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Exploring the microbial twilight zone:
Adaptations to genetic code ambiguity in *Methanosarcina acetivorans*

By

Katharine Elizabeth Shalvarjian

A dissertation submitted in partial satisfaction of the

requirements for the degree of

Doctor of Philosophy

in

Microbiology

in the

Graduate Division

of the

University of California, Berkeley

Committee in charge:

Professor Dipti D. Nayak, Chair
Professor Karine A. Gibbs
Professor Michiko E. Taga
Professor N. Cecilia Martinez-Gomez

Summer 2025

Abstract

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By

Katharine Elizabeth Shalvarjian
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University of California, Berkeley
Professor Dipti Nayak, Chair

The ability to transfer information from DNA to RNA to protein is a fundamental characteristic of life. The flow of information between biomolecules was first described using a model termed the "central dogma," through which genetic information, stored in the four nucleotides of DNA, is transcribed to mRNA, and the resulting three base-pair codons are decoded during protein synthesis, or translation[1]. Contemporarily, the organization of the central dogma is used as a scaffold for the diverse and varied mechanisms of cellular information flow across the tree of life[1–3]. It follows that the genetic code is fundamental to the central dogma, as it defines the framework for how the codons of mRNA are interpreted and decoded into protein sequence[4]. Given its universality and essentiality to protein synthesis, the genetic code was first proposed to be immutable, a "frozen accident in time"[5] that was incapable of evolution. This is due in part to the diverse suite of translational machinery—ribosomes, release factors, tRNA's, and their cognate tRNA synthetases[6]—that is required to decode mRNA. Any change to the canonical encoding of twenty amino acids in sixty-one sense codons would necessarily require compensatory changes to this translational machinery, which was initially thought to be an insurmountable evolutionary challenge. Yet, the discovery of over thirty alternative genetic codes[7–10] in the years since the genetic code was proposed 1961, demonstrates that it is subject to the same pressures that govern cellular evolution.

An alternative genetic code encapsulates myriad types of codon reassignments, where either a sense or nonsense (i.e., stop) codon is captured and assigned to a meaning that deviates from the standard genetic code[11]. These alternative genetic codes are found across all domains of the tree of life and can range in complexity. Most involve single codon changes, wherein the genetic code degeneracy allows for a sense codon to be reassigned to a pre-existing amino acid, as in the case of certain fungi, like *Candida albicans*[8,12,12] and members of *Saccharomycotina*[13,14]. In other, more extreme cases, like the yeast mitochondrial genome, six codons (five sense codons and one stop codon) have been reassigned to standard amino acids[15,16]. The co-option of one of the three stop codons (TAG/UAG, TGA/UGA, and TAA/UAA) as a sense codon is a common form that alternative genetic codes take and is characteristic of several bacterial[7], archaeal[17,18], eukaryotic[19], and even phage[9] genetic codes. Yet, in contrast to sense-to-sense codon reassignments, nonsense-to-sense genetic codes present a unique challenge in how cells adapt to complete or partial re-assignment of one of its stop codons. In the former, complete stop re-assignment typically co-occurs with the gain of a codon-specific suppressor tRNA for the given codon, and, sometimes, loss of release factor activity[11]. In theory, this buffers the cell from the challenge of balancing between truncated and elongated protein forms: a conundrum that arises when partial, or

ambiguous, codon reassignment allows for a nonsense codon to be interpreted as both a stop and sense codon.

Natural genetic code expansions represent a unique case of nonsense-to-sense codon reassignment, under which a stop codon is co-opted to either conditionally or stochastically encode an amino acid outside of the standard twenty[20]. While there are only two known natural genetic code expansions to date—Selenocysteine (Sec)[21] and Pyrrolysine (Pyl)[17]—these two code expansions are emblematic of the molecular strategies that are used to navigate partial stop codon reassignment. In the former, charged Sec-tRNA^{Sec} is formed through the post transcriptional modification of a charged Ser-tRNA^{Sec}[22]. Sec's incorporation at UGA sites is contingent upon a proximal sequence motif, the Sec insertion sequence (SECIS) and is facilitated by Sec-tRNA^{Sec} binding by a specialized elongation factor called SelB[23]. Together, the coordination of these two processes allows for partial UGA reassignment to Sec by splitting UGA sites into two pools: 1) true stops, which *lack* the SECIS cue, and 2) true Sec sequences, which *contain* the proximal SECIS element. In contrast, Pyl is freely biosynthesized[24] in the cell, and its incorporation at UAG sites is, to date, independent of either sequence motif or specialized elongation factor[25]. Thus, how Pyl-encoding organisms navigate ambiguous interpretation of UAG sites, as either Pyl or stop, remains largely unknown. In this dissertation, I use Pyl as a system to address how ambiguity in information transfer (i.e., ambiguous UAG decoding) is productively maintained in the Pyl-encoding, methane-producing archaeon *Methanosarcina acetivorans*.

Chapter 1 of this thesis discusses and reviews literature pertaining to the transcriptional regulation of methane metabolism in the domain Archaea, a class of organisms to which *M. acetivorans* belongs. This chapter begins by summarizing what is known of archaeal transcription and genomic organization. It proceeds to review known regulators, their targets, and their influence on methane metabolism in two model methane-producing archaea, (methanogens) with different energy conservation strategies. The first, *Methanococcus maripaludis*, relies on flavin-based electron transport to regenerate reducing equivalents in the absence of cytochromes and the quinone-like molecule, methanophenazine. We contrast regulatory responses during growth on reduced compounds like H_2 and formate, highlighting outstanding questions related to signal detection and transduction. The second model organism addressed in this review, *M. acetivorans*, contains a complete electron transport chain. In this section we synthesize what is known of regulators, sensor kinases, and the interactions therein, which tune the expression of enzymes involved in methylotrophic and acetoclastic methanogenesis. Moreover, we discuss evidence for post-transcriptional regulation in *M. acetivorans*. We conclude by discussing how methodological advances can be applied to the questions raised in this chapter. Since transcriptional regulation represents one of many regulatory valves that tune the extent and degree of information transfer between DNA and mRNA, this chapter offers a framework for the regulatory trends discussed in subsequent chapters.

Chapter 2 explores the world of Pyrrolysine and addresses how methanogenic archaea, like *Methanosarcina acetivorans* have adapted to an ambiguous genetic code. First, we examine the distribution and diversity of Pyl systems across the archaea (using a bioinformatic tool described in Appendix A). With data from this survey, we 1) establish the co-occurrence between *pyl* genes and associated metabolic machinery for methylamine methanogenesis, 2) evaluate the evolutionary history of Pyl biosynthetic and incorporation machinery, and 3) determine that while TAG usage decreases in Pyl users, patterns of stop codon usage are poor predictors for Pyl usage.

We then test the functionality of diverse Pyl systems from uncultured archaea that break from Pyl's co-occurrence trends and confirm that *pyl* genes in ANME-3 and *Borrarchaeum weybense* are likely vestiges of previously functional systems. Next, we sought to understand how genetic code ambiguity affects the physiology of Pyl-encoding methanogens like *M. acetivorans*. To this end, we provide conclusive evidence that *M. acetivorans* has an ambiguous genetic code where the amber codon (UAG) is decoded as both stop and Pyl. We use RNA-Seq to observe transcriptional changes that occur under *pyl* deletion and find that deletion mutants grown on methanol override substrate-specific transcriptional control and exhibit transcriptional profiles akin to wildtype cells grown on trimethylamine. Using our transcriptomic data, we present a model for how an ambiguous code, like that of *M. acetivorans*, might be tolerated. We posit that readthrough efficiency, or the suppression of UAG stop codons by Pyl, dictates the balance between the elongated and truncated forms of UAG-containing proteins. Under this model, we propose that Pyl demand outpaces Pyl supply during growth on trimethylamine, resulting in relatively low readthrough efficiency that drives UAG-containing proteins to their truncated forms. We conclude by proposing that readthrough efficiency is detected as a transcriptional cue via Pyl's incorporation in regulatory proteins. Together, this chapter offers insights into how genetic code ambiguity can be productively integrated in an organism's transcriptional regime.

Chapter 3 tests the hypothesis that Pyl-containing sensor kinase, called RdmS, acts as a sensor module for readthrough efficiency, driving the transcriptional effects we observe in Chapter 2. If the failure to incorporate Pyl into RdmS is causal to transcriptional dysregulation observe in *pyl* deletion mutants, we expect a Δ*rdmS* strain to exhibit similar growth defects to Δ*pyl* strains on permissive substrates like methanol. Instead, Δ*rdmS* grows akin to wildtype cells on both methanol and trimethylamine. Simultaneously, we investigated whether truncations of *rdmS* to its sensory, ATPase, and first two PAS domains produced a detectable phenotype. While we observed alterations to growth in the ATPase and PAS_2 domain complements, neither strain produced a significant defect relative to controls, likely due to the wide range of observed growth rates. To investigate whether RdmS's role manifests at a transcriptional level, unobservable by growth, we performed RNA-Seq on a Δ*pyl* strain complemented with a constitutively long form of *rdmS.* Our results rule out RdmS as a candidate sensory module for readthrough efficiency. While it is unlikely that RdmS plays a role in Pyl homeostasis, our results offer additional insights into the *in vivo* physiology of RdmS and underscore its relationship to methylsulfide methyltransferases.

Together, this dissertation dissects adaptations to code ambiguity across several steps in the central dogma. Using large-scale genomic surveys, we demonstrate that Pyl-based code expansion is widespread across the archaea, where it strongly co-occurs with a methylamine methanogenesis, a microbial metabolism of environmental importance. We establish that Pyl-encoding organism like *Methanosarcina acetivorans* jointly decode UAG residues as Pyl and stop, providing conclusive evidence that pools of UAG-encoding proteins are split into two forms: elongated and truncated. Insights derived from transcriptional profiling of a suite of Pyl mutants, complements, and wildtype strains enabled us to develop a model for how cells overcome the conundrum posed by ambiguous decoding of UAG as Pyl and stop by integrating this ambiguity in its transcriptional regime. Although the readthrough detection module remains elusive, we highlight candidates for future work and provide evidence ruling out RdmS's involvement in this process. Through this, and future work, we will be able to draw a mechanistic throughline between genetic code ambiguity and its role in organismal physiology.

Dedication

Dedicated to my family, of all shapes and forms.

Three apples fell from the sky:
One for the storyteller,
One for the listener,
And the third for the one who took it to heart.

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1. Transcriptional Regulation of Methanogenic Metabolism in Archaea

Transcriptional regulation is a critical valve in modulating how information stored in DNA template is transferred to mRNA transcript. Transcription in the domain Archaea is often conceptualized as a chimera of the eukaryotic and bacterial systems, as they use machinery homologous to that of Eukarya to transcribe genomic information organized in an operonic structure like the Bacteria. At the time of this chapter's publication (2021), little was known about how regulatory mechanisms integrate such chimeric machinery in a uniquely archaeal transcriptional regime. It is worth noting that since this review's publication, substantial work has been done to dissect this question. For instance, we now know that methanogenic archaea can employ single-component regulatory systems to streamline signal detection and DNA binding in a single regulator. The remainder of my dissertation builds on the idea presented in this review—that methanogens employ dynamic transcriptional strategies to navigate a changing environment—and addresses how these strategies can be used to overcome ambiguity in codon interpretation.

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Abstract

Methanogenesis is a widespread, ancient metabolism of evolutionary and environmental importance. Microorganisms that perform methanogenesis, termed methanogens, belong exclusively to the domain Archaea. Despite maintaining eukaryotic transcription machinery and homologs of bacterial regulators, archaeal transcription and gene regulation appear to be distinct from either domain. While genes involved in methanogenic metabolism have been identified and characterized, their regulation in response to both extracellular and intracellular signals is less understood. Here, we review recent reports on transcriptional regulation of methanogenesis using two model methanogens, *Methanococcus maripaludis* and *Methanosarcina acetivorans,* and highlight directions for future research in this nascent field.

1.1 Introduction

Methanogens are a polyphyletic group of archaea that couple growth and energy conservation to the generation of methane gas through a process called methanogenesis[26–28]. These microbes are typically found in anoxic environments such as wetlands and sewage treatment plants, as well as the digestive tract of diverse hosts like termites, cows, and humans[29]. As the predominant source of methane, a potent greenhouse gas, methanogenic archaea rank as a highly influential group of organisms in the context of global climate regulation[27,30–32]. By now, many of the enzymes and respiratory complexes involved in methanogenesis have been identified and characterized in intricate biochemical detail[26,26]. Yet very little is known about how these genes are regulated in response to biotic or abiotic signals. As the climate crisis exacerbates, the need to understand how methanogens regulate their metabolism in response to environmental cues is crucial to forecast how they will adapt to and impact the warming planet.

Since all known methanogens are members of the Archaea, the third domain of Life, their transcriptional machinery contains elements related to that of Bacteria and Eukarya, while remaining distinct from either (**Fig 1.1**)[33,34]. For instance, the archaeal RNA polymerase (RNAP) is structurally and evolutionarily related to PolII in *Saccharomyces cerevisiae* (**Fig 1.1C**)[35]. Similarly, transcription initiation relies on homologs of eukaryotic TATA-binding proteins (TBPs) and transcription factor B (TFB) binding to the TATA box and B-recognition element in the core promoter sequence, respectively (**Fig 1.1A**)[35,36]. However, following coordination of RNAP with the promoter, elongation proceeds akin to Bacteria, with transcription of the nascent mRNA coupled directly to its translation (**Fig 1.1B**)[37]. This is particularly relevant within the context of polarity as archaeal genomes are generally organized in operons[34]. Although homologs of the canonical, bacterial two component system (TCS) and some eukaryotic transcription factors have been identified in methanogens, the fundamental mechanisms of signal transduction and gene regulation in archaea are distinct and largely uncharacterized *in vivo*[38–40]. However, with the advent of new genetic techniques, these questions are becoming more feasible to address within the context of the cell.

This review summarizes current knowledge and identifies future directions for research related to the regulation of methanogenesis in *Methanoccocus maripaludis* and *Methanosarcina acetivorans*. These well-studied species have emerged as genetically tractable model organisms that represent two distinct groups of methanogens. *M. maripaludis* lacks cytochromes and is restricted to growth on H_2+CO_2 or formate[41]; whereas *M. acetivorans* contains cytochromes and has a broader substrate range, which can include acetate and methylated compounds like methanol or methylamines[42]. Together, these two species provide an ideal genetic framework to identify signaling cascades and transcription factors that regulate methanogenesis *in vivo.*

1.2 Methanogens without cytochromes

Methanogens belonging to the Orders *Methanococcales, Methanobacteriales, Methanomicrobiales,* and *Methanopyrales* within the *Euryarchaeota*, lack cytochromes and differ in their energy metabolism from members of *Methanosarcinales*. The vast majority of these methanogens are restricted to growth on CO_2 with H_2 or formate as the electron donor[27,29]. A few notable exceptions can use methylated compounds as a carbon source and short-chain alcohols, like ethanol, as an electron donor as discussed in several papers[43,44]. Although methanogens with and without cytochromes share a conserved seven-step pathway for the step-wise reduction of CO_2 to methane, the two differ significantly in their energy conservation strategies. Methanogens without cytochromes, like *M. maripaludis,* also lack the quinone-like compound methanophenazine, and rely on flavin-based electron bifurcation (FBEB) for the regeneration of coenzyme M (CoM) and coenzyme B (CoB) from the oxidized heterodisulfide (CoM-CoB) produced during the final step of methanogenesis[27,45–47]. As a result, the Na^+-dependent N^5-methyl-tetrahydrosarcinopterin:CoM methyltransferase (Mtr) singularly generates the ion gradient for ATP synthesis by the membrane-bound ATPase[27]. Until recently, *M. maripaludis* was the only genetically tractable member of this group of methanogens[48,49]. While its nitrogen regulon has been characterized and reviewed in detail in, regulation of methanogenesis in *M. maripaludis* has only been inferred from genome-wide transcriptomic data[50,51]. Therefore, despite extensive evidence for the regulation of methanogenic enzymes (as discussed below) transcriptional regulators involved in this process are yet to be characterized.

1.2.1 H_2 dependent gene regulation

Whole cell transcriptomic analyses of *M. maripaludis* in chemostat cultures where growth was limited by H_2 revealed extensive regulation in core methanogenesis genes[52–54]. Significantly, expression of metabolic genes that use F_{420}, an NAD(P) analog used by methanogens as a redox carrier, is linked to extracellular H_2 levels[54]. Two enzymes can carry out the fourth step of the methanogenesis pathway: an F_{420}-dependent tetrahydromethanopterin dehydrogenase (Mtd) or a H_2-dependent tetrahydromethanopterin dehydrogenase (Hmd) (**Fig 1.2A**). As H_2 levels drop, transcripts for Mtd become more abundant relative to Hmd, favoring the use of F_{420} as an intermediate under low H_2 conditions (**Fig 1.2A**)[54,55]. Similarly, transcripts for the F_{420}-dependent methylene tetrahydromethanopterin reductase (Mer) and F_{420}-dependent hydrogenase (Fru) are more abundant under H_2-limiting conditions (**Fig 1.2A**). This upregulation of genes encoding F_{420}-dependent enzymes under H_2-limiting conditions might be beneficial to sustain metabolic flux for methanogenesis fueled by reduced F_{420} rather than H_2[41,45,55]. Similar studies with other Class I methanogens like *Methanocaldococcus janaschii* and *Methanothermobacter thermoautotrophicum* Δ*H*, have also revealed substantial transcriptional regulation of Mtd versus Hmd—along with other methanogenic enzymes—as a function of H_2 availability[56,57]. Altogether, while it is clear that there is an an extensive H_2 regulon in *M. maripaludis*, a H_2 sensor and the downstream signaling cascade remains elusive.

1.2.2 Formate Dependent Gene Regulation

In methanogens without cytochromes, formate dehydrogenase (encoded by *fdhAB*) catalyzes the oxidation of formate to CO_2 with the concomitant reduction of F_{420}. *M. maripaludis* encodes two copies of *fdhAB* where only *fdh1* is essential for growth on formate and the Δ*fdh2* mutant is indistinguishable from wildtype[55,58]. Whole cell transcriptomics and gene specific lacZ fusions have shown that *fdh1* is upregulated during H_2 limitation and in the presence of formate,

whereas *fdh2* is only upregulated under formate limiting conditions (**Fig 1.2B**)[58]. Likewise, many core methanogenesis genes appear to be regulated in response to formate (**Fig 1.2B**)[55]. Whether the regulatory signals for formate and H_2 are the same, somewhat overlapping, or completely distinct is yet to be determined.

1.3 Class II Methanogens

Members of the Order *Methanosarcinale*s encode cytochromes and a membrane bound electron transport chain for energy conservation during methanogenesis[27–29]. These methanogens are metabolically diverse[29,59], providing a unique opportunity for the characterization of genes involved in the substrate specific regulation of methanogenesis. While many species within the Genus *Methanosarcina* are genetically tractable[60,61], *M. acetivorans* is emerging as a preeminent model system for understanding gene regulation in methanogens and perhaps, even more broadly, in the Archaea. Consequently, *M. acetivorans* encodes the largest number of transcription factors (TFs) in an archaeal genome[38] and substantial work has been done to show that several members of the ArsR family TFs act as both activators and repressors of genes involved in methanogenic metabolism[62,63].

1.3.1 Methylotrophic methanogenesis

During growth on methylated compounds, also referred to as methylotrophic methanogenesis, 1/4th of the C_1 substrate is oxidized to CO_2 via a reversal of six steps of the core methanogenesis pathway and 3/4th is reduced to methane using the enzyme methyl coenzyme reductase (**Fig 1.3A**)[26,64]. During this process, the methyl group from the substrate enters core methanogenesis at the level of methyl-CoM via two stepwise methyl-transfer reactions mediated by two different methyltransferases, referred to as MT1 and MT2 (**Fig 1.3A**)[65]. The MT1 complex is substrate-specific and consists of a methyltransferase that transfers the methyl group to its associated corrinoid containing protein, whereas MT2 catalyzes the transfer of the methyl group from the corrinoid protein to CoM to form methyl-CoM (**Fig 1.3A**)[66–69]. For the purpose of this review, we will focus *only* on the regulation of MT1 and MT2 during methylotrophic methanogenesis.

Methanosarcina spp. often encode multiple copies of the substrate-specific MT1 that are dynamically regulated (**Fig 1.3B**)[42,70]. In *M. acetivorans,* the three copies of methanol-specific MT1 operons, *mtaCB1, mtaCB2,* and *mtaCB3* are differentially regulated with respect to changes in growth phase and substrate availability[62]. Several members of the ArsR family of TFs that are in the genomic proximity of these operons have been designated as members of the Msr (**m**ethanol **s**pecific **r**egulator) family upon functional characterization (**Fig 1.3B**)[63]. Unlike members of the ArsR family in Bacteria, which act only as transcriptional activators, Msr proteins can both activate and repress the expression of *mtaCB* in *M. acetivorans*. Mutational analyses coupled to transcriptional fusions have revealed that MsrA and MsrB act as positive regulators of *mtaCB1* while MsrD and MsrE function in the dual activation and repression of *mtaCB2* and *mtaCB3,* respectively (Fig 1.3B). This model of Msr-mediated regulation can be extended to a class of fused MT1/MT2 proteins (MtsD, MtsF, MtsH) that are required for the production of methylated sulfur compounds during growth on carbon monoxide, or for growth on methylated sulfur compounds[71,72]. Genetic studies have shown that MsrF, MsrC, and MsrG are required for the transcriptional activation of MtsD, MtsF, and MtsH respectively (**Fig 1.3B**)[73]. While each of the Msr proteins contains a DNA-binding domain, whether these proteins directly bind to the promoter

region of the corresponding MTs or interact with other TFs to regulate transcription is unknown and warrants further investigation[63].

Recent work has identified two redox-active cytoplasmic sensor kinases that are likely involved in the regulation of MTs[74,75]. A methylsulfide-specific sensor, named MsmS, is encoded directly upstream of the regulator MsrG and undergoes autophosphorylation when the iron in its covalently bound heme group is oxidized from Fe(II) to Fe(III) (**Fig 1.3B**)[74]. Interestingly, a *ΔmsmS* knockout constitutively produces MtsF, indicating that MsmS may act as a negative effector of *mtsF* expression[74]. Similarly, another sensor kinase, RdmS, is autophosphorylated at a conserved tyrosine residue when intramolecular disulfide bonds between two cysteine residues are formed under oxidizing conditions[75]. These sensor kinases are promising models for understanding archaeal two-component systems, but whether they interact with Msr family regulators to fine-tune the expression of MTs remains unclear.

Beyond transcription initiation, regulation of methylotrophic methanogenesis also occurs at the post-transcriptional level. Curiously, when the *mtaCBA* genes are expressed from a tetracycline-inducible $P_{mcrB(tetO1)}$ promoter, RNA and protein levels can vary substantially (>10 fold) depending on the growth conditions[76]. This observation is supported by recent work identifying that global changes in mRNA half-life in *M. acetivorans* depend on its growth conditions[77], in addition to work characterizing small RNAs that regulate expression of MTs in *M. mazei*[78]. However, a model describing the extent to which post-transcriptional regulation fine tunes gene expression and cellular protein levels has yet to be uncovered.

1.3.2 Acetoclastic methanogenesis

In *Methanosarcina spp.* growth on acetate proceeds through the dismutation of acetate to CO_2 and methane using two dedicated enzymes: acetate kinase (Ack) and phosphotransacetylase (Pta)[26,79]. First, acetate is activated to acetyl-CoA by Ack and Pta, after which it is split into enzyme-bound methyl and CO groups by acetyl-CoA decarbonylase/synthase (ACDS). The methyl group then enters the central pathway as methyl-tetrahydrosarcinopterin (methyl-H_4SPT), and the CO group is oxidized to CO_2[26,79].

Mutational analyses coupled with RNA-seq have revealed that a TrmB family regulator, named MreA, plays a role in the dual activation and repression of acetoclastic and methylotrophic methanogenesis, respectively[80]. RNA-seq analyses of the *ΔmreA* mutant reveals wholesale downregulation of genes required for acetoclastic methanogenesis with concurrent upregulation of MTs and the Msr family regulatory proteins involved in methylotrophic methanogenesis[80]. Additionally, purified MreA has been shown to bind the promoter region of *pta* and *fpo*; the former is essential to acetoclastic methanogenesis, while the latter is a membrane bound energy conservation complex upregulated during methylotrophic growth. Taken with the observation of a substantial growth defect in a *ΔmreA* mutant, these results indicate that MreA may play a role in the global regulation of methanogenesis[80]. However, the underlying mechanism of MreA mediated regulation is yet to be characterized.

1.4 Discussion and Future Directions

Methanogenesis is a widespread, environmentally relevant, and evolutionarily important metabolism. While there is considerable phenomenological evidence of regulation in methanogens, a clear picture of transcriptional and post-transcriptional regulatory processes in these pivotal organisms has yet to emerge. The work outlined in this review represents a foundation for future research threads that will shed light on how methanogens sense their environment and tune their metabolism in response. Recent methodological advances, such as genome-wide functional screens coupled with high-throughput global gene expression profiling, are likely to facilitate future efforts to map the complex regulatory network in methanogens. Furthermore, besides its myriad practical applications, studying the regulation of methanogenesis also presents an opportunity to deepen our fundamental understanding of gene regulation in the domain Archaea.

1.4.1 Highlights

- Transcriptional regulation in Archaea is distinct from that of Bacteria or Eukarya.
- Methanogens present a unique opportunity to study archaeal regulation.
- Methanogenesis is regulated in response to substrate availability.
- Msr family regulators tune expression of methyltransferase isozymes.
- Post-transcriptional regulation contributes to gene expression in methanogens.

1.4.2 Concluding Remarks

The majority of atmospheric methane emission is of biological origin, due primarily to the activity of a group of methane-producing archaea called methanogens. While substantial work has been done to describe the mechanism by which methane is produced, our understanding of how environmental signals are interpreted to tune the regulation of methanogenesis is still fledgling. In this chapter, I review substrate-responsive regulatory mechanisms in two subgroups of methanogens—those with and without cytochromes—and highlight outstanding questions in how information transfer is regulated at the level of transcription.

1.4.3 Acknowledgements

The authors would like to acknowledge members of the Nayak lab for their feedback and input. Molecular graphics were produced using the UCSF Chimera package from the Resources for Biocomputing, Visualization, and Informatics at the University of California, San Francisco (supported by NIH P41 RR-01081).

