Pl'* ; *rmr1-3* / *rmr1-3* showed complete complementation (49 / 49 Pl' types; Table 2).

The above results present an apparent paradox that *rmr1-3* can both complement and non-complement *rpd1-1*. This does not appear to be due to parent of origin effects as both results have been observed when *rmr1-3* is homozygous in either parent. The original non-complementation results are not a simple failure of the test as a single *Pl'* / *Pl'* ; *rmr1-3* / + plant showed complementation with *rmr2-1* and non-complementation with *rpd1-1*. The discrepancy between the two results may be due to the background of the individual stocks used for the two sets of complementation test crosses. The original test was performed using stocks only one generation removed from the EMS mutagenesis screen while subsequent tests were performed using stocks that had undergone multiple rounds of outcrossing, sibling crossing, and selfing. Perhaps the *Pl'* alleles used in the original crosses were more sensitive to perturbations in the *rmr1-3* ; *rpd1-1* double heterozygote.

While I found that the original *rmr1-3* ; *rpd1-1* results were not replicable, an additional example of non-complementation was observed between *rmr1-4* and *rmr7-1* / *rpd2a* (Table 3). As described in the previous chapter, *rmr7-1* / *rpd2a* encodes the second largest subunit of either Pol IV and / or Pol V. Two independent test crosses showed that *rmr1-4* specifically non-complements alleles of *rmr1* and *rpd2a-1* while complementing other *rmr* mutations. In total, these results indicate that certain trans-heterozygous combinations involving mutant alleles of *rmr1* and specific mutant alleles encoding RNAP subunits can destabilize the *Pl'* state.

Putative *rmr1-3* ; *rpd1-1* double mutants have severe developmental phenotypes.

I performed crosses to produce *rmr1* ; *rpd1* double mutants in an effort to further understand the genetic relationship of *rmr1* and *rpd1* functions. Homozygous *rmr1-3* mutants were crossed by homozygous *rpd1-1* mutants to generate a family of *rmr1-3* / + ; + / *rpd1-1* plants. These double heterozygotes were selfed to generate F2 progenies segregating for *rmr1-3* / *rmr1-3* ; *rpd1-1* / *rpd1-1* double mutants. Seeds from six F2 ears progenies were grown out and scored for anther phenotype and plant morphology. At the time this experiment was performed, the molecular lesions responsible for *rmr1* and *rpd1* had not been determined, so putative double mutants were inferred by visual phenotype.

In total, 800 F2 seeds were planted and 440 surviving plants were examined. Anther color was graded on a scale of 1-7 with ACS1-4 types considered Pl' and ACS7 types considered Pl [Hollick *et al.* 1995]. ACS5 (3 individuals) and ACS6 (14 individuals) plants are not included in the Pl' / Pl categories because they are metastable and can either increase or decrease ACS in the next generation. Assuming full complementation we expect 247 Pl' types and 193 Pl types, but the Pl types would be further subdivided based on plant morphology. Homozygous *rpd1-1* mutants have characteristic morphological defects including reduced plant height (90-170 cm for mutants vs. 140-220 cm for heterozygous siblings [Parkinson *et al.* 2007]), compact tassel morphology (Figure 2A), and feminized tassel [Parkinson *et al.* 2007]. Therefore one would expect ~ 83 plants (28 + / + ; *rpd1-1* / *rpd1-1* and 55 + / *rmr1-3* ; *rpd1-1* / *rpd1-1*) to be Pl and exhibit homozygous *rpd1-1* morphological characteristics. Because homozygous *rmr1-3* mutants are of normal height with normal tassel morphology (Figure 2B), one would expect ~ 83 plants to be Pl with no morphological defects. Finally, we would expect 27-28 double mutants were expected which could either look like *rpd1-1* mutants, *rmr1-3* mutants, or have a new phenotype depending on the relationship between the loci (additive, epistatic, or synergistic, respectively).

In total, 234 Pl' types and 114 Pl types were recorded indicating that full complementation occurred in the F2 families as it did in the F1 double heterozygotes. 76 Pl types were record as morphologically normal (Table 4), which is close to what was expected for the *rmr1-3* single mutant class. However, only 22 Pl types were recorded as having a compact tassel phenotype (Table 4). This number roughly correlates with the number of expected + / + ; *rpd1-1* / *rpd1-1* mutants (27-28) suggesting that + / *rmr1-3*; *rpd1-1* / *rpd1-1* mutants may have exhibited a different phenotype. Feminized tassels were observed for a smaller number of plants (11, Table 4) but the tassel seed phenotype is not completely penetrant in *rpd1* mutants [Parkinson *et al.* 2007].

In general, fewer Pl types than expected were recorded. This is in part due to 32 plants which were recorded as colorless and 44 which could not be scored (Table 4). Colorless anthers differ from Pl' anthers in that there is absolutely no color produced and the anthers have a greenish hue instead of the usual yellow. This phenotype is similar to that observed when plants are homozygous for recessive *r-g* alleles, but a pedigree search did not detect a source for *r-g* in either the *rmr1-3* or *rpd1-1* parent. Alternatively, these colorless anthers could represent developmentally delayed anthers which have not matured enough to produce pigmentation.

The majority of plants with colorless and non-scorable anthers exhibited morphological phenotypes which were more severe than individual *rpd1-1* and *rmr1-3* homozygous mutants. These plants with morphological defects were further sub-divided into two classes based on the severity of their phenotypes. Class I plants were reduced to 66 to 86 cm in height, beyond the normal range of *rpd1-1* mutants. In addition to the height reduction, some Class I plants had reduced tassel size and floret production and wrinkled instead of smooth leaf blades (Figure 2C).

In total, 34 plants were identified as Class I. The majority of these Class I plants had either colorless anthers (14) or were not scorable (13) although 6 ACS7 and 1 ACS1 types were recorded (Table 5). The single ACS1 plant may have been an incorrectly scored colorless type. Class II plants, were distinguished from Class I by a further reduction in height (less than 66 cm, Figure 2D), narrow and wrinkled leaves which remained wrapped around the tassel (Figure 2E), and more severe tassel defects (Figure 2F, 2G) including plants with complete absence of a tassel. 36 plants were identified as Class II, and the majority had non-scorable tassels (Table 4).

The number of observed Class II plants (36) is greater than would be expected for the double mutant class (27-28). Alternatively, the double mutant class may not be viable (the germination rate was ~55%), and Class I and Class II plants could represent mutants with triple *rmr* doses (*rmr1-3* / *rmr1-3* ; + / *rpd1-1* or + / *rmr1-3* ; *rpd1-1* / *rpd1-1*). While an absolute correlation between genotype and phenotype cannot be determined, these results are consistent with the idea that the severity of morphological defects increases as dosage of *rmr1-3* and *rpd1-1* alleles is increased. The putative double mutants exhibit stronger phenotypes than would be expected through a simple additive relationship between the two single mutants. Availability of molecular markers for the *rmr1-3* and *rpd1-1* alleles can now be used to unambiguously address this apparent dosage issue.

Different rates of *Pl'* to *Pl* reversion highlight variation in *rmr1* alleles.

The *rmr1* locus is defined by four recessive alleles which are required to maintain repression of the *Pl'* state. As described above, the *rmr1-3* and *rmr1-4* alleles exhibit non-allelic non-complementation with mutant alleles of *rpd1* and *rpd2a,* respectively, while *rmr1-1* and *rmr1-2* alleles have never demonstrated non-allelic non-complementation with any other *rmr* allele. Curious to see if the mutant *rmr1* alleles had different affects on other phenotypes, I crossed homozygous *Pl'* ; *rmr1* mutants to *Pl* / *Pl* plants to test meiotic stability of the *Pl'* state. Any alleles which reverted from *Pl'* to *Pl* in *rmr1* mutants would produce Pl type progeny while non-reverted alleles would produce Pl' types.

Previous analysis showed stable reversion of *Pl'* to *Pl* at a rate of 12-89% in *rmr1-1* and *rmr1-2* homozygous mutants [Hollick and Chandler 2001]. Cross direction and *Pl* / *Pl* tester background has not been shown to impact reversion rate, but some *rmr* factors show increased reversion when the *Pl'* allele is kept in a mutant background for multiple generations [Hollick and Chandler 2001; Hollick *et al*. 2005; Stonaker *et al*. 2009]. To control for these different conditions, I set up reciprocal crosses between both *rmr1-3* and *rmr1-1* homozygous mutants at various levels of inbreeding and *Pl* / *Pl* testers in two different backgrounds, A632 and A619. The two mutant *rmr1* alleles were in similar backgrounds derived from the original mutagenesis screen. As controls, I crossed *rmr1-3* mutants to *Pl'* / *Pl'* testers and heterozygous siblings to both *Pl'* / *Pl'* and *Pl* / *Pl* testers. No progeny with Pl types were observed from any of the control crosses.

My progeny test results indicate that *rmr1-3* homozygous mutants show no reversion of *Pl'* to *Pl* when crossed to an A632 *Pl* / *Pl* tester regardless of the direction of the cross or number of generations of inbreeding (Table 5). Reversion in A619 testcrosses ranged from 0-33% with an average 8.5% (Table 5). There did not appear to be a correlation between reversion rate and number of generations kept in a mutant background. In contrast, *rmr1-1* homozygous mutants showed reversion of *Pl'* to *Pl* when crossed to both A632 and A619 *Pl* / *Pl* testers, but reversion detected by crosses to the A619 tester was greater. Reversion in A632 ranged from 0-89% with an average of 58.7% while reversion in A619 ranged from 58-100% and averaged 86.8% (Table 5). Again, there did not appear to be a correlation between reversion rate and number of generations kept in a mutant background. These results show that reverted *Pl* states are transmitted more frequently from *rmr1-1* mutants than from *rmr1-3* mutants, and that the *Pl* state is more recalcitrant to paramutation in A619 than A632. This interpretation is supported by the rates of spontaneous *Pl* to *Pl'* conversion in the two lines (A619, ~1 / 5000; A632, ~1 / 10; [Gross and Hollick 2007]).

Establishment of the *Pl'* state in *rmr1* mutants.

In addition to analysis of *Pl'* stability in *rmr1* mutants, I tested the ability of the *Pl'* state to be established in *Pl'* / *Pl* ; *rmr1-3* / *rmr1-3* mutants. Linking *Pl1-Rhoades* alleles in either the *Pl'* or *Pl* state to a *T6-9* translocation chromosome (*T*) allows specific alleles to be tracked and thus allows one to discriminate between meiotic reversion of an already established *Pl'* state from failure to established the *Pl'* state upon testcrossing to a *Pl* / *Pl* plant [Hollick *et al*. 2005]. Previous studies with a *rmr1-1* / *rmr1-2* mutant showed that the *Pl'* state could be established, but some Pl types were observed, likely due to reversion [Hale *et al*. 2007].

Reciprocal crosses were made between *Pl' T* / *Pl' T* ; + / *rmr1-3* and *Pl* / *Pl* ; + / *rmr1-3* plants to combine the *Pl'* and *Pl* state in *rmr1-3* mutants (Figure 3). The resulting dark-anthered *Pl' T* / *Pl* ; *rmr1-3* / *rmr1-3* plants were then reciprocally crossed to *Pl* / *Pl* testers (A619 background). Testcross progeny with semi-sterile pollen received the *Pl' T* chromosome, and were expected to have Pl' anthers unless reversion of the *Pl'* allele to *Pl* had occurred. Progeny with fully-fertile pollen received the non-translocation chromosome carrying the original *Pl* allele. If establishment occurred in the mutant, *Pl* would have been converted to *Pl'* and all the testcross progeny would be Pl'. If establishment failed to occur in the mutant then the *Pl* state would be transmitted resulting in Pl progeny. Light-anthered *Pl' T* / *Pl* ; *Rmr1* / - plants were also reciprocally crossed to *Pl* / *Pl* testers as a control. Both the semi-sterile and fully-fertile progeny from the control crosses should be Pl'.

Testcross progeny were grown to maturity and scored for pollen sterility and anther color (Table 6). Of the 97 fully-fertile test progeny, 40 were ACS7. Two plants had Pl' anthers but could not be assigned a discrete ACS. These plants had chimeric tassels containing anthers which varied from ACS1 to ACS4. This is unusual as pigment is typically uniform within a given plant [Hollick *et al.* 1995]. The remaining 55 plants also had chimeric tassels encompassing at least two different ACS scores including 4 plants with ACS1 through ACS7 anthers. Of the 96 semi-sterile test progeny, 9 were fully ACS7, 6 were fully ACS2, 1 was fully ACS3, and 6 others had chimeric tassels with only *Pl'*-type color scores. The remaining 74 plants had chimeric tassels encompassing at least two different ACS scores that were not exclusively Pl' types.

The control crosses, which should have produced progeny of only Pl' types, also had a large proportion of ACS7 and chimeric tassels (Table 6). Of 47 fully-fertile control progeny, 7 were ACS7, 2 were ACS1, 4 were ACS2, and 4 were ACS3. 4 plants had chimeric tassels with exclusively Pl' type anthers while the remaining 26 plants had chimeric tassels that were not exclusively Pl' types. Of the 48 semi-sterile control progeny, 12 were ACS7, 2 were Pl' only chimerics, and the remaining 34 were chimerics that were not exclusively Pl'.

The presence of Pl-type progeny from in the control crosses suggests instability of the *Pl' T* allele or recalcitrance of the *Pl* allele to new paramutation. Neither of these two situations have been observed in mutants or non-mutants previously. The original *Pl' T* / *Pl' T* ; + / *rmr1-3* plant was generated by crossing a homozygous mutant and heterozygous sibling. Perhaps the *Pl'* T allele reverted to *Pl* in the mutant, but the *Pl'* state should have been successfully re-established in the heterozygote. Additionally, this plant was recorded as Pl' with no observed chimerism in the tassel. It is also unclear if this instability is due to the *rmr1-3* allele as control crosses performed with + / *rmr1-3* or + / + plants also showed chimerism, but the *Pl' T* chromosome had been used in other mutant backgrounds, even with other *rmr1* alleles, with no apparent problems [Hollick *et al.* 2005; Hale *et al.* 2007]. From these tests, it is impossible to determine if establishment is inhibited in *rmr1-3* homozygous mutants given the unexpected results of the controls. However, these results, along with the non-allelic non-complementation of *rpd1-1*, highlight the unusual effects *rmr1-3* can have on paramutant *pl1* alleles.

Production of peptide antibodies against RMR1.

To better understand the nature of the *rmr* allelic series differences and functional characteristics of the RMR1 protein I began to develop immunoreagents against RMR1. The initial goal was to generate antibodies against full-length RMR1 which would require cloning the *rmr1* cDNA into an expression vector. Since the *rmr1* cDNA is large (>4.5kb) it would be difficult to amplify by RT-PCR, and attempts to amplify the *rmr1* cDNA using a RT-PCR kit optimized for long templates were not successful. To work around the PCR size limitation, fragments of *rmr1* cDNA were amplified separately, but attempts to clone portions of *rmr1* into normal and his-tagged vectors was met with variable results (Figure 4, Table 7). The region covering the Snf2 domain was never successfully cloned, but the region immediately 5' to the Snf2 domain was cloned into a standard vector and used as a molecular probe. No amplicons from the N-terminal portion of the *rmr1* cDNA were successfully cloned into standard vectors, but *rmr1* RACE products were cloned into a pSMART vector with transcriptional terminators flanking the cloning site to prevent unwanted transcription. These results indicate that *rmr1* is toxic to *E. coli*, and provide another possible explanation for why *rmr1* cDNA was never identified in publicly available cDNA libraries. Specialized vectors such as pSMART should be used for future cloning projects.

Given the difficulties with cloning *rmr1*, I worked with Covance Antibody Services (www.abservices.crpinc.com) to have peptide antibodies raised against RMR1. Peptide chemists selected four 11-12 amino acid long peptides from different regions of RMR1 (Figure 5, Table 8). Two were specifically designed to the N-terminal region to detect a truncated RMR1-3 (T1 and T2) while the other two were designed to the C-terminal region to detect only full length RMR1 (F1 and F2). Peptides were synthesized and conjugated to carrier protein keyhole limpet hemoglobin (KLH) to increase the immune response. Sixteen rabbits were prescreened for background, and eight were selected for injection with peptides (two rabbits / peptide; Table 8). Antibodies were produced according to the standard 118-day rabbit protocol and I then affinity purified these for use in immunoblots and immunolocalization. Initial immunoblots showed high levels of background, and it was determined that the goat anti-rabbit IgG secondary antibody was cross reacting with all maize proteins, perhaps due to corn in the goat diet. This issue was corrected by performing subsequent immunoblots with protein A as the secondary detection reagent.

Peptide antibodies are not effective for either immunoblotting or immunolocalization.

RMR1 is predicted to be a nuclear localized protein with a molecular weight of 161 kD, and if a truncated RMR1-3 peptide is produced it is predicted to be 47.8 kD. If the peptide antibodies specifically recognize RMR1 then anti-F1, anti-F2, anti-T1, and anti-T2 antibodies should recognize a 161 kD protein in all non-mutant samples and potentially in homozygous *rmr1-1*, *rmr1-2*, and *rmr1-4* samples, depending on mutant protein stability. Anti-T1 and anti-T2 could recognize a 47.8 kD protein from homozygous *rmr1-3* mutant samples while anti-T1 and anti-T2 should not recognize any proteins in those samples. Immature ears were selected as the tissue for analysis due to RT-PCR-based evidence for expression of *rmr1* in the tissue and their relatively larger size and cell density compared to other tissues that express *rmr1* (immature tassels, root tips, and shoot apical meristems).

Immunoblots were performed on both total and nuclear proteins isolated from immature ears (Figure 6A). A Pol II antibody was used as a positive control for protein and immunoblotting quality. Pol II was detected in the total protein sample but was enriched in the nuclear protein sample (Figure 6A) indicating that the nuclear fraction was enriched for nuclear proteins, high molecular weight proteins had been transferred during blotting, and immunodetection was successful. As a positive control for immunodetection with the RMR1 peptide antibodies, the corresponding conjugated peptides were included and a different conjugated peptide was included as a negative control. In this immunoblot, the F1 and T1 antibodies did not recognize their respective peptides and are not included in the figure. The F2 and T2 antibodies showed selective detection of their respective peptides (Figure 6A) indicating that the antibodies could recognize their purified epitopes.

Anti-T2 did not detect any proteins in the nuclear protein fraction, yet a faint ~50kD band was observed in both homozygous mutant and heterozygous non-mutant total protein samples (Figure 6A). While this protein roughly corresponds to the size of the predicted RMR1-3 peptide it should not be detected in the *rmr1-1* samples. This likely indicates that anti-T2 is not recognizing RMR1, but alternatively it could be recognizing an unknown processed form of the protein. Anti-F2 detected a ~65-70kD protein and a ~30kD protein in total protein mutant and non-mutant samples. As anti-F2 should not recognize any proteins in the *rmr1-3* sample, this result indicates that anti-F2 is not binding to RMR1 in total protein samples. However, in the nuclear protein fraction, anti-F2 recognized a ~30kD protein in non-mutant samples only (Figure 6A). While the size of this protein does not correspond to RMR1 it could represent a processed form, and the failure to recognize protein in the *rmr1-3* sample is as expected for the anti-F2 antibody.

Since the anti-F2 antibody had produced a promising result, a new immunoblot was performed using the same *rmr1-1* and *rmr1-3* samples with the addition of *rmr1-2* and *rmr1-4* samples. Anti-F2 recognized multiple proteins in the total protein homogenate from homozygous mutant and heterozygous non-mutant samples. None of these proteins corresponded to the predicted size of RMR1 or truncated RMR1-3 (Figure 6B) and are likely not RMR1. In the nuclear protein fraction ~30 kD and ~65-70kD proteins were detected in all heterozygous non-mutant and homozygous *rmr1-2* and *rmr1-4* mutant samples (the *rmr1-4* mutant band is faint but detectable in the original film). Again, no proteins were recognized in the homozygous *rmr1-1* and *rmr1-3* mutant samples. To check protein quality in these lanes the blots were stripped and re-detected with anti-Pol II resulting in a similar pattern as the anti-F2 detection indicating that protein quality was poor in nuclear fractions isolated from homozygous *rmr1-1* and *rmr1-3* mutant samples, and to a lesser extent in the *rmr1-4* mutant sample. Therefore, anti-F2 is likely not detecting RMR1 protein but rather cross-reacting with other maize proteins.

One possible explanation for the failure of the peptide antibodies to detect RMR1 is that the levels of RMR1 protein are below the limits of detection. To enrich for RMR1, I used a combined mixture of anti-F1, F2, T1, and T2 antibodies to immunoprecipitate total protein samples which were then detected with the individual antibodies by immunoblotting (Figure 6C). This resulted in identification of a ~50kD protein in all samples by each antibody. This protein cannot be RMR1 or a processed form of RMR1 as anti-F1 and anti-F2 should not have recognized any protein in the homozygous *rmr1-3* mutant samples. This result indicates that the peptide antibodies are not able to detect RMR1 protein by immunoblotting. The peptide antibodies were also used for immunolocalization on isolated root tip cells, but no RMR1 specific staining patterns were observed. Immunological analysis of RMR1 will require additional antibodies preferentially generated against the whole protein sequence.

***rmr1* is required for post-transcriptional regulation of *pl1*.**

Snf2 proteins are often characterized as transcriptional regulators [Flaus *et al*. 2006]. Previously, *rmr1-1* mutants were shown to have a 26-fold increase in *pl1* RNA levels in floret tissue over heterozygous siblings, but it was not clear if this increase in *pl1* RNA was due to increased transcription from the *pl1* locus [Hollick and Chandler 2001]. In vitro transcription assays using husk leaf nuclei showed no statistically significant difference in *pl1* transcription rates between *rmr1-1* mutants and heterozygous siblings, but a direct downstream target of PL1, *anthocyaninless1* (*a1*), showed a ~4-fold increase in transcription in *rmr1-1* mutants demonstrating increased PL1 activity [Hale *et al.* 2007]. Similarly, nuclei isolated from *rmr1-3* mutants showed no significant change in *pl1* transcription and an ~6-fold increase in transcription of *a1* compared to heterozygous siblings [Hale *et al*. 2007].

I performed RNase protection experiments using husk RNA isolated from the same plants used for the in vitro transcription assays that showed a 5.7-fold increase in *pl1* RNA for *rmr1-3* mutants compared to heterozygous siblings (Figure 7A and 7B; n=2, two-tailed two-sample *t*-test, $t = 10.8$, $p < 0.01$). The increase in *pl1* RNA in *rmr1-3* mutants is much lower than what is observed for *rmr1-1* mutants, but the difference could be due to the different tissues used in the respective experiments (floret vs. husk leaf) or allele specific effects. Regardless of the variation between alleles, together these results show that *rmr1* is not required for transcription repression of *Pl1-Rhoades* but rather functions at a post-transcriptional level to regulate *Pl1-Rhoades* RNA. These results stand in contrast to those observed for similar experiments which show that *rpd1* is required for transcriptional repression of *Pl1-Rhoades* [Hollick *et al*. 2005].

Discussion

In this chapter, I present genetic and molecular characterization of the *rmr1-3* allele. These results demonstrate that *rmr1-3* can both stabilize and destabilize the *Pl'* state depending on combination with other background modifiers and / or differential conditioning of the *Pl1-Rhoades* allele. The apparently paradoxical role of *rmr1-3* in the maintenance of *Pl'* may help dissect the complex mechanisms required for paramutation at *pl1*.

To date, all mutant alleles identified from our genetic screens have been recessive [Hollick and Chandler 2001; Hollick *et al*. 2005; Stonaker *et al*. 2009]. However, double heterozygous combinations of specific *rmr1* and RNAP subunit alleles can destabilize the *Pl'* state resulting in *Pl*-like plants. Two different models have been proposed to explain such examples of non-allelic non-complementation (NANC). In the poison complex model, mutant proteins inhibit function of a large macromolecular complex because they retain the ability to interact with the complex but lack other enzymatic functions [Yook 2005]. The dosage model postulates that while individual loci are haplosufficient, the double heterozygote combination is haploinsufficient [Yook 2005].

Alleles in the dosage model are usually, but not always, nulls while alleles in the poison complex model are by definition not nulls because the gene products must physically interact [Yook 2005]. As discussed in Chapter 2, the *rmr1-3* is expressed and potentially produces a truncated protein that contains a large proportion of the intrinsic disorder regions but lacks a Snf2 domain. The *rpd1-1* allele harbors a nonsense mutation which truncates the final third of the protein. It is unknown if *rpd1-1* is expressed or makes a stable protein, but if the RPD1-1 peptide is produced it would contain RNAP domains A through F, including the active site, but lack domains G and H. Thus, both *rmr1-3* and *rpd1-1* have the potential to encode mutant proteins that could retain some functional regions.

I propose that a combination of the poison complex and dosage models is consistent with the NANC observed between *rmr1-3* and *rpd1-1*. In the + / *rmr1-3* ; *rpd1-1* / + double heterozygote, interaction of truncated RMR1-3 with RPD1 would sequester functional RPD1 into inactive Pol IV complexes, and, if the *rpd1-1* allele is expressed, RPD1-1 could sequester normal RMR1 into inactive Pol IV complexes. Either or both of these interactions could reduce the number of functional Pol IV complexes below the critical threshold required to maintain *Pl'* repression. Differing threshold levels in different maize lines could explain why NANC is observed in some, but not all, genetic backgrounds and why partial NANC is observed in other backgrounds.

NANC is also observed in + / *rmr1-4* ; *rpd2a-1* / + double heterozygotes. The *rmr1-4* allele has a missense mutation in the Snf2 domain predicted to inhibit ATP hydrolysis and, therefore, DNA translocation activity, but with unknown effect on protein stability. The *rpd2a-1* allele has a nonsense mutation which, if translated, would result in a 205 amino acid protein which lacks conserved RNAP domains C through I, including the active site. As with *rmr1-3* / *rpd1-1*, translation of either the RMR1-4 or RPD2a-1 mutant protein could result in sequestration of non-mutant proteins into inactive RNAP complexes and destabilization of the *Pl'* state.

The question remains why NANC is only observed between these specific allele combinations. The *rmr1-1* and *rmr1-2* alleles complement all other RNAP alleles, and *rpd2a-2* and *rpd2a-3* complement all *rmr1* alleles [Hollick and Chandler 2001; Stonaker *et al*. 2009] indicating that these alleles are either true nulls (no protein interactions to poison complexes) or do not result in haploinsufficiency when in combination with any other alleles. The *rmr1-3* allele may complement *rpd2a* because RMR1-3 lacks the regions required for interaction with RPD2a while full length RMR1-4 would retain those regions. However, if RMR1-4 has the ability to interact with both RPD1 and RPD2a, one might expect *rmr1-4* to also non-complement alleles of *rpd1*, which has not been documented [Hale *et al*. 2007]. Alternatively, the non-complementation between *rmr1-4* and *rpd2a-1* is simply the result of combined haploinsufficiency while double heterozygous combinations of *rmr1-4* with other RNAP subunits are all haplosufficient. Regardless, the NANC results observed between *rmr1*, *rpd1*, and *rpd2a* indicate that the proteins encoded by these loci are functioning together to maintain *Pl'* repression even if they aren't forming direct physical interactions.

We have proposed a function of RPD1 / Pol IV in inhibition of Pol II transcription at RdDM target loci [Erhard *et al*. 2009; Hale *et al*. 2009; this work, Chapter 3]. The developmental phenotypes observed in homozygous *rpd1* mutants may be the result of increased Pol II transcription from repetitive regions up-regulating nearby genes important for development. Accordingly, in homozygous *rpd1-1* mutants, hypomethylation and loss of 24 nt siRNAs at the *doppia* element ~100 bp upstream of *pl1* [Hale *et al*. 2007; Erhard *et al*. 2009] correlates with an increase in transcription of the *pl1* locus [Hollick *et al*. 2005]. However, while homozygous *rmr1* mutants also hypomethylate and reduce 24 nt siRNA accumulation at *doppia*, *pl1* stability rather than transcription is increased [this chapter, Hale *et al*. 2007]. The exact nature of this increase is unknown but indicates that *RMR1* may interact with RNA processing factors in addition to Pol IV. Failure to recruit RNA processing factors, such as RdDM component RDR2 [Xie *et al*. 2004] or exosome components [Belostotsky and Sieburth 2009], would result in an increase in transcript stability without a concurrent increase in transcription rate. Since *rmr1* mutants do not display developmental defects, these results indicate that transcription, rather than 24 nt siRNA accumulation, is the critical function for genome homeostasis.

Plants with developmental phenotypes drastically more severe than normal *rpd1* mutants were observed in the progeny set segregating for double mutants of *rmr1-3* and *rpd1-1*. Unfortunately, the molecular lesions responsible for the individual mutations was not known at the time of the experiment, but genetic analysis indicates that developmental phenotypes increase in severity as the dosage of either *rpd1-1* or *rmr1-3* increases. Molecularly, some of these plants have both increased transcription from and increased RNA stability of RdDM target loci and potentially attendant genes, amplifying the effect on developmentally important loci. This indicates that *rmr1-3*, and potentially other *rmr1* alleles, can enhance the *rpd1* phenotype. The effect with the *rmr1-3* allele may be stronger due to poison complex type-interactions between the two alleles.

The strange result of the *rmr1-3* establishment test may also represent a type of phenotype enhancement by the *rmr1-3* allele. In the establishment test, progeny with chimeric tassels were produced from both control and test crosses which is unusual because anther pigment is typically consistent within a tassel [Hollick *et al*. 1995]. Additionally, control crosses produced progeny with *Pl* anthers when *Pl'* anthers were exclusively expected. These results indicate that there was some instability in the *pl1* alleles which was enhanced upon exposure to *rmr1-3*. Sequestration of functional Pol IV complexes by + / *rmr1-3*, as proposed for the complementation test results, would likely not be sufficient to destabilize the *Pl'* state. However, combination of *rmr1-3* with an additional factor, such as an alterations to the *cis*-acting elements which control the acquisition and maintenance of the *Pl'* state, may have sufficiently destabilized *Pl'*.

The *Pl* alleles tested for ability to acquire the *Pl'* state in *rmr1-3* homozygous mutants came from one of two potential sources (1) *Pl* A619 or (2) a heritable revertant of *Pl'* to *Pl*. *Pl* alleles in the A619 background will invariantly convert to *Pl'* in *Pl'* / *Pl* heterozygotes, but A619 *Pl* alleles are relatively recalcitrant to spontaneous paramutation compared to *Pl* alleles in other backgrounds [Gross and Hollick 2007]. The A619 inbred line does not naturally contain a *Pl1-Rhoades* allele, but rather *Pl1-Rhoades* has been introgressed into A619 (98.5%). During the introgression process, the *cis*-acting elements may have been slightly modified, not enough to inhibit paramutation establishment, but enough to make the allele slightly more recalcitrant. This recalcitrance, in combination with the *rmr1-3* allele, could have destabilized the *Pl'* state during the establishment test which could have been further reinforced by test crossing the establishment test progeny to A619 *Pl* plants to assay the state of the *pl1* alleles.

However, *rmr1-3* alleles and A619 *Pl* have been combined many times with no apparent unusual effects (see reversion tests, this chapter). Alternatively, the heritably reverted *Pl* allele may have been recalcitrant to reestablishment of paramutation, although this has not been observed previously. The *Pl' T* allele used in the establishment tests had also not previously demonstrated any unusual behavior [Hollick *et al*. 2005; Hale *et al*. 2007], but perhaps it too had been destabilized in the *rmr1-3* background. Identification and molecular characterization of the *cis*-acting elements and additional grow outs of the establishment test progeny in combination with crosses to appropriate *pl1* testers may help determine the forces behind the observed result.

In addition to establishment, reversion, the ability of the *Pl'* state to heritably revert to *Pl*, was tested in homozygous *rmr1-3* mutants and compared the results to homozygous *rmr1-1* mutants. One might expect the *rmr1-3* mutants to show higher levels of reversion compared to *rmr1-1*, but instead, lower levels of reversion, 0% in most cases, were observed. Homozygous *rmr1-1* mutants showed higher rates of reversion, averaging at 87%. This result is unexpected because of the general destabilization of *Pl'* alleles when in combination with *rmr1-3* and would suggest that *rmr1-1* is the stronger allele. This result is consistent with *rmr1-1* being a true null and *rmr1-3* only destabilizing the *Pl'* state through interactions with other *trans*- or *cis*-acting factors. The material used for the reversion tests may have had a lower threshold for Pol IV function, and any sequestration by *rmr1-3* was not enough to produce a phenotype. Interestingly, keeping the *Pl'* allele in the mutant background did not increase the rate of reversion to *Pl* for either *rmr1-1* or *rmr1-3* indicating that loss of RMR1 function does not have a cumulative function.

Potential interactions between *rmr1* and other RdDM components are likely mediated by the regions of intrinsic disorder in the N-terminal region of the protein. RMR1-3, predicted to contain only intrinsically disordered (ID) regions but no Snf2 domain, would have the ability to bind other proteins but not function as a DNA translocase. RMR1-3 could inactivate Pol IV resulting in destabilization of *Pl'* in certain backgrounds. However, the stickiness of the intrinsic disordered regions may also explain, in part, the toxicity of *rmr1* to *E. coli* and the failure to identify RMR1 protein by immunoblotting and *rmr1* mRNA by Northern blotting (see Chapter

2). ID proteins must be tightly regulated at all levels because of the ability of the ID regions to form interactions with multiple protein partners [Uversky and Dunker 2010]. Inappropriate or ectopic interactions can result in atypical phenotypes [Uversky and Dunker 2010].

If *rmr1* is normally tightly regulated, mRNA and protein amounts may not accumulate to a level which can be detected by Northern or immuno-blotting. To date, expression of *rmr1* has only been detected by RT-PCR optimized for high amplification. I used multiple methods to increase both the sensitivity of the RMR1 peptide antibodies and the levels of RMR1, but I was not able to detect any RMR1 specific proteins. The amount of RMR1 protein is well below the detection levels of the peptide antibodies. Additionally, as the predicted RMR1-3 protein is truncated it potentially lacks the sequences required for regulation and could accumulate to abnormally high levels in the cells, exacerbating the ability of the *rmr1-3* to destabilize the *Pl'* state. Maize stocks which do not demonstrate this phenotype (such as the stocks used for reversion testing and later complementation tests) may better compensate for the higher levels of protein.

Finally, the stickiness problem may be part of the reason that *rmr1* is toxic to *E. coli*. Leaky expression from the cloning vector could produce RMR1 protein, and the ID regions could interfere with endogenous *E. coli* proteins. Attempts to clone just the Snf2 domain were potentially unsuccessful because the modular Snf2 domain was able to fold independently and interfere with endogenous nuclear functions, perhaps by inducing unwanted torsional strain in the bacterial chromosome. The internal segment of *rmr1* which was successfully cloned into a typical vector contains only small regions of intrinsic disorder and a portion of the Snf2 domain limiting any unwanted interactions with endogenous *E. coli* functions. Specially designed cloning vectors which prevent unwanted expression will facilitate cloning *rmr1*, but given the characteristic of the RMR1 protein, future expression of *rmr1* for biochemical analysis may prove difficult in both bacterial and eukaryotic systems.

rmr1 is a key component of the maize RdDM-like pathway and paramutation. While many questions about *rmr1* function remain, the analyses presented here highlight a role for *rmr1* in interacting with Pol IV and components required for RNA stability. The sticky nature of the ID regions likely facilitate normal RMR1 function, but in the *rmr1-3* allele these same regions are deregulated, released from the Snf2 domain, and able to destabilize the paramutation mechanism under certain conditions. Additional analysis of the *rmr1* allele series will continue to unravel this unusual nature of the paramutation mechanism.

Materials and Methods

Genetic stocks

General stock descriptions can be found in Chapter 2. Descriptions of the *rmr1-3* stocks used for the various genetic analyses are shown in Figure 8.

Complementation Tests

Crosses were performed between *rmr* factors as indicated in Tables 1, 2, and 3. When possible, at least one heterozygous individual was used to minimize effects of reversion of *Pl'* to *Pl-Rh* in mutant homozygotes. Progeny seeds were grown to maturity, and anthers were scored using the ACS. Individuals with ACS 1-4 were noted as *Pl'* while ACS 7 individuals were noted as *Pl-Rh*. For most allelic combinations, one or two independent crosses were analyzed. For crosses indicated in Table 1, progeny from one ear were analyzed in two different growouts to verify that field specific effects did not influence the original results.

Double Mutant Analysis

Double mutants were generated by crossing homozygous *rpd1-1* mutants (family 03-139) by homozygous *rmr1-3* mutants (family 03-770). The resulting trans-heterozygotes were selfed, and families segregating for double mutants were grown out in the following field season. Plants were screened for developmental phenotypes several times a week throughout the growing season. Upon flowering, ACS scores, tassel morphology, and plant heights were recorded. For plants which did not flower, phenotypes were last recorded two weeks after sibling plants flowered.

Meiotic Reversion Tests

Inbred *rmr1-1* and *rmr1-3* lines were initiated by selfing homozygous mutant plants from a segregating F2 family. Lines of single seed descent were propagated by selfing over the following growing seasons resulting in 10 generations of *rmr1-1* (F2S10) and 8 generations of *rmr1-3* (F2S8). Families from each selfed generation were grown out concurrently and crossed to color converted A619 or A632 *Pl-Rh* testers. Anther color scores of the progeny were evaluated the following year. % reversion was calculated by dividing the number of ACS 7 plants by the total number of plants in a given family.

Pl' Establishment Tests

The *Pl'* allele was linked to the translocation chromosome (*Pl'* T6-9) while the *Pl* allele was linked to the normal chromosome (*Pl*). Description of the T6-9 translocation chromosome can be found in Hollick *et al*. [2005]. *Pl'* T6-9 / *Pl* plants display 50% pollen sterility which can be assayed using a pocket microscope. Establishment of the *Pl'* state on the *Pl* allele was assayed by testcrossing *Pl'* T6-9 / *Pl* ; *rmr1-3* / *rmr1-3* plants and *Pl'* T6-9 / *Pl* ; *Rmr1-3* / *rmr1-3* controls to an *Pl* A619 tester. The resulting progeny were grown out in the following families: test: 08-117 (ear 72416), 08-118 (72421), 08-119 (72422), 08-120 (72413), 08-123 (72419), 08-125 (72414), 08-127 (72404); control: 09-121 (72407), 08-122 (72401), 08-124 (72410), 08-126 (72408) and scored for anther phenotype.

Cloning *rmr1* cDNA

PCR and RT-PCR were performed as described in Chapter 2. Long-template RT-PCR (Invitrogen, www.invitrogen.com) was performed according to manufacturer protocol. Cloning primers can be found in Appendix 1. Vector ligation and bacterial transformation was performed according to manufacturer protocol for the following plasmids: pSMART (Lucigen, www.lucigen.com), pGEM T-Easy (Promega, www.promega.com), pCR4-TOPO, pCR8/GW/TOPO, and pET30x (Invitrogen, www.invitrogen.com).

Antibodies

Peptides were selected as described in the text with the assistance of a peptide chemist at

New England Peptides (www.newenglandpeptides.com) to minimize cross reactivity and maximize antigenicity. Peptides were synthesized by New England Peptides, purified to at least 80% purity, and conjugated to carrier protein keyhole limpet hemocyanin. Antibodies were produced by Covance (www. crpinc.com). Serum from 16 rabbits was prescreened for peptide background by Covance, and 8 rabbits were selected for injection with peptides following the standard 118-day protocol. Specific rabbit / peptide combinations can be found in Table 8. 10 mLs of exsanguination bleed serum from each rabbit was affinity purified using the appropriate synthetic peptide coupled to Sulfolink coupling gel (Pierce, www.piercenet.com) as described in Onodera *et al*. [2005]. Affinity purified antibodies from the two rabbits used for each peptide were pooled for subsequent blotting.

Immunoblotting and Immunolocalization

Total protein was isolated by grinding immature ears in a coffee grinder with dry ice and mixing the resulting powder in extraction buffer (1mM EDTA; 10% glycerol; 75% NaCl; Protease inhibitor cocktail, 1 tablet / 10mL, Roche (www.roche.com); 0.05% SDS; 100mM Tris-Cl, pH 7.4; 0.1% Triton X-100) at proportions of 1-2 mLs / g ear tissue. The slurry was filtered through cheesecloth and spun at 10,000 x g at 4 degrees for 15 minutes. Nuclear proteins were isolated as per Steinmuller *et al*. [1986]. Proteins were quantified with the RCDC Kit (Biorad, www3.bio-rad.com). Samples for IP were treated with Benzonase endonuclease (Merck, www.merck.com) to release DNA-binding proteins and IP was performed as described in Fiil *et al*. [2008].

Gel electrophoresis was performed using the Invitrogen NuPAGE system (www.invitrogen.com) with 4-12% Bis-Tris gels. Blotting was performed by wet transfer onto 0.45 um nitrocellulose (Bio-Rad) using a transfer buffer optimized for high-molecular weight proteins (0.38M glycine; 0.05M Tris base; 0.2% Methanol; 0.1% SDS) at 30V overnight in the cold room. Membranes were blocked in 5% non-fat dry milk and incubated with 1:1000 dilutions of affinity purified primary antibody and 1:80,000 dilutions of protein A-peroxidase (Sigma-Aldrich, www.sigmaaldrich.com) in PBST. Washes were performed with PBST, and the ECL Western Blotting Analysis System was used for protein detection (GE Healthcare, www.gehealthcare.com). Immunolocalizations were performed on three-day old root tips as described in Golubovskaya *et al*. [2002].

RNase protection assay

RNA was isolated from *rmr1-3* mutant and heterozygous husk leaves using Trizol (Invitrogen) per manufacturers instructions. Anti-sense riboprobes for *pl1* and *actin1* were generated from 250 ng of linearized DNA template with T3 or T7 RNA polymerase (as applicable to template) and labeled with 2.5 µL of α^{32}P UTP (800 Ci/mmole) in a 10 µL reaction. Probe synthesis was stopped after 1 hour and remaining DNA was degraded with RNase-free DNase I (Roche). Probe was purified from unincorporated nucleotides and short synthesis products by running on a 6% acrylamide gel at ~600 V for 2-3 hours. Purified probe was hybridized with 5-10 µg of total RNA sample at 50°C overnight. ~500 U of T1 RNase (BRL) in 200 µL of RNase digestion mix (10mM Tris pH 7.8, 150 mM NaCl, 5mM EDTA) were added to the hybridized samples and incubated at 35 C for 1-2 hours. RNase was degraded with proteinase

K / SDS (8% SDS, 2μg/μL proteinase K) and extracted with 1:1 phenol/chloroform mixture. Samples were resuspended in loading buffer, denatured at 65-70°C for 10 minutes, and then run on a 6% acrylamide gel at 700-900 V. After ~3.5 hours gels were dried and placed in a phosphoimager cassette for 1-3 days. Riboprobe information can be obtained from Hollick *et al.* [2000].

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Figures

Figure 1. *rmr1-3* complementation test pedigree. Dark plants from 99-45B (bold), the initial isolate of the *rmr1-3* mutation, were crossed by *Pl'* and *Pl* testers to generate families 99-460 and 99-461, and these heterozygous + / *rmr1-3* plants were crossed with *rmr1-1*, *rmr2-1*, and *rpd1-1* mutants to test complementation. Results can be found in Table 1.

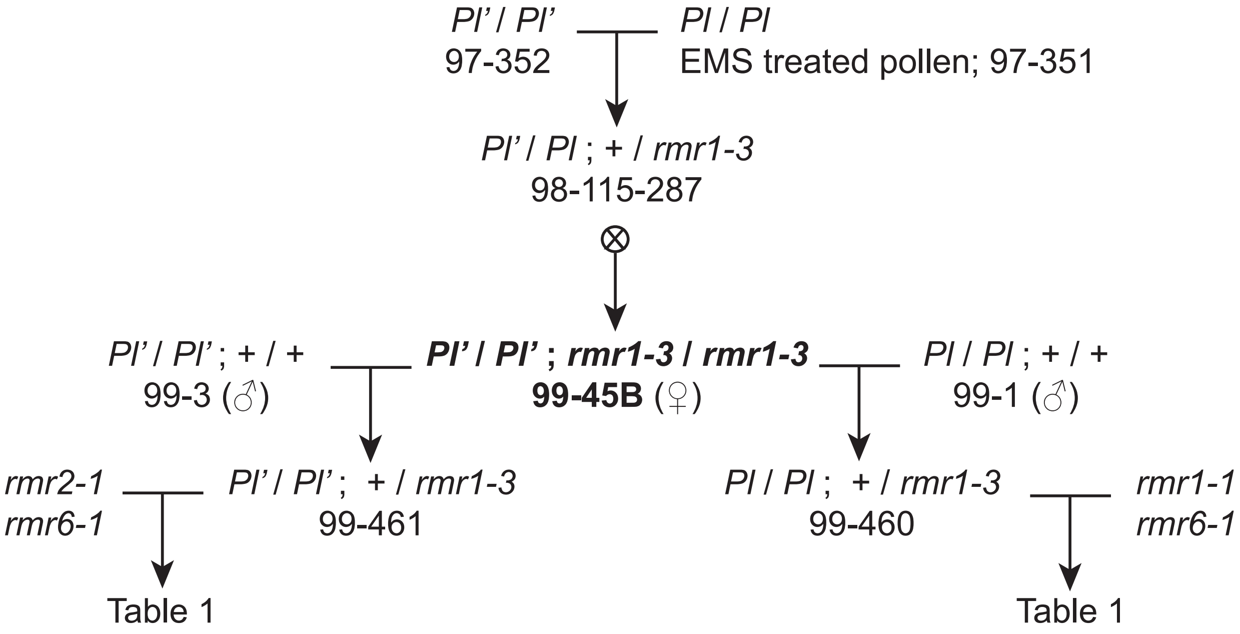


Figure 2. Phenotypes of plants from families segregating for *rmr1-3* ; *rpd1-1* double mutants.

(A) *rpd1-1* / *rpd1-1* tassel showing compact structure. (B) *rmr1-3* / *rmr1-3* tassel showing normal development of lateral branches and florets. (C) Wrinkled leaf phenotype characteristic of some Class I and Class II plants. (D) Class II plant flanked by Class I plants to show size difference. (E) Enveloped tassel characteristic of some Class II plants. (F) Tassel from Class II plant showing reduced lateral branching and floret development. (G) Class II plant showing a more severe tassel defect with no lateral branches or florets.

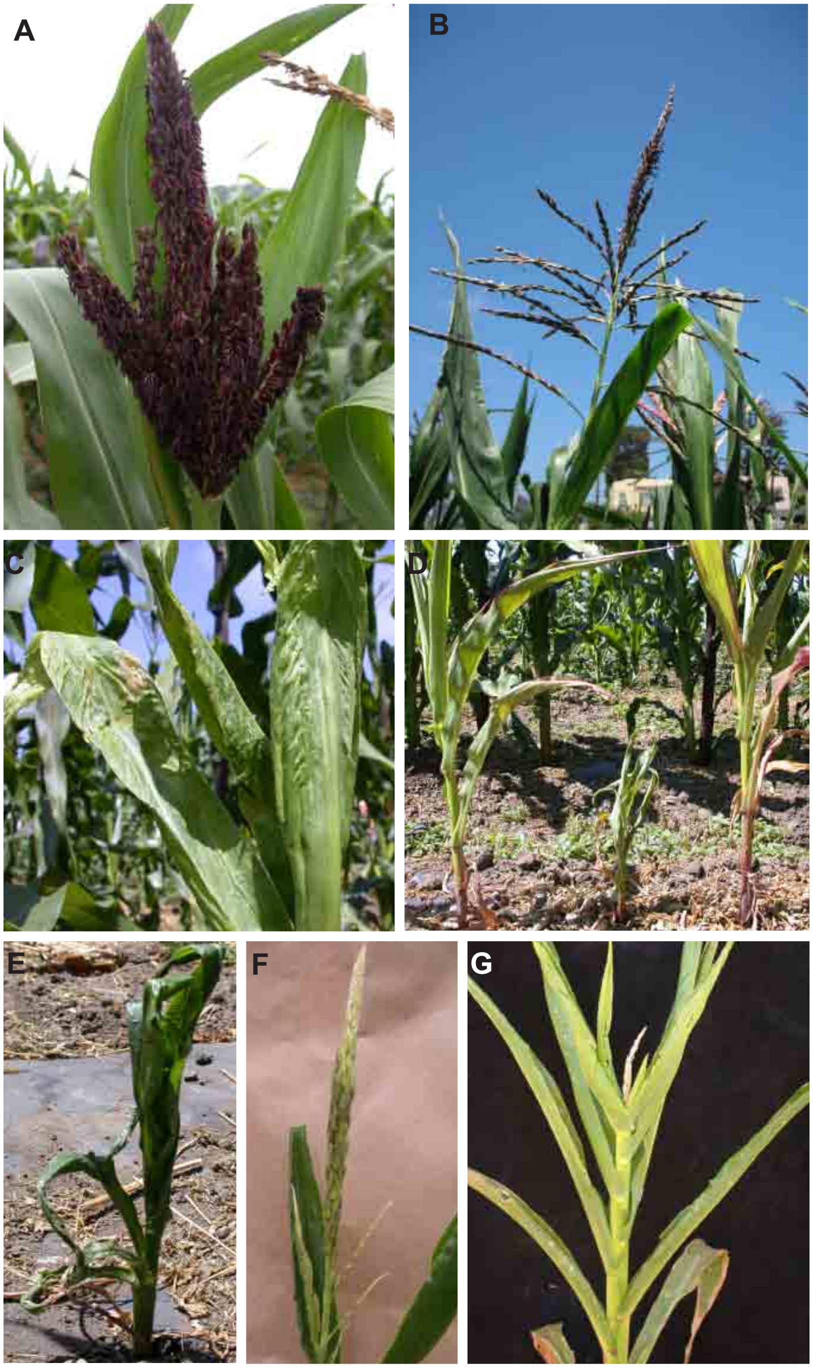


Figure 3. ***Pl′*** **establishment in** ***rmr1-3*** **mutants.** Pedigree information including family and ear numbers. (A) The *Pl′* allele was provided by a family segregating 1:1 for *rmr1-3* heterozygotes and homozygous mutant siblings. The *Pl* allele was generated from a reversion event occurring in a *rmr1-3* mutant. A heterozygous stock was generated by crossing the revertant plant to a *Pl* tester. (B) Light-anthered, heterozygous *rmr1-3* plants carrying *Pl′* on a translocation chromosome were crossed to dark-anthered heterozygous *rmr1-3* plants carrying *Pl* on a normal chromosome. (C) Dark, semi-sterile plants were crossed to a *Pl* tester to test establishment of the *Pl′* state while light, semi-sterile plants were crossed to a *Pl* tester as a control. (D) No Pl types are expected in the control cross. Pl types in the semi-sterile progeny class of the test cross represent *Pl′* alleles which have reverted to *Pl* while Pl types in the fully-fertile progeny class would represent failure to establish the *Pl′* state. Results can be found in Table 6.

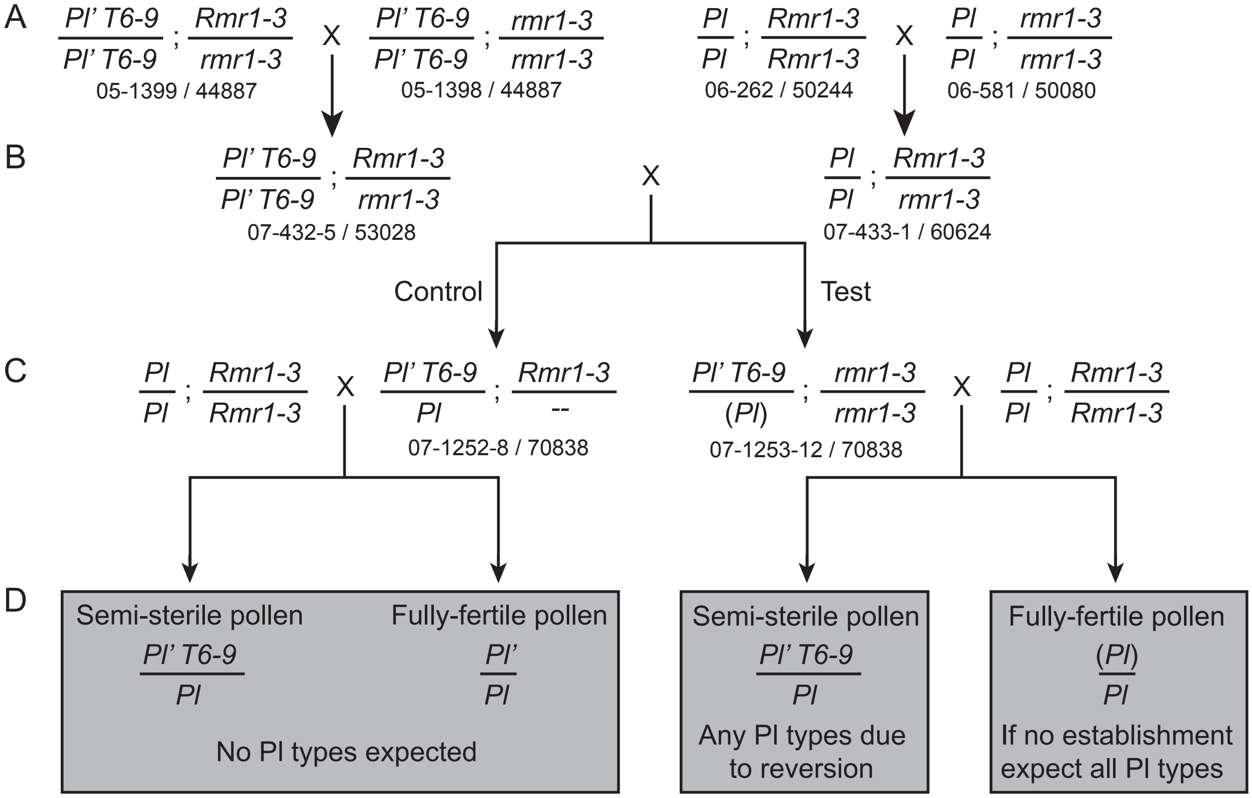


Figure 4. Cloning success of different *rmr1* regions. The *rmr1* cDNA is represented by the gray box with splice junctions represented by black bars and the Snf2 domain by black boxes. Regions for which cloning was attempted are highlighted below the cDNA model. Filled bars represent regions that were successfully cloned while open bars represent regions which were not successfully cloned. Description of regions and cloning vectors can be found in Table 7.

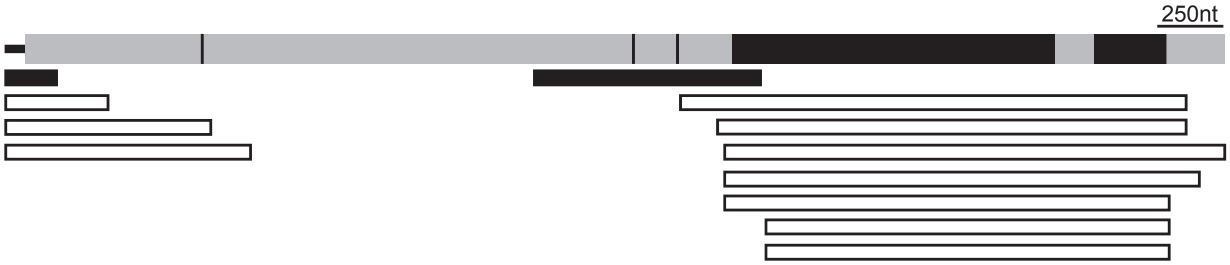


Figure 5. Peptide antibodies designed against four regions of RMR1. The RMR1 protein model is represented by the gray box. The hashed boxes highlight regions of intrinsic disorder and the black boxes represent the conserved SNF2 domain. The nuclear localization signal (NLS) and cysteine-rich region (Cys) are noted by white bars. Location of peptides T1, T2, F1, and F2 used to generate antibodies are indicated by purple bars. Peptide sequences can be found in Table 8.

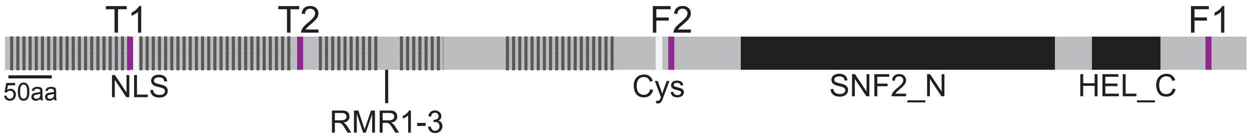


Figure 6. Immunoblots using peptide antibodies. (A) Immunoblots of total (upper panels) and nuclear (lower panels) proteins isolated from B73 (abbreviated B), *rmr1-1* (*1-1*), and *rmr1-3* (*1-3*) heterozygous (H) and homozygous mutant (M) immature ears. (+) and (-) signs refer to conjugated peptide positive and negative controls. Molecular weight ladder is indicated. (B) Immunoblot of immature ears isolated from indicated genotypes and detected with either anti-F2 (upper panels) or anti-Pol II (lower panel). (+) control lane is F2-conjugated peptide. (C) Immunoblot following immunoprecipitation of total protein samples from indicated genotypes with anti-F1, F2, T1, and T2 and then detected with individual antibodies as indicated.

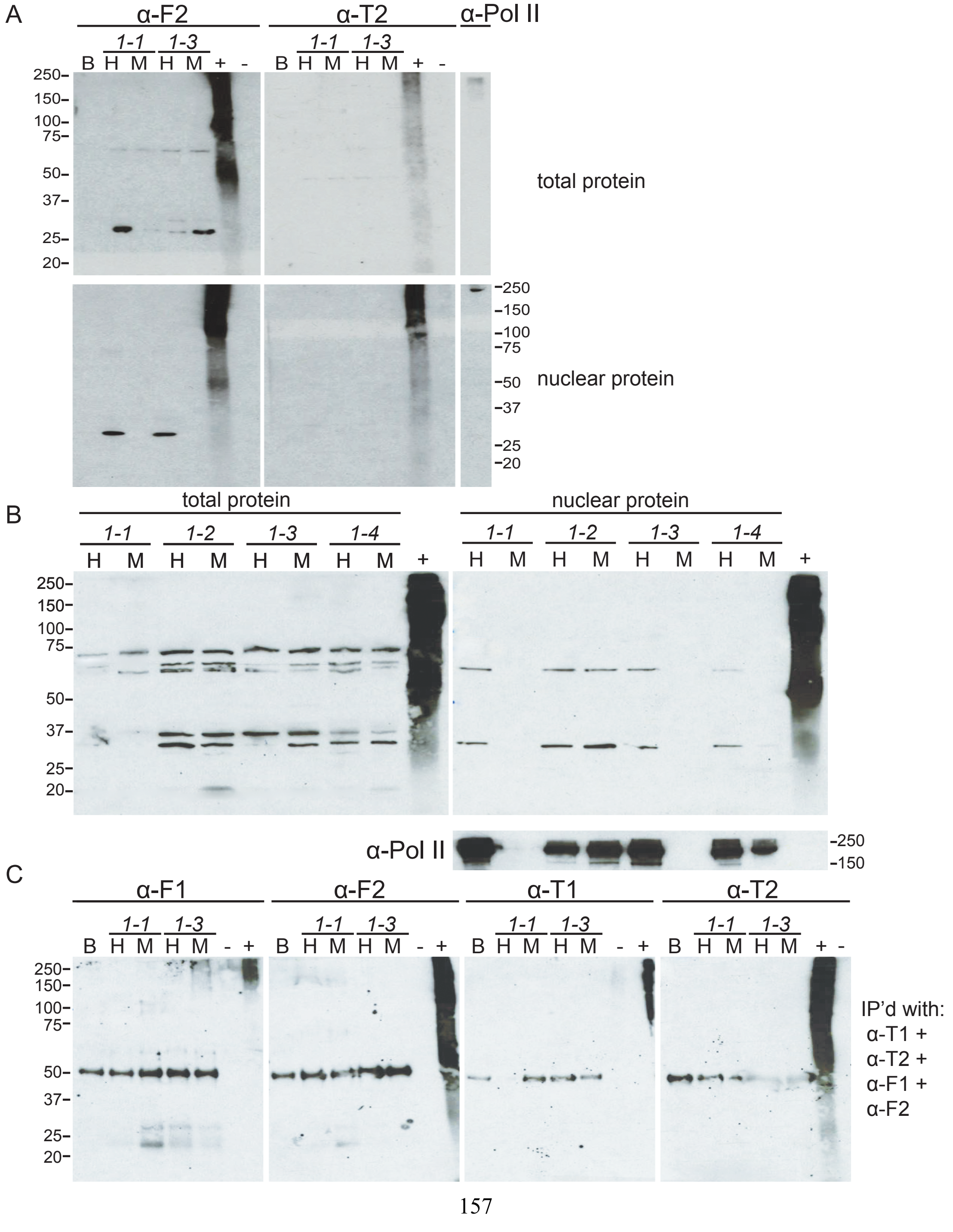


Figure 7. Comparison of *pl1* RNA levels between *rmr1-3* mutants and heterozygous siblings. (A) RNase protection analysis comparing *pl1* and *actin1* RNA levels in husk leaf tissue. (B) Quantification of relative *pl1* RNA levels from + / *rmr1-3* (open) and *rmr1-3* / *rmr1-3* (closed) siblings +/- s.e.m. (n = 2). Panels reprinted from Hale *et al.* 2007.

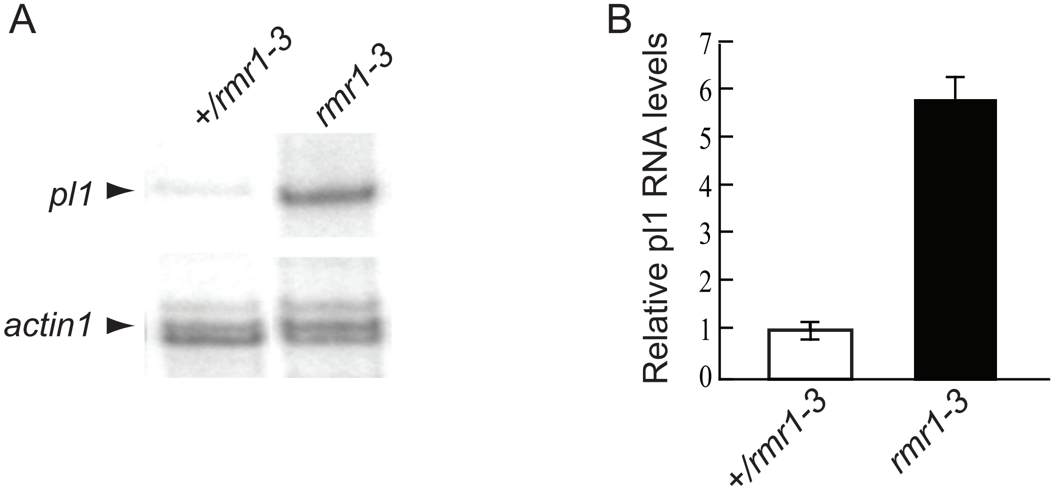
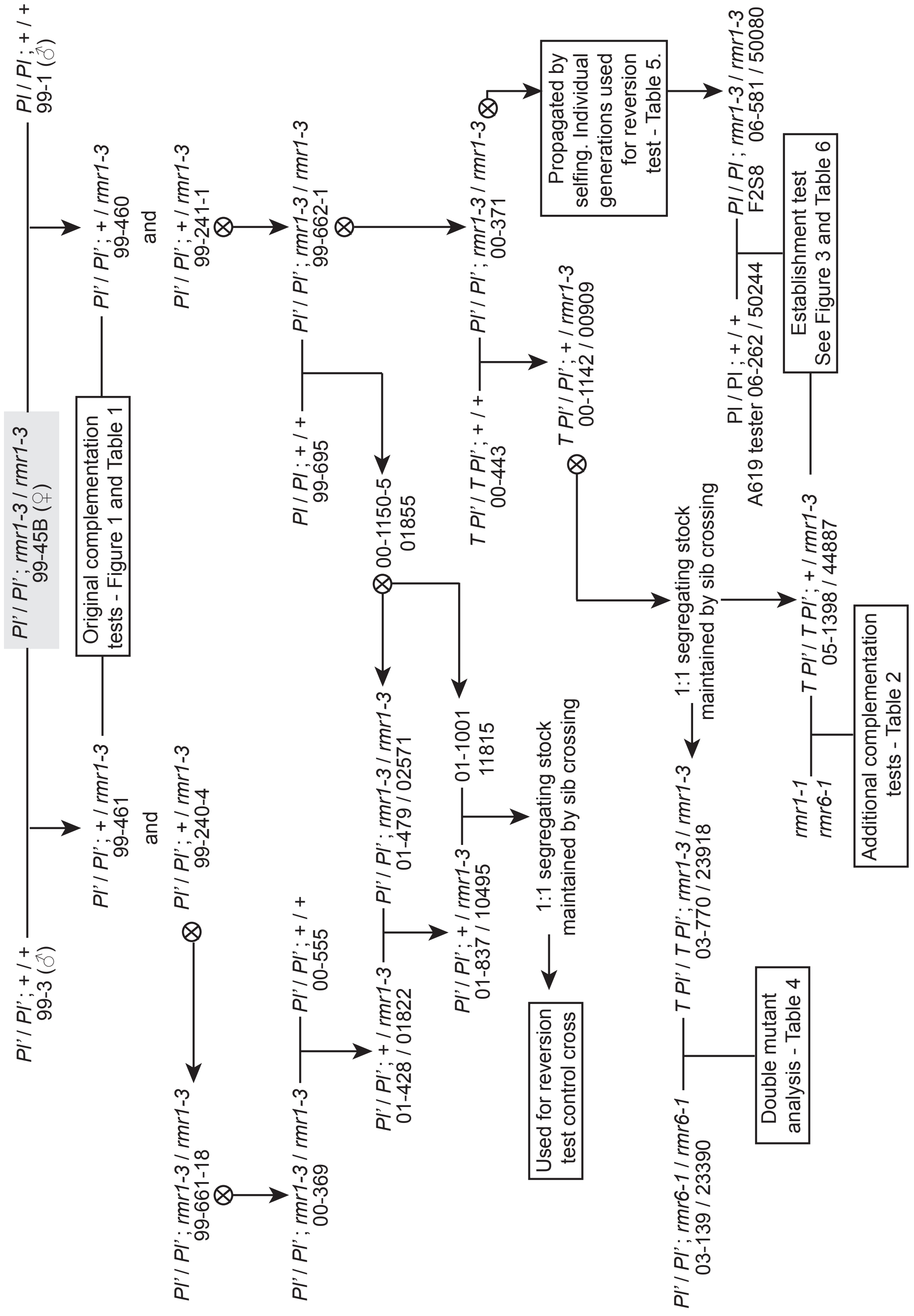


Figure 8. Pedigree of *rmr1-3* stocks used for genetic analyses. Stocks are described by their genotypic information, year and family number (ex: 01-428), and five digit ear number (ex: 01822) when available. Outcrossing is depicted by a horizontal bar while selfing is indicated by a ⊗ symbol.



Tables

Table 1. Original *rmr1-3* complementation tests. Progeny anthers from indicated crosses were scored Pl' vs Pl in two different growouts. Significantly more progeny with Pl types were observed for *rmr1-3* / + X *rmr1-1* / *rmr1-1* than expected by non-complementation alone (χ^2=18.132, p=0.0001). Progeny from *rmr1-3* / + X *rmr2-1* / *rmr2-1* showed complete complementation. Progeny generated from crosses between plants carrying *rmr1-3* and *rpd1-1* mutations showed non-allelic non-complementation. Data from 2000 growout collected by J. Hollick.

Parent Genotypes		Year	Progeny Phenotypes	
Pistillate	Staminate		Pl'	Pl
Pl / Pl ; rmr1-3 / +	*Pl' / Pl'* ; *rmr1-1 / rmr1-1*	2000	6	17
		2005	5	25
		Total	11	42
Pl' / Pl' ; rmr1-3 / +	*Pl' / Pl'* ; *rmr2-1 / rmr2-1*	2000	26	0
Pl' / Pl' ; *rpd1-1 / rpd1-1*	*Pl' / Pl' ; rmr1-3 / +*	2000	18	5
		2005	14	8
		Total	32	13
Pl / Pl ; rmr1-3 / +	*Pl' / Pl'* ; *rpd1-1 / +*	2000	12	3
		2005	28	5
		Total	40	8

Table 2. New *rmr1-3* complementation tests. Additional crosses between *rmr1-3* and *rmr1-1* and *rpd1-1*. Pl' and Pl phenotypes were scored in the anthers. All parents are *Pl'* / *Pl'*. [1]Ear generated for double mutant analysis.

Parent Genotypes		No. ears	Progeny Phenotypes	
Pistillate	Staminate		Pl'	Pl
rmr1-3 / *rmr1-3*	+ / *rmr1-1*	2	29	20
+ / *rmr1-1*	*rmr1-3* / *rmr1-3*	1	13	15
rmr1-3 / *rmr1-3*	*rpd1-1* / *rpd1-1*	1 [1]	20	0
+ / *rpd1-1*	*rmr1-3* / *rmr1-3*	2	49	0

Table 3. *rmr1-4* complementation tests. Complementation tests for *rmr1-4* allele. Pl' and Pl phenotypes were scored in the anthers. All parents are *Pl'* / *Pl'*. Specific non-allelic non-complementation observed among the progeny generated between *rmr1-4* / *rmr1-4* and *rpd2a-1* / + parents.

Parent Genotypes		No. ears	Progeny Phenotypes	
Pistillate	Staminate		Pl'	Pl
+ / *rmr1-1*	*rmr1-4* / *rmr1-4*	1	14	13
+ / *rmr1-3*	*rmr1-4* / *rmr1-4*	1	12	15
+ / *rmr2-1*	*rmr1-4* / *rmr1-4*	1	29	0
+ / *rpd1-1*	*rmr1-4* / *rmr1-4*	1	28	0
+ / *rpd2a-1*	*rmr1-4* / *rmr1-4*	2	13	11
+ / *rmr8-1*	*rmr1-4* / *rmr1-4*	2	31	0
+ / *mop1-4*	*rmr1-4* / *rmr1-4*	1	25	0

Table 4. Phenotypes of plants from families segregating for *rmr1-3* ; *rpd1-1* double mutants. ACS and developmental phenotypes of plants from the *rmr1-3* ; *rpd1-1* double mutant screen. The majority of plants were normal with no developmental phenotypes. A subset showed compact tassel and / or feminized tassel, mild developmental phenotypes characteristic of *rpd1-1* / *rpd1-1* mutants. Another group showed more severe developmental phenotypes. Class I plants were 66-86 inches tall, and some exhibited defects in tassel and / or leaf development. Class II plants were less than 66 inches tall, had narrow, wrinkled leaves, enveloped tassels, and tassel defects. A subset of these plants did not produce an apical inflorescence. [1]Colorless
[2]Not scorable. [3]One ACS7 plant was had both compact tassel and tassel seed.

Morphological phenotypes	Anther color phenotype								
	1	2	3	4	5	6	7	cl [1]	n.s. [2]
Normal	176	39	12	1	3	13	76	10	0
Compact tassel	3	0	0	0	0	0	22 [3]	4	1
Feminized tassel	0	0	0	0	0	0	9 [3]	0	2
Class I:	0	0	0	0	0	0	4	2	0
with tassel defects	0	0	0	0	0	0	0	3	6
with leaf defects	0	0	0	0	0	0	0	5	0
with tassel and leaf defects	1	0	0	0	0	0	2	4	7
Class II:	2	0	0	0	0	0	2	4	19
with no tassel	0	0	0	0	0	0	0	0	9
Total	182	39	12	1	3	13	114	32	44

Table 5. Meiotic reversion of *Pl'* to *Pl-Rh* in inbred *rmr1* mutants. The range of reversion in *rmr1-1* is 0-100% with an average of 87% when crossed to A619 testers and 59% when crossed to A632 testers. No reversion was observed when *rmr1-3* was crossed to A632 testers. When *rmr1-3* was crossed to A619 testers, the range was 0-33% which an average of 8.5%. *rmr1-1* allows higher rates of reversion than *rmr1-3* indicating that *rmr1-1* is a stronger mutant allele.

Parents		Progeny ACS							Reversion
Staminate	Pistillate	1	2	3	4	5	6	7	
A619 *Pl-Rh*	*rmr1-3*/*rmr1-3*								
	F2S1	1	1	2	2	1	1	4	33%
	F2S2	5	10	3	3	3	0	0	0%
	F2S4	5	3	3	1	0	0	0	0%
	F2S6	0	1	0	0	8	4	1	7%
	F2S7	0	2	0	1	1	0	0	0%
	F2S8	0	0	0	5	2	3	2	17%
A632 *Pl-Rh*	*rmr1-3*/*rmr1-3*								
	F2S2	5	4	0	0	0	0	0	0%
	F2S4	9	4	0	0	0	0	0	0%
	F2S5	4	4	0	0	0	0	0	0%
	F2S6	15	2	0	0	0	0	0	0%
	F2S7	3	7	0	0	0	0	0	0%
	F2S8	3	11	0	0	0	0	0	0%
rmr1-3/*rmr1-3*	A619 *Pl-Rh*								
F2S1		3	10	3	2	1	1	3	13%
F2S2		0	3	2	5	1	0	0	0%
F2S3		0	3	4	3	2	2	1	7%
F2S4		0	2	10	0	0	0	0	0%
F2S6		0	3	2	3	2	2	1	8%
F2S8		0	2	3	2	1	2	2	17%
rmr1-3/*rmr1-3*	A632 *Pl-Rh*								
F2S1		4	17	0	0	1	1	0	0%
F2S3		8	5	0	0	0	0	0	0%

F2S4		9	5	0	0	0	0	0	0%
F2S6		0	8	4	0	0	0	0	0%
F2S8		7	8	0	0	0	0	0	0%
A619 *Pl-Rh*	*rmr1-1*/*rmr1-1*								
	F2S1	0	0	0	0	0	1	10	91%
	F2S2	0	0	0	0	0	0	12	100%
	F2S3	0	0	0	0	0	3	10	77%
	F2S5	0	0	0	0	0	3	11	79%
	F2S6	0	0	0	0	1	4	7	58%
	F2S7	0	0	0	0	0	0	15	100%
	F2S8	0	0	0	0	0	0	17	100%
	F2S9	0	0	0	0	0	0	14	100%
	F2S10	0	0	0	0	0	3	10	77%
A632 *Pl-Rh*	*rmr1-1*/*rmr1-1*								
	F2S1	0	3	4	0	1	0	0	0%
	F2S2	0	1	3	0	0	0	6	60%
	F2S3	0	0	0	0	1	0	1	50%
	F2S5	0	0	0	1	0	0	8	89%
	F2S6	0	0	1	1	1	1	6	60%
	F2S7	0	0	1	0	0	2	11	79%
	F2S8	0	0	0	0	3	2	8	62%
	F2S9	0	0	0	0	0	2	7	78%
	F2S10	0	2	1	0	1	2	6	50%

Table 6. *rmr1-3* establishment test results. Anther phenotypes of establishment and control test crosses. Pedigree information is described in Figure 3. All plants were expected to be Pl' unless there was a failure to establish the *Pl'* state (Pl types in test, fully-fertile class) or *Pl'* reverted to *Pl* (Pl types in the test, semi-sterile class). Most plants displayed anthers with chimeric tassel phenotypes making it difficult to interpret the results.

		Anther phenotype			
	Pollen phenotype	Pl'	Chimeric, Pl' ACS types only	Chimeric, any ACS types	Pl
Test	Fully-fertile	0	2	55	40
	Semi-sterile	7	6	74	9
Control	Fully-fertile	10	4	26	7
	Semi-sterile	0	2	34	12

Table 7. Cloning *rmr1* cDNA. cDNA regions for which cloning was attempted are listed in the first column. Numbers represent cDNA nucleotides with the predicted translational start site as the +1 position. Vectors used for each insert are listed in the second column, and cloning success is noted in the third column. The Δ 1921 - 2776 insert in pCR4-TOPO has been named pJS1. See also Figure 4.

Insert	Vector	Cloned?
Δ -85 - 127	pSMART	Yes
Δ -75 - 343	pGEM T-Easy	No
Δ -75 - 682	pGEM T-Easy	No
Δ -75 - 857	pGEM T-Easy	No
Δ 1921 - 2776	pCR4-TOPO	Yes
Δ 2464 - 4372	pCR8/GW/TOPO	No
Δ 2616 - 4372	pGEM T-Easy	No
Δ 2655 - 4525	pET302 and pET303	No
Δ 2658 - 4305	pCR4-TOPO and pGEM T-Easy	No
Δ 2658 - 4435	pCR4-TOPO and pGEM T-Easy	No
Δ 2767 - 4221	pCR8/GW/TOPO	No

Table 8. Peptide antibodies against RMR1. Peptide names, abbreviations, sequence and amino acid positions are indicated. Underlined cysteine residues in the peptide sequence are not found in RMR1 but were added to facilitate conjugation of the peptides to KLH. Rabbit ID numbers describe the rabbits used to generate the respective antibodies. See also Figure 5.

Peptide name	Abbreviation	Sequence	Amino acid position	Rabbit ID numbers
RMR1-Trnc1	T1	CRAGTSRSTSRDK	141-152	CA3722SCR; CA3725SCR
RMR1-Trnc2	T2	NSKPIQNHAKLEC	333-344	CA3726SCR; CA3727SCR
RMR1-Full2	F2	HEFVIDDQIGIRC	763-775	CA3720SCR; CA3721SCR
RMR1-Full1	F1	CRNMLSKEMEH	1379-1389	CA3733SCR; CA3734SCR

Chapter 5 – Molecular Models and Future Directions

Paramutation describes an epigenetic interaction between specific alleles which results in heritable changes in gene regulation. At the *pl1* locus in maize, *Pl1-Rhoades* alleles in the highly expressed *Pl* state can be heritably repressed when combined with *Pl1-Rhoades* alleles in the weakly expressed *Pl'* state [Hollick *et al.* 1995; Hollick *et al.* 2000]. This epigenetic change is identified by changes in pigmentation in the seedling, plant body, and anthers [Hollick *et al.* 1995]. The *cis*-acting elements required for paramutation include both locus-specific features, either *pl1* transcription or RNA, and elements 3' distal to the coding sequence, of which the specific molecular features are not known [Gross and Hollick 2007]. *Trans*-acting factors *required to maintain repression* (*rmr*) of the *Pl'* state have now been identified in forward genetic screens [Hollick and Chandler 2001; Hollick *et al.* 2005; Stonaker *et al.* 2009]. My research has identified and characterized many of these trans-acting molecules and this has led to novel insights regarding the relationship of paramutation to normal genome function.

In this dissertation, I presented my contributions to the mapping and characterization of four *rmr* factors: *rmr1*, *rmr2*, *rmr6*, and *rmr7*. The identification of *RMR1*, *RMR6/RPD1*, and *RMR7/RPD2a* has implicated a RNA-directed DNA Methylation (RdDM) type pathway in the maintenance of the *Pl'* state [Hale *et al.* 2007; Erhard *et al.* 2009; Stonaker *et al.* 2009]. In *Arabidopsis*, the RdDM pathway uses 24 nt siRNAs to facilitate DNA methylation and subsequent repression of repetitive target sequences [Matzke *et al.* 2009; Pikaard *et al.* 2008]. Aberrant RNA transcripts produced from target loci are made double stranded by RNA DEPENDENT RNA POLYMERASE2 (RDR2) and cut into 24 nt siRNAs by DICER-LIKE3 (DCL3) [Xie *et al.* 2004]. 24 nt siRNA accumulation also depends on Snf2 protein CLSY1 [Smith *et al.* 2007] and subunits of RNA Polymerase IV (Pol IV), although no Pol IV dependent transcripts have been identified [Matzke *et al.* 2009; Pikaard *et al.* 2008]. 24 nt siRNAs are then loaded into ARGONAUTE4 (AGO4) [Zilberman *et al.* 2003] where they presumably interact with the nascent non-coding transcripts produced at low levels by RNA Polymerase V (Pol V) to direct *de novo* asymmetric cytosine methylation through recruitment of DOMAINS REARRANGED METHYLASE1 and 2 (DRM1 and DRM2) and CHROMOMETHYLASE3 (CMT3) [Wierzbicki *et al.* 2008; Cao *et al.* 2003]. Pol V localization and transcription depends on another Snf2 protein, DEFECTIVE IN RNA-DIRECTED DNA METHYLATION1 (DRD1) [Wierzbicki *et al.* 2008; Kanno *et al.* 2004].

A diagram of the presumed RdDM pathway in maize is presented in Figure 1. The *mop1* / *rdr2* locus, alleles of which were identified in the *rmr* genetic screens, encodes a RDR2 ortholog [Hale *et al.* 2007; Alleman *et al.* 2006; Woodhouse *et al.* 2006]. Mutations in *mop1* / *rdr2* prevent 24 nt siRNA accumulation [Nobuta *et al.* 2008], and therefore MOP1 / RDR2 has been placed in a similar position in the maize RdDM model as in *Arabidopsis*. The *rmr1* locus encodes a Snf2 protein which is neither the structural ortholog of CLSY1 or DRD1 but which highlights a novel group of plant-specific Snf2 proteins [see Chapter 2, this work]. Analysis of *rmr1-3* mutants indicates that *RMR1* genetically interacts with Pol IV, but it is unclear if there is direct physical interaction. The placement of RMR1 in the model (Figure 1) is consistent with this data. Given the position of RMR1 and CLSY1 in the model, and the role of RMR1 in RNA stability, it is tempting to speculate that these Snf2 proteins may function on an RNA template [Smith *et al.*

2007]. The phylogenetic evidence I presented does not support this function for the Snf2 domain [see Chapter 2], but perhaps the variable N-terminal regions of these proteins are involved in RNA-binding interactions in addition to mediating protein-protein interactions.

The *rmr6* / *rpd1* and *rmr7* / *rpd2a* loci encode the largest and second largest subunits of Pol IV [Erhard *et al*. 2009; Stonaker *et al.* 2009], although *rmr7* / *rpd2a* may also function in the Pol V complex (indicated by blue and gray hashed oval in Figure 1 diagram) [Stonaker *et al.* 2009]. Based on the phylogenetic analysis presented here [see Chapter 3] and additional molecular characterization by other lab members [Erhard *et al*. 2009; Hale *et al*. 2009], Pol IV appears to be an inefficient, error-prone polymerase which functions mainly to inhibit Pol II transcription. This inhibition could occur through blocking Pol II access to templates or by titration of Pol II accessory subunits. Regardless, Pol IV likely produces extremely low level transcripts. Given the alterations to the RPD1 domain G, these hypothetical Pol IV transcripts likely contain numerous errors, including incorporation of dNTPs and potentially represent the elusive "aberrant RNA" which initiates RdDM at a particular target.

24 nt siRNA molecules produced by the inducing (paramutagenic) allele could facilitate *trans*-homolog interactions via homology with the responding (paramutable) allele. Loss of functions from *rmr1*, *rpd1*, *rpd2a*, and *rdr2* specifically affect the small RNA accumulation and cytosine methylation patterns of a *doppia* transposon element ~100 bp upstream of *pl1* [Hale *et al*. 2007]. However, no differences in *doppia* methylation are observed between alleles in the *Pl'* and *Pl* states, and, despite loss of siRNAs, establishment of the *Pl'* state still occurs in *rmr1-1* and *rmr1-2* mutants [Hale *et al*. 2007]. This result indicates that the RdDM pathway may not be acting directly on the elements that control paramutation but rather indirectly on the general chromatin environment around *pl1*. In mutant conditions, derepression of the *doppia* element results in changes to the immediate chromatin environment which allow increased transcription (*rpd1* mutants [Hollick *et al*. 2005]) and RNA stability (*rmr1* mutants [see Chapter 4; Hale *et al*. 2007]) from *pl1* and, ultimately, increased plant pigmentation. In some cases, these changes can feedback on the heritable maintenance of the *Pl'* state resulting in reversion of *Pl'* to *Pl*, but this does not occur in every mutant background [Hollick and Chandler 2001; Hollick *et al*. 2005; Stonaker *et al*. 2009]. As either *pl1* RNA or *pl1* transcription is required for heritable maintenance of paramutation [Gross and Hollick 2007], the differing effect of *rmr* mutants on these processes could result in different rates of heritable reversion and effects on establishment.

Interestingly, no RdDM components in the downstream portion of the pathway (AGO4 / DRD1 / Pol V / DRM) have been identified to date in our genetic screens yet we have several alleles each of *rmr1*, *rpd1*, and *rpd2a*. This could be due to these factors currently being in our mapping pipeline or functional redundancy. There is only one copy of RPE1 (the largest subunit of Pol V), but there are multiple potential second largest subunits. There are also two potential DRD1 orthologs, although there is a non-redundant duplicate DRD1 protein in *Arabidopsis* as well. The composition of the DRM family in maize is unknown. It is tempting to speculate that this result reflects on the fundamental biology of the paramutation mechanism. The genetic screen which identified RPE1 and DRD1 in *Arabidopsis* used a hairpin construct as the silencing inducer and did not identify Pol IV, RDR2 or DCL3 because siRNAs could be produced independently from the construct. Perhaps the paramutation mechanism does not require the downstream portion of the pathway due to maintain cytosine methylation or just does not require cytosine methylation at all. This question can be explored once the 3' functional sequences are identified.

Identification of the maize RdDM components has not provided the definitive molecular mechanism for paramutation, but my work has provided a better understanding of the molecular components at work at the *pl1* locus. Additionally, my work has shown a RdDM-like pathway functions in maize and has provided evidence for RdDM-like pathways in other plants [see Chapters 2 and 3]. Basal plants such as *Selaginella* have a relatively simple RdDM-like pathway in that they only contain Pol IV, CLSY1, and a basal RMR1 while angiosperms contain specific RMR1 and DRD1 homologs, an expanded DRD1 subfamily, and a largest subunit for Pol V. In the grasses, further duplications have produced multiple second largest subunits which could function in either Pol IV or Pol V. This specialization with regard to RNA polymerase function may provide plants with exquisite control over RNA-mediated epigenetic repression. Additionally, the variability of N-terminal regions might allow different DRD1 subfamily members to specifically interact with different nuclear proteins, and thus facilitate fine-tuning of the RdDM pathway for specific environmental, developmental, or genomic conditions.

Finally, plants which lose *rpd1* function show pleiotrophic developmental phenotypes including reduced height, delayed flowering, delayed internode elongation, polarity reversals, and ectopic outgrowths [Parkinson *et al.* 2007; Parkinson 2007]. Mutations in Pol IV and Pol V subunits in *Arabidopsis* do not display the gross developmental abnormalities observed in *rpd1* mutants, but they do exhibit delayed flowering time due to derepression of repetitive elements in the promoter / 3' UTR of *FLOWERING LOCUS C* (*FLC*) [Matzke *et al.* 2007]. Interestingly, however, loss of *rmr1* does not result in developmental abnormalities, although *rmr1-3* does appear to enhance the *rpd1* developmental phenotype [Chapter 4], indicating that loss of siRNAs alone is not enough to produce these phenotypes [Hale *et al.* 2009]. True repression of repetitive sequences may depend on both siRNAs and Pol IV-mediated Pol II inhibition as proposed here [Chapters 3 and 4] and previously [Erhard *et al.* 2009; Hale *et al.* 2009]. The loci underlying the *rpd1* phenotypes are not known, but combined these results indicate that differential regulation of repetitive elements in euchromatic regions do effect development and normal functioning of the plant, as proposed by McClintock almost 60 years ago [McClintock 1951]. Additionally, the potential for fine-tuning the pathway via the diversity among RdDM components has important evolutionary implications. Maize, which contains a much larger proportion of repetitive elements than *Arabidopsis* [Liu *et al.* 2007], provides the perfect model system in which to study the role of repetitive elements in regulating developmentally important genes and plant evolution.

Many questions remain about the RdDM pathway and its role in paramutation and normal maize development. Other *rmr* factors are in the positional cloning pipeline and identification of these will be greatly facilitated by the release of the draft maize genome sequence. These new factors could represent additional RdDM components or novel factors, such as the protein recently identified as encoded by *rmr2*. Identification of additional DRD1 subfamily members or RPD2 proteins could help determine the specific functionality of these duplicate factors. Specific models of RdDM function in maize could be tested by analyzing the subunit composition of the Pol IV complex for Pol II specific components or direct interactions with RMR1 or the predicted ZmCLSY1, and further analysis of RMR1 through biochemical tests of Snf2 enzymatics could support its predicted function in the RdDM pathway. Assays could also be designed to specifically look for the unique molecular signature of Pol IV transcripts given the current understanding of altered domain G function. This might finally allow identification of these extremely low level transcripts. Additionally, identification of the 3' distal elements required for the establishment and heritable maintenance of paramutant states at *pl1* will provide new target sequences for analysis. These functional 3' sequences could also be targeted by the RdDM pathway or instead could rely on direct-pairing based interactions, or some combination of the two mechanisms. Finally, identification of additional RdDM targets in the maize genome could provide the first large scale analysis of the relationship between repetitive elements and developmentally important genes and describe how these elements help drive the evolution and domestication of maize.

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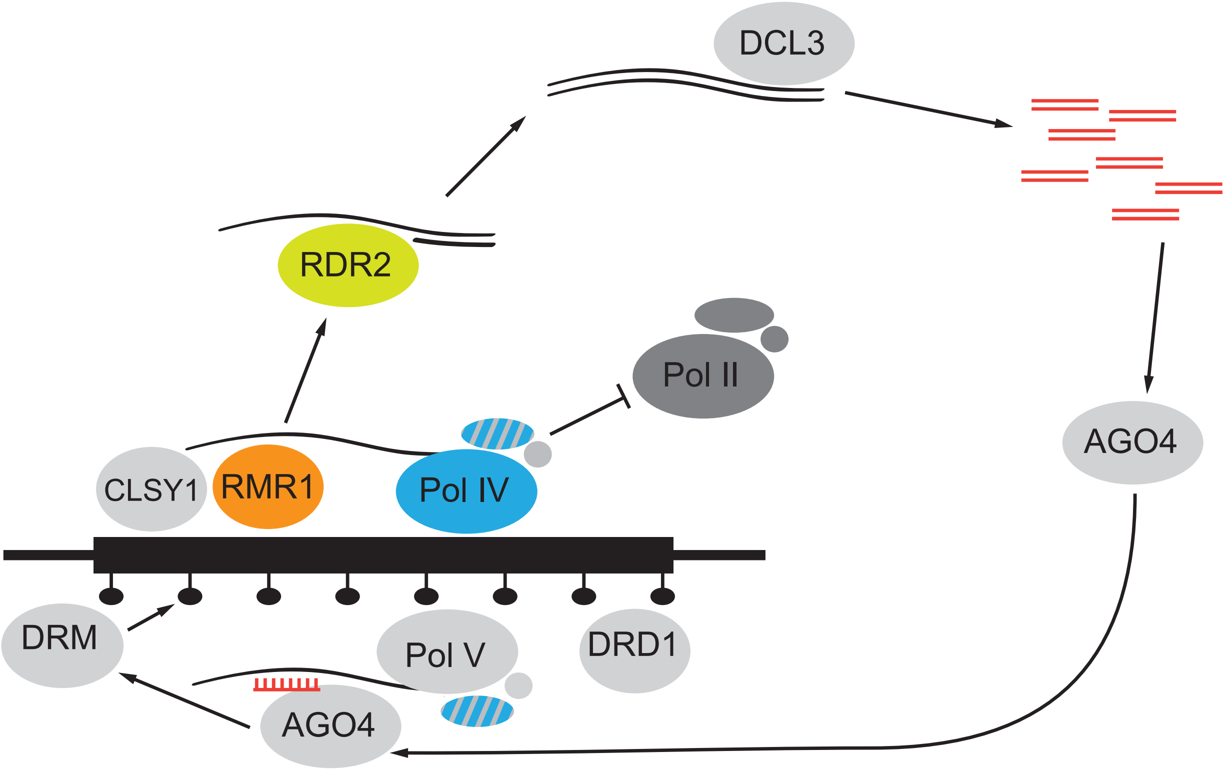
Figures

Figure 1. Model for role of RdDM-like pathway in maize. Map of a putative RdDM target in maize (black box). Proteins and functions only identified in *Arabidopsis* have been shaded light gray while proteins identified in maize are colored. Pol IV functions at the target locus to exclude Pol II. RMR1 and CLSY1 both function upstream of RDR2 action and potentially in contact with Pol IV. RDR2 converts the aberrant ssRNA transcript into dsRNA which can then be cut into 24 nt siRNAs (red) by DCL3. siRNAs are then loaded into the AGO4 complex which interacts with nascent Pol V transcripts and DRM methyltransferases to mediate cytosine methylation of target loci. DRD1 functions to localize and promote transcription of Pol V.



Appendix 1: Primer information.

Name	Dir.	Sequence	Notes
2map1	F	ACAGGGTGGACAGGACAGAG	EST CF637444 by Clarissa Lee
2map1	R	AGTGCAATCCCGTTCGTATC	EST CF637444 by Clarissa Lee
2map2	F	TCGGCTCAGCTCCTTGGT	EST CD650821 by Clarissa Lee
2map2	R	CCAGCAATGTCGTGTTCCT	EST CD650821 by Clarissa Lee
2map3	F	GGAGCGGTTGACACGAGTAT	EST CK370377 by Clarissa Lee
2map3	R	CTGGGGAGTGACCATGAAAT	EST CK370377 by Clarissa Lee
2map4	F	CGTCACTGGGAAGCCAATAG	EST CK370377 by Clarissa Lee
2map4	R	TAGGGCCTCGGTAGCATACA	EST CK370377 by Clarissa Lee
2map5	F	TGCAGTGAAGGCATCAATATG	EST CD440054 by Clarissa Lee
2map5	R	TGGCTATGCTTTAAAGGCTCT	EST CD440054 by Clarissa Lee
2map6	F	GTTGGAGCGGTTTTCCTAAA	EST BQ485194 by Clarissa Lee
2map6	R	TGCATTTCAAGCCATTTCTG	EST BQ485194 by Clarissa Lee
2map7	F	TCTTGCACTTCAACGACAGG	EST AW066777 by Clarissa Lee
2map7	R	GCCGTCTCCTCTCTCCAAC	EST AW066777 by Clarissa Lee
2map8	F	TCTGCTCAAAAGTGGTCAGG	EST BM498426 by Clarissa Lee
2map8	R	AATGGTCCTTCCTCCAACAA	EST BM498426 by Clarissa Lee
2map9	F	CGGTGCTCGAGGATAGCTT	EST CF647259 by Clarissa Lee
2map9	R	CCTGTTCTGGAACCACACCT	EST CF647259 by Clarissa Lee
2map10	F	GCCTGATACGGTTACAGGAGA	EST CA398302 by Clarissa Lee
2map10	R	CAGTGCATGCAGAACTGAGA	EST CA398302 by Clarissa Lee
2map11	F	CTCACCGGCATCCTCTACTG	EST CK347688 by Clarissa Lee
2map11	R	CCCAGGGACCCCTTCTTC	EST CK347688 by Clarissa Lee
2map12	F	ATGATTGCGGTAAGGATGGA	EST CN070734 by Clarissa Lee
2map12	R	CGTCGATGCAGGAGATGAT	EST CN070734 by Clarissa Lee
2map13	F	AGCCCGTCTATCGCGTACT	EST BU499437 by Clarissa Lee
2map13	R	CAAGAACATCGAGGACAGCA	EST BU499437 by Clarissa Lee
2map14	F	AGCAGTATCGTGGGCTCAAT	EST BU499437 by Clarissa Lee
2map14	R	CCACTTCGAGAGGCTGAGTAA	EST BU499437 by Clarissa Lee
2map15	F	CCATTGAGCACCTGTAGAGC	EST AW288927 by Clarissa Lee
2map15	R	TGCAGGTTTTCAGATGGAAG	EST AW288927 by Clarissa Lee
2map16	F	CGAGGACCGAGGTCTGAATA	EST CF034137 by Clarissa Lee
2map16	R	GTTGAAGCGGCCCATAGATA	EST CF034137 by Clarissa Lee
2map17	F	TCAGGTTGGTGCTCTTCTTG	EST CD440054 by Clarissa Lee
2map17	R	TGGGAATTGAGCCAATTATG	EST CD440054 by Clarissa Lee
2map18	F	TGCTTCACTAACAGCTAGCAGAC	EST CD440054 by Clarissa Lee
2map18	R	ACCCAGCTTTCTTTCGGTTA	EST CD440054 by Clarissa Lee
2map19	F	GGTACGACCAGGAGGTTCAA	EST BQ485194 by Clarissa Lee
2map19	R	TGCACGCCAGTTACATGATT	EST BQ485194 by Clarissa Lee
2map20	F	CATCTCAGCGAGAGGTCAAA	EST CD527818 by Clarissa Lee
2map20	R	TTGGCCTTTTTGTGAAGAATC	EST CD527818 by Clarissa Lee
2map21	F	GCAAACACTTGTTTCCACAGA	EST CF038398 by Clarissa Lee
2map21	R	ACTGGCAAACAAGCATGACA	EST CF038398 by Clarissa Lee

Name	Dir.	Sequence	Notes
2map22	F	CCCTGTGCATTGTGAAGAGA	EST BE510846 by Clarissa Lee
2map22	R	AAAGACTCAGCAAATTCAGCAA	EST BE510846 by Clarissa Lee
2map23	F	TCCGTTGACGAAGCTCTTG	EST BI135304 by Clarissa Lee
2map23	R	CACCTACTTCGACAGCGTCA	EST BI135304 by Clarissa Lee
sdg104-170	F	GTGCGGAGGTGCAAAATACT	seq, binds sdg104 at cDNA bp 170
sdg104-747	F	AGGGTTTGAAGAAGCCGTTT	seq, binds sdg104 at cDNA bp 747
sdg104-818	R	ACTCGAGTCCTGGAGCAGAA	seq, binds sdg104 at cDNA bp 818
sdg104-1023	F	AGCGATCGTTCTCTGATGCT	seq, binds sdg104 at cDNA bp 1023
sdg104-1158	R	CCAGAATGAGCACTCGCATA	seq, binds sdg104 at cDNA bp 1158
sdg104-1383	R	AGATCAGGCCGCACATTAAG	seq, binds sdg104 at cDNA bp 1383
sdg104-1648	F	GGCTGTTGCAGTCAATCAGA	seq, binds sdg104 at cDNA bp 1648
sdg104-2217	R	CACTTGCAAGAAGGACCACA	seq, binds sdg104 at cDNA bp 2217
sdg104-2216	F	TGCCCTCCTACATGTCACAA	seq, binds sdg104 at cDNA bp 2216
sdg104-2781	R	TACAGCCAGCCATCACACTC	seq, binds sdg104 at cDNA bp 2781
sdg104-gen	F	CGGACGAAGAGCCGGCTCGG	seq, binds sdg104 genomic DNA
sdg104-196	R	GGCACGAGTATTTTGCACCT	seq, binds sdg104 at base 196
sdg104-1322	F	CGGGACCTTTTAGATGAAGAAG	seq; binds sdg104 at base 1322
sdg104-1900	F	CTGCAAACAGGGAACTCTGG	seq; binds sdg104 at base 1900
sdg104-2455	R	TAGGCCCTCCCAAAGAGACT	seq; binds sdg104 at base 2455
sdg104-1836	R	CGGTCTCCATGCTCTTTCTC	seq; binds sdg104 at base 1836
sdg104-382	R	CCTACCCGATCCGAATTTTT	seq; binds sdg104 at base 382
SNP2ApaI	F	TTTAGGATCACAGACTCACGGGCC	rmr6 dCAPS, cuts A632 amplicon
SNP3HfI	F	GAGTCAACACAAAACTGATCATGGTGTTGAAT	rmr6 dCAPS, cuts A632 amplicon
SNP3EcoV	F	GAGTCAACACAAAACTGATCATGGTGTGATAT	rmr6 dCAPS, cuts A632 amplicon
SNP4PstI	F	AGGAACATTACTCTGCA	rmr6 dCAPS, cuts *rmr6-1* amplicon
SNP3/4HnfI	F	TGATCATGGTGTTGAAT	rmr6 dCAPS, cuts A632 amplicon
SNP3/4EcoV	F	TGATCATGGTGTTGAAT	rmr6 dCAPS, cuts A632 amplicon
umc1395	F	TGAATGAGTGGCATTCAAAATCTG	1.05
umc1395	R	CAGATTGCATGTGTGAGTGTGTGT	1.05
umc1281	F	TCAGAATGAGAACATATGGTGGATG	1.06
umc1281	R	GTCTGTGTCGACCATTTTGACTTG	1.06
umc1197a	F	GGTGTAATTTAGGGAGTGTTTGTTCG	1.08
umc1197a	R	CCGCATAGATGTGCTTTCTAGGAG	1.08
bnlg1175	F	ACTTGCACGGTCTCGCTTAT	2.04
bnlg1175	R	GCACTCCATCGCTATCTTCC	2.04
umc1635	F	GCTGAGCAGATCTTTCCTTGTTTC	2.05
umc1635	R	AAGGAGCAGAACTCGGAGACG	2.05
umc2178	F	GTATCGAGACACGTACGCACGAA	2.06
umc2178	R	GCGCAGTGATTTCTTACCATGC	2.06
bnlg2077	F	GACCAGAGGATGGGGAAATT	2.07
bnlg2077	R	GTAGGCACATGCACATGAGG	2.07
mmc0381	F	GTGGCCCTGTTGATGAG	2.08
mmc0381	R	CGACGAGTACCAGGCAT	2.08
umc1252	F	GCGTCGGAGAAGTACATCAAGTTT	2.09

Name	Dir.	Sequence	Notes
umc1252	R	CTTCTGCATCATCATCATCGTCTT	2.09
umc2105	F	ACATACATAGGCTCCCTTTTTCCG	3.00
umc2105	R	TCCCGTGACACTCTCTTTCTCTCT	3.00
umc2071	F	ACTGATGGTGTTCTTGGGTGTTTT	3.01
umc2071	R	ATACACGCAGTTACCCGAAGGTT	3.01
bnlg1523	F	GAGCACAGCTAGGCAAAAGG	3.02
bnlg1523	R	CTCGCACGCTCTCTCTTCTT	3.02
umc1458	F	CCAATAAACAAATCATCTCCCCCT	3.02
umc1458	R	TGCTATGCTATGTACAGGGACAGG	3.02
bnlg1144	F	TACTCGTCGTGTGGCGTTAG	3.02
bnlg1144	R	AGCCGAGGCTATCTAACGGT	3.02
umc1647	F	TAAAGCCACAGGCACGAACTTAAT	3.02
umc1647	R	CTTCGCATTTGCACCCAAAC	3.02
bnlg1447	F	GAGAGGAGAGGCTGAGCTGA	3.03
bnlg1447	R	TCCTCCCACTGAATTTCCAC	3.03
umc2000	F	CTGTTGTCAAGCCAAGCCAGT	3.04
umc2000	R	AGGCTTGTGAGACTCAGCAGTTTT	3.04
umc1223	F	TTCAACAGATTCAGAGAAAGCACA	3.04
umc1223	R	TTGATAATTAATCCGCAGCTCTCTC	3.04
mmc0312	F	CCTGATGAAACAGTCCAATT	3.04
mmc0312	R	ATCTGCTGGTGATACCTCC	3.04
umc1759	F	GTGAGGAGAGGAGACGGAGAGAG	4.01
umc1759	R	GAAGCTCCTGTGGAACGTGTG	4.01
umc1829	F	GTTGATTGGTTGATGTGGAAACAA	5.09
umc1829	R	CAGTTTGATGTTCATGGCTCTCTC	5.09
bnlg1154	F	GGGTGATCACATGGGTTAGG	6.04
bnlg1154	R	AAATCAATGCTCCAAATCGC	6.04
bnlg2249	F	AGGATCCCCTAGCAAAAGGA	6.05
bnlg2249	R	CCCCCTAGTTCGTTGCATAA	6.05
umc2141	F	ATTAGCACCACCGTGTAGCAAGTT	6.05
umc2141	R	GGCAGTGTGAGTGGTTGTGTG	6.05
bnlg1174a	F	CGCATTCCAAGAACAATGAA	6.05
bnlg1174a	R	TTCGATTGGTGGGAAGATTC	6.05
bnlg1732	F	AACTTTTGGCATTGCACTGG	6.05
bnlg1732	R	CGTAAGTGCACACGGCATTA	6.05
umc2165	F	AGAACACCAAATGGTGACGTTATGT	6.07
umc2165	R	CTAGCTCGTCTTCCCTGTGGTCT	6.07
umc2323	F	TTCCCTATCAACTTCCATCCTGAA	6.07
umc2323	R	ATCTGAAGCCAACTGTGTTCATTG	6.07
umc1248	F	CTTTGTCCATCGGCTTTATTCTTT	6.07
umc1248	R	CACATTAAGTTACAAATACAAATCACCG	6.07
umc1695	F	CAGGTAATAACGACGCAGCAGAA	7.00
umc1695	R	GTCCTAGGTTACATGCGTTGCTCT	7.00
umc2160	F	TAAAACCTTTACCCCATCCAGCAT	7.01

Name	Dir.	Sequence	Notes
umc2160	R	TGTGCTCGTGCTTCTCTCTGAGTA	7.01
umc1409	F	GCTAGTAGACATCGACGGATCGAC	7.01
umc1409	R	ATGACGTCCAGGAGGATGACC	7.01
bnlg1380	F	ACAATTCGATCGAGAGCGAG	7.02
bnlg1380	R	CCTTTCTTGCTGGTTCTTGC	7.02
umc1359	F	GCAGAGCCAGAATTCGACCTT	8.00
umc1359	R	CATCGTCATCATTCGAGCAGAG	8.00
umc1592	F	GACCATATGTGCTCCAAAACCTTC	8.01
umc1592	R	AAGCTTCTTCGGTCTTTGTAGGGT	8.01
umc1786	F	ACCGTGACTTCCTCCTCATAACTG	8.01
umc1786	R	CATTTTTCGCATTTAGGAAATCCA	8.01
bnlg1194	F	GCGTTATTAAGGCAAGCTGC	8.01
bnlg1194	R	ACGTGAAGCAGAGGATCCAT	8.01
bnlg2235	F	ATCCGGAGACACATTCTTGG	8.02
bnlg2235	R	CTGCAAGCAACTCTCATCGA	8.02
umc1910	F	AGCTCACGAGACAGAGCAGAAAAT	8.03
umc1910	R	TGAATTGATGAGTGACGAGTTGTG	8.03
umc1778	F	GTGAACCATTGTAGCTGTCCCTG	8.03
umc1778	R	GAGCTCGTACCTGTTCATGAGGAT	8.03
umc1149	F	TACAGTAGGGATTCTTGCAGCCTC	8.05
umc1149	R	GTGGGACCTTGTTGCTTCCTTT	8.05
bnlg2181	F	CCAATTCACCAATCATGCAA	8.05
bnlg2181	R	TTGGGGTGAAGCAATGTGTA	8.05
umc1724	F	GTCTCAAGTGAAACAACCACGCTT	8.06
umc1724	R	CCACATGAGATGAGATTGCCATT	8.06
umc1807	F	CAGAAGTTGCGTTTATGCTACCAC	8.07
umc1807	R	GGTATTTTCTAATCAACGCTCACCTC	8.07
bnlg1056	F	ATCGTTGTTGGGTACACGGT	8.08
bnlg1056	R	ACGGGTAGTGGTGAAGATGC	8.08
phi233376	F	CCGGCAGTCGATTACTCC	8.09
phi233376	R	CGAGACCAAGAGAACCCTCA	8.09
umc1810	F	TCTCCACGACGATTAAAAGGCTAA	9.01
umc1810	R	AGCAGTAGCAAGAGGGATAGAGCA	9.01
umc1583	F	AAAGGGCGACTTGTTTTTGTTTTT	9.01
umc1583	R	GCCTGCTTTTGTGTATCTTAGGCA	9.01
umc1636	F	GTACTGGTACAGGTCGTCGCTCTT	9.02
umc1636	R	CATATCAGTCGTTCGTCCAGCTAA	9.02
umc1366	F	GTCACTCGTCCGCATCGTCT	9.06
umc1366	R	CCTAACTCTGCAAAGACTGCATGA	9.06
umc1506	F	AAAAGAAACATGTTCAGTCGAGCG	9.07
umc1506	R	ATAAAGGTTGGCAAAACGTAGCCT	9.07
umc1137	F	ATCAGTCACTCTTCTGCCTCCACT	9.07
umc1137	R	GGCTGGATAATGTTGTAGCTGGTC	9.07
umc2163	F	AAGCGGGAATCTGAATCTTTGTTC	10.04

Name	Dir.	Sequence	Notes
umc2163	R	GAAATTGCTGGGGTTCTCATTTCT	10.04
phi323152	F	TCAGGGAGCTCACCTACTACGG	10.05
phi323152	R	CACGACTGCACCGATTAGC	10.05
umc1993	F	CTTTTCTGCTACTCCTGCCTGC	10.06
umc1993	R	CTAGCTGATGGAGGCTGTAGCG	10.06
umc2122	F	TTGACAAGCTAGTGTGCAACTGTG	10.06
umc2122	R	TGAAAGCCCACTGGACAAACTAAT	10.06
umc1084	F	GATAAAAAGGCAAGTGCAACAAGG	10.07
umc1084	R	ATATCAACCAGAGGCTGGAACTTG	10.07
umc1038	F	CGTCACACTCCTCTGCCACTT	10.07
umc1038	R	GAGGATTCAGAACTCGACTCGG	10.07
umc1640	F	ACTACACGGTGTGAGATGTGATCG	10.07
umc1640	R	GTCGTCGCAAGAACAACAAGG	10.07
CAPS10F	F	ATGAGTAGTGCCCCATCCAG	CAPS marker for rmr1-3 lesion
CAPS10R	R	TCAGCCTCTTCTTCCTCTTCC	CAPS marker for rmr1-3 lesion
CAPS6F	F	GCATCTTCGCAAGTTCTTCA	CAPS marker for rmr1-1 lesion
CAPS6R	R	TCGTGGGAAGTCATCTCCTC	CAPS marker for rmr1-1 lesion
exon F	F	GTGTCAGTGTTTGCCGAGAA	rmr1 sequencing
exon R	R	CTATAGTTACAATCAAATTGCTACTGAG	rmr1 sequencing
far 5'F	F	GTTGCAGCAACAGAATCTAGC	rmr1 sequencing
intron F	F	GTCGTTTCCCAGAATAGAGTAACTTTG	rmr1 sequencing
intron F2	F	ATCTGGCACAAGGGCAAAG	rmr1 sequencing
intron F3	F	AGGGCAAAGATGCAGGAGAT	rmr1 sequencing
intron F4	F	AGGGCGTGGAAATTCTTTCT	rmr1 sequencing
intron R	R	CTCAAACATATGTAGTATTCTGCATATC	rmr1 sequencing
intron R2	R	CCCTTGACAAACACCACAGA	rmr1 sequencing
iPCR2F	F	TTATGAGTAAGTAACCACAAAAGAACC	rmr1 sequencing
iPCR2R	R	CCAGGTTCTGATAAAAGGGTCTT	rmr1 sequencing
iPCRF	F	GATCACAAAGAGCACAGCAGG	rmr1 sequencing
iPCRR	R	GCAGTTAGAAATCCTAGGTTCCG	rmr1 sequencing
JS1	F	GAATTCATGGATCGCGCCACGCCG	rmr1 cloning
JS1.1	F	GAATTCATGGATCGCGCCACGC	rmr1 cloning
JS1.2	F	GAATTCATGGACCGCGCCACGCCG	rmr1 cloning
JS1.3	F	GAATTCATGGACCGCGCCACGC	rmr1 cloning
JS10	F	GAATTCATGCTGCCGCCGATGATGGTG	rmr1 cloning
JS11	F	GAATTCATGGTGCCAGCGGGAGCGG	rmr1 cloning
JS12	F	GAATTCATGCTGGCGGCGGCAGTGG	rmr1 cloning
JS13	F	GAATTCATGGCGACGTCGAGTCATAAGC	rmr1 cloning
JS2	R	CCCGGGCTCAGTAGCAATTTGATTGTAAC	rmr1 cloning
JS2.1	R	CCCGGGCTCAGTAGCAATTTGATTG	rmr1 cloning
JS3	F	GGATCCCCCATCAGCGTGAAGCATTTG	rmr1 cloning
JS4	F	GGATCCCCCAATATGGAACGGTGTGGA	rmr1 cloning
JS5	R	GCGGCCGCTGACCTATCCTAAATGC	rmr1 cloning
JS5.1	R	GCGGCCGCCTGACCTATCCTAAATGC	rmr1 cloning

Name	Dir.	Sequence	Notes
JS6	R	GCGGCCGTTTGTCACCTTCACCTGT	rmr1 cloning
JS6.1	R	GCGGCCGCTTTGTCACCTTCACCTGT	rmr1 cloning
JS7	F	CTAAAGCGGCAGTCTCTTTTGAAGCTTTTG	rmr1 cloning
JS8	R	CCAACATCTTGCTCTGGCCTGTCAGC	rmr1 cloning
JS9	F	GAATTCATGGACCTTGGCGACGACGAC	rmr1 cloning
mid 5'F	F	CAAAAGGAACGAGTTGGAGG	rmr1 sequencing
near 5'F	F	GAGATGTGATTCGTGCTTACAG	rmr1 sequencing
near 5'R	R	CTGTAAGCACGAATCACATCTC	rmr1 sequencing
Os01 F	F	GTTAAAAGGTCTAGCGTTCTGCC	Os05g32610
Os01 R	R	CGAAGTCAGCAAGCTTGAGC	Os05g32610
Os02 F	F	TCCAAAAGCAAGAATCAGTGC	Os05g32610
Os02 R	R	GTCTTGTTGCTGCAGGTAACG	Os05g32610
Os03 F	F	GCACCTAGGCCAACATTGAAC	Os05g32610
Os03 R	R	ACGAGACTTGTCCGCACTGC	Os05g32610
Os04 F	F	TCGAACCTGATGCAAGCTGAC	Os05g32610
Os04 R	R	GGAACAGTAACCCAAGAATGGC	Os05g32610
Os05 F	F	GAAATCAGATTTATTTTACCATTGC	Os05g32610
Os05 R	R	GCAAGCATAGGTTTATCAATAAGTG	Os05g32610
Os06 F	F	CACTTATTGATAAACCTATGCTTGC	Os05g32610, Maize GSS BZ681915
Os06 R	R	TCAGACAGAGAACAGAACATTACTCC	Os05g32610, Maize GSS CG882444
Os07 F	F	GTTTCTCAGAAGAGGATCAAGAGTG	Os05g32610
Os07 R	R	TCAAGGATAACCTCAGGACTTCC	Os05g32610
Os08 F	F	TGAAGATCTTCTTGCCCTTGC	Os05g32610
Os08 R	R	CAACTTTTCGAGAGAGTTCATCAGC	Os05g32610
Os09 F	F	CAAACTTTGAAAGTTGAAATCC	Os05g32610
Os09 R	R	TTCTCAAGGTGTGTAATTATCATGTG	Os05g32610
Os10F	F	GAAGAGTTGGGTGTGGGAAA	Os05g32610, Sb EST AW287235
Os10R	R	AACATCTTGCTCTGGCCTGT	Os05g32610, Maize GSS CG068341
Os11F	F	AAGCATACATCGCCCAAATC	Os05g32610, Maize GSS CG068341
Os11R	R	CCTGCAGGTCCTCCAAAATA	Os05g32610, Maize GSS CG068341
Os11Rb	R	GTTTGATGGTGCATCTCCAA	Os05g32610, Maize GSS CG068341
Os12F	F	CCCAATCATGCAACTCCTCT	Os05g32610, Maize GSS CG068341
Os12R	R	GATGGCCCCTGGAATAAGAT	Os05g32610, Maize GSS CG886593
Os13F	F	CTGTAGTGCAGGTTGCGAGA	Os05g32610, Maize GSS CG886593
Os13R	R	GCCAGGTTTTTCAGAGGTCA	Os05g32610, Maize GSS BZ668661
Os13Rb	R	CCATAACTTATTCCAAGAATACC	Os05g32610, Maize GSS BZ668661
Os14F	F	GAGGATCGGGAGATATGCAA	Os05g32610, Maize GSS BZ668661
Os14R	R	CTGGCGATATCTTGGAAGGA	Os05g32610, Maize GSS BZ681915
Os15F	F	TTGGAGATGCACCATCAAAC	Os05g32610, Maize GSS CG068341
Os15R	R	CACGCTGATGCTCATACATA	Os05g32610, Maize GSS CG886593
Os16F	F	CCCAATCATGCAACTCCTCT	rmr1 sequencing
Os16R	R	TGATCTCCAGGTTTACCAAGG	rmr1 sequencing
Os17F	F	AGGGCAAAGATGCAGGAGAT	rmr1 sequencing
Os17R	R	TTCTCGGCAAACACTGACAC	rmr1 sequencing

Name	Dir.	Sequence	Notes
OS18F	F	GGGCATTTGTCTCTCCTTGT	rmr1 sequencing
OS18R	R	GGATCGCTCCTTCCTTCTTC	rmr1 sequencing
OS19F	F	CCAGGAAGACGGTTGGTG	rmr1 sequencing
OS19R	R	GATGATCCCCGTTAACCAGA	rmr1 sequencing
rmr1-3'F	F	AGGCAAGCAGAAAAGGATCA	rmr1 cloning
rmr1-3'F2	F	TGACTCAGTTGGTGGATAATGG	rmr1 cloning
rmr1-5'R	R	CTACTCTGGGTCCGTTCGAC	rmr1 cloning
rmr1-5'R2	R	ACCCGCATCCTCTTTTTCTT	rmr1 cloning
rmr1-A619F	F	ATGGGTCGCGCCACGCCGCGCGTTT	rmr1 cloning
rmr1-BamR	R	GGATCCTCACTCAGTAGCAATTTGATTGTA	rmr1 cloning
rmr1-CD-F	F	ATGTTTCATGATCTTTATGAACAAGG	rmr1 cloning
rmr1-CD-R1	R	TGATCCTTTTCTGCTTGCCTA	rmr1 cloning
rmr1-CD-R2	R	GTGGGAAGTCATCTCCTCCA	rmr1 cloning
rmr1-ctermF	F	TCTCTTGCCCCAGTAACACCCTG	rmr1 cloning
rmr1-ctermF2	F	GCATGGCCAAATGACAAAGGCGTG	rmr1 cloning
rmr1-ctermR	R	AGCTTTAGATAACATGTTCCTAACATTATTG	rmr1 cloning
rmr1-exon3	F	GTGTCAGTGTTTGCCGAGAA	rmr1 cloning
rmr1-hel F	F	CATCAGCGTGAAGCATTTGAATTT	rmr1 cloning
rmr1-hel R	R	CTGACCTATCCTAAATGCTCTGC	rmr1 cloning
rmr1-NsiF	F	ATGCATTTTCATGATCTTTATGAACAAGGA	rmr1 cloning
rmr1-nterm R	R	CTCATACATAGTACTGATGACCCC	rmr1 cloning
rmr1-start	F	ATGGATCGCGCCACGCCGCGCGTTT	rmr1 cloning
rmr1-stop	F	GTTACAATCAAATTGCTACTGAGTGA	rmr1 cloning
rmr1-stop	R	TCACTCAGTAGCAATTTGATTGTAACTATAG	rmr1 cloning
rmr1-XhoF	F	CTCGAGTTTCATGATCTTTATGAACAAGGA	rmr1 cloning
rmr1-XhoR	R	CTCGAGCTCAGTAGCAATTTGATTGTAACT	rmr1 cloning
rmr1_+1F	F	ATGGATCGCGCCACGCCGC	rmr1 cloning
rmr1_-329F	F	ACATTTCGGCCTAGGGAAAG	rmr1 sequencing
rmr1_-75F	F	TACCCCCTTCAATTCCTCTG	rmr1 sequencing
rmr1_2767F	F	CTCTTTGCTTGGGATGAGGA	rmr1 cloning
rmr1_2851F	F	GAGGATCGGGAGATATGCAA	rmr1 cloning
rmr1_3020F	F	GCCAGGTTTTTCAGAGGTCA	rmr1 cloning
rmr1_3030R	R	CTTCTGTGCAGCCAGGTTTT	rmr1 cloning
SacI_+1F	F	GAGCTCATGGATCGCGCCACGCCGC	rmr1 cloning
stopR_EcoRI	R	GAGCTCTCACTCAGTAGCAATTTGATTGTAAC	rmr1 cloning
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RACE 1.2	R	TCGCCAAGGTCCATGACAAC	RACE
RACE 2.1	R	ATCGCTCCTTCCTTCTTCTTC	RACE
RACE 2.2	R	CGCTCCTTCCTTCTTCTTCTT	RACE
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RACE 3.2	R	GCCTCCAACTCGTTCCTTTT	RACE

Appendix 2: DNA sequences

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Appendix 3. Alignment of RMR1 and related sequences over the SNF2 conserved domain. The lightest level of shading represents conserved residues in at least 60% of the sequences, the middle level is conserved residues is at least 80% of the sequences, and the darkest level is amino acid identity in all sequences. Most sequences are identified by their NCBI GI number. Information for other sequences can be found in Appendix 4.

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239977156      VQLAALGFIVERTN----------------------------------------------
146081173      VQLAALGFIVERTE----------------------------------------------
Sm441121       HQRRAVRFMKRNIV----------------------------------------------
```

```
Bd3g18910    HQFEGFKFLVKNLM----------------------------------------------
Bd1g74070    HQLEGFNFLVKNLA----------------------------------------------
Os03g06920   HQVEGFNFLVKNLA----------------------------------------------
Sb01g046180  HQVEGFNFLIKNLA----------------------------------------------
Bd3g19890    HQLEGFHFLVKNLV----------------------------------------------
Os06g14440   HQLEGFSFLVKNLV----------------------------------------------
Sb07g002945  HQLEGFNFLVKNLI----------------------------------------------
ZM093940     HQVEGFNFLVKNLI----------------------------------------------
ZM064574     HQLEGFNFLVKNLI----------------------------------------------
Bd2g21430    HQLEGFHFLVKNLV----------------------------------------------
Bd2g21450    HQLEGFEFLVKNLV----------------------------------------------
Os08g14610   HQLEGFKFLVNNLV----------------------------------------------
Vv35918      HQVEGFNFLVSNLV----------------------------------------------
Pt195587     HQVEGFNFLRNNLV----------------------------------------------
AtDRD1       HQIEGFQFLCSNLV----------------------------------------------
At2g21450    HQTEGFRFLCNNLA----------------------------------------------
Bd2g26500    HQREAFEFMWTNLVGD--------------------------------------------
Os05g32610   HQREAFEFMWTNLVGD--------------------------------------------
Sb09g019410  HQREAFEFMWTNLVGG--------------------------------------------
RMR1         HQREAFEFMWTNLVGD--------------------------------------------
Bd2g43500    HQREGFEFMWKKLAGG--------------------------------------------
Os02g43460   HQQEGFEFMWRKLAGG--------------------------------------------
Bd3g50300    YQAAAVEFMWKNLAGG--------------------------------------------
Sb04g033300  HQQDAFEFLWTKLAGG--------------------------------------------
ZM178435     HQQDAFEFMWTKLAGG--------------------------------------------
Vv15867      HQCEGFEFIWKNVAGG--------------------------------------------
Pt28648      HQREGFEFLWKNIAGG--------------------------------------------
Cp76.2       HQREGFEFIWKNIAGG--------------------------------------------
At1g05490    HQQEGFEFIWKNLAGT--------------------------------------------
At3g24340    HQQEGFEFIWKNLAGT--------------------------------------------
Bd1g16720    HQKEAFEFIWKNLAGS--------------------------------------------
Os07g49210   HQRKALDFLWKNLAGS--------------------------------------------
Sb02g043870  HQRKAFEFIWKNLAGS--------------------------------------------
ZM108166     HQRKAFEFIWKNLAGS--------------------------------------------
Vv29366      ------------------------------------------------------------
Pt832603     HQKKAFEFLWKNTAGS--------------------------------------------
Pt567214     HRKKAFECLWRNIAGS--------------------------------------------
Cp19.123     HQKRAYEFLWRNIAGD--------------------------------------------
AtCLSY1      HQKKAFEFLWKNLAGS--------------------------------------------
At5g20420    HQRRAFEFLWRNVAGS--------------------------------------------
Sm84719      HQREAFIFISRNLL----------------------------------------------

                               80                 100                 120
15898471     ------------------------------------------------------------
256419642    ------------------------------------------------------------
237794935    ------------------------------------------------------------
187779742    ------------------------------------------------------------
ScSNF2       ------L-----------------------------------------------------
83286649     ------------------------------------------------------------
124803472    ------------------------------------------------------------
74008371     ------V-----------------------------------------------------
14028669     ------I-----------------------------------------------------
56118945     ------I-----------------------------------------------------
47217344     ------I-----------------------------------------------------
```

```
157103787     ------I-----------------------------------------------------
170572145     ------I-----------------------------------------------------
255719682     ------L-----------------------------------------------------
145610651     ------I-----------------------------------------------------
145353082     ------C-----------------------------------------------------
225436589     ------T-----------------------------------------------------
189521245     ------T-----------------------------------------------------
47206539      ------T-----------------------------------------------------
113678140     ------T-----------------------------------------------------
156717248     ------T-----------------------------------------------------
73997410      ------T-----------------------------------------------------
115939069     ------I-----------------------------------------------------
221120608     ------D-----------------------------------------------------
256052547     ------I-----------------------------------------------------
24666729      ------I-----------------------------------------------------
170592228     ------T-----------------------------------------------------
17569817      ------T-----------------------------------------------------
256072692     ------I-----------------------------------------------------
145341798     ------R-----------------------------------------------------
145491053     ------R-----------------------------------------------------
118367847     ------R-----------------------------------------------------
145484966     ------R-----------------------------------------------------
239899054     ------------------------------------------------------------
291001481     ------R-----------------------------------------------------
211853152     ------R-----------------------------------------------------
189521372     ------R-----------------------------------------------------
260834763     ------R-----------------------------------------------------
196012568     ------------------------------------------------------------
242011216     ------R-----------------------------------------------------
193599122     ------R-----------------------------------------------------
19112177      ------------------------------------------------------------
259147500     ------C-----------------------------------------------------
254582697     ------C-----------------------------------------------------
255720394     ------C-----------------------------------------------------
50309923      ------C-----------------------------------------------------
146416597     ------T-----------------------------------------------------
68483838      ------T-----------------------------------------------------
149235383     ------T-----------------------------------------------------
199432721     ------T-----------------------------------------------------
254568884     ------V-----------------------------------------------------
19075591      ------A-----------------------------------------------------
261358370     ------V-----------------------------------------------------
70982085      ------V-----------------------------------------------------
225682364     ------V-----------------------------------------------------
239615027     ------V-----------------------------------------------------
212536498     ------V-----------------------------------------------------
255936215     ------V-----------------------------------------------------
189204870     ------V-----------------------------------------------------
66813000      ------T-----------------------------------------------------
242056785     ------A-----------------------------------------------------
85014197      ------K-----------------------------------------------------
Cr13231       ---ERHRLQAQDPDNS--------------------------------------------
ScRAD54       -----------------------------DPLKSDEKAL-------------TESQKTEQ
50302399      MEKADTQADSNITGSK-------------SPVETDVSSL-------------KDVIKINE
```

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156845511    KEKNNGEKIQEEENPIPKTKGKKKKSNSKESKSTTDSTI-------------EIKIT---
45190309     -DGTGKDPGSKDSEPIVVEVLEETPTPTPTPTPTPSPEI-------------LDANAAMT
255718981    ---TADAATTKEPTPPPHTQSSSTESPASSPASTPSSATPPPAAQAPALQQCTVATEVSE
238878261    ------------------------------------------------------------
255728815    ------------------------------------------------------------
149239498    ------------------------------------------------------------
149388940    ------------------------------------------------------------
190348945    ------------------------------------------------------------
254570653    ------------------------------------------------------------
189211141    ------------------------------------------------------------
46127169     ------------------------------------------------------------
225684006    ------------------------------------------------------------
259485020    ------------------------------------------------------------
238840822    ------------------------------------------------------------
19115202     ------------------------------------------------------------
50546160     ------------------------------------------------------------
58266612     ------------------------------------------------------------
164660184    ------------------------------------------------------------
41055574     ------------------------------------------------------------
118094595    ------------------------------------------------------------
281351942    ------------------------------------------------------------
195539537    ------------------------------------------------------------
47575794     ------------------------------------------------------------
156369786    ------------------------------------------------------------
238814383    ------------------------------------------------------------
170041242    ------------------------------------------------------------
189238349    ------------------------------------------------------------
195161916    ------------------------------------------------------------
193591979    ------------------------------------------------------------
71033369     ---G--F-----N-----------------------------------------------
221488620    ---E--F-----Q-----------------------------------------------
157128256    ------------------------------------------------------------
241602475    ------------------------------------------------------------
194214970    ------------------------------------------------------------
281347253    ------------------------------------------------------------
119906776    ------------------------------------------------------------
194037038    ------------------------------------------------------------
149045437    ------------------------------------------------------------
149638830    ------------------------------------------------------------
45382655     ------------------------------------------------------------
148230804    ------------------------------------------------------------
156379220    ---RNFN-----------------------------------------------------
193661957    ------------------------------------------------------------
110760280    ---KVPN-----------------------------------------------------
242023203    ---KDIN-----------------------------------------------------
66811190     ------------------------------------------------------------
71651467     ------------ERMP--------------------------------------------
50311185     MVHTKGDESMILERDD--------------------------------------------
254585925    ------SKSLVLENDS--------------------------------------------
50294037     ------DKSCRLERDS--------------------------------------------
255725568    -------------RDF--------------------------------------------
241952408    -------------RDF--------------------------------------------
260941370    -------------HQP--------------------------------------------
254567481    ------------SKEL--------------------------------------------
```

```
145230930     -------------RSF--------------------------------------------
238484253     -------------RSF--------------------------------------------
119494890     -------------RSF--------------------------------------------
225681829     -------------RSF--------------------------------------------
258563128     -------------RPF--------------------------------------------
242778005     -------------RDY--------------------------------------------
212533393     -------------RDY--------------------------------------------
189209013     -------------RC---------------------------------------------
71019185      -------HADGTK-----------------------------------------------
290982366     -------------KDF--------------------------------------------
281209956     -------------RHQ--------------------------------------------
167385507     ------------------------------------------------------------
170577655     ------------------------------------------------------------
145350886     ------------------------------------------------------------
224013540     ------------------------------------------------------------
145482121     ------------------------------------------------------------
145338703     ------------HGSA--------------------------------------------
20336209      ---------ESVKKTK--------------------------------------------
242018945     ------ESLKRMEE-D--------------------------------------------
196005243     ------ESVDRIA--E--------------------------------------------
81916664      ------ESLERFKTS---------------------------------------------
75026277      ------ESLERFKTS---------------------------------------------
193580055     ---------ETVEKTN--------------------------------------------
193610723     ---------ETVEKTN--------------------------------------------
145335288     ------QSISRVKSGD--------------------------------------------
258572168     ---------------K--------------------------------------------
171685718     ---------------V--------------------------------------------
289615990     ------------VESN--------------------------------------------
164425263     ------------VESN--------------------------------------------
72391587      ------------------------------------------------------------
71662347      ------------------------------------------------------------
239977156     ------------------------------------------------------------
146081173     ------------------------------------------------------------
Sm441121      ------------------------------------------------------------
Bd3g18910     ---------------S--------------------------------------------
Bd1g74070     ---------------D--------------------------------------------
Os03g06920    ---------------D--------------------------------------------
Sb01g046180   ---------------D--------------------------------------------
Bd3g19890     --------------SD--------------------------------------------
Os06g14440    --------------GD--------------------------------------------
Sb07g002945   --------------GD--------------------------------------------
ZM093940      --------------GD--------------------------------------------
ZM064574      --------------GD--------------------------------------------
Bd2g21430     --------------CD--------------------------------------------
Bd2g21450     --------------SD--------------------------------------------
Os08g14610    --------------TD--------------------------------------------
Vv35918       --------------AE--------------------------------------------
Pt195587      --------------AD--------------------------------------------
AtDRD1        --------------AD--------------------------------------------
At2g21450     --------------AD--------------------------------------------
Bd2g26500     ---IRLDELKHGAKPD--------------------------------------------
Os05g32610    ---IRLNEIKHGAKPD--------------------------------------------
Sb09g019410   ---IRLDELKHGAKPD--------------------------------------------
RMR1          ---IRLDEIKHGAKPD--------------------------------------------
```

```
Bd2g43500    ---IDIQQVKHTVNTD--------------------------------------------
Os02g43460   ---TSIEQLRNNANT---------------------------------------------
Bd3g50300    ---TKIQDVKNNINSD--------------------------------------------
Sb04g033300  ---TTIEQLKQTVKSD--------------------------------------------
ZM178435     ---TTIEQLKHTIKSD--------------------------------------------
Vv15867      ---IYLDELKRSSFSD--------------------------------------------
Pt28648      ---IYLDKLKENANLN--------------------------------------------
Cp76.2       ---IILDKMKVPPQFD--------------------------------------------
At1g05490    ---IMLNELKDFENSD--------------------------------------------
At3g24340    ---TKINELNSVG-VK--------------------------------------------
Bd1g16720    ------LQLEEMDNPT--------------------------------------------
Os07g49210   ------IQVEGMDNSN--------------------------------------------
Sb02g043870  ------LQLEEMDDST--------------------------------------------
ZM108166     ------LQLEEMDGST--------------------------------------------
Vv29366      ------------------------------------------------------------
Pt832603     ---LVPAHMEKTS-K---------------------------------------------
Pt567214     ---LVPALMEKAS-K---------------------------------------------
Cp19.123     ---LVPAQMESKS-D---------------------------------------------
AtCLSY1      ---VVPAMMDPSS-D---------------------------------------------
At5g20420    ---VEPSLMDPTS-G---------------------------------------------
Sm84719      ------------------------------------------------------------

                              140                 160                 180
15898471     -----LGFGICLADDMGLGKTLQT-IAVFSDAKKENELT-----------P---------
256419642    -----VKWGGILADDMGLGKTIQA-LTFIQHYKNKHDDKCL-------------------
237794935    -----MKFGGILADEMGLGKTIQT-ISFLLSEKGTR------------------------
187779742    -----MKFGGILADEMGLGKTIQT-ISFLLSEKGAK------------------------
ScSNF2       --------NGILADEMGLGKTIQT-ISLLTYLYEMKNIRG----------P---------
83286649     -----HKINGILADEMGLGKTLQT-ISLLCYLRFNKNIKR----------K---------
124803472    -----FKINGILADEMGLGKTLQT-ISLLCYLRFNKNIKK----------K---------
74008371     --------NGILADEMGLGKTLQT-IALLGYLKHYRNIPG----------P---------
14028669     --------NGILADEMGLGKTLQT-ISLLGYMKHYRNIPG----------P---------
56118945     --------NGILADEMGLGKTLQT-ISLLGYMKHYRSIPG----------P---------
47217344     --------NGILADEMGLGKTLQT-IALLGYMKHYRNIPG----------P---------
157103787    --------NGILADEMGLGKTLQT-ISLLGYLKNFRNNPG----------P---------
170572145    --------NGILADEMGLGKTLQT-VAVIGFMKHYKNASG----------P---------
255719682    --------AGILADEMGLGKTLQT-ISFIGYMRYVEKKRG----------P---------
145610651    --------SGILADEMGLGKTLQT-ISFLGYLRHIMGITG----------P---------
145353082    --------SCILADEMGLGKTLQS-ISFLACIKEMRHANG----------P---------
225436589    --------NVILADEMGLGKTVQS-VSMLGFLQNAQQIYG----------P---------
189521245    --------DTILADEMGLGKTIQT-IVFLYSLFKEGHTKG----------P---------
47206539     --------DTILADEMGLGKTVQT-IVFLYSLYKEGHSKG----------P---------
113678140    --------DTILADEMGLGKTVQT-AVFLYSLYKEGHSKG----------P---------
156717248    --------DTILADEMGLGKTVQT-AVFLYSLYKEGHSKG----------P---------
73997410     --------DTILADEMGLGKTVQT-AVFLYSLYKEGHSKG----------P---------
115939069    --------CTILADEMGLGKTIQT-IAFLYSLYKEGHSKG----------P---------
221120608    --------NTILADEMGLGKTIQT-ITFLNSLLSEGRSEG----------P---------
256052547    --------DTILADEMGLGKTIQT-IAFLYSLYKEGHCRG----------P---------
24666729     --------PTILADEMGLGKTIQT-VVFLYSLFKEGHCRG----------P---------
170592228    --------DAILADEMGLGKTIQS-MVFLYSLVKEGHTRG----------P---------
17569817     --------DAILADEMGLGKTVQS-LTFLYTLMKEGHTKG----------P---------
256072692    --------NAILADEMGLGKTVQV-IALLYSLWKEENDYG----------P---------
145341798    --------GCILADEMGLGKTAQA-LALIHHCLQVR--PG---------LP---------
145491053    --------NVILADEMGLGKTIQT-IAFLNHLYNFENYRG----------P---------
```

```
118367847     --------NVILADEMGLGKTIQS-TAFINHLYTFENVRG----------P---------
145484966     --------NVLLADEMGLGKTIQS-IAFLNHLVSMESCRG----------P---------
239899054     -----QYRGSILADEMGMGKTVQT-AVFLSAVMATVGGTG----------P---------
291001481     --------NSILADEMGLGKTVQT-VATLEYLRAFEHIRG----------P---------
211853152     --------NCILADEMGLGKTIQS-ITFLQEIYLN-RIPG----------P---------
189521372     --------NCILADEMGLGKTIQS-ITFLEEIYRT-GIKG----------P---------
260834763     --------NCILADEMGLGKTVQS-ITFLKEIQEQ-GILG----------P---------
196012568     ---------------MGLGKTIQS-LSFLNHLLNY-NIRG----------P---------
242011216     --------NCILADEMGLGKTIQS-LAFVNSVYNY-GIRG----------P---------
193599122     --------NCILADEMGLGKTIQS-LTFIHAVHEY-GVRG----------P---------
19112177      -----THHPCILADEMGLGKTVQV-ISFISVLFYRHKCF-----------P---------
259147500     --------GGIIGDEMGLGKTIQV-IAFIAALHHSGLLTG----------P---------
254582697     --------GGIIGDEMGLGKTIQV-IAFLAALHHSNQLDG----------P---------
255720394     --------GGIIGDEMGLGKTIQI-IAFLASLHHSGKLNG----------P---------
50309923      --------GGIIGDEMGLGKTIQI-IAFLATLHHSRKLNG----------P---------
146416597     --------GGIIGDEMGLGKTIQV-VSFIAGLHYSGLLDK----------P---------
68483838      --------GGIIGDEMGLGKTIQI-ISFLAGLHYSGLLDK----------P---------
149235383     --------GGIIGDEMGLGKTIQI-ISFIAGLHYSGLLEK----------P---------
199432721     --------GGIIGDEMGLGKTIQI-ISFLAGLHYSGLLEK----------P---------
254568884     --------GGILGDEMGLGKTVQI-ISFIAGLHYTKKLNK----------P---------
19075591      --------GGIIGDEMGLGKTIQI-VSFLSSLHHSGKFQK----------P---------
261358370     --------GGIVGDEMGLGKTVQA-IAFIAALHYSKKLTK----------P---------
70982085      --------GGIIGDEMGLGKTIQA-IAFLAGLHYSKKLDR----------P---------
225682364     --------GGIIGDEMGLGKTIQV-IAFLAGLHYSKKLTK----------P---------
239615027     --------GGIIGDEMGLGKTIQV-IAFLAGLHHSRILTK----------P---------
212536498     --------GGIIGDEMGLGKTIQV-ISFLAGLHHSRKLTK----------P---------
255936215     --------GGIIGDEMGLGKTIQA-ISYLAALHHSKKFTK----------P---------
189204870     --------GGIIGDEMGLGKTIQA-IGLVAGLHYSKKLTK----------P---------
66813000      --------GGIVGDEMGLGKTVQI-VSFLASLHYSRRLGG----------P---------
242056785     --------GGIIGDEMGLGKTVQV-LSFLGSLHNSS-MYK----------P---------
85014197      --------GGVLADDMGLGKTIQV-IVFLGALLHSRVVSK--------------------
Cr13231       ---CLDAGGCILAHSMGLGKTLST-IALLHMFLGQGLAAGPGPGSQPQA-TTGADPAAAD
ScRAD54       N--NRGAYGCIMADEMGLGKTLQC-IALMWTLLRQG--------------P---------
50302399      NSRNRGAYGCIMADEMGLGKTLQC-LALMWTMLKQG--------------P---------
156845511     ---NKGAYGCIMADEMGLGKTLQC-IALMWTLLKQG--------------P---------
45190309      RESNRGAYGCIMADEMGLGKTLQC-IALMWTLLRQG--------------S---------
255718981     IAQNRGAYGCIMADEMGLGKTLQC-IALMWTLLRQG--------------P---------
238878261     ---DARAKGCIMADEMGLGKTLQC-LTLMWTLLRQS--------------P---------
255728815     ---DAKAKGCIMADEMGLGKTLQC-LTLMWTLLRQS--------------P---------
149239498     ---DPRAKGCIMADEMGLGKTLQC-LTLMWTLLRQS--------------P---------
149388940     ---DARAKGCIMADEMGLGKTLQC-IALMWTLLKQS--------------P---------
190348945     ---DPRAKGCIMADEMGLGKTLQC-IALMWTLLRQG--------------P---------
254570653     ---DASAKGCIMADEMGLGKTLQC-IALLWTLLRQS--------------P---------
189211141     ---DPKANGCIMADEMGLGKTLQC-IALMWTLLKQS--------------P---------
46127169      ---DEKANGCIMADEMGLGKTLQC-ISLMWTLLKQS--------------P---------
225684006     ---DPKANGCIMADEMGLGKTLQC-ITLLWTLLKQS--------------P---------
259485020     ---DRNAHGCIMADGMGLGKTLQC-ISLMWTLLKQS--------------P---------
238840822     ---DKNASGCIMADGMGLGKTLQC-ITLMWTLLKQS--------------P---------
19115202      ---DRCANGCIMADEMGLGKTLQC-IALLWTLLKQS--------------P---------
50546160      ---NPKAHGCIMADEMGLGKTLQC-IALLWTLLKQS--------------P---------
58266612      ---ADGAWGCIMADEMGLGKTLQC-IALLWTLLKQS--------------P---------
164660184     ---SENAHGCIMADEMGLGKTLQC-ITLLWTLLKQS--------------P---------
41055574      ---IENSYGCIMADEMGLGKTLQC-ITLIWTLLKQS--------------P---------
118094595     ---IPGSHGCIMADEMGLGKTLQC-ITLMWTLLRQS--------------P---------
```

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281351942     ---VPGSHGCIMADEMGLGKTLQC-ITLMWTLLRQS--------------P---------
195539537     ---IPGSHGCIMADEMGLGKTLQC-ITLMWTLLRQS--------------P---------
47575794      ---ISGSHGSIMADEMGLGKTLQC-ITLIWTLLRQS--------------P---------
156369786     ---IQGSYGCIMADEMGLGKTLQC-ITLIWTLLRQG--------------P---------
238814383     ---IEEAYGCIMADEMGLGKTLQC-ITLLWTLLKQG--------------P---------
170041242     ----GDFQGCIMADEMGLGKTLQC-ITLLWTLLRQS--------------P---------
189238349     ---IPNSFGCIMADEMGLGKTLQC-ITLLWTLVRQG--------------P---------
195161916     ----GNFNGCIMADEMGLGKTLQC-VALVWTLLKQS--------------A---------
193591979     ---IEGAYGCIMADEMGLGKTLQC-ITLMWTLLKQG--------------P---------
71033369      ------GRGCILADDMGLGKTLQS-ITVMWTLLNQG--------------LDNKPG--KA
221488620     ------GEGCILADDMGLGKTLQS-ITILWTLLEQN--------------IEG-------
157128256     ------RFGAILADEMGLGKTLQC-ISLIYTLMKQG--------------PY--------
241602475     ------GGGAILADEMGLGKTLQC-ITLVWTLLRQG--------------PYG-------
194214970     ------RYGAILADEMGLGKTIQC-ISLIWTLQCQG--------------PYG-------
281347253     ------RCGAILADEMGLGKTLQC-ISLIWTLQCQG--------------PYG-------
119906776     ------RCGAILADEMGLGKTLQC-ISLIWTLQCQG--------------PYG-------
194037038     ------RCGAILADEMGLGKTLQC-ISLIWTLQCQG--------------PYG-------
149045437     ------KCGAILADEMGLGKTLQC-ISLIWTLQCQG--------------PYG-------
149638830     ------RFGAILADEMGLGKTLQC-ISLIWTLLRQG--------------PYG-------
45382655      ------RFGAILADEMGLGKTLQC-ISLVWTLLRQG--------------VYG-------
148230804     ------RFGAILADEMGLGKTLQC-ISLIWTLLRQG--------------PYG-------
156379220     ------GNGAILADEMGLGKTLQC-IALIWTLHKQG--------------PYG-------
193661957     ------CFGAILADEMGLGKTLQT-ICLVWMLLKRG--------------PYG-------
110760280     ------YFGAILADEMGLGKTLQC-ITIIWTLLKKG--------------P---------
242023203     ------YNGVILADEMGLGKTLQC-ISLIWTLLKQG--------------P---------
66811190      -----KGNGCILADDMGLGKSIQA-ITILWTLLKQG--------------PK--------
71651467      -----GYHGAILADEMGLGKTIQT-VATIYTCLRQG------------------------
50311185      -----DIKGCLLADEMGLGKTLMT-ITLIWTLLKQT--------------PYPTII--NQ
254585925     -----DIQGCILADEMGLGKTLMT-ITLIWTLLKQT--------------PMASKVSCSQ
50294037      -----DIKGCILADDMGLGKTLMT-ITLIWTLLKQT--------------PFASKVQCSQ
255725568     -----QGHGCLLADEMGLGKTLMT-ITTIWTLLKQN--------------P---------
241952408     -----DGNGCLLADEMGLGKTLMT-ITTIWTLLKQN--------------P---------
260941370     -----NYFGALLADEMGLGKTLMT-ITVIWTLLKQS--------------P---------
254567481     -----PHKGCILADEMGLGKTLTT-ITLIWTLLKQN------------------------
145230930     -----NGEGAILADDMGLGKTLQT-ITLLWTLLKQN--------------P---------
238484253     -----NGQGAILADDMGLGKTLQT-ITLLWTLLKQN--------------P---------
119494890     -----NGEGAILADDMGLGKTLQT-ITLLWTLLKQN--------------P---------
225681829     -----NGEGAILADEMGLGKTLQT-IALIWTLLKQN--------------P---------
258563128     -----NGEGAVLADEMGLGKTLQT-IALLWTLMKQN--------------P---------
242778005     -----NGEGAILADEMGLGKTLQT-ITLLWTLLKQN--------------F---------
212533393     -----NGEGAILADEMGLGKTLQT-ITLLWTLLKQN--------------P---------
189209013     -----EGEGAIMADEMGLGKTLQT-IALLWTLMKQN--------------P---------
71019185      ------GKGAILADEMGLGKTLQT-IALILTLIKQS--------------C----YYTSK
290982366     -----VGKGCLLADEMGLGKTLQT-ITLIYTLLRRG--------------P---------
281209956     -----FGNGCILADQMGLGKTVMT-LTTLWTLLKQS--------------P---------
167385507     ---RGGECGCILADEMGLGKTLQT-ITLIWTVYKQC------------------------
170577655     ----NSHGGALLADEMGLGKTVQT-ISLITALVKKR------------------------
145350886     -----AHTGCLLAHEMGLGKTLQV-IALVWTLLKQS--------------P---------
224013540     -----VPRGAVLADEMGLGKTLMT-IATIYAFHRRQ------------------------
145482121     -----SIRGCILADSMGLGKTLQA-ITLMWILIQSH------------------------
145338703     -----NINGCILADDMGLGKTLQS-ITLLYTLLCQG------------------------
20336209      ---KSPGSGCILAHCMGLGKTLQV-VSFLHTVLLCD------------------------
242018945     -----SGSGCILAHCMGLGKTLQV-ITLSHTLLTNN------------------------
196005243     -----PGSGCIIAHSMGLGKTLQV-IAFIDAVLNYG------------------------
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81916664       -----SGFGCILAHSMGLGKTLQV-ISFIDVLFRHT--------------P---------
75026277       -----SGFGCILAHSMGLGKTLQV-ISFIDVLFRHT--------------P---------
193580055      ---TTEGTGCVLAHRMGIGKTLQI-ITLMYTLLCHT------------------------
193610723      ---TTEGTGCVLAHRMGIGKTLQI-ITIIYTILCHT------------------------
145335288      -----KGLGCILAHTMGLGKTFQV-IAFLYTAMRCV------------------------
258572168      ---DEKRQGCLLAHTMGLGKTMQV-ISLLVTIANVANSQD----------P------ELR
171685718      -----SGQGCLLAHTMGLGKTMQV-ITLLVVIAEAAASDD----------P------AVV
289615990      -----SRQGCLLAHTMGLGKTMQV-ITLLVAIAEASQSDD----------P------RMV
164425263      -----SRQGCLLAHTMGLGKTMQV-ITLLVAIAEASQSDD----------P------RVV
72391587       -----EGDGCVLALTMGLGKTLVS-LTICYSYIYNNGPCD--------------------
71662347       -----KGNGCVIALTMGLGKTLLS-LALCYSHMYDQNPRD--------------------
239977156      -----KQSGCVVAMTMGLGKTLVA-LTLCFSHLHLAPQAD--------------------
146081173      -----KQSGCVVAMTMGLGKTLVA-LTLCFSQLHLAPQAD--------------------
Sm441121       ----DEEGGCILAHAPGTGKTFAT-VYFYLKYKEIM--------------A---------
Bd3g18910      ---TSDPGGCIIAHAPGSGKTFMV-ISFIQSFLAKH--------------S---------
Bd1g74070      ---EKNPGGCILAHAPGSGKTFML-ISFVQSYLTKY--------------P---------
Os03g06920     ---ENNPGGCILAHAPGSGKTFLI-ISFVHSFLAKY--------------P---------
Sb01g046180    ---EDNPGGCILAHAPGSGKTFLL-ISFVHSFLARY--------------P---------
Bd3g19890      -----KPGGCILAHAPGSGKTFMV-ISFIQSFLAKY--------------P---------
Os06g14440     -----KPGGCILAHAPGSGKTFML-ISFIQSFLAKY--------------P---------
Sb07g002945    -----KPGGCILAHAPGSGKTFML-ISFIQSFMARY--------------P---------
ZM093940       -----KPGGCILAHAPGSGKTFLL-ISFIQSFMARY--------------P---------
ZM064574       -----KPGGCILAHAPGTGKTFML-ISFIQSFMARY--------------P---------
Bd2g21430      -----KPGGCILAHAAGSGKTFMI-ICFIQSFLAKH--------------P---------
Bd2g21450      -----KPGGCILAHAPGSGKTFMI-ICFIQSFLAKD--------------P---------
Os08g14610     -----EPGGCILVHAPGSGEIFML-ISFIQGFMARH--------------F---------
Vv35918        -----NPGGCILAHAPGSGKTFMI-ISFMQSFLAKY--------------P---------
Pt195587       -----NPGGCILAHAPGSGKTFMI-ISFMQSFLAKY--------------P---------
AtDRD1         -----DPGGCIMAHAPGSGKTFMI-ISFMQSFLAKY--------------P---------
At2g21450      -----EPGGCILAHAPGSGKTFLL-ISFLQSFMAMD--------------P---------
Bd2g26500      -----VVGGCVICHAPGTGKTRLA-IVFIQTYMKVF--------------P---------
Os05g32610     -----VVGGCVICHAPGTGKTRLA-IVFIQTYMKVF--------------P---------
Sb09g019410    -----VVGGCVICHAPGTGKTRLA-IVFIQTYMKVF--------------P---------
RMR1           -----VVGGCVICHAPGTGKTRLA-IVFIQTYMKVF--------------P---------
Bd2g43500      -----STSGCVISHAPGTGKTRLA-ITFVQSYLELF--------------P---------
Os02g43460     -----IEGGCVISHAPGTGKTRLA-ITFVQSYFAFF--------------P---------
Bd3g50300      -----DLRGCWISHAPGTGKTRST-IAFLQSYRVLF--------------P---------
Sb04g033300    -----VGGGCVISHAPGTGKTRLA-ITFVQSYLEVF--------------P---------
ZM178435       -----AGGGCVISHAPGTGKTRLA-ITFVQSYLEVF--------------P---------
Vv15867        -----GGSGCIISHAPGTGKTRLT-IVFLQTYMELY--------------P---------
Pt28648        -----GGTGCIISHAPGTGKTRLT-IVFLQTYMQLY--------------P---------
Cp76.2         -----GGNGCIISHAPGTGKTRLT-IVFLQSYMMLY--------------P---------
At1g05490      -----ETGGCIMSHAPGTGKTRLT-IIFLQAYLQCF--------------P---------
At3g24340      -----GSGGCIISHKAGTGKTRLT-VVFLQSYLKRF--------------P---------
Bd1g16720      ---ASSTGGCVVAHTPGSGKTLLL-ISFLVSYLKVH--------------P---------
Os07g49210     ---V-STGGCVIAHTPGSGKTLLL-ISFLVSYMKAH--------------P---------
Sb02g043870    -----SRGGCVVAHTPGAGKTLLL-ISFLVSYLKVH--------------P---------
ZM108166       -----SRGGCVVAHTPGAGKTLLL-ISFLVSYLKVH--------------P---------
Vv29366        -------GGCVISHSPGAGKTFLV-ISFLVSYLKLF--------------P---------
Pt832603       -----KIGGCVVSHTPGAGKTFLI-IAFLVSYLKLF--------------P---------
Pt567214       -----KIGGCVISHTPGAGKTFLK-IAFLVSYLKLF--------------P---------
Cp19.123       -----NIGGCVVSHSPGAGKTFLI-IAFLVSYLKLF--------------P---------
AtCLSY1        -----KIGGCVVSHTPGAGKTFLI-IAFLASYLKIF--------------P---------
At5g20420      -----NIGGCVISHSPGAGKTFLI-IAFLTSYLKLF--------------P---------
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Sm84719          ---SKEPGGVILHHAPGTGKTFLV-ISFLTSFFANF--------------Q----------

                                   200                 220                 240
15898471         ------------SLVICPLSVLKNWEEELSKFA-P-----HLRFAVFHEDRSKIKLEDYD-
256419642        ------------ALVVCPTTLIYNWENEIRKFT-P-----SMTYHIHHGPTRLKTAEELMK
237794935        ------------SLIVTPTSLIYNWQDEFQKFA-E-----TLKIGVIHGS-KEERMKVLDG
187779742        ------------SLIVTPTSLIYNWQDEFQKFA-K-----TLKIGVIHGS-KEERMKVLDD
ScSNF2           ------------YLVIVPLSTLSNWSSEFAKWA-P-----TLRTISF-KG-SPNERK----
83286649         ------------NIIICPRSTLDNWYEEIKKWC-S-----EMKPFKY-YG-SKEQRKELNK
124803472        ------------SIIICPRSTLDNWYEEIKKWC-T-----PMKAFKY-YG-NKDQRKELNR
74008371         ------------HMVLVPKSTLYNWMNEFKRWV-P-----SLRVICF-VG-DKDARA----
14028669         ------------HMVLVPKSTLHNWMSEFKRWV-P-----TLRSVCL-IG-DKEQRA----
56118945         ------------HMVLVPKSTLHNWMAEFKRWV-P-----SLCAICL-IG-DKDHRA----
47217344         ------------HMVLVPKSTLYNWMNEFKRWV-P-----SLRAVCL-IG-DRDERT----
157103787        ------------HIVIVPKSTLQNWVNEFGRWC-P-----SLRAVCL-IG-DQETRN----
170572145        ------------HLVIAPKSTLQNWINEFGKWC-P-----SLKAIAL-IG-IAEARA----
255719682        ------------FVVIAPKSTLNNWLREINRWT-P-----EVNAFIL-QG-DKEERAKLVS
145610651        ------------HLVIVPKSTLDNWKREFGKWT-P-----EVNVLVL-QG-AKEERAALIA
145353082        ------------HLVVCPLSVLSSWMDELQKWA-P-----SFRVVRLHSG-DENERV----
225436589        ------------FLVVVPLSTLSNWAKEFKKWL-P-----DLNVIVY-VG-TRASREVC--
189521245        ------------FLVSAPLSTIINWEREFEMWA-P-----DFYVVTY-TG-DKDSRAII--
47206539         ------------FLVSAPLSTIINWEREFEMWA-P-----DFYVVTY-TG-DKDSRAII--
113678140        ------------FLVSAPLSTIINWEREFEMWA-P-----DMYVVTY-VG-DKDSRAVI--
156717248        ------------FLVSAPLSTIINWEREFEMWA-P-----DMYVVTY-VG-DKDSRAVI--
73997410         ------------FLVSAPLSTIINWEREFEMWA-P-----DMYVVTY-VG-DKDSRAII--
115939069        ------------FLISAPLSTIINWEREFEFWA-P-----DFYVVTY-TG-DKDSRAII--
221120608        ------------FLICAPLSTIVNWEREFEFWA-P-----NMYVVTY-SG-NRENRQVI--
256052547        ------------FLVAAPLSTIINWEREFEFWA-P-----DLYVVSY-IG-DKDSRTVI--
24666729         ------------FLISVPLSTLTNWERELELWA-P-----ELYCVTY-VG-GKTARAVI--
170592228        ------------FLVAAPLSTLINWEREAEFWC-P-----DFYVVTY-VG-DKDSRTVI--
17569817         ------------FLIAAPLSTIINWEREAELWC-P-----DFYVVTY-VG-DRESRMVI--
256072692        ------------FIIMTPLSTLQNWDREFSIWA-P-----DFYIVVY-SG-DKQVRAML--
145341798        ------------ALVVVPLSTIVNWEREAQRWV-P-----DAYVVTH-VG-KQAGREFA--
145491053        ------------FLIIAPLSTLQHWKRTVEEWT-N-----LNAVLYYDQE-SSAGRALC--
118367847        ------------FLIIAPLSTLEHWKRSVEDWT-N-----LNAVLYYDHS-GQEGRNCC--
145484966        ------------FLIIAPLSTLQHWKRSCEDWT-S-----LNAVLYYDQQ-GQPGRQAI--
239899054        ------------CLIVAPLSTLRHWQRELRKWA-P-----ELNVVVM-AG-SSEDRDII--
291001481        ------------FIVIAPLSTVEHWKREFENWT-------DMNVLVF-HG-NTQSREVM--
211853152        ------------FLIIAPLSTIANWEREFRTWT-------DLNVVVY-HG-SMISRQMI--
189521372        ------------FLIIAPLSTIANWEREFRTWT-------HLNVIVY-HG-SVVSRQML--
260834763        ------------FLIIAPLSTIANWQREFETWT-------NVNVVVY-HG-SSASRQMI--
196012568        ------------FLVIAPLSTIANWQREIEAWT-------DMNVVVY-HG-SSASRQLI--
242011216        ------------FLVIAPLSTIPNWQREFEAWT-------DLNVVVY-HG-SAASLQMI--
193599122        ------------FLVIAPLSTIPNWQREFEAWT-------DLNVIVY-HG-SSHSRNMV--
19112177         ------------VLVIVPHATVANWERELKKWA-P-----FLQINVLVGS-EKNRSLVRDY
259147500        ------------VLIVCPATVMKQWCNEFHHWW-P-----PLRTVIL-HS-MGSGMASD--
254582697        ------------VLIVCPATVMKQWCTEFHHWW-P-----PFRTVIL-HS-IGAGMAS---
255720394        ------------ILVVCPATVLRQWCKEFHTWW-P-----PFRAIIL-HS-IGAGMTQ---
50309923         ------------VLVVCPATVMKQWCNEFHTWW-P-----PFRAVIL-HS-IGAGMNK---
146416597        ------------VIVVVPATVMMQWVNEFHTWW-P-----PLRCAIL-HS-IGSGM--S--
68483838         ------------VLVVVPATVLNQWVNEFHRWW-P-----PLRCIIL-HS-IGSGM--N--
149235383        ------------VLVVVPATVLNQWVNEFHRWW-P-----PLRCVIL-HS-IGSGM--S--
199432721        ------------VLVVVPATVMNQWVNEFHRWW-P-----PLRCVIL-HS-IGSGM--G--
254568884        ------------VIVVCPATVLRQWCNEFHRWW-P-----PLRVVIL-HA-IGTGLSGS--
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19075591       -----------ALIVCPATLMKQWVNEFHTWW-A-----PLRVVVL-HA-TGSGQRAS--
261358370      -----------VIIVAPATVLRQWVNEFHRWW-P-----ALRVSIL-HS-SGSGMINL--
70982085       -----------VIVVCPATVMKQWVNEFHRWW-P-----PFRVSIL-HT-SGSGMVNI--
225682364      -----------IIVVCPPTVMKQWVNEFHRWW-A-----PFRVSIL-HT-SGSGMINL--
239615027      -----------VIVVCPPTVMKQWVNEFHRWW-A-----PFRVSIL-HT-SGSGMVNL--
212536498      -----------VIVVAPATVMKQWVTEFHRWW-P-----PFRVSIL-HT-SGSGMINV--
255936215      -----------AIVVCPATLMKQWVNEFHRWW-P-----PFRVSIL-HS-SGSGMINI--
189204870      -----------VIVVCPATVMKQWVNEFHRWW-P-----ALRVSIL-HT-SGSGMLDT--
66813000       -----------ALIVAPATLLSNWIKEFHKWW-P-----PFRVGLF-HS-SGSGGGGN--
242056785      -----------SIVICPVTLLQQWQREASRWY-P-----KFKVEIL-HD-SANGSSKK--
85014197       -----------ALILCPATIVSQWMDEWKRFY-P-----FVRIFF--------GFPN---
Cr13231        GDEDGLAGRRRALVVTPANVASTFRVEFERWL-PERGSEDEQLSRLTGNKTRR-------
ScRAD54        --Q-GKRLIDKCIIVCPSSLVNNWANELIKWL-G-----PNTLTPLAVDGKKSSM-GGGN
50302399       --Q-GRRSIDKCIIVCPSSLVNNWANEIDKWL-G-----PGSLSSLAIDGKKSSL-NNG-
156845511      --Q-GKSLIDKCIIVCPSSLVNNWANELIKWL-G-----PGTLSPLAIDGKKSSITNGGN
45190309       --Q-GRPTIEKCIIVCPSSLVNNWANEIVKWL-G-----PDALSPLAIDGRKSSL-SNG-
255718981      --Q-GKPTIDKCIIVCPSSLVNNWANEIVKWL-G-----RGTLASLPIDGKKSSL-SNG-
238878261      --R-GKRTIEKCIIVCPSSLVRNWANEIVKWL-G-----EGALTPLAVDGKSTKN-----
255728815      --R-GKKTIDKCIIVCPSSLVRNWANEIVKWL-G-----EGALTPLAVDGKSTKS-----
149239498      --R-GKRTIEKCIIVCPSSLVRNWANEIVKWL-G-----EGVLTPLAVDGKSTKS-----
149388940      --R-GKRTIEKCIIVCPSSLVRNWANEIIKWL-G-----EGVLTPLAVDGKSTKN-----
190348945      --R-GTKTISKCIIVCPSSLVRNWANEIVKWL-G-----EGVLTPLAVDGKSTKS-----
254570653      --R-GTKTIEKAIVVCPSSLVKNWANEFDKWL-G-----KGTLTPLAIDGKSAKG-----
189211141      --EAGKSTIQKCVIACPSSLVRNWANELIKWL-G-----KDAVTPFAIDGKASK------
46127169       --DAGKSTIQKAIVVCPASLVKNWANELTKWL-G-----ANAINPFAIDGKASK------
225684006      --EAGKTTIQKCVIACPSTLVKNWANELVKWL-G-----KDAVTPFVVDGKATK------
259485020      --EAGKTTIQKCIIACPSSLVGNWANELGKWL-G-----KDTITPFAVDGKASK------
238840822      --EAGKSTVQKAVIACPATLVGNWANELVKWL-G-----KDAINPFVIDGKASK------
19115202       --QAGKPTIEKAIITCPSSLVKNWANELVKWL-G-----KDAITPFILDGKSSK------
50546160       --Q-GKGTISKAIVVCPSSLVRNWAAEFVKWL-G-----EGVVVPYAVDG-SQKP-----
58266612       --VAGKPTCEKVIIACPTSLVGNWANELVKWL-G-----TGAVSPMVVDGKGGK------
164660184      --NAGKSTIQKAIVVCPSSLVRNWANELVKWL-G-----ASAPGSLALDGRLSR------
41055574       --D-CKPEIDKVIVVSPSSLVRNWYNEVGKWL-G------GRVQPVAIDGGSK-------
118094595      --D-CKPEIEKAMVVSPSSLVRNWYNEVEKWL-G------GRIQPLAIDGGSK-------
281351942      --E-CRPEIDKAVVVSPSSLVKNWYNEVGKWL-G------GRIQPLAIDGGSK-------
195539537      --D-CKPEIDKAVVVSPSSLVRNWYNEVGKWL-G------GRIQPLAIDGGSK-------
47575794       --D-AKPEIEKAVVVCPSSLVKNWYNEVSKWL-G------GRIQPLAIDGGSK-------
156369786      --S-AQPIVSKVIIVAPSSLVKNWYNELYKWL-G------NRINALAIDSGSK-------
238814383      --E-AKPLIEKAIIVAPSSLVKNWYNEIFKWL-Q------NRVKPLAIDGGSK-------
170041242      --D-CKPEINKAVIVCPSSLVKNWYKEFGKWL-G------CRVNCLSIDGGSK-------
189238349      --E-CKPTIDKGIIVCPSSLVRNWSNEIDKWL-K------GRLSCLIMDGGP--------
195161916      --E-CKPTINKCIIVSPSSLVKNWEKEFTKWL-H------GRMHCLAMEGGSK-------
193591979      --D-ASPTIHKAIIVTPSSLVKNWCNEIKKWL-G------GRIGALPVDGGGK-------
71033369       LNYSSSTAARKCAIICPASLVNNWESEIKKWLRG-----RCPCTPVAES-SK--------
221488620      ----TQPAVRRAVVVCPASLVNNWAAEIQKWLQG-----RCGCTPVADN-CK--------
157128256      ----SQPILKRILIVTPSSLMENWDREISKWL-K-----TERIFTFIVS-PTNPL-----
241602475      ----GYPVLRRIIIITPSSLVKNWVKEFKKWL-P-----NSNLRIYYVG-QKNKV-----
194214970      ----GKPVIKKTLIVTPGSLVNNWRKEFQKWL-G-----SERIKIFAVG-QDHKI-----
281347253      ----GKPVIKKTLIVTPGSLVNNWRKEFQKWL-G-----SERIKIFPVD-QDHKV-----
119906776      ----GKPIVKKTLIVTPGSLVNNWKKEFQKWL-G-----IERIKIFTVD-QDHKV-----
194037038      ----GKPVIKKTLIVHL-KLGDNWRKEFQKWL-G-----SERIKIFTVD-PDHKV-----
149045437      ----GKPIVKRTLIVTPGSLVNNWRKEFQKWL-G-----SERIKIFTVD-QDHKV-----
149638830      ----GKPIIKQTLVVTPGSLVNNWKKEFQKWL-G-----TERIKVFSVD-QEHKV-----
45382655       ----CKPVLKRALIVTPGSLVKNWKKEFQKWL-G-----SERIKVFTVD-QDHKV-----
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148230804       ----AKPVIKRALIVTPGSLVKNWRKEFQKWL-G-----TERIRVFAVD-QDHKV-----
156379220       ----GQPVCNRILIITPGSLVKNWCAEFRKWL-G-----NERMRVFPVT-SDMRV-----
193661957       ----GIPLAKRVLIVAPSSLVGNWENEFTRWL-G-----RDRLRLFSVD-QKKKP-----
110760280       ---YGYPILKYVLIVTPSSLCNNWNKEFKHWL-G-----FHRISPYVVN-AKNKP-----
242023203       --YNKKPVIKRVLIVTPTSLIMNWYNEFIKWL-G-----RVKIVPYVVN-QKNKP-----
66811190        ----GESTAKKAVIVAPCTLVGNWGQELKKWL-------GDGVNTVAIG-EST-------
71651467        --KHGVPTARKCLVVTPSSLVKNWCNEFDKWL-G-----EGAVKYFSISESTPKGDRIIS
50311185        RGVTLAGEISKVLIVCPVTLIGNWKKEFKKWL-P-----MNRIGVLTLH-SRNSP-----
254585925       NGVPLQGLCKKIIIVCPVTLIANWKREFGKWL-N-----LSRIGILTLS-PQNNA-----
50294037        LGVPLSGMISKVVIVCPVTLIGNWKREFKKWL-G-----LNRIGILTLN-PKNNV-----
255725568       FPEQKKPVINKVLVVCPATLISNWRQEFKKWL-G-----ANKLNVLTLN-NAM-------
241952408       FLDQKNAVVNKVLVVCPVTLISNWRQEFKKWL-G-----ANKLNVLTLN-NAM-------
260941370       -FPGQKKVASKVLICCPVSLIDNWRREFTKWL-G-----TYRIGVLCLN-NKQVSP----
254567481       QVDHKRPAVKKVLVVCPVTLIHNWKREFRKWL-G-----MNRVSILEMS-SASNV-----
145230930       VY-DSPPVVKKALIVCPVTLINNWRKEFRKWL-G-----NERIGVFVFD-DKRKRLTDFT
238484253       IY-ENPPEVKKALIVCPVTLINNWRKEFRKWL-G-----NERIGVFVFD-DKRKRLTDFT
119494890       IH-ESPPVIKKALIVCPVTLINNWRKEFRKWL-G-----NERIGVFVFD-DKRKRLTDFT
225681829       IY-EAPPVIKKALIVCPVTLIDNWKKEFRKWL-G-----NERIGVFVAD-AKRTRLTDFT
258563128       IH-EAPPVVKKALIVCPVTLIKNWQKEFKKWL-G-----NDRLGVFVAD-GKHMRLTDFT
242778005       IY-EAAPVVKKALIVCPVTLINNWRKEFRKWL-G-----NERIGVFVFD-DKRKKLTDFT
212533393       IY-EASPVIKKALIVCPVTLINNWRKEFRKWL-G-----NERIGVFVFD-DKRKKLTDFT
189209013       IH-GASPVIKKALIVCPAGLVDNWKREFKKWL-G-----NERIGVYVLD-AKNKKIANFT
71019185        -----SSTIERAMIVCPLTLVKNWKREFRKWI-G-----SNSLNVLCID-EDC-------
290982366       ---FGSPIIKKAIVVTNSSLVKNWTSEFDKWV-G-----EDKIKVLTVT-TKTAK-----
281209956       ---TGQPTCKKAIIVTPAGLVGNWKREIKRWF-G-----AERLKPFTLN-DSVS------
167385507       -------NIKKIVIVCPQSLIGNWEKEFKKWL-G-----VERIPVQTGS-----------
170577655       --LNQKPIIRKCIIVVPTSLLNNWYAEFMRWS-P-----QTQTMLFRILKSTDVKKLISY
145350886       -FKRGQPTCRRVVVCVPASLTGNWALEFRKWL-G-----EERCDPKVVEGGDKEARKSFE
224013540       -------RDRRFIVVCPSSLVSNWAKEFDKWL-G----------------KASQPKRVIA
145482121       -------EISKIVITCPVSLIGNWEKEIKKWL-G-----PMRLQPLSAIGTKDEVNKQVK
145338703       --FDGTPMVKKAIIVTPTSLVSNWEAEIKKWV-------GDRIQLIALC-----------
20336209        -----KLDFSTALVVCPLNTALNWMNEFEKWQEGLKDDEKLEVSELATV-----------
242018945       ------TGVQSILILCPLSTVQNWVKEFYYWL------------------------KKCK
196005243       -----NESIQSVLVVCPKNVLLNWALEFKKWL------------------------KREN
81916664        --------AKTVLAIVPVNTLQNWLAEFNMWLPAPEALPA----------DSKPEEVQPR
75026277        --------VKTVLAIVPVNTLQNWLAEFNMWLPPPEALPA----------DNKPEEVQPR
193580055       -----QINIKTFLIICPSGLVYNWMDEIYKWLKDVDIDKVVKVYDLPKT-----------
193610723       -----QINIKTFLIICPPGLIYNWMDEIYKWLKDIDIDEVVKVYDLPKT-----------
145335288       -----DLGLKTALIVTPVNVLHNWRSEFEKWMPS--EVKPLRIFMLGDV-----------
258572168       KQIPDTFRESRTLILCPSSLIENWWEEFLMWR-PGDPESVSNLGPIRKI---------LQ
171685718       EQIPEKLRRSRTLILCPSGLVDNWVDEVNMWA-P-----EGSLGPVYKV---------DA
289615990       AQIPKDLQNGRALILCPSGLVENWADEVDMWA-P-----GGILGEIFTI-VRDERDTRTQ
164425263       AQIPKDLRVGRPLILCPSGLVENWIDEICKWA-P-----KDILGTITKI--------DAS
72391587        -----------ILIVAPKTLLQHWMQEAKKWK-------DYGLVFPGFI-VLNNVDSSSF
71662347        -----------VLILAPKIVLTHWTGEKQKWE-------KYGLVFSHFV-VSDGTDSVSF
239977156       -----------ILILTPKPIISHWVDEKNKWG-------MYGLHFPHFV-ASDGLNSLEF
146081173       -----------ILILTPKPIISHWVDEKNKWG-------MHGLHFPHFV-ASDGLNSLEF
Sm441121        --------GCRLLVLCPKMVQNVWREEFRKSQME------TPFFLSSRK-----------
Bd3g18910       --------SAR-------------------WLLH--------------------------
Bd1g74070       --------EGRPLIVLPVGILATWRTEFLRWQIE-----DIPLYDFYSS-KANNR-----
Os03g06920      --------AGRPLIILPKGILSTWRTEFLHWQVD-----DIPLYDFYSS-KADKR-----
Sb01g046180     --------AGRPLIMLPKGILGTWKSEFLCWQVE-----NIPLYDFYSS-KASSR-----
Bd3g19890       --------SGRPLVILPKGILGTWKKEFQQWQVE-----DIPLYDFYSV-KAEKR-----
Os06g14440      --------SARPLVVLPKGILGTWKREFQRWQVE-----DIPLYDFYSV-KADKR-----
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Sb07g002945  --------SARPLVVLPKGILGTWKKEIQRWQVQ-----DIPLYDFYSV-KAEKR-----
ZM093940     --------SARPLVVLPKGILVIWKKEIQRWQVQ-----DIPVYDFYSV-KAEKR-----
ZM064574     --------SARPLVVLPKGILGIWKTEIKRWQVQ-----DIPVYDFYSV-KAEKR-----
Bd2g21430    --------SARPLVVLPKGIVGTWKREFQRWQVE-----DIPLYDFYSV-NATKR-----
Bd2g21450    --------SARPLVVLPKGIVGTWKREFQRWQVE-----DMPVYDFYSV-NATKR-----
Os08g14610   --------TARPLVVLPEGILGTWKREFQQWQVE-----DIPLYDFDSI-KADNR-----
Vv35918      --------QARPLVVLPKGILATWKKEFLTWQVE-----DIPLYDFYSV-KADSR-----
Pt195587     --------HAKSLVVLPKGILPTWKREFQIWQIE-----DIPLYDFYSV-KADSR-----
AtDRD1       --------QAKPLVVLPKGILPTWKKEFVRWQVE-----DIPLLDFYSA-KAENR-----
At2g21450    --------QARPLVVLPKGIIESWKREFTLWEVE-----KIPLLDFYSV-KAESR-----
Bd2g26500    --------DCRPVIIAPRGMLFAWEEEFKKWDVN------VPFHILNTT-EYSGK-----
Os05g32610   --------DCRPVIIAPRGMLFAWEQEFKKWNVN------VPFHIMNTT-DYSGK-----
Sb09g019410  --------DCRPVIIAPRGMLFAWDEEFKKWNVD------VPFHIMNTT-DYTGK-----
RMR1         --------DCRPVIIAPRGMLFAWDEEFKKWNVD------VPFHILNTT-DYTGK-----
Bd2g43500    --------WCRPVIIAPRGMLATWEQEFKKWNVK------LPFHLLSSS-GIHWD-----
Os02g43460   --------ECCPVIIAPRGMLATWEQEFRKWKVK------VPFHVLNSK-EINWK-----
Bd3g50300    --------RSCVLIIAPKAMLATWQDEIGKWNAK------VPIHVYSSC-DINWG-----
Sb04g033300  --------RCRPVIIAPRGMLATWEKEFRKWK----------------------------
ZM178435     --------HCSPVIIAPRGMLATWEKEFRKWK----------------------------
Vv15867      --------ACRPVIIAPRTMLLTWEEEFKKWNVD------IPFHNLNKL-EYSGK-----
Pt28648      --------TSRPVIVAPCSMLLTWEAEFLKWGVD------IPFHIMNKK-NLSGK-----
Cp76.2       --------RCRPVIVAPRSMLLTWEEEFIKWRVG------IPFHNLNKS-EFSGA-----
At1g05490    --------DCKPVIIAPASLLLTWAEEFKKWNIS------IPFHNLSSL-DFTGK-----
At3g24340    --------NSHPMVIAPATLMRTWEDEVRKWNVN------IPFYNMNSL-----------
Bd1g16720    --------RSRPLIIAPKSAIHTWKREFEKWGIS------LPLHVLHHA-DSRGRSMGAI
Os07g49210   --------RSRPLVLTPKAAIHTWKREFEKWGIS------LPLHVFHHA-NRSGKPLGAM
Sb02g043870  --------RSRPLVLTPKAAIHTWRREFQKWGIL------LPLHVLHHS-NRTSKLMRGL
ZM108166     --------RSRPLVLTPKAAIHTWRTEFQKWGIL------LPLHVLHHS-NRTSKLMGGL
Vv29366      --------GKRPLVLAPKTTLYTWYKEIIKWKVP------VPVYQI-HG-CRTYRYEIYK
Pt832603     --------GKRPLVLAPKTTLYTWYKEFIKWEIP------VPVHLI-HG-TRSSR--AFK
Pt567214     --------GKRPLVLAPKTTLYTWYKEFIKWEIP------VPVLLI-HG-TRSSR--VFR
Cp19.123     --------GKRPLVLAPKTTLYTWHKEFIKWKIP------IPVHLI-HG-RRSYR--IIK
AtCLSY1      --------GKRPLVLAPKTTLYTWYKEFIKWEIP------VPVHLL-HG-RRTYC--MSK
At5g20420    --------GKRPLVLAPKTTLYTWYKEFIKWEIP------VPVHLI-HG-RRTYC--TFK
Sm84719      --------SARAMILAPKGMLLRWEEEFHKWEVA-----SLPVYILDGD-----------

                              260                 280                 300
15898471     ------------------------------------------------------------
256419642    FD----------------------------------------------------------
237794935    REEYD-------------------------------------------------------
187779742    REKYD-------------------------------------------------------
ScSNF2       ---------------------------------------------------AKQAKIRAG
83286649     TVLHS-------------------------------------------------------
124803472    NLLHS-------------------------------------------------------
74008371     ----AF--------------------------------------------IRDEMMPG--
14028669     ----AF--------------------------------------------VRDVLLPG--
56118945     ----AF--------------------------------------------VRDVLLPG--
47217344     ----AL--------------------------------------------IRDVLLPG--
157103787    ----AF--------------------------------------------IRDVLMPG--
170572145    ----DL--------------------------------------------IRNEILPG--
255719682    NKLMAC------------------------------------------------------
145610651    ERLVDE------------------------------------------------------
145353082    ----RL---------------------------------------------RKEVVPNTE
225436589    -QQYEFYTNKKTGRTI--------------------------------------------
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189521245    -RENEFTFDDTAVKGGKK--------------------------------AFKLRREAPI
47206539     -RENEFTFEDSAVKSGRK--------------------------------VFRMKKDTPI
113678140    -RENEFSFENNAIRGGKK--------------------------------PSKMKKEASV
156717248    -RENEFSFEDNAIRGGKK--------------------------------ASRMKKEASV
73997410     -RENEFSFEDNAIRGGKK--------------------------------ASRMKKEASV
115939069    -RENEFSFEDDAVKGGKK--------------------------------AYKMRQGSLV
221120608    -RNYEMTFDDDSMRKGQK--------------------------------AYKVKKDVIC
256052547    -REHEFSFDEGAVRGGAK--------------------------------AMKMRTGTSV
24666729     -RKHEISFEEVTTKTMRE-------------------------------------NQTQY
170592228    -REHEFSFIEGAVRGGPK--------------------------------PSRLKTDQGI
17569817     -REHEFSFVDGAVRGGPK--------------------------------VSKIKTLENL
256072692    -REYEFRLRN---------------------------------------------AGGIP
145341798    -REHDW--YH-PVDETQS--------------------------------ISRAF-----
145491053    -RQYEFFYTDISMKGIVL--------------------------------QASEIY----
118367847    -RFYEWLYTDISTKGTVL--------------------------------QSNEIY----
145484966    -RDYEWFYTDISLKGNTL--------------------------------PSQELY----
239899054    -ADFDMSWININNGHREKEPLKHRADPQFCP-----------------------------
291001481    -KNHEFFFKHPKTGNLIYHQKTY-------------------------------------
211853152    -QQYEMYFRDSQ-GRIIW----------------------------------GSY-----
189521372    -QQYEMYCRDSQ-GRVIR----------------------------------GAY-----
260834763    -HRYEMFHRDEL-GNIIP----------------------------------ECY-----
196012568    -RDYELYYRDSN-G--VP--------------------------------NLNAI-----
242011216    -QEYEFYFKNDK-GNLMK----------------------------------DLH-----
193599122    -QQYEMYYRNEK-GAIIK----------------------------------DIS-----
19112177     RLINQKDPKHVSTH----------------------------------------------
259147500    -QKFK-----MDENDLENLIMNSKPSDFSYEDWKNSTRTKKALESSYH--LDKLIDKVV-
254582697    --KKK-----MSEDELEDMIMSGDPNQFSYGDLENSSKTKAQVESDNL--LQTLIDKVA-
255720394    --KEN-----LSEQKLEELFMNSNPEEFSFDAYTNSKRTKSILESSLT--RDNLINKVV-
50309923     --GTQ-----IPEEELEKMLMTSNYGTFTYNDYEKKEKTRTSLESRKS--VKKLLEKVI-
146416597    -KSAL-----TSEEKIENMMANDDFD-------LNEDKFLAQQKGLSN--AKNIVDRVV-
68483838     --G-S-----VSESKLEEYLESTDPD-------ATQS-SLHGIKSQIN--AQEIVDRVM-
149235383    -KDKK-----ISEEKLEEFMEDWDPK-------TSKS-SLKGIKSQIN--AREILDKVQ-
199432721    -KNAI-----HSEEKIEAFLETTDPS-------SVKNDSFKGINSHMR--AKEIIDTVM-
254568884    -RTSL-----QNEASIEKLLEEEEYG-------STK--SLASLKAESR--VKELIDSVF-
19075591     -REKRQYESDASESEAEE---------------SKTSIKLRGASSSFHRYAKNLVESVF-
261358370    -RED--------DTDEET-----H-----------SGRRDK------S--VRKIVDRVV-
70982085     -RSES-----SREDALLSQTYSSNS--------RGITSNQK------A--ARKVVKRVV-
225682364    -RSES-----YADARLESQIWDPDQP-------RRATKEQK------A--AKKILDRVL-
239615027    -RRES-----YADARLESQLWEPDQP-------RGLTKEQK------A--AKRILKRVL-
212536498    -RNES-----NRENALNDEMWDPSRP-------YTMTKAQK------T--AKKIVQRVV-
255936215    -GKES-----SRENALTSEMMGSHSS-------RHLSAGQK------A--AKKIIKRVT-
189204870    -RRED-----RLEQEMELRKYG-DYD-------TTLTGAGK------A--AKKVLEKVK-
66813000     -DGSD---------------------------------------------KEDIVKKIA-
242056785    -SKAY-------NDSDSEGSWDSDQE------------GVRRAKPAKK--WDDLISRVV-
85014197     ------------------------------------------------------------
Cr13231      ------------------------------------------------------------
ScRAD54      TTVSQAIHAWAQAQGRNIVKP---------------------------------------
50302399     -NVADSVSHWASAQGRNIVKP---------------------------------------
156845511    ATVAHAIKSWAQAKGRNIVKP---------------------------------------
45190309     -SVAQSVRQWAIAQGRNVVKP---------------------------------------
255718981    -TVAQAVRSWALAQGRSVVKP---------------------------------------
238878261    SELGTALQQWSTAQGRNIVRP---------------------------------------
255728815    SDLGTALQQWASAQGRNIVRP---------------------------------------
149239498    NDLGLALQQWSTAQGRNIVRP---------------------------------------
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149388940    SELGGALQQWSVARGRNIVRP---------------------------------------
190348945    ADLGPALQQWSVASGRNIVRP---------------------------------------
254570653    STISSQLSQWAMATGRNIVRP---------------------------------------
189211141    EELIQQIRQWSIASGRSVVRP---------------------------------------
46127169     EELTRQLRQWANATGRSVTRP---------------------------------------
225684006    AELTSQLRQWAISSGRAVVRP---------------------------------------
259485020    TELTSQLKQWAISSGRSIVRP---------------------------------------
238840822    TELISQLRQWAIASGRSVVRP---------------------------------------
19115202     QELIMALQQWASVHGRQVTRP---------------------------------------
50546160     AELTAGLRQWAEAEGRKVTRP---------------------------------------
58266612     AELIPAVRRWVQAHGRNVTLP---------------------------------------
164660184    EQMFESVQRWADCSGRAIVHP---------------------------------------
41055574     DEIDSKLVNFISQQGMRIPTP---------------------------------------
118094595    EEIDRKLVGFMNQRGLRVPSP---------------------------------------
281351942    DEIDQKLEGFMNQRGARVPSP---------------------------------------
195539537    DEIDQKLEGFMNQRGARVPSP---------------------------------------
47575794     EEIDKKLSGFMNQHGMRVPSA---------------------------------------
156369786    DEIDRNLERYMSQQGSRTPTP---------------------------------------
238814383    SEIDAKLTGFMKTYGRRCATP---------------------------------------
170041242    EQTTKQLEQFMANQSARQGTP---------------------------------------
189238349    -DARKKLTQFMQGFG-RTAIP---------------------------------------
195161916    ENTVRALEQFSMNASTRLGTP---------------------------------------
193591979    EQVDKVITGFVQARGRRTVDP---------------------------------------
71033369     ----EKVISSFQGFKYDRTS-R--------------------------------------
221488620    ----EKVVSKFEGFKYDRQS-R--------------------------------------
157128256    ----KKYAQSAHIP----------------------------------------------
241602475    ----EGFLRQPSLYP---------------------------------------------
194214970    ----EEFTKSPFYS----------------------------------------------
281347253    ----EEFTKSPFYS----------------------------------------------
119906776    ----EEFTKSPFYS----------------------------------------------
194037038    ----EEFTKSPLYS----------------------------------------------
149045437    ----EEFINSAFHS----------------------------------------------
149638830    ----EEFIKSPFYS----------------------------------------------
45382655     ----EEFISSPLYS----------------------------------------------
148230804    ----EEFVNSPLYS----------------------------------------------
156379220    ----KEFIISP------------IYP----------------------------------
193661957    ----SEFARLPARSYP--------------------------------------------
110760280    ----NNFKKQIRNS----------------------------------------------
242023203    ----SEIKYHS-------------------------------------------------
66811190     ----KTGRAKLTELEFGKAD----------------------------------------
71651467     RFDGEGD-----------------------------------------------------
50311185     ----TEDKAQV----RSFLKVPRTYQ----------------------------------
254585925    ----ERDIYDV----KSFLRVQRTYQ----------------------------------
50294037     ----DMDKISV----RNFIKVNRTYQ----------------------------------
255725568    ----SDEKRDI----LNFGK-LNVYQ----------------------------------
241952408    ----TNEKRDI----LNFGK-LNVYQ----------------------------------
260941370    ----AKDKDDI----VNFGK-NNVYQ----------------------------------
254567481    ----EEDKRSV----INFGR-TRVYQ----------------------------------
145230930    RGRAYS------------------------------------------------------
238484253    RGRAYN------------------------------------------------------
119494890    MGRAYS------------------------------------------------------
225681829    MGQSYS------------------------------------------------------
258563128    MGMSYN------------------------------------------------------
242778005    MGKAYN------------------------------------------------------
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212533393    MGKAYN------------------------------------------------------
189209013    MGKSYN------------------------------------------------------
71019185     ------GREHVERFARSKAYH---------------------------------------
290982366    ----QSPSETLKIFKAGYHQ----------------------------------------
281209956    ----KNTKQMLEDFNTSTVNP---------------------------------------
167385507    --SDSSMKEKVNDFIRDYIP----------------------------------------
170577655    RNTSM-------------------------------------------------------
145350886    EFALPSQRRYN-------------------------------------------------
224013540    KNGGEEGLRNLRSFVPPKPQQAE-------------------------------------
145482121    YFLYSPYN----------------------------------------------------
145338703    ----ESTRDDVLSGIDSFTRPRSALQ----------------------------------
20336209     -----------KRPQERSYMLQRWQEDGG-------------------------------
242018945    KRIKIFEVVTCKTKKLKIKKIKSWKENGG-------------------------------
196005243    SYSVHTFSATLSSTKDRLRPLRLWNATKG-------------------------------
81916664     FFKVHILNDEHKTVASRAKVTADWVSEGG-------------------------------
75026277     FFKVHILNDEHKTMASRAKVMADWVSEGG-------------------------------
193580055    ------------QKLYNVTNIATWKSNGG-------------------------------
193610723    ------------QKLYNITNIATWKSKGG-------------------------------
145335288    ------------SRERRFDLLTKWRKKGG-------------------------------
258572168    SMEPWERLKEIAAWHSEGG-----------------------------------------
171685718    SLTAYVRVEVVKKWASGGG-----------------------------------------
289615990    EVKTRERILTVKQWTRSRG-----------------------------------------
164425263    TVPPSERVLLIKEWARSRG-----------------------------------------
72391587     EDDLSNYEQQGTTTNPKKSY----------------------------------------
71662347     EIALKRYKQQLNGELPRTSH----------------------------------------
239977156    EQQLLEYERQKNNEKPKAGH----------------------------------------
146081173    EQQLLEYERQRNNEKPKLGH----------------------------------------
Sm441121     ----------------------------------------SRRLEVLSRWHRQRG-----
Bd3g18910    ------------------------------------------------------------
Bd1g74070    -------------SDQ---------------------------LKVLNLWEENRS-----
Os03g06920   -------------SEQ---------------------------LKVLNLWEESRS-----
Sb01g046180  -------------PEQ---------------------------LKVLKLWEESKS-----
Bd3g19890    -------------EDQ---------------------------LKILNSWQSKMS-----
Os06g14440   -------------VEQ---------------------------LEVLKSWEAQMS-----
Sb07g002945  -------------VEQ---------------------------LQILKSWEDKMS-----
ZM093940     -------------VEQ---------------------------LQILKSWEDKMG-----
ZM064574     -------------VEQ---------------------------LQILKSWEDKMS-----
Bd2g21430    -------------EDQ---------------------------LKILYSWQSNMS-----
Bd2g21450    -------------EDQ---------------------------LKILNSWQSNMS-----
Os08g14610   -------------VEQ---------------------------LEVLKSWSSKRS-----
Vv35918      -------------PQQ---------------------------LEVLKQWVAEKS-----
Pt195587     -------------QQQ---------------------------LEVLNQWVEQKS-----
AtDRD1       -------------AQQ---------------------------LSILKQWMEKKS-----
At2g21450    -------------KQQ---------------------------LKVLGQWIKERS-----
Bd2g26500    -----------------------EDRDICRLIKKEHRTDKLTRLVKLLSWNKGHG-----
Os05g32610   -----------------------EDRDICRLIKKEHRTEKLTRLVKLFSWNRGHG-----
Sb09g019410  -----------------------EDREICKLIKKEHRTEKLTRLVKLLSWNKGHG-----
RMR1         -----------------------EDREICKLIKKEHRTEKLTRLVKLLSWNKGHG-----
Bd2g43500    -------------EDKTIKKLVAQDESLGQKLSMNKLSQKSRLMLKLASWYEGSC-----
Os02g43460   -------------EDRTIKQLAIMDENLAQSLARNKLDHKFRRKLKLASWRKGSS-----
Bd3g50300    -------------GDETIKRIVDNDEDFAQRLSVNKFGPKVRKVLKVRSWCEGSS-----
Sb04g033300  ------------------------------------------------------------
ZM178435     ------------------------------------------------------------
Vv15867      -------------ENITALNFLRRIS-------HQGQSAKSIRMVKLYSWKKDRS-----
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Pt28648      -------------ENRTAMDLFRELK-------PAERGLNAIRMVKLYSWKKERS-----
Cp76.2       -------------ENQKVINYLSQAR-------KGVRSINAIRMVKLYSWKKDGG-----
At1g05490    -------------ENSAALGLLMQKN-------ATARSNNEIRMVKIYSWIKSKS-----
At3g24340    -------------------QLSGYEDAEAVSRLEGNRHHNSIRMVKLVSWWKQKS-----
Bd1g16720    DPRMQEILSKFHRSSWKNMRFVDC-------------------MDKLCKWHASPS-----
Os07g49210   DSKLRSLLNNFHRPTWTNMRLMDS-------------------LDKLFKWHAHPS-----
Sb02g043870  SSKLQVVLKNFHQPTWKTMRIMDC-------------------LDKLCKWHEEPS-----
ZM108166     SSKLQAVLKSFHQPSWKTMRIMHC-------------------LDKLCKWHEEPS-----
Vv29366      H-KVETSPGI-PRPNQDVMHVLDC-------------------LEKIQKWHAHPS-----
Pt832603     Q-TPAALRGSGPRPSQDVVHILDC-------------------LEKMQKWHAQPS-----
Pt567214     Q-TPVALRGSCPRPSQDVVHILDC-------------------LEKMQKWHAQPS-----
Cp19.123     Q-KTVKFQGV-PRPSQDVMHVLDC-------------------LEKIHKWHAEPS-----
AtCLSY1      E-KTIQFEGI-PKPSQDVMHVLDC-------------------LDKIQKWHAQPS-----
At5g20420    QNKTVQFNGV-PKPSRDVMHVLDC-------------------LEKIQKWHAHPS-----
Sm84719      ------------------------------------------SDIKVYKWATERS-----

                               320                 340                 360
15898471     -------IILTTYAVL--------------------------------------------
256419642    -------ILITTYGTL---------------------------------------R----
237794935    -------VLLTTYGTL---------------------------------------K----
187779742    -------VLLTTYGTL---------------------------------------K----
ScSNF2       ---EFD-VVLTTFEYI---------------------------------------IK---
83286649     ---DYD-VLLTTYEIV---------------------------------------I----
124803472    ---DFD-VLLTTYEIV---------------------------------------I----
74008371     ---EWD-VCVTSYEMV---------------------------------------IK---
14028669     ---EWD-VCVTSYEML---------------------------------------IK---
56118945     ---EWD-VCVTSYEML---------------------------------------IK---
47217344     ---EWD-VCVTSYEML---------------------------------------II---
157103787    ---EWD-VCITSYEMC---------------------------------------IR---
170572145    ---KWD-VLVTSYEMV---------------------------------------LK---
255719682    ---DFD-IVVASYEII---------------------------------------IK---
145610651    ---SFD-VCITSYEMI---------------------------------------LR---
145353082    ---SYD-VAVTTYEMA---------------------------------------CNPAF
225436589    ---LFN-ALLTTYEVV---------------------------------------L----
189521245    ---KFH-VLLTSYELV---------------------------------------TI---
47206539     ---KFH-ILLTSYELI---------------------------------------TI---
113678140    ---KFH-VLLTSYELI---------------------------------------TI---
156717248    ---KFH-VLLTSYELI---------------------------------------TI---
73997410     ---KFH-VLLTSYELI---------------------------------------TI---
115939069    ---KFH-VLLTSYELI---------------------------------------SI---
221120608    ---KFH-VLLTSYELV---------------------------------------AI---
256052547    ---RFH-VLLTSYELI---------------------------------------SI---
24666729     ---KFN-VMLTSYEFI---------------------------------------SV---
170592228    ---KFH-VLLTSYELI---------------------------------------NI---
17569817     ---KFH-VLLTSYECI---------------------------------------NM---
256072692    ---AFH-VLITSHELA---------------------------------------CI---
145341798    ---KAN-IVLTTYETI---------------------------------------TA---
145491053    ---KFQ-ILITSYEVF---------------------------------------MQ---
118367847    ---KFQ-VLITSNEVF---------------------------------------LS---
145484966    ---KFQ-ILITSFEVF---------------------------------------NQ---
239899054    ---KFD-VVVTSYEIFLTCSNR--------------------------------------
291001481    ---KFN-VLITTYEIV---------------------------------------M----
211853152    ---KFH-AIITTFEMI---------------------------------------LG---
189521372    ---RFQ-AVITTFEMI---------------------------------------LG---
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260834763     ---KFQ-SLITTYEVI----------------------------------------IS---
196012568     ---KFQ-IIITTYEII----------------------------------------LS---
242011216     ---KFN-VLITTFELI----------------------------------------IT---
193599122     ---KFD-VLITTFETI----------------------------------------IS---
19112177      -------VLVISASNV----------------------------------------E----
259147500     --TDGH-ILITTYVGL----------------------------------------R----
254582697     --KDGH-VLITTYVGL----------------------------------------R----
255720394     --TDGH-VLITTYVGL----------------------------------------R----
50309923      --TDGH-IIITTYVGL----------------------------------------R----
146416597     --SKGH-VLITTYVGL----------------------------------------R----
68483838      --EKGH-VLVTTYVGL----------------------------------------R----
149235383     --EKGH-VLVTTYVGL----------------------------------------R----
199432721     --EKGH-VLVTTYVGL----------------------------------------R----
254568884     --TRGH-VIITTYVGL----------------------------------------R----
19075591      --TRGH-ILITTYAGL----------------------------------------R----
261358370     --KHGH-VLVTTYNGL----------------------------------------Q----
70982085      --EEGH-VLVTTYSGL----------------------------------------Q----
225682364     --AKGH-VLVTTYSGL----------------------------------------Q----
239615027     --EEGH-VLVTTYSGL----------------------------------------Q----
212536498     --EEGH-VLVTTYSGL----------------------------------------Q----
255936215     --EDGH-VLVTTYSGL----------------------------------------Q----
189204870     --RDGH-VLVTTYSGL----------------------------------------Q----
66813000      --EKGH-ILLTTFDSI----------------------------------------R----
242056785     --NSGSGLLLTTYEQL----------------------------------------R----
85014197      --EDCEGVYLMSYEKF----------------------------------------K----
Cr13231       -------LLLEG-------------------------------------------------
ScRAD54       -------VLIISYETL----------------------------------------R----
50302399      -------VLIISYDTL----------------------------------------R----
156845511     -------VLIISYETL----------------------------------------R----
45190309      -------VLIISYETL----------------------------------------R----
255718981     -------VLIISYETL----------------------------------------R----
238878261     -------VLIISYETL----------------------------------------R----
255728815     -------VLIISYETL----------------------------------------R----
149239498     -------VLIISYETL----------------------------------------R----
149388940     -------VLIISYETL----------------------------------------R----
190348945     -------VLIISYETL----------------------------------------R----
254570653     -------VLIVSYETL----------------------------------------R----
189211141     -------VLIVSYETL----------------------------------------R----
46127169      -------VIIVSYETL----------------------------------------R----
225684006     -------VLIVSYETL----------------------------------------R----
259485020     -------VLIVSYETL----------------------------------------R----
238840822     -------VLIVSYETL----------------------------------------R----
19115202      -------VLIASYETL----------------------------------------R----
50546160      -------VLIISYDTL----------------------------------------R----
58266612      -------VMIVSYETL----------------------------------------R----
164660184     -------VMIVSYETL----------------------------------------R----
41055574      -------ILIISYETF----------------------------------------R----
118094595     -------ILIISYETF----------------------------------------R----
281351942     -------ILIISYETF----------------------------------------R----
195539537     -------ILIISYETF----------------------------------------R----
47575794      -------ILIISYETF----------------------------------------R----
156369786     -------VLIISYETF----------------------------------------R----
238814383     -------ILIISYETF----------------------------------------R----
170041242     -------VLIISYETF----------------------------------------R----
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189238349    -------VLIISYETF---------------------------------------R----
195161916    -------VLLISYETF---------------------------------------R----
193591979    -------ILVISYETF---------------------------------------R----
71033369     -------VIISSYETY---------------------------------------R----
221488620    -------ILIASYETF---------------------------------------R----
157128256    -------ILIISYELL---------------------------------------S----
241602475    -------VLILSYEMY---------------------------------------L----
194214970    -------VLIISYEML---------------------------------------L----
281347253    -------VLIISYEML---------------------------------------L----
119906776    -------VLIISYEML---------------------------------------L----
194037038    -------VLIISYEML---------------------------------------L----
149045437    -------VLIISYEML---------------------------------------L----
149638830    -------VLIISYEML---------------------------------------L----
45382655     -------VMIISYEML---------------------------------------L----
148230804    -------VLIISYEML---------------------------------------L----
156379220    -------VLIISYEMF---------------------------------------I----
193661957    -------VMITSYEML---------------------------------------V----
110760280    -------IMIISYEML---------------------------------------I----
242023203    -------VVIISYEML---------------------------------------I----
66811190     -------VLIISYDQL---------------------------------------R----
71651467     -------VLVISYDQL---------------------------------------R----
50311185     -------VLIVGYEKL---------------------------------------L----
254585925    -------VLIIGYEKL---------------------------------------L----
50294037     -------VLILGYEKV---------------------------------------L----
255725568    -------VLVVNYEKI---------------------------------------T----
241952408    -------VLVVNYEKI---------------------------------------M----
260941370    -------VLIMSYEKT---------------------------------------L----
254567481    -------ILILGYEKL---------------------------------------Q----
145230930    -------VMIVGYEKL---------------------------------------R----
238484253    -------IMIVGYEKL---------------------------------------R----
119494890    -------VMIVGYEKL---------------------------------------R----
225681829    -------VMIIGYERL---------------------------------------R----
258563128    -------VMIIGYERL---------------------------------------R----
242778005    -------VMIIGYEKL---------------------------------------R----
212533393    -------IMIVGYEKL---------------------------------------R----
189209013    -------ILIVGYEML---------------------------------------R----
71019185     -------VMVIGYEKL---------------------------------------R----
290982366    -------VLIISYNLC---------------------------------------T----
281209956    -------VLIISYDQC---------------------------------------R----
167385507    -------VLIISYEQV---------------------------------------R----
170577655    -------IAIVSYEMI---------------------------------------A----
145350886    -------VLITSYETL---------------------------------------R----
224013540    -------VLILSYELF---------------------------------------R----
145482121    -------LLLTSYETF---------------------------------------R----
145338703    -------VLIISYETF---------------------------------------R----
20336209     -------VMIIGYEMYRNLAQGRNVKSR--------------------------------
242018945    -------VLIMSYNGFRLMTNNKKNENS--------------------------------
196005243    -------LMIISYNMYTRLLSPDKSNFDRSCND---------------------------
81916664     -------VLLMGYEMY-RLLTLKKSLATSRPKKTKKRSHPVIIDLDEEDRQQEFRR----
75026277     -------VLLMGYEMY-RLLTLKKSFATGRPKKTKKRSHPVIIDLDEEDRQQEFRR----
193580055    -------ILILSYGNFKSLVNCKQS-----------------------------------
193610723    -------ILILSYENFKSLVNCKQS-----------------------------------
145335288    -------VFLMGYTNFRNLSLGRGV-----------------------------------
258572168    -------VLLLSYDIFRAFILNRATKSRGSSLGAKVHETIKKQLLDG-------------
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171685718      -------VLIVGYSLFGNLVED--------------------------------------
289615990      -------LLIIGYEMFRTLVSKNE------------------------------------
164425263      -------VLVMGYELFRSLVSGNE------------------------------------
72391587       -------VFVINPGYI---------------------------------------K----
71662347       -------VFVINPEYI---------------------------------------R----
239977156      -------VFVINSEYL---------------------------------------A----
146081173      -------IFVINGEYL---------------------------------------A----
Sm441121       -------VLVMGFTLFMKMSLKKE------------------------YRSYMLES----
Bd3g18910      -------------------------------------------------KDKLLVI----
Bd1g74070      -------IMLLGYEHF-ARIVSEHTCDTETVK----------------CRKKLLKV----
Os03g06920     -------ILLLGYQQF-ACIVSDHTSDTEAIM----------------CQEKLLKV----
Sb01g046180    -------ILLLGYQQF-AHIISDNSSDRETIM----------------CKEKLLRV----
Bd3g19890      -------ILFLGYKQF-STIICGDGGGTVAAA----------------CRDMLLMV----
Os06g14440     -------ILFLGYKQF-SRIICGDGDGNIAAA----------------CRDRLLMV----
Sb07g002945    -------ILFLGYKQF-ATIVTDDGGSNVTAA----------------CRDRLLKV----
ZM093940       -------ILFLGYKQF-STIVTDDGGSKVTAA----------------CRDRLLKV----
ZM064574       -------ILFLGYKQF-STIVTDDGGSNVTAA----------------CRDRLLKV----
Bd2g21430      -------ILFLGYEQF-SKIICFNGDEIAGAA----------------CRDMLLMA----
Bd2g21450      -------ILFVGYEQF-SKIVCCKGDEITAPV----------------CRDMLLMV----
Os08g14610     -------ILFVGSKHF-TQIVCDDRDENAVAE----------------CRDTLLMV----
Vv35918        -------ILFLGYKQF-SSIVCGDGASKATIA----------------CQEILLKA----
Pt195587       -------ILFLGYKQF-SSIVCDDGKNQVSVT----------------CQEILLRR----
AtDRD1         -------ILFLGYQQF-STIVCDDTTDSLS------------------CQEILLKV----
At2g21450      -------ILFLGYQQF-TRIICDDNFEAASED----------------CKLILLEK----
Bd2g26500      -------ILGISYGLY-MKLTSEKSVCTEENK----------------VRSILLEN----
Os05g32610     -------VLGISYGLY-MKLTSEKVGCTGENK----------------VRTILLEN----
Sb09g019410    -------ILGISYGLY-TKLTSEKPGCTEENK----------------VRSILLDN----
RMR1           -------ILGISYGLY-TKLTSEKPGCTEENK----------------VRSILLDN----
Bd2g43500      -------IIGLSYSLY-RNLAKGED--MDGET----------------VRNLLLKN----
Os02g43460     -------IIGVSYTLF-RKLANQSS--MDGNM----------------VRNLLLEM----
Bd3g50300      -------VLGMSYEMF-SKLAKQNS--ND-ET----------------MRKLLLEK----
Sb04g033300    -------AIGEVRVLDEWKLANHEGMDGDK------------------VRKLLLEK----
ZM178435       -------ATGEARVLDERKLANHEGMDGDK------------------VRKLLLEK----
Vv15867        -------ILGISYTLF-EKLAGERDYTKVQ------------------VRKILLEL----
Pt28648        -------ILGISYRLFEELVGEEKSKTKVSDKTEDDQ-----------VRKVLLEL----
Cp76.2         -------VLGVSYRLF-EELAGEEERVKGKAKKVKARRKAKDEK----VRKVLLEL----
At1g05490      -------ILGISYNLY-EKLAGVKDEDKKTKMVREVKPDKELDD----IREILMGR----
At3g24340      -------ILGISYPLY-EKLAANKNTEGMQV-----------------FRRMLVEL----
Bd1g16720      -------VLIMTYSSF-LGLTREGSRMQQRAS----------------MVQVLINN----
Os07g49210     -------VLLMTYSSF-LGMTKQDSKVRNRYREF--------------IAEVLMNN----
Sb02g043870    -------ILLMTYSSF-LSLTKEDSKLHHQEF----------------ITKVLMNN----
ZM108166       -------ILLMTYSSF-LSLTKEDSKLRHQAF----------------ITKVLMNN----
Vv29366        -------ILLMGYTSF-LSLMREDSKF--IHRRY--------------MGEVLRQS----
Pt832603       -------VLVMGYTSF-LTLMREDSKY--NHRKY--------------MAKVLRES----
Pt567214       -------VLVMGYTSF-LTLMREDSKY--NRRKY--------------MAKVLRES----
Cp19.123       -------VLVMGYTSF-LTLMREDAKF--AHRKY--------------MAKVLRES----
AtCLSY1        -------VLVMGYTSF-LTLMREDSKF--AHRKY--------------MAKVLRES----
At5g20420      -------VLVMGYTSF-TTLMREDSKF--AHRKY--------------MAKVLRES----
Sm84719        -------VLIMTPQLLASKLAGGQGEEGDESW-------------------LLARA----

                                380                 400                 420
15898471       LRDTRL----KEVE--WKYIVIDEAQNIKNP-QT-KIFKAVKE-LKSKYRIALTGTPIEN
256419642      SDVQTL----MKLD--LDYVVLDESQAIKNP-QS-KVTKAAQL-LNTRNKLALSGTPMQN
237794935      NDIQLY----KDIT--FDYCIIDEGQNIKNP-LA-QSTDSVKR-INSKVRFALTGTPIEN
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187779742     NDFQLY----KDII--FDYCIIDEGQNIKNP-LA-QNTDSVKR-INSKVRFALTGTPIEN
ScSNF2        E-RALL----SKVK--WVHMIIDEGHRMKNA-QS-KLSLTLNTHYHADYRLILTGTPLQN
83286649      KDKSAL----YDID--WFFLVIDEAHRIKND-KS-VLSSSVRF-LKSENRLLITGTPLHN
124803472     KDKSAL----YDID--WFFLVIDEAHRIKNE-KS-VLSSSVRF-LRSENRLLITGTPLHN
74008371      E-KSVF----KKFH--WRYLVIDEAHRIKNE-KS-KLSEIVRE-FKSTNRLLLTGTPLQN
14028669      E-KSVF----KKFN--WRYLVIDEAHRIKNE-KS-NLSEIVRE-FKTTNRLLLTGTPLQN
56118945      E-KSVF----KKFN--WRYLVIDEAHRIKNE-KS-KLSEIVRE-FKTTNRLLLTGTPLQN
47217344      E-KAVF----KKFN--WRYLVIDEAHRIKNE-KS-KLSEIVRE-FKTTNRLLLTGTPLQN
157103787     E-KAVF----KKFN--WRYMVIDEAHRIKNE-KS-KLSEILRE-FKTANRLLLTGTPLQN
170572145     E-KSLL----RKYV--WQYLVIDEAHRIKNE-HS-KLSEIVRE-FKSKHRLLITGTPLQN
255719682     E-KSSF----KKID--WEYIIIDEAHRIKNE-ES-MLSQVLRE-FTSRNRLLITGTPLQN
145610651     E-KSHL----KKFA--WEYIIIDEAHRIKNE-ES-SLAQVIRL-FNSRNRLLITGTPLQN
145353082     N-VTLT----QKVM--WRCLILDEGHRVKNE-ET-AAHQVLKR-IKRQHTLLLTGTPIQN
225436589     KDKAVL----SKIK--WNYLMVDEAHRLKNS-EA-QLYTTLSE-FSAKNKLLITGTPLQN
189521245     D-QNVL----KSID--WACLVVDEAHRLKNN-QS-KFFRRLND-YKIDHKLLLTGTPLQN
47206539      D-QAIL----GSVT--WACLVVDEAHRLKNN-QS-KFFRILNG-YKIYYKLLLTGTPLQN
113678140     D-TAVL----GSID--WACLVVDEAHRLKNN-QS-KFFRILNN-YPLQHKLLLTGTPLQN
156717248     D-MAVL----GSID--WACLVVDEAHRLKNN-QS-KFFRVLNG-YSLQHKLLLTGTPLQN
73997410      D-MAIL----GSID--WACLIVDEAHRLKNN-QS-KFFRVLNG-YSLQHKLLLTGTPLQN
115939069     D-AGTL----QSVN--WDVLVVDEAHRLKNN-QS-RFFRILSG-YNIRFRLLLTGTPLQN
221120608     D-ANTL----QSID--WKVLVIDEAHRLKNN-QS-RFFRTMTS-YNIDYTLLLTGTPLQN
256052547     D-QALL----GSID--WEVLVVDEAHRLKNN-QS-KFFRILTT-YKIGYKLLLTGTPLQN
24666729      D-AAFL----GCID--WAALVVDEAHRLRSN-QS-KFFRILSK-YRIGYKLLLTGTPLQN
170592228     D-KSIL----SSIE--WAGLVVDEAHRLKNN-QS-LFFRTLRD-FRINYRLLLTGTPLQN
17569817      D-KAIL----SSID--WAALVVDEAHRLKNN-QS-TFFKNLRE-YNIQYRVLLTGTPLQN
256072692     D-RSFL----KSFD--WSVLVVDEAHRLKNK-QS-RFFRYTSQ-YHTKFKILLTGTPLQN
145341798     D-RQSF----AKAK--WSTMVVDEAHRLKRV-GG-KLGNDLNS-LAVERICLLTGTPLQN
145491053     DFQAIF----INIP--FQYIVVDEAHKLKNS-NA-RILQSLKK-LCCQRTLLLTGTPIQN
118367847     DTNNFL----INIP--FQFIVVDEAHRLKNQ-NA-KILATLKR-LPCKRTLLLTGTPIQN
145484966     DHSTYI----QQIP--FQFIIVDEAHRLKNQ-NA-KILASLKR-LVCSRIMILTGTPVQN
239899054     SNITSL----TNYN--WRVLVLDEGHRVKNH-LS-HSTKALAHIANVQHTVILTGTPIQN
291001481     AESSYL----SKIP--WQYLVVDEGHRLKNH-NS-KLAQILKN-FNAVHKLLLTGTPIQN
211853152     G-CPEL----NAIE--WRCVIFDEAHRLKNK-NC-KLLEGLKL-MNLEHKVLLTGTPLQN
189521372     G-CPEL----NAID--WRCVIIDEAHRLKNK-NC-KLLEGFKL-MSLEHKVLLTGTPLQN
260834763     D-CLEL----RDIP--WRAVIIDEAHRLKNR-NC-KLLEGLKI-LDLEHRVLLTGTPLQN
196012568     D-NPDL----RAIP--WKVVVIDEAHRLKNR-HC-KLLEGLKL-LHMDHRILLTGTPLQN
242011216     H-SQEL----KSFN--WRLCVIDEAHRLKNR-NC-KLLEGLRL-LNMEHRVLLSGTPLQN
193599122     D-CMEL----RDIG--WRLCVIDEAHRLKNR-NC-KLLEGLRA-LNLEHRVLLSGTPLQN
19112177      REISLL----RKFQ--WKVLIVDEGQRLKND-QS-SLFYYLSS-VKSDFKLLLTGTPLQN
259147500     IHSDKL----LKVK--WQYAVLDEGHKIRNP-DS-EISLTCKK-LKTHNRIILSGTPIQN
254582697     IHADKL----LKIN--WAYGILDEGHKIRNP-DS-DISLTCKK-LKTPNRLILSGTPIQN
255720394     IHSDKL----LNVR--WGYAVLDEGHKIRNP-DA-DISLTCKQ-LKTKNRIILSGTPIQN
50309923      LHSEAL----LNVR--WGYAILDEGHKIRNP-DS-DISLTCKQ-LKTQNRIILSGTPIQN
146416597     VYSKYI----LPHQ--WGYAVLDEGHKIRNP-NS-HITLTCKQ-LKTHNRIILSGTPIQN
68483838      IYSKHI----LPRE--WGYVVLDEGHKIRNP-DS-DISLTCKK-IKTVNRIILSGTPIQN
149235383     MYSKYI----LPRQ--WGYCILDEGHKIRNP-DS-DISLTCKQ-IKTVNRVILSGTPIQN
199432721     IYSKFI----LPRQ--WGYVVLDEGHKIRNP-DS-DISLTCKQ-IKTYNRIILSGTPIQN
254568884     IYSKHL----LKRD--WGYAILDEGHKIRNP-NS-DISLTCKQ-LRTPNRVILSGTPIQN
19075591      IYGDLI----LPRE--WGYCVLDEGHKIRNP-DS-EISISCKQ-IRTVNRIILSGTPIQN
261358370     TYQDEL----LHVE--WDYAVLDEGHKIRNP-NA-EITVLCKE-LRTPNRIILSGTPVQN
70982085      TYSHFL----IPVE--WGCAILDEGHKIRNP-NT-SITIHCKE-LRTPHRIILSGTPMQN
225682364     TYSSLL----IPVD--WGCSILDEGHKIRNP-DT-AITIHCKE-LRTAHRLILSGTPMQN
239615027     TYCSLL----IPVD--WGCAILDEGHKIRNP-DT-AITIHCKE-LRTAHRLILSGTPMQN
212536498     TYAPVL----IPVD--WDCAILDEGHKIRNP-NT-SITIHCKE-LRTPHRLILSGTPMQN
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255936215     SYADAL----VDVE--WGCAILDEGHKIRNP-DA-GITFSCKE-LRTPHRIILSGTPMQN
189204870     TYAEFL----IPTE--WECAILDEGHKIRNP-NT-AITIHCKE-LRTPNRIILSGTPMQN
66813000      INQEIL----LKYH--WEYVILDEGHKIRNP-DA-EITLSCKQ-LQTPHRVILSGSPIQN
242056785     ILGEKL----LDIE--WGYAVLDEGHRIRNP-NA-EITLVCKQ-LQTVHRIIMTGAPIQN
85014197      AGVKNF----L-----WDVLILDEGHRIKNK-NA-QITLSVKK-ARSRGRFVLSGTPIQN
Cr13231       ----------------CGLVVVDEAHELKNP-ES-QYYKAMQQ-VSTPRRLALTGYPLQN
ScRAD54       RNVDQL----KNCN--VGLMLADEGHRLKNG-DS-LTFTALDS-ISCPRRVILSGTPIQN
50302399      RNVEQL----KNCE--VGLMLADEGHRLKNA-DS-LTFTALDS-IRCPRRVILSGTPIQN
156845511     RNVDQL----VNCD--VGLMLADEGHRLKNA-DS-LTFTALDS-INCPRRIILSGTPIQN
45190309      RNVENL----KGCK--VGLMLADEGHRLKNG-DS-LTFTSLDS-INCPRRVILSGTPIQN
255718981     RNVEHL----RHCD--VGLLLADEGHRLKNA-DS-QTFTSLNS-IRCPRRVILSGTPIQN
238878261     RNVDKL----AGTE--VGLMLADEGHRLKNG-DS-LTFTALNS-LRCERRVILSGTPIQN
255728815     RNVDKL----AGTE--VGLMLADEGHRLKNG-ES-LTFTALNS-LRCERRVILSGTPIQN
149239498     RNVDKL----AGTE--VGLMLADEGHRLKNG-DS-LTFTALNS-LRCERRVILSGTPIQN
149388940     RNVDKL----AGTE--VGLMLADEGHRLKNG-DS-LTFTALNS-LRCERRVILSGTPIQN
190348945     RNVDKL----AGTE--VGLMLADEGHRLKNG-DS-LTFTALNA-LRCERRVILSGTPIQN
254570653     RNVESL----KGTK--VGLMLADEGHRLKNG-DS-LTFTALNS-LDCERRVILSGTPIQN
189211141     LYADEF----GQTP--IGLMLCDEGHRLKNG-DS-LTFTALNN-LNVQRRVILSGTPIQN
46127169      LNVEEL----KNTK--IGLLFCDEGHRLKNS-DS-NTFNALNS-LNVSRRVILTGTPIQN
225684006     LNVDEI----KDTQ--IGLLLCDEGHRLKNG-DS-QTFTALNS-LNVDRRVILSGTPIQN
259485020     MYVDTL----KDSP--IGLLLCDEGHRLKNK-ES-LTWTALNS-LNVQRRVILSGTPIQN
238840822     MNSDEL----RDTQ--IGLLLCDEGHRLKNA-DS-QTYVALNK-LNVQKRVILSGTPIQN
19115202      SYVEHL----NNAE--IGMLLCDEGHRLKNS-DS-LTFTALDK-LNVQRRVILSGTPIQN
50546160      RQVGAI----ADSE--VGLLLADEGHKLKNG-DS-QTFTALNQ-LNVKRRVILSGTPIQN
58266612      TLQEEL----ASCE--IGLLLADEGHRLKNA-ET-LTFQALTS-LKVQRRVILTGTPIQN
164660184     NLQELL----GNTE--IGLLLCDEGHRLKNA-DS-MTFQSLAM-LKVKRRVILSGTPIQN
41055574      LHAEVL----HKGK--VGLVICDEGHRLKNS-DN-QTYLALNS-MNAQRRVLISGTPIQN
118094595     LHAEAL----QKGS--VGLVICDEGHRLKNS-EN-QTYQALNS-LNTPRRVLISGTPIQN
281351942     LHVGVL----QKGS--VGLVICDEGHRLKNS-EN-QTYQALDS-LNTSRRVLISGTPIQN
195539537     LHVGVL----QKGS--VGLVICDEGHRLKNS-EN-QTYQALDS-LNTSRRVLISGTPIQN
47575794      LHAEVL----HRGS--VGLVICDEGHRLKNS-EN-QTYQALNS-LNTVRRVLISGTPIQN
156369786     LHAAAL----HNGS--VGLVICDEGHRLKNL-ES-QTYQALNK-LNATRRVLLSGTPIQN
238814383     LHAHVL----HQDD--VGLVLCDEGHRLKNS-EN-QTYQALMG-LKAKRRVLLSGTPIQN
170041242     LYAGIL----NNSE--VGAVLCDEGHRLKNC-EN-LTYQALMG-LKTKRRVLLSGTPIQN
189238349     MHAEIL----HKSE--IGLVLCDEGHRLKNC-EN-QTYKALMG-LKARRRVLLSGTPIQN
195161916     IYAEIL----CKYE--VGMVICDEGHRLKNS-DN-LTYQALMG-LKTKRRVLLSGTPIQN
193591979     SHASLL----QNAE-DIGLVLCDEGHRLKNC-EN-QTYRSLMA-LKAKRRVLLSGTPIQN
71033369      LHCSYL----EGVN--IDLLICDEAHRLKND-KT-RTSQSISN-SSAKMRLMLSGTPIQN
221488620     MHVHRL----EGVP--IDMVVCDEAHRLKND-KT-KTSLAIIE-LPAKKRLLLSGTPIQN
157128256     KQIREL----DSVK--FDLMICDEGHRLKNS-AI-KTSSILDA-VECPRRILLTGTPIQN
241602475     RVSDSL----ANIN--FDLLICDEAHRLKNA-NI-KIAGSLQN-LGITRKILVTGTPVQN
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281347253     RSLDQV----KNVK--FDLLICDEGHRLKNS-AI-KTTTALIS-LSCEKRIILTGTPVQN
119906776     RSLDQI----KNVK--FDLLICDEGHRLKNS-TI-KTTTALIS-LSCEKRIILTGTPVQN
194037038     RSLDQI----KNIK--FDLLICDEGHRLKNS-AI-KTTTALFS-LPCEKRIILTGTPVQN
149045437     RSLDRI----KTIT--FGLLICDEGHRLKNS-GI-KTTAALSS-LSCEKRVILTGTPVQN
149638830     RSLDQI----KNID--FNLLICDEGHRLKNN-SI-KTTTALIS-LSCDRRIILTGTPVQN
45382655      RSLDQI----QAIE--FNLLICDEGHRLKNS-SI-KTTTALTN-LSCERRIILTGTPIQN
148230804     RCLEQI----ESLD--FDLVICDEGHRLKNT-SI-KTTTSLTS-LTCSKRIILSGTPVQN
156379220     RSQDDI----MNIK--FDLFICDEAHRLKNS-AI-KTTTLISG-LKTRRRVLLTGTPIQN
193661957     RYIEEI----EKLH--FDLMVCDEGHRLKNN-ST-NTYLALTK-IECKRRVLLTGTPIQN
110760280     KYQQEI----EQIA--FDLIICDEGHRLKNN-DI-KTTKVLSN-LNCKRRILLTGTPVQN
242023203     RCVNNV----MEHN--VDLLVCDEAHRIKNS-NI-KTAQVLNQ-LNCKKKILLTGTPLQN
66811190      IYCEDI----CKIT-SIGLVICDEGHRLKNA-EI-KTTKAVSM-IPTARRVILSGTPIQN
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71651467       KYITRI----STLR-SVELVVCDEGHRLKNA-EV-KTTKAVDM-LPTRNRIILSGTPIQN
50311185       SIKDEL----QNEKRNLDLVICDEGHRLKNK-DS-KILKVLQS-LDIEKKIVLSGTPIQN
254585925      SVAQEL----ENGKNLIDLLVCDEGHRLKNG-SS-KVLNILKN-LEIPRKIILSGTPIQN
50294037       TVQEEL----LKQKDKLDLLICDEGHRLKNG-AS-KILKVLKS-LDIDKKVILTGTPIQN
255725568      IHYEEL----STIK--FDLLVCDEGHRLKNS-AN-KVLNHLIK-LNIPKKIVLTGTPIQN
241952408      AHFDEL----STVS--FDLLVCDEGHRLKNS-AN-KVLNNLIK-LNIPKKVVLTGTPIQN
260941370      SCSKEL----DALN--LDILVCDEGHRLKSG-SN-RVFKVLSA-LSVEKRLLLTGTPIQN
254567481      KLTNEI----SQIN--VDLLVCDEGHRLKNS-NN-KVMKSLTS-FQIPRKIILTGTPIQN
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238484253      TVQEGL----AQGA-GVDIIIADEGHRLKTL-QN-KSGQAIQS-LNATKRVILSGTPIQN
119494890      TVQEGL----ARGA-GVDIIIADEGHRLKTL-QN-KSGQAIQS-LNATKRIILSGTPIQN
225681829      TVQEEL----SKGS-GIDIVIADEGHRMRTV-QN-KSAQAIQT-LNTSKRVILSGTPIQN
258563128      TVQEEL----TKGR-GIDIVIADEGHRLKTV-QN-KSAQAIQS-LNTARRIILSGTPIQN
242778005      TVQEGL----LKGH-GIDIVIADEGHRLKTV-QN-KSGQAIQA-LNTAKRIILSGTPIQN
212533393      TVQDGL----LKGH-GVDIVIADEGHRLKTV-QN-KSGQAIQA-LNTAKRIILSGTPIQN
189209013      VYQEEL----KRGS-GVDIVIADEGHRLKTA-NN-KAMLAIQS-LNTERRIILSGTPLQN
71019185       SCIDIV----KTAQPPVDLIVCDEGHRLKSK-DA-QTTKMFDE-LSTERKIILSGTPIQN
290982366      NYVEEL----QDCQ--CDILICDEGHKLKNA-NI-KIFQTLKK-ISTPRRIVLSGTPLQN
281209956      IFSSIL----CTMS--CGVLVCDEGHRLKNM-ES-QTTQSIAS-IKTKAKIILSGTPIQN
167385507      SHVETL----KKTK--IGLIVCDEGHRIKNL-MS-KTNSSLKA-LGAPRHIILSGTPVQN
170577655      RTAAKL----SVVS--VDLLVCDEAHRIKNL-NG-RLREQLQI-LHAQRRLLLTGTPMQN
145350886      AQADVV----ARAN--VDLLVCDEAHRLKNATQSTKGAQALAS-LKCHRRVLLTGTPIQN
224013540      LHAKII----SKAT-RIGILVVDEGHRLKNTAGS-QTLSALNS-VDAEARILITGTPIQN
145482121      NICNEI----DKV---IDLLICDEGHRLKNS-NI-KTVQAMNQ-LKCKRRIVLSGTPIQN
145338703      MHSSKF----CQSE-SCDLLICDEAHRLKND-QT-LTNRALAS-LTCKRRVLLSGTPMQN
20336209       KLKEIFNKALVDPG--PDFVVCDEGHILKNE-AS-AVSKAMNS-IRSRRRIILTGTPLQN
242018945      KYLTAF----LNPG--PDLVVCDEGHLLKNE-KS-CLALCVSQ-LKTLRRIVLTGTPLQN
196005243      FLTQVL----LEPG--PDIVICDEGHLLKSQ-KT-KTSEILNR-IRTKRRIILTGTPLQN
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75026277       EFEKAL----CRPG--PDVVICDEGHRIKNC-QA-STSQALKN-IRSRRRVVLTGYPLQN
193580055      DLREAFYHTLVDPG--PDVVILDEGHYIKNT-RS-ILLKSLTQ-IRTKRRIVLTGTPMQN
193610723      DLREAFYHTLVDPG--PDVVILDEGHYIKNT-QT-ILLKSLTQ-IRTKRRIVLTGTPMQN
145335288      KDLNAARGICNALRDGPDILVCDEAHIIKNT-KA-DTTQALKQ-VKCQRRIALTGSPLQN
258572168      ----------------PNIIVADEAHKMKNR-NT-GIAEAASG-FKSKSRIALTGSPLAN
171685718      EELEKL----LQEK--PNIVVGDETHLIKNQ-NT-KRSRAAAH-FHTKSRIAMTGSPLTN
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164425263      DNVAEL----LHSS--PSIVICDEAHRFKNK-TS-KLYAVVQD-FHTMSRIATTGSPLTR
72391587       SFLSRV----KGFR--PALIVVDEGHCISSK-ES-KLREVLDS-LYCSARVVLTGTPVQN
71662347       TVLKKL----TGFR--PSLIIVDEGHRVSSK-GS-KLKDWLEG-LRCTARVILSGTPVQN
239977156      GFLRRF----RRFT--PFLIIVDEGHRVAAK-GN-KLTESLDR-LRCNLRVVLSGTPLQN
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Pt567214     ----------------PGMLVLDEGHNPRST-KS-RLRKVLMK-VETDLRILLSGTLFQN
Cp19.123     ----------------PGLLVLDERHNPRS------------------------------
AtCLSY1      ----------------PGLLVLDEGHNPRST-KS-RLRKALMK-VDTDLRILLSGTLFQN
At5g20420    ----------------PGLLVLDEGHNPRST-KS-RLRKALMK-VGTDLRILLSGTLFQN
Sm84719      ----------------ADVLVFDEAHYARND-NT-RIAEALKT-VRTPRRIFLSGTVFQN

                              440                 460                 480
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256419642    NTFDIYAQMNFLNPGM--LGSV---------DFF--------------------------
237794935    NLMELWSIFDFIMPGY--LYSE---------ERF--------------------------
187779742    NLMELWSIFDFIMPGY--LYSE---------ERF--------------------------
ScSNF2       NLPELWALLNFVLPKI--FNSV---------KSF--------------------------
83286649     NLKELWSLLNFLMPKI--FDNS---------EEF--------------------------
124803472    NLKELWSLLNFLMPKI--FDNS---------EEF--------------------------
74008371     NLHELWALLNFLLPDV--FNSA---------DDF--------------------------
14028669     NLHELWSLLNFLLPDV--FNSA---------DDF--------------------------
56118945     NLHELWALLNFLLPDV--FNSA---------EDF--------------------------
47217344     NLHELWALLNFLLPDV--FNSS---------EDF--------------------------
157103787    NLHELWALLNFLLPDI--FNSA---------DDF--------------------------
170572145    NLHELWALLNFLLPDM--FALA---------SDF--------------------------
255719682    NLHELWALLNFLLPDV--FSDS---------QAF--------------------------
145610651    NIHELWALLNFLLPDV--FGDS---------EAF--------------------------
145353082    NLHELYAILSFLHPDV--FTSS---------EPF--------------------------
225436589    SVEELWALLHFLDPDK--FKNK---------DDF--------------------------
189521245    NLEELFHLLNFLTPNR--FNNL---------EGF--------------------------
47206539     NLEELFHLLNFLTPER--FNNL---------EGF--------------------------
113678140    NLEELFHLLNFLTPER--FSNL---------EGF--------------------------
156717248    NLEELFHLLNFLTPER--FNNL---------EGF--------------------------
73997410     NLEELFHLLNFLTPER--FHNL---------EGF--------------------------
115939069    NLEELFHLLNFMSPDE--FNNL---------QHF--------------------------
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256052547     NLEELFHLLHFMTPEK--FNDM---------QGF--------------------------
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170592228     NLEELFHLLNFLSPDR--FYDM---------DSF--------------------------
17569817      NLEELFHLLNFLAPDR--FNQL---------ESF--------------------------
256072692     SLEELFHLLNFVEPKK--FTDF---------RAL--------------------------
145341798     NTTELWSLLNFVDSKH--FSNA---------EEF--------------------------
145491053     NTEELFSLLNFIEPYQ--FSNL---------ISF--------------------------
118367847     NTEELWTLLNYIEPNK--FASL---------QEF--------------------------
145484966     NPEELWSLLNFIEPYQ--FPNL---------NQF--------------------------
239899054     NLRELWSILHLVDKKR--FATF---------EGV--------------------------
291001481     NLTELFSLLQFLDPET--FYDL---------DVF--------------------------
211853152     TVEELFSLLHFLEPQR--FPSE---------STF--------------------------
189521372     TVEELFSLLHFLEPTR--FPSE---------NTF--------------------------
260834763     NVEELFSLLNFLEPDQ--FDSE---------ADF--------------------------
196012568     NVEELFSLLNFLEPAR--FASD---------VMF--------------------------
242011216     NVNELFSLLNFLEPAQ--FSSS---------DAF--------------------------
193599122     NVNELFSLLNFLEPTQ--FSSC---------EDF--------------------------
19112177      NVRELFNLLQFLNPMK--INAA---------EL---------------------------
259147500     NLTELWSLFDFIFPGK--LGTL---------PVF--------------------------
254582697     NLTELWSLFDFIFPGK--LGTL---------PIF--------------------------
255720394     NLTELWSLFDFIFPGR--LGTL---------PVF--------------------------
50309923      NLTELWSLFDFVYPGK--LGTL---------PVF--------------------------
146416597     NLIELWSLFDFVFPGR--LGTL---------PVF--------------------------
68483838      NLIELWSLFDFVFPGR--LGTL---------PVF--------------------------
149235383     NLTELWSLFDFVFPGR--LGTL---------PVF--------------------------
199432721     NLIELWSLFDFIFPGR--LGTL---------PVF--------------------------
254568884     NLTELWSLFDFIFPGR--LGTL---------PVF--------------------------
19075591      NLTELWNLFDFVFPGR--LGTL---------PVF--------------------------
261358370     NLSELWSLFDFIYPMR--LGTL---------VTF--------------------------
70982085      NLTELWSLFDFVFPMR--LGTL---------VNF--------------------------
225682364     NLTELWSLFDFVFPMR--LGTL---------VNF--------------------------
239615027     SLTELWSLFDFVFPMR--LGTL---------VNF--------------------------
212536498     NLSELWSLFDFVFPMR--LGTL---------VDF--------------------------
255936215     SLVDLWSLFDFVFPMR--LGNL---------VTF--------------------------
189204870     NLTELWSLFDFVFPMR--LGTL---------VNF--------------------------
66813000      KLTELWSLFDFVFPGR--LGTL---------PIF--------------------------
242056785     KLSELWSLFDFVFPGK--LGVL---------PVF--------------------------
85014197      NLGELWSIFDFVNPGL--LGSH---------TSF--------------------------
Cr13231       NLEEYFAMISWAQPDL--LGTQ---------QQF--------------------------
ScRAD54       DLSEYFALLSFSNPGL--LGSR---------AEF--------------------------
50302399      DLSEYFALLNFSNPGL--LGSR---------NDF--------------------------
156845511     DLSEYFALLNFSNPGL--LGSR---------SEF--------------------------
45190309      DLSEYFALLNFSNPGL--LGTR---------AQF--------------------------
255718981     DLSEYFALLNFSNPGL--LGSR---------LEF--------------------------
238878261     DLSEYFSLLNFANPGY--LGTR---------IEF--------------------------
255728815     DLSEYFALLNFANPGY--LGTR---------NEF--------------------------
149239498     DLSEYFSLLNFANPGY--LGTR---------NDF--------------------------
149388940     DLSEYFSLLNFANPGY--LGTR---------NDF--------------------------
190348945     DLSEYFSLLNFSNPGY--LGTR---------NDF--------------------------
254570653     DLSEYFSLLTFANPGL--LGTR---------NEF--------------------------
189211141     DLSEYFALLNFANPNY--LGTR---------MEF--------------------------
46127169      DLTEYFSLTSFANPDL--LGTR---------LEF--------------------------
225684006     DLSEYFSLLNFANPNI--LGTR---------SEF--------------------------
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259485020      DLSEYFALLNFANPDL--LGSQ---------NEF--------------------------
238840822      DLSEYFSLLDFANPGI--LGSR---------SEF--------------------------
19115202       DLSEYFSLLNFANPGL--LGSR---------QEF--------------------------
50546160       DLLEYFSLLNFSNPGL--LGTK---------GEF--------------------------
58266612       DLSEYFALLNFANPEY--LGSK---------LDF--------------------------
164660184      DLSEYFALINFAIPDM--LGNR---------NEF--------------------------
41055574       DLLEYFSLVHFVNSGI--LGTA---------QEF--------------------------
118094595      DLLEYFSLVHFVNSGI--LGTA---------QEF--------------------------
281351942      DLLEYFSLVHFVNSGL--LGTA---------HEF--------------------------
195539537      DLLEYFSLVHFVNSGI--LGTA---------QEF--------------------------
47575794       DLLEYFSLVHFVNAGI--LGTA---------QEF--------------------------
156369786      DLLEYFSLVHFVNQGI--LGTV---------SEF--------------------------
238814383      DLLEYFSLIHFVNSGL--LGTA---------AEF--------------------------
170041242      DLTEYYSLLHFVNPGM--LGSS---------NEF--------------------------
189238349      DLLEYFSLVHFVNEGL--LGSA---------QEF--------------------------
195161916      DLTEYFSLVNFVNPEM--LGTA---------ADF--------------------------
193591979      DLLEYFSLVHFVNEGI--LGTA---------QEF--------------------------
71033369       DLNEFYSLVSLCNPDV--LGDV---------NSF--------------------------
221488620      DLDEFFALVSLCNPNV--VGDA---------HTF--------------------------
157128256      DLQEFYSLITFVNPGL--LGTY---------SEF--------------------------
241602475      DLQEFFTLIDFCNPGI--LGKYPYVCQRIGPSSF--------------------------
194214970      DLQEFFALIDFVNPGI--LGPL---------SSY--------------------------
281347253      DLQEFFALIDFVNPGI--LSSL---------SSY--------------------------
119906776      DLQEFFTLIDFVNPGI--LGSL---------SAY--------------------------
194037038      DLQEFFSLIDFVNPGI--LGSL---------SCY--------------------------
149045437      DLQEFFALVDFVNPGI--LGSL---------SSY--------------------------
149638830      DLQEFYALIEFVNPGI--LGSL---------STY--------------------------
45382655       DLQEFYALIEFVNPGV--LGSL---------STY--------------------------
148230804      DLQEFFALIEFVNPAV--LGSL---------STY--------------------------
156379220      DLKEFHTLIELCNPGV--LGTL-----------F--------------------------
193661957      ELAEFYALIDFVNPGI--LGTY---------SMF--------------------------
110760280      DLQEFFALIDFVNPVI--LGSS---------SEF--------------------------
242023203      DLQELYTLIDFANPNI--LGSP---------SQF--------------------------
66811190       DLTEFYAMVNFVNPGV--LKNV---------ATF--------------------------
71651467       DLSEFHAMVGFVNPGI--LGSR---------DVF--------------------------
50311185       DLEEFYTIIDFINPGI--LGSF---------GRF--------------------------
254585925      DLNEFFTIIDFINPGV--LGSY---------PFF--------------------------
50294037       DLNEFFTIIDFVNPGV--LGTY---------ASF--------------------------
255725568      ELIEFHTLISFLNPGV--LPEL---------KTF--------------------------
241952408      ELVEFHTLISFLNPKV--LPEL---------KLF--------------------------
260941370      DLNEFYTIINFINPGI--LGTQ---------SEF--------------------------
254567481      DLNEFYNIINFVQPGI--VGDF---------ASF--------------------------
145230930      DLKEFFAAVDLVNPGV--LGTF---------KSF--------------------------
238484253      DLKEFFAAVDLVNPGV--LGNF---------KAF--------------------------
119494890      DLKEFFAAVDLVNPGI--LGNF---------KAF--------------------------
225681829      DLTEFFAMVDFVNPGI--LGTF---------KMF--------------------------
258563128      DLSEFFAMVDFVNPGL--LGTF---------KMF--------------------------
242778005      DLSEFFAAVDLVNPGI--LGTY---------KNF--------------------------
212533393      DLSEFFAAVDLVNPGI--LGTY---------RNF--------------------------
189209013      DLGEFYTAIDFVNPGL--LGQR---------AAF--------------------------
71019185       NLSELYAMIDFVIPDL--LGKP---------ESF--------------------------
290982366      DLNEFFTICDFINPGL--LGDA---------TSF--------------------------
281209956      DLIEFYSMVDFCNPGS--LGTL---------SQF--------------------------
167385507      GLEDFYSLIEFCSPGC--LGTL---------SSF--------------------------
```

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170577655     DLEEFYSLVNFARPDL--FISF---------LEF--------------------------
145350886     NLDELWGVMDFAAPGL--LGDL---------DSF--------------------------
224013540     NLSEFYNVANFALPGI--LGEL---------SDF--------------------------
145482121     NMKEFYACCDFVNPGI--FSSY---------KTF--------------------------
145338703     DLEEFFAMVNFTNPGS--LGDA---------AHF--------------------------
20336209      NLIEYHCMVNFIKENL--LGSI---------KEF--------------------------
242018945     NLIEYFCMVEFVKPSI--LGTK---------REF--------------------------
196005243     NLSEYYYMVNFVKPRL--LGSM---------SEF--------------------------
81916664      NLIEYWCMVDFVRPDF--LGTR---------QEF--------------------------
75026277      NLIEYWCMVDFVRPDF--LGTR---------QEF--------------------------
193580055     SLKEYYTLVEFVKPNI--LGNF---------TDF--------------------------
193610723     SLKEYHTLVEFVKPNI--LGNL---------TDF--------------------------
145335288     NLMEYYCMVDFVREGF--LGSS---------PEF--------------------------
258572168     HLEEYYSMINWIAPGY--LGDF---------VQF--------------------------
171685718     NVMDYYAMINWVSPGY--LSDI---------EEF--------------------------
289615990     NVMDYYSMINWVAPNY--LSDV---------GEF--------------------------
164425263     NVMDYYSMINWVAPNY--LSDV---------GEF--------------------------
72391587      NAEELYRLVGWVDDKVHSTLPQ---------RDF--------------------------
71662347      NAEELYRLIGWINSDVHSVLPP---------RVF--------------------------
239977156     DASELYRLVGWVNKGVSKVLPP---------KRF--------------------------
146081173     DASELYRLVGWVNKGVSRVLPP---------KRF--------------------------
Sm441121      TFEELFNLIFLARPNF--IQQL--------------------------------------
Bd3g18910     HVKEVFNILNLVRPKFLKMRSS----------------RRIVRRIM--SQAIV-AGCSSS
Bd1g74070     HVSEVFNILNLVRPNFLKMERS----------------RAIVKRIL--SKVDM-FGKSAW
Os03g06920    HVREVFNILKLVRSKFLKMDKS----------------RAIVNCIL--SKVDL-MGKSAR
Sb01g046180   HVSEVFNILNLVRPRFLKMQRS----------------RAIMKSIL--TKLDM-SGMAIR
Bd3g19890     HVGEVFNILNLVRPKFLRMESS----------------RPIVRRIM--SQVAI-SGTRVS
Os06g14440    HVSEVFNILDLVRPKFLKMESS----------------RPIARRIM--SQVAI-SGIRSL
Sb07g002945   HVEEVFNILNLVRPKFLRMESS----------------RPIARRIM--SQVEI-SG-RGS
ZM093940      HVEEVFNILNLVRPKFLRMESS----------------RPIARRIM--SQVEI-FG-RSS
ZM064574      HVEEVFNILNLVRPKFLRMESS----------------RPTARRIM--SQVEI-VG-RSS
Bd2g21430     HVKEVVSILNLVRPKFLNTGST----------------RPIARRSM--SQVAI-SGKKIP
Bd2g21450     HVKEVVSILNLVRPKFLNTGSS----------------RLIARRIM--SQVAI-SGRRIP
Os08g14610    HVKEVFNTLDLVRPGFLKTETF----------------WPIVTRMM--GQLEI-------
Vv35918       HVKEVFNILNLVRPKFLKLESS----------------RAVVKRIM--SKVDI-MGVRKQ
Pt195587      HAKEVFNVLNLVRPKFLRMDTS----------------RAIVKRIL--SKVNI-PGARKQ
AtDRD1        HVKEVFNILNLVRPKFLKLDTS----------------KSAVKRILAYTPCDV-RGRLTG
At2g21450     NVEEVFNILDLVRPKFLKRPGT----------------REIVSRIM--SKAEIPRGKQVN
Bd2g26500     NFLELYNILCLVRPRF------------------------------GEMFLTKTKVGRRH
Os05g32610    NFLELYNILCLVRPRF------------------------------GEMFLTKTRVGRRH
Sb09g019410   NFLELYNILCLVRPRF------------------------------GEMFLTKGRVGRRH
RMR1          NFLELYNILCLVRPRF------------------------------GEMFLTKSRVGRRH
Bd2g43500     NFLELYNILCLVKPKF------------------ARDFACTRLNKKDFSSKRTCQSRATH
Os02g43460    SFLELSNVLYLIRPKF-------------------------------------ARHFASK
Bd3g50300     NFEELYNVLCLLQGTC---------------------------------------DADSK
Sb04g033300   NFEELKNTLRLVRTKE----------------------------------ADGPKEADAV
ZM178435      NFEELYNTLRLVRPKD----------------------------------------ADAL
Vv15867       NFKELYNTLCLVRPKF--ADRI--------------------------AVEQYGGFRGKR
Pt28648       NFDELYNTLCLVKPKF--ADE--------------I------S-----SKHHRACPKRRR
Cp76.2        NFDELFNTLCLVLPKF-----------------------------GDTISPGDDKDHKRH
At1g05490     NFLELCNVLGLARPKY--LER---------------------------------------
At3g24340     NFKELSNVLCLARPAD--------------------------------------------
Bd1g16720     NFEEYFNTLSLARPRF--------------------VDDVMAALVMERKKEMRGRRAKHR
Os07g49210    NFEEYFNTLCLARPRF--------------------IGDIMSELVPERKRETVGRRAKHQ
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Sb02g043870  NFEEYFNTLSLARPRF--------------------VNDVMTTLVPESEKKTRSRTGKHQ
ZM108166     NFEEYFNTLSLARPRF--------------------VNDVMTTLVTESEKRTRSRTGKHQ
Vv29366      NFSEYFNTLCLARPKF--------------------VNEVLRELDPKFKRNKNRRKRRYS
Pt832603     NFCEYFNTLTLARPMF--------------------IKEVLKALDPKFKRKKKGAQKARH
Pt567214     NFCEYFNTLCLARPLF--------------------IREVLKALDPKFKRKKKGAQKARH
Cp19.123     ------------------------------------------------------------
AtCLSY1      NFCEYFNTLCLARPKF--------------------VHEVLVELDKKFQTNQ-AEQKAPH
At5g20420    NFCEYFNTLCLARPKF--------------------IHEVLMELDQKFKTNH-GVNKAPH
Sm84719      NLDELYNLFTLCRPSF--------------------------------LTPVLERFEFDA

                               500                 520                 540
15898471     ------KSKFATPIKKGD------------------------------------------
256419642    ------RNEFATPIDKFQ------------------------------------------
237794935    ------QEKFIDEVEENI------------------------------------------
187779742    ------QEKFIDEVETNI------------------------------------------
ScSNF2       ------DEWFNTPFANTG------------------------------------------
83286649     ------DNLFNIS-----------------------------------------------
124803472    ------DNLFNIS-----------------------------------------------
74008371     ------DSWFD-------------------------------------------------
14028669     ------DSWFD-------------------------------------------------
56118945     ------DSWFD-------------------------------------------------
47217344     ------DSWFD-------------------------------------------------
157103787    ------DSWFD-------------------------------------------------
170572145    ------DSWFT-------------------------------------------------
255719682    ------DDWFS-------------------------------------------------
145610651    ------DQWFS-------------------------------------------------
145353082    ------DKAFNLNTSEH-------------------------------------------
225436589    ------VQNYK-NLSSFN------------------------------------------
189521245    ------LEEFA-------------------------------------------------
47206539     ------LEEFA-------------------------------------------------
113678140    ------LEEFA-------------------------------------------------
156717248    ------LEEFA-------------------------------------------------
73997410     ------LEEFA-------------------------------------------------
115939069    ------LAEFA-------------------------------------------------
221120608    ------LAEFE-------------------------------------------------
256052547    ------LDEFA-------------------------------------------------
24666729     ------QAEFT-------------------------------------------------
170592228    ------THEFA-------------------------------------------------
17569817     ------TAEFS-------------------------------------------------
256072692    ------SEQWA-------------------------------------------------
145341798    ------EEAFGGMAKAAQ------------------------------------------
145491053    ------KREYG-------------------------------------------------
118367847    ------KEQFG-------------------------------------------------
145484966    ------KSQFG-------------------------------------------------
239899054    ------VAELQKDTPDEG------------------------------------------
291001481    ------SEEYG-------------------------------------------------
211853152    ------MQEFGDLKTEEQ------------------------------------------
189521372    ------MQEFGDLKTEEQ------------------------------------------
260834763    ------LSEFGDLKTEDQ------------------------------------------
196012568    ------LSEFGNLKTEAQ------------------------------------------
242011216    ------LQEFGALKTESE------------------------------------------
193599122    ------LQEFGALKSETE------------------------------------------
19112177     ------EKRYSII-----------------------------------------------
259147500    ------QQQFVIPINIGC------------------------------------------
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254582697     ------QQQFVQPINMGG------------------------------------------
255720394     ------QQQFSVPINMGG------------------------------------------
50309923      ------QQQFANPINMGG------------------------------------------
146416597     ------EQQFSIPINMGG------------------------------------------
68483838      ------QQEFSIPINIGG------------------------------------------
149235383     ------EQQFSVPIKIGG------------------------------------------
199432721     ------EQQFSVPINMGG------------------------------------------
254568884     ------QNQFAIPINVGG------------------------------------------
19075591      ------QNQFALPINIGG------------------------------------------
261358370     ------RTQFEVPIKQGG------------------------------------------
70982085      ------RNQFEFPIRQGG------------------------------------------
225682364     ------RNQFEFPIRQGG------------------------------------------
239615027     ------RNQFEFPIRQGG------------------------------------------
212536498     ------RNQFEFPIRQGG------------------------------------------
255936215     ------KNQFEIPIRQGG------------------------------------------
189204870     ------RNQFEFPIKRGG------------------------------------------
66813000      ------KSQFSLPISVGG------------------------------------------
242056785     ------ETEFSVPITVGG------------------------------------------
85014197      ------NEEFEEVIRRGG------------------------------------------
Cr13231       ------RAEFATIIRKGGWKLAGAGGAGSTEGAGEGVRTGAGGRLGGDGWGRGARGGADS
ScRAD54       ------RKNFENPILRGR------------------------------------------
50302399      ------RKNFELPILQSR------------------------------------------
156845511     ------RRNFEIPILAGR------------------------------------------
45190309      ------RKNFEIPILRGR------------------------------------------
255718981     ------RKNFELPILRGR------------------------------------------
238878261     ------KKNYENAILKGR------------------------------------------
255728815     ------KKNFENAILRGR------------------------------------------
149239498     ------RRNFENAILRGR------------------------------------------
149388940     ------KKNFENKILKGR------------------------------------------
190348945     ------RKNFENAILRGR------------------------------------------
254570653     ------RKNYENPILRGR------------------------------------------
189211141     ------RKHYEIPILKGR------------------------------------------
46127169      ------RKRYEIPILRGR------------------------------------------
225684006     ------HKKFEMPILRGR------------------------------------------
259485020     ------RKRFEIPILKGR------------------------------------------
238840822     ------HKTYEIPILRGR------------------------------------------
19115202      ------RKNYEIPILKGR------------------------------------------
50546160      ------RKNYEIPILKGR------------------------------------------
58266612      ------KKNFESKILRGR------------------------------------------
164660184     ------RKHFELDILRGR------------------------------------------
41055574      ------KKRFEIPILKGR------------------------------------------
118094595     ------KRHFELPILKGR------------------------------------------
281351942     ------KKHFELPILKGR------------------------------------------
195539537     ------KKHFELPILKGR------------------------------------------
47575794      ------KKRFEIPILKGR------------------------------------------
156369786     ------KRKFETPILRGR------------------------------------------
238814383     ------RKKFENPILRGQ------------------------------------------
170041242     ------RRQFENPILRGQ------------------------------------------
189238349     ------KKKFENPILRGQ------------------------------------------
195161916     ------KRNFENCILRGQ------------------------------------------
193591979     ------RRQYETPIVRGQ------------------------------------------
71033369      ------RRNFA-------------------------------------------------
221488620     ------RRRYANPILVGR------------------------------------------
157128256     ------KTKFENPILQSQ------------------------------------------
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241602475    ------RRVYEEPILQSR------------------------------------------
194214970    ------RKIYEEPIILSR------------------------------------------
281347253    ------RKIYEEPIIISR------------------------------------------
119906776    ------RKIYEEPIIISR------------------------------------------
194037038    ------RKIYEEPIITSR------------------------------------------
149045437    ------RRIYEEPIVMSR------------------------------------------
149638830    ------RKIYEEPIIRSR------------------------------------------
45382655     ------RKIYEEPIVRSR------------------------------------------
148230804    ------RKVFEEPIVRSR------------------------------------------
156379220    ------RRVYEQPIVNGQ------------------------------------------
193661957    ------KREFEDKIVESQ------------------------------------------
110760280    ------KNYYEKPIVASQ------------------------------------------
242023203    ------RIQFADPIIASR------------------------------------------
66811190     ------KNVYDAPIVASR------------------------------------------
71651467     ------ARVFEEPVMQGR------------------------------------------
50311185     ------KREYILPIARSR------------------------------------------
254585925    ------KKRFMTPITKAR------------------------------------------
50294037     ------KKLYINPISRAR------------------------------------------
255725568    ------QRNYVNPISRAR------------------------------------------
241952408    ------QRNFITPISRAR------------------------------------------
260941370    ------QKNYLRPILRAR------------------------------------------
254567481    ------NRDYMRPILQAR------------------------------------------
145230930    ------VREFEGPIVKSR------------------------------------------
238484253    ------VREFEVPIVKSR------------------------------------------
119494890    ------VREFEGPIVKSR------------------------------------------
225681829    ------MKQFEGPIVKSQ------------------------------------------
258563128    ------MKEFEGPIVKSR------------------------------------------
242778005    ------MKEFEGPIVRSQ------------------------------------------
212533393    ------MKEFEGPIVRSQ------------------------------------------
189209013    ------KRTFEAPIIRSR------------------------------------------
71019185     ------KTLFEEPILRSR------------------------------------------
290982366    ------KNLFTEPIKKSQ------------------------------------------
281209956    ------KKDYANPIIRGR------------------------------------------
167385507    ------KRVFAIPIQKAQ------------------------------------------
170577655    ------------------------------------------------------------
145350886    ------RKIYSGPIEKAS------------------------------------------
224013540    ------RRLYERPMSQAN------------------------------------------
145482121    ------KLVFQDPIEMSM------------------------------------------
145338703    ------RHYYEAPIICGR------------------------------------------
20336209     ------RNRFINPIQNGQ------------------------------------------
242018945    ------MNGFVNPIKNGQ------------------------------------------
196005243    ------KNRFINPIRNGL------------------------------------------
81916664     ------SNMFERPILNGQ------------------------------------------
75026277     ------SNMFERPILNGQ------------------------------------------
193580055    ------ITTFIKPIDAGQ------------------------------------------
193610723    ------VTTFIKPIDAGQ------------------------------------------
145335288    ------RNRFQNPIENGQ------------------------------------------
258572168    ------KAKYVEPIEAGL------------------------------------------
171685718    ------RSRFGNPIKEGL------------------------------------------
289615990    ------NQKYAEPISLGL------------------------------------------
164425263    ------NQKYAEPISLGL------------------------------------------
72391587     -------NEFSNSINRYV------------------------------------------
71662347     -------TDLAGTINRYI------------------------------------------
239977156    -------QELANSINQFV------------------------------------------
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146081173      -------QELANDINQFV------------------------------------------
Sm441121       QMEDRARRWFIKEIGRKF------------------------------------------
Bd3g18910      KK---ADEVFAESVEATL------------------------------------------
Bd1g74070      SKNT-SDKCFYDMVEENL------------------------------------------
Os03g06920     SKNI-SDKDFFDLVQEHL------------------------------------------
Sb01g046180    SKMI-SEKVFFELIEENL------------------------------------------
Bd3g19890      KGVP--DNVFTESVEETL------------------------------------------
Os06g14440     KGVH--DSAFTESVEDTL------------------------------------------
Sb07g002945    KGFA--DSAFTEAVEGTL------------------------------------------
ZM093940       KGLA--DGAFTEAVEGTL------------------------------------------
ZM064574       KGLA--DGAFTKAVEETL------------------------------------------
Bd2g21430      KDPRKFDKVFAESVEETL------------------------------------------
Bd2g21450      KDPRKFDKAFAESVEETL------------------------------------------
Os08g14610     -SSARSITEISESMEDTL------------------------------------------
Vv35918        LKSN-AADAFYDLVENTL------------------------------------------
Pt195587       FKAG-ADAAFYDLVEQTI------------------------------------------
AtDRD1         SNSD-MASMFNETVEHTL------------------------------------------
At2g21450      QSSSSIEGTFFAAVELTL------------------------------------------
Bd2g26500      YVSKKQRDKFSDKYEKGV------------------------------------------
Os05g32610     CVSKKQRDKFSDKYEKGV------------------------------------------
Sb09g019410    YVSKKQKDKFSDKYEKGV------------------------------------------
RMR1           YVSKKQKDKFSDKYEKGV------------------------------------------
Bd2g43500      HLEEDEGKEFWKSLRMSN------------------------------------------
Os02g43460     SFKKIGLEDYWTSLTLNN------------------------------------------
Bd3g50300      LLGKDEDKGFWTSMSVDN------------------------------------------
Sb04g033300    HLETDEGKDFWSSLRLND------------------------------------------
ZM178435       HLETDESKDFWSSLRLND------------------------------------------
Vv15867        GRKSNAARGKWDLLTSSI------------------------------------------
Pt28648        CKRNTDARRNWASLTTAI------------------------------------------
Cp76.2         ARKRSEAKGKWTSLTSSM------------------------------------------
At1g05490      -LTSTLKKSGMTVTKRGK------------------------------------------
At3g24340      ------KDTISSRIHELS------------------------------------------
Bd1g16720      --EAVARRIFVERVAQKM------------------------------------------
Os07g49210     --EAVARRAFVEKVGQKI------------------------------------------
Sb02g043870    --EALARRIFVERVGQKI------------------------------------------
ZM108166       --EALARHVFVERVGHKI------------------------------------------
Vv29366        STESRARKFFTDEIAKRI------------------------------------------
Pt832603       LLESRARKFFIDNIASKI------------------------------------------
Pt567214       FLESRARKFFIDNIASKI------------------------------------------
Cp19.123       ------------------------------------------------------------
AtCLSY1        LLENRARKFFLDIIAKKI------------------------------------------
At5g20420      LLENRARKLFLDIIAKKI------------------------------------------
Sm84719        SKDDAERHFFKEMIENRL------------------------------------------

                                560                 580                 600
15898471       ------------------------------------NMAKEELKAIISP--FIL-RRTKY
256419642      -----------------------------------DEERKDHLRKLIYP--FIL-RRTKE
237794935      ----------------------------------------DKLKTLIRP--FIL-RREKK
187779742      -----------D------------------------KLKT-----LIRP--FIL-RREKK
ScSNF2         ---------GQD-------------K--IELSEEETLLVIRRLHKVLRP--FLL-RRLKK
83286649       -------------------------K--ISTNDNKQSEIITQLHTILKP--FML-RRLKV
124803472      -------------------------K--ISTNDNKQSEIITQLHTILKP--FML-RRLKV
74008371       -------------------------T--KNCLGD--QKLVERLHAVLKP--FLL-RRIKT
14028669       -------------------------T--NNSLGD--QKLVERLHMVLRP--FLL-RRIKA
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56118945       -------------------------T--NNCLGD--QKLVERLHMVLKP--FLL-RRIKA
47217344       -------------------------T--NNCLGD--QKLVERLHTVLRP--FLL-RRIKA
157103787      -------------------------A--NECIGD--NKLIERLHAVLKP--FLL-RRLKS
170572145      ----------------------------NDMMGN--QDLVARLHKVLKP--FLL-RRLKS
255719682      ----------------------------SESSEEDKGTIVKQLHTVLQP--FLL-RRLKN
145610651      ------------------------------GEGQDSDTVVQQLHRVLRP--FLL-RRVKA
145353082      -------------------------KVDSNL--------LEKAHFLMRP--FIL-RRVKG
225436589      ---------EME---------------------------LANLHMELRP--HIL-RRVIK
189521245      ---------DIS-------------K--EDQ--------IKKLHDLLGP--HML-RRLKA
47206539       ---------DIS-------------K--EDQ--------IKKLHDLLGP--HML-RRLKA
113678140      ---------DIA-------------K--EDQ--------IKKLHDMLGP--HML-RRLKA
156717248      ---------DIA-------------K--EDQ--------IKKLHDMLGP--HML-RRLKA
73997410       ---------DIA-------------K--EDQ--------IKKLHDMLGP--HML-RRLKA
115939069      ---------DIS-------------K--EDQ--------IKKLHDMLGP--HML-RRLKA
221120608      ---------DIA-------------K--EDQ--------IKKLHEMLGP--HML-RRLKG
256052547      ---------DIS-------------K--EEQ--------VKKLHDMLGQ--HLL-RRLKA
24666729       ---------DVS-------------K--EEQ--------VKRLHEILEP--HML-RRLKA
170592228      ---------EIS-------------K--EDQ--------IQKLHSLLGP--HML-RRLKA
17569817       ---------EIS-------------K--EDQ--------IEKLHNLLGP--HML-RRLKA
256072692      ---------EMP-------------K--TDR--------IKHLHDLLNR--HLL-RRLKC
145341798      ---------------------------------------VERLQKVLGP--YLL-RRLKR
145491053      ---------QLE-------------T--SDQ--------VEKLNVLLKP--YIL-RRQKE
118367847      ---------ELQ-------------N--KEQ--------VDNLQVKIKP--FLL-RRMKE
145484966      ---------DLN-------------T--AEQ--------IEKLNKTLKP--YIL-RRQKE
239899054      ---------QSGSATSNHGDGSSEGK--KSEIDSVANLDLDKVTEVLRP--YML-RRYKS
291001481      ------------------------------NLGESGSEKLEGLHKLISP--YIL-RRLKE
211853152      ---------------------------------------VQKLQAILKP--MML-RRLKE
189521372      ---------------------------------------VQKLQAILKP--MML-RRLKE
260834763      ---------------------------------------VSKLQALLKP--MML-RRLKE
196012568      ---------------------------------------VDKLQTILKP--MML-RRLKE
242011216      ---------------------------------------VNKLQAILKP--MML-RRMKE
193599122      ---------------------------------------VQKLQLLLKP--MML-RRLKE
19112177       -------------------------D--TEK--------VTELHQILKP--FFL-RRVKS
259147500      ---------YAN-------------A--TNIQVQTGYKCAVALRDLISP--YLL-RRVKA
254582697      ---------YAN-------------A--TNIQVQTGYKCAVALRDLISP--YLL-RRVKA
255720394      ---------YAN-------------A--TNIQVQTGYKCAVALRNLISP--YLL-RRIKA
50309923       ---------YAN-------------A--SNIQVKTGYKCAVALRDLISP--YLL-RRVKS
146416597      ---------YAN-------------A--SNVQVQTGYKCAVVLRDLISP--YLL-RRLKS
68483838       ---------YAN-------------S--NNLQVKTAYKCAVVLRDLISP--YML-RRLKS
149235383      ---------YAN-------------S--NNLQVKTAYKCAVVLRDLISP--YLL-RRLKK
199432721      ---------YAN-------------A--SNVQVQTGYKCAVILRDLISP--YLL-RRLKS
254568884      ---------YAN-------------A--TNLQVQVGYKCAVTLKDLISP--YLL-RRVKA
19075591       ---------YAN-------------A--SNVQVQTAYKCACMLRDLISP--YLL-RRMKL
261358370      ---------YAG-------------A--TNLQILTAEKCAETLKEAISQ--YLL-QRLKI
70982085       ---------YAN-------------A--SNLQVQTAAKCAETLKDAISP--YLL-QRFKI
225682364      ---------YAN-------------A--SNLQVQTAAKCAETLKDAISP--YLL-QRFKI
239615027      ---------YAN-------------A--SNLQVQTAAKCAETLKDAISP--YLL-QRFKI
212536498      ---------YAN-------------A--SNLQVQTAARCAETLKEAISP--YLL-QRFKV
255936215      ---------YAS-------------A--SNLQVQTAAKCAETLKDAISP--YLL-QRFKA
189204870      ---------YAN-------------A--SNLEFETAVQCAETLKDAVSP--YLL-QRFKV
66813000       ---------FAN-------------A--SPIQVQAAYKCAVALRDLISP--YML-RRVKS
242056785      ---------YAN-------------A--TPLQVSTAYRCAVVLRDLIMP--YLL-RRMKA
85014197       ---------YRN-------------A--SNLQVEKAYRHSLMLRSLIEP--YIL-RRTKS
Cr13231        APLQLITYTHTCIYTPLLRITRTGQQ--PDASRADREACAKKL--------YLLTERLTK
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ScRAD54      ---------DAD-------------A--TDKEITKGEAQLQKLSTIVSK--FII-RR-TN
50302399     ---------DSL-------------A--TDEEVTLGKDRLRQLSNIVSK--FII-RR-TN
156845511    ---------EAD-------------A--TDEALKKSTLQLQKLSEVVSK--FII-RR-TN
45190309     ---------DAD-------------A--TDKEIAAGEVKLHELSQIVSK--FII-RR-TN
255718981    ---------DAD-------------A--MDEDVKKGDERLQALSTIVSK--FII-RR-TN
238878261    ---------DST-------------A--SDEEREKGDKKLNELSQMVSK--FII-RR-TN
255728815    ---------DAD-------------A--TEKEREKGDQKLVELSQLVSK--FII-RR-TN
149239498    ---------DAD-------------A--TDKEREKGDQKLSELSQLVSK--FII-RR-TN
149388940    ---------DAI-------------A--TDKEREVGDEKLAELSQLVSK--FII-RR-TN
190348945    ---------DAD-------------A--TDKEKEIGDQKLSDLSKLVSK--FII-RR-TN
254570653    ---------DSL-------------A--DDKEREKGDQKLKELTEIVAR--FII-RR-TN
189211141    ---------DAN-------------G--TDEDVKKGTERLTELLGLVNK--FII-RR-TN
46127169     ---------DAD-------------A--SEADRKKGDECTAALLGVVNK--FLI-RR-TN
225684006    ---------DAD-------------G--TDEDRKKGDETVAELLAIVNK--FII-RR-TN
259485020    ---------DAA-------------G--TEEDRKKGDERLAELSSIVNK--FII-RR-TN
238840822    ---------DAD-------------G--TEEQQKKGNERLAELLNLVNK--FII-RR-SN
19115202     ---------DAD-------------G--TEKDKENGDAKLAELAKIVNR--FII-RR-TN
50546160     ---------DAD-------------G--TDKDVEKAEAKLLEMASIVSP--LII-RR-TN
58266612     ---------DAD-------------A--TEKEKLESDAKLKELGGLVSK--FII-RR-TN
164660184    ---------DAG-------------A--TEKEKEVGREKLQQLSGMVSP--FII-RR-TN
41055574     ---------DAD-------------A--SDKDRAAGEQKLQELISIVNR--CLI-RR-TS
118094595    ---------DAD-------------A--SEAERQKGEERLKELISIVNR--CLI-RR-TS
281351942    ---------DAA-------------A--SEADRQLGEERLRELTSIVNR--CLI-RR-TS
195539537    ---------DAA-------------A--SEEDRRVGEERLRELTSIVNR--CLI-RR-TS
47575794     ---------DAD-------------A--SAADRQKGEEKLKELIGVVNR--CLI-RR-TS
156369786    ---------DAD-------------A--TDAEHKKGIERLTELASLVNK--CII-RR-TA
238814383    ---------DAG-------------A--TDKERQIAQERLTELVTVVNK--CLI-RR-TS
170041242    ---------DAN-------------S--TESEREKATERLQELSALVNR--CMI-RR-TS
189238349    ---------DST-------------A--TDSERQKAVERLKELSDLVNR--CLI-RR-TS
195161916    ---------NAD-------------S--TDKERDRALEKTQELIKLVDQ--CII-RR-TN
193591979    ---------DSC-------------A--TDSERKKAAERLEQLISLVNR--CLI-RR-TS
71033369     -----------------------------------ASERLAELSNITNQ--FVL-RR-TN
221488620    ---------EPD-------------A--TEDQQQLAAERLTELSSLTNL--FIL-RR-TN
157128256    ---------QPG-------------V--LPMFANLGKARLEELNSITSS--FIL-RR-TQ
241602475    ---------LPQ-------------A--TEEQKELGQARANELSRITAL--FVL-RR-TQ
194214970    ---------QPS-------------A--SEEEKELGERRAAELTCLTGL--FIL-RR-TQ
281347253    ---------QPS-------------A--SEEEKELGEKRAAELTCLTGL--FIL-RR-TQ
119906776    ---------QPS-------------A--SEEERELGEQRAAELTCLTGL--FIL-RR-TQ
194037038    ---------QPS-------------A--SQEEKELGERRACELTCLTGL--FIL-RR-TQ
149045437    ---------EPS-------------A--SKEERELGERRTTELTRLTGC--FIL-RR-TQ
149638830    ---------EPS-------------A--TREEKELGEKRAAELTRLTGL--FIL-RR-TQ
45382655     ---------EPS-------------A--TKEEKDLGEKRAAELTRLTGL--FIL-RR-TQ
148230804    ---------EPT-------------A--TPEEKNLGEERAAELARLTGL--FIL-RR-TQ
156379220    ---------QPG-------------A--TSEDKLLGQTRASELNRLTRL--FFL-RR-TS
193661957    ---------QPE-------------C--HPQIISLGKRKASELNEVTEK--FIL-RR-TQ
110760280    ---------CPN-------------A--SCHVISLGTERANELHEKTKC--FIL-RR-TQ
242023203    ---------QPD-------------S--NEDVVKKGNERSINLKKIINK--FLL-RR-TR
66811190     ---------NPD-------------A--SDEEKEIGRQRSLELSRLTSQ--FIL-RR-TA
71651467     ---------DPD-------------C--PEHLRSLGSDRAHYLSNLTQR--FIL-RR-TQ
50311185     ---------DVN-------------AKQNQTLVEQGLLRSDQLIEITKR--FIL-RR-TN
254585925    ---------DPA-------------NRFNLHVVEKGQERSEEMISITRR--FIL-RR-TN
50294037     ---------DIN-------------NKFNTKVIEQGEEKSNQLIEFTKR--FIL-RR-SN
255725568    ---------DVN--------------CFDPEVKRRGEEISQQLIGLTSQ--FIL-RR-TQ
241952408    ---------DVN--------------CFDPEVKKRGEEISQQLIKLTQS--FIL-RR-TQ
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260941370     ---------DVN--------------CHDLKIIREGKDKSAELIQLTKS--FIL-RR-TK
254567481     ---------EIN--------------CLNRKIIKAGNEKSNSLVELTQK--FIL-RRKAK
145230930     ---------QPE-------------A--TRKDIEKGEARNEELRELTSK--FML-RR-TA
238484253     ---------QPE-------------A--TRKDIEKGEARNEELRELTSQ--FML-RR-TA
119494890     ---------QPE-------------A--TKKEIEKGEARNEELRELTSK--FML-RR-TA
225681829     ---------QPG-------------A--LKRDIEKGKARSEELASLTSL--FIL-RR-TA
258563128     ---------QPG-------------A--SRKEIEKGKARSEELASLTSL--FIL-RR-TA
242778005     ---------QPE-------------A--TIRDIEKGETRGEELRELTSM--FIL-RR-TA
212533393     ---------QPE-------------A--TMRDIEKGEARGEELRELTSM--FIL-RR-TA
189209013     ---------QPD-------------A--SESDLEKGEARWKELVSLTSQ--FMI-RR-TA
71019185      ---------AKH-------------A--SKHAKAVGQARLGALMTVTKD--IIL-RR-TA
290982366     ---------EPN-------------A--KKQDKVIGENRSKELNKIVSQ--FVL-RR-TN
281209956     -----------------------------EDSTKEGIAKAMQLSKITSS--FIL-RR-KS
167385507     ---------DGN-------------A--SIEEIQLGTERAKELTNKLND--YVL-RR-TS
170577655     --------------------------------KNLCEMESTRFNELLSE--VML-RR-TA
145350886     ---------ERG-------------A--KEEVVRIGNARREEVGRLIGP--FIH-SRKAD
224013540     ---------QKN-------------S--SKTQNEKGREQSKKLDAITST--FVI-RRLQK
145482121     ---------EKG-------------S--SAETVELGKLRSQELSSLTSQ--FIL-RR-KP
145338703     ---------EPT-------------A--TEEEKNLAADRSAELSSKVNQ--FIL-RR-TN
20336209      ---------CAD-------------S--TMVDVRVMKKRAHILYEMLAG--CV--QRKDY
242018945     ---------FED-------------S--TQSDVRIMKRRAHVLHSLVEG--FI--QRFGY
196005243     ---------HAD-------------S--TRDDVKYMKKRTYVLNLKVKA--FV--QRYDY
81916664      ---------CID-------------S--TPQDVRLMRYRSHVLHSLLEG--FV--QRRGH
75026277      ---------CID-------------S--TPQDVRLMRYRSHVLHSLLEG--FV--QRRGH
193580055     ---------FID-------------S--HDEDVKIMKQRAFILHKLLQN--TV--HRIDD
193610723     ---------FID-------------S--HDEDVKIMKQRTFILHKLLQN--TV--HRIDD
145335288     ---------HMN-------------S--TAEDVKIMNQRSHILYEQLKG--FV--QRMDM
258572168     ---------YRE-------------S--TRAERRESLKRLQVLKKDLDP--KV--NRADI
171685718     ---------YAD-------------S--NPSAKRQARKLLVILKETMSP--KV--HRRDV
289615990     ---------HAD-------------C--SASEKKLSRERLQILKAIVAP--KV--NRRDI
164425263     ---------HAD-------------S--TDAQKRLARERLQILKAIVAP--KV--NRKDI
72391587      -----------N-------------G--DDSAFCDALFAQRYIHEWMSP--YVF-TVMKV
71662347      -----------N-------------G--DDSALAAAVSAQRYIQEWMCS--YVF-SVMKT
239977156     -----------E-------------G--DDGAFYNAVMAQEYIQDWMRG--FVF-REMEN
146081173     -----------E-------------G--DDGAFYNAVMAQEYIQDWMRG--FVF-REMEN
Sm441121      -------------------------D--DGHGHREMQAAQMKLVKMTQG--FT--DHYTG
Bd3g18910     -------------------------L--ADDNFERKSHVISGLRELTED--VL--HYYKG
Bd1g74070     -------------------------Q--KDANDKIREMIIENLRELTAN--VL--HYYQG
Os03g06920    -------------------------Q--KDGNDKMRAVIIQNLRELTAD--VL--HYYQG
Sb01g046180   -------------------------Q--KDSK-TMRVMIIQNLRKLTEN--IL--HYYQG
Bd3g19890     -------------------------L--HDENFTRKAHIIRSLRELTND--VL--HYYKG
Os06g14440    -------------------------L--NDDNFTRKAHVIRSLRELTKD--VL--HYYKG
Sb07g002945   -------------------------L--NDENFKRKAHVIRGLRELTKD--VL--HYYKG
ZM093940      -------------------------L--NDENFKRKVHVIRGLRELTRD--VL--HYYKG
ZM064574      -------------------------L--NDENFKRKAHVIRGLRELTKD--VL--HYYKG
Bd2g21430     -------------------------L--HDVNFTRKKHVIRSLRELTEG--VI--HYYKG
Bd2g21450     -------------------------L--HDENFTRKKHVIRSLKELTED--VI--HYYKG
Os08g14610    -------------------------L--NDDNFTRKVNVIRSLGELTKD--VL--HYCKG
Vv35918       -------------------------Q--KDDNFRRKITVIQDLREMTSK--VL--HYYKG
Pt195587      -------------------------Q--KDQDFKRKVTVIRDLHEMTSK--VL--HYYKG
AtDRD1        -------------------------Q--KSEDFTVKIKVIQDLREMTKK--VL--HYYKG
At2g21450     -------------------------Q--RSTNFSAKASLIKDLREMTRN--IL--HYHKA
Bd2g26500     -------------------------W--ASLTSNVTDDNAEKVRSILKP--FV--HIHNG
Os05g32610    -------------------------W--ASLTSNVTDDNAEKVRSILKP--FV--HIHNG
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Sb09g019410     -------------------------W--ASLTSNVTDDNAEKVRSILKP--FV--HIHNG
RMR1            -------------------------W--ASLTSNVTDDNAEKVRSILKP--FV--HIHNG
Bd2g43500       ----------------------------------ITDDHLSEIREKLDP--FV--HIHNG
Os02g43460      ----------------------------------ITEKKIDEIRQILDP--IV--HIHNG
Bd3g50300       ----------------------------------ITDERVNEIRDKLKP--FL--HIYNG
Sb04g033300     ----------------------------------ITEADINEVRKKLDP--IV--HIHSG
ZM178435        ----------------------------------ITKANINEVRKKLDP--IV--HIHSG
Vv15867         --------------------------------GKIADDKVEELRAMIEP--FV--HIHKG
Pt28648         -------------------------G--KVTDDKLEAQRVEELRKMIWQ--FV--HVHKG
Cp76.2          -----------------------------GKFLDVKADNLKVIRDVIAP--FV--HVHKG
At1g05490       ----------------------------KNLGNEINNRGIEELKAVMLP--FV--HVHKG
At3g24340       -----------------------KCSQEGEHGRVNEENRIVDLKAMIAH--FV--HVHEG
Bd1g16720       ----------------------------ESSSSRDRIDGLNLLNKLTCG--FI--DSFEG
Os07g49210      ----------------------------ESDNKHIRSDGISLLNKLTRG--FI--DSFEG
Sb02g043870     ----------------------------ESSSKHDRMDGISLLNDLTHG--FI--DSFEG
ZM108166        ----------------------------ESSSKHDRMDGISLLNELTQG--FI--DSFEG
Vv29366         ----------------------------NSNVPEEQIEGLNMLRNLTSK--FI--DVYEG
Pt832603        ----------------------------NSDEAEEKMQGLNMLRNMTNG--FI--DVYEG
Pt567214        ----------------------------NLDEAEEKMQGLNMLRNMTNG--FI--DVYEG
Cp19.123        ------------------------------------------------------------
AtCLSY1         ----------------------------DTKVGDERLQGLNMLRNMTSG--FI--DNYEG
At5g20420       ----------------------------DASVGDERLQGLNMLKNMTNG--FI--DNYEG
Sm84719         --------------------------------ENNLGAAVRFFRKLTAP--FL--HWHGG

                                 620                 640                 660
15898471        DKAIIND--LPDKIETNVYCNLTPEQAAMYKAEVENLFNNIDSVTGIK------------
256419642       QVA--KE--LPEKIETVIFCEMDAEQRHIYDAYRNSYRSKILGVIEDQGMER--------
237794935       DVL--KD--LPHKIEKKFLVEMTTNQERIYKAYMKSIKEKLKNNKE--------------
187779742       NVL--KD--LPHKIEKKFLVEMTTNQERIYKAYMKSIKEKLKNNKED-------------
ScSNF2          DVE--KE--LPDKVEKVVKCKMSALQQIMYQQMLK-------------------------
83286649        EVE--QS--LPPKREIYIFVGMSKLQKKLYSDILS-------------------------
124803472       EVE--QS--LPPKREIYIFVGMSKLQKKLYSDILS-------------------------
74008371        DVE--KS--LPPKKEIKVYLGLSKMQREWYTKILM-------------------------
14028669        DVE--KS--LPPKKEVKIYVGLSKMQREWYTRILM-------------------------
56118945        DVE--KS--LPPKKEIKIYVGLSKMQREWYTKILM-------------------------
47217344        DVE--KT--LLPKKEIKIYVGLSKMQREWYTKILM-------------------------
157103787       EVE--KR--LLPKKEVKIFVGLSKMQREWYTKILM-------------------------
170572145       DVE--KT--LLPKKEVKIYVGLSKMQREWYTRILM-------------------------
255719682       EVE--TS--LLPKKELNLYIGMSAMQKRWYKQILE-------------------------
145610651       DVE--KS--LLPKKEVNLYLKMTEMQRTWYQKILE-------------------------
145353082       EVE--VS--LPPKTETKIMCPLSEAQTFWYRRLLL-------------------------
225436589       DVE--KS--LPPKIERILRVEMSPLQKQYYKWILE-------------------------
189521245       DVF--KN--MPAKTELIVRVELSPMQKKYYKFILT-------------------------
47206539        DVF--KN--MPAKTELIVRVELSPMQKKYYKFILT-------------------------
113678140       DVF--KH--MPSKTELIVRVELSPMQKKYYKFILT-------------------------
156717248       DVF--KN--MPSKTELIVRVELSPMQKKYYKFILT-------------------------
73997410        DVF--KN--MPSKTELIVRVELSPMQKKYYKYILT-------------------------
115939069       DVL--KG--MPSKSEFIVRVELSPLQKKYYKYILT-------------------------
221120608       DVL--KD--MPSKSEFIVRVELSPMQKKYYKYILT-------------------------
256052547       DVL--QD--MPSKGEFIVRVELSPMQKRYYKFILT-------------------------
24666729        DVL--KS--MPPKSEFIVRVELSSMQKKFYKHILT-------------------------
170592228       DVL--SG--MPSKSELIVRVELSPMQKKYYKNILT-------------------------
17569817        DVL--TG--MPSKQELIVRVELSAMQKKYYKNILT-------------------------
256072692       DVI--QD--LPKKTEIVVPVDMTLLQRRLYKYILT-------------------------
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145341798     DVE--QK--LPPRSETLVECELAPLQKKCYRALFE-------------------------
145491053     DVE--QM--IPPLQETIIDIEMTTIQKHIYKALYE-------------------------
118367847     DVE--DS--IPPLQETIIDIEMTTLQKTLYRAIYE-------------------------
145484966     DVE--QS--IPPLQENIIDVELTNVQKTLYRALYE-------------------------
239899054     DAM--KK--VPPKLEHIIEVEFTTLQRRVYKSVYE-------------------------
291001481     DVE--KS--IPPKEEIVVEVVPTSIQKAYEQAIFK-------------------------
211853152     DVE--KK--LAPKEETIIEVELTNIQKKYYRAILE-------------------------
189521372     DVE--KK--LAPKEETIIEVELTNIQKKYYRAILE-------------------------
260834763     DVE--KN--LAPKEETIIEVELTNIQKKYYRAILE-------------------------
196012568     DVE--KN--LAPKEETIIEVELTPIQKKFYRAILE-------------------------
242011216     DVE--KS--LAPKEETVVEVELTNIQKKYYRGILE-------------------------
193599122     DVE--KS--IAPKEETVVEVELTNIQKKYYRGILE-------------------------
19112177      EVL--DN--FPTKVEVIIPLSMTPVQKGLYKSILS-------------------------
259147500     DVA--KD--LPPKKEMVLFCKLTKYQRSKYLEFLHSSDLNQIQN----------------
254582697     DVA--KD--LPEKKEMVLFCKLTQVQRRKYLEFLHSRELEDIKG----------------
255720394     DVA--KD--LPRKNEMVLFCKLTQYQRNKYLQFLNSEDLVKIKN----------------
50309923      DVA--KD--LPKKNEMVLFCKLTQYQKSKYLEFLHSDELMKIRK----------------
146416597     DVA--QD--LPKKEEMVLFVKLTQYQQDMYEKFLSSEDLHAILK----------------
68483838      DVA--QD--LPKKNEMVLFVKLTKIQQELYESFLQSEDLESILK----------------
149235383     DVA--QD--LPKKNEMVLFVRLTKEQQELYEKFLDSEEMDSIVK----------------
199432721     DVA--QD--LPKKNEMVLFVKLTQYQQDLYEKFLSSEDLHAILK----------------
254568884     DVA--KD--LPKKSEMVLFCKLTAPQHALYEKFLRSDELSRILQ----------------
19075591      DVA--AD--LPKKSEQVLFCKLTPLQRKAYQDFLQGSDMQKILN----------------
261358370     DVA--AD--LPSKTERVLFCKMTDRQLEAYKQFLNSDAVNQILS----------------
70982085      DVA--AD--LPKKTEQVLFCKLTKPQRMAYESFLKSEEMESILK----------------
225682364     DVA--AD--LPKKSEQVLFCKLTKIQRSAYQAFLGSNEMSSILR----------------
239615027     DVA--AD--LPKKSEQVLFCKLTKIQRSAYEAFLGSNEMSSILR----------------
212536498     DVA--SD--LPKKSEQVLFCKLSPLQRKAYEQFLNSQECNSILA----------------
255936215     DVT--SD--LPLKSEQVIFCKLTQLQRTIYKRFLGSDDMKSIIR----------------
189204870     DVA--TD--LPQKKEQVLFCKLTRQQRQAYEAFLASEDMKSIAN----------------
66813000      DVL--KS--LPSKNEQVLMCPLTPFQEKLYLEFLDSNDIKSVLD----------------
242056785     DVN--AQ--LPKKTEHVLFCSLTPEQRSTYRAFLASSEVEQIFD----------------
85014197      QVS--HK--LPSKEDKIVFCSLTPAQIELYNRVLESKHIMKVLT----------------
Cr13231       DCI--HRPMLPPKSDVVLFLDMTPRQRAMYTAY---------------------------
ScRAD54       DIL--AKY-LPCKYEHVIFVNLKPLQNELYNKLIK---SREVKKVVKGV-----------
50302399      NIL--AKY-LPCKYEHVIFINLTPFQQSLYQHFIE---SRAVKKIVK--G----------
156845511     DIL--SKY-LPCKYEHVIFVNMKPFQRDLYKSYIELRKDDSFEK----------------
45190309      DIL--SKY-LPCKYEHILFVNLSPMQKAIYEHFVR---SREVAKLMKG------------
255718981     DIL--SKY-LPCKYEHVIFVNLKPFQRSLYEHMLK---SRDIKLLVKDA-----------
238878261     DIL--SKY-LPIKYEYVLFTGLSPMQKDIYNHFIT---SPEIKKLMK--G----------
255728815     DIL--SKY-LPVKYEYVLFTGLSPMQKSLYSHFIN---SPDMKKLIR--G----------
149239498     DIL--SKY-LPVKYEYVLFTGLAPMQKKLYHHFIT---SPEIKKLLK--G----------
149388940     DIL--SKY-LPVKYEYVLFTGLSPMQKDLYRHFIT---SPEIKKLLK--G----------
190348945     DIL--SKY-LPIKYEYVVFVKLSPLQKALYKHFLT---SPEVRKLLK--G----------
254570653     DIL--SKY-LPVKYEYVIFCNLSETQKSLYQRFTA---SKSISKLVKEVG----------
189211141     DIL--SKY-LPVKYEHVVFCNLAPFQKDLYNHFIK---SPDVQSLLR--G----------
46127169      DIL--SKY-LPVKYEHVVFCNLAPFQFDLYNYFIK---SPEIQALLR--G----------
225684006     DIL--SKY-LPVKYEHVVFCGLAPFQTDLYNYFIQ---SPDIKSLLR--G----------
259485020     DIL--SKY-LPVKYEHVVFCNLSQFQLDLYKHFID---SPEIKSLLR--G----------
238840822     DLL--SKY-LPVKYEHVVFCNLAPFQLDLYNHFIQ---SPEIKSLLR--G----------
19115202      DIL--SKY-LPVKYEHVVFCNLSEFQLSLYKHFIT---SPEINKILR--G----------
50546160      DIL--SKY-LPVKYEHVVFCNLAPFQKSLYVQFRT---SKEARSLLK--GEKSS------
58266612      DLL--SKY-LPVKYEHVVFCRPSPLQASLYNLFVT---SKDVQRLLR--G----------
164660184     DIL--SKY-LPVKYEHVVFCRLSPFQVDLYNLFLR---SPVIARLLR--G----------
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41055574     DIL--SKY-LPVKIEQVVCCNLTPLQKELYKLFLK---QAKPVESLQ----TGK------
118094595    DIL--SKY-LPVKIEQVVCCRLTPLQAELYKNFLK---QAKPVEELK----EGK------
281351942    DIL--SKY-LPVKIEQVVCCRLTPLQTELYKRFLR---QAKPAEELR----EGK------
195539537    DIL--SKY-LPVKIEQVVCCRLTPLQIELYKRFLR---QAKPAEELR----EGK------
47575794     DIL--SKY-LPVKIEQVVCCRLTPLQSELYKLFLK---QAKPAEDLN----EGK------
156369786    AIL--SKY-LPIKVEQVVCCRLTALQTAIYKRLIH---SKALKIKLA----EGSKGKPGG
238814383    ALL--SKY-LPLKHELVVCIKMTPLQTQLYKNFIK---SDSIKKSMQDDGTAKK------
170041242    SLL--TKY-LPIKFEMVVCVKMTDVQTELYKSFLQ---SDSIRRSVL----EKSEVK---
189238349    NLL--TKY-LPVKFEMIVICQLTPLQKQIYLNYIN---SEGLRKGVLNDV-EVK------
195161916    QIL--TKY-LPVKFEMVICAKLTPIQLQLYTNFLK---SDQVRRSLADC--KEK------
193591979    ALL--SKY-LPVKTEHVVCIKLTPLQTDLYLHLLK---SDMVTKSIKGN--DGK------
71033369     ALL--AKV-LPPKIILNVFCNLTDVQKDIYKSFVT---SRRWKNIMNQDT----------
221488620    SLL--AKV-LPPKVVLNVFCRLTPLQKEFYRSFLS---SKSCRKMFTAEAEGKGG-----
157128256    EVI--NKY-LPGKQEAVIFCHPSKLQETLLRTAIQFYEKSDR------------------
241602475    DVV--QSY-LPGKAECVVFCRPTSLQLTVYRELLA---SNAVQACLSSYLSC--------
194214970    EVI--NKY-LPPKIENVVFCQPAALQIELYRKLLN---SRAVRFCLQG--LL--------
281347253    EVI--NKY-LPPKIENVVFCRPGALQIELYRKLLN---SQAVRFCLQG--LL--------
119906776    EVI--NQY-LPPKIENVVFCRPGALQIALYRKLLN---SQAVRFCLQG--LL--------
194037038    EVI--NKY-LPPKIENVVFCRPGALQIELYRKLLN---SQAVRFCLQG--LM--------
149045437    EVI--NKY-LPPKIENVVFCRPGALQIELYRKLLS---SQSVRFCLQG--LL--------
149638830    EVI--NKY-LPPKIESVVFCRPAALQIELYRKLLN---SRAISFCLQG--ML--------
45382655     EVI--NKF-LPPKKENIIFCQPTALQLELYRKLLS---SRVISSCLQG--RL--------
148230804    EVI--NKF-LPPKIENIVFCQPSQFQLDLYRRLLN---SRAVKSCLLG--NG--------
156379220    EIN--EKY-LPPKVEMVVFCRPAHLQVTLYRHLLT---SRFLRGCLRA--SC--------
193661957    DVN--NKY-LPSKYESVVFCAMAPIQCRLYEETVSYWENRVQEFGL--------------
110760280    EII--NKY-LPSKHELVIFCRLSDEQEDLYSRITNLWFSKSVLPN---------------
242023203    NIL--KNY-LPPRHDIVVFCKITEPQRNMYNSLVNSFLNAKESEEFI-------------
66811190     FVN--TQY-LPPKVEYVIFCKLTPLQLSIYKHLIKEAKDSAFA-----------------
71651467     SIN--ESY-LPPKVDVTVFVRLGELQSVAYEKLSDLVEG---------------------
50311185     EIL--QQY-LPPRTDLIIFCKPTAEQVEAFHKILT---EGQLNFSNM-------------
254585925    SIL--SKY-LPPKMDIILFCKPTNHQISAFKDILQ---GANIDLQRL-------------
50294037     NIL--SKF-LPPKTDIILFCRPTIEQIKAFRDIIE---NVRVDMNNI-------------
255725568    SIL--SKY-LTTKTDILLFVPPSDLQVKLFKYITNLKKFNQIN-----------------
241952408    SIL--ANY-LTQKTDILLFVPPTSSQLELFNYITNLKKFNQFN-----------------
260941370    DII--SNC-LTRKTDVIIFCAPTKVQKSLFEAVSK---SSKFNSVMRS------------
254567481    DIN--TNF-LPPKTELILMVPMTELQQELYKDIIE-------------------------
145230930    DIL--AKY-LPPKTEYVLFCKATRTQATIYQNVLA---SPVFQSALG-------------
238484253    DIL--ANY-LPPKSEYILFCDPTPTQANIYQNVLA---SPVFQCAVG-------------
119494890    DIL--AKY-LPPKTEYVLFCNPTSTQANIYKNVLA---SPVFQCAIG-------------
225681829    DLL--SNY-LPPKTEYVLFCNPTSSQANIYRHVLS---SPVFQCALG-------------
258563128    DIL--LKH-LPPKTEYILFCNPTPAQANIYRHVLA---SPIFQSALG-------------
242778005    DIL--SRY-LPPKTEYVILCNPTSVQASIYRHVLG---SPIFQTALG-------------
212533393    DVL--SKY-LPPKTEYVILCNPTSVQASIYRHVLG---SPIFQSALG-------------
189209013    EVL--SKY-LPPKTEHIVFCRPTKGQAEAYRAVLD---SPTFRLAMG-------------
71019185     DIL--TKF-LPPKHEMVLFCSPSEEQLRIYQAILG---SSQVRSLLQG------------
290982366    LLL--RQH-LPPKMEIVLFCGMTELQENLYKHFVL---SKALRGVINGTL----------
281209956    NVL--EEY-LPTKTIHVVFCRLSEFQKKLYRAVLD---NNGVDSIIA-------------
167385507    QVN--EKY-LPDKTEIVLFIKPSHLQIKLYKIMLKELDKKKL------------------
170577655    EVI--HDL-LPPKIDYIVWCRPSALQCSIYKNLKKF------------------------
145350886    EIN--ASL-LPPKTEYVVFVRLSEVQKGLYVDQLK---QKSMLSMLGRIGKTQDA-----
224013540    DVL--KSL-LPPRTELLLFCRPTERQCELYREISNRA-SRSIGSIRGRD-----------
145482121    EIL--SKF-LPSKFEYLIFCTMTPQQQVLYKRSLQLCPNSVM------------------
145338703    ALL--SNH-LPPKIIEVVCCKMTTLQSTLYNHFIS---SKNLKRALADNA----------
20336209     TAL--TKF-LPPKHEYVLAVRMTSIQCKLYQYYLDHLTGVGNNSEGGRGK----------
```

```
242018945     YVL--KSL-LPEKQEYVIKICLTETQEELYRTFVKNYANFS-------------------
196005243     DVL--ESE-LPPKHEYVIYIRMSRKQCELYKSYLEKFASDDHLHF---------------
81916664      TVL--KIH-LPAKEENVILVRLSQIQRDLYTQFMDRFRDCGTSG-----W----------
75026277      TVL--KIH-LPAKEENVILVRLSKIQRDLYTQFMDRFRDCGSSG-----W----------
193580055     KNL--KPL-FTNKIEYTIEVNLTKFQCELYEKFLHSIKHKVSI-----------------
193610723     KNL--KPL-FTNKIEYTIEVNLTKFQCELYEKFLHYNKASN-------------------
145335288     NVV--KKD-LPPKTVFVISVKLSPLQRILYQRFLELYGFSDGRTDER-------------
258572168     SVL--KGD-LPPKVEFVITLPLTAIQEEAYKIYVATLSTGKDDV----------------
171685718     QVL--RDE-LPTKKEFIIMLPLTPLQRTLYEIYIERVNNPTITGSDR-------------
289615990     QVL--VDE-LPQKREFILTIQMTKVQRDAYKEYLETAERNKGNDLY--------------
164425263     QVL--VDE-LPQKREFILTIQMTKVQRDAYQEYLETAQRNKGNDLY--------------
72391587      D--------LPPLHDYIIICNFSAVQQKMFEERIKVDAT---------------------
71662347      D--------LPPLNDYIIICGFSSIQRKMLEDHFGMEGI---------------------
239977156     D--------LPPLHDYLLVCGSSNVQRE-YEEKLGLTE----------------------
146081173     D--------LPPLHDYLLICGSSDVQRE-YEEKLGLTE----------------------
Sm441121      AIL--TEV-LPGLRDYEITTAMTELQHKLVAAVA--------------------------
Bd3g18910     DVL--DK--LLGLVDFSVFLKLTQKQKDIL-DTLE-------------------------
Bd1g74070     ELS--EE--LPGLVDFTVFLNMTTKQEESI-KSFV-------------------------
Os03g06920    KLL--DE--LPGIVDFTVFLNMSSKQEHII-KGLD-------------------------
Sb01g046180   EIL--KE--LPGLVDFTVLLNMSSKQEDII-KGLA-------------------------
Bd3g19890     DIL--DE--LPGLVDFSVFLKLSPRQKEIV-HKLE-------------------------
Os06g14440    DIL--DE--LPGLVDFSVFLKLSTKQKEIV-HKIE-------------------------
Sb07g002945   DIL--DE--LPGLVDFSVFLKLTPKQKDIIRNKLE-------------------------
ZM093940      AIL--DE--LPGLVDFSVFLKLTPKQKDIV-HKLE-------------------------
ZM064574      DIL--DE--LPGLVDFSVFLKLTPKQKDII-YKLE-------------------------
Bd2g21430     DIL--HE--LPGLIDFSVFLKLSPMQKESI-QKLE-------------------------
Bd2g21450     DIL--HE--LPGLIDFSVFLKLSPRQNELV-QKLE-------------------------
Os08g14610    EDL--NE--FPVLLDFSVFLELSPKQKDIL-CKLE-------------------------
Vv35918       DFL--DE--LPGLVDFTVLLNLSARQKKEV-GNLN-------------------------
Pt195587      DFL--DE--LPGLVDFTLMLNLSSRQKHEV-KKLK-------------------------
AtDRD1        DFL--DE--LPGLADFTVVLNLSPKQLNEV-KKLR-------------------------
At2g21450     DFS--GL--LPGLSEFTVMLNLSSIQRDEV-KGLR-------------------------
Bd2g26500     TIL--RT--LPGLRESVIVLKPPPLQKSIIRKVENI------------------------
Os05g32610    TIL--RT--LPGLRECVIVLKPLPLQKSIIRKVENV------------------------
Sb09g019410   NIL--RT--LPGLRESVIILKPLPLQKSIIRKVENI------------------------
RMR1          NIL--RT--LPGLRESVIILKPLPLQKSIIKKVENI------------------------
Bd2g43500     DIL--QKS-LPGLKESVVILNPLPHQKEIITMMEKSAGK---------------------
Os02g43460    DIL--QKS-LPGLRESVVILNPLPHQKEIITAMENTVTM---------------------
Bd3g50300     EFL--QKS-LPGLRESVVILNPFPHQKKIIKMLEDSRTKS--------------------
Sb04g033300   KFL--QKS-LPGLGESVVILNPLPYQKEVIATMEKTVAT---------------------
ZM178435      RFL--QKS-LPGLRESVVILNPLLYQKEVIASMEKTVA----------------------
Vv15867       TIL--QEN-LPGLKDSVVVLQPSDLQRRLLESIR--------------------------
Pt28648       GVL--RER-LPGLRDSVVILQPVHLQKTLL-ENV-----KQINGL---------------
Cp76.2        KIL---KDSLPGLRHSVVVLRPVDLQKSLLDGLQ--------------------------
At1g05490     SIL--QSS-LPGLRECVVVLNPPELQRRVL-ESIEVTHNRKTK-----------------
At3g24340     TIL---QESLPGLRDCVVVLNPPFQQKKILDRID--------------------------
Bd1g16720     AKL--SN--LPGIHVYTVFMKPGKIQEEILAKVSMSTSC---------------------
Os07g49210    AKL--IN--LPGIHVYTVFMKPTDIQEEMLAKVTMPKLG---------------------
Sb02g043870   TKL---NI-LPGIHVYTLFMKPTDVQEEVLAKLSMPLAD---------------------
ZM108166      TKL---NI-LPGIRVYTLFMKPTDVQEEVLAKLLMPLSG---------------------
Vv29366       GSS---DN-LPGLQVYTLLMKSTTIQQQFLSKLQKKDE----------------------
Pt832603      TAS---DT-LPGIQIYTILMNPTDIQHQILVKLHKIMEK---------------------
Pt567214      TAS---DT-LPGLQIYTIMINPTDIQHEILVKLHKIMEK---------------------
Cp19.123      ------------------------------------------------------------
```

```
AtCLSY1       SGSGSGDV-LPGLQIYTLLMNSTDVQHKSLTKLQNIMST---------------------
At5g20420     SGSGSGDA-LPGLQIYTLVMNSTDIQHKILTKLQDVIKT---------------------
Sm84719       KVL---DS-LPGIEEVLVTLNLTEAHKALVLNAGKSYTKE--------------------

                                680                 700                 720
15898471      RKGMIL-----------------------------STLLKLKQ-------IVDHPAL---
256419642     SQLTIL-----------------------------QGLMKLRQ-------ICDSPAI---
237794935     DKITIF-----------------------------SYLTRLRQ-------LCLDPSI---
187779742     -KITIF-----------------------------SYLTRLRQ-------LCLDPSL---
ScSNF2        YRRLFI-------GDQ-NNKKM------VGLRGFNNQIMQLKK-------ICNHPFV---
83286649      KNIDVI-------NAMTGSKNQML-----------NILMQLRK-------CCNHPYL---
124803472     KNIDVL-------NAMTGSKNQML-----------NILMQLRK-------CCNHPYL---
74008371      KDIDVL-----------NSAGKMDK---MRLL---NILMQLRK-------CCNHPYL---
14028669      KDIDIL-----------NSAGKMDK---MRLL---NILMQLRK-------CCNHPYL---
56118945      KDIDIL-----------NSSGKTDK---MRLL---NILMQLRK-------CCNHPYL---
47217344      KDIDIL-----------NSAGKMDK---MRLL---NILMQLRK-------CCNHPYL---
157103787     KDIDIV-----------NGAGKMEK---MRLQ---NILMQLRK-------CTNHPYL---
170572145     KDIDVV-----------NGAGKLEK---ARIM---NILMHLRK-------CCNHPYL---
255719682     KDLDAV-----------NGA-NGSKESKTRLL---NIMMQLRK-------CCNHPYL---
145610651     KDIDAV------------NGANGKRESKTRLL---NIVMQLRK-------CCNHPYL---
145353082     REATALQSLEKATKGEGGADNF------QKLN---SLLMQLRK-------CCNHPFL---
225436589     RNFHDL-------NKG-V--RGNQ----VSLL---NIVVELKK-------CCNHPFL---
189521245     RNFEAL-------NSK-GGGNQ------VSLL---NIMMDLKK-------CCNHPYL---
47206539      RNFEAL-------NSK-GGGNQ------VSLL---NIMMDLKK-------CCNHPYL---
113678140     RNFEAL-------NTR-GGGNQ------VSLL---NVVMDLKK-------CCNHPYL---
156717248     RNFEAL-------NAR-GGGNQ------VSLL---NVVMDLKK-------CCNHPYL---
73997410      RNFEAL-------NAR-GGGNQ------VSLL---NVVMDLKK-------CCNHPYL---
115939069     RNFQAL-------NTKAAGGGS------VSLL---NIMMDLKK-------CCNHPYL---
221120608     KNFGAL-------NTR--GSQQ------VSLL---NIVMELKK-------CCNHPYL---
256052547     RNFEAL-------SCR-SGGSQ------VSLI---NIMMDLKK-------CCNHPFL---
24666729      KNFKAL-------NQK-GGGRV------CSLL---NIMMDLRK-------CCNHPYL---
170592228     RNFEAL-------SPK-GGGSQ------ISLI---NIIMDLKK-------CCNHPYL---
17569817      RNFDAL-------NVK-NGGTQ------MSLI---NIIMELKK-------CCNHPYL---
256072692     SNYEEL-------RCG-------------NLM---NSIVHLQK-------VCNHPYL---
145341798     RNFSFL-------RQGCDSRESFANFA--------NIMMEVRK-------CCQHPFL---
145491053     RNKSML-------EQGFSQWAANA----ASLN---NLEIQLRK-------CCNHPFL---
118367847     RNKSML-------QKNFSSMAMN-----TSLN---NLEMQLRK-------CCNHPFL---
145484966     RNKSAL-------IQGFSQQTAQI----ASLN---NLDMHLRK-------LCNHPLL---
239899054     GKIYSL-------VNGKGGKSS--------LN---NIAMELRK-------CCAHPYL---
291001481     RNREFL-------MKGVSKSQNV-----PKLN---NVLMELRK-------VCNHPFL---
211853152     KNFAFL-------SKG-AGQANV-----PNLV---NTMMELRK-------CCNHPYL---
189521372     KNFSFL-------AKG-AGQANV-----PNLL---NTMMELRK-------CCNHPYL---
260834763     RNFTFL-------AKGCGSSSNV-----PNLM---NTMMELRK-------CCNHPYL---
196012568     RNFNFL-------SKG-ANTSNL-----PNLM---NTMMELRK-------CCNHPFL---
242011216     RNFSFL-------SKG-TTSSNI-----PNLM---NTMMELRK-------CCIHPYL---
193599122     KNFSFL-------SKG-TTSANV-----PNLM---NTMMELRK-------CCIHPYL---
19112177      KNLSLLRNITGYANTSSSGGQRT-----TSLN---NILMQLRK-------TLAHPYI---
259147500     GKRNVL-----------------------------FGIDILRK-------ICNHPDL---
254582697     GKRRVL-----------------------------YGIDILRK-------ICNHPDL---
255720394     GKRQVL-----------------------------FGIDILRK-------ICNHPDL---
50309923      GKRQVL-----------------------------YGIDILRK-------ICNHPDL---
146416597     GKRNML-----------------------------TGVDTLRK-------ICNHPDL---
68483838      GKRNVL-----------------------------MGVDILRK-------ICNHPDL---
149235383     GKRNVL-----------------------------VGVDTLRK-------ICNHPDL---
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199432721     GKRNIL-----------------------------MGVDILRK-------ICNHPDL---
254568884     GKRQVL-----------------------------YGIDILRK-------ICNHPDL---
19075591      GKRQML-----------------------------YGIDILRK-------ICNHPDL---
261358370     ARRKSL-----------------------------YGIDILRK-------ICNHPDL---
70982085      GRRQIL-----------------------------YGVDILRK-------ICNHPDL---
225682364     GRREAL-----------------------------YGIDMLRK-------ICNHPDL---
239615027     GRREAL-----------------------------YGIDMLRK-------ICNHPDL---
212536498     GRRQVL-----------------------------YGVDMLRK-------ICNHPDL---
255936215     GRRNSL-----------------------------YGIDILRK-------ISNHPDL---
189204870     GKRQML-----------------------------FGVDFLRK-------ICNHPDL---
66813000      GRRNAL-----------------------------YGIDILKK-------ICNHPDI---
242056785     GNRNSL-----------------------------YGIDVLRK-------ICNHPDL---
85014197      GKANLL-----------------------------SGISMLRK-------VCNHPRL---
Cr13231       ----------------------------------------LRA-------LQGRP-----
ScRAD54       GGSQPL-----------------------------RAIGILKK-------LCNHPNL---
50302399      DSNQPL-----------------------------KAIGLLKK-------LCNHPDL---
156845511     ----PL-----------------------------KAIGVLKK-------LCNHPDL---
45190309      TGSQPL-----------------------------KAIGLLKK-------LCNHPDL---
255718981     KHTQPL-----------------------------KHIGVLKK-------LCNHPDL---
238878261     TGSQPL-----------------------------KAIGMLKK-------LCNHPDL---
255728815     IGSQPL-----------------------------KAIGLLKK-------LCSHPDL---
149239498     IGSQPL-----------------------------KAIGMLKK-------LCNHPDL---
149388940     VGSQPL-----------------------------KAIGMLKK-------LCNHPDL---
190348945     AGSQPL-----------------------------KAIGMLKK-------LCTHPEL---
254570653     GGAQSL-----------------------------QSIGLLKK-------LCTHPNL---
189211141     KGSQPL-----------------------------KVIGMLKK-------LCNHPDL---
46127169      KGSQPL-----------------------------KAINILKK-------LCNHPDL---
225684006     KGSQPL-----------------------------KAIGILKK-------LCNHPDL---
259485020     KGSQPL-----------------------------KAIGILKK-------LCNHPDL---
238840822     KGSQPL-----------------------------KAIGILKK-------LCNHPDL---
19115202      TGSQPL-----------------------------KAIGLLKK-------ICNHPDL---
50546160      EGTTTL-----------------------------NAIGILKK-------LCNHPDL---
58266612      KDSQPL-----------------------------KAIGLLRK-------LVNHPDL---
164660184     IGSQPL-----------------------------KAIGILKK-------LCNHPDL---
41055574      ISVSSL-----------------------------SSITSLKK-------LCNHPAL---
118094595     INVSSL-----------------------------SSITSLKK-------LCNHPAL---
281351942     MSVSSL-----------------------------SSITLLKK-------LCNHPAL---
195539537     MSVSSL-----------------------------SSITSLKK-------LCNHPAL---
47575794      ISVSSL-----------------------------SSITSLKK-------LCNHPSL---
156369786     VSTSSL-----------------------------GFITSLKK-------LCNHPEL---
238814383     GSLSAL-----------------------------SAITLLKK-------LCNHPDL---
170041242     ASLTAL-----------------------------SNITALKK-------LCNHPDL---
189238349     ASLSAL-----------------------------ASITTLKK-------LCNHPDL---
195161916     ASLTAL-----------------------------ADITTLKK-------LCSHPNL---
193591979     VTSNAL-----------------------------AAITLLKK-------LCAHPDL---
71033369      VVSRAL-----------------------------SAIQSLMK-------LCNHPFL---
221488620     FTGRVL-----------------------------SSIQGLMK-------LCNHPSL---
157128256     STYFPL-----------------------------QLITVLKK-------ICNHPSL---
241602475     DANHHL-----------------------------ACILALRK-------LCNHPSLVTP
194214970     ENSPHL-----------------------------ICIGALKK-------LCNHPCL---
281347253     GNSPHL-----------------------------ICIGALKK-------LCNHPCL---
119906776     ENTSHL-----------------------------ICIGALKK-------LCNHPCL---
194037038     ENSSHL-----------------------------ICIGALKK-------LCNHPCL---
149045437     GNSAHL-----------------------------ICIGALKK-------LCNHPRL---
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149638830      ENSPHL-----------------------------VCIGALKK-------LCNHPCL---
45382655       ENSPHL-----------------------------ICIGALKK-------LCNHPCL---
148230804      ENSPHL-----------------------------VCIGALKK-------LCNHPCL---
156379220      PSSTHL-----------------------------ECIGALKK-------LCNHPTL---
193661957      STISHF-----------------------------SVITMLKK-------VCNHPEL---
110760280      NNISHL-----------------------------TLITALKK-------ICNHPEL---
242023203      EGSSHL-----------------------------ELITSLKK-------ICNYPSL---
66811190       STTGAL-----------------------------PLITTLKK-------LSNCAEL---
71651467       SSCPPL-----------------------------VLISALRK-------LCNHMDL---
50311185       TFNSSL-----------------------------GLITLFKK-------ICNSTRL---
254585925      NFNSSL-----------------------------ALITLLKK-------ICNSPTL---
50294037       TFNTSL-----------------------------GLINLMKK-------VCNSPSL---
255725568      SGSDSF-----------------------------TLINLFKK-------ICNSPSL---
241952408      SGSDSF-----------------------------TMINLFKK-------ICNSPSL---
260941370      ETKDVL-----------------------------SMILMFRK-------ICNSPSL---
254567481      TNQAKLGLINDRNFFL-------------------QKILILRK-------ICNSPSL---
145230930      NSESAL-----------------------------QLITILKK-------LCNSPSL---
238484253      NSENAL-----------------------------QLITILKK-------LCNSPSL---
119494890      NSENAL-----------------------------QLITILKK-------LCNSPSL---
225681829      NSDSAL-----------------------------QLITILKK-------LCNSPSL---
258563128      N-----------------------------------------------------------
242778005      NTEGAF-----------------------------SLLTILKK-------LCNSPSL---
212533393      NTEGAF-----------------------------SLLTVLKK-------LCNSPSL---
189209013      SSDIAL-----------------------------QLINVLKK-------ICNSPSL---
71019185       APGNGL-----------------------------LQIGVLRK-------LCNSPEL---
290982366      DSNNAL-----------------------------ACIMHLKK-------LLAHPNM---
281209956      GKQNAL-----------------------------TTMTTLKQ-------LCNYPSL---
167385507      DQCGAL-----------------------------KYIQLFTK-------LCNHPAL---
170577655      LPYDHL-----------------------------TLIDALRK-------LCNHPFL---
145350886      ESISPL-----------------------------QAIQTLQK-------LCNAAAL---
224013540      DNDTPL-----------------------------TLLTEVRK-------LCTHPSL---
145482121      -----------------------------------MQLNLLRK-------VTTHPKL---
145338703      KQTKVL-----------------------------AYITALKK-------LCNHPKL---
20336209       AGAKLF-----------------------------QDFQMLSR-------IWTHPWCLQ-
242018945      ENKSLF-----------------------------NTFSWLQK-------IWTHPRVFHH
196005243      RTYSLF-----------------------------GDFSNLTS-------IWTYPWN---
81916664       LGLNPL-----------------------------KAFCVCCK-------IWNHPDVLYE
75026277       LGLNPL-----------------------------KAFCVCCK-------IWNHPDVLYE
193580055      DGYNVF-----------------------------LCLHVLTL-------ITLHPLT---
193610723      DGHNVF-----------------------------LCLHVLTL-------ITLHPLT---
145335288      MRKNFF-----------------------------AAYQVLAQ-------ILNHPGI---
258572168      PNARLW-----------------------------AWLAILSL-------LCNHPSC---
171685718      SSAQVW-----------------------------SMVAKLGT-------VLAHPKI---
289615990      RTACVW-----------------------------EFIAALKL-------LLAHPKI---
164425263      RTACVW-----------------------------GLIASLKL-------LLAHPKI---
72391587       -----------------------------------DNLLCLKASEHRPYHLSTHPLCFLG
71662347       -----------------------------------DGLTSIKASEHRPYHLSTHPLCFLG
239977156      -----------------------------------TAMTALRATEHRPHHLSTHPACYLA
146081173      -----------------------------------TAMTALKATEHRPHHLSTHPACYLA
Sm441121       ---GTL-----------------------------EMDITRTR-------ISIHPLL---
Bd3g18910      A-YGSL-----------------------------KRAAVETA-------VYIHPCLKDI
Bd1g74070      G-QNKF-----------------------------SKRSNCNA-------VSLHPCLKDI
Os03g06920     G-INKF-----------------------------AKRSRCNA-------VSLHPCLKNA
Sb01g046180    G-LKRF-----------------------------EAHAKCNA-------VSLHPCLKDV
```

```
Bd3g19890    A-YEKF-----------------------------KRSAVGTA-------LYMHPCLSEM
Os06g14440   A-YEKF-----------------------------KRSAVGTA-------LYIHPCLSEI
Sb07g002945  S-HDRF-----------------------------KRSAVGTA-------LYIHPCLSQL
ZM093940     M-HDRF-----------------------------KRSAVGSA-------LYIHPCLSGL
ZM064574     A-HDRF-----------------------------KRNAVGSA-------LYIHPCLSEL
Bd2g21430    A-YEYL-----------------------------KSSAVGTA-------LYVHPCLFEM
Bd2g21450    G-YEYL-----------------------------KRSAVGTA-------LYMHPCLSEM
Os08g14610   EDHGML-----------------------------KTSAVGAA-------LYVHPCLSEI
Vv35918      KFERKF-----------------------------KKNSVGSA-------VYLHPQLKYF
Pt195587     KLAMKF-----------------------------KRSSVGSA-------VYLHPKLNSF
AtDRD1       REKRKF-----------------------------KVSAVGSA-------IYLHPKLKVF
At2g21450    K-MELF-----------------------------KQISLGAA-------LYIHPKLKSF
Bd2g26500    GSGNNF-----------------------------EHEYVISL-------ASTHPSL---
Os05g32610   GSGNNF-----------------------------EHEYVISL-------ASTHPSL---
Sb09g019410  GSGNNF-----------------------------EHEYVISL-------ASTHPSL---
RMR1         GSGNNF-----------------------------EHEYVISL-------ASTHPSL---
Bd2g43500    ---GFL-----------------------------DAEYKISL-------ASIHPFL---
Os02g43460   ---GTL-----------------------------DAEYKISL-------ASIHPFL---
Bd3g50300    GTNGHL-----------------------------DFEYKISL-------ASVHPSL---
Sb04g033300  ---TGL-----------------------------DEEYKISI-------ASIHPSL---
ZM178435     ---MGL-----------------------------DAEYKISL-------ASIHPSL---
Vv15867      EKKNPL-----------------------------ELGYLVSL-------ISVHPSL---
Pt28648      ---DHF-----------------------------EMEYLLSV-------LSVHPSL---
Cp76.2       GTRNTI-----------------------------LLDFRVSL-------VSVHPSL---
At1g05490    ---NVF-----------------------------ETEHKLSL-------VSVHPSL---
At3g24340    TSQNTF-----------------------------EFEHKLSA-------VSVHPSL---
Bd1g16720    TGRYPL-----------------------------EIELLITV-------GSIHPWL---
Os07g49210   SSRFPL-----------------------------EVELLITI-------GSIHPWL---
Sb02g043870  NARYLL-----------------------------EIELLITI-------ASIHPWL---
ZM108166     NARYPL-----------------------------EYELLITI-------ASIHPWL---
Vv29366      YKGYPL-----------------------------ELELLVTL-------GSIHPWL---
Pt832603     CPGYPL-----------------------------EVELLITL-------ASIHPSL---
Pt567214     CPGYPL-----------------------------EVELLITL-------ASIHPSI---
Cp19.123     ------------------------------------------------------------
AtCLSY1      YHGYPL-----------------------------ELELLITL-------AAIHPWL---
At5g20420    YFGYPL-----------------------------EVELQITL-------AAIHPWL---
Sm84719      KKKGFL-----------------------------AEDSRLAR-------ACVHPCF---

                              740                 760                 780
15898471     ------------------------------------------------------------
256419642    ------------------------------------------------------------
237794935    ------------------------------------------------------------
187779742    ------------------------------------------------------------
ScSNF2       --------------------------------FEEV-ED---------------------
83286649     --------------------------------FDGI-E----------------------
124803472    --------------------------------FDGI-E----------------------
74008371     --------------------------------FDGA-EP---------------------
14028669     --------------------------------FDGA-EP---------------------
56118945     --------------------------------FDGA-EP---------------------
47217344     --------------------------------FDGA-EP---------------------
157103787    --------------------------------FDGA-EP---------------------
170572145    --------------------------------FDGA-EP---------------------
255719682    --------------------------------FDGA-EP---------------------
145610651    --------------------------------FEGA-EP---------------------
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145353082    --------------------------------FTGT-DV---------------------
225436589    --------------------------------FESA-DH---------------------
189521245    --------------------------------FPVA-AA---------------------
47206539     --------------------------------FPVA-AVVRTSCPPL-SF----------
113678140    --------------------------------FPAA-AM---------------------
156717248    --------------------------------FPVA-AM---------------------
73997410     --------------------------------FPVA-AM---------------------
115939069    --------------------------------FPTA-AA---------------------
221120608    --------------------------------FSTA-SL---------------------
256052547    --------------------------------FPSA-AE---------------------
24666729     --------------------------------FPSA-AE---------------------
170592228    --------------------------------FPKA-SI---------------------
17569817     --------------------------------FMKA-CL---------------------
256072692    --------------------------------MQIG-DS---------------------
145341798    --------------------------------LDGV-EAAI-------------------
145491053    --------------------------------IQEM-QNDLTKGC---------------
118367847    --------------------------------IKEM-EIE-LTQNF--------------
145484966    --------------------------------LKEM-HSDILEKSK--------------
239899054    --------------------------------ISGV-EDSHLEAL---------------
291001481    --------------------------------ISGA-EENITRG----------------
211853152    --------------------------------IKGA-EEKILGEF----RETYNQM----
189521372    --------------------------------IKGA-EEKIMEDF----KEVYSPA----
260834763    --------------------------------INGA-EEKILGEY----KDQHGEN----
196012568    --------------------------------INGA-EEKIVGEFTA-NNQVNGINAA--
242011216    --------------------------------LNGA-EEQIQIDY----RNVNGDD----
193599122    --------------------------------LNGA-EDQIQYDY----RNLNGDD----
19112177     --------------------------------YSPD-IEDRNLPYEL-AM----------
259147500    ------------------------------------------------------------
254582697    ------------------------------------------------------------
255720394    ------------------------------------------------------------
50309923     ------------------------------------------------------------
146416597    ------------------------------------------------------------
68483838     ------------------------------------------------------------
149235383    ------------------------------------------------------------
199432721    ------------------------------------------------------------
254568884    ------------------------------------------------------------
19075591     ------------------------------------------------------------
261358370    ------------------------------------------------------------
70982085     ------------------------------------------------------------
225682364    ------------------------------------------------------------
239615027    ------------------------------------------------------------
212536498    ------------------------------------------------------------
255936215    ------------------------------------------------------------
189204870    ------------------------------------------------------------
66813000     ------------------------------------------------------------
242056785    ------------------------------------------------------------
85014197     ------------------------------------------------------------
Cr13231      ------------------------------------------------------------
ScRAD54      --------------------------------L-----NFEDEFDDE-DD----------
50302399     --------------------------------L-----ELSEDIPGS-EE----------
156845511    --------------------------------L-----DLESELPEMGDS----------
45190309     --------------------------------L-----DLPDEIAGS-TN----------
255718981    --------------------------------L-----RLPDDIEGS-ED----------
238878261    --------------------------------L-----DLPEDVEGS-EE----------
```

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255728815     --------------------------------L-----DLPDDIEGC-DH----------
149239498     --------------------------------L-----NLPDDIEGC-DD----------
149388940     --------------------------------L-----NLPDDFEGS-EK----------
190348945     --------------------------------L-----RLPEEVSGS-ED----------
254570653     --------------------------------L-----NLPEDIEGC-EN----------
189211141     --------------------------------L-----NLPEDLPGC-EN----------
46127169      --------------------------------L-----NMSDDLPGS-EK----------
225684006     --------------------------------L-----NLGADLPGC-EQ----------
259485020     --------------------------------L-----NLSTDLPGC-EH----------
238840822     --------------------------------L-----KLSEDLPGC-EK----------
19115202      --------------------------------L-----NLTEDLEGC-EA----------
50546160      --------------------------------L-----KLPDEIEGC-RK----------
58266612      --------------------------------L-----NLPEDLPGS-EA----------
164660184     --------------------------------L-----NLPADLEGS-EE----------
41055574      --------------------------------IYEKCLTGEEGFDGA-LD----------
118094595     --------------------------------IYDKCVEEEEGFMGA-LD----------
281351942     --------------------------------IYDKCVEEEDGFEGA-LE----------
195539537     --------------------------------IYDKCVEEEDGFEGT-LD----------
47575794      --------------------------------IYEKCVEEEEGFQGA-LN----------
156369786     --------------------------------IYEKAQMEDEGFEGV-LE----------
238814383     --------------------------------VYEKIQENSDGFEGA-AK----------
170041242     --------------------------------VYEKIKERAEGFEEA-YK----------
189238349     --------------------------------IMDKILEGGEGFEKS-RH----------
195161916     --------------------------------ICEKIAAGEKGFENS-QN----------
193591979     --------------------------------IIDKIMNGSDGFENS-KH----------
71033369      ------------------------------------------------------------
221488620     ------------------------------------------------------------
157128256     --------------------------------IASTEKIDVGGSLIK-LL----------
241602475     RHMSLWGCFRSSQ--------DLLPTKSQKQFSLDM-SKLAAESL---------------
194214970     ----------------------LFNSIKEKECSSTW-DKNEERSLYE-GL----------
281347253     ----------------------LFNSIKEKEYSSTW-DGNEERSLYE-GL----------
119906776     ----------------------LFGSIKEKESNSTW-DESEERNLYE-GL----------
194037038     ----------------------LFSSVKEKECSSAW-DENEERRLYE-DL----------
149045437     ----------------------LFSFVKGKEFNSSR-DENEERSLCQ-GL----------
149638830     ----------------------LFKAIKEKECNSTH-DGFEETNLYE-GL----------
45382655      ----------------------LFKALKEKCCDPKS-DEHVESSLYE-GL----------
148230804     ----------------------LFRTIQEKSTNPDQ-G---EHSLYE-SI----------
156379220     ----------------------LYSASQGANTLGDE-D---QVSLYD-GL----------
193661957     --------------------------------ILNN-RNNSDTTEET-LN----------
110760280     --------------------------------F---------------------------
242023203     --------------------------------LNKDDNYLEK------------------
66811190      --------------------------------VYTP------------------------
71651467      --------------------------------FYEA-VLNSSKEEVR-EG----------
50311185      --------------------------------IKTDPYYEERLSQVQ-TS----------
254585925     --------------------------------I-------QTDSYYK-SS----------
50294037      --------------------------------L-------CNDPYYQ-SN----------
255725568     --------------------------------LIDD------------------------
241952408     --------------------------------LADD------------------------
260941370     --------------------------------LHND------------------------
254567481     --------------------------------LKDE-PDFARYNLGN-RF----------
145230930     --------------------------------LTPR-DVNETPSETI-AA----------
238484253     --------------------------------LSPR-NVDEKPSETI-AA----------
119494890     --------------------------------LSPK-TGDEKPSETI-AA----------
225681829     --------------------------------LNPK-SSDEDSTSTL-SS----------
```

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258563128     -------------------------------------SETENSNSTI-SS----------
242778005     --------------------------------LNAK-TDDEPQNSTV-AT----------
212533393     --------------------------------LTAK-AGDEPPNATM-EA----------
189209013     --------------------------------LKSSKDNDDTPSEML-Q-----------
71019185      --------------------------------LLKD-TEADADSPTK-AL----------
290982366     --------------------------------IYPQ-ENNEEKEEED-NE----------
281209956     ------------------------------------------------------------
167385507     --------------------------------ISKY-LMEEKISLNE-ND----------
170577655     --------------------------------LYQSMVVKRQTCKVE-ER----------
145350886     ------------------------------------------------------------
224013540     --------------------------------LNKD-DSSLS------------------
145482121     --------------------------------IEDD-ESQAAEKLVV-QD----------
145338703     --------------------------------IYDT-IKSGNPGTVG-FE----------
20336209      -LDYISKENKGYF--------DEDSMDEFIASDSD---------ETS-MSLSSDDYTKKK
242018945     ALDTVSNDVDKTS--------QFAMAFADCNKI---------------------------
196005243     ---WKRDNNNSMT--------DMVSENDEVSTVSDG-GCSTTWKDSS-LAEDCDHLQNDT
81916664      ALQKENLANEQDL--------DVEELGSAGTSARC----------------------PPH
75026277      ALQKESLANEQDL--------DVEELGSAGTSARC----------------------PPQ
193580055     ------------------------------------------------------------
193610723     ------------------------------------------------------------
145335288     ------------------------------------------------------------
258572168     --------------------------------FMEK-ILKKNRDKKQ-QGVLQDSENESV
171685718     --------------------------------FKTV-AERQKDAKGK-AKSGKSEDEDEL
289615990     --------------------------------FKSKVQE---------------------
164425263     --------------------------------FRSKMEE---------------------
72391587      FLTGIWRTGQVD--------------------IEEE-PGEFEELGTY-RLSRDDDALAKD
71662347      FISGVYKSLNGNH--------KLTPEAEEELESQEY-A-----SQLY-SLTEDDIGLIDE
239977156     FISNCYQSMVSGW-------------------TVRA-QSNTSRLRTT-QLEEIDAMRLEQ
146081173     FISDSYQSMVSGW-------------------TVRA-QSNTSRPRVS-QLEEIDTMRLEQ
Sm441121      ----------------------------------------------------------RS
Bd3g18910     SEADSNEK--NWT--------DAE-----IDSLIES------------------------
Bd1g74070     KNICEKNE--NTTYQKIFLRNHEK-----ISSVMSG------------------------
Os03g06920    NKADADDG--NVT--------NRK-----IGSIISG------------------------
Sb01g046180   KIVDKKNR--NIN--------KRM-----MDSIVCG------------------------
Bd3g19890     SEGDATDRANNLT--------DAA-----VDSMVQS------------------------
Os06g14440    SEGDAADRASNLT--------DAT-----VDSLIES------------------------
Sb07g002945   SEVNAENRANTLR--------DDL-----VDSLLDS------------------------
ZM093940      SEVNAENRAHTLR--------DDS-----VDSLMDS------------------------
ZM064574      SEVNAEHRANTFR--------DDL-----VDSLVDS------------------------
Bd2g21430     SEAGAADRAKNLT--------DAT-----VDTLVES------------------------
Bd2g21450     SEAGAADKANILT--------DAT-----VDTLFES------------------------
Os08g14610    SEANDVDR-------------DDR-----VDSLVNS------------------------
Vv35918       AEKLAANE--SKT--------DEMTCQKKMDEILEQ------------------------
Pt195587      SK----NS--AIT--------DDM-----MDDLLET------------------------
AtDRD1        SDK---SD--DVS--------DTT-----MDEMVEK------------------------
At2g21450     LEENPSNGEKGFS--------DNNTTVMKLDKMLKK------------------------
Bd2g26500     --------------------------------VTAI-NMSDEEASLI-DK----------
Os05g32610    --------------------------------VNAI-NMTEEEASLI-DK----------
Sb09g019410   --------------------------------VTAI-NMSEEEASLI-DK----------
RMR1          --------------------------------VTAI-NMSEEEASLI-DK----------
Bd2g43500     --------------------------------LTSV-KLSDEEASIV-NK----------
Os02g43460    --------------------------------VTCA-KLSEKETSSV-DV----------
Bd3g50300     --------------------------------ITSTQKLPYQLTSVM-DK----------
Sb04g033300   --------------------------------LASA-KLSEQEESIL-DI----------
```

```
ZM178435          --------------------------------LASA-KLSMKEESIL-DK----------
Vv15867           -------------------------------------LPSDERKLFF-DQ----------
Pt28648           --------------------------------LP---EKSVGTLEFK-FV--------DR
Cp76.2            -----------------------------------------------------LIDCHPE
At1g05490         -------------------------------------------------VSRCKISEKER
At3g24340         -------------------------------------------------YLCCNPTKKED
Bd1g16720         ----------------------------------------------------IKTTNCAS
Os07g49210        ----------------------------------------------------IKTTKAVS
Sb02g043870       ----------------------------------------------------INTTRCAS
ZM108166          ----------------------------------------------------INTTKCAS
Vv29366           ----------------------------------------------------ITTAACAD
Pt832603          ----------------------------------------------------VNSSVCVK
Pt567214          ----------------------------------------------------INSSVCVK
Cp19.123          ------------------------------------------------------------
AtCLSY1           ----------------------------------------------------VKTTTCCA
At5g20420         ----------------------------------------------------VTSSNCCT
Sm84719           ------------------------------------------------------------

                                   800                 820                 840
15898471          ------------------------------------------------------------
256419642         ------------------------------------------------------------
237794935         ------------------------------------------------------------
187779742         ------------------------------------------------------------
ScSNF2            -------------QINPTR-----------------------------------------
83286649          ------------------------------------------------------------
124803472         ------------------------------------------------------------
74008371          ------------------------------------------------------------
14028669          ------------------------------------------------------------
56118945          ------------------------------------------------------------
47217344          ------------------------------------------------------------
157103787         ------------------------------------------------------------
170572145         ------------------------------------------------------------
255719682         ------------------------------------------------------------
145610651         ------------------------------------------------------------
145353082         ------------------------------------------------------------
225436589         ------------GYGGNRS-----------------------------------------
189521245         --------------EAPKT-----------------------------------------
47206539          -HQKHTSAYHVPFQEAPVL-----------------------------------------
113678140         --------------EAAKM-----------------------------------------
156717248         --------------EAPKM-----------------------------------------
73997410          --------------EAPKM-----------------------------------------
115939069         --------------DAQRL-----------------------------------------
221120608         --------------EAPRY-----------------------------------------
256052547         --------------EAQRM-----------------------------------------
24666729          --------------EATIS-----------------------------------------
170592228         --------------EAPKL-----------------------------------------
17569817          --------------EAPKL-----------------------------------------
256072692         --------------IAPRLNL---------------------------------------
145341798         ------------------------------------------------------------
145491053         ------------------------------------------------------------
118367847         ------------------------------------------------------------
145484966         ------------------------------------------------------------
239899054         ----GVK-----------------------------------------------------
291001481         ------------------------------------------------------------
```