1.5 Figures

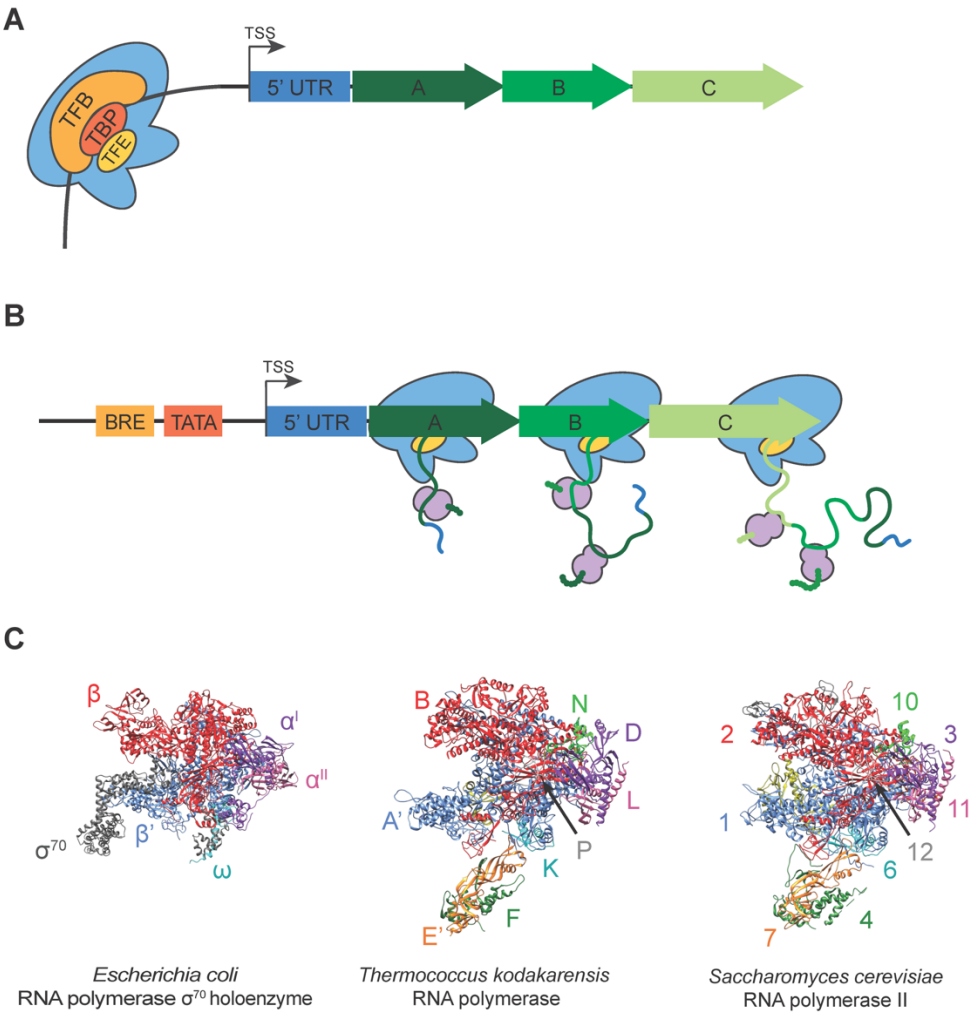

Fig 1.1. Transcription in Methanogenic Archaea. A) Two transcription factors, TBP (TATA binding protein; in orange-red) and TFB (transcription factor B; in orange), that bind to the TATA-box and the B-recognition element (BRE) in the promoter region respectively are required to recruit the RNA polymerase (in light blue) for transcription initiation in methanogenic archaea. A third transcription factor, Transcription factor E (TFE; in yellow) is not essential but enhances the recruitment of RNA polymerase *in vitro.* **B)** Genes in methanogenic archaea are arranged in operons and transcription of a multi-gene operon (in green) produces polycistronic RNA. Assembly of the corresponding polypeptide is facilitated by a translating ribosome (light purple). **C)** Structural overview of RNA polymerase (RNAP) derived from a bacterium (*Escherichia coli*; PDB ID: 4YG2), an archaeon (*Thermococcus kodakarensis* PDB ID: 4QIW) and a eukaryote (Polymerase II from *Saccharomyces cerevisiae* PDB ID: 1WCM). Orthologous subunits of RNAP are shown using the same color.

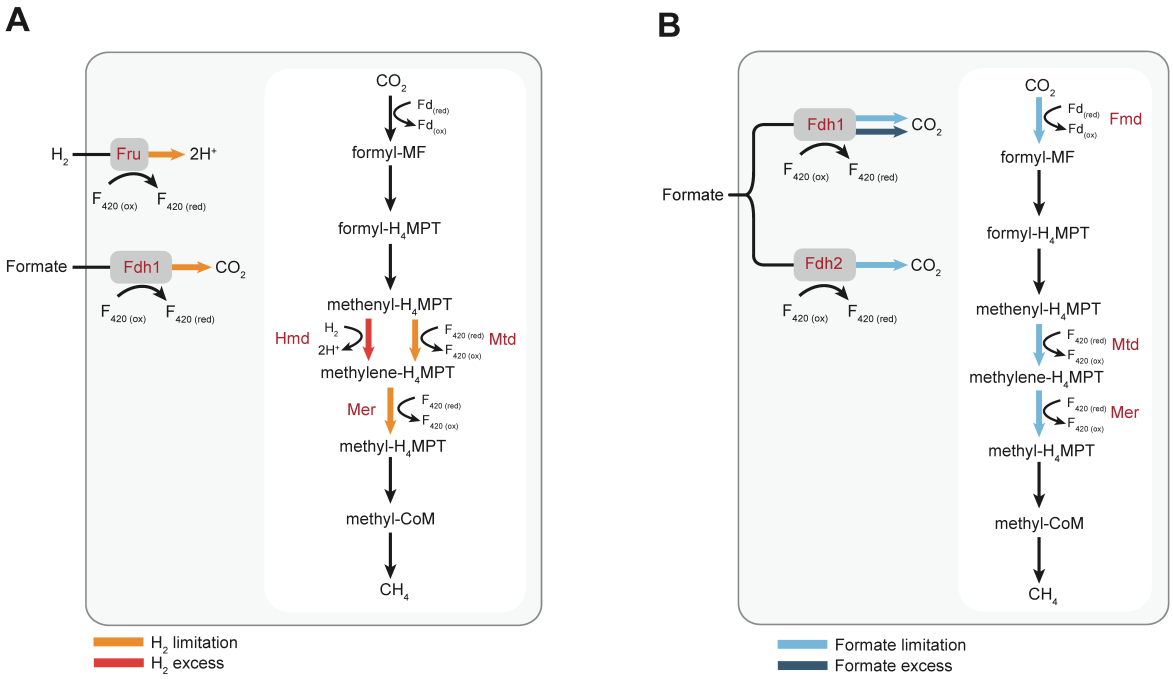

Fig 1.2. Regulation of Methanogenesis in *Methanococcus maripaludis.* A) Transcriptomic analyses of methanogenesis in H_2-replete and H_2-limited conditions has shown that genes catalyzing the fourth and the fifth step in the sequential reduction of CO_2 to methane are transcriptionally regulated as a function of H_2 availability. Additionally, the F_{420} reducing hydrogenase complex (Fru) and formate dehydrogenase (Fdh1) are upregulated upon H_2 limitation. **B)** During growth on formate, three steps of the seven-step pathway for CO_2 reduction are regulated as a function of substrate concentration. In addition, the two formate dehydrogenase orthologs are differently expressed: Fdh1 is expressed in formate replete media whereas Fdh2 is only expressed when formate concentrations are growth limiting.

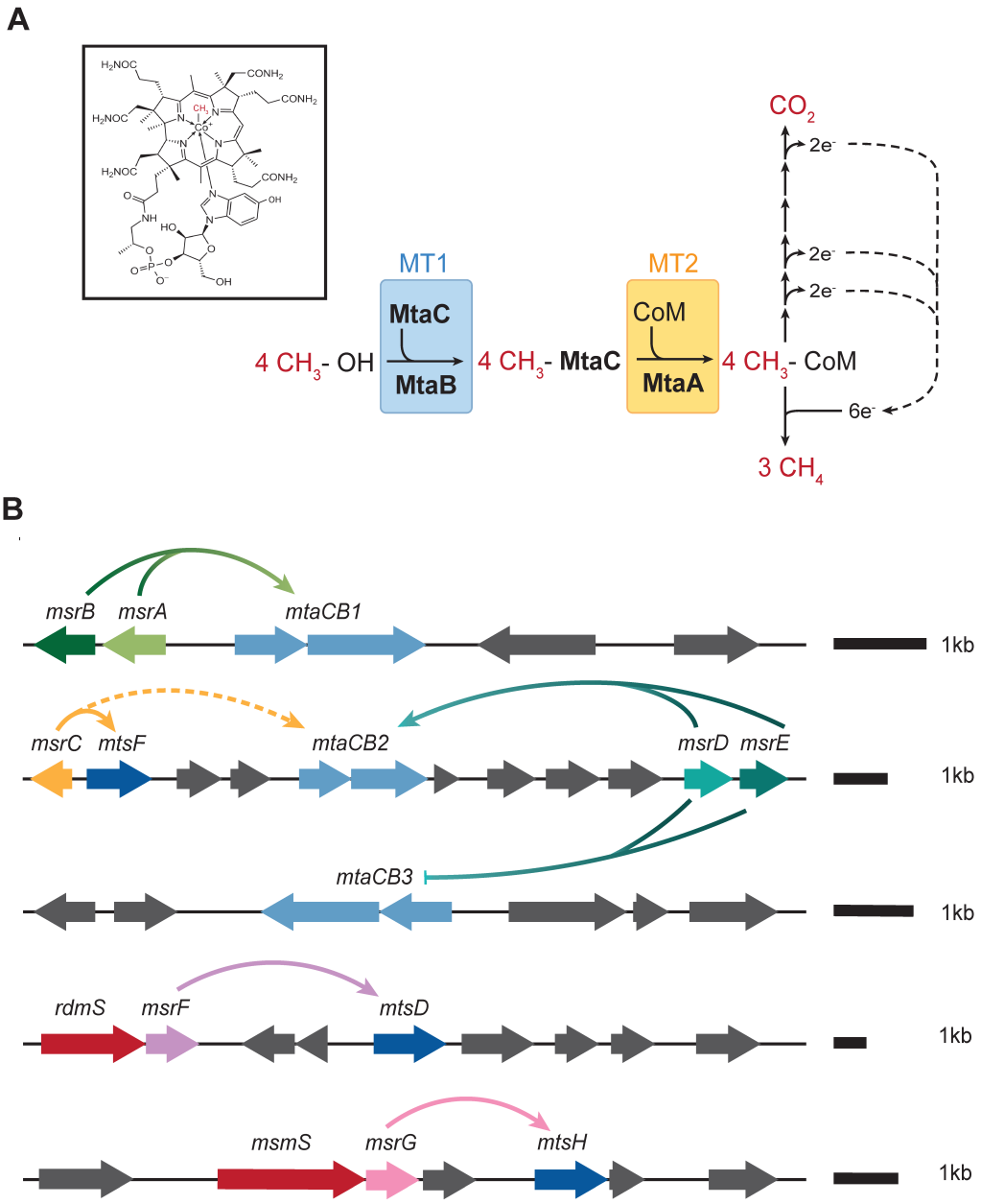

Fig 1.3. Methylotrophic Methanogenesis in *Methanosarcina acetivorans*. A) A substrate-specific methyltransferase (MtaB) catalyzes a methyl-transfer reaction from methanol to a corrinoid-containing protein (MtaC). The heterodimer of MtaB and MtaC (in blue) is called the MTI. A second methyltransferase (MtaA2; in yellow) catalyzes a methyl-transfer reaction from methyl-MtaC to form methyl-coenzyme M (CoM), which is disproportionated in a 3:1 ratio to methane and CO_2 using the conserved seven-step methanogenesis pathway. The MtaC corrinoid cofactor, methylated 5-hydroxybenzimidazolylcobamide, is depicted in the inset above MT1. **B)** Msr proteins regulate the expression of three different MtaCB operons in *M. acetivorans.* The dashed arrow indicates that MsrC is a weak activator of MtaCB2 compared to MsrDE.

2. An Ambiguous Genetic Code is Prevalent in Methanogenic Archaea that Grow on Methylamines

In this chapter, I use a combination of experimental and computational biology to dissect the evolution and physiology of genetic code expansion in methanogen archaea. My results demonstrate, conclusively, that methanogens like *Methanosarcina acetivorans* have an ambiguous genetic code, wherein the amber codon (TAG/UAG) can be decoded as both a stop codon and a Pyrrolysine (Pyl) residue. We conclude this chapter by presenting a model under which Pyl-encoding Archaea, like *Methanosarcina acetivorans,* maintain an ambiguous genetic code by incorporating such ambiguity in its transcriptional program.

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Abstract

Natural genetic code expansion is a phenomenon wherein an additional amino acid is encoded by a stop codon. These non-standard amino acids are beneficial as they facilitate novel biochemical reactions. However, code expansion leads to ambiguity at the recoded stop codon, which can either be read through or terminated. Pyrrolysine (Pyl) is encoded by the amber codon (TAG/UAG) and is widespread in archaea, where it is required for methylamine-mediated methanogenesis, an environmentally important metabolism. Mechanisms to conditionally suppress the amber stop codon for Pyl installation during protein synthesis have not been identified. Using the model methanogen, *Methanosarcina acetivorans,* we demonstrate that Pyl-encoding archaea maintain an ambiguous genetic code wherein UAG encodes dual meaning as stop and Pyl. Our data suggest that expression of Pyl biosynthesis and incorporation genes is tuned to the cellular demand for Pyl, which allows these archaea to navigate ambiguous stop decoding in response to environmental cues.

2.1 Introduction

The genetic code is a core feature of life on Earth; through this triplet code, information stored in the four nucleotides of mRNA are translated into the twenty standard amino acids found in peptides/proteins. While initially proposed to be immutable[5], it is now well established that the genetic code is flexible and subject to evolutionary pressure. At least 33 alternative genetic codes have been identified across the tree of life—in ciliates[81], bacteria[7,82,83], archaea[84,85], fungi[8], and phage[9]—where either a sense or a stop codon is reassigned to deviate from the standard genetic code. Natural genetic code expansion is a distinct case of codon reassignment, wherein a stop codon is recoded to an amino acid beyond the standard twenty amino acids[86]. Natural genetic code expansion is beneficial because the non-standard amino acids can enhance reaction rates or facilitate novel biochemistry[17,87–89]. But, it also presents a unique challenge due to the ambiguous interpretation of the recoded stop codon: the ribosome can either read through the recoded stop codon to add the non-standard amino acid to the peptide chain or terminate translation by recruiting a release factor instead. This ambiguity likely leads to the production of two pools of proteins—an extended form and a truncated form—for all transcripts containing the recoded stop codon. In the case of Selenocysteine (Sec), the 21st amino acid, a Sec-tRNA^{Sec} specific elongation factor called SelB directs the ribosome to incorporate Sec at a UGA codon contingent on the presence of a proximal structural motif called SECIS (selenocysteine insertion sequence)[22,23,25]. In contrast, neither a sequence motif nor a specialized elongation factor has been found for Pyrrolysine (Pyl), the 22nd proteinogenic amino acid. Thus, the molecular mechanisms that Pyl-encoding microorganisms use (if at all) to tolerate ambiguous stop decoding remains unclear.

Pyl is biosynthesized from two molecules of lysine[24] and is installed in elongating polypeptides using a dedicated UAG-decoding tRNA^{Pyl} that is charged by a cognate tRNA synthetase (PylRS)[90]. Pyl was first identified in the active site of methylamine-specific methyltransferases in methanogenic archaea (methanogens)[17], where it is hypothesized to play an essential role during the methyltransfer reaction from methylamines to a corrinoid-containing protein[89]. Since then, Pyl has been identified across both archaea[85,91–93] and bacteria[94,95]. However, a mechanism for targeted insertion of Pyl is not known in any of these microorganisms.

Here, we address the conundrum of how Pyl-encoding archaea have evolved to navigate a potentially ambiguous genetic code. First, we use an *in silico* approach to assess the distribution of Pyl across archaea and identify features that are unique to Pyl^{+} genomes. Although Pyl-encoding archaea have lower TAG stop codon usage overall, it can vary substantially from 1 to 27%. Hence, the pattern of stop codon usage is neither a universal solution for the ambiguous genetic code created by Pyl nor is it a reliable predictor for its presence. Next, we engineer a heterologous expression system in *Methanosarcina acetivorans*, a native Pyl user, to test the functionality of Pyl systems from metabolically and taxonomically diverse archaea *in vivo*. Our functional assays add a layer of nuance to computational predictions and demonstrate that the presence of the *pyl* genes alone is not sufficient evidence for genetic code expansion. Finally, we provide conclusive evidence that *M. acetivorans* has an ambiguous genetic code in which the amber codon can be interpreted either as a stop codon or as Pyl. To this end, we describe possible mechanisms through which *M. acetivorans* maintains an ambiguous genetic code without a detrimental impact to organismal fitness.

2.2 Results

2.2.1 Pyrrolysine is present in archaea that perform anaerobic methylamine and methane metabolism

To map the distribution of Pyl in archaea, we searched for genes involved in its biosynthesis and incorporation in reference genomes available in the Genome Taxonomy Database (n=4,416; GTDB 214.0)[96]. The biosynthesis genes for Pyl (*pylBCD*)[24] are typically encoded in an operon[97,98] and are generally found in close proximity to the incorporation machinery, comprised of $tRNA^{Pyl}$ (*pylT*)[99] and its cognate aminoacyl tRNA synthetase (*pylRS*, denoted as *pylS* hereafter)[90,91,98] (**Fig 2.1**). We observe a strong correlation between the presence of the biosynthesis (*pylBCD*) and incorporation (*pylTS*) modules (p=1.4e-273, χ^2=1249, **Table S2.1**); genomes encoding both sets of genes were annotated as Pyl^+ (putative Pyl users) and the remainder as Pyl^-. Consistent with previous reports[85], the Pyl^+ genomes are broadly distributed across archaea (**Fig S2.1, Table S2.2**) but can be discontinuous at the Genus level. For instance, among the *Asgardarchaeota*, only a few strains within the Genus *Borrarchaeum* are Pyl^+ (**Fig S2.1, S2.2A**)[85,92]. Likewise, even though 92% of *Methanosarcina* genomes are Pyl^+, a few strains have lost Pyl (**Fig S2.1, S2.2B**).

The Pyl machinery (i.e. PylBCD and PylTS) strongly co-occurs with two markers of methane metabolism in archaea: methyl-coenzyme M reductase (MCR) and component A2[100] (p=3.1e-49, χ^2=218, **Table S2.1**). If we survey only methanogens, the co-occurrence metric strengthens (p=1.1e-51, χ^2=288 **Table S2.1**), a trend that does not hold true for **an**aerobic **met**hanotrophic archaea (ANME) (p=1.0, Fisher's exact test). Pyl also co-occurs with genes encoding methylamine methyltransferases (p= 2.9e-231, χ^2=1054, **Table S2.1**), although some Pyl^+ archaea with these methyltransferases lack markers for methanogenesis (**Fig S2.2**) and are instead likely to perform acetogenesis[92]. Often, genes involved in methylamine metabolism[42] are in close genomic proximity to the Pyl machinery (**Fig 2.1C, Fig S2.3**), which further corroborates their functional association.

Methanosarcinaceae from diverse environments commonly encode genes for methylamine-mediated methanogenesis and, thus, can be used to investigate fine-scale evolutionary events associated with Pyl-mediated genetic code expansion. To this end, we compared the gene trees for *pylS* and *pylBCD* to the 16S rRNA tree for this Family. While the *pylBCD* tree is in strong agreement with vertical inheritance (**Fig S2.4A**), the *pylS* tree diverges substantially (**Fig S2.4B, S2.5**). These data suggest that the Pyl biosynthesis and incorporation modules can have distinct evolutionary histories despite being functionally interlinked.

2.2.2 Pyl-mediated genetic code expansion does not lead to universal patterns of stop codon compensation

Given that Pyl incorporation relies on read through of the TAG codon, we examined differences in stop codon usage between Pyl^+ and Pyl^- genomes. As expected, TAG usage is significantly lower in Pyl^+ genomes (median=5.0%) compared to Pyl^- genomes (median=22.0%) (Welch's t-test, p=5.6e-47) (**Fig 2.2A**). However, taxon-specific features, like GC content[101], can be major confounders in these global trends. To control for these biases, we analyzed the distribution of stop codon usage and GC content within the *Methanosarcinaceae* and the *Methanomethylophilaceae*, two groups that have a relatively high distribution of Pyl^+ and Pyl^- genomes. Despite a large difference in GC content, TAG usage in Pyl^+ genomes from *Methanosarcinaceae* (median=4.9%) and *Methanomethylophilaceae* (median=4.1%) is similar

(**Fig 2.2B**). Further, within *Methanosarcinaceae,* we observe a marked increase in TAG stop codon usage for Pyl^- strains to their Pyl^+ counterparts (Pyl^-: 13.5%; Pyl^+: 7.8%) (**Fig 2.2C, Table S2**).

We did not detect a global pattern of compensation for decreased TAG usage in the Pyl^+ genomes. While there are significant differences in TGA and TAA usage between Pyl^+ and Pyl^- genomes across archaea (Welch's t-test, p=8.3e-7 and p=5.9e-5, respectively) (**Fig 2.2A**), these are likely driven by taxon-specific factors. For instance, the Pyl^+ genomes in *Methanomethylophilaceae* have higher TGA usage relative to *Methanosarcinaceae*, likely due to their heightened GC content (**Fig 2.2B)**. Hence, even though reduced TAG usage correlates with the presence of Pyl, there is no global compensation pattern. Rather, changes in TAA and TGA usage are contingent on factors like GC content.

Although TAG codon usage is substantially lower in Pyl^+ genomes, it can be highly variable, from 1% to 27% (**Table S2**), in agreement with previous reports[85,92]. We hypothesized that differences in TAG codon usage might be associated with the putative extension length of TAG-containing ORFs across Pyl^+ genomes. Hence, we predicted ORFs with internal TAG codons and measured their putative readthrough lengths within each Pyl^+ genome (**Table S2.3**). Overall, we observe that heightened TAG usage (>15%) is associated with an increase in the density of putative Pyl-containing proteins, whereas low TAG usage (<5%) is associated with an increase in readthrough length of TAG-containing ORFs (**Fig 2.2D, Fig S2.6**).

2.2.3 Genetic studies of diverse Pyl systems defy computational predictions

Although Pyl is broadly distributed in archaea, its role in genetic code expansion has only been studied in the context of a few methanogens[85,102,103]. To broaden our functional understanding of Pyl across the domain, we expressed the Pyl machinery from two non-methanogens in the genetically tractable model organism, *Methanosarcina acetivorans.* The first strain, *Borrarchaeum weybense*, is an *Asgardarchaeon* hypothesized to use Pyl to perform methylamine-mediated acetogenesis[92]. The second strain, ANME-3 S7, contains Pyl despite lacking methylamine metabolism. Axenic cultures are currently unavailable for both these strains, which prevents attempts to investigate their Pyl machinery in its native context[93,104]. Moreover, these strains are unusual because they break from the strong co-occurrence patterns shown in (**Fig S2.1, Table S2.1**) and thus might offer additional insights into the role of Pyl in archaea.

To develop *M. acetivorans* as a heterologous host, we generated deletion mutants lacking either the biosynthetic operon (Δ*pylBCD*) or the incorporation genes (Δ*pylTS*) using our well-established CRISPR-Cas9 editing system[61]. Neither mutant had off-target effects or suppressor mutations based on whole genome resequencing (**Table S2.4**). We observed that both mutants have a mild growth defect (slower by 15%; **Fig 2.3A, Table S2.5**) when Pyl is not essential i.e., on methanol, and are unable to grow when Pyl is essential i.e., on trimethylamine (TMA). Complementation of each deletion mutant with the native locus *in trans* restored growth across all conditions (**Fig 2.3A, Fig S2.7, Table S2.5**), indicating that no extragenic effects stem from the chromosomal deletions. To validate the proposed catalytic role for Pyl in methylamine methyltransferases[17,89,105], we generated a suite of non-synonymous point mutations at the Pyl residue in the TMA-specific methyltransferase, *mttB1.* We expressed these point mutants *in trans* from a tetracycline-inducible promoter[106] in the Δ*pylBCD* background, where the chromosomal copy of *mttB1* would be prematurely truncated at the TAG codon (**Fig 2.3B)**. If Pyl (O) is catalytically essential, then the mutant alleles of *mttB1* will not be able to rescue growth on TMA (**Fig 2.3A, Table S2.5**). Indeed, neither the $mttB1_{O334A}$ nor the $mttB1_{O334K}$ mutants restored growth

on TMA (**Fig 2.3C, Fig S2.7, Table S2.5**). To control for polar effects caused by premature translational termination of chromosomal *mttB1,* we jointly expressed *mttB1*$_{O334K}$ with its cognate corrinoid containing protein, *mttC1*, and observed the same lethal phenotype (**Fig 2.3C, Fig S2.7, Table S2.5**). Together these data affirm the hypothesis that Pyl is essential for the activity of methylamine methyltransferases, which underlies the lethal phenotype for the Δ*pyl* mutants on TMA.

Next, to test the functionality of non-native Pyl machinery, we complemented each deletion mutant with the *pyl* genes from *B. weybense* or ANME-3 S7 under the control of a tetracycline-inducible promoter. Even when fully induced, *pylTS*, *pylBCD* or *pylTS*+*pylBCD* from *B. weybense* were unable to restore growth on TMA (**Fig 2.3D**). Given that *pyl* genes from archaea have been successfully expressed in bacteria[107], these data suggest that the *B. weybense* Pyl system is likely non-functional. In contrast, *pylBCD* from ANME-3 S7 could restore growth of the Δ*pylBCD* mutant on TMA (**Fig 2.3D, Table S2.5**). We tested both copies of the *pylT* locus (*pylT1* and *pylT2*) from ANME-3 S7 with their cognate synthetase, and neither could support growth of the Δ*pylTS* mutant on TMA (**Fig 2.3D**). In an alignment of ANME-3 S7 *pylT* sequences with *M. acetivorans pylT,* we identified a 3bp insertion at the 3' end of the tRNA that could alter its secondary structure and disrupt its function (**Fig 2.3E**). To test this hypothesis, we generated Δ3bp deletions of *pylT1* and *pylT2* from ANME-3 S7 (**Fig 2.3D**) and introduced it with its cognate synthetase in *M. acetivorans*. However, we were still unable to rescue growth on TMA. Altogether, our heterologous expression platform suggests that only the Pyl biosynthetic machinery derived from ANME-3 S7 is functional in *M. acetivorans*. However, despite retaining the capacity to produce Pyl, it seems unlikely that ANME-3 S7 can incorporate it into proteins.