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211853152    ------------------------------------------------------------
189521372    ------------------------------------------------------------
260834763    ------------------------------------------------------------
196012568    ------------------------------------------------------------
242011216    ------------------------------------------------------------
193599122    ------------------------------------------------------------
19112177     ------------------------------------------------------------
259147500    ------------------------------------------------------------
254582697    ------------------------------------------------------------
255720394    ------------------------------------------------------------
50309923     ------------------------------------------------------------
146416597    ------------------------------------------------------------
68483838     ------------------------------------------------------------
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70982085     ------------------------------------------------------------
225682364    ------------------------------------------------------------
239615027    ------------------------------------------------------------
212536498    ------------------------------------------------------------
255936215    ------------------------------------------------------------
189204870    ------------------------------------------------------------
66813000     ------------------------------------------------------------
242056785    ------------------------------------------------------------
85014197     ------------------------------------------------------------
Cr13231      ----------------PPGAA---------------------------------------
ScRAD54      ------------------------------------------------------------
50302399     ------------------------------------------------------------
156845511    ------------------------------------------------------------
45190309     ------------------------------------------------------------
255718981    ------------------------------------------------------------
238878261    ------------------------------------------------------------
255728815    ------------------------------------------------------------
149239498    ------------------------------------------------------------
149388940    ------------------------------------------------------------
190348945    ------------------------------------------------------------
254570653    ------------------------------------------------------------
189211141    ------------------------------------------------------------
46127169     ------------------------------------------------------------
225684006    ------------------------------------------------------------
259485020    ------------------------------------------------------------
238840822    ------------------------------------------------------------
19115202     ------------------------------------------------------------
50546160     ------------------------------------------------------------
58266612     ------------------------------------------------------------
164660184    ------------------------------------------------------------
41055574     ------------------------------------------------------------
118094595    ------------------------------------------------------------
281351942    ------------------------------------------------------------
195539537    ------------------------------------------------------------
47575794     ------------------------------------------------------------
156369786    ------------------------------------------------------------
```

```
238814383     ------------------------------------------------------------
170041242     ------------------------------------------------------------
189238349     ------------------------------------------------------------
195161916     ------------------------------------------------------------
193591979     ------------------------------------------------------------
71033369      -------------------------------------------------------LKRGG
221488620     -----------------------------------------------------VKSQAQM
157128256     ------------------------------------------------------------
241602475     ------------------------------------------------------------
194214970     -----------------INV-FP---ADYNP-----------------------------
281347253     -----------------VDV-FP---ADYNP-----------------------------
119906776     -----------------MNV-FP---ADYNP-----------------------------
194037038     -----------------LKV-FP---PDYNP-----------------------------
149045437     -----------------LTV-FP---AGYNL-----------------------------
149638830     -----------------IDV-FP---PDYSP-----------------------------
45382655      -----------------TDV-FP---QDYTS-----------------------------
148230804     -----------------AEL-FP---QDYDG-----------------------------
156379220     -----------------LKL-FP---ECNDA-----------------------------
193661957     ------------------------------------------------------------
110760280     ------------------------------------------------------------
242023203     ------------------------------------------------------------
66811190      ------------------------------------------------------------
71651467      ------------------------------------------------------------
50311185      ------------------------------------------------------------
254585925     ------------------------------------------------------------
50294037      ------------------------------------------------------------
255725568     ------------------------------------------------------------
241952408     ------------------------------------------------------------
260941370     ------------------------------------------------------------
254567481     ------------------------------------------------------------
145230930     ------------------------------------------------------------
238484253     ------------------------------------------------------------
119494890     ------------------------------------------------------------
225681829     ------------------------------------------------------------
258563128     ------------------------------------------------------------
242778005     ------------------------------------------------------------
212533393     ------------------------------------------------------------
189209013     ------------------------------------------------------------
71019185      ------------------------------------------------------------
290982366     ------------------------------------------------------------
281209956     ------------------------------------------------------------
167385507     -ENCIKG-----------------------------------------------------
170577655     ------------------------------------------------------------
145350886     ------------------------------------------------------------
224013540     ------------------------------------------------------------
145482121     ------------------------------------------------------------
145338703     ------------------------------------------------------------
20336209      KKGKKGKKDSSSSGSGSDNDVEVIKVWNSRSRGGGEGNVDETGNNPSVSLKLEESKATSS
242018945     ------------------------------------------------------------
196005243     GIIDATRLDLGDTTKGNENDSANTRVNS------------DDGSKKAVTVDQLVLNTTIN
81916664      GTKVKGEDSALPSSMGEATNSKFLQ-------GVGFNPFQERGNNIVTYE----------
75026277      GTKGKGEDSTLASSMGEATNSKFLQ-------GVGFNPFQERGNNIVTYE----------
193580055     ----------------------------------------------LYRLKHFRSSKQRE
193610723     ----------------------------------------------LYRLKHFKNSKQRE
```

```
145335288    ------------------PQLRSEDSKNGRRGSIVDIPDDCSSDENIDYNMVTGEKQRTM
258572168    IDDITDS-----------------------------------------------------
171685718    ILPQDIL-----------------------------------------------------
289615990    ------------------------------------------------------------
164425263    ------------------------------------------------------------
72391587     CSSLLENGKLADFVA---------------------------------------------
71662347     CLSLVSSGFLTEFVG---------------------------------------------
239977156    YAQMIENEQLDAFIN---------------------------------------------
146081173    YVQLVENEQLDAFID---------------------------------------------
Sm441121     AEAAGGDFSAVAAEVVDVRASM--------------------------------------
Bd3g18910    ---------------INIRDGV--------------------------------------
Bd1g74070    ---------------IDINDGA--------------------------------------
Os03g06920   ---------------IDINDGV--------------------------------------
Sb01g046180  ---------------IDISDGV--------------------------------------
Bd3g19890    ---------------INVRDGV--------------------------------------
Os06g14440   ---------------IIIKDGV--------------------------------------
Sb07g002945  ---------------INVKDGV--------------------------------------
ZM093940     ---------------INVRDGV--------------------------------------
ZM064574     ---------------ITVRDGV--------------------------------------
Bd2g21430    ---------------VQLSDGV--------------------------------------
Bd2g21450    ---------------VHVGDGV--------------------------------------
Os08g14610   ---------------INLGDGV--------------------------------------
Vv35918      ---------------LDVRDGV--------------------------------------
Pt195587     ---------------VDVRDGV--------------------------------------
AtDRD1       ---------------LDLNEGV--------------------------------------
At2g21450    ---------------INVRDGV--------------------------------------
Bd2g26500    --------PMLERLRSNPYEGV--------------------------------------
Os05g32610   --------PMLERLRSNPYEGV--------------------------------------
Sb09g019410  --------HMLGKLRSNPYEGV--------------------------------------
RMR1         --------PMLAKVRSNPYEGV--------------------------------------
Bd2g43500    ----------LKSSRLDPCEGV--------------------------------------
Os02g43460   --------SLLKSLRPNPCVGV--------------------------------------
Bd3g50300    --------PLLESLRLNPCEGV--------------------------------------
Sb04g033300  --------PKLESLRSRPSEGV--------------------------------------
ZM178435     --------PKLESLRSNPSGGV--------------------------------------
Vv15867      --------TKLEKIKLNPDIGV--------------------------------------
Pt28648      --------MELEMLRSKPEAGV--------------------------------------
Cp76.2       MDHGYIDWKKLEKCRMIPNAGV--------------------------------------
At1g05490    LSIDEALLAQLKKVRLDPNQSV--------------------------------------
At3g24340    LVIGPATLGTLKRLRLKYEEGV--------------------------------------
Bd1g16720    TFFTSAELDKVDKYKKDFAAGC--------------------------------------
Os07g49210   TFFSPAEVKKVERYKRDFAAGC--------------------------------------
Sb02g043870  TYFTPAEVARVGKYKRNFAVGC--------------------------------------
ZM108166     TYFTPAEVASVDKYKRNFAAGC--------------------------------------
Vv29366      KYFSREELLELKKHKDDVKKGS--------------------------------------
Pt832603     KFYNLEELMELEKLRFDCKKGS--------------------------------------
Pt567214     KFYEQEELMELEKLRFDCKKGS--------------------------------------
Cp19.123     ------------------------------------------------------------
AtCLSY1      KFFNPQELLEIEKLKHDAKKGS--------------------------------------
At5g20420    KFFNPQELSEIGKLKHDAKKGS--------------------------------------
Sm84719      ----AVDVESPELEQQDPKAGA--------------------------------------

                              860                 880                 900
15898471     --------------------LKGGE---------Q-------------------------
```

```
256419642    --------------------LNEAE---------Q-------------------------
237794935    ----------------------IID---------E-------------------------
187779742    --------------------I--ID---------E-------------------------
ScSNF2       -----------------ETN----D---------D-------------------------
83286649     -----------------EPPYIEGN---------H-------------------------
124803472    -----------------EPPYIEGN---------H-------------------------
74008371     -----------------GPPYTTDE---------H-------------------------
14028669     -----------------GPPYTTDM---------H-------------------------
56118945     -----------------GPPYTTDM---------H-------------------------
47217344     -----------------GPPYTTDL---------H-------------------------
157103787    -----------------GPPYTTDY---------H-------------------------
170572145    -----------------GPPYTTDQ---------H-------------------------
255719682    -----------------GPPYTTDE---------H-------------------------
145610651    -----------------GPPYTTDE---------H-------------------------
145353082    -----------------PEDGVPIE---------D-------------------------
225436589    -----------------TNDCGKLE---------R-------------------------
189521245    -----------------PSGAYEGV---------G-------------------------
47206539     -----------------PNGSYDGN---------L-------------------------
113678140    -----------------PNGMYEGG---------G-------------------------
156717248    -----------------PNGMYDGS---------A-------------------------
73997410     -----------------PNGMYDGS---------A-------------------------
115939069    -----------------QNGAFEVV---------S-------------------------
221120608    -----------------ANNAYEVK---------G-------------------------
256052547    -----------------PNGAYEGV---------G-------------------------
24666729     -----------------PSGLYEMS---------S-------------------------
170592228    -----------------KSGIYEGT---------A-------------------------
17569817     -----------------KNGMYEGS---------A-------------------------
256072692    --------------NDETNGPYEPK---------A-------------------------
145341798    -----------------APEGASTT---------A-------------------------
145491053    -----------------SNKNDYIL---------K-------------------------
118367847    -----------------KTSEERYK---------C-------------------------
145484966    -----------------GNEGEYQK---------I-------------------------
239899054    -----------------PDSAVAMQ---------N-------------------------
291001481    -----------------MSDVEVNE---------A-------------------------
211853152    ------------------AADFYLQ---------A-------------------------
189521372    ------------------AVDFHLQ---------A-------------------------
260834763    ------------------HGK-YLH---------C-------------------------
196012568    -----------------I------H---------A-------------------------
242011216    -------------------PDAYFK---------A-------------------------
193599122    -------------------PDVYYK---------A-------------------------
19112177     ------------------------R---------S-------------------------
259147500    -----------------------------------------------LDRDTKRHNP---
254582697    -----------------------------------------------LDRDERSKEA---
255720394    -----------------------------------------------LEREQRQNED---
50309923     -----------------------------------------------LDLKRKKMNDYED
146416597    -----------------------------------------------VDRELLLRKK--G
68483838     -----------------------------------------------VYRDTLMKRK---
149235383    -----------------------------------------------IYREALMHRA---
199432721    -----------------------------------------------VDREILQRRK--N
254568884    -----------------------------------------------VDVHAKRRSK-KD
19075591     -----------------------------------------------VTREYLLHKE--D
261358370    -----------------------------------------------ID-PHLQNKA--G
70982085     -----------------------------------------------QNHKMQSHQS---
225682364    -----------------------------------------------PEHKTLSTKP--G
```

```
239615027     -----------------------------------------------PEHKTLSKKS--S
212536498     -----------------------------------------------VTHKLFSATT---
255936215     -----------------------------------------------ADHTLRSREA---
189204870     -----------------------------------------------TEHKTLSKKP--G
66813000      -----------------------------------------------LHMDASDEDR--P
242056785     ---------LEREHAAQNP----DY---------G-------------------------
85014197      ---------------------------LFPRKLGVSEDCEEEASDEKNGEDEALELPGAD
Cr13231       --------------GGTGTSGEGAE---------G-------------------------
ScRAD54       ----------------------------------LELP---DDYN--------MPGSKAR
50302399      ----------------------------------L-IP---DDYQSSV----DSRTSRNR
156845511     ----------------------------------VSIP---DGYV-------ISKNGKSK
45190309      ----------------------------------L-IP---DDYQSAMTH--NSRGGRSH
255718981     ----------------------------------L-MP---EDYQS------STVSKRGR
238878261     ----------------------------------F-IP---DDYQSSIA---GGSASRNR
255728815     ----------------------------------L-IP---DDYESSISHNGGRGGFRNS
149239498     ----------------------------------L-IP---EDYVSSIHG--HGGGGRNR
149388940     ----------------------------------F-IP---EDYCSSI-----GSGGRNR
190348945     ----------------------------------I-LP---DDYES---------SGRDK
254570653     ----------------------------------L-LP---DDYDY------GHGNRRNR
189211141     ----------------------------------T-LP---DDFVQ------KDARGRDR
46127169      ----------------------------------C-YP---DDYVP------KEARGRDR
225684006     ----------------------------------F-FP---DDYIP------IESRGRDR
259485020     ----------------------------------A-FP---DDYVP------VEARGRDR
238840822     ----------------------------------Y-FP---EDMAS------SNGRRGDR
19115202      ----------------------------------L-FP---PGFIP------RELRGRDR
50546160      ----------------------------------V-FP---DDYAPP-----DERGSRDR
58266612      ----------------------------------L-LP---DGYNG---------KGRDR
164660184     ----------------------------------L-YP---EGYRP---------GDR-R
41055574      ----------------------------------L-FP---QNY-------------STK
118094595     ----------------------------------L-FP---AGY-------------STK
281351942     ----------------------------------I-FP---PGY-------------SSK
195539537     ----------------------------------I-FP---PGY-------------NSK
47575794      ----------------------------------L-FP---SGY-------------STK
156369786     ----------------------------------M-FP---QKF-------------DLK
238814383     ----------------------------------L-LP---ANY-------------STK
170041242     ----------------------------------I-LP---ANY-------------SAK
189238349     ----------------------------------L-LP---PNY-------------NDK
195161916     ----------------------------------I-LP---INY-------------NPK
193591979     ----------------------------------L-LP---PTYIA----------AHSK
71033369      --SSPDVDSLLLDIENATKSSKYKC---------C-------------------------
221488620     LQGFEKCEKYFSELDLEGQKARSRM---------V-------------------------
157128256     ----------------NDNLPPWQD---------M-------------------------
241602475     ------------------------------------------------------------
194214970     -----------------------FM---------F-------------------------
281347253     -----------------------LM---------F-------------------------
119906776     -----------------------IM---------F-------------------------
194037038     -----------------------LM---------F-------------------------
149045437     -----------------------LQ---------L-------------------------
149638830     -----------------------VT---------F-------------------------
45382655      -----------------------DT---------F-------------------------
148230804     -----------------------AK---------I-------------------------
156379220     -----------------------SE---------L-------------------------
193661957     --------------QHLNRTITLKH---------S-------------------------
110760280     ------------------------------------------------------------
```

```
242023203       ----------------------------------I-------------------------
66811190        ---DKETDVGTSILKLFPKEWNPKV---------F-------------------------
71651467        ---------HGIPKSVLPKGYKSGT---------L-------------------------
50311185        -----------------------ST---------S-------------------------
254585925       ---------------MQNSRISQKY---------Q-------------------------
50294037        ----------------VDSNIFTVS---------N-------------------------
255725568       -----------------------AFFKRIVEEKFH-------------------------
241952408       -----------------------EFFKKIVEQKFN-------------------------
260941370       ---------------------------PLFASFLH-------------------------
254567481       ------------------------------------------------------------
145230930       -------------LLSSLPPNLLRH---------F-------------------------
238484253       -------------LLSSLPPNLLRH---------F-------------------------
119494890       -------------LLSSLPPNLLRH---------F-------------------------
225681829       -------------LVASLPSSITRR---------L-------------------------
258563128       -------------LLSTLPPNLLRH---------F-------------------------
242778005       -------------LLSTLSPSLRRQ---------F-------------------------
212533393       -------------LLSTLTPSLRRQ---------F-------------------------
189209013       -----------------------SILPLIPNNILN-------------------------
71019185        -----------VGDLTRFFPPNFVR---------N-------------------------
290982366       -LFDDIWTQSKKHFPSDYNPNDKKE---------Y-------------------------
281209956       ----IKSDDYSKYFTDSNDTTTPTD---------F-------------------------
167385507       -----------------------VT---------I-------------------------
170577655       -------EFYNAFLQSFPNTFNAFS---------L-------------------------
145350886       --------------------ATEVS---------D-------------------------
224013540       -----------------------AS---------D-------------------------
145482121       ------------------------------------------------------------
145338703       --NCLEFFPAEMFSGRSGAWTGGDG---------A-------------------------
20336209        SNPSSPAPD-----WYKDFVTDADA---------E-------------------------
242018945       -------------------LKEEEF---------T-------------------------
196005243       SASDKDAVDRHKKRWLEQLAKVPQE---------D-------------------------
81916664        --------------WAKELLTNYQT---------G-------------------------
75026277        --------------WAKDLLTNYQT---------G-------------------------
193580055       LGTAVDEKLSKDLSWIDSYGEDPRF---------F-------------------------
193610723       LGTAVDEKLSKDLSWIDSYGEDPRF---------F-------------------------
145335288       NDLQDKVDGYLQKDWWVDLLQKNNY---------K-------------------------
258572168       --------------QTLGPEVIKEV---------Q-------------------------
171685718       -----------------------SE---------L-------------------------
289615990       ------------------------------------------------------------
164425263       ------------------------------------------------------------
72391587        ------------------------------------------------------------
71662347        ------------------------------------------------------------
239977156       ------------------------------------------------------------
146081173       ------------------------------------------------------------
Sm441121        ------------------------------------------------------------
Bd3g18910       ------------------------------------------------------------
Bd1g74070       ------------------------------------------------------------
Os03g06920      ------------------------------------------------------------
Sb01g046180     ------------------------------------------------------------
Bd3g19890       ------------------------------------------------------------
Os06g14440      ------------------------------------------------------------
Sb07g002945     ------------------------------------------------------------
ZM093940        ------------------------------------------------------------
ZM064574        ------------------------------------------------------------
Bd2g21430       ------------------------------------------------------------
```

```
Bd2g21450    ------------------------------------------------------------
Os08g14610   ------------------------------------------------------------
Vv35918      ------------------------------------------------------------
Pt195587     ------------------------------------------------------------
AtDRD1       ------------------------------------------------------------
At2g21450    ------------------------------------------------------------
Bd2g26500    ------------------------------------------------------------
Os05g32610   ------------------------------------------------------------
Sb09g019410  ------------------------------------------------------------
RMR1         ------------------------------------------------------------
Bd2g43500    ------------------------------------------------------------
Os02g43460   ------------------------------------------------------------
Bd3g50300    ------------------------------------------------------------
Sb04g033300  ------------------------------------------------------------
ZM178435     ------------------------------------------------------------
Vv15867      ------------------------------------------------------------
Pt28648      ------------------------------------------------------------
Cp76.2       ------------------------------------------------------------
At1g05490    ------------------------------------------------------------
At3g24340    ------------------------------------------------------------
Bd1g16720    ------------------------------------------------------------
Os07g49210   ------------------------------------------------------------
Sb02g043870  ------------------------------------------------------------
ZM108166     ------------------------------------------------------------
Vv29366      ------------------------------------------------------------
Pt832603     ------------------------------------------------------------
Pt567214     ------------------------------------------------------------
Cp19.123     ------------------------------------------------------------
AtCLSY1      ------------------------------------------------------------
At5g20420    ------------------------------------------------------------
Sm84719      ------------------------------------------------------------

                                920                 940                 960
15898471     ----SVRRSG----------KMIRTMEIIE-EALD--EGDKIAIFTQFVDMGKIIR-NII
256419642    ----YPNHSV----------KLHELTREMSENI----SNHKVLIFSQFLGMLGLIR-EKL
237794935    ----YKGGSS----------KLRIAMELVE-EGVD--EGKKILLFSQFISVLKNIS-KLL
187779742    ----YKGGSS----------KLRIAMELVQ-EGVD--EGKKILLFSQFTSVLKNIS-KLL
ScSNF2       ----IWRVAG----------KFELLDRILP-KLKA--TGHRVLIFFQMTQIMDIME-DFL
83286649     ----LIETSG----------KMSLLDKLLP-RLKK--ENSRVLLFSQMTRLLDIID-DYC
124803472    ----LIETSG----------KMSLLDKLLP-RLKK--ENSRVLLFSQMTRLLDIID-DYC
74008371     ----IVSNSG----------KMVVLDKLLA-KLKE--QGSRVLIFSQMTRLLDILE-DYC
14028669     ----LVTNSG----------KMVVLDKLLP-KLKE--QSSRVLIFSQMTRVLDILE-DYC
56118945     ----LVTNSG----------KMVVLDKLLP-RLKE--QGSRVLIFSQMTRVLDILE-DYC
47217344     ----LVVNSG----------KMVVLDKLLP-KLKE--QGSRVLIFSQMTRVLDILE-DYC
157103787    ----LLENSG----------KMVVLDKLLT-KLQE--QGSRVLVFSQMTRMLDILE-DYC
170572145    ----LVDNSG----------KMVLLDKLLV-KLKA--QGSRVLIFSSMSRMLDLLE-DYC
255719682    ----LVYNSA----------KLKVLDKLLR-KFKE--EGSRVLIFSQMSRLLDILE-DYC
145610651    ----LVYNSG----------KMVVLDKLLK-RLKA--QGSRVLIFSQMSRVLDILE-DYC
145353082    ----LISASG----------KLAVLDRMLQ-KLKE--GGHRVVLFSQFTSMLDILQ-DFL
225436589    ----LILSSG----------KLVLLDKLLE-KLHE--TNHRVLIFSQMVRMLDILA-EYM
189521245    ----LTKASG----------KLMLLQKMLR-KLKE--QGHRVLVFSQMTKMLDLLE-DFL
47206539     ----LVKSSG----------KLTLLQKMLK-KLKD--EGHRVLIFSQMTKMLDLLE-DFL
113678140    ----LTKSSG----------KLLLLQKMLR-KLKE--GGHRVLIFSQMTKMLDLLE-DFL
156717248    ----LIKGAG----------KLLLLQKMLR-KLKD--DGHRVLIFSQMTKMLDLLE-DFL
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73997410      ----LIRASG-----------KLLLLQKMLK-NLKE--GGHRVLIFSQMTKMLDLLE-DFL
115939069     ----LIKSCG-----------KLVLLCKMLR-MLKK--DNHRVLIFSQMTRMLDLLE-DFL
221120608     ----LTEASG-----------KLVLLYKMLK-KLKE--QGHRVLIFSQMTRVLDLLE-DFM
256052547     ----LRKGSG-----------KLELMSKMLR-KLYE--TKHRVLIFSQMTKMLDLLE-DFL
24666729      ----LTKASG-----------KLDLLSKMLK-QLKA--DNHRVLLFSQMTKMLNVLE-HFL
170592228     ----LVKASG-----------KFVLLQKMLK-KLKE--QGHRVLIFSQMTKMLDIME-DFC
17569817      ----LIKNAG-----------KFVLLQKMLR-KLKD--GGHRVLIFSQMTMMLDILE-DFC
256072692     ----LVQVSS-----------KLVVLMELLR-GLFV--DDHRVLIFSRFTMMLDLLE-QVM
145341798     ----LVSSAG-----------KLQLLDKLLP-HLRE--GGHRALIFSQMTRVLDVLE-DYC
145491053     ----LVECSG-----------KMILLDKLLN-KFRN--EGKKMLIFSQFTMMLSILE-EYL
118367847     ----LVDTSG-----------KMILLDKLVQ-KYKI--EGKKILIFSQFVYMLNLLE-EYL
145484966     ----LIEYSG-----------KMVLLDKMLK-KFLK--EDKKMLIFSQFTNMLALLE-EYL
239899054     ----LTEMSG-----------KLVFLEKLIP-QLRE--KKEKLLIFSQFKIVLDIIE-DWL
291001481     ----LIKSSS-----------KMILVDKLLR-KLRE--GGHKVLIFSQMVLVLNILE-DYM
211853152     ----MIQSAG-----------KLVLIDKLLP-KMKA--GGHKVLIFSQMVRCLDILE-DYL
189521372     ----MIQSAG-----------KLVLIDKLLP-KMKA--GGHKVLIFSQMVRCLDILE-DYL
260834763     ----MVQASG-----------KLVLIDKLLP-KLRA--GGHKVLIFSQMVRCLDILE-DYL
196012568     ----MIQASG-----------KLVLIDKLLP-KLKD--GGHKVLIFSQMVRCLDILE-DYL
242011216     ----LIHSSG-----------KMVLVDKLLP-KLKS--NGHRVLIFSQMVKCLDILE-DYL
193599122     ----LIHSSG-----------KMVLIDKLLP-KLKD--NGHRVLIFSQMVRCLDIIE-DYL
19112177      ----LEEASC-----------KFLILRLLVP-KLIT--RGHRILLFSQFIQQLDILE-DWF
259147500     -DYGDPKRSG-----------KMQVVKQLLL-LWHK--QGYKALLFTQSRQMLDILE-EFI
254582697     -SYGDPKRSG-----------KMQVVKQLLL-LWRK--EGHKALLFTQSRQMLDILQ-EFI
255720394     -SYGDPKRSG-----------KMQVVKQLLK-LWHS--QGHKTLLFTQSRQMLDILE-RFI
50309923      ADYGNPARSG-----------KMQVVKQLLL-LWHS--QGHKTLLFTQSRQMLDILQ-EFI
146416597     YNYGIPNKSG-----------KMLVLKGLLQ-LWQS--QGHRTLLFCQTKQMLDILE-KLL
68483838      -NYGDPAKSG-----------KMQVLKNLLR-LWQS--ENHKTLLFCQTRQMLDILE-KFV
149235383     -NYGDPSKSG-----------KMQVLKNLLQ-LWQS--EDHKTLLFCQTRQMLDILE-KFV
199432721     YNYGNPAKSG-----------KLQVLKNLLQ-LWQM--QGHRTLLFCQTKQMLDILE-KFV
254568884     PTYGSASKSG-----------KMQVVKKLLE-LWKS--QGHKTLLFTQTRQMLDILE-SFL
19075591      YNYGDPEKSG-----------KLKVIRALLT-LWKK--QGHRTLLFSQTRQMLDILE-IGL
261358370     YDWGDPEKSG-----------KMLVVRNLLQ-IWKK--LGHKTLLFSQSKMMLNVIE-KFL
70982085      -GYGNANKSG-----------KMQVVKSLLE-LWRD--TGHKTLLFAQHRIMLDILE-KFV
225682364     YNYGSAAKSG-----------KMQVVKALLE-LWKE--TGHKSLLFAQHRIMLDILE-RFI
239615027     YNYGSASKSG-----------KMQIVKSLLE-LWRD--TGHKTLLFAQHRIMLDILE-RFI
212536498     -GYGEPSKSG-----------KMKVVKALLE-LWRD--TGHKTLLFAQHRIMLNILE-KFV
255936215     -DYGDAERSG-----------KMKVLKGLLE-VWRD--TGHKTLLFTQGRLMLDIIE-KFL
189204870     YDYGNPNRSG-----------KMQVVKELLS-LWKK--GGHKTLLFAQHRIMLDILQ-KFI
66813000      HDYGNIERSA-----------KLKVVETILP-LWFK--QGDKVLLFCQTRQMLDIVE-QYI
242056785     ----NPERSG-----------KMKVVEQVLK-VWKD--QGHRVLLFTQTQQMLDILE-NFL
85014197      VSYDLVSSSC-----------KIKILVDLLK-KWRS--EGNKVLVFSQTIRMLDIIE-RCV
Cr13231       ----GGGGSGGVLERRLFFRDLRVLGMLVDVGELE--EAEKLVIFSQHLAVLDDLQ-ALL
ScRAD54       -DV-QTKYSA-----------KFSILERFLH-KIKTE-SDDKIVLISNYTQTLDLIE-KMC
50302399      -SVIQTAFSS-----------KFSVLARFLY-KIKTE-SNDKIVLISNYTQTLDLIE-KMC
156845511     -DV-QPQFSG-----------KFAILERFLH-KINTE-SDDKIVLISNYTQTLDLVE-RLC
45190309      VEV-QTTHSS-----------KFAILERFLF-KIKHE-SNDKIVLISNYTQTLDLIE-KMC
255718981     SEL-QTWHSG-----------KFSILGRFLH-KIKTE-SDDKIVIISNYTQTLDLIE-KMC
238878261     -EI-QTWFSG-----------KFLILERFLQ-KINKE-TDDKIVLISNYTQTLDLIE-KMC
255728815     -EV-QTWFSV-----------KFMILERFLH-KIKKE-TNDKIVLISNYTQTLDLIE-KMC
149239498     -EI-QTWFSG-----------KFQVLERFLH-KIKRE-TNDKIVLISNYTQTLDLIE-KMC
149388940     -EV-QSWYSG-----------KFMILERFLY-QIRSQ-TNDKIVLISNYTQTLDLIE-RMC
190348945     -EI-RTWYSG-----------KFAMLERFLH-QIRTE-TDDKIVLISNYTQTLDLIE-RMC
254570653     -EV-QVWHSS-----------KFLILQRFLY-KINKE-TNDKIVIISNYTQTLDLIE-KLC
189211141     -EV-KTWYSG-----------KMAVLDRMLA-RIRAE-TNDKIVLISNYTQTLDIFA-MLC
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46127169      -EV-KSWYSG----------KMAVLDRMLA-RIRQD-TNDKIVLISNYTSTLDLFE-KLC
225684006     -DV-RSWYSG----------KMMVLDRMLA-RIRQD-TNDKIVLISNYTQTLDLFE-RLC
259485020     -DV-RPWYSG----------KMMVLDRMLA-RIRQD-TNDKIVLISNYTQTLDLFE-KLC
238840822     -EV-KSWYSG----------KMMVLDRMLA-RIRQD-TNDKIVLISNYTQTLDLFE-RLC
19115202      -NI-DSSLSG----------KMLVLERMLY-QIKQE-TDDKIVLISNYTSTLDLFE-QLC
50546160      -DI-YPHFSA----------KFLILERMLR-SINAE-TNDKIVIISNYTATLDLIE-KMC
58266612      -TV-NCQYSG----------KFVVLERMLD-HINHH-TNDKIVLISNATQTLDLME-KLC
164660184     -NV-AVGLSG----------KLAVLERFLT-SMRAK-TDDKIVLISNYTQTLDLFE-RLC
41055574      -AV-EPQLSG----------KMLVLDYILA-MTRTT-TSDKVVLVSNYTQTLDLFE-KLC
118094595     -SV-EPQLSG----------KMLVLDYILA-VTKST-SNDKVVLVSNYTQTLDLFE-KLC
281351942     -AL-EPQLSG----------KMLVLDYILA-VTRSR-SSDKVVLVSNYTQTLDLFE-KLC
195539537     -AL-EPQLSG----------KMLVLDYILA-VTRSR-SSDKVVLVSNYTQTLDLFE-KLC
47575794      -SV-EPQLSG----------KMLVLDYILA-VTRST-SSDKVVLVSNYTQTLDLFE-KLC
156369786     -NV-QPELSG----------KMQVLDYILA-VTKAT-SDDKVVLVSNYTQTLDLFE-KLC
238814383     -EV-MPELSG----------KLMVLDCLLA-FIKST-TTDKIVLVSNYTQTLDLFE-RLC
170041242     -EV-RPEFGG----------KLMVLDCMLA-SIKMN-TNDKIVLVSNYTQTLDLFE-KLC
189238349     -DV-MPQLSG----------KLMLLDCFLA-NLKNN-YNDKVVLVSNYTQTLDLFE-KLC
195161916     GEI-NPELSG----------KFKLLDFMLA-AIRAH-GNDKVVLISNYTQTLDLFE-LLA
193591979     KKL-MIELSS----------KLMVLDTMLA-VIKTT-TTDRVVLISNYTQTLELFE-RLA
71033369      ----RCDLSG----------KFLVLYRLLY-QIRRH-GNDRVVIISNYTQTLDLFE-RLC
221488620     ----RTEISG----------KLLLLARLLD-VIRTT-TNDKIVLISNYTQTLDLFD-RMC
157128256     ----GPTDSG----------KLAVLDSLLE-TLIQ--RQEKAVIVSYYGKTLDMIM-GLC
241602475     -----EASSG----------KLKVLAAMLA-SLWDSSPREKIVVVSNFTRMLNVVQ-ELC
194214970     ----TEEESG----------KLQVLSKLLA-VIRELCPAEKVVLVSNYTQTLNILQ-EVC
281347253     ----MEEESG----------KLQVLMKLLA-VIHELRPTEKVVLVSNYTQTLNILQ-EVC
119906776     ----TEEESG----------KLQVLSKLLA-VIRELRPAEKVVLVSNYTRTLDILQ-EVC
194037038     ----AEEESG----------KLQVLSKLLA-VIHELRPAEKVVLVSNYTQTLNILQ-EVC
149045437     ----SESESG----------KLQVLVKLLA-AISELRPTEKVILVSNYRQTLNLLE-EVC
149638830     ----PEVDSG----------KLRVLIKLLA-VIRELSPSEKVVLVSNYTQTLTILQ-EIC
45382655      ----SEIDSG----------KLQVLVKLLA-AIRELSSSERVVLVSNYTQTLNVLL-ETC
148230804     ----SESESG----------KLLVLSKLLS-GIRELSPSERVVLVSHYTQTLNILQ-ALC
156379220     ----SIAQSG----------KLTVLNSMLE-EIH--CTGERVVLVSNYSQTLDILQ-KLC
193661957     ----LIESSG----------KLIVVDNLLK-ELHKN-GSEKTVLISYYTQTLDIFV-KLC
110760280     --------------------YISIVQTLIK-NLKK--TNEKLVLISYYTQTLDLLE-RVC
242023203     ----DIDTSG----------KLKVTVNFLK-ELQMTSVKEKVLIVSNATQTLNLLE-KVF
66811190      ----QPQYSS----------KLLFVDRLLA-NIRNSKSGDKTVIISNYTQTLEVLA-TMC
71651467      ----SEAAGG----------KMHFVSLMLD-ELRNNGDRDKLVIVSNFTQTLDVIA-NMC
50311185      ----GKFTSG----------KLRILLSLLH-ELKTK-TDEKVVVISNYTQTLDIIE-GHC
254585925     ----NEYNSG----------KLRVLMKLLN-QIKIETTSDKVVVISNYTQTLDIIE-NLM
50294037      ----KSNSSG----------KLTVLLELLL-EIKATSPMEKVVIVSNYTQSLDIIQ-GLM
255725568     ----LTLSSG----------KINVLIPLLL-EIVA--QKEKIVLISNYTQTLDLLE-KVL
241952408     ----LGMSSG----------KLNILVPLLL-EIVS--LKEKIVLISNYTKTLDLLE-TVL
260941370     ----DTELSSSPLSSRTTGSKVNVLVPLLL-EFRT--VGEKVVLVSNYAQTLDFLE-TVL
254567481     -------NSG----------KIKLTVLLLR-KLFET-TNEKCVIVSNFTKTLDVLQ-LII
145230930     ----TPSSSA----------KLRVLDQLLD-GLRTK-TSEKIVLVSNYTSTLNLLA-NLL
238484253     ----SPSSSA----------KIRVLDQLLH-ILHTS-TSEKVVLVSNYTSTLNLLA-TLL
119494890     ----SPSCSA----------KIRVLDQLLH-NLRTS-TSEKIVLVSNYTSTLNMLA-NLL
225681829     ----TPASSG----------KIRVLDQLLH-NIRHT-TSEKVVLISNYTSTLDLLG-KLL
258563128     ----SPASSG----------KIRVLDQLLH-NLRST-TSEKVVLVSNYTSTLNLLA-ALL
242778005     ----SPSSSG----------KIRVLDQLLH-NLRTS-TSEKIVIVSNYTSTLNLLG-VLL
212533393     ----SPSSSG----------KIRVLDQLLH-NLQTT-TSEKIVLVSNYTSTLNLLG-ILL
189209013     ----SSASSA----------KLRLLDSLVH-RIYTT-TEEKIVIVSNYTTTLDMIE-RLL
71019185      ----EARFGG----------KLICVMNLLQ-TVRAQ-TDDKVVLVSNFTSTLDIIE-AMM
290982366     ----HSQYSG----------KLLVLDNLLR-EIRE--VGDRVVIVSNFKSILNEIE-KLC
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281209956     ----DASQSG----------KMEFVEQLLI-TLKS--LGDRAVLVSNYTQTLDVFE-LLL
167385507     ----NEESSN----------KFNITIQFIK-EIIIK-SKEKVVLVSNYTKTLDLFE-MYF
170577655     ----STTDSG----------KLNVFVELLA-TFRE--QEEKVVIVSNFTQTLDLIE-ELC
145350886     ----PVASSS----------KLAVLRAMFR-ALA---NDERIVVVSGFTTTLDLIA-KLC
224013540     ----DASLSG----------KLIVLSSLIE-SIREHHPTDKVIITSNFTTALTVVENSIL
145482121     ------YQSV----------KFNCLKILVD-QCKE--QNEKVVINSYYRQTLDQIEHNLI
145338703     ----WVELSG----------KMHVLSRLLA-NLRRK-TDDRIVLVSNYTQTLDLFA-QLC
20336209      ----VLEHSG----------KMVLLFEILR-MAEE--IGDKVLVFSQSLISLDLIE-DFL
242018945     ----EIRASG----------KLVLLFQILK-ICHQ--AGDKLLVFSQYLTTLNLIE-YFL
196005243     ----LMTYCN----------KMKVVVKIID-LAYK--LQEKVIIFSHSLCCLTLIE-EVL
81916664      ----VLENSP----------KMVLLFHLIE-ESVK--LGDKILVFSQSLSTLALIE-EFL
75026277      ----VLENSP----------KMVLLFHLIE-ESVK--LGDKILVFSQSLSTLALIE-EFL
193580055     ----EAKQSN----------KITYVLNTIH-ECSK--RNEKVLCFLKSLLALDALE-YFL
193610723     ----EAKQSN----------KITYVLNTIH-ECSK--RNEKILCFLKSPLALDALE-HFL
145335288     ----VSDFSG----------KMILLLDILS-MSAD--VGDKALVFSQSIPTLDLIE-LYL
258572168     ----RVFEGISDLKSTALSHRATMLEQIVK-ESVS--AGDKVLVFSHSIPTLNYLE-HIL
171685718     ----LTPTTCRDIDNDAHSYKIVALMFLLG-EFRK--VGDKALIFTQSIPALDFLE-SIF
289615990     --------------------RLNTNQAPAKRKKRI--INDEDPDNNESDEPLDLSR-DML
164425263     --------------------RLSTNPALVKGKQRI--TNDEDPESDEVDEPLDLSR-DTL
72391587      -------LSG----------KLTALISILH-SIFE--KMEKAVIFSQYIGSQDFIA-RTL
71662347      -------LSG----------KMTVLISILH-SIRE--KKEKAIIFSQYVGSQDFIS-RTL
239977156     -------VSG----------KMRVLVDIVL-RVQA--RKEKLIIFSLYVGSQDLIH-RTL
146081173     -------LSG----------KMRVLVDIVL-RVQA--RKEKLIIFSLYVGSQDLIH-RTL
Sm441121      --------------------KTAFVMKLIE-LCQC--ANEKVLVFGEFLAPFHLLL-RML
Bd3g18910     --------------------KARFFLNILS-LADS--AGEKLIAFSR-------------
Bd1g74070     --------------------KLKFIHNLLS-LSES--AGEKVLVFSQYVCSLLFLE-MLF
Os03g06920    --------------------KAKFVHNLLS-LSEA--TGGKVLVFSQYVRSLIFLE-KLV
Sb01g046180   --------------------KAKFIHNLLS-LSEA--AGEKVLVFSQYVRSLHFLE-TLF
Bd3g19890     --------------------KASFFINILR-LASC--AGEKLIAFSQYILPMKFLE-RLL
Os06g14440    --------------------KAKFFFNILS-LANS--AGEKLIAFSQYILPMKFLE-RLL
Sb07g002945   --------------------KANFFMNILS-LANS--AGEKVIAFSQYILPMKFFE-RLL
ZM093940      --------------------KANFFMNILS-LANS--AGEKVIAFSQYILPMTFFE-RLL
ZM064574      --------------------KANFFMNILS-LANS--AGEKVIAFSQYISPMIFFE-RLL
Bd2g21430     --------------------KANFFINILK-LASS--AGEKLIAFSQHILPMKFLE-RLL
Bd2g21450     --------------------KAKFFINILK-LASS--AGEKLIAFSQHILPMKFLE-RLL
Os08g14610    --------------------KARFFLNILA-LANS--AGEKLVAFSQYTLPMKFLE-RLL
Vv35918       --------------------KAKFFLNVLA-LCQS--SGEKLLVFSQYLLPLRFLE-KLT
Pt195587      --------------------KAKFFLNILS-LCES--AGEKLLVFSQYLTPLKFLE-RLV
AtDRD1        --------------------KAKFFLNLIN-LCDS--AGEKLLVFSQYLIPLKFLE-RLA
At2g21450     --------------------KMKFFLNLLA-LCES--TGEKLLVFSQYIVPIKTLE-RLM
Bd2g26500     --------------------KTRFVIEVVR-LCEA--LKEKVLIFSQFIQPLELIK-EHL
Os05g32610    --------------------KTRFVMEVVR-LCEA--LKEKVLIFSQFIQPLELIK-EHL
Sb09g019410   --------------------KTRFVMEVVR-LCEA--LREKVLIFSQYIQPLELIK-EHL
RMR1          --------------------KTRFVIEVVR-LSEA--LREKVLIFSQFIQPLELIK-EHL
Bd2g43500     --------------------KTRFVLEIVR-LCKP--LKERVLVFSQYLEPLSLIM-DQL
Os02g43460    --------------------KTKFVLEIVR-LCEA--MKERVLVFSQYLEPLSLIM-DQL
Bd3g50300     --------------------KTKFVFEIVR-LCQP--LKERVLVFSQYLQPLDLIM-QQL
Sb04g033300   --------------------KTRFVLEIVR-LCEA--LNERVLVFSQYLGPLSLIM-EQL
ZM178435      --------------------KTRFVLEIVR-LCEA--LNERVLVFSQYLEPLSLIM-EQL
Vv15867       --------------------KTKFLMAFIR-FSET--MNEKVLVFSQFLDPLTYLM-DQL
Pt28648       --------------------KTKFLMELIR-LCQA--RNEKVLVFSQYLEPLNLVI-KQL
Cp76.2        --------------------KTKFVNELLH-LSEA--LGEKVLIFAQYLEPLTLIM-DQL
At1g05490     --------------------KTRFLMEFVE-LCEV--IKEKVLVFSQYIDPLKLIM-KHL
At3g24340     --------------------KTKFLIDFIR-ISGT--VKEKVLVYSQYIDTLKLIM-EQL
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Bd1g16720    --------------------KAKFVIDLLH-KCSF--RGERVLIFCHNVSPINFLV-KLI
Os07g49210   --------------------KAKFVIDLLH-KSSF--RGERVLIFCHNVSPITFLV-KLI
Sb02g043870  --------------------KAKFVIDLLH-KSSF--RGERVLIFCHNVAPITFLV-KLI
ZM108166     --------------------KAKFVIDLLH-KSSF--RGERVLVFCHNVAPIAFLV-TLI
Vv29366      --------------------KVKFVLSLVN-RCII--RKEKILIFCHNISPINLFV-DIF
Pt832603     --------------------KVMFVLNLVY-R-VV--KNEKVLIFCHNIAPIKLFL-ELF
Pt567214     --------------------KVMFVLNLVY-R-VV--KKDKVLIFCHNIAPIKLFL-ELF
Cp19.123     ------------------------------------------------------------
AtCLSY1      --------------------KVMFVLNLVF-RVV---KREKILIFCHNIAPIRLFL-ELF
At5g20420    --------------------KVMFVLNLIF-RVV---KREKILIFCHNIAPIRMFT-ELF
Sm84719      --------------------KTAFVMELLR-FLRN--KPEKLIIFGQYRQPLELLK-NMI

                               980                1000               1020
15898471     EKE----------------------------LNTEVPFLYGELSKKERD-----------
256419642    QHM----------------K-------VPFE------YFDGSTSATERERAIQNFQT--N
237794935    EKE----------------G-------IEYF------YLDGSTNASERIKLVNEFNK--N
187779742    EKE----------------G-------IEYF------YLDGSTNASERIKLVNEFNK--N
ScSNF2       RYI----------------N-------IKYL------RLDGHTKSDERSELLRLFNAP-D
83286649     RWK----------------K-------YEYL------RIDGSTVGDERQIRINKFNEP-N
124803472    RWK----------------N-------YPYL------RIDGSTPGDERQVRINQFNEP-N
74008371     MWR----------------G-------YEYC------RLDGQTPHEEREEAIEAFNAP-N
14028669     MWR----------------N-------YEYC------RLDGQTPHDERQDSINAYNEP-N
56118945     MWR----------------N-------YEYC------RLDGQTPHEERQDSIIAYNAP-G
47217344     MWR----------------N-------YGYC------RLDGQTPHEERQISINAFNEP-N
157103787    YWR----------------G-------YQYC------RLDGQTPHEDRTKMIDEYNAE-N
170572145    WWR----------------G-------YRYC------RLDGQTVHDERQKSIDEFNKP-D
255719682    FFR----------------N-------YEYC------RIDGSTAHEDRIEAIDEYNAP-D
145610651    VFR----------------E-------YKYS------RIDGGTAHEDRIAAIDEYNKP-G
145353082    TLR----------------G-------YTYA------RLDGSTNRVQRSIDIAAFNRP-D
225436589    SLR----------------G-------FQFQ------RLDGSTKAELRQQAMDHFNAP-G
189521245    DSE----------------G-------YKYE------RIDGGITGALRQEAIDRFNAP-G
47206539     EFE----------------G-------YKYE------RIDGGITGGLRQEAIDRFNAP-G
113678140    ENE----------------G-------YKYE------RIDGGITGGMRQEAIDRFNAP-G
156717248    EHE----------------G-------YKYE------RIDGGITGNMRQEAIDRFNAP-G
73997410     EHE----------------G-------YKYE------RIDGGITGNMRQEAIDRFNAP-G
115939069    EGE----------------G-------YKYE------RIDGGVTGGLRQEAIDRFNAP-G
221120608    EGH----------------G-------WRYE------RLDGTITGGIRQSAIDRFNLP-N
256052547    DSE----------------G-------YKFE------RIDGAVTGQLRQDAIDRFNAP-D
24666729     EGE----------------G-------YQYD------RIDGSIKGDLRQKAIDRFNDP-V
170592228    ENE----------------G-------YKYE------RIDGSITGQARQDAIDRFNAA-N
17569817     DVE----------------G-------YKYE------RIDGSITGQQRQDAIDRYNAP-G
256072692    INA----------------R-------YKYV------RIDGRVRGPLRQVTIDRFNAP-D
145341798    RAR----------------G-------HSYV------RLDGSITGKARQEAIDKYCAE-D
145491053    KFR----------------Q-------VKYE------KIDGQIKARERQNAIDRFNDP-Q
118367847    RYR----------------Q-------LKYE------KIDGSVKSKERQNAIDRFNDP-D
145484966    QFN----------------Q-------IKYE------KITGDIKQIDRQNAIDRFNDQ-K
239899054    TWK----------------K-------LPVE------RLDGSVSGGKRQAAIDRFNDK-K
291001481    RYR----------------N-------FTYV------RLDGTIKGSIRQQAIDRFNDP-N
211853152    MHK----------------R-------YLYE------RIDGRVRGNLRQAAIDRFSKP-D
189521372    IQR----------------R-------YLYE------RIDGRVRGNLRQAAIDRFSKP-D
260834763    VQN----------------V-------YPYE------RIDGRVRGNLRQAAIDRFSKP-D
196012568    VYR----------------R-------YQYE------RIDGRVRGNLRQAAIDRFCKP-E
242011216    IYR----------------K-------YSFE------RIDGRIRGDLRQAAIDRFCRP-D
193599122    VYR----------------K-------YPFE------RLDGRIRGNLRQAAIDRFCKP-D
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19112177     EYK----------------N-------IAYA------RFDGASSEMERQSAIDSFNAP-N
259147500    STK-----------DPDLSH-------LNYL------RMDGTTNIKGRQSLVDRFNN---
254582697    AFK-----------DQELTG-------LKFL------RMDGTTTISIRQSLVDEFNR---
255720394    SYK-----------DPELEE-------LTYL------RMDGTTSIGARQALVDSFNN---
50309923     SYK-----------DPELSD-------LKFL------RMDGTTNIGSRQSLVDKFNN---
146416597    VNL-----------TRISDGTEY----FNYM------RMDGSTPISKRQGLVDMFNN--N
68483838     ANL-----------SLINGGD------FNYL------RMDGSTPISKRQMLVDAFNQ--D
149235383    ANL-----------HLLGDESKK----FNYL------RMDGNTPISRRQQLVDTFNN--S
199432721    TNL-----------PSLNENGEEVRGTFNYL------RMDGSTNIGRRQALVDTFNE--D
254568884    ERL-----------NAKGAEEEDFV-PFKFL------RMDGTTSIGVRQSLVDVFNN--D
19075591     K---------------DLPD-------VHYC------RMDGSTSIALRQDLVDNFNK--N
261358370    G---------------GLET-------VKYV------RMDGETSIEKRQSLIDQFNT--D
70982085     R---------------SLSG-------FNYR------RMDGTTPIQNRQTMVDEFNN--D
225682364    K---------------SMTG-------FKYQ------RMDGNTPIKLRQSLVDEFNN--N
239615027    K---------------SLSG-------FKYQ------RMDGNTPIKLRQSMVDEFNN--N
212536498    N---------------TLSG-------FNYR------RMDGETPIHRRQLLVDEFNN--S
255936215    G---------------VLGG-------FNCR------RMDGTTPIKERQSLVNDFNN--D
189204870    S---------------QLPD-------INWR------RMDGDTPIKDRQNLVDEFNN--N
66813000     R---------------DSTQ-------FNYL------RMDGTTSIRQRQCLVEQFNI--D
242056785    TAC----------------D-------YQYR------RMDGLTPAKQRMALIDEFNN--T
85014197     RK-------------------------YTYL------RMDGRTPTSSRPGLVDRFNE--D
Cr13231      TSP----------------G-------QGYVPGRHLFRIDGSVDTNKRKQVIDGFND--G
ScRAD54      RYK----------------H-------YSAV------RLDGTMSINKRQKLVDRFND-PE
50302399     FSN----------------H-------YGVL------RLDGTMNINKRQKLVDRFND-PE
156845511    RRK----------------Q-------YGSV------RLDGSMTINKRQKLVDRFNS-PD
45190309     RYN----------------H-------YGVL------RLDGTMTINKRQKLVDKFND-PS
255718981    RSS----------------T-------YPVV------RLDGTMTINKRQKLVDRFND-PE
238878261    RYK----------------K-------YGVL------RLDGTMNINKRQKLVDKFND-PN
255728815    RNK----------------K-------YGVL------RLDGTLSINKRQKLVDKFNN-PD
149239498    RYK----------------K-------YGAL------RLDGTMNINKRQKLVDRFND-PD
149388940    RHK----------------K-------YGSL------RLDGTLSINKRQKLVDKFND-PE
190348945    RYK----------------R-------YQCC------RLDGTMNINKRQKLVDRFND-PE
254570653    ISS----------------R-------YGSL------RLDGTMNINKRQKLVDKFNN-PE
189211141    RSR----------------G-------YGCF------RLDGTMNVSKRQKLVDKFND-PE
46127169     RSR----------------Q-------YGSL------RLDGTMNVNKRQKLVDRFND-PE
225684006    RSR----------------Q-------YGCL------RLDGSMNVTKRQKLVDKFND-PE
259485020    RSR----------------A-------YGCL------RLDGTMNVKKRQKLVDKFND-PD
238840822    RSR----------------G-------YGCI------RLDGTMGVKKRSKLVDRFND-PN
19115202     RAR----------------G-------YKAL------RLDGTMNVNKRQRLVDTFND-PE
50546160     RQR----------------R-------YGCL------RLDGTMNINKRAKLVTQFND-PE
58266612     RSK----------------R-------YGYL------RLDGSMSVPKRSKIVAQFNQ-PE
164660184    RSR----------------R-------WGFF------RLDGTMNINKRQNLVDRFNN-PE
41055574     RNR----------------R-------YLYV------RLDGTMSIKKRAKIVERFNN-PS
118094595    RNR----------------R-------YLYV------RLDGTMSIKKRAKVVERFNS-PS
281351942    RAR----------------R-------YLYV------RLDGTMSIKKRAKVVERFNN-PL
195539537    RAR----------------R-------YLYV------RLDGTMSIKKRAKVVERFNN-PS
47575794     RTR----------------R-------YLYV------RLDGTMSIKKRAKIVERFNS-PS
156369786    RQR----------------R-------YQHV------RLDGSMSIKKRQKIVDRFND-PK
238814383    AKR----------------K-------YKYV------RLDGTMSIKKRAKVVDNFNN-PD
170041242    RKR----------------G-------YGYV------RLDGTMTIKKRGKVVDEFNK-PD
189238349    RKR----------------G-------YRYV------RLDGTMSIKKRAKVVANFND-PE
195161916    RKR----------------K-------YGFV------RLDGTMSIKKRSKVVDRFND-PE
193591979    KLR----------------N-------YTFV------RLDGSMTAKKRAKAVDDINS-PT
71033369     KEC----------------N-------YPFE------RLDGTTSIKKRHKLVTTFNDP-N
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221488620      RDC----------------G-------YPVM------RLDGQTSIKKRHAMITKFNDPMN
157128256      EHY----------------N-------YKYC------RLDGSTPSQDRCKIVSSFNSP-S
241602475      ACK----------------G-------YTFV------RLDGSTSSTQRLEIVERFNSA-H
194214970      KRH----------------G-------YAYT------RLDGQTPVSQRQQIVDSFNSK-Y
281347253      KRH----------------G-------YTYT------RLDGQTPISQRQQIVDGFNSK-Y
119906776      KRH----------------G-------YAYT------RLDGQTPISQRQQIVDGFNSK-Y
194037038      RRH----------------G-------YGCT------RLDGQTPISQRQQIVDGFNSK-Y
149045437      KCH----------------G-------YACA------RLDGQTPVSQRQQIVDNFNSK-Y
149638830      KRY----------------G-------YAHT------RLDGQTPISQRQHIIDGFNSK-H
45382655       KCY----------------G-------YSYT------RLDGNTPVSQRQQIVDSFNSK-F
148230804      VQH----------------G-------YSCT------RLDGQTPVTQRQHIVDGFNSK-Y
156379220      TVK----------------K-------YRYL------RLDGSTPTAKRQSLVERFNAK-H
193661957      DMK----------------H-------YKYL------RLDGSTATAQRTDIVKKFNN-SN
110760280      NME----------------C-------LQFL------RLDGNTTSSTRSKIIEQFNS-TN
242023203      HVL----------------N-------YSTC------RLDGNTPSAQRNKIVEDFNT--S
66811190       KTR----------------G-------YAYF------QLDGSTANAKRQQLVNLYNDP-A
71651467       RQK----------------R-------ISFF------QLDGSMPVKRRQEVVDRFNVP-E
50311185       SSE----------------G-------YTSA------RLDGSTATKTRDQIVTSFNN--D
254585925      ASA----------------G-------MSSC------RLDGSTPAKQRDAIVNNFNH--N
50294037       NSN----------------Q-------LSNC------RLDGATPAKQRDMLVNTFNN--N
255725568      SKI----------------N-------LTFS------RLDGSTATNIRSKIVKQFNS--N
241952408      RKI----------------N-------LTFS------RLDGSTPNNVRSKLVNQFNT--N
260941370      SKL----------------N-------LQYC------RLDGSTPAKVRDKLVLDFNK--C
254567481      EHN----------------N-------WKYH------RLDGSS--KGRDKIVRDFNESPQ
145230930      TSL----------------S-------LPFL------RLDGSTPAQKRQSLVEDFNRLPS
238484253      TSL----------------S-------LPFL------RLDGSTPAQKRQSLVEDFNRFPT
119494890      NSL----------------S-------LPFL------RLDGSTPAQKRQALVEDFNRLPP
225681829      TSL----------------S-------LPFL------RLDGSTPAAKRQALVDDFNRSSP
258563128      TSL----------------A-------LPFL------RLDGSTPANKRQYLVDDFNRSSS
242778005      TSL----------------S-------LPFL------RLDGSTPSSKRQSLVDDFNRAPA
212533393      TSL----------------S-------LPFL------RLDGSTPSAKRQSLVDDFNRAPA
189209013      VSL----------------S-------YTYL------RLDGSTPASKRQALVEKFNKTPK
71019185       RKK----------------R-------YPYL------RLDGKTPQDERMAMVNQFNREGV
290982366      KIR----------------D-------YPLS------RLDGSTQSEKRMVIVNSFNS-PK
281209956      KKL----------------S-------IQSY------RIDGQVKATERQDRVDKFNDPSN
167385507      KQE----------------EEYKQKKIFNYL------RLDGKTSQKQRDIIVEKIND-KS
170577655      RTL----------------Y-------YTIL------RLDGSTEAKKRMEIVEEFNS-LS
145350886      ESE----------------H-------LKYD------RLQGSTPPKERTSIVRTFNN---
224013540      RKK----------------N-------LPFI------RLDGSVDNASRQPIVDSFNNNSV
145482121      QWN------------------------LKFL------RLDGKVVQKQRLTLVDEFNK--D
145338703      RER----------------R-------YPFL------RLDGSTTISKRQKLVNRLNDP-T
20336209       ELASREKTEDKDKPLIYKGE-------GKWLRNIDYYRLDGSTTAQSRKKWAEEFNDETN
242018945      RFVNDNNNKNDEC--------------NTWVTGVDYYRIDGTTNSQSRFDYCKKFNDKNN
196005243      REN----------------C-------TPSLSYEDYCRMDGRTSAELRQRYIDKFNNSNS
81916664       GKRDMPCLPGAEG----QGT-------QKWVRNVSYFRLDGSTPAFERERLINQFNDPSN
75026277       GKREVPCPPGTEG----QGA-------QKWVRNISYFRLDGSTPAFERERLINQFNDPSN
193580055      QQE------------------------KKWILGEDYLRMDGKTSLSIRNKMCEAFNN-PE
193610723      QQE------------------------KRWILGEDYLRMDGKTPLSIRNQMCEAFNN-PE
145335288      SRVPRHGKQG-----------------KFWKKGKDWYRIDGKTESSERQKLVDRFNEPDN
258572168      KQN----------------G-------WTYC------RLDGTTPISSRQVATKYFNR-TD
171685718      KRR----------------Q-------IGYQ------RLDGHTPINTRQASIKKFNS--N
289615990      RSVLAKVSIRGIDDIDLFKRPGMK---ILHK------RLDGSTPVGKRQAAIKDFNT--D
164425263      RNVLAKVSIRGIDDIDLFKLKK-----INYR------KLDGKTPVSQRQAAVKEFNA--V
72391587       TAY----------------K-------ISVV------TIRGKDCQQRRRVVEMFRD--D
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71662347     TSF----------------D-------IVSS------TIRGRDCHERRRRTIEKFRE--D
239977156    TAL----------------R-------VCTF------TVRGRDSQDRRRRAMHEFSE--N
146081173    TAL----------------R-------VCTF------TVRGRDSQDRRRRAMQEFSE--N
Sm441121     ELE------------------------RGWSRDKEVVFLHGALVTEERHELMDRFNA-EG
Bd3g18910    ---------------------------------------------------MDKFNS--S
Bd1g74070    TRM------------------------KGWKPDMHMFMIHGGSV--QRDKTIERFNH--S
Os03g06920   SRM------------------------KGWKSEVHIFRVTGGSTQDQREQAVHRFNN--S
Sb01g046180  TKM------------------------KGWKPGVNTFLMDGSSTQEQREQAIERFNN--S
Bd3g19890    VKT------------------------WGWHVGKEIFVISGDTSPEDRELAMDQFNN--S
Os06g14440   VKR------------------------LGWHVGKEIFMISGDTSADDREVAMDQFNN--S
Sb07g002945  VKM------------------------KGWHVGKEIFMISGDTSQEDREVAVDHFNN--S
ZM093940     VKK------------------------KGWHVGREIFMISGDTSQEDREAAVDRFNS--S
ZM064574     VKK------------------------KGWHVGKEIFMISGDTSQEDRELATDHFNN--S
Bd2g21430    VNM------------------------FGWRVGKEIFAITGDTSAADRELAMDKFNN--S
Bd2g21450    VKM------------------------FGWHVGMEIFVITGDTSAVDRELAMDKFNN--S
Os08g14610   VKE------------------------MGWHVGKEIFVINGDTSMEDGQLAMDQFNG--S
Vv35918      MKV------------------------KGWSPGKEIFAISGESSSEQREWSMERFNT--S
Pt195587     MKV------------------------KGWILGKEIFVISGESSSDHREWSMERFNN--S
AtDRD1       ALA------------------------KGWKLGKEVFVLTGNTSSEQREWSMETFNS--S
At2g21450    SSM------------------------KGWRLGKEMFTITGDSSNEQREWSMERFNN--S
Bd2g26500    RKF------------------------FKWREGKEILQMDGKILPRYRQNSIEVFNNPD-
Os05g32610   RKI------------------------FKWREGKEILQMDGKILPRYRQNSIEVFNNPD-
Sb09g019410  RKF------------------------FKWREGKEILQMDGKILPRYRQASIEAFNNPN-
RMR1         RKF------------------------FKWREGKEILQMDGKILPRYRQASIEAFNNPN-
Bd2g43500    TKK------------------------FNWTEGKEILLMSGNVRVKQREALMEAFND-MN
Os02g43460   SKM------------------------FNWIEGEEILLMSGNVLVQNREALMEAFND-MK
Bd3g50300    RSE------------------------FLWTKDKEILSMSGDDDAETRQKLMNDFNN-ME
Sb04g033300  KAK------------------------FNWAEGKEILLMSGKVPVKNRQTMMEVFND-MK
ZM178435     KER------------------------FSWAEGEEILLMSGKVLVKKRQTMMEVFNN-MK
Vv15867      KYH------------------------FHWIVGKEVLYMDGQRDVKQRQSSINTFND-PA
Pt28648      ESN------------------------FSWIQGEDILYMHGKLKIDERQILIKHFNNAN-
Cp76.2       RDR------------------------KKWTQGKEVLYMDGKYDIMHRQTLISTFNN--S
At1g05490    VSR------------------------FKWNPGEEVLYMHGKLEQKQRQTLINEFNDPK-
At3g24340    IAE------------------------CDWTEGEQILLMHGKVEQRDRQHMIDNFNK-PD
Bd1g16720    ENV------------------------FGWRLGEEVLVLQGDQDLPVRSDVMDKFNSDGE
Os07g49210   EMV------------------------FGWRLGEEVLVLQGDQELPVRSDVMDKFNGDSA
Sb02g043870  EIV------------------------FGWRLGQEVLVLQGDQELPVRSDVMDKFNSDRE
ZM108166     EIV------------------------FGWRLGQEVLVLQGDQELHVRSDVMDKFNSDRR
Vv29366      DKL------------------------YKWKKGEDVLVLQGDLELFERGRVMDQFEEPG-
Pt832603     ENI------------------------FRWQQGKEILVLTGELELFERGRVMDKFEELG-
Pt567214     ENV------------------------FRWQ------------------LEMDKFEELG-
Cp19.123     ---------------------------------RELLVLTGDLELFERGRVMDKFEEPG-
AtCLSY1      ENV------------------------FRWKRGRELLTLTGDLELFERGRVIDKFEEPG-
At5g20420    ENI------------------------FRWQRGREILTLTGDLELFERGRVIDKFEEPG-
Sm84719      MER------------------------LGWRELHEVLYMSGETATNERVRISSTFNS-KS

                             1040                1060                1080
15898471     -----------------DRECSHAVILFD-------------------------------
256419642    DDCRVFLISLKAGGVGLNLTAADYVYIVDPWWNPAVEQQAIDRTHRIGQTK---------
237794935    SHVKVFLISLKAGGTGLNLTSANLVIHFDPWWNPAIEDQATDRAHRIGQKN---------
187779742    SNVKVFLISLKAGGTGLNLTSANLVIHFDPWWNPAVEDQATDRAHRIGQKN---------
ScSNF2       SEYLCFILSTRAGGLGINLQTADTVIIFDTDWNPHQDLQAQDRAHRIGQKN---------
83286649     SKYFIFLLSTRAGGIGINLTTADIVILFDSDYNPQMDIQAMDRAHRIGQKK---------
124803472    SKYFIFLLSTRAGGIGINLTTADIVILFDSDYNPQMDIQAMDRAHRIGQKK---------
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74008371        SSKFIFMLSTRAGGLGINLASADVVILYDSDWNPQVDLQAMDRAHRIGQKK----------
14028669        STKFVFMLSTRAGGLGINLATADVVILYDSDWNPQVDLQAMDRAHRIGQTK----------
56118945        SSKFIFMLSTRAGGLGINLATADVVIIYDSDWNPQVDLQAMDRAHRIGQTK----------
47217344        SSKFIFMLSTRAGGLGINLATADVVILYDSDWNPQVDLQAMDRAHRIGQQK----------
157103787       SSKFIFMLSTRAGGLGINLATADVVIIYDSDWNPQMDLQAMDRAHRIGQKK----------
170572145       SDKFIFMLTTRAGGLGINLTAADVVIIYDSDWNPQVDLQAMDRAHRIGQKK----------
255719682       SKKFVFLLTTRAGGLGINLTTADVVVLYDSDWNPQADLQAMDRAHRIGQKK----------
145610651       SEKFVFLLTTRAGGLGINLTTADIVILFDSDWNPQADLQAMDRAHRIGQTK----------
145353082       SPMFAFLLSTRAGGLGVNLQTADTCILFDSDWNPQVDLQAMARVHRIGQKK----------
225436589       SDDFCFLLSTRAGGLGINLATADTVIIFDSDWNPQNDLQAMSRAHRIGQRE----------
189521245       AVQFCFLLSTRAGGLGINLATADTVIIFDSDWNPHNDIQAFSRAHRIGQAN----------
47206539        AQQFCFLLSTRAGGLGINLASADTVIIYDSDWNPHNDIQAFSRAHRIGQNK----------
113678140       APQFVFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNK----------
156717248       AQQFCFLLSTRAGGLGINLATADTVVIYDSDWNPHNDIQAFSRAHRIGQNK----------
73997410        AQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQNK----------
115939069       AEQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQSN----------
221120608       SEIFSFLLSTRAGGLGINLATADTVFIYDSDWNPHNDIQAFSRAHRIGQQN----------
256052547       SLSFAFLLSTRAGGLGINLASADTVIIYDSDWNPHNDIQAFSRAHRIGQSN----------
24666729        SEHFVFLLSTRAGGLGINLATADTVIIFDSDWNPHNDVQAFSRAHRMGQKK----------
170592228       AQQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRIGQQK----------
17569817        AKQFVFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQAFSRAHRLGQKH----------
256072692       SEYFIFLLSTRAGGEGINLASADTVVLYDSDWNPQWDLQALSRAHRIGQSK----------
145341798       SDTFLFLLSTRAGGQGINLVQADTVVMFDSDWNPQNDAQALARAHRIGQTR----------
145491053       KKREVFLLSTKAGGQGINLTAAEIVVIYDSDWNPQNDVQATARAHRIGQSK----------
118367847       KKRDVFLLSTKAGGLGINLTSANIVIIFDSDWNPQNDVQATARAHRIGQKQ----------
145484966       KGRQVFLLSTKAGGQGINLTAAEIVVIFDSDWNPQNDIQATARAHRIGQDK----------
239899054       HDSFAFLLTTRAGGVGINLTSASVVVIYDSDWNPQNDNQAQARCHRIGQTK----------
291001481       IDTFVFLVSTKAGGVGINLTSADTVIIYDSDWNPQNDLQAQARCHRIGQTK----------
211853152       SDRFVFLLCTRAGGLGINLTAADTCIIFDSDWNPQNDLQAQARCHRIGQNK----------
189521372       SDRFVFLLCTRAGGLGINLTAADTCIIFDSDWNPQNDLQAQARCHRIGQNK----------
260834763       SDRFVFLLCTRAGGLGINLTAADTVIIFDSDWNPQNDLQAQARCHRIGQSK----------
196012568       SDRFVFLLCTRAGGLGINLTAADTVVIFDSDWNPQNDLQAQARCHRIGQSK----------
242011216       SDRFVFLLCTKAGGLGINLTAADTVIIYDSDWNPQNDLQAQARCHRIGQQK----------
193599122       SDRFVFLLCTKAGGLGINLTAADTVIIYDSDWNPQNDLQAQARCHRIGQQK----------
19112177        SELSCFLLSTRAGGVGINLASADTVIILDPDFNPHQDMQAIARAHRYGQKK----------
259147500       ESFDVFLLTTRVGGLGVNLTGANRIIIFDPDWNPSTDMQARERAWRIGQKR----------
254582697       GDYNVFLLTTRVGGIGVNLTGANRIIIFDPDWNPSTDMQARERAWRIGQKR----------
255720394       GSYDVFLLTTRVGGLGVNLTGANRIIIFDPDWNPSTDMQARERAWRIGQRR----------
50309923        EPYDVFLLTTRVGGLGINLTGANRIIIFDPDWNPSTDMQARERAWRIGQKR----------
146416597       TNYDVFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDIQARERAWRLGQKR----------
68483838        PDMHVFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDIQARERAWRLGQKR----------
149235383       PDLHVFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDIQARERAWRLGQKK----------
199432721       KQYHVFLLTTKVGGLGINLTGADRVIIYDPDWNPSTDIQARERAWRLGQKK----------
254568884       PSYNVFLLTTRVGGLGVNLTGANRVIIYDPDWNPSTDVQARERAWRLGQKK----------
19075591        EYFDVFLLTTRVGGLGVNLTGADRVILFDPDWNPSTDAQARERAWRLGQKK----------
261358370       PEIDIFLLTTRTGGLGVNLTGANRIIIFDPDWNPSTDMQARERAWRLGQTR----------
70982085        PNIHVFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDVQARERAWRLGQKR----------
225682364       PEIHIFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDVQARERAWRLGQKR----------
239615027       PDIHVFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDVQARERSWRLGQKR----------
212536498       PDIHVFLLTTKVGGLGVNLTGADRVIIYDPDWNPSTDMQARERAWRLGQKR----------
255936215       PNIHVFLLTTRVGGIGVNLTGADRVIIYDPDWNPSTDLQARERAWRLGQKR----------
189204870       PDLHVFLLTTKVGGLGVNLTGANRVIIYDPDWNPSTDIQARERSWRLGQKR----------
66813000        PSLFIFLLTTKVGGLGLNLTGANRVILFDPDWNPSTDMQARERVYRIGQKK----------
242056785       DEIFVFILTTKVGGLGTNLTGANRIIIYDPDWNPSTDMQARERAWRIGQTR----------
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85014197     EDVFLFLLTTKVGGLGLNLTGASRIVIYDPDWNPSTDTQAKERAWRYGQKK---------
Cr13231      REARVMLGSLRAASLGINLTTAYRMVLFDLEWNPVYSAQAVARIHRLGQRR---------
ScRAD54      GQEFIFLLSSKAGGCGINLIGANRLILMDPDWNPAADQQALARVWRDGQKK---------
50302399     GQEFIFLLSSKAGGCGINLIGANRLILLDPDWNPAADQQALARVWRDGQKK---------
156845511    SHEFIFLLSSKAGGCGINLIGANRLILLDPDWNPAADQQALARVWRDGQKK---------
45190309     GEEFIFLLSSKAGGCGINLIGANRLILMDPDWNPAADQQALARVWRDGQKK---------
255718981    GQEFIFLLSSKAGGCGINLIGANRLILMDPDWNPAADQQALARVWRDGQKK---------
238878261    GPEFIFLLSSKAGGCGINLIGANRLVLMDPDWNPASDQQALARVWRDGQKK---------
255728815    GSEFIFLLSSKAGGCGINLIGANRLVLIDPDWNPASDQQALARVWRDGQKK---------
149239498    GAEFIFLLSSKAGGCGINLIGANRLVLIDPDWNPASDQQALARVWRDGQKK---------
149388940    GNEFIFLLSSKAGGCGINLIGANRLILMDPDWNPAADQQALARVWRDGQKK---------
190348945    GQEFIFLLSSKAGGCGINLIGANRLILLDPDWNPAADQQALARVWRDGQKK---------
254570653    GKEFVFLLSSKAGGCGINLIGANRLILVDPDWNPASDQQALARVWRDGQTK---------
189211141    SPEFVFLLSSKAGGCGLNLIGANRLVLFDPDWNPAADQQALARVWRDGQKK---------
46127169     GDEFIFLLSSKAGGCGINLIGANRLVLFDPDWNPAADQQALARVWRDGQKK---------
225684006    GEEFVFLLSSKAGGCGINLIGANRLVLFDPDWNPAADQQALARVWRDGQKK---------
259485020    GEEFVFLLSSKAGGCGLNLIGANRLVLFDPDWNPAADQQALARVWRDGQKK---------
238840822    GEEFVFLLSSKAGGCGINLVGANRLVLFDPDWNPAADQQALARVWRDGQSK---------
19115202     KDAFVFLLSSKAGGCGINLIGANRLILFDPDWNPAADQQALARVWRDGQKK---------
50546160     GQEFIFLLSSKAGGCGLNLIGANRLILMDPDWNPAADQQALARVWRDGQKK---------
58266612     SKEFVFLLSSKAGGCGINLIGANRLVLFDPDWNPASDQQALARVWRDGQKK---------
164660184    GSEFIFLLSSKAGGCGLNLIGANRLVLFDPDWNPASDQQALARVWRDGQKK---------
41055574     SPEFIFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDEQAMARVWRDGQKK---------
118094595    SPEFIFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDEQAMARVWRDGQKK---------
281351942    SPDFVFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDEQAMARVWRDGQKK---------
195539537    SPDFVFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDEQAMARVWRDGQKK---------
47575794     SPEFIFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDEQAMARVWRDGQKK---------
156369786    GGDFIFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDDQAMARVWRDGQKK---------
238814383    SGDFIFMLSSKAGGCGLNLVGANRLVMFDPDWNPANDDQAMARVWRDGQKK---------
170041242    SKEFIFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDEQAMARVWRDGQKK---------
189238349    SGEFIFMLSSKAGGCGLNLIGANRLIMFDPDWNPANDDQAMARVWRDGQQK---------
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193591979    SGVFLFMLSSKAGGCGLNLIGANRLVMFDPDWNPANDDQAMARVWRDGQKK---------
71033369     SNSFIFLLSSKAGGCGINLIGANRLVLFDPDWNPANDKQALARVWRDGQTK---------
221488620    PHSFVFLLSSKAGGCGVNLIGANRLVLFDPDWNPANDKQALARVWRDGQKK---------
157128256    SDTFIFLLSAKAGGIGLNLTGASRLILYDNDWNPASDLQAMSRIWRDGQTR---------
241602475    SDCFVFLLSCKAGGVGLNLIGASRIVLYDVDWNPANDLQAMARVWRDGQGR---------
194214970    SSDFIFLLSSKAGGVGLNLIGGSHLILYDIDWNPATDIQAMSRVWRDGQKH---------
281347253    SSDFIFLLSSKAGGVGLNLIGGSHLILYDIDWNPATDIQAMSRVWRDGQKH---------
119906776    SSDFIFLLSSKAGGVGLNLIGGSHLILYDIDWNPATDIQAMSRVWRDGQKH---------
194037038    SSDFIFLLSSKAGGVGLNLIGGSHLILYDIDWNPATDIQAMSRVWRDGQKH---------
149045437    STDFIFLLSSKAGGVGLNLIGGSHLILYDIDWNPATDIQAMARVWRDGQKH---------
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242023203    RDLFIFLLSSKAGGVGLNVTGASRLILFDSDWNPATDLQAISRIWRDGQKF---------
66811190     RPEFVFLLSSKAGGVGLNLIGGNHLVLFDADWNPANDAQSMARVWREGQKK---------
71651467     SQEIVFLLSSKAGGVGLNLIGANRLILFDPDWNPANDAQAMGRVWRDGQKK---------
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254585925    PSIFAFLLSAKSGGVGLNLIGACRLILFDNDWNPSVDLQAMSRIHRDGQKK---------
50294037     PNIFGFLLSAKAGGVGLNLIGASRLVLFDNDWNPAVDLQAMSRIHREGQKR---------
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260941370    PTHKIFLLSAKAGGVGLNLVGASRLILFDNDWNPSVDLQAMARVHRYGQTK----------
254567481    KDRFIMLLSSKAGGVGLNLIGASRLILFDNDWNPSVDIQAMARVHRDGQKR----------
145230930    NLCFAFLLSAKAGGTGLNLIGASRLVLFDVDWNPATDIQAMARIHRDGQKR----------
238484253    NRCFAFLLSAKAGGTGLNLIGASRLILFDVDWNPATDIQAMARIHRDGQKR----------
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225681829    TSVFAFLLSAKAGGTGLNLIGASRLVLFDVDWNPATDMQAMARIHRDGQKR----------
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290982366    SNDFIFLLSSKAGGCGLNLIGANRLIMIDPDWNPSNDEQAMARVWRDGQKK----------
281209956    KTHTVFLLSSKAGGVGLNLIGANHIVLYDPDWNPAIDIQAMERVWREGQTK----------
167385507    SNFNILLLSSKAGGVGLNLIGCSRLILFDPDWNPAKDKQAMARIWRDGQQK----------
170577655    NKNYAFLLSAKAGGLGLNLVGANRMILFDSDWNPAVDMQAMARIWRQGQEK----------
145350886    -SGKILLLSTKAGGVGLNLVGANRLVLVDSSWNPAHDLQAQARVWREGQTK----------
224013540    NHSFAFTLSSKAGGCGLNLIGANRLIMVDADWNPATDQQVMARVYRQGQKK----------
145482121    KDITVFLLNGKSGGTGLNLVGANKMICVEVDWNPANDSQVMGRIWRDGQQK----------
145338703    KDEFAFLLSSKAGGCGLNLIGANRLVLFDPDWNPANDKQAAARVWRDGQKKHQ--------
20336209     VRGRLFIISTKAGSLGINLVAANRVIIFDASWNPSYDIQSIFRVYRFGQTK----------
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81916664     LTTWLFLLSTRAGCLGVNLIGANRVVVFDASWNPCHDAQAVCRVYRYGQKK----------
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193610723    NTAKVFLLSMGTGVLGYNMVGANRVLLLSTSWNPSNDLQAIYRCLRFGQQK----------
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71662347     ENITCLLLSTQIGAYGLDFTAANHVILWDSWWNPQVESQAIARAYRRNQTR----------
239977156    KDLTVLVLSTKIAAYGLEFTAANHVVLFDSWWNPQADAQAIARAYRRNQRK----------
146081173    KDLIVLVLSTKIAAYGLDFTAANHVVLFDSWWNPQVDAQAIARAYRRNQRK----------
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Sb01g046180  PKAKVFFGSIKACGEGISLVGASRIVILDVHENPAVMRQAIGRAFRPGQSK----------
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ZM093940     ADAKVLFGSIRACGEGISIVGASRVVILDVHLNPSVTRQAIGRAFRPGQQK----------
ZM064574     ADAKIMFGSIKACGEGISLVGASRVVILDVHLNPSVTRQAIGRAFRPGQQK----------
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Vv35918      PDARVFFGSIKACGEGISLVGASRVLILDVHLNPSVTRQAIGRAFRPGQKK----------
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Cp76.2        NEVKVLLASTRACSEGINLSGASRVILIDVAWNPSVERQAISRAYRLGQKK----------
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Cp19.123      GSSKVLLASITACAEGISLTAASRVIFLDSEWNPSKTKQAMARAFRPGQQK----------
AtCLSY1       GQSRVLLASITACAEGISLTAASRVIMLDSEWNPSKTKQAIARAFRPGQQK----------
At5g20420     NPSRVLLASITACAEGISLTAASRVIMLDSEWNPSKTKQAIARAFRPGQQK----------
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Appendix 4: Sequence information for phylogenetic analyses. Title information:
>Protein name | NCBI accession or Phytozome locus name | Genomic region used for prediction if original gene model incorrect

A. SNF2 protein sequences:

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LSCDSSEQRESSDEEALENPRSMAAEHKYPVKRNQCSLPVKEKQISMEIKKNTTDQGCSDSYIPHTPAKNTERPRFR
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EAKDIFPPMFTGKDHERPERNHFGQDGHVLDLSFFEICAPEFSKIKESGNVWASITDLEPKLLAHQRKAFEFIWKNL
AGSLQLEEMDGSTSRGGCVVAHTPGAGKTLLLISFLVSYLKVHPRSRPLVLTPKAAIHTWRTEFQKWGILLPLHVLH
HSNRTSKLMGGLSSKLQAVLKSFHQPSWKTMRIMHCLDKLCKWHEEPSILLMTYSSFLSLTKEDSKLRHQAFITKVL
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SRTGKHQEALARHVFVERVGHKIESSSKHDRMDGISLLNELTQGFIDSFEGTKLNILPGIRVYTLFMKPTDVQEEVL
AKLLMPLSGNARYPLEYELLITIASIHPWLINTTKCASTYFTPAEVASVDKYKRNFAAGCKAKFVIDLLHKSSFRGE
RVLVFCHNVAPIAFLVTLIEIVFGWRLGQEVLVLQGDQELHVRSDVMDKFNSDRRGKRKVLIASTTACAEGISLTGA
SRLVMLDSEWNHSKTRQAIARAFRPGQERMVFVYLLVASGTWEEDKYNSNRRKAWIAKMVFFGRHFDDPLQNRVTEI
DDEVLKELADEDETNTFHMIVKQD

>ZM000342 | GRMZM2G000342
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LQNLQPEELQDGSVRWNSAVDCFHHNRSKLLSARFSLEVAYLIVLSSLRRMEFNIKMVDGNIIYQIIKGDQARDSID
SMSIPPGFGKNMDIISFKPRGEALRPITRTVPVTQVEEGNLTEDGCIAVKGESDSAQDVEILYAHVDIRRSKRMKTQ
PDRFTSYDARNFNRTYNKKEADGPSTKYEDSESGLSCDSSEQRESSDEEALENPRSMAAEHKYPVKRNQCSLPVKEK
QISMEIKKNTTDQGCSDSYIPHTPAKNTERPRFRLKPFASSRSLDGNSEPAFCQKRGRKRKKHMCQIEYKRMIDQCI
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ICAPEFSKIKESGNVWASITDLEPKLLAHQRKAFEFIWKNLAGSLQLEEMDGSTSRGGCVVAHTPGAGKTLLLISFL
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>ZM093940 | GRMZM2G093940
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CGTVKLSEDFIVADIAIHPRHAQAMKPHQVEGFNFLVKNLIGDKPGGCILAHAPGSGKTFLLISFIQSFMARYPSAR
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CRDRLLKVPNLLILDEGHTPRNKETDVLESLSRVETPRKVVLSGTLFQNHVEEVFNILNLVRPKFLRMESSRPIARR
IMSQVEIFGRSSKGLADGAFTEAVEGTLLNDENFKRKVHVIRGLRELTRDVLHYYKGAILDELPGLVDFSVFLKLTP
KQKDIVHKLEMHDRFKRSAVGSALYIHPCLSGLSEVNAENRAHTLRDDSVDSLMDSINVRDGVKANFFMNILSLANS
AGEKVLAFSQYILPMTFFERLLVKKKGWHVGREIFMISGDTSQEDREAAVDRFNSSADAKVLFGSIRACGEGISIVG
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>ZM064574 | GRMZM2G064574
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GTVHTYGDKNTQIVPYGQCSALVNQFPLQTSWQPSIQFERVVLQKRPEEQRMQDLVAASIAEKRAETQVFLSLPTEK
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ARPLVVLPKGILGIWKTEIKRWQVQDIPVYDFYSVKAEKRVEQLQILKSWEDKMSILFLGYKQFSTIVTDDGGSNVT
AACRDRLLKVPNLLILDEGHTPRNRETNVLESLNRVETPRKVVLSGTLFQNHVEEVFNILNLVRPKFLRMESSRPTA
RRIMSQVEIVGRSSKGLADGAFTKAVEETLLNDENFKRKAHVIRGLRELTKDVLHYYKGDILDELPGLVDFSVFLKL
TPKQKDIIYKLEAHDRFKRNAVGSALYIHPCLSELSEVNAEHRANTFRDDLVDSLVDSITVRDGVKANFFMNILSLA
NSAGEKVLAFSQYISPMIFFERLLVKKKGWHVGKEIFMISGDTSQEDRELATDHFNNSADAKIMFGSIKACGEGISL
VGASRVVILDVHLNPSVTRQAIGRAFRPGQQKKVFVYRLVAADSDEVKVHETAFKKEVIPKLWFEWSEHCTTEDFKL
GQIDIDDSGDELLDTKAIRKDIKALYR

>Vv15867 | GSVIVT00015867001 | Predicted from chr2:5790000..5830000 with
CLSY1
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GGENSDEDVTDVVSISDDSEASDYEEEEDDDDDDYIVDPTIDRDERGNQASKLGKKKVELGTSSHPFCVDVDEGEGD
GDGEGEEEWEEEEEEEEEEEGRDSSSGHAEFPKTIGRKDKGELGKHTKRKRIRALKHCDALKILVDSIWAKNSGLLE
ELVSPRGSDSIEETAPAFTELPLKFKFGVDESIPLGKSQPEIGMNQLWAEFDFDGEEDFGSAEVEIDQAVLCHQGNH
QLVLDEQIGMTCCFCSFVQLEIKYILPSFSRNPWGGSEKGNAGKEDCNSIFDELQFQKPGCGSQSGSDHGLHPEGTV
WDIIPGIRNSMYRHQCEGFEFIWKNVAGGIYLDELKRSSFSDGGSGCIISHAPGTGKTRLTIVFLQTYMELYPACRP
VIIAPRTMLLTWEEEFKKWNVDIPFHNLNKLEYSGKENITALNFLRRISHQGQSAKSIRMVKLYSWKKDRSILGISY
TLFEKLAGERDYTKVQVRKILLELPGLLVLDEGHTPRNEQSLIWKALSKIDTERRIILSGTPFQNNFKELYNTLCLV
RPKFADRIAVEQYGGFRGKRGRKSNAARGKWDLLTSSIGKIADDKVEELRAMIEPFVHIHKGTILQENLPGLKDSVV
VLQPSDLQRRLLESIREKKNPLELGYLVSLISVHPSLLPSDERKLFFDQTKLEKIKLNPDIGVKTKFLMAFIRFSET
MNEKVLVFSQFLDPLTYLMDQLKYHFHWIVGKEVLYMDGQRDVKQRQSSINTFNDPASQVRVLLASTKACSEGISLV
GASRVILLDVVWNPSVERQAISRAYRLGQRKVVYIYHLLTSGTMEEEKYCRQAKKDRLSELVFSSKDKTINVLVVTN
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>Vv29366 | GSVIVT00029366001 | Predicted from chr13:1048180..1068179 with
CLSY1
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SIERRPHEPECSCQFFVNFYITQDPLGTEKGTLSKDISVVELDQISILQKLGKYPCEDEHYRWKFSEDCSLLQRTKL
FLGKFSSDLSWLVVTSVLKQAVFDVRSVQNRIVYQIVGGDHDKVSLNAVNFRVDNGISTPVIFPFVPADTIEADPLN
GTNEAGPLPFCDIVDLRRSKRRNVQPDRFFSLGGFSESDIGSVRAGIHKVDYWRKEEMPLALPDEGDVHSIFSEKHI
IDYEKGAHSLQIDSYEDFLVCKSKDRSREVKPILAAQNEDQHQFAIVPVPLIIEPIAHGEDHLHDETPWNESGEIGE
ISPKYYCTNGVPKLQRKNMSDLYMEVESRWEGKGPIRKLRRKRGFTIRTKTESYGEVRPHKKRPFSEPGYKEVIEAY
MKNIESTINKEQPLVIDQWKELQVRNDLNQRRDCNSPSSVGDQEESSETEMLWREMEFSIASSYLLEENEGSNVEVL
KEVVQESSNISEQVCQHEYILDEEIGVLCQLCGFVSTEIKDVSPPFVIKRRGGCVISHSPGAGKTFLVISFLVSYLK
LFPGKRPLVLAPKTTLYTWYKEIIKWKVPVPVYQIHGCRTYRYEIYKHKVETSPGIPRPNQDVMHVLDCLEKIQKWH
AHPSILLMGYTSFLSLMREDSKFIHRRYMGEVLRQSPGILVLDEGHNPRSTGSRLRKALMKVKTNLRILLSGTLFQN
NFSEYFNTLCLARPKFVNEVLRELDPKFKRNKNRRKRRYSSTESRARKFFTDEIAKRINSNVPEEQIEGLNMLRNLT
SKFIDVYEGGSSDNLPGLQVYTLLMKSTTIQQQFLSKLQKKKDEYKGYPLELELLVTLGSIHPWLITTAACADKYFS
REELLELKKHKDDVKKGSKVKFVLSLVNRCIIRKEKILIFCHNISPINLFVDIFDKLYKWKKGEDVLVLQGDLELFE
RGRVMDQFEEPGGASKVLLASITACAEGISLTAASRVILLDTEWNPSKQKQAVARAFRPGQERVVYVYQLLETDTLE
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>Vv35918 | GSVIVT00035918001 | Predicted from chr3:17397..57396 with DRD1
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RFGSVTKEIEALCARRMQMLQPYYVMYPSLSYMCTDLGKKQGKKASKLVNREASHLAHEDVIDLEDDHVVDDALTAT
AVEDATLPVVIIDSDDEDCGDQKVSHPPQETAWPSFSYQEVVLRKPSVGLLANNPVVRDYVGSIAPKVEEGSLMGAT
EIRKDKDVYIGVGEKSLVANLEMKKVQGEYVGVEDDMETNEGNLRAKTEDDGLADMWQEFDLALQSSKDVAVDPGED
EKESKEECEHSFVLKDDIGSVCRICGVVNKSIETIIEYQYTKVKRSRTYMYEPRNTKDREPTDDPSDGLGFSEHNLT
VTEIHAHPRHSMQMKPHQVEGFNFLVSNLVAENPGGCILAHAPGSGKTFMIISFMQSFLAKYPQARPLVVLPKGILA
TWKKEFLTWQVEDIPLYDFYSVKADSRPQQLEVLKQWVAEKSILFLGYKQFSSIVCGDGASKATIACQEILLKAPQI
LILDEGHTPRNENTDVLYSLAKVQTPRKVVLSGTLYQNHVKEVFNILNLVRPKFLKLESSRAVVKRIMSKVDIMGVR
KQLKSNAADAFYDLVENTLQKDDNFRRKITVIQDLREMTSKVLHYYKGDFLDELPGLVDFTVLLNLSARQKKEVGNL
NKFERKFKKNSVGSAVYLHPQLKYFAEKLAANESKTDEMTCQKKMDEILEQLDVRDGVKAKFFLNVLALCQSSGEKL
LVFSQYLLPLRFLEKLTMKVKGWSPGKEIFAISGESSSEQREWSMERFNTSPDARVFFGSIKACGEGISLVGASRVL
ILDVHLNPSVTRQAIGRAFRPGQKKKVHVYKLVAADSPEEEDHNSCFKKELISKMWFEWNEYCGHHEFEAETVDVSD
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>Vv23895 | GSVIVT00023895001 | Predicted from chr6:9332680..9372679 with DRD1
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KKASKLVNRHASHLGHEDVIDLEDDHIVYDVPTATAVADAALPVVIIDSDDEESGDQKVRDYVESIAPKKEERSLTA
SSEIRKDKGGLYIAVGERSLAANHEMKNVKGEYVGVEDDMEASEGNLQAKTKDDDLADMWQEFDLALQSSKDVAVDP
EEDGKEGEEECEHSFVLKDDIGSVCRICGVVNKSIETIIEYQYSKVKRSRTYMYEPRNTKDREPTDDPSDGLRFSEH
SLIVTEIHAHPRHSMQMKPHQVEGFNFLVSNLVADNPGGCILAHAPGSGKTFMIISFMQSFLAKYPQARPLVVLPKG
ILATWKKEFLTWQVEDIPLYDFYSVKADSRPQQLEVLKQWVAEKSILFLGYKQFSSIVCGDGASKAAMACQEILLKA
PQILILDEGHTPRNENTDVLYSLAKVQTPRKVVLSGTLYQNHVKEVFNILNLVRPKFLKLESSRAIVKRIMSKVDIM
GVRKQLKSNAADAFYDLVENTLQKDDNFRRKITVIQDLREMTSKVLHYYKGDFLDELPGLVDFTVLLNLSARQKKEV
GNLNKFERKFKKNSVGSAVYLHPQLKYFAEKLAANESKTDEMTYQKKMDEILEQLDVREGVKVKFFLNVLALCQSAG
EKLLVFSQYLLPLRFLEKLTMKVNGWSSGKEIFVISGESSSEQREWSMERFNTSPDARVFFGSIKACGEGISLVGAS
RVLILDVHLNPSVTRQAIGRAFRPGQKKKVHVYKLVAADSPEEEDHNTCFKKELISKMWFEWNEYCGNHEFEAETVN
VSDSGDLFLESPLLREDVTVLYKSGGCHEPIAAPIRLNDAIWEEAAAFFRTRPLVPA

>Pt286483 | 286483 | Predicted from scaffold_40:736704..756703 with DRD1
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TDVGGSCSGVKSDGEESGRSKVPLPRWQRIVNESYNGDVFAHERNEGGVCFLSSGIGNGSGGVGLKGRESNGVAGRT
ELRSGFCEKKKDGNVVVVVDDDDDDACIILEKDAEELQSSSSGEEETFKDDSDDDDYRVELPESFMVEEEEKEEDGD
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DNDEDDTEAYEAVDVAQKVRSKKGKTKPTGGNGGDVDDGDETCDHKSQRRTIESREGSRDEHGHGVCRRKPSKRRRK
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LDENEDDAHEVEPDTVTLCHQGNHELYLDEEIGLLCKYCSFVDLEIKYYVPPFDRYPRGKSARRDFVTMQHNIFNDL
HHQDSGHDTHPDYDPCTLVQGTVWNLIPGIGKGMHGHQREGFEFLWKNIAGGIYLDKLKENANLNGGTGCIISHAPG
TGKTRLTIVFLQTYMQLYPTSRPVIVAPCSMLLTWEAEFLKWGVDIPFHIMNKKNLSGKENRTAMDLFRELKPAERG
LNAIRMVKLYSWKKERSILGISYRLFEELVGEEKSKTKVSDKTEDDQVRKVLLELPGLLVLDEGHTPRNDRSRIWKA
LSKVQTQKRIILSGTPFQNNFDELYNTLCLVKPKFADEISSKHHRACPKRRRCKRNTDARRNWASLTTAIGKVTDDK
LEAQRVEELRKMIWQFVHVHKGGVLRERLPGLRDSVVILQPVHLQKTLLENVKQINGLDHFEMEYLLSVLSVHPSLL
PEKSVGTLEFKFVDRMELEMLRSKPEAGVKTKFLMELIRLCQARNEKVLVFSQYLEPLNLVIKQLESNFSWIQGEDI
LYMHGKLKIDERQILIKHFNNANSNAKVLLASTRACSEGINLVGASRVVLLDVLWNPSVERQAISRAYRLGQEKVVY
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>Pt832603 | 8326023 656302 | Predicted from LG_VIII:4535905..4605904 with
CLSY1
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GIDVCVLSSSERAKNTGEGNSEPVWVDAKISSIKRKPHVSHCSCQFFVNLYVNQGPLGSERARLSKETEAVGINEIS
VLQKLDNDPCEADNNQQEAQFYRWEFCEDCSLVQRSKLFLGRFSADLTWLLVASVLKQVEFNVRSVQNKIVYQILGG
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DAPAETEIGWVRSLPYTPLKWKAEEEEEEEMHLPLAYLFGTHAGASCAEEQTCNEVGASSPKLELLEGIPVSRTKTY
LKEIKSNVVNRRDHQTEPGEVRAGMAKRRECQKSTMADRIEHQTRLGDAESGMANRKKHGTQIREVKSGVANRREHQ
DQLAIVPVHTEDVLATFEQFDSPVKTPEPYSQAFIEFPISYYRKKSSPAAHRKNDRDEDLMFGNGWGGKFSTKKVQR
ARYRSTHLKQDGSCAPMTYKRTALSAGAYNKLISSYMKNIDATIKSKEVPRIIDQWEEFKAKHSSDQKEKMEPSSVK
DDGESSETEMLWREMELCLASAYILEDNEVELCVVFIYSYHLYRIFFFITVSDWLKDLQALLSTRTTQKNCQHEFKL
DEEIGILCQICGFVKTEIKYVSAPFMEHTGWTAESKPQNEEDLELKPDEDEGSSLFGNHTSGEDVPVSEVNDNVWDL
IPELRPKLHMHQKKAFEFLWKNTAGSLVPAHMEKTSKKIGGCVVSHTPGAGKTFLIIAFLVSYLKLFPGKRPLVLAP
KTTLYTWYKEFIKWEIPVPVHLIHGTRSSRAFKQTPAALRGSGPRPSQDVVHILDCLEKMQKWHAQPSVLVMGYTSF
LTLMREDSKYNHRKYMAKVLRESPGMLILDEGHNPRSAKSRLRKVLMKVETDLRILLSGTLFQNNFCEYFNTLTLAR
PMFIKEVLKALDPKFKRKKKGAQKARHLLESRARKFFIDNIASKINSDEAEEKMQGLNMLRNMTNGFIDVYEGTASD
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CKKGSKVMFVLNLVYRVVKNEKVLIFCHNIAPIKLFLELFENIFRWQQGKEILVLTGELELFERGRVMDKFEELGGP
SRVLLASITACAEGISLTAASRVILLDSEWNPSKTKQAIARAFRPGQQKMVYVYQLLATGTVEEDKYRRTAWKEWVS
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QVVQAVSLSAG

>Pt567214 | 567214 567215 659448 | Predicted from LG_X:16473610..16513609
with CLSY1
MKRKHLHQSKHPYNAHPFEALYGGSWQSVELIEIRDGAMTLHFADSHHRIEEKGPFSNIRVKSRKSTLSDCTCFLRP
GIDVCVLSFSERAKSSEEGNSEPVWVDARINSIKRKPHESQCSCQFFVNLYVNQGPLGSERATLSKETEAVGIDQIS
ILQKLDNDPCEADNNRHETQFYRWEFCEDCSLVQRTSIPKQVAFDVRSVQNKIAYQIFGGDDDHCSLKSNNHINCVT
FKVEDGISTPFVVQLDPIDTCNTPAETEIGWVRSLPYTPLKWKEEEELHLPLAYLFGTHADASCAEEKPGNEVRVNS
PKLEFLEGPPVSRTKTNSRKIKSNVFNRREHQAELGEVESGIDNRRERQKSTVANRIKHQTRLGEAKSGMANRKKHG
TQIREVKLGVANRIEHQDQLAIVPVPTEDDLVTFEQYDSPLKTPDNFPQECIEFPIRSYSKKGYSVQRKNDFDEDMM
FGSGWGGKSSRKKVQRARYQSTHLKRDDSCKPKTYKQTALSAGAYDKLISFYMKNFDSTIKSKEVTRIIDQWEEFKA
KHSSDQKETMEPSLVEDDGESSETEMLWREMELCLTSAYIFEDNESRVSTQTTQNSSECCQHEFKLDEEIGILCHKC
SFVKTEKKYVSAPFVFSVFLLSFMSPLDRQVSMQGRHFLFVIRGYSARNPIAHLFNVCKISPLVPFEVNDNVWDLIP
ELRAKLHMHRKKAFECLWRNIAGSLVPALMEKASKKIGGCVISHTPGAGKTFLKIAFLVSYLKLFPGKRPLVLAPKT
TLYTWYKEFIKWEIPVPVLLIHGTRSSRVFRQTPVALRGSCPRPSQDVVHILDCLEKMQKWHAQPSVLVMGYTSFLT
LMREDSKYNRRKYMAKVLRESPGMLVLDEGHNPRSTKSRLRKVLMKVETDLRILLSGTLFQNNFCEYFNTLCLARPL
FIREVLKALDPKFKRKKKGAQKARHFLESRARKFFIDNIASKINLDEAEEKMQGLNMLRNMTNGFIDVYEGTASDTL
PGLQIYTIMINPTDIQHEILVKLHKIMEKCPGYPLEVELLITLASIHPSIINSSVCVKKFYEQEELMELEKLRFDCK
KGSKVMFVLNLVYRVVKKDKVLIFCHNIAPIKLFLELFENVFRWQLEMDKFEELGGPLRVLLASITACAKGISLTAA
SRVILLDSEWNPSKTKQAIARAFRPGQQKMVYVYQLLATGTVEEDKYHRTAWKNWVSRMIFSEESVEDPSRWQAEKI
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>Pt195587 | 195587 195591 | Predicted from LG_IV:14796532..14836531 with DRD1
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EPDSKKDKGVYVGVEDDEVDTEIKDDGLQVSDNVGRRIQGEAASLAGEPDSKKDNGVYVGVEDDEVDTEIKYDGLGD
IWKEMSFALECSKDVVENSPSDENMEEDEDYCDHSFVLKDDIGYVCRICGVIERAIYTIIEIQFNKVKRNTRTYISE
SRNAKDRDSNGTVGADLFEEDLMVTDIPAHPRHMKQMKPHQVEGFNFLRNNLVADNPGGCILAHAPGSGKTFMIISF
MQSFLAKYPHAKSLVVLPKGILPTWKREFQIWQIEDIPLYDFYSVKADSRQQQLEVLNQWVEQKSILFLGYKQFSSI
VCDDGKNQVSVTCQEILLRRPSILILDESHTPRNENTDVLQSLAKVQTPRKVVLSGTLYQNHAKEVFNVLNLVRPKF
LRMDTSRAIVKRILSKVNIPGARKQFKAGADAAFYDLVEQTIQKDQDFKRKVTVIRDLHEMTSKVLHYYKGDFLDEL
PGLVDFTLMLNLSSRQKHEVKKLKKLAMKFKRSSVGSAVYLHPKLNSFSKNSAITDDMMDDLLETVDVRDGVKAKFF
LNILSLCESAGEKLLVFSQYLTPLKFLERLVMKVKGWILGKEIFVISGESSSDHREWSMERFNNSMDAKVFFGSIKA
CGEGISLVGASRIIILDVHLNPSVTCQAIGRAFRPGQTKKVYAYRLVAADSPEEEDHTTCFRKEAIAKMWFEWNEYC
GYQDFEVGTVELDDSGDRFLESLLVREDVRVLYKRSVHIGNSVNFP

>Cp19.123 | evm.model.supercontig_19.123 | Predicted from
supercontig_19:775024..815023 with CLSY1
MRKRRLYESRHPFGLHPFEAFSRGSWRMVDCIRIEDGTMSLRFVDGRHVIKRKRPFSELRVRSRQANLTDCTCFLRP
GIDVCVLIPSKDLASSDEANLELVLIDAKIRSIERKPHESQCSCQFYVNLYVNQGPLGSEKLELDKDTKVLGIDQIL
ILQRLEKHPCEGQYYRWSLSEDCSSLSRTKLFLGKFSSDLSWLLVASVLKQVAFEVRTEQYKIVYQILADDDGSPSK
SNNYISATMFINGGWWELRRSKRRNVQPERFIGGQGLTESDSVWVRQMPIKTDKWKEKMKCLPLSRLFKMQPLYLKE
QPKNETRDLVVYKSNKYSKDVKSGLADQVEHQNKLAIIPVPNVPELEPEPLASEHHDYHANLSANNSKRVEELSFRY
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>Cp76.2 | evm.model.supercontig_76.2 | Predicted from
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SLTSSMGKFLDVKADNLKVIRDVIAPFVHVHKGKILKDSLPGLRHSVVVLRPVDLQKSLLDGLQGTRNTILLDFRVS
LVSVHPSLLIDCHPEMDHGYIDWKKLEKCRMIPNAGVKTKFVNELLHLSEALGEKVLIFAQYLEPLTLIMDQLRDRK
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>At3g24340
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KVLLASTKACSEGISLVGASRVVILDVVWNPSVESQAISRAFRIGQKRAVFIYHLMVKDTSEWNKYCKQSEKHRISE
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>At1g05490
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KEVVGDNRDDDDLRKASSPIKRVSLVERKALVRYKRSGSSLTKPRERDNKIQKLNHREEEKKERQREVVRVVTKQPS
NVVYTCAHCGKENTGNPESHSSFIRPHSIRDEIEDVNNFASTNVSKYEDSVSINSGKTTGAPSRPEVENPETGKELN
TPEKPSISRPEIFTTEKAIDVQVPEEPSRPEIYSSEKAKEVQAPEMPSRPEVFSSEKAKEIQVPEMPSIPEIQNSEK
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RLLVNSVWEKGQLGEEDEADELVSSAEDQSQEQAREDHRKYDDAGLLIIRPPPLIEKFGVEEPQSPPVVSEIDSEED
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TRERRKFDRFEEEEGSSFIGKLGFDAPNNSLNEGCVSSEGTVWDKIPGVKSQMYPHQQEGFEFIWKNLAGTIMLNEL
KDFENSDETGGCIMSHAPGTGKTRLTIIFLQAYLQCFPDCKPVIIAPASLLLTWAEEFKKWNISIPFHNLSSLDFTG
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RGKKNLGNEINNRGIEELKAVMLPFVHVHKGSILQSSLPGLRECVVVLNPPELQRRVLESIEVTHNRKTKNVFETEH
KLSLVSVHPSLVSRCKISEKERLSIDEALLAQLKKVRLDPNQSVKTRFLMEFVELCEVIKEKVLVFSQYIDPLKLIM
KHLVSRFKWNPGEEVLYMHGKLEQKQRQTLINEFNDPKSKAKVFLASTKACSEGISLVGASRVILLDVVWNPAVERQ
AISRAYRIGQKRIVYTYHLVAKGTPEGPKYCKQAQKDRISELVFACSSRHDKGKEKIAEAVTEDKVLDTMVEHSKLG
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>AtCLSY1 | At3g42670
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KEQSLDRYYRWRYSEDCSSLVKTRLNLGKFLPDLTWLLVTSVLKNIVFQIRTVHEKMVYQIVTDEDCEGSSSSLSAM
NITVEDGVVMSKVVLFNPAEDTCQDSDVKEEIEEEVMELRRSKRRSGRPERYGDSEIQPDSKDGWVRMMPYRYNIWN
VSSDDDDEEEDCEDDKDTDDDLYLPLSHLLRKKGSKKGFSKDKQREIVLVDKTERKKRKKTEGFSRSCELSVIPFTP
VFEPIPLEQFGLNANSLCGGVSGNLMDEIDKYRSKAAKYGKKKKKKIEMEEMESDLGWNGPIGNVVHKRNGPHSRIR
SVSRETGVSEEPQIYKKRTLSAGAYNKLIDSYMSRIDSTIAAKDKATNVVEQWQGLKNPASFSIEAEERLSEEEEDD
GETSENEILWREMELCLASSYILDDHEVRVDNEAFHKATCDCEHDYELNEEIGMCCRLCGHVGTEIKHVSAPFARHK
KWTTETKQINEDDINTTIVNQDGVESHTFTIPVASSDMPSAEESDNVWSLIPQLKRKLHLHQKKAFEFLWKNLAGSV
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LDEGHNPRSTKSRLRKALMKVDTDLRILLSGTLFQNNFCEYFNTLCLARPKFVHEVLVELDKKFQTNQAEQKAPHLL
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CHNIAPIRLFLELFENVFRWKRGRELLTLTGDLELFERGRVIDKFEEPGGQSRVLLASITACAEGISLTAASRVIML
DSEWNPSKTKQAIARAFRPGQQKVVYVYQLLSRGTLEEDKYRRTTWKEWVSSMIFSEEFVEDPSQWQAEKIEDDVLR
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>At5g20420
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IPFTPVFEPIPLEQFGLNANSFGGGGSFSRSQYFDETEKYRSKGMKYGKKMTEMEEMMEADLCWKGPNQVKSFQKRT
SRSSRSVAPKTEDSDEPRVYKKVTLSAGAYNKLIDTYMNNIESTIAAKDEPTSVVDQWEELKKTNFAFKLHGDMEKN
LSEDGEGETSENEMLWREMELCLASSYILDDNEVRVDNEAFEKARSGCEHDYRLEEEIGMCCRLCGHVGSEIKDVSA
PFAEHKKWTIETKHIEEDDIKTKLSHKEAQTKDFSMISDSSEMLAAEESDNVWALIPKLKRKLHVHQRRAFEFLWRN
VAGSVEPSLMDPTSGNIGGCVISHSPGAGKTFLIIAFLTSYLKLFPGKRPLVLAPKTTLYTWYKEFIKWEIPVPVHL
IHGRRTYCTFKQNKTVQFNGVPKPSRDVMHVLDCLEKIQKWHAHPSVLVMGYTSFTTLMREDSKFAHRKYMAKVLRE
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SRVIMLDSEWNPSKTKQAIARAFRPGQQKVVYVYQLLSRGTLEEDKYRRTTWKEWVSCMIFSEEFVADPSLWQAEKI
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>AtDRD1 | At2g16390
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STLVQHQKNQGDVTPLIPQCSFEEVDLGRGKEMPSAIKAIVEGQTSRGKVLPIENGVVNEKGVYVGVEEDDSDNESE
AADEDLGNIWNEMALSIECSKDVARETSHKEKADVVEDCEHSFILKDDMGYVCRVCGVIEKSILEIIDVQFTKAKRN
TRTYASETRTKRFGESDNELKFSEEGLMIGGLAAHPTHAAEMKPHQIEGFQFLCSNLVADDPGGCIMAHAPGSGKTF
MIISFMQSFLAKYPQAKPLVVLPKGILPTWKKEFVRWQVEDIPLLDFYSAKAENRAQQLSILKQWMEKKSILFLGYQ
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RDGVKMKFFLNLLALCESTGEKLLVFSQYIVPIKTLERLMSSMKGWRLGKEMFTITGDSSNEQREWSMERFNNSLEA
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B. Polymerase largest subunit sequences:

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FAMGKSPGGVFEAAAMNREVDYLAGANELAFCGKSPSLGTGANIELFFKEDKGPVSRFPDFESLVFSRRVVDDTV
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DGPSLAYDDRTKAYKRTVDASKKIDDYRQHPQFSVLASSFVTSRVMECLQSSKLYSKKTDKESSTDSYGTSDAIL
SKRSDYAFRSIMVGDPKIRLHEIGIPMDLADLFVPEHVSIYNFKSINLKCNLHLLAKELLIARRNGKLIYVRKEN
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LKCQKGTNSLDHFGLLFLSKNLKKYRYGFEYASLYVQNYLEPMDFSELVNTVMIQYDGGGVQKTKGSPWITHFHI
SKEMMKRKRLGLRLLVEDLTEHYNAKRDQLNNVIPKVYISKCKCSDDDDCINNQTCCITVVAQDESNSTSTSQLD
DLKKRAIPVLLATPVKGFLEFKDVEIQCQRDNELVVKVNMSKHCKSGIFWTTLKKACIGIMGLIDWERSRPGSVY
DIFCPCGIDSAWKYFVESLRSKTDDIGRNIHREHLLVVADTLSPHEPVQNENIYGFLHNPEVWGPEKNHMETDST
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KLHRNTSVMDKMSIIAEVAGGVAHKSKNKAPHETLPQDFWDFIPDDNQPPIFNVTKKILSPYQVFHMLKKLDPEL
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QVEINSMSQLDVIKERVIPSILATLLKGFLEFKNVKVQCQEDNELVLKVGMSEHCKSGKFWATLQNACIPIMELI
DWERSRPERVYDNFCSYGIDSAWKFFVESVRSTTDAIGRNIHRQHLLVVADCLSVSGQFHGLSSQGLKQQRTWLS
ISSPFSEACFSRPAHSFINAAKRDSVDNLSGTLDAIAWGKEPCAGSSGPFKILYSGKSHETKQNEHIYDFLHNPE
VQALEKNVMDTYRKRTEKTSKRRSALNSEGNATINGGAISFNQKFLNAKVGIWENIIDMRTSLQNMLREYTLNEV
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>OsRPD1b | Os09g38268 | Predicted from chr9:2201469..22034062
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KLHRNTSVMDKISIIAEVAGGVTHNSKNKAPHETLPQDFWDFVPDDNQPPQSNVAKKILSPYQVFHMLKNLDPEL
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YSLATGNWGQANAAGTRAGVSQVLNRLTYASTLSHLRRLNSPIGREGKLAKPRQLHNSQWGMMCPAETPEGQACG
LVKNLALMVYITVGSAAYPILEFLEEWGTENFEEISPSVIPQATKIFVNGMWVGVHRDPDMLVKTLRRLRRRVDV
NTEVGVVRDIRLKELRIYTDYGRCSRPLFIVDNQKLLIKKRDIYALQQRESAEEDGWHHLVAKGFIEYIDTEEEE
TTMISMTISDLVQARLRPEEAYTENYTHCEIHPSLILGVCASIIPFPDHNQSPRNTYQSAMGKQAMGIYVTNYQF
RMDTLAYVLYYPQKPLVTTRAMEHLHFRQLPAGINAIVAISCYSGYNQEDSVIMNQSSIDRGFFRSLFFRSYRDE
EKKMGTLVKEDFGRPDRGSTMGMRHGSYDKLDDDGLAPPGTRVSGEDVIIGKTTPISQDEAQGQSSRYTRRDHSI
SLRHSETGMVDQVLLTTNADGLRFVKVRVRSVRIPQIGDKFSSRHGQKGTVGMTYTQEDMPWTIEGVTPDIIVNP
HAIPSRMTIGQLIECIMGKVAAHMGKEGDATPFTDVTVDNISKALHKCGYQMRGFERMYNGHTGRPLTAMIFLGP
TYYQRLKHMVDDKIHSRGRGPVQILTRQPAEGRSRDGGLRFGEMERDCMIAHGAAHFLKERLFDQSDAYRVHVCE
VCGLIAIANLKKNSFECRGCKNKTDIVQVYIPYACKLLFQELMSMAIAPRMLTKHLKSAKGRQ
```

Appendix 5. Alignment of DRD1 subfamily members over N-terminal region using (A) MAFFT, (B) Satchmo, (C) MUSCLE, and (D) TCOFFEE. The lightest level of shading represents conserved residues in at least 60% of the sequences, the middle level is conserved residues is at least 80% of the sequences, and the darkest level is amino acid identity in all sequences.

(A) MAFFT

```
                             20                  40                  60
RMR1       MDRATP------------------------------------------------------
Sb09g19410 MDRAAP------------------------------------------------------
Bd2g26500  MDRSGR------------------------------------------------------
Os05g32610 MDRAAR------------------------------------------------------
Pt286483   MSKSPI------------------------------------------------------
Vv15867    MDFSS-------------------------------------------------------
Cp76.2     MEGKRL------------------------------------------------------
ZM178435   MPAPPS------------------------------------------------------
Sb04g33300 MPAPPS------------------------------------------------------
Os02g43460 MPRRKG------------------------------------------------------
Bd2g43500  MPKNK-------------------------------------------------------
Bd3g50300  MPPAAD------------------------------------------------------
At3g24340  MDMTS-------------------------------------------------------
ZM000342   MMIKKK------------------------------------------------------
ZM108166   MV----------------------------------------------------------
Sb02g43870 MV----------------------------------------------------------
Os07g49210 MAGKKMSGEVRSVPAFDFAEWLKRTVSEQDYVVMKMDVEGTEFDLIPRLFDTGAICLIDE
Bd1g16720  MAGKTL------------------------------------------------------
At5g20420  MKKRGF------------------------------------------------------
AtCLSY1    MKRKHY------------------------------------------------------
Pt567214   MKRKHL------------------------------------------------------
Pt832603   MKRKRL------------------------------------------------------
Cp19.123   MRKRRL------------------------------------------------------
Vv29366    M-----------------------------------------------------------
Sm441121   MS----------------------------------------------------------
At1g05490  MECIGK------------------------------------------------------
Sm84719    MASNGP------------------------------------------------------
ZM064574   M-----------------------------------------------------------
ZM093940   M-----------------------------------------------------------
Sb07g02945 M-----------------------------------------------------------
Os07g25390 M-----------------------------------------------------------
Os06g14440 M-----------------------------------------------------------
Bd3g19890  M-----------------------------------------------------------
Bd2g21450  M-----------------------------------------------------------
Bd2g21430  M-----------------------------------------------------------
Os08g14610 M-----------------------------------------------------------
Bd3g18910  M-----------------------------------------------------------
At2g21450  M-----------------------------------------------------------
AtDRD1     M-----------------------------------------------------------
Pt195587   M-----------------------------------------------------------
Vv23895    M-----------------------------------------------------------
Vv35918    M-----------------------------------------------------------
Sb01g46180 M-----------------------------------------------------------
Os03g06920 MARYPA------------------------------------------------------
Bd1g74070  M-----------------------------------------------------------
```

```
                              80                 100                 120
RMR1       ------------------------------------------------------------
Sb09g19410 ------------------------------------------------------------
Bd2g26500  ------------------------------------------------------------
Os05g32610 ------------------------------------------------------------
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   ------------------------------------------------------------
Sb04g33300 ------------------------------------------------------------
Os02g43460 -----------------------------------------------------KGKGVED
Bd2g43500  ------------------------------------------------------------
Bd3g50300  ------------------------------------------------------------
At3g24340  ------------------------------------------------------------
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 LFLECHYNRWQKCCPDRAEAFEMAKGVSCFYWSIQFPNFKDHLCFRNCSNASSTRHFSYR
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   ------------------------------------------------------------
Pt832603   ------------------------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                             140                 160                 180
RMR1       ---------------------------------------------------RVCG--RRG
Sb09g19410 ---------------------------------------------------RARGRRRRG
Bd2g26500  ----------------------------------------------------------RG
Os05g32610 -------------------------------------------------------LARRG
Pt286483   -------------------------------------------------GHRKPTPYQTR
Vv15867    ------------------------------------------------------------
```

```
Cp76.2     -------------------------------------------------KLDNQ------
ZM178435   -------------------------------------------------TEAGRSRTMTR
Sb04g33300 -------------------------------------------------AVPGKGRTKPR
Os02g43460 EVEVYEPASPPERVLIILDSSEDDLDLQEVRRSLMITGRGRARAAERVGEEAPRGSGRRA
Bd2g43500  ------------------------------------------------------------
Bd3g50300  -------------------------------------------------FPASKRKSRIE
At3g24340  ------------------------------------------------------------
ZM000342   -------------------------------------------------SGRCHLLAGHL
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 SLLIRTEKPVTTRNHAYAEVVVFVLDQNPMFFLFLRFFYPAIQRGPNCWSSANSTVMRQA
Bd1g16720  -------------------------------------------KGPS--RAAGHPICATP
At5g20420  -------------------------------------------------YNLKHPFDPCP
AtCLSY1    -------------------------------------------------FEFNHPFNPCP
Pt567214   -------------------------------------------------HQSKHPYNAHP
Pt832603   -------------------------------------------------HQSKHPFNAHP
Cp19.123   -------------------------------------------------YESRHPFGLHP
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 -------------------------------------------------PTSSRAIGAPI
Bd1g74070  ------------------------------------------------------------

                            200                 220                 240
RMR1       VSQAAVEAAPSSSRARRRDKAPAVVMDLGDD---DC-GGGGARKTVGGAAGRCEGSTKAP
Sb09g19410 VSQ----AAPSSSRARRRDKAPVVVVDLGDDEDEDCGGGGGARKTVGGAAGGRGGSTEAS
Bd2g26500  RARGRGETLAEASPRTRRRHAETIVIDLDSE------DGGGGSSTAAAAASSSSSR----
Os05g32610 GGVTVAEYRMVRGRRRGGDAGPVVVIDVEDDGEDAADDSAGGGGGAAAAVKRR-------
Pt286483   EANSNVPVTKDNIYSTHRSPS---------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   V---------------------IILLDSDKE-------DDGTGRQAGRELG-GAAIASAG
Sb04g33300 E---------------------IIVIDSDEE------GVGGGGRQAGRDLGSGAAIGAAG
Os02g43460 APVVASRRRRRRSRSRSRSP----------------------------------------
Bd2g43500  ------------------------------------------------------------
Bd3g50300  IPDSDDDADRRRESRS--------------------------------------------
At3g24340  ------------------------------------------------------------
```

```
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 FEVFYDGSWHGVNCIRIRNGNLFVKF----------------------------------
Bd1g16720  FEAFHHGSWHGVNCIRVQNSRLFVRF----------------------------------
At5g20420  FEFFCSGTWKPVEYMRIEDGMMTIRL----------------------------------
AtCLSY1    FEVFCWGTWKAVEYLRIENGTMTMRL----------------------------------
Pt567214   FEALYGGSWQSVELIEIRDGAMTLHF----------------------------------
Pt832603   FEALCCGSWQSVELIQIRDGAMTVHF----------------------------------
Cp19.123   FEAFSRGSWRMVDCIRIEDGTMSLRF----------------------------------
Vv29366    ---------------RIEDGTVALHL----------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 QPTEPHAPLPNTGGEGAPPPARTMPPPSSQA------ATSTPPAAATPLQRPPAQATAQP
Bd1g74070  ------------------------------------------------------------

                              260                 280                 300
RMR1       ------------------------------------------------------------
Sb09g19410 ------------------------------------------------------------
Bd2g26500  ------------------------------------------------------------
Os05g32610 ------------------------------------------------------------
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   EASKLVKPEVVDDVGSNPVRPGA-------------------------------------
Sb04g33300 EAVKLVKPEPVDDAGFHPVLPGAPRLGAVPVPPRAQNPRAPSSPRAQAQNPRAPSSPRTP
Os02g43460 ------------------------------------------------------------
Bd2g43500  ------------------------------------------------------------
Bd3g50300  ------------------------------------------------------------
At3g24340  ------------------------------------------------------------
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 ------------------------------------------------------------
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
```

```
Pt567214   ------------------------------------------------------------
Pt832603   ------------------------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 STQRYYVGVQRDKGTGKWAACVVDPSNPTKHRLVGAFPDEHAAALAHDRLDLAFRGGGHR
Bd1g74070  ------------------------------------------------------------

                            320                 340                 360
RMR1       ------------------------------------------------------------
Sb09g19410 ------------------------------------------------------------
Bd2g26500  ------------------------------------------------------------
Os05g32610 ------------------------------------------------------------
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   ------------------------------------------------------------
Sb04g33300 SPRAPSLPSLVAAHPLGPGAPRLGV-----------------------------------
Os02g43460 ------------------------------------------------------------
Bd2g43500  ------------------------------------------------------------
Bd3g50300  ------------------------------------------------------------
At3g24340  ------------------------------------------------------------
ZM000342   --------------------------------------ELEDLTVDSTPLPFLPQGP---
ZM108166   ------------------------------------------------------KGS---
Sb02g43870 ------------------------------------------------------KGS---
Os07g49210 ------------------------------------------------------------
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   ------------------------------------------------------------
Pt832603   ------------------------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
```

```
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 GAGDNFRPAFHAVELEFLRLCAATSSPGSHCGLVAGGDKYDEKYSEFLRKIYHGVMDNSP
Bd1g74070  ------------------------------------------------------------

                            380                 400                 420
RMR1       -----------------LPLLPPMMVPAGAVALRTRSRRR--------------------
Sb09g19410 -----------------PPPPPPMMVPAGAVAMRTRSRRR--------------------
Bd2g26500  -----------------RSSAPLTLVTSGSVATRTRSRSL--------------------
Os05g32610 ------------------------VVVPGAVATRTRSRRM--------------------
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   -----------------LPTSLRVQGHRAPSSPSPVPAAVRKQPEIIAISDEDNDGSRF-
Sb04g33300 -----------------VPVPPRAQNPRAPSSPSPVAPEDRHQPEIIAISDDDG-GSRFR
Os02g43460 -----------------RAARPRAESSRRPTARRARARARSPSLEIIDVDSGSD------
Bd2g43500  ------------------------------------------------------------
Bd3g50300  ----SVGTGGQRERSAEAGRSGGLERRLAAAIARRRTRAAAASRPEVVNLTGDDDDDIRD
At3g24340  -----------------------------CVARRTRSRTESYLNSILNKSKGIS------
ZM000342   -------NGQPIFFTVQRPVA--VQHDIDGSYLRVRSRKATCSDCSHVLKPGADVCVW--
ZM108166   -------TGHH-----SNPIAPVLQHDIDGSYLRVRSRKATCSDCSHVLKPGADVCVW--
Sb02g43870 -------TGHH-----NNPIGSVLQHDIDGSYLRIRSRKATCSDCSHVLKPGADVCVW--
Os07g49210 -----------------IYSGSTVEHNVDGDCLRLRSRRATCSDCSNVLKPGVDVCVQSS
Bd1g16720  -----------------VYSGSTVERNIDRDHLRLRSRRATCFDCSHVLKPGVDVCVQSP
At5g20420  -----------------LENGYVLEDIRPFQRLRLRSRKAALSDCICFLRPDIDVCVL--
AtCLSY1    -----------------LENGQVLDDIKPFQRLRIRSRKATLIDCTSFLRPGIDVCVL--
Pt567214   -----------------ADSHHRIEEKGPFSNIRVKSRKSTLSDCTCFLRPGIDVCVLSF
Pt832603   -----------------VDSHHRIEEKGPFSNVRVKSRKATSSDCTCFLRPGIDVCVLSS
Cp19.123   -----------------VDGRHVIKRKRPFSELRVRSRQANLTDCTCFLRPGIDVCVLIP
Vv29366    -----------------AESEYVIEEKSPIPNLRIRPRKATLSDCTCFLRPGTEITVLWT
Sm441121   ------------------------------------------------------------
At1g05490  ---------------------------------RVKSRSWQRLQ----------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
```

```
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    -----------------------------------------------------EPTNGGL
Sb01g46180 ------------------------------------------------------------
Os03g06920 SYKKFFDVILDFFIARAREIGREALEDGGDMLVERFVAMHKNKAVTPRWRAWYRSDSRKV
Bd1g74070  ------------------------------------------------------------

                            440                 460                 480
RMR1       ---------------------------------------AMLAAAVVEEAPTKKKKK---
Sb09g19410 ---------------------------------------AMQAAAVVEETPTTKRRK---
Bd2g26500  --------------------------------------AMKSPVAEAEAAPRAKRRR---
Os05g32610 ---------------------------------AMAQQAPVTPPAAAEEAPSRRRKR---
Pt286483   ---------------------------------PSLQWTRLREAEVYKKLHDEIRKG---
Vv15867    ---------------------------------PVAKRTRLQEALVYRRLYEEKKRN---
Cp76.2     ---------------------------------PVARRTRLKEAQFFKEYYERRRKE---
ZM178435   ------------RRVRRVKDEA-----SDWVLSAKAKRAMVSGVPPGSSDVKRKRKRGSS
Sb04g33300 GAVPLDMIEESGRRVRPVKEEALDDLDCDWVRSAEAKRALVAVLPPGSSHAKRKRKRASS
Os02g43460 ------------RGVVRVKEEPRSGSDSDYNGARGRARARARAPVAATAAKKKKRKRGKE
Bd2g43500  -----------------------------------------------SPLVETPRRR---
Bd3g50300  EEAAGRREVLGRVKEEPLDDRGLDPEASVAR--RGRGRGRARAAAASAPVASRKRRR---
At3g24340  -------------------GEEEDQSLGCVNSRTEKRRVNMRDACSPSPRKKKRRRR---
ZM000342   ---QAVY--------------------------RGETKDSVLLCCRDARLIKIKRNH---
ZM108166   ---QAVY--------------------------RGETKDSVLLCCRDARLIKIKRNH---
Sb02g43870 ---QATY--------------------------GGETKDSVPL-CRDARLIKIKRNH---
Os07g49210 HTPEASS--------------------------QGGTNASVLL-RHDARLITIKKNH---
Bd1g16720  HPLQACS--------------------------TGDQKSSISL-CHDARIVTIKRNH---
At5g20420  ---------------------------------YRIHEDDLEPVWVDARIVSIERKP---
AtCLSY1    ---------------------------------YQRDEETPEPVWVDARVLSIERKP---
Pt567214   SERA-----------------------------KSSEEGNSEPVWVDARINSIKRKP---
Pt832603   SERA-----------------------------KNTGEGNSEPVWVDAKISSIKRKP---
Cp19.123   SKDL-----------------------------ASSDEANLELVLIDAKIRSIERKP---
Vv29366    LQQS-----------------------------ESSDEENREPVWIDAKISSIERRP---
Sm441121   ------------------------------------------------------------
At1g05490  ---------------------------------AVNKRKKMETVAPVTSPPKKRRQK---
Sm84719    ---------------------------------CSAIHSCVMLQLSHTPLASKAVRF---
ZM064574   ---------------------SQSPGGREGIYYSRQRKP-ERNGSVFTPIAAMYSSG---
ZM093940   ---------------------SQSPGGREGIYYSRQRKPSERNGSVFTPIAAMYPSG---
Sb07g02945 ------------------------------------------------------------
Os07g25390 ---------------AAAGRDPPATPSSRMYYCRQRKASSEVNANVFVPGGQNG------
Os06g14440 -------------------------DLISMYYRRQRKASSEANANVFMPGGPND------
Bd3g19890  ------------------------------YYRRKNRASDPISG----------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  -----------------------------------------DAAAAATKIFRRNHRL---
Os08g14610 ------------------------------------------------------------
Bd3g18910  ----------------------------------GGEMPNANMTNCFMEQTEKKK-----
At2g21450  --------------------------------FTAWNLRSRSRSITQEELAKRPDPF---
AtDRD1     -------------GFVYIVMTGYYKNVHKRKQNQVDDGPEAKRVKSSAKVIDYSNPF---
Pt195587   -------------------------------------------KDTKEKVTDYAKPF---
Vv23895    -----------------------------------HSEPKQKRQKAGSNVVDYSDPF---
```

```
Vv35918    SSNYGNPIPVNFEPYKLTEFNSTKHKRIWTFEENMHSEPKQKRQKAGPNVVDYSDPF---
Sb01g46180 ----------NLRGDYLSDKYTRMGSAGQKRQKLGSEHTSSPGTQSQSNIFLANKR----
Os03g06920 LQIPLSLRGGGGEIDHSTQKEARMDSDSCKRRKHESGHDSSSRVQSQSSILSRNRI----
Bd1g74070  ------------------------DPSGCKRQKHEIEHDSSPGNQSQATIISHNSS----

                              500                 520                 540
RMR1       -----------EGA-IPDAAEAPRGHGSKAAATSMATSSHKRRAGTSRSTSRD-----KR
Sb09g19410 -----------RGATTPDAAEASRGRGSKAAAASRATSRDKRRAGASRSTSRD-----KR
Bd2g26500  ---------------KGTSAEADGGGGSKGAEASESASKGNRR-GRSRTASEPPDRALAR
Os05g32610 ---------------KGAASAEAGGGGPSKRRVRSSGSAGGRG---------------AR
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   GA--------GDFHALDRNLSASGAGRRTSWMAEDAGSSRNVSSSELSRGGVGDRSGSTK
Sb04g33300 GRAKPDKRADGGVHALDRNSSASGAGHPTAWMSDDARSSRGVKSRESSRGVAGDRPGSAK
Os02g43460 APSRAQESREVVRVKEEPNSDGNGAGGRARARSPVAAAAKQRKRGGREAPSRAQESRVPV
Bd2g43500  -------IRRLLIDDDDDDDDSGDGGRAREAISPSVAAGGSRRVGAEISGWLVRDPLAPS
Bd3g50300  -----------------EDDSGSRGRGGRRATRSAKQCTRGRRGGLRSLPSRPSSSDEPL
At3g24340  ------------------------------------------------------------
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 ------------------------------------------------------------
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   ------------------------------------------------------------
Pt832603   ------------------------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ---------------------------KPKNYDSDIEDITPTCNDSVPPPQVSNMYSVPN
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                              560                 580                 600
RMR1       RARSGRASEPARVGRARKRK------RNELEAPARRERVKAPCVSESDD--NSGRGDDAS
```

```
Sb09g19410 RARSGRASEPARAARACKRKGIELGAETEVDAPARSERAKAPCVSESDD--DGGRGDDAS
Bd2g26500  KSKDADAEEEAEAEAEE---------EAEAEAPACGKRVE---VSRVDGCANSERGEDPL
Os05g32610 KRKEAEADEEEAEAEAEEEA------EAEAGTPARGESME---VSQVDGGGSSGRADDAS
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   KA----------------------------------------------------------
Sb04g33300 KA----------------------------------------------------------
Os02g43460 QIKEEPYSGSDSDGNVAGGRAVVPAADAKQGKRGKK------------------------
Bd2g43500  SSAQPG------------------------------------------------------
Bd3g50300  ------------------------------------------------------------
At3g24340  ------------------------------------------------------------
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 ------------------------------------------------------------
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   ------------------------------------------------------------
Pt832603   ------------------------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  NSVKESFSRIMRDLNVEKKSGPSSSRLTDGSEQNPCLKERSFRVSDLGVEKKCSPEITDL
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                            620                 640                 660
RMR1       HDGDAEPRVGVAIGTDLVNGD------------------HPAAK----------------
Sb09g19410 DDGNAEPRAGVAIGADLVNGD------------------RRTAKGEDHIEEHGGDQENS-
Bd2g26500  DDHNNGSNAREACGIGHGNEE------------------HHNAAGKNRIGEPCGNGVAS-
Os05g32610 HNGNGESRVCNADGIDQASEERPSVAGGDLIEEEHYGNGEASVAGGDRIEEHCGNVEAS-
Pt286483   -------------------------------------------RNQGKESNAAATGSTN-
Vv15867    --------------------------------------AGVSSSGSHNDDGVEFLGEAG-
Cp76.2     --------------------------------------------DGKNVARPSGQSEDR-
ZM178435   ------------------------------------------RGAPGKTRRGGGTRRER-
```

```
Sb04g33300 -----------------------------------LVSSEESRGAPGKARSGGGARRER-
Os02g43460 -----------------TPSRGKGRRVVVRETSTPAAPSNGAPSVGRGKGRGPGRGRQRS
Bd2g43500  ------------------------------------------------------------
Bd3g50300  ------------------------------------GDSGRAKRVRRGHAEGGGSGRHG-
At3g24340  ---------------------------------------------KDDDDDVVFVRTEY-
ZM000342   -----------------QSDRCLCLFAVIFYKDQCPGSKEK--VISGTIADVVTIDDIC-
ZM108166   -----------------QSDRCLCLFAVIFYKDQCPGSKEK--VISGTIADVVTIDDIC-
Sb02g43870 -----------------QLDRCLCLFAVIFYKDQCPGSKEK--VISGTIADVVTIDDVC-
Os07g49210 -----------------QEDKCLCLFVVILYKNQCPGNAEK--VITDRRAEVVTINDIF-
Bd1g16720  -----------------NADQCLCLFLVILDDSQCPGNTEKGGKATDRRQEVVTLNNIF-
At5g20420  -----------------HESECSCKINVRIYIDQGCIGSEK--QRINRDSVVIGLNQIS-
AtCLSY1    -----------------HESECLCTFHVSVYIDQGCIGLEK--HRMNKVPVLVGLNEIA-
Pt567214   -----------------HESQCSCQFFVNLYVNQGPLGSER--ATLSKETEAVGIDQIS-
Pt832603   -----------------HVSHCSCQFFVNLYVNQGPLGSER--ARLSKETEAVGINEIS-
Cp19.123   -----------------HESQCSCQFYVNLYVNQGPLGSEK--LELDKDTKVLGIDQIL-
Vv29366    -----------------HEPECSCQFFVNFYITQDPLGTEK--GTLSKDISVVELDQIS-
Sm441121   ------------------------------------------------------------
At1g05490  DVGIPVPRFSKLKDVSEQKNTCLMQKSSPEIADLDLVISVPSSSVLKDVSEEIRFLKDKC
Sm84719    ------------------------------------------------------------
ZM064574   -------------------------------------------------------HALP-
ZM093940   -------------------------------------------------------HALP-
Sb07g02945 ------------------------------------------------------------
Os07g25390 -------------------------------------------------------ISFP-
Os06g14440 -------------------------------------------------------ISFP-
Bd3g19890  -------------------------------------------------------LSLP-
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  -------------------------------------------------------CLPN-
AtDRD1     -------------------------------------------------------AVSN-
Pt195587   -------------------------------------------------------AIRG-
Vv23895    -------------------------------------------------------AIPN-
Vv35918    -------------------------------------------------------AIPN-
Sb01g46180 -------------------------------------------------------LRLQ-
Os03g06920 -------------------------------------------------------LCHQ-
Bd1g74070  -------------------------------------------------------VRLR-

                            680                 700                 720
RMR1       --------------------EVVEGAGDEDTGDGGNSGLASTA-----------------
Sb09g19410 -------AVNLNDDLVSGDAEAVEGAGDEDT--RGNSGLASTA-----------------
Bd2g26500  -------ILNSSHGMNVVASGHA-----EGVKDWGNKGGELDD-----------------
Os05g32610 -------VANSNRDGGEIIAG-------EGTEDRGNTELSVVD-----------------
Pt286483   -------GLNGAQEESVGGLSYKGSKSPVVLDDSEDDAFL--------------------
Vv15867    -------VFDSVQKFVAESDGKNSDRKNSSRK----------------------------
Cp76.2     -------GVNGSKLGRVGLKGTNMETRDLGLNCKGSAGLENRA-----------------
ZM178435   -------STSAAPANLVGGSATVGSRIRLRSRQQGRVQCATYS-----------------
Sb04g33300 -------STSVAPANWIGTS--IGSRIRSRSRKQGTGQYS--------------------
Os02g43460 KG-----AVRGRATPVNRVSTGVGSRTRSRLAEQGRAFAQEEE---------------EQ
Bd2g43500  ------------------------------------------------------------
Bd3g50300  -------AAPSKQAGSLVASSSRSRKGKQRAALPPKHQFPLVS-----------------
At3g24340  -------PEGKRDDENVGSTSGNLQSKSFDFG----------------------------
ZM000342   -------ILQNLQPEEL-------QDGSVRWNSAVDCFHHNRS-------------KLLS
ZM108166   -------ILQNLQPEEL-------QDGSVRWNSAVDCFHHNRS-------------KLLS
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Sb02g43870 -------ILQNLQSEEL-------QDGSVQWNSAVDCFHHNRS-------------KLLS
Os07g49210 -------LLQKLQPEV--------HEGSMKWSFSKDRLSLNKG-------------RLIS
Bd1g16720  -------LLQKLQPKEL-------QEGSVQWNSAEDCLYQNRS-------------RLLS
At5g20420  -------ILQKFYKEQS-------TDQFYRWRFSEDCTSLMKT--------------RLS
AtCLSY1    -------ILQKFCKEQS-------LDRYYRWRYSEDCSSLVKT--------------RLN
Pt567214   -------ILQKLDNDPCEADNNRHETQFYRWEFCEDCSLVQRT-----------------
Pt832603   -------VLQKLDNDPCEADNNQQEAQFYRWEFCEDCSLVQRS--------------KLF
Cp19.123   -------ILQRLEKHPC-------EGQYYRWSLSEDCSSLSRT--------------KLF
Vv29366    -------ILQKLGKYPC-------EDEHYRWKFSEDCSLLQRT--------------KLF
Sm441121   ------------------------------------------------------------
At1g05490  SPEIRGLVLEKSVPGEIEILSDSESETEARRRASAKKKLFEES------------SRIVE
Sm84719    -------TLHLPEPIQPSSRPPPPCAARALLTSSSSYFLSLP------------------
ZM064574   -------VANRSHGLVFGSLSKDWDDIRQRKDQLVNFLASLERASGDSAA-AGKIEDSKL
ZM093940   -------DANRNHSLVFGGTSKDWDNIRQ-------FIASLERASENSSAIASKTGGGKS
Sb07g02945 ------------------------------------------------------------
Os07g25390 -------ASNRAHDWGYGGVREEWEASYARKLQLINFLSSLHQRTANSLITTRMDANMDT
Os06g14440 -------ASNRDHDWGYGGVGKEWEASYARKLQLMNFLSSLHQRTANPLVTTRMDANMDT
Bd3g19890  -------AGSGVHSWGCGSVTKDMEDIYARNVQLINFLSTLHEPTRSSVPMVETNVKYCS
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  -------LLDGLEDGLYGRLADDVKRLCKLRQEYLNGSISLEDI----------------
AtDRD1     -------MLEALDSGKFGSVSKELEEIADMRMDLVKRSIWLYP------------SLAYT
Pt195587   -------LLERLDSGRYGSVTDDIRSLFYRRAQLIHPCLAMHP--------------TLS
Vv23895    -------LLEGLDAGKFGSMTKEIEALCARRMQMLHPYYVMYP-SLSYMSTDLGKQPSKK
Vv35918    -------LLEGLDAGRFGSVTKEIEALCARRMQMLQPYYVMYP-SLSYMCTDLGKKQGKK
Sb01g46180 -------FLEQVNELKAWSVTKDLKAITAKRRELFGIIERLRQVPIEQLYSSPFPKPSDA
Os03g06920 -------LLEQCDDLKYGSSTNDYKAISMKRLELISILQKLQEVPIQLPYASPLKSSETN
Bd1g74070  -------FLEQFDDLKYASATKDYKAVNAKMHELLSTLEKLKEVPIKLPYVSPVLKTSDA

                             740                 760                 780
RMR1       ----------DVFAEEMAPFEDD-------YDDEMLEEQLVGDVIRAYSNGRNFDSDGVD
Sb09g19410 ----------DVVAEEMAPFEDD-------YDDEMLEEQLVGDVIRAYSNGRNFDADEAD
Bd2g26500  --------GFEVDEEYMNEEDTE-------DDDEMLEEKLVGDLIRAYSNGDDLDADGVD
Os05g32610 -----------PVNEELASDEDD-------YDDEMLEEKLVGDVIRAYSNGADLDTNGVD
Pt286483   ------------------------------DDCEKGGLEEGLDVVSLDDSDDDDQSEGVE
Vv15867    ------------------------------KNGGENSDEDVTDVVSISDDSEAS------
Cp76.2     --------RRIKTREKVTDENKDRVREMNAKDCGDLNPEKCRDVIVIDDDDNEAIAADAS
ZM178435   -ARVSSEDTGEDEKHMQEQTRVEDVEFMEVDDDYD-DVNVAGNVIDQESEQDEALEGRSS
Sb04g33300 -ARVSSEDTGEDEVQEQKQKRVEDVESMDVDDDDDNNTNEAGNGIQKESEQDEALEGRSR
Os02g43460 VEEREEEEEEEEQGRAFAQVKEEQVEEQEEDEEEGEEEMEMEVEVEVRSDDNDHGNGGIR
Bd2g43500  ------------------------------TLLRSREQEQPEIIVISDDDHEDEEEDGAR
Bd3g50300  ---------------------------------------QSESSSESDDDDDDEEGDDGL
At3g24340  ----------------------DRVCDFDADDRNLGCEEKASNFNPIDDDDDVVFVGTVQ
ZM000342   -ARFSLEVAYLIVLSSLRRME---------FNIKMVDGNIIYQIIKGDQARDSIDSMSIP
ZM108166   -ARFSLEVAYLIVLSSLRRME---------FNIKMVDGNIIYQIIKGDQARDSIDSMSIP
Sb02g43870 -ARFSLEVAYLIVLSSLRGME---------FSIKLVDGNIIYQIIKGDQARYSIDSMSIP
Os07g49210 -ARFSSEITHLIVLSILRGME---------FNIKLVEGQIVYQIIKGDQAQWNLDSMAIP
Bd1g16720  AARFSSEISHLIVLSALRGME---------FSIKLVEGNIIYRVIKGDQARRGVDCMSIP
At5g20420  LGKFLPDLSWLTVTSTLKSIV---------FQIRTVQTKMVYQIVTDEEGSSST-----L
AtCLSY1    LGKFLPDLTWLLVTSVLKNIV---------FQIRTVHEKMVYQIVTDEDCEGSSSS---L
Pt567214   --------------SIPKQVA---------FDVRSVQNKIAYQIFGGDDDHCSLKSNNHI
Pt832603   LGRFSADLTWLLVASVLKQVE---------FNVRSVQNKIVYQILGGENEHCSLKSNNHI
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Cp19.123   LGKFSSDLSWLLVASVLKQVA---------FEVRTEQYKIVYQIIADDDGSPS-KSNNYI
Vv29366    LGKFSSDLSWLVVTSVLKQAV---------FDVRSVQNRIVYQIVGGDHDKVS------L
Sm441121   ------------------------------------------------------------
At1g05490  SISDGEDSSSETDEEEEENQDSEDNNTKDNVTVESLSSEDPSSSSSSSSSSSSSSSSSSS
Sm84719    ------------------------------LDEAASLENHLSIVVAVDGETSRTER----
ZM064574   A-----------------------------SPVEPTEQKEKAAIIVLDSDDEDGNGSG--
ZM093940   TN----------------------------HSVEPAEQKGKGDIIVLDSDDEDGDGNSPE
Sb07g02945 ------------------------------------------------------------
Os07g25390 PLEQ--------------------------------KQKDSSAIIVLDSDDED-EAER--
Os06g14440 PLEQ--------------------------------KQKDSSAIIVLDSDDEDGYTEG--
Bd3g19890  IKQE--------------------------TKVTDCSVKQTEPIIIPDSDDEDGST----
Bd2g21450  ------------------------------------------------------------
Bd2g21430  -----------------------------------------PPVVQQKRFPPSGGASFLP
Os08g14610 --------------------------------SGSGNSLDTVALIVGGGSDSSGIVGRKR
Bd3g18910  ------------------------------YNVLLILDSPPKELIILDSDDEDGNSGKTQ
At2g21450  ------------------------------EARQDNKRAKSSHNLIIDSDDE--------
AtDRD1     VFEAEKTMDNQQVVEGVINLDDDDDDDTDVEKKALCVVPSSSEIVLLDSDDEDN------
Pt195587   NEPRGRGMSFGEGKCNVIDLDDDEIEGV--GDSVGNVAVGRTPVVVIDSDDDES------
Vv23895    ASKLVNRHASHLGHEDVIDLEDDHIVYD--VPTATAVADAALPVVIIDSDDEES------
Vv35918    ASKLVNREASHLAHEDVIDLEDDHVVDD--ALTATAVEDATLPVVIIDSDDEDC------
Sb01g46180 RLDNFGKMESSYNPDNVINLDADEENVEYHTQVNAGNTEADSTASADDSGDKDR------
Os03g06920 RL---VQDGRNSSCRNIIDLDSD--NDEDYTFANVDNIGANTTVVLVDSDDGDS------
Bd1g74070  RLHSATQSGSNFSSDNIIDLDPD--NVGDHTHPNMENTGAHNTTYLVDSGDGDM------

                            800                 820                 840
RMR1       WEAEDEMEFNDDADNSDFMDDADD-------------------SDFMDDAY---------
Sb09g19410 WEAEDEMEFDDDADNSDFMDDAHDSDFVNDADEGGKSGDDAENSDFMDDAHDSDFVNDAD
Bd2g26500  WEAEDEMEFDD-------------------------------------DGDDDYFVHDAD
Os05g32610 WEAEDEMEFADLDTNVVDWEAEDEMEFDDD-------------NDNDADDDGDNFGGDAD
Pt286483   SKSFDVGGKKSGGTDVGGSCSGVKSDGEESGRSKVPLPR---------------------
Vv15867    ------------------------------------------------------------
Cp76.2     GDDDDDCDENHDDEDDD-------------------------------------------
ZM178435   QDSHGYSEDKEG------------------------------------------------
Sb04g33300 QDSH--------------------------------------------------------
Os02g43460 GEGGGTDDV---------------------------------------------------
Bd2g43500  GG----------------------------------------------------------
Bd3g50300  DDVCSETSDESWQPRYNSEFQVAMKGEKKVEGRRNSVEEEATEKELGENGNGIPVLEE--
At3g24340  RENDHVEDDDNVGSASVIS-----------------------------------------
ZM000342   PGFGKNMDIISFKPRGEALRPITRTVPVTQVEEGNLTEDGCIAVKG--------------
ZM108166   PGFGKNMDIISFKPRGEALRPITRTVPVTQVEEGNLTEDGCIAVKG--------------
Sb02g43870 PGFGKSMDIISFKPRAEALRPIIRTVLITQVKEDNLIEDGCTAVKH--------------
Os07g49210 PGFGNTMEIISFQLRDEALRPTITNIPITHVKKNNITEDMRFTVKS--------------
Bd1g16720  PGFGRNMEIVSFQLHDKNLRPTIRNIPVTHAKKHNLTEDNRFTLKTELDDQLEYIRVAVK
At5g20420  SSMNITLEDGVSLSKVVKFNPADILDDSQDLEIKQETDYYQEEDEV--------------
AtCLSY1    SAMNITVEDGVVMSKVVLFNPAE--DTCQDSDVKEEIEEEV-------------------
Pt567214   NCVTFKVEDGISTPFVVQLDPIDT------------------------------------
Pt832603   NCVTFKVKDSISTPFVVQLVPTDACSEAGHISDTNGTEQSPCYDV---------------
Cp19.123   SATMFI------------------------------------------------------
Vv29366    NAVNFRVDNGISTPVIFPFVPADT-IEADPLNGTNEAGPLPFCDI---------------
Sm441121   ------------------------------------------------------------
At1g05490  DDESYVKEVVGDNRDDDDLRKASSPIKRVSLVER--------------------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
```

```
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  PRCEAL------------------------------------------------------
Os08g14610 RRCDLIRERWCCLCPVWC------------------------------------------
Bd3g18910  VPSYPTKELIIL------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                            860                 880                 900
RMR1       EGGNSKPIQNHAKLEIQDWVNQKVVLSGGRCEARGEGDLEEELDVGKEA-DEEDVEPKSE
Sb09g19410 EGGKSEPIKSHAKMEIQDLVNQKVVLCGGGCEE--EGGEKEELGVGKEAGKKEDVEPKSE
Bd2g26500  ECGMSEPMCDDYKVGTQYLSDHEVVVGEVSCQL-------------EEDVVKDEVDPKRE
Os05g32610 EGDKSVQMHDFSKVETQDLVSHNVNVSEVRPHE-------------DEEAIKDEMESKGK
Pt286483   --------------------------------------------------WQRIVNESYN
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   ------------------------------------------------------------
Sb04g33300 ------------------------------------------------------------
Os02g43460 ------------------------------------------------------------
Bd2g43500  -------------------------------------------------------EIRHG
Bd3g50300  --------------------------------------------------AAEKELRENG
At3g24340  ------------------------------------------------------------
ZM000342   -ESDS----AQDVEILYAH-------------------------------VDIRRSKRMK
ZM108166   -ESDS----AQDVEILYAH-------------------------------VDIRRSKRMK
Sb02g43870 -ESDS----AQDVEVLYEH-------------------------------VDIRRSKRMK
Os07g49210 -EMDSELDRALDVEILYEH-------------------------------VDLRRSKRLK
Bd1g16720  IELDDQLEDQFDVGLLYKH-------------------------------VDLRRSKRLK
At5g20420  --------------------------------------------------VELRRSKRRN
AtCLSY1    --------------------------------------------------MELRRSKRRS
Pt567214   ------------------------------------------------------------
Pt832603   --------------------------------------------------MSLRRSKRRN
Cp19.123   ----------------------------------------------NGGWWELRRSKRRN
Vv29366    --------------------------------------------------VDLRRSKRRN
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
ZM064574   -------------------------------------------------------NSKLA
ZM093940   -------------------------------------------------------HNKLA
Sb07g02945 ------------------------------------------------------------
Os07g25390 -------------------------------------------------------CEQLA
Os06g14440 -------------------------------------------------------CEQLT
Bd3g19890  --------------------------------------------------------AELA
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
```

```
Bd3g18910  --------------------------------------------------DSNDRKTLLP
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                            920                 940                 960
RMR1       AAPGSDKRVLQLEILGSDEEIKVLENMSSAPSRKASVQSKLPTIPSCVAWRTRSSWGVNQ
Sb09g19410 AAPGSDKGGSHLETMSSDEEIKVLENMSSAPSRKASVQSKLPTIPSCVAWRTRSSWGINR
Bd2g26500  GTTCFDQGRLHIEILESDDEVKVLSDASNPLKRKPLPQAKIPVLP-CVAWRTRSLWGVKQ
Os05g32610 GSLSFNEGSSYIEILDSDEEVKVVNDTGNALRRKPLVPAKLPIVPSCVAWRTRSSWGMKE
Pt286483   GDVFAHERNEGGVCFLSSGIGNGSGGVGLKGRESNGVAGRTELRSGFCEKKKDGNVVVVV
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   ------------------------------------------------------------
Sb04g33300 ------------------------------------------------------------
Os02g43460 ------------------------------------------------------------
Bd2g43500  EIPARVKDEESEEGSSVDWDALMLSDDESTAAAPPGTATGVPDEEEEAELEDKDNLEEEQ
Bd3g50300  NSIPVQEEAAEKELGENGNSIPVLEEAAEKELRENGKSIPVEEEAAEKELGENGNS----
At3g24340  ------------------------------------------------------------
ZM000342   TQPDRFTS----------------------------------------------------
ZM108166   TQPDRFTS----------------------------------------------------
Sb02g43870 TQPDRFTS----------------------------------------------------
Os07g49210 TQPDRFTS----------------------------------------------------
Bd1g16720  TQPERFTS----------------------------------------------------
At5g20420  VRPDIYTG-----------------------------------------------CDYEP
AtCLSY1    GRPERYGD-----------------------------------------------SEIQP
Pt567214   -------------------------------------------------------CNTPA
Pt832603   VQPERFLA-----------------------------------------------CDAPA
Cp19.123   VQPERFIG-----------------------------------------------GQGLT
Vv29366    VQPDRFFS-----------------------------------------------LGGFS
Sm441121   ------------------------------------------------------------
At1g05490  ------------------------------------------------------------
Sm84719    ------------------------------------------------------------
ZM064574   SETNKELG-----------TSGLINNIAERMTFNGSQAFG-------TVHTY-GDKNTQI
ZM093940   SEMNKELG-----------TSVLASNIAERMATNGSQTFE-------TVHAYGGSKNTQI
Sb07g02945 ------------------------------------------------------------
Os07g25390 SENNKQQA-----------PSGPTSPCTTWIVSSAKDQVNGTLHV-------DGVQSTQI
Os06g14440 SENNKQQA-----------PSGLTSPYTTWIVSSAKDQVNGTLHV-------DGVQSTQI
Bd3g19890  PEKNKELI-----------PLGLAGTLTAHVTSKGKDQVNETRHY--------GYQNSQI
Bd2g21450  ------------------------------------------------------------
Bd2g21430  -------------------SVNFVATYFLRCTCESKKLYTHNLFF---------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  PYPTKELIILDSYDEDRNPPCQRKRKISEVSSQVNRDASN------DPRQK--KLKNEPT
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
```

```
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                             980                1000                1020
RMR1       DR-LSYDTYFEELSDEPKEDDDDTEVELDEVEDDNNDDDSSDAY-----DKDDEEK----
Sb09g19410 DR-LSYNTYFEALSDEPKEDDDDTEVELDEDEDGNNDDGSSDAY-----DKDDEEKEE--
Bd2g26500  DR-ISYNAYFEELSDEPIE-DDDTEVELDDE--DDNDDDSASF------EEEEEEE----
Os05g32610 ER-ISYNTYFEVLSDEPKEDDDDTEVELDDEEDDENDDDCNSASCDEEDEEEEEER----
Pt286483   DD-DDDDACIILEKDAEELQSSSSGEEETFKDDSDDDDYRVELPESFMVEEEEKEEDG--
Vv15867    ----------------------------DYEEEEDDDDDDYIVDPTIDRDERGNQA----
Cp76.2     -------------GDVVWEEDMDDLERTSEEDNDDSDDEDYAVMKTMYRKEKCKPKNH--
ZM178435   -------------KDSAALSDNEEDVGGKELLEEEEEGADQEESHIIYDGEGEQEEDA--
Sb04g33300 -----------------ALIDNEEEVGEKELSEEEEDD-NQEESHSMYDGEGEQEEDA--
Os02g43460 -------------AEIEEEELGTDEDETSDDSDENFSDEEGDEEELEEEEEEEEEEED--
Bd2g43500  EEDEEDEWEEEEEEEREADLEDMVGEEEEEEQGKEEDEWELEEEEEEEHEETEEEESE--
Bd3g50300  ---IQDDRYDGEDEEATDDAHAAEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEEE--
At3g24340  -------------PRVCDFDEDDAKVSGKENPLSPDDDDDVVFLGTIAGENQHVEDVNAG
ZM000342   -------------YDARNFNRTYNKKEADGPSTKYEDSESGLSCD---SSEQRESSDEEA
ZM108166   -------------YDARNFNRTYNKKEADGPSTKYEDSESGLSCD---SSEQRESSDEEA
Sb02g43870 -------------YDAPNFNRTYNKKEAYGPSNKNENSESDLSFY---SSEQTESSDEEV
Os07g49210 -------------YDTPRFLSGYKKKEASSSPTKHVRGAVHCDSPVDDSKKEVESCCVEI
Bd1g16720  -------------YDAPNFNRDTKKKGASASSTMHY-------DHRRASQVKVESSCGED
At5g20420  DTIDGWVRMMPYQFGKCAVNVESDEDEDDNNEDGDTNDDLYIPLSRLFIKKKKTNSREAK
AtCLSY1    DSKDGWVRMMPYRYNIWNVSSDDDDEEEDCEDDKDTDDDLYLPLSHLLRKKGSKKGFS--
Pt567214   ETEIGWVRSLPYTPLKWK-----------------EEEELHLPLAYLFGTHADASCAEEK
Pt832603   ETEIGWVRSLPYTPLKWK-------------AEEEEEEEMHLPLAYLFGTHAGASCAEEQ
Cp19.123   ESDSVWVRQMPIKTDKWK------------------EKMKCLPLSRLFKMQPLYLKEQP-
Vv29366    ESDIGSVRAGIHKVDYWR------KEEMPLALPDEGDVHSIFSEKHIIDYEKGAHSLQ--
Sm441121   ------------------------------------------------------------
At1g05490  ---KALVRYKRSGSSLTKPRERDNKIQKLNHREEEKKERQREVVRVVTKQPSNVVYTCAH
Sm84719    ---LNLCSTEYTLCSCPAFKLSSSYEAVCEEQDLAEDDASKDTEI---------------
ZM064574   VP-YGQ-----------------CSALVNQFPLQTSWQPSIQFERVVLQKRPEEQRMQ--
ZM093940   VP-YGQ-----------------GSALVNQFPLQTSWQPSIQFERVVLTKRPEEQRMQ--
Sb07g02945 ---------------------------------------------------------Q--
Os07g25390 VP-YGQ-----------------NAPLINQSPLQTSWQPSIQYERVILQRRPEEQRVQ--
Os06g14440 VPYYGQ-----------------NAPLINQFPLQTSWQPSIQYERVILQKRPEEQRVQ--
Bd3g19890  VP-YGQ-----------------SAALINHHSLQTSWQPSIQYESVILQTRTEEERIK--
Bd2g21450  ------------------------------------------------------------
Bd2g21430  -----------------------VINVIDNVVNQGGQQP-VRFDRVILHTRTEENIFK--
Os08g14610 ----------------------------------------KEAQEVVVPGRGRNGARQRD
Bd3g18910  YF-GFDEPMEKKKNPRKESDCHFNLAVPSKKLLLSNLWPSESLNKLIIQPKQSEEVAN--
At2g21450  ------------------------------------------------------------
AtDRD1     ----------------------------------ERQRPMYQFQSTLVQHQKNQGDVT--
Pt195587   ----------------------------------NENRMVGHFQGIVLPKPEGQFS----
Vv23895    ----------------------------------GDQK----------------------
Vv35918    ----------------------------------GDQKVSHPPQETAWPSFSYQEVVLRK
Sb01g46180 -----------------------VKSFGDENSS-SNRNDNYIQQNPLLEHPVGHQE----
Os03g06920 -----------------------VASFVDEKSSDSKQNANYIEESVLPEQHAQQQE----
Bd1g74070  -----------------------IKSIRDGNSSGCMQNVNFTQECSLAEQPGQYQD----

                            1040                1060                1080
RMR1       --------EEEEEEAERRKLN--NRICTSDEDMINITVPTSRYDMFKKKN----------
Sb09g19410 --------EEEEEEAERRKLN--NGIYTSDDDMINITVPTSRYDMFERKNISRYDMFKRK
Bd2g26500  --------TKQEEVAEKSKHK--KGIHSSFPEIRSRPMPL----FVNRERRMQTSIPKWR
```

```
Os05g32610 --------EEEEEEAQRRKQK--KGIDSSDDEMIDDAVDC--------------------
Pt286483   --------DREQGEMELKRNKVYGIEVLCDSDIGKFENNDVDMDDSL-------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   --------SEEETQELDETGE----------------------AQPFNPSNTMAGSTMRS
Sb04g33300 --------SEEVEQEMDETGEEDEKELDGTGEEDEQELDGAGKAQPVTPSNTIAGSSMRS
Os02g43460 --------DDDDDEEEEEPGD-----------------------APDQPGEAGEESPPRS
Bd2g43500  --------SEQDEEAAEEPRR-------------------------GGPRNSAAAGRYAH
Bd3g50300  --------EEQDDESDEAGEE-----------------------LHPVPNSNADAGGNAR
At3g24340  SEVCDILLDDANLRGEEKTYV---------------------------------------
ZM000342   L-----------------------------------------------------------
ZM108166   L-----------------------------------------------------------
Sb02g43870 LGNPGVKKKVSRSFVVK-------------------------------------------
Os07g49210 PGNVTQKQTGVHSPMVDEKSNSPEGQHKNTTKRTTCSLVKEKASSPEGQHEKTTKRTTCA
Bd1g16720  P----VKITGASSFMFN-------------------------------------------
At5g20420  P-----------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   PGNEVRVNSPKLEFLEGPPVSRTKTNSRKIKSNVFNRREHQAELGEVESGIDNRRERQKS
Pt832603   TCNEVGASSPKLELLEGIPVSRTKTYLKEIKSNVVNRRDHQTEPGEVRAGMAKRRECQKS
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  CGKENTGNPESHSSFIRPHSIRDEIEDVNNFASTNVSKYEDSVSINSGKTTGAPSRPEVE
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 GGGCALGTTEV-------------------------------------------------
Bd3g18910  --------DEVFNDETQNESE--CFMDAMCDHFDLAIASKKGSEEVANDEAQNESELFVD
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    PSVGLLA-----------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                           1100                1120                1140
RMR1       ----------------------------SSRYDIEWVEDE--DASVDMLQPVSFKKDSSW
Sb09g19410 NTSRYDIFKRKNTSRYDIFKR-----KKTSRYDIEWVEDEDKDANVDTLQPISLRKGSSW
Bd2g26500  GTSKK---ARQPETCHVIYSSDDEIIDDTAKDGLKCEVDE--DPRNNVFQPLNFEKVGSD
Os05g32610 --------------------------------GIDWEEDY---PEVDFTRPLTFQKDGSE
Pt286483   ------------------------------------------------------------
Vv15867    ------------------------------------------------------------
Cp76.2     ------------------------------------------------------------
ZM178435   GGDGKQVFRRRVFEGIYLPENPHRTVGKGIQ-----------------------------
Sb04g33300 GGDDTRVFRRRVFEGICLPQKPRKTVGKGIG-----------------------------
Os02g43460 RIMAMPLMGKRMFEGFSFLQQVDTSTGRDIR-----------------------------
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Bd2g43500  RAEDGEIFAKRLFEGLCISKAADTSAAGKPVA----------------------------
Bd3g50300  SGGEGTPIGKRVFEGLCLVDNADNAVTTKSIR----------------------------
At3g24340  ------------------------------------------------------------
ZM000342   ------------------------------------------------------------
ZM108166   ------------------------------------------------------------
Sb02g43870 ------------------------------------------------------------
Os07g49210 LPVK--------------------------------------------------------
Bd1g16720  ------------------------------------------------------------
At5g20420  ------------------------------------------------------------
AtCLSY1    ------------------------------------------------------------
Pt567214   TVANRIKHQTRLG-----------------------------------------------
Pt832603   TMADRIEHQTRLG-----------------------------------------------
Cp19.123   ------------------------------------------------------------
Vv29366    ------------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  NPETGKELNTPEKPSISRPEIFTTEKAIDVQV----------------------------
Sm84719    ------------------------------------------------------------
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ALCNHFD-----------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                           1160                1180                1200
RMR1       KPVAVGNDTFTEQQKRSRFTWELERRKKLKLEMKTNP-----------------------
Sb09g19410 NPVAVGNDTFTEQQKQSRFTWQLERRKKNKLEMKTNP-----------------------
Bd2g26500  GT--VGNGITTEQQKGSRFTWDLERRKKLKLGIIKSR-----------------------
Os05g32610 AP--VGSEAFTEQQKRSRFTWELERRKKLKLGMMTNH-----------------------
Pt286483   ----------CVAKRTRSHYNLESAKKRMKLETVSRPLCVDEEKLDDNGDNEDDTEAYE
Vv15867    ---------------------SKLGKKKVELGTSSHPFCVDVDEGEGDGDGEGE------
Cp76.2     -------------DVNGRDFSSLEGNKQSPATTFDHHDCDDND-----------------
ZM178435   ----------GRTRSQRKCK----DKKLLKRGTFSKPYNIDIP--DSTSDSEEEIEPPAP
Sb04g33300 ----------ARTRSQRKCK----DKKLLRRGTFSKPYNIDIP--DSTSDSEEDIEPPAP
Os02g43460 ----------ARTRSNFKRKKLL-DKKLLKRGTFAKPYCIDV----SSSGSEEDVPQPEQ
Bd2g43500  ----------GRTRSRRRCL----NTKLLRQGTYNKPYCLDTPSESGSSEAEEGVNKTPP
Bd3g50300  ----------QRTRSNFKDRACL-DKKLLGQGTCSKPYCIDTE-------SEEDVPPPPQ
At3g24340  ----------SDEVVSLSSSSDDEEDPLEELGTDSREEVSGEDRDSGESDMDEDANDSDS
ZM000342   ----------ENPRSMAAEHKYPVKRNQCSLPVKEKQISMEI-KKNTTDQGCSDSYIPHT
ZM108166   ----------ENPRSMAAEHKYPVKRNQCSLPVKEKQISMEI-KKNTTDQGCSDSYIPHT
Sb02g43870 ----------EDPRSMKGQHKYPVKRNQCSLPIKENQTSMET-KKNATDQGCSDSHIPHT
Os07g49210 ----------EKASSPEGQHKNTIKRTTCSLPVKEEPSSVEIEEKSSKEQSAPEFHIPRT
```

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Bd1g16720  ----------ENPSTTKGQHKNTRRRTPCSLPMKEKPSSV--KEESKTEERASDSHIPQT
At5g20420  ----------KSRKGEIVVIDK------RRVHGFGRKERKSELSVIPFTP----VFEPIP
AtCLSY1    ----------KDKQREIVLVDKTERKKRKKTEGFSR---SCELSVIPFTP----VFEPIP
Pt567214   ----------EAKSGMANRKKHGTQIREVKLGVANRIEHQDQLAIVPVPT----EDDLVT
Pt832603   ----------DAESGMANRKKHGTQIREVKSGVANRREHQDQLAIVPVHT----EDVLAT
Cp19.123   ----------KNETRDLVVYKSNKYSKDVKSGLADQVEHQNKLAIIPVPNVPELEPEPLA
Vv29366    ----------IDSYEDFLVCKSKDRSREVKPILAAQNEDQHQFAIVPVPL----IIEPIA
Sm441121   ------------------------------------------------------------
At1g05490  ----------PEEPSRPEIYSSEKAKEVQAPEMPSRPEVFSSEKAKEIQVPEMPSIPEIQ
Sm84719    ----------SHSSALRQSKVSPLTTELTKLSLSSSFEAIHRERASDPSESSKPDLALLD
ZM064574   -----------DLVAASIAEKRAETQVFLSLPTE--------------------------
ZM093940   -----------DLVAATIAEKRAETQMFLSLPTE--------------------------
Sb07g02945 -----------DLVAASIAEKRAETQMFLSLPTE--------------------------
Os07g25390 -----------DLVAASHAEKIAETQVFLTLPTLPNE-----------------------
Os06g14440 -----------DLVAASHAEKIAETQVLLTLPTLPNE-----------------------
Bd3g19890  -----------YLAAASHAEKMAETQVFPDLPRE--------------------------
Bd2g21450  --------------------------EMLKLPQ---------------------------
Bd2g21430  --------------IWSDVEKIAETQTSPALPG---------------------------
Os08g14610 ----------LGRICNSSVEKAEERETVIPAISN--------------------------
Bd3g18910  ----------LAIASKNDSKKVANDEVAHDEPQKESECLVHDTWNHFDHAIASKNLKESE
At2g21450  ----------LPQESVTQINPLEKRLKKLK------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ----------TDVMVSDNVGRRIQGE-VASLTGEPDS-----------------------
Vv23895    --------------VRDYVESIAPKKEERSLTASSEI-----------------------
Vv35918    ----------NNPVVRDYVGSIAPKVEEGSLMGATEI-----------------------
Sb01g46180 ------------ITRPDNCNSSTEPQALVKQVKDAMD-----------------------
Os03g06920 ------------ISMLDNENISSEAQAV-KKGKDSMD-----------------------
Bd1g74070  ------------IIMLGNENINSEDQAVAKQGNDIMD-----------------------

                           1220                1240                1260
RMR1       ---------------------------------LHERDLDSDPNSSGS-------DQIRK
Sb09g19410 ---------------------------------LYERDLNSDSNSSGS-------DQIRK
Bd2g26500  --------------------------------HSYERGLDLDSDSSGS-------GENER
Os05g32610 --------------------------------RLYERDLESDSNSSDS-------SQNRK
Pt286483   AVDVA-----------------------QKVRSKKGKTKPTGGNGGDVDDGDETCDHKSQ
Vv15867    --------------------------------EEWEEEEEEEEEEEGR-------DSSSG
Cp76.2     --------------------------------RIWEHDLNDLVTSSKE-------ENGVS
ZM178435   QQGLLSSSEE----------DNMTFGKRKRRRAAINKRWDKRLSASSD-------EEDYG
Sb04g33300 QQGLLSSSEE----------GNITFGKRKHRRAIKNRR-RKRPSTSSD--------EEYR
Os02g43460 SAYGGDCADD----------DGGSDGNEEHRAVKRRKLNRRQSAHSDS-------EEDTT
Bd2g43500  APALSSSDEEIE--------ADAGGHGRTAARKGRRRGKNPTPSDDDS-------EEHRV
Bd3g50300  PQPSSAECEDDGSGG-----DDRMPAKRRRGKEQITDSDDTQNDSEDS-------DENRT
At3g24340  SDYVGESSDS--------------------------------SDVESSDSDFVCSEDEEG
ZM000342   P-----------------------------------------------------------
ZM108166   P-----------------------------------------------------------
Sb02g43870 P-----------------------------------------------------------
Os07g49210 P-----------------------------------------------------------
Bd1g16720  P-----------------------------------------------------------
At5g20420  LEQFGLNANSFGGGGSFSRSQYFDETE-KYRSKGMKYGKKMTEMEEM--MEADLCWKGP-
AtCLSY1    LEQFGLNANSLCGGVS---GNLMDEID-KYRSKAAKYGKKKKKKIEMEEMESDLGWNGPI
Pt567214   FEQYDSPLKT-----PDNFPQECIEFPIRSYSKKGY-SVQRKNDFDED-MMFGSGWGGK-
Pt832603   FEQFDSPVKT-----PEPYSQAFIEFPISYYRKKSSPAAHRKNDRDED-LMFGNGWGGK-
Cp19.123   SEHHDYHANL-----SANNSKRVEELSFRYNSLKCSRTSSRKKFSQIDDMDLVPRWEGIQ
Vv29366    HGEDHLHDET-----PWNESGEIGEISPKYYCTNGVPKLQRKNMSDLY-MEVESRWEGK-
```

```
Sm441121   ------------------------------------------------------------
At1g05490  NSEKAKEVQA---------NNRMGLTTPAVAEGLNKSVVTNEHIEDDSDSSISSGDGYES
Sm84719    FHGFHLHPQHHLAGLDPGYVLELAAGSHGRDLRPKRDFAPRQLEVVFHLLLEDDPDEARR
ZM064574   ---------------------------------KKRR------RSDPS---------LHA
ZM093940   ---------------------------------RKRR------RTDHS---------LLM
Sb07g02945 ---------------------------------KKRK------RSDLS---------LLM
Os07g25390 ---------------------------------RKRR------KSEPT---------TLV
Os06g14440 ---------------------------------RKRR------KTEPT---------TLV
Bd3g19890  ---------------------------------RKQR------KLDPN---------SQV
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ---------------------------------------------------------SHV
Os08g14610 -------------------------------------------------------TEKMG
Bd3g18910  VVANDEVANDEPQKESEYLVDDMWNHFELAIASENLE------ESEEV-------THDEQ
At2g21450  --------------------------------------EVIVVKNGDS-------SGSDS
AtDRD1     ------------------------------------------------PLIPQCSFEEVD
Pt195587   ---------------------------------KKDKGVYVGVEDDEV--------DTEI
Vv23895    ---------------------------------RKDKGGLYIAVGERS------------
Vv35918    ---------------------------------RKDK-DVYIGVGEKS------------
Sb01g46180 --------------------------------------NDNVSAEAKKIVLFDCHSTSEQ
Os03g06920 ----------------------------------INDVIYNKSGHEEI-------GEEEA
Bd1g74070  --------------------------------------IDNENHDEQK-------GKREG

                           1280                1300                1320
RMR1       YGFKSDGSHKVDRKKKHTSPKSGKK-----------------------------------
Sb09g19410 YGFKRDGSHKVDMKKKHTSSKSGKK-----------------------------------
Bd2g26500  HGYQEGGDNKVGRKKKHLSSKSGKSGKK--------------------------------
Os05g32610 NGCQGSGDHRTGRKRKNPLSKSG-------------------------------------
Pt286483   RRTIESREGSRDEHGHGVCRR---------------------------------------
Vv15867    HAEFPKTIGRKDKGELGKHTK---------------------------------------
Cp76.2     HNNFSSVRKTVS------------------------------------------------
ZM178435   ASAMDAKERPFRRLKKGLSNLQAAKEGCRNYEGSNP----GHARYSGPNGGNLENMSSAQ
Sb04g33300 VYARDGKDRPFRRLKKGLSKLQAGKEGCGRYVGSNP----GHAKYNGPNG---ENQSNEQ
Os02g43460 FVCDVKEGSGSRRVQEGAPRRQVKKEGSNKKKDGSTP---QCVRNNGPKVGRQTNGLNGQ
Bd2g43500  GGRQGTAVRRRRWPKDNTAQCDHEEEED---DEAFVPFRRPKRSGAVPNPRDGYYDQQQQ
Bd3g50300  LARNARKGSSSRRPKNGASYQQNVKEGSRNYDSPSNP---RHVKNYAANAGNPTDRFNMQ
At3g24340  GTRDDATCEKNPSEKVYHHKK---------------------------------------
ZM000342   ----AKNTE---RP--RFRLKPFASSRSLDGNSEPAFCQKR-------------------
ZM108166   ----AKNTE---RP--RFRLKPFASSRSLDGNSEPAFCQKR-------------------
Sb02g43870 ----AKNIEKCNRP--TFRLKSFASSRSLDGNSEPAFCQKR-------------------
Os07g49210 ----AQNKEKHNRPPFSCKPKLFTSSGTLGVNCEPAFCQKV-------------------
Bd1g16720  ----AQNKEKNHRTPSSFHRKSGTSPCSLGGNYEPAFCQKR-------------------
At5g20420  -NQVKSFQKRTSRSSRSVAPKTEDSDEP--------------------------------
AtCLSY1    GNVVHKRNGPHSR-IRSVSRETGVSEEP--------------------------------
Pt567214   ----SSRKKVQRARYQSTHLKRDDSCKP--------------------------------
Pt832603   ----FSTKKVQRARYRSTHLKQDGSCAP--------------------------------
Cp19.123   GK--GSNRKAQIRKHRGISSK-EDFDEP--------------------------------
Vv29366    ----GPIRKLRRKRGFTIRTKTESYGEV--------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  DPTLKDKEVKINNHSDW-------------------------------------------
Sm84719    SHDPAFFHACERQQSGWKSKLVHELHGLLGEDGLASVNFGGFSLILGNTHGDRAKVDGGG
ZM064574   SDDTATVPKQRKSKGATVVAAANLSLVSQQ------------------------------
ZM093940   LD--SFVPKQRRRKGDTGLAPADLSLDLHQ------------------------------
Sb07g02945 LD--SFVPKQ-RRKSDTGLAAADLSLDLQQ------------------------------
Os07g25390 DGDGGTNLGKGKRKNHQNQAAVDSILDLQQ------------------------------
```

```
Os06g14440 DVDGGTNLGKRKRKNHQNQAAVDSNLD---------------------------------
Bd3g19890  DGDAGTAPRKRKRKTGPDPAAVDLPSETYN------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  DGDAETAPRKRKRENERDSAAVDLPSNTYN------------------------------
Os08g14610 EKQQKSIPRDRKRKGELDPA----------------------------------------
Bd3g18910  KKENEYLVRDRWNHFELAIASKNLYFICFLRPRNIWHYPKLS------------------
At2g21450  SPQGYDEEDSSRNSTDI-------------------------------------------
AtDRD1     LGRGKEMPSAIKAIVEGQTSRGKV------------------------------------
Pt195587   KDDGLQVSDNVGRRIQGEAAS---------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 QPLMKQARGNIKTNTENGLKEKGKIGGT--------------------------------
Os03g06920 QAENVQIKGNLKKEI---------------------------------------------
Bd1g74070  EGEDVQSAGSIENNS---------------------------------------------

                           1340                1360                1380
RMR1       ---------------PSSAIILKRQSLLKLLVD--------KMSGDKSLASFP-------
Sb09g19410 ---------------SSSAIMLKRQSLLKLLVD--------KMSGDKSLESFS-------
Bd2g26500  ---------------SSRSTMLKRQSLLKLLMD--------KMTGDKDGECSP-------
Os05g32610 ---------------KKSSRMLKRQSLMKLLMD--------KMCSNDDGKSTP-------
Pt286483   ---------------KPSKRRRKEYEVVKILAN--------SLFLDLEDVPFK-------
Vv15867    ---------------RKRIRALKHCDALKILVD--------SIWAKNSGLLEELVSPRG-
Cp76.2     ---------------KKRKHMHKSHDIVKVVVN--------SMLEEEEMLFEETVASGDV
ZM178435   DDISFKRNVHMI---RIKKRGRAAKAVYDELLD--------SLFSGWENHI---------
Sb04g33300 DGIFFKRTAHKI---RMKKHGPVAKAAYDELLN--------SLFSGWEDHI---------
Os02g43460 GG-VSFKRNVKIAQRRKRRQATADQEKYGHLLD--------PMFNEIESNQ---------
Bd2g43500  AGDAPFKKSSLILP-KKRCGAGQERETYDDLLQ--------SIFDEITNQQNGSAPLD--
Bd3g50300  SGDICFNTNTLLPQ-RMKHGRVWTKQDTDNLLN--------SLLDEIE------------
At3g24340  ---------------SRTFRRKHNFDVINLLAK--------SMLESKDVFKEDIFSWDKI
ZM000342   ---------------GRKRKKHMCQIEYKRMID--------QCIGNIQCEVERDSDFKFG
ZM108166   ---------------GRKRKKHMCQIEYKRMID--------QCIGNIQCEVERDSDFKFG
Sb02g43870 ---------------GRKRKKGMCQREYKRMIE--------QCIGNIQCEVERDSDFKID
Os07g49210 ---------------GGKRKRHMCEREYKQMID--------QCIGNIESEMERDSMFNFD
Bd1g16720  ---------------GRKRKERMCDEEYEKIIN--------QCIGNIQSEMERDYEFNLD
At5g20420  ---------------RVYKKVTLSAGAYNKLID--------TYMNNIESTIAAKDEPTSV
AtCLSY1    ---------------QIYKKRTLSAGAYNKLID--------SYMSRIDSTIAAKDKATNV
Pt567214   ---------------KTYKQTALSAGAYDKLIS--------FYMKNFDSTIKSKEVT-RI
Pt832603   ---------------MTYKRTALSAGAYNKLIS--------SYMKNIDATIKSKEVP-RI
Cp19.123   ---------------ITYKKKSLSAGAYDKLIH--------SYMKNIDSTM-IKEEP-HI
Vv29366    ---------------RPHKKRPFSEPGYKEVIE--------AYMKNIESTI-NKEQP-LV
Sm441121   ------------------------------------------------------------
At1g05490  ---------------RILNGNNKEVDLFRLLVN--------SVWEKGQLGEEDEADELVS
Sm84719    GGGDDLREKPASVGFCLRRATMLVEEGDERAIDWDRLIAKEKRWQRKESTRKNPAPN---
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
```

```
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------

                           1400                1420                1440
RMR1       ---------------------------------------------------FDQNPQLQF
Sb09g19410 ---------------------------------------------------FDQNPQLQF
Bd2g26500  ---------------------------------------------------FDLHSQFEY
Os05g32610 ---------------------------------------------------FDQKPQIEY
Pt286483   ---------------------------------------------------EEREPLEEP
Vv15867    ---------------------------------------------------SDSIEETAP
Cp76.2     LKE------------------------------------------------QGNHPETEP
ZM178435   -----------------------------------------------------GNPVHAE
Sb04g33300 -----------------------------------------------------NDPDHAA
Os02g43460 -----------------------------------------------------YEPVPEE
Bd2g43500  ---------------------------------------------------DGSAPAQEQ
Bd3g50300  ---------------------------------------------------NGSAPAQAQ
At3g24340  AEVDSREDPVVRESSSEKVNEHGKPRERRSFHRVREKNHLNGESFYGGEKLCDGEETINY
ZM000342   DQI---------------------------------------------------------
ZM108166   DQI---------------------------------------------------------
Sb02g43870 AQI---------------------------------------------------------
Os07g49210 ANM---------------------------------------------------------
Bd1g16720  VPM---------------------------------------------------------
At5g20420  VDQWEE------------------------------------------------------
AtCLSY1    VEQWQG------------------------------------------------------
Pt567214   IDQWEE------------------------------------------------------
Pt832603   IDQWEE------------------------------------------------------
Cp19.123   IDQWQE------------------------------------------------------
Vv29366    IDQWKE------------------------------------------------------
Sm441121   ------------------------------------------------------------
At1g05490  ---------------------------------------------------SAEDQSQEQ
Sm84719    ---------------------------------------------------AGKRRAVEE
ZM064574   ------------------------------------------------------------
ZM093940   ------------------------------------------------------------
Sb07g02945 ------------------------------------------------------------
Os07g25390 ------------------------------------------------------------
Os06g14440 ------------------------------------------------------------
Bd3g19890  ------------------------------------------------------------
Bd2g21450  ------------------------------------------------------------
Bd2g21430  ------------------------------------------------------------
Os08g14610 ------------------------------------------------------------
Bd3g18910  ------------------------------------------------------------
At2g21450  ------------------------------------------------------------
AtDRD1     ------------------------------------------------------------
Pt195587   ------------------------------------------------------------
Vv23895    ------------------------------------------------------------
Vv35918    ------------------------------------------------------------
Sb01g46180 ------------------------------------------------------------
Os03g06920 ------------------------------------------------------------
Bd1g74070  ------------------------------------------------------------
```

```
                           1460                1480                1500
RMR1       IFKE-------------MHPLVF-SFGDED---LVAADR--------------PE-QDVG
Sb09g19410 IFKE-------------MHPLVF-SFGDED---LEAADR--------------PE-QDVG
Bd2g26500  NSND-------------SHPLVF-SFGDED---HIPANK--------------AE-QNAE
Os05g32610 SFKD-------------LHPLVF-SFGDDD---PSPTDR--------------SE-QDAA
Pt286483   -----------------VLPLKF-TFGIEE---SSPPVK--------------SE-EEKQ
Vv15867    AFTE--------------LPLKF-KFGVDE---SIPLGK--------------SQ-PEIG
Cp76.2     -----------------TLPLTF-TFQIDE---SSMSKN--------------SD-SDNE
ZM178435   AGNS--------------LPLVF-SFGDED-----AEEN--------------TE-NDKY
Sb04g33300 AGNS--------------LPLVF-SFGDED-----AEEN--------------IE-NDKY
Os02g43460 QIDR-------------RLPLVF-AFGDDD----KLEEK--------------SK-HDKL
Bd2g43500  SVPD-------------TLPLIF-SFGDED---QVVKEK--------------TE-QGKF
Bd3g50300  NEDR--------------LPLVF-SFGDED----QVEEQ--------------SD-HNKL
At3g24340  STED-------------SPPLNL-RFGCEE---PVLIEK--------------TE-EEKE
ZM000342   -----------------LDGCVR-AYQEVDFTWPSSADS--------------QE-EKDE
ZM108166   -----------------LDGCVR-AYQEVDFTWPSSADS--------------QE-EKDE
Sb02g43870 -----------------LNGCGH-AYQEEDFMWPSSADS--------------QE-EKDE
Os07g49210 -----------------MNYVQH-SYREEDFTWPPSADN--------------QEVEEDE
Bd1g16720  -----------------MHCCQG-AYPEEDFTWPSLADS--------------QEEKKDE
At5g20420  ------------------LKKTNFAFKLHGDMEKNLSED--------------GEGETSE
AtCLSY1    ------------------LKNPA-SFSIEAEERLSEEEE--------------DDGETSE
Pt567214   ------------------FKAKH-S-SDQKETMEPSLVE--------------DDGESSE
Pt832603   ------------------FKAKH-S-SDQKEKMEPSSVK--------------DDGESSE
Cp19.123   ------------------FKKA--SFPEQRMEIEQSSSE--------------DEGESSE
Vv29366    ------------------LQVRN-DLNQRRDCNSPSSVG--------------DQEESSE
Sm441121   ------------------------------------------------------------
At1g05490  AREDHRKYDDAGLLIIRPPPLIE-KFGVEEPQSPPVVSE-----------------IDSE
Sm84719    EEEEDDDGDEIYPCLEDSRSWDF-DFDHEK-----------------------LENEDKL
ZM064574   -------------------TATS-----PEPDMVIEEEE--------KHK---NE-SDGL
ZM093940   -------------------TATS-----QEPDIAIEEEE--------KRK---ND-GDGL
Sb07g02945 -------------------PAKS-PEPEPEPDMAIEEEE--------KCK---NE-SDGL
Os07g25390 ----------------TVVPLQQ-NDVPSQSYRTMIEEE--------KPV---KE-SDGL
Os06g14440 --------------------LQQ-NDVPSQSYRTMIEEE--------KPV---KE-SDGL
Bd3g19890  -------------------PVEE---------EEPAEED--------KPE---NK-SDGL
Bd2g21450  ----------------------------EKEREKTICPQ--------------KP-----
Bd2g21430  -------------------PVEE---------EEPMEDG--------KPK---KE-SNGH
Os08g14610 --------------------------------------------------------ADYV
Bd3g18910  ------------------KNATF-VIGKLDKFEEVASDE------------PKKE-SDCL
At2g21450  ---------------------------DNQSLYVDAEEE---------------------
AtDRD1     ------------------LPIEN-GVVNEKGVYVGVEED--------DSDNESEAADEDL
Pt195587   ------------------LAGEP-DSKKDNGVYVGVEDD----------EVDTEIKYDGL
Vv23895    ------------------LAANH-EMKNVKGEYVGVEDD----MEASEGNLQAKTKDDDL
Vv35918    ------------------LVANL-EMKKVQGEYVGVEDD----METNEGNLRAKTEDDGL
Sb01g46180 --------------------IAK-HVGSYEVSCEILQNE--PHSNEGNHHDNGSP-VGEL
Os03g06920 ----------------------I-SVASDELACEVMRSQSPTNGNFDQYDNS-SP-VDEL
Bd1g74070  ---------------------VP-VVDSYDISCEVIQSESTENGNYDRYDNNDSP-VDEL

                           1520                1540                1560
RMR1       L--DMLWADFDFALESEN-------------IGTYY------------------------
Sb09g19410 L--DMLWADFDFALESEN-------------IGTYY------------------------
Bd2g26500  H--DMLWADYDFALELEN-------------IGTYY------------------------
Os05g32610 L--DMLWADLDFTLESEN-------------IGTYY------------------------
Pt286483   L--EELWADMALALCLKD-------------TTDDA------------------------
```

```
Vv15867    M--NQLWAEFDFDGEEDF------------------------------------------
Cp76.2     L--HNLWVEMNFAQRSFE-------------IDSHA------------------------
ZM178435   QEQEDLWMECGIAFQSMN-------------IGSNG------------------------
Sb04g33300 Q--EDLWRECDIAFESMD-------------IGNGS------------------------
Os02g43460 QDEDELWKEFDFALESIN-------------VCSHN------------------------
Bd2g43500  E--DLLWAEFDFALESTN-------------ACSHA------------------------
Bd3g50300  Q--DELWAEMDFCMESTN-------------VCPQS------------------------
At3g24340  L--DSLWEDMNVALTLEG-------------MHSST------------------------
ZM000342   L--DELWKEMDYALATVA-------------ILEQKQM----------------------
ZM108166   L--DELWKEMDYALATVA-------------ILEQKQM----------------------
Sb02g43870 L--QELWKEMDYALATVA-------------IDEQKQLI-KC------------------
Os07g49210 L--EELWKEMDYSLTTLA-------------LLEQKQVMAQSRINMLVDNFDGLRLDCLT
Bd1g16720  L--DELWKEMDFSLTTLE-------------L----------------------------
At5g20420  N--EMLWREMELCLASSY-------------ILDDN------------------------
AtCLSY1    N--EILWREMELCLASSY-------------ILDDH------------------------
Pt567214   T--EMLWREMELCLTSAY-------------IFEDN------------------------
Pt832603   T--EMLWREMELCLASAY-------------ILEDN--------------EVELCVVFIY
Cp19.123   N--EMLWREMELSMASAY-------------FLEDN------------------------
Vv29366    T--EMLWREMEFSIASSY-------------LLEEN------------------------
Sm441121   ------------------------------------------------------------
At1g05490  E--DRLWEELAFFTKSND-------------IGGNE------------------------
Sm84719    ---AAIWHDWDAEIEAER------------------------------------------
ZM064574   ---DDYWKDFALAVESTK------LDEVDE-AAIEK------------------------
ZM093940   ---EDYWKDFALAVESTK------LDDVDEAAANEK------------------------
Sb07g02945 ---EDYWKDFALAVESTK------LDEVDE-AANEK------------------------
Os07g25390 ---EDLWKDFSLAAECTK------LDTNED-MSNEK------------------------
Os06g14440 ---EDLWKDFSLAAECTK------LDTNED-MSNEK------------------------
Bd3g19890  ---EDLWKDFSVAMESSK------LNTFEE-LPDEK------------------------
Bd2g21450  ---TNPWRKRSLQK---KFYFNAQLDTLED-VPNAK------------------------
Bd2g21430  ---QDIWNAFDMALENSKLYFNAQLDTPED-VPNIK------------------------
Os08g14610 ---KDLWDAFYVTAESTH------------------------------------------
Bd3g18910  V--DDLWNHFDLAMASKK----------YEEVANDK------------------------
At2g21450  ---EELWRKMAFAQESIK-------------VTVED------------------------
AtDRD1     ---GNIWNEMALSIECSK------------DVARET------------------------
Pt195587   ---GDIWKEMSFALECSK------------DVVENS------------------------
Vv23895    ---ADMWQEFDLALQSSK------------DVAVDP------------------------
Vv35918    ---ADMWQEFDLALQSSK------------DVAVDP------------------------
Sb01g46180 ---DDLWIGMSVALACSE-----------KNNQVNLSIV---------------------
Os03g06920 ---EGLWMDMYLAMACSK------------TVGSDHNIV---------------------
Bd1g74070  ---EYLWRDMSLALACSK------------TIGSDHSIV---------------------

                           1580                1600                1620
RMR1       ---------------DDECQ-EGNQLDFSLAPVTPCSRGKHEFVIDDQIGIRCKYCSLVN
Sb09g19410 ---------------DDEGQEEGNQLDFSLAPVTPCSRGKHEFIIDDRIGIRCKYCSLVN
Bd2g26500  ---------------DDEHQEESNMLNLGLACTTPCSRGKHEFIIDDQIGIRCKYCSLVN
Os05g32610 ---------------DDEGQEDS-LLDHALAPITPCSRGKHEFIIDEQIGIRCKYCSLVN
Pt286483   --------------ALDENEDDAHEVEPDTV--TLCHQGNHELYLDEEIGLLCKYCSFVD
Vv15867    ---------------------GSAEVEIDQA--VLCHQGNHQLVLDEQIGMTCCFCSFVQ
Cp76.2     ------------CNMVENEYAVCSEVDLDIA--TLCSKGSHHLILDEEIGVKCKYCCFIQ
ZM178435   ------------------CEEDGKEIPPVKV--TSCNIGQHEFIIDEQIGVRCKHCHVVD
Sb04g33300 -------------------EEDGLEIPPVEV--TSCNNGQHEFIIDEQIGVRCKHCNVVD
Os02g43460 --------------CEEGEKEDEQEIPADKA--ASCIQGKHELIIDEQIGLRCKHCNFVD
Bd2g43500  -------------CQEEGEKSNGDEIHADRA--TSCKRGKHDLIMDEQIGIRCKHCDFID
Bd3g50300  -------------CEEGEKSNNGQEKPGDKA--TLCSQGKHDLVTDEQIGVWCRRCNFIQ
```

```
At3g24340  ---------------------------PDKNGDMLCSKGTHDFVLDDEIGLKCVHCAYVA
ZM000342   ---------------TDSEVVHESNTDLGKGGE-HC---HHDCMLDEQLGLTCRLCNVVC
ZM108166   ---------------TDSEVVHESNTDLGKGGE-HC---HHDCMLDEQLGLTCRLCNVVC
Sb02g43870 ----------LDFQTTDSEADHESNTDLGKRGE-HC---HHDCMLDEQLGLTCRLCNVVC
Os07g49210 LTDDYRCYYQKKEKFAESGSVNESTDYFGKVGGIPC---HHECILDEELGLACRLCNVVC
Bd1g16720  ----------DRMQVPDSEDVHESTARLGKNGEIPC---YHDCILDEELGLMCRLCNVVC
At5g20420  --------------------EVRVDNEAFEKARSGC---EHDYRLEEEIGMCCRLCGHVG
AtCLSY1    --------------------EVRVDNEAFHKATCDC---EHDYELNEEIGMCCRLCGHVG
Pt567214   --------------------ESRVSTQTTQNSSECC---QHEFKLDEEIGILCHKCSFVK
Pt832603   SYHLYRIFFFITVSDWLKDLQALLSTRTTQK---NC---QHEFKLDEEIGILCQICGFVK
Cp19.123   --------------------EVRVSYENIQKTTEVC---QHSYRLNEEIGMCCFLCGFIS
Vv29366    -------------EGSNVEVLKEVVQESSNISEQVC---QHEYILDEEIGVLCQLCGFVS
Sm441121   ------------------------------SFDDICE--VHDYVLNELVGLICSVCGYVG
At1g05490  -----------------LFSNVEKNISANETPAAQCKKGKHDLCIDLEVGLKCMHCGFVE
Sm84719    -----------------RRVPDLIKFKDIDVLIDSC---DHEFVFREDCGKVCEICGRVV
ZM064574   ------------------------EDNGK-MEDIDC---NHDIRIHEDLGHVCRVCGMIV
ZM093940   ------------------------EDNGK-MEDIDC---NHDIRIHEDLGHVCRVCGMIV
Sb07g02945 ------------------------EDNGN-MEDIDC---NHDIRIHEDLGHVCRVCGMIV
Os07g25390 ------------------------DVDDENEMDDDC---NHDIRIHEDLGHVCRICGMIV
Os06g14440 ------------------------DVDDENEMDDDC---NHDIRIHEDLGHVCRICGMIV
Bd3g19890  ------------------------ELGEK-DVDNDC---NHDIRIHEDLGHVCRVCGLIV
Bd2g21450  ------------------------EVGRK-EVKIEC---NHQIVIREDLGHVCRVCGMIV
Bd2g21430  ------------------------EVSEK-EVKIDC---NHQIEIHEDLGHVCRICSMIV
Os08g14610 --------------------LDTSEVNNK-KQLDNC---NHDIHVYEDLGHVCHECGLVV
Bd3g18910  ------------------------HVKRKINVDIGC---NHDICLHEDLGEVCRVCGMIV
At2g21450  ------------------------SQSNDHKQIEDC---DHSFICKDDIGEVCRVCGLIK
AtDRD1     ------------------------SHKEKADVVEDC---EHSFILKDDMGYVCRVCGVIE
Pt195587   ----------------------PSDENME-EDEDYC---DHSFVLKDDIGYVCRICGVIE
Vv23895    ------------------------EEDGK-EGEEEC---EHSFVLKDDIGSVCRICGVVN
Vv35918    ------------------------GEDEK-ESKEEC---EHSFVLKDDIGSVCRICGVVN
Sb01g46180 ----------------------PFVSNSE-ETEDAC---NHDFLLKDDLGMVCRICGLIQ
Os03g06920 ----------------------PSENSCE-QAEDEC---QHDFLMKDDLGIVCRVCGLIQ
Bd1g74070  ----------------------PSENTCG-EVVDDC---HHDFLMRDDLGLVCRVCGLIK

                           1640                1660                1680
RMR1       LEIKFMFPSL-------VSVFAEKSAWPNDKGV----------KNTLMF-----------
Sb09g19410 LEIKFMFPSL-------ISGFAEKSAWPNAKGV----------KDTLMF-----------
Bd2g26500  LEIRFVLPSM-------VSNYAEKSAWRNSSCL----------KDALMY-----------
Os05g32610 LEIRFILPLL-------ASNFAEKPAWRNSSCL----------KTALMC-----------
Pt286483   LEIKYYVPPF-------DRYPRGKSARRDFVTM----------QHNIF------------
Vv15867    LEIKYILPSF-------SRNPWGGSEKGNAGKE----------DCNSIF-----------
Cp76.2     QEIKYIVPPF--------------------------------------------------
ZM178435   LEIRDVLPTL----------GKCSAERGSAINP----------EFDRML------KEMLN
Sb04g33300 IEIRHVLPTL----------GKFSAERESAIDP----------ELDKML------KEMLS
Os02g43460 LEIRFVLPSM-------VKSCTERDMRKDH-------------ELDLFF-----------
Bd2g43500  LEIRDVFPSM----------VKFSIEREPAMSL----------NLDLFC-----------
Bd3g50300  LEIRHVVADM-------VSHYSLQHAFTKTLS-----------ELDLSI-----------
At3g24340  VEIKDISPAM-------DKYRPSVNDNKKCSDR----------KGDPLP-----------
ZM000342   IEAKDIFPPMVASNSNQFTGKDH--ERPERNHF----------GQ---------------
ZM108166   IEAKDIFPPM-------FTGKDH--ERPERNHF----------GQ---------------
Sb02g43870 TEAKDIFPPM-------FTGKDH--KRLEQSHF----------GQ---------------
Os07g49210 TEAKDIFPEM-------FNGNDYK-DRPGCSNI----------CL---------------
Bd1g16720  IEAKDIFPQM-------FNGNGYNKDRPGCSNF----------FH---------------
At5g20420  SEIKDVSAPF-------AEHKKWTIETKHIEED----------DIKTKL-----------
```

```
AtCLSY1    TEIKHVSAPF-------ARHKKWTTETKQINED----------DINTTI-----------
Pt567214   TEKKYVSAPF-------VFSVFLLSFMSPLDRQVSMQGRHFLFVIRGYS-----------
Pt832603   TEIKYVSAPF-------MEHTGWTAESKPQNEE----------DLELKP-----------
Cp19.123   TEIKYMTAPF-------MEFRSYVAENRWENEE----------DNKNMT-----------
Vv29366    TEIKDVSPP---------------------------------------------------
Sm441121   IPIEEMAPHP------DWSFRLPQNVLENPDPF----------IRRPEL-----------
At1g05490  REIRSMDVSE-------WGEKTTR-ERRKFDRF----------EEEEGSSFI--------
Sm84719    KLVSDVFDVS-------IISFLSFPARKASSRP----------ATKKLKLHEDYAWKSTL
ZM064574   RRADSIIDYQ-------WKK-ASR-RRTNGYGG----------HSKDADEID---CGTVK
ZM093940   RRADSIIDYQ-------WKK-ASR-RRMNGYGG----------NSKDADEID---CGTVK
Sb07g02945 RRADSIIDYQ-------WKK-ASR-RKTNSYGG----------HSKDADEID---CGTVK
Os07g25390 RKAETIIDYQ-------WKK-ASR-TRTNYYES----------RSKDADDID---TGAVK
Os06g14440 RKAETIIDYQ-------WKK-ASR-TRTNYYES----------RSKDADEID---TGAVK
Bd3g19890  RRADTIIDYQ-------WKK-ASR-SRSYFCGT----------RSKDADEII---IGDIR
Bd2g21450  RKADTIFDYQ-------WEK-ESR-PRSYLYGT----------RSKDAGEIV---VGNVT
Bd2g21430  RKADMIFDFE-------WRKVSSR-SRSYFKET----------RS---SEIV---LGNVT
Os08g14610 RKADSLFHYQ-------WKK-ASR-KRTNVNEV----------CLKKVG------SDAIS
Bd3g18910  RSADKIFDYC-------WWKQLSR-KRSGTHEA----------GSKNADQIEDFGSATAS
At2g21450  KPIESMIEVV-------FNK-QKRSRRTYMREK----------ENGETS----RDFSGIQ
AtDRD1     KSILEIIDVQ-------FTK-AKRNTRTYASET----------RTKRFGESDNE----LK
Pt195587   RAIYTIIEIQ-------FNK-VKRNTRTYISES----------RNAKDRDSNG--TVGAD
Vv23895    KSIETIIEYQ-------YSK-VKR-SRTYMYEP----------RNTKDREPTDDPSDGLR
Vv35918    KSIETIIEYQ-------YTK-VKR-SRTYMYEP----------RNTKDREPTDDPSDGLG
Sb01g46180 QRIDKIFEHS-------WKK-RNQAYRSYPIKQ----------RNSGDPDATMNALGTIL
Os03g06920 QRIENIFEYQ-------WKK-RKQSYRARPSEH----------RNSSDADAIDKTSGAIL
Bd1g74070  KPIDTIIECQ-------WKK-PKQSYRTYPSGH----------RNSNDLDTPINLSRNIL

                           1700                1720
RMR1       ----HDLYEQG---VNDTEQSQDIHQYGTVWNLIPGVISTMYE
Sb09g19410 ----HDLYEQT---GSDIEQISDLHQYGTVWDLISGVISTMYE
Bd2g26500  ----HDLCEQA---GSIDGQSQGFHPYGTVWDLIPGAINTMYQ
Os05g32610 ----PDLYEQT---GTGDGQSQDFHINGTVWDLIPGVITDMYQ
Pt286483   ----NDLHHQDSGHDTHPDYDPCTLVQGTVWNLIPGIGKGMHG
Vv15867    ----DELQFQKPGCGSQSGSDHGLHPEGTVWDIIPGIRNSMYR
Cp76.2     --------------------------QGTVWDMIPGVKDSMYP
ZM178435   VFEQNDVLVSN---GHELPCNFGDHKAGSVWNLIPGVKETMFP
Sb04g33300 VFEQNDVLVSN---GHELPCNFGGHKAGSVWDLIPGVKETMFP
Os02g43460 ----DDILTSA---GYEGPRDFGGKKTGLVWDLVPGVREDMFP
Bd2g43500  ----EDIIKSM---GYEGTSHFDIHESGLVWDLIPGVREHMFP
Bd3g50300  ----NNLLTSM---GYEGTCKIVDHKAGSVWDLIPGVKEGLFT
At3g24340  ----NRLEFDA--SDPSSFVAPLDNIEGTVWQYVPGIKDTLYP
ZM000342   ----DGHVLDLSFFEICAPEFSKIKESGNVWASITDLEPKLLA
ZM108166   ----DGHVLDLSFFEICAPEFSKIKESGNVWASITDLEPKLLA
Sb02g43870 ----DDHVLDLSFFEICAPESSKSKESGNVWSSIPVLEPKLLA
Os07g49210 ----DDDILDPSLLANLAPELSELKNSGSVWSAISDLDPKLLP
Bd1g16720  ----DDHVLDPSLLATFAPEFSEPRGSGNLWSLIPDLEPKLLP
At5g20420  --SHKEAQTKDFSMISDSSEMLAAEESDNVWALIPKLKRKLHV
AtCLSY1    -VNQDGVESHTFTIPVASSDMPSAEESDNVWSLIPQLKRKLHL
Pt567214   ---ARNPIAHLFNVCKISPLVPF-EVNDNVWDLIPELRAKLHM
Pt832603   ---DEDEGSSLFGNHTSGEDVPVSEVNDNVWDLIPELRPKLHM
Cp19.123   ---YAGRELNLVGNHT-SHERLLTEENDNVWALIPELRNKLHL
Vv29366    -------------------------------------------
Sm441121   ----NDLNDDL---------------ADDPYFPSTDTRRSLHA
At1g05490  ----GKLGFDA---PNNSLNEGCVSSEGTVWDKIPGVKSQMYP
```

```
Sm84719    NF--GDVTVDL--------------------VPHPMDSARMYP
ZM064574   LSE-DFIVADI--------------------AIHPRHARIMKP
ZM093940   LSE-DFIVADI--------------------AIHPRHAQAMKP
Sb07g02945 LSE-DFIIADV--------------------AIHPRHAQTMKP
Os07g25390 VSE-DFIVSDI--------------------AIHPRHAKQMRP
Os06g14440 VSE-DFIVSDI--------------------AIHPRHAKQMRP
Bd3g19890  VSD-DLLALDI--------------------AIHPRHKKQIRS
Bd2g21450  VSE-DLIALDV--------------------AIHPRHAQHIKP
Bd2g21430  VYE-DLTALDV--------------------AIHPRHAQHIRP
Os08g14610 LSE-DFIFSDI--------------------AIHPRHAKNIRP
Bd3g18910  AYE-DFIFEDA--------------------AIHPMHAKEIRL
At2g21450  SSHTNILGEKM--------------------FIHPWHDQEMRP
AtDRD1     FSEEGLMIGGL--------------------AAHPTHAAEMKP
Pt195587   LFEEDLMVTDI--------------------PAHPRHMKQMKP
Vv23895    FSEHSLIVTEI--------------------HAHPRHSMQMKP
Vv35918    FSEHNLTVTEI--------------------HAHPRHSMQMKP
Sb01g46180 ----SVAPDTL--------------------SLHPQHSEQMKP
Os03g06920 ----EVVPDAL--------------------CLHPQHSQHMKP
Bd1g74070  ----QMLPDPL--------------------SIHPQHLQQMKP
```

(B) Satchmo

```
                              20                  40                  60
Bd2g21450   ------------------------------------------------------------
Bd2g21430   mdaaaaatkifrrnhrlppvvqqkrfppsggasflpprcealsvnfvatyflrctceskk
Sb07g02945  ------------------------------------------------------------
ZM064574    msqspggregiyysrqrkp-erngsvftpiaamyssghalpvanrshglvfgslskdwdd
ZM093940    msqspggregiyysrqrkpserngsvftpiaamypsghalpdanrnhslvfggtskdwdn
Bd3g19890   --------------------myyrrknrasdpis-------------glslpagsgvhsw
Os06g14440  ---------------mdlismyyrrqrkas---seananvfmpggpndisfpasnrdhdw
Os07g25390  maaagrdppatpssr-----myycrqrkas---sevnanvfvpggqngisfpasnrahdw
Os08g14610  msgsgnsldtvalivgggsdssgivgrkrrrcdlirerwcclcpvwckeaqevvvpgrgr
Bd3g18910   mggempnanmtncfmeqtekkkynvllildsppkeliildsddedgnsgktqvpsyptke
Vv23895     ------------------------------------------mhsepkqkrqkagsnvvd
Vv35918     meptngglssnygnpipvnfepykltefnstkhkriwtfeenmhsepkqkrqkagpnvvd
Pt195587    ------------------------------------------m--------kdtkekvtd
AtDRD1      mgfvyivmtgyyknvhkrkqnq--------------------vddgpeakrvkssakvid
Bd1g74070   ------------------------------------------------------------
Os03g06920  marypaptssraigapiqptephaplpntggegapppartmpppssqaatstppaaatpl
Sb01g46180  mnlrgdylsdkytr----------------------------------------------
At2g21450   mftawnlrsrsrsitqeelakrpdpfclpnlldgledglygrladdvkrlcklrqeylng
Sm84719     masngpcsaihscvmlqlshtplaskavrftlhlpepiqpssrppppcaaralltssssy
Vv15867     ------------------------------------------------------------
Pt286483    mskspighrkptpyqtreansnvpvtkdniysthrspspslqwtrlreaevykklhdeir
Cp76.2      megkrlkldnqpvarrtrlkeaqffkeyyerrrkedgknvarpsgqsedrgvngsklgrv
At3g24340   mdmtscvarrtrsrtesylnsilnkskgisgeeedqslgcvnsrtekrrvnmrdacspsp
ZM178435    ------------------------------------------------------------
Sb04g33300  ------------------------------------------------------------
Os02g43460  mprrkgkgkgvedevevyepasppervliildsseddldlqevrrslmitgrgraraaer
Bd3g50300   mppaadfpaskrksrieipdsdddadrrresrssvgtggqrersaeagrsgg--------
Bd2g43500   ------------------------------------------------------------
Os05g32610  mdraarlar-r--gggv-------------------------------------------
Bd2g26500   mdrsgrrgrar--grge-------------------------------------------
```

```
RMR1        mdratprvc-g--rrgv-------------------------------------------
Sb09g19410  mdraaprar-grrrrgv-------------------------------------------
At1g05490   mecigkrvksrswqrlqavnkrkkmetvapvtsppkkrrqkkpknydsdieditptcnds
AtCLSY1     ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
Pt832603    ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Bd1g16720   ------------------------------------------------------------
Os07g49210  magkkmsgevrsvpafdfaewlkrtvseqdyvvmkmdvegtefdliprlfdtgaiclide
Sb02g43870  ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
ZM000342    mmikkksgrchllaghleledltvdstplpflpqgpngqpifftvqr-------------
Sm441121    ------------------------------------------------------------

                                  80                  100                 120
Bd2g21450   ------------------------------------------------------------
Bd2g21430   lythnlffvinvidnvvnqggqqpvrfdrvilhtrteenifkiwsdvekiaetqtspalp
Sb07g02945  ------------------------------------------------------------
ZM064574    irqrkdqlvnflaslerasgdsaa-agkiedskla--spvepteqkekaaiivldsdded
ZM093940    irq-------fiaslerasenssaiasktgggkstnhs-vepaeqkgkgdiivldsdded
Bd3g19890   gcgsvtkdmediyarnvqlinflstlheptrssvpmvet----nvkycsikqetkvtdcs
Os06g14440  gyggvgkeweasyarklqlmnflsslhq--rtanplvttrmdanm---dtpleqkqkdss
Os07g25390  gyggvreeweasyarklqlinflsslhq--rtanslittrmdanm---dtpleqkqkdss
Os08g14610  ngarqrdgggcalgttevlgricnssvekaeeretvipaisntekmge------------
Bd3g18910   liildsndrktllppyptkeliildsydedrnppcqrkrkisevssqvnrdasndprqkk
Vv23895     ysdpfaipnllegldagkfgsmtkeiealcarrmqmlhpyyvmypslsymstdlgkqpsk
Vv35918     ysdpfaipnllegldagrfgsvtkeiealcarrmqmlqpyyvmypslsymctdlgkkqgk
Pt195587    yakpfairgllerldsgrygsvtddirslfyrraqlihpclamhptlsneprgrgmsfge
AtDRD1      ysnpfavsnmlealdsgkfgsvskeleeiadmrmdlvkrsiwlypslaytvfe-------
Bd1g74070   ------------------------------------------------------------
Os03g06920  qrppaqataqpstqryyvgvqrdkgtgkwaacvvdpsnptkhrlvgafpdehaaalahdr
Sb01g46180  ------------------------------------------------------------
At2g21450   sislediearqdnkraksshnliidsddelpqesvtqinplekrlkklkevivvkngdss
Sm84719     flslpldeaaslenhlsivvavdgetsrterlnlcsteytlcscpafklsssyeavceeq
Vv15867     ------------------------------------------------------------
Pt286483    kgrnqgkesnaaatgstnglngaqeesvgglsykgskspvvlddseddaflddcekggle
Cp76.2      glkgtnmetrdlg-----------------------------------------------
At3g24340   rkkkrrrrkdddddvvfvrteypegkrddenvgstsgnlqsksfdfgdrvcdfdaddrnl
ZM178435    -----------------------------------------mp----appsteagrsr--
Sb04g33300  -----------------------------------------mp----appsavpgkgr--
Os02g43460  vgeeaprgsgrraapvvasrrrrrrsrsrsrspraarpraess----rrptarrarar--
Bd3g50300   -----------------------------------------le----rrlaaaiarrr--
Bd2g43500   -----------------------------------------mp----knksplvetpr--
Os05g32610  -----------------------------------------tv----aeyrmvrgrrrgg
Bd2g26500   -----------------------------------------tl----ae-asprtrrrha
RMR1        -----------------------------------------sqaaveaapsssrarrr--
Sb09g19410  -----------------------------------------sq----aapsssrarrr--
At1g05490   vpppqvsnmysvpnnsvkesfsrimrdlnvekksgpsssrltdgseqnpclkersfrvsd
AtCLSY1     ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
```

```
Pt832603    ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Bd1g16720   ------------------------------------------------------------
Os07g49210  lflechynrwqkccpdraeafemakgvscfywsiqfpnfkdhlcfrncsnasstrhfsyr
Sb02g43870  ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
ZM000342    ------------------------------------------------------------
Sm441121    ------------------------------------------------------------

                             140                 160                 180
Bd2g21450   ------------------------------------------------------------
Bd2g21430   gshvdgdaetaprkrkrenerdsaavdlpsntynpveeeepmedgkpkkesnghqdiwna
Sb07g02945  ------------------------------------------------------------
ZM064574    gngsgns----klasetnkelgtsglinniaermtfngsqafgtvhtygd-kntqivpyg
ZM093940    gd--gnspehnklasemnkelgtsvlasniaermatngsqtfetvhayggskntqivpyg
Bd3g19890   vkqtepilipdsddedgstae----lapeknkeliplglagtltahvtskgkdqvnetrh
Os06g14440  a-----iivldsddedgy-tegceqltsennkqqapsgltspyttwivssakdqvngtlh
Os07g25390  a-----iivldsddede--aerceqlasennkqqapsgptspcttwivssakdqvngtlh
Os08g14610  ------------------------------------------------------------
Bd3g18910   lkneptyfgfdepmekkknprkesdchfnlavpskklllsnlwpseslnkliiqpkqsee
Vv23895     kasklvnrhashlghedvidleddhivydvptatavadaalpvviidsddeesgdqk---
Vv35918     kasklvnreashlahedvidleddhvvddaltatavedatlpvviidsddedcgdqkvsh
Pt195587    --------------gkcnvidldddeiegvgdsvgnavgrtpvvvidsdddesnenrmvg
AtDRD1      -aektmdnqqvvegvin-ldddddddtdvekkalcvvpssseivlldsddednerqrpmy
Bd1g74070   ------------------------------------------------------------
Os03g06920  ldlafrggghrgagdnfrpafhaveleflrlcaatsspgshcglvaggdkydekyseflr
Sb01g46180  ------------------------------------------------------------
At2g21450   gsdsspqgydee------------------------------------------------
Sm84719     dlaeddaskdteishssalrqskvspltteltklslsssfeaihrerasdpsesskpdla
Vv15867     ------------------------------------------------------------
Pt286483    egldvvslddsddddqsegvesksfdvggkksggtdvggscsgvksdgeesgrskvplpr
Cp76.2      ------------------------------------------------------------
At3g24340   gceekasnfnpidddddvvfvgtvqrendhvedddnvgsasvisprvcdfdeddakvsgk
ZM178435    tmtrviilldsdked-dgtgrqa----------grelg-gaaiasage---asklvk---
Sb04g33300  tkpreiividsdeegvggggrqa----------grdlgsgaaigaage---avklvk---
Os02g43460  arspsleiidvdsgs-drgvvrv----------keepr-sgsdsdyng---argrar---
Bd3g50300   traaa----asrpev-vnltgdd----------dddir-deeaagrre---vlgrvk---
Bd2g43500   rrirrlliddddddd-dsgdggr----------areai-spsvaa--g---gsrrvg---
Os05g32610  dagpvvvidvedd--------------------gedaa-ddsaggggg---aaaavk---
Bd2g26500   et---ividl--d--------------------sed--------ggggsstaaaaassss
RMR1        dkapavvmdlgdd-------------dc-ggggarktv-ggaagrceg---stkaplpll
Sb09g19410  dkapvvvvdlgdd----------ededcgggggarktv-ggaaggrgg---steaspppp
At1g05490   lgvekkcspeitdldvgipvprfsklkdvseqkntclmqksspeiadldlvisvpsssvl
AtCLSY1     --------------------------------------------------------m---
At5g20420   --------------------------------------------------------m---
Cp19.123    --------------------------------------------------------m---
Pt567214    --------------------------------------------------------m---
Pt832603    --------------------------------------------------------m---
Vv29366     --------------------------------------------------------m---
Bd1g16720   --------------------------------------------------------magk
Os07g49210  sllirtekpvttrnhayaevvvfvldqnpmfflflrffypaiqrgpncwssanstvm---
Sb02g43870  --------------------------------------------------------m---
ZM108166    --------------------------------------------------------m---
ZM000342    ------------------------------------------------------------
```

```
Sm441121    ------------------------------------------------------------

                             200                 220                 240
Bd2g21450   ------------------------------------------------------------
Bd2g21430   fdma--------------------------------------------------------
Sb07g02945  ------------------------------------------------mqdlvaasiaek
ZM064574    qcsalvnqfplqtswqpsiqfervvlqkrpeeqr--------------mqdlvaasiaek
ZM093940    qgsalvnqfplqtswqpsiqfervvltkrpeeqr--------------mqdlvaatiaek
Bd3g19890   y-gyqnsqivp-ygqsaalinhhslqtswqpsiqyesvilqtrteeerikylaaashaek
Os06g14440  vdgvqstqivpyygqnaplinqfplqtswqpsiqyervilqkrpeeqrvqdlvaashaek
Os07g25390  vdgvqstqivp-ygqnaplinqsplqtswqpsiqyervilqrrpeeqrvqdlvaashaek
Os08g14610  ------------------------------------------------------------
Bd3g18910   vandevfndetqnesecfmdamcdhfdlaiaskkgseevandeaqneselfvdalcnhfd
Vv23895     -------------------------------vrdyvesiapkkeersltas------sei
Vv35918     ppqetawpsfsyqevvlrkpsvgllannpv-vrdyvgsiapkveegslmga------tei
Pt195587    hfqgivlpkpegqfstdvmvsdnvgrriqgevasltgepdskkdkgvyvgveddevdtei
AtDRD1      qfqstlvqhqknqgd----------------vtpli--pqcsfeevdlgrg------kem
Bd1g74070   ------------------------------------------------------------
Os03g06920  kiyhgvmdnspsykkffdvildffiarareigrealedggdmlverfvamhknkavtprw
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     lldfhgfhlhpqhhlagldpgyvlelaagshgrdlrpkrdfaprqlevvfhllleddpde
Vv15867     ------------------------------------------------------------
Pt286483    wqrivnesyngdvfaherneggvcflssgigngsggvglkgresngvagrtelrsgfcek
Cp76.2      ------------------------------------------------------------
At3g24340   enplspdddddv------------------------------------------------
ZM178435    -pevvddvgsnpv------rpga-------------------------------------
Sb04g33300  -pepvddagfhpv------lpgaprlgavpvppraqnprapsspraqaqnprapssprtp
Os02g43460  -ara-----rapv------aata-------------------------------------
Bd3g50300   -eeplddrgldpe------asva-------------------------------------
Bd2g43500   -aeisgwlvrdpl------apss-------------------------------------
Os05g32610  -rrvv------vp------gava-------------------------------------
Bd2g26500   srrss------apltlvtsgsva-------------------------------------
RMR1        ppmmv------pa------gava-------------------------------------
Sb09g19410  ppmmv------pa------gava-------------------------------------
At1g05490   kdvseeirflkdkcspeirglvleksvpgeieilsdsesetearrrasakkklfeessri
AtCLSY1     -krkhyfefnhpfnpcpfevfcwgtwkaveylriengtmtmrllengqvlddikpfqrlr
At5g20420   -kkrgfynlkhpfdpcpfeffcsgtwkpveymriedgmmtirllengyvledirpfqrlr
Cp19.123    -rkrrlyesrhpfglhpfeafsrgswrmvdciriedgtmslrfvdgrhvikrkrpfselr
Pt567214    -krkhlhqskhpynahpfealyggswqsvelieirdgamtlhfadshhrieekgpfsnir
Pt832603    -krkrlhqskhpfnahpfealccgswqsveliqirdgamtvhfvdshhrieekgpfsnvr
Vv29366     --------------------------------riedgtvalhlaeseyvieekspipnlr
Bd1g16720   tlkgpsraaghpicatpfeafhhgswhgvncirvqnsrlfvrfvysgstvernidrdhlr
Os07g49210  ------rqa--------fevfydgswhgvncirirngnlfvkfiysgstvehnvdgdclr
Sb02g43870  -vkgstghhnnpig---------------------------------svlqhdidgsylr
ZM108166    -vkgstghhsnpia---------------------------------pvlqhdidgsylr
ZM000342    -----------pva-----------------------------------vqhdidgsylr
Sm441121    ------------------------------------------------------------

                             260                 280                 300
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  raetqmf---lslptekkrkrsd-lsllmld--sfvpkqrr-ksdtglaaadl-------
ZM064574    raetqvf---lslptekkrrrsd-pslhasddtatvpkqrkskgatvvaaanl-------
```

```
ZM093940        raetqmf---lslpterkrrrtd-hsllmld--sfvpkqrrrkgdtglapadl-------
Bd3g19890       maetqvf---pdlprerkqrkldpnsqvdgd--agtaprkr-krktgpdpaav-------
Os06g14440      iaetqvlltlptlpnerkrrkteptttlvdvd--ggtnlgkr-krknhqnqaavdsnld--
Os07g25390      iaetqvfltlptlpnerkrrksepttlvdgd--ggtnlgkg-krknhqnqaavdsildlq
Os08g14610      ------------------------------------------------------------
Bd3g18910       laiasknds kkvandevahdepqkeseclvhdtwnhfdhaiasknlkesevvandevand
Vv23895         rkdkgglyiavger------slaanhemknvkgeyvg-----------------------
Vv35918         rkdk-dvyigvgek------slvanlemkkvqgeyvg-----------------------
Pt195587        kddglqvsdnvgrriqgeaaslagepdskkdngvyvg-----------------------
AtDRD1          psaikaivegqtsrgk----vlpiengvvnekgvyvg-----------------------
Bd1g74070       ----------------------------------mdpsgckrqkheiehdsspgnqsqat
Os03g06920      rawyrsdsrkvlqiplslrggggeidhstqkearmdsdsckrrkhesghdsssrvqsqss
Sb01g46180      ----------------------------------mgsagqkrqklgsehtsspgtqsqsn
At2g21450       ------------------------------------------------------------
Sm84719         arrshdpaffhacerqqsgwksklvhelhgllgedglasvnfggfslilgnthgdrakvd
Vv15867         ------------------------------------------------------------
Pt286483        kkdgnvvvvvddddddaciilekdaeelqssssgeeetfkddsddddyrvelpesfmvee
Cp76.2          ------------------------------------------------------------
At3g24340       ------------------------------------------------------------
ZM178435        ------lptsl--------------------rvqghrapssp------spvpaavrkqpe
Sb04g33300      sprapslp-slvaahplgpgaprlgvvpvppraqnprapssp------spvapedrhqpe
Os02g43460      ------akkkk--------------------rkrgkeapsra------qesrevvrvkee
Bd3g50300       ------rrgrg--------------------rgraraaaasa-------pvasrkrrre-
Bd2g43500       ------------------------------------saqpg------tllrsreqeqpe
Os05g32610      ------trtrs--------------------rrmamaqqapvtppaaaeeapsrrrkrkg
Bd2g26500       ------trtrs--------------------rslam--kspv---aeaeaaprakrrrkg
RMR1            ------lrtrs--------------------rrramlaaavv------eeaptkkkkkeg
Sb09g19410      ------mrtrs--------------------rrramqaaavv------eetpttkrrkrg
At1g05490       vesisdgedsssetdeeeeenqdsednntkdnvtveslssedpsssssssssssssssss
AtCLSY1         irsrkatlidctsflrpgidvcv--------ly------qrdeetpepv-wvdarvlsie
At5g20420       lrsrkaalsdcicflrpdidvcv--------ly------riheddlepv-wvdarivsie
Cp19.123        vrsrqanltdctcflrpgidvcv--------lipskdlassdeanlelv-lidakirsie
Pt567214        vksrkstlsdctcflrpgidvcv--------lsfseraksseegnsepv-wvdarinsik
Pt832603        vksrkatssdctcflrpgidvcv--------lssserakntgegnsepv-wvdakissik
Vv29366         irprkatlsdctcflrpgteitv--------lwtlqqsessdeenrepv-widakissie
Bd1g16720       lrsrratcfdcshvlkpgvdvcvqsphplqacs------tgdqkssisl-chdarivtik
Os07g49210      lrsrratcsdcsnvlkpgvdvcvqsshtpeass------qggtnasvll-rhdarlitik
Sb02g43870      irsrkatcsdcshvlkpgadvcv-----wqaty------ggetkdsvpl-crdarlikik
ZM108166        vrsrkatcsdcshvlkpgadvcv-----wqavy------rgetkdsvllccrdarlikik
ZM000342        vrsrkatcsdcshvlkpgadvcv-----wqavy------rgetkdsvllccrdarlikik
Sm441121        ------------------------------------------------------------

                                 320                 340                 360
Bd2g21450       ------------------------------------------------------------
Bd2g21430       ------------------------------------------------------------
Sb07g02945      ---------sldlqqpakspep--------------------------------------
ZM064574        ---------slvsqqtats-----------------------------------------
ZM093940        ---------sldlhqtats-----------------------------------------
Bd3g19890       ---------dlpsetynpveee--------------------------------------
Os06g14440      -----lqqndvpsqsyrtmiee--------------------------------------
Os07g25390      qtvvplqqndvpsqsyrtmiee--------------------------------------
Os08g14610      ------------------------------------------------------------
Bd3g18910       epqkeseylvddmwnhfelaiasenleeseevthdeqkkeneylvrdrwnhfelaiaskn
Vv23895         ------------------------------------------------------------
```

```
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   iishnssvrlrfleqfddlkyasatkdykavnakmhellstleklkevpiklpyvspvlk
Os03g06920  ilsrnrilchqlleqcddlkygsstndykaismkrlelisilqklqevpiqlpyasp-lk
Sb01g46180  iflankrlrlqfleqvnelkawsvtkdlkaitakrrelfgiierlrqvpieqlysspfpk
At2g21450   ------------------------------------------------------------
Sm84719     ggggggddlrekpasvgfclrratmlveegderaidwdrliakekrwqrkestrknpapn
Vv15867     ------------------------------------------------------------
Pt286483    eekeedgdreqgemelkrnkvygievlcdsdigkfenndvd-------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    i---iaisdedndgsrf-------------rrvrrvkdea-----sdwv---------ls
Sb04g33300  i---iaisddd-ggsrfrgavpldmieesgrrvrpvkeealddldcdwv---------rs
Os02g43460  -----pnsdgngaggra-------------rarspvaaaa-----kqrk---------rg
Bd3g50300   ----------ddsgsrg-------------rggrratrsa-----kqct---------rg
Bd2g43500   i---ivisddd-------------------------------------------------
Os05g32610  a---asaeaggggpsk--------------rrvrssgsag-----grga---------rk
Bd2g26500   ----tsaeadggggsk-gaeasesaskgn-rrgrs-----------rtaseppdralark
RMR1        a-ipdaaeaprghgsk-aaatsmatssh--krragtsrst-----srdk---------rr
Sb09g19410  attpdaaeasrgrgsk-aaaasratsrd--krragasrst-----srdk---------rr
At1g05490   ssddesyvkevvgdnrddddlrkasspikrvslverkalvrykrsgssltkprerdnkiq
AtCLSY1     rkpheseclctfhvsvyidqgciglek--hrmnkvpvlvglneiailqkfckeqsld---
At5g20420   rkphesecsckinvriyidqgcigsek--qrinrdsvviglnqisilqkfykeqstd---
Cp19.123    rkphesqcscqfyvnlyvnqgplgsek--leldkdtkvlgidqililqrlekhpceg---
Pt567214    rkphesqcscqffvnlyvnqgplgser--atlsketeavgidqisilqkldndpceadnn
Pt832603    rkphvshcscqffvnlyvnqgplgser--arlsketeavgineisvlqkldndpceadnn
Vv29366     rrphepecscqffvnfyitqdplgtek--gtlskdisvveldqisilqklgkypced---
Bd1g16720   rnhnadqclclflvilddsqcpgntekggkatdrrqevvtlnnifllqklqpkelqe---
Os07g49210  knhqedkclclfvvilyknqcpgnaek--vitdrraevvtindifllqklqp-evhe---
Sb02g43870  rnhqldrclclfavifykdqcpgskek--visgtiadvvtiddvcilqnlqseelqd---
ZM108166    rnhqsdrclclfavifykdqcpgskek--visgtiadvvtiddicilqnlqpeelqd---
ZM000342    rnhqsdrclclfavifykdqcpgskek--visgtiadvvtiddicilqnlqpeelqd---
Sm441121    ------------------------------------------------------------

                             380                 400                 420
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   lyficflrprniwhypklsknatfvi----------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   tsda-rlhsatqsgsnfssdniidldpd--nvgdhthpnmentgahntt-ylvdsgdgdm
Os03g06920  ssetnrl---vqdgrnsscrniidldsd--ndedytfanvdniga-nttvvlvdsddgds
Sb01g46180  psda-rldnfgkmessynpdnvinldadeenveyhtqvnagnteadsta-saddsgdkdr
At2g21450   ------------------------------------------------------------
```

```
Sm84719     agkrraveeeeeedddgdeiypcl------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    akak------ramvsgvppgssdvkrkrkrg------ssg-------a-gdfhaldrnl-
Sb04g33300  aeak------ralvavlppgsshakrkrkra------ssgrakpdkradggvhaldrns-
Os02g43460  greaps----raqesrvp---vqikeepysg------sds-------d-gnvaggravv-
Bd3g50300   rrgglrslpsrpsssdeplgdsg-rakrvrr------gha-------e-gggsgrhgaa-
Bd2g43500   --------------------------hedee------edg-------a-rggeirhgei-
Os05g32610  rkea------ea--deeeaeaeaeeeaeaea------gtp-------a-rgesmevsqv-
Bd2g26500   skda------da---eeeaeaeaeeeaeaea--------p-------a-cgkrvevsrv-
RMR1        arsg------ra--separvgrarkrkrnel------eap-------a-rrervkapcvs
Sb09g19410  arsg------ra--separaarackrkgielgaetevdap-------a-rserakapcvs
At1g05490   klnhreeekkerqrevvrvvtkqpsnvvytcahcgkentgnpeshssfirphsirdeied
AtCLSY1     ----ryyrwrysedcsslvktrlnl-gkflpdltwllv------------------tsvlk
At5g20420   ----qfyrwrfsedctslmktrlsl-gkflpdlswltv------------------tstlk
Cp19.123    ----qyyrwslsedcsslsrtklfl-gkfssdlswllv------------------asvlk
Pt567214    rhetqfyrwefcedcslvqr-----------------------------------tsipk
Pt832603    qqeaqfyrwefcedcslvqr------------------sklflgrfsadltwllvasvlk
Vv29366     ----ehyrwkfsedcsllqrtklfl-gkfssdlswlvv------------------tsvlk
Bd1g16720   ----gsvqwnsaedclyqnrsrllsaarfsseishliv------------------lsalr
Os07g49210  ----gsmkwsfskdrlslnkgrlis-arfsseithliv------------------lsilr
Sb02g43870  ----gsvqwnsavdcfhhnrsklls-arfslevayliv------------------lsslr
ZM108166    ----gsvrwnsavdcfhhnrsklls-arfslevayliv------------------lsslr
ZM000342    ----gsvrwnsavdcfhhnrsklls-arfslevayliv------------------lsslr
Sm441121    ------------------------------------------------------------

                             440                 460                 480
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   iksirdgnssgcmqnvnftqecslaeqpgqyqdiimlgneninsedqavakqgndimdid
Os03g06920  vasfvdekssdskqnanyieesvlpeqhaqqqeismldnenisseaqav-kkgkdsmdin
Sb01g46180  vksfgdenss-snrndnyiqqnpllehpvghqeitrpdncnsstepqalvkqvkdamdnd
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    sasgagr-rtswm--aedagssrn-----------vssselsrggv---gdrsgstkka-
Sb04g33300  sasgagh-ptawm--sddarssrg-----------vksressrgva---gdrpgsakkal
```

```
Os02g43460  paadakqgkrgkk--tpsrgkgrr-----------vvvretstpaapsngapsvgrgkg-
Bd3g50300   pskqags-lvass--srsrkgkqraalppkhqfplvsqsesssesd---dddddeegdd-
Bd2g43500   pa---------------------r-----------vkdeeseegss---vdwd-------
Os05g32610  dgggssg-radda--shngngesr-----------vcnadgidqas---eerpsvaggd-
Bd2g26500   dgcanse-rgedplddhn-ng-sn-----------areacgi---------------gh-
RMR1        esddnsg-rgdda--shdgdaepr-----------vgvaigtdlvn---gdhpaak----
Sb09g19410  esdddgg-rgdda--sddgnaepr-----------agvaigadlvn---gdrrtak----
At1g05490   vn----------------------------------------------------------
AtCLSY1     nivfqirtvhekmvyqivtdedcegs-ssslsamnitv--edgvvmsk-vvlfnpae---
At5g20420   sivfqirtvqtkmvyqivtde--egs-sstlssmnitl--edgvslsk-vvkfnpadil-
Cp19.123    qvafevrteqykivyqiladddgsps-ksnnyisatmf--ing-----------------
Pt567214    qvafdvrsvqnkiayqifggdddhcslksnnhincvtfkvedgistpf-vvqldpid---
Pt832603    qvefnvrsvqnkivyqilggenehcslksnnhincvtfkvkdsistpf-vvqlvptdacs
Vv29366     qavfdvrsvqnrivyqivggdhdkvs----lnavnfrv--dngistpv-ifpfvpad---
Bd1g16720   gmefsiklvegniiyrvikgdqarrg------vdcmsi--ppgfgrnmeivsfqlhd---
Os07g49210  gmefniklvegqivyqiikgdqaqwn------ldsmai--ppgfgntmeiisfqlrd---
Sb02g43870  gmefsiklvdgniiyqiikgdqarys------idsmsi--ppgfgksmdiisfkpra---
ZM108166    rmefnikmvdgniiyqiikgdqards------idsmsi--ppgfgknmdiisfkprg---
ZM000342    rmefnikmvdgniiyqiikgdqards------idsmsi--ppgfgknmdiisfkprg---
Sm441121    ------------------------------------------------------------

                               500                 520                 540
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ----nenhdeqk--------------------gkregeged-vqsagsi--ennsvpvvd
Os03g06920  dviynksgheei--------------------geeeaqaen-vqikgnlkkeiis---va
Sb01g46180  ----nvsaeakkivlfdchstseqqplmkqargniktntenglkekgki--ggtiakhvg
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    ------rgapgktrr----gggtrrerstsaapanlvggsatvgs---------------
Sb04g33300  vsseesrgapgkars----gggarrerstsvapanwigts--igs---------------
Os02g43460  ------rgpgrgrqr----skgavrgrat---pvnrvstg--vgs---------------
Bd3g50300   ------glddvcset----sdeswqprynsefqvamkgekkvegr---------------
Bd2g43500   ------------------------------------------------------------
Os05g32610  ------lieeehygngeasvaggdrieehcgnveasvansnrdgg---------------
Bd2g26500   ------gneehh--n----aagknrigepcgngvasilnssh-gm---------------
RMR1        ------------------------------------------------------------
Sb09g19410  ---------------------------------------------gedhieehggdqens
```

```
At1g05490   ------------------------------------------------------------
AtCLSY1     --------------------------------------dtcqd-----sdv---------
At5g20420   --------------------------------------ddsqd-----lei---------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------tcntpae-----teigwvrslpyt
Pt832603    eaghisdtngteqspcydvmslrrskrrnvqperflacdapae-----teigwvrslpyt
Vv29366     --------------------------------------tieadplngtnea---------
Bd1g16720   --------------------------------------knlr------------------
Os07g49210  --------------------------------------ealr------------------
Sb02g43870  --------------------------------------ealr------------------
ZM108166    --------------------------------------ealr------------------
ZM000342    --------------------------------------ealr------------------
Sm441121    ------------------------------------------------------------

                             560                 580                 600
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   sydisceviqs-------------------------------------------------
Os03g06920  sdelacevmrs-------------------------------------------------
Sb01g46180  syevsceilqn-------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    -------------rirl-r--srqqg---rvq--catysarvs-sedtgedek--hmqeq
Sb04g33300  -------------rirs-r--srkqg---tgq-----ysarvs-sedtgedev--qeqkq
Os02g43460  -------------rtrs-r--laeqg---raf--aqeeeeqv---eereeeee--eeeqg
Bd3g50300   -------------rnsv-e--eeate---kel--gengngipv-leeaaekel--rengn
Bd2g43500   --------------alm-l--sddes---taa--appgtatgv-pdeeeeael--edkdn
Os05g32610  -------------eiia-g--egted---rgn--telsvvdpv-neelasded--dydde
Bd2g26500   -------------nvvasghaegvkd---wgnkggelddgfev-deeymneedted-dde
RMR1        -------------evve-g--agdedtgdggn--sglastadvfaeemapfed--dydde
Sb09g19410  avnlnddlvsgdaeave-g--agdedt--rgn--sglastadvvaeemapfed--dydde
At1g05490   ------------------------------------------------------------
AtCLSY1     ----------keei-----eeevmelrrskrrs---------------------------
At5g20420   ----------kqetdyyqeedevvelrrskrrn---------------------------
Cp19.123    ---------------------gwwelrrskrrn---------------------------
Pt567214    plkwk----eeeel-----hlplaylfgthada---------------------------
Pt832603    plkwkaeeeeeeem-----hlplaylfgthaga---------------------------
Vv29366     ----------gplp-----fcdivdlrrskrrn---------------------------
```

```
Bd1g16720   -------------p-----tirnipvthakkhn---------------------------
Os07g49210  -------------p-----titnipithvkknn---------------------------
Sb02g43870  -------------p-----iirtvlitqvkedn---------------------------
ZM108166    -------------p-----itrtvpvtqveegn---------------------------
ZM000342    -------------p-----itrtvpvtqveegn---------------------------
Sm441121    ------------------------------------------------------------

                             620                 640                 660
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    t--rvedvefmevdddyddvnv--agnvidqe--------------seqdealeg-----
Sb04g33300  k--rvedvesmdvddd-ddnntneagngiqke--------------seqdealeg-----
Os02g43460  r--afaqvkeeqveeqeedeee--geeememe--------------vevevrsdd-----
Bd3g50300   sipvqeeaaekelgengnsipv--leeaaekelrengksipveeeaaekelgeng-----
Bd2g43500   l--eeeq------eedeedewe--eeeeeere--------------a-------------
Os05g32610  m--leeklvgdviraysngadl--dtngvdwe--------------aedemefadldtnv
Bd2g26500   m--leeklvgdliraysngddl--dadgvdwe--------------aedemef-------
RMR1        m--leeqlvgdviraysngrnf--dsdgvdwe--------------aedemefnd-----
Sb09g19410  m--leeqlvgdviraysngrnf--dadeadwe--------------aedemefdd-----
At1g05490   ------------------------------------------------------------
AtCLSY1     ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
Pt832603    ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Bd1g16720   ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
ZM000342    ------------------------------------------------------------
Sm441121    ------------------------------------------------------------
```

```
                             680                 700                 720
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    -----------rssqdshgysedk--------------------e--gkdsaa-------
Sb04g33300  -----------rsrqdsh----------------------------------a-------
Os02g43460  -----------ndhgnggirgegg--------------------g--tddvae-------
Bd3g50300   -----------nsiqddrydgede--------------------e--atddah-------
Bd2g43500   ------------------------------------------------------------
Os05g32610  vdweaedemefdddndndadddgd--------------------n--fggdad-------
Bd2g26500   -------------------dddgd--------------------ddyfvhdad-------
RMR1        -----------dadnsdfmddadd-------------------sd--fmdday-------
Sb09g19410  -----------dadnsdfmddahdsdfvndadeggksgddaensd--fmddahdsdfvnd
At1g05490   ------------------------------------------------------------
AtCLSY1     ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
Pt832603    ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Bd1g16720   ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
ZM000342    ------------------------------------------------------------
Sm441121    ------------------------------------------------------------

                             740                 760                 780
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
```

```
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    --lsdneedvggkelleeeeegad-qee--shiiydg-------egeqee------dase
Sb04g33300  --lidneeevgekelseeeed--dnqee--shsmydg-------egeqee------dase
Os02g43460  --ieeeelgtdedetsddsdenfs-deegdeeeleee-------eeeeee------eedd
Bd3g50300   --aaeeeeeeeeeeeeeeeee-----ee--eeeeeee-------eeeeee------eeee
Bd2g43500   ----dledmvgeee---eeeqgke-ede--weleeee-------eeehee------teee
Os05g32610  --egdksvqmhdfskvetqdlvsh-nvn--vsevrph-------edeeai------kdem
Bd2g26500   --ecgmsepmcddykvgtqylsdh-evv--vgevscq-------leedvv------kdev
RMR1        --eggnskpiqnhakleiqdwvnq-kvv--lsggrceargegdleeeldvgkead-eedv
Sb09g19410  adeggksepikshakmeiqdlvnq-kvv--lcgggcee--eggekeelgvgkeagkkedv
At1g05490   ------------------------------------------------------------
AtCLSY1     ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
Pt832603    ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Bd1g16720   ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
ZM000342    ------------------------------------------------------------
Sm441121    ------------------------------------------------------------

                             800                 820                 840
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
```

```
AtDRD1          ------------------------------------------------------------
Bd1g74070       ------------------------------------------------------------
Os03g06920      ------------------------------------------------------------
Sb01g46180      ------------------------------------------------------------
At2g21450       ------------------------------------------------------------
Sm84719         ------------------------------------------------------------
Vv15867         --------------------------------------------mdfsspvakrtr----
Pt286483        --------------------------------------------mddslcvakrtrshyn
Cp76.2          --------------------------------------------lnckgsaglenr----
At3g24340       --------------------------------------------vflgtiagenqh----
ZM178435        eetqeldetge----------------------a-qpfn--psntmagstmrsggd----
Sb04g33300      eveqemdetgeedekeldgtgeedeqeldgagka-qpvt--psntiagssmrsggd----
Os02g43460      ddddeeeeepg----------------------d-apdq--pgeageespprsrim----
Bd3g50300       eqddesdeage----------------------elhpvp--nsnadaggnarsgge----
Bd2g43500       eseseqdeeaa----------------------e-eprrggprnsaaagryahrae----
Os05g32610      eskgkgslsfn----------------------e-gssy--ieildsdeevkvvnd----
Bd2g26500       dpkregttcfd----------------------q-grlh--ieilesddevkvlsd----
RMR1            epkseaapgsd----------------------k-rvlq--leilgsdeeikvlen----
Sb09g19410      epkseaapgsd----------------------k-ggsh--letmssdeeikvlen----
At1g05490       --------------------------------------------nfastnvskyed----
AtCLSY1         --------------------------------------------grperygdseiq----
At5g20420       --------------------------------------------vrpdiytgcdye----
Cp19.123        --------------------------------------------vqperfiggqgl----
Pt567214        --------------------------------------------scaeekpgnevr----
Pt832603        --------------------------------------------scaeeqtcnevg----
Vv29366         --------------------------------------------vqpdrffslggf----
Bd1g16720       --------------------------------------------ltednrftlkte----
Os07g49210      --------------------------------------------itedmrftvkse----
Sb02g43870      --------------------------------------------liedgctavkhe----
ZM108166        --------------------------------------------ltedgciavkge----
ZM000342        --------------------------------------------ltedgciavkge----
Sm441121        ------------------------------------------------------------

                                 860                 880                 900
Bd2g21450       ------------------------------------------------------------
Bd2g21430       ------------------------------------------------------------
Sb07g02945      ------------------------------------------------------------
ZM064574        ------------------------------------------------------------
ZM093940        ------------------------------------------------------------
Bd3g19890       ------------------------------------------------------------
Os06g14440      ------------------------------------------------------------
Os07g25390      ------------------------------------------------------------
Os08g14610      ------------------------------------------------------------
Bd3g18910       ------------------------------------------------------------
Vv23895         ------------------------------------------------------------
Vv35918         ------------------------------------------------------------
Pt195587        ------------------------------------------------------------
AtDRD1          ------------------------------------------------------------
Bd1g74070       ------------------------------------------------------------
Os03g06920      ------------------------------------------------------------
Sb01g46180      ------------------------------------------------------------
At2g21450       ------------------------------------------------------------
Sm84719         ------------------------------------------------------------
Vv15867         lqe-----------a-------lvyrrly--eekkr--nagvsss-gshnddgveflge-
```

```
Pt286483    les-----------akkrmkletvsrplcvdeekl---------------dd--------
Cp76.2      arr-----------i-------ktrekvt--denkd--rvremna-kdcgdlnpekcrd-
At3g24340   ved-----------v-------nagsevc--dilld--------------danlrgeek-
ZM178435    gkq-----------v-------frrrvfe--giylp--enphrtv-gkgiqgrtrsqrk-
Sb04g33300  dtr-----------v-------frrrvfe--giclp--qkprktv-gkgigartrsqrk-
Os02g43460  amp-----------l-------mgkrmfe--gfsfl--qqvdtst-grdirartrsnfk-
Bd3g50300   gtp-----------i--------gkrvfe--glclv--dnadnavttksirqrtrsnfkd
Bd2g43500   dge-----------i-------fakrlfe--glcis--kaadtsaagkpvagrtrsrrr-
Os05g32610  tgn-----------a-------lrrk-------plv--paklpiv-pscvawrtrsswg-
Bd2g26500   asn-----------p-------lkrk-------plp--qakipvl-p-cvawrtrslwg-
RMR1        mss-----------a-------psrk-------asv--qsklpti-pscvawrtrsswg-
Sb09g19410  mss-----------a-------psrk-------asv--qsklpti-pscvawrtrsswg-
At1g05490   svs-----------i-------nsgkttg--apsrp--evenpet-gkelntpekpsisr
AtCLSY1     pds-----------k-------dgwvrmm--pyryn--iwnvssd-dddeeedceddkd-
At5g20420   pdt-----------i-------dgwvrmm--pyqfgkcavnvesd-ed--eddnnedgd-
Cp19.123    tes-----------d-------svwvrqm--pik---------------------tdkw-
Pt567214    vnspkleflegppvs-------rtktnsr--kiksn--vfnrreh-qaelgevesgidn-
Pt832603    asspklellegipvs-------rtktylk--eiksn--vvnrrdh-qtepgevragmak-
Vv29366     ses-----------d-------igsvrag--ihkvd--ywrkeem-plalpdegdvhsi-
Bd1g16720   lddqleyir-----v-------avkield--dqled--qfdvgll-ykhvdlrrskrlk-
Os07g49210  mds-----------------------eld--ral------dveil-yehvdlrrskrlk-
Sb02g43870  sds-----------------------------------aqdvevl-yehvdirrskrmk-
ZM108166    sds-----------------------------------aqdveil-yahvdirrskrmk-
ZM000342    sds-----------------------------------aqdveil-yahvdirrskrmk-
Sm441121    ------------------------------------------------------------

                             920                 940                 960
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ---ag---vfdsv--qkfvaesd-gknsdr---k--n-s---sr--kkngg-ens-----
Pt286483    ------------------------------------------------n-g-dn------
Cp76.2      ---vi---viddd--dneaiaad-asgddd---d--d-c-------denhd-ded-----
At3g24340   ---ty---vsdev--vslssssd-deedpl---e--e-lgtdsr--eevsg-edr-----
ZM178435    ---ck---dkkll--krgtfskp-ynidip---d--s-t---sd--seeei-epp-----
Sb04g33300  ---ck---dkkll--rrgtfskp-ynidip---d--s-t---sd--seedi-epp-----
Os02g43460  ---rkklldkkll--krgtfakp-ycidv-------s-s---sg--seedv-pqp-----
Bd3g50300   ra-cl---dkkll--gqgtcskp-ycidt--------------e--seedvpppp-----
```

```
Bd2g43500    ---cl---ntkll--rqgtynkp-ycldtp---sesg-s---se--aeegv-nkt-----
Os05g32610   ---mk---eeris--yntyfev---lsdep---k--edd---dd--tevel-dde-----
Bd2g26500    ---vk---qdris--ynayfee---lsdep---i--e-d---dd--tevel-dde-----
RMR1         ---vn---qdrls--ydtyfee---lsdep---k--edd---dd--tevel-dev-----
Sb09g19410   ---in---rdrls--yntyfea---lsdep---k--edd---dd--tevel-ded-----
At1g05490    peift---tekai--dvqvpeep-srpeiy---s--s-e---ka--kevqa-pem-----
AtCLSY1      ---td---ddlylplshllrkkg-skkgfs---k--d-k---qr--eivlv-dkt-----
At5g20420    ---tn---ddlyiplsrlfikk---kktnsreak--p-k---srkgeivvi-dkrrvhgf
Cp19.123     ---ke---kmkclplsrlfkmqplylkeqp---k--n-e---tr--dlvvy-ksn-----
Pt567214     ---rr---erqkstvanrikhqt-rlgeak---s--g-m---an--rkkhg-tqi-----
Pt832603     ---rr---ecqkstmadriehqt-rlgdae---s--g-m---an--rkkhg-tqi-----
Vv29366      ---fs---ekhii---dyekgah-slqids---y--e-d---fl--vcksk-drs-----
Bd1g16720    ---tq---perftsydapnfnrd-tkkkga---s--a-s---st--mhydh-rra-----
Os07g49210   ---tq---pdrftsydtprflsg-ykkkea---s--s-s---pt--khv---rgavhcds
Sb02g43870   ---tq---pdrftsydapnfnrt-ynkkea---y--g-p---sn--knens-esdlsfy-
ZM108166     ---tq---pdrftsydarnfnrt-ynkkea---d--g-p---st--kyeds-esglscd-
ZM000342     ---tq---pdrftsydarnfnrt-ynkkea---d--g-p---st--kyeds-esglscd-
Sm441121     ------------------------------------------------------------

                              980                1000                1020
Bd2g21450    ------------------------------------------------------------
Bd2g21430    ------------------------------------------------------------
Sb07g02945   ------------------------------------------------------------
ZM064574     ------------------------------------------------------------
ZM093940     ------------------------------------------------------------
Bd3g19890    ------------------------------------------------------------
Os06g14440   ------------------------------------------------------------
Os07g25390   ------------------------------------------------------------
Os08g14610   ------------------------------------------------------------
Bd3g18910    ------------------------------------------------------------
Vv23895      ------------------------------------------------------------
Vv35918      ------------------------------------------------------------
Pt195587     ------------------------------------------------------------
AtDRD1       ------------------------------------------------------------
Bd1g74070    ------------------------------------------------------------
Os03g06920   ------------------------------------------------------------
Sb01g46180   ------------------------------------------------------------
At2g21450    ------------------------------------------------------------
Sm84719      ------------------------------------------------------------
Vv15867      ----dedvtdv---v--sisdd----s--easdy--eee----eddd--d-d-----dyi
Pt286483     ----de--------------dd----t--ea--y--e----------------------a
Cp76.2       ----ddgdvvw---e--edmdd----l--ertse--edn----ddsd--d-e-----dya
At3g24340    ----dsgesdm---d--edand----s--dssdyvgess----dssd--v-e-----ssd
ZM178435     ----apqqgll---s--sseed----n--mtfgk--rkr----rraa--i-n-----krw
Sb04g33300   ----apqqgll---s--sseeg----n--itfgk--rkh----rrai--k-n-----rr-
Os02g43460   ----eqsaygg---d--caddd----g--gsdgn--eeh-----rav--k-r-----rkl
Bd3g50300    ----qpqpssa---e--ceddg----s--ggddr--mpa----krrr--g-k-----eqi
Bd2g43500    ----ppapals---s--sdeei----e--adagg--hgr----taar--k-g-----rrr
Os05g32610   ----eddendd---dcnsascd----e--edeee--eeereeeeeea--q-r-----rkq
Bd2g26500    ------ddndd---d--sasf----------eee--eeeetkqeeva--e-k-----skh
RMR1         ----eddnndd---d-ssdayd----k--ddeek--eee----eeea--e-r-----rkl
Sb09g19410   ----edgnndd---g-ssdayd----k--ddeekeeeee----eeea--e-r-----rkl
At1g05490    ----psrpevf---s--sekak----e--iqvpe--mps----ipei--q-n-----sek
AtCLSY1      ----erkkrkk---t--egfsr----s--celsv--ipf----tpvf--e-p-----ipl
```

```
At5g20420   ----grkerks-------------------elsv--ipf----tpvf--e-p-----ipl
Cp19.123    ----kyskdvksgla--dqveh----q--nklai--ipvpn--vpel--e-p-----epl
Pt567214    ----revklgv---a--nrieh----q--dqlai--vpv----pted--d-l-----vtf
Pt832603    ----revksgv---a--nrreh----q--dqlai--vpv----hted--v-l-----atf
Vv29366     ----revkpil---a--aqned----q--hqfai--vpv----plii--e-p-----iah
Bd1g16720   ----sqvkves---s--cgedp----v--kitga--ssf----mfne--n-p-----stt
Os07g49210  pvddskkeves---c--cveipgn--vtqkqtgv--hsp----mvdeksnspegqhkntt
Sb02g43870  ----sseqtes---s--deevlgnpgv--kkkvs--rsf----vvke--d-p-----rsm
ZM108166    ----sseqres---s--deeal------------------------e--n-p-----rsm
ZM000342    ----sseqres---s--deeal------------------------e--n-p-----rsm
Sm441121    ------------------------------------------------------------

                            1040                1060                1080
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     v---------------------------------------dpti----------------
Pt286483    v---------------------------------------d--v----------------
Cp76.2      v---------------------------------------mktm----------------
At3g24340   s---------------------------------------dfvc----------------
ZM178435    d---------------------------------------krls----------------
Sb04g33300  r---------------------------------------krps----------------
Os02g43460  n---------------------------------------rrqs----------------
Bd3g50300   t---------------------------------------dsdd----------------
Bd2g43500   g---------------------------------------knptp---------------
Os05g32610  k---------------------------------------kgid----------------
Bd2g26500   k---------------------------------------kgihssfpeirsrpmplfvn
RMR1        n---------------------------------------nric----------------
Sb09g19410  n---------------------------------------ngiy----------------
At1g05490   a---------------------------------------kevq----------------
AtCLSY1     e---------------------------------------qfgl----------------
At5g20420   e---------------------------------------qfgl----------------
Cp19.123    a---------------------------------------sehh----------------
Pt567214    e---------------------------------------qyds----------------
Pt832603    e---------------------------------------qfds----------------
Vv29366     g---------------------------------------edhl----------------
Bd1g16720   k---------------------------------------gqhk----------------
Os07g49210  krttcslvkekasspegqhekttkrttcalpvkekasspegqhk----------------
```

```
Sb02g43870  k---------------------------------------gqhk----------------
ZM108166    a---------------------------------------aehk----------------
ZM000342    a---------------------------------------aehk----------------
Sm441121    ------------------------------------------------------------

                            1100                1120                1140
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     -----------------------------drdergnqa----------------------
Pt286483    -----------------------------aqkvr--------------------------
Cp76.2      -----------------------------yrkekckpk----------------------
At3g24340   -----------------------------sedeeggtr----------------------
ZM178435    -----------------------------assdee-------------------------
Sb04g33300  -----------------------------tssdee-------------------------
Os02g43460  -----------------------------ahsdse-------------------------
Bd3g50300   -----------------------------tqndse---dsd-------------------
Bd2g43500   -----------------------------sdddse-------------------------
Os05g32610  -----------------------------ssddem---idd-avd---------------
Bd2g26500   rerrmqtsipkwrgtskkarqpetchviyssddei---iddtakdglk------------
RMR1        -----------------------------tsdedm---ini-tvptsrydmfkkkn----
Sb09g19410  -----------------------------tsdddm---ini-tvptsrydmferknisry
At1g05490   -----------------------------annrmgltt----------------------
AtCLSY1     -----------------------------nanslc-gg----------------------
At5g20420   -----------------------------nansfg-gg----------------------
Cp19.123    -----------------------------dyhanl-sa----------------------
Pt567214    -----------------------------plktpd-nf----------------------
Pt832603    -----------------------------pvktpe-py----------------------
Vv29366     -----------------------------hdetpw-ne----------------------
Bd1g16720   -----------------------------ntrrrt-pc----------------------
Os07g49210  -----------------------------ntikrt-tc----------------------
Sb02g43870  -----------------------------ypvkrn-qc----------------------
ZM108166    -----------------------------ypvkrn-qc----------------------
ZM000342    -----------------------------ypvkrn-qc----------------------
Sm441121    ------------------------------------------------------------

                            1160                1180                1200
Bd2g21450   ------------------------------------------------------------
```

```
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
Pt286483    ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
At3g24340   ------------------------------------------------------------
ZM178435    ------------------------------------------------------------
Sb04g33300  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Bd3g50300   ------------------------------------------------------------
Bd2g43500   ------------------------------------------------------------
Os05g32610  --------------------------------cgidweedy---pevdftrpltfqkdgs
Bd2g26500   --------------------------------cevd--ed----prnnvfqplnfekvgs
RMR1        -----------------------------ssrydiewvede--dasvdmlqpvsfkkdss
Sb09g19410  dmfkrkntsrydifkrkntsrydifkrkktsrydiewvededkdanvdtlqpislrkgss
At1g05490   ------------------------------------------------------------
AtCLSY1     ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
Pt832603    ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Bd1g16720   ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
ZM000342    ------------------------------------------------------------
Sm441121    ------------------------------------------------------------

                            1220                1240                1260
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
```

```
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     --sk---lgkkkve-l-g-t-ss--h-pfcvd---vdegegdgdg-e-geeew-eeeeee
Pt286483    --sk---kgktkpt-g-g-n-gg--------d---vd----dgd----------------
Cp76.2      --nh---dvngrdf-s-s-l-eg--n-kqspa---ttfdhhdcd--d-ndriw-ehdlnd
At3g24340   --dd---atceknp-s-e-k-vy--h-hkksr---tfrrkhnfd------vin-llaksm
ZM178435    --dy---gasamda-k-e-r-pf--r-rlkkg---lsnlqaakeg-c-rnyeg-snpgha
Sb04g33300  ---y---rvyardg-k-d-r-pf--r-rlkkg---lsklqagkeg-c-gryvg-snpgha
Os02g43460  --ed---ttfvcdv-k-egs-gs--r-rvqeg---aprrqvkkeg-snkkkdg-stpqcv
Bd3g50300   --en---rtlarnark-g-s-ss--r-rpkng---asyqqnvkeg-s-rnydspsnprhv
Bd2g43500   --eh---rvggrqg-t-a-v-rr--r-rwpkd----ntaqcdhee-e-eddea-fvpfrr
Os05g32610  --ea---pvgseaf-t-e-q-qk--rsrftwe---lerrkklklgmm-tnhrl-yerdle
Bd2g26500   --dg---tvgngit-t-e-q-qk--gsrftwd---lerrkklklgii-ksrhs-yergld
RMR1        wkpv---avgndtf-t-e-q-qk--rsrftwe---lerrkklkle-m-ktnpl-herdld
Sb09g19410  wnpv---avgndtf-t-e-q-qk--qsrftwq---lerrkknkle-m-ktnpl-yerdln
At1g05490   --pa---vaeglnk-s-v-v-tn--e-hiedd---sdssissgdg-y-esdpt-lkdkev
AtCLSY1     --vs---gnlmdei-d-k-y-rs--k-aakyg---kkkkkkieme-e-mesdl-gwngpi
At5g20420   --gsfsrsqyfdet-e-k-y-rs--k-gmkyg------kkmteme-emmeadl-cwkgp-
Cp19.123    --nn---skrveel-sfr-y-ns--l-kcsrt---ssrkkfsqid-d-mdlvp-rweg-i
Pt567214    --pq---eciefpi-r-s-y-sk--k-g--ys---vqrk-----n-d-fdedm-mfgsgw
Pt832603    --sq---afiefpi-s-y-y-rk--k-----sspaahrk-----n-d-rdedl-mfgngw
Vv29366     --sg---eigeisp-k-y-y-ct--n-gvpk----lqrknms-------dlym-evesrw
Bd1g16720   --sl---pmkekps-s-v-k-ee--s-kteer---asdshipqtp-a-qnkek-nhrtps
Os07g49210  --sl---pvkeeps-s-v-eieekss-k-eqs---apefhiprtp-a-qnkek-hnrppf
Sb02g43870  --sl---pikenqt-s-m-etkk--n-atdqg---csdshiphtp-a-kniek-cnrp--
ZM108166    --sl---pvkekqi-s-m-eikk--n-ttdqg---csdsyiphtp-a-knte----rp--
ZM000342    --sl---pvkekqi-s-m-eikk--n-ttdqg---csdsyiphtp-a-knte----rp--
Sm441121    ------------------------------------------------------------

                                1280                1300                1320
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
```

```
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     e-----------eeeeg-r---dsssghae-fp----ktigrkdkgelgk-ht----krk
Pt286483    etcdhksqrrtiesregsr---d-ehghg----------vcrr------k-ps----krr
Cp76.2      l-----------vtssk-e---engvshnn-f-------------ssvrk-tv----skk
At3g24340   l-----------eskdv-f---kedifswd-ki----aevdsredpvvre-ss----sek
ZM178435    r-----------ysgpn-g---gnlenmss-aq----ddisfkrnvhmir-ik----krg
Sb04g33300  k-----------yngpn-g------enqsn-eq----dgiffkrtahkir-mk----khg
Os02g43460  r-----------nngpk-v---grqtngln-gq----ggvsfkrnvkiaq-rr----krr
Bd3g50300   k-----------nyaan-a---gnptdrfn-mqs---gdicfntntllpq-rm----khg
Bd2g43500   p-----------krsga-v---pnprdgyy-dqqqqagdapfkksslilp-kk----rcg
Os05g32610  s-----------dsnss-d---ssqnrkng-cq----gsgdhrtgrkrknpls----ksg
Bd2g26500   l-----------dsdss-g---sgenerhg-yq----eggdnkvgrkkkh-lssksgksg
RMR1        s-----------dpnss-g---sdqirkyg-fk----sdgshkvdrkkkhtsp----ksg
Sb09g19410  s-----------dsnss-g---sdqirkyg-fk----rdgshkvdmkkkhtss----ksg
At1g05490   k-----------innhs-d---wrilngnn-ke----vdlfrllvnsvwe-kg----qlg
AtCLSY1     g-------------nvv-h---krngphsr-ir----svsretgvseepq-iy----kkr
At5g20420   --------------nqv-ksfqkrt---srssr----svapktedsdepr-vy----kkv
Cp19.123    q-------------gkg-s---nrkaqirk-hr----gissk-edfdepi-ty----kkk
Pt567214    g-------------gks-s---rkkvqrar-yq----sthlkrddsckpk-ty----kqt
Pt832603    g-------------gkf-s---tkkvqrar-yr----sthlkqdgscapm-ty----krt
Vv29366     e-------------gkg-p---irklrrkr-gf----tirtktesygevr-ph----kkr
Bd1g16720   ---------------sf-h---rksgtspc-sl----ggnyepafcqkrg-rk----rke
Os07g49210  ---------------sc-k---pklftssg-tl----gvncepafcqkvg-gk----rkr
Sb02g43870  ---------------tf-r---lksfassr-sl----dgnsepafcqkrg-rk----rkk
ZM108166    ---------------rf-r---lkpfassr-sl----dgnsepafcqkrg-rk----rkk
ZM000342    ---------------rf-r---lkpfassr-sl----dgnsepafcqkrg-rk----rkk
Sm441121    ------------------------------------------------------------

                            1340                1360                1380
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Vv15867     ri-r--al----khcdalkilvdsiwaknsgll--------eelvsprgsds--------
Pt286483    r-----------keyevvkila------nslfldledvpfkee----r--ep--------
Cp76.2      rk-h--mh----kshdivkvvvnsmleeeemlf--------eetvasgdvlk--------
```

```
At3g24340   vn-e--hg----kpre--rrsfhrvreknhlng--------esfyggeklcd--------
ZM178435    ra-a--ka----vydelldslfsgwenhig------------------------------
Sb04g33300  pv-a--ka----aydellnslfsgwedhin------------------------------
Os02g43460  qa-tadqe----kyghlldpmfneiesnqy------------------------------
Bd3g50300   rvwt--kq----dtdnllnslldeieng-s------------------------------
Bd2g43500   ag-qe-re----tyddllqsifdeitnqqn----------------------gsapldddg
Os05g32610  kk-s--sr--mlkrqslmkllmdkmcsndd----------------------gkstpfdq
Bd2g26500   kk-s--srstmlkrqsllkllmdkmtgdkd----------------------gecspfdl
RMR1        kk-p--ssaiilkrqsllkllvdkmsgdks----------------------lasfpfdq
Sb09g19410  kk-s--ssaimlkrqsllkllvdkmsgdks----------------------lesfsfdq
At1g05490   e-----ed----eadelvssaedqsqeqar----------------edhrky--------
AtCLSY1     tl-s--ag----aynklidsymsridstiaakd--------katnvveqwqg--------
At5g20420   tl-s--ag----aynklidtymnniestiaakd--------eptsvvdqwee--------
Cp19.123    sl-s--ag----aydklihsymknidstmi--k--------eephiidqwqe--------
Pt567214    al-s--ag----aydklisfymknfdstiksk---------evtriidqwee--------
Pt832603    al-s--ag----aynklissymknidatiksk---------evpriidqwee--------
Vv29366     pf-s--ep----gykevieaymkniestin--k--------eqplvidqwke--------
Bd1g16720   rm-c--de----eyekiinqcigniqsemerdy--------efnl---dvpm--------
Os07g49210  hm-c--er----eykqmidqcigniesemerds--------mfnf---danm--------
Sb02g43870  gm-c--qr----eykrmieqcigniqceverds--------dfki---daqi--------
ZM108166    hm-c--qi----eykrmidqcigniqceverds--------dfkf---gdqi--------
ZM000342    hm-c--qi----eykrmidqcigniqceverds--------dfkf---gdqi--------
Sm441121    ------------------------------------------------------------

                            1400                1420                1440
Bd2g21450   ----------------------MEMLKLPQE--KEREKTI-C--PQKP-TNPWRKR----
Bd2g21430   ----------------------LENSKL--------------------------------
Sb07g02945  ----------------------EPEPDMAIE--EEEKCKN-E--SDGL-EDYWKDF----
ZM064574    -----------------------PEPDMVIE--EEEKHKN-E--SDGL-DDYWKDF----
ZM093940    -----------------------QEPDIAIE--EEEKRKN-D--GDGL-EDYWKDF----
Bd3g19890   ----------------------EP------A--EEDKPEN-K--SDGL-EDLWKDF----
Os06g14440  ----------------------E-------------KPVK-E--SDGL-EDLWKDF----
Os07g25390  ----------------------E-------------KPVK-E--SDGL-EDLWKDF----
Os08g14610  ----------------------KQQKSIPRD--RKRKGEL-DpaADYV-KDLWDAF----
Bd3g18910   ----------------------GKLDKFEEV--ASDEPKK-E--SDCLvDDLWNHF----
Vv23895     ----------------------VEDDMEASE--GNLQAKT-K--DDDL-ADMWQEF----
Vv35918     ----------------------VEDDMETNE--GNLRAKT-E--DDGL-ADMWQEF----
Pt195587    ----------------------VEDD--------EVDTEI-K--YDGL-GDIWKEM----
AtDRD1      ----------------------VEED----D--SDNESEA-A--DEDL-GNIWNEM----
Bd1g74070   ----------------------ESTENGNYD--RYDNNDS-P--VDEL-EYLWRDM----
Os03g06920  ----------------------QSPTNGNFD--QYDNS-S-P--VDEL-EGLWMDM----
Sb01g46180  ----------------------EPHSNEG----NHHDNGS-P--VGEL-DDLWIGM----
At2g21450   ----------------------DSSRNSTDI--DNQSLYV-D--AEEE-EELWRKM----
Sm84719     ----------------------EDSRSWDFD--FDHEKLE-N--EDKL-AAIWHDW----
Vv15867     -ie--e-tap-aft--el--plKFKFGVDES--IPLGKSQ-P--EIGM-NQLWAEF----
Pt286483    -le--e---p-v-----l--plKFTFGIEES--SPPVKSE-E--EKQL-EELWADMalal
Cp76.2      -eq--g-nhp-etep-tl--plTFTFQIDES--SMSKNSD-S--DNEL-HNLWVEMnfaq
At3g24340   -ge--e-tin-yst--edspplNLRFGCEEP--VLIEKTE-E--EKEL-DSLWEDM----
ZM178435    -np--v-hae-agn--sl--plVFSFGDEDA--EENTEND-K--YQEQ-EDLWMEC----
Sb04g33300  -dp--d-haa-agn--sl--plVFSFGDEDA--EENIEND-K--Y--Q-EDLWREC----
Os02g43460  -ep--vpeeq-idr--rl--plVFAFGDDDKl-EEKSKHD-K--LQDE-DELWKEF----
Bd3g50300   -ap--a-qaq-ned--rl--plVFSFGDEDQv-EEQSDHN-K--L--Q-DELWAEM----
Bd2g43500   sap--a-qeqsvpd--tl--plIFSFGDEDQvvKEKTEQG-K--F--E-DLLWAEF----
Os05g32610  -kp--qieys-fkd--lh--plVFSFGDDDP--SPTDRSE-Q--DAAL-DMLWADL----
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Bd2g26500     -hs--qfeyn-snd--sh--plVFSFGDEDH--IPANKAE-Q--NAEH-DMLWADY----
RMR1          -np--qlqfi-fke--mh--plVFSFGDEDL--VAADRPE-Q--DVGL-DMLWADF----
Sb09g19410    -np--qlqfi-fke--mh--plVFSFGDEDL--EAADRPE-Q--DVGL-DMLWADF----
At1g05490     -dd--a-gll-iir--pp--plIEKFGVEEPq-SPPVVSE-I--DSEE-DRLWEEL----
AtCLSY1       -lk--n-pas-fsi--ea--------EERLS--EEEEDDG-E--TSEN-EILWREM----
At5g20420     -lkktn-fa--fklhgdm--------EKNLS--EDGE--G-E--TSEN-EMLWREM----
Cp19.123      -fk--k--as-fpe--qr--------MEIEQ--SSSEDEG-E--SSEN-EMLWREM----
Pt567214      -fk--a-khs--sd--qk--------ETMEP--SLVEDDG-E--SSET-EMLWREM----
Pt832603      -fk--a-khs--sd--qk--------EKMEP--SSVKDDG-E--SSET-EMLWREM----
Vv29366       -lq--v-rnd-lnq--rr--------DCNSP--SSVGDQE-E--SSET-EMLWREM----
Bd1g16720     -mh--c-cqg-ayp--ee--------DFTWP--SLADSQEeK--KDEL-DELWKEM----
Os07g49210    -mn--y-vqh-syr--ee--------DFTWP--PSADNQEvE--EDEL-EELWKEM----
Sb02g43870    -ln--g-cgh-ayq--ee--------DFMWP--SSADSQE-E--KDEL-QELWKEM----
ZM108166      -ld--g-cvr-ayq--ev--------DFTWP--SSADSQE-E--KDEL-DELWKEM----
ZM000342      -ld--g-cvr-ayq--ev--------DFTWP--SSADSQE-E--KDEL-DELWKEM----
Sm441121      ----------------------MSSFD---------------------------------

                              1460                1480                1500
Bd2g21450     ----------S--LQKKFYFNA-QLDT-LEDV-PN-------------------------
Bd2g21430     ------------------YFNA-QLDT-PEDV-PN-------------------------
Sb07g02945    ----------A--LAVE---ST-KLDE-VDEA-AN-------------------------
ZM064574      ----------A--LAVE---ST-KLDE-VDEA-AI-------------------------
ZM093940      ----------A--LAVE---ST-KLDD-VDEA-AAn------------------------
Bd3g19890     ----------S--VAME---SS-KLNT-FEEL-PD-------------------------
Os06g14440    ----------S--LAAE---CT-KLDT-NEDM-SN-------------------------
Os07g25390    ----------S--LAAE---CT-KLDT-NEDM-SN-------------------------
Os08g14610    ----------Y--VTAE---ST-HLDT-S-------------------------------
Bd3g18910     ----------D--LAMA-------SKK-YEEV-AN-------------------------
Vv23895       ----------D--LALQ---------S-SKDV-AV-------------------------
Vv35918       ----------D--LALQ---------S-SKDV-AV-------------------------
Pt195587      ----------S--FALE---------C-SKDV-VE-------------------------
AtDRD1        ----------A--LSIE---------C-SKDV-AR-------------------------
Bd1g74070     ----------S--LALA---CS-KTIG-SDHS-IV-------------------------
Os03g06920    ----------Y--LAMA---CS-KTVG-SDHN-IV-------------------------
Sb01g46180    ----------S--VALA---CSeKNNQ-VNLS-IV-------------------------
At2g21450     ----------A--FAQE---------S-IKVT-VE-------------------------
Sm84719       ----------D--AEIE----A-ERRR-VPDL-IK-------------------------
Vv15867       ----------D--FDGE-----------EDFG-SA-------------------------
Pt286483      clkdttd---DaaLDEN-----------ED-D-AH-------------------------
Cp76.2        rsfeidshacN--MVEN-----------EYAV-CS-------------------------
At3g24340     ----------N--VALT----------lEGMH-SS-------------------------
ZM178435      ----------G--IAFQ-----------SMNI-GSngce----e-----d-gk-------
Sb04g33300    ----------D--IAFE-----------SMDI-G-ngse----e-----d-gl-------
Os02g43460    ----------D--FALE-----------SINV-CShnceegeke-----d-eq-------
Bd3g50300     ----------D--FCME-----------STNV-CPqsce----egeksnn-gq-------
Bd2g43500     ----------D--FALE-----------STNA-CShacq----eegeksn-gd-------
Os05g32610    ----------D--FTLE-----------SENI-GTyydd----egq-eds-ll-------
Bd2g26500     ----------D--FALE-----------LENI-GTyydd----ehq-eesnml-------
RMR1          ----------D--FALE-----------SENI-GTyydd----ecq-egn-ql-------
Sb09g19410    ----------D--FALE-----------SENI-GTyydd----egqeegn-ql-------
At1g05490     ----------A--FFTK-----------SNDI-GGnelfsnvekni--------------
AtCLSY1       ----------E--LCLA-----------SSYI-LDdhev---------------------
At5g20420     ----------E--LCLA-----------SSYI-LDdnev---------------------
Cp19.123      ----------E--LSMA-----------SAYF-LEdnev---------------------
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Pt567214    ----------E--LCLT-----------SAYI-FEdnes---------------------
Pt832603    ----------E--LCLA-----------SAYI-LEdnevelcvvfiysyhly--------
Vv29366     ----------E--FSIA-----------SSYL-LEenegsnvevlk--------------
Bd1g16720   ----------D--FSLT-----------TLE--LDrmqv---------------------
Os07g49210  ----------D--YSLT-----------TLA-lLEqkqvmaqsrinmlvdnfdglrldcl
Sb02g43870  ----------D--YALA-----------TVA-iDEqkqlikcldfqt-------------
ZM108166    ----------D--YALA-----------TVA-iLEqkqm---------------------
ZM000342    ----------D--YALA-----------TVA-iLEqkqm---------------------
Sm441121    ----------D--ICEV-------------------------------------------

                            1520                1540                1560
Bd2g21450   -------------------------------------------AKEV-GRK-E-V-KIE-
Bd2g21430   -------------------------------------------IKEV-SEK-E-V-KID-
Sb07g02945  -------------------------------------------EKED-NGN-M-E-DID-
ZM064574    -------------------------------------------EKED-NGK-M-E-DID-
ZM093940    -------------------------------------------EKED-NGK-M-E-DID-
Bd3g19890   -------------------------------------------EKEL-GEK-D-V-DND-
Os06g14440  -------------------------------------------EKDVdDEN-E-M-DDD-
Os07g25390  -------------------------------------------EKDVdDEN-E-M-DDD-
Os08g14610  ---------------------------------------------EV-NNK-K-Q-LDN-
Bd3g18910   -------------------------------------------DKHV-KRKiN-V-DIG-
Vv23895     -------------------------------------------DPEE-DGK-E-G-EEE-
Vv35918     -------------------------------------------DPGE-DEK-E-S-KEE-
Pt195587    -------------------------------------------NSPS-DEN-M-E-EDEd
AtDRD1      -------------------------------------------ETSH-KEK-A-DvVED-
Bd1g74070   -------------------------------------------PSEN-TCG-E-V-VDD-
Os03g06920  -------------------------------------------PSEN-SCE-Q-A-EDE-
Sb01g46180  -------------------------------------------PFVS-NSE-E-T-EDA-
At2g21450   -------------------------------------------DSQS-NDH-K-Q-IED-
Sm84719     -------------------------------------------FKDI-DV----L-IDS-
Vv15867     -------------------------------------------EVEI-DQA-V-L-CHQ-
Pt286483    -------------------------------------------EVEP-DTV-T-L-CHQ-
Cp76.2      -------------------------------------------EVDL-DIA-T-L-CSK-
At3g24340   -------------------------------------------TPDK-NGD-M-L-CSK-
ZM178435    -------------------------------------------EIPP-VKV-T-S-CNI-
Sb04g33300  -------------------------------------------EIPP-VEV-T-S-CNN-
Os02g43460  -------------------------------------------EIPA-DKA-A-S-CIQ-
Bd3g50300   -------------------------------------------EKPG-DKA-T-L-CSQ-
Bd2g43500   -------------------------------------------EIHA-DRA-T-S-CKR-
Os05g32610  -------------------------------------------DHAL-API-T-P-CSR-
Bd2g26500   -------------------------------------------NLGL-ACT-T-P-CSR-
RMR1        -------------------------------------------DFSL-APV-T-P-CSR-
Sb09g19410  -------------------------------------------DFSL-APV-T-P-CSR-
At1g05490   -------------------------------------------SANE-TPA-A-Q-CKK-
AtCLSY1     ----------------------rv-----------------dnEAFH-KAT-C-D-CE--
At5g20420   ----------------------rv-----------------dnEAFE-KAR-S-G-CE--
Cp19.123    ----------------------rv-----------------syENIQ-KTT-E-V-CQ--
Pt567214    ----------------------rv-----------------stQTTQ-NSS-E-C-CQ--
Pt832603    ----------------------rifffitvsdwlkdlqallstRTTQkN-------CQ--
Vv29366     ----------------------ev-----------------vqESSN-ISE-Q-V-CQ--
Bd1g16720   ----------------pdsedvhe-----------------stARLG-KNG-EiP-CY--
Os07g49210  tltddyrcyyqkkekfaesgsvne-----------------stDYFG-KVG-GiP-CH--
Sb02g43870  ----------------tdseadhe-----------------snTDLG-KRG-E-H-CH--
ZM108166    ----------------tdsevvhe-----------------snTDLG-KGG-E-H-CH--
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ZM000342    ----------------tdsevvhe-----------------snTDLG-KGG-E-H-CH--
Sm441121    ------------------------------------------------------------

                            1580                1600                1620
Bd2g21450   -CNHQIVIREDLGHVCRVCGMIVRKAD--TIFDY---------Q----------------
Bd2g21430   -CNHQIEIHEDLGHVCRICSMIVRKAD--MIFDF---------E----------------
Sb07g02945  -CNHDIRIHEDLGHVCRVCGMIVRRAD--SIIDY---------Q----------------
ZM064574    -CNHDIRIHEDLGHVCRVCGMIVRRAD--SIIDY---------Q----------------
ZM093940    -CNHDIRIHEDLGHVCRVCGMIVRRAD--SIIDY---------Q----------------
Bd3g19890   -CNHDIRIHEDLGHVCRVCGLIVRRAD--TIIDY---------Q----------------
Os06g14440  -CNHDIRIHEDLGHVCRICGMIVRKAE--TIIDY---------Q----------------
Os07g25390  -CNHDIRIHEDLGHVCRICGMIVRKAE--TIIDY---------Q----------------
Os08g14610  -CNHDIHVYEDLGHVCHECGLVVRKAD--SLFHY---------Q----------------
Bd3g18910   -CNHDICLHEDLGEVCRVCGMIVRSAD--KIFDY---------C----------------
Vv23895     -CEHSFVLKDDIGSVCRICGVVNKSIE--TIIEY---------Q----------------
Vv35918     -CEHSFVLKDDIGSVCRICGVVNKSIE--TIIEY---------Q----------------
Pt195587    yCDHSFVLKDDIGYVCRICGVIERAIY--TIIEI---------Q----------------
AtDRD1      -CEHSFILKDDMGYVCRVCGVIEKSIL--EIIDV---------Q----------------
Bd1g74070   -CHHDFLMRDDLGLVCRVCGLIKKPID--TIIEC---------Q----------------
Os03g06920  -CQHDFLMKDDLGIVCRVCGLIQQRIE--NIFEY---------Q----------------
Sb01g46180  -CNHDFLLKDDLGMVCRICGLIQQRID--KIFEH---------S----------------
At2g21450   -CDHSFICKDDIGEVCRVCGLIKKPIE--SMIEV---------V----------------
Sm84719     -CDHEFVFREDCGKVCEICGRVVKLVS--DVFDV---------S----------------
Vv15867     -GNHQLVLDEQIGMTCCFCSFVQLEIK--YILPS---------F----------------
Pt286483    -GNHELYLDEEIGLLCKYCSFVDLEIK--YYVPP---------F----------------
Cp76.2      -GSHHLILDEEIGVKCKYCCFIQQEIK--YIVPP---------F----------------
At3g24340   -GTHDFVLDDEIGLKCVHCAYVAVEIK--DISPA---------M----------------
ZM178435    -GQHEFIIDEQIGVRCKHCHVVDLEIR--DVLPT---------L----------------
Sb04g33300  -GQHEFIIDEQIGVRCKHCNVVDIEIR--HVLPT---------L----------------
Os02g43460  -GKHELIIDEQIGLRCKHCNFVDLEIR--FVLPS---------M----------------
Bd3g50300   -GKHDLVTDEQIGVWCRRCNFIQLEIR--HVVAD---------M----------------
Bd2g43500   -GKHDLIMDEQIGIRCKHCDFIDLEIR--DVFPS---------M----------------
Os05g32610  -GKHEFIIDEQIGIRCKYCSLVNLEIR--FILPL---------L----------------
Bd2g26500   -GKHEFIIDDQIGIRCKYCSLVNLEIR--FVLPS---------M----------------
RMR1        -GKHEFVIDDQIGIRCKYCSLVNLEIK--FMFPS---------L----------------
Sb09g19410  -GKHEFIIDDRIGIRCKYCSLVNLEIK--FMFPS---------L----------------
At1g05490   -GKHDLCIDLEVGLKCMHCGFVEREIRsmDVSEW---------G----------------
AtCLSY1     ---HDYELNEEIGMCCRLCGHVGTEIK--HVSAP---------F-------ar-------
At5g20420   ---HDYRLEEEIGMCCRLCGHVGSEIK--DVSAP---------F-------ae-------
Cp19.123    ---HSYRLNEEIGMCCFLCGFISTEIK--YMTAP---------F-------me-------
Pt567214    ---HEFKLDEEIGILCHKCSFVKTEKK--YVSAPfvfsvfllsF-------ms-------
Pt832603    ---HEFKLDEEIGILCQICGFVKTEIK--YVSAP---------F-------mehtgwtae
Vv29366     ---HEYILDEEIGVLCQLCGFVSTEIK--DVSPP--------------------------
Bd1g16720   ---HDCILDEELGLMCRLCNVVCIEAK--DIFPQ---------M-------fn-------
Os07g49210  ---HECILDEELGLACRLCNVVCTEAK--DIFPE---------M-------fn-------
Sb02g43870  ---HDCMLDEQLGLTCRLCNVVCTEAK--DIFPP---------M-------ft-------
ZM108166    ---HDCMLDEQLGLTCRLCNVVCIEAK--DIFPP---------M-------ft-------
ZM000342    ---HDCMLDEQLGLTCRLCNVVCIEAK--DIFPP---------Mvasnsnqft-------
Sm441121    ---HDYVLNELVGLICSVCGYVGIPIE--EMAPH---------Pd---------------

                            1640                1660                1680
Bd2g21450   ---------------WEK-----E-SR-P-RSY-------LYG------TRSKDAGEIV-
Bd2g21430   ---------------WRKv----S-SR-S-RSY-------FKE------TRSS---EIV-
Sb07g02945  ---------------WKK-----A-SR-R-KTN-------SYG------GHSKDADEID-
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ZM064574    ---------------WKK-----A-SR-R-RTN-------GYG------GHSKDADEID-
ZM093940    ---------------WKK-----A-SR-R-RMN-------GYG------GNSKDADEID-
Bd3g19890   ---------------WKK-----A-SR-S-RSY-------FCG------TRSKDADEII-
Os06g14440  ---------------WKK-----A-SR-T-RTN-------YYE------SRSKDADEID-
Os07g25390  ---------------WKK-----A-SR-T-RTN-------YYE------SRSKDADDID-
Os08g14610  ---------------WKK-----A-SR-K-RTN-------VNE------VCLK---KVG-
Bd3g18910   ---------------WWK-----QlSR-K-RSG-------THE------AGSKNADQIEd
Vv23895     ---------------YSK-----V-KR-S-RTY-------MYE------PRNTKDREPT-
Vv35918     ---------------YTK-----V-KR-S-RTY-------MYE------PRNTKDREPT-
Pt195587    ---------------FNK-----V-KRnT-RTY-------ISE------SRNAKDRDS--
AtDRD1      ---------------FTK-----A-KRnT-RTY-------ASE------TRTKRFGESD-
Bd1g74070   ---------------WKK-----P-KQ-SyRTY-------PSG------HRNSNDLDTP-
Os03g06920  ---------------WKK-----R-KQ-SyRAR-------PSE------HRNSSDADAI-
Sb01g46180  ---------------WKK-----R-NQ-AyRSY-------PIK------QRNSGDPDAT-
At2g21450   ---------------FNK-----Q-KR-SrRTY-------MRE------KENGETSRDF-
Sm84719     ---------------IISflsfpA-RK-A-SSR-------PAT------KKLKLHEDYA-
Vv15867     ---------------SRN-----P-WG-G-SEK-------GNAg-kedcNSIFDELQFQk
Pt286483    ---------------DRY-----P-RG-K-SARrdfvtmqHN---------IFNDLHHQ-
Cp76.2      ------------------------------------------------------------
At3g24340   ---------------DKY-----R-PS-V-NDN-------KKCs-drkgDPLPNRLEFDa
ZM178435    ---------------GKC-----S-AE-R-GSA-------INPefdrmlKEMLNVFEQNd
Sb04g33300  ---------------GKF-----S-AE-R-ESA-------IDPeldkmlKEMLSVFEQNd
Os02g43460  ---------------VKS-----C-TE-R-DMR-------KDHeldlff---------Dd
Bd3g50300   ---------------VS-------------HYS-------LQHaftktlSEL--DLSINn
Bd2g43500   ---------------VKF-----S-IE-R-EPA-------MSLnldlfc---------Ed
Os05g32610  ---------------ASN-----F-AE-K-PAW-------RNS------SCLKTALMCPd
Bd2g26500   ---------------VSN-----Y-AE-K-SAW-------RNS------SCLKDALMYHd
RMR1        ---------------VSV-----F-AE-K-SAW-------PND------KGVKNTLMFHd
Sb09g19410  ---------------ISG-----F-AE-K-SAW-------PNA------KGVKDTLMFHd
At1g05490   ---------------EKT-----T-RE-R-RKF-------DRFe-eeegSSFIGKLGFDa
AtCLSY1     ---------------HKK-----W-TT-E-TKQ-------INEd-dintTIVNQDGVESh
At5g20420   ---------------HKK-----W-TI-E-TKH-------IEEd-diktKL-------Sh
Cp19.123    ---------------FRS-----Y-VA-E-NRW-------ENEe-dnknMTYAGRELN--
Pt567214    --p-------l----DRQ-----V-SM-Q-GRH-------FL----fviRGYSARNPIAh
Pt832603    skpqneedlelkpdeDEG-----S-SL-F-GNH------------------TSGED----
Vv29366     ------------------------------------------------------------
Bd1g16720   ---------------GNG-----Y-----------------NKd-rpgcSNFFHDDHVLd
Os07g49210  ---------------GND-----Y------------------Kd-rpgcSNICLDDDILd
Sb02g43870  ---------------GKD-----H-------------------k-rleqSHFGQDDHVLd
ZM108166    ---------------GKD-----H-------------------e-rperNHFGQDGHVLd
ZM000342    ---------------GKD-----H-------------------e-rperNHFGQDGHVLd
Sm441121    ---------------WSF-----R-LP-Q-NVL-------ENP------DPFIRRPELN-

                            1700                1720
Bd2g21450   ------------VG----NVTVSE-DLI--------ALDVAIHPRHAQHIKP
Bd2g21430   ------------LG----NVTVYE-DLT--------ALDVAIHPRHAQHIRP
Sb07g02945  ------------CG----TVKLSE-DFI--------IADVAIHPRHAQTMKP
ZM064574    ------------CG----TVKLSE-DFI--------VADIAIHPRHARIMKP
ZM093940    ------------CG----TVKLSE-DFI--------VADIAIHPRHAQAMKP
Bd3g19890   ------------IG----DIRVSD-DLL--------ALDIAIHPRHKKQIRS
Os06g14440  ------------TG----AVKVSE-DFI--------VSDIAIHPRHAKQMRP
Os07g25390  ------------TG----AVKVSE-DFI--------VSDIAIHPRHAKQMRP
Os08g14610  ------------SD----AISLSE-DFI--------FSDIAIHPRHAKNIRP
Bd3g18910   fg----------SA----TASAYE-DFI--------FEDAAIHPMHAKEIRL
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Vv23895     ------------DDpsdgLRFSEH-SLI--------VTEIHAHPRHSMQMKP
Vv35918     ------------DDpsdgLGFSEH-NLT--------VTEIHAHPRHSMQMKP
Pt195587    -------------NgtvgADLFEE-DLM--------VTDIPAHPRHMKQMKP
AtDRD1      ------------NE----LKFSEE-GLM--------IGGLAAHPTHAAEMKP
Bd1g74070   ------------IN----LSRNIL-QML--------PDPLSIHPQHLQQMKP
Os03g06920  ------------DK----TSGAIL-EVV--------PDALCLHPQHSQHMKP
Sb01g46180  ------------MN----ALGTIL-SVA--------PDTLSLHPQHSEQMKP
At2g21450   ------------SG----IQSSHT-NIL--------GEKMFIHPWHDQEMRP
Sm84719     ------------WK----STLNFG-DVT--------V-DLVPHPMDSARMYP
Vv15867     -------pgcgsQS----GSDHGL-HPE--------GTVWDIIPGIRNSMYR
Pt286483    ------------DS----G--HDT-HPDydpctlvqGTVWNLIPGIGKGMHG
Cp76.2      ---------------------------Q--------GTVWDMIPGVKDSMYP
At3g24340   -------sdpssFV----APLDNI---E--------GTVWQYVPGIKDTLYP
ZM178435    vl-----vsnghEL----PCNFGD-HKA--------GSVWNLIPGVKETMFP
Sb04g33300  vl-----vsnghEL----PCNFGG-HKA--------GSVWDLIPGVKETMFP
Os02g43460  il-----tsagyEG----PRDFGG-KKT--------GLVWDLVPGVREDMFP
Bd3g50300   ll-----tsmgyEG----TCKIVD-HKA--------GSVWDLIPGVKEGLFT
Bd2g43500   ii-----ksmgyEG----TSHFDI-HES--------GLVWDLIPGVREHMFP
Os05g32610  ly-----eqtgtGD----GQSQDF-HIN--------GTVWDLIPGVITDMYQ
Bd2g26500   lc-----eqagsID----GQSQGF-HPY--------GTVWDLIPGAINTMYQ
RMR1        ly-----eqgvnDT----EQSQDI-HQY--------GTVWNLIPGVISTMYE
Sb09g19410  ly-----eqtgsDI----EQISDL-HQY--------GTVWDLISGVISTMYE
At1g05490   -------pnnslNE----GC---V-SSE--------GTVWDKIPGVKSQMYP
AtCLSY1     ----t--ftipvAS----SDMPSA-EES--------DNVWSLIPQLKRKLHL
At5g20420   keaqtkdfsmisDS----SEMLAA-EES--------DNVWALIPKLKRKLHV
Cp19.123    -------lvgnhTS----HERLLT-EEN--------DNVWALIPELRNKLHL
Pt567214    ----l--fnvckIS-----PLVPF-EVN--------DNVWDLIPELRAKLHM
Pt832603    ---------------------VPVsEVN--------DNVWDLIPELRPKLHM
Vv29366     ----------------------------------------------------
Bd1g16720   ----p--sllatFA----PEFSEP-RGS--------GNLWSLIPDLEPKLLP
Os07g49210  ----p--sllanLA----PELSEL-KNS--------GSVWSAISDLDPKLLP
Sb02g43870  ----l--sffeiCA----PESSKS-KES--------GNVWSSIPVLEPKLLA
ZM108166    ----l--sffeiCA----PEFSKI-KES--------GNVWASITDLEPKLLA
ZM000342    ----l--sffeiCA----PEFSKI-KES--------GNVWASITDLEPKLLA
Sm441121    ------------DL----NDDLAD-DPY--------FPSTDT----RRSLHA
```

(C) MUSCLE

```
                               20                  40                  60
Sb02g43870  ------------------------------------------------------------
ZM000342    ------------------------------------------------------------
ZM108166    ------------------------------------------------------------
Os07g49210  MAGKKMSGEVRSVPAFDFAEWLKRTVSEQDYVVMKMDVEGTEFDLIPRLFDTGAICLIDE
Bd1g16720   ------------------------------------------------------------
Sm441121    ------------------------------------------------------------
At5g20420   ------------------------------------------------------------
AtCLSY1     ------------------------------------------------------------
Vv29366     ------------------------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    ------------------------------------------------------------
Pt832603    ------------------------------------------------------------
Sm84719     ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Bd1g74070   ------------------------------------------------------------
```

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Sb01g46180      ------------------------------------------------------------
Bd3g18910       ------------------------------------------------------------
Os08g14610      ------------------------------------------------------------
Os07g25390      ------------------------------------------------------------
Os06g14440      ------------------------------------------------------------
ZM064574        ------------------------------------------------------------
ZM093940        ------------------------------------------------------------
Sb07g02945      ------------------------------------------------------------
Bd3g19890       ------------------------------------------------------------
Bd2g21450       ------------------------------------------------------------
Bd2g21430       ------------------------------------------------------------
At2g21450       ------------------------------------------------------------
AtDRD1          ------------------------------------------------------------
Pt195587        ------------------------------------------------------------
Vv23895         ------------------------------------------------------------
Vv35918         ------------------------------------------------------------
At1g05490       ------------------------------------------------------------
At3g24340       ------------------------------------------------------------
Bd2g26500       ------------------------------------------------------------
Os05g32610      ------------------------------------------------------------
RMR1            ------------------------------------------------------------
Sb09g19410      ------------------------------------------------------------
Pt286483        ------------------------------------------------------------
ZM178435        ------------------------------------------------------------
Sb04g33300      ---------------------------MPAPPSAVPGKGRTKPREIIVIDSDEEGVGGGG
Bd3g50300       MPPAADFPASKRKSRIEIPDSDDDADRRRESRSSVGTGGQRERSAEAGRSGGLERRLAAA
Os02g43460      MPRRKGKGKGVEDEVEVYEPASPPERVLIILDSSEDDLDLQEVRRSLMITGRGRARAAER
Bd2g43500       ------------------------------------------------------------
Cp76.2          ------------------------------------------------------------
Vv15867         ------------------------------------------------------------

                                  80                 100                 120
Sb02g43870      ------------------------------------------------------------
ZM000342        ------------------------------------------------------------
ZM108166        ------------------------------------------------------------
Os07g49210      LFLECHYNRWQKCCPDRAEAFEMAKGVSCFYWSIQFPNFKDHLCFRNCSNASSTRHFSYR
Bd1g16720       ------------------------------------------------------------
Sm441121        ------------------------------------------------------------
At5g20420       ------------------------------------------------------------
AtCLSY1         ------------------------------------------------------------
Vv29366         ------------------------------------------------------------
Cp19.123        ------------------------------------------------------------
Pt567214        ------------------------------------------------------------
Pt832603        ------------------------------------------------------------
Sm84719         ------------------------------------------------------------
Os03g06920      ------------------------------------------------------------
Bd1g74070       ------------------------------------------------------------
Sb01g46180      ------------------------------------------------------------
Bd3g18910       ------------------------------------------------------------
Os08g14610      ------------------------------------------------------------
Os07g25390      ------------------------------------------------------------
Os06g14440      ------------------------------------------------------------
ZM064574        ------------------------------------------------------------
ZM093940        ------------------------------------------------------------
```

```
Sb07g02945      ------------------------------------------------------------
Bd3g19890       ------------------------------------------------------------
Bd2g21450       ------------------------------------------------------------
Bd2g21430       ------------------------------------------------------------
At2g21450       ------------------------------------------------------------
AtDRD1          ------------------------------------------------------------
Pt195587        ------------------------------------------------------------
Vv23895         ------------------------------------------------------------
Vv35918         ------------------------------------------------------------
At1g05490       ------------------------------------------------------------
At3g24340       ------------------------------------------------------------
Bd2g26500       ------------------------------------------------------------
Os05g32610      ------------------------------------------------------------
RMR1            ------------------------------------------------------------
Sb09g19410      ------------------------------------------------------------
Pt286483        ------------------------------------------------------------
ZM178435        ------------------------------------------------------MPAPPS
Sb04g33300      RQAGRDLGSGAAIGAAGEAVKLVKPEPVDDAGFHPVLPGAPRLGAVPVPPRAQNPRAPSS
Bd3g50300       IARRRTRAAAASRPEVVNLTGDDDDDIRDEEAAGRR------------------------
Os02g43460      VGEEAPRGSGRRAAPVVASRRRRRRSRSRSRSPRAARPRAESSRRPTARRARARARSPSL
Bd2g43500       ------------------------------------------------------------
Cp76.2          ------------------------------------------------------------
Vv15867         ------------------------------------------------------------

                                 140                 160                 180
Sb02g43870      ------------------------------------------------------------
ZM000342        ---------------------------------------------MMIKKKSGRCHLLAG
ZM108166        ------------------------------------------------------------
Os07g49210      SLLIRTEKPVTTRNHAYAEVVVFVLDQNPMFFLFLRFFYPAIQRGPNCWSSANSTVMRQA
Bd1g16720       ---------------------------------------MAGKTLKGPSRAAGHPICATP
Sm441121        ------------------------------------------------------------
At5g20420       -------------------------------------------MKKRGFYNLKHPFDPCP
AtCLSY1         -------------------------------------------MKRKHYFEFNHPFNPCP
Vv29366         ------------------------------------------------------------
Cp19.123        -------------------------------------------MRKRRLYESRHPFGLHP
Pt567214        -------------------------------------------MKRKHLHQSKHPYNAHP
Pt832603        -------------------------------------------MKRKRLHQSKHPFNAHP
Sm84719         ------------------------------------------------------------
Os03g06920      ----------------------------------------------------------MA
Bd1g74070       ------------------------------------------------------------
Sb01g46180      ------------------------------------------------------------
Bd3g18910       ------------------------------------------------------------
Os08g14610      ------------------------------------------------------------
Os07g25390      ------------------------------------------------------------
Os06g14440      ------------------------------------------------------------
ZM064574        ------------------------------------------------------------
ZM093940        ------------------------------------------------------------
Sb07g02945      ------------------------------------------------------------
Bd3g19890       ------------------------------------------------------------
Bd2g21450       ------------------------------------------------------------
Bd2g21430       ------------------------------------------------------------
At2g21450       ------------------------------------------------------------
AtDRD1          ------------------------------------------------------------
Pt195587        ------------------------------------------------------------
```

```
Vv23895     ------------------------------------------------------------
Vv35918     -----------------------------------------------------MEPTNGG
At1g05490   --------MECIGKRVKSRSWQRLQAVNKRKKMETVAPVTSPPKKRRQKKPKNYDSDIED
At3g24340   -------------------------------------------MDMTSCVARRTRSRTES
Bd2g26500   ---------------------------MDRSGRRGRARGRGETLAEASPRTRRRHAETIV
Os05g32610  -----------------------------MDRAARLARRGGVTVAEYRMVRGRRRGGDAG
RMR1        -----------MDRATPRVCGRRGVSQAAVEAAPSSSRARRRDKAPAVVMDLGDDDCGGG
Sb09g19410  ---------MDRAAPRARGRRRRGVSQAAPSSSRARRRDKAPVVVVDLGDDEDEDCGGGG
Pt286483    -----------------------------------------------MSKSPIGHRKPTP
ZM178435    TEAGRSRTMTRVIILLDSDKEDDGTGRQAGRELGGAAIASAGEASKLVKPEVVDDVGSNP
Sb04g33300  PRAQAQNPRAPSSPRTPSPRAPSLPSLVAAHPLGPGAPRLGVVPVPPRAQNPRAPSSPSP
Bd3g50300   --------------------------EVLGRVKEEPLDDRGLDPEASVARRGRGRGRARA
Os02g43460  EIIDVDSGSDRGVVRVKEEPRSGSDSDYNGARGRARARARAPVAATAAKKKKRKRGKEAP
Bd2g43500   ------------------------------------------------------------
Cp76.2      ------------------------------------------------------------
Vv15867     ------------------------------------------------------------