2.2.4 The amber codon can be read as a stop or as a Pyl residue in Methanosarcina acetivorans

Although Pyl$^+$ genomes have lower TAG usage, it is not clear if this codon has been obligately recoded to Pyl. Our genomic analyses show that *M. acetivorans* exists at an inflection point on the spectrum of Pyl$^+$ genomes (**Fig 2.2D**), which uniquely positions it as a model system to experimentally test for TAG recoding. To this end, we evaluated readthrough versus translational termination at the TAG codon in RdmS, a non-essential Pyl-containing sensor kinase[75,103]. We fused a 1xFLAG tag at the N-terminus of *rdmS* and expressed it *in trans* in either a Δ*rdmS* or a Δ*pylBCD* background. In the latter, RdmS would be obligately truncated at the TAG codon located in its second PAS domain (**Fig 2.4A**). As expected, we only detected this "short-form" protein of approximately 25 kDa by α-FLAG western blot in the Δ*pylBCD* mutant (**Fig 2.4B, Fig S2.8**). In contrast, both the "long -form" and "short -form" of FLAG-tagged RdmS were detected in the Pyl$^+$ Δ*rdmS* background (**Fig 2.4B, Fig S2.8**). Since a UAG codon retains the ability to recruit a release factor for translation termination, even in the presence of Pyl-tRNA^{Pyl}, we searched for genes that might use it as a bona fide stop codon in *M. acetivorans* (see Methods). One candidate is *rnfA*, a membrane integral subunit of the energy conservation complex RNF[108,109]. If TAG is read as Pyl in lieu of a stop, RnfA would have a putative 28 AA C-terminal extension. Yet, *rnfA* homologs across *Methanosarcinaceae* lack the 28 AA C-terminal extension and use either TAA or TGA as a stop codon instead (**Fig S2.9, Table S2.6**), supporting a stop interpretation for TAG in *rnfA* from *M. acetivorans*. Taken together, these data support the hypothesis that the amber codon encodes a dual meaning in *M. acetivorans*.

In the absence of any sequence-specific cues for conditional suppression of the amber codon, we hypothesized that *M. acetivorans* might use the environmental context to dynamically tune the expression of the *pyl* genes i.e. produce more *pyl* transcripts in the presence of

methylamines. Indeed, when we compare the global transcriptome, we observe that all *pyl* genes are substantially upregulated on TMA compared to methanol (**Fig 2.4C**, **Table S2.7**). Interestingly, even in the absence of TMA, *pylTS* is upregulated in the Δ*pylBCD* mutant and vice versa (**Fig 2.4C, Table S2.7**). These transcriptional profiles suggest that the *pyl* genes are dynamically expressed based on the cellular demand for Pyl in both a substrate-dependent and -independent manner.

2.2.5 Archaeal release factor copy number is not correlated with Pyl

Besides the expression of the *pyl* genes, the abundance and/or specificity of the archaeal release factor, aRF1, could, in principle, bias translation termination of the amber codon. A previous study showed that *Methanosarcina barkeri* has two copies of aRF1 and that one of them recognizes all three stop codons *in vitro*[110]. *M. acetivorans* also encodes two copies of aRF1, aRF1-1 (MA_RS00215) and aRF1-2 (MA_RS05270), but their functions have not been investigated. Thus, we reasoned that Pyl^+ archaea might encode more than one aRF1, perhaps with distinct affinities for stop codons and expression levels, which could bias how UAG is decoded. We mapped the distribution of aRFs across all archaea and found that 4.3% of sampled genomes encode two copies of aRF1 (n=81, **Table S2.8**). However, most Pyl^+ genomes with two copies of aRF1 belong to the Genus *Methanosarcina* (**Table S2.8**). Thus, it is likely that the additional aRF1 copy in *Methanosarcina* spp. arose from gene duplication due to lineage-specific genome expansion. Accordingly, we found that aRF1 copy number increases with genome size in archaea (p=2e-21, **Fig S2.10A**), independent of predicted Pyl use (**Fig S2.10B**). Finally, our transcriptomics analyses indicate that the aRF1 genes are constitutively expressed in *M. acetivorans* across all tested conditions (**Fig S2.10C**). While our data do not rule out the possibility for post-transcriptional regulation or differing affinities of aRF1s, it seems unlikely that aRF1 duplications play a universal role in streamlining an ambiguous code in Pyl^+ archaea.

2.3 Discussion

Pyl-based code expansion is a double-edged sword: the Pyl residue enables methylamine-metabolism but also leads to ambiguous interpretation of the amber codon. Here, we outline two co-occurring processes that allow Pyl^+ archaea to maintain Pyl in their proteome. First, the acquisition of *pyl* genes selects for the genome-wide redistribution of stop codons to lower TAG usage (**Fig 2.2**). This process is relatively swift and can be observed in archaea that have recently gained Pyl, like *Hydrothermarchaeum profundi* (**Fig S2.1**), or in archaea that have recently lost Pyl, like ANME-3 S7, which encodes partially functional *pyl* genes (**Fig 2.3D**), or the *Methanosarcina spp.* that have entirely lost *pyl* genes (**Fig 2.2C**). Given the speed and ease at which this process occurs, lowering TAG usage is likely the first step in maintaining Pyl.

Once TAG usage stabilizes, the ability to tolerate ambiguous decoding at all remaining amber codons is essential to maintaining Pyl homeostasis. Using RdmS, a gene with an in-frame TAG codon, we provide evidence that, at least in *M. acetivorans,* the amber codon can be simultaneously read as both a sense and nonsense codon *in vivo* (**Fig 2.4**). These data reinforce previous findings that show the co-existence of the extended and truncated forms of the Pyl-containing monomethylamine-methyltransferases (MtmB) in *Methanosarcina barkeri* MS[102]. Hence, unlike Sec, an ambiguous code is not an evolutionary intermediate but an endpoint in Pyl-mediated genetic code expansion.

To address how an ambiguous code might be tolerated, we present a heuristic model for *M. acetivorans* using our transcriptome data. In the absence of a sequence-specific suppression mechanism, we assume that the likelihood of readthrough and truncation are equal for all UAG-containing transcripts in the cell. Hence, we can define readthrough efficiency for a given UAG-containing transcripts as the ratio of the readthrough rate to the truncation rate, which is proportional to the ratio of Pyl supply and demand in the cell, respectively (see Methods). We can estimate Pyl supply by measuring the abundance of transcripts for the *pyl* genes, and Pyl demand by measuring the total number of UAG-containing transcripts (Eq. 1, see methods, FPKM: fragments per kilobase per million mapped reads):

$$readthrough\ efficiency = \frac{readthrough\ rate}{truncation\ rate} \propto \frac{Pyl\ supply}{Pyl\ demand} \propto \frac{FPKM_{Pyl\ transcripts}}{\sum FPKM_{UAG\ transcripts}} \quad (1)$$

Based on equation 1, the readthrough efficiency is *ca.* two-times higher on methanol than on TMA i.e. there is a higher fraction of the long-form of the protein for all UAG-containing transcripts on methanol than on TMA (**Table S2.9**). At first glance, this outcome might seem counterintuitive, as the cells needs to produce Pyl-containing methylamine methyltransferases on TMA. However, a 4.0-fold increase in expression of the *pyl* genes (i.e. Pyl supply) is far surpassed by the dramatic increase in UAG-containing transcripts (i.e. Pyl demand) on TMA, *ca.* 188.0-fold, primarily due to the upregulation of methylamine methyltransferases (**Fig 2.4C, Table S2.7**). Hence, even though Pyl supply increases during growth on TMA, its demand far outpaces its supply, leading to lower readthrough efficiency (**Fig. 5**).

In our Δ*pylBCD* and Δ*pylTS* knockouts, we eliminate Pyl supply and effectively reduce the readthrough efficiency to zero. Under this regime, we observe that *pylBCD* is upregulated in the absence of *pylTS*, and vice versa, on methanol (**Fig 2.3C**). While the cue(s) leading to an upregulation of the complementary *pyl* genes in the knockout mutants is unknown, we rule out sensing of free Pyl, as the transcriptomes of Δ*pylBCD* and Δ*pylTS* are nearly overlapping (**Table S2.7**). Instead, we hypothesize that these transcriptional changes stem from an inability to incorporate Pyl in a UAG-containing transcript, i.e. by sensing a diminishingly low readthrough efficiency. This artificially low readthrough efficiency, and its resulting transcriptional response, is likely akin to what occurs in wildtype cells upon initial exposure to TMA. Here, the rapid increase in demand for Pyl (due to expression of methylamine methyltransferases) results in a transiently low readthrough efficiency, which is partially recovered by increased expression in *pyl* genes (**Fig 2.5**).

Given the enrichment of TAG codons in genes with proposed regulatory function, one hypothesis for how cells sense readthrough efficiency is through a Pyl-containing repressor that is active when there is readthrough and inactive in its truncated form. In this scenario, high readthrough efficiency on methanol maintains the repressor in its elongated form and partially represses *pyl* genes. In contrast, during growth on TMA, the repressor is prematurely truncated at its UAG site, which results in de-repression of *pyl* genes (**Fig 2.5**). Therefore, when we impose a readthrough efficiency of zero through deletion of either *pylTS* or *pylBCD,* the repressor is fully inactive. This leads to a TMA-like transcriptional response on methanol, complete with upregulation of the remaining *pyl* genes and methylamine methyltransferases (**Fig 2.4C, Table S2.7**). Alternately, other mechanisms like attenuation or transcript stability may play a role in regulation too. It is worth noting that *pylB* has an in-frame TAG codon at the C-terminus. While the functional consequence (if at all) of Pyl in $PylB^{103}$ is unknown, it is tempting to hypothesize that it plays a role in tuning Pyl biosynthesis.

Our model also explains the counterintuitive growth data wherein overexpression of the *pyl* genes is tolerated on methanol but leads to a growth defect on TMA (**Fig 2.3A**). An increase in Pyl supply likely elevates the readthrough efficiency across all growth conditions. This is tolerated on methanol since the readthrough efficiency is already high. In contrast, on TMA, where the readthrough efficiency is low, elevated Pyl incorporation in some UAG-containing transcripts might lead to a buildup of the "long form" of certain proteins that are detrimental to growth.

Altogether, we propose that Pyl^+ archaea, like *M. acetivorans,* are expert funambulists that navigate the tightrope of Pyl homeostasis through transcriptional regulation of Pyl supply and demand. While we cannot rule out unknown mechanisms for sequence-specific Pyl insertion, we show that the ambiguity imposed by its presence can be tolerated successfully.

2.4 Materials and Methods

2.4.1 Bioinformatic screen for Pyl and Pyl-associated genes

All archaeal genomes from GTDB Release 214.0[111] were annotated with Prokka[112] v.1.14.6 using the prokaryotic genetic code 11 to identify homologs of the Pyl biosynthetic genes (*pylBCD*), Pyl incorporation gene (*pylS*), methyl-coenzyme M reductase catalytic subunits (*mcrABG*), component A2, and methylamine-specific methyltransferases (*mttB, mtbB,* and *mtmB*). The Pyl-$tRNA^{Pyl}$ sequences (*pylT*) were predicted in the Prokka pipeline using Aragorn[113], and hits were counted for each genome using a custom script that can be found at https://github.com/kshalv/pyl. Gene identification was performed using a command line tool developed for automated gene searching with profile HMM's (accessions can be found in **Table S2.10**) using the 'hmm' option, as previously described in [[1]14] and can be found at: https://github.com/kshalv/hmm_tools. Pyl^+ genomes were strictly defined as those containing a full suite of biosynthetic genes (*pylBCD*) and incorporation genes (*pylS*, *pylT*). In principle, a genome with just *pylTS* (0.2% of genomes) could be Pyl^+ but there are no known Pyl transporters, so we also classified this group as Pyl^-.

2.4.2 Phylogenetic analyses

Phylogenetic trees depicted in **Fig 2.1C**, **Fig S2.1**, **Fig S2**, and **Fig S2.3** were generated using ete3 and a custom python script to parse the ar53_r214.tree available through Genome Taxonomy Database (GTDB). Genomes with a checkM ≥90% were used for all trees except for Fig S2.1 for which genomes with a checkM completeness scores of ≥80% were used. The CheckM score was calculated using a concatenated biomarker set described in [111]. The trees depicted in all figures, except for Fig S2.3-S2.5, were visualized using iTol v7.1[115]. Genomic neighborhood diagrams for genes +/- 7.5 kb up and downstream of *pylB* in Fig. S2.3 were generated using BioPython and overlaid on the GTDB tree using a custom script found at https://github.com/kshalv/pyl. Amino acid sequences used to generate gene trees for the Pyl biosynthetic and incorporation machinery within the Family *Methanosarcinaceae* were extracted from the corresponding GTDB 214.0 genomes (code 11) using the 'seq' option of the hmm_tools CLI described above with the 'trusted cutoff' threshold. Sequences were aligned using MAFFT and trimmed to 90% with TrimAl. The trimmed alignments were then concatenated using a custom script (https://github.com/kshalv/pyl). Gene trees were generated using the Geneious RAxML plug-in 8.2.11 and GAMMA BLOSUM62 substitution matrix with n_bootstraps=100. The 16S rRNA tree for the Family *Methanosarcinaceae* was generated using an alignment provided in GTDB r214.0 and assembled using the Geneious RAxML 8.2.11 plug-in. Tanglegrams were visualized using Dendroscope

3.5.9[116]. Sequences used to generate methyltransferase gene trees were extracted using the protocol described above from GTDB 214.0 genomes (annotated to code 15, with TAG recoding to Pyl using a custom script (https://github.com/kshalv/pyl). Sequences were dereplicated to 90% sequence identity using MMSeqs2[117] easy-cluster. The tree was built using the Geneious RAxML 8.2.11 plug-in and was rooted to the methanol-specific methyltransferase family in iTol (v 7.1).

2.4.3 Evaluation of stop codon usage and GC content

Stop codon usage was calculated for all genomes available in GTDB 214.0 using BioPython to extract the last three nucleotides of each annotated open reading frame (i.e., "CDS" designation) in the corresponding code 11 Genbank files generated by Prokka's annotation pipeline. Usage for each stop codon was calculated as a fraction of the total number of predicted stop codons and was recorded for each genome. The GC content for each genome was derived from GTDB r214.0 metadata. Taxonomic groups were classified by binning accessions in accordance with the taxonomy designated by GTDB 214.0. All genomes used in this analysis exceeded a checkM genome completeness score of ≥90%. A Welch's t-test was performed for each comparison group depicted in Figure 2 using the scipy.stats Python package.

2.4.4 Identification of putative Pyl-containing proteins

Predictions for putative Pyl containing proteins were performed for each genome predicted to be Pyl^+ based on the presence of 2/3 Pyl biosynthetic genes, the presence of *pylS,* and *pylT*. Each Pyl^+ genome was reannotated using the Blepharisma Nuclear Code (code 15) in Prokka v1.14.6, effectively recoding each TAG codon to Glutamine (Gln, Q). For each genome, we identified putative Pyl proteins using a custom script, where CDS's containing an in-frame 'TAG' codon were defined as putative Pyl proteins. For each Pyl protein, extension length was calculated as the difference between total length of the protein and the 'TAG' position and recorded in a genome-specific CSV file. We recorded the total number of putative Pyl proteins, the average and median extension lengths, and the density of putative Pyl proteins (i.e., normalized Pyl hits per Mb) for each genome. A CDS containing the TAG codon as putative stop codon was identified as a sequence where TAG readthrough results in a >5 AA extension for which there is 1) no predictable domain, and 2) is absent in sequence homologs.

2.4.5 Media and culture conditions

All *Methanosarcina acetivorans* strains were grown without shaking at 37 °C in bicarbonate-buffered high salt (HS) liquid medium containing either 50 mM trimethylamine hydrochloride (TMA) or 125 mM methanol as growth substrates. All growth substrates were added to the medium prior to sterilization, along with NH_4Cl, Cysteine-HCl, and $Na_2S.9H_2O$ to final concentrations of 19 mM, 2.8 mM, and 0.4 mM, respectively. Each strain was grown in a hermetically sealed Balch tube with N_2/CO_2 (80%/20%) in the headspace at 8-10 psi. All *Escherichia coli* strains were grown in lysogeny broth (LB) with antibiotic concentrations of 20 µg/mL chloramphenicol and/or 25 µg/mL kanamycin.

2.4.6 Plasmid construction

Plasmids for Cas9-mediated genome editing were designed using the method previously described in [118]. PCR fragments containing the promoter (P_{mtaCB1}), scaffolds, and terminator (T_{mtaCB1}), were amplified with overhangs containing single guide RNAs (sgRNAs) that target Pyl genes (Δ*pylBCD,* MA_RS00820-MA_RS00810; Δ*pylTS* MA_RS00815). All sgRNAs were designed using the CRISPR site finder tool in Geneious Prime version 2023.2.1 and are provided in **Table**

S2.11. PCR fragments containing the sgRNA scaffold were assembled into pDN201 linearized with *AscI* using the Gibson assembly method described previously in [118]. The repair template was assembled into the sgRNA containing derivative of pDN201 at the *PmeI* site. All complementation constructs were built using either pJK027A or pJK029A as described in **Table S2.11**. PCR fragments containing the genes of interest and if applicable, affinity-purification tags, were fused to the appropriate tetracycline-inducible promoter (**Table S2.11**) by linearizing pJK027A or pJK029A with *NdeI* and *HindIII*. Cointegrates of all plasmids with pAMG40 for expression in *M. acetivorans* were obtained using the Gateway BP Clonase II Enzyme Mix (Thermo Fisher, Waltham, MA, USA) and verified by restriction endonuclease digest. All cloning was performed in WWM4489[119], a DH10B derivative, which was transformed by electroporation at 1.8 kV using an *E. coli* Gene Pulser (Bio-Rad, Hercules, USA), and the growth medium was supplemented with 10 mM Rhamnose to induce copy number as previously described [119]. All plasmids were extracted using Zyppy Miniprep Kit (Zymo Research, Tustin, CA, USA) and verified by Sanger sequencing at the UC Berkeley DNA Sequencing Facility. All primers and plasmids used in this study are listed in **Table S2.11** and **Table S2.12**, respectively.

2.4.7 Methanosarcina acetivorans mutant generation

Liposome-mediated transformation was used to generate *M. acetivorans* mutants as previously described in [120]. Briefly, 20 mL cultures of *M. acetivorans* were grown in HS-Methanol (MeOH) medium until they reached mid-late exponential phase and were harvested for transformation. Transformants were plated and selected for on agar-solidified HS medium with 125 mM MeOH and 2 µg/mL puromycin. Plates were incubated in an intra-chamber anaerobic incubator maintained at 37°C with $N_2/CO_2/H_2S$ (1000 ppm/20%/balance) in the headspace. For all complementation strains, plasmids were screened by PCR and resulting products were verified by Sanger sequencing at the UC Berkeley DNA Sequencing Facility. For deletion mutants, individual colonies were picked and screened at the chromosomal locus using primers designated in **Table S2.12** for the desired mutation. Colonies that were positive for the desired mutation were then streaked on solid HS-MeOH medium with 20 µg/mL 8ADP (Carbosynth, San Diego, CA, USA) to cure the plasmid; single plasmid cured colonies were screened for the absence of the *pac* gene on the mutagenic plasmid with PCR. Chromosomal deletion mutants were sent for whole genome re-sequencing (described below) to screen for the deletion and suppressor mutations elsewhere on the chromosome. All strains used and generated in this study are listed in **Table S2.13**.

2.4.8 DNA extraction and sequencing

Genomic DNA for whole genome re-sequencing of deletion strains was extracted from 10 mL of stationary phase culture of the *M. acetivorans* strain using the Qiagen blood and tissue kit following the manufacturer's instructions (Qiagen, Hilden, Germany). Genomic DNA was sent to SeqCenter (Pittsburgh, PA) where it was further processed using the Illumina DNA Prep kit and sequenced (150 bp paired end reads). Sequencing reads were mapped to the *M. acetivorans* C2A reference genome using breseq[121] version 0.35.5 using default parameters. All mutations identified through this analysis are listed in **Table S2.5**. Illumina sequencing reads for DDN121 (Δ*pylBCD*), and DDN146 (Δ*pylTS*) have been deposited in the Sequencing Reads Archive (SRA) and the project number will be made available upon publication.

2.4.9 Cultivation for growth assays

All growth curves generated for this work were performed by pre-culturing strains in 10 mL HS-MeOH media at 37°C without shaking (HeraTherm General Protocol Microbiological Incubator,

Thermo Fisher Scientific, Waltham, MA, USA) in hermetically sealed Balch tubes with N_2/CO_2 (80%/20%) in the headspace at 8-10 psi. All growth experiments were inoculated with 500 µl of the pre-culture at late exponential phase (OD_{600} ~0.9-1.0). Growth of three independent biological replicates was measured by monitoring the optical density of cultures at 600 nm using a UV-Vis Spectrophotometer (Genesys 50, Thermo Fisher Scientific, Waltham, MA, USA) with an uninoculated "blank" containing 10 mL HS medium with the appropriate growth substrate. All strains harboring a plasmid for gene expression *in trans* also contained 2 µg/mL puromycin in the medium for plasmid maintenance and 100 µg/mL tetracycline for promoter induction. All cultures with tetracycline were wrapped in aluminum foil to prevent degradation over time. Growth rates were calculated as the slope of the linear fit of the log-transformed optical density versus time plot with a minimum five points with the highest R^2 value (minimum cut-off ≥0.95).

2.4.10 RNA extraction, sequencing, and analysis

10 mL cultures of WWM60 (parental strain), DDN121 (Δ*pylBCD*), and DDN146 (Δ*pylTS*) were grown in triplicate on HS + 125 mM MeOH at 37˚C; an additional triplicate set of WWM60 was grown on HS+ 50 mM TMA at g. When cultures reached mid-exponential phase (OD_{600}~ 0.45-0.65), 1 mL culture was removed for RNA extraction and mixed 1:1 with Trizol (Life Technologies, Carslbad, CA, USA) that was pre-warmed to 37˚C. After a five-minute incubation at room temperature, 2 mL of 100% ethanol was added to each sample and RNA extraction was performed according to the manufacturer's instructions using the Qiagen RNeasy Mini Kit (Qiagen, Hilden, Germany). RNA concentration was determined using Nanodrop One UV Spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA) before storage at -80˚C. Samples were sent to SeqCenter (Pittsburg, PA) where each replicate underwent DNase treatment, rRNA depletion, library preparation, and Illumina paired-end sequencing (600 bp read length). Transcriptome analysis was performed using the KBase bioinformatics platform. Raw transcript reads (in FastQ format) were used as an input for read alignment to the *M. acetivorans* C2A reference genome using HISAT2 (v.2.1.0). The resulting read alignment was assembled using Cufflinks (v.2.2.1) and fold changes, significance values were calculated using DESeq2 (v.1.20.0). We considered changes in transcript abundance between pairwise comparison to be significantly differentially expressed if they exceeded a $\log_2$ fold change of ±2.0 and a *q*-value of ≤0.05. All DESeq2 data is recorded in **Table S2.7**. Raw transcript reads for DDN121 and DDN146 have been deposited in Sequencing Read Archive (SRA) and the project number will be made available upon publication; raw transcript reads for WWM60 grown on MeOH and on TMA have been deposited in the SRA.

2.4.11 Immunoblotting of FLAG-tagged proteins

Immunoblotting was performed with cell lysates from a 10 mL culture in HS medium + 125 mM MeOH grown to late-exponential phase (OD600 ~0.9-1.0). For strains harboring plasmids with tetracycline inducible genes, 2 µg/mL puromycin was added to maintain the plasmid and 100 µg/mL tetracycline was added to induce gene expression. Crude cell lysates were prepared from cultures using the method described in [122, 123]. Briefly, the culture was spun down at 5,000 x *g* at 4˚C for 10 minutes using the Sorvall Legend XTR centrifuge (Thermo Fischer Scientific, Waltham, MA, USA). The culture supernatant was decanted, and the pellets were resuspended in 200 µL lysis buffer (50 mM Na_2HPO_4) and kept on ice for ten minutes prior to adding 1 µL of DNase along with 12 µl 5M NaCl. After mixing gently, the lysate was stored at room temperature for two minutes prior to centrifugation at 14,000 x *g* for ten minutes twice to obtain cleared lysate. Near-equal loading of 30 µg of protein was estimated using Bradford reagent (Sigma-Aldrich, St

Louis, MO) with bovine serum albumin (BSA) standards per the manufacturer's instructions. Cell lysates were run on a 12% mini-Protean TGX Gels (Bio-Rad, Hercules, USA) and transferred to a Trans-Blot Turbo Mini 0.2 μM PVDF membrane using the Bio-Rad Trans-Blot Turbo Transfer System (Bio-Rad, Hercules, USA). FLAG-tagged proteins were probed by immunoblotting using monoclonal anti-FLAG M2-Peroxidase (HRP) antibody (Sigma-Aldrich, St Louis, MO, USA) at a 1/50,000x dilution. Subsequent signal detection was performed using Immobilon Western Chemiluminescent HRP Substrate (Millipore, Burlington, MA, USA). Imaging was performed with ChemiDoc MP Imaging System (Bio-Rad, Hercules, CA, USA) with a 1 second exposure time. Imaging was also performed with a 13.5 second exposure time and a paper towel occluding the high molecular weight portion of the gel to gain better resolution of the short form RdmS bands in **Fig 2.4**. Coomassie blue dye (Thermo Fisher, Waltham, MA, USA) was used to evaluate near-equal loading of all cell lysates. All blots and Coomassie stained gel images are available in **Fig S2.8**.