                             200                 220                 240
Sb02g43870  ------------------MVKGSTGHHNNPIGSV-LQHDIDGSYLRI-------------
ZM000342    HLELEDLTVDSTPLPFLPQGPNGQPIFFTVQRPVAVQHDIDGSYLRV-------------
ZM108166    ------------------MVKGSTGHHSNPIAPV-LQHDIDGSYLRV-------------
Os07g49210  FEVFYDGSWHGV--NCIRIRNGNLFVKFIYSGST-VEHNVDGDCLRL-------------
Bd1g16720   FEAFHHGSWHGV--NCIRVQNSRLFVRFVYSGST-VERNIDRDHLRL-------------
Sm441121    ------------------------------------------------------------
At5g20420   FEFFCSGTWKPV--EYMRIEDGMMTIRLLENGYV-LEDIRPFQRLRL-------------
AtCLSY1     FEVFCWGTWKAV--EYLRIENGTMTMRLLENGQV-LDDIKPFQRLRI-------------
Vv29366     -----------------MRIEDGTVALHLAESEYVIEEKSPIPNLRI-------------
Cp19.123    FEAFSRGSWRMV--DCIRIEDGTMSLRFVDGRHV-IKRKRPFSELRV-------------
Pt567214    FEALYGGSWQSVELIEIRDGAMTLHFADSHHR---IEEKGPFSNIRV-------------
Pt832603    FEALCCGSWQSVELIQIRDGAMTVHFVDSHHR---IEEKGPFSNVRV-------------
Sm84719     -----------------MASNGPCSAIHSCVMLQLSHTPLASKAVRF-------------
Os03g06920  RYPAPTSSRAIGAPIQPTEPHAPLPNTGGEGAPPPARTMPPPSSQAA-------------
Bd1g74070   ----------------------MDPSGCKRQKHEIEHDSSPGNQS---------------
Sb01g46180  ------------------MNLRGDYLSDKYTRMGSAGQKRQKLGSEH-------------
Bd3g18910   -------MGGEMPNANMTNCFMEQTEKKKYNVLLILDSPPKELIILD-------------
Os08g14610  ------------------------------------------------------------
Os07g25390  -----------------MAAAGRDPPATPSSRMYYCRQRKASSEVNA-------------
Os06g14440  ---------------------------MDLISMYYRRQRKASSEANA-------------
ZM064574    ------------------MSQSPGGREGIYYS---RQRKPERNGSVF-------------
ZM093940    ------------------MSQSPGGREGIYYSR--QRKPSERNGSVF-------------
Sb07g02945  ------------------------------------------------------------
Bd3g19890   ----------------------------MYYRR---------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
At2g21450   --------------------------------MFTAWNLRSRSRSIT-------------
AtDRD1      -------------MGFVYIVMTGYYKNVHKRKQNQVDDGPEAKRVKS-------------
Pt195587    -----------------------------------MKDT---------------------
Vv23895     -----------------------------------MHSEPKQKRQKA-------------
Vv35918     LSSNYGNPIPVNFEPYKLTEFNSTKHKRIWTFEENMHSEPKQKRQKA-------------
At1g05490   ITPTCNDSVPPPQVSNMYSVPNNSVKESFSRIMRDLNVEKKSGPSSSRLTDGSEQNPCLK
At3g24340   YLNSILNKSKGISGEEEDQSLGCVNSRTEKRRVNMRDACSPSPRKKK-------------
Bd2g26500   IDLDSEDGGGGSSTAAAAASSSSSRRSSAPLTLVTSGSVATRTRSRS-------------
Os05g32610  PVVVIDVEDDGEDAADDSAGGGGGAAAAVKRRVVVPGAVATRTRSRRMAMAQ--------
RMR1        GARKTVGGAAGRCEGSTKAPLPLLPPMMVPAGAVALRTRSRRRAMLAAAVVEEAPTKKKK
```

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Sb09g19410  GARKTVGGAAGGRGGSTEASPPPPPPMMVPAGAVAMRTRSRRRAMQAAAVVEETPTTKRR
Pt286483    YQTREANSNVPVTKDNIYSTHRSPSPSLQWTRLREAEVYKKLHDEIR-------------
ZM178435    VRPGALPTSLRVQGHRAPSSPSPVPAAVRKQPEIIAISDEDNDGSRF----RRVRRVKDE
Sb04g33300  VAPEDRHQPEIIAISDDDGGSRFRGAVPLDMIEESGRRVRPVKEEALDDLDCDWVRSAEA
Bd3g50300   AAASAPVASRKRRREDDSGSRGRGGRRATRSAKQCTRGRRGGLRSLP-------------
Os02g43460  SRAQESREVVRVKEEPNSDGNGAGGRARARSPVAAAAKQRKRGGREA-------------
Bd2g43500   -----------MPKNKSPLVETPRRRIRRLLIDDDDDDDDSGDGGRA-------------
Cp76.2      ------MEGKRLKLDNQPVARRTRLKEAQFFKEYYERRRKEDGKNVA-------------
Vv15867     ------------MDFSSPVAKRTRLQEALVYRRLYEEKKRNAGV----------------

                                     260                 280                 300
Sb02g43870  ---------------RSRKATCSDCSHVLKPGADVCVWQATY-------GGETK-DSV--
ZM000342    ---------------RSRKATCSDCSHVLKPGADVCVWQAVY-------RGETK-DSV--
ZM108166    ---------------RSRKATCSDCSHVLKPGADVCVWQAVY-------RGETK-DSV--
Os07g49210  ---------------RSRRATCSDCSNVLKPGVDVCVQSSHTPEASS--QGGTN-ASV--
Bd1g16720   ---------------RSRRATCFDCSHVLKPGVDVCVQSPHPLQACS--TGDQK-SSI--
Sm441121    ------------------------------------------------------------
At5g20420   ---------------RSRKAALSDCICFLRPDIDVCVLYRIHE------DDLEP-VWV--
AtCLSY1     ---------------RSRKATLIDCTSFLRPGIDVCVLYQRDE------ETPEP-VWV--
Vv29366     ---------------RPRKATLSDCTCFLRPGTEITVLWTLQQSESSDEENREP-VWI--
Cp19.123    ---------------RSRQANLTDCTCFLRPGIDVCVLIPSK-------DLASS-DEANL
Pt567214    ---------------KSRKSTLSDCTCFLRPGIDVCVLSFSERAKSSEEGNSEP-VWV--
Pt832603    ---------------KSRKATSSDCTCFLRPGIDVCVLSSSERAKNTGEGNSEP-VWV--
Sm84719     ---------------TLHLPEPIQPSSRPPPPCAARALLTSSSSYFL--SLPLD-EAA--
Os03g06920  ---------------TSTPPAAATPLQRPPAQATAQPSTQRYYVGVQRDKGTGK--WAAC
Bd1g74070   ---------------QATIISHNSSVRLR--------FLEQFDDLKY--ASATK-DYK--
Sb01g46180  ---------------TSSPGTQSQSNIFLANKRLRLQFLEQVNELKA--WSVTK-DLK--
Bd3g18910   ---------------SDDEDGNSGKTQVPSYPTKELIILDSNDRKTLLPPYPTK------
Os08g14610  ---------------MSGSGNSLDTVALIV-------------------GGGSD-SSGIV
Os07g25390  ---------------NVFVPGGQNGISFP--------ASNRAHDWGY--GGVRE-EWE--
Os06g14440  ---------------NVFMPGGPNDISFP--------ASNRDHDWGY--GGVGK-EWE--
ZM064574    ---------------TPIAAMYSSGHALP--------VANRSHGLVF--GSLSK-DWD--
ZM093940    ---------------TPIAAMYPSGHALP--------DANRNHSLVF--GGTSK-DWD--
Sb07g02945  ------------------------------------------------------------
Bd3g19890   ---------------KNRASDPISGLSLP--------AGSGVHSWGC--GSVTK-DME--
Bd2g21450   ------------------------------------------------------------
Bd2g21430   -------------------------------------------------MDAAA-AAT--
At2g21450   ---------------QEELAKRPDPFCLP-------NLLDGLEDGLY--GRLAD-DVK--
AtDRD1      ---------------SAKVIDYSNPFAVS-------NMLEALDSGKF--GSVSK-ELE--
Pt195587    ---------------KEKVTDYAKPFAIR-------GLLERLDSGRY--GSVTD-DIR--
Vv23895     ---------------GSNVVDYSDPFAIP-------NLLEGLDAGKF--GSMTK-EIE--
Vv35918     ---------------GPNVVDYSDPFAIP-------NLLEGLDAGRF--GSVTK-EIE--
At1g05490   ERSFRVSDLGVEKKCSPEITDLDVGIPVPRFSKLKDVSEQKNTCLMQKSSPEIA-DLDLV
At3g24340   ---------------RRRRKDDDDDVVFVRTEYPEGKRDDENVGSTS--GNLQS------
Bd2g26500   ---------------LAMKSPVAEAEAAPRAKRRRKGTSAEADGGGGSKGAEASESASKG
Os05g32610  ---------------QAPVTPPAAAEEAPSRRRKRKGAASAEAGGGGPSKRRVRSSGSAG
RMR1        KEGAIPDAAEAPRGHGSKAAATSMATSSHKRRAGTSRSTSRDKRRAR--SGRASEPARVG
Sb09g19410  KRGATTPDAAEASRGRGSKAAAASRATSRDKRRAGASRSTSRDKRRARSGRASE-PARAA
Pt286483    ---------------KGRNQGKESNAAATGSTNGLNGAQEESVGGLS--YKGSK-SPVVL
ZM178435    ASDWVLSAKAKRAMVSGVPPGSSDVKRKRKRGSSGAGDFHALDRNLSASGAGRRTSWMAE
Sb04g33300  KRALVAVLPPGSSHAKRKRKRASSGRAKPDKRADGGVHALDRNSSASG-AGHPT-AWMSD
Bd3g50300   -----------SRPSSSDEPLGDSGRAKRVRRGHAEGGGSGRHGAAP--SKQAG-SLVAS
Os02g43460  -------------------PSRAQESRVPVQIKEEPYSGSDSDGNVA--GGRAV-VPAAD
Bd2g43500   ---------------REAISPSVAAGGSRRVGAEISGWLVRDPLAPS--SSAQP-GTLLR
```

```
Cp76.2      ------------RPSGQSEDRGVNGSKLGRVGLKGTNMETRDLGLNC--KGSAGLENRAR
Vv15867     ---------------SSSGSHNDDGVEFL--------------------GEA--------

                             320                 340                 360
Sb02g43870  -PLCRDARLIKIKRN---HQLDRCLCLFAVIFYKDQCPGSKEK-----------------
ZM000342    LLCCRDARLIKIKRN---HQSDRCLCLFAVIFYKDQCPGSKEK-----------------
ZM108166    LLCCRDARLIKIKRN---HQSDRCLCLFAVIFYKDQCPGSKEK-----------------
Os07g49210  -LLRHDARLITIKKN---HQEDKCLCLFVVILYKNQCPGNAEK-----------------
Bd1g16720   -SLCHDARIVTIKRN---HNADQCLCLFLVILDDSQCPGNTEKGG---------------
Sm441121    ------------------------------------------------------------
At5g20420   -----DARIVSIERK---PHESECSCKINVRIYIDQGCIGSEK-----------------
AtCLSY1     -----DARVLSIERK---PHESECLCTFHVSVYIDQGCIGLEK-----------------
Vv29366     -----DAKISSIERR---PHEPECSCQFFVNFYITQDPLGTEK-----------------
Cp19.123    ELVLIDAKIRSIERK---PHESQCSCQFYVNLYVNQGPLGSEK-----------------
Pt567214    -----DARINSIKRK---PHESQCSCQFFVNLYVNQGPLGSER-----------------
Pt832603    -----DAKISSIKRK---PHVSHCSCQFFVNLYVNQGPLGSER-----------------
Sm84719     SLENHLSIVVAVDGE---TSRTERLNLCSTEYTLCSC-----------------------
Os03g06920  VVDPSNPTKHRLVGAFPDEHAAALAHDRLDLAFRGGGH----------------------
Bd1g74070   AVNAKMHELLSTLEK---LKEVPIKLPYVSPVLKTSD-----------------------
Sb01g46180  AITAKRRELFGIIER---LRQVPIEQLYSSPFPKPSD-----------------------
Bd3g18910   -----ELIILDSYDE---DRNPPCQRKRKISEVSSQVN----------------------
Os08g14610  GRKRRRCDLI--------RERWCCLCP---------------------------------
Os07g25390  ASYARKLQLINFLSS---LHQRTANSLITTRMDANMD-----------------------
Os06g14440  ASYARKLQLMNFLSS---LHQRTANPLVTTRMDANMD-----------------------
ZM064574    DIRQRKDQLVNFLAS---LERASGDSAAAGKIED--------------------------
ZM093940    -------NIRQFIAS---LERASENSSAIASKTGGG------------------------
Sb07g02945  ------------------------------------------------------------
Bd3g19890   DIYARNVQLINFLST---LHEPTRSSVPMVETNVKYCS----------------------
Bd2g21450   ------MEMLKLPQE---KEREKTIC----------------------------------
Bd2g21430   KIFRRNHRLPPVVQQ---KRFPPSGGASFLPPRCEALS----------------------
At2g21450   ----RLCKLRQEYLN---------------------------------------------
AtDRD1      EIADMRMDLVKRSI----WLYPSLAYTVFEAEKTMDN-----------------------
Pt195587    SLFYRRAQL---------IHPCLAMHPTLSNEPRGRG-----------------------
Vv23895     ALCARRMQMLHPYY----VMYPSLSYMSTDLGKQPSK-----------------------
Vv35918     ALCARRMQMLQPYY----VMYPSLSYMCTDLGKKQGK-----------------------
At1g05490   ISVPSSSVLKDVSEE---IRFLKDKCSPEIRGLVLEKSVPGEIEILSDSESET-------
At3g24340   KSFDFGDRVCDFDAD---DRNLGCEEKASNFNPIDDD-----------------------
Bd2g26500   NRRGRSRTASEPPDRALARKSKDADAEEEAEAEAEEEAEAE-------------------
Os05g32610  GRGARKRKEAEADEEEAEAEAEEEAEAEAGTPARGESMEVSQVDGGG-------------
RMR1        RARKRKRNELEAPAR---RERVKAPCVSESDDNSGRGDDASHDGDAEPRVG---------
Sb09g19410  RACKRKGIELGAETE---VDAPARSERAKAPCVSESDDDGGRGDDASDDGNAEPRAGVAI
Pt286483    DDSEDDAFLDDCEKG---GLEEGLDVVSLDDSDDDDQSEGVESKSF--------------
ZM178435    DAGSSRNVSSSELSRGGVGDRSGSTKKARGAPGKTRRGGGTRRE----------------
Sb04g33300  DARSSRGVKSRESSRGVAGDRPGSAKKALVSSEESRGAPGKARSGGGARRERSTSVAPAN
Bd3g50300   SSRSRKGKQRAALPP---KHQFPLVSQSESSSESDDDDDDEEGDDGLDDVCSETSDESWQ
Os02g43460  AKQGKRGKKTPSRGK---GRRVVVRETSTPAAPSNGAPSVGRGKGRGPGRGRQRSKGAVR
Bd2g43500   SREQEQPEIIVISDD---DHEDEEEDGARGGEIRHGEIPA--------------------
Cp76.2      RIKTREKVTDENKDR---VREMNAKDCGDLNPEKCRDVIVIDD-----------------
Vv15867     GVFDSVQKFVAESDG---KNSDRKNSSRKKNGGENSD-----------------------

                             380                 400                 420
Sb02g43870  ------------------VISGTIADVVTIDDVCILQNLQSEELQD-------------G
ZM000342    ------------------VISGTIADVVTIDDICILQNLQPEELQD-------------G
ZM108166    ------------------VISGTIADVVTIDDICILQNLQPEELQD-------------G
```

```
Os07g49210  ------------------VITDRRAEVVTINDIFLLQKLQPEVHE--------------G
Bd1g16720   ------------------KATDRRQEVVTLNNIFLLQKLQPKELQE-------------G
Sm441121    ------------------------------------------------------------
At5g20420   ------------------QRINRDSVVIGLNQISILQKFYKEQSTD-------------Q
AtCLSY1     ------------------HRMNKVPVLVGLNEIAILQKFCKEQSLD-------------R
Vv29366     ------------------GTLSKDISVVELDQISILQKLGKYPCED-------------E
Cp19.123    ------------------LELDKDTKVLGIDQILILQRLEKHPCEG-------------Q
Pt567214    ------------------ATLSKETEAVGIDQISILQKLDNDPCEADN------NRHETQ
Pt832603    ------------------ARLSKETEAVGINEISVLQKLDNDPCEADN------NQQEAQ
Sm84719     ---------------------PAFKLSSSYEAVCEEQDLAEDDASKDT------EISHSS
Os03g06920  ------------------RGAGDNFRPAFHAVELEFLRLCAATSSPGSHCGLVAGGDKYD
Bd1g74070   ------------------ARLHSATQSGSNFSSDNIIDLDPDNV---------------G
Sb01g46180  ------------------ARLDNFGKMESSYNPDNVINLDADEENV-------------E
Bd3g18910   ------------------RDASNDPRQKKLKNEPTYFGFDEPMEKKKN-----------P
Os08g14610  --------------------------VWCKEAQEVVVPGRGR-----------------N
Os07g25390  -----------------------TPLEQKQKDSSAIIVLDSDDEDE--------------
Os06g14440  -----------------------TPLEQKQKDSSAIIVLDSD----D------------E
ZM064574    ------------------SKLASPVEPTEQKEKAAIIVLDSDD----------------E
ZM093940    ------------------KSTNHSVEPAEQKGKGDIIVLDSDDED--------------G
Sb07g02945  ------------------------------------------------------------
Bd3g19890   ------------------IKQETKVTDCSVKQTEPILIPDSDDEDG--------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   -----------------------------------------------------------V
At2g21450   -----------------------------------------------------------G
AtDRD1      -----------------------------QQVVEGVINLDDDDDDD-------------T
Pt195587    --------------------------MSFGEGKCNVIDLDDDEIEG--------------
Vv23895     ------------------KASKLVNRHASHLGHEDVIDLEDD------------------
Vv35918     ------------------KASKLVNREASHLAHEDVIDLEDD------------------
At1g05490   ------------------EARRRASAKKKLFEESSRIVESISDGEDSS------SETDEE
At3g24340   ---------------------DDVVFVGTVQRENDHVEDDDNVGS--------------A
Bd2g26500   ------------------APACGKRVEVSRVDGCANSERGEDPLDDHNNGSNAREACGIG
Os05g32610  ------------------SSGRADDASHNGNGESRVCNADGIDQASEERPSVAGGDLIEE
RMR1        ------------------VAIGTDLVNGDHPAAKEVVEGAGDEDTGDG------GNSGLA
Sb09g19410  GADLVNGDRRTAKGEDHIEEHGGDQENSAVNLNDDLVSGDAEAVEGAGDEDTRGNSGL-A
Pt286483    ------------------DVGGKKSGGTDVGGSCSGVKSDGEESGRSKVPLPRWQRIVNE
ZM178435    ------------------RSTSAAPANLVGGSATVGSRIRLRSRQQGRVQCATYSARVSS
Sb04g33300  WIGTSIGSR---------IRSRSRKQGTGQYSARVSSEDTGEDEVQEQ------KQKRVE
Bd3g50300   PRYNSEFQVAMKGEKKVEGRRNSVEEEATEKELGENGNGIPVLEEAAE------KELREN
Os02g43460  GRATPVNRVSTGVGSRTRSRLAEQGRAFAQEEEEQVEEREEEEEEEE------------Q
Bd2g43500   ------------------RVKDEESEEGSSVDWDALMLSDDESTAA--------APPGTA
Cp76.2      ------------------DDNEAIAADASGDDDDDCDENHDDEDDD-------------G
Vv15867     ---------------------EDVTDVVSISDDSEASDYEEEEDDDDD------DYIVDP

                             440                 460                 480
Sb02g43870  SVQWNSAVDCFHHNRSKLL-SARFSLEVAYLIVLSSLRGMEFSIKLVDGNIIYQIIK---
ZM000342    SVRWNSAVDCFHHNRSKLL-SARFSLEVAYLIVLSSLRRMEFNIKMVDGNIIYQIIK---
ZM108166    SVRWNSAVDCFHHNRSKLL-SARFSLEVAYLIVLSSLRRMEFNIKMVDGNIIYQIIK---
Os07g49210  SMKWSFSKDRLSLNKGRLIS-ARFSSEITHLIVLSILRGMEFNIKLVEGQIVYQIIK---
Bd1g16720   SVQWNSAEDCLYQNRSRLLSAARFSSEISHLIVLSALRGMEFSIKLVEGNIIYRVIK---
Sm441121    ------------------------------------------------------------
At5g20420   FYRWRFSEDCTSLMKTRLS-LGKFLPDLSWLTVTSTLKSIVFQIRTVQTKMVYQIVT---
AtCLSY1     YYRWRYSEDCSSLVKTRL-NLGKFLPDLTWLLVTSVLKNIVFQIRTVHEKMVYQIVTDED
Vv29366     HYRWKFSEDCSLLQRTKLF-LGKFSSDLSWLVVTSVLKQAVFDVRSVQNRIVYQIVG---
Cp19.123    YYRWSLSEDCSSLSRTKLF-LGKFSSDLSWLLVASVLKQVAFEVRTEQYKIVYQILA---
```

```
Pt567214    FYRWEFCEDCSLVQRTSIPKQVAFDVRSVQNKIAYQIFGGDDDHCSLKSNNHINCVTFKV
Pt832603    FYRWEFCEDCSLVQRSKLF-LGRFSADLTWLLVASVLKQVEFNVRSVQNKIVYQILG---
Sm84719     ALRQSKVSPLTTELTKLSLSSSFEAIHRERASDPSESSKPDLALLDFHGFHLH-------
Os03g06920  EKYSEFLRKIYHGVMDNSPSYKKFFDVILDFFIARAREIGREALEDGGDMLVERFVAMHK
Bd1g74070   DHTHPNMENTGAHNTTYLVDSGDGDMIKSI------------------------------
Sb01g46180  YHTQVNAGNTEADSTASADDSGDKDRVKSFGDENSSSNR---------------------
Bd3g18910   RKESDCHFNLAVPSKKLLLSNLWPSESLNKLIIQPKQSEEVANDEVFNDETQNESECFMD
Os08g14610  GARQRDGGGCALGTTEVLG-----------------------------------------
Os07g25390  ---AERCEQLASENNKQQAPSGPTSPCTTWIVSSAKDQVN--------------------
Os06g14440  DGYTEGCEQLTSENNKQQAPSGLTSPYTTWIVSSAKDQVN--------------------
ZM064574    DGNGSGNSKLASETNKELGTSGLINNIAERMTFNGSQAF---------------------
ZM093940    DGNSPEHNKLASEMNKELGTSVLASNIAERMATNGSQTFE--------------------
Sb07g02945  ------------------------------------------------------------
Bd3g19890   -----STAELAPEKNKELIPLGLAGTLTAHVTSKGKDQV---------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   NFVATYFLRCTCESKKLYTHNLFFVI----------------------------------
At2g21450   SISLEDIEARQDNKRAKSSHNLII------------------------------------
AtDRD1      DVEKKALCVVPSSSEIVLLDSDDEDNERQ-------------------------------
Pt195587    ------VGDSVGNVAVGRTPVVVID-----------------------------------
Vv23895     ----HIVYDVPTATAVADAALPVVII----------------------------------
Vv35918     ----HVVDDALTATAVEDATLPVVII----------------------------------
At1g05490   EEENQDSEDNNTKDNVTVESLSSEDPSSSSSSSSSSSSSSSSSSSDDESYVKEVVGDNRD
At3g24340   SVISPRVCDFDEDDAKVSGKENPLSPDDDDDVVFLGTIAGENQHVEDVNAGSEVCDILLD
Bd2g26500   HGNEEHHNAAGKNRIGEPCGNGVASILNSSHGMNVVASGHAEGVKDWGNKGGELDDGFEV
Os05g32610  EHYGNGEASVAGGDRIEEHCGNVEASVANSNRDGGEIIAGEGTEDRGNTELSVVDPVNEE
RMR1        STADVFAEEMAPFEDDYDDEMLEEQLVGDVIRAYSNGRNFDSDGVDWEAEDEMEFNDDAD
Sb09g19410  STADVVAEEMAPFEDDYDDEMLEEQLVGDVIRAYSNGRNFDADEADWEAEDEMEFDDDAD
Pt286483    SYNGDVFAHERNEGGVCFLSSGIGNGSGGVGLKGRESNGVAGRTELRSGFCEKKKDGNVV
ZM178435    EDTGEDEKHMQEQTRVEDVEFMEVDDDYDDVNVAGNVIDQESEQDEALEGRSSQDSHGYS
Sb04g33300  DVESMDVDDDDDNNTNEAGNGIQKESEQDEALEGRSRQDSHALIDNEEEVGEKELSEEEE
Bd3g50300   GNSIPVQEEAAEKELGENGNSIPVLEEAAEKELRENGKSIPVEEEAAEKELGENGNSIQD
Os02g43460  GRAFAQVKEEQVEEQEEDEEEGEEEMEMEVEVEVRSDDNDHGNGGIRGEGGGTDDVAEIE
Bd2g43500   TGVPDEEEEAELEDKDNLEEEQEEDEEDEWEEEEEEEREADLED----------MVGEEE
Cp76.2      DVVWEEDMDDLERTSEEDNDDSDDEDYAVMKTMYRKEKCKP-------------------
Vv15867     TIDRDERGNQASKLGKKKVELGTSSHPFCVDVDEGEGDGDG-------------------

                               500                 520                 540
Sb02g43870  -----GDQARYSIDSMSI------------------PPGFGKSMDIISFKPRAEALR---
ZM000342    -----GDQARDSIDSMSI------------------PPGFGKNMDIISFKPRGEALR---
ZM108166    -----GDQARDSIDSMSI------------------PPGFGKNMDIISFKPRGEALR---
Os07g49210  -----GDQAQWNLDSMAI-----------------PPGF-GNTMEIISFQLRDEALR---
Bd1g16720   -----GDQARRGVDCMSI-----------------PPGF-GRNMEIVSFQLHDKNLR---
Sm441121    ------------------------------------------------------------
At5g20420   -----DEEGSSSTLSSMN-----------------ITLEDGVSLSKVVKFNPADILD---
AtCLSY1     -----CEGSSSSLSAMNI-----------------TVEDGVVMSKVVLFNPAEDTCQ---
Vv29366     -----GDHDKVSLNAVN------------------FRVDNGISTPVIFPFVPADTIE---
Cp19.123    -----DDDGSPSKSNNYI---------------------------SATMFINGGWWE---
Pt567214    EDGISTPFVVQLDPIDTC-----------------NTPAETEIGWVRSLPYTPLKWK---
Pt832603    ----GENEHCSLKSNNHI-----------------NCVTFKVKDSISTPFVVQLVPT---
Sm84719     -----PQHHLAGLDPGYV-----------------LELAAGSHGRDLRPKRDFAPRQ---
Os03g06920  NKAVTPRWRAWYRSDSRKVLQ--------------IPLSLRGGGGEIDHSTQKEARM---
Bd1g74070   -----------------------------------RDGNSSGCMQNVNFTQECSLAE---
Sb01g46180  -----------------------------------NDNYIQQNPLLEHPVGHQEITR---
Bd3g18910   AMCDHFDLAIASKKGSEE-----------------VANDEAQNESELFVDALCN------
```

```
Os08g14610  ----------------------------------------RICNSSVEKAEERETVI---
Os07g25390  -----GTLHVDGVQSTQI-----------------VPY--GQNAPLINQSPLQTSWQ---
Os06g14440  -----GTLHVDGVQSTQI-----------------VPYY-GQNAPLINQFPLQTSWQ---
ZM064574    -----GTVHTYGDKNTQI-----------------VPY--GQCSALVNQFPLQTSWQ---
ZM093940    -----TVHAYGGSKNTQI-----------------VPY--GQGSALVNQFPLQTSWQ---
Sb07g02945  ------------------------------------------------------------
Bd3g19890   -----NETRHYGYQNSQI-----------------VPY--GQSAALINHHSLQTSWQ---
Bd2g21450   ------------------------------------------------------------
Bd2g21430   --------------------------------------------NVIDNVVNQGGQQ---
At2g21450   -----------------------------------DSDDELPQESVTQINPLEKRLK---
AtDRD1      -----------------------------------RPMYQFQSTLVQHQKNQGDVTP---
Pt195587    -----------------------------------SDDDESNENRMVGHFQGIVLPK---
Vv23895     -----------------------------------DSDDEESGDQKVRDYVESIAPK---
Vv35918     -----------------------------------DSDDEDCGDQKVSHPPQETAW----
At1g05490   DDD--LRKASSPIKRVSLVERKALVRYKRSGSSLTKPRERDNKIQKLNHREEEKKER---
At3g24340   DANLRGEEKTYVSDEVVS-----------------LSSSSDDEEDPLEELGTDSREEVSG
Bd2g26500   DEEYMNEEDTEDDDEMLEEKL--------------VGDLIRAYSNGDDLDADGVDWE---
Os05g32610  LASDEDDYDDEMLEEKLVGDVIRAYSNGADLDTNGVDWEAEDEMEFADLDTNVVDWEAED
RMR1        N----SDFMDDADDSDFM-----------------DDAYEGGNSKPIQNHAKLEIQDWVN
Sb09g19410  NSDFMDDAHDSDFVNDAD-----------------EGGKSGDDAENSDFMDDAHDSDFVN
Pt286483    VVVDDDDDDACIILEKDA-----------------EELQSSSSGEEETFKDDSDDDDYRV
ZM178435    EDKEGKDSAALSDNEEDVGGKELL-----------EEEEEGADQEESHIIYDGEGEQ---
Sb04g33300  DDNQEESHSMYDGEGEQ------------------EEDASEEVEQEMDETGEEDEKE---
Bd3g50300   DRYDGEDEEATDDAHAAE-----------------EEEEEEEEEEEEEEEEEEEEEE---
Os02g43460  EEELGTDEDETSDDSDEN-----------------FSDEEGDEEELEEEEEEEEEEE---
Bd2g43500   EEEQGKEEDEWELEEEEE-----------------EEHEETEEEESESEQDEEAAEE---
Cp76.2      -----KNHDVNGRDFSSL-----------------EGNKQSPATTFDHHDCDDNDRI---
Vv15867     -----EGEEEWEEEEEEE-----------------EEEEGRDSSSGHAEFPKTIGRK---

                             560                 580                 600
Sb02g43870  --P-IIRTVLITQVKEDNLIEDGCT------------------------------AVKHE
ZM000342    --P-ITRTVPVTQVEEGNLTEDGCI------------------------------AVKGE
ZM108166    --P-ITRTVPVTQVEEGNLTEDGCI------------------------------AVKGE
Os07g49210  --P-TITNIPITHVKKNNITEDMRF-----------TVKS---------------EMDSE
Bd1g16720   --P-TIRNIPVTHAKKHNLTEDNRF-----------TLKTELDDQLEYIRVAVKIELDDQ
Sm441121    ------------------------------------------------------------
At5g20420   --D-SQDLEIKQETDYYQE-----------------------------------------
AtCLSY1     --D-SDVKEEI-------------------------------------------------
Vv29366     --ADPLNGTNEAGPLP--------------------------------------------
Cp19.123    ------------------------------------------------------------
Pt567214    --E-EEELHLPLAYLFGTHADASCA-------------EEKPGNEVRVNSPKLEFLEGPP
Pt832603    --D-ACSEAGHISDTNGTEQSP--------------------------------------
Sm84719     --L-EV------------------------------------------------------
Os03g06920  --D-SDSCKRRKHESGHDSSSRV-------------------------------------
Bd1g74070   --Q-PG------------------------------------------------------
Sb01g46180  --PDNCNS----------------------------------------------------
Bd3g18910   ------------------------------------------------------------
Os08g14610  --P-AIS-----------------------------------------------------
Os07g25390  --P-SI------------------------------------------------------
Os06g14440  --P-SI------------------------------------------------------
ZM064574    --P-SI------------------------------------------------------
ZM093940    --P-SI------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Bd3g19890   --P-SI------------------------------------------------------
```

```
Bd2g21450   ------------------------------------------------------------
Bd2g21430   --P-VR------------------------------------------------------
At2g21450   ------------------------------------------------------------
AtDRD1      LIP-QC------------------------------------------------------
Pt195587    --P-EG------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     --P-SF------------------------------------------------------
At1g05490   --Q-REVVRVVTKQPSNVVYTCAHCGKENTGNPESHSSFIRPHSIRDEIEDVNNFASTNV
At3g24340   EDR---------------------------------------------------------
Bd2g26500   --A-EDEMEFDDDGDDDYFVHDADECGMSEPMCDDYKVGTQYLSDHEVVVGEVSCQLEED
Os05g32610  EMEFDDDNDNDADDDGDNFGGDADEGDKSVQMHDFSKVETQDLVSHNVNVSEVRPHEDEE
RMR1        QKV-VLSGGRCEARGEGDLEEELDV---------------------------GKEADEED
Sb09g19410  DAD-EGGKSEPIKSHAKMEIQDLVNQKVVLCGGGCEEEGGEKEELGVGKEAGKKEDVEPK
Pt286483    ELP-ESFMVEEEEKEEDGDR----------------------------------------
ZM178435    --E-EDASEEETQELDETGEAQPFN-------------------------------PSNT
Sb04g33300  --L-DGTGEEDEQELDGAGKAQPVT-------------------------------PSNT
Bd3g50300   --E-EEEEEEEEEEEEEQDDESDEA------------------------GEELHPVPNSN
Os02g43460  --D-DDDDDEEEEEPGDAPDQPGEA-----------------------------------
Bd2g43500   --P-RRGGPRNSAAAGRYAHR---------------------------------------
Cp76.2      ------------------------------------------------------------
Vv15867     ------------------------------------------------------------

                              620                 640                 660
Sb02g43870  SDSAQDVEVLYEHVDIRRSK---------RMKTQPDRFTSYDAPN--------------F
ZM000342    SDSAQDVEILYAHVDIRRSK---------RMKTQPDRFTSYDARN--------------F
ZM108166    SDSAQDVEILYAHVDIRRSK---------RMKTQPDRFTSYDARN--------------F
Os07g49210  LDRALDVEILYEHVDLRRSK---------RLKTQPDRFTSYDTPRFLSGYKKKEASSSPT
Bd1g16720   LEDQFDVGLLYKHVDLRRSK---------RLKTQPERFTSYDAPN-------------FN
Sm441121    ------------------------------------------------------------
At5g20420   ---------EDEVVELRRSK---------RRNVRPDIYTGCDYEP---------------
AtCLSY1     ---------EEEVMELRRSK---------RRSGRPERYGDSEIQP---------------
Vv29366     ---------FCDIVDLRRSK---------RRNVQPDRFFSLGGFSESDIGSVRAGIHKVD
Cp19.123    ---------------LRRSK---------RRNVQPERFIGGQGLT---------------
Pt567214    VSRTKTNSRKIKSNVFNRRE---------HQAELGEVESGIDNRR---------------
Pt832603    ---------CYDVMSLRRSK---------RRNVQPERFLACDAPA---------------
Sm84719     ----------VFHLLLEDDP---------DEARRSHDPAFFHACE---------------
Os03g06920  ---------QSQSSILSRNRILCH-----QLLEQCDDLKYGSSTNDYKAISMKRLELISI
Bd1g74070   ---------QYQDIIMLGN----------ENINSEDQAVAKQGND---------------
Sb01g46180  ---------STEPQALVKQV---------KDAMDNDNVSAEAKKI--------------V
Bd3g18910   ---------HFDLAIASKND---------SKKVANDEVAHDEPQK---------------
Os08g14610  -----------------------------NTEKMGEKQQKSIPRD---------------
Os07g25390  ---------QYERVILQRRP---------EEQRVQDLVAASHAEK---------------
Os06g14440  ---------QYERVILQKRP---------EEQRVQDLVAASHAEK---------------
ZM064574    ---------QFERVVLQKRP---------EEQRMQDLVAASIAEK---------------
ZM093940    ---------QFERVVLTKRP---------EEQRMQDLVAATIAEK---------------
Sb07g02945  ---------------------------------MQDLVAASIAEK---------------
Bd3g19890   ---------QYESVILQTRT---------EEERIKYLAAASHAEK---------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ----------FDRVILHTRT---------EENIFK---IWSDVEK---------------
At2g21450   ---------KLKEVIVVKNG---------DSSGSDSSPQGYDEED---------------
AtDRD1      ---------SFEEVDLGRGK---------EMPSAIKAIVEGQTSR---------------
Pt195587    ---------QFSTDVMVSDN---------VGRRIQGEVASLTGEP---------------
Vv23895     ----------KEERSLTASS---------EIRKDKGGLYIAVGER---------------
Vv35918     ---------SYQEVVLRKPSVGLLA----NNPVVRDYVGSIAPKV---------------
```

```
At1g05490       SKYEDSVSINSGKTTGAPSRPEVENPETGKELNTPEKPSISRPEI---------------
At3g24340       ---------DSGESDMDEDA---------NDSDSSDYVGESSDSS---------------
Bd2g26500       VVKDEVDPKREGTTCFDQGRLHIEILESDDEVKVLSDASNPLKRK-PLPQAKIPVLPCVA
Os05g32610      AIKDEMESKGKGSLSFNEGSSYIEILDSDEEVKVVNDTGNALRRKPLVPAKLPIVPSCVA
RMR1            VEPKSEAAPGSDKRVLQLEILGSD-----EEIKVLENMSSAPSRKASVQSKLPTIPSCVA
Sb09g19410      SEAAPGSDKGGSHLETMSSD---------EEIKVLENMSSAPSRKASVQSKLPTIPSCVA
Pt286483        ---------EQGEMELKRN----------KVYGIEVLCDSDIGKF---------------
ZM178435        MAGSTMRSGGDGKQVFRRRVF--------EGIYLPENPHRTVGKG---------------
Sb04g33300      IAGSSMRSGGDDTRVFRRRVF--------EGICLPQKPRKTVGKG---------------
Bd3g50300       ADAGGNARSGGEGTPIGKRVF--------EGLCLVDNADNAVTTK------------SIR
Os02g43460      GEESPPRSRIMAMPLMGKRMF--------EGFSFLQQVDTSTGRD-------------IR
Bd2g43500       ---------AEDGEIFAKRLF--------EGLCISKAADTSAAGK---------------
Cp76.2          -----------------------------WEHDLNDLVTSSKEEN---------------
Vv15867         -----------DKGELGKHT---------KRKRIRALKHCDALKI---------------

                                 680                 700                 720
Sb02g43870      NRTYNKKEAYGPSNKNENSESDLSFYSSEQTESSDE------------------------
ZM000342        NRTYNKKEADGPSTKYEDSE----------------------------------------
ZM108166        NRTYNKKEADGPSTKYEDSE----------------------------------------
Os07g49210      KHVRGAVHCDSPVDDSKKEVESCCVEIPGNVTQKQTGVHSPMVDEKSNSPEGQHKNTTKR
Bd1g16720       RDTKKKGASASSTMHYDHRRASQVK-----------------------------------
Sm441121        ------------------------------------------------------------
At5g20420       -DTIDGWVRMMPYQFGKCAVNVESDEDEDDNNEDGDTNDD--------------------
AtCLSY1         -DSKDGWVRMMPYRYNIWNVSSDDDDEEEDCEDDKDTDDDLYLPLSHLLRKKGS------
Vv29366         YWRKEEMPLALPDEGDVHSIFSEKHIIDYEKGAHSLQIDSYEDFLVC-------------
Cp19.123        -ESDSVWVRQMPIKTDKWKEKMKCLPLSRLFKMQPLYLKEQPKNETRDLVVYKSNKYSKD
Pt567214        ERQKSTVANRIKHQTRLGE-----------------------------------------
Pt832603        -ETEIGWVRSLPYTPLKWKAEEEEEEEMHLPLAYLFGTHAGASCAEEQTCNEVGASSPKL
Sm84719         -RQQSGWKSKLVHELHGLL-----------------------------------------
Os03g06920      LQKLQEVPIQLPYASPLKS-----------------------------------------
Bd1g74070       -------IMDIDNENHDEQ-----------------------------------------
Sb01g46180      LFDCHSTSEQQPLMKQARG-----------------------------------------
Bd3g18910       -ESECLVHDTWNHFDHAIA-----------------------------------------
Os08g14610      ------------------------------------------------------------
Os07g25390      -IAETQVFLTLPTLPNERK-----------------------------------------
Os06g14440      -IAETQVLLTLPTLPNERK-----------------------------------------
ZM064574        -RAETQVFLSLPTEKK--------------------------------------------
ZM093940        -RAETQMFLSLPTERK--------------------------------------------
Sb07g02945      -RAETQMFLSLPTEKK--------------------------------------------
Bd3g19890       -MAETQVFPDLPRERK--------------------------------------------
Bd2g21450       ------------------------------------------------------------
Bd2g21430       -IAETQTSPALPGSHVDGD-----------------------------------------
At2g21450       ------------------------------------------------------------
AtDRD1          -------GKVLPIENGVVN-----------------------------------------
Pt195587        -DSKKDKGVYVGVEDDEVD-----------------------------------------
Vv23895         ---------SLAANHEMKN-----------------------------------------
Vv35918         -EEGSLMGATEIRKDKDVY-----------------------------------------
At1g05490       FTTEKAIDVQVPEEPSRPEIYSSEKAKEVQAPEMPSRPE---------------------
At3g24340       -DVESSDSDFVCSEDEEGG-----------------------------------------
Bd2g26500       WRTRSLWGVKQDRISYNAYFEELSDEPIEDDDTEVELDDEDDNDDDSASFEEEEEEETKQ
Os05g32610      WRTRSSWGMKEERISYNTYFEVLSDEPKEDDDDTEVELDDEEDDENDDDCNS--------
RMR1            WRTRSSWGVNQDRLSYDTYFEELSDEPKEDDDDTEVELDEVEDDNNDDDSSDAYDKDDEE
Sb09g19410      WRTRSSWGINRDRLSYNTYFEALSDEPKEDDDDTEVELDEDEDGNNDDGSSDAYDKDDEE
Pt286483        ENNDVDMDDSLCVAKRTRS-----------------------------------------
```

```
ZM178435    -IQGRTRSQRKCKDKKLLKRGTFSKPYNIDIPDSTSDSE---------------------
Sb04g33300  -IGARTRSQRKCKDKKLLRRGTFSKPYNIDIPDSTSDSE---------------------
Bd3g50300   QRTRSNFKDRACLDKKLLGQGTCSKPYCIDTESEEDVPPPP-------------------
Os02g43460  ARTRSNFKRKKLLDKKLLKRGTFAKPYCIDVSSSGSEEDVPQPEQSA-------------
Bd2g43500   PVAGRTRSRRRCLNTKLLRQGTYNKPYCLDTPSESGSSEAE-------------------
Cp76.2      ----GVSHNNFSSVRKTVS-----------------------------------------
Vv15867     -LVDSIWAKNSGLLEELVS-----------------------------------------

                             740                 760                 780
Sb02g43870  ------------------------------------------EVLGNPGVKKKVSRSFVV
ZM000342    ------------------------------------------SGLSCDSSEQRESSDEEA
ZM108166    ------------------------------------------SGLSCDSSEQRESSDEEA
Os07g49210  TTCSLVKEKASS------------------------------PEGQHEKTTKRTTCALPV
Bd1g16720   ------------------------------------------VESSCGEDPVKITGASSF
Sm441121    ------------------------------------------------------------
At5g20420   ------------------------------------------LYIPLSRLFIKKKKTNSR
AtCLSY1     ------------------------------------------KKGFSKDKQREIVLVDKT
Vv29366     ------------------------------------------KSKDRSREVKPILAAQNE
Cp19.123    VKSGLADQVEHQ------------------------------NKLAIIPVPNVPELEPEP
Pt567214    ---------------------------------------------------AKSGMANRK
Pt832603    ELLEGIPVSRTKTYLKEIKSNVVNRRDHQTEPGEVR------AGMAKRRECQKSTMADRI
Sm84719     ------------------------------------------------------------
Os03g06920  ------------------------------------------SETNRLVQDGRNSSCRNI
Bd1g74070   ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Bd3g18910   ----------------------------------------------------------SK
Os08g14610  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
ZM064574    ------------------------------------------------------------
ZM093940    ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Bd3g19890   ------------------------------------------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ------------------------------------------------------------
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
At1g05490   ------------------------------------------VFSSEKAKEIQVPEMPSI
At3g24340   -------------------------------------------------TRDDATCEKNP
Bd2g26500   EEVAEKSKHKKGIHSSFPEIRSRPMPLFVNRERR--------MQTSIPKWRGTSKKARQP
Os05g32610  ------------------------------------------ASCDEEDEEEEEEREEEE
RMR1        KEEEE-------------------------------------EEAERRKLNNRICTSDED
Sb09g19410  KEEEEEEEEAERRKLNNGIYTSDDDMINITVPTSRYDMFERKNISRYDMFKRKNTSRYDI
Pt286483    ----------------------------------------------------HYNLESAK
ZM178435    ------------------------------------------EEIEPPAPQQGLLSSSEE
Sb04g33300  ------------------------------------------EDIEPPAPQQGLLSSSEE
Bd3g50300   ------------------------------------------QPQPSSAECEDDGSGGDD
Os02g43460  ------------------------------------------YGGDCADDDGGSDGNEEH
Bd2g43500   ------------------------------------------EGVNKTPPAPALSSSDEE
Cp76.2      ------------------------------------------------------------
Vv15867     ------------------------------------------------------------
```

```
                                 800                 820                 840
Sb02g43870  KEDPRSMKGQHKYPVKRNQCSLPIKENQTSME----------------------------
ZM000342    LENPRSMAAEHKYPVKRNQCSLPVKEKQISME----------------------------
ZM108166    LENPRSMAAEHKYPVKRNQCSLPVKEKQISME----------------------------
Os07g49210  KEKASSPEGQHKNTIKRTTCSLPVKEEPSSVE-------------IEEK-----------
Bd1g16720   MFNENPSTTKGQHKNTRRRTPCSLPMKEKPSS-------------VKEE-----------
Sm441121    ------------------------------------------------------------
At5g20420   EAKPKSRKGEIVVIDKRRVHGFGRKERKSELSVIPFTPVFEPIPLEQFGLNANSFGGGGS
AtCLSY1     ERKKRKKTEGFSRSCELSVIPFTPVFEPIPLEQFGLNANSLCGGVSGNL-----------
Vv29366     DQHQFAIVPVPLIIEPIAHGEDHLHDETPWNE----------------------------
Cp19.123    LASEHHDYHANLSANNSKRVEELSFRYNSLKC-------------SRTS-----------
Pt567214    KHGTQIREVKLGVANRIEHQDQLAIVPVPTEDDLVTFEQYDSPLKTPDN-----------
Pt832603    EHQTRLGDAESGMANRKKHGTQIREVKSGVANRREHQDQLAIVPVHTEDVLATFEQFDSP
Sm84719     ---------GEDGLASVNFGGFSLILGNTHGD-------------RAKV-----------
Os03g06920  IDLDSDNDEDYTFANVDNIGANTTVVLVDSDD--------------------------GD
Bd1g74070   ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Bd3g18910   NLKESEVVANDEVANDEPQKESEYLVDDMWNH----------------------------
Os08g14610  ------------------------------------------------------------
Os07g25390  ----------------RRKSEPTTLVDGDGGT----------------------------
Os06g14440  ----------------RRKTEPTTLVDVDGGT----------------------------
ZM064574    ----------------RRRSDPSLHASDDTAT----------------------------
ZM093940    ----------------RRRTDHSLLMLDSF------------------------------
Sb07g02945  ----------------RKRSDLSLLMLDSFVP----------------------------
Bd3g19890   ----------------QRKLDPNSQVDGDAGT----------------------------
Bd2g21450   ------------------------------------------------------------
Bd2g21430   ---------------------------------------------AETA-----------
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ----------------TEIKDDGLQVSDNVG-----------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ----------------IGVGEKSLVANLEM------------------------------
At1g05490   PEIQNSEKAKEVQANNRMGLTTPAVAEGLNKS-------------VVTN-----------
At3g24340   SEKVYHHKKSRTFRRKHNFDVINLLAKSMLES----------------------------
Bd2g26500   ETCHVIYSSDDEIIDDTAKDGLKCEVDEDPRNNVFQPLNFEKVGSDGTVGNGITTEQQKG
Os05g32610  EEAQRRKQKKGIDSSDDEMIDDAVDCGIDWEEDYPEVDFTRPLTFQKDGSEAPVGSEAFT
RMR1        MINITVPTSRYDMFKKKNSSRYDIEWVEDEDASVDMLQPVSFKKDSSWKPVAVGNDTFTE
Sb09g19410  FKRKNTSRYDIFKRKKTSRYDIEWVEDEDKDANVDTLQPISLRKGSSWNPVAVGNDTFTE
Pt286483    KRMKLETVSRPLCVDEEKLDDNGDNDEDDTEA----------------------------
ZM178435    DNMTFGKRKRRRAAINKRWDKRLSASSDEEDY-------------GASA-----------
Sb04g33300  GNITFGKRKHRRAIKNRRRKRPSTSSDEEYRV-------------YARD-----------
Bd3g50300   RMPAKRRRGKEQITDSDDTQNDSEDSDENRTL-------------ARNA-----------
Os02g43460  RAVKRRKLNRRQSAHSDSEEDTTFVCDVKEGS-------------GSRR-----------
Bd2g43500   IEADAGGHGRTAARKGRRRGKNPTPSDDDSEEHRVGGRQGTAVRRRRWP-----------
Cp76.2      ------------------------------------------------------------
Vv15867     ------------------------------------------------------------

                                 860                 880                 900
Sb02g43870  -------------TKKNATDQGCSDSHIPHTPAKNIEKCNRPTFRLKSFASSRSLDGNSE
ZM000342    ----------------IKKNTTDQGCSDSYIPHTPAKNTERPRFRLKPFASSRSLDGNSE
ZM108166    ---------IKKN-TTDQGCSDSYIPHTPAK------NTERPRFRLKPFASSRSLDGNSE
Os07g49210  --------------SSKEQSAPEFHIPRTPAQNKEKHNRPPFSCKPKLFTSSGTLGVNCE
Bd1g16720   ------SKTEE---RASDSHIPQTPAQNKEK--NHRTPSSFHRKSGTSP---CSLGGNYE
```

```
Sm441121    ------------------------------------------------------------
At5g20420   FSRSQYFDETEKYRSKGMKYGKKMTEMEEMMEADLCWKGPNQVKSFQKRTSRSSRSVAPK
AtCLSY1     ------MDEIDKYRSKAAKYGKKKKKKIEMEEMESDLGWNGPIGNVVHKRNGPHSRIRSV
Vv29366     -------SGEIGEISPKYYCTNGVPKLQRKNMSDLYMEVESRWEGKGPIRKLRRKRGFTI
Cp19.123    --------------SRKKFSQIDDMDLVPRW-------EGIQGKGSNRKAQIRKHRGISS
Pt567214    -------FPQECIEFPIRSYSKKGYSVQRKNDFDEDMMFGSGWGGKSSRKKVQRARYQST
Pt832603    VKTPEPYSQAFIEFPISYYRKKSSPAAHRKNDRDEDLMFGNGWGGKFSTKKVQRARYRST
Sm84719     --------------DGGGGGGDDLREKPASVGFCLRRATMLVEEGDERAIDWDRLIAKEK
Os03g06920  SVASFVDEKSSDSKQNANYIEESVLPEQHAQQQEISMLDNENISSEAQAVKKGKDSMDIN
Bd1g74070   ------------------------------------------------------------
Sb01g46180  -----------------------------------------------------------N
Bd3g18910   ---------------------------------------------------FELAIASEN
Os08g14610  ------------------------------------------------------------
Os07g25390  -----------------------------------------------------------N
Os06g14440  -----------------------------------------------------------N
ZM064574    -----------------------------------------------------------V
ZM093940    -----------------------------------------------------------V
Sb07g02945  ------------------------------------------------------------
Bd3g19890   -----------------------------------------------------------A
Bd2g21450   --------------PQKP------------------------------------------
Bd2g21430   --------------PRK-------------------------------------------
At2g21450   ------------------------------------------------------------
AtDRD1      ------------------------------------------------------------
Pt195587    ------------------------------------------------------------
Vv23895     ------------------------------------------------------------
Vv35918     ------------------------------------------------------------
At1g05490   --------------EHIEDDSDSSISSGDGYESDPTLKDKEVKINNHSDWRILNGNNKEV
At3g24340   ------------------------KDVFKEDIFSWDKIAEVDSREDPVVRESSSEKVNEH
Bd2g26500   SRFTWDLERRKKLKLGIIKSRHSYERGLDLDSDSSGSGENERHGYQEGGDNKVGRKKKHL
Os05g32610  EQQKRSRFTWELERRKKLKLGMMTNHRLYERDLESDSNSSDSSQNRKNGCQGSGDHRTGR
RMR1        QQKRSRFTWELERRKKLKLEMKTNPLHERDLDSDPNSSGSDQIRKYGFKSDGSHKVDRKK
Sb09g19410  QQKQSRFTWQLERRKKNKLEMKTNPLYERDLNSDSNSSGSDQIRKYGFKRDGSHKVDMKK
Pt286483    --------------YEAVDVAQKVRSKKGKTKPTGGNGGDVDDGDETCDHKSQRRTIESR
ZM178435    ------MDAKERPFRRLKKGLSNLQAAKEGCRNYEGSNPGHARYSGPNGGNLENMSSAQD
Sb04g33300  ------GKDRPFRRLKK-----GLSKLQAGKEGCGRYVGSNPGHAKYNGPNGENQSNEQD
Bd3g50300   ------RKGSSSRRPKNGASYQQNVKEGSRNYDSPSNPRHVKNYAANAGNPTDRFNMQSG
Os02g43460  --------------VQEGAPRRQVKKEGSNKKKDGSTPQCVRNNGPKVGRQTNGLNGQGG
Bd2g43500   ------KDNTAQCDHEEEEDDEAFVPFRRPKRSGAVPNPRDGYYDQQQQAGDAPFKKSSL
Cp76.2      -----------------------------------------------------------K
Vv15867     ------------------------------------------------------------

                             920                 940                 960
Sb02g43870  PAFCQKRGR---KRKKGMCQREYKRMIEQCIGNIQCEVERDSDFKIDAQILNGCGHAYQ-
ZM000342    PAFCQKRGR---KRKKHMCQIEYKRMIDQCIGNIQCEVERDSDFKFGDQILDGCVRAYQ-
ZM108166    PAFCQKRGR---KRKKHMCQIEYKRMIDQCIGNIQCEVERDSDFKFGDQILDGCVRA-YQ
Os07g49210  PAFCQKVGG---KRKRHMCEREYKQMIDQCIGNIESEMERDSMFNFDANMMNYVQHS-YR
Bd1g16720   PAFCQKRGR---KRKERMCDEEYEKIINQCIGNIQSEMERDYEFNLDVPMMHCCQGA-YP
Sm441121    ------------------------------------------------------------
At5g20420   TEDSDEPRV---YKKVTLSAGAYNKLIDTYMNNIESTIAAKDEPTSVVDQWEELKKTNFA
AtCLSY1     SRETGVSEEPQIYKKRTLSAGAYNKLIDSYMSRIDSTIAAKDKATNVVEQWQGLKNP-AS
Vv29366     RTKTESYGEVRPHKKRPFSEPGYKEVIEAYMKNIESTINKEQPLVIDQWKELQVRNDLNQ
Cp19.123    KEDFDEPIT---YKKKSLSAGAYDKLIHSYMKNIDSTMI--KEEPHIIDQWQEFKKASFP
Pt567214    HLKRDDSCKPKTYKQTALSAGAYDKLISFYMKNFDSTIKSKEVTRIIDQWEEFKAKHSSD
Pt832603    HLKQDGSCAPMTYKRTALSAGAYNKLISSYMKNIDATIKSKEVPRIIDQWEEFKAKHSSD
```

```
Sm84719        RWQRKESTR---KNPAPNAGKRRAVEEEEEEDDDGDEIYPCLEDSRSWD-----------
Os03g06920     DVIYNKSGH---EEIGEEEAQAENVQIKGNLKKEIISVASDELA------CEVMRSQSPT
Bd1g74070      --KGKREGE---GEDVQSAGSIENNSVPVVDSYDISCEVIQSES----------------
Sb01g46180     IKTNTENGL---KEKGKIGGTIAKHVGSYEVSCEILQNEPHSN-----------------
Bd3g18910      LEESEEVTHDEQKKENEYLVRDRWNHFELAIASKNLYFICFLRPRNIWHYPKLSKNATFV
Os08g14610     ---RKRKGE---------------------------------------------------
Os07g25390     LGKGKRKNH---QNQAAVDSILDLQQTVVPLQQNDVPSQSYRTM----------------
Os06g14440     LGKRKRKNH---QNQAAVDSNLD-------LQQNDVPSQSYRTM----------------
ZM064574       PKQRKSKGA---TVVAAANLSLVSQQTATSPEPDMVI-----------------------
ZM093940       PKQRRRKGD---TGLAPADLSLDLHQTATSQEPDIAI-----------------------
Sb07g02945     --KQRRKSD---TGLAAADLSLDLQQPAKSPEPEPEP----------------------D
Bd3g19890      PRKRKRKTG---PDPAAVDLPSETYNPVEEEEPAEE------------------------
Bd2g21450      ------------------------------------------------------------
Bd2g21430      ---RKRENE---RDSAAVDLPSN-------TYNPVEE----EEP----------------
At2g21450      ------------SSRNSTDIDNQSLYVDA-------------------------------
AtDRD1         -----EKGV---YVGVEEDDS---------------------------------------
Pt195587       ---RRIQGEAASLAGEPDSKKDNGVYVGVE------------------------------
Vv23895        -----VKGE---YVGVEDDMEAS-------------------------------------
Vv35918        ---KKVQGE---YVGVEDDMETN-------------------------------------
At1g05490      DLFRLLVNSVWEKGQLGEEDEADELVSSAEDQSQEQAREDHRKYDDAGLLIIRPPPLIEK
At3g24340      GKPRERRSFHRVREKNHLNGESFYGGEKLCDGEETINYSTEDSP-----------PLNLR
Bd2g26500      SSKSGKSGKKSSRSTMLKRQSLLKLLMDKMTGDKDGECSPFDLHSQFEYNSNDSHPLVFS
Os05g32610     KRKNPLSKSGKKSSRMLKRQSLMKLLMDKMCSNDDGKSTPFDQKPQIEYSFKDLHPLVFS
RMR1           KHTSPKSGKKPSSAIILKRQSLLKLLVDKMSGDKSLASFPFDQNPQLQFIFKEMHPLVFS
Sb09g19410     KHTSSKSGKKSSSAIMLKRQSLLKLLVDKMSGDKSLESFSFDQNPQLQFIFKEMHPLVFS
Pt286483       EGSRDEHGHGVCRRKPSKRRRKEYEVVKILANSLFLDLEDVPFKEEREPLEEPVLPLKFT
ZM178435       DISFKRNVH---MIRIKKRGRAAKAVYDELLDSLFSGWENHIGNPVHAEAGNSLPLV-FS
Sb04g33300     GIFFKRTAH---KIRMKKHGPVAKAAYDELLNSLFSGWEDHINDPDHAAAGNSLPLV-FS
Bd3g50300      DICFNTNTL---LPQRMKHGRVWTKQDTDNLLNSLLDEIENGSAPAQAQNEDRLPLV-FS
Os02g43460     VSFKRNVKIA--QRRKRRQATADQEKYGHLLDPMFNEIESNQYEPVPEEQIDRRLPLVFA
Bd2g43500      ILPKKRCGAG--QERETYDDLLQSIFDEITNQQNGSAPLDDGSAPAQEQSVPDTLPLIFS
Cp76.2         KRKHMHKSHDIVKVVVNSMLEEEEMLFEETVASGDVLKEQGNHP-----ETEPTLPLTFT
Vv15867        PRGSDSIEE---TAPAFTELPLK-----------------------------------FK

                                980                1000                1020
Sb02g43870     ---EEDFMWPSSADSQEEKDEL-QELWKEMDYALATVAIDEQKQLIKCLD----FQTTD-
ZM000342       ---EVDFTWPSSADSQEEKDEL-DELWKEMDYALATVAILEQKQ----------MTDSE-
ZM108166       EVDFTW---PSSADSQEEKDEL-DELWKEMDYALATVAILEQKQ----------MTDSE-
Os07g49210     EEDFTW--PPSADNQEVEEDEL-EELWKEMDYSLTTLALLEQKQVMAQSRINMLVDNFDG
Bd1g16720      EEDFTW--PSLADSQEEKKDEL-DELWKEMDFSLTTLELDRMQV----------PDSED-
Sm441121       ------------------------------------------------------MSSFD-
At5g20420      FKLHGDMEKNLSEDGEGETSEN-EMLWREMELCLASSYI---------------LDDNE-
AtCLSY1        FSIEAEERLSEEEEDDGETSEN-EILWREMELCLASSYI---------------LDDHE-
Vv29366        RRDCNS---PSSVGDQEESSET-EMLWREMEFSIASSYL---------------LEENE-
Cp19.123       EQRMEI--EQSSSEDEGESSEN-EMLWREMELSMASAYF---------------LEDNE-
Pt567214       QKETME---PSLVEDDGESSET-EMLWREMELCLTSAYI---------------FEDNE-
Pt832603       QKEKME---PSSVKDDGESSET-EMLWREMELCLASAYI---------------LEDNE-
Sm84719        ---FDF------DHEKLENEDKLAAIWHDWDAEIEAER----------------RRVPD-
Os03g06920     NGNFDQ------YDNSSPVDEL-EGLWMDMYLAMACSK----------------TVGSD-
Bd1g74070      ---TENGNYDRYDNNDSPVDEL-EYLWRDMSLALACSK----------------TIGSD-
Sb01g46180     ---EGN------HHDNGSPVGELDDLWIGMSVALACSEK---------------NNQVN-
Bd3g18910      IGKLDKFEEVASDEPKKESDCLVDDLWNHFDLAMASKK----------------YEEVA-
Os08g14610     ---------------LDPAADYVKDLWDAFYVTAESTH----------------LDTSE-
Os07g25390     ---IEE------EKPVKESDGL-EDLWKDFSLAAECTK----------------LDTNE-
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Os06g14440  ---IEE------EKPVKESDGL-EDLWKDFSLAAECTK----------------LDTNE-
ZM064574    ---EEE------EKHKNESDGL-DDYWKDFALAVESTK----------------LDEVD-
ZM093940    ---EEE------EKRKNDGDGL-EDYWKDFALAVESTK----------------LDDVD-
Sb07g02945  MAIEEE------EKCKNESDGL-EDYWKDFALAVESTK----------------LDEVD-
Bd3g19890   ------------DKPENKSDGL-EDLWKDFSVAMESSK----------------LNTFE-
Bd2g21450   -----------------------TNPWRKRSL---QKKFYFNAQ----------LDTLE-
Bd2g21430   ---MED------GKPKKESNGH-QDIWNAFDMALENSKLYFNAQ----------LDTPE-
At2g21450   ---EEE-----------------EELWRKMAFAQESIK----------------VTVED-
AtDRD1      ------------DNESEAADEDLGNIWNEMALSIECSK-----------------DVAR-
Pt195587    ---DDE------VDTEIKYDGL-GDIWKEMSFALECSK-----------------DVVE-
Vv23895     ---EGN------LQAKTKDDDL-ADMWQEFDLALQSSK----------------DVAVD-
Vv35918     ---EGN------LRAKTEDDGL-ADMWQEFDLALQSSK----------------DVAVD-
At1g05490   FGVEEP----QSPPVVSEIDSEEDRLWEELAFFTKSNDIGGNEL----------FSNVE-
At3g24340   FGCEEP----VLIEKTEEEKEL-DSLWEDMNVALT-------------------LEGMH-
Bd2g26500   FGDEDH-----IPANKAEQNAEHDMLWADYDFALELENIGTYYD----------DEHQE-
Os05g32610  FGDDDP-----SPTDRSEQDAALDMLWADLDFTLESENIGTYYD----------DEGQE-
RMR1        FGDEDL----VAADRPEQDVGL-DMLWADFDFALESENIGTYY-----------DDECQ-
Sb09g19410  FGDEDL----EAADRPEQDVGL-DMLWADFDFALESENIGTYYD----------DEGQE-
Pt286483    FGIEES-----SPPVKSEEEKQLEELWADMALALCLKDTTDDAA----------LDENE-
ZM178435    FGDEDA-----EENTENDKYQEQEDLWMECGIAFQSMNIG--------------SNGCE-
Sb04g33300  FGDEDA-------EENIENDKYQEDLWRECDIAFESMDIGNGSE----------EDGLE-
Bd3g50300   FGDEDQ------VEEQSDHNKLQDELWAEMDFCMESTNVCPQSC-----------EEGE-
Os02g43460  FGDDDK----LEEKSKHDKLQDEDELWKEFDFALESINVCSHNC-----------EEGE-
Bd2g43500   FGDEDQ-----VVKEKTEQGKFEDLLWAEFDFALESTNACSHAC----------QEEGE-
Cp76.2      FQIDES-----SMSKNSDSDNELHNLWVEMNFAQRSFEIDSHACN---------MVENE-
Vv15867     FGVDES----IPLGKSQPEIGM-NQLWAEFDFDGEED-----------------FGSAE-

                            1040                1060                1080
Sb02g43870  -------------------------SEADHESNTDLGKRGEHCH-HDCMLDEQLGLTCRL
ZM000342    ---------------------------VVHESNTDLGKGGEHCH-HDCMLDEQLGLTCRL
ZM108166    ---------------------------VVHESNTDLGKGGEHCH-HDCMLDEQLGLTCRL
Os07g49210  LRLDCLTLTDDYRCYYQKKEKFAESGSVNESTDYFGKVGGIPCH-HECILDEELGLACRL
Bd1g16720   ---------------------------VHESTARLGKNGEIPCY-HDCILDEELGLMCRL
Sm441121    ----------------------------------------DICEVHDYVLNELVGLICSV
At5g20420   ----------------------------VRVDNEAFEKARSGCE-HDYRLEEEIGMCCRL
AtCLSY1     ----------------------------VRVDNEAFHKATCDCE-HDYELNEEIGMCCRL
Vv29366     ---------------------GSNVEVLKEVVQESSNISEQVCQ-HEYILDEEIGVLCQL
Cp19.123    ----------------------------VRVSYENIQKTTEVCQ-HSYRLNEEIGMCCFL
Pt567214    ----------------------------SRVSTQTTQNSSECCQ-HEFKLDEEIGILCHK
Pt832603    -VELCVVFIYSYHLYRIFFFITVSDWLKDLQALLSTRTTQKNCQ-HEFKLDEEIGILCQI
Sm84719     -----------------------------LIKFKDIDVLIDSCD-HEFVFREDCGKVCEI
Os03g06920  --------------------------HNIVPSENSCEQAEDECQ-HDFLMKDDLGIVCRV
Bd1g74070   --------------------------HSIVPSENTCGEVVDDCH-HDFLMRDDLGLVCRV
Sb01g46180  --------------------------LSIVPFVSNSEETEDACN-HDFLLKDDLGMVCRI
Bd3g18910   ----------------------------NDKHVKRKINVDIGCN-HDICLHEDLGEVCRV
Os08g14610  ---------------------------------VNNKKQLDNCN-HDIHVYEDLGHVCHE
Os07g25390  -------------------------DMSNEKDVDDENEMDDDCN-HDIRIHEDLGHVCRI
Os06g14440  -------------------------DMSNEKDVDDENEMDDDCN-HDIRIHEDLGHVCRI
ZM064574    --------------------------EAAIEKEDNGKMEDIDCN-HDIRIHEDLGHVCRV
ZM093940    -------------------------EAAANEKEDNGKMEDIDCN-HDIRIHEDLGHVCRV
Sb07g02945  --------------------------EAANEKEDNGNMEDIDCN-HDIRIHEDLGHVCRV
Bd3g19890   --------------------------ELPDEKELGEKDVDNDCN-HDIRIHEDLGHVCRV
Bd2g21450   --------------------------DVPNAKEVGRKEVKIECN-HQIVIREDLGHVCRV
Bd2g21430   --------------------------DVPNIKEVSEKEVKIDCN-HQIEIHEDLGHVCRI
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At2g21450   -------------------------------SQSNDHKQIEDCD-HSFICKDDIGEVCRV
AtDRD1      -----------------------------ETSHKEKADVVEDCE-HSFILKDDMGYVCRV
Pt195587    ----------------------------NSPSDENMEEDEDYCD-HSFVLKDDIGYVCRI
Vv23895     -------------------------------PEEDGKEGEEECE-HSFVLKDDIGSVCRI
Vv35918     -------------------------------PGEDEKESKEECE-HSFVLKDDIGSVCRI
At1g05490   ---------------------------KNISANETPAAQCKKGK-HDLCIDLEVGLKCMH
At3g24340   ----------------------------SSTPDKNGDMLCSKGT-HDFVLDDEIGLKCVH
Bd2g26500   -------------------------ESNMLNLGLACTTPCSRGK-HEFIIDDQIGIRCKY
Os05g32610  --------------------------DSLLDHALAPITPCSRGK-HEFIIDEQIGIRCKY
RMR1        -------------------------EGNQLDFSLAPVTPCSRGK-HEFVIDDQIGIRCKY
Sb09g19410  -------------------------EGNQLDFSLAPVTPCSRGK-HEFIIDDRIGIRCKY
Pt286483    --------------------------DDAHEVEPDTVTLCHQGN-HELYLDEEIGLLCKY
ZM178435    --------------------------EDGKEIPPVKVTSCNIGQ-HEFIIDEQIGVRCKH
Sb04g33300  -------------------------------IPPVEVTSCNNGQ-HEFIIDEQIGVRCKH
Bd3g50300   ------------------------KSNNGQEKPGDKATLCSQGK-HDLVTDEQIGVWCRR
Os02g43460  -------------------------KEDEQEIPADKAASCIQGK-HELIIDEQIGLRCKH
Bd2g43500   -------------------------KSNGDEIHADRATSCKRGK-HDLIMDEQIGIRCKH
Cp76.2      -------------------------YAVCSEVDLDIATLCSKGS-HHLIIDEEIGVKCKY
Vv15867     -------------------------------VEIDQAVLCHQGN-HQLVIDEQIGMTCCF

                            1100                1120                1140
Sb02g43870  CNVVCTEAKDIFPP-------MFTGKD-HKRLEQSHF----------------GQDDHVL
ZM000342    CNVVCIEAKDIFPPMVASNSNQFTGKD-HERPERNHF----------------GQDGHVL
ZM108166    CNVVCIEAKDIFPP-------MFTGKD-HERPERNHF----------------GQDGHVL
Os07g49210  CNVVCTEAKDIFPE-------MFNGND-YKDRPGCSNI---------------CLDDDIL
Bd1g16720   CNVVCIEAKDIFPQ-------MFNGNGYNKDRPGCSNF---------------FHDDHVL
Sm441121    CGYVGIPIEEMAPH------PDWSFRL--------------------------PQNVLEN
At5g20420   CGHVGSEIKDVSAP-----FAEHKKWT-IETKHIEEDDIKTKLS---------HKEAQTK
AtCLSY1     CGHVGTEIKHVSAP-----FARHKKWT-TETKQINEDDINTTIV---------NQDGVES
Vv29366     CGFVSTEIKDVSPP----------------------------------------------
Cp19.123    CGFISTEIKYMTAP-----FMEFRSYV-AENRWENEEDNKNM-----------TYAGREL
Pt567214    CSFVKTEKKYVSAPFVFS-VFLLSFMS-PLDRQVSMQGRHFLFVIR-------GYSARNP
Pt832603    CGFVKTEIKYVSAP-----FMEHTGWT-AESKPQNEEDLELK-----------PDEDEGS
Sm84719     CGRVVKLVSDVFDVSIIS-FLSFPARK-ASSRP--------------------ATKKLKL
Os03g06920  CGLIQQRIENIFEY-------QWKKRK-QSYRARPSE----------------HRNSSDA
Bd1g74070   CGLIKKPIDTIIEC-------QWKKPK-QSYRTYPSG----------------HRNSNDL
Sb01g46180  CGLIQQRIDKIFEH-------SWKKRN-QAYRSYPIK----------------QRNSGDP
Bd3g18910   CGMIVRSADKIFDY-------CWWKQL-SRKRSGTHE----------------AGSKNAD
Os08g14610  CGLVVRKADSLFHY-------QWKK-A-SRKRTN----------------------VNEV
Os07g25390  CGMIVRKAETIIDY-------QWKK-A-SRTRTN-------------------YYESRSK
Os06g14440  CGMIVRKAETIIDY-------QWKK-A-SRTRTN-------------------YYESRSK
ZM064574    CGMIVRRADSIIDY-------QWKK-A-SRRRTN-------------------GYGGHSK
ZM093940    CGMIVRRADSIIDY-------QWKK-A-SRRRMN-------------------GYGGNSK
Sb07g02945  CGMIVRRADSIIDY-------QWKK-A-SRRKTN-------------------SYGGHSK
Bd3g19890   CGLIVRRADTIIDY-------QWKK-A-SRSRSY-------------------FCGTRSK
Bd2g21450   CGMIVRKADTIFDY-------QWEK-E-SRPRSY-------------------LYGTRSK
Bd2g21430   CSMIVRKADMIFDF-------EWRKVS-SRSRSY----------------------FKET
At2g21450   CGLIKKPIESMIEV-------VFNKQK-RSRRTYMREK---------------ENGETSR
AtDRD1      CGVIEKSILEIIDV-------QFTKAK-RNTRTY-------------------ASETRTK
Pt195587    CGVIERAIYTIIEI-------QFNKVK-RNTRTYI------------------SESRNAK
Vv23895     CGVVNKSIETIIEY-------QYSK-V-KRSRTYMYE----------------PRNTKDR
Vv35918     CGVVNKSIETIIEY-------QYTK-V-KRSRTYMYE----------------PRNTKDR
At1g05490   CGFVEREIRSMDVS-------EWGEKT-TRERRKFDRFEE--------------EEGSSFI
At3g24340   CAYVAVEIKDISPA-----MDKYRPSV-NDNKKCSDRKG--------------DPLPNRL
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Bd2g26500    CSLVNLEIRFVLPS---M-VSNYAEKS-AWRNSSC------------------LKDALMY
Os05g32610   CSLVNLEIRFILPL-------LASNFA-EKPAWRNSSC---------------LKTALMC
RMR1         CSLVNLEIKFMFPS-------LVSVFA-EKSAWPNDKGV--------------KNTLMFH
Sb09g19410   CSLVNLEIKFMFPS-------LISGFA-EKSAWPNAKG---------------VKDTLMF
Pt286483     CSFVDLEIKYYVPP-----FDRYPRGK-SARRDFVTMQHNIFNDLHH------QDSGHDT
ZM178435     CHVVDLEIRDVLPT--------LGKCS-AERGSAINP--EFDRMLKEMLNVFEQNDVLVS
Sb04g33300   CNVVDIEIRHVLPT--------LGKFS-AERESAIDP--ELDKMLKEMLSVFEQNDVLVS
Bd3g50300    CNFIQLEIRHVVAD---M-VSHYSLQH-AFTKTLSELDL--------------SINNLLT
Os02g43460   CNFVDLEIRFVLPS-------MVKSCT-ERDMRKDHELDL-------------FFDDILT
Bd2g43500    CDFIDLEIRDVFPS-------MVKFSI-EREPAMSLNLDL-------------FCEDIIK
Cp76.2       CCFIQQEIKYIVPP----------------------------------------------
Vv15867      CSFVQLEIKYILPS--FS-RNPWGGSE-KGNAGKEDC----------------NSIFDEL

                                  1160
Sb02g43870   DLSFFEICAPESSKSKE--SGNVWSSIPVLEPKLLA
ZM000342     DLSFFEICAPEFSKIKE--SGNVWASITDLEPKLLA
ZM108166     DLSFFEICAPEFSKIKE--SGNVWASITDLEPKLLA
Os07g49210   DPSLLANLAPELSELKN--SGSVWSAISDLDPKLLP
Bd1g16720    DPSLLATFAPEFSEPRG--SGNLWSLIPDLEPKLLP
Sm441121     PDPFIRRPELNDLNDDL--ADDPYFPSTDTRRSLHA
At5g20420    DFSMISDSSEMLAAEE---SDNVWALIPKLKRKLHV
AtCLSY1      HTFTIPVASSDMPSAEE--SDNVWSLIPQLKRKLHL
Vv29366      ------------------------------------
Cp19.123     NLVGNHTSHERLLT-EE--NDNVWALIPELRNKLHL
Pt567214     IAHLFNVCKISPLV-PFEVNDNVWDLIPELRAKLHM
Pt832603     SLFGNHTSGEDVPVSEV--NDNVWDLIPELRPKLHM
Sm84719      HEDYAWKSTLNFGD-----VTVDLVPHPMDSARMYP
Os03g06920   DAIDKTSGAIL----EV--VPDALCLHPQHSQHMKP
Bd1g74070    DT---PINLSRNIL-QM--LPDPLSIHPQHLQQMKP
Sb01g46180   DATMNALGTILSV------APDTLSLHPQHSEQMKP
Bd3g18910    QIEDFGSATASAYE-DF--IFEDAAIHPMHAKEIRL
Os08g14610   CLKKVGSDAISLSE-DF--IFSDIAIHPRHAKNIRP
Os07g25390   DADDIDTGAVKVSE-DF--IVSDIAIHPRHAKQMRP
Os06g14440   DADEIDTGAVKVSE-DF--IVSDIAIHPRHAKQMRP
ZM064574     DADEIDCGTVKLSE-DF--IVADIAIHPRHARIMKP
ZM093940     DADEIDCGTVKLSE-DF--IVADIAIHPRHAQAMKP
Sb07g02945   DADEIDCGTVKLSE-DF--IIADVAIHPRHAQTMKP
Bd3g19890    DADEIIIGDIRVSD-DL--LALDIAIHPRHKKQIRS
Bd2g21450    DAGEIVVGNVTVSE-DL--IALDVAIHPRHAQHIKP
Bd2g21430    RSSEIVLGNVTVYE-DL--TALDVAIHPRHAQHIRP
At2g21450    DFSGIQSSHTNI-------LGEKMFIHPWHDQEMRP
AtDRD1       RFGESD-NELKFSEEGL--MIGGLAAHPTHAAEMKP
Pt195587     DRDSNGTVGADLFEEDL--MVTDIPAHPRHMKQMKP
Vv23895      EPTDDPSDGLRFSEHSL--IVTEIHAHPRHSMQMKP
Vv35918      EPTDDPSDGLGFSEHNL--TVTEIHAHPRHSMQMKP
At1g05490    GKLGFDAPNNSLNEGCVSSEGTVWDKIPGVKSQMYP
At3g24340    EFDASDPSSFVAPLDNI--EGTVWQYVPGIKDTLYP
Bd2g26500    HDLCEQAGSIDGQSQGFHPYGTVWDLIPGAINTMYQ
Os05g32610   PDLYEQTGTGDGQSQDFHINGTVWDLIPGVITDMYQ
RMR1         DLYEQGVNDTEQSQ-DIHQYGTVWNLIPGVISTMYE
Sb09g19410   HDLYEQTGSDIEQISDLHQYGTVWDLISGVISTMYE
Pt286483     HPDYDPCTLV---------QGTVWNLIPGIGKGMHG
ZM178435     NGHELPCNFGDHK------AGSVWNLIPGVKETMFP
Sb04g33300   NGHELPCNFGG----HK--AGSVWDLIPGVKETMFP
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```
Bd3g50300   SMGYEGTCKIVDHK-----AGSVWDLIPGVKEGLFT
Os02g43460  SAGYEGPRDFGGKK-----TGLVWDLVPGVREDMFP
Bd2g43500   SMGYEGTSHFDIHE-----SGLVWDLIPGVREHMFP
Cp76.2      ----------------F--QGTVWDMIPGVKDSMYP
Vv15867     QFQKPGCGSQSGSDHGLHPEGTVWDIIPGIRNSMYR
```

(D) TCOFFEE

```
                              20                  40                  60
At1g05490/  MECIGKRVKS-R-SWQ-------RLQAV--------------------------------
At2g21450/  MFTAWNLRSR--------------------------------------------------
At3g24340/  MDMTSCVARRTR-SRTE-----SYLNSILNKSKGIS----------GEEEDQ-----SLG
At5g20420/  MKKRGFYNLK-H------------------------------------------------
AtCLSY1/1-  MKRKHYFEFN-H------------------------------------------------
AtDRD1/1-3  MGFVYIVMTG-Y-YK-N-------------------------------------------
Bd1g16720/  MAGKTLKGPS-R-AAGH-------------------------------------------
Bd1g74070/  MDPSGCKRQK-H-EIEH-------------------------------------------
Bd2g21430/  MDAAAAATKI--------------------------------------------------
Bd2g21450/  MEMLKLPQEK--------------------------------------------------
Bd2g26500/  MDRSGRRGRA-R-GRGETLAEAS-------------------------------------
Bd2g43500/  MPKNKSPLVE------------T-------------------------------------
Bd3g18910/  MGGEMPNANM--------------------------------------------------
Bd3g19890/  MYYRRKNRA---------------------------------------------------
Bd3g50300/  MPPAADFPAS--------------------------------------------------
Cp19.123/1  MRKRRLYESR-H------------------------------------------------
Cp76.2/1-4  MEGKRLKLDN------------Q-------------------------------------
Os02g43460  MPRRKGKGKG-V---EDEVEVYE-------------------------------------
Os03g06920  MARYPAPTSS-R-AIGA-------------------------------------------
Os05g32610  MDRAARLAR--R-GGGVTVAEYR-------------------------------------
Os06g14440  MDLISMY-----------------------------------------------------
Os07g25390  MAAAGRDPPA-T------------------------------------------------
Os07g49210  MAGKKMSGEV-R-SVPA-----FDFAEWLKRTVSEQDYVVMKMDVEGTEFDLIPRLFDTG
Os08g14610  MSGSGNSLDT-V------------------------------------------------
Pt195587/1  MKDTKEKVT---------------------------------------------------
Pt286483/1  MSKSPIGHRK---P--------T-------------------------------------
Pt567214/1  MKRKHLHQSK-H------------------------------------------------
Pt832603/1  MKRKRLHQSK-H------------------------------------------------
RMR1/1-850  MDRATPRVCG-RRGVSQAAVEAA-------------------------------------
Sb01g46180  MNLRGDYLSD-K-YT-R-------------------------------------------
Sb02g43870  MVKGSTGHHN-N------------------------------------------------
Sb04g33300  MPAPPSAVPG-K------------------------------------------------
Sb07g02945  MQDLVAA-----------------------------------------------------
Sb09g19410  MDRAAPRARG-RRRRGV--SQAA-------------------------------------
Sm441121/1  MSSF--------------------------------------------------------
Sm84719/1-  MASNGPCSAI-H-SCVMLQLSHT-------------------------------------
Vv15867/1-  MDFSSPVAKR-TR-LQEALVY---------------------------------------
Vv23895/1-  MHSEPKQ-----------------------------------------------------
Vv29366/1-  MRIEDGT-----------------------------------------------------
Vv35918/1-  MEPTNGGLSS-N-YG-N-------------------------------------------
ZM000342/1  MMIKKKSGRC-H-LLAG-----HL-------------------ELE--------------
ZM064574/1  MSQSPGGREG--------------------------------------------------
ZM093940/1  MSQSPGGREG--------------------------------------------------
ZM108166/1  MVKGSTGHHS-N------------------------------------------------
ZM178435/1  MPAPPSTEAG-R------------------------------------------------
```

```
                              80                 100                 120
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  C---------------------------------------------------------VN
At5g20420/  ------------------------------------------------------------
AtCLSY1/1-  ------------------------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------------------------------------------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ------------------------------------------------------------
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ------------------------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Os05g32610  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  AICLIDELFLECHYNRWQKCCPDRAEAFEMAKGVSCFYWSIQFPNFKDHLCFRNCSNASS
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  ------------------------------------------------------------
Pt832603/1  ------------------------------------------------------------
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ------------------------------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  ------------------------------------------------------------

                             140                 160                 180
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  SR----------------------------------------------------------
At5g20420/  ---------------P--------------------------------------------
AtCLSY1/1-  ---------------P--------------------------------------------
```

```
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ---------------P--------------------------------------------
Bd1g74070/  ---------------D--------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ------------------------------------------------------------
Bd2g43500/  ---------------P--------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ---------------P--------------------------------------------
Cp76.2/1-4  ---------------P--------------------------------------------
Os02g43460  ---------------P--------------------------------------------
Os03g06920  ---------------P--------------------------------------------
Os05g32610  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ---------------P--------------------------------------------
Os07g49210  TRHFSYRSLLIRTEKPVTTRNHAYAEVVVFVLDQNPMFFLFLRFFYPAIQRGPNCWSSAN
Os08g14610  ---------------A--------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ---------------P--------------------------------------------
Pt567214/1  ---------------P--------------------------------------------
Pt832603/1  ---------------P--------------------------------------------
RMR1/1-850  ---------------P--------------------------------------------
Sb01g46180  ---------------M--------------------------------------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  ---------------G--------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ---------------P--------------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ---------------P--------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ---------------P--------------------------------------------
ZM000342/1  -----------------------------------------------------------D
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  ---------------S--------------------------------------------

                             200                 220                 240
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  --FDP-------------------------------------------------------
AtCLSY1/1-  --FNP-------------------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  --ICA-------------------------------------------------------
Bd1g74070/  ---------------------------------------------S--------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ----PRTRRRH--A-ETIVIDLDS-ED------------------GGGGS-STAA-A-AA
Bd2g43500/  -------RRRI--R-RLL-IDDDD-DDDD-----S----------GDG-GRAREAIS--P
```

```
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  --------KRK--S-RIE-IPDSD-DDAD-----RRRESRSSVG--TG-GQRERSAE--A
Cp19.123/1  --FGL-------------------------------------------------------
Cp76.2/1-4  --VA--------------------------------------------------------
Os02g43460  -------ASPP-ER-VLIILDSSE-DDLD-----LQEVRRSLMITGRGRARAAERVG--E
Os03g06920  --IQP----------------------------------------T--------------
Os05g32610  ---MVRGRRRGGDAGPVVVIDVED-DGEDAADDSA----------GGGGG-AAAA-----
Os06g14440  ------------------------------------------------------------
Os07g25390  --SS---R----------------------------------------------------
Os07g49210  STVMR-------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  --YQTR---EANSNVPVTKDNIY-------------------------------------
Pt567214/1  --YNA-------------------------------------------------------
Pt832603/1  --FNA-------------------------------------------------------
RMR1/1-850  --SSSRARRR--DKAPAVVMDLGD---DD-----C----------GGGG--ARKTVG-GA
Sb01g46180  ---------------------------------------------G--------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  -------RTKP--R-EIIVIDSDE-EGV-----------------GGGGRQAGRDLGSGA
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --SSSRARRR--DKAPVVVVDLGDDEDED-----C----------GGGGG-ARKTVG-GA
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  --LASKAVRF-TLHL---------------------------------------------
Vv15867/1-  -------RR---------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  --I-P-------------------------------------------------------
ZM000342/1  LTVDS-------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  -------RTMT--R-VIILLDSDK-EDD-----------------GT-GRQAGRELG-GA

                             260                 280                 300
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  ------------CP-------------------------------------F--EFFCSG
AtCLSY1/1-  ------------CP-------------------------------------F--EVFCWG
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------TP-------------------------------------F--EAFHHG
Bd1g74070/  ------------SPG---------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  SSS---SSRRSS------------------------------------------APL---
Bd2g43500/  SV-AAGGSRRV-------------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  GR-SGGLERRL-------------------------------------------------
Cp19.123/1  ------------HP-------------------------------------F--EAFSRG
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  EA-PRGSGRR--------------------------------------------------
Os03g06920  ------------EPHAPLPNTGGEGAPPPARTMPPPSSQAATSTPPAAATPLQRPPAQAT
```

```
Os05g32610  ------VK------------------------------------------------R---
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------QA-------------------------------------F--EVFYDG
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------STHRS----------------------------------------P--SP----
Pt567214/1  ------------HP-------------------------------------F--EALYGG
Pt832603/1  ------------HP-------------------------------------F--EALCCG
RMR1/1-850  AGRCE-GSTKAPLP-------------------------------------L--LPP---
Sb01g46180  ------------SAG---------------------------------------------
Sb02g43870  -------------P-------------------------------------I--G-----
Sb04g33300  AIGAAGEAVKLV------------------------------------------KPE---
Sb07g02945  ------------------------------------------------------------
Sb09g19410  AGGRG-GSTEASPP-------------------------------------P--PPP---
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -----------PEP-------------------------------------I--------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ---------------------------------------------------VNFEPYKLT
ZM000342/1  ------------TP-------------------------------------L--PFLPQG
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  -------------P-------------------------------------I--A-----
ZM178435/1  AIASAGEASKLV------------------------------------------KPE---

                             320                 340                 360
At1g05490/  ---------------NKRK-----KMETVAPV---------TSPPK-KRRQKK-------
At2g21450/  --------------------------------------------------SRS-------
At3g24340/  ---------------TEKR-----RVNMRDAC---------SPSPRKKKRRRR-------
At5g20420/  TWKPVEYM-------RIED-----GMMTIRLLENGYVLEDIRPFQRLRLRSRK-------
AtCLSY1/1-  TWKAVEYL-------RIEN-----GTMTMRLLENGQVLDDIKPFQRLRIRSRK-------
AtDRD1/1-3  ------------------------------------------------VHKRK-------
Bd1g16720/  SWHGVNCI-------RVQN-----SRLFVRFVYSGSTVERNIDRDHLRLRSRR-------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  -----------------------------------------------FRRNHR-------
Bd2g21450/  -----------------------------------------------ERE--K-------
Bd2g26500/  -------T-------LVTS-----G------------------SVATRTRSRS-------
Bd2g43500/  ------------------------GAE---------------I---------S-------
Bd3g18910/  --------------------------------------------------TNC-------
Bd3g19890/  --------------------------------------------------S---------
Bd3g50300/  ------------------------------------------AAAIARRRTRA-------
Cp19.123/1  SWRMVDCI-------RIED-----GTMSLRFVDGRHVIKRKRPFSELRVRSRQ-------
Cp76.2/1-4  ----------------------------------------------RRTRLKE-------
Os02g43460  ------------------------AAP---------------VVASRRRRRRS-------
Os03g06920  A-------------------------------------QPSTQRYYVGVQRDK-------
Os05g32610  -------R-------VVVP-----G------------------AVATRTRSRR-------
Os06g14440  -----------------------------------------------YRRQRK-------
Os07g25390  ---------------------------------------------MYYCRQRK-------
Os07g49210  SWHGVNCI-------RIRN-----GNLFVKFIYSGSTVEHNVDGDCLRLRSRR-------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  --------------------------------------------SLQWTRLRE-------
```

```
Pt567214/1  SWQSVELI-------EIRD-----GAMTLHFADSHHRIEEKGPFSNIRVKSRK-------
Pt832603/1  SWQSVELI-------QIRD-----GAMTVHFVDSHHRIEEKGPFSNVRVKSRK-------
RMR1/1-850  -------M-------MVPA-----G------------------AVALRTRSRR-------
Sb01g46180  -------------------------------------------------QKRQ-------
Sb02g43870  -----------------------------------SVLQHDIDGSYLRIRSRK-------
Sb04g33300  -------PVDDAGFHPVLPGAPRLGAV---------------PVPPRAQNPRAPSSPRAQ
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -------M-------MVPA-----G------------------AVAMRTRSRR-------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  --------------------------VALHLAESEYVIEEKSPIPNLRIRPRK-------
Vv35918/1-  E-------------------------------------------FNSTKHKRI-------
ZM000342/1  -----------------PN-----GQPIFFTVQRPVAVQHDIDGSYLRVRSRK-------
ZM064574/1  ---------------------------------------------IYYSRQRK-------
ZM093940/1  ---------------------------------------------IYYSRQRK-------
ZM108166/1  -----------------------------------PVLQHDIDGSYLRVRSRK-------
ZM178435/1  -------VVDDVGSNPVRP-----GAL---------------P-----------------

                             380                 400                 420
At1g05490/  --------PKNYDSD----IEDITPT-CND-SVPP-P---QV------------------
At2g21450/  --------IT--QEE------------LA--KRPD-P-----------------------
At3g24340/  --------K-D-DDD----DVVF--------VRT--------------------------
At5g20420/  --------AA--LSD------------CICFLRPD-I---DV------------------
AtCLSY1/1-  --------AT--LID------------CTSFLRPG-I---DV------------------
AtDRD1/1-3  --------QN--Q----------------VDDGPE-------------------------
Bd1g16720/  --------AT--CFD------------CSHVLKPG-V---DV------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  --------LP--PVV------------QQKRFPPS-GG----------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  --------LA--MK--------------SPV-----------------------------
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  --------FM--EQT------------EK--KKYNVL-----------------------
Bd3g19890/  ------------DPI------------S---------G----------------------
Bd3g50300/  --------AA--ASR---------------------------------------------
Cp19.123/1  --------AN--LTD------------CTCFLRPG-I---DV------------------
Cp76.2/1-4  ---------------------------AQ-------------------------------
Os02g43460  --------RS--RSR---------------------------------------------
Os03g06920  --------GT--GKW------------AACVVDPS-N---PTKHRLVGAFPDEHAAALAH
Os05g32610  --------MA--MAQ------------QAPVTPP--------------------------
Os06g14440  --------AS--SEA------------NANVFMPG-G---PN------------------
Os07g25390  --------AS--SEV------------NANVFVPG-G---QN------------------
Os07g49210  --------AT--CSD------------CSNVLKPG-V---DV------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ---------------------------AE-------------------------------
Pt567214/1  --------ST--LSD------------CTCFLRPG-I---DV------------------
Pt832603/1  --------AT--SSD------------CTCFLRPG-I---DV------------------
RMR1/1-850  --------RA--MLA------------AA-------------------------------
Sb01g46180  --------KL--GS--------------EHTSSPG-------------------------
Sb02g43870  --------AT--CSD------------CSHVLKPG-A---DV------------------
Sb04g33300  AQNPRAPSSP--RTPSPR-APSLPSLVAAHPLGPG-A---PR------------------
Sb07g02945  ------------------------------------------------------------
```

```
Sb09g19410  --------RA--MQA------------AA-------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -----QPS-S--RPPPPCAARALLTSSSSYFLSL--------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  --------AT--LSD------------CTCFLRPG-T---EI------------------
Vv35918/1-  --------WT--FEE-------------NMHSEPK-------------------------
ZM000342/1  --------AT--CSD------------CSHVLKPG-A---DV------------------
ZM064574/1  --------P----ER------------NGSVFTPI-AAMYSS------------------
ZM093940/1  --------PS---ER------------NGSVFTPI-AAMYPS------------------
ZM108166/1  --------AT--CSD------------CSHVLKPG-A---DV------------------
ZM178435/1  ------------------------------------------------------------

                             440                 460                 480
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  ------------------------------------------------------------
AtCLSY1/1-  ------------------------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------------------------------------------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ------------------------------------------------------------
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ------------------------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  DRLDLAFRGGGHRGAGDNFRPAFHAVELEFLRLCAATSSPGSHCGLVAGGDKYDEKYSEF
Os05g32610  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  ------------------------------------------------------------
Pt832603/1  ------------------------------------------------------------
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ------------------------------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
```

```
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  ------------------------------------------------------------

                             500                 520                 540
At1g05490/  -----------------------------------------------------------S
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  -----------------------------------------------------------C
AtCLSY1/1-  -----------------------------------------------------------C
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  -----------------------------------------------------------C
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  -----------------------------------------------------------A
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ------------------------------------------------------------
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  -----------------------------------------------------------C
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  LRKIYHGVMDNSPSYKKFFDVILDFFIARAREIGREALEDGGDMLVERFVAMHKNKAVTP
Os05g32610  ------------------------------------------------------------
Os06g14440  -----------------------------------------------------------D
Os07g25390  -----------------------------------------------------------G
Os07g49210  -----------------------------------------------------------C
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  -----------------------------------------------------------C
Pt832603/1  -----------------------------------------------------------C
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Sb02g43870  -----------------------------------------------------------C
Sb04g33300  -----------------------------------------------------------L
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ------------------------------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  -----------------------------------------------------------T
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  -----------------------------------------------------------C
ZM064574/1  -----------------------------------------------------------G
ZM093940/1  -----------------------------------------------------------G
ZM108166/1  -----------------------------------------------------------C
ZM178435/1  ------------------------------------------------------------

                             560                 580                 600
```

```
At1g05490/  -----NMYS-------------VPNN------SVKE--------------SFSRIMR---
At2g21450/  -------FC-------------LPNL----------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  -----VLYR-------------I---------HEDD--------------LEP-VWV---
AtCLSY1/1-  -----VLYQ-------------R---------DEET--------------PEP-VWV---
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  -----VQSP-------------HPLQACST-GDQKS--------------SIS-LCH---
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -------------AEAEA-AP---------------------------------------
Bd2g43500/  -----GWLVRDPLAPSSSAQPG-TLLR--SR-----------------------------
Bd3g18910/  -------LI-------------LD------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ----------------------------------P----------------EV-VNLTGD
Cp19.123/1  -----VLIP-------------SKDLA--S-SDEAN--------------LEL-VLI---
Cp76.2/1-4  --------------FFKE-YY---------------------------------------
Os02g43460  -----SPRAARPRAESSR-RPTARRAR--ARARSPS--------------LEI-IDV---
Os03g06920  -----RWRA-------------WYR------SDSRKVLQIPLSLRGGGGEIDHSTQK---
Os05g32610  -------------AAAEE-AP---------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  -----VQSS-------------HTPEASSQ-GGTNA--------------SVL-LRH---
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  --------------VYKK-LH---------------------------------------
Pt567214/1  -----VLSF-------------SERAK--S-SEEGN--------------SEP-VWV---
Pt832603/1  -----VLSS-------------SERAK--N-TGEGN--------------SEP-VWV---
RMR1/1-850  --------------VVEE-AP---------------------------------------
Sb01g46180  ------------------------------------------------------------
Sb02g43870  -----VWQA-------------T-----YG-GETKD--------------SVP-LCR---
Sb04g33300  GVVPVPPRAQNPRAPSSP-SPVAPEDR--HQ---P----------------EI-IAISDD
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --------------VVEE-TP---------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -----------P----------LDEAA--S-LENHL--------------SIV-VAV---
Vv15867/1-  -------------------LY---------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  -----VLWT-------------LQQSE--S-SDEEN--------------REP-VWI---
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  -----VWQA-------------V-----YR-GETKD--------------SVLLCCR---
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  -----VWQA-------------V-----YR-GETKD--------------SVLLCCR---
ZM178435/1  ----TSLRVQGHRAPSSP-SPVPAAVR--KQ---P----------------EI-IAISDE

                             620                 640                 660
At1g05490/  --D---------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  --DA--------------------------------------------------------
AtCLSY1/1-  --DA--------------------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  --DA--------------------------------------------------------
```

```
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ------------------------------------------------------------
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  DDDDIRD-------EEAAGRREVLGRVKEEPLDDRGLDPEASVARRGRGRGRARAAA--A
Cp19.123/1  --DA--------------------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  --DS-------------GSDRG-VVRVKEEPRSGSDSDYNGA---RGRARARARAPV--A
Os03g06920  --EA--------------------------------------------------------
Os05g32610  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  --DA--------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  --DA--------------------------------------------------------
Pt832603/1  --DA--------------------------------------------------------
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  ------------------------------------------------------------
Sb02g43870  --DA--------------------------------------------------------
Sb04g33300  DG-GSRFRGAVPLDMIEESGRR-VRPVKEEALDDLDCDWVRSA-----EAKRALVAVLPP
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ------------------------------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  --DG--------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  --DA--------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  --DA--------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  --DA--------------------------------------------------------
ZM178435/1  DNDGSRF-------------RR-VRRVKDEA-----SDWVLSA-----KAKRAMVSGVPP

                             680                 700                 720
At1g05490/  ----------------------------------------------LNVEKKSGPS----
At2g21450/  ------------------------------------------------------------
At3g24340/  ----------------------------------------------------EYPE----
At5g20420/  ------------------------------------------RI--VSIERK--PH----
AtCLSY1/1-  ------------------------------------------RV--LSIERK--PH----
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------------------------------------RI--VTIKRN--HN----
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ----RA--KRRRKGTS----A----EADGG-GGSKGAEAS------------------ES
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
```

```
Bd3g50300/  SAPVAS--RKRRREDD----SG--------------------------------------
Cp19.123/1  ------------------------------------------KI--RSIERK--PH----
Cp76.2/1-4  ----ER--RRKEDGKN--VARPSGQSEDRGVNGSKLGRVGLKGT--NMETRDL--GLNCK
Os02g43460  ATAAKK--KKRKRGKE----APSR------------------------------------
Os03g06920  ------------------------------------------RMDSDSCKRR--KH----
Os05g32610  ----SR--RRKRKGAA----S----AEAGG-GGPSKRRVR------------------SS
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------------------------------RL--ITIKKN--HQ----
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ----DEIRKGRNQGKESNAAATGST---NGLNGAQEESV-------------G--GLS--
Pt567214/1  ------------------------------------------RI--NSIKRK--PH----
Pt832603/1  ------------------------------------------KI--SSIKRK--PH----
RMR1/1-850  ----TK--KKKKEGA-----IPDAAEAPRG-HGSKAAATSM-AT--SSHKRRA--GTSRS
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------------------RL--IKIKRN--HQ----
Sb04g33300  GSSHAK--RKRKRASS----GRA-------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ----TT--KRRKRGAT----TPDAAEASRG-RGSKAAAASR-AT--SRDKRRA--GASRS
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------ET--SRTERL--------
Vv15867/1-  ----EE--KKRNAGVS----SSGSHN-------------------------DD--GVEFL
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------KI--SSIERR--PH----
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ------------------------------------------RL--IKIKRN--HQ----
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------RL--IKIKRN--HQ----
ZM178435/1  GSSDVK--RKRKRGSS----GA--------------------------------------

                             740                 760                 780
At1g05490/  ---------------SS--------------------------------RLT--DGSEQN
At2g21450/  ---------------------------------------------------L--D-----
At3g24340/  ---------------GK--------------------------------RDDENVGSTSG
At5g20420/  ---------------ES--------------------------------E---------C
AtCLSY1/1-  ---------------ES--------------------------------E---------C
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ---------------AD--------------------------------Q---------C
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ---ASKGNRRGRSRTASEPPD--RALARKSKDADAEEEAEAEAEEE--AE---------A
Bd2g43500/  --------------E---------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ---------------ES--------------------------------Q---------C
Cp76.2/1-4  GSA----------------GLENRARRI------------------KTR-----------
Os02g43460  --------------A---------------------------------------------
Os03g06920  ---------------ES--------------------------------G---------H
Os05g32610  ---GSAGGRGARKRKEAE--------------AD-EEEAEAEAEEEAEAE---------A
Os06g14440  ------------------------------------------------------------
```

```
Os07g25390  ------------------------------------------------------------
Os07g49210  ---------------ED--------------------------------K---------C
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  ---------------ES--------------------------------Q---------C
Pt832603/1  ---------------VS--------------------------------H---------C
RMR1/1-850  ---TSRDKRRARSGRASEPARVGRARKR------------------KRNE---------L
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ---------------LD--------------------------------R---------C
Sb04g33300  ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ---TSRDKRRARSGRASEPARAARACKRKGIELG------------AETE---------V
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ---------NLCSTEYT--------------------------------L---------C
Vv15867/1-  GEAGVFDSVQ--------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ---------------EP--------------------------------E---------C
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ---------------SD--------------------------------R---------C
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ---------------SD--------------------------------R---------C
ZM178435/1  ------------------------------------------------------------

                             800                 820                 840
At1g05490/  ------------PCLKERSFRVS--DL---------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  NLQSKSFDFGDRVCDFDA---DDR-NL---------------------------------
At5g20420/  ------------SCKINVRIYIDQGCIGSEKQR--INRDSVVIGL---------------
AtCLSY1/1-  ------------LCTFHVSVYIDQGCIGLEKHR--MNKVPVLVGL---------------
AtDRD1/1-3  ---------------------------AK---R--VKSSAKVIDY---------------
Bd1g16720/  ------------LCLFLVILDDSQCPGNTEKGGKATDRRQEVVTL---------------
Bd1g74070/  -----------------------------------NQSQATIISH---------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -----------------------EAPACGKR--------VEVSRVD-G-----------C
Bd2g43500/  ----------------------------QEQ--------PEIIVISDD-----------D
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ------------SCQFYVNLYVNQGPLGSEKLE--LDKDTKVLGI---------------
Cp76.2/1-4  ------------------------------------------EKVTDE-----------N
Os02g43460  ----------------------------QES--------REVVRVKEE-----------P
Os03g06920  ------------DS-------------SS---R--VQSQSSILSR---------------
Os05g32610  -----------------------GTPARGES--------MEVSQVD-G-----------G
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------LCLFVVILYKNQCPGNAEKVI--TDRRAEVVTI---------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  -------------------------------------------DY---------------
Pt286483/1  ----------------------------YKG--------SKSPVVLDD-----------S
Pt567214/1  ------------SCQFFVNLYVNQGPLGSERAT--LSKETEAVGI---------------
Pt832603/1  ------------SCQFFVNLYVNQGPLGSERAR--LSKETEAVGI---------------
```

```
RMR1/1-850  -----------------------EAPARRER--------VKAPCVSES-----------D
Sb01g46180  -----------------------------------TQSQSNIFLA---------------
Sb02g43870  ------------LCLFAVIFYKDQCPGSKEKVI--SGTIADVVTI---------------
Sb04g33300  ---------------------------------------------KPDKRADGGVHALDR
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -----------------------DAPARSER--------AKAPCVSES-----------D
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -----------------------SCPAFKLS--------SSYEAVCEE-----------Q
Vv15867/1-  ------------------------------------------KFVAES-----------D
Vv23895/1-  ----------------------------K---R--QKAGSNVVDY---------------
Vv29366/1-  ------------SCQFFVNFYITQDPLGTEKGT--LSKDISVVEL---------------
Vv35918/1-  ---------------------------QK---R--QKAGPNVVDY---------------
ZM000342/1  ------------LCLFAVIFYKDQCPGSKEKVI--SGTIADVVTI---------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------LCLFAVIFYKDQCPGSKEKVI--SGTIADVVTI---------------
ZM178435/1  ----------------------------------------------------GDFHALDR

                             860                 880                 900
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  ------------------------------------------------------------
AtCLSY1/1-  ------------------------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------------------------------------------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  A--NSERGEDPL--------D---DHNNGSNAREACGIGHGNEEHHNAA-----------
Bd2g43500/  H--EDEE-EDGARGGEI-------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  -----SR-GRGGRRATRSAK----------------------------------------
Cp19.123/1  ------------------------------------------------------------
Cp76.2/1-4  K--DRVREM--------NAK----------------------------------------
Os02g43460  N--SDGN-GAGGRARARSPV----------------------------------------
Os03g06920  ------------------------------------------------------------
Os05g32610  G--SSGRADDAS--------H---NGNGESRVCNADGIDQASEERPSVAGGDLIEEEHYG
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  E--DDA-----------FLD----------------------------------------
Pt567214/1  ------------------------------------------------------------
Pt832603/1  ------------------------------------------------------------
RMR1/1-850  D--NSGRGDDAS--------H---DGDAEPRVGVAIGTDLVNGDHPA-------------
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  N--SSAS-GAG-HPTAWMSDDARSSRGVKSRES---------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  D--DGGRGDDAS--------D---DGNAEPRAGVAIGADLVNGDRRTAK-----------
Sm441121/1  ------------------------------------------------------------
```

```
Sm84719/1-  DLAED----DAS--------K---DTEI--------------------------------
Vv15867/1-  G-KNSDRKN-SS-----RKKN---------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  N--LSAS-GAG-RRTSWMAEDAGSSRNVSSSEL---------------------------

                             920                 940                 960
At1g05490/  -----------------------------------------------GVE-------KKC
At2g21450/  -----------------------------------------------GLE-------D--
At3g24340/  -----------------------------------------------GCE-------EKA
At5g20420/  ---------------------------------NQISILQKFY--KEQST-------DQ-
AtCLSY1/1-  ---------------------------------NEIAILQKFC--KEQSL-------DR-
AtDRD1/1-3  ---------------------------------SNPFAVSNML---EALD-------S--
Bd1g16720/  ---------------------------------NNIFLLQKLQ--PKELQ-------EG-
Bd1g74070/  ---------------------------------NSSVRL-RFL---EQFD-------D--
Bd2g21430/  ------------------------------------SFLPPR----CEAL-------S--
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -------GKNRIGEPCG----N--------------------------------------
Bd2g43500/  ---------------------------------RHGEIPARVK--DEESE-------EGS
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------LSLPAG----SGVH-------S--
Bd3g50300/  --------------QCTR-GRR-GGLRSLPSRPSSSD-----------------------
Cp19.123/1  ---------------------------------DQILILQRLE--KHPCE-------GQ-
Cp76.2/1-4  --------------DCGDLNPE--------------------------------------
Os02g43460  --------------AAAA-KQRKRGGREAPSRAQESRVPVQIK--E-EPY-------SGS
Os03g06920  ---------------------------------NRILCH-QLL---EQCD-------D--
Os05g32610  NGEASVAGGDRIEEHCG----N--------------------------------------
Os06g14440  ------------------------------------ISFPAS----NRDH-------D--
Os07g25390  ------------------------------------ISFPAS----NRAH-------D--
Os07g49210  ---------------------------------NDIFLLQKLQ--PE-VH-------EG-
Os08g14610  --------------------------------------LIVG----GGSD-------S--
Pt195587/1  ---------------------------------AKPFAIRGLL---ERLD-------S--
Pt286483/1  --------------DCEKGGLE--------------------------------------
Pt567214/1  ---------------------------------DQISILQKLD--NDPCEADNNRHETQ-
Pt832603/1  ---------------------------------NEISVLQKLD--NDPCEADNNQQEAQ-
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  ---------------------------------NKRLRL-QFL---EQVN-------E--
Sb02g43870  ---------------------------------DDVCILQNLQ--SEELQ-------DG-
Sb04g33300  -------------SRGVA-GDR-PGSA---------K-----------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -------GEDHIEEHGG----D--------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ---------------------------------SHSSALRQSKVSPLTTE-------LT-
Vv15867/1-  ---------------GGENSDE--------------------------------------
Vv23895/1-  ---------------------------------SDPFAIPNLL---EGLD-------A--
Vv29366/1-  ---------------------------------DQISILQKLG--KYPCE-------DE-
Vv35918/1-  ---------------------------------SDPFAIPNLL---EGLD-------A--
ZM000342/1  ---------------------------------DDICILQNLQ--PEELQ-------DG-
ZM064574/1  ------------------------------------HALPVA----NRSH-------G--
```

```
ZM093940/1  ------------------------------------HALPDA----NRNH-------S--
ZM108166/1  ---------------------------------DDICILQNLQ--PEELQ-------DG-
ZM178435/1  -------------SRGGV-GDR-SGST---------K-----------------------

                               980                 1000                1020
At1g05490/  SPEITDLDVGIPVPR-F-------------------------------------------
At2g21450/  -------------GL-Y-------------------------------------------
At3g24340/  S-----------------------------------------------------------
At5g20420/  -------------FY-R-------------------------------------------
AtCLSY1/1-  -------------YY-R-------------------------------------------
AtDRD1/1-3  -------------GK-F-------------------------------------------
Bd1g16720/  -------------SV-Q-------------------------------------------
Bd1g74070/  -------------LK-Y-------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  --------------G-VASI---------LNSSH-------------------G-----
Bd2g43500/  -------------SV-DWDA---------LMLSDD-------------------ESTA--
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  -------------WG-C-------------------------------------------
Bd3g50300/  --------------------------EPL-------------------------------
Cp19.123/1  -------------YY-R-------------------------------------------
Cp76.2/1-4  --------------K-CRDV---------IVIDDD-------------------DN----
Os02g43460  -------------DS-DGNVAGGRAVVPAADAKQGKRGKKTPSRGKGRRVVVRETSTP--
Os03g06920  -------------LK-Y-------------------------------------------
Os05g32610  --------------V-EASV---------ANSNRD-------------------G-----
Os06g14440  -------------WG-Y-------------------------------------------
Os07g25390  -------------WG-Y-------------------------------------------
Os07g49210  -------------SM-K-------------------------------------------
Os08g14610  -------------SGIV-------------------------------------------
Pt195587/1  -------------GR-Y-------------------------------------------
Pt286483/1  --------------E-GLDV---------VSLDDS-------------------DDDDQS
Pt567214/1  -------------FY-R-------------------------------------------
Pt832603/1  -------------FY-R-------------------------------------------
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  -------------LK-A-------------------------------------------
Sb02g43870  -------------SV-Q-------------------------------------------
Sb04g33300  --------------------------K--------------------ALVSSE-------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --------------Q-ENSA---------VNLNDD-------------------LVS---
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -------------KL-S-------------------------------------------
Vv15867/1-  --------------D-VTDV---------VSISDD-------------------SE----
Vv23895/1-  -------------GK-F-------------------------------------------
Vv29366/1-  -------------HY-R-------------------------------------------
Vv35918/1-  -------------GR-F-------------------------------------------
ZM000342/1  -------------SV-R-------------------------------------------
ZM064574/1  -------------LV-F-------------------------------------------
ZM093940/1  -------------LV-F-------------------------------------------
ZM108166/1  -------------SV-R-------------------------------------------
ZM178435/1  --------------------------K---------------------------------

                              1040                 1060                1080
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
```

```
At3g24340/   ------------------------------------------------------------
At5g20420/   ------------------------------------------------------------
AtCLSY1/1-   ------------------------------------------------------------
AtDRD1/1-3   ------------------------------------------------------------
Bd1g16720/   ------------------------------------------------------------
Bd1g74070/   ------------------------------------------------------------
Bd2g21430/   ------------------------------------------------------------
Bd2g21450/   ------------------------------------------------------------
Bd2g26500/   -----------------------M------------------------------------
Bd2g43500/   ----------------------AAP-------------------PGTAT-----------
Bd3g18910/   ------------------------------------------------------------
Bd3g19890/   ------------------------------------------------------------
Bd3g50300/   ---------------------------GDSGRAKRVRRGHAE-G--------GGSGRHGA
Cp19.123/1   ------------------------------------------------------------
Cp76.2/1-4   ------------------------------------------------------------
Os02g43460   ----------------------AAPSNGAPS----VGRGKGR-GPGRGRQRSKGAVRGRA
Os03g06920   ------------------------------------------------------------
Os05g32610   -----------------------G------------------------------------
Os06g14440   ------------------------------------------------------------
Os07g25390   ------------------------------------------------------------
Os07g49210   ------------------------------------------------------------
Os08g14610   ------------------------------------------------------------
Pt195587/1   ------------------------------------------------------------
Pt286483/1   EGVESKSFDVGGKKSGGTDVGG--------------------------------------
Pt567214/1   ------------------------------------------------------------
Pt832603/1   ------------------------------------------------------------
RMR1/1-850   ----------------------AK------------------------------------
Sb01g46180   ------------------------------------------------------------
Sb02g43870   ------------------------------------------------------------
Sb04g33300   -------------------------------ESRG-APGKARSGGGARRER-----STSV
Sb07g02945   ------------------------------------------------------------
Sb09g19410   ---------------------GDA------------------------------------
Sm441121/1   ------------------------------------------------------------
Sm84719/1-   ------------------------------------------------------------
Vv15867/1-   ------------------------------------------------------------
Vv23895/1-   ------------------------------------------------------------
Vv29366/1-   ------------------------------------------------------------
Vv35918/1-   ------------------------------------------------------------
ZM000342/1   ------------------------------------------------------------
ZM064574/1   ------------------------------------------------------------
ZM093940/1   ------------------------------------------------------------
ZM108166/1   ------------------------------------------------------------
ZM178435/1   --------------------------------ARG-APGKTRRGGGTRRER-----STSA

                             1100                1120                1140
At1g05490/   -----------------SKLKDVSEQKNTCLMQKSSP---EI-AD----L----------
At2g21450/   -----------------GRLAD-----DVKRLCKLRQ---EY-LN----G----------
At3g24340/   ------------------NFNPIDDDDDVVFVGTVQRENDHV-EDDDNVG----------
At5g20420/   -----------------WRFSE-----DCTSLMKTRL---SL-GK----F----------
AtCLSY1/1-   -----------------WRYSE-----DCSSLVKTRL---NL-GK----F----------
AtDRD1/1-3   -----------------GSVSK-----ELEEIADMRM---DL-VK----R----------
Bd1g16720/   -----------------WNSAE-----DCLYQNRSRL---LSAAR----F----------
Bd1g74070/   -----------------ASATK-----DYKAVNAKMH---EL-LS----T----------
Bd2g21430/   -------------------------------------------VN----F----------
```

```
Bd2g21450/       ------------------------------------------------------------
Bd2g26500/       --------NV-VASGHA-------------------------------------------
Bd2g43500/       ----------GV------------------------------------------------
Bd3g18910/       ------------------------------------------------------------
Bd3g19890/       -----------------GSVTK-----DMEDIYARNV---QL-IN----F----------
Bd3g50300/       APSKQAGS--LV------------------------------------------------
Cp19.123/1       -----------------WSLSE-----DCSSLSRTKL---FL-GK----F----------
Cp76.2/1-4       ------------------------------------------------------------
Os02g43460       TPVNRVST--GV------------------------------------------------
Os03g06920       -----------------GSSTN-----DYKAISMKRL---EL-IS----I----------
Os05g32610       --------EI-IA---G-------------------------------------------
Os06g14440       -----------------GGVGK-----EWEASYARKL---QL-MN----F----------
Os07g25390       -----------------GGVRE-----EWEASYARKL---QL-IN----F----------
Os07g49210       -----------------WSFSK-----DRLSLNKGRL---IS-AR----F----------
Os08g14610       -----------------GR-------------KRRRC---DL-IRE---R----------
Pt195587/1       -----------------GSVTD-----DIRSLFYRRA---QL-IH----P----------
Pt286483/1       ---------------SCSGVKS-----DGEESGRSKV---PL-PR----WQRIVNESYNG
Pt567214/1       -----------------WEFCE-----DCSLVQRT-------------------------
Pt832603/1       -----------------WEFCE-----DCSLVQRSKL---FL-GR----F----------
RMR1/1-850       --------EV-VE---G-------------------------------------------
Sb01g46180       -----------------WSVTK-----DLKAITAKRR---EL-FG----I----------
Sb02g43870       -----------------WNSAV-----DCFHHNRSKL---LS-AR----F----------
Sb04g33300       APANWIGT--SI------------------------------------------------
Sb07g02945       ------------------------------------------------------------
Sb09g19410       --------EA-VE---G-------------------------------------------
Sm441121/1       ------------------------------------------------------------
Sm84719/1-       ------------------------------------------------------------
Vv15867/1-       ------------------------------------------------------------
Vv23895/1-       -----------------GSMTK-----EIEALCARRM---QM-LH----P----------
Vv29366/1-       -----------------WKFSE-----DCSLLQRTKL---FL-GK----F----------
Vv35918/1-       -----------------GSVTK-----EIEALCARRM---QM-LQ----P----------
ZM000342/1       -----------------WNSAV-----DCFHHNRSKL---LS-AR----F----------
ZM064574/1       -----------------GSLSK-----DWDDIRQRKD---QL-VN----F----------
ZM093940/1       -----------------GGTSK-----DWDNIRQ---------------F----------
ZM108166/1       -----------------WNSAV-----DCFHHNRSKL---LS-AR----F----------
ZM178435/1       APANLVGGSATV------------------------------------------------

                                 1160                1180                1200
At1g05490/       ------------------------------------------------------------
At2g21450/       ------------------------------------------------------------
At3g24340/       ------------------------------------------------------------
At5g20420/       ------------------------------------------------------------
AtCLSY1/1-       ------------------------------------------------------------
AtDRD1/1-3       ------------------------------------------------------------
Bd1g16720/       ------------------------------------------------------------
Bd1g74070/       ------------------------------------------------------------
Bd2g21430/       ------------------------------------------------------------
Bd2g21450/       ------------------------------------------------------------
Bd2g26500/       -----------------EG--VK---D-----------WGNKGGEL-DDG--------FE
Bd2g43500/       ------------------PD----------------------------------E-----
Bd3g18910/       ------------------------------------------------------------
Bd3g19890/       ------------------------------------------------------------
Bd3g50300/       ------------------ASSSR---S-----------RKGKQ------RAALPPKHQFP
Cp19.123/1       ------------------------------------------------------------
```

```
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------GSRTR---S-----------RLAEQ------GRAFAQ-----
Os03g06920  ------------------------------------------------------------
Os05g32610  -----------------EG--TE---D-----------RGNTE--L-SVV--------DP
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  DVFAHERNEGGVCFLSSGI--GNGSGGVGLKGRESNGVAGRTE--L--------------
Pt567214/1  ------------------------------------------------------------
Pt832603/1  ------------------------------------------------------------
RMR1/1-850  -----------------AG--DEDTGD-----------GGNSG--LASTA--------DV
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  ------------------GSRIR---S-----------RSRKQ------GTG--------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -----------------AG--DEDT-------------RGNSG--LASTA--------DV
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ---------------------------------------------LSSSF--------EA
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  ------------------GSRIR---L-----------RSRQQ------GRV-----QCA

                            1220                1240                1260
At1g05490/  -------------DLVI-SVPSSSVLKDVS--EEIRFLK--DKC----------------
At2g21450/  -------------SIS---------LED--------------------------------
At3g24340/  -------------SASV-ISP---------------------------------------
At5g20420/  -------------LPDLSWLTVTSTLKSIV--FQIRTVQ--TKM----------------
AtCLSY1/1-  -------------LPDLTWLLVTSVLKNIV--FQIRTVH--EKM----------------
AtDRD1/1-3  -------------SIWL-----YPSLAYTV--FEAEKTM--D------------------
Bd1g16720/  -------------SSEISHLIVLSALRGME--FSIKLVE--GNI----------------
Bd1g74070/  -------------LEKL-----KEVPIKLPYVSPVLKTS--DAR----------------
Bd2g21430/  -------------VATY--------------------------------------FLRCT
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  VDEEYMNEEDTE--------------------DDDEMLE--EKL----------------
Bd2g43500/  --EEEAELEDK---------------------DNLE--EEQ-------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  -------------LSTL-----HEPTRSSV-----PMVE--TNVKYCSIK-QETKVTDCS
Bd3g50300/  LVSQSESSSES---------------------DDDDDDEEGDDG----------------
Cp19.123/1  -------------SSDLSWLLVASVLKQVA--FEVRTEQ--YKI----------------
Cp76.2/1-4  -----------------------------------E------------------------
Os02g43460  --EEEEQVEER---------------------EEEEEEEEQ-------------------
Os03g06920  -------------LQKL-----QEVPIQLPYASPLKSSE--TN-----------------
Os05g32610  VNEELASDED-D--------------------YDDEMLE--EKL----------------
Os06g14440  -------------LSSL-----HQRTANPL-----V--T--TR---MDANM-DTPLE-QK
Os07g25390  -------------LSSL-----HQRTANSL-----I--T--TR---MDANM-DTPLE-QK
Os07g49210  -------------SSEITHLIVLSILRGME--FNIKLVE--GQI----------------
```

```
Os08g14610  -------------WCCL-----C-------------------------------P---VW
Pt195587/1  -------------CLAM-----HPTLSNEP--RGRGMS----------------------
Pt286483/1  ---------------------------------RSGFCE--KKK----------------
Pt567214/1  -----------------------SIPKQVA--FDVRSVQ--NKI----------------
Pt832603/1  -------------SADLTWLLVASVLKQVE--FNVRSVQ--NKI----------------
RMR1/1-850  FAEEMAPFED-D--------------------YDDEMLE--EQL----------------
Sb01g46180  -------------IERL-----RQVPIEQLYSSPFPKPS--DAR----------------
Sb02g43870  -------------SLEVAYLIVLSSLRGME--FSIKLVD--GNI----------------
Sb04g33300  QYSARVSSEDT---------------------GEDEVQEQKQKR----------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  VAEEMAPFED-D--------------------YDDEMLE--EQL----------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  IHRERASDPSESSKPDLALLDFHGFHLHPQ--HHLAGLD--PGY----------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  -------------YYVM-----YPSLSYMS--TDLGKQP--SKK----------------
Vv29366/1-  -------------SSDLSWLVVTSVLKQAV--FDVRSVQ--NRI----------------
Vv35918/1-  -------------YYVM-----YPSLSYMC--TDLGKKQ--GKK----------------
ZM000342/1  -------------SLEVAYLIVLSSLRRME--FNIKMVD--GNI----------------
ZM064574/1  -------------LASL-----ERASGDSA-----A--A--GK--IEDSKL-ASPVEPTE
ZM093940/1  -------------IASL-----ERASENSS-----AI-A--SK--TGGGKSTNHSVEPAE
ZM108166/1  -------------SLEVAYLIVLSSLRRME--FNIKMVD--GNI----------------
ZM178435/1  TYSARVSSEDT---------------------GEDEKHMQEQTR----------------

                             1280                1300               1320
At1g05490/  --------SPEIRGLVLEKSVPGEIEILSDSESETEARRRASAKKKLFEESSRIVESISD
At2g21450/  ----------------------------------IEARQDNKR-----AKSSHNLIIDSD
At3g24340/  ------------------------------------------------------RVCDFD
At5g20420/  --------VYQIVT----------------------------------------------
AtCLSY1/1-  --------VYQIVT----------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  --------IYRVIK----------------------------------------------
Bd1g74070/  --------LHSA-T----------------------------------------------
Bd2g21430/  CESKKLYTH------------------------------------------NLFFVINVI
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  --------VGDLIR-----------------------------------------AYSNG
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  -----------------------------------------------SPPKELIIILDSD
Bd3g19890/  VKQ-----T------------------------------------------EPILIPDSD
Bd3g50300/  --------LDDV------------------------------------------------
Cp19.123/1  --------VYQILA----------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  ----------RL-V----------------------------------------------
Os05g32610  --------VGDVIR-----------------------------------------AYSNG
Os06g14440  QKD-----S------------------------------------------SAIIVLDSD
Os07g25390  QKD-----S------------------------------------------SAIIVLDSD
Os07g49210  --------VYQIIK----------------------------------------------
Os08g14610  CKE-----A------------------------------------------QEVVVPG-R
Pt195587/1  ------------------------------------------------------------
Pt286483/1  --------DGNVVV-----------------------------------------VVDDD
Pt567214/1  --------AYQIFG----------------------------------------------
Pt832603/1  --------VYQILG----------------------------------------------
RMR1/1-850  --------VGDVIR-----------------------------------------AYSNG
Sb01g46180  --------LDNF-G----------------------------------------------
```

```
Sb02g43870  --------IYQIIK----------------------------------------------
Sb04g33300  --------VEDV------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --------VGDVIR-----------------------------------------AYSNG
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  --------VLELAA-----------------------------------------G-SHG
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  --------ASKLVN----------------------------------------------
Vv29366/1-  --------VYQIVG----------------------------------------------
Vv35918/1-  --------ASKLVN----------------------------------------------
ZM000342/1  --------IYQIIK----------------------------------------------
ZM064574/1  QKE-----K------------------------------------------AAIIVLDSD
ZM093940/1  QKG-----K------------------------------------------GDIIVLDSD
ZM108166/1  --------IYQIIK----------------------------------------------
ZM178435/1  --------VEDV------------------------------------------------

                            1340                1360                1380
At1g05490/  GEDS--------------------------------------------S--------SE-
At2g21450/  DELP--------------------------------------------------------
At3g24340/  EDDA--------------------------------------------K--------V--
At5g20420/  DEEG--------------------------------------------S-----------
AtCLSY1/1-  DEDC--------------------------------------------E--------GS-
AtDRD1/1-3  ---N--------------------------------------------Q-----------
Bd1g16720/  GDQA--------------------------------------------R--------RG-
Bd1g74070/  QSGS--------------------------------------------N-----------
Bd2g21430/  DNV---------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ---------------------------------------------------------DDL
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  DEDG--------------------------------------------------------
Bd3g19890/  DEDGSTA-----ELAPEKNKELIPLGLAGTLTAHVTSKGKDQVNETRH---------YG-
Bd3g50300/  -------------------------------------------------CS--------E
Cp19.123/1  DDDG--------------------------------------------S--------PS-
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  QDGR--------------------------------------------N-----------
Os05g32610  ---------------------------------------------------------ADL
Os06g14440  DEDGYTEG--CEQLTSENNKQQAPSGLTSPYTTWIVSSAKDQVNGTLHV--------DG-
Os07g25390  DEDEAE-R--CEQLASENNKQQAPSGPTSPCTTWIVSSAKDQVNGTLHV--------DG-
Os07g49210  GDQA--------------------------------------------Q--------WN-
Os08g14610  GRNGAR----------------------------QRDGG-GCALGTTEV--------LG-
Pt195587/1  ---F--------------------------------------------G-----------
Pt286483/1  -DDD--------------------------------------------ACIILEKDAEEL
Pt567214/1  GDDD--------------------------------------------H--------CS-
Pt832603/1  GENE--------------------------------------------H--------CS-
RMR1/1-850  ---------------------------------------------------------RNF
Sb01g46180  KMES--------------------------------------------S-----------
Sb02g43870  GDQA--------------------------------------------R--------YS-
Sb04g33300  ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ---------------------------------------------------------RNF
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ---------------------------------------------------------RD-
Vv15867/1-  ------------------------------------------------------------
```

```
Vv23895/1-  RHAS--------------------------------------------H-----------
Vv29366/1-  GDHD--------------------------------------------K--------VS-
Vv35918/1-  REAS--------------------------------------------H-----------
ZM000342/1  GDQA--------------------------------------------R--------DS-
ZM064574/1  DEDGNGSG--NSKLASETNKELGTSGLINNIAERMTFNG-SQAFGTVHT--------YG-
ZM093940/1  DEDGDGNSPEHNKLASEMNKELGTSVLASNIAERMATNG-SQTFETVHA--------YGG
ZM108166/1  GDQA--------------------------------------------R--------DS-
ZM178435/1  ------------------------------------------------------------

                            1400                1420                1440
At1g05490/  ------------------------------TDEEEEENQDSEDNNTKDNVT---------
At2g21450/  --------------------------------------Q-------ESVT----------
At3g24340/  ---------------------------------SGKEN------------PLSPDDDDDV
At5g20420/  ---------------------------SSTLSS---------------------------
AtCLSY1/1-  ---------------------------SSSLSA---------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------------------------VDC----------------MSIPPGFGRNM
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -------------------------------DA----------------DGVDWEA----
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  --------------------------------------N-------SGKTQVPSYPTKEL
Bd3g19890/  ------------------------------YQN----------------SQIVP-YGQSA
Bd3g50300/  TSDESWQPRYNSEFQVAMKGEKKVEGRRNSVEE----------------EATEKELGENG
Cp19.123/1  ------------------------------KS-----------------N-------NYI
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  ------------------------------------------------------------
Os05g32610  -------------------------------DT----------------NGVDWEAEDEM
Os06g14440  ------------------------------VQS----------------TQIVPYYGQNA
Os07g25390  ------------------------------VQS----------------TQIVP-YGQNA
Os07g49210  ------------------------------LDS----------------MAIPPGFGNTM
Os08g14610  ------------------------------R-----------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  -------------------------------QS----------------SS---SG----
Pt567214/1  ------------------------------LKS----------------N-------NHI
Pt832603/1  ------------------------------LKS----------------N-------NHI
RMR1/1-850  -------------------------------DS----------------DGVDWEA----
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------IDS----------------MSIPPGFGKSM
Sb04g33300  ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -------------------------------DA----------------DEADWEA----
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------LNA---------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ------------------------------IDS----------------MSIPPGFGKNM
ZM064574/1  ------------------------------DKN----------------TQIVP-YGQCS
ZM093940/1  ------------------------------SKN----------------TQIVP-YGQGS
ZM108166/1  ------------------------------IDS----------------MSIPPGFGKNM
```

```
ZM178435/1  ------------------------------------------------------------
                            1460                1480                1500
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  VFLG--------------------------------------------------------
At5g20420/  --MNIT--LEDGVSLSKVVKFNPADI-L--------------------------------
AtCLSY1/1-  --MNIT--VEDGVVMSKVVLFNPAE-----------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  EIVSFQ--LHDKNLRPTI-RNIPVTH-A--------------------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  --------VNQGGQQP-V-R----------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  --------------E--------------D-EMEF-----------DD-DGDD-------
Bd2g43500/  -----------------------------------E----------ED-EEDEWE-----
Bd3g18910/  IILDSN--DRKTLLPPYP-TKE--------------------------------------
Bd3g19890/  ALINHH--SLQTSWQPSI-Q----------------------------------------
Bd3g50300/  NGIPVLEEAAEKELRENG-NSIPVQEEA-A-EKELGENGNSIPVLEEA-AEKEL------
Cp19.123/1  SATM--------------------------------------------------------
Cp76.2/1-4  -------------AI--------------AADASG-----------DD-DDDC-------
Os02g43460  --------------------GRAFAQ-V-K-EEQVE----------EQ-EEDEEE-----
Os03g06920  ------------------------------------------------------------
Os05g32610  EFADLDTNVVDWEAE--------------D-EMEF-----------DD-DNDND---AD-
Os06g14440  PLINQF--PLQTSWQPSI-Q----------------------------------------
Os07g25390  PLINQS--PLQTSWQPSI-Q----------------------------------------
Os07g49210  EIISFQ--LRDEALRPTI-TNIPITH-V--------------------------------
Os08g14610  --------ICNSS-----------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  --------------E----------------EETF-----------KDDSDDDD-YRV--
Pt567214/1  NCVTFK--VEDGISTPFVVQLDPIDT-C--------------------------------
Pt832603/1  NCVTFK--VKDSISTPFVVQLVPTDA-C--------------------------------
RMR1/1-850  --------------E--------------D-EMEF-----------ND-DADNS-DFMD-
Sb01g46180  ------------------------------------------------------------
Sb02g43870  DIISFK--PRAEALRPII-RTVLITQ-V--------------------------------
Sb04g33300  -----------------------------E-SMDV-----------DD-DDDNNTNEAGN
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --------------E--------------D-EMEF-----------DD-DADNS-DFMD-
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -------------LRPKR-DFAPRQLEVVF-HLLL-----------E-DDPDEA-RR---
Vv15867/1-  -------------AS--------------D-YEEE-----------ED-DDDDD-YIVD-
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  --VNFR--VDNGISTPVIFPFVPADT-I--------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  DIISFK--PRGEALRPIT-RTVPVTQ-V--------------------------------
ZM064574/1  ALVNQF--PLQTSWQPSI-Q----------------------------------------
ZM093940/1  ALVNQF--PLQTSWQPSI-Q----------------------------------------
ZM108166/1  DIISFK--PRGEALRPIT-RTVPVTQ-V--------------------------------
ZM178435/1  -----------------------------E-FMEV-----------DD-DYDDV-NVAGN

                            1520                1540                1560
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  ------------------------------------------------------------
AtCLSY1/1-  ------------------------------------------------------------
```

```
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ------------------------------------------------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -------------------------------------------------DYFVHDADECG
Bd2g43500/  -EEEEEEREADLE-----------------------------------------------
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ---RENGKSIPVEEEA--------------------------------------------
Cp19.123/1  ------------------------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  -GEEEMEMEVEVEVRSDD-----------------------------NDHGNGGIRGEGG
Os03g06920  ------------------------------------------------------------
Os05g32610  -----------------D-----------------------------DGDNFGGDADEGD
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------------------------------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  ------------------------------------------------------------
Pt832603/1  ------------------------------------------------------------
RMR1/1-850  -----------------DAD----------------------------DSDFMDDAYEGG
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ------------------------------------------------------------
Sb04g33300  GIQKESEQDEALEGRSRQ-----------------------------DSH----------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -----------------DAHDSDFVNDADEGGKSGDDAENSDFMDDAHDSDFVNDADEGG
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  -----------------PTID----------------------------------RDERG
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  VIDQESEQDEALEGRSSQ-----------------------------DSHGYSEDKEGKD

                            1580                1600                1620
At1g05490/  ----------------------------------------VES--L--------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------T--I--------------
At5g20420/  -------------------------------DD-----SQDLEIKQ--------------
AtCLSY1/1-  -------------------------------DT-----CQDSDVKE--------------
AtDRD1/1-3  -----------------------------------QVVEGVIN--L--------------
Bd1g16720/  -------------------------------KKHNLTEDNRFTLKT--------------
Bd1g74070/  -----------------------------------FSSDNIID--L--------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  MSEPMCDDYKVGTQYLSDHEVVVGEVSCQLE---------------EDVVKDEVDPKREG
Bd2g43500/  ------------------------------------------------------------
```

```
Bd3g18910/  ----------------------------------------LII--L--------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ------------------------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  -GT---------------------------------------------------------
Os03g06920  -----------------------------------SSCRNIID--L--------------
Os05g32610  KSVQMHDFSKVETQDLVSHNVNVSEVRPHED---------------EEAIKDEMESKGKG
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  -------------------------------KKNNITEDMRFTVKS--------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  -----------------------------------EGKCNVID--L--------------
Pt286483/1  ---------------------ELPESFMVEE---------------EEKEEDGDREQGEM
Pt567214/1  ------------------------------------------------------------
Pt832603/1  -------------------------------SE-----AGHISDTN--------------
RMR1/1-850  NSKPIQNHAKLEIQDWVNQKVVLSGGRCEARGEGDLEEE--LDVGKEA-DEEDVEPKSEA
Sb01g46180  -----------------------------------YNPDNVIN--L--------------
Sb02g43870  -------------------------------KEDNLIEDGCTAVKH--------------
Sb04g33300  ------------------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  KSEPIKSHAKMEIQDLVNQKVVLCGGGCEE--EGGEKEE--LGVGKEAGKKEDVEPKSEA
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  NQASKLGKK----------KVELG----------T-------------------------
Vv23895/1-  -----------------------------------LGHEDVID--L--------------
Vv29366/1-  -------------------------------EA-----D-PLNGTN--------------
Vv35918/1-  -----------------------------------LAHEDVID--L--------------
ZM000342/1  -------------------------------EEGNLTEDGCIAVKG--------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  -------------------------------EEGNLTEDGCIAVKG--------------
ZM178435/1  -SA---------------------------------------------------------

                            1640                1660                1680
At1g05490/  ---SSEDPSSSSSSSSSSSSSSSSSS--------------SDDESYV---------KEVV
At2g21450/  ------------------------------------------------------------
At3g24340/  ----------------------------------------AGENQHVEDVNAGSEVCDIL
At5g20420/  ---ETDY------------------------------------------Y-------QEE
AtCLSY1/1-  ---E------------------------------------------------------IE
AtDRD1/1-3  ---DDDD---------------------------------------DDDT-------DVE
Bd1g16720/  ---ELDD------------------QLEYIRVAVKIELDDQ--LEDQFDV-------GLL
Bd1g74070/  ---DPDN---------------------------------------VGD---------HT
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  TTCF---------------------------------------DQGRLHI-------EIL
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ---DSYDEDRNPPCQRKRKIS----E--------------VSSQV--------------N
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------------------------------------------------
Cp19.123/1  ---------------------------------------------------------FIN
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------------------------------------------------------------
Os03g06920  ---DSDN---------------------------------------DED---------YT
```

```
Os05g32610  SLSF---------------------------------------NEGSSYI-------EIL
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ---EMDS------------------E-----------------LDRALDV-------EIL
Os08g14610  ------------------------------------------------------------
Pt195587/1  ---DDDE---------------------------------------IEGV---------G
Pt286483/1  ELKR----------------------------------------NKVYGI-------EVL
Pt567214/1  ------------------------------------------------------------
Pt832603/1  ---GTE-------------------------------------------Q-------SPC
RMR1/1-850  APGS---------------------------------------DKRVLQL-------EIL
Sb01g46180  ---DADE---------------------------------------ENVE-------YHT
Sb02g43870  ---ESDS---------------------------------------AQDV-------EVL
Sb04g33300  ---------------------------------------------------------ALI
Sb07g02945  ------------------------------------------------------------
Sb09g19410  APGS---------------------------------------DKGGSHL-------ETM
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ---EDDH---------------------------------------IVYD-------VP-
Vv29366/1-  ---EAG-------------------------------------------P-------LPF
Vv35918/1-  ---EDDH---------------------------------------VVDD-------AL-
ZM000342/1  ---ESDS---------------------------------------AQDV-------EIL
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ---ESDS---------------------------------------AQDV-------EIL
ZM178435/1  ---------------------------------------------------------ALS

                            1700                1720                1740
At1g05490/  GDNRDDDDLRKASSPIKRVSLVERKALVRYKR-SGSSLTKPRERDNKIQKLNHREEEKKE
At2g21450/  ------------------------------------------------------------
At3g24340/  LD------------------------DANLRG-EEKTY----------------------
At5g20420/  DE------------------------VVELRR-SKRRN----------------------
AtCLSY1/1-  EE------------------------VMELRR-SKRRS----------------------
AtDRD1/1-3  KK------------------------AL--------------------------------
Bd1g16720/  YK------------------------HVDLRR-SKRLK----------------------
Bd1g74070/  HP------------------------NM--------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ES------------------------DDEVKV-LSDAS----------------------
Bd2g43500/  DM------------------------VGEE--EEEEQG----------------------
Bd3g18910/  RD------------------------ASNDPR-QKKLK----------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ---------------------------AEKELGENGNS----------------------
Cp19.123/1  GG------------------------WWELRR-SKRRN----------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  DD------------------------VAEI--EEEELG----------------------
Os03g06920  FA------------------------NV--------------------------------
Os05g32610  DS------------------------DEEVKV-VNDTG----------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  YE------------------------HVDLRR-SKRLK----------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  DS------------------------VG--------------------------------
Pt286483/1  CD------------------------SDIGKF-ENNDV----------------------
```

```
Pt567214/1  ------------------------------------------------------------
Pt832603/1  YD------------------------VMSLRR-SKRRN----------------------
RMR1/1-850  GS------------------------DEEIKV-LENMS----------------------
Sb01g46180  QV------------------------NA--------------------------------
Sb02g43870  YE------------------------HVDIRR-SKRMK----------------------
Sb04g33300  DN------------------------EEEV--GEKELS----------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  SS------------------------DEEIKV-LENMS----------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -------------------------------------S----------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  -T------------------------AT--------------------------------
Vv29366/1-  CD------------------------IVDLRR-SKRRN----------------------
Vv35918/1-  -T------------------------AT--------------------------------
ZM000342/1  YA------------------------HVDIRR-SKRMK----------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  YA------------------------HVDIRR-SKRMK----------------------
ZM178435/1  DN------------------------EEDV--GGKELL----------------------

                            1760                1780                1800
At1g05490/  RQREVVRVVTKQPSNVVYTCAHCGKENTGNPESHSSFIR---------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  ----------------------------VRPDIYTGCDY---------------------
AtCLSY1/1-  ----------------------------GRPERYGDSEI---------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  ----------------------------TQPERFTSYDA---------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ----------------------------NPLKRKPLPQAKIPVLP-CVAWRTRSLWGVKQ
Bd2g43500/  ----------------------------KE-----------------------------E
Bd3g18910/  ----------------------------NEPTYF-GFDE---------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ----------------------------IQDDRYDG-----------------------E
Cp19.123/1  ----------------------------VQPERFIGGQG---------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ----------------------------TD-----------------------------E
Os03g06920  ------------------------------------------------------------
Os05g32610  ----------------------------NALRRKPLVPAKLPIVPSCVAWRTRSSWGMKE
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ----------------------------TQPDRFTSYDT---------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ----------------------------D------------MDDSLCVAKRTRSHYNLES
Pt567214/1  -------------------------------------NT---------------------
Pt832603/1  ----------------------------VQPERFLACDA---------------------
RMR1/1-850  ----------------------------SAPSRKASVQSKLPTIPSCVAWRTRSSWGVNQ
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ----------------------------TQPDRFTSYDA---------------------
Sb04g33300  ----------------------------EE-----------------------------E
Sb07g02945  ------------------------------------------------------------
```

```
Sb09g19410  ----------------------------SAPSRKASVQSKLPTIPSCVAWRTRSSWGINR
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ----------------------------HDPA----------------------------
Vv15867/1-  -----------------------------------------SSHPFC-------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ----------------------------VQPDRFFSLGG---------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ----------------------------TQPDRFTSYDA---------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ----------------------------TQPDRFTSYDA---------------------
ZM178435/1  ----------------------------EE-----------------------------E

                            1820                1840                1860
At1g05490/  -----PHSI-RDEIEDVNNFAS--------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  --------------------VSDEVVSLSSSSDD---------------------EEDPL
At5g20420/  -----EPDTID-------GW------------VRMMPY-Q-----FGKCA---V------
AtCLSY1/1-  -----QPDSKD-------GW------------VRMMPY-R-----YNIWN---V------
AtDRD1/1-3  ---------------------------------------CVVPSSSEIVL---L------
Bd1g16720/  -----PNFN-R-------DT------------KKKGAS-A-----SSTMH---YDHR---
Bd1g74070/  ---------------------------------------ENTGAHNTTYL---V------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  --DR-I-SY-N-------AY------------FEELSD-E-----PI---ED-DDTE---
Bd2g43500/  ---------------------------------------------DE---WELEEEE---
Bd3g18910/  -----PMEK-K-------KNPR--------------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  --DE-EATD-D-------AH------------AAEEEE-E-----EE---EEEEEEE---
Cp19.123/1  -----LTESDS-------VW------------VRQMPI-K-----TDKWK---E------
Cp76.2/1-4  --------D-E-------NH------------DDEDDD-G-----DVVWEEDMDDLE---
Os02g43460  --DE-TSDD-S-------DE------------NFSDEE-G-----DE---EELEEEE---
Os03g06920  ---------------------------------------DNIGANTTVVL---V------
Os05g32610  --ER-I-SY-N-------TY------------FEVLSD-E-----PK---EDDDDTE---
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  -----PRFL-S-------GY------------KKKEAS-S-----SPTKH---VRGA---
Os08g14610  ------------------------------------------------------------
Pt195587/1  ---------------------------------------NVAVGRTPVVV---I------
Pt286483/1  AKKR-M-KL-E-------TV------------S------R-----PL---CVD---E---
Pt567214/1  -----PAETEI-------GW------------VRSLPY-T-----PLKWK---E------
Pt832603/1  -----PAETEI-------GW------------VRSLPY-T-----PLKWK---A------
RMR1/1-850  --DR-L-SY-D-------TY------------FEELSD-E-----PK---EDDDDTE---
Sb01g46180  ---------------------------------------GNTEADSTASA---D------
Sb02g43870  -----PNFN-R-------TY------------NKKEAY-G-----PSNKN---ENSE---
Sb04g33300  --ED-DNQE-E-------SH------------SMYDGE-G-----EQ---EEDASEE---
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --DR-L-SY-N-------TY------------FEALSD-E-----PK---EDDDDTE---
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  --------------------------------FFHACERQ-----QSGWK------S---
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ---------------------------------------AVADAALPVVI---I------
Vv29366/1-  -----FSESDI-------GS------------VRAGIH-K-----VDYWR---K------
Vv35918/1-  ---------------------------------------AVEDATLPVVI---I------
```

```
ZM000342/1  -----RNFN-R-------TY------------NKKEAD-G-----PSTKY---EDSE---
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  -----RNFN-R-------TY------------NKKEAD-G-----PSTKY---EDSE---
ZM178435/1  --EEGADQE-E-------SH------------IIYDGE-G-----EQ---EEDASE----

                              1880                1900                1920
At1g05490/  ------------------T-------------------------N---------------
At2g21450/  ------------------------------------------------------------
At3g24340/  EELGTDSREEVSGEDRDSG-------------------------E---------------
At5g20420/  --------------------------NVESDEDEDDN---NEDGDT-------ND----D
AtCLSY1/1-  --------------------------SSDDDDEEEDC---EDDKDT-------DD----D
AtDRD1/1-3  --------------------------DSDDEDNERQR---------------------PM
Bd1g16720/  ------------------R-------A---------S---QVKVES-------SC----G
Bd1g74070/  --------------------------DSGDGDMIKSI---RDGN-S-------SGCMQNV
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  ------------------VELDDEDD--NDDD--SASFEEE--EEEE--T---KQ----E
Bd2g43500/  ------------------EEE-------------HEETEEEESESEQDEE---AA----E
Bd3g18910/  ------------------K-------------------------E---------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ------------------EEE-------------EEE-EEEEEEEEEEEE---EE----E
Cp19.123/1  ----------------------------K-----M-------------------------
Cp76.2/1-4  ------------------RTSEEDNDDSDDEDYAV-------------------------
Os02g43460  ------------------EEE-----------------EEEEDDDD-DDE---EE----E
Os03g06920  --------------------------DSDDGDSVASF---VDEK-S-------SDSKQNA
Os05g32610  ------------------VELDDEEDDENDDDCNSASCDEEDEEEEEERE---EE----E
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------V-------HC--DSPVDDS---KKEVES-------CC----V
Os08g14610  ------------------------------------------------------------
Pt195587/1  --------------------------DSDDDESNENR---M------------------V
Pt286483/1  ------------------EKLDDNGD--ND----------EDDT---EAY---EA----V
Pt567214/1  --------------------------------EEE-------------------------
Pt832603/1  ----------------------------EEEEEEE-------------------------
RMR1/1-850  ------------------VELDEVEDDNNDDD-SSDAYDKDDEEKE-------EE----E
Sb01g46180  --------------------------DSGDKDRVKSF---GDEN-S-------S-SNRND
Sb02g43870  ------------------S-----------DLSFYS----SEQTES-------SD----E
Sb04g33300  ------------------VEQ-----------------EMDETGEEDEKELDGTG----E
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ------------------VELDEDEDGNNDDG-SSDAYDKDDEEKEE--E---EE----E
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------KLVHELHGLL-----------------------GE-------
Vv15867/1-  ------------------VDVDEGE---GDGD--GEG--EEEWE-EEEEE---EE----E
Vv23895/1-  --------------------------DSDDEESGDQK---V-------------------
Vv29366/1-  ----------------------------E-----E-------------------------
Vv35918/1-  --------------------------DSDDEDCGDQK---VSHP-P-------QETAWPS
ZM000342/1  ------------------S-----------GLSCDS----SEQRES-------SD----E
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------S-----------GLSCDS----SEQRES-------SD----E
ZM178435/1  ------------------------------------------------------------

                              1940                1960                1980
```

```
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  LY---IPLSRLFIKKKKTNSREAK-PKS--------------------------------
AtCLSY1/1-  LY---LPLSHLL-RKKG--SKKGF-SKD--------------------------------
AtDRD1/1-3  YQ---FQS-TLV-QH----------Q-K--------------------------------
Bd1g16720/  ED---------PVK--------------I-TGA-SSF------------MF---------
Bd1g74070/  NF---TQECSLA-EQ----------P-G--------------------------------
Bd2g21430/  -----FDR-VIL-HTR---------T-E--------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  EV--AEK------------------SKH-KKGIHSSFPE------------IRSRPMPLF
Bd2g43500/  EPRR--G------------------GPRNSAAA-GRYA-------------HRAEDGEIF
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  -----YES-VIL-QTR---------T-E--------------------------------
Bd3g50300/  EE--QDD------------------ESDE-AGE-ELHPVPNSNADAGGNARSGGEGTP-I
Cp19.123/1  KC---LPLSRLFKMQ--PLYLKEQ-PKN--------------------------------
Cp76.2/1-4  MK--TMY------------------RKE-K-----CKP--------------KNHDVNG-
Os02g43460  EPGDAPD------------------QPGE-AGE-ESPPR------------SRIMAMPLM
Os03g06920  NY---IEESVLP-EQ----------H-A--------------------------------
Os05g32610  EE--AQR------------------RKQ-KKGIDSS------------------------
Os06g14440  -----YER-VIL-QKR---------P-E--------------------------------
Os07g25390  -----YER-VIL-QRR---------P-E--------------------------------
Os07g49210  EI---P--GNVTQK--------------Q-TGV-HSP------------MV---------
Os08g14610  --------------VE---------K-A--------------------------------
Pt195587/1  GH---FQG-IVL-PK----------P-E--------------------------------
Pt286483/1  DV--AQK------------------VRS-KKGKT--------------------------
Pt567214/1  LH---LPLAYLFGTHADASCAEEK-PGNE-VRV-NSP------------KL---------
Pt832603/1  MH---LPLAYLFGTHAGASCAEEQ-TCNE-VGA-SSP------------KL---------
RMR1/1-850  EE--AER------------------RKL-NNRICTSDED------------MINITVPT-
Sb01g46180  NY---IQQNPLL-EH----------P-V--------------------------------
Sb02g43870  EV---L--GNPGVK--------------K-KVS-RSF------------VV---------
Sb04g33300  E---DEQ------------------ELDG-AGK-AQ-PVTPSNTIAGSSMRSGGDDTRVF
Sb07g02945  ------------------------------------------------------------
Sb09g19410  EE--AER------------------RKL-NNGIYTSDDD------------MINITVPT-
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------DG----------------------------
Vv15867/1-  EE--G--------------------RDS-S------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  MP---LALPDEG--DVHSIFSEKHIIDYE-KGA-HSL------------QI---------
Vv35918/1-  FS---YQE-VVL-RK----------P-S--------------------------------
ZM000342/1  EA---L------------------------------------------------------
ZM064574/1  -----FER-VVL-QKR---------P-E--------------------------------
ZM093940/1  -----FER-VVL-TKR---------P-E--------------------------------
ZM108166/1  EA---L------------------------------------------------------
ZM178435/1  E---ETQ------------------ELDE-TGE-AQ-PFNPSNTMAGSTMRSGGDGKQVF

                            2000                2020                2040
At1g05490/  --------------------------------------------------VSK--YEDS-
At2g21450/  ------------------------------------------------------------
At3g24340/  -------------------------------SDMDEDANDSDSSDYVGESSDSSDVESSD
At5g20420/  ---RKGEIVVIDKRRVHGF-----------------------------------------
AtCLSY1/1-  ---KQREIVLVDKTERKKR-----------------------------------------
AtDRD1/1-3  ---NQGDV----------------------------------------------------
Bd1g16720/  --NEN-------------------------------------------------------
```

```
Bd1g74070/  ---QYQDIIMLGNENI--------------------------------------------
Bd2g21430/  ----ENI-----------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  VNR---------------------------------------------------------
Bd2g43500/  AKRLFEGLCIS-------------------------------------------------
Bd3g18910/  --------------------------------------------------SDC--HFNL-
Bd3g19890/  ----EER-----------------------------------------------------
Bd3g50300/  GKRVFEGLCLV-------------------------------------------------
Cp19.123/1  ---ETRDLVVYKSNKYSK------------------------------------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  GKRMFEGFSFL-------------------------------------------------
Os03g06920  ---QQQEISMLDNENI--------------------------------------------
Os05g32610  ------------------------------------------------------------
Os06g14440  ----EQR-----------------------------------------------------
Os07g25390  ----EQR-----------------------------------------------------
Os07g49210  --DEKSNSPEGQHKNTTKRTTCSLVKEK--------------------------------
Os08g14610  ----EER-----------------------------------------------------
Pt195587/1  ----GQFS----------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  --EFLEGPPVSRTKTNSRKIKSNVFNRREHQAELGEV----------------------E
Pt832603/1  --ELLEGIPVSRTKTYLKEIKSNVVNRRDHQTEPGEV----------------------R
RMR1/1-850  ------------------------------------------------------------
Sb01g46180  ---GHQEITRPDNCNS--------------------------------------------
Sb02g43870  --K---------------------------------------------------------
Sb04g33300  RRRVFEGICLP-------------------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ------------------------------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  --DSYEDFLVCKSKDRSRE-----------------------------------------
Vv35918/1-  ---VGLLA----------------------------------------------------
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ----EQR-----------------------------------------------------
ZM093940/1  ----EQR-----------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  RRRVFEGIYLP-------------------------------------------------

                            2060                2080                2100
At1g05490/  --VSINSGKTTGAPSR--------------PEVENPET----G--KELNTP---E-----
At2g21450/  ------------------------------------------------------------
At3g24340/  SDFVCSEDEEGGTRDDA-------------TCEKNPSE-KVYH--HKKSRT---FR--RK
At5g20420/  ------------------------------------------------------------
AtCLSY1/1-  ------------------------------------------------------------
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  -----------------------------------PST-TKGQ--HK-NTR---RR--TP
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -------------------------------------------------------ERRMQ
Bd2g43500/  ---------------------------------KAADTSAAGKPVAG-RTRS---RRRCL
Bd3g18910/  --AVP--------------------------------S----K--KLLLSN---L-----
Bd3g19890/  ------------------------------------------------------------
```

```
Bd3g50300/  ---------------------------------DNADNAVTTKSIRQ-RTRSNFKDRACL
Cp19.123/1  ------------------------------------------------------------
Cp76.2/1-4  --------------------------------------------------------RDFS
Os02g43460  ---------------------------------QQVDT-STGRDIRA-RTRSNFKRKKLL
Os03g06920  ------------------------------------------------------------
Os05g32610  ------------------------------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  -----------ASSPEGQHEKTTKRTTCALPVKEKASS-PEGQ--HK-NTI---KR--TT
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  SGIDNRRERQKS--------------T-VANRIKHQTR-LGEA--KS-GMA---NR--KK
Pt832603/1  AGMAKRRECQKS--------------T-MADRIEHQTR-LGDA--ES-GMA---NR--KK
RMR1/1-850  --------------------------------------------------------SRYD
Sb01g46180  ------------------------------------------------------------
Sb02g43870  ---------------------------------EDPRS-MKGQ--HK-YPV---KR--NQ
Sb04g33300  ---------------------------------QKPRK-TVGKGIGA-RTRS---QRKCK
Sb07g02945  ------------------------------------------------------------
Sb09g19410  --------------------------------------------------------SRYD
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ------------------------------------------------------------
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  ---------------------------------ENPRS-MAAE--HK-YPV---KR--NQ
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ---------------------------------ENPRS-MAAE--HK-YPV---KR--NQ
ZM178435/1  ---------------------------------ENPHR-TVGKGIQG-RTRS---QRKCK

                            2120                2140                2160
At1g05490/  ------------------------------------KPSISR------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  HNFDVIN---------------LL------AKSMLESKDVFK------------------
At5g20420/  ----------------------------------------------------------G-
AtCLSY1/1-  ----------------------------------------------------------K-
AtDRD1/1-3  ------------------------------------------------------------
Bd1g16720/  C-----S---------------LP-----------------MKE-----KP---SSVK--
Bd1g74070/  -----------------------N-----------------SED-----QA---VAKQG-
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  T-----SIPKWRGTS------KKA--------RQPETCHVIYSSDDEIIDDTAKDGLKCE
Bd2g43500/  N-----TKLLRQGTY------NKP------------------------------YCLDT-
Bd3g18910/  ------------------------------------WPSESL------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  D-----KKLLGQGTC------SKP------------------------------YCIDT-
Cp19.123/1  ---------------------------------------------------------DV-
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  D-----KKLLKRGTF------AKP------------------------------YCIDV-
Os03g06920  -----------------------S-----------------SEA-----QA---V-KKG-
Os05g32610  --------------------------------------------DDEMIDDAVDCGIDWE
Os06g14440  ------------------------------------------------------------
```

```
Os07g25390  ------------------------------------------------------------
Os07g49210  C-----S---------------LP-----------------VKE-----EP---SSVEI-
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------------------------
Pt286483/1  ------------------------------------------------------------
Pt567214/1  H-----G---------------TQ-----------------IR--------------EV-
Pt832603/1  H-----G---------------TQ-----------------IR--------------EV-
RMR1/1-850  M-----FK--K--------------------------------------KNSSRYDIEWV
Sb01g46180  -----------------------S-----------------TEP-----QA---LVKQV-
Sb02g43870  C-----S---------------LP-----------------IKE-----NQ---TSMET-
Sb04g33300  D-----KKLLRRGTF------SKP------------------------------YNIDI-
Sb07g02945  ------------------------------------------------------------
Sb09g19410  M-----FE--RKNISRYDMFKRKNTSRYDIFKRKNTSRYDIFKR-----KKTSRYDIEWV
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------------------------
Vv29366/1-  ----------------------------------------------------------V-
Vv35918/1-  ------------------------------------------------------------
ZM000342/1  C-----S---------------LP-----------------VKE-----KQ---ISMEI-
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  C-----S---------------LP-----------------VKE-----KQ---ISMEI-
ZM178435/1  D-----KKLLKRGTF------SKP------------------------------YNIDI-

                            2180                2200                2220
At1g05490/  -PEIF-T---TEKAIDVQVPEEPSRPEIY------------------SS-EK--AKEV--
At2g21450/  ----------------QINPLEKRLKKL--------------------------------
At3g24340/  -EDIF-S---WDKIAE----VDSREDPVV------------------R------------
At5g20420/  R-K-------ERKSELSVI---------P------------------F--TP--VFEP--
AtCLSY1/1-  K-TEG-F---SRSCELSVI---------P------------------F--TP--VFEP--
AtDRD1/1-3  T---------------PLI---------P------------------Q--CS--FEEV--
Bd1g16720/  -EESK-T---EERASDSHI---------P------------------Q--TP--AQNK--
Bd1g74070/  N-D-------------IMD------IDNE-------------------------------
Bd2g21430/  ------------------------FK---IWSDVEKIAETQTSP---A--LP--GS----
Bd2g21450/  ----------------------------------------TICP---Q--KP--TN----
Bd2g26500/  V---DE-----DPRNNV------------------------------------F----QP
Bd2g43500/  P-SESGS---SEAEEGV-----------N------------------------K----TP
Bd3g18910/  -N----------KLIIQPKQSEEVANDEV------------------FNDET--QNES--
Bd3g19890/  ------------------------IKYLAAASHAEKMAETQVFP---D--LP--RER---
Bd3g50300/  E-S----------EEDV------------------------------------P----PP
Cp19.123/1  K-SGL-ADQVEHQNKLAII---------P------------------V--PNVPELEPEP
Cp76.2/1-4  ------------SLE---------------------------------------------
Os02g43460  S-S--S-----GSEEDV------------------------------------P----QP
Os03g06920  K-D-------------SMD------INDV-------------------------------
Os05g32610  ----ED-----YPEVDF------------------------------------T----RP
Os06g14440  ------------------------VQDLVAASHAEKIAETQVLLTLPT--LP--NER---
Os07g25390  ------------------------VQDLVAASHAEKIAETQVFLTLPT--LP--NER---
Os07g49210  EEKSS-K---EQSAPEFHI---------P------------------R--TP--AQNK--
Os08g14610  ------------------------ETVIPAISNTEKMGEKQQ-K---S--I---------
Pt195587/1  T-D-------------VMV------S------------------------DN--VGRR--
Pt286483/1  ----------------------------------------------------------KP
Pt567214/1  K-LGV-ANRIEHQDQLAIV---------P------------------V--PTED----DL
Pt832603/1  K-SGV-ANRREHQDQLAIV---------P------------------V--HTED----VL
```

```
RMR1/1-850  E-DE-------DASVDM------------------------------------L----QP
Sb01g46180  K-D-------------AMD------NDNV------------------S--AE--AKKI--
Sb02g43870  K-KNA-T---DQGCSDSHI---------P------------------H--TP--AKNI--
Sb04g33300  P-DSTS-----DSEEDI-----------------------------------------EP
Sb07g02945  -------------------------------SIAEKRAETQMFLSLP-------TEK---
Sb09g19410  E-DEDK-----DANVDT------------------------------------L----QP
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ------------------------------------------------------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  -------------------------RDYV------------------E--SI--APKK--
Vv29366/1-  K-PIL-AAQNEDQHQFAIV---------P------------------V--PLII----EP
Vv35918/1-  N-N-------------PVV------RDYV------------------G--SI--APKV--
ZM000342/1  K-KNT-T---DQGCSDSYI---------P------------------H--TP--AKNT--
ZM064574/1  ------------------------MQDLVAASIAEKRAETQVFLSLP-------TEK---
ZM093940/1  ------------------------MQDLVAATIAEKRAETQMFLSLP-------TER---
ZM108166/1  K-KNT-T---DQGCSDSYI---------P------------------H--TP--AKNT--
ZM178435/1  P-DSTS-----DSEEEI-----------------------------------------EP

                            2240                2260                2280
At1g05490/  ------------------------------------------QAPEMPS--------RPE
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  IPLEQF-G----------------LNANSFGGGG----SFSRS-----------------
AtCLSY1/1-  IPLEQF-G----------------LNANSLCGGV----S---G-----------------
AtDRD1/1-3  -DL---------------------------------------G-----------------
Bd1g16720/  ------------------------------------------E-----------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  LNFEKV-G----------------SDGT--VGNGITTE-Q--Q-----------------
Bd2g43500/  PAPAL--S----------------SSDE--EIEADAGGHG--R-----------------
Bd3g18910/  ------------------------------------------EC--FMDAMCDHFDLAI-
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  PQPQP--S----------------SAEC--EDDGSG---G--D-----------------
Cp19.123/1  LASEHH-D----------------YHANLS-ANN----S---K-----------------
Cp76.2/1-4  --------------------------------GNKQS-----------------------
Os02g43460  EQSAY--G----------------GDCA----DDDGGSDG--N-----------------
Os03g06920  ------------------------------------------------------------
Os05g32610  LTFQKD-G----------------SEAP--VGSEAFTE-Q--Q-----------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ------------------------------------------E-----------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ------------------------------------------I-----------------
Pt286483/1  --TGGN------------------------------------------------------
Pt567214/1  VTFEQY-D----------------SPLKTP-DNF----P---Q-----------------
Pt832603/1  ATFEQF-D----------------SPVKTP-EPY----S---Q-----------------
RMR1/1-850  VSFKKD-S----------------SWKPVAVGNDTFTE-Q--Q-----------------
Sb01g46180  ------------------------------------------V-----------------
Sb02g43870  ------------------------------------------E-----------------
Sb04g33300  PAPQQGLL----------------SSSE--EGNITFGK----R-----------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  ISLRKG-S----------------SWNPVAVGNDTFTE-Q--Q-----------------
Sm441121/1  ------------------------------------------------------------
```

```
Sm84719/1-  ------LASVNFGGFSLILGNTHGDRA-----KVDGGGGG--G-----------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ------------------------------------------E-----------------
Vv29366/1-  IAHGED-H----------------LHDETP-WNE----S---G-----------------
Vv35918/1-  ------------------------------------------E-----------------
ZM000342/1  ------------------------------------------E-----------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------E-----------------
ZM178435/1  PAPQQGLL----------------SSSE--EDNMTFGK----R-----------------

                            2300                2320                2340
At1g05490/  VFSS--------------------------------------EKAKEIQV-PEMPSIPEI
At2g21450/  ------------------------------------------------------------
At3g24340/  ESSS--------------------------------------EKVNEH------------
At5g20420/  -------------------------------------------QY-F-------------
AtCLSY1/1-  -------------------------------------------NL-M-------------
AtDRD1/1-3  ----------------------------------------------RGK-----------
Bd1g16720/  -------------------------------------------KN-H-------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  -------------------------------------------K----------------
Bd2g43500/  ------------------------------------------------------------
Bd3g18910/  ---ASKKGSEEVANDEAQNESELFVDALCNHFDLAIASKNDSKKVANDEVAHDEPQKESE
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  -------------------------------------------D----------------
Cp19.123/1  -------------------------------------------RV-E-------------
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  -------------------------------------------E----------------
Os03g06920  ------------------------------------------------------------
Os05g32610  -------------------------------------------K----------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  -------------------------------------------KH-N-------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ----------------------------------------------QGEV----ASL---
Pt286483/1  ------------------------------------------------------------
Pt567214/1  -------------------------------------------EC-I-------------
Pt832603/1  -------------------------------------------AF-I-------------
RMR1/1-850  -------------------------------------------K----------------
Sb01g46180  ----------------------------------------------LFDCH---STS---
Sb02g43870  -------------------------------------------KC-N-------------
Sb04g33300  -------------------------------------------K----------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  -------------------------------------------K----------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -------------------------------------------D----------------
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  ----------------------------------------------ERS-------L---
Vv29366/1-  -------------------------------------------EI-G-------------
Vv35918/1-  ----------------------------------------------EGS-------L---
ZM000342/1  ------------------------------------------------------------
ZM064574/1  ------------------------------------------------------------
```

```
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ------------------------------------------------------------
ZM178435/1  -------------------------------------------K----------------

                            2360                2380                2400
At1g05490/  -------------QNSEKAKEVQANNRMGLTT---PAV-AEGLNKS------------VV
At2g21450/  -------------------KEVI-----------------------------------VV
At3g24340/  ------------------------------GK---PRE-RR-------------------
At5g20420/  --------------------D-ETEKYRSKGM---KYGK---KMTE------------M-
AtCLSY1/1-  --------------------D-EIDKYRSKAA---KYGKKKKKKIE------------M-
AtDRD1/1-3  --------------------EMPSA-----------------------------------
Bd1g16720/  --------------------RTPSS-FHRKS-----------------------------
Bd1g74070/  ------------------------------------------------------------
Bd2g21430/  ----------------------------------------------H-------------
Bd2g21450/  ----------------------------------------------P-------------
Bd2g26500/  ---------------------------GSRFTW--DLE-RRKKLKLGIIKSR------HS
Bd2g43500/  ----------------------------TAARK--GRR-RGKNPTPS-------------
Bd3g18910/  CLVHDTWNHFDHAIASKNLKESE-----------------------------------VV
Bd3g19890/  ------------------------------------KQ-RKLDPNSQ-------------
Bd3g50300/  ----------------------------RMPAK--RRR-GKEQITDS-------------
Cp19.123/1  --------------------ELSFRYNSLKCS---RTS-SRKKFSQ------------I-
Cp76.2/1-4  ---------------------------PATTFDHHDCD----------D-ND------RI
Os02g43460  ---------------------------EHRAVK--RRK-LNRRQSAH-------------
Os03g06920  ------------------------------------------------------------
Os05g32610  ---------------------------RSRFTW--ELE-RRKKLKLGMMTNH------RL
Os06g14440  ------------------------------------KR-RKTEPTTL-------------
Os07g25390  ------------------------------------KR-RKSEPTTL-------------
Os07g49210  --------------------RPPFS-CKPKL-----------------------------
Os08g14610  ------------------------------------------------------------
Pt195587/1  --------------------TGEPD-----------------------------------
Pt286483/1  ---------------------------------GGDV-----------------------
Pt567214/1  --------------------EFPIRSYSKKGY----SV-QRKNDFD--------------
Pt832603/1  --------------------EFPISYYRKKSS---PAA-HRKNDRD--------------
RMR1/1-850  ---------------------------RSRFTW--ELE-RRKKLKLEMKTN-------PL
Sb01g46180  --------------------EQQPL-----------------------------------
Sb02g43870  --------------------RPT---FRLKS-----------------------------
Sb04g33300  ---------------------------HRRAI---KNR-RRKRPSTS-------------
Sb07g02945  ------------------------------------KR-KRSDLSLL-------------
Sb09g19410  ---------------------------QSRFTW--QLE-RRKKNKLEMKTN-------PL
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  ---------------------------DL----------REKPASVGFCLRRATMLVEEG
Vv15867/1-  ------------------------------------------------------------
Vv23895/1-  --------------------TASSE-----------------------------------
Vv29366/1-  --------------------EISPKYYCTNGV---PKL-QRKNMSD--------------
Vv35918/1-  --------------------MGATE-----------------------------------
ZM000342/1  --------------------RPR---FRLKP-----------------------------
ZM064574/1  ------------------------------------KR-RRSDPSLH-------------
ZM093940/1  ------------------------------------KR-RRTDHSLL-------------
ZM108166/1  --------------------RPR---FRLKP-----------------------------
ZM178435/1  ---------------------------RRRAAI--NKR-WDKRLSAS-------------

                            2420                2440                2460
At1g05490/  TNEHIEDDSDSSI--SSG--------DGY---ESD--PTL--------------------
At2g21450/  K------NGDSSGSDSSP--------Q---------------------------------
```

```
At3g24340/  -------------------------------------SFH--------------------
At5g20420/  -EEMMEADL-------CW--------KGP---NQV-KSFQK--RTSRSS-----------
AtCLSY1/1-  --EEMESDL-------GW--------NGP---IGN-VVHKR-NGPHSRI-----------
AtDRD1/1-3  ---------------------------------------------IKAI-----------
Bd1g16720/  ---------------------------------------------GTSP-----------
Bd1g74070/  ---------------------------------------------NHDE-----------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  YERGLDLDS-------DSSGSGENERHGY---QEG-GDN-K-VGR--KKKH---------
Bd2g43500/  ----D-------------DDSEEHRVGG---RQGT-AVR-RRRWP---KDNTAQCDHEEE
Bd3g18910/  A------NDEVA-N-DEP--------Q---------------------------------
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  ----DDTQN-------DSEDSDENRTLARNARKGS-SSR-RP------KNG---------
Cp19.123/1  --DDMDLVP-------RW--------EGI---QGK-GSN-R-KAQIRKH-----------
Cp76.2/1-4  WEHDLND-----------LVTSSKEENGVSHNNFSSVRK-T-VSK--KRK----------
Os02g43460  ------------------SDSEEDTTFVCDVKEGS-GSR-RV------QEG---------
Os03g06920  ---------------------------------------------IYNK-----------
Os05g32610  YERDLESDS-------NSSDSSQNRKNGC---QGS-GDH-R-TGR--KRKN---------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  ---------------------------------------------FTSS-----------
Os08g14610  ------------------------------------------------------------
Pt195587/1  ---------------------------------------------SKKD-----------
Pt286483/1  ----DDGDE-------TCDHKSQRRT----------IES-R-EGS--RDEH---------
Pt567214/1  --EDMMFGS-------GW--------G------GK-SSR-K-KVQRARY-----------
Pt832603/1  --EDLMFGN-------GW--------G------GK-FST-K-KVQRARY-----------
RMR1/1-850  HERDLDSDP-------NSSGSDQIRKYGF---KSD-GSH-K-VDR--KKKH---------
Sb01g46180  ---------------------------------------------MKQA-----------
Sb02g43870  ---------------------------------------------FASS-----------
Sb04g33300  ------------------SDE-EYRVYARDGKD-R-PFR-RL------KKG---------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  YERDLNSDS-------NSSGSDQIRKYGF---KRD-GSH-K-VDM--KKKH---------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  DERAIDWDR-------L---------IAKE-----KRWQ-R-KES--TRKN---------
Vv15867/1-  ------------------SGHAE-------------FPK-T-IGR--KDKG---------
Vv23895/1-  ---------------------------------------------IRKD-----------
Vv29366/1-  --LYMEVES-------RW--------E------GK-GPI-R-KLRRKRG-----------
Vv35918/1-  ---------------------------------------------IRKD-----------
ZM000342/1  ---------------------------------------------FASS-----------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  ---------------------------------------------FASS-----------
ZM178435/1  ------------------SDEEDYGASAMDAKE-R-PFR-RL------KKG---------

                            2480                2500                2520
At1g05490/  ------------------------------------------------------------
At2g21450/  ------------------------------------------------------------
At3g24340/  ------------------------------------------------------------
At5g20420/  ------------------RSVAPKTE-D----------------------------SDEP
AtCLSY1/1-  ------------------RSVSRETG-V----------------------------SEEP
AtDRD1/1-3  --------------------VEGQT-----------------------------------S
Bd1g16720/  ------------------CSLGGNYEPA----------------------------FCQK
Bd1g74070/  -------------------------Q------------------------------KGKR
Bd2g21430/  --------------------VDGD---A----------------------------ETAP
```

```
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  --------------------------------LSSKSG------------KSGK------
Bd2g43500/  EDDEAFVPFRRPKRSGA--------VP------NPRDGYY-DQQQQA-GDAPFKKSSLIL
Bd3g18910/  ------------------------------------------------------------
Bd3g19890/  --------------------VDGD---A----------------------------GTAP
Bd3g50300/  ------ASYQQNVKEGSR-NYDSPSNPRHVKNYAANAGNPTDRFNMQSGDICFNTNTLLP
Cp19.123/1  ------------------RGISSK-E-D----------------------------FDEP
Cp76.2/1-4  ------------------------------------------------------------
Os02g43460  ------APRRQVKKEGSNKKKD-GSTPQCVRNNGPKVGRQTNGLNGQ-GGVSFKRNVKIA
Os03g06920  ---------------------SGHEE------------------------------IGEE
Os05g32610  --------------------------------PLSKSG---------------K------
Os06g14440  --------------------VDVD---G----------------------------GTNL
Os07g25390  --------------------VDGD---G----------------------------GTNL
Os07g49210  ------------------GTLGVNCEPA----------------------------FCQK
Os08g14610  -----------------------------------------------------------P
Pt195587/1  ---------------------K-GV----------------------------------Y
Pt286483/1  --------------------------------GH---G------------VCRR------
Pt567214/1  ------------------QSTHLKRD-D----------------------------SCKP
Pt832603/1  ------------------RSTHLKQD-G----------------------------SCAP
RMR1/1-850  --------------------------------TSPKSG---------------K------
Sb01g46180  ---------------------RGNIK------------------------------TNTE
Sb02g43870  ------------------RSLDGNSEPA----------------------------FCQK
Sb04g33300  ------LSKLQAGKEGCG-RYV-GSNPGHAKYNGPNG---ENQSNEQ-DGIFFKRTAHKI
Sb07g02945  --------------------MLD---------------------------------SFVP
Sb09g19410  --------------------------------TSSKSG---------------K------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  --------------------------------PAPNAG---------------K------
Vv15867/1-  --------------------------------ELG---------------KHTK------
Vv23895/1-  ---------------------KGGL----------------------------------Y
Vv29366/1-  ------------------FTIRTKTE-S----------------------------YGEV
Vv35918/1-  ---------------------K-DV----------------------------------Y
ZM000342/1  ------------------RSLDGNSEPA----------------------------FCQK
ZM064574/1  --------------------ASDD---T----------------------------ATVP
ZM093940/1  --------------------MLD---------------------------------SFVP
ZM108166/1  ------------------RSLDGNSEPA----------------------------FCQK
ZM178435/1  ------LSNLQAAKEGCR-NYE-GSNPGHARYSGPNGGNLENMSSAQ-DDISFKRNVHMI

                            2540                2560                2580
At1g05490/  -KDKEVKI-NNHSDWRILNGNNKEVDLFRLLVNSVWE------------KGQLGEE---D
At2g21450/  ------------------------------GY----------------------------
At3g24340/  -RV---RE-KNHLNGESFY-----------GGEKL------------------------C
At5g20420/  RV----YK-KVTLSA----------GAYNKLIDTYMN------------NIESTIA----
AtCLSY1/1-  QI----YK-KRTLSA----------GAYNKLIDSYMS------------RIDSTIA----
AtDRD1/1-3  R--------G--------------------------------------------------
Bd1g16720/  RGR---KR-KERMCD----------EEYEKIINQCIG------------NIQSEME----
Bd1g74070/  EGE----G-EDVQSA----------G-----------------------SIENNS-----
Bd2g21430/  RKR---KR-ENERDS----------AAVDLPSNT-----------------YN-------
Bd2g21450/  W-R---KR----------------------------------------------------
Bd2g26500/  -KS---SRSTMLKRQ----------SLLKLLMDKMTG------------DKDGE----CS
Bd2g43500/  P-K---KRCGAGQER----------ETYDDLLQSIFD------------EITNQQN-GSA
Bd3g18910/  --K-ES----------------------EYLVDDMWN------------HFELAIA---S
Bd3g19890/  RKR---KR-KTGPDP----------AAVDLPSET-----------------YN-------
Bd3g50300/  QR----MKHGRVWTK----------QDTDNLLNSLLD------------EIEN-------
Cp19.123/1  IT----YK-KKSLSA----------GAYDKLIHSYMK------------NIDSTMI----
```

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Cp76.2/1-4  ---------HMHKSH----------DIVKVVVNSMLE------------EEEMLFEETVA
Os02g43460  QRR---KRRQATADQ----------EKYGHLLDPMFN------------EIESNQY----
Os03g06920  EAQ----A-ENVQIK----------G-----------------------NLKKEI-----
Os05g32610  -KS-----SRMLKRQ----------SLMKLLMDKMCS------------NDDGK----ST
Os06g14440  GKR---KR-KNHQNQ----------AAVDSNLDL-----------------Q--------
Os07g25390  GKG---KR-KNHQNQ----------AAVDSILDL-----------------QQTVV----
Os07g49210  VGG---KR-KRHMCE----------REYKQMIDQCIG------------NIESEME----
Os08g14610  RDR---KR-KG-------------------------------------------------
Pt195587/1  VGV----E-D---------------D----EVDTEIKDDGLQVSDNVGRRIQGEA-----
Pt286483/1  -K----PSKRRRKEY----------EVVKILANSLFL------------DLE------DV
Pt567214/1  KT----YK-QTALSA----------GAYDKLISFYMK------------NFDSTIK----
Pt832603/1  MT----YK-RTALSA----------GAYNKLISSYMK------------NIDATIK----
RMR1/1-850  -KP---SSAIILKRQ----------SLLKLLVDKMSG------------DKSLA----SF
Sb01g46180  NGL----K-EKGKIG----------G-----------------------TIAK-------
Sb02g43870  RGR---KR-KKGMCQ----------REYKRMIEQCIG------------NIQCEVE----
Sb04g33300  R-M---KK-HGPVAK----------AAYDELLNSLFS------------GWEDHIN----
Sb07g02945  KQR----R-KSDTGL----------AAADLSLDL-----------------QQPAK----
Sb09g19410  -KS---SSAIMLKRQ----------SLLKLLVDKMSG------------DKSLE----SF
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  -R-------RA---------------------------------------VEEEEE----
Vv15867/1-  -R----KRIRALKHC----------DALKILVDSIWA------------KNSGLLEELVS
Vv23895/1-  IAV----G-E--------------------------------------------------
Vv29366/1-  RP----HK-KRPFSE----------PGYKEVIEAYMK------------NIESTIN----
Vv35918/1-  IGV----G-E--------------------------------------------------
ZM000342/1  RGR---KR-KKHMCQ----------IEYKRMIDQCIG------------NIQCEVE----
ZM064574/1  KQR---KS-KGATVV----------AAANLSLVS-----------------QQTAT----
ZM093940/1  KQR---RR-KGDTGL----------APADLSLDL-----------------HQTAT----
ZM108166/1  RGR---KR-KKHMCQ----------IEYKRMIDQCIG------------NIQCEVE----
ZM178435/1  R-I---KK-RGRAAK----------AVYDELLDSLFS------------GWENHIG----

                            2600                2620                2640
At1g05490/  E-AD--ELVSSAEDQSQEQARE-------------------------------DHRKYDD
At2g21450/  ------------D-EEDSS--R--------------------------------------
At3g24340/  D-GE--ET-----------IN---------------------------------------
At5g20420/  A-KD--EP---------TSVV---------------------------------------
AtCLSY1/1-  A-KD--KA---------TNVV---------------------------------------
AtDRD1/1-3  ------KV---------LPIE---------------------------------------
Bd1g16720/  R--D--YE---------FNLD---------------------------------------
Bd1g74070/  -----------------VP-V---------------------------------------
Bd2g21430/  ------------------------------------------------------------
Bd2g21450/  ------------------------------------------------------------
Bd2g26500/  P---FDLH---------SQFE---------------------------------------
Bd2g43500/  PLD-DGSA---------PAQE---------------------------------------
Bd3g18910/  E-NL--EESEEVTHDEQKK--ENEYLVRDRWNHFELAIASKNLYFICFLRPRNIW-----
Bd3g19890/  ------------------------------------------------------------
Bd3g50300/  -----GSA---------PA-Q---------------------------------------
Cp19.123/1  K--E--EP----------HII---------------------------------------
Cp76.2/1-4  S-GDVLKE---------QGNH---------------------------------------
Os02g43460  -------E---------PVPE---------------------------------------
Os03g06920  -----------------IS-----------------------------------------
Os05g32610  P---FDQK---------PQIE---------------------------------------
Os06g14440  ------------------------------------------------------------
Os07g25390  ------------------------------------------------------------
Os07g49210  R--D--SM---------FNFD---------------------------------------
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Os08g14610  ------------------------------------------------------------
Pt195587/1  ------AS---------LAGE---------------------------------------
Pt286483/1  P---FK-----------EERE---------------------------------------
Pt567214/1  S-KE--VT----------RII---------------------------------------
Pt832603/1  S-KE--VP----------RII---------------------------------------
RMR1/1-850  P---FDQN---------PQLQ---------------------------------------
Sb01g46180  --------------------H---------------------------------------
Sb02g43870  R--D--SD---------FKID---------------------------------------
Sb04g33300  -------D---------PD-H---------------------------------------
Sb07g02945  ------------------------------------------------------------
Sb09g19410  S---FDQN---------PQLQ---------------------------------------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  E---DDDG---------DEIY---------------------------------------
Vv15867/1-  PRG-SDSI---------EETA---------------------------------------
Vv23895/1-  ------RS---------LAAN---------------------------------------
Vv29366/1-  K--E--QP----------LVI---------------------------------------
Vv35918/1-  ------KS---------LVAN---------------------------------------
ZM000342/1  R--D--SD---------FKFG---------------------------------------
ZM064574/1  ------------------------------------------------------------
ZM093940/1  ------------------------------------------------------------
ZM108166/1  R--D--SD---------FKFG---------------------------------------
ZM178435/1  -------N---------PV-H---------------------------------------

                            2660                2680                2700
At1g05490/  AGLLII--R-PPPLIEKFGVE------EPQSPPVVSEIDSEEDRLWEELAFFTKSNDIGG
At2g21450/  ------------------NS-TDI--D---NQSLYVDA-EEEEELWRKMAFAQESIKVTV
At3g24340/  --YSTE--D-SPPLNLRFGCE------EPVL-IEKTEEEKELDSLWEDMNVALTLEGMHS
At5g20420/  --DQWE--EL-KKTNFAFKLHGDM--EKNLSED-GEGETSENEMLWREMELCLASSYILD
AtCLSY1/1-  --EQWQ--GLKNPASFSIEA--EE--RLSEEEE-DDGETSENEILWREMELCLASSYILD
AtDRD1/1-3  --NGV----V-NEKGVYVGVEEDD-----SDN-ESEAADEDLGNIWNEMALSIECSKDVA
Bd1g16720/  --VPM----M-HCCQGAYPE-EDF--TWPSLADSQEEKKDELDELWKEMDFSLTTLELDR
Bd1g74070/  --VDS----Y-DISCEVIQSESTENGNYDRYD-NNDSPVDELEYLWRDMSLALACSKTIG
Bd2g21430/  --PVE----------------EE---EPMEDG-KPKKESNGHQDIWNAFDMALENSKLYF
Bd2g21450/  -------------------------------------------SLQKKFYFNA-------
Bd2g26500/  --YNSN--D-SHPLVFSFGDE------DHIP-ANKAEQNAEHDMLWADYDFALELENIGT
Bd2g43500/  --QSVP--D-TLPLIFSFGDE------DQVV-KEKTEQGKFEDLLWAEFDFALESTNACS
Bd3g18910/  ----HYPKL-SKNATFVIGKLDKF--EEVASDEPKKESDCLVDDLWNHFDLAMASKKYEE
Bd3g19890/  --PVE----------------EE---EPAEED-KPENKSDGLEDLWKDFSVAMESSKLNT
Bd3g50300/  --AQNE--D-RLPLVFSFGDE------DQVEE--QSDHNKLQDELWAEMDFCMESTNVCP
Cp19.123/1  --DQWQ--EFK-KASFP-EQ-RME--IEQSSSE-DEGESSENEMLWREMELSMASAYFLE
Cp76.2/1-4  --PETE--P-TLPLTFTFQID------ESSM-SKNSDSDNELHNLWVEMNFAQRSFEIDS
Os02g43460  --EQID--R-RLPLVFAFGDD------DKLEEKSKHDKLQDEDELWKEFDFALESINVCS
Os03g06920  --VAS----D-ELACEVMRSQSPTNGNFDQ-Y-DNSSPVDELEGLWMDMYLAMACSKTVG
Os05g32610  --YSFK--D-LHPLVFSFGDD------DPSP-TDRSEQDAALDMLWADLDFTLESENIGT
Os06g14440  -----Q--N-DVP----S--QSYR--TMIEEE-KPVKESDGLEDLWKDFSLAAECTKLDT
Os07g25390  --PLQQ--N-DVP----S--QSYR--TMIEEE-KPVKESDGLEDLWKDFSLAAECTKLDT
Os07g49210  --ANM----M-NYVQHSYRE-EDF--TWPPSADNQEVEEDELEELWKEMDYSLTTLALLE
Os08g14610  ---------------------------------ELDPAADYVKDLWDAFYVTAESTHLDT
Pt195587/1  --PDS----K-KDNGVYVGVEDD-------EV-DTEIKYDGLGDIWKEMSFALECSKDVV
Pt286483/1  --PLEE--P-VLPLKFTFGIE------ESSP-PVKSEEEKQLEELWADMALALCLKDTTD
Pt567214/1  --DQWE--EFK-AKHSS-DQ-KET--MEPSLVE-DDGESSETEMLWREMELCLTSAYIFE
Pt832603/1  --DQWE--EFK-AKHSS-DQ-KEK--MEPSSVK-DDGESSETEMLWREMELCLASAYILE
RMR1/1-850  --FIFK--E-MHPLVFSFGDE------DLVA-ADRPEQDVGLDMLWADFDFALESENIGT
Sb01g46180  --VGS----Y-EVSCEILQNE-PH-SNEGNHH-DNGSPVGELDDLWIGMSVALACSEKNN
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Sb02g43870  --AQI----L-NGCGHAYQE-EDF--MWPSSAD-SQEEKDELQELWKEMDYALATVAIDE
Sb04g33300  --AAAG--N-SLPLVFSFGDE------DA-EE--NIENDKYQEDLWRECDIAFESMDIGN
Sb07g02945  --------S-PEP----EP-EPDM--AIEEEE-KCKNESDGLEDYWKDFALAVESTKLDE
Sb09g19410  --FIFK--E-MHPLVFSFGDE------DLEA-ADRPEQDVGLDMLWADFDFALESENIGT
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  --PCLE--D-SRSWDFDF------------D-HEKLENEDKLAAIWHDWDAEIEAERRRV
Vv15867/1-  --P-AF--T-ELPLKFKFGVD------ESIP-LGKSQPEIGMNQLWAEFDFDGEED-FGS
Vv23895/1-  --HEM----K-NVKGEYVGVEDDMEAS-EGNL-QAKTKDDDLADMWQEFDLALQSSKDVA
Vv29366/1-  --DQWK--ELQ-VRNDL-NQRRDC--NSPSSVG-DQEESSETEMLWREMEFSIASSYLLE
Vv35918/1-  --LEM----K-KVQGEYVGVEDDMETN-EGNL-RAKTEDDGLADMWQEFDLALQSSKDVA
ZM000342/1  --DQI----L-DGCVRAYQE-VDF--TWPSSAD-SQEEKDELDELWKEMDYALATVAILE
ZM064574/1  -----------------SP-EPDM--VIEEEE-KHKNESDGLDDYWKDFALAVESTKLDE
ZM093940/1  -----------------SQ-EPDI--AIEEEE-KRKNDGDGLEDYWKDFALAVESTKLDD
ZM108166/1  --DQI----L-DGCVRAYQE-VDF--TWPSSAD-SQEEKDELDELWKEMDYALATVAILE
ZM178435/1  --AEAG--N-SLPLVFSFGDE------DA-EENTENDKYQEQEDLWMECGIAFQSMNIGS
                            2720                2740                2760
At1g05490/  N-E------LF-------------------------------------SN----------
At2g21450/  E-----------------------------------------------------------
At3g24340/  S-T------P--------------------------------------------------
At5g20420/  D-N------EVR-------------------------------------V----------
AtCLSY1/1-  D-H------EVR-------------------------------------V----------
AtDRD1/1-3  R-E------T--------------------------------------------------
Bd1g16720/  M--------QVP-------------------------------------D----------
Bd1g74070/  S-D------HSI------------------------------------------------
Bd2g21430/  N-AQLDTPEDV-------------------------------------PN----------
Bd2g21450/  ---QLDTLEDV-------------------------------------PN----------
Bd2g26500/  Y-Y------DD-------------------------------------EHQ---------
Bd2g43500/  H-A------CQE------------------------------------EGE---------
Bd3g18910/  V-A---------------------------------------------------------
Bd3g19890/  F-E------EL-------------------------------------PD----------
Bd3g50300/  Q-S------CE-------------------------------------EGE---------
Cp19.123/1  D-N------EVR-------------------------------------V----------
Cp76.2/1-4  H-A------CN-------------------------------------MVE---------
Os02g43460  H-N------CE-------------------------------------EGE---------
Os03g06920  S-D------HNI------------------------------------------------
Os05g32610  Y-Y------DD-------------------------------------EGQ---------
Os06g14440  N-E------DM-------------------------------------SN----------
Os07g25390  N-E------DM-------------------------------------SN----------
Os07g49210  Q-K------QVMAQSRINMLVDNFDGLRLDCLTLTDDYRCYYQKKEKFAE----------
Os08g14610  S-----------------------------------------------------------
Pt195587/1  E-N------S--------------------------------------------------
Pt286483/1  D-A------AL-------------------------------------D-E---------
Pt567214/1  D-N------ESR-------------------------------------V----------
Pt832603/1  D-N------EVE-------------------------------------LCVVFIYSYHL
RMR1/1-850  Y-Y------DD-------------------------------------ECQ---------
Sb01g46180  QVN------LSI------------------------------------------------
Sb02g43870  Q-K------QLIKCLDF----------------------------Q-TTD----------
Sb04g33300  G-S------E-E------------------------------------------------
Sb07g02945  V-D------EA-------------------------------------AN----------
Sb09g19410  Y-Y------DD-------------------------------------EGQ---------
Sm441121/1  ------------------------------------------------------------
Sm84719/1-  P--------DLI-------------------------------------KF---------
Vv15867/1-  A-----------------------------------------------E-----------
Vv23895/1-  V-D------P--------------------------------------------------
```

```
Vv29366/1-  E-N------EGS-------------------------------------N----------
Vv35918/1-  V-D------P--------------------------------------------------
ZM000342/1  Q-K------QM-------------------------------------TD----------
ZM064574/1  V-D------EA-------------------------------------AI----------
ZM093940/1  V-D------EAA------------------------------------AN----------
ZM108166/1  Q-K------QM-------------------------------------TD----------
ZM178435/1  N-G------CEE------------------------------------------------

                            2780                2800                2820
At1g05490/  ------------VEKNISA--NETPA-AQCKKG-KHDLCIDLEVGLKCMHCGFVEREIRS
At2g21450/  -------------DSQSN---DH----KQIEDC-DHSFICKDDIGEVCRVCGLIKKPIES
At3g24340/  ---------------DK------NGD-MLCSKG-THDFVLDDEIGLKCVHCAYVAVEIKD
At5g20420/  -----------------D---NEAFE-KARSGC-EHDYRLEEEIGMCCRLCGHVGSEIKD
AtCLSY1/1-  -----------------D---NEAFH-KATCDC-EHDYELNEEIGMCCRLCGHVGTEIKH
AtDRD1/1-3  --------------------SHKEKA-DVVEDC-EHSFILKDDMGYVCRVCGVIEKSILE
Bd1g16720/  ------------SEDVHES--TARLGKNGEIPC-YHDCILDEEIGLMCRLCNVVCIEAKD
Bd1g74070/  ---------------V-P--SENTCG-EVVDDC-HHDFLMRDDIGLVCRVCGLIKKPIDT
Bd2g21430/  -----------------IKE-V-SE-KEVKIDC-NHQIEIHEDIGHVCRICSMIVRKADM
Bd2g21450/  -----------------AKE-V-GR-KEVKIEC-NHQIVIREDIGHVCRVCGMIVRKADT
Bd2g26500/  -------------EESNMLNLGLACT-TPCSRG-KHEFIIDDQIGIRCKYCSLVNLEIRF
Bd2g43500/  -------------KSN-GDEIHADRA-TSCKRG-KHDLIMDEQIGIRCKHCDFIDLEIRD
Bd3g18910/  ------------NDKHVK---RK--I-NVDIGC-NHDICLHEDLGEVCRVCGMIVRSADK
Bd3g19890/  -----------------EKE-L-GE-KDVDNDC-NHDIRIHEDLGHVCRVCGLIVRRADT
Bd3g50300/  -------------KSNNGQEKPGDKA-TLCSQG-KHDLVTDEQIGVWCRRCNFIQLEIRH
Cp19.123/1  -----------------S---YENIQ-KTTEVC-QHSYRLNEEIGMCCFLCGFISTEIKY
Cp76.2/1-4  ------------NEYAVCSEVDLDIA-TLCSKG-SHHLILDEEIGVKCKYCCFIQQEIKY
Os02g43460  -------------KED-EQEIPADKA-ASCIQG-KHELIIDEQIGLRCKHCNFVDLEIRF
Os03g06920  ---------------V-P--SENSCE-QAEDEC-QHDFLMKDDLGIVCRVCGLIQQRIEN
Os05g32610  -------------ED-SLLDHALAPI-TPCSRG-KHEFIIDEQIGIRCKYCSLVNLEIRF
Os06g14440  -----------------EKD-VDDE-NEMDDDC-NHDIRIHEDLGHVCRICGMIVRKAET
Os07g25390  -----------------EKD-VDDE-NEMDDDC-NHDIRIHEDLGHVCRICGMIVRKAET
Os07g49210  ------------SGSVNES--TDYFGKVGGIPC-HHECILDEELGLACRLCNVVCTEAKD
Os08g14610  -------------------E--VNN-KKQLDNC-NHDIHVYEDLGHVCHECGLVVRKADS
Pt195587/1  -----------------P--SDENME-EDEDYC-DHSFVLKDDIGYVCRICGVIERAIYT
Pt286483/1  ------------NED-DAHEVEPDTV-TLCHQG-NHELYLDEEIGLLCKYCSFVDLEIKY
Pt567214/1  -----------------S---TQTTQ-NSSECC-QHEFKLDEEIGILCHKCSFVKTEKKY
Pt832603/1  YRIFFFITVSDWLKD-LQA--LLSTR-TTQKNC-QHEFKLDEEIGILCQICGFVKTEIKY
RMR1/1-850  -------------E-GNQLDFSLAPV-TPCSRG-KHEFVIDDQIGIRCKYCSLVNLEIKF
Sb01g46180  ---------------V-P--FVSNSE-ETEDAC-NHDFLLKDDLGMVCRICGLIQQRIDK
Sb02g43870  ------------SEADHES--NTDLG-KRGEHC-HHDCMLDEQLGLTCRLCNVVCTEAKD
Sb04g33300  ---------------D-GLEIPPVEV-TSCNNG-QHEFIIDEQIGVRCKHCNVVDIEIRH
Sb07g02945  -----------------EKE--DNG-NMEDIDC-NHDIRIHEDLGHVCRVCGMIVRRADS
Sb09g19410  -------------EEGNQLDFSLAPV-TPCSRG-KHEFIIDDRIGIRCKYCSLVNLEIKF
Sm441121/1  -----------------------------DDICEVHDYVLNELVGLICSVCGYVGIPIEE
Sm84719/1-  ----------------------KDID-VLIDSC-DHEFVFREDCGKVCEICGRVVKLVSD
Vv15867/1-  --------------------VEIDQA-VLCHQG-NHQLVIDEQIGMTCCFCSFVQLEIKY
Vv23895/1-  --------------------EE-DGK-EGEEEC-EHSFVLKDDIGSVCRICGVVNKSIET
Vv29366/1-  ------------VEVLKEV-VQESSN-ISEQVC-QHEYILDEEIGVLCQLCGFVSTEIKD
Vv35918/1-  --------------------GE-DEK-ESKEEC-EHSFVLKDDIGSVCRICGVVNKSIET
ZM000342/1  ------------SEVVHES--NTDLG-KGGEHC-HHDCMLDEQLGLTCRLCNVVCIEAKD
ZM064574/1  -----------------EKE--DNG-KMEDIDC-NHDIRIHEDLGHVCRVCGMIVRRADS
ZM093940/1  -----------------EKE--DNG-KMEDIDC-NHDIRIHEDLGHVCRVCGMIVRRADS
ZM108166/1  ------------SEVVHES--NTDLG-KGGEHC-HHDCMLDEQLGLTCRLCNVVCIEAKD
ZM178435/1  ---------------D-GKEIPPVKV-TSCNIG-QHEFIIDEQIGVRCKHCHVVDLEIRD
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                            2840                2860                2880
At1g05490/  MDVSE-WGEK---T----------TRER-RK----FDRFE-EEE-------GSSF-IGKL
At2g21450/  MIEVV-FNKQ--------------KRSRRTY----MREKE---N-------GETS-R---
At3g24340/  ISPAM-DKYR---P----------SVNDNKK----CSD----RK-------GDPL-PNRL
At5g20420/  VSAPF-AEHK--------------KWTIETKHIEEDDIKTKLSH-------KEAQ---TK
AtCLSY1/1-  VSAPF-ARHK--------------KWTTETKQINEDDINTTIVN-------QDGV-E-SH
AtDRD1/1-3  IIDVQ-FTKA--------------KRNTRTY----ASETRTK-R-------FGES-D---
Bd1g16720/  IFPQM-FNGN--------------GYNK-----DRPGCSNFFHD-------DHVL-D-PS
Bd1g74070/  IIECQ-WKKP--------------KQSYRTY----PSGHRNSND-------LDTP-I---
Bd2g21430/  IFDFE-WRKV--------------SSRSRSY----FKETR-SS----------EI-V---
Bd2g21450/  IFDYQ-WEKE--------------SR-PRSY----LYGTR-SKD-------AGEI-V---
Bd2g26500/  VLPSM-VSN----Y----------AEKSAWRNSSCLKDAL---------MYHDL-CE-Q-
Bd2g43500/  VFPSM-VKF----S----------IEREP-AMS--LNLDL---------FCEDI-IK-S-
Bd3g18910/  IFDYC-WWKQ---L----------SRK-RSG----THEAG-SKN-------ADQI-E---
Bd3g19890/  IIDYQ-WKKA--------------SR-SRSY----FCGTR-SKD-------ADEI-I---
Bd3g50300/  VVADM-VSH----Y----------SLQHAFTKTL-SELDL---------SINNL-LT-S-
Cp19.123/1  MTAPF-MEFR--------------SYVAENRWENEEDNKNMTYA-------GRE----LN
Cp76.2/1-4  IVPPF-------------------------------------------------------
Os02g43460  VLPSM-VKS----C----------TERDM-RKD--HELDL---------FFDDI-LT-S-
Os03g06920  IFEYQ-WKKR--------------KQSYRAR----PSEHRNSSD-------ADAI-D---
Os05g32610  ILPLL-ASN----F----------AEKPAWRNSSCLKTAL---------MCPDL-YE-Q-
Os06g14440  IIDYQ-WKKA--------------SR-TRTN----YYESR-SKD-------ADEI-D---
Os07g25390  IIDYQ-WKKA--------------SR-TRTN----YYESR-SKD-------ADDI-D---
Os07g49210  IFPEM-FNGN--------------DYK------DRPGCSNICLD-------DDIL-D-PS
Os08g14610  LFHYQ-WKKA--------------SR-KRTN----VNEVC-LKK----------V-G---
Pt195587/1  IIEIQ-FNKV--------------KRNTRTY----ISESRNAKD-------RDS----N-
Pt286483/1  YVPPF-DRY----P----------RGKSARRDFVTMQHN----------IFNDLH-H-Q-
Pt567214/1  VSAPF-VFSV---FLLSFMSPLDRQVSMQGRHFLFV-IR--GYS-------ARNP-I-AH
Pt832603/1  VSAPF-MEHT--------------GWTAESKPQNEEDLE--LKP-------DEDE-G-SS
RMR1/1-850  MFPSL-VSV----F----------AEKSAWPNDKGVKNTL---------MFHDL-YE-Q-
Sb01g46180  IFEHS-WKKR--------------NQAYRSY----PIKQRNSGD-------PDAT-M---
Sb02g43870  IFPPM-FTGK--------------DHK-------RLEQSHFGQD-------DHVL-D-LS
Sb04g33300  VLPTL-GKF----S----------AERES-AID--PELDKMLKEMLSVFEQNDV-LV-S-
Sb07g02945  IIDYQ-WKKA--------------SR-RKTN----SYGGH-SKD-------ADEI-D---
Sb09g19410  MFPSL-ISG----F----------AEKSAWPNAKGVKDTL---------MFHDL-YE-Q-
Sm441121/1  MAPHPDWSFR---L----------PQNVLEN--------------------PDPF-IRRP
Sm84719/1-  VFDVS-IISFLSFP----------ARKASSRPAT-KK--------LKLH--EDYA-----
Vv15867/1-  ILPSF-SRN----P----------WGGSEKGNAGKEDCNS---------IFDELQFQ-KP
Vv23895/1-  IIEYQ-YSKV--------------KRS-RTY----MYEPRNTKD-------REPT-D-D-
Vv29366/1-  VS----------------------------------------------------------
Vv35918/1-  IIEYQ-YTKV--------------KRS-RTY----MYEPRNTKD-------REPT-D-D-
ZM000342/1  IFPPM-VASN--------------SNQFTGKDHERPERNHFGQD-------GHVL-D-LS
ZM064574/1  IIDYQ-WKKA--------------SR-RRTN----GYGGH-SKD-------ADEI-D---
ZM093940/1  IIDYQ-WKKA--------------SR-RRMN----GYGGN-SKD-------ADEI-D---
ZM108166/1  IFPPM-FTGK--------------DHE-------RPERNHFGQD-------GHVL-D-LS
ZM178435/1  VLPTL-GKC----S----------AERGS-AIN--PEFDRMLKEMLNVFEQNDV-LV-S-

                            2900
At1g05490/  GFDAPNN-SLNEGCVSSEGTVWDK--IPGVKSQMYP
At2g21450/  DFSGIQ--SSHTN---ILGEKMFI--HPWHDQEMRP
At3g24340/  EFDASDPSSFVAPLDNIEGTVWQY--VPGIKDTLYP
At5g20420/  DFSMIS-DSSEMLAAEESDNVWAL--IPKLKRKLHV
AtCLSY1/1-  TFTIPV-ASSDMPSAEESDNVWSL--IPQLKRKLHL
```

```
AtDRD1/1-3  ----N---ELKFSEEGLMIGGLAA--HPTHAAEMKP
Bd1g16720/  LLA--T-FAPEFSEPRGSGNLWSL--IPDLEPKLLP
Bd1g74070/  ----N---LSR-NILQMLPDPLSI--HPQHLQQMKP
Bd2g21430/  -LGN--V---T-VYEDLTALDVAI--HPRHAQHIRP
Bd2g21450/  -VGN--V---T-VSEDLIALDVAI--HPRHAQHIKP
Bd2g26500/  -AGSID-GQ--SQGFHPYGTVWDL--IPGAINTMYQ
Bd2g43500/  -MGYEG-TS--HFDIHESGLVWDL--IPGVREHMFP
Bd3g18910/  DFGSATA-SAYED---FIFEDAAI--HPMHAKEIRL
Bd3g19890/  -IGD--I---R-VSDDLLALDIAI--HPRHKKQIRS
Bd3g50300/  -MGYEG-TC--KIVDHKAGSVWDL--IPGVKEGLFT
Cp19.123/1  LVGNHT-SHER-LLTEENDNVWAL--IPELRNKLHL
Cp76.2/1-4  -----------------QGTVWDM--IPGVKDSMYP
Os02g43460  -AGYEG-PR--DFGGKKTGLVWDL--VPGVREDMFP
Os03g06920  ----K---TSG-AILEVVPDALCL--HPQHSQHMKP
Os05g32610  -TGTGD-GQ--SQDFHINGTVWDL--IPGVITDMYQ
Os06g14440  -TGA--V---K-VSEDFIVSDIAI--HPRHAKQMRP
Os07g25390  -TGA--V---K-VSEDFIVSDIAI--HPRHAKQMRP
Os07g49210  LLA--N-LAPELSELKNSGSVWSA--ISDLDPKLLP
Os08g14610  -SDA--I---S-LSEDFIFSDIAI--HPRHAKNIRP
Pt195587/1  --GTV---GADLFEEDLMVTDIPA--HPRHMKQMKP
Pt286483/1  DSGHDT-HPDYDPCTLVQGTVWNL--IPGIGKGMHG
Pt567214/1  LFNVCK-ISP-LVPFEVNDNVWDL--IPELRAKLHM
Pt832603/1  LFGNHT-SGEDVPVSEVNDNVWDL--IPELRPKLHM
RMR1/1-850  -GVNDT-EQ--SQDIHQYGTVWNL--IPGVISTMYE
Sb01g46180  ----N---ALG-TILSVAPDTLSL--HPQHSEQMKP
Sb02g43870  FFE--I-CAPESSKSKESGNVWSS--IPVLEPKLLA
Sb04g33300  -NGHEL-PC--NFGGHKAGSVWDL--IPGVKETMFP
Sb07g02945  -CGT--V---K-LSEDFIIADVAI--HPRHAQTMKP
Sb09g19410  -TGSDI-EQ--ISDLHQYGTVWDL--ISGVISTMYE
Sm441121/1  EL--N---D---LNDDLADDPYFP--STDTRRSLHA
Sm84719/1-  ---WKS-------TLNFGDVTVDLVPHPMDSARMYP
Vv15867/1-  GCGSQS-GS--DHGLHPEGTVWDI--IPGIRNSMYR
Vv23895/1-  --PSD---GLRFSEHSLIVTEIHA--HPRHSMQMKP
Vv29366/1-  ----------------------------------PP
Vv35918/1-  --PSD---GLGFSEHNLTVTEIHA--HPRHSMQMKP
ZM000342/1  FFE--I-CAPEFSKIKESGNVWAS--ITDLEPKLLA
ZM064574/1  -CGT--V---K-LSEDFIVADIAI--HPRHARIMKP
ZM093940/1  -CGT--V---K-LSEDFIVADIAI--HPRHAQAMKP
ZM108166/1  FFE--I-CAPEFSKIKESGNVWAS--ITDLEPKLLA
ZM178435/1  -NGHEL-PC--NFGDHKAGSVWNL--IPGVKETMFP
```

Appendix 6. Full-length alignments of polymerase largest subunits using (A) ClustalW, (B) Satchmo, (C) MUSCLE, and (D) TCOFFEE. These alignments were determined to be less accurate than the MAFFT alignment (Chapter 3, Figure 2).

(A) ClustalW

```
PtRPE1a         --MD------EIPQSSIFEGEITGIRFGLASQKEICTASIS-----DCPISHSIQLT-NP 46
PtRPE1b         --MD------ENSQSSIFDGEITGIRFGLATQKEICTASIS-----DCPISHSSQLT-NP 46
VvRPE1          --ME------EDS-STILDGEISGIRFGLATRQEICIASVS-----DCPISHASQLT-NP 45
CpRPE1          ------------------------------------------------------------
AtRPE1          --ME------EESTSEILDGEIVGITFALASHHEICIQSIS-----ESAINHPSQLT-NA 46
BdRPE1          --ME-----EDQSAVLVAEGAIKSIKLSLSTEDEI--------------------LG-NP 32
OsRPE1b         --ME-----EDQSAIPVAEGAIKSIKLSLSTEDEIRTYSIN-----DCPVTHPSQLG-NP 47
SbRPE1b         --ME-----EDHSATLVSEGAIKSIKLSLSTGEEVCTYSVN-----ECPVTHPSQLG-NP 47
ZmRPE1          --ME-----EDHSVILISEGAIKSIKLSLSTGEEICTYSIN-----ECPVTHPSQLG-NP 47
OsRPE1a         --MEGHPDPTSAATAMIPEASIRRINLSITSNEEILKAQPVNELEKPIPITHQSQLLNNP 58
SbRPE1a         --ME--DDDPAAAGLTVPEAFIRRVKLSVTSNQEIKLMAHP--VEDPIPITHCSQLQDNP 54
OsRPD1a         -------MEEPSLEVNNPVAELNAIKFSLMTSSDMEKLSSAT--------IIEMCDVTNA 45
OsRPD1b         -------MEEPSLEVKMPEADLKAVKFSLMTSSDMEKLSSAS--------IIEMCDVTNA 45
BdRPD1          ------------------------------------------------------------
SbRPD1          ----------MELHRELPEATLNAIKFDLMTSTDMEKLSSMS--------VIEVSDVTSP 42
ZmRPD1          ----------MELHREPPEAILNAIKFDLMTSTDMEKLSSMS--------IIEVSDVTSP 42
VvRPD1          ------MDNDFLEEQQVPSGLLIGIKFDVSTEEDMEKISVMK--------IDAVNEITDP 46
PtRPD1          ------MEIDFSEEQQVPSALITGMAFGVLTEAETEKLSVLN--------IDAVSEVTDP 46
CpRPD1          ------------------------------------MALWIL--------LGSWIEVTDP 16
AtRPD1          -------MEDDCEELQVPVGTLTSIGFSISNNNDRDKMSVLE--------VEAPNQVTDS 45
ZmRPB1          -------MDARFPYSPAEVAKVEFVQFGILSPDEIRQMSVIQ------IEHAETMERGKP 47
AtRPB1          -------MDTRFPFSPAEVSKVRVVQFGILSPDEIRQMSVIH------VEHSETTEKGKP 47
SmRPD1          MASSKRRSSHRDRALEEATGTLIALDFRPLTSEEIIRASVYE--------VKTVRALQNN 52


PtRPE1a         YLGLPLEFG--------KCESCGTSEPGQCEG---------------------------- 70
PtRPE1b         FLGLPLEFG--------KCESCGTSEPGKCEG---------------------------- 70
VvRPE1          FLGLPLEFG--------KCESCGTAEPGQCEG---------------------------- 69
CpRPE1          ------------------------------------------------------------
AtRPE1          FLGLPLEFG--------KCESCGATEPDKCEG---------------------------- 70
BdRPE1          FLGLPLETG--------KCESCGASENGKCEG---------------------------- 56
OsRPE1b         FLGLPLETG--------KCESCGASENGKCEG---------------------------- 71
SbRPE1b         FLGLPLEAG--------KCESCGASENDKCEG---------------------------- 71
ZmRPE1          FLGLPLEAG--------KCESCGASENDKCEG---------------------------- 71
OsRPE1a         YLGLPLQVG--------SCQSCGSNAIEECEG---------------------------- 82
SbRPE1a         SLGLPLQDGS-------TCESCGATQLDKCDG---------------------------- 79
OsRPD1a         KLGLPNGAP--------QCATCGSRSIRDCD----------------------------- 68
OsRPD1b         KLGLPNGAP--------QCATCGSQSVRDCD----------------------------- 68
BdRPD1          ------------------------------------------------------------
SbRPD1          KLGLPNASP--------QCETCGSKSGRDCD----------------------------- 65
ZmRPD1          KLGLPNGSL--------QCETCGSQRGRDCD----------------------------- 65
VvRPD1          KLGVPNPSC--------QCSTCGAKDTKKCE----------------------------- 69
PtRPD1          KLGLPNPSS--------QCSTCGSRDLKSCEGIVDVDLNSADRLASIATGDCANILLSLS 98
CpRPD1          KLGLPNPSS--------ECLTCGAKDLKHCE----------------------------- 39
AtRPD1          RLGLPNPDS--------VCRTCGSKDRKVCE----------------------------- 68
ZmRPB1          KPGGLSDPRLGTIDRKIKCETCMAG-MAECPG---------------------------- 78
AtRPB1          KVGGLSDTRLGTIDRKVKCETCMAN-MAECPG---------------------------- 78
SmRPD1          RFGLPNLSD--------CCTSCGAKRTDASNSACP------------------------- 79


PtRPE1a         -HFGYIDLPVPIYHPSHISELKRMLSLLCLKCLKLKRNKIQIKS-NGVAERLL------- 121
PtRPE1b         -HFGFIHLPIPIYHPSHISELKRMLSLICLKCLKLKRNKIQIKS-NGVAERLL------- 121
VvRPE1          -HFGYIELPIPIYHPGHVSELKRMLSLLCLKCLKIRKSKVTN---NGITEQLL------- 118
CpRPE1          ----------------------MVYSLLGINWIMAGTSKVKN---AGVAERLF------- 28
AtRPE1          -HFGYIQLPVPIYHPAHVNELKQMLSLLCLKCLKIKKAKGTS---GGLADRLL------- 119
BdRPE1          -HFGYIELPVPIYHPCHVSELRQLLSLVCLKCLRIKKG---------------------- 93
OsRPE1b         -HFGYIELPVPIYHPCHVTELRQILNVVCLKCLRVKKGKVKQTEGKDNTSALS------- 123
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SbRPE1b         -HFGYIELPVPIFHPCHVSELRQLLSLICLKCLRIKKGKVKQSNGKGNLSATL------- 123
ZmRPE1          -HFGYIELPVPIYHPCHVTELRQLLSLICLKCLRIKKGKVKQSNGKGNAAPTL------- 123
OsRPE1a         -HFRFIELPMPIFHPSHVTELSQILNLICLRCLKIKNRKKSTLKG---SKFTS------- 131
SbRPE1a         -HFGFIKLPEPIYHPSHIAELGKILNLVCLRCLRLKKPKKVTGKE---SRFTS------- 128
OsRPD1a         GHFGVIKLAATVHNSYFIEEVVQLLNQICPGCLTLKQNGDTKKADGTTIQGT--CKYCSK 126
OsRPD1b         GHFGVIKLAATVHNPCFIEEVVQLLNQICPGCLTLKQNGDTKKTDGTTIQTT--CKYCSK 126
BdRPD1          --------------------MLILL-------LLLK------RSDAATIQEP--CKYCSK 25
SbRPD1          GHFGVTKLAATVHNPYFIDDVVHFLNQICPGCLSPREGINMKRLGRETVQATSTCKYCSK 125
ZmRPD1          GHFGVTKLAATVHNPYFIDDVVHFLNRICPGCLSPREGIDTKRLEREKVQAT--CKYCSK 123
VvRPD1          GHFGVIKFPFTILHPYFLTEVVQILNKICPGCKSTRQG---QWVKVRRLRSKG-CKYCAA 125
PtRPD1          GHFGVINFPYTIVHPYFLSEVVQILNKICPGCKSIRLAKATELITKENPQRKG-CKYCAG 157
CpRPD1          GHFGVIQFPYTILHPYYLSEVVQILNKVCPALIHAIQG---------------------- 77
AtRPD1          GHFGVINFAYSIINPYFLKEVAALLNKICPGCKYIRKK----QFQITEDQPER-CRYCTL 123
ZmRPB1          -HFGHLELAKPMFHIGFIKTVLSIMRCVCFNCSKILADEDETKFKQALKIRNP------- 130
AtRPB1          -HFGYLELAKPMYHVGFMKTVLSIMRCVCFNCSKILAD-------EAMKIKNP------- 123
SmRPD1          GHSGHIELPVLVYHWDRISALEAILNRVCLHCYSFKHKGRKKELRTLSSLEQVASG--VD 137
                                       .