2.4.12 Readthrough efficiency calculation

We generated Eq. 1 by representing the rates of readthrough and truncation for the cellular proteome assuming second order kinetics as described in Eqs. 2 and 3. The rate of readthrough of any UAG codons in the cell depends on the concentration of Pyl-tRNA^{Pyl}, the number of UAG-containing transcripts, and the rate constant $k_{readthrough}$ as shown in Eq. 2. The rate of truncation of any UAG codon is a function of archaeal release factor (aRF1) concentration, the number of UAG-containing transcripts, and the rate constant $k_{truncation}$ as shown in Eq. 3.

$$\frac{d[readthrough]}{dt} = k_{readthrough}[Pyl \cdot tRNA^{Pyl}][UAG\ transcript] \quad (2)$$

$$\frac{d[truncation]}{dt} = k_{truncation}[aRF1][UAG\ transcript] \quad (3)$$

The rate of change of Pyl-tRNA^{Pyl} can be described by:

$$\frac{d[Pyl \cdot tRNA^{Pyl}]}{dt} = k_{production}[Pyl][tRNA^{Pyl}] - k_{readthrough}[Pyl \cdot tRNA^{Pyl}][UAG\ transcript] \quad (4)$$

Where the first term on the right side of Eq. 4 represents the rate of production of Pyl-tRNA^{Pyl} and is dependent on the concentration of free pyrrolysine [Pyl], the uncharged tRNA^{pyl} [tRNA^{pyl}] and the rate constant $k_{production}$. The second term on the right represents the rate of consumption of Pyl-tRNA^{Pyl} due to readthrough of a UAG codon (i.e. the readthrough rate, Eq. 2). If we assume steady state concentrations of Pyl-tRNA^{Pyl} during growth on a given substrate then the production and consumption of Pyl-tRNA^{Pyl} are balanced, i.e.:

$$k_{production}[Pyl][tRNA^{Pyl}] = k_{readthrough}[Pyl \cdot tRNA^{Pyl}][UAG\ transcript] \quad (5)$$

To determine the readthrough efficiency, we take the ratio of the readthrough rate—equivalent to the production rate in steady state (Eq. 5)—over the truncation rate (Eq. 3), yielding Eq. 6.

$$readthrough\ efficiency = \frac{readthrough\ rate}{truncation\ rate} = \frac{Production\ rate}{k_{truncation}[aRF1][UAG\ transcript]} \quad (6)$$

Since we observe that aRF1 transcription does not significantly change between MeOH and TMA growth conditions (**Fig S2.10C**, **Table S2.7**), we assume $k_{truncation}$[aRF1] remains constant and find that:

$$\frac{readthrough\ efficiency\ (MeOH)}{readthrough\ efficiency\ (TMA)} \propto \left(\frac{Production\ rate\ MeOH}{Production\ rate\ TMA}\right) \times \left(\frac{[UAG\ transcript]\ TMA}{[UAG\ transcript]\ MeOH}\right) \quad (7)$$

We refer to the Pyl-tRNA^{Pyl} production rate as the "Pyl supply" and estimate this value to be proportional to the FPKM (fragments per kilobase per million mapped reads) of the *pyl* genes for a given condition. We refer to the concentration of UAG transcripts as the "Pyl demand" and estimate it as the sum FPKM values for transcripts containing a UAG, using gene IDs identified in our Pyl ID script, for a given condition. This leads us from Eq. 7 to the relationship represented in Eq. 1 and illustrated in **Fig. 2.5**. This heuristic model for readthrough efficiency allows us to compare the ratio of Pyl-containing proteins to their truncated counterparts without quantifying the precise proportion of readthrough to truncation in any single condition. All FPKM values can be found in **Table S2.10**, along with the calculations used to determine ratio of readthrough efficiencies between substrates.

2.4.13 Data and code availability

Raw Illumina reads associated genome-wide DNA and RNA sequencing have been deposited to the Sequencing Reads Archive (SRA) and the project number will be made available upon publication. All custom scripts described can be found at the following repository: https://github.com/kshalv/pyl.

2.5 Figures

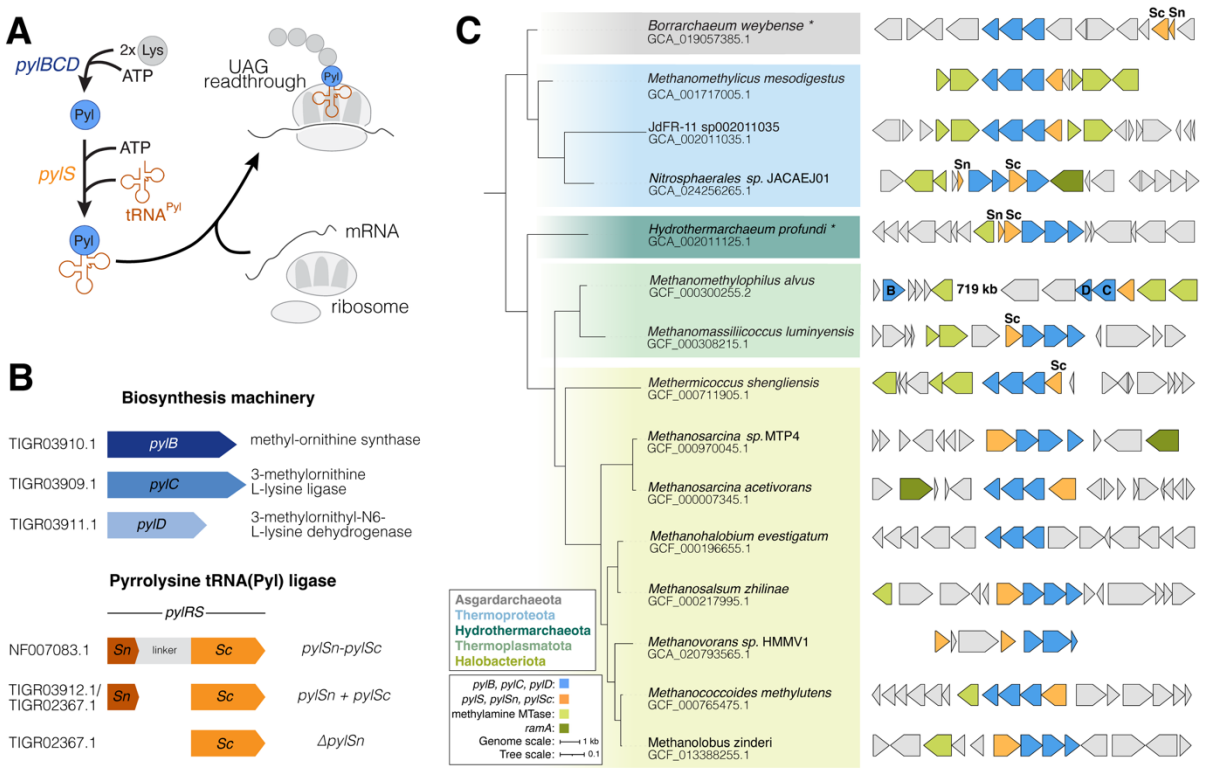

Figure 2.1. Distribution of Pyrrolysine (Pyl) in archaea. **A)** Proposed mechanism for Pyl biosynthesis (blue), and incorporation (orange) into elongating polypeptides by a Pyl-tRNA^{Pyl} charged by its cognate aminoacyl tRNA synthetase (PylS). **B)** Pyl^{+} archaea were annotated based on the presence of the biosynthesis genes encoded by *pylBCD* (in blue) and the Pyl aminoacyl tRNA synthetase (PylS; in orange). Genes and their corresponding Hidden Markov Models (HMM's) accessions used for the bioinformatic survey are shown. Domain architecture and class distinctions are noted for each of the *pylS* classes. **C)** Pyrrolysine biosynthesis (blue) and incorporation (orange) genes and their genome neighborhood (±7.5 kb of *pylB,* unless otherwise noted) across different Phyla of Pyl^{+} archaea. The genome accession number is provided below the strain names. The corrinoid reductive activase *ramA* (dark green) and methylamine methyltransferases (light green) that often co-occur with the *pyl* genes are indicated. Strains denoted with an asterisk lack genes involved in methane metabolism. **Pyl:** pyrrolysine; **MTase**: methyltransferase; ***pylB****:* methyl-ornithine synthase; ***pylC****:* 3-methylornithine L-lysine ligase; ***pylD****:* 3-methylornithyl-N6-L-lysine dehydrogenase; ***pylS***: pyrrolysine tRNA(pyl) ligase; ***ramA****:* corrinoid protein reductive activase.

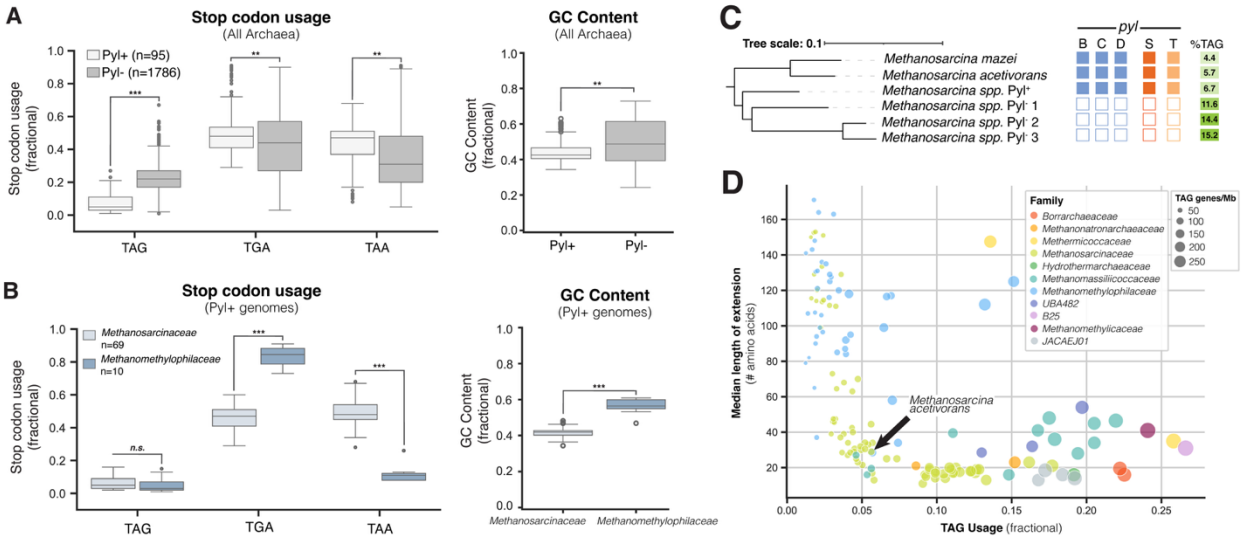

Figure 2.2. Stop codon usage in response to Pyl-mediated genetic code expansion. **A)** Box and whisker plots of stop codon usage and GC content in Pyl^+ (light gray) and Pyl^- (dark gray) genomes within the archaea. **B)** Box and whisker plots of stop codon usage and GC content in Pyl^+ genomes within the *Methanosarcinaceae* (light blue) and *Methanomethylophilaceae* (dark blue). Stop codon usage was calculated as fraction of total stop codons in protein encoding genes. All statistical tests for panels A and B were performed using Welch's t-test (***p<1.0e-10, **p<1.0e-5, ***n.s.*** not significant). **C)** TAG usage in select *Methanosarcina* strains. The presence of a given gene is indicated by a filled-in square corresponding to the gene noted above the box; %TAG usage is indicated by the opacity of green box and denoted numerically. *Methanosarcina spp.* accessions are as follows: Pyl^+: GCA_00171414685.2; Pyl^-1: CA_017883485.1; Pyl^-2: GCA_003157235.1; Pyl^-_3: GCA_003164755.1 **D)** Genome-specific traits of Pyl^+ archaea. A graph showing the relationship between the fractional TAG usage and the median extension length (# of amino acids) of putative Pyl-encoding proteins. The size of the genome dot indicates the relative abundance of putative Pyl containing genes (genes/Mb). The Family-level taxonomy is indicated by the color of the genome dot, and *Methanosarcina acetivorans* is indicated with the black arrow.

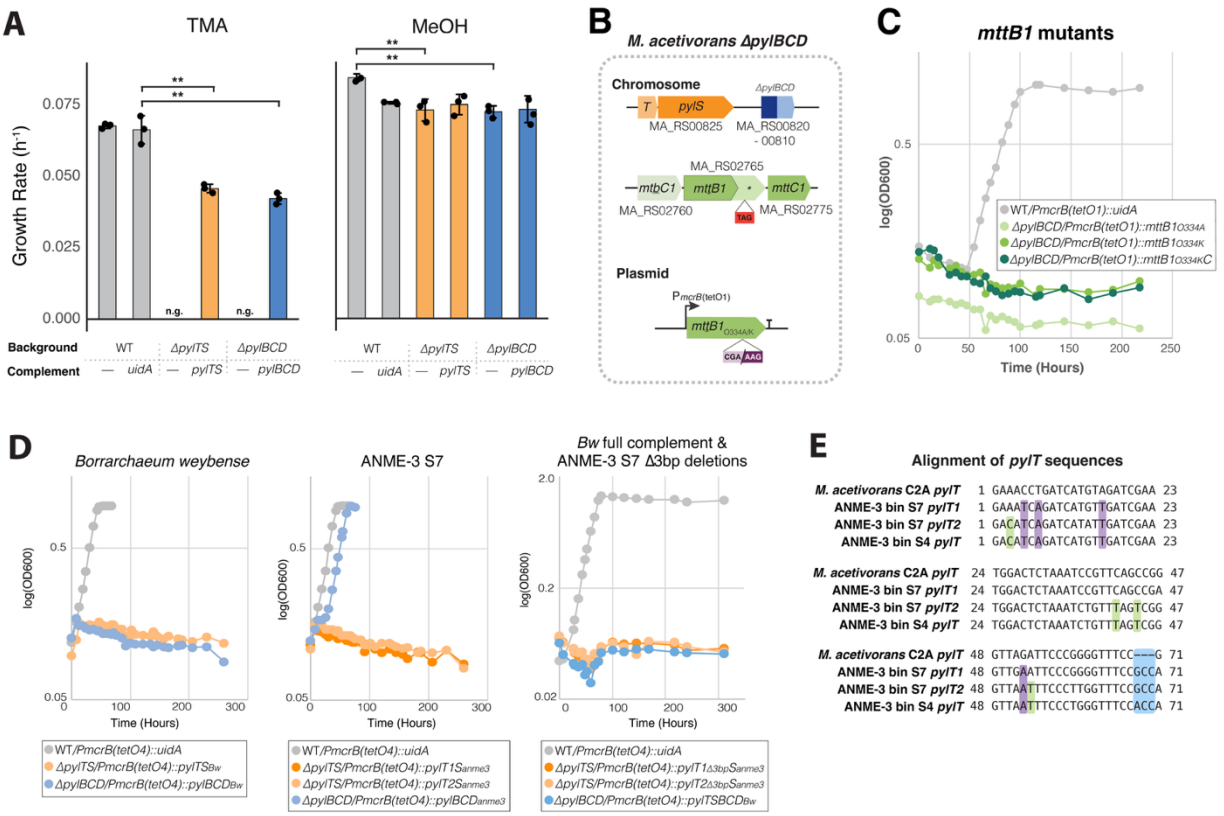

Figure 2.3. Heterologous expression of *pyl* genes from uncultivated archaea in *Methanosarcina acetivorans*. **A)** Growth rates of the parent strain (WWM60, denoted as wildtype or WT; in gray), the Δ*pylTS* (in orange), Δ*pylBCD* (in blue) mutants and the corresponding complementation strains in minimal media with either trimethylamine (TMA) or methanol (MeOH). In the WT strain, a control gene (*uidA)* was expressed from the tetracycline inducible promoter (P*mcrB*(*tetO1*)) on a plasmid like the genes complemented in *trans.* A two-sided t-test with unequal variances was used to compare mean growth rate from three biological replicates (**p<0.005). Error bars represent the standard deviation of three replicates. **B)** Diagram representing the genomic background for *mttB1* point mutation experiments. In the Δ*pylBCD* background, the chromosomal copy of *mttB1* is maintained, but TAG is obligately read as a stop codon due to the absence of Pyl biosynthesis machinery. A point mutated form of *mttB1* is complemented *in trans* under the control of the tetracycline inducible promoter, P*mcrB*(*tetO1*). **C)** Growth of WT with a control gene (*uidA*; in gray) or the Δ*pylBCD* strain with the *mttB1* point mutants (in green) after transferring MeOH-grown cells into TMA. **D)** Growth of strains expressing *pyl* genes from *Borrarchaeaum weybense* or ANME-3 bin S7 (including Δ3bp deletion in *pylT).* Complements were expressed *in trans* under a tetracycline-inducible promoter (P*mcrB*(*tetO4*)) as indicated. WT with a control gene (*uidA*) are shown in gray. **E)** Alignment of *pylT* sequences from two members of ANME-3 (bin S7 and bin S3) with *M. acetivorans*. Blue box highlights the 3 bp insertion identified and deleted in panel D. Purple box highlights point mutations shared amongst all ANME *pylT* sequences. Green box highlights point mutations shared between S7 *pylT2* and S3 *pylT.* In panels A, C, and D, all strains bearing a plasmid for expression were cultivated with puromycin to maintain the plasmid and 100 µg/ml tetracycline to induce full expression of the complement from the tetracycline-inducible promoter. All growth curves shown are representative curves of triplicate curves.

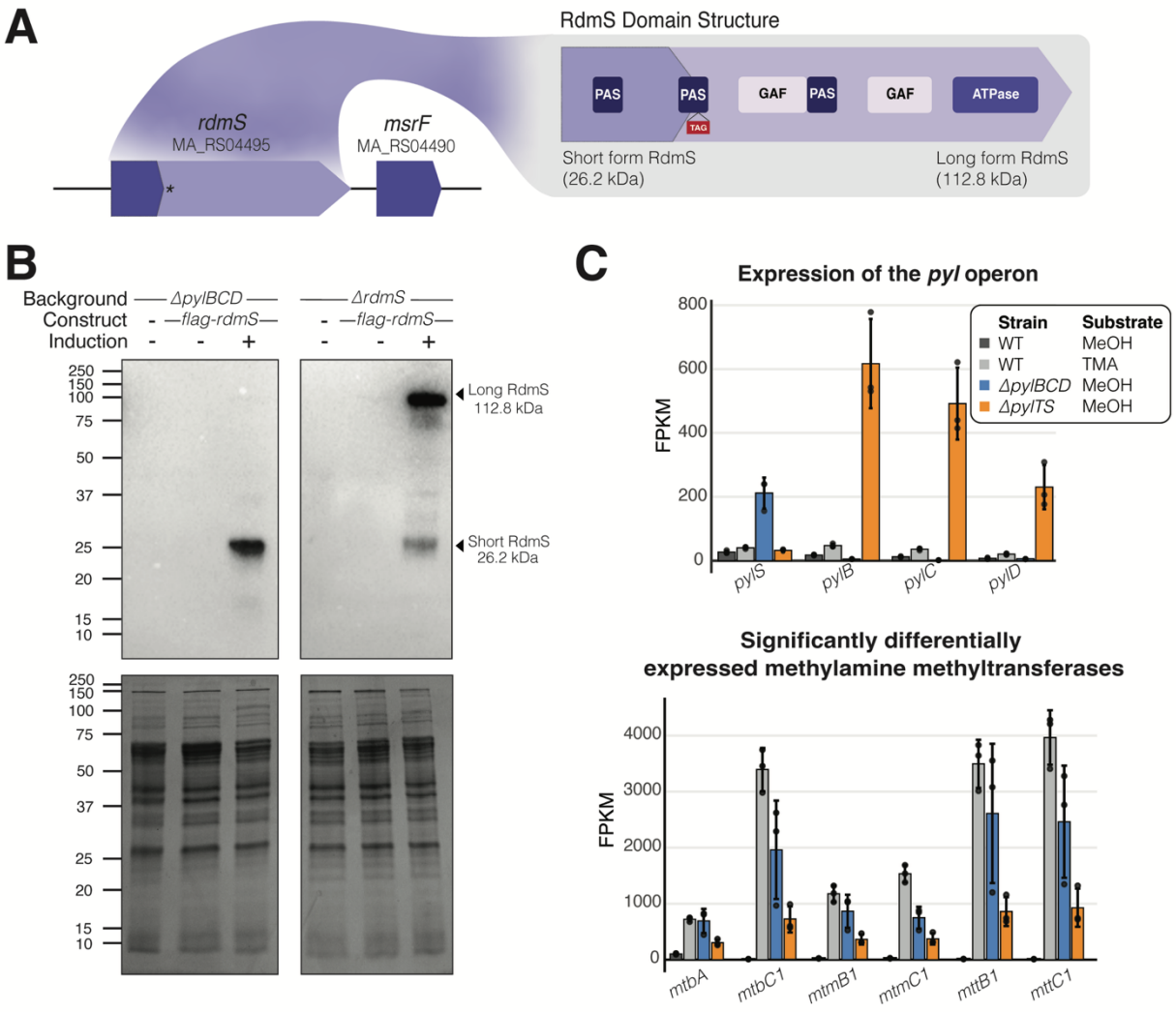

Fig 2.4. The amber codon can be interpreted as a stop codon or Pyl in *Methanosarcina acetivorans*. **A)** Diagram of RdmS domain structure and genomic organization. RdmS is a predicted sensor kinase located upstream of *msrF*[73], a Msr (methanol-specific regulator) family protein likely involved in the regulation of methylsulfide methyltransferases. Asterisk and TAG box indicate the location of the Pyl residue, where truncation would result in a ~26.2 kDa protein. **PAS: P**er-**A**rnt-**S**im domain; **GAF:** c**G**MP-specific phosphodiesterases, **A**denylyl cyclases and **F**hlA; **ATPase**: **ATP** hydrolyzing domain. **B)** α-FLAG western blot for a N-terminal 1xFLAG translational fusion of *rdmS* expressed *in trans* from tetracycline inducible promoter, P*mcrB*(*tetO4*). Induction is indicated as no induction (-) at 0 µg/ml tetracycline or maximum induction (+) at 100 µg/ml tetracycline. Coomassie stained SDS-PAGE gels shown beneath western blot as loading control. **C)** FPKM values of the *pyl* genes (top) and methylamine methyltransferase genes (bottom) in the Δ*pylBCD* mutant on methanol (MeOH) (blue), Δ*pylTS* mutant on MeOH (orange), WWM60 (parent strain also referred to as wildtype or WT) on MeOH (light gray) or trimethylamine (TMA) (dark gray). Error bars represent the standard deviation amongst plotted FPKM values for three replicates. The DESeq2 data can be found in Table S2.8.

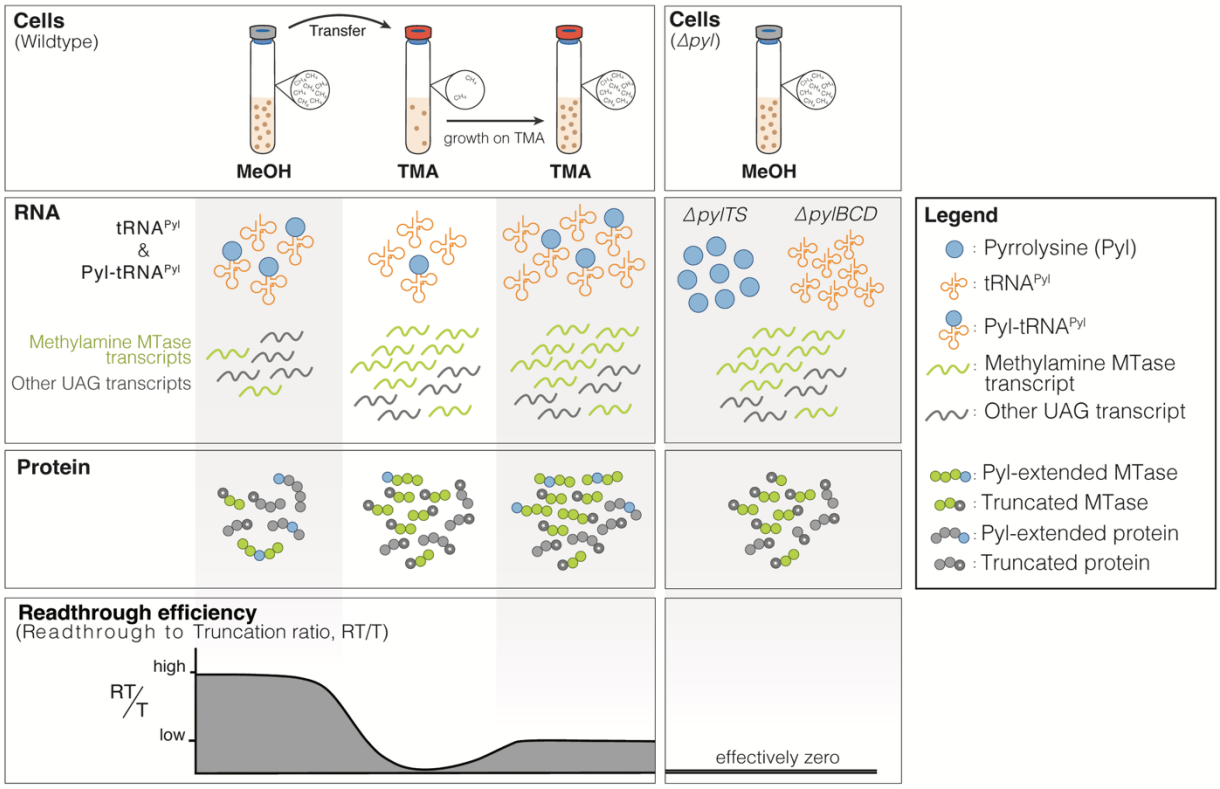

Fig 2.5. A model for Pyrrolysine (Pyl) homeostasis in *Methanosarcina acetivorans*. During growth on methanol (MeOH), the pool of UAG-containing transcripts is lower, leading to the higher readthrough efficiency (RT/T, bottom panel). We hypothesize that as cells switch from MeOH to trimethylamine (TMA), they encounter a transient state wherein the expression of methylamine methyltransferases (MTase) increases rapidly and Pyl demand outpaces its production. As a result, the readthrough efficiency transiently decreases. This decrease in RT/T likely leads to an increase in expression of *pyl* genes, and methylamine MTases, however, because the MTases have an outsized contribution to the total UAG transcript pool, MTase transcripts effectively outcompete other UAG transcripts for Pyl. We suggest our *pyl* knockouts have a readthrough efficiency that is close to zero and that they respond to this by upregulating the *pyl* genes as well as the methylamine-specific MTases as seen in **Fig 2.4C**.

3. Probing the regulatory role of RdmS, a putative Pyl-responsive sensor kinase

In this chapter, I present a series of experiments focused on understanding whether RdmS, a sensor kinase with an internal TAG residue, functions as a Pyl-responsive regulator in *Methanosarcina acetivorans*. Through complementation assays, western blots, and transcriptomics, we demonstrate that RdmS is likely not the primary regulatory protein through which Pyl-responsive physiology is mediated. We close by identifying other TAG-containing genes with regulatory function that could putatively act as a sensor module for readthrough efficiency.

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Abstract

Pyrrolysine (Pyl), the 22nd proteinogenic amino acid, is essential to methanogenic growth on methylamines. The incorporation of Pyl into methylamine-specific methyltransferases is critical for the catalytic function of these enzymes, which facilitate methyl-transfer into the core methanogenic pathway. While Pyl's catalytic role during growth on methylamines is well-mapped, its role in the physiology and regulation of methanogenesis during growth on other substrates, like methanol, is poorly understood. In previous work, we posit that UAG sites represent a translational fork, where competition between the Pyl-tRNA^{Pyl} and archaeal release factor result in one of two outcomes: elongation and truncation, respectively. Here, we investigate the hypothesis that the balance between the two protein forms resulting from this competition (elongated and truncated) affects whole cell regulation. Our work focuses on a dissecting the contribution of a Pyl-containing sensor kinase, called RdmS, to the growth and transcriptome of *Methanosarcina acetivorans* during growth on methanol. While our results demonstrate that RdmS is unlikely to behave as a Pyl-responsive regulatory protein, we identify additional Pyl-containing candidate genes for future work and contextualize our results with the broader cellular role of RdmS in *M. acetivorans.*

3.1 Introduction

Natural genetic code expansions are an evolutionary innovation that can unlock novel catalytic mechanisms[86]. Natural code expansions involve co-option of a stop codon, i.e. the amber (UAG/TAG) or opal codon (UGA/TGA), to encode an amino acid outside of the standard twenty. Pyrrolysine (Pyl) is emblematic of this kind of cellular innovation. First discovered in the active site of monomethylamine methyltransferases belonging to *Methanosarcina barkeri*, Pyl has since been irrevocably tied to methanogenic growth on methylamines. Several data support this assertion: 1) Pyl is essential during growth on methylamines[97,124], 2) *pyl* genes strongly co-occur with those for methylamine methanogenesis[124], and 3) Pyl activates methylamines for methyl transfer[89]. While Pyl's essentiality to methylamine methanogenesis is well-described, the growth defect that we and others[103] observe for *Methanosarcina acetivorans pyl* mutants during growth on Methanol (MeOH) is less understood. In the previous chapter, we demonstrate that Pyl's incorporation into polypeptides involves competition between the charged Pyl-$tRNA^{Pyl}$ and the archaeal release factor (aRF1). This manifests in cellular readthrough efficiency, defined as the propensity to incorporate Pyl into elongating polypeptides at UAG sites. We posit that readthrough efficiency may act as a sensory cue in the regulation of substrate-specific transcriptional responses, via Pyl incorporation into proteins with regulatory function (**Fig 3.1)**. We hypothesize that deviation from the native readthrough efficiency under *pyl* deletion produces the MeOH growth defect.