PtRPE1a         -------------------------S-CCEECAQISIREVKNTDGACFLELKLPSRSR-L 154
PtRPE1b         -------------------------S-CCEECAQISIREVKNTDGACFLELKLPSRSR-L 154
VvRPE1          -------------------------APCCQDSPQVSVREFRPTEGACFLELKIPSRSR-P 152
CpRPE1          -------------------------SLCCEEVSQVSIKEGKTPDDACYLQLKLPSMSR-L 62
AtRPE1          -------------------------GVCCEEASQISIKD-RASDGASYLELKLPSRSR-L 152
BdRPE1          -----------------------------KDVPALSLKEVKTADGAFRLELRAPPRRL-M 123
OsRPE1b         -------------------------CYYCRDLPALSLKEIKTADGAFRLELKMPPRKF-M 157
SbRPE1b         -------------------------CSYCRDIPALSVKEVKTADGAIRLELSAPHKRH-M 157
ZmRPE1          -------------------------CSYCRDIPALSLKEIKTTDGAIRLELRAPHNKH-M 157
OsRPE1a         -------------------------CSHCQELPPLCVAEVKKSNGARGLELRAPIKKE-L 165
SbRPE1a         -------------------------CSYCQELSPLCVSQVKKSNGARSLELKLPLKQE-V 162
OsRPD1a         DGSKLYPSIIFKMLTSPRVTLSRSKLHRNTSVMDKMSIIAEVAGGVAHKSKNKAPHET-L 185
OsRPD1b         DGAKLYPSVIFKMLTSPRVTLSRSKLHRNTSVMDKISIIAEVAGGVTHNSKNKAPHET-L 185
BdRPD1          DG--LYPSVIFKVLTSPRITLSKSKLQRNTSVMDKVSVTAEVIN----MSKNKSSLEV-L 78
SbRPD1          DGSKLYPSVIFKTLSSPRVLLSKSKLHRSPSVMERISIVAEAAERVSNRSKGKGLLEG-L 184
ZmRPD1          DGSKLYPSIVFKTLSSPRVLLFKSKLHRNASVMERISIVAEAADRMPNRSKGKGSLEG-L 182
VvRPD1          NSNDWYPTMKFKVSSK--------------DLFRKTAIIVEMNEKLPKKLQKKSFRPV-L 170
PtRPD1          NSLGWYPPMKFKVSSK--------------EIFRKTAIIAEIRETLSKKPQK-GFKKI-L 201
CpRPD1          NSLNWYPPMKFKVLSE--------------DIFRLSAIMVEVNENVLRKFQK-RRKEA-L 121
AtRPD1          NTG--YPLMKFRVTTK--------------EVFRRSGIVVEVNEESLMKLKK-RGVLT-L 165
ZmRPB1          --KNRLKRIYDACKSKKVCAGGDDLD-VQEQDTDEPIKK-RGGCGAQQPNITVDGMKM-V 185
AtRPB1          --KNRLKKILDACKNKTKCDGGDDIDDVQSHSTDEPVKKSRGGCGAQQPKLTIEGMKM-I 180
SmRPD1          AHQADIGAVPNGARAPEAEENPGKCTGPAAAVKKIFKKVGTANVPALLLEIDGKVRREDI 197


PtRPE1a         RDGCWNFLERYGFRYVFVTFEKYSYIHMPKVYAFMSKGVCAFRSDWYFIYAPATMLASPR 214
PtRPE1b         RDGCWNFLERYGFRYG-------------------------------------------- 170
VvRPE1          KDGFWDFLARYGYRYG-------------------------------------------- 168
CpRPE1          RESFWNFLEKYGFSLRLCGLGSQISALTLKVLG--------------------------- 95
AtRPE1          QPGCWNFLERYGYRYG-------------------------------------------- 168
BdRPE1          KDSSWNFLDKYGFHHG-------------------------------------------- 139
OsRPE1b         TEGSWNFLDKYGFHHG-------------------------------------------- 173
SbRPE1b         TERSWNFLDKYGFHHG-------------------------------------------- 173
ZmRPE1          TERSWNFLDKYGFHHG-------------------------------------------- 173
OsRPE1a         EEGFWSFLDQFGSCTR-------------------------------------------- 181
SbRPE1a         ADGFWSFLDQFGFHTS-------------------------------------------- 178
OsRPD1a         PQDFWDFIPDDNQPPI-------------------------------------------- 201
OsRPD1b         PQDFWDFVPDDNQPPQ-------------------------------------------- 201
BdRPD1          PHDYWNFVP-HNQPPQ-------------------------------------------- 93
SbRPD1          PQDYWDFVPSENKQVQ-------------------------------------------- 200
ZmRPD1          PLDFWDFVPSENKQVQ-------------------------------------------- 198
VvRPD1          PLDYWDFIPKDPQQEE-------------------------------------------- 186
PtRPD1          AADYWDIFPKDEQEEEEE------------------------------------------ 219
CpRPD1          PADYWDFLPKDSHQEE-------------------------------------------- 137
AtRPD1          PPDYWSFLPQDSNIDE-------------------------------------------- 181
ZmRPB1          AEFKAPKKKTDDQDQLP------------------------------------------- 202
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AtRPB1          AEYKNSKEENDEPDQLP------------------------------------------- 197
SmRPD1          PPGFQSLILKDEMTPQ-------------------------------------------- 213


PtRPE1a         NLVWSYVLLTRLGTGYLFNASVSELLVNDSNFRTVLVYIQSFTFSAYACYFLVMQILKTI 274
PtRPE1b         ---------------------------------------DDFTRPLLPC--EVMQILKRI 189
VvRPE1          ---------------------------------------HNLSRILLPS--EVMEILRRI 187
CpRPE1          --------------------------LLAFWVAFTSLCEGSCKEISKVIGQVVMKMIRSI 129
AtRPE1          ---------------------------------------SDYTRPLLAR--EVKEILRRI 187
BdRPE1          ----------------------------------------GASHFRTLLPEEALNILKKI 159
OsRPE1b         ----------------------------------------GTSHCRTLLPEEALNILKKI 193
SbRPE1b         ----------------------------------------GCSQFRSLLPEEALNILKKV 193
ZmRPE1          ----------------------------------------GCSHHRTLLPEEALNILKKV 193
OsRPE1a         ----------------------------------------GTSHCRPLLPEEVQNIIKKI 201
SbRPE1a         ----------------------------------------GTSHRRPLHPKEVQDIMKKI 198
OsRPD1a         ----------------------------------------FNVTKKILSPYQVFHMLKKL 221
OsRPD1b         ----------------------------------------SNVAKKILSPYQVFHMLKNL 221
BdRPD1          ----------------------------------------PNTTKILLSPYQVFHILKQV 113
SbRPD1          ----------------------------------------SNMTKIILSPYQVFHMLKKS 220
ZmRPD1          ----------------------------------------SNMTKIILSPYQVFYMLKKS 218
VvRPD1          --------------------------------------NCLNPNRRVLSHAQVHYLLKDI 208
PtRPD1          --------------------------------------TNAKPNRRVLSHSQVRHMLKDV 241
CpRPD1          --------------------------------------SGTRPNRRILSHAQVHFLLKAI 159
AtRPD1          --------------------------------------SCLKPTRRIITHAQVYALLLGI 203
ZmRPB1          ---------------------------------------EPVERKQILSAERVLNVLKRI 223
AtRPB1          ---------------------------------------EPAERKQTLGADRVLSVLKRI 218
SmRPD1          ------------------------------------------WRSKMLDPNQVLRILKCL 231
                                                    .  ::   

PtRPE1a         PAETRKKLGGKGYFP--QDGYILQQLPVPPNCLSVPAVSDGISIMSS-DLSISILKKVLK 331
PtRPE1b         PAETRKKLSGKGYFP--QDGYILQQLPVPPNCLSVPVVSDGITVMSS-DLSISMLKKVLK 246
VvRPE1          PEDTRKKLVRKGYFP--QDGYILQYLPVPPNCLSVPDISDGVSIMSS-DLSVSMLKKVLK 244
CpRPE1          PEDTRRKLAGKGYFP--QDGYILQVLPVPPNCLSVPDISDGVSTMSS-DPSTPLLKKVLE 186
AtRPE1          PEESRKKLTAKGHIP--QEGYILEYLPVPPNCLSVPEASDGFSTMSV-DPSRIELKDVLK 244
BdRPE1          PDDTRKKLAARGYIA--QSGYVMKYLPVPPNCLYIPEFTDGQSIMSY-DISISLLKKILH 216
OsRPE1b         PEETKRKLAARGYIA--QSGYVMKYLPVPPNCLYIPEFTDGQSIMSY-DISISLLKKVLQ 250
SbRPE1b         PDDTRRKLAARGYIV--QTGYVMKYLPVPPNCLYIPEFTDGQSIMSY-DISIALLKKVLQ 250
ZmRPE1          PDDTRRKLAARGYIV--QTGYVMKYLPVPPNCLYIPEFTDGQSIMSY-DISIALLKKVLQ 250
OsRPE1a         PEETRRWLSVRGYIP--QDGFILSYLCVPPNCLRVSNVLDGNTFSCS-GTSTNLLRKALR 258
SbRPE1a         TEKTRARLAARGYNL--QDGFVMDNMSIPPNCLQISNMLDENTEMCPPDTSKGLLHKVLR 256
OsRPD1a         DPELINQVTRR------RELLFLSCLPVTPNCHRVAEMP--YGHLDGPRLAFDDRTKAYK 273
OsRPD1b         DPELINQVTPR------RELLFLSCLPVTPNCHRVAEMQ--YGHSDGPRLAFDDRTKAYK 273
BdRPD1          DLELITKFAPR------RELLFLSCLPVTPNRHRVAEMP--YRFSDGPSLAYDDRTKAYK 165
SbRPD1          DPELIKQFVSR------RELLFLSCLPVTPNCHRVVEIG--YGLSDG-RVTFDDRTKAYK 271
ZmRPD1          DPELIKQFVSR------RELLFLSCLPVTPNCHRVVEIG--YGLPDG-RLTFDDRTKAYK 269
VvRPD1          DPGFIKEFVSR------MDSFFLNCLPVTPNNHRVTEIT--HALSNGQTLIFDQHSRAYK 260
PtRPD1          DPNFIKLSILK------TDTIFLNCFPVTPNSHRVTEVT--HAFSNGQRLIFDERTRAYK 293
CpRPD1          DPKLIRKFILR------PDSLFLNYFPVTPNSHRVTELT--YMFSSGQRLFFDERTGAYK 211
AtRPD1          DQRLIKKDIPM------FNSLGLTSFPVTPNGYRVTEIV--HQFN-GARLIFDERTRIYK 254
ZmRPB1          SDEDCLLLGLNPKYAR-PDWMILQVLPVPPPPVRPSVMMDTSSRSED--DLTHQLAMIIR 280
AtRPB1          SDADCQLLGFNPKFAR-PDWMILEVLPIPPPPVRPSVMMDATSRSED--DLTHQLAMIIR 275
SmRPD1          PQETIDKLRDEKLPSIPAEDYFIKSLPVPPNWMRYSTNEFYFQDKTT-----KNLKHLLT 286
                                      :  : :.*                              

PtRPE1a         QVEVIKSSRSGAPNFDAHKDEANSLQSMVDRYLQVRGTTKTSRDVDVRYGV-KKDSSESS 390
PtRPE1b         QAEVIRSSRSGAPNFDAHKDEATSLQSMVDQYLQVRGTTKTSRDVDTRYGV-KKESSEST 305
VvRPE1          QIEVIKGSRSGEPNFESHKIEANNLQSSIEQYLEVRGTAKTSRSLDTRFGS-SKEPNESS 303
CpRPE1          KVENIKSSRCGEPNFESHSVEANELQSAVNKYLQARGTAKASRE-DTRYGV-SKNSNDCS 244
AtRPE1          KVIAIKSSRSGETNFESHKAEASEMFRVVDTYLQVRGTAKAARNIDMRYGV-SKISDSSS 303
BdRPE1          RIEQIKKSRAGTPNFESHEAESSDLQISIAQYIHLRGTT-------KRFTI-STDSSHLS 268
OsRPE1b         KIEQIKKSRAGSPNFESHEVESCDLQLSIAQYIHLRGTTRGPQDNTKRFAI-STDPSALS 309
SbRPE1b         KIEQIKRSRSGSPNFDSHDAESCDLQLAIGQYIRLRGTTRGPQDNTKRFTVGSADSAALS 310
ZmRPE1          KIEQIKRSRSGSPNFESHDAESCDLQLAIGQYIRLRGTTRGPQDNTKRFTVGSADSAALS 310
OsRPE1a         KIQQIRGSRIGSSNIQVDQV-ADDLQVDVANYINLGGTT--------KGHGDDTFTSQPT 309
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SbRPE1a         TIEQIESLNISHPNIEARELGADDLQVAVADYMNMGGAA--------KVSQHVTFTRQPA 308
OsRPD1a         RMVDVSR--------RIDDYHQHPQFGVFASSVVTSRVMECLKSSKLYSKKSDDESSAST 325
OsRPD1b         RMVDVSK--------RIDDCRQHPQFSVFASSVVTSRVMECLKSSKLYSRKSDGEDPTSP 325
BdRPD1          RTVDASK--------KIDDYRQHPQFSVLASSFVTSRVMECLQSSKLYSKKTDKES--ST 215
SbRPD1          RMVDVSR--------RIDDYRQHPQFSVLASSLVSGRVSECLKSSKLYSKKTDGET--ST 321
ZmRPD1          RMVDVSR--------RIDDYRQHPHFSVLASSLVSSRVSECLKSSKLYSKKADGET--ST 319
VvRPD1          KLVDFRG--------TANELSCHS----------------------------------AS 278
PtRPD1          KMVDFRG--------VANTLSFHVMDCLKTSKLNP----DKSGNIDPWTAQPKKSNDYVN 341
CpRPD1          KLVDFRG--------TSNELSSRLHTFKSSSKD---------------ATTALLKNEDSS 248
AtRPD1          KLVGFEG--------NTLELSSRVMECMQYSRLFS----ETVSSSKD-SANPYQKKSDTP 301
ZmRPB1          HNENLRRQERNGAPAHIITEFAQLLQFHIATYFDNDLPG---QPRATQRSGRPIKSICSR 337
AtRPB1          HNENLKRQEKNGAPRHIISRFTQLLQFHIATYFDNELPG---QPRATQKSGRPIKSICSR 332
SmRPD1          KIKSIVYTRDEDKISLLTEQKVMEIQAAATQCIRANPLYGNVSDEDPRYGNVSDESKPLS 346


PtRPE1a         TKAWLEKMRTLFIRKGSGFSSRSVITGDAYTKVNQVGIPYEIAQRITFEERVSVHN--MR 448
PtRPE1b         TKAWLEKMRTLFIRKGSGFSSRSVITGDAYTLVNQVGIPYEIAQRITFEERVSVHN--MR 363
VvRPE1          TKAWLEKMRTLFIRKGSGFSSRSVITGDAYKRVNEIGLPFEIAQRITFEERVNVHN--MK 361
CpRPE1          TKAWLEKMRTLFIRKGSGFSSRSVITGDPYKKVNEIGIPFEIAQRITFEERVNLHN--MK 302
AtRPE1          SKAWTEKMRTLFIRKGSGFSSRSVITGDAYRHVNEVGIPIEIAQRITFEERVSVHN--RG 361
BdRPE1          TKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGVDVVGLPSEVAKRITFEEQVTDIN--IK 326
OsRPE1b         TKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGVDVIGLPSEVAKRITFEEQVTDIN--LN 367
SbRPE1b         TKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGLGVVGLPSEVAKRMTFEEQVTDIN--IN 368
ZmRPE1          TKQWLEKMRTLFISKGSGFSSRSVLTGDPYIGLGVVGLPSEVAKRMTFEEQVTDIN--IN 368
OsRPE1a         AMQWKQKMKTLFISKSSSFSSRGVITGDPYIGLNVVGVPEEVAKRMSVEEKVTDHN--IA 367
SbRPE1a         PKQWHKKMKTLFLSKSSSYTCRAVITGDPYIGLDVVGVPDEIARRMSVQECVTNYN--IA 366
OsRPD1a         DTYGTKWLKDIILSKRSDNAFRSIMVGDPKINLNEIGIPMGLALNLVVSEQVSSYN---- 381
OsRPD1b         DTYGTKWLKDIILSKRSDNAFRSIMVGDPKINLNEIGIPTDLALNLVVSEQVSFYN---- 381
BdRPD1          DSYGT---SDAILSKRSDYAFRSIMVGDPKIRLHEIGIPMDLAD-LFVPEHVSIYN---- 267
SbRPD1          DPSGMKWLKDAVLSKRSDNAFRSTMVGDPKIKLWEIGIPEDLASNLVVSDHVNSYN---- 377
ZmRPD1          DTYGMKWLKDVVLSKRSDNVFRSIMVGDPKIKLWEIGIPEDLSSSLVVSEHVSSYN---- 375
VvRPD1          KMSGLKWIKEVLLGKRTNHSFRMIVVGDPKLRLSEIGIPCHIAEELLISEHLNSWN---- 334
PtRPD1          NASGLRWIKDVVLGKRNDHSFRMVIVGDPHLQLHEIGIPCHIAERLQISESLTAWN---- 397
CpRPD1          NMVGLRYMKDVLLGKRNDSSFRTVVIGDRSLKLSEIGIPCHIAESLQISENLNNWN---- 304
AtRPD1          KLCGLRFMKDVLLGKRSDHTFRTVVVGDPSLKLNEIGIPESIAKRLQVSEHLNQCN---- 357
ZmRPB1          LKAKEGRIRGNLMGKRVDFSARTVITPDPNINIDELGVPWSIALNLTYPETVTPYN--IE 395
AtRPB1          LKAKEGRIRGNLMGKRVDFSARTVITPDPTINIDELGVPWSIALNLTYPETVTPYN--IE 390
SmRPD1          GLHFLRSLTGKYCG----SSARAVVIGDPALKLEEIGISARIAAGLVVLETVTSSN---- 398
                                     *  :  *    :  :*:.  ::  :   : :.  *

PtRPE1a         YLQELVDNKLCLTYRDG-SSTYSLREGSK---------GHTFLRPGQ------------- 485
PtRPE1b         YLQELVDNKLCLTYKDG-SSTYSLREGSK---------GHTFLRPGQ------------- 400
VvRPE1          HLQNLVDEKLCLTYRDG-LSTYSLREGSK---------GHTFLRPGQ------------- 398
CpRPE1          YLQELVDKKLCLTYRDG-GSTYSLREGSK---------GHTFLRPGQ------------- 339
AtRPE1          YLQKLVDDKLCLSYTQG-STTYSLRDGSK---------GHTELKPGQ------------- 398
BdRPE1          RLQEVVDKGLCLTYRDG-QTTYAITVGSK---------GYTTLKVGQ------------- 363
OsRPE1b         RLQEIVDKGLCLTYRDG-QATYAITVGSK---------GHTTLKVGQ------------- 404
SbRPE1b         RLQEVVDKGLCLTYRDG-QATYAITVGSK---------GHTTLKVGQ------------- 405
ZmRPE1          RLQDVVDKGLCLTYRDG-QATYAITVGSK---------GYTTLKVGQ------------- 405
OsRPE1a         QLQDMMNKGLCLTYTDANSITYSLDAGKDNPN-----KKHTILKVGE------------- 409
SbRPE1a         RLQDMMNKGLCLTYTDLNTNTYDLDGKKG--N-----KKCIMLRVGE------------- 406
OsRPD1a         --FETINLKCNLHLLTK-EVLLVRRNGNLIFV-----RKANQLEIGD------------- 420
OsRPD1b         --FETINLKCNLHLLTK-EVLLVRRNGKLIFV-----RKANKLEIGD------------- 420
BdRPD1          --FKSINLKCNLHLLAK-ELLIARRNGKLIYV-----RKENQLEIGD------------- 306
SbRPD1          --FENINLKCNLHLLTK-EELFIRRNGKLMFL-----RKADQLEIGD------------- 416
ZmRPD1          --FQSTNLKCNLHLLAK-QELFIRRNGKLMFL-----RKADQLEIGD------------- 414
VvRPD1          --WEKVTNGCNLRLLEK-GQTYVRRKGTLAPV-----RRMNDFQAGD------------- 373
PtRPD1          --WEKLNACFEKSRFEK-GDMHVRREGNLVRV-----RHMKELRLGD------------- 436
CpRPD1          --WDKLISSCDLRLLEK-GEIHVRRKNSLISL-----RRISDLRMGD------------- 343
AtRPD1          --KERLVTSFVPTLLDN-KEMHVRRGDRLVAI-----Q-VNDLQTGD------------- 395
ZmRPB1          RLKELVEYGPHPPPGKTGAKYIIREDGQRLDLRYVKKSSDQHLELGY------------- 442
AtRPB1          RLKELVDYGPHPPPGKTGAKYIIRDDGQRLDLRYLKKSSDQHLELGYRYVLLSYSIHSTH 450
SmRPD1          -------IIFLQSYAYNNPGLKVVRGGEVCTAR-----SCKKLQVGD------------- 433
                                                          :. *
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PtRPE1a         ---------------VVHRRIIDGDVVFINRPPTTHKHSLQALSVYVH-DDHTVKINPLI 529
PtRPE1b         ---------------VVHRRIMDGDIVFINRPPTTHKHSLQALSVYVH-DDHAVKINPLI 444
VvRPE1          ---------------VVHRRIMDGDIVFINRPPTTHKHSLQALSVYVH-DDHTVKINPLI 442
CpRPE1          ---------------VVHRRIMDGDTVFINRPPTTHKHSLQALSVYIH-DDHTVKINPLI 383
AtRPE1          ---------------VVHRRVMDGDVVFINRPPTTHKHSLQALRVYVH-EDNTVKINPLM 442
BdRPE1          ---------------TISRRIVDGDVVFLNRPPSTHKHSLQAFYVYIH-DDHTVKINPLI 407
OsRPE1b         ---------------TISRRIVDGDVVFLNRPPSTHKHSLQAFRVYVH-EDHTVKINPLI 448
SbRPE1b         ---------------TISRRIVDGDVVFLNRPPSTHKHSLQAFYAYVH-DDHTVKINPLM 449
ZmRPE1          ---------------TISRRIVDGDVVFLNRPPSTHKHSLQAFYAYVH-DDHTVKINPLM 449
OsRPE1a         ---------------IVNRRVFDGDIVFLNRPPSTDKHSVEAFYVQVH-NDHTIKINPLI 453
SbRPE1a         ---------------TVDRRVLDGDLVFLNKPPSTDMHSIQALYVHVH-DDHTIKINPLI 450
OsRPD1a         ---------------IAYRLLQDGDLVLVNSPPSVHQHSLIALSAKLLSTQSAVSINPLC 465
OsRPD1b         ---------------IAYRLLQDGDLVLVNRPPSVHQHSLIALSAKLLPIQSAVAINPLC 465
BdRPD1          ---------------IVYRPLQDGDLILVNRPPSVHQHSLIALSAKLLPVQSVVAINPLN 351
SbRPD1          ---------------IAYRPLQDGDLILINRPPSVHQHSLIAFSAKILPIHSVVSINPLC 461
ZmRPD1          ---------------IAYRPLQDGDIILINRPPSVHQHSLIALSAKILPIHSVVSINPLC 459
VvRPD1          ---------------IIYRPLTDGDIVLINRPPSIHQHSVIALSVKVLPLNSVVSINPLC 418
PtRPD1          ---------------IIYRPLNDGDTVLINRPPSIHQHSLIALSVKVLPVPSVLAINPLC 481
CpRPD1          ---------------IISRPLKDGDILLINRPPSIHPHSLIALSVKVLPISSVVSINPIC 388
AtRPD1          ---------------KIFRSLMDGDTVLMNRPPSIHQHSLIAMTVRILPTTSVVSLNPIC 440
ZmRPB1          ---------------KVERHLNDGDFVLFNRQPSLHKMSIMGHRIKIM-PYSTFRLNLSV 486
AtRPB1          KRLFLEVVIFMLSWSQVERHLQDGDFVLFNRQPSLHKMSIMGHRIRIM-PYSTFRLNLSV 509
SmRPD1          ---------------VIHRSLKDGDQVFVNRPPTFHKHALIGLKSKVI-RNNVFAVNPLI 477
                                  * : *** ::.*  *: .  :: .    :     .. :*

PtRPE1a         CGPLSADFDGDCVHLFYPQSLAAKAEVLELFSVEKQLLSSHSGNLNLQLTTDSLLSLKMI 589
PtRPE1b         CGPLSADFDGDCVHLFYPQSLAAKAEVLELFSVEKQLLSSHSGNLNLQLTTDSLLSLKMM 504
VvRPE1          CGPLSADFDGDCVHLFYPQSLGAKAEVLELFSVEKQLLSSHSGNLNLQLATDSLLSLKVL 502
CpRPE1          CGPLSADFDGDCVHLFYPQSPAARAEVLELFSVEKQLLSSHSGNLNLQLAADSLLSLKVM 443
AtRPE1          CSPLSADFDGDCVHLFYPQSLSAKAEVMELFSVEKQLLSSHTGQLILQMGSDSLLSLRVM 502
BdRPE1          CSPLAADFDGDCVHIYYPQSLAAKAEALELFSVEKQLTNSHNGKVNLQLSNDSLLALKHM 467
OsRPE1b         CAPFAADFDGDCVHIYYPQSLAAKAEALELFSVEKQLTSSHSGKVNLQLVSDSLLALKHM 508
SbRPE1b         CGPFSADFDGDCVHIYYPQSLAAKAEALELFSVERQLISSHSGKVNLQLGNDCLVAMKAM 509
ZmRPE1          CGPFSADFDGDCVHIYYPQSLAAKAEALELFSVERQLISSHSGKVNLQLGNDSLVAMKAM 509
OsRPE1a         CDPLGADFDGDCVQIFYPRSLSARAEAKELYTVDKQLVSSHNGKLNFQFKNDFSLALKIM 513
SbRPE1a         CGPLEADFDGDCVHIFFPRSVLARVEAAELFAVEKQLLNSHNAKLNFQIKNDYLLALRIM 510
OsRPD1a         CDPFKGDFDGDCLHGYIPQCLQSRIELEELVGLSGQLLNQQDGRSLVSLTHDSLAAAHQL 525
OsRPD1b         CDPFKGDFDGDCLHGYVPQTLQSRVELDGLVSLSGQMLNAQDGRSLVSLTHDSLAAAHQL 525
BdRPD1          CAPLSGDFDGDCLHGYVPQSIGSRVELGELVSLSHQLLNMQDGRSLVSLTHDSLAAAHLL 411
SbRPD1          CTPFLGDFDGDCLHGYIPQSVRSRIELGELVSLHHQLLNMQDGRSLVSLTHDSLAAAHLL 521
ZmRPD1          CTPFAGDFDGDCLHGYIPQSIRSRVELEELVSLHNQLLNMQDGRNLVSLTHDSLAAAHLL 519
VvRPD1          CSPFRGDFDGDCLHGYIPQSVDSRVELSELVALNRQLINRQSGRNLLSLSQDSLSAAHLV 478
PtRPD1          CPPFRADFDGDCLHGYVPQSVDTRVELTELVSLDKQLTNWQSGRNLLSLSQDSLTAAHLV 541
CpRPD1          CSPFRGDFDGDCFHGYIPQSIEARVELHELVALDRQLTNWLSGRNLLCLGQDSLTAAHLI 448
AtRPD1          CLPFRGDFDGDCLHGYVPQSIQAKVELDELVALDKQLINRQNGRNLLSLGQDSLTAAYLV 500
ZmRPB1          TSPYNADFDGDEMNMHVPQSFETRAEVLELMMVPKCIVSPQSNRPVMGIVQDTLLGCRKI 546
AtRPB1          TSPYNADFDGDEMNMHVPQSFETRAEVLELMMVPKCIVSPQANRPVMGIVQDTLLGCRKI 569
SmRPD1          CPPLFADFDGDTLALYLPQSLQVRAEVAELVALPKQLVSSQGGQSIIGLTQDALLGAHLM 537
                  *  .***** .  . *:    : *   *  :   : .    .  . :  *   .   :

PtRPE1a         --FKACFLDKSAAQQLA--MFVSPDLPQPALLKVNC--IRPYWTAHQILQMALPTCFNCS 643
PtRPE1b         --FKACFLGKSAAQQLA--MFISPYLPQPALLKVNC--FFPHWTAHQILQMALPACFNCS 558
VvRPE1          --FERYFLNKAAAQQLV--MFVSMSLPRPALLKSPC--SGPCWTALQILQTALPSYFDCI 556
CpRPE1          --FEKFFLGKTAAQQLA--MFGSLSLLWPALFKSHS--SGSFWTASQIIQTALPACFDCN 497
AtRPE1          --LERVFLDKATAQQLA--MYGSLSLPPPALRKSSK--SGPAWTVFQILQLAFPERLSCK 556
BdRPE1          --SSRTVLSKESANQLA--MLLSFSLPDPAVVKL-----KPCWTITQIIQGALPAALTCE 518
OsRPE1b         --SSRTMLSKEAANQLA--MLVTCSLPDPAVIKS-----KPYWTISQIVQGALPKALTSQ 559
SbRPE1b         --SDRTVLHKELANQLA--MFVPFSLLAPAVMKP-----IPSWTITQIVQGALPAKLTCQ 560
ZmRPE1          --SHTTMLHKELANQLA--MFVPFSLLAPAVIKP-----VPSWTISQIVQGAFPANLTCQ 560
OsRPE1a         --CGR-EYSEREANQITNAMFSSGMYP-QKPLIG-----GPYWTFPQILETTKSNAITLA 564
SbRPE1a         --CDR-SYSKEKANQIA--MFSSGMIPPCNPWTI-----CDRWTIPQILQTTDALRIVPS 560
OsRPD1a         -TNADVFLEKAEFQQLQMLSSSISLTPMPSVFKSTN-SQGPLWTGKQLFGMLLPYGMNIS 583
OsRPD1b         -TSADVFLQKAEFQQLQLLCSSISPTPEPSVVKSAN-FQGSLWTGKQLFGMLLPSGMNIS 583
```

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BdRPD1          -TSSGVLLNKTEFQQLQMLCVSLSPTPVPSVIKSIN-PQGPLWTGKQLFGMLLPSGMNFS 469
SbRPD1          -TSTDVFLKKSEFQQLQMLCLSVL-TPVPAVIKSMN-FQGSRWTGKQLFSMLLPSGMKFS 578
ZmRPD1          -TSTDVFLKKSELQQLQMLCLSVS-TPAPAVIKSMN-FQGSLWTGKQLFSMLLPSGMNFS 576
VvRPD1          -MEDGVLLNLFQMQQLEMFCPYQL--QSPAIIK--------------------------- 508
PtRPD1          -LEDDVFLSSFELQQLQMFRPERF--LLPAVKAPS--ANALVWTGKQLISMLLPVGFDHD 596
CpRPD1          -KEDGFLLNKYQMQQLKMYCPYEL--PPPALVKAPR-LNSSVWTGKQLFSMLLPPGFNYY 504
AtRPD1          NVEKNCYLNRAQMQQLQMYCPFQL--PPPAIIKASPSSTEPQWTGMQLFGMLFPPGFDYT 558
ZmRPB1          TKRDTLIEKDVFMNILMWWQDFDGKIPAPTILKP-----RPIWTGKQVFNLIIPKQINLI 601
AtRPB1          TKRDTFIEKDVFMNTLMWWEDFDGKVPAPAILKP-----RPLWTGKQVFNLIIPKQINLL 624
SmRPD1          -TRKNVFLDKLDMDQLR-MWCPSAEVPVPAIVKSPR--KSPLWTGQQLFQMTLPTTFDWE 593
                             : :

PtRPE1a         GERFLINNSNVLKVDFNRDVVAS----------------MIN-EILISIFFEKGSGAVLK 686
PtRPE1b         GERFLIINSNFLKVDFNRDVVAS----------------VIN-EILISMFFEKGSGAVLK 601
VvRPE1          GERHWISKSAILKVDYNRDVLQS----------------LVN-EIVTSIFSEKGPNEVLK 599
CpRPE1          EDRYLIRKSEILNIDFNKDSVQS----------------VVG-EVVNSIFYEKGPKEVLE 540
AtRPE1          GDRFLVDGSDLLKFDFGVDAMGS----------------IIN-EIVTSIFLEKGPKETLG 599
BdRPE1          GGRFLVKDSTVIKLDLAKESVQA----------------SFS-DLVSSILCVKGPGGALQ 561
OsRPE1b         GDKHVVRDSTIIKLDLDKESVQT----------------SFS-DLVYSTLSVKGPGEALQ 602
SbRPE1b         GDTHLVRDSTIIKLDLDKESVQD----------------SFP-DLVSSILREKGPREALQ 603
ZmRPE1          GDTHLVRDSTIIRLDLGKESVQD----------------SFP-DLVSSILREKGPKEALQ 603
OsRPE1a         -------------DHLDRESVGA----------------LATGTTISSILSTKGPREATE 595
SbRPE1a         -------------HPN---TVGA----------------SVT-AIITSTLSEKGPREAIK 587
OsRPD1a         FDQ-KLHIKDSEVLTCSSGSFWL----------------QNNTSSLFSVMFKEYGCKALE 626
OsRPD1b         FDQ-KLHIKDSEVLTCSSGSFWL----------------QNNTSSVFSVMFKEYGSKALE 626
BdRPD1          PDP-KLHIKDSEVLACSGGSFWL----------------QNNTSGLFSVLFKQYGGEALE 512
SbRPD1          CDR-MLHILNGEVLTCSLGSSWL----------------QNNTSGLFSVMFKQYGCKALD 621
ZmRPD1          CDT-ELHIMDSEVLTCSLGSSWL----------------QNNTSGLFSVMFKQYGCKALD 619
VvRPD1          ------------------------------------------------------------
PtRPD1          FPSCNVCIRDGDLVSS-EGSFWL----------------WDTDGNLFQSLVKHCHGQVLD 639
CpRPD1          FSQNGVCIINGELTSSSDGSAWL----------------RDNDGNLFQSLVKYDKSMVLN 548
AtRPD1          YPLNNVVVSNGELLSFSEGSAWL----------------RDGEGNFIERLLKHDKGKVLD 602
ZmRPB1          RFSAWHSEEEKGFITPGDTMVRIEKGELLSGTLCKKSLGTGSGSLIHVIWEEVGPDAARK 661
AtRPB1          RYSAWHADTETGFITPGDTQVRIERGELLAGTLCKKTLGTSNGSLVHVIWEEVGPDAARK 684
SmRPD1          SDDGGLIIRQGEILRTSDKSSAWLG----------------KDGLMTTICRRYGPDRALE 637


PtRPE1a         FFNALQPLLMENLFSEGFSVSLKDFSISQAVKQSIQ-ESFKVISPLLCNLRSTYNELVEL 745
PtRPE1b         FFNSLQPMLMENLFSEGFSVSLEDFSISRAVKQRIP-ESFKAISPLLCNLRSTFNELVEL 660
VvRPE1          FFDSLQPLLMENLFSEGFSVSLEDFSIPSEVTQNIQ-KNVEDISSLLYNLRSMYNELLQL 658
CpRPE1          FFASLQPLLMENLFVEGFSVGLKDFSMPKSDMQAIQ-KLIHDTSLFLSCLGSTYNE--EL 597
AtRPE1          FFDSLQPLLMESLFAEGFSLSLEDLSMSRADMDVIHNLIIREISPMVSRLRLSYRD--EL 657
BdRPE1          FLNALQPLLMEYLLLDGFSVSLQDFNVPKVLLEEVH-KSIQEQSLVLEQSRCSKSQFVEM 620
OsRPE1b         FLNVLQPLLMELILLDGFSVSLQDFNVPKVLLEEAQ-KNIEKQSLILEQSRFAENQVVEM 661
SbRPE1b         FLNVLEPLLMEFLVLGGLSISLRDFNVPKALLEEAQ-KNIQNQSLVLEQSRCSTSQFVEL 662
ZmRPE1          FLNVLEPLLMEFLLLDGLSISLRDFNVPKALLEEAQ-KDIRNQSLILEQSRCSTSQFVEF 662
OsRPE1a         FLNLLQPLLMESLLIDCFSINLGDFTVPSPILEAIQ-NNP------LELNKYREP----- 643
SbRPE1a         LINLLQPLLMESLLMDGFSISLKDLDGQSAMQKANQ-SIS------LEIDKFSKS----- 635
OsRPD1a         FLSSTQDVLCEFLTMWGLSVSLSDLYLFSDHYSRRKLSEEVHLALDEAEEAFQIKQILLN 686
OsRPD1b         FLSSTQDVLCEFLTMKGLSVSLSDFYLFSDHYSRKKLSEEIHLALDEAEEAFQIKQILLN 686
BdRPD1          FLSSAQDMLCEFLTMRGLSVSLSDIYLFSDHYSRRKFAEEVNLALDEAEEAFRVTQILLS 572
SbRPD1          FLSSAQEVLCEFLTMRGLSVSLSD--MFSDHYSRRKLTEGVKLALDEAEEAFRIKQILLD 679
ZmRPD1          FLSSAQEVLCEFLTMRGLSVSLSDLYMFSDHYSRRKLAEGVKLALYEAEEAFRVKKILLD 679
VvRPD1          ----APLLDTQWLSMRGLSVSLSDIYLSSDSISRKNMIDEVFCGLLVAEQTCHFKQLLVD 564
PtRPD1          FLYAAQRVLCEWLSMRGLSVSLSDLYLCPDSNSRKNMMDEIWYGLQDADYACNLKHLMVD 699
CpRPD1          FLYAAQEVLCDWLSDRGFSISLSDLYLSSDLHSRENLMDEISWGLLEAEQTCNFKQLMVD 608
AtRPD1          IIYSAQEMLSQWLLMRGLSVSLADLYLSSDLQSRKNLTEEISYGLREAEQVCNKQQLMVE 662
ZmRPB1          FLGHTQWLVNYWLLQNGFSIGIGDTIADASTMETINDTISKAKNAVKELIKKAHEKQLEA 721
AtRPB1          FLGHTQWLVNYWLLQNGFTIGIGDTIADSSTMEKINETISNAKTAVKDLIRQFQGKELDP 744
SmRPD1          HLDIAQGIAVDWISERGFSVGLCDFYMAADAVSRRKLEEETLCAVEEAKISSLAHQIVSD 697
                       :    :    :::.: *        .

PtRPE1a         Q---------------------------------------------------------VE 748
PtRPE1b         Q---------------------------------------------------------VE 663
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VvRPE1          Q---------------------------------------------------------AE 661
CpRPE1          Q---------------------------------------------------------LE 600
AtRPE1          Q---------------------------------------------------------LE 660
BdRPE1          R---------------------------------------------------------VD 623
OsRPE1b         R---------------------------------------------------------VD 664
SbRPE1b         R---------------------------------------------------------VE 665
ZmRPE1          R---------------------------------------------------------VE 665
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
OsRPD1a         SVSIPNLKYYDGGDDRSNT-------------------DEQSGFTQVSLPIIRSSMTSFK 727
OsRPD1b         TVSIPNLKHYDGPDNLSNS-------------------HGQSDFTQVSLPIIKSSITGFK 727
BdRPD1          PNFIPHLKCYDDCDDLSDS-------------------YEQSDFVQSNLPIIKSSIMAFK 613
SbRPD1          PINIPVLKCQDETEDVT---------------------YRQSDCIQNNPSVIRSSIMAFK 718
ZmRPD1          PINIPVLKCHDETEDVT---------------------YRQSDCIQSNPSVIRSSIMAFK 718
VvRPD1          SSQNFLIGSGENNQNGVVP-----------------DVQSLWYERQGSAALCQSSVCAFK 607
PtRPD1          SCRDFLTGNNEEDQCNVERLRFLSGCSEEDYCVMAFDGERLCYEKQRSAALSQSSVDAFR 759
CpRPD1          SCRDLLAGNDEESQNVITF-----------------DVERLCYEKQGSAVLSQASVDAFK 651
AtRPD1          SWRDFLAVNGEDKEEDSVS-----------------DLARFCYERQKSATLSELAVSAFK 705
ZmRPB1          EPGRTMMESFENRVN-----------------------------------------QVLN 740
AtRPB1          EPGRTMRDTFENRVN-----------------------------------------QVLN 763
SmRPD1          PRFQVNSVSRPRCNSWNER---------------------VQPVTSVNEATQQAAISAFQ 736


PtRPE1a         NHIQDVKTPVLEFI---LTSSALGYLIDSKSDGAVAKLVQQIGFLGLQVSDRGKLYSKTL 805
PtRPE1b         NHIRDVKQPVREFI---LTSSALGYLIDSKSDAAVTKVVQQIGFLGLQVSDRGKLYSKTL 720
VvRPE1          NHLRLTKVPVANFI---LNSSALGNLIDSKSDSAINKVVQQIGFLGQQLSEKGKFYSRTL 718
CpRPE1          NRIRCLKETAENFI---IKS-SLRNLIDFRSDSAVNKVVQQIGFLGLQLSDKGKFYSKNL 656
AtRPE1          NSIHKVKEVAANFM---LKSYSIRNLIDIKSNSAITKLVQQTGFLGLQLSDKKKFYTKTL 717
BdRPE1          NNLKDVKQQISDFV---VESSHLGLLIDPKSEPSMSKVVQQLGFVGLQLYREGKFYSSRL 680
OsRPE1b         NNLKDIKQQISDFV---VKRSHLGLLIDPKSDSSVSKVVQQLGFVGLQLYREGKFYSRRL 721
SbRPE1b         NNLKSVKQQISDYV---GKFSGLGLLIDPKKEASMAKVVQQVGFVGLQLYREGKLYSRRL 722
ZmRPE1          NNLKNVKQQISDSV---GKFSDLGLLIDPKKEASMSKVVQQVGFVGLQLYREGKLYSRRL 722
OsRPE1a         ---------IMDFI---THSSAIGLLVDPKSDSNMNKVVEQLGFLGPQLQHNGRLYSSRL 691
SbRPE1a         ---------IVDFI---ANSSALGLLVDPKNDSALMNLVEQVGFLGYQLQSTDRLYSNNL 683
OsRPD1a         SVFNDLLKMVQQYV---SKDNSMMTMINSGSKGSVLKFVQQTACVGLQLPASKFPFRIPS 784
OsRPD1b         SVFNDLLKMVLQHV---SKDNSMMAMINSGSKGSVLKFVQQTACVGLQLPASTFPFRIPS 784
BdRPD1          SVFSDLLKMVQQHT---PKDNSMMAMINAGSKGSMLKFVQQAACVGLQLPAGKFPFRIPS 670
SbRPD1          DVFSDLLKMVQQHV---SNDNSMMVMINAGSKGSMLKYAQQTACVGLQLPASKFPFRVPS 775
ZmRPD1          DVFRDLLKMVQQHV---SNDNSMMVMINAGSKGSMLKYAQQTACIGLQLPASKFPFRIPS 775
VvRPD1          QKFRDIQNLVYQYA---NKDNSLLAMLKAGSKGNLLKLVQQGLCLGLQHSLVPLSFKIPH 664
PtRPD1          LVFRDIQSLVYKYA---SQDNSFLAMFKAGSKGNLLKLVQHSMCLGLQHALASLSFRIPH 816
CpRPD1          QVFRDIQTLAFKYA---SKENSLLAMYKAGSKGSLPKLVQHSMCLGLQHSLVPLSFRFPH 708
AtRPD1          DAYRDVQALAYRYG---DQSNSFLIMSKAGSKGNIGKLVQHSMCIGLQNSAVSLSFGFPR 762
ZmRPB1          KARDDAGSSAQNSL---SESNNLKAMVTAGSKGSFINISQMTACVGQQNVEGKRIPFGFI 797
AtRPB1          KARDDAGSSAQKSL---AETNNLKAMVTAGSKGSFINISQMTACVGQQNVEGKRIPFGFD 820
SmRPD1          STMKAFERTIEEHVRENSRENSLLRMVEANSKGSFSKMMQQGGCLGLQLRQGEFVYHRVK 796
                                      :  :    ..  . :  :    :* *

PtRPE1a         VEDLASHFQSKYPTNL-------LNYPSAQYGLIQSSFFHGLDAYEEMAHSISTREVIVR 858
PtRPE1b         VEDLASHFLSKYPANL-------FDYPSAQYGLIQNSFFHGLDAYEEMAHSISTREVIVR 773
VvRPE1          VEGMAYLFKSKYPFHG-------ADYPSGEFGLIRSCFFHGLDPYEEMVHSISTREIIVR 771
CpRPE1          VEDVAFLFRSKHPG-A-------GHYPSANFGLIKSCFIHGLDPYEEMAHSISTREVIVR 708
AtRPE1          VEDMAIFCKRKYGR----------ISSSGDFGIVKGCFFHGLDPYEEMAHSIAAREVIVR 767
BdRPE1          VEDCFSSFVDKHPPIVG------NQHPPEAYGLVQNSYFHGLNPYEELVHSISTREAIVR 734
OsRPE1b         VEDCYYTFVNKHPAVR-------EEHSPEAYGLVRSSYFHGLNPYEELVHAISTREAIVR 774
SbRPE1b         VEDCFSSFVNKHSAIG-------DEYSPEAFGLVQSSYFHGLNPYEELVHAICTRETMIR 775
ZmRPE1          VEDCFTNFVNKHLAIG-------DEYPPEAYGLVQSSYFHGLNPYEELIHAISTREAMIR 775
OsRPE1a         VEDCLSKSLHRCCGSTN------CCNPLEEYGTVRSSIYHGLNPYEALLHSICEREKIMR 745
SbRPE1a         VEDCYN-FLEKRSGSTK------CYDPPKGHDFVTSSFYNGLNPYEELLHSISVREKIER 736
OsRPD1a         QLSCVSWNRHKSRNCEITDGTSECVGGQDMYAVVRNSFLDGLNPLECLLHAISGRANFFS 844
OsRPD1b         ELSCVSWNRQKSLNCEITNNTSECMAGQNMYAVIRNSFLDGLNPLECLLHAISGRANFFS 844
BdRPD1          ELTCASWNRHKSLDCDISEGARKRLGGQNSHAVIRNSFIEGLNPLECLLHSISGRANFFS 730
SbRPD1          QLSCIRWNRQKSLNYEAEG-TNERVGGQNLYAVIRNSFIEGLNPLECLLHAISGRANFFS 834
ZmRPD1          QLSCISWNGQKSLNYEAES-TSERVGGQNLYAVIKNSFIEGLNPLECLLHAISGRANFFS 834
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VvRPD1          QLSCAAWNKQKVPGL-IQNDTSEYAESYIPYAVVENSFLMGLNPLECFVHSVTSRDSSFS 723
PtRPD1          QLSCAGWNKQKA------DDATESAKRYIPHAVVEGSFLSGLNPIECFVHSVTSRDSSFS 870
CpRPD1          QLSCAAWNKQKR------------------------------------------------ 720
AtRPD1          ELTCAAWNDPNSPLRGAKGKDSTTTESYVPYGVIENSFLTGLNPLESFVHSVTSRDSSFS 822
ZmRPB1          DRTLPHFTKDDYG--------------PESRGFVENSYLRGLTPQEFFFHAMGGREGLID 843
AtRPB1          GRTLPHFTKDDYG--------------PESRGFVENSYLRGLTPQEFFFHAMGGREGLID 866
SmRPD1          SLFPRAVENESRGYLTS-------SELWKSMGLVESSFLDGLDPREFFIHSLSSRKGNDG 849


PtRPE1a         -SSRGLSEPGTLFKNLMAILRDVVICYDGTVRNVCSNSIIQSEYGVKVGAESQS------ 911
PtRPE1b         -SSRGLSEPGTLFKNLMAILRDVVICYDGTVRNVSSNSIIQFEYGVKVGTESQS------ 826
VvRPE1          -SSRGLSEPGTLFKNLMAILRDVVICYDGTVRNVCSNSIIQFEYGVKARTKPQH------ 824
CpRPE1          -SSRGLTEPGTLFKNMMAVLRDIIVCYDGTVRNICSNSVIQFKYGLKADNEPLR------ 761
AtRPE1          -SSRGLAEPGTLFKNLMAVLRDIVITNDGTVRNTCSNSVIQFKYGVDSERGHQG------ 820
BdRPE1          -SSRGLTEPGTLFKNLMAILRDVVICYDGTVRNICSNSIMQLKYNEDDATDIPS------ 787
OsRPE1b         -SSRGLTEPGTLFKNLMALLRDVVICYDGTVRNVCSKSIIQLNYTEDDALDFPS------ 827
SbRPE1b         -SSRGLSEPGTLFKNLMAILRDVVICYDGTVRNICSNSIIQLKYGEDDEADSSS------ 828
ZmRPE1          -SSRGLSEPGTLFKNLMAILRDVVICYDGTVRNICSNSIIQLKYGEDDETDSSS------ 828
OsRPE1a         -ASKGLVEPGSLFKNMMSRLRDVTACYDGSIRTSSGNLVLQFGS-----RDASN------ 793
SbRPE1a         SSSKGLAEAGNLFKNMMAMLRDVTVCYDGTMRTSYNNSIVQFDS-----TNVSS------ 785
OsRPD1a         ---ENADVPGTLTRKLMYHLRDTYVAYDGTVRSSYGQQIVRFSYDTADGM------YSDH 895
OsRPD1b         ---ENADVPGTLTRKLMYHLRDTYVAYDGTVRSSYGRQIVQFSYDTADGM------NNDH 895
BdRPD1          ---ENADVPGTLTKNLMYHLRDIYVAYDGTVRSSYGQQIVQFTYDTAEDI------YTDC 781
SbRPD1          ---ENADVPGTLTRKLMYHLRDIHVAYDGTVRSSYGQQIVQFSYDSAD------------ 879
ZmRPD1          ---ENADVPGTLTRKLMYHLRDIHVAYDGTVRSSYGQQIVQFSYDSVD------------ 879
VvRPD1          ---DNADLPGTLTRRLMFFMRDLYIAYDGTVRNAYGNQLVQFSYNIEHTSTPSDGINEDT 780
PtRPD1          ---DNADLPGTLFRRMMFFMRDLHGAYDGTVRNAYGNQLVQFSYNIDDMD-PSGSVDEIN 926
CpRPD1          ------------------------------------------------------------
AtRPD1          ---GNADLPGTLSRRLMFFMRDIYAAYDGTVRNSFGNQLVQFTYETDG------------ 867
ZmRPB1          -TAVKTSETGYIQRRLVKAMEDIMVKYDGTVRNSLG-DVIQFLYGEDGMDAVWIE-SQKL 900
AtRPB1          -TAVKTSETGYIQRRLVKAMEDIMVKYDGTVRNSLG-DVIQFLYGEDGMDAVWIE-SQKL 923
SmRPD1          ----SQQRCASFFRFLMSYMKDIRVEYDNTIRSTHGGHIFQFSYGATAE----------- 894


PtRPE1a         --LFPAGEPVGVLAATAMSNPAYKAVLDSTPSSNSSWDMMKEILLCKVGFKNDQADRRVI 969
PtRPE1b         --LFPAGEPVGVLAATAMSNPAYKAVLDSTPSSNCSWDMMKEILLCKVGFKNDLADRRVI 884
VvRPE1          --FFPAGEPVGVLAATAMSNPAYKAVLDSSPSSNSSWELMKEILLCQVNFKNDLIDRRVI 882
CpRPE1          --LFPAGEPVGVLAATAMSNPAYKAVLDSTPSSNSSWELMKEILLSKISFKNDLNDRRVI 819
AtRPE1          --LFEAGEPVGVLAATAMSNPAYKAVLDSSPNSNSSWELMKEVLLCKVNFQNTTNDRRVI 878
BdRPE1          --ALTPGEPVGVLAATAISNPAYKAVLDASQSNNTSWASMKEILQTKVSYKNDTNDRKVI 845
OsRPE1b         --AIGPGEPVGVLAATAISNPAYKAVLDASQSNNTSWERMKEILQTTSRYKNDMKDRKVI 885
SbRPE1b         --AVPPGEPVGVLAATAISNPAYKAVLDSSQSNNASWESMKEILQTRTSYKNDAKDRKVV 886
ZmRPE1          --VVPPGEPVGVLAATAISNPAYKAVLDSSQSNNASWESMKEILQTRTSYKNDVKDRKVV 886
OsRPE1a         --CVTPGDPVGILAATAVANAAYKAVLAPNQNNIISWDSMKEVLLTRASTKADANHRKVI 851
SbRPE1a         --SLTPGDSIGILAATVFANAAYKAVLVPNQKNMTSWDSMKEVLLTNACSKTGTIDQKAI 843
OsRPD1a         DLEGEPGAPVGSWAACSISEAAYGALDHPV-NSLEDSPLMNLQEVLKCHKGTNSLDHTGL 954
OsRPD1b         DLEGEPGAPVGSWAACSISEAAYGALDHPV-NALEDSPLMNLQEVLKCHKGTKSAVHTGL 954
BdRPD1          GQEGEFGAPVGSWAACSISEAAYGALDHPV-NVIEDSPLMNLQEVLKCQKGTNSLDHFGL 840
SbRPD1          DPVDKLGAPVGCWAACSISEAAYGALEHPV-NGLEDSPLMNLQEVFKCHKATNSGDHIGL 938
ZmRPD1          DLVDKLGAPVGCRAACSISEAAYGALEHPV-NGLEDSPLMNLQEVFKCHKATNSGDHIGL 938
VvRPD1          CAYDMGGQPVGSISACAISEAAYSALDQPI-SLLEPSPLLNLKRVLECGLRKSTADRTVS 839
PtRPD1          NSDGIAGRPVGPLAACAISEAAYSALDQPI-SLLEKSPLLNLKNVLECGLKRNSAHQTMS 985
CpRPD1          --------------ECPIDDGPR------------------------------------- 729
AtRPD1          PVEDITGEALGSLSACALSEAAYSALDQPI-SLLETSPLLNLKNVLECGSKKGQREQTMS 926
ZmRPB1          DSLKMKKPEFDNVFRYELDDENWRPNYMLPEHVDDLKTIREFRNVFEAEVQKLEADRYQL 960
AtRPB1          DSLKMKKSEFDRTFKYEIDDENWNPTYLSDEHLEDLKGIRELRDVFDAEYSKLETDRFQL 983
SmRPD1          -----PGEPVGLLAGTAVIEPVYDQVMSSS---PQASTMLKTLQNILFSNSFKDIDRCVT 946
                                 . :

PtRPE1a         LYFNYCGCGREHCQEKAAFLVKNHLEKVSLKDVAKCFMIEYK------------------ 1011
PtRPE1b         LYLNDCGCGRNYCQERAAYLVKNHLEKVSLKDIAKCFMIEYK------------------ 926
VvRPE1          LYLNDCDCGRKYCRENAAYLVKNQLKKASLKDTAVEFMIEYV------------------ 924
CpRPE1          LYLNDCNCARRHCQEKAACLVRNQLNKVTLKDAAVQFLVEYK------------------ 861
AtRPE1          LYLNECHCGKRFCQENAACTVRNKLNKVSLKDTAVEFLVEYR------------------ 920
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BdRPE1          LFLNDCSCPKKFCKEKAAIAVQNRLKRVTLEDCATDICIEY------------------- 886
OsRPE1b         LFLNDCSCAKKFCKEKAAIAVQGCLRRITLEDCATDICIEDGNWAAPAGFQHPVPPPQCK 945
SbRPE1b         LFLSDCSCAKKFCKERAALAVQSCLKRVTLGDCATDICIEH------------------- 927
ZmRPE1          LFLNDCSCAKKFCKERAALAVQSCLKRVTLGDCATDICIEH------------------- 927
OsRPE1a         LYLNQCSC-ENECMERALT-IRACLRRIKLEDCTTEISIKY------------------- 890
SbRPE1a         LYLNKCFCGLKFCSELAAHRVQSCLKRIKLEYCAIEVSIKY------------------- 884
OsRPD1a         LFLSKHLRKYRYGFEYASLEVKDHLERVDFSDMVDT------------------------ 990
OsRPD1b         LFLSKYLKKYRYGFEYASLEVKDHLERVDFSDLVDTVMILL------------------- 995
BdRPD1          LFLSKNLKKYRYGFEYASLYVQNYLEPMDFSELVNTVMIQYD------------------ 882
SbRPD1          LFLSRHLKKYRYGLEYASLEVKNHLEQVNFSDLVETIMIIYD------------------ 980
ZmRPD1          LFLSRHLKKYRYGLEYASLEVKNHLERVNFSDLVETIMIIYD------------------ 980
VvRPD1          LFLSKKLEKRKHGFEYGALEVKNHLEKLLFSDIVSTVMIVFS------------------ 881
PtRPD1          LFLSEKLGRQRHGFEYAALEVQNHLERLLFSDIVSFVRIIFS------------------ 1027
CpRPD1          ------------------------------------------------------------
AtRPD1          LYLSEYLSKKKHGFEYGSLEIKNHLEKLSFSEIVSTSMIIFS------------------ 968
ZmRPB1          GSEITTTGDNSWPMPVNLKRLIWNAQKTFKIDFRRPSDMHPMEIVEAIDKLQER------ 1014
AtRPB1          GTEIATNGDSTWPLPVNIKRHIWNAQKTFKIDLRKISDMHPVEIVDAVDKLQER------ 1037
SmRPD1          LKLQKLPVQP----EWIALQVQDFLKPVTIGMLASKIWIEYS------------------ 984


PtRPE1a         -------------------------------------NQQ-IPESFGSDAGLVGHVHLEK 1033
PtRPE1b         -------------------------------------SQQ-IPESFGSDAGLVGHVHLDK 948
VvRPE1          -------------------------------------KQHAVSGSSEPGTGLVGHIHLNK 947
CpRPE1          -------------------------------------NHRTVSEGLEIDAGLAGHVHLNK 884
AtRPE1          -------------------------------------KQPTISEIFGIDSCLHGHIHLNK 943
BdRPE1          ----------------------------------------ILDGSSEATPALVGHIHLEK 906
OsRPE1b         ILPVPIPIPAHGSVKFPPVPIPAPEHLKYNIHVVRYQKQIGLDGTSEAAPALVGHIHLDR 1005
SbRPE1b         ------------------------------------QKQINLDGTSEAAPTLVGHIHLDK 951
ZmRPE1          ------------------------------------QKQINLDGTSEAAPTLVGHIHLDK 951
OsRPE1a         -----------------------------------------QQQATQAAHHLVGHIHLDK 909
SbRPE1a         -----------------------------------------QQEATQAAQCLVGHIHLDK 903
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ----------------------------------------GGGVQKTKGSPWITHFHISK 902
SbRPD1          ----------------------------------------GHDKIRKEG-TWTTHFHISK 999
ZmRPD1          ----------------------------------------GHDKIRNEG-MWTTHFHINK 999
VvRPD1          ----------------------------------------PQNGSKTHFSPWVCHFHVCE 901
PtRPD1          ----------------------------------------PQSDGRMHFSPWVCHFHVYK 1047
CpRPD1          ------------------------------------------------------------
AtRPD1          ----------------------------------------PSSNTKVPLSPWVCHFHISE 988
ZmRPB1          --------------------------------------LKVVPGDDAMSIEAQKNATLFF 1036
AtRPB1          --------------------------------------LLVVPGDDALSVEAQKNATLFF 1059
SmRPD1          --------------------------------------PCSEVGGQKKRVPWIGCFQLRA 1006


PtRPE1a         RILQELNISAQVILEKCQETVNSFR--KKKKVGNLFKKTTLSISECCSFEQ-CTD----E 1086
PtRPE1b         RKLQDLNITAQVILEKCQETVNTFR--KKKKVGNLFKKTILLVSESCSFQQ-CID----E 1001
VvRPE1          LLLQDLNVSMQEVCQKCEETINSFR--KKKNVGPFFKKIILSFRECCTFQH-SCQSKGSD 1004
CpRPE1          TLLQVLNIDMQEILQQCRERISLFR--KKKKVGHCFKKIILSVSKCCSFQQ-SCEENSSD 941
AtRPE1          TLLQDWNISMQDIHQKCEDVINSLGQKKKKKATDDFKRTSLSVSECCSFRD-PCGSKGSD 1002
BdRPE1          ARLDMINVSTEDILQKCQEVSLKHG-KKKGHLGHLFKKITFSTCDCSFTQKPMIDGKLPK 965
OsRPE1b         AHLERINISTEDILQKCQEVSGKYG-KKKGHLSNLFKNITFSTCDCLFTQK-LVDGKLPK 1063
SbRPE1b         GQLERINISIQDILQKCQEVSGRYG-KKKGHLCHLLKKITFATC-----------GKLHK 999
ZmRPE1          GHLERINISTQDILQKCQEVSGRFG-KKKGHLCHIFKKITFATCDCSFTQM-PIDGKLHK 1009
OsRPE1a         KQLNQIETIMDSVLHKCQETFRNNI-KKKGSMREILKTVTFISST-SLCDQHTDDDKKFQ 967
SbRPE1a         EQLNWMEITMGNILQTCQKNVNKHV-MKNRQLMQILKTTEIISSEYCLCGQDIGDERALQ 962
OsRPD1a         ETMKIKRLRLEFIVREIIDQYNTLR----KQLNNAIPSVSISNSKCSVGNE---CVKNQT 1043
OsRPD1b         ETMKIKRLRLGFIVRELIDQYNALR----KKLNNMIPSVCISYSKCSVGNE---CVKNRS 1048
BdRPD1          EMMKRKRLGLRLLVEDLTEHYNAKR----DQLNNVIPKVYISKCKCSDDDD---CINNQT 955
SbRPD1          EMMKKKRLGLRFVIEELTKEYNATR----DQLKNAIPSICISRRKCVVGDE---GVKISA 1052
ZmRPD1          AMMKKKRLGLRFVVDELAKEYDTTR----DQLNNAIPSIRISRRKCLVGDE---GVKSSS 1052
VvRPD1          EIAKKRSLKPHSIIDALYMKCNSAR----AESKINLPDLQITSKDC-FVDM---EKEDSD 953
PtRPD1          EIVKKRSLKVHYIIDALEKQCK---------SKTRFPKVQITSRYCTVADT---WKEKKE 1095
CpRPD1          ---------------------------------------------------------QED 732
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AtRPD1          KVLKRKQLSAESVVSSLNEQYKSRN----RELKLDIVDLDIQNTNHCSSDD---QAMKDD 1041
ZmRPB1          NILLRSTFASKRVLKEYRLTKEAFEWVIGEIESRFLQSLVAPGEMIGCVAAQSIGEPATQ 1096
AtRPB1          NILLRSTLASKRVLEEYKLSREAFEWVIGEIESRFLQSLVAPGEMIGCVPAQSIGEPATQ 1119
SmRPD1          EAMERCSLNIDTIVCHLRKLLPTSL----DDPDAFIQGLHFFSR-------------DVE 1049


PtRPE1a         LLCLMFFWQDAND-------VHLERTSNILADMICP---VLLETTIKGDHR-ISCANIIW 1135
PtRPE1b         SPCLMFFWQGADD-------VHLERTSNILADMICP---VLLETIIKGDHR-ISCANIIW 1050
VvRPE1          MPCLLFFWQGNRD-------DNLEQILHILAHKICP---VLLQTIIKGDSR-VCTVNIIW 1053
CpRPE1          LPCLIFCWHDTSD-------IHLERTSYVLANMIYP---VLLETVIKGDPR-ICSANIIW 990
AtRPE1          MPCLTFSYN-ATD-------PDLERTLDVLCNTVYP---VLLEIVIKGDSR-ICSANIIW 1050
BdRPE1          VPCLQFSFSEDIP----MLSESVERAVSVLANSLCDSATIFWSICSAGDPR-IQEAKIMW 1020
OsRPE1b         LPCLQFFVSDNM-----IVSESVERAVSVLADSLCG---VLLNTIIKGDPR-IQEAKIVW 1114
SbRPE1b         VPCVQFSFSDEST----VLSESVERAVNVIADSVCS---VLLDTIIKGDPR-IQAAKVIW 1051
ZmRPE1          VPCVQFAFSDD-I----VLSESIERAVNVIADSVCS---VLLDTIIKGDPR-IQAAKVIW 1060
OsRPE1a         VSCLQFFLPGSITK---NISESTERVIDFMTNAIFP---IILDTVIKGDPR-VEEANLVR 1020
SbRPE1a         VSCLQCFIHASTTT---VQPES--NVIQMMTNTIFP---ILLDTVIKGDPQ-VQEAKLIW 1013
OsRPD1a         CCVTMVVQVEIN----------SMSQLDVIKERVIP---SILATLLKGFLE-FKNVKVQC 1089
OsRPD1b         CCVTMVAQVESN----------STSQLDIIKERVIP---SILATLLKGFLE-FENVKVEC 1094
BdRPD1          CCITVVAQDESNS--------TSTSQLDDLKKRAIP---VLLATPVKGFLE-FKDVEIQC 1003
SbRPD1          CCIAVVALAEPN----------SMSQLDTIKKRVIP---IILDTLLKGFLE-FKDVEIQC 1098
ZmRPD1          CCIAVVAHAERN----------SISQLDTIKTRVIP---SILDTLLKGFLE-FKDVEIQC 1098
VvRPD1          CFCITVSIVN-SK--------KSCIQLDTVRDLVIP---FLLGAVVKGLLD-VKKVDILW 1000
PtRPD1          TFCITVTIVETSK--------NEFIELETIQDLMIP---FLLETVIKGFME-IQKVDILW 1143
CpRPD1          SFCISVTVVKKSK--------DSSVQLDTVRGLVMP---FLLRAVIKGFPE-IKKVDILW 780
AtRPD1          NVCITVTVVEASK--------HSVLELDAIRLVLIP---FLLDSPVKGDQG-IKKVNILW 1089
ZmRPB1          MTLNTFHYAGVSAKNVTLGVPRLREIINVAKKIKTPSLSVYLKPQVNQKKE-LAKNVQCA 1155
AtRPB1          MTLNTFHYAGVSAKNVTLGVPRLREIINVAKRIKTPSLSVYLTPEASKSKE-GAKTVQCA 1178
SmRPD1          VLCFFPITSSVSN-------YDSKQIHKHMIGTMFG---NLLQVVVKGCPRGIEFVNVKW 1099


PtRPE1a         ASQETTTWIRNPSRTQKGELALDIVLEKSVVKQSGDAWRIVLDSCLPVLHLIDTTRSVPY 1195
PtRPE1b         ATPETNTWIRNPSRTQKGELALDIVLEKSVVKKSGDAWRIVLDSCLPVLHLINTTRSIPY 1110
VvRPE1          ISPDTTTWIRNPCKSRKGELALDIVLEKAAVKQRGDAWRIVLDACLPVLHLIDTRRSIPY 1113
CpRPE1          ASPDTMTWIRKPSRTRKGEWVLDVVVEKSMVKRSGDAWRIVMDSCLPVFHLIDSRRSIPY 1050
AtRPE1          NSSDMTTWIRNRHASRRGEWVLDVTVEKSAVKQSGDAWRVVIDSCLSVLHLIDTKRSIPY 1110
BdRPE1          VGSDAQSWVKNTRKVSKGEPTVEIVVEKNEASKQGDAWRIAMDACIPVIDLIDTRRSIPY 1080
OsRPE1b         VGSDATSWVKNTQKASKGEPAVEIIVEEEEALHIGDAWRTTMDACIPVLNLIDIRRSIPY 1174
SbRPE1b         VESDATAWVKNTRKVSKGEPALEIIVEKDHAVSNGDAWRTTIDACLPVLDLIDTRRSIPY 1111
ZmRPE1          VESDAASWVKHTRKVSKGESALEIIVEKDDAVSNGDAWRTAIDACLPVLNLIDTRRSIPY 1120
OsRPE1a         IEPESTFWVQSSGAEQKGEAALEITVEEAAAAESGNAWGVAMNACIPVMDLIDTTRSMPY 1080
SbRPE1a         VEPKLTRWVKNSSAEQKGELAVEITVEKIAAAENGGTWGVVMDACVPVMDLIDTTRSAPC 1073
OsRPD1a         QE----------------DNELVLKVGMSEHCKSGKFWATLQNACIPIMELIDWERSRPE 1133
OsRPD1b         QQ----------------DSELVVKVGMSEHCKTGKFWATLQNACIPIMELIDWERSRPE 1138
BdRPD1          QR----------------DNELVVKVNMSKHCKSGIFWTTLKKACIGIMGLIDWERSRPG 1047
SbRPD1          QH----------------DGELLVKVCMSHHCKGGRFWATLQNACIPVMELIDWELSRPS 1142
ZmRPD1          PH----------------DGELLVKVCMSEHCKGGRFWPTLQNACIPVMELIDWELSQPS 1142
VvRPD1          NDNPDS--DVLKSS----SGRLYLRVYVSGDCGKKNFWGVLMDACLQIMDMIDWERSHPD 1054
PtRPD1          NDKPKIP-KSHNRL----RGELFLRVHMSRGSDKTRLWNQLMDDCLSIMDLIDWARSHPD 1198
CpRPD1          KDRPKLS-KSYDS-----RGELYLRVSMSEEHGTRTSWNALMDGCLPIMDMIDWARSYPD 834
AtRPD1          TDRPKAPKRNGNHL----AGELYLKVTMYGDRGKRNCWTALLETCLPIMDMIDWGRSHPD 1145
ZmRPB1          LEYTTLRSVTHATEIWYDPDPLGTIIEEDTEFVQSYYEMPDEDIDPDKISPWLLRIELNR 1215
AtRPB1          LEYTTLRSVTQATEVWYDPDPMSTIIEEDFEFVRSYYEMPDEDVSPDKISPWLLRIELNR 1238
SmRPD1          ED------------------ELCIEVAFLS-RTRGVPWTHALEACGSISHLVDWQKSTPL 1140
                                     :   :                .             .

PtRPE1a         AIKQVQELLGVSCAFDQA-------------VQRLSKSVTMVAKGVLKEHLILLGNSMTC 1242
PtRPE1b         AIKQVQELLGVSCAFDTA-------------VQRLSKSVTMVAKGVLKEHLILLGNSMTC 1157
VvRPE1          AIKQVQELLGISCAFDQA-------------VQRLSKSVTMVAKGVLKEHLILLANSMTC 1160
CpRPE1          STKQVQELLGISCAFDQA-------------VQRLSTSVAMVAKGVLREHLILLANSMTC 1097
AtRPE1          SVKQVQELLGLSCAFEQA-------------VQRLSASVRMVSKGVLKEHIILLANNMTC 1157
BdRPE1          GIQQVRELLGISCSFDQI-------------VQRLSTTMKTVAKGILKDHLILVANSMTC 1127
OsRPE1b         GIQQVRELLGISCAFDQV-------------VQRLSTTVRMVAKDVLKDHLVLVANSMTF 1221
SbRPE1b         GIQQVKELIGISCAFDQV-------------VQRLSSTVKMVNKGVLKDHLILVANSMTC 1158
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ZmRPE1          GIQQVRELIGISCAFDQV-------------VQRLSTTVKMVNKGVLKDHLILVANSMTC 1167
OsRPE1a         DIQQVRQVFGISSAFEKVTQVQLFPFLLLAEIQYLSKSVGMITKSVLQEHLTTVASSMTC 1140
SbRPE1a         NIQEVQKVFGISSVFDRV-------------VQHLSKAVGMVTKSVLMEHLITVASSMTC 1120
OsRPD1a         RVYDNFCSYGIDSAWKFF-------------VESVRSTTDAIGRNIHRQHLLVVADCLSV 1180
OsRPD1b         RVYDIFCSYGIDSAWKYF-------------VESLRSTTDAIGRNIHRQHLLVVADCLSI 1185
BdRPD1          SVYDIFCPCGIDSAWKYF-------------VESLRSKTDDIGRNIHREHLLVVADTLSP 1094
SbRPD1          NVADIFCSYGIDSAWKYF-------------VESLKSATTDIGRNIRREHLLVIADSMSV 1189
ZmRPD1          NVSDIFCSYGIDSAWKYF-------------VESLKSATTDTGRNIRREHLLVIADSLSV 1189
VvRPD1          NIHDIFVVYGIDAGWKYF-------------LNSLKSAISDIGKTVLPEHLLLVASCLSA 1101
PtRPD1          NIHECCLAYGIDAGWKFF-------------LNNLQSAMSDVGKTVLPEHLLLVANCLSV 1245
CpRPD1          NIHHFCSANGIDAGWKLF-------------LNNLDSAISDVGKTILPEHLLLIANCLSA 881
AtRPD1          NIRQCCSVYGIDAGRSIF-------------VANLESAVSDTGKEILREHLLLVADSLSV 1192
ZmRPB1          EMMVDKKLSMADIAEKIN--------------REFDDDLSCIFNDDNADKLILRIRITND 1261
AtRPB1          EMMVDKKLSMADIAEKIN--------------LEFDDDLTCIFNDDNAQKLILRIRIMND 1284
SmRPD1          SIQEVHVAFGIEAAYQYL-------------LEKLKEFTKGSG-------------VLRK 1174
                           .   .                  .

PtRPE1a         AGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRKCFEKAAEKCHTDYLSSIVASCSWGK 1302
PtRPE1b         AGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRKCFEKAAEKCHTDSLSSIVASCAWGK 1217
VvRPE1          AGNLIGFNSGGYKALSRALNLQVPFTEATLFTPRKCFEKASEKCHTDSLSSIVASCSWGK 1220
CpRPE1          AGNLVGFNPGGYKAISRSLNIQAPFMEATLFTPRKCFERAAEKCHTDSLSSVVGSCSWGK 1157
AtRPE1          SGTMLGFNSGGYKALTRSLNIKAPFTEATLIAPRKCFEKAAEKCHTDSLSTVVGSCSWGK 1217
BdRPE1          TGNLYGFNTGGYRATFRALKVQVPFTESTLFTPMKCFEKAAEKCHSDALGCVVSSCSWGK 1187
OsRPE1b         TGNLNGFNNAGYKATFRSLKVQVPFTESTLITPMKCFEKAAEKCHSDSLGCVVSSCSWGK 1281
SbRPE1b         TGSLIGFNIAGYKATFRSLKVQVPFTESTLFTPMKCFEKAAEKCDSDSLGCVVSSSSWGK 1218
ZmRPE1          TGNLIGFNIAGYKATFRSLKVQVPFTESTLFTPMKCFEKAAEKCDSDSLGCVVSSSAWGK 1227
OsRPE1a         TGDLHGFNNSGYKATCQSLKVQAPFMEATLSRSIQCFEKAAAKAYSDQLGNVVSACSWGN 1200
SbRPE1a         TGSLHGFNRSGSKATFQSLKVQAPFTEATLSRPMQCFRKSAEKVDSDQLDSVVSTCSWGN 1180
OsRPD1a         SGQFHGLSSQGLKQQRTWLSISSPFSEACFSRPAHSFINAAKRDSVDNLSGTLDAIAWGK 1240
OsRPD1b         SGQFHGLSSQGLKQQRAWLSISSPFSEACFSRPAYSFINAAKRDSVDNLSGALDAIAWGK 1245
BdRPD1          ------------------------------------------------------------
SbRPD1          TGQFHAISSHGLKQQRTRLSISSPFSEACFSRPAQSFIDAAKQCSVDNLCGSLDAIAWGK 1249
ZmRPD1          TGQFHALSSQGLKQQRTRLSISSPFSEACFSRPAQSFINAAKQCSVDNLCGSLDAVAWGK 1249
VvRPD1          TGEFVGLNAKGMARQKELTSISSPFMQGCFSSPGSCFIKAGKRAVADNLHGSLDALAWGK 1161
PtRPD1          TGEFVGLNAKGLKRQREHASVSTPFVQACFSNPGDCFIRAAKAGVVDDLQGSIDALAWGK 1305
CpRPD1          TGEFVGLSSRGLAQQRKHASVVSPFTQACFSNPSTCFVKAAKAGVTDDLQGSIDALAWGK 941
AtRPD1          TGEFVALNAKGWSKQRQVESTPAPFTQACFSSPSQCFLKAAKEGVRDDLQGSIDALAWGK 1252
ZmRPB1          EAPKGEIQDESAEDDVFLKKIEGNMLTEMALRGIPDINKVFIKEGKVNTFYQDDGFKAAN 1321
AtRPB1          EGPKGELQDESAEDDVFLKKIESNMLTEMALRGIPDINKVFIKQVRKSRFDEEGGFKTSE 1344
SmRPD1          PWKNIDANESGYEAFVKNLSGCSPLAFAMGKSPGGVFEAAAMNREVDYLAGANELAFCGK 1234


PtRPE1a         HVTVGTGSR--FDVLWDTKEACLNPEGG--IDAYSFLNMVRSTAGGEESVTACLGAEVDD 1358
PtRPE1b         HVTVGTGSH--FDVLWDTKEACLNPEGS--MDVYSFLNMVRSTAGGEESVTACLGAEVDD 1273
VvRPE1          HVTVGTGSR--FDVLWDTKEIGPAQDGG--IDIYSFLHLVRSGSYGKEPDTACLGAEVED 1276
CpRPE1          NVAVGTGSR--FDVLWDTKEARFNEGGK--LDVYTFLHMVRSSSHGEDLSTACLGEEIDD 1213
AtRPE1          RVDVGTGSQ--FELLWNQKETGLDDKEE--TDVYSFLQMVISTTN-ADAFVSSPGFDVT- 1271
BdRPE1          HAALGTGSS--FQILWNENQVNCNKEYG--DGLYDFLAMVRTDQEKARYTFLD---DVDY 1240
OsRPE1b         HAASGTGSS--FQILWNESQLKSNKEYG--DGLYDYLALVRTDEEKARYTFFD---DVDY 1334
SbRPE1b         HAAVGTGSS--FQILWNENQLKSNKDYG--DGLYDFLALVRTDQEKTGYMFLD---DVDY 1271
ZmRPE1          HAAVGTGSS--FQILWNENQLKSNKEYG--DGLYDFLALVRTDQEKTDYMFLD---DVDY 1280
OsRPE1a         NAEIGTGSA--FEILWNDENMSSSKSILGGYGLYDFLEAVETTGATKDKAIVP---HNYC 1255
SbRPE1a         HAAIGTGSA--FKIHWNDENQSASNEILREYNLYDFLEAVGRIGATEQKTDAP---HSLC 1235
OsRPD1a         EPCAGSSGP--FKILYSGKSHETKQNEH----IYDFLHNPE------------------- 1275
OsRPD1b         EPCAGTSGP--FKVLYSGKSQKTKQNKN----IYDFLHNPE------------------- 1280
BdRPD1          --------------------HEPVQNEN----IYGFLHNPE------------------- 1111
SbRPD1          EPFNGTSGP--FEIMHSGKPHEPEQDES----IYDFLRSPK------------------- 1284
ZmRPD1          EPFNGTSGP--FEIMHSGKPHEPEQNES----IYDFLCSSK------------------- 1284
VvRPD1          IPSVGSGGH--FDILYSAKGHELARPED----IYKLLGSQT------------------- 1196
PtRPD1          VPAIGTG-Q--FDIVYSGKGLEFSKPVD----VYNLLGSQM------------------- 1339
CpRPD1          PPCFGTGGQ--FDIIYS------WRPVD----VYDLLNSIV------------------- 970
AtRPD1          VPGFGTGDQ--FEIIISPKVHGFTTPVD----VYDLLSSTK------------------- 1287
ZmRPB1          EWMLDTEGVNLLAVMCHEDVDATRTTSNHLIEVIEVLGIEAVRRSLLDELRVVISFDGSY 1381
AtRPB1          EWMLDTEGVNLLAVMCHEDVDPKRTTSNHLIEIIEVLGIEAVRRALLDELRVVISFDGSY 1404
```

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SmRPD1          SPSLGTGAN--IELFFKEDKGPVSRFPD-----FESLVFSR------------------- 1268
                                                    *

PtRPE1a         LILEDE--DWNLSPEHHSSSDKPTFEDSAEFQDFLGN-QPAESNWGKASSLKDGSWSAGN 1415
PtRPE1b         LMLEDE--DWNLSPEHNSSSDKPTFEDSAEFQDFLGN-QPAESNWEKISSLKDRSRSSGN 1330
VvRPE1          LILEDENLELGMSPEHSSNFEKPVFEDSAEFQNTWEN-HVPGS--------------GGD 1321
CpRPE1          LVPDEETFDWSPSPEHYSTSGKPVFEDGEDILENLET-QPTKP----------------S 1256
AtRPE1          ---EEEMAEWAESPERDSALGEPKFEDSADFQNLHDEGKPSGANWEKSSSWDNGCSGGSE 1328
BdRPE1          LVEDNAMDDICLSPELNGTHGVPTFEDNFEHQDTQNG----------------------- 1277
OsRPE1b         LAEENEAD-VCLSPELDGTIGQPIFDDNLEEQDVQNN----------------------- 1370
SbRPE1b         LLEENAIDDMCLSPEPDGTVGKPTFEDNFEEQNIQKG----------------------- 1308
ZmRPE1          LVEENAADDMCLSPEPDGTLGKPTFEDNFEEQNIQKG----------------------- 1317
OsRPE1a         LYD----------------------VDCIPED---------------------------- 1265
SbRPE1a         LYD----------------------VGQLPEDEVQED----------------------- 1250
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          VNYRHLAILCDTMTYRGHLMAITRHGINRNDTGPLMR----------------------- 1418
AtRPB1          VNYRHLAILCDTMTYRGHLMAITRHGINRNDTGPLMR----------------------- 1441
SmRPD1          ------------------------------------------------------------

PtRPE1a         WDVDKNDSAGKEKPWSLGMSSAETNDVG---WDTAATRKINSSWNSENDVTQSNSLSGWA 1472
PtRPE1b         WDVDKNDGAVKEKPWSLGMNTAEANDVASSGWDTAAARTTNNSWNSENNVAQSNSFSGWA 1390
VvRPE1          WAVNQNKETTASTLKPSAWSSWGTDKVT--MKDTFSTREPDESSRS----AGWDDKGTWG 1375
CpRPE1          WEHLNNGRADLQK--QSSWSSWSTDRAHS--QDVCSTKTLEECLNS----AGGTGVIGSD 1308
AtRPE1          WGVSKSTGGEANPESNWEKTTNVEKEDAWSSWNTRKDAQESSKSDSGGAWGIKTKDADAD 1388
BdRPE1          -------------------NSWENGTKANASWEQNASAGNDSDNWGGWSNAAAAADTGAA 1318
OsRPE1b         -------------------SSWDNGTTTNASWEQNGSAGNDSDKWGGWNDAAAGADTGVT 1411
SbRPE1b         -------------------SSWENGITMKSSWEQDASAANDSGDWGGWSSGGGAS----A 1345
ZmRPE1          -------------------SSWEIGITTNSSWEQNASVANDSGDWGGWSSGGGAA----A 1354
OsRPE1a         --------------------KVCLEENNQITWTDKPKAEFLMESEGRRAGMHSTG---QK 1302
SbRPE1a         -------------------EVVCFGGTSPISWTDKPKGDSLLHDFMGRAGMWSTV---QK 1288
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          ---------------------CSFEETVDILLDAAVYAESDHLRGVTENIMLGQLAPIGT 1457
AtRPB1          ---------------------CSFEETVDILLDAAAYAETDCLRGVTENIMLGQLAPIGT 1480
SmRPD1          ------------------------------------------------------------

PtRPE1a         TKKSETHNGFAT--KVQEKPARSNDWDVGTAWGRKAGDNKFAN--VTKSWWGKVTDGDES 1528
PtRPE1b         TKKPEPHNGFAT--KVQEEPTTSNDWDAGAAWGRKDRDNKFAETNASKSWWGKVTDGDES 1448
VvRPE1          TDK--AQNTAFR--RTHEDSPRSSGRDETFRDGRP----QFAS----SAWGKKIDEADKT 1423
CpRPE1          KTNLDSQNTWAN--WNTKGSYPTKASE---------------------------DSPKSC 1339
AtRPE1          TTPNWETSPAPKDSIVPENNEPTSDVWGHKSVSDKSWDKKNWGTESAPAAWGSTDAAVWG 1448
BdRPE1          KPADQGNSSWDVPATAENDST---------------------------------DWGGWG 1345
OsRPE1b         KPANQGNSCWDVPATVEKSSS---------------------------------DWGGWG 1438
SbRPE1b         KPADQDNS-WEVHAKVQDNSTDWGGWSSGVGAAAKPADQDNSWEVHAKAQDNCTDWGGWS 1404
ZmRPE1          KPADQDNS-WEVHAKVQDNST--------------------------------TDWGGWS 1381
OsRPE1a         HPRKP---------NWHEGN---------------------------------------- 1313
SbRPE1a         HQEMQNKTKWNSVANWKNDKP-------------------------------------MG 1311
```

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OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          GGCALYLN---------------------------------------------------- 1465
AtRPB1          GDCELYLN---------------------------------------------------- 1488
SmRPD1          ------------------------------------------------------------


PtRPE1a         EQNKNKQHQ-EDQELGTHGWDDKMSPDQLISGWASTTTQEATTESCSSKAASVWGTKNTN 1587
PtRPE1b         GQNKSKNKRPEDQDVGTHGWDDKMSQDQSISGWASKTTQEATTESLG------------- 1495
VvRPE1          GWNKNDGKPQMDKLRESYDWDCKVAQEK-----TTQSTYGGISSTTG------------- 1465
CpRPE1          GWVADKCGSGETNAKGEHNWSNWTAVKGGSQDFTATKTWEESSKAGG------------- 1386
AtRPE1          SSDKKNSETESDAAAWGSRDKNNSDVGSGAGVLGPWNKKSSETESNG------------- 1495
BdRPE1          NEKAKDNRTVSTEPAELDTWSDRGAKKGTDGGGGSWGKQTNTCEDSGTNLERN------- 1398
OsRPE1b         TEKAKEKEKISEEPAQHDAWSVQGPKRATDGG-ASWKKQSSTQNDGNSWKENKGR----- 1492
SbRPE1b         TDKPTGEATVSGQPAEMDTWADKGTKMESGAGDANWEKKSSTPEASNKNDPWG------- 1457
ZmRPE1          VEKPTGEATVSGEPAETDTWADKGAKMESDAGDGNWEK-SSTPEASKKND---------- 1430
OsRPE1a         --------TKSSPNSTAVEFTGQVFQRRQLKTKSNWNSDATQQDDK-------------- 1351
SbRPE1a         PPRTAFAESTSTRGQNKRQFTGQVYARKQPK--HSWSQAATHQNNK-------------- 1355
OsRPD1a         --VQALEKNVMDTYRKRTEKT-SKRRSALNSEGNATINGGAISFN--------------- 1317
OsRPD1b         --VQALEKNFMDTYKQRTEKP-SKQRSAFSSKGNATINGGTISVN--------------- 1322
BdRPD1          --VWGPEKNHMETDSTRTKNA-SER----WSSGNATFNGGTISVE--------------- 1149
SbRPD1          --VQNVEKNHLDTRRQSTENASICRLACKS-KGSATVNGVAITSD--------------- 1326
ZmRPD1          --VRNFEKNHLDTRRQSTENASICRLACKSSKGSTTVNGVAITID--------------- 1327
VvRPD1          --SCHEQNLKVKVPITCYQTTTKCGAQLVYANGDSASKGCKSLEK--------------- 1239
PtRPD1          --ISTEQNTEFGVLDAQIYKSDKCGAQFLHKFGGCGPKGFKVKEG--------------- 1382
CpRPD1          --TPLKQNVKSDLPNSMNIKSDKYGDRSIYVHSGSISLGLKKLEG--------------- 1013
AtRPD1          --TMRRTNSAP--------KSDKATVQPFGLLHSAFLKDIKVLDGKG------------- 1324
ZmRPB1          -DQMLQQAIELQLPSYVEGLDFGMTPARSPITGTPYHEGMMSPSYLLSPN---------- 1514
AtRPB1          -DEMLKNAIELQLPSYMDGLEFGMTPARSPVSGTPYHEGMMSPNYLLSPN---------- 1537
SmRPD1          ---RVVDDTVSATLS--------------------------------------------- 1280


PtRPE1a         VDEQGSENHVLLNQAKESSDWNKKSNSNQTDAACGSKAASSWGAKNTDADKRWGRKVDLN 1647
PtRPE1b         --------------------WDSKGNSNPGDAACGWKAASTWGAENTDGDKLWGKEVSSN 1535
VvRPE1          -----------------------DWKKNELQMEVVQHDESPVNEHSWDAN---LPEDPLA 1499
CpRPE1          -----------------------WGSKKSGNGESNVGEGSPWSNWKTNKGNSQGTHPQKA 1423
AtRPE1          --------------------ATWGSSDKTKSGAAAWNSWDKKNIETDSEPAAWGSQGKKN 1535
BdRPE1          -----------------------SWAK----RPSSPSLSTWAKKNSDGGDGTWDKQANSC 1431
OsRPE1b         ------------------GSNGGSWEKDNAQKGSWGRGNDEAENNNDVQNKSWETVAADA 1534
SbRPE1b         --------------------------------KSENTWDKRKGDGGDGGDGAWEKKSVDG 1485
ZmRPE1          --------------------------------SSENTWDKRKGDGGD---GAWGNRSDDG 1455
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------
```

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PtRPE1a         QADTS--CSWGRSKTP---------------DRGWGLSNYGGSNGSEMENKTENQSLLDR 1690
PtRPE1b         QADTA--SGWGKPKSPEISLGWGSTKESVKSDRGWGVSSSGGGR----DKKTENQSLAGQ 1589
VvRPE1          QATTS--VGWDSSTGK-----------------DWTKR------------KLQSPSEQQR 1528
CpRPE1          QEESSDFGGWGSNKFS-----------------------------------RCETNLKEQ 1448
AtRPE1          SETESGPAAWGAWDKK---------------------------------KSETEPGPAGW 1562
BdRPE1          KKNVEQD-SWKNMPVSPARNAWN---KKESSRGD-ATWEMRASTLEEKKTSESNEGSWEK 1486
OsRPE1b         HASTEK--SWGNVTASPSDNAWS---AAPVSQGN-GSSDTKQSDSWDGWKSAGVDKAINK 1588
SbRPE1b         HGNWDHPGNWNGQSLNVDQDTWGNARGKKKADGN-CQWEEQPSTYRRKKTNADHNSSYNN 1544
ZmRPE1          HGNWEHPSNWNGQSLDVDQDTWGNARGKKKADGNYCQWEEQPSNYKQKKTNADHDSSYNN 1515
OsRPE1a         -------PSWYSS----------------------------------------------- 1357
SbRPE1a         -------LSWCGE----------------------------------------------- 1361
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------


PtRPE1a         GKESVGWGGKNT-DADKPWSNKVNSNQADTASGWGKSKSLDR---GWGVSNSGGGNGSEM 1746
PtRPE1b         GKESGGWGNKVTSNQADTASGWGKPKSSENSQGWGLSKESGKEVHEWGVPNSAGGNGSET 1649
VvRPE1          DPAIKSWSSSHN-------VMKEQSNQPASTHGWD----------------SPGAKG--- 1562
CpRPE1          STWSKWNSNKGDNQDAYATMLENNDNDTGKEKGWS------------SWARDDSINGSVL 1496
AtRPE1          GMGDKKNSETELGPAAMGNWDKKKSDTKSGPAAWG--------------STDAAAWGSSD 1608
BdRPE1          SN------AQKDSWGNTQHGSSDKMAVKDNDMQQDPWG----HIATQNINAQDDLWGSVA 1536
OsRPE1b         DKESLGNVPASPSFSAWNASPVSQGNERSDAKQSDSWDGWKSAGVDKAINKDKESLGNVP 1648
SbRPE1b         VMP-----SSDNAWNAGER--FGRSNAKSN--AGSSWGEKDKMESDEHPKVPKESDTWNT 1595
ZmRPE1          VMP-----SSEIAWNAGDG--TGRPNAKSN--AESSWGEEDKMESDDHPKVPKESDTWNT 1566
OsRPE1a         -------------------------------------------------NSAGTQNFTIA 1368
SbRPE1a         -------------------------------------------------NVAGAQDFANA 1372
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          -------------------------------------------------IRASPINTDAS 1525
AtRPB1          -------------------------------------------------MRLSPMS-DAQ 1547
SmRPD1          ------------------------------------------------------------


PtRPE1a         EDKTENQSLLDRGKESGGW-GGKNTDADKPWSNKVNSNQADTASGWGKSKSLDRGWGVSN 1805
PtRPE1b         NNNNENQSLVEQGKESG-------------WDNKASSNQEGTASGWGKPKSP-------- 1688
VvRPE1          WNDVEEQSQWNQ------------------RGSAVKNDQSESSHGWGPSNEQ-------- 1596
CpRPE1          PEGDSSKSNGLDAGTVG--------------DGSWEQTPTGTSDGWGVLSES-------- 1534
AtRPE1          KNNSETESDAAAWGSRN-------------KKTSEIESGAGAWGSWGQPSPTAE------ 1649
BdRPE1          AKAQTSTAENT----------DAQDDSWG--AVAAKAQTSTAQESWGNVAASPSDNAWKA 1584
OsRPE1b         ASPSFSAWNAAPVSQGNERLDAKQSDSWDGWKSAGVDDSVKDKESWGNVPASPSDSAWNA 1708
SbRPE1b         GKSNESPWDNT----------DALQDSWG--VNSATHDNNTEDGSWDKVVAIKDPVSQQD 1643
ZmRPE1          GRSNESPWDNT----------DALQDSW---VKSAARNNNTQDGSWDKVVSMKDLDSLQD 1613
OsRPE1a         GSSRPGEWNRK---------------------NNNRGQGGGR------------------ 1389
SbRPE1a         ESSK-GGWNRK---------------------NSGFGRGGHRGGGRGMAFA--------- 1401
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
```

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SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          FSPYVGHMAFSPFPSPGGYSPSSGGYSPSSPVFTPEKGYSPLSPSYSPASPS-------- 1577
AtRPB1          FSPYVGGMAFSPSSSPG---------------------YSPSSPGYSPTSPG-------- 1578
SmRPD1          ------------------------------------------------------------


PtRPE1a         SGGGNGSEMEDKTENQSLLDRGKESGGWGKPKSISQGWGSSKDSVKAVDGWGVPNSAGSN 1865
PtRPE1b         --------------------------------ALSEGWGSPREPVKAVHGWGVPNSGGGN 1716
VvRPE1          ------------------------------------------NQLPSSQGWGSPNAGAGH 1614
CpRPE1          ------------------------------------------TEPAGCHGWGLPNNEDIT 1552
AtRPE1          ---------------------------------------DKDTNEDDRNPWVSLKETKSR 1670
BdRPE1          PP------------------------------------ISQTSAAEHTDAHNDSWGIVAA 1608
OsRPE1b         AP------------------------------------VSQGNESSDAKQSDSWDGWKSA 1732
SbRPE1b         S--------------------------------------WSNVAIQKNDAQNDSWDNVAE 1665
ZmRPE1          S--------------------------------------WSKATIQTNDAQNDSWDNVAK 1635
OsRPE1a         -------------------------------------------EVWKSEGPHRGGSSSNR 1406
SbRPE1a         -----------------------------------------NAESSSSGGWNRKNSGFGR 1420
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------


PtRPE1a         GSERDQQWGQQSGEF--------------------------------------------- 1880
PtRPE1b         GSGRDQQWGQQSREF--------------------------------------------- 1731
VvRPE1          ESETQSQWGQPSG----------------------------------------------- 1627
CpRPE1          QNESQGRRTWEFS----------------------------------------------- 1565
AtRPE1          EKDDKERSQWGNP----------------------------------------------- 1683
BdRPE1          KAQTSTAQ-QESWGNATASPSDN----------AWNAAPMDLDAKQPGSWDGWSSALAED 1657
OsRPE1b         GVDASTNKDKESWGNVPASPSDS----------AWNAAPVSQGD------DVWNSAEANE 1776
SbRPE1b         KALNSASQ--DSWGHLAATPVSNSDAKQSDSWDGWNAVPAENSQ------GTAQWKERTD 1717
ZmRPE1          NAPDSAAE--DSWG--AATPA-----------------------------------ETTD 1656
OsRPE1a         N--QGGGR---------------------------------------------------- 1412
SbRPE1a         GGRRGGGR---------------------------------------------------- 1428
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------


PtRPE1a         --------KKNRTEGSRGWGSNN-GHWK-KRNRPSKP----HEDSSSSGLFTMTRQWLDI 1926
PtRPE1b         --------KKDRFEGSRGWGSNN-GDWKNKRNRPSKP----HEDLNASGIFTTTRQRLDV 1778
VvRPE1          --------KKSRPEGSRGWGSNN-TEWKNKKNRPNKPQGPLNDDYSAGGIFTATRQRVDI 1678
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CpRPE1          --------KKKRNEGSRGWSSNS-GDWKGKKNLPGKLAGNVKDDFGAGRLYTHTRQRLDM 1616
AtRPE1          ---------AKKFPSSGGWSNGGGADWKGNRNHTPRPP---RSEDNLAPMFTATRQRLDS 1731
BdRPE1          SNKADDSSNKNKGWKSDGWGAKG-NRRDQRDNPSMPPMRPDER----------PPRPRFE 1706
OsRPE1b         S--------RNKDWKSDGWGARGGNWRGQRNNPGRPPRKPDGRGLPRRPDERGPPRRHFD 1828
SbRPE1b         S--------GNKDWKSDGWGAKSGNWSSQRNNPGRPPRRPDERGPP-------PPRQRFE 1762
ZmRPE1          S--------GNKEWKSDGWGAKSGNWSSQRNNPGRPPRRPDERGPP-------PPRQRFE 1701
OsRPE1a         -----------AVWKSEASHRGSGNNRNRGGGRAVWKSEASRRGGSM------RQVASCA 1455
SbRPE1a         -----------GMWKSEGSHRGGSNSTN---WRAQNNNSARQCG------------ISYS 1462
OsRPD1a         ----------------------------------------------------------QK 1319
OsRPD1b         ----------------------------------------------------------QK 1324
BdRPD1          ----------------------------------------------------------QN 1151
SbRPD1          ----------------------------------------------------------QD 1328
ZmRPD1          ----------------------------------------------------------QD 1329
VvRPD1          ---------------------------------------------------------ISK 1242
PtRPD1          ---------------------------------------------------------IPR 1385
CpRPD1          ---------------------------------------------------------ISR 1016
AtRPD1          ---------------------------------------------------------IPM 1327
ZmRPB1          -----------YSPTSPSYTPGSPTYSPTSPNYSPTSPTYSPTSPSYSPTSPSYSPTSPS 1626
AtRPB1          -----------YSPTSPGYSPTSPGYSPTSPTYSPSSPGYSPTSPAYSPTSPSYSPTSPS 1627
SmRPD1          ------------------------------------------------------------


PtRPE1a         FTSQEQDILSDVEPLMLSIRRIMHQTGYSDGDPLSADDQSYVLDNVFNYHPDKAVKMGAG 1986
PtRPE1b         FTSQEQDILSDIEPLMLSIRRIMHQTGYNDGDPLSADDQSYVLDNVFHYHPDKAVKMGAG 1838
VvRPE1          FTSEEQDILLDVEPIMQSIRRIMHQAGYNDGDPLSADDQSYILDKVFNNHPDKAVKMGTG 1738
CpRPE1          FTSEEQDVLSDVEPLMQSIRRIMHQSGYNDGDPLSVDDQSFVIDKVFMYHPDRAVKMGAG 1676
AtRPE1          FTSEEQELLSDVEPVMRTLRKIMHPSAYPDGDPISDDDKTFVLEKILNFHPQKETKLGSG 1791
BdRPE1          VPAEAKKILREIEPIVSMVRKIFRES--CDGVRLPLEDEKFIKESILEHHPEKERKVPGE 1764
OsRPE1b         LTAEEEKILGEIEPTVLSIRKIFRES--IDSIKLSPEDEKFIKENVLEHHPEKQSKVSGE 1886
SbRPE1b         LTIEEKKILLEVEPLIFRVRRIFREA--CDGVRLKPEDEKFIQEKILEHHPEKQSKVSSE 1820
ZmRPE1          LTVAEKNILLEVEPIKLRVRSIFREA--CDGVRLNPEDEKFILEKVLEHHPEKQSKVSGE 1759
OsRPE1a         FTPVEQQIFEQIEPITKNVKRIIRES--RDGIKLPPDDEKFIVTNVLMYHPERKKKIAGN 1513
SbRPE1a         FTPVEQQIYTQVEPIIKNVKRIIRES--RDGMKLSQDDEMFIMNKILMYHPEKEKKMAGQ 1520
OsRPD1a         FLNAKVGIWENIIDMRTSLQNMLREY---TLNEVVTEQDKSCLMEALKFHPRGYDKIGVG 1376
OsRPD1b         FLDSKVGIWENIIDMRTCLQNMLREY---TLNEVVTEQDKSCLIEALKFHPRGYDKIGVG 1381
BdRPD1          YLGAKVGVWDSIIDMRTCLQNMLREY---QLDEYVVELDKSRVIEALRFHPRGREKIGVG 1208
SbRPD1          FLHAKVSIWDNIIDMRASLQNMLREY---PLNGYVMEPDKSKLIEALKFHPRGAEKIGVG 1385
ZmRPD1          FLHAKVSIWDNIIDMRTSLQNMLREY---PLNGYVAEPDKSQLIEALKFHSRGAEKIGVG 1386
VvRPD1          SVLRSFLSLNDIQKLSRRLKFILQKY---PINHQLSEIDKTTLMMALYFHPRRDEKIGPG 1299
PtRPD1          SFLRRLLTYDDIQRMSYTVRKILNKY---SVDQQLNESDKSVLMMTLYFHPRRDEKIGIG 1442
CpRPD1          AYLRTVLTWKDIQKLYHASKKILNKY---PIDHRLNEGEKKILMMALYFHPQSYEKIGTG 1073
AtRPD1          SLLRTIFTWKNIELLSQSLKRILHSY---EINELLNERDEGLVKMVLQLHPNSVEKIGPG 1384
ZmRPB1          YSPTSPSYSPTSPSYSPTSPSYSPTSPVYSPTSPAYSPTSPAYSPTSPSYSPTSPSYSPT 1686
AtRPB1          YSPTSPSYSPTSPSYSPTSPSYSPTSPSYSPTSPAYSPTSPAYSPTSPAYSPTSPSYSPT 1687
SmRPD1          -AKDREIVWARIDQRSQKLHDILRKS---LTGTPVSAANEAVILDTLKYHPMMDSKVGCG 1336
                                                                 :.    .

PtRPE1a         INHVTVSRHSNFQESRCFYIVSTDDCKQDIFPTANVWRTSSGENNLTWQMNSSESILQE- 2045
PtRPE1b         IDHVTVSRHSNFQESRCFYIVSTDGCKQDFSYRKCLENFIKGKYPDLADEFIAKYFARR- 1897
VvRPE1          IDYVMVSRHSSFLESRCFYVVSTDGHKEDFSYRKCLENFIKEKYPDNAETFIGKYFRRPR 1798
CpRPE1          IDFVTVSRHSNFQDSRCFYIVSTDGRKQDFSYRKCLDNFIKGKYPDIAEQFIGKYFRKPR 1736
AtRPE1          VDFITVDKHTIFSDSRCFFVVSTDGAKQDFSYRKSLNNYLMKKYPDRAEEFIDKYFTKPR 1851
BdRPE1          IDHIMVNKHHIFQESRCFYVVLADGTHTDFSYNKCMDNYVRKTYTDAAEHADL------- 1817
OsRPE1b         IDHIMVDKHQVFQDSRCLFVVSSDGTRSDFSYLKCMENFVRKTYPEHGDSFCKKYFKRRR 1946
SbRPE1b         IDHIMVNKHHTFEDTRCFFVVSTDGSQADFSYLKCLENFVRKNYTEDVDSFCMKYLRPRR 1880
ZmRPE1          IDYLTVNKHQTFQDTRCFFVVSTDGSQADFSYLKCLENFVRKSYTEDADTFCMKYLRP-- 1817
OsRPE1a         GNYITVDRHQVFHGSRCLYVMSSDGSRKDFSYKKCLENYIRAQYPDAADSFCRKYFK--- 1570
SbRPE1a         GNYIMVNKHQTFPSSRCLYVASSDGSSSDFSYKKCLENFIRIHYPHAAESFCRKYFK--- 1577
OsRPD1a         IREIKIGVNPGHPSSRCFIVLRNDDTTADFSYNKCVLGAANSISPELG------------ 1424
OsRPD1b         IREIKIGVNPGHPNSRCFIVQRSDDTSADFSYNKCVLGAANSISPELGSYIEKILSNRAI 1441
BdRPD1          IRDIK------------------------------------------------------- 1213
SbRPD1          VREIKVGLNPNHPGTRCFILLRNDDTTEDFSYHKCVHGAANSISPQLGSYLKKLYHRA-- 1443
ZmRPD1          VREIKIGLNPSHPGTRCFILLRNDDTTEDFSYHKCVQGAADSISPQLGSYLKKLYYRA-- 1444
VvRPD1          AQNIKVRYHSKYHNTRCFSLVRTDGTEEDFSYHKCVHGALEIIDPRRARSYQSRWLPYSE 1359
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PtRPD1          AKDIKVINHPEYQDTRCFSLVRTDGTIEDFSYRKCLHNALEIIAPQRAKRYCEKYLTSKV 1502
CpRPD1          AQYIKVLKTE-------------------------------------------------- 1083
AtRPD1          VKGIRVAKSKHG-DSCCFEVVRIDGTFEDFSYHKCVLGATKIIAPKKMNFYKSKYLKNGT 1443
ZmRPB1          SPSYSPTSPSYSPTSPSYSPTSPSYSPTSPAYSPTSPGYSPTSPSYSPTSPSYSPTSPSY 1746
AtRPB1          SPSYSPTSPSYSPTSPSYSPTSPSYSPTSPAYSPTSPGYSPTSPSYSPTSPSYGPTSPSY 1747
SmRPD1          VRHIRVDN-HHSFGGRCFHIVRLDGSVEDFSYHKCLLERIKG-NTVLVQRYKKKFMGGKN 1394


PtRPE1a         --EAIGSAPLLQREPRRNRPRDV------------------------------------- 2066
PtRPE1b         --GNRQRTPAPEGTEEEKQAL--------------------------------------- 1916
VvRPE1          AGGNRERSVIPEDGGNREQSVVPEETGSENRQ---------------------------- 1830
CpRPE1          SSGNQQKPVLEETENML------------------------------------------- 1753
AtRPE1          PSGNRDRNNQDATPPGEEQSQPPNQSIGNGGDDFQTQTQSQSPSQTRAQSPSQAQAQSPS 1911
BdRPE1          ------------------------------------------------------------
OsRPE1b         DQPPAADGGTAPGTPAGATQSTAVDTQEGTSQQTQPDIATAPAATQQETLQD-------- 1998
SbRPE1b         RQAPPPDVGTAPGTPAEVPPSTAAETEQGTP-APPAEVPQETLGSPAVALEG-THNPRTD 1938
ZmRPE1          -----------------------PETEQGTPPAPQAEVPQETWGSPAVPLEGGTHIAGPD 1854
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         RPHQL------------------------------------------------------- 1446
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          V----------------------------------------------------------- 1360
PtRPD1          SATDNSGCTDLPLDN--------------------------------------------- 1517
CpRPD1          ------------------------------------------------------------
AtRPD1          LESGGFSENP-------------------------------------------------- 1453
ZmRPB1          NPSSAKYSPSHAYSPSSPRMS---PYSQTSPSYSPTSPTYSPTSPSYSQPSPSYSPTS-- 1801
AtRPB1          NPQSAKYSPSIAYSPSNARLSPASPYSPTSPNYSPTSPSYSPTSPSYSPSSPTYSPSSPY 1807
SmRPD1          GRKEEVPVEIFSQKNDTGRMYDKKTHGFLLVENHFVPVKTLKKT---------------- 1438


PtRPE1a         ------------------------------------------------------------
PtRPE1b         ------------------------------------------------------------
VvRPE1          ------------------------------------------------------------
CpRPE1          ------------------------------------------------------------
AtRPE1          QTQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSQSPSQTQTQSPSQTQAQAQSPSSQSP 1971
BdRPE1          ------------------------------------------------------------
OsRPE1b         --------------TPAPPADDGLLGKGPSPSD--------------------------- 2017
SbRPE1b         PTDDTELLGKDSDLTPASPAVAPQEAPKPDPTDDTELLGNEKPDLTPSSPGEALQATADP 1998
ZmRPE1          STGDAVILGEQHDLTPASPAVAPQVASEPDTTDGTGLLG--------KAPQADWGPRFDA 1906
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
ZmRPB1          ---------PSGSYSPTAPGYSPSSTGQGN----DKDDKSAR------------------ 1830
AtRPB1          SSGASPDYSPSAGYSPTLPGYSPSSTGQYTPHEGDKKDKTGKKDASKDDKGNP------- 1860
SmRPD1          ------------------------------------------------------------


PtRPE1a         -------
PtRPE1b         -------
VvRPE1          -------
CpRPE1          -------
AtRPE1          SQTQT-- 1976
BdRPE1          -------
```

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OsRPE1b         -------
SbRPE1b         DSTLTDI 2005
ZmRPE1          D------ 1907
OsRPE1a         -------
SbRPE1a         -------
OsRPD1a         -------
OsRPD1b         -------
BdRPD1          -------
SbRPD1          -------
ZmRPD1          -------
VvRPD1          -------
PtRPD1          -------
CpRPD1          -------
AtRPD1          -------
ZmRPB1          -------
AtRPB1          -------
SmRPD1          -------
```

(B) Satchmo

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VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
BdRPD1          ............................................................
OsRPD1a         meepslevnnpvaelnaikfslmtssdmeklssatiiemcdvtnaklglpngapqcatcg
OsRPD1b         meepslevkmpeadlkavkfslmtssdmeklssasiiemcdvtnaklglpngapqcatcg
ZmRPD1          melhreppeailnaikfdlmtstdmeklssmsiievsdvtspklglpngslqcetcgsqr
SbRPD1          melhrelpeatlnaikfdlmtstdmeklssmsvievsdvtspklglpnaspqcetcgsks
VvRPE1          ............................................................
PtRPE1b         ............................................................
PtRPE1a         ............................................................
CpRPE1          ............................................................
AtRPE1          ............................................................
BdRPE1          ............................................................
OsRPE1b         ............................................................
ZmRPE1          ............................................................
SbRPE1b         ............................................................
OsRPE1a         meghpdp.....................................................
SbRPE1a         medd.dp.....................................................
ZmRPB1          ............................................................
AtRPB1          ............................................................
SmRPD1          masskr......................................................

VvRPD1          .................................................MDNDF.LEEQQ
PtRPD1          .................................................MEIDF.SEEQQ
AtRPD1          .................................................MEDD-.CEELQ
CpRPD1          .................................................M----.-----
BdRPD1          .................................................MLILL.LLLKR
OsRPD1a         srsirdcdghfgviklaatvhnsyfieevvqllnqicpgcltlkqngdt-----.---KK
OsRPD1b         sqsvrdcdghfgviklaatvhnpcfieevvqllnqicpgcltlkqngdt-----.---KK
ZmRPD1          grdcdghfgvtklaatvhnpyfiddvvhflnricpgcl...........SPREG.IDTKR
SbRPD1          grdcdghfgvtklaatvhnpyfiddvvhflnqicpgcl...........SPREG.INMKR
VvRPE1          .................................................MEEDS.STIL-
PtRPE1b         .................................................MDENSqSSIF-
PtRPE1a         .................................................MDEIPqSSIF-
CpRPE1          .................................................M----.-----
AtRPE1          .................................................MEEEStSEIL-
BdRPE1          .................................................MEEDQ.SAVL-
OsRPE1b         .................................................MEEDQ.SAIP-
ZmRPE1          .................................................MEEDH.SVIL-
SbRPE1b         .................................................MEEDH.SATL-
OsRPE1a         .................................................TSAAT.AMIP-
SbRPE1a         .................................................-AAAG.LTVP-
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ZmRPB1        .................................................MDARF.PYSP-
AtRPB1        .................................................MDTRF.PFSP-
SmRPD1        .................................................RSSHR.DRALE

VvRPD1        VP..SGLLIGIKFDVSTEEDM.EK.......ISVMKIDAVNE...............I.T
PtRPD1        VP..SALITGMAFGVLTEAET.EK.......LSVLNIDAVSE...............V.T
AtRPD1        VP..VGTLTSIGFSISNNNDR.DK.......MSVLEVEAPNQ...............V.T
CpRPD1        --..-ALWILLGSWI------.--.......----------E...............V.T
BdRPD1        SD..AATIQE-----------.--.......-----------...............-.-
OsRPD1a       AD..GTTIQG-----------.--.......-----------...............-.-
OsRPD1b       TD..GTTIQT-----------.--.......-----------...............-.-
ZmRPD1        LE..REKVQA-----------.--.......-----------...............-.-
SbRPD1        LG..RETVQA-----------.--.......-----------...............-.-
VvRPE1        --..DGEISGIRFGLATRQEI.CIas.....VSDCPISHASQ...............L.T
PtRPE1b       --..DGEITGIRFGLATQKEI.CTas.....ISDCPISHSSQ...............L.T
PtRPE1a       --..EGEITGIRFGLASQKEI.CTas.....ISDCPISHSIQ...............L.T
CpRPE1        --..-----------------.--.......-----------...............-.-
AtRPE1        --..DGEIVGITFALASHHEI.CIqs.....ISESAINHPSQ...............L.T
BdRPE1        --vaEGAIKSIKLSLSTEDEI.--.......-----------...............L.G
OsRPE1b       --vaEGAIKSIKLSLSTEDEI.--.......-----------rtysindcpvthpsqL.G
ZmRPE1        --isEGAIKSIKLSLSTGEEI.--.......-----------ctysinecpvthpsqL.G
SbRPE1b       --vsEGAIKSIKLSLSTGEEV.--.......-----------ctysvnecpvthpsqL.G
OsRPE1a       --..EASIRRINLSITSNEEI.LKaqpvnelEKPIPITHQSQ...............LlN
SbRPE1a       --..EAFIRRVKLSVTSNQEIkLMahpv...EDPIPITHCSQ...............LqD
ZmRPB1        AE..VAKVEFVQFGILSPDEI.RQ.......MSVIQIEHAETmergkpkpgg.....L.S
AtRPB1        AE..VSKVRVVQFGILSPDEI.RQ.......MSVIHVEHSETtekgkpkvgg.....L.S
SmRPD1        EA..TGTLIALDFRPLTSEEI.IR.......ASVYEVKTVRA...............L.Q

VvRPD1        DPKLGVPNPSC..Q.CSTCGAKDT..K....KCE..........................
PtRPD1        DPKLGLPNPSS..Q.CSTCGSRDL..K....SCEgivdvdlnsadrlasiatgdcanill
AtRPD1        DSRLGLPNPDS..V.CRTCGSKDR..K....VCE..........................
CpRPD1        DPKLGLPNPSS..E.CLTCGAKDL..K....HCE..........................
BdRPD1        -----------..P.CKYC-SKDG..L....YPS..........................
OsRPD1a       -----------..T.CKYC-SKDGskL....YPS..........................
OsRPD1b       -----------..T.CKYC-SKDGakL....YPS..........................
ZmRPD1        -----------..T.CKYC-SKDGskL....YPS..........................
SbRPD1        -----------tsT.CKYC-SKDGskL....YPS..........................
VvRPE1        NPFLGLPLEFG..K.CESCGTAEP..G....QCE..........................
PtRPE1b       NPFLGLPLEFG..K.CESCGTSEP..G....KCE..........................
PtRPE1a       NPYLGLPLEFG..K.CESCGTSEP..G....QCE..........................
CpRPE1        -----------..-.---------..-....---..........................
AtRPE1        NAFLGLPLEFG..K.CESCGATEP..D....KCE..........................
BdRPE1        NPFLGLPLETG..K.CESCGASEN..G....KCE..........................
OsRPE1b       NPFLGLPLETG..K.CESCGASEN..G....KCE..........................
ZmRPE1        NPFLGLPLEAG..K.CESCGASEN..D....KCE..........................
SbRPE1b       NPFLGLPLEAG..K.CESCGASEN..D....KCE..........................
OsRPE1a       NPYLGLPLQVG..S.CQSCGSNAI..E....ECE..........................
SbRPE1a       NPSLGLPLQDG..StCESCGATQL..D....KCD..........................
ZmRPB1        DPRLGTIDRKI..K.CETC-MAGM..A....ECP..........................
AtRPB1        DTRLGTIDRKV..K.CETC-MANM..A....ECP..........................
SmRPD1        NNRFGLPNLSD..C.CTSCGAKRT..DasnsACP..........................

VvRPD1        ...GHFGVIKFPFTILHPYFLTEVVQILNKICPGCKSTRQGQWV..KV.....RRL....
PtRPD1        slsGHFGVINFPYTIVHPYFLSEVVQILNKICPGCKSIR---LA..KA.....TELitke
AtRPD1        ...GHFGVINFAYSIINPYFLKEVAALLNKICPGCKYIRKKQF-..QI.....TED....
CpRPD1        ...GHFGVIQFPYTILHPYYLSEVVQILNKVCPALIHAIQG---..--.....---....
BdRPD1        ...VIFKVLTSPRITLSKSKLQRNTSVMDKV-------------..--.....---....
OsRPD1a       ...IIFKMLTSPRVTLSRSKLHRNTSVMDKM-------------..--.....---....
OsRPD1b       ...VIFKMLTSPRVTLSRSKLHRNTSVMDKI-------------..--.....---....
ZmRPD1        ...IVFKTLSSPRVLLFKSKLHRNASVMERI-------------..--.....---....
SbRPD1        ...VIFKTLSSPRVLLSKSKLHRSPSVMERI-------------..--.....---....
VvRPE1        ...GHFGYIELPIPIYHPGHVSELKRMLSLLCLKCLKIRKSKVT..NN.....GIT....
PtRPE1b       ...GHFGFIHLPIPIYHPSHISELKRMLSLICLKCLKLKRNKIQikSN.....GVA....
PtRPE1a       ...GHFGYIDLPVPIYHPSHISELKRMLSLLCLKCLKLKRNKIQikSN.....GVA....
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CpRPE1          ...-----------------------VYSLLGINWIMAGTSKVK..NA.....GVA....
AtRPE1          ...GHFGYIQLPVPIYHPAHVNELKQMLSLLCLKCLKIKKAKGT..SG.....GLA....
BdRPE1          ...GHFGYIELPVPIYHPCHVSELRQLLSLVCLKCLRIKKGK--..--.....---....
OsRPE1b         ...GHFGYIELPVPIYHPCHVTELRQILNVVCLKCLRVKKGK--..--.....---....
ZmRPE1          ...GHFGYIELPVPIYHPCHVTELRQLLSLICLKCLRIKKGK--..--.....---....
SbRPE1b         ...GHFGYIELPVPIFHPCHVSELRQLLSLICLKCLRIKKGK--..--.....---....
OsRPE1a         ...GHFRFIELPMPIFHPSHVTELSQILNLICLRCLKIKNRKKS..TL.....KGS....
SbRPE1a         ...GHFGFIKLPEPIYHPSHIAELGKILNLVCLRCLRLKKPKKV..TG.....KES....
ZmRPB1          ...GHFGHLELAKPMFHIGFIKTVLSIMRCVCFNCSKILADE-D..ET.....KFK....
AtRPB1          ...GHFGYLELAKPMYHVGFMKTVLSIMRCVCFNCSKILADE--..--.....---....
SmRPD1          ...GHSGHIELPVLVYHWDRISALEAILNRVCLHCYSFKHKGRK..KElrtlsSLE....

VvRPD1          ...RSKGCKYCAANSNDWYPTMKFKVSSK...................DLFRK.TAIIVE
PtRPD1          npqR-KGCKYCAGNSLGWYPPMKFKVSSK...................EIFRK.TAIIAE
AtRPD1          ...QPERCRYCTLNTG--YPLMKFRVTTK...................EVFRR.SGIVVE
CpRPD1          ...----------NSLNWYPPMKFKVLSE...................DIFRL.SAIMVE
BdRPD1          ...--------------------------...................-----.-SVTAE
OsRPD1a         ...--------------------------...................-----.-SIIAE
OsRPD1b         ...--------------------------...................-----.-SIIAE
ZmRPD1          ...--------------------------...................-----.-SIVAE
SbRPD1          ...--------------------------...................-----.-SIVAE
VvRPE1          ...EQLLAPCCQ-----------------...................DSPQV.SVREFR
PtRPE1b         ...ERLLS-CCE-----------------...................ECAQI.SIREVK
PtRPE1a         ...ERLLS-CCE-----------------...................ECAQI.SIREVK
CpRPE1          ...ERLFSLCCE-----------------...................EVSQV.SIKEGK
AtRPE1          ...DRLLGVCCE-----------------...................EASQI.SIKD-R
BdRPE1          ...--------------------------...................DVPAL.SLKEVK
OsRPE1b         ...--------------------------vkqtegkdntsalscyycrDLPAL.SLKEIK
ZmRPE1          ...--------------------------vkqsngkgnaaptlcsycrDIPAL.SLKEIK
SbRPE1b         ...--------------------------vkqsngkgnlsatlcsycrDIPAL.SVKEVK
OsRPE1a         ...KFTSCSHCQ-----------------...................ELPPL.CVAEVK
SbRPE1a         ...RFTSCSYCQ-----------------...................ELSPL.CVSQVK
ZmRPB1          ...QALKIRNPKNRLKRIYDACKSKKVCA...................GGDDL.DVQEQD
AtRPB1          ...-AMKIKNPKNRLKKILDACKNKTKCD...................GGDDIdDVQSHS
SmRPD1          ...QVASGVDAHQADIGAVPNGARAPEAE...................ENPGK.CTGPAA

VvRPD1          MN....EKLPK.K....LQKKSF............RPVLPLDYWDFIPKDP.QQ.E....
PtRPD1          IR....ETLSK.K....PQ-KGF............KKILAADYWDIFPKDE.QE.E....
AtRPD1          VN....EESLM.K....LKKRGV............LT-LPPDYWSFLPQDS.NI.D....
CpRPD1          VN....ENVLR.K....FQKRR-............KEALPADYWDFLPKDS.HQ.E....
BdRPD1          VI....NM---.-....SKNKSS............LEVLPHDYWNFVP---.HN.Q....
OsRPD1a         VA....GG---.-vahkSKNKAP............HETLPQDFWDFIP---dDN.Q....
OsRPD1b         VA....GG---.-vthnSKNKAP............HETLPQDFWDFVP---dDN.Q....
ZmRPD1          AAdrmpNR---.-....SKGKGS............LEGLPLDFWDFVP---sEN.K....
SbRPD1          AAervsNR---.-....SKGKGL............LEGLPQDYWDFVP---sEN.K....
VvRPE1          PT....EGACF.L....ELKIPS............RSRPKDGFWDFLARYG.YR.Y....
PtRPE1b         NT....DGACF.L....ELKLPS............RSRLRDGCWNFLERYG.FR.Y....
PtRPE1a         NT....DGACF.L....ELKLPS............RSRLRDGCWNFLERYG.FR.Yvfvt
CpRPE1          TP....DDACY.L....QLKLPS............MSRLRESFWNFLEKYG.FS.Lrlcg
AtRPE1          AS....DGASY.L....ELKLPS............RSRLQPGCWNFLERYG.YR.Y....
BdRPE1          TA....DGAFR.L....ELRAPP............RRLMKDSSWNFLDKYG.FH.H....
OsRPE1b         TA....DGAFR.L....ELKMPP............RKFMTEGSWNFLDKYG.FH.H....
ZmRPE1          TT....DGAIR.L....ELRAPH............NKHMTERSWNFLDKYG.FH.H....
SbRPE1b         TA....DGAIR.L....ELSAPH............KRHMTERSWNFLDKYG.FH.H....
OsRPE1a         KS....NGARG.L....ELRAPI............KKELEEGFWSFLDQFG.SCtR....
SbRPE1a         KS....NGARS.L....ELKLPL............KQEVADGFWSFLDQFG.FHtS....
ZmRPB1          TD....EPIKK.R....GGCGAQ............QPNITVDGMKMVAEFK.AP.K....
AtRPB1          TD....EPVKKsR....GGCGAQ............QPKLTIEGMKMIAEYK.NS.K....
SmRPD1          AV....KKIFK.K....VGTANVpallleidgkvrREDIPPGFQSLILKDE.MT.P....

VvRPD1          .......................................................E....
PtRPD1          .......................................................E....
AtRPD1          .......................................................E....
CpRPD1          .......................................................E....
```

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BdRPD1         .......................................................P....
OsRPD1a        .......................................................P....
OsRPD1b        .......................................................P....
ZmRPD1         .......................................................Q....
SbRPD1         .......................................................Q....
VvRPE1         .......................................................G....
PtRPE1b        .......................................................G....
PtRPE1a        fekysyihmpkvyafmskgvcafrsdwyfiyapatmlasprnlvwsyvlltrlgtGylfn
CpRPE1         lgsqisaltlkvlgllafwvaftslceg...........................S....
AtRPE1         .......................................................G....
BdRPE1         .......................................................Gg...
OsRPE1b        .......................................................Gg...
ZmRPE1         .......................................................Gg...
SbRPE1b        .......................................................Gg...
OsRPE1a        .......................................................G....
SbRPE1a        .......................................................G....
ZmRPB1         .......................................................K....
AtRPB1         .......................................................E....
SmRPD1         .......................................................Q....

VvRPD1         ........NC............LN..PN........RRVLSHAQ..VHYLLKDIDPGFIK
PtRPD1         ........EE............TNakPN........RRVLSHSQ..VRHMLKDVDPNFIK
AtRPD1         ........SC............LK..PT........RRIITHAQ..VYALLLGIDQRLIK
CpRPD1         ........SG............TR..PN........RRILSHAQ..VHFLLKAIDPKLIR
BdRPD1         ........PQ............PN..TT........KILLSPYQ..VFHILKQVDLELIT
OsRPD1a        ........PI............FN..VT........KKILSPYQ..VFHMLKKLDPELIN
OsRPD1b        ........PQ............SN..VA........KKILSPYQ..VFHMLKNLDPELIN
ZmRPD1         ........VQ............SN..MT........KIILSPYQ..VFYMLKKSDPELIK
SbRPD1         ........VQ............SN..MT........KIILSPYQ..VFHMLKKSDPELIK
VvRPE1         ........HN............LS..--........-RILLPSE..VMEILRRIPEDTRK
PtRPE1b        ........DD............FT..--........-RPLLPCE..VMQILKRIPAETRK
PtRPE1a        asvsellvNDsnfrtvlvyiqsFT..--........-FSAYACYflVMQILKTIPAETRK
CpRPE1         ........CK............EI..--........-SKVIGQV..VMKMIRSIPEDTRR
AtRPE1         ........SD............YT..--........-RPLLARE..VKEILRRIPEESRK
BdRPE1         ........AS............HF..--........-RTLLPEE..ALNILKKIPDDTRK
OsRPE1b        ........TS............HC..--........-RTLLPEE..ALNILKKIPEETKR
ZmRPE1         ........CS............HH..--........-RTLLPEE..ALNILKKVPDDTRR
SbRPE1b        ........CS............QF..--........-RSLLPEE..ALNILKKVPDDTRR
OsRPE1a        ........TS............HC..--........-RPLLPEE..VQNIIKKIPEETRR
SbRPE1a        ........TS............HR..--........-RPLHPKE..VQDIMKKITEKTRA
ZmRPB1         ........KT............DD..QDqlpepverKQILSAER..VLNVLKRISDEDCL
AtRPB1         ........EN............DE..PDqlpepaerKQTLGADR..VLSVLKRISDADCQ
SmRPD1         ........WR............SK..--........--MLDPNQ..VLRILKCLPQETID

VvRPD1         EF.....VSR......MDSFFLNCLPVTPNNHRVTEITHALSNGQTLI.FDQHSRAYKKL
PtRPD1         LS.....ILK......TDTIFLNCFPVTPNSHRVTEVTHAFSNGQRLI.FDERTRAYKKM
AtRPD1         KD.....IPM......FNSLGLTSFPVTPNGYRVTEIVHQF-NGARLI.FDERTRIYKKL
CpRPD1         KF.....ILR......PDSLFLNYFPVTPNSHRVTELTYMFSSGQRLF.FDERTGAYKKL
BdRPD1         KF.....APR......RELLFLSCLPVTPNRHRVAEMPYRFSDGPSLA.YDDRTKAYKRT
OsRPD1a        QV.....TRR......RELLFLSCLPVTPNCHRVAEMPYGHLDGPRLA.FDDRTKAYKRM
OsRPD1b        QV.....TPR......RELLFLSCLPVTPNCHRVAEMQYGHSDGPRLA.FDDRTKAYKRM
ZmRPD1         QF.....VSR......RELLFLSCLPVTPNCHRVVEIGYGLPDG-RLT.FDDRTKAYKRM
SbRPD1         QF.....VSR......RELLFLSCLPVTPNCHRVVEIGYGLSDG-RVT.FDDRTKAYKRM
VvRPE1         KL.....VRKgyfp..QDGYILQYLPVPPNCLSVPDISDGVS---IMS.SDLSVSMLKKV
PtRPE1b        KL.....SGKgyfp..QDGYILQQLPVPPNCLSVPVVSDGIT---VMS.SDLSISMLKKV
PtRPE1a        KL.....GGKgyfp..QDGYILQQLPVPPNCLSVPAVSDGIS---IMS.SDLSISILKKV
CpRPE1         KL.....AGKgyfp..QDGYILQVLPVPPNCLSVPDISDGVS---TMS.SDPSTPLLKKV
AtRPE1         KL.....TAKghip..QEGYILEYLPVPPNCLSVPEASDGFS---TMS.VDPSRIELKDV
BdRPE1         KL.....AARgyia..QSGYVMKYLPVPPNCLYIPEFTDGQS---IMS.YDISISLLKKI
OsRPE1b        KL.....AARgyia..QSGYVMKYLPVPPNCLYIPEFTDGQS---IMS.YDISISLLKKV
ZmRPE1         KL.....AARgyiv..QTGYVMKYLPVPPNCLYIPEFTDGQS---IMS.YDISIALLKKV
SbRPE1b        KL.....AARgyiv..QTGYVMKYLPVPPNCLYIPEFTDGQS---IMS.YDISIALLKKV
OsRPE1a        WL.....SVRgyip..QDGFILSYLCVPPNCLRVSNVLDGNT---FSC.SGTSTNLLRKA
SbRPE1a        RL.....AARgynl..QDGFVMDNMSIPPNCLQISNMLDENT---EMCpPDTSKGLLHKV
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ZmRPB1          LLglnpkYAR......PDWMILQVLPVPPPPVRPSVMMDTSS----RS.EDDLTHQLAMI
AtRPB1          LLgfnpkFAR......PDWMILEVLPIPPPPVRPSVMMDATS----RS.EDDLTHQLAMI
SmRPD1          KL.....RDEklpsipAEDYFIKSLPVPPNWMR-------YSTNEFYF.QDKTTKNLKHL

VvRPD1          VDFRGTANELS.................................................
PtRPD1          VDFRGVANTLSfhvmd............................................
AtRPD1          VGFEGNTLELSsrvme............................................
CpRPD1          VDFRGTSNELSsrlhtfksssskdattallk..............................
BdRPD1          VDASKKIDDYRqhpqfsvlassfvtsrvme..............................
OsRPD1a         VDVSRRIDDYHqhpqfgvfassvvtsrvme..............................
OsRPD1b         VDVSKRIDDCRqhpqfsvfassvvtsrvme..............................
ZmRPD1          VDVSRRIDDYRqhphfsvlasslvssrvse..............................
SbRPD1          VDVSRRIDDYRqhpqfsvlasslvsgrvse..............................
VvRPE1          LKQIEVIKGSRsgepnfeshkie.annlqssieqylevrgt.......aktsrsldtrfg
PtRPE1b         LKQAEVIRSSRsgapnfdahkde.atslqsmvdqylqvrgt.......tktsrdvdtryg
PtRPE1a         LKQVEVIKSSRsgapnfdahkde.anslqsmvdrylqvrgt.......tktsrdvdvryg
CpRPE1          LEKVENIKSSRcgepnfeshsve.anelqsavnkylqargt.......akasre.dtryg
AtRPE1          LKKVIAIKSSRsgetnfeshkae.asemfrvvdtylqvrgt.......akaarnidmryg
BdRPE1          LHRIEQIKKSRagtpnfesheae.ssdlqisiaqyihlrgt.......tk.......rft
OsRPE1b         LQKIEQIKKSRagspnfesheve.scdlqlsiaqyihlrgttrgpqdntk.......rfa
ZmRPE1          LQKIEQIKRSRsgspnfeshdae.scdlqlaigqyirlrgttrgpqdntk.......rft
SbRPE1b         LQKIEQIKRSRsgspnfdshdae.scdlqlaigqyirlrgttrgpqdntk.......rft
OsRPE1a         LRKIQQIRGSRigssniqvdqv..addlqvdvanyinlggt.......tkghgd......
SbRPE1a         LRTIEQIESLNishpniearel.gaddlqvavadymnmgga.......akvsqh......
ZmRPB1          IRHNENLRRQErngapahiitefaqllqfhiatyfdndlpgqpratqrsgrpik......
AtRPB1          IRHNENLKRQEkngaprhiisrftqllqfhiatyfdnelpgqpratqksgrpik......
SmRPD1          LTKIKSIVYTRdedkisllteqkvmeiqaaatqciranplygnvsdedprygnv......

VvRPD1          ..CHSASKM.........................SGLKW...I....KEVLLGKRTNHSF
PtRPD1          ..CLKTSKLnpdksgnidpwtaqpkksndyvnnaSGLRW...I....KDVVLGKRNDHSF
AtRPD1          ..CMQYSRLfsetvssskdsanpyqkksdtpkl.CGLRF...M....KDVLLGKRSDHTF
CpRPD1          ..NEDSSNM.........................VGLRY...M....KDVLLGKRNDSSF
BdRPD1          ..CLQSSKLyskktdkes................STDSY...Gt...SDAILSKRSDYAF
OsRPD1a         ..CLKSSKLyskksddessa..............STDTY...GtkwlKDIILSKRSDNAF
OsRPD1b         ..CLKSSKLysrksdgedpt..............SPDTY...GtkwlKDIILSKRSDNAF
ZmRPD1          ..CLKSSKLyskkadget................STDTY...GmkwlKDVVLSKRSDNVF
SbRPD1          ..CLKSSKLyskktdget................STDPS...GmkwlKDAVLSKRSDNAF
VvRPE1          s.SKEPNES.........................STKAWlekM....RTLFIRKGSGFSS
PtRPE1b         v.KKESSES.........................TTKAWlekM....RTLFIRKGSGFSS
PtRPE1a         v.KKDSSES.........................STKAWlekM....RTLFIRKGSGFSS
CpRPE1          v.SKNSNDC.........................STKAWlekM....RTLFIRKGSGFSS
AtRPE1          v.SKISDSS.........................SSKAWtekM....RTLFIRKGSGFSS
BdRPE1          i.STDSSHL.........................STKQWlekM....RTLFISKGSGFSS
OsRPE1b         i.STDPSAL.........................STKQWlekM....RTLFISKGSGFSS
ZmRPE1          vgSADSAAL.........................STKQWlekM....RTLFISKGSGFSS
SbRPE1b         vgSADSAAL.........................STKQWlekM....RTLFISKGSGFSS
OsRPE1a         ..DTFTSQP.........................TAMQWkqkM....KTLFISKSSSFSS
SbRPE1a         ..VTFTRQP.........................APKQWhkkM....KTLFLSKSSSYTC
ZmRPB1          ..SICSRLK.........................AKEGR...I....RGNLMGKRVDFSA
AtRPB1          ..SICSRLK.........................AKEGR...I....RGNLMGKRVDFSA
SmRPD1          ..SDESKPL.........................SGLHF...L....RSLT-GKYCGSSA

VvRPD1          RMIVVGDPKLRLSEIGIPCHIAE.ELLISEHLNSWNWEKVTNGC..NLR..........L
PtRPD1          RMVIVGDPHLQLHEIGIPCHIAE.RLQISESLTAWNWEKL-NACfeKSR..........-
AtRPD1          RTVVVGDPSLKLNEIGIPESIAK.RLQVSEHLNQCNKERLVTSF..VPT..........L
CpRPD1          RTVVIGDRSLKLSEIGIPCHIAE.SLQISENLNNWNWDKLISSC..DLR..........L
BdRPD1          RSIMVGDPKIRLHEIGIPMDLA-.DLFVPEHVSIYNFKSINLKC..NLH..........L
OsRPD1a         RSIMVGDPKINLNEIGIPMGLA-lNLVVSEQVSSYNFETINLKC..NLH..........L
OsRPD1b         RSIMVGDPKINLNEIGIPTDLA-lNLVVSEQVSFYNFETINLKC..NLH..........L
ZmRPD1          RSIMVGDPKIKLWEIGIPEDLS-sSLVVSEHVSSYNFQSTNLKC..NLH..........L
SbRPD1          RSTMVGDPKIKLWEIGIPEDLA-sNLVVSDHVNSYNFENINLKC..NLH..........L
VvRPE1          RSVITGDAYKRVNEIGLPFEIAQ.RITFEERVNVHNMKHLQNLV..DEK..........L
PtRPE1b         RSVITGDAYTLVNQVGIPYEIAQ.RITFEERVSVHNMRYLQELV..DNK..........L
PtRPE1a         RSVITGDAYTKVNQVGIPYEIAQ.RITFEERVSVHNMRYLQELV..DNK..........L
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CpRPE1          RSVITGDPYKKVNEIGIPFEIAQ.RITFEERVNLHNMKYLQELV..DKK..........L
AtRPE1          RSVITGDAYRHVNEVGIPIEIAQ.RITFEERVSVHNRGYLQKLV..DDK..........L
BdRPE1          RSVLTGDPYIGVDVVGLPSEVAK.RITFEEQVTDINIKRLQEVV..DKG..........L
OsRPE1b         RSVLTGDPYIGVDVIGLPSEVAK.RITFEEQVTDINLNRLQEIV..DKG..........L
ZmRPE1          RSVLTGDPYIGLGVVGLPSEVAK.RMTFEEQVTDININRLQDVV..DKG..........L
SbRPE1b         RSVLTGDPYIGLGVVGLPSEVAK.RMTFEEQVTDININRLQEVV..DKG..........L
OsRPE1a         RGVITGDPYIGLNVVGVPEEVAK.RMSVEEKVTDHNIAQLQDMM..NKG..........L
SbRPE1a         RAVITGDPYIGLDVVGVPDEIAR.RMSVQECVTNYNIARLQDMM..NKG..........L
ZmRPB1          RTVITPDPNINIDELGVPWSIAL.NLTYPETVTPYNIERLKELV..EYGphpppgktgaK
AtRPB1          RTVITPDPTINIDELGVPWSIAL.NLTYPETVTPYNIERLKELV..DYGphpppgktgaK
SmRPD1          RAVVIGDPALKLEEIGISARIAA.GLVVLETVTSSNIIFLQSYA..---..........-

VvRPD1          LEKGQTYVR.RKGT...LAP.VRRMNDFQAGDI...........................
PtRPD1          FEKGDMHVR.REGN...LVR.VRHMKELRLGDI...........................
AtRPD1          LDNKEMHVR.RGDR...LVA.I-QVNDLQTGDK...........................
CpRPD1          LEKGEIHVR.RKNS...LIS.LRRISDLRMGDI...........................
BdRPD1          LAKELLIAR.RNGK...LIY.VRKENQLEIGDI...........................
OsRPD1a         LTKEVLLVR.RNGN...LIF.VRKANQLEIGDI...........................
OsRPD1b         LTKEVLLVR.RNGK...LIF.VRKANKLEIGDI...........................
ZmRPD1          LAKQELFIR.RNGK...LMF.LRKADQLEIGDI...........................
SbRPD1          LTKEELFIR.RNGK...LMF.LRKADQLEIGDI...........................
VvRPE1          CLTYRDGLS.TYSL...REG.SKGHTFLRPGQV...........................
PtRPE1b         CLTYKDGSS.TYSL...REG.SKGHTFLRPGQV...........................
PtRPE1a         CLTYRDGSS.TYSL...REG.SKGHTFLRPGQV...........................
CpRPE1          CLTYRDGGS.TYSL...REG.SKGHTFLRPGQV...........................
AtRPE1          CLSYTQGST.TYSL...RDG.SKGHTELKPGQV...........................
BdRPE1          CLTYRDGQT.TYAI...TVG.SKGYTTLKVGQT...........................
OsRPE1b         CLTYRDGQA.TYAI...TVG.SKGHTTLKVGQT...........................
ZmRPE1          CLTYRDGQA.TYAI...TVG.SKGYTTLKVGQT...........................
SbRPE1b         CLTYRDGQA.TYAI...TVG.SKGHTTLKVGQT...........................
OsRPE1a         CLTYTDANSiTYSLdagKDNpNKKHTILKVGEI...........................
SbRPE1a         CLTYTDLNTnTYDLd.gKKG.NKKCIMLRVGET...........................
ZmRPB1          YIIREDGQR.LDLR...YVK.KSSDQHLELGYK...........................
AtRPB1          YIIRDDGQR.LDLR...YLK.KSSDQHLELGYRyvllsysihsthkrlflevvifmlsws
SmRPD1          YNNPGLKVV.RGGE...VCT.ARSCKKLQVGDV...........................