Previous work[103] demonstrated that deletion of the $tRNA^{Pyl}$ induces dysregulation of the proteome during growth on methanol (MeOH). Proteomic dysregulation manifests in the upregulation of methylsulfide methyltransferases concomitant with downregulation of proteins involved in translation initiation, amino acid metabolism, and methanogenesis[103]. Our work indicates that rearrangement of the proteome under *pyl* deletion co-occurs with transcriptional changes that are conserved between both Pyl biosynthetic (Δ*pylBCD*) and incorporation (Δ*pylTS*) knockouts. We interpret the substantial overlap in transcriptome between these mutants to mean that the inability to incorporate Pyl into elongating polypeptides, rather than the absence of cellular Pyl, drives cellular dysregulation during growth on MeOH. While the phenotype of genetic code collapse is well-established, the underlying mechanism and genes (if any) that contribute to this dysregulation remains unmapped.

Genomic work indicates that TAG codons, or putative Pyl residues, are enriched in genes annotated with regulatory function[103]. Moreover, several of these genes have been experimentally demonstrated to incorporate Pyl in their coding sequences. This includes RdmS (MA_RS04495, MA_0863), a sensor kinase with an in-frame Pyl residue in its second PAS domain (see, **Fig 2.4**). Since its first demonstration as a Pyl-protein, *in vitro* work has mapped its biochemical characteristics, autophosphorylation at a tyrosine residue[75]. Interestingly, RdmS putatively interacts with MsrF, a response regulator that activates expression of the methylsulfide methyltransferase, *mtsD*[75]. Indeed, we observe significant upregulation of *msrF*, concurrent with *mtsD* upregulation, under *pyl* deletion (**Fig S3.1**). Given these data, we tested the hypothesis that RdmS behaves as a sensory cue for readthrough efficiency in *Methanosarcina acetivorans*: under low readthrough efficiency (growth on TMA), RdmS is truncated, and under high readthrough efficiency (growth on MeOH), RdmS is elongated. In this chapter, we demonstrate that *rdmS* is dispensable for growth on these substrates and that complementation of Δ*pylBCD* with a constitutively long-form does not complement for the transcriptional dysregulation we observe, ruling it out as sensory candidate.

3.2 Results

*3.2.1 Δrdm*S *does not produce a growth defect across diverse substates*

While substantial work has been done to characterize whole cell physiological responses to *pyl* deletion[103], none have directly tested genetic components beyond the *pyl* genes themselves that could contribute to the growth defect observed during growth on methanol (MeOH). Conceivably, the deletion of *pyl* genes (either the biosynthetic, *pylBCD*, or incorporation, *pylTS* machinery) collapses the cellular genetic code from 21 to 20 amino acids and restricts readthrough of all UAG-containing transcripts, resulting in premature translational termination for these proteins. For instance, during growth on TMA, the inability to incorporate Pyl in elongating polypeptides of the methylamine-specific methyltransferases likely drives the lethal growth phenotype on this substrate. In contrast, it is unknown which, if any, of the upwards of two-hundred TAG-containing genes in *Methanosarcina acetivorans* (**Table S3.1**) might contribute to the MeOH growth defect that we and others observe.

Two lines of evidence led us to hypothesize that a putative Pyl-containing regulatory protein, like a sensor kinase or response regulator, might contribute to the reduced growth rate we and others observe for Δ*pyl* strains on MeOH. First, genomic and proteomic work has demonstrated that Pyl is enriched in substrate-sensing histidine kinases and may have been selectively maintained in this group of proteins[103]. Second, we observed substantial dysregulation of the cellular transcriptome for both Δ*pylBCD* and Δ*pylTS* strains when cultivated on MeOH (**Fig S3.1**). Within this group of differentially expressed genes (n=37, **Fig S3.1**), we observed a substantial reduction in expression of the expression of *msrF*, a positive regulator methylsulfide-specific methyltransferases that is located directly downstream of a *rdmS,* a Pyl-containing sensor kinase. Pyl is located in the second PAS domain of RdmS, where truncation conceivably produces a short-form product that is unable to transmit its sensed signal.

To test the role that RdmS plays in *M. acetivorans*, we assayed growth of a Δ*rdms* deletion strain in tandem with its parental strain (WWM60; Wildtype, hereafter) across routine growth substrates used in the cultivation of *M. acetivorans.* Based on whole genome resequencing, the Δ*rdmS* strain lacked off-target effects or suppressor mutations (**Table S3.2**). We observed that during growth on either MeOH or trimethylamine (TMA), the Δ*rdmS* strain lacked a replicable phenotype (**Fig 3.2, Table 3.1**). While it appears that expression of the wildtype *rdmS* complement under full induction of the tetracycline-inducible promoter (P*mcrB*(tetO4)) reduces growth rate on TMA, the observed growth rate does not vary substantially from that of the expression control strain (**Fig 3.2, Table 3.1**). Since the Δ*rdmS* strain does not phenocopy the Δ*pylTS* or Δ*pylBCD* strain during growth on MeOH, it is unlikely that truncation of RdmS is causal to the MeOH growth defect we observe for Δ*pyl* strains.

3.2.2 Complementation with diverse RdmS *forms produces a growth defect on MeOH*

In tandem with our initial growth experiments, we sought to understand whether engineered truncations of RdmS might affect its growth on MeOH. To this end, we complemented Δ*rdmS* with alternate forms of *rdmS* (**Fig 3.3A**), in which 1) all sensory domains are maintained (i.e., sensor, or signal perception), 2) the putative ATPase domain (i.e., ATPase) is maintained, or 3) it is locked into its truncated, short form at its internal TAG codon (i.e.,

truncation). Each complement was expressed off the tetracycline-inducible promoter (PmcrB(tetO4)) at maximum induction.

We limited our growth assays to MeOH only, as we initially hypothesized that RdmS function would be most affected by *pyl* deletion due to the relatively lower readthrough efficiency for TAG codons on MeOH compared to TMA. In line with our previous observations, neither Δ*rdmS* nor its wildtype complemented form produce a substantial defect. Similarly, the signal domain complement maintains a near wildtype growth rate (**Fig 3.3B**). In contrast, expression of the ATPase and the truncation forms of *rdmS* produce a substantial growth defect (**Fig 3.3B**). Yet, it is worth noting that for both strains, the observed growth defect has substantial range between biological replicates in the same experiment (**Fig 3.3B**) and thus the growth defect is not significant between any pairwise comparisons of strains.

3.2.3 Constitutively long-form RdmS *does not induce notable transcriptional changes*

In previous work, we demonstrate that both our Δ*pylBCD* and Δ*pylTS* strains, which are pre-grown on MeOH, have transcriptional profiles like that of Wildtype cells pre-grown on TMA. It follows that deletion of either the Pyl biosynthetic or incorporation machinery results overrides the substrate-specific regulatory control of certain genes, like methylamine methyltransferases, resulting in a whole cell transcriptional response akin to that of growth on TMA. We hypothesized that RdmS might contribute to this cellular response: when Pyl is incorporated at its TAG residue, the protein is read through and functional, whereas when RdmS is truncated at its TAG residue (i.e., in a Δ*pylBCD* background), it is prematurely truncation. To test whether the form of RdmS acts as a detection module for the transcriptional response we observe in Δ*pylBCD*, we complemented this strain with a constitutively long form of *rdmS* where the Pyl residue is point mutated to Lysine ($rdmS_{O216K}$). Subsequently, we performed RNA-Seq of cells pre-grown on MeOH and compared their transcriptional profile to that of Δ*pylBCD.* Our transcriptomic work reveals that 70 genes are significantly changed in expression ($q<0.01$ and $-2.5 \leq \log_2\text{fold change} \geq 2.5$) in a comparison of the Δ*pylBCD/*P*mcrB*(tetO4)-$rdmS_{O216K}$ strain to Δ*pylBCD* (**Table S3.3**). While many genes are changed in expression, these are primarily small hypothetical proteins located near transposases. The most notable transcriptional changes that we observe in Δ*pylBCD* alone (i.e., methylamine methyltransferases) are conserved with the $rdmS_{O216K}$ strain (**Fig 3.4**). Taken together, we conclude that complementation with the constitutively long form of *rdmS* in unable to return Δ*pylBCD* to its native transcriptional profile during growth on MeOH.

3.2.4 Identification of candidates for future work

Our experimental data indicates that RdmS is unlikely to behave as a sensor for readthrough efficiency under the cultivation conditions that we tested. Given that we rule out RdmS as a Pyl-responsive sensor under TMA and MeOH growth conditions, we sought to identify additional candidates that may contribute to the detection of readthrough efficiency. We parsed our UAG-containing protein predictions (**Table S3.1**) for sequences with putative regulatory function and predicted their domain topology using Interpro (**Table 3.2)**. We classified these sequences as three "types" of UAG-containing proteins those with: 1) C-terminal UAG extensions, 2) internal UAG's, and 3) new UAG-based fusions. Of the seventeen candidate proteins, readthrough of UAG as Pyl in five of these sequences (excluding RdmS) produce predictable domains downstream of the UAG codon (**Table 3.2**). In three genes—MA_RS12290, MA_RS07955, and MA_RS25720)—Pyl readthrough at UAG putatively enables translation of

transcriptional repressor, helix-turn-helix, or C-terminal dimerization domains, respectively (**Table 3.2**). MA_RS25720 is an enticing candidate as it contains an internal UAG, where truncation would likely result in a partial loss of functionality. Given that dimerization at the C-terminal domain of TetR family repressors, like MA_RS25720, is thought to influence ligand binding[125], truncation at the UAG codon could possibly render the MA_RS25720 gene product non-functional.

3.3 Discussion

It is well-established that Pyrrolysine is closely tied to methylamine methanogenesis, yet its physiological role during growth on other substrates, like methanol, is less well defined. Here, we tested whether a Pyl incorporation in a TAG-containing sensor kinase, called RdmS, behaves as a cue for readthrough efficiency during growth on methanol. Under all the conditions tested, we were unable to discern a significant growth defect for the deletion of *rdmS*. While we are unable to rule out that its deletion carries a defect under cultivation conditions yet tested (i.e. alternate growth substrates, substrate-depletion, etc.), our results indicate that RdmS is unlikely to behave as the sensor module for readthrough efficiency in *M. acetivorans*. This assertion is supported by our growth data for domain truncations of *rdmS* complemented in the Δ*rdmS* background. While the $rdmS_{ATPase}$ and $rdmS_{truncation}$ complements produced a notable growth defect, neither were significantly different from the $rdmS_{WT}$ complement, likely due to the substantial range in observed growth rates. It is possible that the observed growth defect for these strains is due to expression of non-functional protein segments, like the constitutively truncated RdmS form. To account for regulatory mechanisms not captured by growth rates alone, we performed RNA-Seq on both Δ*pylBCD* and Δ*pylBCD* expressing a constitutively long-form *rdmS,* $rdmS_{O216K}$, and compared the transcriptomes in both. We observed that the constitutively long-form *rdmS* was unable to restore the wildtype transcriptome during growth on MeOH. Instead, we observe the predominant Δ*pylBCD* type transcriptome, characterized by its similarity to that of wildtype cells grown on TMA.

Although we rule out truncation of RdmS as causal to the transcriptional and proteomic dysregulation that we and others observe in *pyl* mutants, our work offers additional insight into RdmS functionality *in vivo.* For instance, our growth data constrains the range of substrates under which RdmS is affects growth by ruling out MeOH and TMA. In our transcriptomic data, we observe that both *mtsH* and *mtsF* are significantly upregulated upon complementation of constitutively long *rdmS* ($rdmS_{O216K}$) in the Δ*pylBCD* background, indicating that there may be regulatory crosstalk in the expression of methylsulfide methyltransferases, as previously suggested[126]. Future work may further address the *in vivo* role of *rdmS* in a context agnostic of Pyl and directly assay its functionality under methylsulfide cultivation.

While our work rules out RdmS as a Pyl-responsive regulatory protein, there are several additional UAG-containing regulatory proteins that may serve as candidates for future work. As noted, MA_RS25720, annotated as a TetR family repressor, is a particularly interesting candidate. In this gene, truncation at the UAG codon by aRF1 terminates translation ahead of its C-terminal domain. The function of the C-terminal domain in TetR family proteins varied[127], but has been demonstrated to enable DNA binding[128]; thus, it stands to reason that UAG truncation could potentially abrogate MA_RS25720 function. Indeed, this functionality is more closely aligned with the model put forth in Chapter 2 (**Fig 3.4**). Under this regime, truncation of a

repressor results in de-repression of both the *pyl* operon and methylamine methyltransferases, driving their overexpression in both Δ*pylBCD* and Δ*pylTS* knockouts during growth on MeOH. Future work addressing the functionality of this protein in context of Pyl-mediated regulation may better resolve the growth defect observed under MeOH cultivation.

3.4 Materials and Methods

3.1.1 Media and culture conditions

M. acetivorans strains were grown in bicarbonate-buffered high salt (HS) liquid medium containing 125 mM methanol or 50 mM trimethylamine as growth substrates, without shaking at 37 °C. All growth substrates were added to media prior to sterilization. Similarly, NH_4Cl, Cysteine-HCl, and $Na_2S.9H_2O$ to final concentrations of 19 mM, 2.8 mM, and 0.4 mM, respectively. Each strain was growh in a hermetically sealed Balch tube, where the headspace was adjusted to 8-10 psi with N_2/CO_2 (80%/20%). *Escherichia coli* strains were grown in lysogeny broth (LB) with antibiotic concentrations of 20 µg/mL chloramphenicol and/or 25 µg/mL kanamycin.

3.1.2 Strain generation and plasmid construction

M. acetivorans Δ*rdmS, ΔpylBCD, and* Δ*pylTS* strains were generated in previous studies[124,129]. We acknowledge and thank Dr. Lopez-Munoz and Dr. William Metcalfe for sharing the *M. acetivorans* Δ*rdmS* strain for our use. All complementation strains were generated by Gibson assembly of PCR fragments to the PmcrB(tetO4) promoter in pJK029A, linearized with *NdeI* and *HindIII*. Cointegrates of all plasmids with pAMG40 were generated using Gateway BP Clonase II Enzyme Mix (ThermoFisher, Waltham, MA, USA) for expression in *M. acetivorans* and were verified by restriction enzyme digest. All cloning was performed in the WWM4489 background[119], which was transformed at 1.8 kV using an *E. coli* Gene pulser. Medium for plasmid extraction (Zyppy MiniPrep Kit, Zymo Research, Tustin, CA, USA) contained 10 mM Rhamnose to induce plasmid copy number as previously descried. Liposome mediated transfection[120] was used to generate *M. acetivorans* mutants as previously described, under HS-Methanol (MeOH) growth conditions. Transformants were selected and plated for on HS medium with agar and 2 µg/ml puromycin. All resulting strains were screened by PCR and the products were sequenced by Sanger sequencing at the UC Berkeley DNA Sequencing facility. All primers, plasmids, and strains are listed in **Table S3.4, S3.5,** and **S3.6,** respectively.

3.1.3 Growth assays

All growth curves were performed by first pre-culturing strains in the appropriate growth substrate at 37°C without shaking (HeraTherm General Protocol Microbiological Incubator, Thermo Fisher Scientific, Waltham, MA, USA). All growth experiments were inoculated in triplicate with 500 µl of the pre-culture at late exponential phase (OD_{600} ~0.9-1.0), and optical density at 600 nm was measured using a UV-Vis Spectrophotometer (Genesys 50, Thermo Fisher Scientific, Waltham, MA, USA) with an uninoculated "blank" containing 10 mL HS medium with the appropriate growth substrate. All strains with plasmids were induced for gene expression *in trans* with 100 µg/ml tetracycline and 2 µg/ml puromycin for plasmid maintenance. All culture tubes with tetracycline were wrapped in aluminum foil to prevent tetracycline degradation over time. Growth rates were calculated as the slope of the linear fit of

the log-transformed OD versus time plot. Minimum of five time points in the linear range were used with the highest R^2 value and minimum cut-off of 0.95.

3.1.4 RNA extraction, sequencing, and analysis

RNA-sequencing data for Δ*pylBCD* was generated in a previous study. Triplicate 10 mL cultures of Δ*pylBCD* expressing $rdmS_{O216K}$ were grown on HS-MeOH media at 37˚C with 2 µg/ml puromycin and 100 µg/ml tetracycline. Upon reaching mid-exponential phase (OD_{600}~ 0.45-0.65), 1 mL of culture was removed and mixed with 1:1 Trizol (Life Technologies, Carslbad, CA, USA) that was pre-warmed to 37˚C for RNA extraction. After a shrot incubation (5 min), 2 mL of 100% ethanol was added to each sample and RNA extraction was performed using the Qiagen RNeasy Mini Kit (Qiagen, Hilden, Germany). Resulting RNA concentrations were evaluated using Nanodrop One UV Spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA) before storage at -80˚C. Samples were sent to SeqCenter (Pittsburg, PA) where each replicate underwent DNase treatment, rRNA depletion, library preparation, and Illumina paired-end sequencing (600 bp read length). Transcriptome analysis was performed using the KBase bioinformatics platform. Raw transcript reads (in FastQ format) were used as an input for read alignment to the *M. acetivorans* C2A reference genome using HISAT2 (v.2.1.0). The resulting read alignment was assembled using Cufflinks (v.2.2.1) and fold changes, significance values were calculated using DESeq2 (v.1.20.0). We considered changes in transcript abundance between pairwise comparison to be significantly differentially expressed if they exceeded a $\log_2$ fold change of ±2.0 and a *q*-value of ≤0.05.

3.1.5 Computational screen for targets

To predict TAG-containing genes with regulatory function, we parsed **Table S3.1** (generated in Chapter 1) to include only genes with helix-turn-helix domains, sensory domains, and DNA domain binding domains. Using a custom BioPython script, we pulled sequences from the prokka code 15 annotated fasta file to copy candidate sequences and metadata to a new fasta file. The resulting file was uploaded to Interpro for domain prediction. Genes where functional domains were predicted downstream of the putative Pyl residue were targeted for downstream analysis and are documented in **Table 3.2**.

3.5 Figures

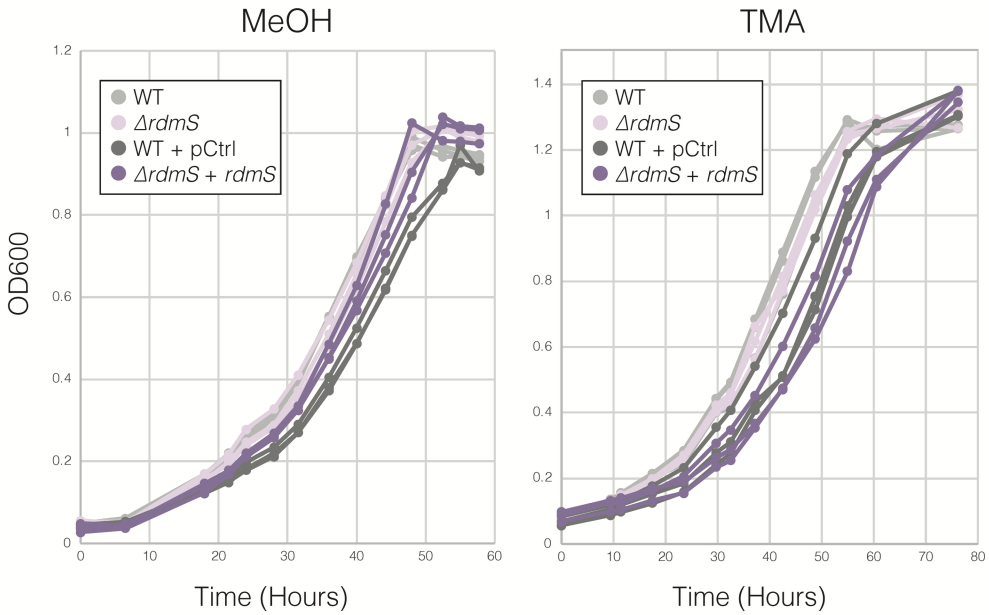

Fig 3.1 *rdmS* deletion does not produce a substantial growth defect during cultivation on either Methanol or Trimethylamine. Growth curves are shown for triplicate cultures grown in either 125 mM methanol (MeOH) or 50 mM trimethylamine (TMA). WT is used to describe the parental strain, WWM60 (**Table S3.x**). Cultures harboring plasmids were cultivated with 2 µg/ml puromycin to maintain the plasmid, alongside 100 µg/ml tetracycline to induce expression of either a control gene, *uidA* (pCtrl), or wildtype *rdmS,* complement off of the P*mcrB*(tetO4) promoter.

		MeOH			TMA		
Background	Complement	Doubling Time (Hrs)	Average	StDev	Doubling Time (Hrs)	Average	StDev
WT	--	9.2 8.9 9.2	9.1	0.2	9.68 8.78 9.04	9.2	0.5
ΔrdmS	--	9.1 9.7 9.4	9.4	0.3	9.84 9.35 9.93	9.7	0.3
WT	*uidA*	10.3 10.4 9.8	10.2	0.3	9.62 8.67 9.59	9.3	0.5
ΔrdmS	*rdmSwt*	10.8 9.8 8.7	9.8	1.1	12.54 10.27 9.26	10.7	1.7

Table 3.1 Doubling Times for Wildtype, Δ*rdmS*, and corresponding complements during growth on either MeOH or TMA. All doubling times were calculated using five time points through linear phase with a R^2 minimum of 0.95.

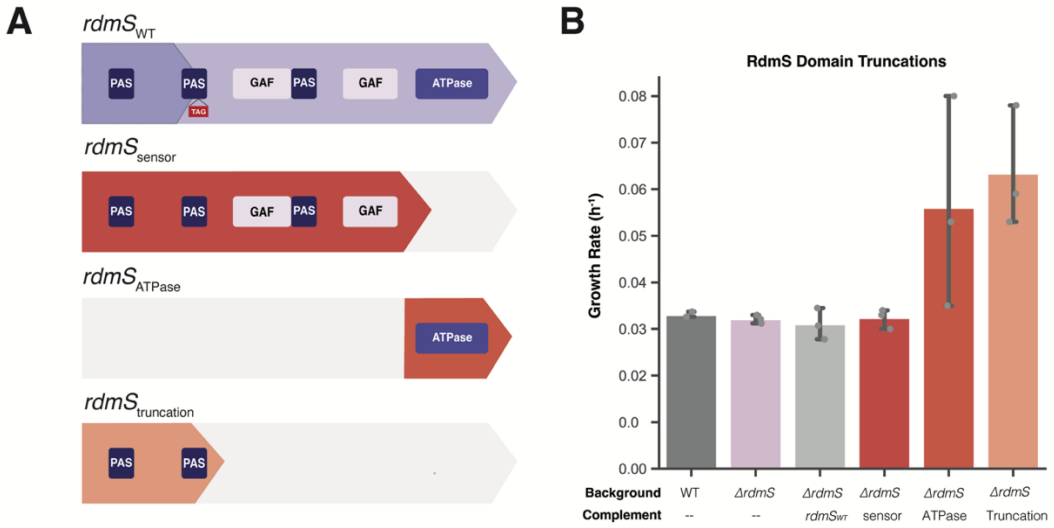

Fig 3.2 Domain truncations of RdmS do not significantly affect growth on MeOH. **A)** Domain structure in the wildtype chromosomal copy of *rdmS*, alongside all domain truncations used for growth experiments. **B)** Growth rates for all mutant strains used in assessing *rdmS* domain truncations. Strains with a complement were cultured in 100 µg/ml tetracycline to induce complement expression from the P*mcrB*(tetO4) promoter, alongside 2 µg/ml puromycin to maintain the plasmid.

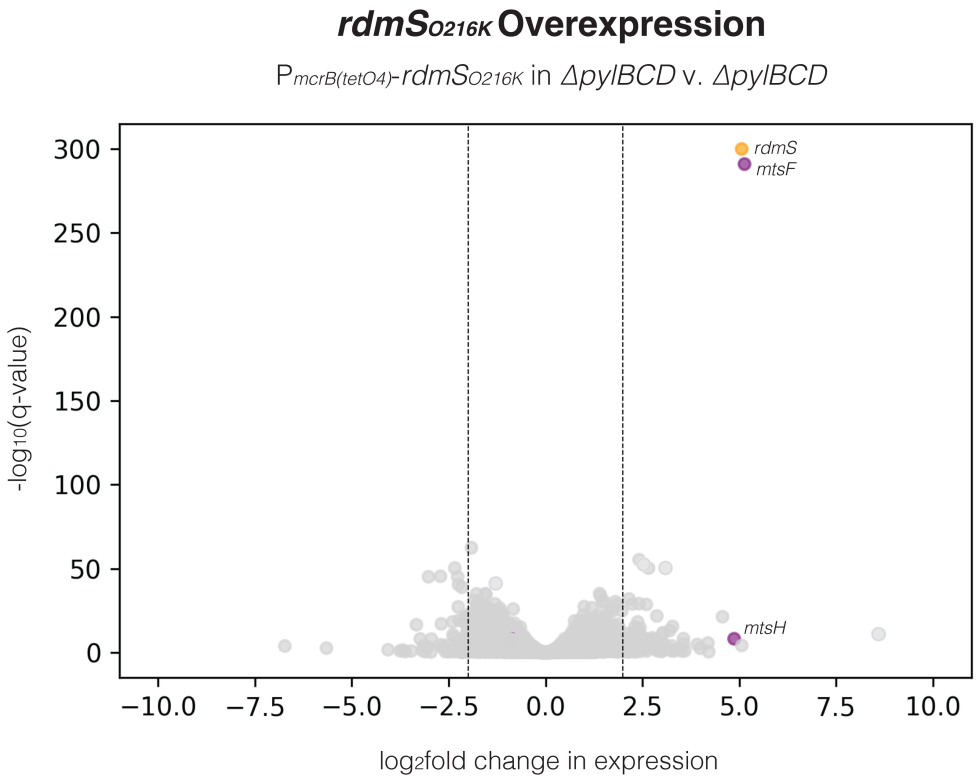

Fig 3.3 Complementation of Δ*pylBCD* with a constitutively long form of *rdmS* does not substantially change its transcriptional profile. Volcano plot is shown for all genes, their DESeq2 fold change expression (x-axis) versus their significance (-$\log_{10}$(q-value)). Points designated in purple are methylsulfide methyltransferases, whereas points in orange represent the *rdmS*$_{O216K}$ complement. Full DESeq2 values for genes defined as significantly differentially expressed (q-value ≤0.05 and $\log_2$ fold change of ±2.0 can be found in **Table S3.3**.

new_locus	old_locus	description	pyl_position	full_length	extension_length	type	post-UAG domain
MA_RS10815	MA_2082	putative sensor histidine kinase	698	735	12	c-terminal extension	No domain
MA_RS06615	MA_1274	putative sensor histidine kinase	1355	1360	5	c-terminal extension	No domain
MA_RS06945	MA_1339	putative HTH-type transcriptional regulator	113	147	34	c-terminal extension	Transmembrane domain
MA_RS01870	MA_0356	Transcriptional regulator, HTH, AF0396-type	237	239	2	c-terminal extension	No domain
MA_RS11915	MA_2294	PAS domain containing protein	548	614	66	c-terminal extension	No domain
MA_RS10480	MA_2013	PAS domain containing protein	940	966	26	c-terminal extension	No domain
MA_RS24890	MA_4619	Transcriptional regulator, HTH, AF0396-type	251	292	41	c-terminal extension	No domain
MA_RS20675	MA_3962	Sensor Histidine Kinase Regulatory	361	402	41	c-terminal extension	Intinsically disordered region
MA_RS01915	MA_0364	HTH-type Transcriptional Regulator	192	202	10	c-terminal extension	No domain
MA_RS24765	MA_3370	putative sensor histidine kinase	1126	1128	2	c-terminal extension	No domain
MA_RS21010	MA_4026	putative sensor histidine kinase	727	767	40	c-terminal extension	No domain
MA_RS14295	MA_2732	putative sensor histidine kinase	495	498	3	c-terminal extension	No domain
MA_RS25720	MA_2902	HTH-type, TetR-like transcriptional regulator	96	225	129	internal UAG	C-terminal dimerization domain
MA_RS04495	MA_0863	Two-component sensor kinase/Photoreceptor **(RdmS)**	215	976	761	internal UAG	PAS-GAF-PAS-GAF-ATPase domain
MA_RS28290	MA_0354	HTH-type, TetR-like transcriptional regulator	95	122	27	new CDS fusion	No domain
MA_RS12290	MA_2370	DNA binding domain protein	41	110	69	new CDS fusion	GLPR-related Tx repressor domain
MA_RS07955	MA_1531	winged HTH transcriptional regulator	7	284	277	new CDS fusion	HTH domain

Table 3.2 TAG-containing containing genes with putative regulatory function. All genes containing an in-frame TAG sequence are depicted alongside the putative Pyl position (pyl_position), the protein length assuming readthrough (in amino acids), and putative extension length (in amino acids).

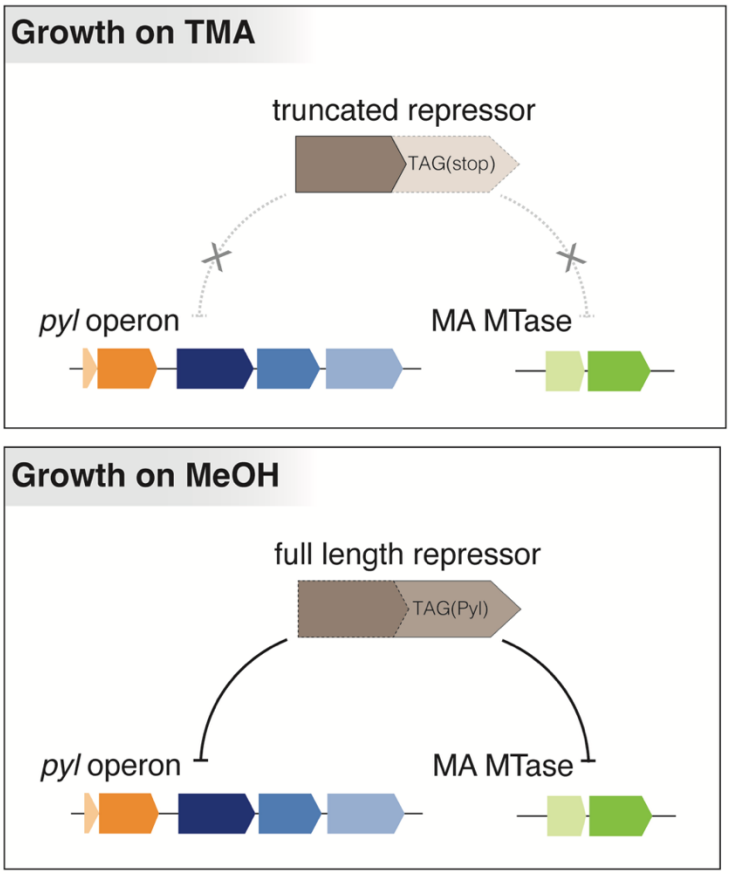

Fig 3.4 A Pyl-responsive repressor may function as a sensor for readthrough efficiency. During growth on trimethylamine (TMA), where we propose low readthrough efficiency, a putative repressor is biased towards its truncated form, resulting in de-repression of methylamine methyltransferases and the *pyl* operon. In contrast, during growth on methanol (MeOH), where we propose higher relative readthrough efficiency, the repressor exists primarily in its elongated form, resulting in repression of its targets.

Conclusions

Natural genetic code expansions can unlock myriad benefits for cells, yet stop codon reassignment, which is required for all known code expansions, presents a unique challenge in how organisms adapt to tolerate a new genetic code. For stop codon recoding to occur, the cell must undergo two essential processes: 1) first, it must acquire all genetic components required for an expanded genetic code, 2) then, its coding sequences must adapt to tolerate codons with changed or ambiguous meaning[11]. While some systems, like Selenocysteine, have discrete mechanisms to toggle codon meaning between stop and amino acid[22,23], how cells navigate ambiguous stop decoding in the absence of incorporation cues, as in the case of Pyrrolysine, remained relatively unknown. Prior to this dissertation, substantial work had been done to map the genetic components required for Pyrrolysine-based genetic code expansion, alongside its distribution and evolution across the tree of life[85,91,92]. Yet, despite previous reports[102] that UAG could be decoded as both stop and Pyl, the reigning paradigm was that most UAG-containing proteins in methanogenic archaea were decoded as Pyl alone. In this work, we conclusively demonstrate that methanogenic archaea, like *Methanosarcina acetivorans*, have an ambiguous genetic code under which the amber stop codon is interpreted as both Pyl and stop. We use this system as a model to address a fundamental question in Pyrrolysine-based genetic code expansion: how do cells tolerate the Pyl-imposed code ambiguity in their transcriptional and translational regimes? Together, this work helps unravel the evolution and adaptation to ambiguous UAG decoding in the domain Archaea.

The genomic work in this dissertation provides new insights into how pyrrolysine biosynthesis and incorporation modules are distributed across the Archaea. It also reveals that while Pyl's association with genes involved in methylamine methanogenesis is conserved, UAG ambiguity varies by genomic and evolutionary context. In line with previous reports[85,91,92], we find that Pyl machinery is found widespread in the Archaea and is strongly associated with methylamine-based methanogenesis. While Pyl's catalytic role in methylamine methanogenesis is well-known, this work establishes the functional co-occurrence between Pyl and this metabolism. Although there is evidence that Pyl can be both vertically and horizontally inherited, prior practices of concatenating the biosynthetic and incorporation machinery into a single set of Pyl genes for phylogenetic inference has the potential to obfuscate evolutionary nuance manifest in its individual modules. Indeed, we observe that the biosynthetic and incorporation modules follow different evolutionary trajectories, even between closely related genera in the Pyl-encoding family *Methanosarcinaceae*. Moreover, within Pyl-containing genomes, we observe an inverse relationship between TAG usage and the median Pyl-extension length and density of Pyl genes in each genome. Our comparative genomics work points towards several major, outstanding questions in Pyl physiology: Do all Pyl-encoding organisms have an ambiguous code? Or just those within TAG usage in range of *M. acetivorans*? Without cultured representatives and genetic tools for many of these organisms, it is difficult to assay stop and Pyl recognition at UAG sites. Future studies focused on *Methanimicrococcus* spp. and *Methanolobus* spp. may provide insights to this question: as culturable members of the *Methanosarcinaceae* with extremely low (<3%) and high TAG usage (9.1-16.2%), respectively, members of these Genus's exist along a yet characterized gradient.

The ability to tolerate ambiguous decoding at UAG sites is essential to the successful acquisition of Pyl. Despite reports that both translation termination and Pyl-readthrough occur at UAG sites, it was widely accepted that UAG sites were biased towards Pyl-readthrough rather than stop recognition. Our work conclusively demonstrates that UAG can be read as either a Pyl residue or a stop codon. Therefore, UAG codons represent an inflection point in translation, where aRF1 and

$tRNA^{Pyl}$ compete for occupancy of UAG site, resulting in translation termination or readthrough, respectively. We propose that readthrough efficiency, or the incorporation of Pyl at UAG sites, depends on the balance between Pyl supply (i.e., Pyl availability) and Pyl demand (i.e., UAG-containing transcripts). Our work estimates that readthrough efficiency during growth on TMA is relatively lower than during growth on MeOH. This is counterintuitive, as one might expect that heightened *pyl* expression on TMA increases Pyl supply; yet, we observe that Pyl demand dramatically outpaces its supply, resulting in lower readthrough efficiency. This observation explains several phenotypes observed in our knockout experiments: removing Pyl supply via *pylBCD* or *pylTS* deletion triggers compensatory upregulation of other *pyl* module and methylamine methyltransferases, possibly due to sensing of low readthrough efficiency. This aligns with our observation that *pyl* overexpression on TMA produces a defect on TMA, and not MeOH, possibly due to greater deviation from its native readthrough efficiency. This regulatory feedback may involve a Pyl-containing repressor whose function depends on UAG readthrough, thus linking readthrough efficiency to gene expression. Together, our results suggest that *M. acetivorans* finely tunes Pyl homeostasis through cellular detection of readthrough efficiency, thus incorporating genetic code ambiguity without sequence-specific decoding strategies.

While we were able to partially validate our model using transcriptomic data, further mechanistic studies are certainly warranted. To this end, we used a candidate approach focused on RdmS to investigate the sensor hypothesis. While we were unable to demonstrate that RdmS play a role in fine-tuning Pyl homeostasis, we identified several promising candidates for future work. The TetR-family repressor, MA_RS05270, is an auspicious candidate for mechanistic work, as UAG-truncation is predicted to interrupt formation of its C-terminal domain. Although, whether this domain functions in DNA- or ligand-binding is yet known. Genetic dissection and quantitative studies of elongated and truncated protein forms of this repressor under growth conditions with varied readthrough efficiencies may offer unique insights into Pyl-$tRNA^{Pyl}$ and aRF1 competition.

Although the work in this dissertation has advanced our understanding of how archaea adapt to genetic code ambiguity, it has similarly highlighted aspects of *M. acetivorans* physiology that require further investigation. As our work focuses primarily on Pyl readthrough as facilitated by the Pyl incorporation machinery, *in vivo* studies of aRF1-1 and aRF1-2 would be well suited for future work. In Bacteria, there is a division of labor between two the two release factors—RF1 and RF2—which recognize UAG/UAA and UGA/UAA, respectively[130]. In contrast, *in vitro* work demonstrated that aRF1-1 recognizes all three stop codons[110]. Analogous work on aRF1-2 is unable to detect stop recognition activity for any of the three codons, albeit in a hybrid *in vitro* system with eRF1 components. Thus, it is currently unknown whether aRF1-2 encodes a functional release factor *in vivo*. Western blotting of the tagged RdmS complement used in Chapter 2 of this dissertation is an appropriate readout for stop recognition in single gene deletions of either release factor (assuming these strains are viable), as we have demonstrated detection of both protein forms. Understanding the *in vivo* role of aRF1 copies is essential to developing a more robust model for Pyl competition between the elongation and truncation of UAG proteins.

Overall, Pyl-containing organisms are representative of dynamic cellular processes consisting of competition at different levels within the central dogma—between transcripts, proteins, and tRNA's—ultimately biasing how UAG is translationally interpreted under a regime in which it encodes dual meaning as both Pyl and stop. The work I have described in this thesis indicates that methanogens are uniquely poised to navigate ambiguous decoding of the amber codon through a diverse cellular landscape.

References

1. Crick, F. Central Dogma of Molecular Biology. *Nature* **227**, 561–563 (1970).
2. Koonin, E. V. Does the central dogma still stand? *Biol. Direct* **7**, 27 (2012).
3. Tamura, K. The Genetic Code: Francis Crick's Legacy and Beyond. *Life* **6**, 36 (2016).
4. Crick, F. H. On protein synthesis. *Symp. Soc. Exp. Biol.* **12**, 138–163 (1958).
5. Crick, F. H. C. The origin of the genetic code. *J. Mol. Biol.* **38**, 367–379 (1968).
6. Yuan, S., Zhou, G. & Xu, G. Translation machinery: the basis of translational control. *J. Genet. Genomics* **51**, 367–378 (2024).
7. Shulgina, Y. & Eddy, S. R. A computational screen for alternative genetic codes in over 250,000 genomes. *eLife* **10**, e71402 (2021).
8. Santos, M. A., Keith, G. & Tuite, M. F. Non-standard translational events in Candida albicans mediated by an unusual seryl-tRNA with a 5′-CAG-3′ (leucine) anticodon. *EMBO J.* **12**, 607–616 (1993).
9. Borges, A. L. *et al.* Widespread stop-codon recoding in bacteriophages may regulate translation of lytic genes. *Nat. Microbiol.* **7**, 918–927 (2022).
10. Ivanova, N. N. *et al.* Stop codon reassignments in the wild. *Science* **344**, 909–913 (2014).
11. Santos, M. A. S., Moura, G., Massey, S. E. & Tuite, M. F. Driving change: the evolution of alternative genetic codes. *Trends Genet.* **20**, 95–102 (2004).
12. Santos, M. A. S., Cheesman, C., Costa, V., Moradas-Ferreira, P. & Tuite, M. F. Selective advantages created by codon ambiguity allowed for the evolution of an alternative genetic code in Candida spp. *Mol. Microbiol.* **31**, 937–947 (1999).
13. Mühlhausen, S., Findeisen, P., Plessmann, U., Urlaub, H. & Kollmar, M. A novel nuclear genetic code alteration in yeasts and the evolution of codon reassignment in eukaryotes. *Genome Res.* **26**, 945–955 (2016).
14. Mühlhausen, S. *et al.* Endogenous Stochastic Decoding of the CUG Codon by Competing Ser- and Leu-tRNAs in Ascoidea asiatica. *Curr. Biol. CB* **28**, 2046-2057.e5 (2018).
15. Freel, K. C., Friedrich, A. & Schacherer, J. Mitochondrial genome evolution in yeasts: an all-encompassing view. *FEMS Yeast Res.* **15**, fov023 (2015).
16. Martin, N. C., Pham, H. D., Underbrink-Lyon, K., Miller, D. L. & Donelson, J. E. Yeast mitochondrial tRNATrp can recognize the nonsense codon UGA. *Nature* **285**, 579–581 (1980).
17. Hao, B. *et al.* A New UAG-Encoded Residue in the Structure of a Methanogen Methyltransferase. *Science* **296**, 1462–1466 (2002).
18. Longstaff, D. G. *et al.* A natural genetic code expansion cassette enables transmissible biosynthesis and genetic encoding of pyrrolysine. *Proc. Natl. Acad. Sci.* **104**, 1021–1026 (2007).
19. Swart, E. C., Serra, V., Petroni, G. & Nowacki, M. Genetic Codes with No Dedicated Stop Codon: Context-Dependent Translation Termination. *Cell* **166**, 691–702 (2016).
20. Ling, J., O'Donoghue, P. & Söll, D. Genetic code flexibility in microorganisms: novel mechanisms and impact on physiology. *Nat. Rev. Microbiol.* **13**, 707–721 (2015).
21. Cone, J. E., Del Río, R. M., Davis, J. N. & Stadtman, T. C. Chemical characterization of the selenoprotein component of clostridial glycine reductase: identification of selenocysteine as the organoselenium moiety. *Proc. Natl. Acad. Sci.* **73**, 2659–2663 (1976).

22. Berry, M. J. *et al.* Recognition of UGA as a selenocysteine codon in Type I deiodinase requires sequences in the 3′ untranslated region. *Nature* **353**, 273–276 (1991).
23. Leibundgut, M., Frick, C., Thanbichler, M., Böck, A. & Ban, N. Selenocysteine tRNA-specific elongation factor SelB is a structural chimaera of elongation and initiation factors. *EMBO J.* **24**, 11–22 (2005).
24. Gaston, M. A., Zhang, L., Green-Church, K. B. & Krzycki, J. A. The complete biosynthesis of the genetically encoded amino acid pyrrolysine from lysine. *Nature* **471**, 647–650 (2011).
25. Zhang, Y., Baranov, P. V., Atkins, J. F. & Gladyshev, V. N. Pyrrolysine and selenocysteine use dissimilar decoding strategies. *J. Biol. Chem.* **280**, 20740–20751 (2005).
26. Thauer, R. K. Biochemistry of methanogenesis: a tribute to Marjory Stephenson:1998 Marjory Stephenson Prize Lecture. *Microbiology* **144**, 2377–2406 (1998).
27. Thauer, R. K., Kaster, A.-K., Seedorf, H., Buckel, W. & Hedderich, R. Methanogenic archaea: ecologically relevant differences in energy conservation. *Nat. Rev. Microbiol.* **6**, 579–591 (2008).
28. Borrel, G. *et al.* Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. *Nat. Microbiol.* **4**, 603–613 (2019).
29. Liu, Y. & Whitman, W. B. Metabolic, Phylogenetic, and Ecological Diversity of the Methanogenic Archaea. *Ann. N. Y. Acad. Sci.* **1125**, 171–189 (2008).
30. Offre, P., Spang, A. & Schleper, C. Archaea in Biogeochemical Cycles. *Annu. Rev. Microbiol.* **67**, 437–457 (2013).
31. Reeburgh, W. S. Oceanic Methane Biogeochemistry. *Chem. Rev.* **107**, 486–513 (2007).
32. Allen, G. Rebalancing the global methane budget. *Nature* **538**, 46–48 (2016).
33. Bell, S. D. & Jackson, S. P. Mechanism and regulation of transcription in archaea. *Curr. Opin. Microbiol.* **4**, 208–213 (2001).
34. Langer, D., Hain, J., Thuriaux, P. & Zillig, W. Transcription in archaea: similarity to that in eucarya. *Proc. Natl. Acad. Sci.* **92**, 5768–5772 (1995).
35. Hirata, A., Klein, B. J. & Murakami, K. S. The X-ray crystal structure of RNA polymerase from Archaea. *Nature* **451**, 851–854 (2008).
36. Hausner, W., Wettach, J., Hethke, C. & Thomm, M. Two transcription factors related with the eucaryal transcription factors TATA-binding protein and transcription factor IIB direct promoter recognition by an archaeal RNA polymerase. *J. Biol. Chem.* **271**, 30144–30148 (1996).
37. French, S. L., Santangelo, T. J., Beyer, A. L. & Reeve, J. N. Transcription and Translation are Coupled in Archaea. *Mol. Biol. Evol.* **24**, 893–895 (2007).
38. Pérez-Rueda, E. & Janga, S. C. Identification and Genomic Analysis of Transcription Factors in Archaeal Genomes Exemplifies Their Functional Architecture and Evolutionary Origin. *Mol. Biol. Evol.* **27**, 1449–1459 (2010).
39. Kim, D. & Forst, S. Genomic analysis of the histidine kinase family in bacteria and archaea. *Microbiology* **147**, 1197–1212 (2001).
40. Galperin, M. Y., Makarova, K. S., Wolf, Y. I. & Koonin, E. V. Phyletic Distribution and Lineage-Specific Domain Architectures of Archaeal Two-Component Signal Transduction Systems. *J. Bacteriol.* **200**, 10.1128/jb.00681-17 (2018).
41. Hendrickson, E. L. *et al.* Complete genome sequence of the genetically tractable hydrogenotrophic methanogen Methanococcus maripaludis. *J. Bacteriol.* **186**, 6956–6969 (2004).

42. Galagan, J. E. *et al.* The Genome of M. acetivorans Reveals Extensive Metabolic and Physiological Diversity. *Genome Res.* **12**, 532–542 (2002).
43. Borrel, G. *et al.* Phylogenomic data support a seventh order of Methylotrophic methanogens and provide insights into the evolution of Methanogenesis. *Genome Biol. Evol.* **5**, 1769–1780 (2013).
44. Imachi, H., Sakai, S., Nagai, H., Yamaguchi, T. & Takai, K. Methanofollis ethanolicus sp. nov., an ethanol-utilizing methanogen isolated from a lotus field. *Int. J. Syst. Evol. Microbiol.* **59**, 800–805 (2009).
45. Costa, K. C. & Leigh, J. A. Metabolic versatility in methanogens. *Curr. Opin. Biotechnol.* **29**, 70–75 (2014).
46. Kaster, A.-K., Moll, J., Parey, K. & Thauer, R. K. Coupling of ferredoxin and heterodisulfide reduction via electron bifurcation in hydrogenotrophic methanogenic archaea. *Proc. Natl. Acad. Sci.* **108**, 2981–2986 (2011).
47. Costa, K. C. *et al.* Protein complexing in a methanogen suggests electron bifurcation and electron delivery from formate to heterodisulfide reductase. *Proc. Natl. Acad. Sci.* **107**, 11050–11055 (2010).
48. Susanti, D., Frazier, M. C. & Mukhopadhyay, B. A Genetic System for Methanocaldococcus jannaschii: An Evolutionary Deeply Rooted Hyperthermophilic Methanarchaeon. *Front. Microbiol.* **10**, (2019).
49. Fonseca, D. R., Halim, M. F. A., Holten, M. P. & Costa, K. C. Type IV-Like Pili Facilitate Transformation in Naturally Competent Archaea. *J. Bacteriol.* **202**, 10.1128/jb.00355-20 (2020).
50. Leigh, J. A. & Dodsworth, J. A. Nitrogen Regulation in Bacteria and Archaea. *Annu. Rev. Microbiol.* **61**, 349–377 (2007).
51. Leigh, J. A. Nitrogen fixation in methanogens: the archaeal perspective. *Curr. Issues Mol. Biol.* **2**, 125–131 (2000).
52. Karr, E. A. Chapter Three - Transcription Regulation in the Third Domain. in *Advances in Applied Microbiology* (eds. Sariaslani, S. & Gadd, G. M.) vol. 89 101–133 (Academic Press, 2014).
53. Hendrickson, E. L., Haydock, A. K., Moore, B. C., Whitman, W. B. & Leigh, J. A. Functionally distinct genes regulated by hydrogen limitation and growth rate in methanogenic Archaea. *Proc. Natl. Acad. Sci.* **104**, 8930–8934 (2007).
54. Hendrickson, E. L. *et al.* Global Responses of Methanococcus maripaludis to Specific Nutrient Limitations and Growth Rate. *J. Bacteriol.* **190**, 2198–2205 (2008).
55. Costa, K. C. *et al.* Effects of H2 and Formate on Growth Yield and Regulation of Methanogenesis in Methanococcus maripaludis. *J. Bacteriol.* **195**, 1456–1462 (2013).
56. Morgan, R. M., Pihl, T. D., Nölling, J. & Reeve, J. N. Hydrogen regulation of growth, growth yields, and methane gene transcription in Methanobacterium thermoautotrophicum deltaH. *J. Bacteriol.* **179**, 889–898 (1997).
57. Pihl, T. D., Sharma, S. & Reeve, J. N. Growth phase-dependent transcription of the genes that encode the two methyl coenzyme M reductase isoenzymes and N5-methyltetrahydromethanopterin:coenzyme M methyltransferase in Methanobacterium thermoautotrophicum delta H. *J. Bacteriol.* **176**, 6384–6391 (1994).
58. Wood, G. E., Haydock, A. K. & Leigh, J. A. Function and Regulation of the Formate Dehydrogenase Genes of the Methanogenic Archaeon Methanococcus maripaludis. *J. Bacteriol.* **185**, 2548–2554 (2003).

59. Evans, P. N. *et al.* An evolving view of methane metabolism in the Archaea. *Nat. Rev. Microbiol.* **17**, 219–232 (2019).
60. Kohler, P. R. A. & Metcalf, W. W. Genetic manipulation of Methanosarcina spp. *Front. Microbiol.* **3**, (2012).
61. Nayak, D. D. & Metcalf, W. W. Cas9-mediated genome editing in the methanogenic archaeon Methanosarcina acetivorans. *Proc. Natl. Acad. Sci.* **114**, 2976–2981 (2017).
62. Bose, A., Pritchett, M. A., Rother, M. & Metcalf, W. W. Differential Regulation of the Three Methanol Methyltransferase Isozymes in Methanosarcina acetivorans C2A. *J. Bacteriol.* **188**, 7274–7283 (2006).
63. Bose, A. & Metcalf, W. W. Distinct regulators control the expression of methanol methyltransferase isozymes in Methanosarcina acetivorans C2A. *Mol. Microbiol.* **67**, 649–661 (2008).
64. Hippe, H., Caspari, D., Fiebig, K. & Gottschalk, G. Utilization of trimethylamine and other N-methyl compounds for growth and methane formation by Methanosarcina barkeri. *Proc. Natl. Acad. Sci.* **76**, 494–498 (1979).
65. Ferry, J. G. Enzymology of one-carbon metabolism in methanogenic pathways. *FEMS Microbiol. Rev.* **23**, 13–38 (1999).
66. van der Meijden, P., te Brömmelstroet, B. W., Poirot, C. M., van der Drift, C. & Vogels, G. D. Purification and properties of methanol:5-hydroxybenzimidazolylcobamide methyltransferase from Methanosarcina barkeri. *J. Bacteriol.* **160**, 629–635 (1984).
67. Wassenaar, R. W., Daas, P. J., Geerts, W. J., Keltjens, J. T. & van der Drift, C. Involvement of methyltransferase-activating protein and methyltransferase 2 isoenzyme II in methylamine:coenzyme M methyltransferase reactions in Methanosarcina barkeri Fusaro. *J. Bacteriol.* **178**, 6937–6944 (1996).
68. Ferguson, D. J., Krzycki, J. A. & Grahame, D. A. Specific Roles of Methylcobamide:Coenzyme M Methyltransferase Isozymes in Metabolism of Methanol and Methylamines in Methanosarcina barkeri. *J. Biol. Chem.* **271**, 5189–5194 (1996).
69. Sauer, K. & Thauer, R. K. Methanol : coenzyme M methyltransferase from Methanosarcina barkeri. *Eur. J. Biochem.* **253**, 698–705 (1998).
70. Maeder, D. L. *et al.* The Methanosarcina barkeri Genome: Comparative Analysis with Methanosarcina acetivorans and Methanosarcina mazei Reveals Extensive Rearrangement within Methanosarcinal Genomes. *J. Bacteriol.* **188**, 7922–7931 (2006).
71. Lessner, D. J. *et al.* An unconventional pathway for reduction of CO2 to methane in CO-grown Methanosarcina acetivorans revealed by proteomics. *Proc. Natl. Acad. Sci.* **103**, 17921–17926 (2006).
72. Oelgeschläger, E. & Rother, M. In vivo role of three fused corrinoid/methyl transfer proteins in Methanosarcina acetivorans. *Mol. Microbiol.* **72**, 1260–1272 (2009).
73. Bose, A., Kulkarni, G. & Metcalf, W. W. Regulation of putative methyl-sulphide methyltransferases in Methanosarcina acetivorans C2A. *Mol. Microbiol.* **74**, 227–238 (2009).
74. Molitor, B. *et al.* A Heme-based Redox Sensor in the Methanogenic Archaeon *Methanosarcina acetivorans**. *J. Biol. Chem.* **288**, 18458–18472 (2013).
75. Fiege, K. & Frankenberg-Dinkel, N. Thiol-based redox sensing in the methyltransferase associated sensor kinase RdmS in Methanosarcina acetivorans. *Environ. Microbiol.* **21**, 1597–1610 (2019).