VvRPD1          .IYRPLTDGDIVLINRPPSIHQHSVIALSVKVLPLNSVVSINPLCCSPFRGDFDGDCLHG
PtRPD1          .IYRPLNDGDTVLINRPPSIHQHSLIALSVKVLPVPSVLAINPLCCPPFRADFDGDCLHG
AtRPD1          .IFRSLMDGDTVLMNRPPSIHQHSLIAMTVRILPTTSVVSLNPICCLPFRGDFDGDCLHG
CpRPD1          .ISRPLKDGDILLINRPPSIHPHSLIALSVKVLPISSVVSINPICCSPFRGDFDGDCFHG
BdRPD1          .VYRPLQDGDLILVNRPPSVHQHSLIALSAKLLPVQSVVAINPLNCAPLSGDFDGDCLHG
OsRPD1a         .AYRLLQDGDLVLVNSPPSVHQHSLIALSAKLLSTQSAVSINPLCCDPFKGDFDGDCLHG
OsRPD1b         .AYRLLQDGDLVLVNRPPSVHQHSLIALSAKLLPIQSAVAINPLCCDPFKGDFDGDCLHG
ZmRPD1          .AYRPLQDGDIILINRPPSVHQHSLIALSAKILPIHSVVSINPLCCTPFAGDFDGDCLHG
SbRPD1          .AYRPLQDGDLILINRPPSVHQHSLIAFSAKILPIHSVVSINPLCCTPFLGDFDGDCLHG
VvRPE1          .VHRRIMDGDIVFINRPPTTHKHSLQALSVYVHD-DHTVKINPLICGPLSADFDGDCVHL
PtRPE1b         .VHRRIMDGDIVFINRPPTTHKHSLQALSVYVHD-DHAVKINPLICGPLSADFDGDCVHL
PtRPE1a         .VHRRIIDGDVVFINRPPTTHKHSLQALSVYVHD-DHTVKINPLICGPLSADFDGDCVHL
CpRPE1          .VHRRIMDGDTVFINRPPTTHKHSLQALSVYIHD-DHTVKINPLICGPLSADFDGDCVHL
AtRPE1          .VHRRVMDGDVVFINRPPTTHKHSLQALRVYVHE-DNTVKINPLMCSPLSADFDGDCVHL
BdRPE1          .ISRRIVDGDVVFLNRPPSTHKHSLQAFYVYIHD-DHTVKINPLICSPLAADFDGDCVHI
OsRPE1b         .ISRRIVDGDVVFLNRPPSTHKHSLQAFRVYVHE-DHTVKINPLICAPFAADFDGDCVHI
ZmRPE1          .ISRRIVDGDVVFLNRPPSTHKHSLQAFYAYVHD-DHTVKINPLMCGPFSADFDGDCVHI
SbRPE1b         .ISRRIVDGDVVFLNRPPSTHKHSLQAFYAYVHD-DHTVKINPLMCGPFSADFDGDCVHI
OsRPE1a         .VNRRVFDGDIVFLNRPPSTDKHSVEAFYVQVHN-DHTIKINPLICDPLGADFDGDCVQI
SbRPE1a         .VDRRVLDGDLVFLNKPPSTDMHSIQALYVHVHD-DHTIKINPLICGPLEADFDGDCVHI
ZmRPB1          .VERHLNDGDFVLFNRQPSLHKMSIMGHRIKIMP-YSTFRLNLSVTSPYNADFDGDEMNM
AtRPB1          qVERHLQDGDFVLFNRQPSLHKMSIMGHRIRIMP-YSTFRLNLSVTSPYNADFDGDEMNM
SmRPD1          .IHRSLKDGDQVFVNRPPTFHKHALIGLKSKVIR-NNVFAVNPLICPPLFADFDGDTLAL

VvRPD1          YIPQSVDSRVELSELVALNRQLINRQSGRNLLSLSQDSLSAAHLV.MEDGVLLNLFQMQQ
PtRPD1          YVPQSVDTRVELTELVSLDKQLTNWQSGRNLLSLSQDSLTAAHLV.LEDDVFLSSFELQQ
AtRPD1          YVPQSIQAKVELDELVALDKQLINRQNGRNLLSLGQDSLTAAYLVnVEKNCYLNRAQMQQ
CpRPD1          YIPQSIEARVELHELVALDRQLTNWLSGRNLLCLGQDSLTAAHLI.KEDGFLLNKYQMQQ
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BdRPD1          YVPQSIGSRVELGELVSLSHQLLNMQDGRSLVSLTHDSLAAAHLL.TSSGVLLNKTEFQQ
OsRPD1a         YIPQCLQSRIELEELVGLSGQLLNQQDGRSLVSLTHDSLAAAHQL.TNADVFLEKAEFQQ
OsRPD1b         YVPQTLQSRVELDGLVSLSGQMLNAQDGRSLVSLTHDSLAAAHQL.TSADVFLQKAEFQQ
ZmRPD1          YIPQSIRSRVELEELVSLHNQLLNMQDGRNLVSLTHDSLAAAHLL.TSTDVFLKKSELQQ
SbRPD1          YIPQSVRSRIELGELVSLHHQLLNMQDGRSLVSLTHDSLAAAHLL.TSTDVFLKKSEFQQ
VvRPE1          FYPQSLGAKAEVLELFSVEKQLLSSHSGNLNLQLATDSLLSLKVL.FER-YFLNKAAAQQ
PtRPE1b         FYPQSLAAKAEVLELFSVEKQLLSSHSGNLNLQLTTDSLLSLKMM.FKA-CFLGKSAAQQ
PtRPE1a         FYPQSLAAKAEVLELFSVEKQLLSSHSGNLNLQLTTDSLLSLKMI.FKA-CFLDKSAAQQ
CpRPE1          FYPQSPAARAEVLELFSVEKQLLSSHSGNLNLQLAADSLLSLKVM.FEK-FFLGKTAAQQ
AtRPE1          FYPQSLSAKAEVMELFSVEKQLLSSHTGQLILQMGSDSLLSLRVM.LER-VFLDKATAQQ
BdRPE1          YYPQSLAAKAEALELFSVEKQLTNSHNGKVNLQLSNDSLLALKHM.SSR-TVLSKESANQ
OsRPE1b         YYPQSLAAKAEALELFSVEKQLTSSHSGKVNLQLVSDSLLALKHM.SSR-TMLSKEAANQ
ZmRPE1          YYPQSLAAKAEALELFSVERQLISSHSGKVNLQLGNDSLVAMKAM.SHT-TMLHKELANQ
SbRPE1b         YYPQSLAAKAEALELFSVERQLISSHSGKVNLQLGNDCLVAMKAM.SDR-TVLHKELANQ
OsRPE1a         FYPRSLSARAEAKELYTVDKQLVSSHNGKLNFQFKNDFSLALKIM.CGR-EY-SEREANQ
SbRPE1a         FFPRSVLARVEAAELFAVEKQLLNSHNAKLNFQIKNDYLLALRIM.CDR-SY-SKEKANQ
ZmRPB1          HVPQSFETRAEVLELMMVPKCIVSPQSNRPVMGIVQDTLLGCRKI.TKRDTLIEKDVFMN
AtRPB1          HVPQSFETRAEVLELMMVPKCIVSPQANRPVMGIVQDTLLGCRKI.TKRDTFIEKDVFMN
SmRPD1          YLPQSLQVRAEVAELVALPKQLVSSQGGQSIIGLTQDALLGAHLM.TRKNVFLDKLDMDQ

VvRPD1          L..EMFCP...YQ..LQSPAIIKAP...................................
PtRPD1          L..QMFRP...ER..FLLPA-VKAPsanalvwtgkqlismllpvgfdhdfpscnvcirdg
AtRPD1          L..QMYCP...FQ..LPPPAIIKASpsstepqwtgmqlfgmlfppgfdytyplnnvvvsn
CpRPD1          L..KMYCP...YE..LPPPALVKAPrlnssvwtgkqlfsmllppgfnyyfsqngvciing
BdRPD1          L..QMLCV...SLspTPVPSVIKSInpqgplwtgkqlfgmllpsgmnfspdpklhikdse
OsRPD1a         L..QMLSS...SIslTPMPSVFKSTnsqgplwtgkqlfgmllpygmnisfdqklhikdse
OsRPD1b         L..QLLCS...SIspTPEPSVVKSAnfqgslwtgkqlfgmllpsgmnisfdqklhikdse
ZmRPD1          L..QMLCL...SVs.TPAPAVIKSMnfqgslwtgkqlfsmllpsgmnfscdtelhimdse
SbRPD1          L..QMLCL...SVl.TPVPAVIKSMnfqgsrwtgkqlfsmllpsgmkfscdrmlhilnge
VvRPE1          L..VMFVS...MS..LPRPALLKSPcsgpc.....wtalqilqtalpsyfdcigerhwis
PtRPE1b         L..AMFIS...PY..LPQPALLKVNcffph.....wtahqilqmalpacfncsgerflii
PtRPE1a         L..AMFVS...PD..LPQPALLKVNcirpy.....wtahqilqmalptcfncsgerflin
CpRPE1          L..AMFGS...LS..LLWPALFKSHssgsf.....wtasqiiqtalpacfdcnedrylir
AtRPE1          L..AMYGS...LS..LPPPALRKSSksgpa.....wtvfqilqlafperlsckgdrflvd
BdRPE1          L..AMLLS...FS..LPDPAVVKL-..kpc.....wtitqiiqgalpaaltceggrflvk
OsRPE1b         L..AMLVT...CS..LPDPAVIKS-..kpy.....wtisqivqgalpkaltsqgdkhvvr
ZmRPE1          L..AMFVP...FS..LLAPAVIKP-..vps.....wtisqivqgafpanltcqgdthlvr
SbRPE1b         L..AMFVP...FS..LLAPAVMKP-..ips.....wtitqivqgalpakltcqgdthlvr
OsRPE1a         ItnAMFSS...GM..YPQ----KPLiggpy.....wtfpqilett..............k
SbRPE1a         I..AMFSS...GM..IP------PC..npwticdrwtipqilqtt...............
ZmRPB1          I..LMWWQdfdGK..IPAPTILKPRpiwtgkqvfnliipkqinlirfsawhseeekgfit
AtRPB1          T..LMWWEdfdGK..VPAPAILKPRplwtgkqvfnliipkqinllrysawhadtetgfit
SmRPD1          L..RMWCP...SAe.VPVPAIVKSPrksplwtgqqlfqmtlpttfdwesddggliirqge

VvRPD1          ........................................LLDT................
PtRPD1          dlvssegsfw..............................LWDTdgnlfqslvkhchgqv
AtRPD1          gellsfsegsawlrdgegnfierllkhdkgkvldiiysaqEMLS................
CpRPD1          eltsssdgsawlrdndgnlfqslvkydksmvlnflyaaq.EVLC................
BdRPD1          vlacsggsfwlqnntsglfsvlfkqyggealeflssaq..DMLC................
OsRPD1a         vltcssgsfwlqnntsslfsvmfkeygckaleflsstq..DVLC................
OsRPD1b         vltcssgsfwlqnntssvfsvmfkeygskaleflsstq..DVLC................
ZmRPD1          vltcslgsswlqnntsglfsvmfkqygckaldflssaq..EVLC................
SbRPD1          vltcslgsswlqnntsglfsvmfkqygckaldflssaq..EVLC................
VvRPE1          ksailkvdyn.r......dvlqslvn..............EIVT................
PtRPE1b         nsnflkvdfn.r......dvvasvin..............EILI................
PtRPE1a         nsnvlkvdfn.r......dvvasmin..............EILI................
CpRPE1          kseilnidfn.k......dsvqsvvg..............EVVN................
AtRPE1          gsdllkfdfg.v......damgsiin..............EIVT................
BdRPE1          dstvikldla.k......esvqasfs..............DLVS................
OsRPE1b         dstiikldld.k......esvqtsfs..............DLVY................
ZmRPE1          dstiirldlg.k......esvqdsfp..............DLVS................
SbRPE1b         dstiikldld.k......esvqdsfp..............DLVS................
OsRPE1a         snaitladhldr......esvgalatg.............TTIS................
SbRPE1a         .......dal.rivpshpntvgasvt..............AIIT................
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ZmRPB1          pgdtmvriekgellsgtlckkslgtgsg............SLIH................
AtRPB1          pgdtqvriergellagtlckktlgtsng............SLVH................
SmRPD1          ilrtsdkssawlgkdglmtticrrygpdralehldiaq..GIAV................

VvRPD1          .......Q.....WLSMRGLSVSLSDIYLSSDSISRKNMIDEVFCGLLVAEQTCHFKQLL
PtRPD1          ldflyaaQrvlceWLSMRGLSVSLSDLYLCPDSNSRKNMMDEIWYGLQDADYACNLKHLM
AtRPD1          .......Q.....WLLMRGLSVSLADLYLSSDLQSRKNLTEEISYGLREAEQVCNKQQLM
CpRPD1          .......D.....WLSDRGFSISLSDLYLSSDLHSRENLMDEISWGLLEAEQTCNFKQLM
BdRPD1          .......E.....FLTMRGLSVSLSDIYLFSDHYSRRKFAEEVNLALDEAEEAFRVTQIL
OsRPD1a         .......E.....FLTMWGLSVSLSDLYLFSDHYSRRKLSEEVHLALDEAEEAFQIKQIL
OsRPD1b         .......E.....FLTMKGLSVSLSDFYLFSDHYSRKKLSEEIHLALDEAEEAFQIKQIL
ZmRPD1          .......E.....FLTMRGLSVSLSDLYMFSDHYSRRKLAEGVKLALYEAEEAFRVKKIL
SbRPD1          .......E.....FLTMRGLSVSLSD--MFSDHYSRRKLTEGVKLALDEAEEAFRIKQIL
VvRPE1          .......S.....IFSEKGPNEVLKFFDSLQPLLMENLFSEGFSVSLED----FSIPSEV
PtRPE1b         .......S.....MFFEKGSGAVLKFFNSLQPMLMENLFSEGFSVSLED----FSISRAV
PtRPE1a         .......S.....IFFEKGSGAVLKFFNALQPLLMENLFSEGFSVSLKD----FSISQAV
CpRPE1          .......S.....IFYEKGPKEVLEFFASLQPLLMENLFVEGFSVGLKD----FSMPKSD
AtRPE1          .......S.....IFLEKGPKETLGFFDSLQPLLMESLFAEGFSLSLED----LSMSRAD
BdRPE1          .......S.....ILCVKGPGGALQFLNALQPLLMEYLLLDGFSVSLQD----FNVPKVL
OsRPE1b         .......S.....TLSVKGPGEALQFLNVLQPLLMELILLDGFSVSLQD----FNVPKVL
ZmRPE1          .......S.....ILREKGPKEALQFLNVLEPLLMEFLLLDGLSISLRD----FNVPKAL
SbRPE1b         .......S.....ILREKGPREALQFLNVLEPLLMEFLVLGGLSISLRD----FNVPKAL
OsRPE1a         .......S.....ILSTKGPREATEFLNLLQPLLMESLLIDCFSINLGD----FTVPSPI
SbRPE1a         .......S.....TLSEKGPREAIKLINLLQPLLMESLLMDGFSISLKD----LDGQSAM
ZmRPB1          .......V.....IWEEVGPDAARKFLGHTQWLVNYWLLQNGFSIGIGDTIADASTMETI
AtRPB1          .......V.....IWEEVGPDAARKFLGHTQWLVNYWLLQNGFTIGIGDTIADSSTMEKI
SmRPD1          .......D.....WISERGFSVGLCDFYMAADAVSRRKLEEETLCAVEE----AKISSLA

VvRPD1          VDSSQNF.LIGSGENNQNGV.................VPDVQSLWYERQGSAALCQSSVC
PtRPD1          VDSCRDF.LTGNNEEDQCNVerlrflsgcseedycvmAFDGERLCYEKQRSAALSQSSVD
AtRPD1          VESWRDF.LAVNGEDKEEDS.................VSDLARFCYERQKSATLSELAVS
CpRPD1          VDSCRDL.LAGNDEESQNVI.................TFDVERLCYEKQGSAVLSQASVD
BdRPD1          LSPNFIP.HLKCYDDCDDLS.................DSYEQSDFV--QSNLPIIKSSIM
OsRPD1a         LNSVSIP.NLKYYDGGDDRS.................NTDEQSGFT--QVSLPIIRSSMT
OsRPD1b         LNTVSIP.NLKHYDGPDNLS.................NSHGQSDFT--QVSLPIIKSSIT
ZmRPD1          LDPINIP.VLKCHDETEDV-.................-TYRQSDCI--QSNPSVIRSSIM
SbRPD1          LDPINIP.VLKCQDETEDV-.................-TYRQSDCI--QNNPSVIRSSIM
VvRPE1          TQNIQKN.VEDISSLLYNLR.................SMYNE--LLQLQAENHL------
PtRPE1b         KQRIPES.FKAISPLLCNLR.................STFNE--LVELQVENHI------
PtRPE1a         KQSIQES.FKVISPLLCNLR.................STYNE--LVELQVENHI------
CpRPE1          MQAIQKL.IHDTSLFLSCLG.................STYNE----ELQLENRI------
AtRPE1          MDVIHNLiIREISPMVSRLR.................LSYRD----ELQLENSI------
BdRPE1          LEEVHKS.IQEQSLVLEQSR.................CSKSQ--FVEMRVDNNL------
OsRPE1b         LEEAQKN.IEKQSLILEQSR.................FAENQ--VVEMRVDNNL------
ZmRPE1          LEEAQKD.IRNQSLILEQSR.................CSTSQ--FVEFRVENNL------
SbRPE1b         LEEAQKN.IQNQSLVLEQSR.................CSTSQ--FVELRVENNL------
OsRPE1a         LEAIQNN.------------.................-------------PLEL------
SbRPE1a         QKANQSI.------------.................-------------SLEI------
ZmRPB1          NDTISKA.KNAVKELIKKAH.................EKQLEAEPGRTMME-SFENRVNQ
AtRPB1          NETISNA.KTAVKDLIRQFQ.................GKELDPEPGRTMRD-TFENRVNQ
SmRPD1          HQIVSDP.RFQVNSVSRPRC.................NSWNERVQPVTSVNEATQQAAIS

VvRPD1          AFKQKFRDIQNLVYQYA...NKDNSLLAMLKAGSKGN.LLKLVQQGLCLGLQHSLVPLSF
PtRPD1          AFRLVFRDIQSLVYKYA...SQDNSFLAMFKAGSKGN.LLKLVQHSMCLGLQHALASLSF
AtRPD1          AFKDAYRDVQALAYRYG...DQSNSFLIMSKAGSKGN.IGKLVQHSMCIGLQNSAVSLSF
CpRPD1          AFKQVFRDIQTLAFKYA...SKENSLLAMYKAGSKGS.LPKLVQHSMCLGLQHSLVPLSF
BdRPD1          AFKSVFSDLLKMVQQHT...PKDNSMMAMINAGSKGS.MLKFVQQAACVGLQLPAGKFPF
OsRPD1a         SFKSVFNDLLKMVQQYV...SKDNSMMTMINSGSKGS.VLKFVQQTACVGLQLPASKFPF
OsRPD1b         GFKSVFNDLLKMVLQHV...SKDNSMMAMINSGSKGS.VLKFVQQTACVGLQLPASTFPF
ZmRPD1          AFKDVFRDLLKMVQQHV...SNDNSMMVMINAGSKGS.MLKYAQQTACIGLQLPASKFPF
SbRPD1          AFKDVFSDLLKMVQQHV...SNDNSMMVMINAGSKGS.MLKYAQQTACVGLQLPASKFPF
VvRPE1          ------RLTKVPVANFI...LNSSALGNLIDSKSDSA.INKVVQQIGFLGQQLSEKGKFY
PtRPE1b         ------RDVKQPVREFI...LTSSALGYLIDSKSDAA.VTKVVQQIGFLGLQVSDRGKLY
PtRPE1a         ------QDVKTPVLEFI...LTSSALGYLIDSKSDGA.VAKLVQQIGFLGLQVSDRGKLY
```

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CpRPE1          ------RCLKETAENFI...IKSS-LRNLIDFRSDSA.VNKVVQQIGFLGLQLSDKGKFY
AtRPE1          ------HKVKEVAANFM...LKSYSIRNLIDIKSNSA.ITKLVQQTGFLGLQLSDKKKFY
BdRPE1          ------KDVKQQISDFV...VESSHLGLLIDPKSEPS.MSKVVQQLGFVGLQLYREGKFY
OsRPE1b         ------KDIKQQISDFV...VKRSHLGLLIDPKSDSS.VSKVVQQLGFVGLQLYREGKFY
ZmRPE1          ------KNVKQQISDSV...GKFSDLGLLIDPKKEAS.MSKVVQQVGFVGLQLYREGKLY
SbRPE1b         ------KSVKQQISDYV...GKFSGLGLLIDPKKEAS.MAKVVQQVGFVGLQLYREGKLY
OsRPE1a         ------NKYREPIMDFI...THSSAIGLLVDPKSDSN.MNKVVEQLGFLGPQLQHNGRLY
SbRPE1a         ------DKFSKSIVDFI...ANSSALGLLVDPKNDSAlMN-LVEQVGFLGYQLQSTDRLY
ZmRPB1          VLNKARDDAGSSAQNSL...SESNNLKAMVTAGSKGS.FINISQMTACVGQQNVEGKRI-
AtRPB1          VLNKARDDAGSSAQKSL...AETNNLKAMVTAGSKGS.FINISQMTACVGQQNVEGKRI-
SmRPD1          AFQSTMKAFERTIEEHVrenSRENSLLRMVEANSKGS.FSKMMQQGGCLGLQLRQGEFVY

VvRPD1          KIPHQLSC...AAW..NKQKV.P.GLI.QNDTSEYAESYIPYAVVENSFLMGLNPLECFV
PtRPD1          RIPHQLSC...AGW..NKQKA.-.---.-DDATESAKRYIPHAVVEGSFLSGLNPIECFV
AtRPD1          GFPRELTC...AAW..NDPNS.PlRGA.KGKDSTTTESYVPYGVIENSFLTGLNPLESFV
CpRPD1          RFPHQLSC...AAW..NKQK-.-.---.--------------------------------
BdRPD1          RIPSELTC...ASW..NRHKS.L.DCDiSEGARKRLGGQNSHAVIRNSFIEGLNPLECLL
OsRPD1a         RIPSQLSC...VSW..NRHKS.R.NCEiTDGTSECVGGQDMYAVVRNSFLDGLNPLECLL
OsRPD1b         RIPSELSC...VSW..NRQKS.L.NCEiTNNTSECMAGQNMYAVIRNSFLDGLNPLECLL
ZmRPD1          RIPSQLSC...ISW..NGQKS.L.NYE.AESTSERVGGQNLYAVIKNSFIEGLNPLECLL
SbRPD1          RVPSQLSC...IRW..NRQKS.L.NYE.AEGTNERVGGQNLYAVIRNSFIEGLNPLECLL
VvRPE1          SRTLVEGM...AYL..FKSKY.P.FHG.ADYPSGE------FGLIRSCFFHGLDPYEEMV
PtRPE1b         SKTLVEDL...ASH..FLSKY.P.ANL.FDYPSAQ------YGLIQNSFFHGLDAYEEMA
PtRPE1a         SKTLVEDL...ASH..FQSKY.P.TNL.LNYPSAQ------YGLIQSSFFHGLDAYEEMA
CpRPE1          SKNLVEDV...AFL..FRSKH.P.GAG.-HYPSAN------FGLIKSCFIHGLDPYEEMA
AtRPE1          TKTLVEDM...AIF..CKRKY.G.RIS.---SSGD------FGIVKGCFFHGLDPYEEMA
BdRPE1          SSRLVEDC...FSS..FVDKHpP.IVG.NQHPPEA------YGLVQNSYFHGLNPYEELV
OsRPE1b         SRRLVEDC...YYT..FVNKH.P.AVR.EEHSPEA------YGLVRSSYFHGLNPYEELV
ZmRPE1          SRRLVEDC...FTN..FVNKH.L.AIG.DEYPPEA------YGLVQSSYFHGLNPYEELI
SbRPE1b         SRRLVEDC...FSS..FVNKH.S.AIG.DEYSPEA------FGLVQSSYFHGLNPYEELV
OsRPE1a         SSRLVEDC...LSK.sLHRCC.G.STN.CCNPLEE------YGTVRSSIYHGLNPYEALL
SbRPE1a         SNNLVEDCynfLEKrs-----.G.STK.CYDPPKG------HDFVTSSFYNGLNPYEELL
ZmRPB1          ------PF...GFI..DRTLP.H.FTK.DDYGPES------RGFVENSYLRGLTPQEFFF
AtRPB1          ------PF...GFD..GRTLP.H.FTK.DDYGPES------RGFVENSYLRGLTPQEFFF
SmRPD1          HR-----V...KSL..FPRAV.E.NES.RGYLTSS-ELWKSMGLVESSFLDGLDPREFFI

VvRPD1          HSVTSRDSSFS.DNADL..PGTLTRRLMFFMRDLYIAYDGTVRNAYGNQLVQFSYNIEHT
PtRPD1          HSVTSRDSSFS.DNADL..PGTLFRRMMFFMRDLHGAYDGTVRNAYGNQLVQFSYNIDDM
AtRPD1          HSVTSRDSSFS.GNADL..PGTLSRRLMFFMRDIYAAYDGTVRNSFGNQLVQFTY-----
CpRPD1          -----------.-----..-----------------------------------------
BdRPD1          HSISGRANFFS.ENADV..PGTLTKNLMYHLRDIYVAYDGTVRSSYGQQIVQFTYD----
OsRPD1a         HAISGRANFFS.ENADV..PGTLTRKLMYHLRDTYVAYDGTVRSSYGQQIVRFSYD----
OsRPD1b         HAISGRANFFS.ENADV..PGTLTRKLMYHLRDTYVAYDGTVRSSYGRQIVQFSYD----
ZmRPD1          HAISGRANFFS.ENADV..PGTLTRKLMYHLRDIHVAYDGTVRSSYGQQIVQFSYD----
SbRPD1          HAISGRANFFS.ENADV..PGTLTRKLMYHLRDIHVAYDGTVRSSYGQQIVQFSYD----
VvRPE1          HSISTREIIVR.SSRGLsePGTLFKNLMAILRDVVICYDGTVRNVCSNSIIQFEYG----
PtRPE1b         HSISTREVIVR.SSRGLsePGTLFKNLMAILRDVVICYDGTVRNVSSNSIIQFEYG----
PtRPE1a         HSISTREVIVR.SSRGLsePGTLFKNLMAILRDVVICYDGTVRNVCSNSIIQSEYG----
CpRPE1          HSISTREVIVR.SSRGLtePGTLFKNMMAVLRDIIVCYDGTVRNICSNSVIQFKYG----
AtRPE1          HSIAAREVIVR.SSRGLaePGTLFKNLMAVLRDIVITNDGTVRNTCSNSVIQFKYG----
BdRPE1          HSISTREAIVR.SSRGLtePGTLFKNLMAILRDVVICYDGTVRNICSNSIMQLKYN----
OsRPE1b         HAISTREAIVR.SSRGLtePGTLFKNLMALLRDVVICYDGTVRNVCSKSIIQLNYT----
ZmRPE1          HAISTREAMIR.SSRGLsePGTLFKNLMAILRDVVICYDGTVRNICSNSIIQLKYG----
SbRPE1b         HAICTRETMIR.SSRGLsePGTLFKNLMAILRDVVICYDGTVRNICSNSIIQLKYG----
OsRPE1a         HSICEREKIMR.ASKGLvePGSLFKNMMSRLRDVTACYDGSIRTSSGNLVLQF-------
SbRPE1a         HSISVREKIERsSSKGLaeAGNLFKNMMAMLRDVTVCYDGTMRTSYNNSIVQF-------
ZmRPB1          HAMGGREGLID.TAVKTseTGYIQRRLVKAMEDIMVKYDGTVRNSLGD-VIQFLYGEDGM
AtRPB1          HAMGGREGLID.TAVKTseTGYIQRRLVKAMEDIMVKYDGTVRNSLGD-VIQFLYGEDGM
SmRPD1          HSLSSRKGN-D.GSQQR..CASFFRFLMSYMKDIRVEYDNTIRSTHGGHIFQFSYG----

VvRPD1          STPS...DGINE.DTCAYDMGGQPVGSISACAISEAAYSALDQPISLLEPSPLLNLKRVL
PtRPD1          D-PSgsvDEINNsDGIA----GRPVGPLAACAISEAAYSALDQPISLLEKSPLLNLKNVL
AtRPD1          ----...---ET.DGPVEDITGEALGSLSACALSEAAYSALDQPISLLETSPLLNLKNVL
CpRPD1          ----...-----.-------------------------------------------------
```

```
BdRPD1              --TA...EDIYT.DCGQEGEFGAPVGSWAACSISEAAYGALDHPVNVIEDSPLMNLQEVL
OsRPD1a             --TA...DGMYS.DHDLEGEPGAPVGSWAACSISEAAYGALDHPVNSLEDSPLMNLQEVL
OsRPD1b             --TA...DGMNN.DHDLEGEPGAPVGSWAACSISEAAYGALDHPVNALEDSPLMNLQEVL
ZmRPD1              --SV...DDLVD.------KLGAPVGCRAACSISEAAYGALEHPVNGLEDSPLMNLQEVF
SbRPD1              --SA...DDPVD.------KLGAPVGCWAACSISEAAYGALEHPVNGLEDSPLMNLQEVF
VvRPE1              ----...VKART.KPQHFFPAGEPVGVLAATAMSNPAYKAVLDSSPSSNSSWEL-MKEIL
PtRPE1b             ----...VKVGT.ESQSLFPAGEPVGVLAATAMSNPAYKAVLDSTPSSNCSWDM-MKEIL
PtRPE1a             ----...VKVGA.ESQSLFPAGEPVGVLAATAMSNPAYKAVLDSTPSSNSSWDM-MKEIL
CpRPE1              ----...LKADN.EPLRLFPAGEPVGVLAATAMSNPAYKAVLDSTPSSNSSWEL-MKEIL
AtRPE1              ----...VDSER.GHQGLFEAGEPVGVLAATAMSNPAYKAVLDSSPNSNSSWEL-MKEVL
BdRPE1              ----...EDDAT.DIPSALTPGEPVGVLAATAISNPAYKAVLDASQSNNTSWAS-MKEIL
OsRPE1b             ----...EDDAL.DFPSAIGPGEPVGVLAATAISNPAYKAVLDASQSNNTSWER-MKEIL
ZmRPE1              ----...EDDET.DSSSVVPPGEPVGVLAATAISNPAYKAVLDSSQSNNASWES-MKEIL
SbRPE1b             ----...EDDEA.DSSSAVPPGEPVGVLAATAISNPAYKAVLDSSQSNNASWES-MKEIL
OsRPE1a             ----...--GSR.DASNCVTPGDPVGILAATAVANAAYKAVLAPNQNNIISWDS-MKEVL
SbRPE1a             ----...--DST.NVSSSLTPGDSIGILAATVFANAAYKAVLVPNQKNMTSWDS-MKEVL
ZmRPB1              DAVW...IESQK.LDSLKMKKPEFDNVFRYELDDENWRPNYMLPEHVDDLKTIREFRNVF
AtRPB1              DAVW...IESQK.LDSLKMKKSEFDRTFKYEIDDENWNPTYLSDEHLEDLKGIRELRDVF
SmRPD1              ----...-----.---ATAEPGEPVGLLAGTAVIEPVYDQVMSSSPQASTMLKT-LQNIL

VvRPD1              ECGL..RKSTADRTVSLFLSKKLEKRKH.GFE...Y.GALEVKNHLEKLLFSDIVSTVMI
PtRPD1              ECGL..KRNSAHQTMSLFLSEKLGRQRH.GFE...Y.AALEVQNHLERLLFSDIVSFVRI
AtRPD1              ECGS..KKGQREQTMSLYLSEYLSKKKH.GFE...Y.GSLEIKNHLEKLSFSEIVSTSMI
CpRPD1              ----..----------------------.---...-.-----------------------
BdRPD1              KCQK..GTNSLDHFGLLFLSKNLKKYRY.GFE...Y.ASLYVQNYLEPMDFSELVNTVMI
OsRPD1a             KCHK..GTNSLDHTGLLFLSKHLRKYRY.GFE...Y.ASLEVKDHLERVDFSDMVDT---
OsRPD1b             KCHK..GTKSAVHTGLLFLSKYLKKYRY.GFE...Y.ASLEVKDHLERVDFSDLVDT---
ZmRPD1              KCHK..ATNSGDHIGLLFLSRHLKKYRY.GLE...Y.ASLEVKNHLERVNFSDLVETIMI
SbRPD1              KCHK..ATNSGDHIGLLFLSRHLKKYRY.GLE...Y.ASLEVKNHLEQVNFSDLVETIMI
VvRPE1              LCQVnfKNDLIDRRVILYLNDCDCGRKY.CRE...N.AAYLVKNQLKKASLKDTAVEFMI
PtRPE1b             LCKVgfKNDLADRRVILYLNDCGCGRNY.CQE...R.AAYLVKNHLEKVSLKDIAKCFMI
PtRPE1a             LCKVgfKNDQADRRVILYFNYCGCGREH.CQE...K.AAFLVKNHLEKVSLKDVAKCFMI
CpRPE1              LSKIsfKNDLNDRRVILYLNDCNCARRH.CQE...K.AACLVRNQLNKVTLKDAAVQFLV
AtRPE1              LCKVnfQNTTNDRRVILYLNECHCGKRF.CQE...N.AACTVRNKLNKVSLKDTAVEFLV
BdRPE1              QTKVsyKNDTNDRKVILFLNDCSCPKKF.CKE...K.AAIAVQNRLKRVTLEDCATDICI
OsRPE1b             QTTSryKNDMKDRKVILFLNDCSCAKKF.CKE...K.AAIAVQGCLRRITLEDCATDICI
ZmRPE1              QTRTsyKNDVKDRKVVLFLNDCSCAKKF.CKE...R.AALAVQSCLKRVTLGDCATDICI
SbRPE1b             QTRTsyKNDAKDRKVVLFLSDCSCAKKF.CKE...R.AALAVQSCLKRVTLGDCATDICI
OsRPE1a             LTRAstKADANHRKVILYLNQCSCENE-.CME...-.RALTIRACLRRIKLEDCTTEISI
SbRPE1a             LTNAcsKTGTIDQKAILYLNKCFCGLK-fCSE...-lAAHRVQSCLKRIKLEYCAIEVSI
ZmRPB1              EAEV..QKLEADRYQLGSEITTTGDNSW.PMPvnlK.RLIWNAQKTFKIDFRRPSDMHPM
AtRPB1              DAEY..SKLETDRFQLGTEIATNGDSTW.PLPvniK.RHIWNAQKTFKIDLRKISDMHPV
SmRPD1              FSNS..FKD-IDRCVTLKLQKLPVQPEW.---...-.IALQVQDFLKPVTIGMLASKIWI

VvRPD1              V.......................................................F...
PtRPD1              I.......................................................F...
AtRPD1              I.......................................................F...
CpRPD1              -.......................................................-...
BdRPD1              Q.......................................................Y...
OsRPD1a             -.......................................................-...
OsRPD1b             -.......................................................-...
ZmRPD1              I.......................................................Y...
SbRPD1              I.......................................................Y...
VvRPE1              E.......................................................Y...
PtRPE1b             E.......................................................Y...
PtRPE1a             E.......................................................Y...
CpRPE1              E.......................................................Y...
AtRPE1              E.......................................................Y...
BdRPE1              E.......................................................Y...
OsRPE1b             EdgnwaapagfqhpvpppqckilpvpipipahgsvkfppvpipapehlkynihvvrYqkq
ZmRPE1              E.......................................................H...
SbRPE1b             E.......................................................H...
OsRPE1a             K.......................................................Y...
SbRPE1a             K.......................................................Y...
```

```
ZmRPB1          E.......................................................I...
AtRPB1          E.......................................................I...
SmRPD1          E.......................................................Y...

VvRPD1          SPQNG.............SKTHFSPWV.....CHFHVCE.....EIAKKRSLKPHSII..
PtRPD1          SPQSD.............GRMHFSPWV.....CHFHVYK.....EIVKKRSLKVHYII..
AtRPD1          SPSSN.............TKVPLSPWV.....CHFHISE.....KVLKRKQLSAESVV..
CpRPD1          -----.............---------.....-------.....--------------..
BdRPD1          DGGGV.............QKTKGSPWI.....THFHISK.....EMMKRKRLGLRLLV..
OsRPD1a         -----.............---------.....-------.....ETMKIKRLRLEFIV..
OsRPD1b         -----.............---------.....-------vmillETMKIKRLRLGFIV..
ZmRPD1          DGHDK.............IRNEGM-WT.....THFHINK.....AMMKKKRLGLRFVV..
SbRPD1          DGHDK.............IRKEGT-WT.....THFHISK.....EMMKKKRLGLRFVI..
VvRPE1          VKQHA....vs......gSSEPGTGLV.....GHIHLNK.....LLLQDLNVSMQEVC..
PtRPE1b         KSQ--......qipesfgSD---AGLV.....GHVHLDK.....RKLQDLNITAQVIL..
PtRPE1a         KNQ--......qipesfgSD---AGLV.....GHVHLEK.....RILQELNISAQVIL..
CpRPE1          KNHRT....vs......eGLEIDAGLA.....GHVHLNK.....TLLQVLNIDMQEIL..
AtRPE1          RKQPT....is......eIFGIDSCLH.....GHIHLNK.....TLLQDWNISMQDIH..
BdRPE1          I----....ld......gSSEATPALV.....GHIHLEK.....ARLDMINVSTEDIL..
OsRPE1b         I----g...ld......gTSEAAPALV.....GHIHLDR.....AHLERINISTEDIL..
ZmRPE1          Q----kqinld......gTSEAAPTLV.....GHIHLDK.....GHLERINISTQDIL..
SbRPE1b         Q----kqinld......gTSEAAPTLV.....GHIHLDK.....GQLERINISIQDIL..
OsRPE1a         QQQAT.............--QAAHHLV.....GHIHLDK.....KQLNQIETIMDSVL..
SbRPE1a         QQEAT.............--QAAQCLV.....GHIHLDK.....EQLNWMEITMGNIL..
ZmRPB1          VEAID.............KLQERLKVVpgddaMSIEAQK.....NATLFFNILLRSTFas
AtRPB1          VDAVD.............KLQERLLVVpgddaLSVEAQK.....NATLFFNILLRSTLas
SmRPD1          SPCSEvg...........GQKKRVPWI.....GCFQLRA.....EAMERCSLNIDTIV..

VvRPD1          DALYMKCNSA..RAE...SKI.....NLPDLQI.TSKD.CFV.DM....EKEDSD.CFCI
PtRPD1          DALEKQC---..--K...SKT.....RFPKVQI.TSRY.CTVaDT....WKEKKE.TFCI
AtRPD1          SSLNEQYKSR..NRE...LKL.....DIVDLDIqNTNH.CSS.DD....QAMKDD.NVCI
CpRPD1          ----------..---...---.....-------.--RE.CPI.DD....GPRQED.SFCI
BdRPD1          EDLTEHYNAK..RDQ...LNN.....VIPKVYI.SKCK.CSD.DD....DCINNQ.TCCI
OsRPD1a         REIIDQYNTL..RKQ...LNN.....AIPSVSI.SNSK.CSV.GN....ECVKNQ.TCCV
OsRPD1b         RELIDQYNAL..RKK...LNN.....MIPSVCI.SYSK.CSV.GN....ECVKNR.SCCV
ZmRPD1          DELAKEYDTT..RDQ...LNN.....AIPSIRI.SRRK.CLV.GD....EGVKSS.SCCI
SbRPD1          EELTKEYNAT..RDQ...LKN.....AIPSICI.SRRK.CVV.GD....EGVKIS.ACCI
VvRPE1          QKCEETINSF..RKKk.nVGP.....FFKKIIL.SFRE.CCT.FQh.scQSKGSD.MPCL
PtRPE1b         EKCQETVNTF..RKKk.kVGN.....LFKKTIL.LVSE.SCS.FQ..qc----IDeSPCL
PtRPE1a         EKCQETVNSF..RKKk.kVGN.....LFKKTTL.SISE.CCS.FE..qc----TDeLLCL
CpRPE1          QQCRERISLF..RKKk.kVGH.....CFKKIIL.SVSK.CCS.FQq.scEENSSD.LPCL
AtRPE1          QKCEDVINSLgqKKKk.kATD.....DFKRTSL.SVSE.CCS.FRd.pcGSKGSD.MPCL
BdRPE1          QKCQEVSLKH..GKKkghLGH.....LFKKITF.STCD.CSF.TQkpmiDGKLPK.VPCL
OsRPE1b         QKCQEVSGKY..GKKkghLSN.....LFKNITF.STCD.CLF.TQk.lvDGKLPK.LPCL
ZmRPE1          QKCQEVSGRF..GKKkghLCH.....IFKKITF.ATCD.CSF.TQmp.iDGKLHK.VPCV
SbRPE1b         QKCQEVSGRY..GKKkghLCH.....LLKKITF.ATC-.---.--....-GKLHK.VPCV
OsRPE1a         HKCQETFRNN..IKKkgsMRE.....ILKTVTF.ISST.SLC.DQh.tdDDKKFQ.VSCL
SbRPE1a         QTCQK----N..VNKh.vMKNrqlmqILKTTEI.ISSEyCLC.GQd.igDERALQ.VSCL
ZmRPB1          KRVLKEYRLT..KEA...FEW.....VIGEIES.RFLQ.SLV.AP....GEM---.IGCV
AtRPB1          KRVLEEYKLS..REA...FEW.....VIGEIES.RFLQ.SLV.AP....GEM---.IGCV
SmRPD1          CHLRKLLPTS..LDD...PDA.....FIQGLHF.FSRD.VEV.LC....------.FFPI

VvRPD1          TVSIVN.S....KK..SCIQ..LDTVRDLVI.....PFLLGAVVKGLLD.VKKVDILWND
PtRPD1          TVTIVEtS....KN..EFIE..LETIQDLMI.....PFLLETVIKGFME.IQKVDILWND
AtRPD1          TVTVVEaS....KH..SVLE..LDAIRLVLI.....PFLLDSPVKGDQG.IKKVNILWTD
CpRPD1          SVTVVKkS....KD..SSVQ..LDTVRGLVM.....PFLLRAVIKGFPE.IKKVDILWKD
BdRPD1          TVVAQD.E....SNstSTSQ..LDDLKKRAI.....PVLLATPVKGFLE.FKDVEI----
OsRPD1a         TMVVQV.E....IN..SMSQ..LDVIKERVI.....PSILATLLKGFLE.FKNVKV----
OsRPD1b         TMVAQV.E....SN..STSQ..LDIIKERVI.....PSILATLLKGFLE.FENVKV----
ZmRPD1          AVVAHA.E....RN..SISQ..LDTIKTRVI.....PSILDTLLKGFLE.FKDVEI----
SbRPD1          AVVALA.E....PN..SMSQ..LDTIKKRVI.....PIILDTLLKGFLE.FKDVEI----
VvRPE1          LFFWQG.N....RD..DNLEqiLHILAHKIC.....PVLLQTIIKGDSR.VCTVNIIWIS
PtRPE1b         MFFWQG.A....DD..VHLErtSNILADMIC.....PVLLETIIKGDHR.ISCANIIWAT
PtRPE1a         MFFWQD.A....ND..VHLErtSNILADMIC.....PVLLETTIKGDHR.ISCANIIWAS
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CpRPE1          IFCWHD.T....SD..IHLErtSYVLANMIY.....PVLLETVIKGDPR.ICSANIIWAS
AtRPE1          TFSY-N.A....TD..PDLErtLDVLCNTVY.....PVLLEIVIKGDSR.ICSANIIWNS
BdRPE1          QFSFSE.Di.pmLS..ESVEraVSVLANSLCds..aTIFWSICSAGDPR.IQEAKIMWVG
OsRPE1b         QF-FVS.Dn.miVS..ESVEraVSVLADSLCgvllnTII-----KGDPR.IQEAKIVWVG
ZmRPE1          QFAFSD.D..ivLS..ESIEraVNVIADSVC.....SVLLDTIIKGDPR.IQAAKVIWVE
SbRPE1b         QFSFSD.E.stvLS..ESVEraVNVIADSVC.....SVLLDTIIKGDPR.IQAAKVIWVE
OsRPE1a         QFFLPG.SitknIS..ESTErvIDFMTNAIF.....PIILDTVIKGDPR.VEEANLVRIE
SbRPE1a         QCFIHA.StttvQP..ESN-.vIQMMTNTIF.....PILLDTVIKGDPQ.VQEAKLIWVE
ZmRPB1          AAQSIG.E....PA..TQMT..LNTFHYAGV.....SA--KNVTLGVPR.LR--EIINVA
AtRPB1          PAQSIG.E....PA..TQMT..LNTFHYAGV.....SA--KNVTLGVPR.LR--EIINVA
SmRPD1          TSSVSN.Y....DS..KQIH..KHMI-GTMF.....GNLLQVVVKGCPRgIEFVNVKWED

VvRPD1          NPDS....DVLKSSS...GRLYLRVYVSGD..CGKKNFWGVLMDACLQIMDMIDWERSHP
PtRPD1          KP--....KIPKSHNrlrGELFLRVHMSRG..SDKTRLWNQLMDDCLSIMDLIDWARSHP
AtRPD1          RPKA....PKRNGNHla.GELYLKVTMYGD..RGKRNCWTALLETCLPIMDMIDWGRSHP
CpRPD1          RPKL....SKSYDSR...GELYLRVSMSEE..HGTRTSWNALMDGCLPIMDMIDWARSYP
BdRPD1          ----....--QCQRD...NELVVKVNMSKH..CKSGIFWTTLKKACIGIMGLIDWERSRP
OsRPD1a         ----....--QCQED...NELVLKVGMSEH..CKSGKFWATLQNACIPIMELIDWERSRP
OsRPD1b         ----....--ECQQD...SELVVKVGMSEH..CKTGKFWATLQNACIPIMELIDWERSRP
ZmRPD1          ----....--QCPHD...GELLVKVCMSEH..CKGGRFWPTLQNACIPVMELIDWELSQP
SbRPD1          ----....--QCQHD...GELLVKVCMSHH..CKGGRFWATLQNACIPVMELIDWELSRP
VvRPE1          PDTTtwirNPCKSRK...GELALDIVLEKAavKQRGDAWRIVLDACLPVLHLIDTRRSIP
PtRPE1b         PETNtwirNPSRTQK...GELALDIVLEKSvvKKSGDAWRIVLDSCLPVLHLINTTRSIP
PtRPE1a         QETTtwirNPSRTQK...GELALDIVLEKSvvKQSGDAWRIVLDSCLPVLHLIDTTRSVP
CpRPE1          PDTMtwirKPSRTRK...GEWVLDVVVEKSmvKRSGDAWRIVMDSCLPVFHLIDSRRSIP
AtRPE1          SDMTtwirNRHASRR...GEWVLDVTVEKSavKQSGDAWRVVIDSCLSVLHLIDTKRSIP
BdRPE1          SDAQswvkNTRKVSK...GEPTVEIVVEKNeaSKQGDAWRIAMDACIPVIDLIDTRRSIP
OsRPE1b         SDATswvkNTQKASK...GEPAVEIIVEEEeaLHIGDAWRTTMDACIPVLNLIDIRRSIP
ZmRPE1          SDAAswvkHTRKVSK...GESALEIIVEKDdaVSNGDAWRTAIDACLPVLNLIDTRRSIP
SbRPE1b         SDATawvkNTRKVSK...GEPALEIIVEKDhaVSNGDAWRTTIDACLPVLDLIDTRRSIP
OsRPE1a         PESTfwvqSSGAEQK...GEAALEITVEEAaaAESGNAWGVAMNACIPVMDLIDTTRSMP
SbRPE1a         PKLTrwvkNSSAEQK...GELAVEITVEKIaaAENGGTWGVVMDACVPVMDLIDTTRSAP
ZmRPB1          KKIK....TPS----..----LSVYLKPQ..VNQKKELAKNVQCALEYTTL----RSVT
AtRPB1          KRIK....TPS----..----LSVYLTPE..ASKSKEGAKTVQCALEYTTL----RSVT
SmRPD1          ----...-------...-ELCIEVAFL-S..RTRGVPWTHALEACGSISHLVDWQKSTP

VvRPD1          DNIHDIFVVYGIDAGWKYF............LNSLKSAISDIGKTVLPEHLLLVASCL.
PtRPD1          DNIHECCLAYGIDAGWKFF............LNNLQSAMSDVGKTVLPEHLLLVANCL.
AtRPD1          DNIRQCCSVYGIDAGRSIF............VANLESAVSDTGKEILREHLLLVADSL.
CpRPD1          DNIHHFCSANGIDAGWKLF............LNNLDSAISDVGKTILPEHLLLIANCL.
BdRPD1          GSVYDIFCPCGIDSAWKYF............VESLRSKTDDIGRNIHREHLLVVADTL.
OsRPD1a         ERVYDNFCSYGIDSAWKFF............VESVRSTTDAIGRNIHRQHLLVVADCLs
OsRPD1b         ERVYDIFCSYGIDSAWKYF............VESLRSTTDAIGRNIHRQHLLVVADCLs
ZmRPD1          SNVSDIFCSYGIDSAWKYF............VESLKSATTDTGRNIRREHLLVIADSL.
SbRPD1          SNVADIFCSYGIDSAWKYF............VESLKSATTDIGRNIRREHLLVIADSM.
VvRPE1          YAIKQVQELLGISCAFDQA............VQRLSKSVTMVAKGVLKEHLILLANSM.
PtRPE1b         YAIKQVQELLGVSCAFDTA............VQRLSKSVTMVAKGVLKEHLILLGNSM.
PtRPE1a         YAIKQVQELLGVSCAFDQA............VQRLSKSVTMVAKGVLKEHLILLGNSM.
CpRPE1          YSTKQVQELLGISCAFDQA............VQRLSTSVAMVAKGVLREHLILLANSM.
AtRPE1          YSVKQVQELLGLSCAFEQA............VQRLSASVRMVSKGVLKEHIILLANNM.
BdRPE1          YGIQQVRELLGISCSFDQI............VQRLSTTMKTVAKGILKDHLILVANSM.
OsRPE1b         YGIQQVRELLGISCAFDQV............VQRLSTTVRMVAKDVLKDHLVLVANSM.
ZmRPE1          YGIQQVRELIGISCAFDQV............VQRLSTTVKMVNKGVLKDHLILVANSM.
SbRPE1b         YGIQQVKELIGISCAFDQV............VQRLSSTVKMVNKGVLKDHLILVANSM.
OsRPE1a         YDIQQVRQVFGISSAFEKVtqvqlfpflllaeIQYLSKSVGMITKSVLQEHLTTVASSM.
SbRPE1a         CNIQEVQKVFGISSVFDRV............VQHLSKAVGMVTKSVLMEHLITVASSM.
ZmRPB1          HATEIWYDPDPLGTIIEED............TEFVQSYYEMPDEDIDPDKISPWLLRI.
AtRPB1          QATEVWYDPDPMSTIIEED............FEFVRSYYEMPDEDVSPDKISPWLLRI.
SmRPD1          LSIQEVHVAFGIEAAYQYL............LEKLKEFTK--GSGVLRK---PWKN--.

VvRPD1          ......................SATGEFVGLNAKGMARQKELTSISSPFMQGCFSSPGS
PtRPD1          ......................SVTGEFVGLNAKGLKRQREHASVSTPFVQACFSNPGD
AtRPD1          ......................SVTGEFVALNAKGWSKQRQVESTPAPFTQACFSSPSQ
CpRPD1          ......................SATGEFVGLSSRGLAQQRKHASVVSPFTQACFSNPST
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BdRPD1          .......................SPH----------------------------------
OsRPD1a         vsgqfhglssqglkqqrtwlsisSPF----------------------------------
OsRPD1b         isgqfhglssqglkqqrawlsisSPF----------------------------------
ZmRPD1          .......................SVT----------------------------------
SbRPD1          .......................SVT----------------------------------
VvRPE1          .......................TCAGNLIGFNSGGYKALSRALNLQVPFTEATLFTPRK
PtRPE1b         .......................TCAGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRK
PtRPE1a         .......................TCAGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRK
CpRPE1          .......................TCAGNLVGFNPGGYKAISRSLNIQAPFMEATLFTPRK
AtRPE1          .......................TCSGTMLGFNSGGYKALTRSLNIKAPFTEATLIAPRK
BdRPE1          .......................TCTGNLYGFNTGGYRATFRALKVQVPFTESTLFTPMK
OsRPE1b         .......................TFTGNLNGFNNAGYKATFRSLKVQVPFTESTLITPMK
ZmRPE1          .......................TCTGNLIGFNIAGYKATFRSLKVQVPFTESTLFTPMK
SbRPE1b         .......................TCTGSLIGFNIAGYKATFRSLKVQVPFTESTLFTPMK
OsRPE1a         .......................TCTGDLHGFNNSGYKATCQSLKVQAPFMEATLSRSIQ
SbRPE1a         .......................TCTGSLHGFNRSGSKATFQSLKVQAPFTEATLSRPMQ
ZmRPB1          .......................ELNREMMVDKKLSMADIAEKINREFDDDLSCIFND--
AtRPB1          .......................ELNREMMVDKKLSMADIAEKINLEFDDDLTCIFND--
SmRPD1          .......................------IDANESGYEAFVKNLSGCSPLAFAMGKSPGG

VvRPD1          CFIKAGKRAVADNLHGSLDALAWGKIPSVGSGGHFDILYSAKGH................
PtRPD1          CFIRAAKAGVVDDLQGSIDALAWGKVPAIGT-GQFDIVYSGKGL................
AtRPD1          CFLKAAKEGVRDDLQGSIDALAWGKVPGFGTGDQFEIIISPKVH................
CpRPD1          CFVKAAKAGVTDDLQGSIDALAWGKPPCFGTGGQFDIIYS----................
BdRPD1          --------------------------------------------................
OsRPD1a         --------------------------------------------seacfsrpahsfinaa
OsRPD1b         --------------------------------------------seacfsrpaysfinaa
ZmRPD1          --------------------------------------------gqfhalssqglkqqrt
SbRPD1          --------------------------------------------gqfhaisshglkqqrt
VvRPE1          CFEKASEKCHTDSLSSIVASCSWGKHVTVGTGSRFDVLWDTKEI................
PtRPE1b         CFEKAAEKCHTDSLSSIVASCAWGKHVTVGTGSHFDVLWDTKEA................
PtRPE1a         CFEKAAEKCHTDYLSSIVASCSWGKHVTVGTGSRFDVLWDTKEA................
CpRPE1          CFERAAEKCHTDSLSSVVGSCSWGKNVAVGTGSRFDVLWDTKEA................
AtRPE1          CFEKAAEKCHTDSLSTVVGSCSWGKRVDVGTGSQFELLWNQKET................
BdRPE1          CFEKAAEKCHSDALGCVVSSCSWGKHAALGTGSSFQILWNENQV................
OsRPE1b         CFEKAAEKCHSDSLGCVVSSCSWGKHAASGTGSSFQILWNESQL................
ZmRPE1          CFEKAAEKCDSDSLGCVVSSSAWGKHAAVGTGSSFQILWNENQL................
SbRPE1b         CFEKAAEKCDSDSLGCVVSSSSWGKHAAVGTGSSFQILWNENQL................
OsRPE1a         CFEKAAAKAYSDQLGNVVSACSWGNNAEIGTGSAFEILWNDENM................
SbRPE1a         CFRKSAEKVDSDQLDSVVSTCSWGNHAAIGTGSAFKIHWNDENQ................
ZmRPB1          ------DNADKLILRIRITNDEAPKGEIQDESAEDDVFLKKIEG................
AtRPB1          ------DNAQKLILRIRIMNDEGPKGELQDESAEDDVFLKKIES................
SmRPD1          VFEAAAMNREVDYLAGANELAFCGKSPSLGTGANIELFFKEDKG................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
BdRPD1          ............................................................
OsRPD1a         krdsvdnlsgtldaiawgk.........................................
OsRPD1b         krdsvdnlsgaldaiawgk.........................................
ZmRPD1          rlsisspfseacfsrpaqsfinaakqcsvdnlcgsldavawgkepfngtsgpfeimhsgk
SbRPD1          rlsisspfseacfsrpaqsfidaakqcsvdnlcgsldaiawgkepfngtsgpfeimhsgk
VvRPE1          ............................................................
PtRPE1b         ............................................................
PtRPE1a         ............................................................
CpRPE1          ............................................................
AtRPE1          ............................................................
BdRPE1          ............................................................
OsRPE1b         ............................................................
ZmRPE1          ............................................................
SbRPE1b         ............................................................
OsRPE1a         ............................................................
SbRPE1a         ............................................................
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ZmRPB1        ............................................................
AtRPB1        ............................................................
SmRPD1        ............................................................

VvRPD1        ..ELA...................RP....EDIYKLL.GSQTSCHEQN.....LKVKVPI
PtRPD1        ..EFS...................KP....VDVYNLL.GSQMISTEQNtefgvLDAQI--
AtRPD1        ..GFT...................TP....VDVYDLL.SSTKTMRRTN.....SAPKSDK
CpRPD1        ..--W...................RP....VDVYDLL.NSIVTPLKQN.....VKSDLPN
BdRPD1        ..EPV...................QN....ENIYGFLhNPEVWGPEKN.....HMETDST
OsRPD1a       ..EPCagssgpfkilysgkshetkQN....EHIYDFLhNPEVQALEKN.....VMDTYRK
OsRPD1b       ..EPCagtsgpfkvlysgksqktkQN....KNIYDFLhNPEVQALEKN.....FMDTYKQ
ZmRPD1        phEPE...................QN....ESIYDFLcSSKVRNFEKN.....HLDTRRQ
SbRPD1        phEPE...................QD....ESIYDFLrSPKVQNVEKN.....HLDTRRQ
VvRPE1        ..GPA...................QD..ggIDIYSFL.HLVRSGS--Y.....GKEPDTA
PtRPE1b       ..CLN...................PE..gsMDVYSFL.NMVRSTA--G.....GEESVTA
PtRPE1a       ..CLN...................PE..ggIDAYSFL.NMVRSTA--G.....GEESVTA
CpRPE1        ..RFN...................EG..gkLDVYTFL.HMVRSSS--H.....GEDLSTA
AtRPE1        ..GLD...................DK..eeTDVYSFL.QMVISTT--N.....ADAFVSS
BdRPE1        ..NCN...................KE..ygDGLYDFL.AMVRT-----.....DQEKARY
OsRPE1b       ..KSN...................KE..ygDGLYDYL.ALVRT-----.....DEEKARY
ZmRPE1        ..KSN...................KE..ygDGLYDFL.ALVRT-----.....DQEKTDY
SbRPE1b       ..KSN...................KD..ygDGLYDFL.ALVRT-----.....DQEKTGY
OsRPE1a       ..SSS...................KSilggYGLYDFL.EAVETTG--A.....TKDKAIV
SbRPE1a       ..SAS...................NEilreYNLYDFL.EAVGRIG--A.....TEQKTDA
ZmRPB1        ..NML...................TEmal.RGIPDIN.KVFIKEGKVN.....TFYQDDG
AtRPB1        ..NML...................TEmal.RGIPDIN.KVFIKQVRKS.....RFDEEGG
SmRPD1        ..PVS...................R-....--FPDFE.SLVFS--RRV.....VDDTVSA

VvRPD1        TCYQTTTKC.....GA....QL.VYANGDSASKGC......KSLEKISKSVLRSFLSLND
PtRPD1        --YK-SDKC.....GA....QF.LHKFGGCGPKGF......KVKEGIPRSFLRRLLTYDD
AtRPD1        ATVQPFGLL.....HS....AF.LKDIKVLDGKG-......-----IPMSLLRTIFTWKN
CpRPD1        SMNIKSDKY.....GD....RS.IYVHSGSISLGL......KKLEGISRAYLRTVLTWKD
BdRPD1        RTKNASERW.....SS....GN.ATFNGGTISVEQ......NYLGA-------KVGVWDS
OsRPD1a       RTEKTSKRR.....SAlnseGN.ATINGGAISFNQ......KFLNA-------KVGIWEN
OsRPD1b       RTEKPSKQR.....SAfsskGN.ATINGGTISVNQ......KFLDS-------KVGIWEN
ZmRPD1        STENASICRlacksSK....GS.TTVNGVAITIDQ......DFLHA-------KVSIWDN
SbRPD1        STENASICRlack.SK....GS.ATVNGVAITSDQ......DFLHA-------KVSIWDN
VvRPE1        CLGAEVEDL.....IL....ED.ENLELGMSPEHS......SNFEK---------PVFED
PtRPE1b       CLGAEVDDL.....ML....ED.EDWNL--SPEHN......SSSDK---------PTFED
PtRPE1a       CLGAEVDDL.....IL....ED.EDWNL--SPEHH......SSSDK---------PTFED
CpRPE1        CLGEEIDDL.....VP....DE.ETFDWSPSPEHY......STSGK---------PVFED
AtRPE1        PGFD-----.....VT....EE.EMAEWAESPERD......SALGE---------PKFED
BdRPE1        TFLDDVDYL.....VE....DN.AMDDICLSPELN......GTHGV---------PTFED
OsRPE1b       TFFDDVDYL.....AE....ENeA--DVCLSPELD......GTIGQ---------PIFDD
ZmRPE1        MFLDDVDYL.....VE....EN.AADDMCLSPEPD......GTLGK---------PTFED
SbRPE1b       MFLDDVDYL.....LE....EN.AIDDMCLSPEPD......GTVGK---------PTFED
OsRPE1a       P--------.....-H....NY.CLYDVDCIPEDK......VCLEE--------------
SbRPE1a       P--------.....-H....SL.CLYDVGQLPEDEvqedevVCFGG--------------
ZmRPB1        FKAANEWML.....DT....EG.VNLLAVMCHEDV......DATRTTSNHLIEVIEVLGI
AtRPB1        FKTSEEWML.....DT....EG.VNLLAVMCHEDV......DPKRTTSNHLIEIIEVLGI
SmRPD1        TLSAKDREI.....--....--.------------......---------------VWAR

VvRPD1        IQKLSRRLKFIL...........................QKYPIN.HQLS....EI....
PtRPD1        IQRMSYTVRKIL...........................NKYSVD.QQLN....ES....
AtRPD1        IELLSQSLKRIL...........................HSYEIN.ELLN....ER....
CpRPD1        IQKLYHASKKIL...........................NKYPID.HRLN....EG....
BdRPD1        IIDMRTCLQNML...........................REYQLD.EYVV....EL....
OsRPD1a       IIDMRTSLQNML...........................REYTLN.EVVT....EQ....
OsRPD1b       IIDMRTCLQNML...........................REYTLN.EVVT....EQ....
ZmRPD1        IIDMRTSLQNML...........................REYPLN.GYVA....EP....
SbRPD1        IIDMRASLQNML...........................REYPLN.GYVM....EP....
VvRPE1        SAEFQNTWENHVpg.........................SGGDWA.VNQN....KE....
PtRPE1b       SAEFQDFLGNQ-paesnwekisslkdrsr..........SSGNWD.VDKNdgavKEkpws
PtRPE1a       SAEFQDFLGNQ-paesnwgkasslkdgsw..........SAGNWD.VDKNdsagKEkpws
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CpRPE1         GEDILENLETQ-.p.........................TKPSWE.HLNN....--....
AtRPE1         SADFQNLHDEGKpsganwekssswdngcsggsewgvsksTGGEAN.PESN....WE....
BdRPE1         NFEHQDTQNGNSwe.........................NGTKAN.ASWE....QN....
OsRPE1b        NLEEQDVQNNSSwd.........................NGTTTN.ASWE....QN....
ZmRPE1         NFEEQNIQKGSSwe.........................IGITTN.SSWE....QN....
SbRPE1b        NFEEQNIQKGSSwe.........................NGITMK.SSWE....QD....
OsRPE1a        ------------...........................------.----....--....
SbRPE1a        ------------...........................------.----....--....
ZmRPB1         EAVRRSLLDELR...........................VVISFDgSYVN....YR....
AtRPB1         EAVRRALLDELR...........................VVISFDgSYVN....YR....
SmRPD1         IDQRSQKLHDIL...........................RKSLTG.TPVS....AA....

VvRPD1         ................DKTTLMM.ALYF............HPRRDEKIGPGAQN....IK
PtRPD1         ................DKSVLMM.TLYF............HPRRDEKIGIGAKD....IK
AtRPD1         ................DEGLVKM.VLQL............HPNSVEKIGPGVKG....IR
CpRPD1         ................EKKILMM.ALYF............HPQSYEKIGTGAQY....IK
BdRPD1         ................DKSRVIE.ALRF............HPRGREKIGVGIRD....IK
OsRPD1a        ................DKSCLME.ALKF............HPRGYDKIGVGIRE....IK
OsRPD1b        ................DKSCLIE.ALKF............HPRGYDKIGVGIRE....IK
ZmRPD1         ................DKSQLIE.ALKF............HSRGAEKIGVGVRE....IK
SbRPD1         ................DKSKLIE.ALKF............HPRGAEKIGVGVRE....IK
VvRPE1         ................TTASTLK.PSAW............SSWGTDKVTM----....KD
PtRPE1b        lgmntaeandvassgwDTAAARTtNNSWnsennvaqsnsfSGWATKKPEP----....HN
PtRPE1a        lgmssaetndv...gwDTAATRKiNSSWnsendvtqsnslSGWATKKSET----....HN
CpRPE1         ................GRADLQK.QSSW............SSWSTDRAHS----....QD
AtRPE1         ................KTTNVEK.EDAW............SSWNTRKDAQ----....ES
BdRPE1         ................ASAG-ND.SDNW............GGWSNAAAAA----dtgaAK
OsRPE1b        ................GSAG-ND.SDKW............GGWNDAAAGA----dtgvTK
ZmRPE1         ................ASVA-ND.SGDW............GGWSSGGGAA----....AK
SbRPE1b        ................ASAA-ND.SGDW............GGWSSGGGAS----....AK
OsRPE1a        ................-----NN.QITW............--------------....--
SbRPE1a        ................-----TS.PISW............--------------....--
ZmRPB1         ................HLAILCD.TMTY............RGHLMAITRHGINR....ND
AtRPB1         ................HLAILCD.TMTY............RGHLMAITRHGINR....ND
SmRPD1         ................NEAVILD.TLKY............HPMMDSKVGCGVRH....IR

VvRPD1         VRYHSKYHNTRCFSL...........VRTD..............................
PtRPD1         VINHPEYQDTRCFSL...........VRTD..............................
AtRPD1         VA-KSKHGDSCCFEV...........VRID..............................
CpRPD1         VLKTE----------...........----..............................
BdRPD1         ---------------...........----..............................
OsRPD1a        ---------------...........----..............................
OsRPD1b        ---------------...........----..............................
ZmRPD1         ---------------...........----..............................
SbRPD1         ---------------...........----..............................
VvRPE1         TFSTREPDESSRSAG...........WDDK..............................
PtRPE1b        GFATKVQEEPTTSND...........WDAG..............................
PtRPE1a        GFATKVQEKPARSND...........WDVG..............................
CpRPE1         VCSTKTLEECLNSAGgtgvigsdktnLDSQ..............................
AtRPE1         SKSDSGGAWGIKTKD...........ADAD..............................
BdRPE1         PADQGNSSWDVPATA...........ENDS..............................
OsRPE1b        PANQGNSCWDVPATV...........EKSS..............................
ZmRPE1         PADQDNS-WEVHAKV...........QDNSt.............................
SbRPE1b        PADQDNS-WEVHAKV...........QDNStdwggwssgvgaaakpadqdnswevhakaq
OsRPE1a        ---------------...........----..............................
SbRPE1a        ---------------...........----..............................
ZmRPB1         TGPLMRCSFEETVDI...........LLDA..............................
AtRPB1         TGPLMRCSFEETVDI...........LLDA..............................
SmRPD1         VDNHHSF-GGRCFHI...........VRLD..............................

VvRPD1         ...GTEEDFSYHKCVHGALEIIDPRRARSYQSRWLPYSEV....................
PtRPD1         ...GTIEDFSYRKCLHNALEIIAPQRAKRYCEKYLT-SKVsatdnsgctdlpldn.....
AtRPD1         ...GTFEDFSYHKCVLGATKIIAPKKMNFYKSKYLKNGTLesggfsenp...........
CpRPD1         ...-------------------------------------....................
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BdRPD1              ...-------------------------------------....................
OsRPD1a             ...-------------------------------------igvnpghpssrcfivlrndd
OsRPD1b             ...-------------------------------------igvnpghpnsrcfivqrsdd
ZmRPD1              ...-------------------------------------iglnpshpgtrcfillrndd
SbRPD1              ...-------------------------------------vglnpnhpgtrcfillrndd
VvRPE1              ...GTWGTDKAQNTAFRRTHEDSPRSSGRDETFRDGRPQF.a.....ss...........
PtRPE1b             ...AAWGRKDRDN-------------------------KF.aetnasks...........
PtRPE1a             ...TAWGRKAGDN-------------------------KF.a..nvtks...........
CpRPE1              ...NTWANWNTKGSYPTKASEDSPKSCGWVADKCGSGETN.a.....kg...........
AtRPE1              ...TTPNWETSPAPKDSIVPENNEPTSDVWGHKSVSDKSW.d.....kk...........
BdRPE1              ...TDWGGWGNEKAKDNRTVSTEPAELDTWSDRGAKKGTDgg.....gg...........
OsRPE1b             ...SDWGGWGTEKAKEKEKISEEPAQHDAWSVQGPKRATD.g.....ga...........
ZmRPE1              ...TDWGGWSVEKPTGEATVSGEPAETDTWADKGAKMESDag.....dg...........
SbRPE1b             dncTDWGGWSTDKPTGEATVSGQPAEMDTWADKGTKMESGag.....da...........
OsRPE1a             ...-------TDKPKAEFLMESEGRRAGMHSTGQKHPRKP....................
SbRPE1a             ...-------TDKPKGDSLLHDFMGRAGMWSTVQKH----.........qemqnktkwns
ZmRPB1              ...AVYAESDHLRGVTENIMLGQLAPIGTGGCALYLNDQMlqqaielqlpsyvegldfgm
AtRPB1              ...AAYAETDCLRGVTENIMLGQLAPIGTGDCELYLNDEMlknaielqlpsymdglefgm
SmRPD1              ...GSVEDFSYHKCLLERIKGNTVLVQRYKKKFMGGKNGRkeevpveifsqkndtgrmyd

VvRPD1              ............................................................
PtRPD1              ............................................................
AtRPD1              ............................................................
CpRPD1              ............................................................
BdRPD1              ............................................................
OsRPD1a             ttadfsynkcvlgaansispelg.....................................
OsRPD1b             tsadfsynkcvlgaansispelgsyiekilsnrairphql....................
ZmRPD1              ttedfsyhkcvqggaadsispqlgsylkklyyra..........................
SbRPD1              ttedfsyhkcvhgaansispqlgsylkklyhra..........................
VvRPE1              ..awg..kkid.eadktgw............nk...n...............dgkpqmdk
PtRPE1b             ..wwg..kvtd..gdesgq............nk...sknkrpedqdvgthgwd.....dk
PtRPE1a             ..wwg..kvtd..gdeseq............nk...nkqhq.edqelgthgwd.....dk
CpRPE1              ..ehn..wsnw.tavkggs............qd...f...............tatktwee
AtRPE1              ..nwg..tesa.paawgst............da...avwgs...........sdkknset
BdRPE1              ..swg..kqtn.tcedsgt............nl...e...............rnswakrp
OsRPE1b             ..swk..kqss.t...............................................
ZmRPE1              ..nwe..ksst.peaskkn............ds...s...............entwdkrk
SbRPE1b             ..nwek.ksst.peasnkn............dpwgks...............entwdkrk
OsRPE1a             ..nwhegntks.spnstav............ef...t...............gqvfqrrq
SbRPE1a             vanwk..ndkpmgpprtafaeststrgqnkrqf...t...............gqvyarkq
ZmRPB1              tparspitgtpyhegmmspsyllspniraspintdasfspyvghmafspfpspggyspss
AtRPB1              tparspvsgtpyhegmmspnyllspnmrlspm.sdaqfspyvggmafspsssp.......
SmRPD1              kkthgfllvenhfvpvktlkkt......................................

VvRPD1              ............................................................
PtRPD1              ............................................................
AtRPD1              ............................................................
CpRPD1              ............................................................
BdRPD1              ............................................................
OsRPD1a             ............................................................
OsRPD1b             ............................................................
ZmRPD1              ............................................................
SbRPD1              ............................................................
VvRPE1              ....lresyd.....wdckvaqekttqs................................
PtRPE1b             ....m..sqdqsisgwaskttqeattes........lg......................
PtRPE1a             ....m..spdqlisgwastttqeattescsskaasvwgtkntnvdeqqsenhvllnqake
CpRPE1              ....sskagg.....wgskksgngesnv................................
AtRPE1              ....esdaaa.....wgsrdknnsdvgsgagvlgpwnkkssetesnga............
BdRPE1              ...sspslst.....wakknsdggdgtwdk..q...........................
OsRPE1b             ..................qn....dg..................................
ZmRPE1              ...gdggdga.....wgnr.sddghgnwehpsn...........................
SbRPE1b             gdggdggdga.....wekk.svdghgnwdhpgn...........................
OsRPE1a             ....lktksn.....wnsdatqqddkps................................
SbRPE1a             ......pkhs.....wsqaathqnnkls................................
```

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ZmRPB1            ggyspsspvftpekgysplspsyspaspsysptspsytpgsptysptspnysptsptysp
AtRPB1            .gyspssp......gysptspgysptspgysptspg.......ysptsptyspsspgysp
SmRPD1            ............................................................

VvRPD1            ............................................................
PtRPD1            ............................................................
AtRPD1            ............................................................
CpRPD1            ............................................................
BdRPD1            ............................................................
OsRPD1a           ............................................................
OsRPD1b           ............................................................
ZmRPD1            ............................................................
SbRPD1            ............................................................
VvRPE1            ...............tyg.......gissttgd..wkk.n........elqmevvqhdes
PtRPE1b           ...wdskgnsnpgdaacgwkaastwgaentdgdklwgk..............ev......
PtRPE1a           ssdwnkksnsnqtdaacgskaasswgakntdadkrwgr..............kv......
CpRPE1            ...............geg.......spwsnwkt..nkg.n........sqgthpqkaqee
AtRPE1            ...............twg.......ssdktksg..aaawn........swdkknietdse
BdRPE1            ...............ans.......ckknveqd..swk.nmpvsparnawnkkessrgda
OsRPE1b           ................................n..swk.e..........nk...grg..
ZmRPE1            ...............wng.......qsldvdqd..twg.n........argkkkadgnyc
SbRPE1b           ...............wng.......qslnvdqd..twg.n........argkkkadgn.c
OsRPE1a           ...............wys.......snsagtqn..fti.a........gssr........
SbRPE1a           ...............wcg.......envagaqd..fan.a........essk........
ZmRPB1            tspsysptspsysptspsysptspsysptspsysptspsysptspvysptspaysptspa
AtRPB1            tspaysptspsysptspsysptspsysptspsysptspsysptspsysptspaysptspa
SmRPD1            ............................................................

VvRPD1            ............................................................
PtRPD1            ............................................................
AtRPD1            ............................................................
CpRPD1            ............................................................
BdRPD1            ............................................................
OsRPD1a           ............................................................
OsRPD1b           ............................................................
ZmRPD1            ............................................................
SbRPD1            ............................................................
VvRPE1            pvnehswdanl...pedplaqattsvgwdsstgk........dw................
PtRPE1b           .......ssn..........qadtasgw....gkpkspeislgwg...............
PtRPE1a           .......dln..........qadtscsw....grsktpd..rgwglsnyggsngsemenk
CpRPE1            ssdfggwgsnkfsrcetnlkeqstwskwnsnkgd........nq................
AtRPE1            paawgsqgkkn...setesgpa.awgawdkkkse........te................
BdRPE1            twemrastlee...kktsesnegsweksnaqkdsw..g....nt................
OsRPE1b           ...................snggswekdnaqkgswgrg....n.................
ZmRPE1            qweeqpsnykq...kktnadhdssynnvmpsseia..w....na................
SbRPE1b           qweeqpstyrr...kktnadhnssynnvmpssdna..w....na................
OsRPE1a           .....................pgewnrknnnrgq........gg................
SbRPE1a           ......................ggwnrknsgfgr........gg................
ZmRPB1            ysptspsysptspsysptspsysptspsysptspsysptspsysptspaysptspgyspt
AtRPB1            ysptspaysptspsysptspsysptspsysptspsysptspsysptspaysptspgyspt
SmRPD1            ............................................................

VvRPD1            ............................................................
PtRPD1            ............................................................
AtRPD1            ............................................................
CpRPD1            ............................................................
BdRPD1            ............................................................
OsRPD1a           ............................................................
OsRPD1b           ............................................................
ZmRPD1            ............................................................
SbRPD1            ............................................................
VvRPE1            .........tkrklqspseqqrdp...ai...............................
PtRPE1b           ....s....tk.......e........sv...............................
PtRPE1a           tenqslldrgk.......e........svgwggkntdadkpwsnkvnsnqadtasgwgks
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CpRPE1          .........dayatmlenndndtg...ke...............................
AtRPE1          .........pgpagwgmgdkknse...te...............................
BdRPE1          .........qhgssdkmavkdndm...qq...............................
OsRPE1b         ..............de.aennndv...qn...............................
ZmRPE1          .........gdgtgrpnaksnaesswgee...............................
SbRPE1b         .........gerfgrsnaksnagsswgek...............................
OsRPE1a         .........gr.................................................
SbRPE1a         ............................................................
ZmRPB1          spsysptspsysptspsynpssakyspshayspssprm...spysqtspsysptsptysp
AtRPB1          spsysptspsygptspsynpqsakyspsiayspsnarlspaspysptspnysptspsysp
SmRPD1          ............................................................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
BdRPD1          ............................................................
OsRPD1a         ............................................................
OsRPD1b         ............................................................
ZmRPD1          ............................................................
SbRPD1          ............................................................
VvRPE1          ks....w......sssh...........................................
PtRPE1b         ks.drgwgv....sssgggr....dkktenqslagqgkesggwg................
PtRPE1a         ksldrgwgv....snsgggngsemedktenqslldrgkesggwggkntdadkpws.....
CpRPE1          kg....w......ss.............................................
AtRPE1          lg....p......aamg...........................................
BdRPE1          dp....w......ghiatq....ni.....na.................qddlw......
OsRPE1b         ks....wetvaadahastekswgnvtaspsdnawsaapvsqgngssdtkqsdswdgwksa
ZmRPE1          dk....m......esddhp....kv.....pk.................esdtw......
SbRPE1b         dk....m......esdehp....kv.....pk.................esdtw......
OsRPE1a         ............................................................
SbRPE1a         ............................................................
ZmRPB1          tspsysqpspsysptsp..sgs.........ysptapgyspsstgq.....gndkddksa
AtRPB1          tspsyspssptyspsspyssgaspdyspsagysptlpgyspsstgqytpheg.dkkdktg
SmRPD1          ............................................................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
BdRPD1          ............................................................
OsRPD1a         ............................................................
OsRPD1b         ............................................................
ZmRPD1          ............................................................
SbRPD1          ............................................................
VvRPE1          ................nvmkeqsn.........qpasth.gwds...pga....k...gw
PtRPE1b         ................n..kvtsn.........qadtas.gwgk...pkssensq...gw
PtRPE1a         ................n..kvnsn.........qadtas.gwgk...sksld..r...gw
CpRPE1          .................warddsi.........ngsvlp.egds...sks....n...gl
AtRPE1          ................nwdkkksd.........tksgpa.awgs...tda....a...aw
BdRPE1          .............gsvaakaqtst.........aentda.qddsw.gava....a...ka
OsRPE1b         gvdkainkdkeslgnvpaspsfsawnaspvsqgnersdakqsdswdgwks....agvdka
ZmRPE1          .............n..tgrsnesp.........wdntda.lqdsw..vks....a...ar
SbRPE1b         .............n..tgksnesp.........wdntda.lqdswg.vns....a...th
OsRPE1a         ............................................................
SbRPE1a         ............................................................
ZmRPB1          r...........................................................
AtRPB1          kkdaskddkgnp................................................
SmRPD1          ............................................................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
```

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BdRPD1         ............................................................
OsRPD1a        ............................................................
OsRPD1b        ............................................................
ZmRPD1         ............................................................
SbRPD1         ............................................................
VvRPE1         ...........................nd.veeqsq........w......nqrgsa...
PtRPE1b        glskesgkevhewgvpnsaggngsetnnn.nenqslveqgkesgwdnkassnqegta...
PtRPE1a        gvs.............nsgggngsemedk.tenqslldrgkesg................
CpRPE1         ...........................dagtvgdgs........w......eqtptg...
AtRPE1         g..........................ss.dknnse........t......esdaaa...
BdRPE1         ...........................qt.staqes........w......gnvaaspsd
OsRPE1b        ............................i.nkdkes........l......gnvpaspsf
ZmRPE1         ...........................nn.ntqdgs........w......dkvvs....
SbRPE1b        ...........................dn.ntedgs........w......dkvva....
OsRPE1a        ..................................ev........w......ksegph...
SbRPE1a        ........................................................h...
ZmRPB1         ............................................................
AtRPB1         ............................................................
SmRPD1         ............................................................

VvRPD1         ............................................................
PtRPD1         ............................................................
AtRPD1         ............................................................
CpRPD1         ............................................................
BdRPD1         ............................................................
OsRPD1a        ............................................................
OsRPD1b        ............................................................
ZmRPD1         ............................................................
SbRPD1         ............................................................
VvRPE1         ............vkndqses...s.h.........gw.g..psneqnqlpssqgwg....
PtRPE1b        ............sgwgkpkspals.e.........gw.g..spre..pvkavhgwg....
PtRPE1a        .............gwgkpks..is.q.........gw.g..sskd..svkavdgwg....
CpRPE1         ............t..........s.d.........gw.g..vlsestepagchgwg....
AtRPE1         ............wgsrnkkt...s.eiesgagawgsw.g..qpsptaedkdtneddrnpw
BdRPE1         nawkappisqtsaaehtdah...n.d.........sw.givaakaqtstaqqeswg....
OsRPE1b        sawnaapvsqgn..erldak...qsd.........swdgwksagvddsvkdkeswg....
ZmRPE1         .............mkdldsl...q.d.........sw.s..katiqtndaqndswd....
SbRPE1b        .............ikdpvsq...q.d.........sw.s..nvaiqkndaqndswd....
OsRPE1a        ............rggsssnr...n.q.........gg.g..ravwkseashrgsgn....
SbRPE1a        ............rgg....................gr.g..mafanaessssggwn....
ZmRPB1         ............................................................
AtRPB1         ............................................................
SmRPD1         ............................................................

VvRPD1         ............................................................
PtRPD1         ............................................................
AtRPD1         ............................................................
CpRPD1         ............................................................
BdRPD1         ............................................................
OsRPD1a        ............................................................
OsRPD1b        ............................................................
ZmRPD1         ............................................................
SbRPD1         ............................................................
VvRPE1         spnagaghes..................etqsqwg..qpsg..k................
PtRPE1b        vpnsgggngs..................grdqqwg..qqsrefk................
PtRPE1a        vpnsagsngs..................erdqqwg..qqsgefk................
CpRPE1         lpnneditqn..................esqgrrt..wefs..k................
AtRPE1         vslketksre..................kddkers..qwgn..p................
BdRPE1         nataspsdnawnaapmdl.....dakqpgswdgws..sala..eds.nk...........
OsRPE1b        nvpaspsdsawnaapvsqgnessdakqsdswdgwk..sagv..dastnkdkeswgnvpas
ZmRPE1         nvaknapdsa...................aedswg..aatp..a................
SbRPE1b        nvaekalnsa...................sqdswghlaatp..v.....snsdakqsdsw
OsRPE1a        nrn.........................................................
SbRPE1a        rkn.........................................................
```

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ZmRPB1            ............................................................
AtRPB1            ............................................................
SmRPD1            ............................................................

VvRPD1            ............................................................
PtRPD1            ............................................................
AtRPD1            ............................................................
CpRPD1            ............................................................
BdRPD1            ............................................................
OsRPD1a           ............................................................
OsRPD1b           ............................................................
ZmRPD1            ............................................................
SbRPD1            ............................................................
VvRPE1            ...................ks........rpe.......gsrgwgsnn.....t.ewkn.
PtRPE1b           ...................kd........rfe.......gsrgwgsnn.....g.dwkn.
PtRPE1a           ...................kn........rte.......gsrgwgsnn.....g.hwk..
CpRPE1            ...................kk........rne.......gsrgwssns.....g.dwkg.
AtRPE1            ...................ak........kfp.......ssggwsngg.....gadwkg.
BdRPE1            ..................add........ssn.......knkgwksdgwgak.g.nrrd.
OsRPE1b           psdsawnaapvsq.....gdd........vwnsaeanesrnkdwksdgwgargg.nwrg.
ZmRPE1            ...................et........tds.......gnkewksdgwgaksg.nwss.
SbRPE1b           dgwnavpaensqgtaqwk.er........tds.......gnkdwksdgwgaksg.nwss.
OsRPE1a           .............................rgg.......gravwksea.....s.rrgg.
SbRPE1a           .....................sgfgrggrrgg.......grgmwkseg.....s.hrggs
ZmRPB1            ............................................................
AtRPB1            ............................................................
SmRPD1            ............................................................

VvRPD1            ............................................................
PtRPD1            ............................................................
AtRPD1            ............................................................
CpRPD1            ............................................................
BdRPD1            ............................................................
OsRPD1a           ............................................................
OsRPD1b           ............................................................
ZmRPD1            ............................................................
SbRPD1            ............................................................
VvRPE1            ...........kknrpn.kp.........qgplnddysaggift...atrqrvdiftsee
PtRPE1b           ...........krnrps.kp.........h....edlnasgift...ttrqrldvftsqe
PtRPE1a           ...........krnrps.kp.........h....edssssglft...mtrqwldiftsqe
CpRPE1            ...........kknlpg.kl.........agnvkddfgagrlyt...htrqrldmftsee
AtRPE1            ...........nrnhtp.rp.........p...rsednlapmft...atrqrldsftsee
BdRPE1            ...........qrdnps.mp.........pmrpder...........pprprfev.paea
OsRPE1b           ...........qrnnpg.rpprkpdgrglprrpder........g..pprrhfdl.taee
ZmRPE1            ...........qrnnpg.rp.........prrpder........gpppprqrfel.tvae
SbRPE1b           ...........qrnnpg.rp.........prrpder........gpppprqrfel.tiee
OsRPE1a           ...........smrqva.sc.........a.........................ftpve
SbRPE1a           nstnwraqnnnsarqcgisy.........s.........................ftpve
ZmRPB1            ............................................................
AtRPB1            ............................................................
SmRPD1            ............................................................

VvRPD1            ............................................................
PtRPD1            ............................................................
AtRPD1            ............................................................
CpRPD1            ............................................................
BdRPD1            ............................................................
OsRPD1a           ............................................................
OsRPD1b           ............................................................
ZmRPD1            ............................................................
SbRPD1            ............................................................
VvRPE1            qdilldvepimqsirrimhqagyndgdplsaddqsyildkvfnnhpdkavkmgtgidyvm
PtRPE1b           qdilsdieplmlsirrimhqtgyndgdplsaddqsyvldnvfhyhpdkavkmgagidhvt
PtRPE1a           qdilsdveplmlsirrimhqtgysdgdplsaddqsyvldnvfnyhpdkavkmgaginhvt
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CpRPE1          qdvlsdveplmqsirrimhqsgyndgdplsvddqsfvidkvfmyhpdravkmgagidfvt
AtRPE1          qellsdvepvmrtlrkimhpsaypdgdpisdddktfvlekilnfhpqketklgsgvdfit
BdRPE1          kkilreiepivsmvrkifresc..dgvrlpledekfikesilehhpekerkvpgeidhim
OsRPE1b         ekilgeieptvlsirkifresi..dsiklspedekfikenvlehhpekqskvsgeidhim
ZmRPE1          knillevepiklrvrsifreac..dgvrlnpedekfilekvlehhpekqskvsgeidylt
SbRPE1b         kkilleveplifrvrrifreac..dgvrlkpedekfiqekilehhpekqskvsseidhim
OsRPE1a         qqifeqiepitknvkriiresr..dgiklppddekfivtnvlmyhperkkkiagngnyit
SbRPE1a         qqiytqvepiiknvkriiresr..dgmklsqddemfimnkilmyhpekekkmagqgnyim
ZmRPB1          ............................................................
AtRPB1          ............................................................
SmRPD1          ............................................................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
BdRPD1          ............................................................
OsRPD1a         ............................................................
OsRPD1b         ............................................................
ZmRPD1          ............................................................
SbRPD1          ............................................................
VvRPE1          vsrhssflesrcfyvvstdghkedfsyrkclenfikekypdnaetfigkyf.rrpraggn
PtRPE1b         vsrhsnfqesrcfyivstdgckqdfsyrkclenfikgkypdladefiakyfarr....gn
PtRPE1a         vsrhsnfqesrcfyivstddckqdi.............fp......ta...........n
CpRPE1          vsrhsnfqdsrcfyivstdgrkqdfsyrkcldnfikgkypdiaeqfigkyf.rkprssgn
AtRPE1          vdkhtifsdsrcffvvstdgakqdfsyrkslnnylmkkypdraeefidkyf.tkprpsgn
BdRPE1          vnkhhifqesrcfyvvladgthtdfsynkcmdnyvrktytdaaehadl............
OsRPE1b         vdkhqvfqdsrclfvvssdgtrsdfsylkcmenfvrkty...pehgds............
ZmRPE1          vnkhqtfqdtrcffvvstdgsqadfsylkclenfvrksytedadtfcm............
SbRPE1b         vnkhhtfedtrcffvvstdgsqadfsylkclenfvrknytedvdsfcm............
OsRPE1a         vdrhqvfhgsrclyvmssdgsrkdfsykkclenyiraqypdaadsfcrkyf.k.......
SbRPE1a         vnkhqtfpssrclyvassdgsssdfsykkclenfirihyphaaesfcrkyf.k.......
ZmRPB1          ............................................................
AtRPB1          ............................................................
SmRPD1          ............................................................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
BdRPD1          ............................................................
OsRPD1a         ............................................................
OsRPD1b         ............................................................
ZmRPD1          ............................................................
SbRPD1          ............................................................
VvRPE1          rersvipedggnreqsvvpeetgsenrq................................
PtRPE1b         rqrtpape..............gteeekqal.............................
PtRPE1a         vwrtssge....................nnltwqmnssesilqeeaigsapllqreprrn
CpRPE1          qqkpvlee...............tenml................................
AtRPE1          rdrnnqdatppgeeqsqppnqsignggddfqtqtqsqspsqtraqspsqaqaqspsqtqs
BdRPE1          ............................................................
OsRPE1b         ............................fckkyfkrrrdqppaadggtapgtpagatqst
ZmRPE1          ............................kylr.....................pp....e
SbRPE1b         ............................kylrprrrqapppdvgtapgtpaevppstaae
OsRPE1a         ............................................................
SbRPE1a         ............................................................
ZmRPB1          ............................................................
AtRPB1          ............................................................
SmRPD1          ............................................................

VvRPD1          ............................................................
PtRPD1          ............................................................
AtRPD1          ............................................................
CpRPD1          ............................................................
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BdRPD1           ............................................................
OsRPD1a          ............................................................
OsRPD1b          ............................................................
ZmRPD1           ............................................................
SbRPD1           ............................................................
VvRPE1           ............................................................
PtRPE1b          ............................................................
PtRPE1a          rprdv.......................................................
CpRPE1           ............................................................
AtRPE1           qsqsqsqsqsqsqsqsqsqsqsqsqsqsqsqspsqtqtqspsqtqaqaqspssqspsqtq
BdRPE1           ............................................................
OsRPE1b          avdtqegtsqqtqpdiatapaatqqetlqdtpappaddgllgkgpspsd...........
ZmRPE1           teqgtppapqaevpqetwgspavpleggthiagpdstgdavilgeqhdltpaspavapqv
SbRPE1b          teqgt.pappaevpqetlgspavale.gthnprtdptddtellgkdsdltpaspavapqe
OsRPE1a          ............................................................
SbRPE1a          ............................................................
ZmRPB1           ............................................................
AtRPB1           ............................................................
SmRPD1           ............................................................

VvRPD1           ........................................................
PtRPD1           ........................................................
AtRPD1           ........................................................
CpRPD1           ........................................................
BdRPD1           ........................................................
OsRPD1a          ........................................................
OsRPD1b          ........................................................
ZmRPD1           ........................................................
SbRPD1           ........................................................
VvRPE1           ........................................................
PtRPE1b          ........................................................
PtRPE1a          ........................................................
CpRPE1           ........................................................
AtRPE1           t.......................................................
BdRPE1           ........................................................
OsRPE1b          ........................................................
ZmRPE1           asepdttdgtgllgkapqadwgprfdad............................
SbRPE1b          apkpdptddtellg..............nekpdltpsspgealqatadpdstltdi
OsRPE1a          ........................................................
SbRPE1a          ........................................................
ZmRPB1           ........................................................
AtRPB1           ........................................................
SmRPD1           ........................................................
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(C) MUSCLE

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ZmRPB1           -------MDARFPYSPAEVAKVEFVQFGILSPDEIRQ-------MSVIQIEHAETMERGK
AtRPB1           -------MDTRFPFSPAEVSKVRVVQFGILSPDEIRQ-------MSVIHVEHSETTEKGK
AtRPE1           --------MEEESTSEILDGEIVGITFALASHHEICIQS-----ISESAINH--------
CpRPE1           -----------------MVYSLLGINWIMAGTSK--------------------------
VvRPE1           ---------MEEDSSTILDGEISGIRFGLATRQEICIAS-----VSDCPISH--------
PtRPE1a          --------MDEIPQSSIFEGEITGIRFGLASQKEICTAS-----ISDCPISH--------
PtRPE1b          --------MDENSQSSIFDGEITGIRFGLATQKEICTAS-----ISDCPISH--------
SbRPE1b          -------MEEDHSATLVSEGAIKSIKLSLSTGEEVCTYS-----VNECPVTH--------
ZmRPE1           -------MEEDHSVILISEGAIKSIKLSLSTGEEICTYS-----INECPVTH--------
BdRPE1           -------MEEDQSAVLVAEGAIKSIKLSLSTEDEI-------------------------
OsRPE1b          -------MEEDQSAIPVAEGAIKSIKLSLSTEDEIRTYS-----INDCPVTH--------
OsRPE1a          --MEGHPDPTSAATAMIPEASIRRINLSITSNEEILKAQPVNELEKPIPITH--------
SbRPE1a          ----MEDDDPAAAGLTVPEAFIRRVKLSVTSNQEIKLMA--HPVEDPIPITH--------
SmRPD1           MASSKRRSSHRDRALEEATGTLIALDFRPLTSEEIIR-------ASVYEVKT--------
SbRPD1           ----------MELHRELPEATLNAIKFDLMTSTDMEK-------LSSMSVIE--------
ZmRPD1           ----------MELHREPPEAILNAIKFDLMTSTDMEK-------LSSMSIIE--------
BdRPD1           ----------------------MLILLLLLKRSD--------------------------
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OsRPD1a         -------MEEPSLEVNNPVAELNAIKFSLMTSSDMEK-------LSSATIIE--------
OsRPD1b         -------MEEPSLEVKMPEADLKAVKFSLMTSSDMEK-------LSSASIIE--------
AtRPD1          -------MEDDCEELQVPVGTLTSIGFSISNNNDRDK-------MSVLEVEA--------
CpRPD1          ----------------------MALWILLGSWIEV-------------------------
VvRPD1          ------MDNDFLEEQQVPSGLLIGIKFDVSTEEDMEK-------ISVMKIDA--------
PtRPD1          ------MEIDFSEEQQVPSALITGMAFGVLTEAETEK-------LSVLNIDA--------
                                        :        .

ZmRPB1          PKPGGL-SDPRLGTIDRKIK-CETCMA-----GMAECP----------------------
AtRPB1          PKVGGL-SDTRLGTIDRKVK-CETCMA-----NMAECP----------------------
AtRPE1          --PSQL-TNAFLGLPLEFGK-CESCGAT----EPDKCE----------------------
CpRPE1          ---------------------VKNAGVA----E---------------------------
VvRPE1          --ASQL-TNPFLGLPLEFGK-CESCGTA----EPGQCE----------------------
PtRPE1a         --SIQL-TNPYLGLPLEFGK-CESCGTS----EPGQCE----------------------
PtRPE1b         --SSQL-TNPFLGLPLEFGK-CESCGTS----EPGKCE----------------------
SbRPE1b         --PSQL-GNPFLGLPLEAGK-CESCGAS----ENDKCE----------------------
ZmRPE1          --PSQL-GNPFLGLPLEAGK-CESCGAS----ENDKCE----------------------
BdRPE1          -----L-GNPFLGLPLETGK-CESCGAS----ENGKCE----------------------
OsRPE1b         --PSQL-GNPFLGLPLETGK-CESCGAS----ENGKCE----------------------
OsRPE1a         --QSQLLNNPYLGLPLQVGS-CQSCGSN----AIEECE----------------------
SbRPE1a         --CSQLQDNPSLGLPLQDGSTCESCGAT----QLDKCD----------------------
SmRPD1          --VRAL-QNNRFGLPNLSDC-CTSCGAKRTDASNSACP----------------------
SbRPD1          --VSDV-TSPKLGLPNASPQ-CETCGSK----SGRDCD----------------------
ZmRPD1          --VSDV-TSPKLGLPNGSLQ-CETCGSQ----RGRDCD----------------------
BdRPD1          --AATI-QEP-----------CKYCSKD----GLYPSV----------------------
OsRPD1a         --MCDV-TNAKLGLPNGAPQ-CATCGSR----SIRDCD----------------------
OsRPD1b         --MCDV-TNAKLGLPNGAPQ-CATCGSQ----SVRDCD----------------------
AtRPD1          --PNQV-TDSRLGLPNPDSV-CRTCGSK----DRKVCE----------------------
CpRPD1          -------TDPKLGLPNPSSE-CLTCGAK----DLKHCE----------------------
VvRPD1          --VNEI-TDPKLGVPNPSCQ-CSTCGAK----DTKKCE----------------------
PtRPD1          --VSEV-TDPKLGLPNPSSQ-CSTCGSR----DLKSCEGIVDVDLNSADRLASIATGDCA
                                        .

ZmRPB1          -------GHFGHLELAKPMFHIGFIKTVLSIMRCVCFNCSKILADEDETKFKQALKIRNP
AtRPB1          -------GHFGYLELAKPMYHVGFMKTVLSIMRCVCFNCSKILADE-------AMKIKNP
AtRPE1          -------GHFGYIQLPVPIYHPAHVNELKQMLSLLCLKC---------------LKIKKA
CpRPE1          -----------------------------RLFSLCCEEV---------------------
VvRPE1          -------GHFGYIELPIPIYHPGHVSELKRMLSLLCLKC---------------LKIRKS
PtRPE1a         -------GHFGYIDLPVPIYHPSHISELKRMLSLLCLKC---------------LKLKRN
PtRPE1b         -------GHFGFIHLPIPIYHPSHISELKRMLSLICLKC---------------LKLKRN
SbRPE1b         -------GHFGYIELPVPIFHPCHVSELRQLLSLICLKC---------------LRIKKG
ZmRPE1          -------GHFGYIELPVPIYHPCHVTELRQLLSLICLKC---------------LRIKKG
BdRPE1          -------GHFGYIELPVPIYHPCHVSELRQLLSLVCLKC---------------LRIKKG
OsRPE1b         -------GHFGYIELPVPIYHPCHVTELRQILNVVCLKC---------------LRVKKG
OsRPE1a         -------GHFRFIELPMPIFHPSHVTELSQILNLICLRC---------------LKIKNR
SbRPE1a         -------GHFGFIKLPEPIYHPSHIAELGKILNLVCLRC---------------LRLKKP
SmRPD1          -------GHSGHIELPVLVYHWDRISALEAILNRVCLHCY-------------SFKHKGR
SbRPD1          -------GHFGVTKLAATVHNPYFIDDVVHFLNQICPGC---------------LSPREG
ZmRPD1          -------GHFGVTKLAATVHNPYFIDDVVHFLNRICPGC---------------LSPREG
BdRPD1          --------IFKVLTSPRITLSKSKLQRNTSVMDKVSVTA---------------------
OsRPD1a         -------GHFGVIKLAATVHNSYFIEEVVQLLNQICPGC---------------LTLKQN
OsRPD1b         -------GHFGVIKLAATVHNPCFIEEVVQLLNQICPGC---------------LTLKQN
AtRPD1          -------GHFGVINFAYSIINPYFLKEVAALLNKICPGC---------------KYIRKK
CpRPD1          -------GHFGVIQFPYTILHPYYLSEVVQILNKVCPAL---------------IHAIQG
VvRPD1          -------GHFGVIKFPFTILHPYFLTEVVQILNKICPGC---------------KSTRQG
PtRPD1          NILLSLSGHFGVINFPYTIVHPYFLSEVVQILNKICPGC---------------KSIRLA
                                              .:   .

ZmRPB1          KNRLKRIYDACKSKKVCAGGDD--------LDVQEQDT-------------------DEP
AtRPB1          KNRLKKILDACKNKTKCDGGDD-----IDDVQSHSTDE--------------------PV
AtRPE1          KGTS--GGLADRLLGVC--CEE-----ASQISIKDRAS----------------------
CpRPE1          ----------------------------SQVSIKEGKT----------------------
VvRPE1          KVTN--NGITEQLLAPC--CQD-----SPQVSVREFRP----------------------
PtRPE1a         KIQIKSNGVAERLLSCCEECAQ--------ISIREVKN----------------------
```

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PtRPE1b         KIQIKSNGVAERLLSCCEECAQ--------ISIREVKN----------------------
SbRPE1b         KVKQS-NGKGNLSATLCSYCRD-----IPALSVKEVKT----------------------
ZmRPE1          KVKQS-NGKGNAAPTLCSYCRD-----IPALSLKEIKT----------------------
BdRPE1          K--------------------D-----VPALSLKEVKT----------------------
OsRPE1b         KVKQT-EGKDNTSALSCYYCRD-----LPALSLKEIKT----------------------
OsRPE1a         KK----STLKGSKFTSCSHCQE-----LPPLCVAEVKK----------------------
SbRPE1a         KK----VTGKESRFTSCSYCQE-----LSPLCVSQVKK----------------------
SmRPD1          KKELRTLSSLEQVASGVDAHQADIGAVPNGARAPEAEE---NPGKCTGPAAAVKKIFKKV
SbRPD1          INMKRLGRETVQATSTCKYCSKDGSKLYPSVIFKTLSSPRVLLSKSKLHRSPSVMERISI
ZmRPD1          IDTK--RLEREKVQATCKYCSKDGSKLYPSIVFKTLSSPRVLLFKSKLHRNASVMERISI
BdRPD1          ------------------------------EVINMSKN----------------------
OsRPD1a         GDTK--KADGTTIQGTCKYCSKDGSKLYPSIIFKMLTSPRVTLSRSKLHRNTSVMDKMSI
OsRPD1b         GDTK--KTDGTTIQTTCKYCSKDGAKLYPSVIFKMLTSPRVTLSRSKLHRNTSVMDKISI
AtRPD1          Q-----FQITEDQPERCRYCTLNTG--YPLMKFRVTTK--------------EVFRRSGI
CpRPD1          N----------------------SLNWYPPMKFKVLSE--------------DIFRLSAI
VvRPD1          QW----VKVRRLRSKGCKYCAANSNDWYPTMKFKVSSK--------------DLFRKTAI
PtRPD1          KATEL-ITKENPQRKGCKYCAGNSLGWYPPMKFKVSSK--------------EIFRKTAI


ZmRPB1          IKKRGGCGAQQPNITVDGMKMVAEFKAPKKKTDDQDQL----------------------
AtRPB1          KKSRGGCGAQQPKLTIEGMKMIAEYKNSKEENDEPDQL----------------------
AtRPE1          ----DGASYLELK-LPSRSRLQPGCWNFLERYGYR-------------------------
CpRPE1          ---PDDACYLQLK-LPSMSRLRESFWNFLEKYGFSLRLCGLGSQISALTLKVLGLLAFWV
VvRPE1          ---TEGACFLELK-IPSRSRPKDGFWDFLARYGYR-------------------------
PtRPE1a         ---TDGACFLELK-LPSRSRLRDGCWNFLERYGFRYVFVTFEKYSYIHMPKVYAFMSKGV
PtRPE1b         ---TDGACFLELK-LPSRSRLRDGCWNFLERYGFR-------------------------
SbRPE1b         ---ADGAIRLELS-APHKRHMTERSWNFLDKYGFH-------------------------
ZmRPE1          ---TDGAIRLELR-APHNKHMTERSWNFLDKYGFH-------------------------
BdRPE1          ---ADGAFRLELR-APPRRLMKDSSWNFLDKYGFH-------------------------
OsRPE1b         ---ADGAFRLELK-MPPRKFMTEGSWNFLDKYGFH-------------------------
OsRPE1a         ---SNGARGLELR-APIKKELEEGFWSFLDQFGSC-------------------------
SbRPE1a         ---SNGARSLELK-LPLKQEVADGFWSFLDQFGFH-------------------------
SmRPD1          GTANVPALLLEIDGKVRREDIPPGFQSLILKDEMT-------------------------
SbRPD1          VAEAAERVSNRSKGKGLLEGLPQDYWDFVPSENKQ-------------------------
ZmRPD1          VAEAADRMPNRSKGKGSLEGLPLDFWDFVPSENKQ-------------------------
BdRPD1          --------------KSSLEVLPHDYWNFVP-HNQP-------------------------
OsRPD1a         IAEVAGGVAHKSKNKAPHETLPQDFWDFIPDDNQP-------------------------
OsRPD1b         IAEVAGGVTHNSKNKAPHETLPQDFWDFVPDDNQP-------------------------
AtRPD1          VVEVNEESLMKLK-KRGVLTLPPDYWSFLPQDSNI-------------------------
CpRPD1          MVEVNENVLRKFQ-KRRKEALPADYWDFLPKDSHQ-------------------------
VvRPD1          IVEMNEKLPKKLQKKSFRPVLPLDYWDFIPKDPQQ-------------------------
PtRPD1          IAEIRETLSKKPQ-KGFKKILAADYWDIFPKDEQE-------------------------
                         .

ZmRPB1          ------PEP--V--ERKQILSAER------------------------------------
AtRPB1          ------PEP--A--ERKQTLGADR------------------------------------
AtRPE1          ------YG---S--DYTRPLLARE------------------------------------
CpRPE1          AFTSLCEGS--C--KEISKVIGQV------------------------------------
VvRPE1          ------YG---H--NLSRILLPSE------------------------------------
PtRPE1a         CAFRSDWYFIYA--PATMLASPRNLVWSYVLLTRLGTGYLFNASVSELLVNDSNFRTVLV
PtRPE1b         ------YG---D--DFTRPLLPCE------------------------------------
SbRPE1b         ------HGG--C--SQFRSLLPEE------------------------------------
ZmRPE1          ------HGG--C--SHHRTLLPEE------------------------------------
BdRPE1          ------HGG--A--SHFRTLLPEE------------------------------------
OsRPE1b         ------HGG--T--SHCRTLLPEE------------------------------------
OsRPE1a         ------TRG--T--SHCRPLLPEE------------------------------------
SbRPE1a         ------TSG--T--SHRRPLHPKE------------------------------------
SmRPD1          ------PQ------WRSKMLDPNQ------------------------------------
SbRPD1          ------VQS--N--MTKIILSPYQ------------------------------------
ZmRPD1          ------VQS--N--MTKIILSPYQ------------------------------------
BdRPD1          ------PQP--N--TTKILLSPYQ------------------------------------
OsRPD1a         ------PIF--N--VTKKILSPYQ------------------------------------
OsRPD1b         ------PQS--N--VAKKILSPYQ------------------------------------
AtRPD1          ------DESCLK--PTRRIITHAQ------------------------------------
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CpRPD1          ------EESGTR--PNRRILSHAQ------------------------------------
VvRPD1          ------EENCLN--PNRRVLSHAQ------------------------------------
PtRPD1          ------EEEETNAKPNRRVLSHSQ------------------------------------


ZmRPB1          ---------------VLNVLKRISDEDCLLL-GLNPKYARPDWMILQVLPVPPPPVRPSV
AtRPB1          ---------------VLSVLKRISDADCQLL-GFNPKFARPDWMILEVLPIPPPPVRPSV
AtRPE1          ---------------VKEILRRIPEESRKKL-TAKG-HIPQEGYILEYLPVPPNCLSVPE
CpRPE1          ---------------VMKMIRSIPEDTRRKL-AGKG-YFPQDGYILQVLPVPPNCLSVPD
VvRPE1          ---------------VMEILRRIPEDTRKKL-VRKG-YFPQDGYILQYLPVPPNCLSVPD
PtRPE1a         YIQSFTFSAYACYFLVMQILKTIPAETRKKL-GGKG-YFPQDGYILQQLPVPPNCLSVPA
PtRPE1b         ---------------VMQILKRIPAETRKKL-SGKG-YFPQDGYILQQLPVPPNCLSVPV
SbRPE1b         ---------------ALNILKKVPDDTRRKL-AARG-YIVQTGYVMKYLPVPPNCLYIPE
ZmRPE1          ---------------ALNILKKVPDDTRRKL-AARG-YIVQTGYVMKYLPVPPNCLYIPE
BdRPE1          ---------------ALNILKKIPDDTRKKL-AARG-YIAQSGYVMKYLPVPPNCLYIPE
OsRPE1b         ---------------ALNILKKIPEETKRKL-AARG-YIAQSGYVMKYLPVPPNCLYIPE
OsRPE1a         ---------------VQNIIKKIPEETRRWL-SVRG-YIPQDGFILSYLCVPPNCLRVSN
SbRPE1a         ---------------VQDIMKKITEKTRARL-AARG-YNLQDGFVMDNMSIPPNCLQISN
SmRPD1          ---------------VLRILKCLPQETIDKLRDEKLPSIPAEDYFIKSLPVPPNWMRYST
SbRPD1          ---------------VFHMLKKSDPELIKQF-VSRR-----ELLFLSCLPVTPNCHRVVE
ZmRPD1          ---------------VFYMLKKSDPELIKQF-VSRR-----ELLFLSCLPVTPNCHRVVE
BdRPD1          ---------------VFHILKQVDLELITKF-APRR-----ELLFLSCLPVTPNRHRVAE
OsRPD1a         ---------------VFHMLKKLDPELINQV-TRRR-----ELLFLSCLPVTPNCHRVAE
OsRPD1b         ---------------VFHMLKNLDPELINQV-TPRR-----ELLFLSCLPVTPNCHRVAE
AtRPD1          ---------------VYALLLGIDQRLIKKD-IPMF-----NSLGLTSFPVTPNGYRVTE
CpRPD1          ---------------VHFLLKAIDPKLIRKF-ILRP-----DSLFLNYFPVTPNSHRVTE
VvRPD1          ---------------VHYLLKDIDPGFIKEF-VSRM-----DSFFLNCLPVTPNNHRVTE
PtRPD1          ---------------VRHMLKDVDPNFIKLS-ILKT-----DTIFLNCFPVTPNSHRVTE
                               .  ::                         :  : :.*

ZmRPB1          MMDTSSRS--EDDLTHQLAMIIRHNENLRRQERNGAPAHIITEFAQL--LQFHIATYFDN
AtRPB1          MMDATSRS--EDDLTHQLAMIIRHNENLKRQEKNGAPRHIISRFTQL--LQFHIATYFDN
AtRPE1          ASDGFSTMS-VDPSRIELKDVLKKVIAIKSS-RSGETNFESHKAEASE-MFRVVDTYLQV
CpRPE1          ISDGVSTMS-SDPSTPLLKKVLEKVENIKSS-RCGEPNFESHSVEANE-LQSAVNKYLQA
VvRPE1          ISDGVSIMS-SDLSVSMLKKVLKQIEVIKGS-RSGEPNFESHKIEANN-LQSSIEQYLEV
PtRPE1a         VSDGISIMS-SDLSISILKKVLKQVEVIKSS-RSGAPNFDAHKDEANS-LQSMVDRYLQV
PtRPE1b         VSDGITVMS-SDLSISMLKKVLKQAEVIRSS-RSGAPNFDAHKDEATS-LQSMVDQYLQV
SbRPE1b         FTDGQSIMS-YDISIALLKKVLQKIEQIKRS-RSGSPNFDSHDAESCD-LQLAIGQYIRL
ZmRPE1          FTDGQSIMS-YDISIALLKKVLQKIEQIKRS-RSGSPNFESHDAESCD-LQLAIGQYIRL
BdRPE1          FTDGQSIMS-YDISISLLKKILHRIEQIKKS-RAGTPNFESHEAESSD-LQISIAQYIHL
OsRPE1b         FTDGQSIMS-YDISISLLKKVLQKIEQIKKS-RAGSPNFESHEVESCD-LQLSIAQYIHL
OsRPE1a         VLDGNTFSC-SGTSTNLLRKALRKIQQIRGS-RIGSSNIQVDQVADD--LQVDVANYINL
SbRPE1a         MLDENTEMCPPDTSKGLLHKVLRTIEQIESL-NISHPNIEARELGADD-LQVAVADYMNM
SmRPD1          NEFYF-----QDKTTKNLKHLLTKIKSIVYT-RDEDKISLLTEQKVME-IQAAATQCIRA
SbRPD1          IGYGLSDG---RVTFDDRTKAYKRMVDVSRR-IDDYRQHPQFSVLASSLVSGRVSECLKS
ZmRPD1          IGYGLPDG---RLTFDDRTKAYKRMVDVSRR-IDDYRQHPHFSVLASSLVSSRVSECLKS
BdRPD1          MPYRFSDG--PSLAYDDRTKAYKRTVDASKK-IDDYRQHPQFSVLASSFVTSRVMECLQS
OsRPD1a         MPYGHLDG--PRLAFDDRTKAYKRMVDVSRR-IDDYHQHPQFGVFASSVVTSRVMECLKS
OsRPD1b         MQYGHSDG--PRLAFDDRTKAYKRMVDVSKR-IDDCRQHPQFSVFASSVVTSRVMECLKS
AtRPD1          IVHQFNG---ARLIFDERTRIYKKLVGFEGN-TLE--------------LSSRVMECMQY
CpRPD1          LTYMFSSG--QRLFFDERTGAYKKLVDFRGT-SNE--------------LSSRLHTFKSS
VvRPD1          ITHALSNG--QTLIFDQHSRAYKKLVDFRGT-ANE--------------LS-----CHSA
PtRPD1          VTHAFSNG--QRLIFDERTRAYKKMVDFRGV-ANT--------------LSFHVMDCLKT
                                                                 :

ZmRPB1          DLP-----GQPRATQRSGRPIKSICSRLKAKE--GRIRGNLMGKRVDFSARTVITPDPNI
AtRPB1          ELP-----GQPRATQKSGRPIKSICSRLKAKE--GRIRGNLMGKRVDFSARTVITPDPTI
AtRPE1          RGTA----KAARNIDMRYGV-SKISDSSSSKAWTEKMRTLFIRKGSGFSSRSVITGDAYR
CpRPE1          RGTA----KASRE-DTRYGV-SKNSNDCSTKAWLEKMRTLFIRKGSGFSSRSVITGDPYK
VvRPE1          RGTA----KTSRSLDTRFGS-SKEPNESSTKAWLEKMRTLFIRKGSGFSSRSVITGDAYK
PtRPE1a         RGTT----KTSRDVDVRYGV-KKDSSESSTKAWLEKMRTLFIRKGSGFSSRSVITGDAYT
PtRPE1b         RGTT----KTSRDVDTRYGV-KKESSESTTKAWLEKMRTLFIRKGSGFSSRSVITGDAYT
SbRPE1b         RGTT----RGPQDNTKRFTVGSADSAALSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYI
ZmRPE1          RGTT----RGPQDNTKRFTVGSADSAALSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYI
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BdRPE1          RGT-----------TKRFTI-STDSSHLSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYI
OsRPE1b         RGTT----RGPQDNTKRFAI-STDPSALSTKQWLEKMRTLFISKGSGFSSRSVLTGDPYI
OsRPE1a         GG------------TTKGHGDDTFTSQPTAMQWKQKMKTLFISKSSSFSSRGVITGDPYI
SbRPE1a         GG------------AAKVSQHVTFTRQPAPKQWHKKMKTLFLSKSSSYTCRAVITGDPYI
SmRPD1          NPLY----GNVSDEDPRYGNVSDESKPLSGLHF---LRSL-TGKYCGSSARAVVIGDPAL
SbRPD1          SKLY----------SKKTD--GETSTDPSGMKW---LKDAVLSKRSDNAFRSTMVGDPKI
ZmRPD1          SKLY----------SKKAD--GETSTDTYGMKW---LKDVVLSKRSDNVFRSIMVGDPKI
BdRPD1          SKLY----------SKKTD--KESSTDSYG------TSDAILSKRSDYAFRSIMVGDPKI
OsRPD1a         SKLY----------SKKSDDESSASTDTYGTKW---LKDIILSKRSDNAFRSIMVGDPKI
OsRPD1b         SKLY----------SRKSDGEDPTSPDTYGTKW---LKDIILSKRSDNAFRSIMVGDPKI
AtRPD1          SRLFSETVSSSKDSANPYQK-KSDTPKLCGLRF---MKDVLLGKRSDHTFRTVVVGDPSL
CpRPD1          SKD-----------ATTALLKNEDSSNMVGLRY---MKDVLLGKRNDSSFRTVVIGDRSL
VvRPD1          SKM-------------------------SGLKW---IKEVLLGKRTNHSFRMIVVGDPKL
PtRPD1          SKLNPDKSGNIDPWTAQPKKSNDYVNNASGLRW---IKDVVLGKRNDHSFRMVIVGDPHL
                                                           *  .   *  :  *

ZmRPB1          NIDELGVPWSIALNLTYPETVTPYNIERLKELVEYGPHPPPGKTGAKYIIREDGQRLDLR
AtRPB1          NIDELGVPWSIALNLTYPETVTPYNIERLKELVDYGPHPPPGKTGAKYIIRDDGQRLDLR
AtRPE1          HVNEVGIPIEIAQRITFEERVSVHNRGYLQKLVDDKLCLSYTQGST-TYSLRDG----SK
CpRPE1          KVNEIGIPFEIAQRITFEERVNLHNMKYLQELVDKKLCLTYRDGGS-TYSLREG----SK
VvRPE1          RVNEIGLPFEIAQRITFEERVNVHNMKHLQNLVDEKLCLTYRDGLS-TYSLREG----SK
PtRPE1a         KVNQVGIPYEIAQRITFEERVSVHNMRYLQELVDNKLCLTYRDGSS-TYSLREG----SK
PtRPE1b         LVNQVGIPYEIAQRITFEERVSVHNMRYLQELVDNKLCLTYKDGSS-TYSLREG----SK
SbRPE1b         GLGVVGLPSEVAKRMTFEEQVTDININRLQEVVDKGLCLTYRDGQA-TYAITVG----SK
ZmRPE1          GLGVVGLPSEVAKRMTFEEQVTDININRLQDVVDKGLCLTYRDGQA-TYAITVG----SK
BdRPE1          GVDVVGLPSEVAKRITFEEQVTDINIKRLQEVVDKGLCLTYRDGQT-TYAITVG----SK
OsRPE1b         GVDVIGLPSEVAKRITFEEQVTDINLNRLQEIVDKGLCLTYRDGQA-TYAITVG----SK
OsRPE1a         GLNVVGVPEEVAKRMSVEEKVTDHNIAQLQDMMNKGLCLTYTDANSITYSLDAGKDNPNK
SbRPE1a         GLDVVGVPDEIARRMSVQECVTNYNIARLQDMMNKGLCLTYTDLNTNTYDLDGKKG--NK
SmRPD1          KLEEIGISARIAAGLVVLETVTSSNIIFLQSYA-------YNNPG--LKVVRGGEVCTAR
SbRPD1          KLWEIGIPEDLASNLVVSDHVNSYNFENINLKCNLHL---LTKEE--LFIRRNGKLMFLR
ZmRPD1          KLWEIGIPEDLSSSLVVSEHVSSYNFQSTNLKCNLHL---LAKQE--LFIRRNGKLMFLR
BdRPD1          RLHEIGIPMDLAD-LFVPEHVSIYNFKSINLKCNLHL---LAKEL--LIARRNGKLIYVR
OsRPD1a         NLNEIGIPMGLALNLVVSEQVSSYNFETINLKCNLHL---LTKEV--LLVRRNGNLIFVR
OsRPD1b         NLNEIGIPTDLALNLVVSEQVSFYNFETINLKCNLHL---LTKEV--LLVRRNGKLIFVR
AtRPD1          KLNEIGIPESIAKRLQVSEHLNQCNKERLVTSFVPTL---LDNKE--MHVRRGDRLVAIQ
CpRPD1          KLSEIGIPCHIAESLQISENLNNWNWDKLISSCDLRL---LEKGE--IHVRRKNSLISLR
VvRPD1          RLSEIGIPCHIAEELLISEHLNSWNWEKVTNGCNLRL---LEKGQ--TYVRRKGTLAPVR
PtRPD1          QLHEIGIPCHIAERLQISESLTAWNWEKLNACFEKSR---FEKGD--MHVRREGNLVRVR
                 :  :*:.  ::  :   : :.  *                 .                .

ZmRPB1          YVKKSSDQHLELG----------------------------YKVERHLNDGDFVLFNRQP
AtRPB1          YLKKSSDQHLELGYRYVLLSYSIHSTHKRLFLEVVIFMLSWSQVERHLQDGDFVLFNRQP
AtRPE1          -----GHTELKPG----------------------------QVVHRRVMDGDVVFINRPP
CpRPE1          -----GHTFLRPG----------------------------QVVHRRIMDGDTVFINRPP
VvRPE1          -----GHTFLRPG----------------------------QVVHRRIMDGDIVFINRPP
PtRPE1a         -----GHTFLRPG----------------------------QVVHRRIIDGDVVFINRPP
PtRPE1b         -----GHTFLRPG----------------------------QVVHRRIMDGDIVFINRPP
SbRPE1b         -----GHTTLKVG----------------------------QTISRRIVDGDVVFLNRPP
ZmRPE1          -----GYTTLKVG----------------------------QTISRRIVDGDVVFLNRPP
BdRPE1          -----GYTTLKVG----------------------------QTISRRIVDGDVVFLNRPP
OsRPE1b         -----GHTTLKVG----------------------------QTISRRIVDGDVVFLNRPP
OsRPE1a         -----KHTILKVG----------------------------EIVNRRVFDGDIVFLNRPP
SbRPE1a         -----KCIMLRVG----------------------------ETVDRRVLDGDLVFLNKPP
SmRPD1          -----SCKKLQVG----------------------------DVIHRSLKDGDQVFVNRPP
SbRPD1          -----KADQLEIG----------------------------DIAYRPLQDGDLILINRPP
ZmRPD1          -----KADQLEIG----------------------------DIAYRPLQDGDIILINRPP
BdRPD1          -----KENQLEIG----------------------------DIVYRPLQDGDLILVNRPP
OsRPD1a         -----KANQLEIG----------------------------DIAYRLLQDGDLVLVNSPP
OsRPD1b         -----KANKLEIG----------------------------DIAYRLLQDGDLVLVNRPP
AtRPD1          ------VNDLQTG----------------------------DKIFRSLMDGDTVLMNRPP
CpRPD1          -----RISDLRMG----------------------------DIISRPLKDGDILLINRPP
VvRPD1          -----RMNDFQAG----------------------------DIIYRPLTDGDIVLINRPP
PtRPD1          -----HMKELRLG----------------------------DIIYRPLNDGDTVLINRPP
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                         :  *                                * : *** ::.*  *

ZmRPB1          SLHKMSIMGHRIKIMP-YSTFRLNLSVTSPYNADFDGDEMNMHVPQSFETRAEVLELMMV
AtRPB1          SLHKMSIMGHRIRIMP-YSTFRLNLSVTSPYNADFDGDEMNMHVPQSFETRAEVLELMMV
AtRPE1          TTHKHSLQALRVYVHE-DNTVKINPLMCSPLSADFDGDCVHLFYPQSLSAKAEVMELFSV
CpRPE1          TTHKHSLQALSVYIHD-DHTVKINPLICGPLSADFDGDCVHLFYPQSPAARAEVLELFSV
VvRPE1          TTHKHSLQALSVYVHD-DHTVKINPLICGPLSADFDGDCVHLFYPQSLGAKAEVLELFSV
PtRPE1a         TTHKHSLQALSVYVHD-DHTVKINPLICGPLSADFDGDCVHLFYPQSLAAKAEVLELFSV
PtRPE1b         TTHKHSLQALSVYVHD-DHAVKINPLICGPLSADFDGDCVHLFYPQSLAAKAEVLELFSV
SbRPE1b         STHKHSLQAFYAYVHD-DHTVKINPLMCGPFSADFDGDCVHIYYPQSLAAKAEALELFSV
ZmRPE1          STHKHSLQAFYAYVHD-DHTVKINPLMCGPFSADFDGDCVHIYYPQSLAAKAEALELFSV
BdRPE1          STHKHSLQAFYVYIHD-DHTVKINPLICSPLAADFDGDCVHIYYPQSLAAKAEALELFSV
OsRPE1b         STHKHSLQAFRVYVHE-DHTVKINPLICAPFAADFDGDCVHIYYPQSLAAKAEALELFSV
OsRPE1a         STDKHSVEAFYVQVHN-DHTIKINPLICDPLGADFDGDCVQIFYPRSLSARAEAKELYTV
SbRPE1a         STDMHSIQALYVHVHD-DHTIKINPLICGPLEADFDGDCVHIFFPRSVLARVEAAELFAV
SmRPD1          TFHKHALIGLKSKVIR-NNVFAVNPLICPPLFADFDGDTLALYLPQSLQVRAEVAELVAL
SbRPD1          SVHQHSLIAFSAKILPIHSVVSINPLCCTPFLGDFDGDCLHGYIPQSVRSRIELGELVSL
ZmRPD1          SVHQHSLIALSAKILPIHSVVSINPLCCTPFAGDFDGDCLHGYIPQSIRSRVELEELVSL
BdRPD1          SVHQHSLIALSAKLLPVQSVVAINPLNCAPLSGDFDGDCLHGYVPQSIGSRVELGELVSL
OsRPD1a         SVHQHSLIALSAKLLSTQSAVSINPLCCDPFKGDFDGDCLHGYIPQCLQSRIELEELVGL
OsRPD1b         SVHQHSLIALSAKLLPIQSAVAINPLCCDPFKGDFDGDCLHGYVPQTLQSRVELDGLVSL
AtRPD1          SIHQHSLIAMTVRILPTTSVVSLNPICCLPFRGDFDGDCLHGYVPQSIQAKVELDELVAL
CpRPD1          SIHPHSLIALSVKVLPISSVVSINPICCSPFRGDFDGDCFHGYIPQSIEARVELHELVAL
VvRPD1          SIHQHSVIALSVKVLPLNSVVSINPLCCSPFRGDFDGDCLHGYIPQSVDSRVELSELVAL
PtRPD1          SIHQHSLIALSVKVLPVPSVLAINPLCCPPFRADFDGDCLHGYVPQSVDTRVELTELVSL
                :    :: .    :     .. :*     *  .***** .  . *.    . *   *  :

ZmRPB1          PKCIVSPQSNRPVMGIVQDTLLGCRKI-TKRDTLIEKDVFMNI--LMWWQDFDGKIPAPT
AtRPB1          PKCIVSPQANRPVMGIVQDTLLGCRKI-TKRDTFIEKDVFMNT--LMWWEDFDGKVPAPA
AtRPE1          EKQLLSSHTGQLILQMGSDSLLSLRVM--LERVFLDKATAQQL--AM-YGSLSL--PPPA
CpRPE1          EKQLLSSHSGNLNLQLAADSLLSLKVM--FEKFFLGKTAAQQL--AM-FGSLSL--LWPA
VvRPE1          EKQLLSSHSGNLNLQLATDSLLSLKVL--FERYFLNKAAAQQL--VM-FVSMSL--PRPA
PtRPE1a         EKQLLSSHSGNLNLQLTTDSLLSLKMI--FKACFLDKSAAQQL--AM-FVSPDL--PQPA
PtRPE1b         EKQLLSSHSGNLNLQLTTDSLLSLKMM--FKACFLGKSAAQQL--AM-FISPYL--PQPA
SbRPE1b         ERQLISSHSGKVNLQLGNDCLVAMKAM--SDRTVLHKELANQL--AM-FVPFSL--LAPA
ZmRPE1          ERQLISSHSGKVNLQLGNDSLVAMKAM--SHTTMLHKELANQL--AM-FVPFSL--LAPA
BdRPE1          EKQLTNSHNGKVNLQLSNDSLLALKHM--SSRTVLSKESANQL--AM-LLSFSL--PDPA
OsRPE1b         EKQLTSSHSGKVNLQLVSDSLLALKHM--SSRTMLSKEAANQL--AM-LVTCSL--PDPA
OsRPE1a         DKQLVSSHNGKLNFQFKNDFSLALKIM--CGRE-YSEREANQITNAM-FSSGMY--PQKP
SbRPE1a         EKQLLNSHNAKLNFQIKNDYLLALRIM--CDRSY-SKEKANQI--AM-FSSGMI--PPCN
SmRPD1          PKQLVSSQGGQSIIGLTQDALLGAHLM-TRKNVFLDKLDMDQL--RM-WCPSAE-VPVPA
SbRPD1          HHQLLNMQDGRSLVSLTHDSLAAAHLL-TSTDVFLKKSEFQQL--QM-LCLSVL-TPVPA
ZmRPD1          HNQLLNMQDGRNLVSLTHDSLAAAHLL-TSTDVFLKKSELQQL--QM-LCLSVS-TPAPA
BdRPD1          SHQLLNMQDGRSLVSLTHDSLAAAHLL-TSSGVLLNKTEFQQL--QM-LCVSLSPTPVPS
OsRPD1a         SGQLLNQQDGRSLVSLTHDSLAAAHQL-TNADVFLEKAEFQQL--QM-LSSSISLTPMPS
OsRPD1b         SGQMLNAQDGRSLVSLTHDSLAAAHQL-TSADVFLQKAEFQQL--QL-LCSSISPTPEPS
AtRPD1          DKQLINRQNGRNLLSLGQDSLTAAYLVNVEKNCYLNRAQMQQL--QM-YCPFQL--PPPA
CpRPD1          DRQLTNWLSGRNLLCLGQDSLTAAHLI-KEDGFLLNKYQMQQL--KM-YCPYEL--PPPA
VvRPD1          NRQLINRQSGRNLLSLSQDSLSAAHLV-MEDGVLLNLFQMQQL--EM-FCPYQL--QSPA
PtRPD1          DKQLTNWQSGRNLLSLSQDSLTAAHLV-LEDDVFLSSFELQQL--QM-FRPERF--LLPA
                   : .    .  . :  *   .   :              :    :

ZmRPB1          ILK--P---RPIWTGKQVFNLIIPKQINLIRFSAWHSEEEKGFITPGDTMVRIEKGELLS
AtRPB1          ILK--P---RPLWTGKQVFNLIIPKQINLLRYSAWHADTETGFITPGDTQVRIERGELLA
AtRPE1          LRK--SSKSGPAWTVFQILQLAFPERLS----------------CKGDRFL-VDGSDLLK
CpRPE1          LFK--SHSSGSFWTASQIIQTALPACFD----------------CNEDRYL-IRKSEILN
VvRPE1          LLK--SPCSGPCWTALQILQTALPSYFD----------------CIGERHW-ISKSAILK
PtRPE1a         LLK--VNCIRPYWTAHQILQMALPTCFN----------------CSGERFL-INNSNVLK
PtRPE1b         LLK--VNCFFPHWTAHQILQMALPACFN----------------CSGERFL-IINSNFLK
SbRPE1b         VMK--P---IPSWTITQIVQGALPAKLT----------------CQGDTHL-VRDSTIIK
ZmRPE1          VIK--P---VPSWTISQIVQGAFPANLT----------------CQGDTHL-VRDSTIIR
BdRPE1          VVK--L---KPCWTITQIIQGALPAALT----------------CEGGRFL-VKDSTVIK
OsRPE1b         VIK--S---KPYWTISQIVQGALPKALT----------------SQGDKHV-VRDSTIIK
OsRPE1a         LIG------GPYWTFPQILET------------------------------TKSNAITL
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SbRPE1a         -----PWTICDRWTIPQILQT----------------------------------TDALR
SmRPD1          IVK--SPRKSPLWTGQQLFQMTLPTTFD--------------WESDDGGLI-IRQGEILR
SbRPD1          VIK-SMNFQGSRWTGKQLFSMLLPSGMK--------------FSCDR-MLH-ILNGEVLT
ZmRPD1          VIK-SMNFQGSLWTGKQLFSMLLPSGMN--------------FSCDT-ELH-IMDSEVLT
BdRPD1          VIK-SINPQGPLWTGKQLFGMLLPSGMN--------------F-SPDPKLH-IKDSEVLA
OsRPD1a         VFK-STNSQGPLWTGKQLFGMLLPYGMN--------------I-SFDQKLH-IKDSEVLT
OsRPD1b         VVK-SANFQGSLWTGKQLFGMLLPSGMN--------------I-SFDQKLH-IKDSEVLT
AtRPD1          IIKASPSSTEPQWTGMQLFGMLFPPGFD--------------YTYPLNNVV-VSNGELLS
CpRPD1          LVK-APRLNSSVWTGKQLFSMLLPPGFN--------------YYFSQNGVC-IINGELTS
VvRPD1          IIK---------------------------------------------------------
PtRPD1          VKA--PSANALVWTGKQLISMLLPVGFD--------------HDFPSCNVC-IRDGDLVS


ZmRPB1          GTL-CKKSLGT-GSGSLIHVIWEEVGPDAARKFLGHTQWLV-NYWLLQNGFSIGIGDTIA
AtRPB1          GTL-CKKTLGT-SNGSLVHVIWEEVGPDAARKFLGHTQWLV-NYWLLQNGFTIGIGDTIA
AtRPE1          FDF-GVDAMGS-IINEIVTSIFLEKGPKETLGFFDSLQPLL-MESLFAEGFSLSLEDLSM
CpRPE1          IDF-NKDSVQS-VVGEVVNSIFYEKGPKEVLEFFASLQPLL-MENLFVEGFSVGLKDFSM
VvRPE1          VDY-NRDVLQS-LVNEIVTSIFSEKGPNEVLKFFDSLQPLL-MENLFSEGFSVSLEDFSI
PtRPE1a         VDF-NRDVVAS-MINEILISIFFEKGSGAVLKFFNALQPLL-MENLFSEGFSVSLKDFSI
PtRPE1b         VDF-NRDVVAS-VINEILISMFFEKGSGAVLKFFNSLQPML-MENLFSEGFSVSLEDFSI
SbRPE1b         LDL-DKESVQD-SFPDLVSSILREKGPREALQFLNVLEPLL-MEFLVLGGLSISLRDFNV
ZmRPE1          LDL-GKESVQD-SFPDLVSSILREKGPKEALQFLNVLEPLL-MEFLLLDGLSISLRDFNV
BdRPE1          LDL-AKESVQA-SFSDLVSSILCVKGPGGALQFLNALQPLL-MEYLLLDGFSVSLQDFNV
OsRPE1b         LDL-DKESVQT-SFSDLVYSTLSVKGPGEALQFLNVLQPLL-MELILLDGFSVSLQDFNV
OsRPE1a         ADHLDRESVGALATGTTISSILSTKGPREATEFLNLLQPLL-MESLLIDCFSINLGDFTV
SbRPE1a         IVPSHPNTVGA-SVTAIITSTLSEKGPREAIKLINLLQPLL-MESLLMDGFSISLKDLDG
SmRPD1          TSDKSSAWLGK---DGLMTTICRRYGPDRALEHLDIAQGIA-VDWISERGFSVGLCDFYM
SbRPD1          CSL-GSSWLQN-NTSGLFSVMFKQYG-CKALDFLSSAQEVL-CEFLTMRGLSVSLSD--M
ZmRPD1          CSL-GSSWLQN-NTSGLFSVMFKQYG-CKALDFLSSAQEVL-CEFLTMRGLSVSLSDLYM
BdRPD1          CSG-GSFWLQN-NTSGLFSVLFKQYG-GEALEFLSSAQDML-CEFLTMRGLSVSLSDIYL
OsRPD1a         CSS-GSFWLQN-NTSSLFSVMFKEYG-CKALEFLSSTQDVL-CEFLTMWGLSVSLSDLYL
OsRPD1b         CSS-GSFWLQN-NTSSVFSVMFKEYG-SKALEFLSSTQDVL-CEFLTMKGLSVSLSDFYL
AtRPD1          FSE-GSAWLRD-GEGNFIERLLKHDK-GKVLDIIYSAQEML-SQWLLMRGLSVSLADLYL
CpRPD1          SSD-GSAWLRD-NDGNLFQSLVK-YDKSMVLNFLYAAQEVL-CDWLSDRGFSISLSDLYL
VvRPD1          -------------------------------------APLLDTQWLSMRGLSVSLSDIYL
PtRPD1          SE--GSFWLWD-TDGNLFQSLVKHCH-GQVLDFLYAAQRVL-CEWLSMRGLSVSLSDLYL
                                                       :     :    :::.: *

ZmRPB1          DAST-------------METINDTISKAKNAVKELIKK-----------------AHEKQ
AtRPB1          DSST-------------MEKINETISNAKTAVKDLIRQ-----------------FQGKE
AtRPE1          SRAD-------------MDVIHNLIIREISPMVSRLR-----------------------
CpRPE1          PKSD-------------MQAIQKL-IHDTSLFLSCLG-----------------------
VvRPE1          PSEV-------------TQNIQKN-VEDISSLLYNLR-----------------------
PtRPE1a         SQAV-------------KQSIQES-FKVISPLLCNLR-----------------------
PtRPE1b         SRAV-------------KQRIPES-FKAISPLLCNLR-----------------------
SbRPE1b         PKAL-------------LEEAQKN-IQNQSLVLEQSR-----------------------
ZmRPE1          PKAL-------------LEEAQKD-IRNQSLILEQSR-----------------------
BdRPE1          PKVL-------------LEEVHKS-IQEQSLVLEQSR-----------------------
OsRPE1b         PKVL-------------LEEAQKN-IEKQSLILEQSR-----------------------
OsRPE1a         PSPI-------------LEAIQNN------------------------------------
SbRPE1a         QSA--------------MQKANQS------------------------------------
SmRPD1          AADAVSRRKLEEETLCAVEEAKIS-SLAHQIVSDPRFQ-----------------VNSVS
SbRPD1          FSDHYSRRKLTEGVKLALDEAEEA-FRIKQILLDPINI-----------------PVLKC
ZmRPD1          FSDHYSRRKLAEGVKLALYEAEEA-FRVKKILLDPINI-----------------PVLKC
BdRPD1          FSDHYSRRKFAEEVNLALDEAEEA-FRVTQILLSPNFI-----------------PHLKC
OsRPD1a         FSDHYSRRKLSEEVHLALDEAEEA-FQIKQILLNSVSI-----------------PNLKY
OsRPD1b         FSDHYSRKKLSEEIHLALDEAEEA-FQIKQILLNTVSI-----------------PNLKH
AtRPD1          SSDLQSRKNLTEEISYGLREAEQV-CNKQQLMVESWRD-----------------FLAVN
CpRPD1          SSDLHSRENLMDEISWGLLEAEQT-CNFKQLMVDSCRD-----------------LLAGN
VvRPD1          SSDSISRKNMIDEVFCGLLVAEQT-CHFKQLLVDSSQN-----------------FLIGS
PtRPD1          CPDSNSRKNMMDEIWYGLQDADYA-CNLKHLMVDSCRDFLTGNNEEDQCNVERLRFLSGC


ZmRPB1          LEAEPG------------RTMMESFENRVNQVLNKARDDAGSSAQNSL---SESNNLKAM
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AtRPB1          LDPEPG------------RTMRDTFENRVNQVLNKARDDAGSSAQKSL---AETNNLKAM
AtRPE1          ----------------------LSYRD--ELQLENSIHKVKEVAANFM---LKSYSIRNL
CpRPE1          ----------------------STYNE--ELQLENRIRCLKETAENFI---IKSS-LRNL
VvRPE1          ----------------------SMYNELLQLQAENHLRLTKVPVANFI---LNSSALGNL
PtRPE1a         ----------------------STYNELVELQVENHIQDVKTPVLEFI---LTSSALGYL
PtRPE1b         ----------------------STFNELVELQVENHIRDVKQPVREFI---LTSSALGYL
SbRPE1b         ----------------------CSTSQFVELRVENNLKSVKQQISDYV---GKFSGLGLL
ZmRPE1          ----------------------CSTSQFVEFRVENNLKNVKQQISDSV---GKFSDLGLL
BdRPE1          ----------------------CSKSQFVEMRVDNNLKDVKQQISDFV---VESSHLGLL
OsRPE1b         ----------------------FAENQVVEMRVDNNLKDIKQQISDFV---VKRSHLGLL
OsRPE1a         ---------------------------------PLELNKYREPIMDFI---THSSAIGLL
SbRPE1a         --------------------------------ISLEIDKFSKSIVDFI---ANSSALGLL
SmRPD1          RPRC----NSWNERVQPVTSVNEATQQAAISAFQSTMKAFERTIEEHVRENSRENSLLRM
SbRPD1          QDETEDV--TYRQSDC--IQNNPSVIRSSIMAFKDVFSDLLKMVQQHV---SNDNSMMVM
ZmRPD1          HDETEDV--TYRQSDC--IQSNPSVIRSSIMAFKDVFRDLLKMVQQHV---SNDNSMMVM
BdRPD1          YDDCDDLSDSYEQSDF--VQSNLPIIKSSIMAFKSVFSDLLKMVQQHT---PKDNSMMAM
OsRPD1a         YDGGDDRSNTDEQSGF--TQVSLPIIRSSMTSFKSVFNDLLKMVQQYV---SKDNSMMTM
OsRPD1b         YDGPDNLSNSHGQSDF--TQVSLPIIKSSITGFKSVFNDLLKMVLQHV---SKDNSMMAM
AtRPD1          GEDKEEDSVSDLARFCYERQKSATLSELAVSAFKDAYRDVQALAYRYG---DQSNSFLIM
CpRPD1          DEESQNVITFDVERLCYEKQGSAVLSQASVDAFKQVFRDIQTLAFKYA---SKENSLLAM
VvRPD1          GENNQNGVVPDVQSLWYERQGSAALCQSSVCAFKQKFRDIQNLVYQYA---NKDNSLLAM
PtRPD1          SEEDYCVMAFDGERLCYEKQRSAALSQSSVDAFRLVFRDIQSLVYKYA---SQDNSFLAM
                                                                        :  :

ZmRPB1          VTAGSKGSFINISQMTACVGQQNVEGKRIP--------FGFIDRTLP------HFTKDDY
AtRPB1          VTAGSKGSFINISQMTACVGQQNVEGKRIP--------FGFDGRTLP------HFTKDDY
AtRPE1          IDIKSNSAITKLVQQTGFLGLQLSDKKKFYTKTLVEDMAIFCKRKY----------GRIS
CpRPE1          IDFRSDSAVNKVVQQIGFLGLQLSDKGKFYSKNLVEDVAFLFRSKHP--------GAGHY
VvRPE1          IDSKSDSAINKVVQQIGFLGQQLSEKGKFYSRTLVEGMAYLFKSKYP-------FHGADY
PtRPE1a         IDSKSDGAVAKLVQQIGFLGLQVSDRGKLYSKTLVEDLASHFQSKYP-------TNLLNY
PtRPE1b         IDSKSDAAVTKVVQQIGFLGLQVSDRGKLYSKTLVEDLASHFLSKYP-------ANLFDY
SbRPE1b         IDPKKEASMAKVVQQVGFVGLQLYREGKLYSRRLVEDCFSSFVNKHS-------AIGDEY
ZmRPE1          IDPKKEASMSKVVQQVGFVGLQLYREGKLYSRRLVEDCFTNFVNKHL-------AIGDEY
BdRPE1          IDPKSEPSMSKVVQQLGFVGLQLYREGKFYSSRLVEDCFSSFVDKHP------PIVGNQH
OsRPE1b         IDPKSDSSVSKVVQQLGFVGLQLYREGKFYSRRLVEDCYYTFVNKHP-------AVREEH
OsRPE1a         VDPKSDSNMNKVVEQLGFLGPQLQHNGRLYSSRLVEDCLSKSLHRCC------GSTNCCN
SbRPE1a         VDPKNDSALMNLVEQVGFLGYQLQSTDRLYSNNLVEDCYNFLEKRS-------GSTKCYD
SmRPD1          VEANSKGSFSKMMQQGGCLGLQLRQGEFVYHR--VKSLFPRAVENESR-----GYLTSSE
SbRPD1          INAGSKGSMLKYAQQTACVGLQLPASKFPFRVPSQLSCIRWNRQKSLNYEAE-GTNERVG
ZmRPD1          INAGSKGSMLKYAQQTACIGLQLPASKFPFRIPSQLSCISWNGQKSLNYEAE-STSERVG
BdRPD1          INAGSKGSMLKFVQQAACVGLQLPAGKFPFRIPSELTCASWNRHKSLDCDISEGARKRLG
OsRPD1a         INSGSKGSVLKFVQQTACVGLQLPASKFPFRIPSQLSCVSWNRHKSRNCEITDGTSECVG
OsRPD1b         INSGSKGSVLKFVQQTACVGLQLPASTFPFRIPSELSCVSWNRQKSLNCEITNNTSECMA
AtRPD1          SKAGSKGNIGKLVQHSMCIGLQNSAVSLSFGFPRELTCAAWNDPNSPLRGAKGKDSTTTE
CpRPD1          YKAGSKGSLPKLVQHSMCLGLQHSLVPLSFRFPHQLSCAAWNKQK---------------
VvRPD1          LKAGSKGNLLKLVQQGLCLGLQHSLVPLSFKIPHQLSCAAWNKQKVP-GLIQNDTSEYAE
PtRPD1          FKAGSKGNLLKLVQHSMCLGLQHALASLSFRIPHQLSCAGWNKQKAD------DATESAK
                    ..  . :  :    :* *

ZmRPB1          GPESRGFVENSYLRGLTPQEFFFHAMGGREGLID-TAVKTSETGYIQRRLVKAMEDIMVK
AtRPB1          GPESRGFVENSYLRGLTPQEFFFHAMGGREGLID-TAVKTSETGYIQRRLVKAMEDIMVK
AtRPE1          SSGDFGIVKGCFFHGLDPYEEMAHSIAAREVIVR-SSRGLAEPGTLFKNLMAVLRDIVIT
CpRPE1          PSANFGLIKSCFIHGLDPYEEMAHSISTREVIVR-SSRGLTEPGTLFKNMMAVLRDIIVC
VvRPE1          PSGEFGLIRSCFFHGLDPYEEMVHSISTREIIVR-SSRGLSEPGTLFKNLMAILRDVVIC
PtRPE1a         PSAQYGLIQSSFFHGLDAYEEMAHSISTREVIVR-SSRGLSEPGTLFKNLMAILRDVVIC
PtRPE1b         PSAQYGLIQNSFFHGLDAYEEMAHSISTREVIVR-SSRGLSEPGTLFKNLMAILRDVVIC
SbRPE1b         SPEAFGLVQSSYFHGLNPYEELVHAICTRETMIR-SSRGLSEPGTLFKNLMAILRDVVIC
ZmRPE1          PPEAYGLVQSSYFHGLNPYEELIHAISTREAMIR-SSRGLSEPGTLFKNLMAILRDVVIC
BdRPE1          PPEAYGLVQNSYFHGLNPYEELVHSISTREAIVR-SSRGLTEPGTLFKNLMAILRDVVIC
OsRPE1b         SPEAYGLVRSSYFHGLNPYEELVHAISTREAIVR-SSRGLTEPGTLFKNLMALLRDVVIC
OsRPE1a         PLEEYGTVRSSIYHGLNPYEALLHSICEREKIMR-ASKGLVEPGSLFKNMMSRLRDVTAC
SbRPE1a         PPKGHDFVTSSFYNGLNPYEELLHSISVREKIERSSSKGLAEAGNLFKNMMAMLRDVTVC
SmRPD1          LWKSMGLVESSFLDGLDPREFFIHSLSSRKG----NDGSQQRCASFFRFLMSYMKDIRVE
SbRPD1          GQNLYAVIRNSFIEGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHLRDIHVA
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ZmRPD1          GQNLYAVIKNSFIEGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHLRDIHVA
BdRPD1          GQNSHAVIRNSFIEGLNPLECLLHSISGRANF---FSENADVPGTLTKNLMYHLRDIYVA
OsRPD1a         GQDMYAVVRNSFLDGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHLRDTYVA
OsRPD1b         GQNMYAVIRNSFLDGLNPLECLLHAISGRANF---FSENADVPGTLTRKLMYHLRDTYVA
AtRPD1          SYVPYGVIENSFLTGLNPLESFVHSVTSRDSS---FSGNADLPGTLSRRLMFFMRDIYAA
CpRPD1          ------------------------------------------------------------
VvRPD1          SYIPYAVVENSFLMGLNPLECFVHSVTSRDSS---FSDNADLPGTLTRRLMFFMRDLYIA
PtRPD1          RYIPHAVVEGSFLSGLNPIECFVHSVTSRDSS---FSDNADLPGTLFRRMMFFMRDLHGA


ZmRPB1          YDGTVRNSLGDVIQFLYGEDGMDAVWIESQKLDSLKMKKPEFDNVFRYELDDENWRPNYM
AtRPB1          YDGTVRNSLGDVIQFLYGEDGMDAVWIESQKLDSLKMKKSEFDRTFKYEIDDENWNPTYL
AtRPE1          NDGTVRNTCSNSVI------------------------------QFKYGVDSER------
CpRPE1          YDGTVRNICSNSVI------------------------------QFKYGLKADN------
VvRPE1          YDGTVRNVCSNSII------------------------------QFEYGVKART------
PtRPE1a         YDGTVRNVCSNSII------------------------------QSEYGVKVGA------
PtRPE1b         YDGTVRNVSSNSII------------------------------QFEYGVKVGT------
SbRPE1b         YDGTVRNICSNSII------------------------------QLKYGEDDEA------
ZmRPE1          YDGTVRNICSNSII------------------------------QLKYGEDDET------
BdRPE1          YDGTVRNICSNSIM------------------------------QLKYNEDDAT------
OsRPE1b         YDGTVRNVCSKSII------------------------------QLNYTEDDAL------
OsRPE1a         YDGSIRTSSGNLVL------------------------------QFGSRDASNC------
SbRPE1a         YDGTMRTSYNNSIV------------------------------QFDSTNVSSS------
SmRPD1          YDNTIRSTHGGHIF------------------------------QFSYGATAE-------
SbRPD1          YDGTVRSSYGQQIV------------------------------QFSYDSADDP------
ZmRPD1          YDGTVRSSYGQQIV------------------------------QFSYDSVDDL------
BdRPD1          YDGTVRSSYGQQIV------------------------------QFTYDTAEDI------
OsRPD1a         YDGTVRSSYGQQIV------------------------------RFSYDTADGM------
OsRPD1b         YDGTVRSSYGRQIV------------------------------QFSYDTADGM------
AtRPD1          YDGTVRNSFGNQLV------------------------------QFTYETDGPV------
CpRPD1          ------------------------------------------------------------
VvRPD1          YDGTVRNAYGNQLV------------------------------QFSYNIEHTSTPSDGI
PtRPD1          YDGTVRNAYGNQLV------------------------------QFSYNIDDMDPSGSVD


ZmRPB1          LPEHVDDLKTIREFRNVFEAEVQKLEADRYQLGSEITTTGDNSWPMPVNLKRLIWNAQKT
AtRPB1          SDEHLEDLKGIRELRDVFDAEYSKLETDRFQLGTEIATNGDSTWPLPVNIKRHIWNAQKT
AtRPE1          --GH--------------------------------------------------------
CpRPE1          --EP--------------------------------------------------------
VvRPE1          --KP--------------------------------------------------------
PtRPE1a         --ES--------------------------------------------------------
PtRPE1b         --ES--------------------------------------------------------
SbRPE1b         --DS--------------------------------------------------------
ZmRPE1          --DS--------------------------------------------------------
BdRPE1          --DI--------------------------------------------------------
OsRPE1b         --DF--------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          YTDC--------------------------------------------------------
OsRPD1a         YSDH--------------------------------------------------------
OsRPD1b         NNDH--------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          NEDT--------------------------------------------------------
PtRPD1          EIN---------------------------------------------------------


ZmRPB1          FKIDFRRPSDMHPMEIVEAIDKLQERLKVVPGDDAMSIEAQKNATLFFNILLRSTFASKR
AtRPB1          FKIDLRKISDMHPVEIVDAVDKLQERLLVVPGDDALSVEAQKNATLFFNILLRSTLASKR
AtRPE1          ------------------------------------------------------------
CpRPE1          ------------------------------------------------------------
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VvRPE1          ------------------------------------------------------------
PtRPE1a         ------------------------------------------------------------
PtRPE1b         ------------------------------------------------------------
SbRPE1b         ------------------------------------------------------------
ZmRPE1          ------------------------------------------------------------
BdRPE1          ------------------------------------------------------------
OsRPE1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          VLKEYRLTKEAFEWVIGEIESRFLQSLVAPGEMIGCVAAQSIGEPATQMTLNTFHYAGVS
AtRPB1          VLEEYKLSREAFEWVIGEIESRFLQSLVAPGEMIGCVPAQSIGEPATQMTLNTFHYAGVS
AtRPE1          ------------------------QGLFEAGEPVGVLAATAMSNPAYKAVLDS-SPNSNS
CpRPE1          ------------------------LRLFPAGEPVGVLAATAMSNPAYKAVLDS-TPSSNS
VvRPE1          ------------------------QHFFPAGEPVGVLAATAMSNPAYKAVLDS-SPSSNS
PtRPE1a         ------------------------QSLFPAGEPVGVLAATAMSNPAYKAVLDS-TPSSNS
PtRPE1b         ------------------------QSLFPAGEPVGVLAATAMSNPAYKAVLDS-TPSSNC
SbRPE1b         ------------------------SSAVPPGEPVGVLAATAISNPAYKAVLDS-SQSNNA
ZmRPE1          ------------------------SSVVPPGEPVGVLAATAISNPAYKAVLDS-SQSNNA
BdRPE1          ------------------------PSALTPGEPVGVLAATAISNPAYKAVLDA-SQSNNT
OsRPE1b         ------------------------PSAIGPGEPVGVLAATAISNPAYKAVLDA-SQSNNT
OsRPE1a         ---------------------------VTPGDPVGILAATAVANAAYKAVLAP-NQNNII
SbRPE1a         ---------------------------LTPGDSIGILAATVFANAAYKAVLVP-NQKNMT
SmRPD1          -----------------------------PGEPVGLLAGTAVIEPVYDQVMSS-SPQAST
SbRPD1          --------------------------VDKLGAPVGCWAACSISEAAYGALEHPVNGLEDS
ZmRPD1          --------------------------VDKLGAPVGCRAACSISEAAYGALEHPVNGLEDS
BdRPD1          ------------------------GQEGEFGAPVGSWAACSISEAAYGALDHPVNVIEDS
OsRPD1a         ------------------------DLEGEPGAPVGSWAACSISEAAYGALDHPVNSLEDS
OsRPD1b         ------------------------DLEGEPGAPVGSWAACSISEAAYGALDHPVNALEDS
AtRPD1          --------------------------EDITGEALGSLSACALSEAAYSALDQPISLLETS
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------CAYDMGGQPVGSISACAISEAAYSALDQPISLLEPS
PtRPD1          ------------------------NSDGIAGRPVGPLAACAISEAAYSALDQPISLLEKS


ZmRPB1          AKNVTLGVPRLREII----NVAKKIKTPSLSVYLKPQVNQKKELAKNVQCALEYTTLRSV
AtRPB1          AKNVTLGVPRLREII----NVAKRIKTPSLSVYLTPEASKSKEGAKTVQCALEYTTLRSV
AtRPE1          S------WELMKEVLLCKVNFQNTTNDRRVILYLNECHCGKRFC-------QENAACTVR
CpRPE1          S------WELMKEILLSKISFKNDLNDRRVILYLNDCNCARRHC-------QEKAACLVR
VvRPE1          S------WELMKEILLCQVNFKNDLIDRRVILYLNDCDCGRKYC-------RENAAYLVK
PtRPE1a         S------WDMMKEILLCKVGFKNDQADRRVILYFNYCGCGREHC-------QEKAAFLVK
PtRPE1b         S------WDMMKEILLCKVGFKNDLADRRVILYLNDCGCGRNYC-------QERAAYLVK
SbRPE1b         S------WESMKEILQTRTSYKNDAKDRKVVLFLSDCSCAKKFC-------KERAALAVQ
ZmRPE1          S------WESMKEILQTRTSYKNDVKDRKVVLFLNDCSCAKKFC-------KERAALAVQ
BdRPE1          S------WASMKEILQTKVSYKNDTNDRKVILFLNDCSCPKKFC-------KEKAAIAVQ
OsRPE1b         S------WERMKEILQTTSRYKNDMKDRKVILFLNDCSCAKKFC-------KEKAAIAVQ
OsRPE1a         S------WDSMKEVLLTRASTKADANHRKVILYLNQCSCENE-C-------MERA-LTIR
SbRPE1a         S------WDSMKEVLLTNACSKTGTIDQKAILYLNKCFCGLKFC-------SELAAHRVQ
SmRPD1          M------LKTLQNILFSN-SFKD--IDRCVTLKLQKLPVQ-----------PEWIALQVQ
SbRPD1          P------LMNLQEVFKC--HKATNSGDHIGLLFLSRHLKKYRYG-------LEYASLEVK
ZmRPD1          P------LMNLQEVFKC--HKATNSGDHIGLLFLSRHLKKYRYG-------LEYASLEVK
BdRPD1          P------LMNLQEVLKC--QKGTNSLDHFGLLFLSKNLKKYRYG-------FEYASLYVQ
OsRPD1a         P------LMNLQEVLKC--HKGTNSLDHTGLLFLSKHLRKYRYG-------FEYASLEVK
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OsRPD1b         P------LMNLQEVLKC--HKGTKSAVHTGLLFLSKYLKKYRYG-------FEYASLEVK
AtRPD1          P------LLNLKNVLEC--GSKKGQREQTMSLYLSEYLSKKKHG-------FEYGSLEIK
CpRPD1          ------------------------------------------------------------
VvRPD1          P------LLNLKRVLEC--GLRKSTADRTVSLFLSKKLEKRKHG-------FEYGALEVK
PtRPD1          P------LLNLKNVLEC--GLKRNSAHQTMSLFLSEKLGRQRHG-------FEYAALEVQ


ZmRPB1          THATEIWYDPDPLGTIIEED----------------------------------------
AtRPB1          TQATEVWYDPDPMSTIIEED----------------------------------------
AtRPE1          NKLNKVSLKDTAVEFLVE------------------------------------------
CpRPE1          NQLNKVTLKDAAVQFLVE------------------------------------------
VvRPE1          NQLKKASLKDTAVEFMIE------------------------------------------
PtRPE1a         NHLEKVSLKDVAKCFMIE------------------------------------------
PtRPE1b         NHLEKVSLKDIAKCFMIE------------------------------------------
SbRPE1b         SCLKRVTLGDCATDICIE------------------------------------------
ZmRPE1          SCLKRVTLGDCATDICIE------------------------------------------
BdRPE1          NRLKRVTLEDCATDICIE------------------------------------------
OsRPE1b         GCLRRITLEDCATDICIEDGNWAAPAGFQHPVPPPQCKILPVPIPIPAHGSVKFPPVPIP
OsRPE1a         ACLRRIKLEDCTTEISIK------------------------------------------
SbRPE1a         SCLKRIKLEYCAIEVSIK------------------------------------------
SmRPD1          DFLKPVTIGMLASKIWIE------------------------------------------
SbRPD1          NHLEQVNFSDLVETIMII------------------------------------------
ZmRPD1          NHLERVNFSDLVETIMII------------------------------------------
BdRPD1          NYLEPMDFSELVNTVMIQ------------------------------------------
OsRPD1a         DHLERVDFSDM-------------------------------------------------
OsRPD1b         DHLERVDFSDLVDTVMIL------------------------------------------
AtRPD1          NHLEKLSFSEIVSTSMII------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          NHLEKLLFSDIVSTVMIV------------------------------------------
PtRPD1          NHLERLLFSDIVSFVRII------------------------------------------


ZmRPB1          -------TEFVQSYYEMPDEDIDPDKISPWLLRIELNREMMVDKKLSMADIAEKINREFD
AtRPB1          -------FEFVRSYYEMPDEDVSPDKISPWLLRIELNREMMVDKKLSMADIAEKINLEFD
AtRPE1          -------------YRKQPTISEIFGIDSCLHGHIHLNKTLLQDWNISMQDIHQKCEDVIN
CpRPE1          -------------YKNHRTVSEGLEIDAGLAGHVHLNKTLLQVLNIDMQEILQQCRERIS
VvRPE1          -------------YVKQHAVSGSSEPGTGLVGHIHLNKLLLQDLNVSMQEVCQKCEETIN
PtRPE1a         -------------YKNQQ-IPESFGSDAGLVGHVHLEKRILQELNISAQVILEKCQETVN
PtRPE1b         -------------YKSQQ-IPESFGSDAGLVGHVHLDKRKLQDLNITAQVILEKCQETVN
SbRPE1b         -------------HQKQINLDGTSEAAPTLVGHIHLDKGQLERINISIQDILQKCQEVSG
ZmRPE1          -------------HQKQINLDGTSEAAPTLVGHIHLDKGHLERINISTQDILQKCQEVSG
BdRPE1          -------------YI----LDGSSEATPALVGHIHLEKARLDMINVSTEDILQKCQEVSL
OsRPE1b         APEHLKYNIHVVRYQKQIGLDGTSEAAPALVGHIHLDRAHLERINISTEDILQKCQEVSG
OsRPE1a         -------------YQQQA-----TQAAHHLVGHIHLDKKQLNQIETIMDSVLHKCQETFR
SbRPE1a         -------------YQQEA-----TQAAQCLVGHIHLDKEQLNWMEITMGNILQTCQKNVN
SmRPD1          -------------YSPCSEVGGQKKRVP-WIGCFQLRAEAMERCSLNIDTIVCHLRKLLP
SbRPD1          -------------YDGHD----KIRKEGTWTTHFHISKEMMKKKRLGLRFVIEELTKEYN
ZmRPD1          -------------YDGHD----KIRNEGMWTTHFHINKAMMKKKRLGLRFVVDELAKEYD
BdRPD1          -------------YDGGG--VQKTKGSP-WITHFHISKEMMKRKRLGLRLLVEDLTEHYN
OsRPD1a         -----------------------------------VDTETMKIKRLRLEFIVREIIDQYN
OsRPD1b         -------------------------------------LETMKIKRLRLGFIVRELIDQYN
AtRPD1          -------------FSPSS--NTKVPLSP-WVCHFHISEKVLKRKQLSAESVVSSLNEQYK
CpRPD1          ------------------------------------------------------------
VvRPD1          -------------FSPQN--GSKTHFSP-WVCHFHVCEEIAKKRSLKPHSIIDALYMKCN
PtRPD1          -------------FSPQS--DGRMHFSP-WVCHFHVYKEIVKKRSLKVHYIIDALEKQCK


ZmRPB1          -------DDLSCIF----------------NDDNADKLILRIRITNDEAPKGEIQDESAE
AtRPB1          -------DDLTCIF----------------NDDNAQKLILRIRIMNDEGPKGELQDESAE
AtRPE1          SLGQKKKKKATDDFKRTSLSVSECCSFRD-PCGSKGSDMPCLTFSYN-----ATDPDLER
CpRPE1          LF--RKKKKVGHCFKKIILSVSKCCSFQQ-SCEENSSDLPCLIFCWHD----TSDIHLER
VvRPE1          SF--RKKKNVGPFFKKIILSFRECCTFQH-SCQSKGSDMPCLLFFWQG----NRDDNLEQ
PtRPE1a         SF--RKKKKVGNLFKKTTLSISECC-----SFEQCTDELLCLMFFWQD----ANDVHLER
PtRPE1b         TF--RKKKKVGNLFKKTILLVSESC-----SFQQCIDESPCLMFFWQG----ADDVHLER
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SbRPE1b         RYG-KKKGHLCHLLKKITFATC-----------GKLHKVPCVQFSFSDEST-VLSESVER
ZmRPE1          RFG-KKKGHLCHIFKKITFATCDCSFTQM-PIDGKLHKVPCVQFAFSDDI--VLSESIER
BdRPE1          KHG-KKKGHLGHLFKKITFSTCDCSFTQKPMIDGKLPKVPCLQFSFSEDIP-MLSESVER
OsRPE1b         KYG-KKKGHLSNLFKNITFSTCDCLFTQK-LVDGKLPKLPCLQFFVSDNM--IVSESVER
OsRPE1a         NNI-KKKGSMREILKTVTFISSTSLCDQH-TDDDKKFQVSCLQFFLPGSITKNISESTER
SbRPE1a         KHV-MKNRQLMQILKTTEIISSEYCLCGQDIGDERALQVSCLQCFIHAST--TTVQPESN
SmRPD1          ----TSLDDPDAFIQGLHFFSRDVEV--------------LCFFPITSS---VSNYDSKQ
SbRPD1          ----ATRDQLKNAIPSICISRRKCV-----VGDEGVKISACCIAVVA-----LAEPNSMS
ZmRPD1          ----TTRDQLNNAIPSIRISRRKCL-----VGDEGVKSSSCCIAVVA-----HAERNSIS
BdRPD1          ----AKRDQLNNVIPKVYISKCKCS-----DDDDCINNQTCCITVVAQD---ESNSTSTS
OsRPD1a         ----TLRKQLNNAIPSVSISNSKCS-----VGNECVKNQTCCVTMVV-----QVEINSMS
OsRPD1b         ----ALRKKLNNMIPSVCISYSKCS-----VGNECVKNRSCCVTMVA-----QVESNSTS
AtRPD1          ----SRNRELKLDIVDLDIQNTNHC-----SSDDQAMKDDNVCITVTVV---EASKHSVL
CpRPD1          ---------------------RECP-----I-DDGPRQEDSFCISVTVV---KKSKDSSV
VvRPD1          ----SARAESKINLPDLQITSKDCF-----V-DMEKEDSDCFCITVSI----VNSKKSCI
PtRPD1          ----SKTR-----FPKVQITSRYCT-----VADTWKEKKETFCITVTIV---ETSKNEFI


ZmRPB1          DDVFLKKIEGN---MLTEMALRGIPD-INKVFIK-----------------EGKVN---T
AtRPB1          DDVFLKKIESN---MLTEMALRGIPD-INKVFI--------------------KQVRKSR
AtRPE1          TLDVLCNTVYP---VLLEIVIKGDSR-ICSANIIWNSSDMTTWIRNRHASRRGEWVLDVT
CpRPE1          TSYVLANMIYP---VLLETVIKGDPR-ICSANIIWASPDTMTWIRKPSRTRKGEWVLDVV
VvRPE1          ILHILAHKICP---VLLQTIIKGDSR-VCTVNIIWISPDTTTWIRNPCKSRKGELALDIV
PtRPE1a         TSNILADMICP---VLLETTIKGDHR-ISCANIIWASQETTTWIRNPSRTQKGELALDIV
PtRPE1b         TSNILADMICP---VLLETIIKGDHR-ISCANIIWATPETNTWIRNPSRTQKGELALDIV
SbRPE1b         AVNVIADSVCS---VLLDTIIKGDPR-IQAAKVIWVESDATAWVKNTRKVSKGEPALEII
ZmRPE1          AVNVIADSVCS---VLLDTIIKGDPR-IQAAKVIWVESDAASWVKHTRKVSKGESALEII
BdRPE1          AVSVLANSLCDSATIFWSICSAGDPR-IQEAKIMWVGSDAQSWVKNTRKVSKGEPTVEIV
OsRPE1b         AVSVLADSLCG---VLLNTIIKGDPR-IQEAKIVWVGSDATSWVKNTQKASKGEPAVEII
OsRPE1a         VIDFMTNAIFP---IILDTVIKGDPR-VEEANLVRIEPESTFWVQSSGAEQKGEAALEIT
SbRPE1a         VIQMMTNTIFP---ILLDTVIKGDPQ-VQEAKLIWVEPKLTRWVKNSSAEQKGELAVEIT
SmRPD1          IHKHMIGTMFG---NLLQVVVKGCPRGIEFVNVKW----------------EDELCIEVA
SbRPD1          QLDTIKKRVIP---IILDTLLKGFLE-FKDVEIQ--------------CQHDGELLVKVC
ZmRPD1          QLDTIKTRVIP---SILDTLLKGFLE-FKDVEIQ--------------CPHDGELLVKVC
BdRPD1          QLDDLKKRAIP---VLLATPVKGFLE-FKDVEIQ--------------CQRDNELVVKVN
OsRPD1a         QLDVIKERVIP---SILATLLKGFLE-FKNVKVQ--------------CQEDNELVLKVG
OsRPD1b         QLDIIKERVIP---SILATLLKGFLE-FENVKVE--------------CQQDSELVVKVG
AtRPD1          ELDAIRLVLIP---FLLDSPVKGDQG-IKKVNILWTDRPKAP--KRNGNHLAGELYLKVT
CpRPD1          QLDTVRGLVMP---FLLRAVIKGFPE-IKKVDILWKDRPKLS----KSYDSRGELYLRVS
VvRPD1          QLDTVRDLVIP---FLLGAVVKGLLD-VKKVDILWNDNPDSDVL----KSSSGRLYLRVY
PtRPD1          ELETIQDLMIP---FLLETVIKGFME-IQKVDILWNDKPK---IPKSHNRLRGELFLRVH
                    :          :      *    .  . :

ZmRPB1          FYQDDGFKAANEWMLDTEGVNLLAVMCHEDVDATRTTSNHLIEVIEVLGIEAVRRSL---
AtRPB1          FDEEGGFKTSEEWMLDTEGVNLLAVMCHEDVDPKRTTSNHLIEIIEVLGIEAVRRAL---
AtRPE1          VEKSAVKQSGDAWRVVIDSC--LSVL--HLIDTKRSIPYSVKQVQELLGLSCAFEQA---
CpRPE1          VEKSMVKRSGDAWRIVMDSC--LPVF--HLIDSRRSIPYSTKQVQELLGISCAFDQA---
VvRPE1          LEKAAVKQRGDAWRIVLDAC--LPVL--HLIDTRRSIPYAIKQVQELLGISCAFDQA---
PtRPE1a         LEKSVVKQSGDAWRIVLDSC--LPVL--HLIDTTRSVPYAIKQVQELLGVSCAFDQA---
PtRPE1b         LEKSVVKKSGDAWRIVLDSC--LPVL--HLINTTRSIPYAIKQVQELLGVSCAFDTA---
SbRPE1b         VEKDHAVSNGDAWRTTIDAC--LPVL--DLIDTRRSIPYGIQQVKELIGISCAFDQV---
ZmRPE1          VEKDDAVSNGDAWRTAIDAC--LPVL--NLIDTRRSIPYGIQQVRELIGISCAFDQV---
BdRPE1          VEKNEASKQGDAWRIAMDAC--IPVI--DLIDTRRSIPYGIQQVRELLGISCSFDQI---
OsRPE1b         VEEEEALHIGDAWRTTMDAC--IPVL--NLIDIRRSIPYGIQQVRELLGISCAFDQV---
OsRPE1a         VEEAAAAESGNAWGVAMNAC--IPVM--DLIDTTRSMPYDIQQVRQVFGISSAFEKVTQV
SbRPE1a         VEKIAAAENGGTWGVVMDAC--VPVM--DLIDTTRSAPCNIQEVQKVFGISSVFDRV---
SmRPD1          FLS---RTRGVPWTHALEAC--GSIS--HLVDWQKSTPLSIQEVHVAFGIEAAYQYL---
SbRPD1          MSHH--CKGGRFWATLQNAC--IPVM--ELIDWELSRPSNVADIFCSYGIDSAWKYF---
ZmRPD1          MSEH--CKGGRFWPTLQNAC--IPVM--ELIDWELSQPSNVSDIFCSYGIDSAWKYF---
BdRPD1          MSKH--CKSGIFWTTLKKAC--IGIM--GLIDWERSRPGSVYDIFCPCGIDSAWKYF---
OsRPD1a         MSEH--CKSGKFWATLQNAC--IPIM--ELIDWERSRPERVYDNFCSYGIDSAWKFF---
OsRPD1b         MSEH--CKTGKFWATLQNAC--IPIM--ELIDWERSRPERVYDIFCSYGIDSAWKYF---
AtRPD1          MYGD--RGKRNCWTALLETC--LPIM--DMIDWGRSHPDNIRQCCSVYGIDAGRSIF---
CpRPD1          MSEE--HGTRTSWNALMDGC--LPIM--DMIDWARSYPDNIHHFCSANGIDAGWKLF---
```

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VvRPD1          VSGD--CGKKNFWGVLMDAC--LQIM--DMIDWERSHPDNIHDIFVVYGIDAGWKYF---
PtRPD1          MSRG--SDKTRLWNQLMDDC--LSIM--DLIDWARSHPDNIHECCLAYGIDAGWKFF---
                .           *    .      :     ::   : .          *:..