76. Opulencia, R. B., Bose, A. & Metcalf, W. W. Physiology and Posttranscriptional Regulation of Methanol:Coenzyme M Methyltransferase Isozymes in Methanosarcina acetivorans C2A. *J. Bacteriol.* **191**, 6928–6935 (2009).
77. Peterson, J. R. *et al.* Genome-wide gene expression and RNA half-life measurements allow predictions of regulation and metabolic behavior in Methanosarcina acetivorans. *BMC Genomics* **17**, 924 (2016).
78. Jäger, D. *et al.* An archaeal sRNA targeting cis - and trans -encoded mRNAs via two distinct domains. *Nucleic Acids Res.* **40**, 10964–10979 (2012).
79. Jetten, M. S. M., Stams, A. J. M. & Zehnder, A. J. B. Methanogenesis from acetate: a comparison of the acetate metabolism in Methanothrix soehngenii and Methanosarcina spp. *FEMS Microbiol. Rev.* **8**, 181–197 (1992).
80. Reichlen, M. J., Vepachedu, V. R., Murakami, K. S. & Ferry, J. G. MreA Functions in the Global Regulation of Methanogenic Pathways in Methanosarcina acetivorans. *mBio* **3**, 10.1128/mbio.00189-12 (2012).
81. Preer, J. R., Preer, L. B., Rudman, B. M. & Barnett, A. J. Deviation from the universal code shown by the gene for surface protein 51A in Paramecium. *Nature* **314**, 188–190 (1985).
82. Yamao, F. *et al.* UGA is read as tryptophan in Mycoplasma capricolum. *Proc. Natl. Acad. Sci.* **82**, 2306–2309 (1985).
83. Campbell, J. H. *et al.* UGA is an additional glycine codon in uncultured SR1 bacteria from the human microbiota. *Proc. Natl. Acad. Sci.* **110**, 5540–5545 (2013).
84. Meng, K., Chung, C. Z., Söll, D. & Krahn, N. Unconventional genetic code systems in archaea. *Front. Microbiol.* **13**, 1007832 (2022).
85. Kivenson, V. *et al.* Sporadic distribution of a new archaeal genetic code with all TAG codons as pyrrolysine. 2024.09.30.615893 Preprint at https://doi.org/10.1101/2024.09.30.615893 (2024).
86. Ling, J., O'Donoghue, P. & Söll, D. Genetic code flexibility in microorganisms: novel mechanisms and impact on physiology. *Nat. Rev. Microbiol.* **13**, 707–721 (2015).
87. Evans, R. M. *et al.* Selective cysteine-to-selenocysteine changes in a [NiFe]-hydrogenase confirm a special position for catalysis and oxygen tolerance. *Proc. Natl. Acad. Sci.* **118**, e2100921118 (2021).
88. Kim, H.-Y. & Gladyshev, V. N. Different Catalytic Mechanisms in Mammalian Selenocysteine- and Cysteine-Containing Methionine-R-Sulfoxide Reductases. *PLOS Biol.* **3**, e375 (2005).
89. Li, J. *et al.* Insights into pyrrolysine function from structures of a trimethylamine methyltransferase and its corrinoid protein complex. *Commun. Biol.* **6**, 1–10 (2023).
90. Polycarpo, C. *et al.* An aminoacyl-tRNA synthetase that specifically activates pyrrolysine. *Proc. Natl. Acad. Sci.* **101**, 12450–12454 (2004).
91. Guo, L.-T. *et al.* Ancestral archaea expanded the genetic code with pyrrolysine. *J. Biol. Chem.* **298**, 102521 (2022).
92. Sun, J. *et al.* Recoding of stop codons expands the metabolic potential of two novel Asgardarchaeota lineages. *ISME Commun.* **1**, 30 (2021).
93. Woods, P. H. *et al.* Convergence and horizontal gene transfer drive the evolution of anaerobic methanotrophy in archaea. 2024.05.23.595608 Preprint at https://doi.org/10.1101/2024.05.23.595608 (2024).
94. Kivenson, V., Paul, B. G. & Valentine, D. L. An Ecological Basis for Dual Genetic Code Expansion in Marine Deltaproteobacteria. *Front. Microbiol.* **12**, 680620 (2021).

95. Prat, L. *et al.* Carbon source-dependent expansion of the genetic code in bacteria. *Proc. Natl. Acad. Sci.* **109**, 21070–21075 (2012).
96. Rinke, C. *et al.* A standardized archaeal taxonomy for the Genome Taxonomy Database. *Nat. Microbiol.* **6**, 946–959 (2021).
97. Srinivasan, G., James, C. M. & Krzycki, J. A. Pyrrolysine Encoded by UAG in Archaea: Charging of a UAG-Decoding Specialized tRNA. *Science* **296**, 1459–1462 (2002).
98. Krzycki, J. A. The direct genetic encoding of pyrrolysine. *Curr. Opin. Microbiol.* **8**, 706–712 (2005).
99. Blight, S. K. *et al.* Direct charging of tRNA(CUA) with pyrrolysine in vitro and in vivo. *Nature* **431**, 333–335 (2004).
100. Borrel, G. *et al.* Wide diversity of methane and short-chain alkane metabolisms in uncultured archaea. *Nat. Microbiol.* **4**, 603–613 (2019).
101. Li, J., Zhou, J., Wu, Y., Yang, S. & Tian, D. GC-Content of Synonymous Codons Profoundly Influences Amino Acid Usage. *G3 GenesGenomesGenetics* **5**, 2027–2036 (2015).
102. James, C. M., Ferguson, T. K., Leykam, J. F. & Krzycki, J. A. The Amber Codon in the Gene Encoding the Monomethylamine Methyltransferase Isolated from Methanosarcina barkeri Is Translated as a Sense Codon *. *J. Biol. Chem.* **276**, 34252–34258 (2001).
103. O'Donoghue, P. *et al.* Reducing the genetic code induces massive rearrangement of the proteome. *Proc. Natl. Acad. Sci.* **111**, 17206–17211 (2014).
104. Chadwick, G. L. *et al.* Comparative genomics reveals electron transfer and syntrophic mechanisms differentiating methanotrophic and methanogenic archaea. *PLOS Biol.* **20**, e3001508 (2022).
105. Mahapatra, A. *et al.* Characterization of a Methanosarcina acetivorans mutant unable to translate UAG as pyrrolysine. *Mol. Microbiol.* **59**, 56–66 (2006).
106. Guss, A. M., Rother, M., Zhang, J. K., Kulkkarni, G. & Metcalf, W. W. New methods for tightly regulated gene expression and highly efficient chromosomal integration of cloned genes for Methanosarcina species. *Archaea* **2**, 193–203 (2008).
107. Longstaff, D. G. *et al.* A natural genetic code expansion cassette enables transmissible biosynthesis and genetic encoding of pyrrolysine. *Proc. Natl. Acad. Sci.* **104**, 1021–1026 (2007).
108. Downing, B. E. & Nayak, D. D. Innovations in the electron transport chain fuel archaeal methane metabolism. *Trends Biochem. Sci.* **50**, 425–437 (2025).
109. Kumar, A. *et al.* Molecular principles of redox-coupled sodium pumping of the ancient Rnf machinery. *Nat. Commun.* **16**, 2302 (2025).
110. Alkalaeva, E. *et al.* Translation termination in pyrrolysine-utilizing archaea. *FEBS Lett.* **583**, 3455–3460 (2009).
111. Parks, D. H. *et al.* GTDB: an ongoing census of bacterial and archaeal diversity through a phylogenetically consistent, rank normalized and complete genome-based taxonomy. *Nucleic Acids Res.* **50**, D785–D794 (2022).
112. Seemann, T. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* **30**, 2068–2069 (2014).
113. Laslett, D. & Canback, B. ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. *Nucleic Acids Res.* **32**, 11–16 (2004).

114. Chadwick, G. L., Williams, M. C., Shalvarjian, K. E. & Nayak, D. D. Methanogenesis marker 16 metalloprotein is the primary coenzyme M synthase in Methanosarcina acetivorans. *PLOS Genet.* **21**, e1011695 (2025).
115. Letunic, I. & Bork, P. Interactive Tree of Life (iTOL) v6: recent updates to the phylogenetic tree display and annotation tool. *Nucleic Acids Res.* **52**, W78–W82 (2024).
116. Huson, D. H. *et al.* Dendroscope: An interactive viewer for large phylogenetic trees. *BMC Bioinformatics* **8**, 460 (2007).
117. Steinegger, M. & Söding, J. MMseqs2 enables sensitive protein sequence searching for the analysis of massive data sets. *Nat. Biotechnol.* **35**, 1026–1028 (2017).
118. Nayak, D. D. & Metcalf, W. W. Genetic techniques for studies of methyl-coenzyme M reductase from *Methanosarcina acetivorans* C2A. in *Methods in Enzymology* (ed. Armstrong, F.) vol. 613 325–347 (Academic Press, 2018).
119. Kim, S. Y. *et al.* Different Biosynthetic Pathways to Fosfomycin in Pseudomonas syringae and Streptomyces Species. *Antimicrob. Agents Chemother.* **56**, 4175–4183 (2012).
120. Metcalf, W. W., Zhang, J. K., Apolinario, E., Sowers, K. R. & Wolfe, R. S. A genetic system for Archaea of the genus Methanosarcina: Liposome-mediated transformation and construction of shuttle vectors. *Proc. Natl. Acad. Sci.* **94**, 2626–2631 (1997).
121. Deatherage, D. E. & Barrick, J. E. Identification of mutations in laboratory evolved microbes from next-generation sequencing data using breseq. *Methods Mol. Biol. Clifton NJ* **1151**, 165–188 (2014).
122. Nayak, D. D. & Metcalf, W. W. Genetic techniques for studies of methyl-coenzyme M reductase from Methanosarcina acetivorans C2A. in *Methods in Enzymology* vol. 613 325–347 (Elsevier, 2018).
123. Chadwick, G. L., Dury, G. A. & Nayak, D. D. Physiological and transcriptomic response to methyl-coenzyme M reductase limitation in Methanosarcina acetivorans. *Appl. Environ. Microbiol.* **90**, e02220-23.
124. Shalvarjian, K. E. *et al.* The Ambiguous Genetic Code of Methanogenic Archaea that Grow on Methylamines. 2025.06.11.659114 Preprint at https://doi.org/10.1101/2025.06.11.659114 (2025).
125. Cuthbertson, L. & Nodwell, J. R. The TetR Family of Regulators. *Microbiol. Mol. Biol. Rev. MMBR* **77**, 440–475 (2013).
126. Munoz, L. & Mayrim, M. Insights into substrate utilization and transcriptional regulation in methanosarcina. (University of Illinois at Urbana-Champaign, 2017).
127. Filipek, J. *et al.* Comprehensive structural overview of the C-terminal ligand-binding domains of the TetR family regulators. *J. Struct. Biol.* **216**, 108071 (2024).
128. Schleif, R. AraC protein, regulation of the l-arabinose operon in Escherichia coli, and the light switch mechanism of AraC action. *FEMS Microbiol. Rev.* **34**, 779–796 (2010).
129. Munoz, L. & Mayrim, M. Insights into substrate utilization and transcriptional regulation in methanosarcina. (University of Illinois at Urbana-Champaign, 2017).
130. Nakamura, Y., Ito, K. & Isaksson, L. A. Emerging Understanding of Translation Termination. *Cell* **87**, 147–150 (1996).
131. Gupta, D., Shalvarjian, K. E. & Nayak, D. D. An Archaea-specific c-type cytochrome maturation machinery is crucial for methanogenesis in Methanosarcina acetivorans. *eLife* **11**, e76970 (2022).

Appendix A. Documentation of an HMM-based gene searching tool

In chapter 2, I describe the use of a Hidden Markov Model-based gene searching tool for use in large scale bioinformatic surveys in the Genome Taxonomy Database. The described tool is available on Github at: github.com/kshalv/hmm_tools. What follows is a brief description of the tool itself alongside documentation of its use within the Nayak Lab.

A.1 Summary

This is a tool for automating HMM-based gene searches using profile hidden markov models. This program takes an input folder of HMMs & and an input folder of Prokka annotated genomes. It searches each genome with each HMM, recording the HMMER output in an intermediate directory (hmm_out). Then, it parses the HMMER output using SimpleHMMER and records all hits, their locus ID, and score/e-value for each pHMM in an hmm_hits directory, where each genome's hits are recorded in a genome-specific ouput csv. Hits beyond the TC score threshold (designated in the profile HMM) are counted and recorded in an output presence/absence matrix, where each genome is a row, and each input HMM is a column. This code all allows you to pull sequences (amino acid) from the hmm hits, recording them in an output .fa or .fna file for downstream phylogenetic analyses. Some aspects of this work are based on the structure put forth by Gray Chadwick, which can be found at: Phylogenomic Gene Cluster Display

A.2 A brief overview of use

A.2.1 Step 1

You'll need a set of genomes (organized in their own directory) and a set of HMMs of interest (organized in their own directory). For the genomes, make sure they have a .fna extension (see step #2 for caveat). The output will use whatever name the HMM file is labelled as (i.e. 'mcrA' for the 'mcrA.HMM' file). For my work, I have used genomes downloaded from GTDB (latest release here & annotated with prokka, as well as Biopython, HMMER (installs with Prokka, otherwise will have to independently install), and SimpleHMMER.

A.2.2 Step 2

The HMMER code runs on any set of genomes, so long as they have been annotated and use the ".fna" extension (though the script can be modified to take in other nucleotide file extensions). If you are using genomes supplied by GTDB, these should download with the "_genomic.fna" extension. This works best when you first annotate your genomes using Prokka; instructions and usage can be found here). If you would like to loop Prokka through a directory of genomes, use the following command (put forth by the prokka dev's here):

```
for F in ./*_genomic.fna; do
N=$(basename $F _genomic.fna) ;
prokka --gcode 15 --locustag $N --outdir $N --prefix $N  $F ;
done
```

A.2.3 Step 3

Running the code. This script has two options: 1. 'hmm' which loops through all hmm's, thresholds, & counts hits, & 2. 'seq' which uses the thresholded hmm hits to pull sequences from the prokka annotated .faa files for downstream phylogenetic analyses. You can customize an e-value for use here, otherwise it uses a default value of 1e-3.

To run '**hmm**':

```
usage: python hmm_tools.py hmm [-h] [-g GENOMES] [-hm HMMS] [-e EVALUE] [-s
{tc,nc}]

options:
  -h, --help            show this help message and exit
  -g GENOMES, --genomes GENOMES
                        Path to genome directory
  -hm HMMS, --hmms HMMS
                        Path to hmm directory. All files should have a .HMM
extension and named
                        according to gene
  -e EVALUE, --evalue EVALUE
                        Specify e-value for parsing hmm output.
  -sc {tc,nc}, --score {tc,nc}
                        Specify filtering threshold. "TC" uses the trusted
cutoff designated in the HMM, whereas "NC" uses the noise cutoff.
```

To run '**seq**':

```
usage: python hmm_tools.py seq [-h] [-hi HITS] [-hm HMMS] [-g GENOMES] [-s
{nt,aa}] [-f {all,tc}]

options:
  -h, --help            show this help message and exit
  -hi HITS, --hits HITS
                        Path to hmm_hits. This is an intermediate directory
produced by hmm searcher.
  -hm HMMS, --hmms HMMS
                        Path to hmm directory
  -g GENOMES, --genomes GENOMES
                        Path to genome directory
  -s {nt,aa}, --sequence {nt,aa}
                        Specify sequence type. Nucleotide (-nt) or amino acid
(-aa)
  -f {all,tc}, --filter {all,tc}
                        Specify filtering threshold. "All" removes score
threshold, whereas "tc" imposes
                        the TC cutoff from the seed HMM.
```

A.3 Use cases

The described HMM tool has been used in several research publications (both published, submitted, and in preparation) within our lab. In the first use case, we map the distribution of *comF* sequences, colloquially known as methanogenesis marker protein, and gauge its co-occurrence with known components of coenzyme M biosynthesis. The publication describing its original use can be found at *PLOS Genetics*. In chapter 2 of this dissertation, we use this tool to map the distribution of Pyl biosynthetic and incorporation machinery, alongside associated metabolic modules like MCR, component A2, and methylamine methyltransferases. As previously mentioned, work pertaining to chapter 2 and the bioinformatic findings therein can be found at *bioRxiv.* Finally, bioinformatic analyses focused on the distribution of energy conservation modules in the *Methanosarcinia* can be found in an upcoming publication.

Appendix B. Supplementary figures to Chapter 2

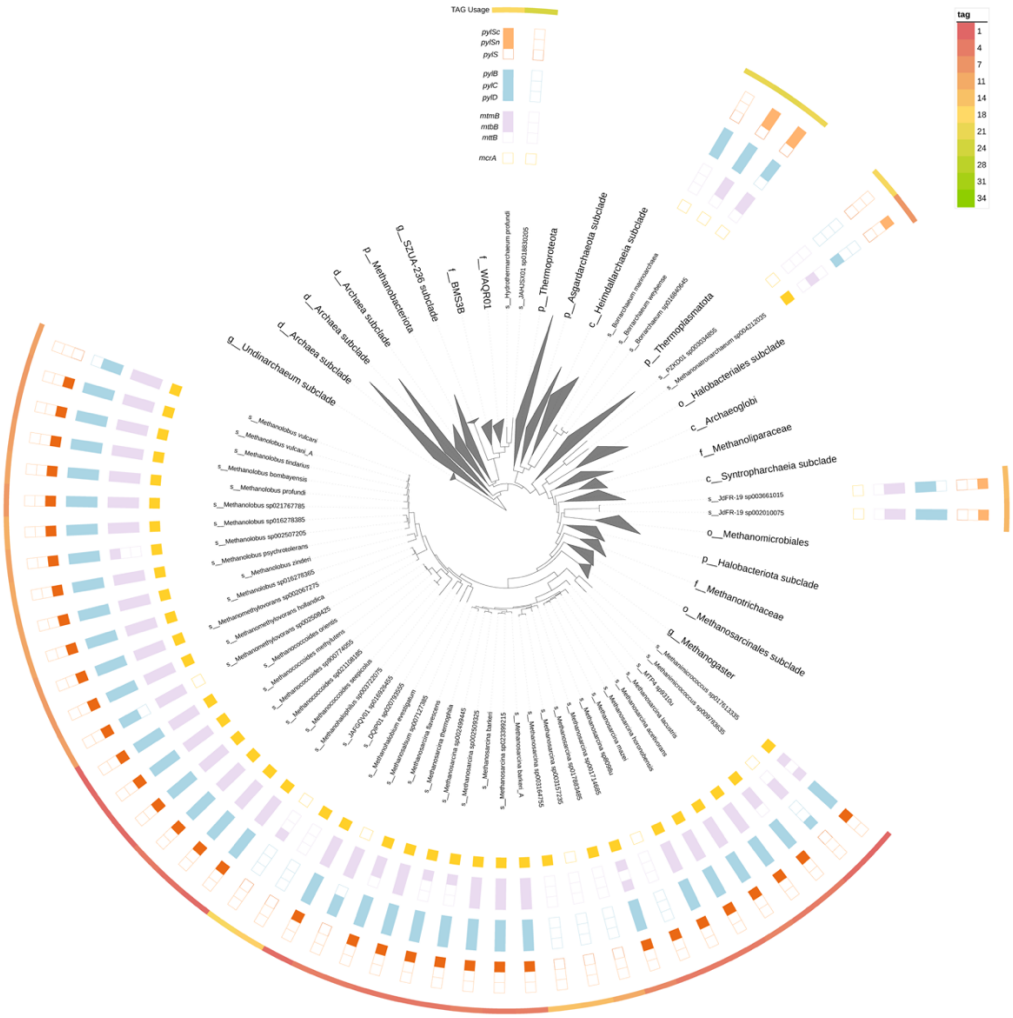

Fig S2.1. Presence and absence of genes encoding the Pyrrolysine (Pyl) biosynthesis (*pylBCD*) and incorporation modules (*pylTS*), methylamine methyltransferases, methyl- coenzyme M reductase subunit A (*mcrA*) overlaid on the archaeal phylogeny from GTDB r214.0. Genomes exceed a checkM completeness threshold of 80% and the completeness score is indicated in blue. TAG stop codon usage is indicated by the red-green gradient and clades universally lacking *pylBCD* and *pylTS* have been collapsed. **mcrA:** methyl coenzyme M reductase subunit Alpha; **mtmB:** mono-methylamine methyltransferase; **mtbB:** di-methylamine methyltransferase; **mttB:** tri-methylamine methyltransferase; **pylB:** methyl-ornithine synthase; **pylC:** 3-methylornithin L-lysine ligase; **pylD:** 3-methylornithyl-N6-L-lysine dehydrogenase; **pylS:** pyrrolysine $tRNA^{Pyl}$ ligase; **pylSn:** N-terminal subunit pyrrolysine $tRNA^{Pyl}$ ligase; **pylSc:** C-terminal subunit pyrrolysine $tRNA^{Pyl}$ ligase.

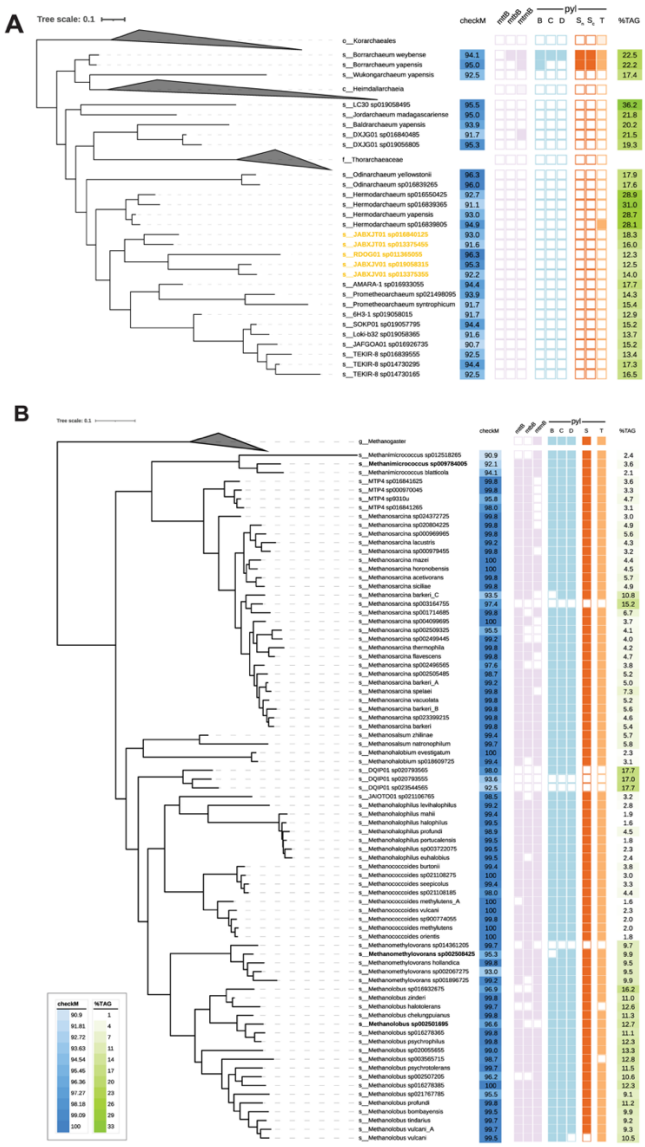

Fig S2.2. Pyl is found sporadically in *Asgardarchaeota* and widely in *Methanosarcinaceae*. All genomes exceed a CheckM threshold of 90%; scales are shared between trees. TAG stop codon usage is indicated by the white-green gradient. **A)** Tree for the phylum *Asgardarchaeota*; bolded yellow text indicates genomes that have the methane metabolism marker genes. **B)** Tree for the family *Methanosarcinaceae*; genomes in bold lack at least one of the following: *mcrA, mcrB, mcrG* or *atwA* (component A2). **mtbB:** di-methylamine methyltransferase; **mttB:** tri-methylamine methyltransferase; **pylB:** methyl-ornithine synthase; **pylC:** 3-methylornithine L-lysine ligase; **pylD:** 3-methylornithyl-N6-L-lysine dehydrogenase; **pylS:** pyrrolysine $tRNA^{Pyl}$ ligase; **pylSn:** N-terminal subunit pyrrolysine $tRNA^{Pyl}$ ligase; **pylSc:** C-terminal subunit pyrrolysine $tRNA^{Pyl}$ ligase; **pylT:** $tRNA^{Pyl}$.