ZmRPB1          ----------LDELRVVISFDGSYVNYRHLAILCDTMTYRGHLMAITRHGINR-----ND
AtRPB1          ----------LDELRVVISFDGSYVNYRHLAILCDTMTYRGHLMAITRHGINR-----ND
AtRPE1          ----------VQRLSASVRMVSKGVLKEHIILLANNMTCSGTMLGFNSGGYKALTRSLNI
CpRPE1          ----------VQRLSTSVAMVAKGVLREHLILLANSMTCAGNLVGFNPGGYKAISRSLNI
VvRPE1          ----------VQRLSKSVTMVAKGVLKEHLILLANSMTCAGNLIGFNSGGYKALSRALNL
PtRPE1a         ----------VQRLSKSVTMVAKGVLKEHLILLGNSMTCAGSLIGFYTGGYKTLSRSLDI
PtRPE1b         ----------VQRLSKSVTMVAKGVLKEHLILLGNSMTCAGSLIGFYTGGYKTLSRSLDI
SbRPE1b         ----------VQRLSSTVKMVNKGVLKDHLILVANSMTCTGSLIGFNIAGYKATFRSLKV
ZmRPE1          ----------VQRLSTTVKMVNKGVLKDHLILVANSMTCTGNLIGFNIAGYKATFRSLKV
BdRPE1          ----------VQRLSTTMKTVAKGILKDHLILVANSMTCTGNLYGFNTGGYRATFRALKV
OsRPE1b         ----------VQRLSTTVRMVAKDVLKDHLVLVANSMTFTGNLNGFNNAGYKATFRSLKV
OsRPE1a         QLFPFLLLAEIQYLSKSVGMITKSVLQEHLTTVASSMTCTGDLHGFNNSGYKATCQSLKV
SbRPE1a         ----------VQHLSKAVGMVTKSVLMEHLITVASSMTCTGSLHGFNRSGSKATFQSLKV
SmRPD1          ----------LEKLKEFTK--GSGVLRKPWKNIDA-----------NESGYEAFVKNLSG
SbRPD1          ----------VESLKSATTDIGRNIRREHLLVIADSMSVTGQFHAISSHGLKQQRTRLSI
ZmRPD1          ----------VESLKSATTDTGRNIRREHLLVIADSLSVTGQFHALSSQGLKQQRTRLSI
BdRPD1          ----------VESLRSKTDDIGRNIHREHLLVVADTLS----------------------
OsRPD1a         ----------VESVRSTTDAIGRNIHRQHLLVVADCLSVSGQFHGLSSQGLKQQRTWLSI
OsRPD1b         ----------VESLRSTTDAIGRNIHRQHLLVVADCLSISGQFHGLSSQGLKQQRAWLSI
AtRPD1          ----------VANLESAVSDTGKEILREHLLLVADSLSVTGEFVALNAKGWSKQRQVEST
CpRPD1          ----------LNNLDSAISDVGKTILPEHLLLIANCLSATGEFVGLSSRGLAQQRKHASV
VvRPD1          ----------LNSLKSAISDIGKTVLPEHLLLVASCLSATGEFVGLNAKGMARQKELTSI
PtRPD1          ----------LNNLQSAMSDVGKTVLPEHLLLVANCLSVTGEFVGLNAKGLKRQREHASV
                          :  :          :       :

ZmRPB1          TGPLMRCSFEETVDILLDAAVYAESDHLRGVTENIMLGQLAPIGTGGC-ALYLNDQMLQQ
AtRPB1          TGPLMRCSFEETVDILLDAAAYAETDCLRGVTENIMLGQLAPIGTGDC-ELYLNDEMLKN
AtRPE1          KAPFTEATLIAPRKCFEKAAEKCHTDSLSTVVGSCSWGKRVDVGTGSQFELLWNQKETGL
CpRPE1          QAPFMEATLFTPRKCFERAAEKCHTDSLSSVVGSCSWGKNVAVGTGSRFDVLWDTKEARF
VvRPE1          QVPFTEATLFTPRKCFEKASEKCHTDSLSSIVASCSWGKHVTVGTGSRFDVLWDTKEIGP
PtRPE1a         QVPFTEATLFTPRKCFEKAAEKCHTDYLSSIVASCSWGKHVTVGTGSRFDVLWDTKEACL
PtRPE1b         QVPFTEATLFTPRKCFEKAAEKCHTDSLSSIVASCAWGKHVTVGTGSHFDVLWDTKEACL
SbRPE1b         QVPFTESTLFTPMKCFEKAAEKCDSDSLGCVVSSSSWGKHAAVGTGSSFQILWNENQLKS
ZmRPE1          QVPFTESTLFTPMKCFEKAAEKCDSDSLGCVVSSSAWGKHAAVGTGSSFQILWNENQLKS
BdRPE1          QVPFTESTLFTPMKCFEKAAEKCHSDALGCVVSSCSWGKHAALGTGSSFQILWNENQVNC
OsRPE1b         QVPFTESTLITPMKCFEKAAEKCHSDSLGCVVSSCSWGKHAASGTGSSFQILWNESQLKS
OsRPE1a         QAPFMEATLSRSIQCFEKAAAKAYSDQLGNVVSACSWGNNAEIGTGSAFEILWNDENMSS
SbRPE1a         QAPFTEATLSRPMQCFRKSAEKVDSDQLDSVVSTCSWGNHAAIGTGSAFKIHWNDENQSA
SmRPD1          CSPLAFAMGKSPGGVFEAAAMNREVDYLAGANELAFCGKSPSLGTGANIELFFKEDKGPV
SbRPD1          SSPFSEACFSRPAQSFIDAAKQCSVDNLCGSLDAIAWGKEPFNGTSGPFEIMHSGKPHEP
ZmRPD1          SSPFSEACFSRPAQSFINAAKQCSVDNLCGSLDAVAWGKEPFNGTSGPFEIMHSGKPHEP
BdRPD1          --------------------------------------------------------PHEP
OsRPD1a         SSPFSEACFSRPAHSFINAAKRDSVDNLSGTLDAIAWGKEPCAGSSGPFKILYSGKSHET
OsRPD1b         SSPFSEACFSRPAYSFINAAKRDSVDNLSGALDAIAWGKEPCAGTSGPFKVLYSGKSQKT
AtRPD1          PAPFTQACFSSPSQCFLKAAKEGVRDDLQGSIDALAWGKVPGFGTGDQFEIIISPKVHGF
CpRPD1          VSPFTQACFSNPSTCFVKAAKAGVTDDLQGSIDALAWGKPPCFGTGGQFDIIYSWRPV--
VvRPD1          SSPFMQGCFSSPGSCFIKAGKRAVADNLHGSLDALAWGKIPSVGSGGHFDILYSAKGHEL
PtRPD1          STPFVQACFSNPGDCFIRAAKAGVVDDLQGSIDALAWGKVPAIGTG-QFDIVYSGKGLEF


ZmRPB1          AIEL----QLPSYVEGLDF----------------------GMTPARSPITGTPYHEGMM
AtRPB1          AIEL----QLPSYMDGLEF----------------------GMTPARSPVSGTPYHEGMM
AtRPE1          DDKE--ETDVYSFLQMVISTTNADAFVSSP-GF---DVT----EEEMAEWAESPERDSAL
CpRPE1          NEGG--KLDVYTFLHMVRSSSHGEDLSTACLGE---EIDDLVPDEETFDWSPSPEHYSTS
VvRPE1          AQDG--GIDIYSFLHLVRSGSYGKEPDTACLGA---EVEDLILEDENLELGMSPEHSSNF
PtRPE1a         NPEG--GIDAYSFLNMVRSTAGGEESVTACLGA---EVDDLILEDEDWNL--SPEHHSSS
PtRPE1b         NPEG--SMDVYSFLNMVRSTAGGEESVTACLGA---EVDDLMLEDEDWNL--SPEHNSSS
SbRPE1b         NKDY--GDGLYDFLALVRT-----DQEKTGYMF-LDDVDYLLEENAIDDMCLSPEPDGTV
ZmRPE1          NKEY--GDGLYDFLALVRT-----DQEKTDYMF-LDDVDYLVEENAADDMCLSPEPDGTL
BdRPE1          NKEY--GDGLYDFLAMVRT-----DQEKARYTF-LDDVDYLVEDNAMDDICLSPELNGTH
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OsRPE1b         NKEY--GDGLYDYLALVRT-----DEEKARYTF-FDDVDYLAEENE-ADVCLSPELDGTI
OsRPE1a         SKSILGGYGLYDFLEAVETTGATKDKAIVPHNYCLYDVDCIPEDKVCLEENNQITWTDKP
SbRPE1a         SNEILREYNLYDFLEAVGRIGATEQKTDAPHSLCLYDVGQLPEDEVQEDEVVCF------
SmRPD1          SRFP----DFESLVFSRRV-----------------------------------------
SbRPD1          EQDE----SIYDFLRSPKV-----------------------------------------
ZmRPD1          EQNE----SIYDFLCSSKV-----------------------------------------
BdRPD1          VQNE----NIYGFLHNPEV-----------------------------------------
OsRPD1a         KQNE----HIYDFLHNPEV-----------------------------------------
OsRPD1b         KQNK----NIYDFLHNPEV-----------------------------------------
AtRPD1          TTPV----DVYDLLSSTKT-----------------------------------------
CpRPD1          --------DVYDLLNSIVT-----------------------------------------
VvRPD1          ARPE----DIYKLLGSQTS-----------------------------------------
PtRPD1          SKPV----DVYNLLGSQMI-----------------------------------------
                             :

ZmRPB1          SPSYLLSPNIRASPINTDASFSPYVGHMAFSPFPSPGGYSPSSGGYSPSSPVFTPEKG--
AtRPB1          SPNYLLSPNMRLSPMSDAQFS-PYVGGMAFSPSSSPG-----------------------
AtRPE1          GEPKFEDSADFQNLHDE-----GKPSGANWEKSSSWDNGCSGGSEWGVSKSTGGEANPE-
CpRPE1          GKPVFEDGEDILENL-E-----TQPTKPSWEHLN--------------------------
VvRPE1          EKPVFEDSAEFQN---------------TWE-----NHVPGSGGDWAVNQNK--------
PtRPE1a         DKPTFEDSAEFQDFL-G-----NQPAESNWGKASSLKDGSWSAGNWDVDKNDSAGKEKPW
PtRPE1b         DKPTFEDSAEFQDFL-G-----NQPAESNWEKISSLKDRSRSSGNWDVDKNDGAVKEKPW
SbRPE1b         GKPTFEDNFEEQNIQKGSSWENGITMKSSWEQDASAANDSGDWGGWSSGGGAS----AK-
ZmRPE1          GKPTFEDNFEEQNIQKGSSWEIGITTNSSWEQNASVANDSGDWGGWSSGGGAA----AK-
BdRPE1          GVPTFEDNFEHQDTQNGNSWENGTKANASWEQNASAGNDSDNWGGWSNAAAAADTGAAK-
OsRPE1b         GQPIFDDNLEEQDVQNNSSWDNGTTTNASWEQNGSAGNDSDKWGGWNDAAAGADTGVTK-
OsRPE1a         KAEFLMESEGRRAGMHSTGQ--KHPRKPNWHEGNTKSSPNSTAVEFTGQVFQRRQLKTK-
SbRPE1a         ----------------------GGTSPISWTDKPKGDSLLHDFMGRAGM-----------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
AtRPE1          --------------SNWEKTTNVEKE----------------------------------
CpRPE1          -----------------NGRADLQKQ----------------------------------
VvRPE1          -----------------ETTASTLKP----------------------------------
PtRPE1a         SLGMSSAETNDV---GWDTAATRKIN----------------------------------
PtRPE1b         SLGMNTAEANDVASSGWDTAAARTTN----------------------------------
SbRPE1b         --------PADQDNS-WEVHAKVQDNSTDWGGWSSGVGAAAKPADQDNSWEVHAKAQDNC
ZmRPE1          --------PADQDNS-WEVHAKVQDNST--------------------------------
BdRPE1          --------PADQGNSSWDVPATAENDS---------------------------------
OsRPE1b         --------PANQGNSCWDVPATVEKSS---------------------------------
OsRPE1a         --------------SNWNSDATQQDDKPS-------------------------------
SbRPE1a         ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
```

```
ZmRPB1          -----------------YSPLSPSYSPASPSYSPTSPSYTPGSPTYSPTSPNYSPTSPTY
AtRPB1          -----------------YSPSSPGYSPTSPGYSPTSPGYSPTSPGYSPTSPTYSPSSPGY
AtRPE1          DAWSS------------WNTRK-------------DAQESSKSDSGGAWGIKTKDADA--
CpRPE1          SSWSS------------WSTDRAHSQDVCSTKTLEECLNSAG--GTGVIGSDKTNL----
VvRPE1          SAWSS------------WGTDKVTMKDTFSTREPDESSRSAGWDDKGTWGTD--------
PtRPE1a         SSWNSENDVTQSNSLSGWATKKSETHNGFATKVQEKPARSNDWDVGTAWGRKAGDNKFA-
PtRPE1b         NSWNSENNVAQSNSFSGWATKKPEPHNGFATKVQEEPTTSNDWDAGAAWGRKDRDNKFAE
SbRPE1b         TDWGG------------WSTDKPTGEATVSG----QPAEMDTWADKGTKMESGAGDANWE
ZmRPE1          TDWGG------------WSVEKPTGEATVSG----EPAETDTWADKGAKMESDAGDGNWE
BdRPE1          TDWGG------------WGNEKAKDNRTVST----EPAELDTWSDRGAKKGTDGGGGSWG
OsRPE1b         SDWGG------------WGTEKAKEKEKISE----EPAQHDAWSVQGPKRATD-GGASWK
OsRPE1a         -----------------WYSSNSAGTQNFTI---AGSSRPGEWNRKNNNRGQGGGREVWK
SbRPE1a         -----------------WSTVQKHQ----------EMQNKTKWNSVANWKNDKPMGPPRT
SmRPD1          ------------------------------------------------------------
SbRPD1          -----------------QNVEKNHLDTRRQSTENASICRLACKSKGSAT-----------
ZmRPD1          -----------------RNFEKNHLDTRRQSTENASICRLACKSSKGSTT----------
BdRPD1          -----------------WGPEKNHMETDSTR----TKNASERWSSGNAT-----------
OsRPD1a         -----------------QALEKNVMDTYRKRTEKTSKRRSALNSEGNAT-----------
OsRPD1b         -----------------QALEKNFMDTYKQRTEKPSKQRSAFSSKGNAT-----------
AtRPD1          -----------------MRRTNSAPKSDKATVQPFGLLHSAFLKDIKVLD----------
CpRPD1          -------------------PLKQNVKSDLPNSMNIKSDKYGDRSIYVHSGSISLGLKK--
VvRPD1          -----------------CHEQNLKVKVPITCYQTTTKCGAQLVYANGDSASKGCKS----
PtRPD1          -----------------STEQNTEFGVLDAQIYKSDKCGAQFLHKFGGCGPKGFKV----


ZmRPB1          SPTSPSYSPTSPSYSPTSPSYSPTSPSYSP------------------------------
AtRPB1          SPTSPAYSPTSPSYSPTSPSYSPTSPSYSP------------------------------
AtRPE1          -DTTPNW--------ETSPAPKDSIVPENNEPTSDVWGHKSVSD---KSWDKKNWGTESA
CpRPE1          -DSQNTWANWNTKGSYPTKASEDSPKS--------------------CGWVADKCGSGET
VvRPE1          -KAQNTAFRRTHEDSPRSSGRDETFRDGRPQFASSAWGKKIDEADK-TGW-NKNDGKPQM
PtRPE1a         -NVTKSWWGKVTDGDESEQNKNKQHQ-EDQELGTHGWDDKMSPDQLISGWASTTTQEATT
PtRPE1b         TNASKSWWGKVTDGDESGQNKSKNKRPEDQDVGTHGWDDKMSQDQSISGWASKTTQEATT
SbRPE1b         KKSSTPEASNKNDPWGKSENTWDKRKGDGGDGGDGAWEKKSVD-GH-GNWDHPGNWNGQS
ZmRPE1          -KSSTPEASKKNDS---SENTWDKRK---GDGGDGAWGNRSDD-GH-GNWEHPSNWNGQS
BdRPE1          KQTNTCEDSGTNL----ERNSWAK-RPSSPSL--STWAKKNSDGGD-GTWDKQANSCKKN
OsRPE1b         KQSSTQNDG----------NSWKENKGRGSNG--GSWEKDNAQ--K-GSWGRGNDEAENN
OsRPE1a         SEGPHRGGSSSNRNQGGGRAVWKSEAS---------------------------------
SbRPE1a         AFAESTSTRGQNKRQFTGQVYARKQPK---------------------------------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
AtRPE1          PAAW--------------------------GSTDAAVWGSSDKKNSETESDAA-----AW
CpRPE1          NAKG------------------------------EHNWSNW-------TAVKG-------
VvRPE1          DKLR-----------------------------ESYDWDCKVAQEKTTQSTYG-------
PtRPE1a         ESCSSKAASVWGTKNTNVDEQGSENHVLLNQAKESSDWNKK-SNSNQTDAACGSKAASSW
PtRPE1b         ESLG---------------------------------WDSK-GNSNPGDAACGWKAASTW
SbRPE1b         LNVD------------------------------QDTWG------------------NAR
ZmRPE1          LDVD------------------------------QDTWG------------------NAR
BdRPE1          --VE------------------------------QDSWKNM-------PV---SPARNAW
OsRPE1b         NDVQ------------------------------NKSWETV-------AADAHASTEKSW
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
```

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SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ---------------------------------------TSPSYSPTSPS----------
AtRPB1          ---------------------------------------TSPSYSPTSPS----------
AtRPE1          GSRDKNNSDVGSGAGVLGPWNK--------KSSETESNGATWGSSDKTKS----------
CpRPE1          GSQDFTATKT---------WEE---------SSKA----GGWGSKKSGNG----------
VvRPE1          GISSTTGD-----------WKKNELQMEVVQHDESPVNEHSWDANLPEDP----------
PtRPE1a         GAKNTDADKR---------WGR---KVDLNQADTS----CSWGRSKTPDRGWGLSNYGGS
PtRPE1b         GAENTDGDKL---------WGK---EVSSNQADTA----SGWGKPKSPEI----------
SbRPE1b         GKKKADGN-CQ--------WEEQPSTYRRKKTNAD----HNSSYNNVMPS----------
ZmRPE1          GKKKADGNYCQ--------WEEQPSNYKQKKTNAD----HDSSYNNVMPS----------
BdRPE1          NKKESSRGDAT--------WEMRASTLEEKKTSES----NEGSWEKSNAQ----------
OsRPE1b         GNVTASPSDNA--------WS----------AAPV----SQGNGSSDTKQ----------
OsRPE1a         ---------------------------------------HRGSGNNRNRG----------
SbRPE1a         ---------------------------------------HSWSQAATHQN----------
SmRPD1          ---------------------------------------VDDTVSATLSA----------
SbRPD1          ---------------------------------------VNGVAITSDQD----------
ZmRPD1          ---------------------------------------VNGVAITIDQD----------
BdRPD1          ---------------------------------------FNGGTISVEQN----------
OsRPD1a         ---------------------------------------INGGAISFNQK----------
OsRPD1b         ---------------------------------------INGGTISVNQK----------
AtRPD1          ---------------------------------------GKGIPMSLLRT----------
CpRPD1          ---------------------------------------LEGISRAYLRT----------
VvRPD1          ---------------------------------------LEKISKSVLRS----------
PtRPD1          ---------------------------------------KEGIPRSFLRR----------


ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
AtRPE1          ----------------GAAAWNSWDKKNIETDSE----------------------PAAW
CpRPE1          -----------ESNVGEGSPWSNWKTNKGNSQGTHPQKAQEESSD-----------FGGW
VvRPE1          --------------LAQATTSVGWDSST----------------------------GKDW
PtRPE1a         NGSEMENKTENQSLLDRGKESVGWGGKNTDADKPWSNKVNSNQADTASGWGKSKSLDRGW
PtRPE1b         --------------------SLGWGSTKESVKS-----------------------DRGW
SbRPE1b         ----------------SDNAWNAGERFGRSNAKSNA--------------------GSSW
ZmRPE1          ----------------SEIAWNAGDGTGRPNAKSNA--------------------ESSW
BdRPE1          ----------------KD-SWGNTQHGSSDKMAVKDNDMQ----------------QDPW
OsRPE1b         ----------------SD-SWDGWKSAGVDKAINKD--------------------KESL
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ----------------NKLSWCGENVAGAQDFANAESS------------------KGGW
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ----------------------YSPTSPVYSPTSPAYSPTSPAYSPTSPSYSPTSPSYS-
AtRPB1          ----------------------YSPTSPSYSPTSPAYSPTSPAYSPTSPAYSPTSPSYS-
```

```
AtRPE1          G-------------SQGKKNSETESGPAAWGAWDKKKSETEPGPAGWGMGDKKNSETELG
CpRPE1          G-S-----------NKFSRCETNLKEQSTWSKWNSNKGDNQDAYATMLENNDNDTGKEKG
VvRPE1          T-------------KRKLQSPSEQQRDPAIKSWSSSHNV------MKEQSNQPAST--HG
PtRPE1a         G-VSNSGGGNGSEMEDKTENQSLLDRGKESGGWGGKNTDADKPWSNKVNSNQADTA--SG
PtRPE1b         G-VSSSGGGR----DKKTENQSLAGQGKESGGWG-----------NKVTSNQADTA--SG
SbRPE1b         GEKDKMESDEHPKVPKESDTWNT--GKSNESPWDNTDALQ-DSWGVNSATHDNNTEDGS-
ZmRPE1          GEEDKMESDDHPKVPKESDTWNT--GRSNESPWDNTDALQ-DSW-VKSAARNNNTQDGS-
BdRPE1          G-----HI-ATQNINAQDDLWGSVAAKAQTSTAENTDAQD-DSWGAVAAKAQTSTAQES-
OsRPE1b         G-----NVPASPSFSA----WNASPVSQGNERSDAKQSDSWDGWKSAGVDKAINKDKES-
OsRPE1a         ---------------------------GGRAVWKSEASRRGGSMRQVASCA---------
SbRPE1a         N------------RKNSGFGRGGHRGGGRGMAFANAESSSSGGWNRKNSGF---------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
AtRPE1          PAAMGNWDKKKSDTKSGPAA-----------WGSTDAAAWGSSDKNNSETESDAAAWGSR
CpRPE1          ------WSS----------------------WARDDSINGSVLPEGDSSKSNGLDAGTVG
VvRPE1          ------WDSPGA--KG---------------W-------------NDVEEQSQWNQRGSA
PtRPE1a         ------WGKSKSLDRG---------------WGVSNSGGGNGSEMEDKTENQSLLDRGKE
PtRPE1b         ------WGKPKSSENSQGWGLSKESGKEVHEWGVPNSAGGNGSETNNNNENQSLVEQGKE
SbRPE1b         ------WDKVVAIKDPVSQQDS---------WSNVAIQK------NDA-QNDSWDNVAEK
ZmRPE1          ------WDKVVSMKDLDSLQDS---------WSKATIQT------NDA-QNDSWDNVAKN
BdRPE1          ------WGNVAA----SPSDNA---------WKAPPISQTSAAEHTDA-HNDSW-GIVAA
OsRPE1b         ------LGNVPA----SPSFSA---------WNAAPVSQ--GNERLDAKQSDSWDGWKSA
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
AtRPE1          NK-KTSEIESGAGAWGSWGQPSPTAEDK---------------DTNEDDRNPWVSLKET-
CpRPE1          DG---SWEQTPTGTSDGWGVLSE--------------------STEPAGCHGWGLPNNE-
VvRPE1          VK------NDQSESSHGWGPSNE--------------------QNQLPSSQGWGSPNAG-
PtRPE1a         SG--------------GWGKPKS--ISQGWGS----------SKDSVKAVDGWGVPNSA-
PtRPE1b         SGWDNKASSNQEGTASGWGKPKSPALSEGWGS----------PREPVKAVHGWGVPNSG-
SbRPE1b         AL------NSAS--QDSWGHLAATPVSNS-------------DAKQSDSWDGWNAVPAEN
ZmRPE1          AP------DSAA--EDSWG--AATPA----------------------------------
BdRPE1          KA------QTSTAQQESWGNATASPSDNAWNAAPMDL-----DAKQPGSWDGWSSALAED
OsRPE1b         GV------DDSVKDKESWGNVPASPSDSAWNAAPVSQGNESSDAKQSDSWDGWKSAGVDA
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
```

```
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ------------------------------------------------------------
AtRPB1          ------------------------------------------------------------
AtRPE1          ---------------------------------KSREKDDKERSQWGNP-----AKKFPS
CpRPE1          ---------------------------------DITQNESQGRRTWEFS----KKKRNEG
VvRPE1          -----------------------------------AGHESETQSQWGQPSG--KKSRPEG
PtRPE1a         -----------------------------------GSNGSERDQQWGQQSGEFKKNRTEG
PtRPE1b         -----------------------------------GGNGSGRDQQWGQQSREFKKDRFEG
SbRPE1b         SQGTA----------------------------QWKERTDSGNKDWKSD-----------
ZmRPE1          ------------------------------------ETTDSGNKEWKSD-----------
BdRPE1          S--------------------------------NKADDSSNKNKGWKSD-----------
OsRPE1b         STNKDKESWGNVPASPSDSAWNAAPVSQGDDVWNSAEANESRNKDWKSD-----------
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ---------------------------------GRGGRRGGGRGMWKSE----------G
SmRPD1          ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------


ZmRPB1          ---------------------------------------PTSPSYSPTSPSYSPTSPSYS
AtRPB1          ---------------------------------------PTSPSYSPTSPSYSPTSPSYS
AtRPE1          SGGWSNGGGADWKGNRNHTPRPP---RSEDNLAPMFT--ATRQRLDSFTSEEQELLSDVE
CpRPE1          SRGWSSNSG-DWKGKKNLPGKLAGNVKDDFGAGRLYT--HTRQRLDMFTSEEQDVLSDVE
VvRPE1          SRGWGSNNT-EWKNKKNRPNKPQGPLNDDYSAGGIFT--ATRQRVDIFTSEEQDILLDVE
PtRPE1a         SRGWGSNNG-HWK-KRNRPSKPH----EDSSSSGLFT--MTRQWLDIFTSQEQDILSDVE
PtRPE1b         SRGWGSNNG-DWKNKRNRPSKPH----EDLNASGIFT--TTRQRLDVFTSQEQDILSDIE
SbRPE1b         --GWGAKSG-NWSSQRNNPGRPPRRPDERGPP-------PPRQRFE-LTIEEKKILLEVE
ZmRPE1          --GWGAKSG-NWSSQRNNPGRPPRRPDERGPP-------PPRQRFE-LTVAEKNILLEVE
BdRPE1          --GWGAK-G-NRRDQRDNPSMPPMRPDER----------PPRPRFE-VPAEAKKILREIE
OsRPE1b         --GWGARGG-NWRGQRNNPGRPPRKPDGRGLPRRPDERGPPRRHFD-LTAEEEKILGEIE
OsRPE1a         -----------------------------------------------FTPVEQQIFEQIE
SbRPE1a         SHRGGSNST-NWRAQNNNSARQCGISYS-------------------FTPVEQQIYTQVE
SmRPD1          -------------------------------------------------KDREIVWARID
SbRPD1          -----------------------------------------------FLHAKVSIWDNII
ZmRPD1          -----------------------------------------------FLHAKVSIWDNII
BdRPD1          -----------------------------------------------YLGAKVGVWDSII
OsRPD1a         -----------------------------------------------FLNAKVGIWENII
OsRPD1b         -----------------------------------------------FLDSKVGIWENII
AtRPD1          ----------------------------------------------------IFTWKNIE
CpRPD1          ----------------------------------------------------VLTWKDIQ
VvRPD1          -----------------------------------------------FLS-----LNDIQ
PtRPD1          ----------------------------------------------------LLTYDDIQ


ZmRPB1          PTSPSYSPTSPAYS-PTSPGYSPTSPSYSPT-SPSYSPTSPSYNPSSAKYSPSHAYSPSS
AtRPB1          PTSPSYSPTSPAYS-PTSPGYSPTSPSYSPT-SPSYGPTSPSYNPQSAKYSPSIAYSP-S
AtRPE1          PVMRTLRKIMHPSAYPDGDPISDDDKTFVLEKILNFHPQKETKLGSGVDFITVDKHTIFS
CpRPE1          PLMQSIRRIMHQSGYNDGDPLSVDDQSFVIDKVFMYHPDRAVKMGAGIDFVTVSRHSNFQ
VvRPE1          PIMQSIRRIMHQAGYNDGDPLSADDQSYILDKVFNNHPDKAVKMGTGIDYVMVSRHSSFL
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PtRPE1a         PLMLSIRRIMHQTGYSDGDPLSADDQSYVLDNVFNYHPDKAVKMGAGINHVTVSRHSNFQ
PtRPE1b         PLMLSIRRIMHQTGYNDGDPLSADDQSYVLDNVFHYHPDKAVKMGAGIDHVTVSRHSNFQ
SbRPE1b         PLIFRVRRIFREA--CDGVRLKPEDEKFIQEKILEHHPEKQSKVSSEIDHIMVNKHHTFE
ZmRPE1          PIKLRVRSIFREA--CDGVRLNPEDEKFILEKVLEHHPEKQSKVSGEIDYLTVNKHQTFQ
BdRPE1          PIVSMVRKIFRES--CDGVRLPLEDEKFIKESILEHHPEKERKVPGEIDHIMVNKHHIFQ
OsRPE1b         PTVLSIRKIFRES--IDSIKLSPEDEKFIKENVLEHHPEKQSKVSGEIDHIMVDKHQVFQ
OsRPE1a         PITKNVKRIIRES--RDGIKLPPDDEKFIVTNVLMYHPERKKKIAGNGNYITVDRHQVFH
SbRPE1a         PIIKNVKRIIRES--RDGMKLSQDDEMFIMNKILMYHPEKEKKMAGQGNYIMVNKHQTFP
SmRPD1          QRSQKLHDILRKS--LTGTPVSAANEAVILD-TLKYHPMMDSKVGCGVRHIRVDNHHSFG
SbRPD1          DMRASLQNMLREY--PLNGYVMEPDKSKLIE-ALKFHPRGAEKIGVGVREIKVGLNPNHP
ZmRPD1          DMRTSLQNMLREY--PLNGYVAEPDKSQLIE-ALKFHSRGAEKIGVGVREIKIGLNPSHP
BdRPD1          DMRTCLQNMLREY--QLDEYVVELDKSRVIE-ALRFHPRGREKIGVGIRDIK--------
OsRPD1a         DMRTSLQNMLREY--TLNEVVTEQDKSCLME-ALKFHPRGYDKIGVGIREIKIGVNPGHP
OsRPD1b         DMRTCLQNMLREY--TLNEVVTEQDKSCLIE-ALKFHPRGYDKIGVGIREIKIGVNPGHP
AtRPD1          LLSQSLKRILHSY--EINELLNERDEGLVKM-VLQLHPNSVEKIGPGVKGIRV-AKSKHG
CpRPD1          KLYHASKKILNKY--PIDHRLNEGEKKILMM-ALYFHPQSYEKIGTGAQYIKVLKTE---
VvRPD1          KLSRRLKFILQKY--PINHQLSEIDKTTLMM-ALYFHPRRDEKIGPGAQNIKVRYHSKYH
PtRPD1          RMSYTVRKILNKY--SVDQQLNESDKSVLMM-TLYFHPRRDEKIGIGAKDIKVINHPEYQ
                                 .      .            .

ZmRPB1          PR----MSPYSQTSPSYSPTSPTYSPTSPSYSQPSPSYSPTS----PSGSYSPTAPGYSP
AtRPB1          NARLSPASPYSPTSPNYSPTSPSYSPTSPSYSPSSPTYSPSSPYSSGASPDYSPSAGYSP
AtRPE1          DSRCFFVVSTDGAKQDFSYRKSLNNYLMKKYPDRAEEFIDKY-FTKPRPSGNRDRNNQDA
CpRPE1          DSRCFYIVSTDGRKQDFSYRKCLDNFIKGKYPDIAEQFIGKY-FRKPRSSGNQQKPVLEE
VvRPE1          ESRCFYVVSTDGHKEDFSYRKCLENFIKEKYPDNAETFIGKY-FRRPRAGGNRERSVIPE
PtRPE1a         ESRCFYIVSTDDCKQDIF-------PTANVWRTSSGENNLTWQMNSSESILQEEAIGSAP
PtRPE1b         ESRCFYIVSTDGCKQDFSYRKCLENFIKGKYPDLADEFIAKY-FARRGNRQRTPAPEGTE
SbRPE1b         DTRCFFVVSTDGSQADFSYLKCLENFVRKNYTEDVDSFCMKY-LRPRRRQAPPPDVGTAP
ZmRPE1          DTRCFFVVSTDGSQADFSYLKCLENFVRKSYTEDADTFCMKY-LRPPETEQGTPPAPQAE
BdRPE1          ESRCFYVVLADGTHTDFSYNKCMDNYVRKTYTDAAEHADL--------------------
OsRPE1b         DSRCLFVVSSDGTRSDFSYLKCMENFVRKTYPEHGDSFCKKY-FKRRRDQPPAADGGTAP
OsRPE1a         GSRCLYVMSSDGSRKDFSYKKCLENYIRAQYPDAADSFCRKY-FK---------------
SbRPE1a         SSRCLYVASSDGSSSDFSYKKCLENFIRIHYPHAAESFCRKY-FK---------------
SmRPD1          G-RCFHIVRLDGSVEDFSYHKCLLERIKGN-TVLVQRYKKKF-MGGKNGRKEEVPVEIFS
SbRPD1          GTRCFILLRNDDTTEDFSYHKCVHGAANSISPQLGSYLKKLY-HRA--------------
ZmRPD1          GTRCFILLRNDDTTEDFSYHKCVQGAADSISPQLGSYLKKLY-YRA--------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         SSRCFIVLRNDDTTADFSYNKCVLGAANSISPELG-------------------------
OsRPD1b         NSRCFIVQRSDDTSADFSYNKCVLGAANSISPELGSYIEKIL-SNRAIRPHQL-------
AtRPD1          DSCCFEVVRIDGTFEDFSYHKCVLGATKIIAPKKMNFYKSKY-L--KNGTLESGGFSENP
CpRPD1          ------------------------------------------------------------
VvRPD1          NTRCFSLVRTDGTEEDFSYHKCVHGALEIIDPRRARSYQSRW----------------LP
PtRPD1          DTRCFSLVRTDGTIEDFSYRKCLHNALEIIAPQRAKRYCEKY-LTSKVSATDNSGCTDLP


ZmRPB1          SSTGQGNDKDDKSAR---------------------------------------------
AtRPB1          TLPGYSPSSTGQYTPHEGDKKDKTGKKDASKDDKGNP-----------------------
AtRPE1          TPPGEEQSQPPNQSIGNGGDDFQTQTQSQSPSQTRAQSPSQAQAQSPSQTQSQSQSQSQS
CpRPE1          TENML-------------------------------------------------------
VvRPE1          DGGNREQSVVPEETGSENRQ----------------------------------------
PtRPE1a         LLQREPRRNRPRDV----------------------------------------------
PtRPE1b         EEKQAL------------------------------------------------------
SbRPE1b         GTPAEVPPSTAAETEQGTPAPPAEVPQETLGSPAVALEGTHNPRTDPTDDTELLGKDSDL
ZmRPE1          VPQETWGSPAVPLEGGTHIAGPDSTGDAVILGEQHDLTPASPAVAPQVASEPDTTDGTGL
BdRPE1          ------------------------------------------------------------
OsRPE1b         GTPAGATQSTAVDTQEGTSQQTQPDIATAPAATQQETLQDTPAPPADDGLLGKGPSPSD-
OsRPE1a         ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SmRPD1          QKNDTGRMYDKKTHGFLLVENHFVPVKTLKKT----------------------------
SbRPD1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
BdRPD1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
```

```
AtRPD1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
VvRPD1          YSEV--------------------------------------------------------
PtRPD1          LDN---------------------------------------------------------


ZmRPB1          -----------------------------------------------------
AtRPB1          -----------------------------------------------------
AtRPE1          QSQSQSQSQSQSQSQSQSQSQSQSPSQTQTQSPSQTQAQAQSPSSQSPSQTQT
CpRPE1          -----------------------------------------------------
VvRPE1          -----------------------------------------------------
PtRPE1a         -----------------------------------------------------
PtRPE1b         -----------------------------------------------------
SbRPE1b         TPASPAVAPQEAPKPDPTDDTELLGNEKPDLTPSSPGEALQATADPDSTLTDI
ZmRPE1          LGKAPQADWGPRFDAD-------------------------------------
BdRPE1          -----------------------------------------------------
OsRPE1b         -----------------------------------------------------
OsRPE1a         -----------------------------------------------------
SbRPE1a         -----------------------------------------------------
SmRPD1          -----------------------------------------------------
SbRPD1          -----------------------------------------------------
ZmRPD1          -----------------------------------------------------
BdRPD1          -----------------------------------------------------
OsRPD1a         -----------------------------------------------------
OsRPD1b         -----------------------------------------------------
AtRPD1          -----------------------------------------------------
CpRPD1          -----------------------------------------------------
VvRPD1          -----------------------------------------------------
PtRPD1          -----------------------------------------------------
```

(D) TCOFFEE

```
AtRPB1          MDTRFP-------FSPAEVSKVRVVQFGILSPDEIRQMS--VIH------VEHSETTEKG
AtRPD1          MEDDC-------EELQVPVGTLTSIGFSISNNNDRDKMS--V------LEVEAP------
AtRPE1          MEEEST--------SEILDGEIVGITFALASHHEICIQS--ISE----SAINHP------
BdRPD1          MLILL-------LLLK--------------------------------------------
BdRPE1          MEEDQS-------AVLVAEGAIKSIKLSLSTEDEI-------------------------
CpRPD1          MALWIL--------------------------------------------LGSW------
CpRPE1          MVYSLL--------GI--------------------------------------------
OsRPD1a         MEEPS-------LEVNNPVAELNAIKFSLMTSSDMEKLS--S------ATIIEM------
OsRPD1b         MEEPS-------LEVKMPEADLKAVKFSLMTSSDMEKLS--S------ASIIEM------
OsRPE1a         MEGHPDPTS--AATAMIPEASIRRINLSITSNEEILKAQ-PVNELEKPIPITHQ------
OsRPE1b         MEEDQS-------AIPVAEGAIKSIKLSLSTEDEIRTYS--IND----CPVTHP------
PtRPD1          MEIDFS------EEQQVPSALITGMAFGVLTEAETEKLS--V------LNIDAV------
PtRPE1a         MDEIPQ--------SSIFEGEITGIRFGLASQKEICTAS--ISD----CPISHS------
PtRPE1b         MDENSQ--------SSIFDGEITGIRFGLATQKEICTAS--ISD----CPISHS------
SbRPD1          MELHR-------E---LPEATLNAIKFDLMTSTDMEKLS--S------MSVIEV------
SbRPE1a         MEDDDPAA----AGLTVPEAFIRRVKLSVTSNQEIKLMAHPVE---DPIPITHC------
SbRPE1b         MEEDHS-------ATLVSEGAIKSIKLSLSTGEEVCTYS--VNE----CPVTHP------
SmRPD1          MASSKRRSSHRDRALEEATGTLIALDFRPLTSEEIIRAS--VY------EVKTV------
VvRPD1          MDNDFL------EEQQVPSGLLIGIKFDVSTEEDMEKIS--V------MKIDAV------
VvRPE1          MEEDSS---------TILDGEISGIRFGLATRQEICIAS--VSD----CPISHA------
ZmRPB1          MDARFP-------YSPAEVAKVEFVQFGILSPDEIRQMS--VIQ------IEHAETMERG
ZmRPD1          MELHR-------E---PPEAILNAIKFDLMTSTDMEKLS--S------MSIIEV------
ZmRPE1          MEEDHS-------VILISEGAIKSIKLSLSTGEEICTYS--INE----CPVTHP------
                *

AtRPB1          KPKVGGL-SDTRLGTIDRK-VKCETCMAN-----MAECP---------------------
AtRPD1          ----NQV-TDSRLGLPNPD-SVCRTCGSKD----RKVCE---------------------
AtRPE1          ----SQL-TNAFLGLPLEF-GKCESCGATE----PDKCE---------------------
BdRPD1          ------------------------------------------------------------
BdRPE1          ------L-GNPFLGLPLET-GKCESCGASE----NGKCE---------------------
CpRPD1          ----IEV-TDPKLGLPNPS-SECLTCGAKD----LKHCE---------------------
CpRPE1          ------------------------------------------------------------
```

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OsRPD1a         ----CDV-TNAKLGLPNGA-PQCATCGSRS----IRDCD---------------------
OsRPD1b         ----CDV-TNAKLGLPNGA-PQCATCGSQS----VRDCD---------------------
OsRPE1a         ----SQLLNNPYLGLPLQV-GSCQSCGSNA----IEECE---------------------
OsRPE1b         ----SQL-GNPFLGLPLET-GKCESCGASE----NGKCE---------------------
PtRPD1          ----SEV-TDPKLGLPNPS-SQCSTCGSRD----LKSCEGIVDVDLNSADRLASIATGDC
PtRPE1a         ----IQL-TNPYLGLPLEF-GKCESCGTSE----PGQCE---------------------
PtRPE1b         ----SQL-TNPFLGLPLEF-GKCESCGTSE----PGKCE---------------------
SbRPD1          ----SDV-TSPKLGLPNAS-PQCETCGSKS----GRDCD---------------------
SbRPE1a         ----SQLQDNPSLGLPLQDGSTCESCGATQ----LDKCD---------------------
SbRPE1b         ----SQL-GNPFLGLPLEA-GKCESCGASE----NDKCE---------------------
SmRPD1          ----RAL-QNNRFGLPNLS-DCCTSCGAKRTDASNSACP---------------------
VvRPD1          ----NEI-TDPKLGVPNPS-CQCSTCGAKD----TKKCE---------------------
VvRPE1          ----SQL-TNPFLGLPLEF-GKCESCGTAE----PGQCE---------------------
ZmRPB1          KPKPGGL-SDPRLGTIDRK-IKCETCMAG-----MAECP---------------------
ZmRPD1          ----SDV-TSPKLGLPNGS-LQCETCGSQR----GRDCD---------------------
ZmRPE1          ----SQL-GNPFLGLPLEA-GKCESCGASE----NDKCE---------------------


AtRPB1          --------GHFGYLELAKPMYHVGFMKTVLSIMRCVCFNCSKILADEAMK-------IKN
AtRPD1          --------GHFGVINFAYSIINPYFLKEVAALLNKICPGCKYIRKKQFQ-I------T--
AtRPE1          --------GHFGYIQLPVPIYHPAHVNELKQMLSLLCLKCLKIKKAKGT--------SGG
BdRPD1          --------------------------------------------------R------SDA
BdRPE1          --------GHFGYIELPVPIYHPCHVSELRQLLSLVCLKCLRIKKGKD------------
CpRPD1          --------GHFGVIQFPYTILHPYYLSEVVQILNKVCPALIHAIQGNSLN----------
CpRPE1          --------------------------------------NWIMAGTSKVK--------NAG
OsRPD1a         --------GHFGVIKLAATVHNSYFIEEVVQLLNQICPGCLTLKQNGDTKK------ADG
OsRPD1b         --------GHFGVIKLAATVHNPCFIEEVVQLLNQICPGCLTLKQNGDTKK------TDG
OsRPE1a         --------GHFRFIELPMPIFHPSHVTELSQILNLICLRCLKIKNRKKST---------L
OsRPE1b         --------GHFGYIELPVPIYHPCHVTELRQILNVVCLKCLRVKKGKVKQT-------EG
PtRPD1          ANILLSLSGHFGVINFPYTIVHPYFLSEVVQILNKICPGCKSIRLAKATEL------ITK
PtRPE1a         --------GHFGYIDLPVPIYHPSHISELKRMLSLLCLKCLKLKRNKIQIK------SNG
PtRPE1b         --------GHFGFIHLPIPIYHPSHISELKRMLSLICLKCLKLKRNKIQIK------SNG
SbRPD1          --------GHFGVTKLAATVHNPYFIDDVVHFLNQICPGCLSPREGINMKR------LGR
SbRPE1a         --------GHFGFIKLPEPIYHPSHIAELGKILNLVCLRCLRLKKPKKVT---------G
SbRPE1b         --------GHFGYIELPVPIFHPCHVSELRQLLSLICLKCLRIKKGKVKQS-------NG
SmRPD1          --------GHSGHIELPVLVYHWDRISALEAILNRVCLHCYSFKHKGRKKE------LRT
VvRPD1          --------GHFGVIKFPFTILHPYFLTEVVQILNKICPGCKSTRQGQWVKV------R--
VvRPE1          --------GHFGYIELPIPIYHPGHVSELKRMLSLLCLKCLKIRKSKVT--------NNG
ZmRPB1          --------GHFGHLELAKPMFHIGFIKTVLSIMRCVCFNCSKILADEDETKFKQALKIRN
ZmRPD1          --------GHFGVTKLAATVHNPYFIDDVVHFLNRICPGCLSPREGIDTKR------LER
ZmRPE1          --------GHFGYIELPVPIYHPCHVTELRQLLSLICLKCLRIKKGKVKQS-------NG


AtRPB1          PKNRLKKILDACKNKT---------------------KCDGGDDIDDVQSHSTDE-----
AtRPD1          -EDQ-PERCRYCTLNT------------------------GYPLMK-FR-VTTK------
AtRPE1          LADRLLG--VCCEEA---------------------------SQIS-IK-----------
BdRPD1          ATI--QEPCKYCSKDG------------------------LYPSVI-FK-VLTSPRITLS
BdRPE1          --------------V---------------------------PALS-LK-----------
CpRPD1          ----------------------------------------WYPPMK-FK-VLSE------
CpRPE1          VAERLFS--LCCEEV---------------------------SQVS-IK-----------
OsRPD1a         TTI--QGTCKYCSKDG---------------------S-KLYPSII-FK-MLTSPRVTLS
OsRPD1b         TTI--QTTCKYCSKDG---------------------A-KLYPSVI-FK-MLTSPRVTLS
OsRPE1a         KGSK-FTSCSHCQEL---------------------------PPLC-VA-----------
OsRPE1b         KDNTSALSCYYCRDL---------------------------PALS-LK-----------
PtRPD1          ENPQ-RKGCKYCAGNS---------------------L-GWYPPMK-FK-VSSK------
PtRPE1a         VAERLL---SCCEEC---------------------------AQIS-IR-----------
PtRPE1b         VAERLL---SCCEEC---------------------------AQIS-IR-----------
SbRPD1          ETVQATSTCKYCSKDG---------------------S-KLYPSVI-FK-TLSSPRVLLS
SbRPE1a         KESR-FTSCSYCQEL---------------------------SPLC-VS-----------
SbRPE1b         KGNLSATLCSYCRDI---------------------------PALS-VK-----------
SmRPD1          LS-SLEQVASGV-DAHQADIGAVPNGARAPEAEENPGKCT-GPAAA-VK-----------
VvRPD1          -RLR-SKGCKYCAANS---------------------N-DWYPTMK-FK-VSSK------
VvRPE1          ITEQLLA--PCCQDS---------------------------PQVS-VR-----------
ZmRPB1          PKNRLKRIYDACKSKK---------------------VCAGGDDLD-VQEQDTDE-----
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ZmRPD1          EKV--QATCKYCSKDG---------------------S-KLYPSIV-FK-TLSSPRVLLF
ZmRPE1          KGNAAPTLCSYCRDI---------------------------PALS-LK-----------
                                                               .

AtRPB1          PVKKSRGGCGAQQPKLTIEGMK---------MIAEYK-NSKEEN---------DEPDQLP
AtRPD1          ---------------EVFRRSGIVVEVNEESLMKL-K-KRGVLTLPPDYWSFLPQDSNID
AtRPE1          D-RASDGA-----------------------SYLELK-LPSRSRLQPGCWNFLERYGYRY
BdRPD1          KSKLQRN-------TSVMDKVSVTAEV----INMSKN-KSSLEVLPHDYWNFVPHNQ-PP
BdRPE1          EVKTADGA-----------------------FRLELR-APPRRLMKDSSWNFLDKYGFHH
CpRPD1          ---------------DIFRLSAIMVEVNENVLRKF-Q-KRRKEALPADYWDFLPKDSHQE
CpRPE1          EGKTPDDA-----------------------CYLQLK-LPSMSRLRESFWNFLEKYGFSL
OsRPD1a         RSKLHRN-------TSVMDKMSIIAEVAGGVAHKSKN-KAPHETLPQDFWDFIPDDNQPP
OsRPD1b         RSKLHRN-------TSVMDKISIIAEVAGGVTHNSKN-KAPHETLPQDFWDFVPDDNQPP
OsRPE1a         EVKKSNGA-----------------------RGLELR-APIKKELEEGFWSFLDQFGSCT
OsRPE1b         EIKTADGA-----------------------FRLELK-MPPRKFMTEGSWNFLDKYGFHH
PtRPD1          ---------------EIFRKTAIIAEIRETLSKK-PQ-KGFKKILAADYWDIFPKDEQEE
PtRPE1a         EVKNTDGA-----------------------CFLELK-LPSRSRLRDGCWNFLERYGFRY
PtRPE1b         EVKNTDGA-----------------------CFLELK-LPSRSRLRDGCWNFLERYGFRY
SbRPD1          KSKLHRS-------PSVMERISIVAEAAERVSNRSKG-KGLLEGLPQDYWDFVPSENKQV
SbRPE1a         QVKKSNGA-----------------------RSLELK-LPLKQEVADGFWSFLDQFGFHT
SbRPE1b         EVKTADGA-----------------------IRLELS-APHKRHMTERSWNFLDKYGFHH
SmRPD1          KI---------------FKKVGT-ANV-PA-LLLEIDGKVRREDIPPGFQSLILKDEMTP
VvRPD1          ---------------DLFRKTAIIVEMNEKLPKKLQK-KSFRPVLPLDYWDFIPKDPQQE
VvRPE1          EFRPTEGA-----------------------CFLELK-IPSRSRPKDGFWDFLARYGYRY
ZmRPB1          PIKK-RGGCGAQQPNITVDGMK---------MVAEFK-APKKKT---------DDQDQLP
ZmRPD1          KSKLHRN-------ASVMERISIVAEAADRMPNRSKG-KGSLEGLPLDFWDFVPSENKQV
ZmRPE1          EIKTTDGA-----------------------IRLELR-APHNKHMTERSWNFLDKYGFHH


AtRPB1          E-----------------------------------------------------------
AtRPD1          ES----------------------------------------------------------
AtRPE1          G-----------------------------------------------------------
BdRPD1          QP----------------------------------------------------------
BdRPE1          G-----------------------------------------------------------
CpRPD1          ES----------------------------------------------------------
CpRPE1          RLCGLGSQISALTLK-V-----LGL----LAFWV--AFT-S-LCE---------------
OsRPD1a         IF----------------------------------------------------------
OsRPD1b         QS----------------------------------------------------------
OsRPE1a         R-----------------------------------------------------------
OsRPE1b         G-----------------------------------------------------------
PtRPD1          EEE-----------------------------------------T---------------
PtRPE1a         VFVTF-EKYSYIHMPKVYAFMSKGVCAFRSD-WYFIYAPATMLASPRNLVWSYVLLTRLG
PtRPE1b         G-----------------------------------------------------------
SbRPD1          QS----------------------------------------------------------
SbRPE1a         S-----------------------------------------------------------
SbRPE1b         G-----------------------------------------------------------
SmRPD1          ------------------------------------------------------------
VvRPD1          EN----------------------------------------------------------
VvRPE1          G-----------------------------------------------------------
ZmRPB1          E-----------------------------------------------------------
ZmRPD1          QS----------------------------------------------------------
ZmRPE1          G-----------------------------------------------------------


AtRPB1          --------------PAERKQTLG-------------ADRVLSVLKRISDADCQLLGFNP-
AtRPD1          -------------CLKPTRRIIT-------------HAQVYALLLGIDQRLIKKDIP---
AtRPE1          ---------------SDYTRPLL-------------AREVKEILRRIPEESRKKLTAK--
BdRPD1          ---------------NTTKILLS-------------PYQVFHILKQVDLELITKFAP---
BdRPE1          --------------GASHFRTLL-------------PEEALNILKKIPDDTRKKLAAR--
CpRPD1          -------------GTRPNRRILS-------------HAQVHFLLKAIDPKLIRKFIL---
CpRPE1          -------------GSCKEISKVI-------------GQVVMKMIRSIPEDTRRKLAGK--
OsRPD1a         ---------------NVTKKILS-------------PYQVFHMLKKLDPELINQVTR---
OsRPD1b         ---------------NVAKKILS-------------PYQVFHMLKNLDPELINQVTP---
OsRPE1a         --------------GTSHCRPLL-------------PEEVQNIIKKIPEETRRWLSVR--
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OsRPE1b         --------------GTSHCRTLL-------------PEEALNILKKIPEETKRKLAAR--
PtRPD1          -------------NAKPNRRVLS-------------HSQVRHMLKDVDPNFIKLSIL---
PtRPE1a         TGYLFNASVSELLVNDSNFRTVLVYIQSFTFSAYACYFLVMQILKTIPAETRKKLGGK--
PtRPE1b         ---------------DDFTRPLL-------------PCEVMQILKRIPAETRKKLSGK--
SbRPD1          ---------------NMTKIILS-------------PYQVFHMLKKSDPELIKQFVS---
SbRPE1a         --------------GTSHRRPLH-------------PKEVQDIMKKITEKTRARLAAR--
SbRPE1b         --------------GCSQFRSLL-------------PEEALNILKKVPDDTRRKLAAR--
SmRPD1          ---------------QWRSKMLD-------------PNQVLRILKCLPQETIDKLRDEKL
VvRPD1          -------------CLNPNRRVLS-------------HAQVHYLLKDIDPGFIKEFVS---
VvRPE1          ---------------HNLSRILL-------------PSEVMEILRRIPEDTRKKLVRK--
ZmRPB1          --------------PVERKQILS-------------AERVLNVLKRISDEDCLLLGLNP-
ZmRPD1          ---------------NMTKIILS-------------PYQVFYMLKKSDPELIKQFVS---
ZmRPE1          --------------GCSHHRTLL-------------PEEALNILKKVPDDTRRKLAAR--
                                     :                 .  ::

AtRPB1          KFARPDWMILEVLPIPPPPVRPSVMMDATS---R-SEDDL-THQLAMIIRHNENLKRQEK
AtRPD1          ---MFNSLGLTSFPVTPNGYRVTEIVHQFN-GARLI-FDERTRIYKKLVGFEGN------
AtRPE1          GHIPQEGYILEYLPVPPNCLSVPEASDGFS---TM-SVDPSRIELKDVLKKVIAIKS-SR
BdRPD1          ---RRELLFLSCLPVTPNRHRVAEMPYRFSDGPSLA-YDDRTKAYKRTVDASKKIDD-YR
BdRPE1          GYIAQSGYVMKYLPVPPNCLYIPEFTDGQS---IM-SYDISISLLKKILHRIEQIKK-SR
CpRPD1          ---RPDSLFLNYFPVTPNSHRVTELTYMFSSGQRLF-FDERTGAYKKLVDFRGT------
CpRPE1          GYFPQDGYILQVLPVPPNCLSVPDISDGVS---TM-SSDPSTPLLKKVLEKVENIKS-SR
OsRPD1a         ---RRELLFLSCLPVTPNCHRVAEMPYGHLDGPRLA-FDDRTKAYKRMVDVSRRIDD-YH
OsRPD1b         ---RRELLFLSCLPVTPNCHRVAEMQYGHSDGPRLA-FDDRTKAYKRMVDVSKRIDD-CR
OsRPE1a         GYIPQDGFILSYLCVPPNCLRVSNVLDGNT---FS-CSGTSTNLLRKALRKIQQIRG-SR
OsRPE1b         GYIAQSGYVMKYLPVPPNCLYIPEFTDGQS---IM-SYDISISLLKKVLQKIEQIKK-SR
PtRPD1          ---KTDTIFLNCFPVTPNSHRVTEVTHAFSNGQRLI-FDERTRAYKKMVDFRGV------
PtRPE1a         GYFPQDGYILQQLPVPPNCLSVPAVSDGIS---IM-SSDLSISILKKVLKQVEVIKS-SR
PtRPE1b         GYFPQDGYILQQLPVPPNCLSVPVVSDGIT---VM-SSDLSISMLKKVLKQAEVIRS-SR
SbRPD1          ---RRELLFLSCLPVTPNCHRVVEIGYGLSDG-RVT-FDDRTKAYKRMVDVSRRIDD-YR
SbRPE1a         GYNLQDGFVMDNMSIPPNCLQISNMLDENT---EMCPPDTSKGLLHKVLRTIEQIES-LN
SbRPE1b         GYIVQTGYVMKYLPVPPNCLYIPEFTDGQS---IM-SYDISIALLKKVLQKIEQIKR-SR
SmRPD1          PSIPAEDYFIKSLPVPPNWMRYSTNE-------FY-FQDKTTKNLKHLLTKIKSIVY-TR
VvRPD1          ---RMDSFFLNCLPVTPNNHRVTEITHALSNGQTLI-FDQHSRAYKKLVDFRGT------
VvRPE1          GYFPQDGYILQYLPVPPNCLSVPDISDGVS---IM-SSDLSVSMLKKVLKQIEVIKG-SR
ZmRPB1          KYARPDWMILQVLPVPPPPVRPSVMMDTSS---R-SEDDL-THQLAMIIRHNENLRRQER
ZmRPD1          ---RRELLFLSCLPVTPNCHRVVEIGYGLPDG-RLT-FDDRTKAYKRMVDVSRRIDD-YR
ZmRPE1          GYIVQTGYVMKYLPVPPNCLYIPEFTDGQS---IM-SYDISIALLKKVLQKIEQIKR-SR
                         :  : :.*                     .         :

AtRPB1          NGAPRHIISR-FTQLLQFHIATYFDN-ELPGQPRATQK----SGR-PIKSICSRLKAKEG
AtRPD1          ------------TLELSSRVMECMQYSRLFSETVSSSK-DSANPYQ--KKSDTPKLCGLR
AtRPE1          SGETNFESHKAEASEMFRVVDTYLQ---VRGTAKAARNIDMRYGV-SKISDSSSSKAWTE
BdRPD1          Q-HPQFSVLA--SSFVTSRVMECLQSSKLYSKK-TDK-------------ESSTDSYG--
BdRPE1          AGTPNFESHEAESSDLQISIAQYIH---LRGTTK-------RFTI-STDSSHLSTKQWLE
CpRPD1          ------------SNELSSRL---------HTF-KSSSK-DATTALL--KNEDSSNMVGLR
CpRPE1          CGEPNFESHSVEANELQSAVNKYLQ---ARGTAKASRE-DTRYGV-SKNSNDCSTKAWLE
OsRPD1a         Q-HPQFGVFA--SSVVTSRVMECLKSSKLYSKK-SDD-----------ESSASTDTYGTK
OsRPD1b         Q-HPQFSVFA--SSVVTSRVMECLKSSKLYSRK-SDG-----------EDPTSPDTYGTK
OsRPE1a         IGSSNIQVDQ-VADDLQVDVANYIN---LGGTTKGHGD--------DTFTSQPTAMQWKQ
OsRPE1b         AGSPNFESHEVESCDLQLSIAQYIH---LRGTTRGPQDNTKRFAI-STDPSALSTKQWLE
PtRPD1          ------------ANTLSFHVMDCLKTSKLNPD-KSGNI-DPWTAQPKKSNDYVNNASGLR
PtRPE1a         SGAPNFDAHKDEANSLQSMVDRYLQ---VRGTTKTSRDVDVRYGV-KKDSSESSTKAWLE
PtRPE1b         SGAPNFDAHKDEATSLQSMVDQYLQ---VRGTTKTSRDVDTRYGV-KKESSESTTKAWLE
SbRPD1          Q-HPQFSVLA--SSLVSGRVSECLKSSKLYSKK-TDG-------------ETSTDPSGMK
SbRPE1a         ISHPNIEARELGADDLQVAVADYMN---MGGAAKVSQH--------VTFTRQPAPKQWHK
SbRPE1b         SGSPNFDSHDAESCDLQLAIGQYIR---LRGTTRGPQDNTKRFTVGSADSAALSTKQWLE
SmRPD1          DEDKISLLTEQKVMEIQAAATQCIRANP---LYGNVSDEDPRYGNV---SDESKPLSGLH
VvRPD1          ------------AN--------------------------------ELSCHSASKMSGLK
VvRPE1          SGEPNFESHKIEANNLQSSIEQYLE---VRGTAKTSRSLDTRFGS-SKEPNESSTKAWLE
ZmRPB1          NGAPAHIITE-FAQLLQFHIATYFDN-DLPGQPRATQR----SGR-PIKSICSRLKAKEG
ZmRPD1          Q-HPHFSVLA--SSLVSSRVSECLKSSKLYSKK-ADG-------------ETSTDTYGMK
ZmRPE1          SGSPNFESHDAESCDLQLAIGQYIR---LRGTTRGPQDNTKRFTVGSADSAALSTKQWLE
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AtRPB1          RIRGNLMGKRVDFSARTVITPDPTINIDELGVPWSIALNLTYPETVTPYNIERLKELVDY
AtRPD1          FMKDVLLGKRSDHTFRTVVVGDPSLKLNEIGIPESIAKRLQVSEHLNQCNKERLVTSFVP
AtRPE1          KMRTLFIRKGSGFSSRSVITGDAYRHVNEVGIPIEIAQRITFEERVSVHNRGYLQKLVDD
BdRPD1          -TSDAILSKRSDYAFRSIMVGDPKIRLHEIGIPMDLAD-LFVPEHVSIYNFKSINLKCNL
BdRPE1          KMRTLFISKGSGFSSRSVLTGDPYIGVDVVGLPSEVAKRITFEEQVTDINIKRLQEVVDK
CpRPD1          YMKDVLLGKRNDSSFRTVVIGDRSLKLSEIGIPCHIAESLQISENLNNWNWDKLISSCDL
CpRPE1          KMRTLFIRKGSGFSSRSVITGDPYKKVNEIGIPFEIAQRITFEERVNLHNMKYLQELVDK
OsRPD1a         WLKDIILSKRSDNAFRSIMVGDPKINLNEIGIPMGLALNLVVSEQVSSYNFETINLKCNL
OsRPD1b         WLKDIILSKRSDNAFRSIMVGDPKINLNEIGIPTDLALNLVVSEQVSFYNFETINLKCNL
OsRPE1a         KMKTLFISKSSSFSSRGVITGDPYIGLNVVGVPEEVAKRMSVEEKVTDHNIAQLQDMMNK
OsRPE1b         KMRTLFISKGSGFSSRSVLTGDPYIGVDVIGLPSEVAKRITFEEQVTDINLNRLQEIVDK
PtRPD1          WIKDVVLGKRNDHSFRMVIVGDPHLQLHEIGIPCHIAERLQISESLTAWNWEKLNACFEK
PtRPE1a         KMRTLFIRKGSGFSSRSVITGDAYTKVNQVGIPYEIAQRITFEERVSVHNMRYLQELVDN
PtRPE1b         KMRTLFIRKGSGFSSRSVITGDAYTLVNQVGIPYEIAQRITFEERVSVHNMRYLQELVDN
SbRPD1          WLKDAVLSKRSDNAFRSTMVGDPKIKLWEIGIPEDLASNLVVSDHVNSYNFENINLKCNL
SbRPE1a         KMKTLFLSKSSSYTCRAVITGDPYIGLDVVGVPDEIARRMSVQECVTNYNIARLQDMMNK
SbRPE1b         KMRTLFISKGSGFSSRSVLTGDPYIGLGVVGLPSEVAKRMTFEEQVTDININRLQEVVDK
SmRPD1          FLRSL-TGKYCGSSARAVVIGDPALKLEEIGISARIAAGLVVLETVTSSNIIFLQSYAYN
VvRPD1          WIKEVLLGKRTNHSFRMIVVGDPKLRLSEIGIPCHIAEELLISEHLNSWNWEKVTNGCNL
VvRPE1          KMRTLFIRKGSGFSSRSVITGDAYKRVNEIGLPFEIAQRITFEERVNVHNMKHLQNLVDE
ZmRPB1          RIRGNLMGKRVDFSARTVITPDPNINIDELGVPWSIALNLTYPETVTPYNIERLKELVEY
ZmRPD1          WLKDVVLSKRSDNVFRSIMVGDPKIKLWEIGIPEDLSSSLVVSEHVSSYNFQSTNLKCNL
ZmRPE1          KMRTLFISKGSGFSSRSVLTGDPYIGLGVVGLPSEVAKRMTFEEQVTDININRLQDVVDK
                        *  .   *  :  *    :  :*:.  ::  :   : :.  *

AtRPB1          GPHPPPGKTGAKYIIRDDGQR-LDLRYLKKSSDQHLELGYRYVLLSYSIHS-THKRLFLE
AtRPD1          TLL-----DNKEMHVRRGDRL-VAI------------------------------Q----
AtRPE1          KLC----------LSYTQGST-TYSLRDG------------------------SKG----
BdRPD1          HLL-----AKELLIARRNGKL-IYV-----------------------------RK----
BdRPE1          GLC----------LTYRDGQT-TYAITVG------------------------SKG----
CpRPD1          RLL-----EKGEIHVRRKNSL-ISL-----------------------------RR----
CpRPE1          KLC----------LTYRDGGS-TYSLREG------------------------SKG----
OsRPD1a         HLL-----TKEVLLVRRNGNL-IFV-----------------------------RK----
OsRPD1b         HLL-----TKEVLLVRRNGKL-IFV-----------------------------RK----
OsRPE1a         GLC----------LTYTDANSITYSLDAGK--------------------DNPNKK----
OsRPE1b         GLC----------LTYRDGQA-TYAITVG------------------------SKG----
PtRPD1          SRF-----EKGDMHVRREGNL-VRV-----------------------------RH----
PtRPE1a         KLC----------LTYRDGSS-TYSLREG------------------------SKG----
PtRPE1b         KLC----------LTYKDGSS-TYSLREG------------------------SKG----
SbRPD1          HLL-----TKEELFIRRNGKL-MFL-----------------------------RK----
SbRPE1a         GLC----------LTYTDLNTNTYDL-DGK--------------------K-GNKK----
SbRPE1b         GLC----------LTYRDGQA-TYAITVG------------------------SKG----
SmRPD1          NP---------GLKVVRGGEV-CTA-----------------------------RS----
VvRPD1          RLL-----EKGQTYVRRKGTL-APV-----------------------------RR----
VvRPE1          KLC----------LTYRDGLS-TYSLREG------------------------SKG----
ZmRPB1          GPHPPPGKTGAKYIIREDGQR-LDLRYVKK------------------------SS----
ZmRPD1          HLL-----AKQELFIRRNGKL-MFL-----------------------------RK----
ZmRPE1          GLC----------LTYRDGQA-TYAITVG------------------------SKG----


AtRPB1          VVIFMLSWSQVERHLQDGDFVLFNRQPSLHKMSIMGHRIRIMPY-STFRLNLSVTSPYNA
AtRPD1          -VNDLQTGDKIFRSLMDGDTVLMNRPPSIHQHSLIAMTVRILPTTSVVSLNPICCLPFRG
AtRPE1          -HTELKPGQVVHRRVMDGDVVFINRPPTTHKHSLQALRVYVHED-NTVKINPLMCSPLSA
BdRPD1          -ENQLEIGDIVYRPLQDGDLILVNRPPSVHQHSLIALSAKLLPVQSVVAINPLNCAPLSG
BdRPE1          -YTTLKVGQTISRRIVDGDVVFLNRPPSTHKHSLQAFYVYIHDD-HTVKINPLICSPLAA
CpRPD1          -ISDLRMGDIISRPLKDGDILLINRPPSIHPHSLIALSVKVLPISSVVSINPICCSPFRG
CpRPE1          -HTFLRPGQVVHRRIMDGDTVFINRPPTTHKHSLQALSVYIHDD-HTVKINPLICGPLSA
OsRPD1a         -ANQLEIGDIAYRLLQDGDLVLVNSPPSVHQHSLIALSAKLLSTQSAVSINPLCCDPFKG
OsRPD1b         -ANKLEIGDIAYRLLQDGDLVLVNRPPSVHQHSLIALSAKLLPIQSAVAINPLCCDPFKG
OsRPE1a         -HTILKVGEIVNRRVFDGDIVFLNRPPSTDKHSVEAFYVQVHND-HTIKINPLICDPLGA
OsRPE1b         -HTTLKVGQTISRRIVDGDVVFLNRPPSTHKHSLQAFRVYVHED-HTVKINPLICAPFAA
PtRPD1          -MKELRLGDIIYRPLNDGDTVLINRPPSIHQHSLIALSVKVLPVPSVLAINPLCCPPFRA
PtRPE1a         -HTFLRPGQVVHRRIIDGDVVFINRPPTTHKHSLQALSVYVHDD-HTVKINPLICGPLSA
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PtRPE1b         -HTFLRPGQVVHRRIMDGDIVFINRPPTTHKHSLQALSVYVHDD-HAVKINPLICGPLSA
SbRPD1          -ADQLEIGDIAYRPLQDGDLILINRPPSVHQHSLIAFSAKILPIHSVVSINPLCCTPFLG
SbRPE1a         -CIMLRVGETVDRRVLDGDLVFLNKPPSTDMHSIQALYVHVHDD-HTIKINPLICGPLEA
SbRPE1b         -HTTLKVGQTISRRIVDGDVVFLNRPPSTHKHSLQAFYAYVHDD-HTVKINPLMCGPFSA
SmRPD1          -CKKLQVGDVIHRSLKDGDQVFVNRPPTFHKHALIGLKSKVIRN-NVFAVNPLICPPLFA
VvRPD1          -MNDFQAGDIIYRPLTDGDIVLINRPPSIHQHSVIALSVKVLPLNSVVSINPLCCSPFRG
VvRPE1          -HTFLRPGQVVHRRIMDGDIVFINRPPTTHKHSLQALSVYVHDD-HTVKINPLICGPLSA
ZmRPB1          -DQHLELGYKVERHLNDGDFVLFNRQPSLHKMSIMGHRIKIMPY-STFRLNLSVTSPYNA
ZmRPD1          -ADQLEIGDIAYRPLQDGDIILINRPPSVHQHSLIALSAKILPIHSVVSINPLCCTPFAG
ZmRPE1          -YTTLKVGQTISRRIVDGDVVFLNRPPSTHKHSLQAFYAYVHDD-HTVKINPLMCGPFSA
                    :       * : *** ::.*  *: .  :: .    :     .. :*     *  .

AtRPB1          DFDGDEMNMHVPQSFETRAEVLELMMVPKCIVSPQANRPVMGIVQDTLLGCRKI-TKRDT
AtRPD1          DFDGDCLHGYVPQSIQAKVELDELVALDKQLINRQNGRNLLSLGQDSLTAAYLVNVEKNC
AtRPE1          DFDGDCVHLFYPQSLSAKAEVMELFSVEKQLLSSHTGQLILQMGSDSLLSLRVM-LER-V
BdRPD1          DFDGDCLHGYVPQSIGSRVELGELVSLSHQLLNMQDGRSLVSLTHDSLAAAHLL-TSSGV
BdRPE1          DFDGDCVHIYYPQSLAAKAEALELFSVEKQLTNSHNGKVNLQLSNDSLLALKHM-SSR-T
CpRPD1          DFDGDCFHGYIPQSIEARVELHELVALDRQLTNWLSGRNLLCLGQDSLTAAHLI-KEDGF
CpRPE1          DFDGDCVHLFYPQSPAARAEVLELFSVEKQLLSSHSGNLNLQLAADSLLSLKVM-FEK-F
OsRPD1a         DFDGDCLHGYIPQCLQSRIELEELVGLSGQLLNQQDGRSLVSLTHDSLAAAHQL-TNADV
OsRPD1b         DFDGDCLHGYVPQTLQSRVELDGLVSLSGQMLNAQDGRSLVSLTHDSLAAAHQL-TSADV
OsRPE1a         DFDGDCVQIFYPRSLSARAEAKELYTVDKQLVSSHNGKLNFQFKNDFSLALKIM-CGR-E
OsRPE1b         DFDGDCVHIYYPQSLAAKAEALELFSVEKQLTSSHSGKVNLQLVSDSLLALKHM-SSR-T
PtRPD1          DFDGDCLHGYVPQSVDTRVELTELVSLDKQLTNWQSGRNLLSLSQDSLTAAHLV-LEDDV
PtRPE1a         DFDGDCVHLFYPQSLAAKAEVLELFSVEKQLLSSHSGNLNLQLTTDSLLSLKMI-FKA-C
PtRPE1b         DFDGDCVHLFYPQSLAAKAEVLELFSVEKQLLSSHSGNLNLQLTTDSLLSLKMM-FKA-C
SbRPD1          DFDGDCLHGYIPQSVRSRIELGELVSLHHQLLNMQDGRSLVSLTHDSLAAAHLL-TSTDV
SbRPE1a         DFDGDCVHIFFPRSVLARVEAAELFAVEKQLLNSHNAKLNFQIKNDYLLALRIM-CDR-S
SbRPE1b         DFDGDCVHIYYPQSLAAKAEALELFSVERQLISSHSGKVNLQLGNDCLVAMKAM-SDR-T
SmRPD1          DFDGDTLALYLPQSLQVRAEVAELVALPKQLVSSQGGQSIIGLTQDALLGAHLM-TRKNV
VvRPD1          DFDGDCLHGYIPQSVDSRVELSELVALNRQLINRQSGRNLLSLSQDSLSAAHLV-MEDGV
VvRPE1          DFDGDCVHLFYPQSLGAKAEVLELFSVEKQLLSSHSGNLNLQLATDSLLSLKVL-FER-Y
ZmRPB1          DFDGDEMNMHVPQSFETRAEVLELMMVPKCIVSPQSNRPVMGIVQDTLLGCRKI-TKRDT
ZmRPD1          DFDGDCLHGYIPQSIRSRVELEELVSLHNQLLNMQDGRNLVSLTHDSLAAAHLL-TSTDV
ZmRPE1          DFDGDCVHIYYPQSLAAKAEALELFSVERQLISSHSGKVNLQLGNDSLVAMKAM-SHT-T
                ***** .  . *:    : *   *  :   : .    .  . :  *   .   :

AtRPB1          FIEKDVFMNT--LMWWEDFDGK-VPAPAILKP-----RPLWTGKQVFNLIIPKQINLLRY
AtRPD1          YLNRAQMQQL--QMYC-P--FQ-LPPPAIIKASPSSTEPQWTGMQLFGMLFPPGFDY---
AtRPE1          FLDKATAQQL--AMYG-S--LS-LPPPALRKSS--KSGPAWTVFQILQLAFPERLSC---
BdRPD1          LLNKTEFQQL--QMLC-V-SLSPTPVPSVIKSI-NPQGPLWTGKQLFGMLLPSGMNF---
BdRPE1          VLSKESANQL--AMLL-S--FS-LPDPAVVKL-----KPCWTITQIIQGALPAALTC---
CpRPD1          LLNKYQMQQL--KMYC-P--YE-LPPPALVKAP-RLNSSVWTGKQLFSMLLPPGFNY---
CpRPE1          FLGKTAAQQL--AMFG-S--LS-LLWPALFKSH--SSGSFWTASQIIQTALPACFDC---
OsRPD1a         FLEKAEFQQL--QMLS-S-SISLTPMPSVFKST-NSQGPLWTGKQLFGMLLPYGMNI---
OsRPD1b         FLQKAEFQQL--QLLC-S-SISPTPEPSVVKSA-NFQGSLWTGKQLFGMLLPSGMNI---
OsRPE1a         Y-SEREANQITNAMFS-S--GM-YPQKP----L--IGGPYWTFPQILETTKSNAITL---
OsRPE1b         MLSKEAANQL--AMLV-T--CS-LPDPAVIKS-----KPYWTISQIVQGALPKALTS---
PtRPD1          FLSSFELQQL--QMFR-P--ER-FLLPAVKAPS--ANALVWTGKQLISMLLPVGFDH---
PtRPE1a         FLDKSAAQQL--AMFV-S--PD-LPQPALLKVN--CIRPYWTAHQILQMALPTCFNC---
PtRPE1b         FLGKSAAQQL--AMFI-S--PY-LPQPALLKVN--CFFPHWTAHQILQMALPACFNC---
SbRPD1          FLKKSEFQQL--QMLC-L-SVL-TPVPAVIKSM-NFQGSRWTGKQLFSMLLPSGMKF---
SbRPE1a         Y-SKEKANQI--AMFS-S--GM-IPPCNP---W--TICDRWTIPQILQTTDALRIVP---
SbRPE1b         VLHKELANQL--AMFV-P--FS-LLAPAVMKP-----IPSWTITQIVQGALPAKLTC---
SmRPD1          FLDKLDMDQL--RMWC-P-SAE-VPVPAIVKSP--RKSPLWTGQQLFQMTLPTTFDW---
VvRPD1          LLNLFQMQQL--EMFC-P--YQ-LQSPAIIKAP--LLD----------------------
VvRPE1          FLNKAAAQQL--VMFV-S--MS-LPRPALLKSP--CSGPCWTALQILQTALPSYFDC---
ZmRPB1          LIEKDVFMNI--LMWWQDFDGK-IPAPTILKP-----RPIWTGKQVFNLIIPKQINLIRF
ZmRPD1          FLKKSELQQL--QMLC-L-SVS-TPAPAVIKSM-NFQGSLWTGKQLFSMLLPSGMNF---
ZmRPE1          MLHKELANQL--AMFV-P--FS-LLAPAVIKP-----VPSWTISQIVQGAFPANLTC---
                        :    :

AtRPB1          SAWHADTETGFITPGDT-QVRIERGELLAGTLCKKTLGTS-NGSLVHVIWEEVGPDAARK
AtRPD1          -------------TYPLNNVVVSNGELLSFSEGSAWLRDG-EGNFIERLLKHDK-GKVLD
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AtRPE1          -------------KGDR-F-LVDGSDLLKFDFGVDAMGSI-INEIVTSIFLEKGPKETLG
BdRPD1          -------------SPDP-KLHIKDSEVLACSGGSFWLQNN-TSGLFSVLFKQYG-GEALE
BdRPE1          -------------EGGR-F-LVKDSTVIKLDLAKESVQAS-FSDLVSSILCVKGPGGALQ
CpRPD1          -------------YFSQNGVCIINGELTSSSDGSAWLRDN-DGNLFQSLVKYDK-SMVLN
CpRPE1          -------------NEDR-Y-LIRKSEILNIDFNKDSVQSV-VGEVVNSIFYEKGPKEVLE
OsRPD1a         -------------SFDQ-KLHIKDSEVLTCSSGSFWLQNN-TSSLFSVMFKEYG-CKALE
OsRPD1b         -------------SFDQ-KLHIKDSEVLTCSSGSFWLQNN-TSSVFSVMFKEYG-SKALE
OsRPE1a         -------------A---------------DHLDRESVGALATGTTISSILSTKGPREATE
OsRPE1b         -------------QGDK-H-VVRDSTIIKLDLDKESVQTS-FSDLVYSTLSVKGPGEALQ
PtRPD1          -------------DFPSCNVCIRDGDLVS-SEGSFWLWDT-DGNLFQSLVKHCH-GQVLD
PtRPE1a         -------------SGER-F-LINNSNVLKVDFNRDVVASM-INEILISIFFEKGSGAVLK
PtRPE1b         -------------SGER-F-LIINSNFLKVDFNRDVVASV-INEILISMFFEKGSGAVLK
SbRPD1          -------------SCDR-MLHILNGEVLTCSLGSSWLQNN-TSGLFSVMFKQYG-CKALD
SbRPE1a         -------------------------------SHPNTVGAS-VTAIITSTLSEKGPREAIK
SbRPE1b         -------------QGDT-H-LVRDSTIIKLDLDKESVQDS-FPDLVSSILREKGPREALQ
SmRPD1          -------------ESDDGGLIIRQGEILRTSD-KSSAWLG-KDGLMTTICRRYGPDRALE
VvRPD1          ------------------------------------------------------------
VvRPE1          -------------IGER-H-WISKSAILKVDYNRDVLQSL-VNEIVTSIFSEKGPNEVLK
ZmRPB1          SAWHSEEEKGFITPGDT-MVRIEKGELLSGTLCKKSLGTG-SGSLIHVIWEEVGPDAARK
ZmRPD1          -------------SCDT-ELHIMDSEVLTCSLGSSWLQNN-TSGLFSVMFKQYG-CKALD
ZmRPE1          -------------QGDT-H-LVRDSTIIRLDLGKESVQDS-FPDLVSSILREKGPKEALQ


AtRPB1          FLGHTQWLVNYWLLQNGFTIGIGDTIADSSTMEKINETI-SNAKTAVKDLIRQFQGKELD
AtRPD1          IIYSAQEMLSQWLLMRGLSVSLADLYLSSDLQ-SRKNLT-EEISYGLREAEQVCNKQQLM
AtRPE1          FFDSLQPLLMESLFAEGFSLSLEDLSMSRADMDVIHNLIIREISPMVSR-----------
BdRPD1          FLSSAQDMLCEFLTMRGLSVSLSDIYLFSDHY-SRRKFA-EEVNLALDEAEEAFRVTQIL
BdRPE1          FLNALQPLLMEYLLLDGFSVSLQDFNVPKVLLEEVHKSI-QEQSLVLEQ-----------
CpRPD1          FLYAAQEVLCDWLSDRGFSISLSDLYLSSDLH-SRENLM-DEISWGLLEAEQTCNFKQLM
CpRPE1          FFASLQPLLMENLFVEGFSVGLKDFSMPKSDMQAIQKLI-HDTSLFLSC-----------
OsRPD1a         FLSSTQDVLCEFLTMWGLSVSLSDLYLFSDHY-SRRKLS-EEVHLALDEAEEAFQIKQIL
OsRPD1b         FLSSTQDVLCEFLTMKGLSVSLSDFYLFSDHY-SRKKLS-EEIHLALDEAEEAFQIKQIL
OsRPE1a         FLNLLQPLLMESLLIDCFSINLGDFTVPSPILEAIQNN-P--------------------
OsRPE1b         FLNVLQPLLMELILLDGFSVSLQDFNVPKVLLEEAQKNI-EKQSLILEQ-----------
PtRPD1          FLYAAQRVLCEWLSMRGLSVSLSDLYLCPDSN-SRKNMM-DEIWYGLQDADYACNLKHLM
PtRPE1a         FFNALQPLLMENLFSEGFSVSLKDFSISQAVKQSIQESF-KVISPLLCN-----------
PtRPE1b         FFNSLQPMLMENLFSEGFSVSLEDFSISRAVKQRIPESF-KAISPLLCN-----------
SbRPD1          FLSSAQEVLCEFLTMRGLSVSLSDMF--SDHY-SRRKLT-EGVKLALDEAEEAFRIKQIL
SbRPE1a         LINLLQPLLMESLLMDGFSISLKDLDGQSAMQKANQSI-S--------------------
SbRPE1b         FLNVLEPLLMEFLVLGGLSISLRDFNVPKALLEEAQKNI-QNQSLVLEQ-----------
SmRPD1          HLDIAQGIAVDWISERGFSVGLCDFYMAADAV-SRRKLE-EETLCAVEEAKISSLAHQIV
VvRPD1          ---------TQWLSMRGLSVSLSDIYLSSDSI-SRKNMI-DEVFCGLLVAEQTCHFKQLL
VvRPE1          FFDSLQPLLMENLFSEGFSVSLEDFSIPSEVTQNIQKNV-EDISSLLYN-----------
ZmRPB1          FLGHTQWLVNYWLLQNGFSIGIGDTIADASTMETINDTI-SKAKNAVKELIKKAHEKQLE
ZmRPD1          FLSSAQEVLCEFLTMRGLSVSLSDLYMFSDHY-SRRKLA-EGVKLALYEAEEAFRVKKIL
ZmRPE1          FLNVLEPLLMEFLLLDGLSISLRDFNVPKALLEEAQKDI-RNQSLILEQ-----------
                            :    :::.: *            .

AtRPB1          PEPGRTMRD------------------------------------------TFENRVNQV
AtRPD1          VESWRDFLAVNGEDKEEDS-----------------VSDLARFCYERQKSATLSELAVSA
AtRPE1          ---LRL---------------------------------------------SYRD--ELQ
BdRPD1          LSPNFIPHLKCYDDCDDLS-----------------DSYEQSDF--VQSNLPIIKSSIMA
BdRPE1          ---SRC---------------------------------------------SKSQFVEMR
CpRPD1          VDSCRDLLAGNDEESQNVI-----------------TFDVERLCYEKQGSAVLSQASVDA
CpRPE1          ---LGS---------------------------------------------TYNE--ELQ
OsRPD1a         LNSVSIPNLKYYDGGDDRS-----------------NTDEQSGF--TQVSLPIIRSSMTS
OsRPD1b         LNTVSIPNLKHYDGPDNLS-----------------NSHGQSDF--TQVSLPIIKSSITG
OsRPE1a         ------------------------------------------------------------
OsRPE1b         ---SRF---------------------------------------------AENQVVEMR
PtRPD1          VDSCRDFLTGNNEEDQCNVERLRFLSGCSEEDYCVMAFDGERLCYEKQRSAALSQSSVDA
PtRPE1a         ---LRS---------------------------------------------TYNELVELQ
PtRPE1b         ---LRS---------------------------------------------TFNELVELQ
SbRPD1          LDPINIPVLKCQDETEDV-------------------TYRQSDC--IQNNPSVIRSSIMA
SbRPE1a         ------------------------------------------------------------
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SbRPE1b         ---SRC---------------------------------------------STSQFVELR
SmRPD1          SDPRFQVNSVSRP--RCNS-----------------WNERVQPV--TSVNEATQQAAISA
VvRPD1          VDSSQNFLIGSGENNQNGV-----------------VPDVQSLWYERQGSAALCQSSVCA
VvRPE1          ---LRS---------------------------------------------MYNELLQLQ
ZmRPB1          AEPGRTMME------------------------------------------SFENRVNQV
ZmRPD1          LDPINIPVLKCHDETEDV-------------------TYRQSDC--IQSNPSVIRSSIMA
ZmRPE1          ---SRC---------------------------------------------STSQFVEFR


AtRPB1          LNKARDDAGSSAQKSL---AETNNLKAMVTAGSKGSFINISQMTACVGQQNVEGKRI-PF
AtRPD1          FKDAYRDVQALAYRYG---DQSNSFLIMSKAGSKGNIGKLVQHSMCIGLQNSAVSLSF--
AtRPE1          LENSIHKVKEVAANFM---LKSYSIRNLIDIKSNSAITKLVQQTGFLGLQLSDKKKFYTK
BdRPD1          FKSVFSDLLKMVQQHT---PKDNSMMAMINAGSKGSMLKFVQQAACVGLQLPAGKFPF--
BdRPE1          VDNNLKDVKQQISDFV---VESSHLGLLIDPKSEPSMSKVVQQLGFVGLQLYREGKFYSS
CpRPD1          FKQVFRDIQTLAFKYA---SKENSLLAMYKAGSKGSLPKLVQHSMCLGLQHSLVPLSF--
CpRPE1          LENRIRCLKETAENFI---IK-SSLRNLIDFRSDSAVNKVVQQIGFLGLQLSDKGKFYSK
OsRPD1a         FKSVFNDLLKMVQQYV---SKDNSMMTMINSGSKGSVLKFVQQTACVGLQLPASKFPF--
OsRPD1b         FKSVFNDLLKMVLQHV---SKDNSMMAMINSGSKGSVLKFVQQTACVGLQLPASTFPF--
OsRPE1a         --LELNKYREPIMDFI---THSSAIGLLVDPKSDSNMNKVVEQLGFLGPQLQHNGRLYSS
OsRPE1b         VDNNLKDIKQQISDFV---VKRSHLGLLIDPKSDSSVSKVVQQLGFVGLQLYREGKFYSR
PtRPD1          FRLVFRDIQSLVYKYA---SQDNSFLAMFKAGSKGNLLKLVQHSMCLGLQHALASLSF--
PtRPE1a         VENHIQDVKTPVLEFI---LTSSALGYLIDSKSDGAVAKLVQQIGFLGLQVSDRGKLYSK
PtRPE1b         VENHIRDVKQPVREFI---LTSSALGYLIDSKSDAAVTKVVQQIGFLGLQVSDRGKLYSK
SbRPD1          FKDVFSDLLKMVQQHV---SNDNSMMVMINAGSKGSMLKYAQQTACVGLQLPASKFPF--
SbRPE1a         --LEIDKFSKSIVDFI---ANSSALGLLVDPKNDSALMNLVEQVGFLGYQLQSTDRLYSN
SbRPE1b         VENNLKSVKQQISDYV---GKFSGLGLLIDPKKEASMAKVVQQVGFVGLQLYREGKLYSR
SmRPD1          FQSTMKAFERTIEEHVRENSRENSLLRMVEANSKGSFSKMMQQGGCLGLQLRQGEFVYH-
VvRPD1          FKQKFRDIQNLVYQYA---NKDNSLLAMLKAGSKGNLLKLVQQGLCLGLQHSLVPLSF--
VvRPE1          AENHLRLTKVPVANFI---LNSSALGNLIDSKSDSAINKVVQQIGFLGQQLSEKGKFYSR
ZmRPB1          LNKARDDAGSSAQNSL---SESNNLKAMVTAGSKGSFINISQMTACVGQQNVEGKRI-PF
ZmRPD1          FKDVFRDLLKMVQQHV---SNDNSMMVMINAGSKGSMLKYAQQTACIGLQLPASKFPF--
ZmRPE1          VENNLKNVKQQISDSV---GKFSDLGLLIDPKKEASMSKVVQQVGFVGLQLYREGKLYSR
                                        :  :    ..  . :  :    :* *

AtRPB1          GFDG--RTLPHF-------------TKDDYGPESRGFVENSYLRGLTPQEFFFHAMGGRE
AtRPD1          GFPRELTCAAWNDPNSPLRGAKGKDSTTTESYVPYGVIENSFLTGLNPLESFVHSVTSRD
AtRPE1          TLVE--DMAIFCKRKYG----------RISSSGDFGIVKGCFFHGLDPYEEMAHSIAARE
BdRPD1          RIPSELTCASWNRHKSLDCDISEGARKRLGGQNSHAVIRNSFIEGLNPLECLLHSISGRA
BdRPE1          RLVE--DCFSSFVDKHPP------IVGNQHPPEAYGLVQNSYFHGLNPYEELVHSISTRE
CpRPD1          RFPHQLSCAAWNKQK---------------------------------------------
CpRPE1          NLVE--DVAFLFRSKHPG------A--GHYPSANFGLIKSCFIHGLDPYEEMAHSISTRE
OsRPD1a         RIPSQLSCVSWNRHKSRNCEITDGTSECVGGQDMYAVVRNSFLDGLNPLECLLHAISGRA
OsRPD1b         RIPSELSCVSWNRQKSLNCEITNNTSECMAGQNMYAVIRNSFLDGLNPLECLLHAISGRA
OsRPE1a         RLVE--DCLSKSLHRCCG------STNCCNPLEEYGTVRSSIYHGLNPYEALLHSICERE
OsRPE1b         RLVE--DCYYTFVNKHPA------V-REEHSPEAYGLVRSSYFHGLNPYEELVHAISTRE
PtRPD1          RIPHQLSCAGWNKQKADD------ATESAKRYIPHAVVEGSFLSGLNPIECFVHSVTSRD
PtRPE1a         TLVE--DLASHFQSKYPT------N-LLNYPSAQYGLIQSSFFHGLDAYEEMAHSISTRE
PtRPE1b         TLVE--DLASHFLSKYPA------N-LFDYPSAQYGLIQNSFFHGLDAYEEMAHSISTRE
SbRPD1          RVPSQLSCIRWNRQKSLNYE-AEGTNERVGGQNLYAVIRNSFIEGLNPLECLLHAISGRA
SbRPE1a         NLVE--DCYNF-LEKRSG------STKCYDPPKGHDFVTSSFYNGLNPYEELLHSISVRE
SbRPE1b         RLVE--DCFSSFVNKHSA------I-GDEYSPEAFGLVQSSYFHGLNPYEELVHAICTRE
SmRPD1          R-VKSL-FPRAVENESRG------YLTSSELWKSMGLVESSFLDGLDPREFFIHSLSSRK
VvRPD1          KIPHQLSCAAWNKQKVPGLI-QNDTSEYAESYIPYAVVENSFLMGLNPLECFVHSVTSRD
VvRPE1          TLVE--GMAYLFKSKYPF------H-GADYPSGEFGLIRSCFFHGLDPYEEMVHSISTRE
ZmRPB1          GFID--RTLPHF-------------TKDDYGPESRGFVENSYLRGLTPQEFFFHAMGGRE
ZmRPD1          RIPSQLSCISWNGQKSLNYE-AESTSERVGGQNLYAVIKNSFIEGLNPLECLLHAISGRA
ZmRPE1          RLVE--DCFTNFVNKHLA------I-GDEYPPEAYGLVQSSYFHGLNPYEELIHAISTRE


AtRPB1          GLIDT-AVKTSETGYIQRRLVKAMEDIMVKYDGTVRNSLGD-VIQFLYGEDGMDAVWIES
AtRPD1          SSFS---GNADLPGTLSRRLMFFMRDIYAAYDGTVRNSFGNQLVQFTYETDGP-------
AtRPE1          VIVRS-SRGLAEPGTLFKNLMAVLRDIVITNDGTVRNTCSNSVIQFKYGVDSERG-----
BdRPD1          NFFS---ENADVPGTLTKNLMYHLRDIYVAYDGTVRSSYGQQIVQFTYDTAEDIY-----
BdRPE1          AIVRS-SRGLTEPGTLFKNLMAILRDVVICYDGTVRNICSNSIMQLKYNEDDATD-----
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CpRPD1            ------------------------------------------------------------
CpRPE1            VIVRS-SRGLTEPGTLFKNMMAVLRDIIVCYDGTVRNICSNSVIQFKYGLKADNE-----
OsRPD1a           NFFS---ENADVPGTLTRKLMYHLRDTYVAYDGTVRSSYGQQIVRFSYDTADGMY-----
OsRPD1b           NFFS---ENADVPGTLTRKLMYHLRDTYVAYDGTVRSSYGRQIVQFSYDTADGMN-----
OsRPE1a           KIMRA-SKGLVEPGSLFKNMMSRLRDVTACYDGSIRTSSGNLVLQFGSR-----D-----
OsRPE1b           AIVRS-SRGLTEPGTLFKNLMALLRDVVICYDGTVRNVCSKSIIQLNYTEDDALD-----
PtRPD1            SSFS---DNADLPGTLFRRMMFFMRDLHGAYDGTVRNAYGNQLVQFSYNIDDMDP----S
PtRPE1a           VIVRS-SRGLSEPGTLFKNLMAILRDVVICYDGTVRNVCSNSIIQSEYGVKVGAE-----
PtRPE1b           VIVRS-SRGLSEPGTLFKNLMAILRDVVICYDGTVRNVSSNSIIQFEYGVKVGTE-----
SbRPD1            NFFS---ENADVPGTLTRKLMYHLRDIHVAYDGTVRSSYGQQIVQFSYDSADD-------
SbRPE1a           KIERSSSKGLAEAGNLFKNMMAMLRDVTVCYDGTMRTSYNNSIVQFDST-----N-----
SbRPE1b           TMIRS-SRGLSEPGTLFKNLMAILRDVVICYDGTVRNICSNSIIQLKYGEDDEAD-----
SmRPD1            GNDG-SQ---QRCASFFRFLMSYMKDIRVEYDNTIRSTHGGHIFQFSYGAT---------
VvRPD1            SSFS---DNADLPGTLTRRLMFFMRDLYIAYDGTVRNAYGNQLVQFSYNIEHTSTP---S
VvRPE1            IIVRS-SRGLSEPGTLFKNLMAILRDVVICYDGTVRNVCSNSIIQFEYGVKARTK-----
ZmRPB1            GLIDT-AVKTSETGYIQRRLVKAMEDIMVKYDGTVRNSLGD-VIQFLYGEDGMDAVWIES
ZmRPD1            NFFS---ENADVPGTLTRKLMYHLRDIHVAYDGTVRSSYGQQIVQFSYDSVDD-------
ZmRPE1            AMIRS-SRGLSEPGTLFKNLMAILRDVVICYDGTVRNICSNSIIQLKYGEDDETD-----


AtRPB1            QKLDSLKMKKSEFDRTFKYEIDDENWNPTYLSDEHLEDLKGIRELRDVFDAEYSKLETDR
AtRPD1            ------------------------------------------------------------
AtRPE1            ------------------------------------------------------------
BdRPD1            ------------------------------------------------------------
BdRPE1            ------------------------------------------------------------
CpRPD1            ------------------------------------------------------------
CpRPE1            ------------------------------------------------------------
OsRPD1a           ------------------------------------------------------------
OsRPD1b           ------------------------------------------------------------
OsRPE1a           ------------------------------------------------------------
OsRPE1b           ------------------------------------------------------------
PtRPD1            GSV---------------------------------------------------------
PtRPE1a           ------------------------------------------------------------
PtRPE1b           ------------------------------------------------------------
SbRPD1            ------------------------------------------------------------
SbRPE1a           ------------------------------------------------------------
SbRPE1b           ------------------------------------------------------------
SmRPD1            ------------------------------------------------------------
VvRPD1            DGI---------------------------------------------------------
VvRPE1            ------------------------------------------------------------
ZmRPB1            QKLDSLKMKKPEFDNVFRYELDDENWRPNYMLPEHVDDLKTIREFRNVFEAEVQKLEADR
ZmRPD1            ------------------------------------------------------------
ZmRPE1            ------------------------------------------------------------


AtRPB1            FQLGTEIATNGDSTWPLPVNIKRHIWNAQKTFKIDLRKISDMHPVEIVDAVDKLQERLLV
AtRPD1            ------------------------------------------------------------
AtRPE1            ------------------------------------------------------------
BdRPD1            ------------------------------------------------------------
BdRPE1            ------------------------------------------------------------
CpRPD1            ------------------------------------------------------------
CpRPE1            ------------------------------------------------------------
OsRPD1a           ------------------------------------------------------------
OsRPD1b           ------------------------------------------------------------
OsRPE1a           ------------------------------------------------------------
OsRPE1b           ------------------------------------------------------------
PtRPD1            ------------------------------------------------------------
PtRPE1a           ------------------------------------------------------------
PtRPE1b           ------------------------------------------------------------
SbRPD1            ------------------------------------------------------------
SbRPE1a           ------------------------------------------------------------
SbRPE1b           ------------------------------------------------------------
SmRPD1            ------------------------------------------------------------
VvRPD1            ------------------------------------------------------------
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VvRPE1          ------------------------------------------------------------
ZmRPB1          YQLGSEITTTGDNSWPMPVNLKRLIWNAQKTFKIDFRRPSDMHPMEIVEAIDKLQERLKV
ZmRPD1          ------------------------------------------------------------
ZmRPE1          ------------------------------------------------------------


AtRPB1          VPGDDALSVEAQKNATLFFNILLRSTLASKRVLEEYKLSREAFEWVIGEIESRFLQSLVA
AtRPD1          --------------------------------------------------------VEDI
AtRPE1          ------------------------------------------------------HQGLFE
BdRPD1          ----------------------------------------------------TDCGQEGE
BdRPE1          ------------------------------------------------------IPSALT
CpRPD1          ------------------------------------------------------------
CpRPE1          ------------------------------------------------------PLRLFP
OsRPD1a         ----------------------------------------------------SDHDLEGE
OsRPD1b         ----------------------------------------------------NDHDLEGE
OsRPE1a         ------------------------------------------------------ASNCVT
OsRPE1b         ------------------------------------------------------FPSAIG
PtRPD1          ---------------------------------------------------DEINNSDGI
PtRPE1a         ------------------------------------------------------SQSLFP
PtRPE1b         ------------------------------------------------------SQSLFP
SbRPD1          --------------------------------------------------------PVDK
SbRPE1a         ------------------------------------------------------VSSSLT
SbRPE1b         ------------------------------------------------------SSSAVP
SmRPD1          ----------------------------------------------------------AE
VvRPD1          ---------------------------------------------------NEDTCAYDM
VvRPE1          ------------------------------------------------------PQHFFP
ZmRPB1          VPGDDAMSIEAQKNATLFFNILLRSTFASKRVLKEYRLTKEAFEWVIGEIESRFLQSLVA
ZmRPD1          --------------------------------------------------------LVDK
ZmRPE1          ------------------------------------------------------SSSVVP


AtRPB1          PGEMIGCVPAQSIGEPATQMTLNTFH-YAGVSAKNVTLGVPRLREIINVAKRIK----TP
AtRPD1          TGEALGSLSACALSEAAYSALDQPISLLETSPL-------LNLKNVLECGS--KKGQREQ
AtRPE1          AGEPVGVLAATAMSNPAYKAVLDSSP-NSNSSW-------ELMKEVLLCKVNFQNTTNDR
BdRPD1          FGAPVGSWAACSISEAAYGALDHPVNVIEDSPL-------MNLQEVLKCQK--GTNSLDH
BdRPE1          PGEPVGVLAATAISNPAYKAVLDASQ-SNNTSW-------ASMKEILQTKVSYKNDTNDR
CpRPD1          ------------------------------------------------------------
CpRPE1          AGEPVGVLAATAMSNPAYKAVLDSTP-SSNSSW-------ELMKEILLSKISFKNDLNDR
OsRPD1a         PGAPVGSWAACSISEAAYGALDHPVNSLEDSPL-------MNLQEVLKCHK--GTNSLDH
OsRPD1b         PGAPVGSWAACSISEAAYGALDHPVNALEDSPL-------MNLQEVLKCHK--GTKSAVH
OsRPE1a         PGDPVGILAATAVANAAYKAVLAPNQ-NNIISW-------DSMKEVLLTRASTKADANHR
OsRPE1b         PGEPVGVLAATAISNPAYKAVLDASQ-SNNTSW-------ERMKEILQTTSRYKNDMKDR
PtRPD1          AGRPVGPLAACAISEAAYSALDQPISLLEKSPL-------LNLKNVLECGL--KRNSAHQ
PtRPE1a         AGEPVGVLAATAMSNPAYKAVLDSTP-SSNSSW-------DMMKEILLCKVGFKNDQADR
PtRPE1b         AGEPVGVLAATAMSNPAYKAVLDSTP-SSNCSW-------DMMKEILLCKVGFKNDLADR
SbRPD1          LGAPVGCWAACSISEAAYGALEHPVNGLEDSPL-------MNLQEVFKCHK--ATNSGDH
SbRPE1a         PGDSIGILAATVFANAAYKAVLVPNQ-KNMTSW-------DSMKEVLLTNACSKTGTIDQ
SbRPE1b         PGEPVGVLAATAISNPAYKAVLDSSQ-SNNASW-------ESMKEILQTRTSYKNDAKDR
SmRPD1          PGEPVGLLAGTAVIEPVYDQVMSSSP-QASTML-------KTLQNILFSN-SFK--DIDR
VvRPD1          GGQPVGSISACAISEAAYSALDQPISLLEPSPL-------LNLKRVLECGL--RKSTADR
VvRPE1          AGEPVGVLAATAMSNPAYKAVLDSSP-SSNSSW-------ELMKEILLCQVNFKNDLIDR
ZmRPB1          PGEMIGCVAAQSIGEPATQMTLNTFH-YAGVSAKNVTLGVPRLREIINVAKKIK----TP
ZmRPD1          LGAPVGCRAACSISEAAYGALEHPVNGLEDSPL-------MNLQEVFKCHK--ATNSGDH
ZmRPE1          PGEPVGVLAATAISNPAYKAVLDSSQ-SNNASW-------ESMKEILQTRTSYKNDVKDR


AtRPB1          SLSVYLTPEASKS----KEGAKTVQCALEYTTLRSVTQATEVWYDPDPMSTII-------
AtRPD1          TMSLYLSEYLSKKKHGFEYGSLEIKNHLEKLSFSEIVSTSMIIF----------------
AtRPE1          RVILYLNECHCGKRFCQENAACTVRNKLNKVSLKDTAVEFLVEY----------------
BdRPD1          FGLLFLSKNLKKYRYGFEYASLYVQNYLEPMDFSELVNTVMIQY----------------
BdRPE1          KVILFLNDCSCPKKFCKEKAAIAVQNRLKRVTLEDCATDICIEY----------------
CpRPD1          ------------------------------------------------------------
CpRPE1          RVILYLNDCNCARRHCQEKAACLVRNQLNKVTLKDAAVQFLVEY----------------
OsRPD1a         TGLLFLSKHLRKYRYGFEYASLEVKDHLERVDFSDMVDTE--------------------
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OsRPD1b         TGLLFLSKYLKKYRYGFEYASLEVKDHLERVDFSDLVDTVMILL----------------
OsRPE1a         KVILYLNQCSCE-NECMER-ALTIRACLRRIKLEDCTTEISIKY----------------
OsRPE1b         KVILFLNDCSCAKKFCKEKAAIAVQGCLRRITLEDCATDICIEDGNWAAPAGFQHPVPPP
PtRPD1          TMSLFLSEKLGRQRHGFEYAALEVQNHLERLLFSDIVSFVRIIF----------------
PtRPE1a         RVILYFNYCGCGREHCQEKAAFLVKNHLEKVSLKDVAKCFMIEY----------------
PtRPE1b         RVILYLNDCGCGRNYCQERAAYLVKNHLEKVSLKDIAKCFMIEY----------------
SbRPD1          IGLLFLSRHLKKYRYGLEYASLEVKNHLEQVNFSDLVETIMIIY----------------
SbRPE1a         KAILYLNKCFCGLKFCSELAAHRVQSCLKRIKLEYCAIEVSIKY----------------
SbRPE1b         KVVLFLSDCSCAKKFCKERAALAVQSCLKRVTLGDCATDICIEH----------------
SmRPD1          CVTLKLQK----LPVQPEWIALQVQDFLKPVTIGMLASKIWIEY----------------
VvRPD1          TVSLFLSKKLEKRKHGFEYGALEVKNHLEKLLFSDIVSTVMIVF----------------
VvRPE1          RVILYLNDCDCGRKYCRENAAYLVKNQLKKASLKDTAVEFMIEY----------------
ZmRPB1          SLSVYLKPQVNQK----KELAKNVQCALEYTTLRSVTHATEIWYDPDPLGTII-------
ZmRPD1          IGLLFLSRHLKKYRYGLEYASLEVKNHLERVNFSDLVETIMIIY----------------
ZmRPE1          KVVLFLNDCSCAKKFCKERAALAVQSCLKRVTLGDCATDICIEH----------------


AtRPB1          ------------------------------EEDFEFVRSYYEMPDEDVSPDKISPWLLRI
AtRPD1          ----------------------------------------SPSSN---TKVPLSPWVCHF
AtRPE1          ----------------------------------------RKQPTISEIFGIDSCLHGHI
BdRPD1          ----------------------------------------DGGGV---QKTKGSPWITHF
BdRPE1          ----------------------------------------IL----DGSSEATPALVGHI
CpRPD1          ------------------------------------------------------------
CpRPE1          ----------------------------------------KNHRTVSEGLEIDAGLAGHV
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ----------------------------------------E-------------------
OsRPE1a         ----------------------------------------QQQA-----TQAAHHLVGHI
OsRPE1b         QCKILPVPIPIPAHGSVKFPPVPIPAPEHLKYNIH-VVRYQKQIGLDGTSEAAPALVGHI
PtRPD1          ----------------------------------------SPQSD---GRMHFSPWVCHF
PtRPE1a         ----------------------------------------KNQQI-PESFGSDAGLVGHV
PtRPE1b         ----------------------------------------KSQQI-PESFGSDAGLVGHV
SbRPD1          ----------------------------------------DGHDK---IRK-EGTWTTHF
SbRPE1a         ----------------------------------------QQEA-----TQAAQCLVGHI
SbRPE1b         ----------------------------------------QKQINLDGTSEAAPTLVGHI
SmRPD1          ----------------------------------------SPCSEVG-GQKKRVPWIGCF
VvRPD1          ----------------------------------------SPQNG---SKTHFSPWVCHF
VvRPE1          ----------------------------------------VKQHAVSGSSEPGTGLVGHI
ZmRPB1          ------------------------------EEDTEFVQSYYEMPDEDIDPDKISPWLLRI
ZmRPD1          ----------------------------------------DGHDK---IRN-EGMWTTHF
ZmRPE1          ----------------------------------------QKQINLDGTSEAAPTLVGHI


AtRPB1          ELNREMMVDKKLSMADIAEKINLEFDD--------------------DLTCIFNDD-NAQ
AtRPD1          HISEKVLKRKQLSAESVVSSLNEQYKS----RNRELKLDIVDLDIQNTNHCSSDDQA-MK
AtRPE1          HLNKTLLQDWNISMQDIHQKCEDVINSLGQKKKKKATDDFKRTSLS-VSECCSFRDP-CG
BdRPD1          HISKEMMKRKRLGLRLLVEDLTEHYNA----KRDQLNNVIPKVYIS-KCKCSDDDDC-IN
BdRPE1          HLEKARLDMINVSTEDILQKCQEVSLKHGK-KKGHLGHLFKKITFS-TCDCSFTQKPMID
CpRPD1          ------------------------------------------------RECPIDDG-PRQ
CpRPE1          HLNKTLLQVLNIDMQEILQQCRERISLFR-K-KKKVGHCFKKIILS-VSKCCSFQQS-CE
OsRPD1a         -----TMKIKRLRLEFIVREIIDQYNT----LRKQLNNAIPSVSIS-NSKCSVGNEC-VK
OsRPD1b         -----TMKIKRLRLGFIVRELIDQYNA----LRKKLNNMIPSVCIS-YSKCSVGNEC-VK
OsRPE1a         HLDKKQLNQIETIMDSVLHKCQETFRNNIK-KKGSMREILKTVTFIS-STSLCDQHT-DD
OsRPE1b         HLDRAHLERINISTEDILQKCQEVSGKYGK-KKGHLSNLFKNITFS-TCDCLFTQKL-VD
PtRPD1          HVYKEIVKKRSLKVHYIIDALEKQCKS---------KTRFPKVQIT-SRYCTVADTWKEK
PtRPE1a         HLEKRILQELNISAQVILEKCQETVNSFR-K-KKKVGNLFKKTTLS-ISECCSFEQC-T-
PtRPE1b         HLDKRKLQDLNITAQVILEKCQETVNTFR-K-KKKVGNLFKKTILL-VSESCSFQQC-I-
SbRPD1          HISKEMMKKKRLGLRFVIEELTKEYNA----TRDQLKNAIPSICIS-RRKCVVGDEG-VK
SbRPE1a         HLDKEQLNWMEITMGNILQTCQKNVNKHVM-KNRQLMQILKTTEIISSEYCLCGQDI-GD
SbRPE1b         HLDKGQLERINISIQDILQKCQEVSGRYGK-KKGHLCHLLKKITFA-TC-----------
SmRPD1          QLRAEAMERCSLNIDTIVCHLRKLLPT----SLDDPDAFIQGLHFFS-------------
VvRPD1          HVCEEIAKKRSLKPHSIIDALYMKCNS----ARAESKINLPDLQIT-SKDCFVDME-KED
VvRPE1          HLNKLLLQDLNVSMQEVCQKCEETINSFR-K-KKNVGPFFKKIILS-FRECCTFQHS-CQ
ZmRPB1          ELNREMMVDKKLSMADIAEKINREFDD--------------------DLSCIFNDD-NAD
ZmRPD1          HINKAMMKKKRLGLRFVVDELAKEYDT----TRDQLNNAIPSIRIS-RRKCLVGDEG-VK
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ZmRPE1          HLDKGHLERINISTQDILQKCQEVSGRFGK-KKGHLCHIFKKITFA-TCDCSFTQMP-ID


AtRPB1          K---LILRIRIMNDEGPKGELQDESAE--DDVFLKKIES---NMLTEMALRGIPD-INKV
AtRPD1          ---DDNVCITVTVVEA--S----KHSVLELDAI-RLVLI---PFLLDSPVKGDQG-IKKV
AtRPE1          SKGSDMPCLTFSYNA---T---DPDLERTLDVL-CNTVY---PVLLEIVIKGDSR-ICSA
BdRPD1          ---NQTCCITVVAQDE--S---NSTSTSQLDDL-KKRAI---PVLLATPVKGFLE-FKDV
BdRPE1          GKLPKVPCLQFSFSED--IPMLSESVERAVSVL-ANSLCDSATIFWSICSAGDPR-IQEA
CpRPD1          ---EDSFCISVTVVKK--S----KDSSVQLDTV-RGLVM---PFLLRAVIKGFPE-IKKV
CpRPE1          ENSSDLPCLIFCWHDT--S---DIHLERTSYVL-ANMIY---PVLLETVIKGDPR-ICSA
OsRPD1a         ---NQTCCVTMVVQVE--I---N--SMSQLDVI-KERVI---PSILATLLKGFLE-FKNV
OsRPD1b         ---NRSCCVTMVAQVE--S---N--STSQLDII-KERVI---PSILATLLKGFLE-FENV
OsRPE1a         DKKFQVSCLQFFLPGSI-TKNISESTERVIDFM-TNAIF---PIILDTVIKGDPR-VEEA
OsRPE1b         GKLPKLPCLQFFVSDN--MI-VSESVERAVSVL-ADSLC---GVLLNTIIKGDPR-IQEA
PtRPD1          ---KETFCITVTIVET--S----KNEFIELETI-QDLMI---PFLLETVIKGFME-IQKV
PtRPE1a         ---DELLCLMFFWQDA--N---DVHLERTSNIL-ADMIC---PVLLETTIKGDHR-ISCA
PtRPE1b         ---DESPCLMFFWQGA--D---DVHLERTSNIL-ADMIC---PVLLETIIKGDHR-ISCA
SbRPD1          ---ISACCIAVVALAE--P---N--SMSQLDTI-KKRVI---PIILDTLLKGFLE-FKDV
SbRPE1a         ERALQVSCLQCFIHAS--TTTV-QPESNVIQMM-TNTIF---PILLDTVIKGDPQ-VQEA
SbRPE1b         GKLHKVPCVQFSFSDE--STVLSESVERAVNVI-ADSVC---SVLLDTIIKGDPR-IQAA
SmRPD1          -RDVEVLCFFPITSSV--S---NYDSKQIHKHM-IGTMF---GNLLQVVVKGCPRGIEFV
VvRPD1          ---SDCFCITVSIVN---S----KKSCIQLDTV-RDLVI---PFLLGAVVKGLLD-VKKV
VvRPE1          SKGSDMPCLLFFWQGN--R---DDNLEQILHIL-AHKIC---PVLLQTIIKGDSR-VCTV
ZmRPB1          K---LILRIRITNDEAPKGEIQDESAE--DDVFLKKIEG---NMLTEMALRGIPD-INKV
ZmRPD1          ---SSSCCIAVVAHAE--R---N--SISQLDTI-KTRVI---PSILDTLLKGFLE-FKDV
ZmRPE1          GKLHKVPCVQFAFSDD---IVLSESIERAVNVI-ADSVC---SVLLDTIIKGDPR-IQAA
                        .                       .           :      *    .  .

AtRPB1          FIKQVR--KSR------------------FDEEGGFKTSEEWMLDTEGVNLLAVMCHEDV
AtRPD1          NILWTDRPKAP--KRNGNHLAGELYLKVTMYG--DRGKRNCWTALLET--CL--PIMDMI
AtRPE1          NIIWNSSDMTTWIRNRHASRRGEWVLDVTVEKSAVKQSGDAWRVVIDS--CL--SVLHLI
BdRPD1          EIQC--------------QRDNELVVKVNMSK--HCKSGIFWTTLKKA--CI--GIMGLI
BdRPE1          KIMWVGSDAQSWVKNTRKVSKGEPTVEIVVEKNEASKQGDAWRIAMDA--CI--PVIDLI
CpRPD1          DILWKDRPKLS---K-SYDSRGELYLRVSMSE--EHGTRTSWNALMDG--CL--PIMDMI
CpRPE1          NIIWASPDTMTWIRKPSRTRKGEWVLDVVVEKSMVKRSGDAWRIVMDS--CL--PVFHLI
OsRPD1a         KVQC--------------QEDNELVLKVGMSE--HCKSGKFWATLQNA--CI--PIMELI
OsRPD1b         KVEC--------------QQDSELVVKVGMSE--HCKTGKFWATLQNA--CI--PIMELI
OsRPE1a         NLVRIEPESTFWVQSSGAEQKGEAALEITVEEAAAAESGNAWGVAMNA--CI--PVMDLI
OsRPE1b         KIVWVGSDATSWVKNTQKASKGEPAVEIIVEEEEALHIGDAWRTTMDA--CI--PVLNLI
PtRPD1          DILWNDKPKIP---KSHNRLRGELFLRVHMSR--GSDKTRLWNQLMDD--CL--SIMDLI
PtRPE1a         NIIWASQETTTWIRNPSRTQKGELALDIVLEKSVVKQSGDAWRIVLDS--CL--PVLHLI
PtRPE1b         NIIWATPETNTWIRNPSRTQKGELALDIVLEKSVVKKSGDAWRIVLDS--CL--PVLHLI
SbRPD1          EIQC--------------QHDGELLVKVCMSH--HCKGGRFWATLQNA--CI--PVMELI
SbRPE1a         KLIWVEPKLTRWVKNSSAEQKGELAVEITVEKIAAAENGGTWGVVMDA--CV--PVMDLI
SbRPE1b         KVIWVESDATAWVKNTRKVSKGEPALEIIVEKDHAVSNGDAWRTTIDA--CL--PVLDLI
SmRPD1          NVKWE----------------DELCIEVAFL---SRTRGVPWTHALEA--CG--SISHLV
VvRPD1          DILWNDNPDSD----VLKSSSGRLYLRVYVSG--DCGKKNFWGVLMDA--CL--QIMDMI
VvRPE1          NIIWISPDTTTWIRNPCKSRKGELALDIVLEKAAVKQRGDAWRIVLDA--CL--PVLHLI
ZmRPB1          FIKEGK--VNT------------------FYQDDGFKAANEWMLDTEGVNLLAVMCHEDV
ZmRPD1          EIQC--------------PHDGELLVKVCMSE--HCKGGRFWPTLQNA--CI--PVMELI
ZmRPE1          KVIWVESDAASWVKHTRKVSKGESALEIIVEKDDAVSNGDAWRTAIDA--CL--PVLNLI
                 :                           .           *    .            :

AtRPB1          DPKRTTSNHLIEIIEVLGIEAVRRAL-------------LDELRVVISFDGSYVNYRHLA
AtRPD1          DWGRSHPDNIRQCCSVYGIDAGRSIF-------------VANLESAVSDTGKEILREHLL
AtRPE1          DTKRSIPYSVKQVQELLGLSCAFEQA-------------VQRLSASVRMVSKGVLKEHII
BdRPD1          DWERSRPGSVYDIFCPCGIDSAWKYF-------------VESLRSKTDDIGRNIHREHLL
BdRPE1          DTRRSIPYGIQQVRELLGISCSFDQI-------------VQRLSTTMKTVAKGILKDHLI
CpRPD1          DWARSYPDNIHHFCSANGIDAGWKLF-------------LNNLDSAISDVGKTILPEHLL
CpRPE1          DSRRSIPYSTKQVQELLGISCAFDQA-------------VQRLSTSVAMVAKGVLREHLI
OsRPD1a         DWERSRPERVYDNFCSYGIDSAWKFF-------------VESVRSTTDAIGRNIHRQHLL
OsRPD1b         DWERSRPERVYDIFCSYGIDSAWKYF-------------VESLRSTTDAIGRNIHRQHLL
OsRPE1a         DTTRSMPYDIQQVRQVFGISSAFEKVTQVQLFPFLLLAEIQYLSKSVGMITKSVLQEHLT
OsRPE1b         DIRRSIPYGIQQVRELLGISCAFDQV-------------VQRLSTTVRMVAKDVLKDHLV
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PtRPD1          DWARSHPDNIHECCLAYGIDAGWKFF-------------LNNLQSAMSDVGKTVLPEHLL
PtRPE1a         DTTRSVPYAIKQVQELLGVSCAFDQA-------------VQRLSKSVTMVAKGVLKEHLI
PtRPE1b         NTTRSIPYAIKQVQELLGVSCAFDTA-------------VQRLSKSVTMVAKGVLKEHLI
SbRPD1          DWELSRPSNVADIFCSYGIDSAWKYF-------------VESLKSATTDIGRNIRREHLL
SbRPE1a         DTTRSAPCNIQEVQKVFGISSVFDRV-------------VQHLSKAVGMVTKSVLMEHLI
SbRPE1b         DTRRSIPYGIQQVKELIGISCAFDQV-------------VQRLSSTVKMVNKGVLKDHLI
SmRPD1          DWQKSTPLSIQEVHVAFGIEAAYQYL-------------LEKLKEFTKG--SGVLRKPWK
VvRPD1          DWERSHPDNIHDIFVVYGIDAGWKYF-------------LNSLKSAISDIGKTVLPEHLL
VvRPE1          DTRRSIPYAIKQVQELLGISCAFDQA-------------VQRLSKSVTMVAKGVLKEHLI
ZmRPB1          DATRTTSNHLIEVIEVLGIEAVRRSL-------------LDELRVVISFDGSYVNYRHLA
ZmRPD1          DWELSQPSNVSDIFCSYGIDSAWKYF-------------VESLKSATTDTGRNIRREHLL
ZmRPE1          DTRRSIPYGIQQVRELIGISCAFDQV-------------VQRLSTTVKMVNKGVLKDHLI
                :   : .    .     *:..                  :  :          :

AtRPB1          ILCDTMTYRGHLMAITRHGINRNDT-----GPLMRCSFEETVDILLDAAAYAETDCLRGV
AtRPD1          LVADSLSVTGEFVALNAKGWSKQRQVESTPAPFTQACFSSPSQCFLKAAKEGVRDDLQGS
AtRPE1          LLANNMTCSGTMLGFNSGGYKALTRSLNIKAPFTEATLIAPRKCFEKAAEKCHTDSLSTV
BdRPD1          VVADTLSPHEP-------------------------------------------------
BdRPE1          LVANSMTCTGNLYGFNTGGYRATFRALKVQVPFTESTLFTPMKCFEKAAEKCHSDALGCV
CpRPD1          LIANCLSATGEFVGLSSRGLAQQRKHASVVSPFTQACFSNPSTCFVKAAKAGVTDDLQGS
CpRPE1          LLANSMTCAGNLVGFNPGGYKAISRSLNIQAPFMEATLFTPRKCFERAAEKCHTDSLSSV
OsRPD1a         VVADCLSVSGQFHGLSSQGLKQQRTWLSISSPFSEACFSRPAHSFINAAKRDSVDNLSGT
OsRPD1b         VVADCLSISGQFHGLSSQGLKQQRAWLSISSPFSEACFSRPAYSFINAAKRDSVDNLSGA
OsRPE1a         TVASSMTCTGDLHGFNNSGYKATCQSLKVQAPFMEATLSRSIQCFEKAAAKAYSDQLGNV
OsRPE1b         LVANSMTFTGNLNGFNNAGYKATFRSLKVQVPFTESTLITPMKCFEKAAEKCHSDSLGCV
PtRPD1          LVANCLSVTGEFVGLNAKGLKRQREHASVSTPFVQACFSNPGDCFIRAAKAGVVDDLQGS
PtRPE1a         LLGNSMTCAGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRKCFEKAAEKCHTDYLSSI
PtRPE1b         LLGNSMTCAGSLIGFYTGGYKTLSRSLDIQVPFTEATLFTPRKCFEKAAEKCHTDSLSSI
SbRPD1          VIADSMSVTGQFHAISSHGLKQQRTRLSISSPFSEACFSRPAQSFIDAAKQCSVDNLCGS
SbRPE1a         TVASSMTCTGSLHGFNRSGSKATFQSLKVQAPFTEATLSRPMQCFRKSAEKVDSDQLDSV
SbRPE1b         LVANSMTCTGSLIGFNIAGYKATFRSLKVQVPFTESTLFTPMKCFEKAAEKCDSDSLGCV
SmRPD1          -----------NIDANESGYEAFVKNLSGCSPLAFAMGKSPGGVFEAAAMNREVDYLAGA
VvRPD1          LVASCLSATGEFVGLNAKGMARQKELTSISSPFMQGCFSSPGSCFIKAGKRAVADNLHGS
VvRPE1          LLANSMTCAGNLIGFNSGGYKALSRALNLQVPFTEATLFTPRKCFEKASEKCHTDSLSSI
ZmRPB1          ILCDTMTYRGHLMAITRHGINRNDT-----GPLMRCSFEETVDILLDAAVYAESDHLRGV
ZmRPD1          VIADSLSVTGQFHALSSQGLKQQRTRLSISSPFSEACFSRPAQSFINAAKQCSVDNLCGS
ZmRPE1          LVANSMTCTGNLIGFNIAGYKATFRSLKVQVPFTESTLFTPMKCFEKAAEKCDSDSLGCV


AtRPB1          TENIMLGQLAPIGTGDCE-LYLNDEMLKNAIEL----QLPSYMD----------------
AtRPD1          IDALAWGKVPGFGTGDQFEIIISPKVHGFT----TPVDVYDLLSSTKTMRRTNSA---P-
AtRPE1          VGSCSWGKRVDVGTGSQFELLWNQKETGLDDK--EETDVYSFLQMVISTTNADAFVSS--
BdRPD1          -----------------------------V----QNENIYGFLHNPEVWGPE---KNHM-
BdRPE1          VSSCSWGKHAALGTGSSFQILWNENQVNCNKE--YGDGLYDFLAMVRTDQEK---ARY--
CpRPD1          IDALAWGKPPCFGTGGQFDIIYSWRP----------VDVYDLLNSIVTPLKQNVKSDLP-
CpRPE1          VGSCSWGKNVAVGTGSRFDVLWDTKEARFNEG--GKLDVYTFLHMVRSSSHGEDLSTA--
OsRPD1a         LDAIAWGKEPCAGSSGPFKILYSGKSHETK----QNEHIYDFLHNPEVQALE---KNVM-
OsRPD1b         LDAIAWGKEPCAGTSGPFKVLYSGKSQKTK----QNKNIYDFLHNPEVQALE---KNFM-
OsRPE1a         VSACSWGNNAEIGTGSAFEILWNDENMSSSKSILGGYGLYDFLEAVETTGATKDKAIVPH
OsRPE1b         VSSCSWGKHAASGTGSSFQILWNESQLKSNKE--YGDGLYDYLALVRTDEEK---ARY--
PtRPD1          IDALAWGKVPAIGTG-QFDIVYSGKGLEFS----KPVDVYNLLGSQMISTEQNTEFGVL-
PtRPE1a         VASCSWGKHVTVGTGSRFDVLWDTKEACLNPE--GGIDAYSFLNMVRSTAGGEESVTA--
PtRPE1b         VASCAWGKHVTVGTGSHFDVLWDTKEACLNPE--GSMDVYSFLNMVRSTAGGEESVTA--
SbRPD1          LDAIAWGKEPFNGTSGPFEIMHSGKPHEPE----QDESIYDFLRSPKVQNVE---KNHL-
SbRPE1a         VSTCSWGNHAAIGTGSAFKIHWNDENQSASNEILREYNLYDFLEAVGRIGATEQKTDAPH
SbRPE1b         VSSSSWGKHAAVGTGSSFQILWNENQLKSNKD--YGDGLYDFLALVRTDQEK---TGY--
SmRPD1          NELAFCGKSPSLGTGANIELFFKEDKGPVSRF----PDFESLVFSRRVV---DDTV--S-
VvRPD1          LDALAWGKIPSVGSGGHFDILYSAKGHELA----RPEDIYKLLGSQTSCHEQNLKVKVP-
VvRPE1          VASCSWGKHVTVGTGSRFDVLWDTKEIGPAQD--GGIDIYSFLHLVRSGSYGKEPDTA--
ZmRPB1          TENIMLGQLAPIGTGGCA-LYLNDQMLQQAIEL----QLPSYVE----------------
ZmRPD1          LDAVAWGKEPFNGTSGPFEIMHSGKPHEPE----QNESIYDFLCSSKVRNFE---KNHL-
ZmRPE1          VSSSAWGKHAAVGTGSSFQILWNENQLKSNKE--YGDGLYDFLALVRTDQEK---TDY--
                                                          :
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AtRPB1          ---------------GLE--FGMTPAR-SPVSGTPYHEGMMSPNYLLSP-NMRLSPM-SD
AtRPD1          ------------------------------------------------------------
AtRPE1          ----P--GFDVTEEEMAE--WAESPER-DSALGEPKFEDSADFQNLHDEGKPSGANWEKS
BdRPD1          ------------------------------------------------------------
BdRPE1          -TFLDDVDYLVEDNAMDD--ICLSPEL-NGTHGVPTFEDNFEHQDTQNG-----------
CpRPD1          ------------------------------------------------------------
CpRPE1          -CLGEEIDDLVPDEETFD--WSPSPEH-YSTSGKPVFEDGEDILENLET-QPTKPSWEHL
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         NYCLYDVDCIPEDKV------CLEENNQITWTDKPKAEFLME--SEG-------------
OsRPE1b         -TFFDDVDYLAEENE-AD--VCLSPEL-DGTIGQPIFDDNLEEQDVQNN-----------
PtRPD1          ------------------------------------------------------------
PtRPE1a         -CLGAEVDDLILEDE--D--WNLSPEH-HSSSDKPTFEDSAEFQDFLGN-QPAESNWGKA
PtRPE1b         -CLGAEVDDLMLEDE--D--WNLSPEH-NSSSDKPTFEDSAEFQDFLGN-QPAESNWEKI
SbRPD1          ------------------------------------------------------------
SbRPE1a         SLCLYDVGQLPEDEVQEDEVVCFGGTSPISWTDKPKGDSLLH--DFM-------------
SbRPE1b         -MFLDDVDYLLEENAIDD--MCLSPEP-DGTVGKPTFEDNFEEQNIQKG-----------
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          -CLGAEVEDLILEDENLE--LGMSPEH-SSNFEKPVFEDSAEFQNTWEN-HV--------
ZmRPB1          ---------------GLD--FGMTPAR-SPITGTPYHEGMMSPSYLLSP-NIRASPINTD
ZmRPD1          ------------------------------------------------------------
ZmRPE1          -MFLDDVDYLVEENAADD--MCLSPEP-DGTLGKPTFEDNFEEQNIQKG-----------


AtRPB1          AQFSPY-VGGMAFSPSSSPG--YSPSSPGYSP------------TSP-------------
AtRPD1          ------------------------------------------------------------
AtRPE1          SSWDNGCSGGSEWGVSKSTGG-EANP----------------------------------
BdRPD1          -------------------------------------------------------ETDST
BdRPE1          NSWENGTKANASWEQNASAGN-DSDNWGGWSNAAAAAD---TGAAKPADQ-GN-------
CpRPD1          -------------------------------------------------------NSMNI
CpRPE1          NNG---------------------------------------------------------
OsRPD1a         -------------------------------------------------------DTYRK
OsRPD1b         -------------------------------------------------------DTYKQ
OsRPE1a         ------------------------RRAGMHSTGQKH---------------------PRK
OsRPE1b         SSWDNGTTTNASWEQNGSAGN-DSDKWGGWNDAAAGAD---TGVTKPANQ-GN-------
PtRPD1          -------------------------------------------------------DAQIY
PtRPE1a         SSLKDGSWSAGNWDVDKNDSAGKEKPWSLGMSSAETND---VG-----------WDTAAT
PtRPE1b         SSLKDRSRSSGNWDVDKNDGAVKEKPWSLGMNTAEANDVASSG-----------WDTAAA
SbRPD1          -------------------------------------------------------DTRRQ
SbRPE1a         ------------------------GRAGMWSTVQKH------------------QEMQNK
SbRPE1b         SSWENGITMKSSWEQDASAAN-DSGDWGGWSSGGGAS-------AKPADQ-DNSWEVHAK
SmRPD1          ------------------------------------------------------------
VvRPD1          -------------------------------------------------------ITCYQ
VvRPE1          ------PGSGGDWAVNQNK-----------------------------------------
ZmRPB1          ASFSPY-VGHMAFSPFPSPGG-YSPSSGGYSP------------SSPVFTPEKGYSPLSP
ZmRPD1          -------------------------------------------------------DTRRQ
ZmRPE1          SSWEIGITTNSSWEQNASVAN-DSGDWGGWSSGGGAA-------AKPADQ-DNSWEVHAK


AtRPB1          ---------GYSP-----TSPGYSPTSPGYSPTSPTYS-PSSPGYSPTSPAYSPTSP---
AtRPD1          KSDK--------------------------------------------------------
AtRPE1          -------------------------ESNWEKTTNVEK-EDAWSSWNTRKDAQE-------
BdRPD1          RTKN--------------------------------------------------------
BdRPE1          --------------------------SSWDVPATAENDSTDWGGWGNEKAKDNRT-V---
CpRPD1          KSDK--------------------------------------------------------
CpRPE1          -------------------------------RADLQK-QSSWSSWSTDRAHSQDV-CSTK
OsRPD1a         RTEK--------------------------------------------------------
OsRPD1b         RTEK--------------------------------------------------------
OsRPE1a         ------------------------------------------PNWHEGNTKSSPNS----
OsRPE1b         --------------------------SCWDVPATVEKSSSDWGGWGTEKAKEKEK-I---
PtRPD1          KSDK--------------------------------------------------------
PtRPE1a         RK----------------------INSSWNSENDVTQ-SNSLSGWATKKSETHNG-FATK
PtRPE1b         RT----------------------TNNSWNSENNVAQ-SNSFSGWATKKPEPHNG-FATK
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SbRPD1          STEN--------------------------------------------------------
SbRPE1a         TKW------------------------------------NSVANWKNDKPMGPPRTA---
SbRPE1b         VQDNSTDWGGWSSGVGAAAKPAD-QDNSWEVHAKAQDNCTDWGGWSTDKPTGEAT-V---
SmRPD1          A-----------------------------------------------------------
VvRPD1          TTTK--------------------------------------------------------
VvRPE1          -----------------------------ETTASTLK-PSAWSSWGTDKVTMKDT-FSTR
ZmRPB1          ---------SYSP-----ASPSYSPTSPSYTPGSPTYS-PTSPNYSPTSPTYSPTSP---
ZmRPD1          STEN--------------------------------------------------------
ZmRPE1          VQDN---------------------------------STTDWGGWSVEKPTGEAT-V---


AtRPB1          -----------------------SY-----------------------------------
AtRPD1          ------------------------------------------------------------
AtRPE1          -------SSK-----------SD----SGGA-WGIKTK-DAD-A--DTTPNWE-TS-PAP
BdRPD1          ------------------------------------------------------------
BdRPE1          -STEPAELDT-----------WS----DRGAKKGTDG-GGGS----------WGKQTNTC
CpRPD1          ------------------------------------------------------------
CpRPE1          TLEECLNSAGGTGVIGSDKTNLD----SQNT-WANWNTKGSYPTKA--------SE-DSP
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------T----------------AVEFTGQV-FQRR------------------------
OsRPE1b         -SEEPAQHDA-----------WS----VQGPKRATDG--GAS----------WKKQSSTQ
PtRPD1          ------------------------------------------------------------
PtRPE1a         VQEKPARSND-----------WD----VGTA-WGRKAG-DNKFA--NVTKSWWGKV-TDG
PtRPE1b         VQEEPTTSND-----------WD----AGAA-WGRKDR-DNKFAETNASKSWWGKV-TDG
SbRPD1          ------------------------------------------------------------
SbRPE1a         -FAESTSTRG-----------QNKRQFTGQV-YARK------------------------
SbRPE1b         -SGQPAEMDT-----------WA----DKGTKMESGA-GDAN----------WEKKSSTP
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          EPDESSRSAG-----------WD----DKGT-WGTDKAQNTAFRRT--------HE-DSP
ZmRPB1          -----------------------SY-----------------------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          -SGEPAETDT-----------WA----DKGAKMESDA-GDGN----------WEKS-STP


AtRPB1          ---------SPTS-----------------PSY-------SPTSPSY-------------
AtRPD1          ---------------ATVQPF------GL------LHSAFLKDIKVLDGK----------
AtRPE1          KDSIVPENNEPTSDVWGHKSVSDKSWD--KKNWGTESA-PA-----------AWGSTDAA
BdRPD1          ---------------ASER--------------------WSSGNATFNGGTI--------
BdRPE1          EDSGTNL-------------------E--RNSWAKR------------------------
CpRPD1          ---------------YGDRSI------YV------HSGSISLGLKKLE------------
CpRPE1          KSCGWVA------DKCGSG--ETNAKG--EHNWSNWTA-VK-----------GGSQ----
OsRPD1a         ---------------TSKRRS---------------AL-NSEGNATINGGAI--------
OsRPD1b         ---------------PSKQRS---------------AF-SSKGNATINGGTI--------
OsRPE1a         -------------------------QLKTKSNWNSDAT-QQDDKPSWYSSNSAGTQ----
OsRPE1b         ND---------------------------GNSWKEN------------------------
PtRPD1          ---------------CGAQFL------HK------FGGCGPKGFKVKE------------
PtRPE1a         DESEQNKNK----Q---HQ--EDQELG--THGWDDKMS-PD-----------QLIS----
PtRPE1b         DESGQNKSK----NK--RP--EDQDVG--THGWDDKMS-QD-----------QSIS----
SbRPD1          ---------------ASICRL---------------AC-KSKGSATVNGVAI--------
SbRPE1a         -------------------------QP--KHSWSQAAT-HQNNKLSWCGENVAGAQ----
SbRPE1b         EASNKNDP-------WG--------KS--ENTWDKR------------------------
SmRPD1          ---------------------------------------------TLS------------
VvRPD1          ---------------CGAQLV------YA------NGDSASKGCKSLE------------
VvRPE1          RSSGRDE------TF---------------------------------------------
ZmRPB1          ---------SPTS-----------------PSY-------SPTSPSY-------------
ZmRPD1          ---------------ASICRL---------------ACKSSKGSTTVNGVAI--------
ZmRPE1          EASKKND------------------SS--ENTWDKR------------------------


AtRPB1          --------SPTSPSY----------------------------SPT--------------
AtRPD1          ------------------------------------------------------------
AtRPE1          VWGSSDKKNSE----TESDAAAWGSRDKNNSD----------------------------
```

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BdRPD1          ------------------------------------------------------------
BdRPE1          ---------PSSPSL-----STWAKKNSDGG---------------DGTWDKQANSCKK-
CpRPD1          ------------------------------------------------------------
CpRPE1          DFTATKTWE------ESSKAGGWGSKKSGNGES--------------------------N
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         NFTI----A------GSSRPGEWNRKNNNRGQ----------------------------
OsRPE1b         ---------KGRGSN--G--GSWEKDNA--Q---------------KGSWGRGNDEAENN
PtRPD1          ------------------------------------------------------------
PtRPE1a         GWASTTTQEATTESCSSKAASVWGTKNTNVDEQGSENHVLLNQAKESSDWNKKSNSNQTD
PtRPE1b         GWASKTTQEATTES---------------------------------LGWDSKGNSNPGD
SbRPD1          ------------------------------------------------------------
SbRPE1a         DFAN----A-------ESSKGGWNRKNSGFGR----------------------------
SbRPE1b         ---------KGDGGD--GGDGAWEKKSVD-G---------------HGNWDHPGNWNGQS
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          --------RDGRPQF---ASSAWGKKIDEAD---------------KTGWNKNDGKPQMD
ZmRPB1          --------SPTSPSY----------------------------SPT--------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          ---------KGDG-----GDGAWGNRSDD-G---------------HGNWEHPSNWNGQS


AtRPB1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
AtRPE1          VGSGAGVLGPWNKKSSET--ESNGATWGSSD--------KTKS-GAAA-WNSWD------
BdRPD1          ------------------------------------------------------------
BdRPE1          ----NVEQ----------------DSWKNMPVSPARNAWNKKESS-RGD-ATWE------
CpRPD1          ------------------------------------------------------------
CpRPE1          V----GEGSPWSN---------------------------------------WK------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         GG----------------------------------------------------------
OsRPE1b         ---NDVQNKSWETVAADAHASTE-KSWGNVTASPSDNAWSAAPVS-QGN-GSS-------
PtRPD1          ------------------------------------------------------------
PtRPE1a         AACGSKAASSWGAKNTDA----D-KRWGRKV--------DLNQ-A-DT-SCSWG------
PtRPE1b         AACGWKAASTWGAENTDG----D-KLWGKEV--------SSNQ-A-DT-ASGWG------
SbRPD1          ------------------------------------------------------------
SbRPE1a         GG----HR----------------------------------------------------
SbRPE1b         ---LNVDQ----------------DTWGNAR--------GKKK-A-DGN-CQWE------
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          ---KLRESYDWDCKVAQE-KTTQ-STYGGIS--------S-------T-TGDWKKNELQM
ZmRPB1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          ---LDVDQ----------------DTWGNAR--------GKKK-A-DGNYCQWE------


AtRPB1          -------SP------------------------------SYS------------------
AtRPD1          ------------------------------------------------------------
AtRPE1          ----KKNI----------------------------ETDSEPA-------------AWGS
BdRPD1          ------------------------------------------------------------
BdRPE1          ----MRA-----------------------------------STLEEKKTSESNEG----
CpRPD1          ------------------------------------------------------------
CpRPE1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
OsRPE1b         ------------------------------------------------------------
PtRPD1          ------------------------------------------------------------
PtRPE1a         ----RSKTPDRGWGLSNYGGSNGSEMENKTENQSLLDRGKESV-------------GWGG
PtRPE1b         ----KPKSP---------------------------------------------------
SbRPD1          ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SbRPE1b         ----EQP-----------------------------------STYRRKKTNADHNSSY--
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SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          EVVQHDESP------------------------------VNEH-------------SWDA
ZmRPB1          -------SP------------------------------SYS------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          ----EQP-----------------------------------SNYKQKKTNADHDSSY--

AtRPB1          --------------------------------P---------TSPSYS------------
AtRPD1          ------------------------------------------------------------
AtRPE1          Q---------GKKNSETESGPAAWGAWDKKKSET----E--PGPAGWGM-----------
BdRPD1          ------------------------------------------------------------
BdRPE1          -------------------------SWEK----------SNAQKDSWGN-----------
CpRPD1          ------------------------------------------------------------
CpRPE1          ----------------------------TNKG---------------------NSQGTHP
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------GR----
OsRPE1b         ---------------------------------------DTKQSDSWDG-----------
PtRPD1          ------------------------------------------------------------
PtRPE1a         KNTDADKPWSNKVNSNQA---DTASGWGKSKS-L---------DRGWGVSNSGGGNGSEM
PtRPE1b         ---------------------EISLGWGSTKE-S----V--KSDRGWGVSSSGGGR----
SbRPD1          ------------------------------------------------------------
SbRPE1a         ----------------------------------------------------GGGRGM--
SbRPE1b         -------------NNVM---PSSDNAWNAGER-FGRSNAKSNAGSSWGE-----------
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          N-----------LPEDPLAQATTSVGWDSSTG------------KDWT------------
ZmRPB1          --------------------------------P---------TSPSYS------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          -------------NNVM---PSSEIAWNAGDG-TGRPNAKSNAESSWGE-----------

AtRPB1          ----------------------P------------T---------S--------------
AtRPD1          ------------------------------------------------------------
AtRPE1          GDKKNSET-------------E-----L-GPAAMGNWDKKKS---------------DTK
BdRPD1          ------------------------------------------------------------
BdRPE1          TQHGSSDKMAVKDNDMQQDPWGHIATQNINAQ-DDLWGSVAA---------K--------
CpRPD1          ------------------------------------------------------------
CpRPE1          ------QK-------------AQ----E-ESSDFGGWGSNKFS--------RCETNLKEQ
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
OsRPE1b         WKSAGVDKAINKDK--ESLGNVP----A-SPS-FSAWNASPV------------------
PtRPD1          ------------------------------------------------------------
PtRPE1a         EDKTENQS-------------LL----D-RGKESGGWGGKNTDADKPWSNKVNSNQADTA
PtRPE1b         DKKTENQS-------------LA----G-QGKESGGWGNK-----------VTSNQADTA
SbRPD1          ------------------------------------------------------------
SbRPE1a         ---------------------------------------A-----------FANAESSS-
SbRPE1b         KDKMESDE-------------HP----K-VPKESDTWNTG-----------K--------
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          KRKLQSPS-------------EQ----Q-RDPAIKSWSSSHNV------MKEQSNQPAST
ZmRPB1          ----------------------P----T-SPVYSPT---------S--------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          EDKMESDD-------------HP----K-VPKESDTWNTG-----------R--------

AtRPB1          PAYS-------P---T-SPAYSPT----------SPAYSP--TS----------------
AtRPD1          ------------------------------------------------------------
AtRPE1          SGPAAWGSTDA------------------------AAWGS--------------------
BdRPD1          ------------------------------------------------------------
BdRPE1          AQTSTAENTDA-Q---------------------DDSWG-------------AVAAKAQT
CpRPD1          ------------------------------------------------------------
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CpRPE1          ---STWSKWNS-NKGDNQDAYATMLENNDNDTGKEKGWS----------SWARDDS--IN
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
OsRPE1b         -SQG-NERSDAKQ---------------------SDSWD----------GWKSAGVDKAI
PtRPD1          ------------------------------------------------------------
PtRPE1a         ---SGWGKSKS-L----------------------------------DRGWGVSNSGGGN
PtRPE1b         ---SGWGKPKS-SE--N-----------------SQGWGLSKESGKEVHEWGVPNSAGGN
SbRPD1          ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SbRPE1b         SNESPWDNTDA-L---------------------QDSWG-------------VNSATHDN
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          ---HGWDSPG------------------------AKGWNDVEE-----------------
ZmRPB1          PAYS-------P---T-SPAYSPT----------SPSYSP--TS----------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          SNESPWDNTDA-L---------------------QDSWV--------------KSAARNN


AtRPB1          --------------------PSYS--PTSP---SYSPTSPSYSPT---------------
AtRPD1          ------------------------------------------------------------
AtRPE1          --SDKN-NSET-----ESDAAAWGSRNKKTSEIE--S----------------------G
BdRPD1          ------------------------------------------------------------
BdRPE1          ----------------STAQESWGNVAASP-------SDNAWKAPPISQTSAAEHTDA-H
CpRPD1          ------------------------------------------------------------
CpRPE1          GSVLPEGDSSKSNGLDAGT-----------------V----------------------G
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         --------------------EVWKSEGP--------------------------------
OsRPE1b         ----------------NKDKESLGNVPASP-------SFSAWNAAPVSQGN--ERLDAKQ
PtRPD1          ------------------------------------------------------------
PtRPE1a         GSEMED-KTENQSLLDRGK----------------------------------------E
PtRPE1b         GSETNN-NNENQSLVEQGKESGWDNKASS--NQE--G----------------------T
SbRPD1          ------------------------------------------------------------
SbRPE1a         -------------------SGGWNRKNS--------------------------------
SbRPE1b         ----------------NTEDGSWDKVVAIK-DPV--SQQDSWSNV------AIQKNDA-Q
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          -------------------QSQWNQRGSA--VKN--D-----------------------
ZmRPB1          --------------------PSYS--PTSP---SYSPTSPSYSPT---------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          ----------------NTQDGSWDKVVSMK-DLD--SLQDSWSKA------TIQTNDA-Q


AtRPB1          SPSY-----------SPTSPSYSPTSPAYSPTSPGYSP-T--------SPSY--------
AtRPD1          ------------------------------------------------------------
AtRPE1          AGAW---------------GSWGQPS--P--TAEDKDT-N--------E-----DDRNPW
BdRPD1          ------------------------------------------------------------
BdRPE1          NDSWGIV-AAKAQTSTAQQESWGNAT--ASPSDNAWNA-APM-----DLDAKQPGSWDGW
CpRPD1          ------------------------------------------------------------
CpRPE1          D------------------GSWEQTP---TGTSDGWGV-L--------SESTEPAGCHGW
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ----------------------------------HRGGSS--------SNRNQ-------
OsRPE1b         SDSWDGWKSAGVDDSVKDKESWGNVP--ASPSDSAWNA-APVSQGNESSDAKQSDSWDGW
PtRPD1          ------------------------------------------------------------
PtRPE1a         S------------------GGWGKPK--S--ISQGWGS-S--------KDS--VKAVDGW
PtRPE1b         A------------------SGWGKPK--SPALSEGWGS-P--------REP--VKAVHGW
SbRPD1          ------------------------------------------------------------
SbRPE1a         ----------------------------------GFGR-----------GGRR-------
SbRPE1b         NDSWDNV-AEKALN-SASQDSWGHLA--ATPVSN--------------SDAKQSDSWDGW
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          ------------------------Q----SESSHGWGP-S--------NEQNQLPSSQGW
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ZmRPB1          SPSY-----------SPTSPSYSPTSPAYSPTSPGYSP-T--------SPSY--------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          NDSWDNV-AKNAPD-SAAEDSWGAA-----------------------------------


AtRPB1          ---------SPTSPSYGPT-----------------------------------------
AtRPD1          ------------------------------------------------------------
AtRPE1          VSLKETKSR---------------------EKDDKERSQWGNPA-----KKFPSSG----
BdRPD1          ------------------------------------------------------------
BdRPE1          SSALA--------------------------EDS------NKADDSSNKNKGWKSD----
CpRPD1          ------------------------------------------------------------
CpRPE1          GLPNNEDIT---------------------QNESQGRRTWEF----SKKKRNEGSR----
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ---------------------------------GGGRAVWK----------SEASHRGSG
OsRPE1b         KSAGVDASTNKDKESWGNVPASPSDSAWNAAPVSQGDDVWNSAEANESRNKDWKSD----
PtRPD1          ------------------------------------------------------------
PtRPE1a         GVPNSAGSN-----------------------GSERDQQWGQQSGEFKKNRTEGSR----
PtRPE1b         GVPNSGGGN-----------------------GSGRDQQWGQQSREFKKDRFEGSR----
SbRPD1          ------------------------------------------------------------
SbRPE1a         ---------------------------------GGGRGMWK----------SEGSH----
SbRPE1b         NAVPA--------------------------ENSQGTAQW--KERTDSGNKDWKSD----
SmRPD1          ------------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          GSPNAGAGH-----------------------ESETQSQWGQPSG--KKSRPEGSR----
ZmRPB1          ---------SPTSPSYSPT-----------------------------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          TP----------------------------------------AETTDSGNKEWKSD----


AtRPB1          ---------SPS---YNP-------------------------QSAKYSPSIAYSPSNAR
AtRPD1          ------------------------------------------------GIPMSLL-RTIF
AtRPE1          ---GWSNGGGADWKGNRNHTPRPPRS-ED--NLAPMF------TATRQR-LDSFTSEEQE
BdRPD1          ------------------------------------------------SVEQNYLGAKVG
BdRPE1          ---GWGAK--GNRRDQRDNPSMPPMR-PD---ER----------PPRPR-FE-VPAEAKK
CpRPD1          ------------------------------------------------GISRAYL-RTVL
CpRPE1          ---GWSSNS-GDWKGKKNLPGKLAGNVKDDFGAGRLY------THTRQR-LDMFTSEEQD
OsRPD1a         ------------------------------------------------SFNQKFLNAKVG
OsRPD1b         ------------------------------------------------SVNQKFLDSKVG
OsRPE1a         NNRNRGGGR-AVWKSEASRRG----------------------GSMRQVASCAFTPVEQQ
OsRPE1b         ---GWGARG-GNWRGQRNNPGRPPRK-PD---GRGLPRRPDERGPPRRH-FD-LTAEEEK
PtRPD1          ------------------------------------------------GIPRSFL-RRLL
PtRPE1a         ---GWGSNN-GHWK-KRNRPSKPHE----DSSSSGLF------TMTRQW-LDIFTSQEQD
PtRPE1b         ---GWGSNN-GDWKNKRNRPSKPHE----DLNASGIF------TTTRQR-LDVFTSQEQD
SbRPD1          ------------------------------------------------TSDQDFLHAKVS
SbRPE1a         ---RGGSNS-TNWRAQNNNSA------------------------RQCGISYSFTPVEQQ
SbRPE1b         ---GWGAKS-GNWSSQRNNPGRPPRR-PD---ERGPP-------PPRQR-FE-LTIEEKK
SmRPD1          -----------------------------------------------------AK-DREI
VvRPD1          ------------------------------------------------KISKSVL-RSFL
VvRPE1          ---GWGSNN-TEWKNKKNRPNKPQGPLNDDYSAGGIF------TATRQR-VDIFTSEEQD
ZmRPB1          ---------SPS---YNP-------------------------SSAKYSPSHAYSPSSPR
ZmRPD1          ------------------------------------------------TIDQDFLHAKVS
ZmRPE1          ---GWGAKS-GNWSSQRNNPGRPPRR-PD---ERGPP-------PPRQR-FE-LTVAEKN


AtRPB1          LSPASPYSPTSPN------------YSPTSPSYSPTSPSYS-PSSPTYSPSSPY------
AtRPD1          T-----WKNIELLSQSLKRILHSY--EINEL-LNERDEGLVK-MVLQLHPNSVEKIGPGV
AtRPE1          L-----LSDVEPVMRTLRKIMHPSAYPDGDP-ISDDDKTFVLEKILNFHPQKETKLGSGV
BdRPD1          V-----WDSIIDMRTCLQNMLREY--QLDEY-VVELDKSRVI-EALRFHPRGREKIGVGI
BdRPE1          I-----LREIEPIVSMVRKIFRES--CDGVR-LPLEDEKFIKESILEHHPEKERKVPGEI
CpRPD1          T-----WKDIQKLYHASKKILNKY--PIDHR-LNEGEKKILM-MALYFHPQSYEKIGTGA
CpRPE1          V-----LSDVEPLMQSIRRIMHQSGYNDGDP-LSVDDQSFVIDKVFMYHPDRAVKMGAGI
OsRPD1a         I-----WENIIDMRTSLQNMLREY--TLNEV-VTEQDKSCLM-EALKFHPRGYDKIGVGI
OsRPD1b         I-----WENIIDMRTCLQNMLREY--TLNEV-VTEQDKSCLI-EALKFHPRGYDKIGVGI
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OsRPE1a         I-----FEQIEPITKNVKRIIRES--RDGIK-LPPDDEKFIVTNVLMYHPERKKKIAGNG
OsRPE1b         I-----LGEIEPTVLSIRKIFRES--IDSIK-LSPEDEKFIKENVLEHHPEKQSKVSGEI
PtRPD1          T-----YDDIQRMSYTVRKILNKY--SVDQQ-LNESDKSVLM-MTLYFHPRRDEKIGIGA
PtRPE1a         I-----LSDVEPLMLSIRRIMHQTGYSDGDP-LSADDQSYVLDNVFNYHPDKAVKMGAGI
PtRPE1b         I-----LSDIEPLMLSIRRIMHQTGYNDGDP-LSADDQSYVLDNVFHYHPDKAVKMGAGI
SbRPD1          I-----WDNIIDMRASLQNMLREY--PLNGY-VMEPDKSKLI-EALKFHPRGAEKIGVGV
SbRPE1a         I-----YTQVEPIIKNVKRIIRES--RDGMK-LSQDDEMFIMNKILMYHPEKEKKMAGQG
SbRPE1b         I-----LLEVEPLIFRVRRIFREA--CDGVR-LKPEDEKFIQEKILEHHPEKQSKVSSEI
SmRPD1          V-----WARIDQRSQKLHDILRKS--LTGTP-VSAANEAVIL-DTLKYHPMMDSKVGCGV
VvRPD1          S-----LNDIQKLSRRLKFILQKY--PINHQ-LSEIDKTTLM-MALYFHPRRDEKIGPGA
VvRPE1          I-----LLDVEPIMQSIRRIMHQAGYNDGDP-LSADDQSYILDKVFNNHPDKAVKMGTGI
ZmRPB1          MSP---YSQTSPS------------YSPTSPTYSPTSPSYS-QPSPSYSPT---------
ZmRPD1          I-----WDNIIDMRTSLQNMLREY--PLNGY-VAEPDKSQLI-EALKFHSRGAEKIGVGV
ZmRPE1          I-----LLEVEPIKLRVRSIFREA--CDGVR-LNPEDEKFILEKVLEHHPEKQSKVSGEI
                                                    .            .

AtRPB1          ---------------------SSGASPDYSPSAGYSPTLP---GYSPSSTGQYTPHEGDK
AtRPD1          KGIRVAKS-KHGDSCCFEVVRIDGTFEDFSYHKCVLGATK---IIAPKKMNFYKSKYLKN
AtRPE1          DFITVDKHTIFSDSRCFFVVSTDGAKQDFSYRKSLNNYLM---KKYPDRAEEFIDKYFTK
BdRPD1          RDI---------------------------------------------------------
BdRPE1          DHIMVNKHHIFQESRCFYVVLADGTHTDFSYNKCMDNYVR---KTYTDAAE---------
CpRPD1          QYIKVLK-----------------------------------------------------
CpRPE1          DFVTVSRHSNFQDSRCFYIVSTDGRKQDFSYRKCLDNFIK---GKYPDIAEQFIGKYFRK
OsRPD1a         REIKIGVNPGHPSSRCFIVLRNDDTTADFSYNKCVLGAAN---SISPEL-----------
OsRPD1b         REIKIGVNPGHPNSRCFIVQRSDDTSADFSYNKCVLGAAN---SISPELGS-YIEKILSN
OsRPE1a         NYITVDRHQVFHGSRCLYVMSSDGSRKDFSYKKCLENYIR---AQYPDAADSFCRKYF--
OsRPE1b         DHIMVDKHQVFQDSRCLFVVSSDGTRSDFSYLKCMENFVR---KTYPEHGDSFCKKYFKR
PtRPD1          KDIKVINHPEYQDTRCFSLVRTDGTIEDFSYRKCLHNALE---IIAPQRAKRYCEKYLTS
PtRPE1a         NHVTVSRHSNFQESRCFYIVSTDDCKQDIFPTANVWRTSSGENNLTWQ-MNSSE-SILQE
PtRPE1b         DHVTVSRHSNFQESRCFYIVSTDGCKQDFSYRKCLENFIK---GKYPDLADEFIAKYFAR
SbRPD1          REIKVGLNPNHPGTRCFILLRNDDTTEDFSYHKCVHGAAN---SISPQLGS-YLKKLY--
SbRPE1a         NYIMVNKHQTFPSSRCLYVASSDGSSSDFSYKKCLENFIR---IHYPHAAESFCRKYF--
SbRPE1b         DHIMVNKHHTFEDTRCFFVVSTDGSQADFSYLKCLENFVR---KNYTEDVDSFCMKYLRP
SmRPD1          RHIRVDNHHSF-GGRCFHIVRLDGSVEDFSYHKCLLERIK---GNTV-LVQRYKKKFMGG
VvRPD1          QNIKVRYHSKYHNTRCFSLVRTDGTEEDFSYHKCVHGALE---IIDPRRARSYQSRWLP-
VvRPE1          DYVMVSRHSSFLESRCFYVVSTDGHKEDFSYRKCLENFIK---EKYPDNAETFIGKYFRR
ZmRPB1          -----------------------------SPSGSYSPTAP---GYSPSSTG---------
ZmRPD1          REIKIGLNPSHPGTRCFILLRNDDTTEDFSYHKCVQGAAD---SISPQLGS-YLKKLY--
ZmRPE1          DYLTVNKHQTFQDTRCFFVVSTDGSQADFSYLKCLENFVR---KSYTEDADTFCMKYLRP


AtRPB1          ------KDK---------------------------------------------------
AtRPD1          GTL----E----------------------------------------------------
AtRPE1          PRPSGNRDRNNQDATPPGEEQSQPPNQSIGNGGDDFQTQTQSQSPSQTRAQSPSQAQAQS
BdRPD1          ------------------------------------------------------------
BdRPE1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
CpRPE1          PRSSGNQQK---------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         RA----------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
OsRPE1b         RRDQP---PAADGGTAPGTP----------------------------------------
PtRPD1          KVSAT--D----------------------------------------------------
PtRPE1a         EA---IGSA---------------------------------------------------
PtRPE1b         RG---NRQR---------------------------------------------------
SbRPD1          ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SbRPE1b         RRRQA---PPPDVGTAPGTPAEVPPSTA-AETEQGTP-APPAE----------------V
SmRPD1          KNG--RKEE--------------------------------------------------V
VvRPD1          ------------------------------------------------------------
VvRPE1          PRAGGNRERS--------------------------------------------------
ZmRPB1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          PETEQ-----------------------------GTPPAPQAE----------------V
```

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AtRPB1          ------------------------------------------------------------
AtRPD1          ------------------------------------------------------------
AtRPE1          PSQTQ----------------------SQSQSQSQSQSQSQSQSQSQSQSQSQSQ-----
BdRPD1          ------------------------------------------------------------
BdRPE1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
CpRPE1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
OsRPE1b         -AGATQSTAVDTQEGT---------------------------------------SQQTQ
PtRPD1          ------------------------------------------------------------
PtRPE1a         ------------------------------------------------------------
PtRPE1b         ------------------------------------------------------------
SbRPD1          ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SbRPE1b         PQETLGSPAVALE-GTHNPRTDPTDDTE-------L----------------LGKDSDLT
SmRPD1          PVEI--------------------------------------------------------
VvRPD1          ------------------------------------------------------------
VvRPE1          ------------------------------------------------------------
ZmRPB1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          PQETWGSPAVPLEGGTHIAGPDSTGDAV-------I----------------LGEQHDLT

AtRPB1          --------------------------------------------------T---------
AtRPD1          ------------------------------------------------------------
AtRPE1          -SQS----QSPSQT---------------Q----------TQSPSQTQAQA---------
BdRPD1          ------------------------------------------------------------
BdRPE1          ------------------------------------------------------------
CpRPD1          ------------------------------------------------------------
CpRPE1          ------------------------------------------------------------
OsRPD1a         ------------------------------------------------------------
OsRPD1b         ------------------------------------------------------------
OsRPE1a         ------------------------------------------------------------
OsRPE1b         PDIATAPAATQQET-------LQDTPAPPADDG---------------------------
PtRPD1          ------------------------------------------------------------
PtRPE1a         ----------P---------------------------------------L---------
PtRPE1b         --------------------------------------------------T---------
SbRPD1          ------------------------------------------------------------
SbRPE1a         ------------------------------------------------------------
SbRPE1b         P---ASPAVAPQEA---------PKPDPTDDTELLGNEKPDLTPSSPGEAL---------
SmRPD1          -------------FSQKNDTGR----------------------------MYDKKTHGFL
VvRPD1          ------------------------------------------------------------
VvRPE1          --------VIPEDG-------------------------------GNREQS---------
ZmRPB1          ------------------------------------------------------------
ZmRPD1          ------------------------------------------------------------
ZmRPE1          P---ASPAVAPQVA---------SEPDTTDGTGLLG------------KAP---------

AtRPB1          --GKKDASKDDKGNP
AtRPD1          -------SGGFSENP
AtRPE1          --QSPSSQSPSQTQT
BdRPD1          --------------K
BdRPE1          -----------HADL
CpRPD1          -------------TE
CpRPE1          ----P-VLEETENML
OsRPD1a         --------------G
OsRPD1b         ---------IRPHQL
OsRPE1a         --------------K
OsRPE1b         ----LLG-KGPSPSD
PtRPD1          ----NSGCTDLPLDN
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PtRPE1a         --LQREPRRNRPRDV
PtRPE1b         --PAPEGTEEEKQAL
SbRPD1          ------------HRA
SbRPE1a         --------------K
SbRPE1b         --QATADPDSTLTDI
SmRPD1          LVENHFVPVKTLKKT
VvRPD1          -----------YSEV
VvRPE1          --VVPEE-TGSENRQ
ZmRPB1          ----QGNDKDDKSAR
ZmRPD1          ------------YRA
ZmRPE1          --Q--ADWGPRFDAD
```