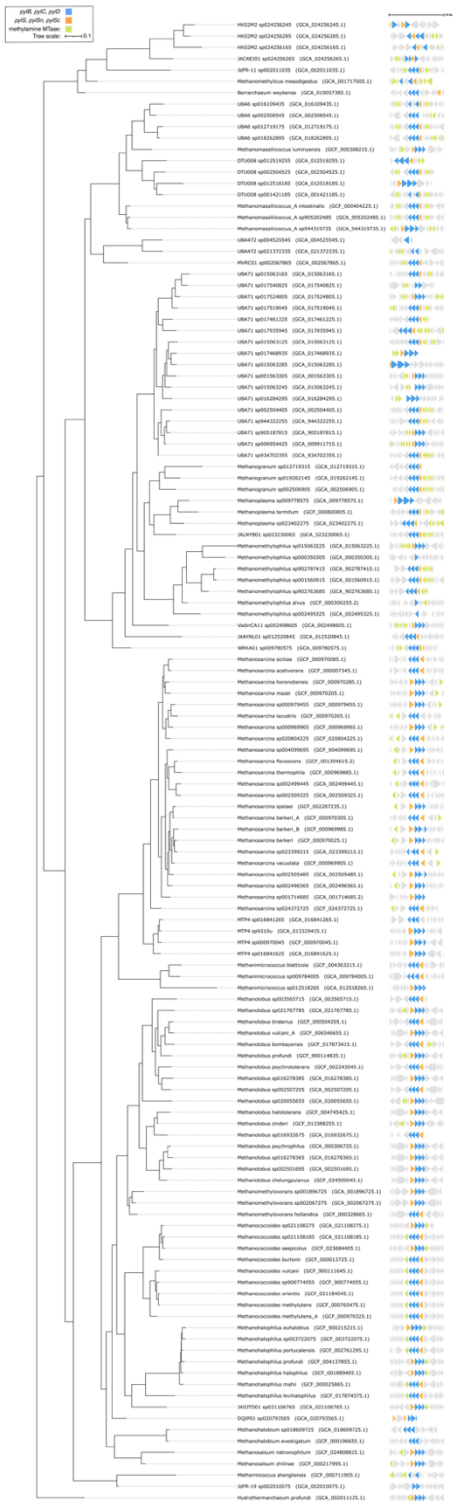

Fig S2.3. Genomic neighborhood of Pyrrolysine (Pyl) biosynthetic machinery in Pyl^{+} genomes (i.e. genomes that encode *pylBCD, pylT,* and *pylRS*). Pyl biosynthetic machinery is in blue, Pyl incorporation genes are in orange, and methylamine-specific methyltransferases are in green. Genome neighborhoods are centered around *pylB* and include 7.5 kb up and downstream of the start and stop sites. **MTase:** methyltransferase; **pylB:** methyl-ornithine synthase; **pylC:** 3-methylornithin L-lysine ligase; **pylD:** 3-methylornithyl-N6-L-lysine dehydrogenase; **pylS:** pyrrolysine tRNA^{Pyl} ligase; **pylSn:** N-terminal subunit pyrrolysine tRNA^{Pyl} ligase; **pylSc:** C-terminal subunit pyrrolysine tRNA^{Pyl} ligase; **pylT:** tRNA^{Pyl}.

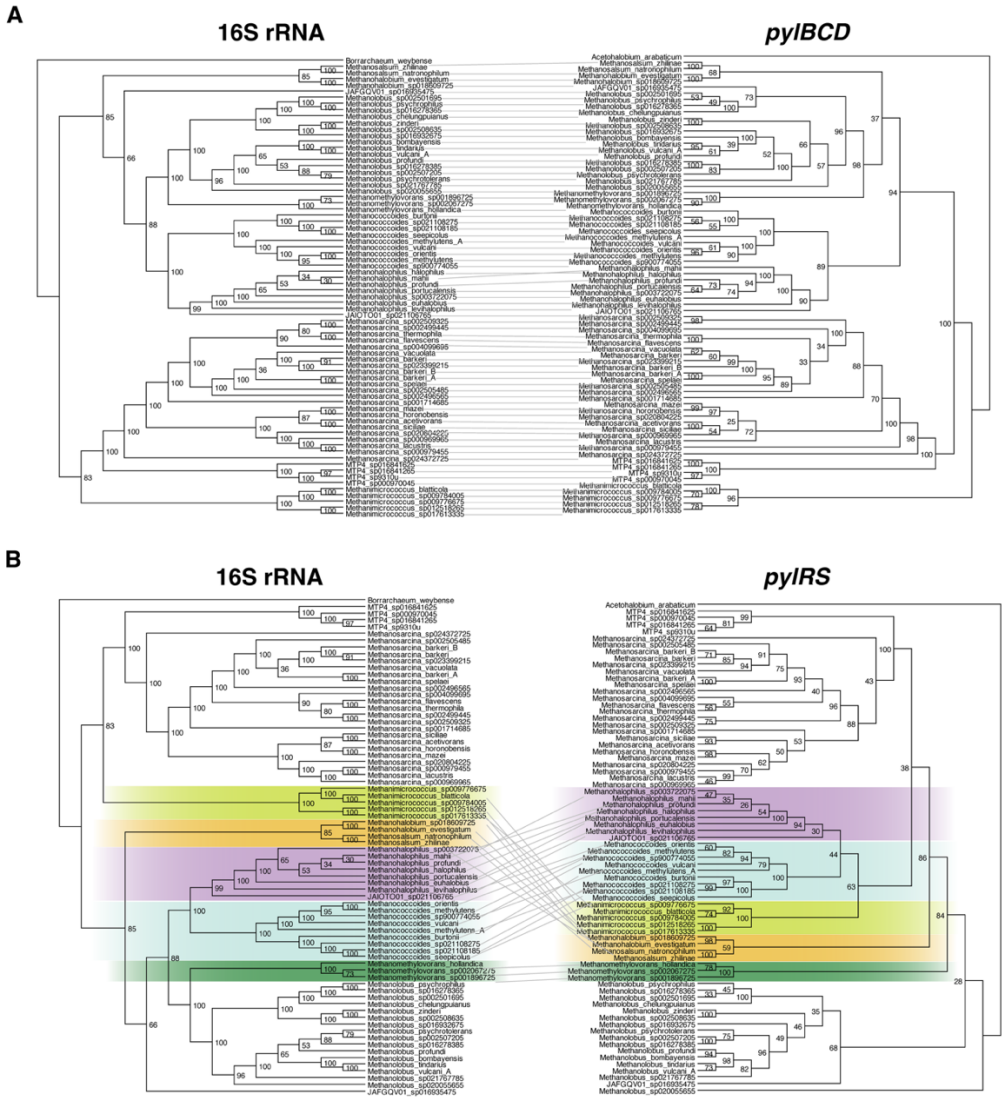

Fig S2.4. Tanglegram comparing the gene trees for the Pyrrolysine (Pyl) biosynthetic and incorporation components and the 16S rRNA tree for members of the family *Methanosarcinaceae.* All 16S ribosomal RNA trees are rooted to the 16S rRNA of *Borrarchaeum weybense*, and gene trees are rooted to the bacterial Pyl sequences from *Acetohalobium arabaticum*. A tanglegram for **A)** concatenated *pylBCD* alignments and **B)** *pylS* alignments, contrasted with the species tree of the family *Methanosarcinaceae.* Notable differences in tree topologies are highlighted in colors distinguished by genus taxonomy. Species tree was generated by RAxML using an alignment of 16S rRNA gene sequences derived from GTDB r214.0. Gene trees were generated using a MAFFT alignment, which was trimmed at 90% with TrimAl, concatenated, and assembled with RAxML 8.2.11 plug-in (GAMMA BLOSUM62 matrix, rapid-hill climbing with bootstrapping, n=100). Node labels represent bootstrap values.

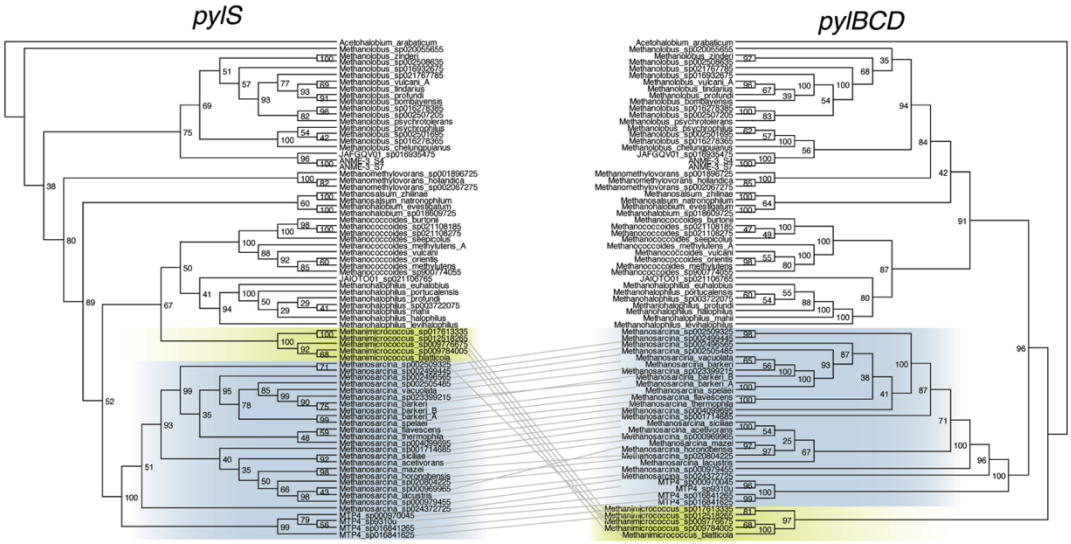

Fig S2.5. A tanglegram contrasting the Pyl incorporation (*pylS*) and biosynthetic (*pylBCD*) components from Fig S4. Both trees are rooted to the bacterial Pyl+ genome, *Acetohalobium arabaticum*. Significant differences in tree topology are highlighted by genus in color. Tree was generated with RAxML 8.2.11 (GAMMA BLOSUM62, n =100). Node labels represent bootstrap values.

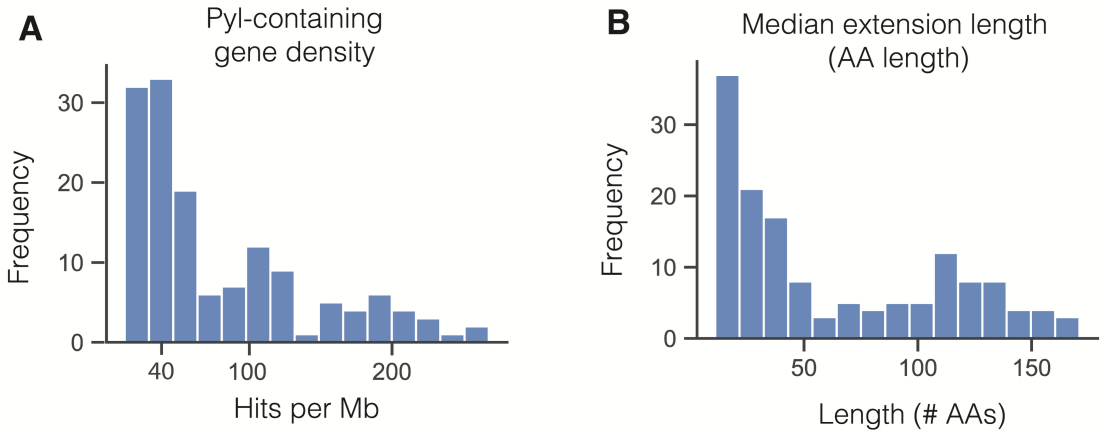

Fig S2.6. Histograms depicting genomic features of predicted Pyrrolysine (Pyl) containing genes. **A)** Pyl-containing gene density. Per genome, putative Pyl-containing genes were counted and normalized to genome size (Mb). **B)** Median extension length for predicted Pyl-containing genes per genome. Extension lengths were calculated as the distance between the first Pyl residue in an open reading frame and a downstream alternate stop codon (TAA or TGA).

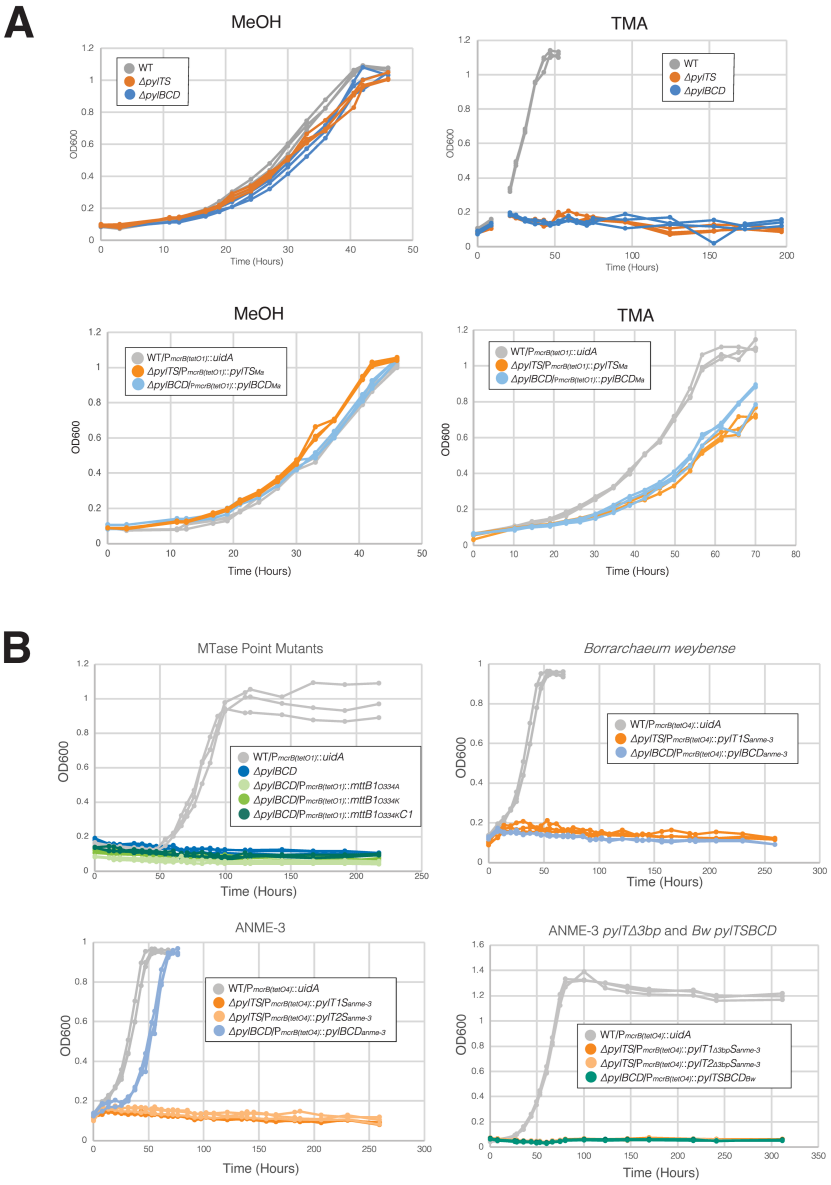

Fig S2.7. Triplicate growth curves for experiments using *Methanosarcina acetivorans* as a heterologous host to express *pyl* genes from archaea. **A)** Growth curves of WWM60 (denoted as wildtype or WT; in gray), single deletion knockouts of the Pyl biosynthetic (Δ*pylBCD;* blue) and incorporation genes (Δ*pylTS;* orange) in the WWM60 background in high-salt (HS) medium supplemented with either 125 mM methanol (MeOH) or 50 mM trimethylamine (TMA) as indicated. All complementation mutants express the deleted genes *in trans* from a tetracycline inducible promoter P*mcrB*(*tetO1*). For WT, a control gene, encoding β-glucuronidase*, uidA*, was expressed *in trans* on a plasmid. Growth curves were conducted in medium supplemented with puromycin at 2 µg/ml (to maintain the plasmid) and tetracycline at 100 µg/ml(to fully induce gene expression). **B)** Growth curves for TMA methyltransferase (*mttB*) point mutants and all heterologous expression mutants. *mttB1* point mutants include: $mttB_{O334A}$ (light green), $mttB_{O334K}$

(green), and $mttB_{O334K}C$ (dark green). Heterologous expression strains include: $pylTS_{Bw}$ (orange), $pylT1S_{anme\text{-}3}$ (dark orange), $pylT2S_{anme\text{-}3}$ (light orange), $pylBCD_{Bw}$ (blue), $pylBCD_{anme\text{-}3}$ (blue), $pylT1_{\Delta 3bp}S_{anme\text{-}3}$ (dark orange), $pylT2_{\Delta 3bp}S_{anme\text{-}3}$ (light orange), and $pylTSBCD_{Bw}$ (teal). All genes were expressed from a tetracycline inducible promoter P*mcrB*(*tetO1*) (*mttB* point mutants) or at P*mcrB*(tetO4) (non-native Pyl machinery) *in* trans on a plasmid. Growth curves were conducted in medium supplemented with puromycin at 2 µg/ml (to maintain the plasmid) and tetracycline at 100 µg/ml(to fully induce gene expression). Each point mutation is indicated in the graphical legend using the following amino acid codes: **O:** Pyrrolysine; **A:** Alanine; **K:** Lysine. ***Ma:*** *Methanosarcina acetivorans;* ***Bw:*** *Borrarchaeum weybense.*

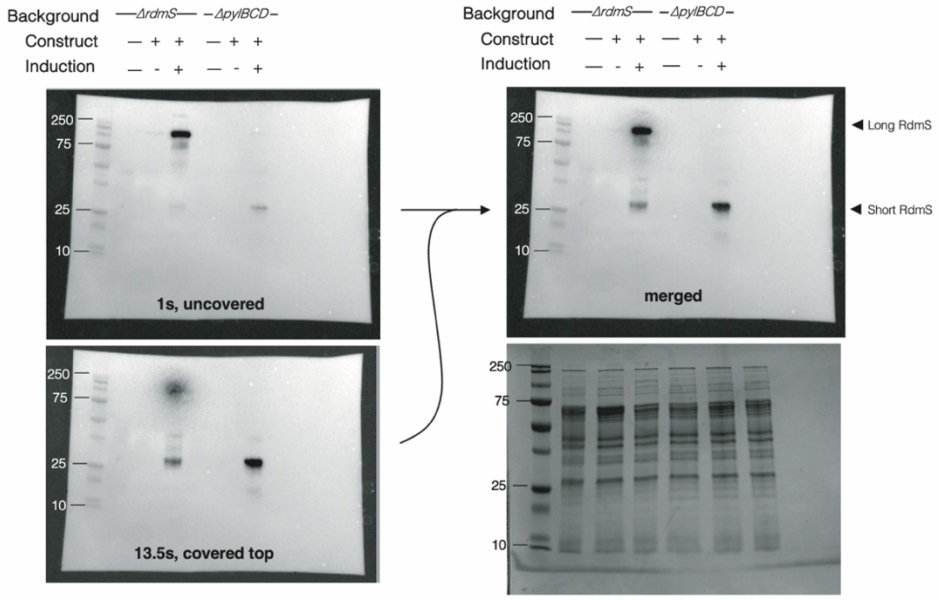

Fig S2.8. Full images for the anti-FLAG Western blot and the Coomassie stained protein gels shown in Fig 4A. The membrane was imaged twice (left) to gain a higher resolution image of the short-form RdmS band. The membrane was first exposed for 1s (top left), then, upper bands were covered to prevent oversaturation, and the membrane was imaged for 13.5s (bottom left). The two images were then merged (top right). Coomassie stained SDS-PAGE gel is shown as a loading control (bottom right), for near equal loading of 30 µg crude cell lysates. Plus symbols indicate the presence of a plasmid construct expressing the target gene from a tetracycline-inducible promoter (PmcrB(tetO4)) at full induction (100 µg/ml tetracycline) with puromycin added to maintain the plasmid.

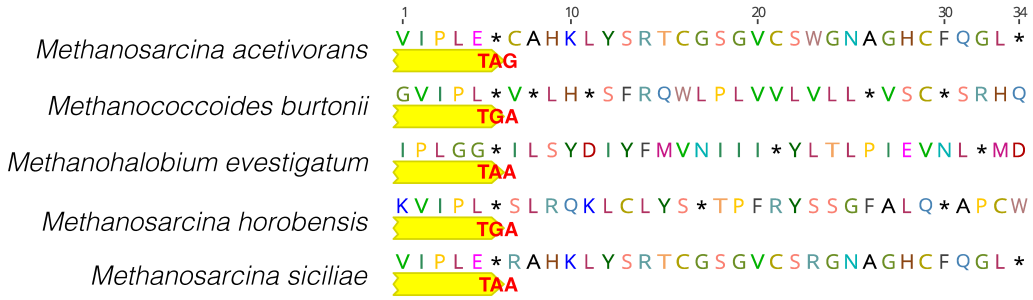

Fig S2.9. RnfA amino acid sequences from members of *Methanosarcinaceae* with different stop codon identities. Sequences shown are from the region five amino acids upstream of the stop codon to 28 amino acids downstream of the stop codon, which corresponds with the predicted 28 AA extension for *rnfA* from *Methanosarcina acetivorans.* The stop codon identity is indicated in bolded red text on the gene annotation beneath the amino acid sequence. Annotations and translations for the downstream *rnfB* sequence were excluded for clarity.

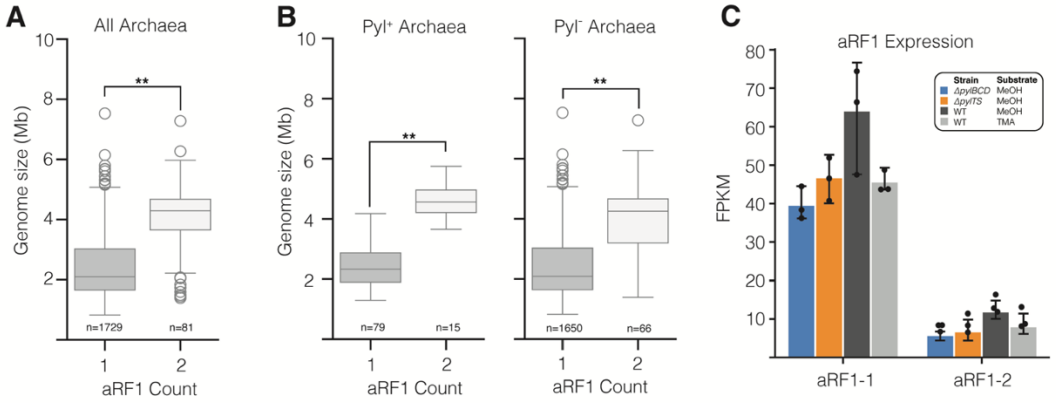

Fig S2.10. Box and whisker plots describing the relationship between archaeal release factor (aRF1) copy number and genome size. **A)** Relationship between aRF1 copy number and genome size across all archaea. **B)** Relationship between aRF1 and genome size within Pyl^+ and Pyl^- genomes within archaea. **C)** FPKM (Fragment per kilobase per million reads) values for aRF1-1 and aRF1-2 in the Δ*pylBCD* mutant on methanol (MeOH) (blue), Δ*pylTS* mutant on MeOH (blue), WWM60 (parent strain also referred to as wildtype or WT) on MeOH (light gray) or trimethylamine (TMA) (dark gray). Error bars represent the standard deviation in triplicate FPKM values. No pairwise comparison of FPKM values for aRF1 copies by DESeq2 were called as significantly differentially expressed (q<0.001 and $\log_2$-fold≤-1.5 or $\log_2$-fold≥1.5); full data can be found in Table S8. All statistical tests in panels A and B were conducted using Welch's t-test where **p<0.001. Note that we only consider hits for aRF1, and not eRF1 in this analysis given that its function in archaea is not yet mapped.

Co-occurrence of Pyl Biosynthetic machinery (*pylBCD*) **and Pyl incorporation machinery** (*pylTS*)**.**

		pylTS +	*pylTS* -
pylBCD	+	95	36
	-	5	1745

p-value = 1.4e-273

Co-occurrence of Pyl with markers of methylamine metabolism (methylamine-specific methyltransferases).

		MA MTase +	MA MTase -
Pyl	+	91	4
	-	57	1729

p-value = 2.9e-231

Co-occurrence of Pyl with markers of methane metabolism (MCR and component A2).

		Methane-metabolism +	Methane-metabolism -
Pyl	+	86	9
	-	396	1390

p-value = 3.1e-49

Co-occurrence of Pyl with markers of methanogenesis (MCR and component A2, corrected for ANME).

		Methanogenesis +	Methanogenesis -
Pyl	+	86	9
	-	371	1729

p-value = 1.1e-51

Table S2.1. Counts for each x2 test used to evaluate the co-occurrence of marker genes within genomes. p-values generated in the testing for co-occurrence are indicated below each table. Pyrrolysine (Pyl) is indicated by the presence of pylBCD (biosynthetic genes), pylT (tRNA(pyl)), and a complete Pyl tRNA synthetase (i.e., pylS, ΔpylSn, pylSn+pylSc). Methylamine methyltransferase (MA MTase) is defined as the presence of at least one methylamine-specific MTase (i.e. monomethylamine, mtmB; dimethylamine, mtbB; trimethylamine, mttB). Methane metabolism refers to the presence of all three catalytic units of Methyl Coenzyme M Reductase (mcrABG) and component A2. Methanogens refer to the group of all putative methane-metabolizers corrected to exclude those belonging to Anaerobic Methanotrophic Archaea (ANME). All genomes used in this analysis surpassed a CheckM completeness threshold of 90%.

genome	GC content	TAG	TGA	TAA	mttB	mtbB	mtmB	pylB	pylC	pylD	pylS	pylSn	pylSc	pylT	mcrA	mcrB	mcrG	component-A2	checkM
GCA_000405245.1	38.6	0.22	0.32	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	47.35
GCA_011773475.1	31.2	0.16	0.28	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.54
GCA_017608545.1	29.1	0.12	0.31	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.29
GCA_018221065.1	33.2	0.21	0.30	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.91
GCA_017609445.1	38.0	0.24	0.34	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.54
GCA_016933455.1	41.4	0.31	0.35	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_021163145.1	27.2	0.13	0.23	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_018901755.1	31.9	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_018901655.1	30.5	0.17	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.78
GCA_013152905.1	45.8	0.16	0.44	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.46
GCA_015521825.1	54.0	0.15	0.55	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.86
GCA_016198755.1	40.3	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.4
GCA_018920255.1	25.7	0.12	0.18	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.93
GCA_018920245.1	47.9	0.25	0.40	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.24
GCA_015521535.1	36.0	0.17	0.33	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.53
GCA_015661515.1	29.9	0.13	0.23	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.67
GCA_002789635.1	37.2	0.25	0.32	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_014728985.1	34.9	0.22	0.28	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_017610225.1	30.7	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	2	0	0	0	0	78.66
GCA_017608955.1	27.8	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.75
GCA_018304545.1	33.8	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.06
GCA_018920345.1	29.1	0.14	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_018920365.1	31.6	0.17	0.31	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_025058005.1	33.4	0.19	0.35	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.89
GCA_001784635.1	47.6	0.27	0.43	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.92
GCA_002254545.1	27.7	0.15	0.27	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.22
GCA_021161745.1	38.3	0.26	0.33	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_014238095.1	24.3	0.07	0.19	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016213525.1	56.3	0.33	0.48	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016177025.1	40.5	0.20	0.31	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.35
GCA_016187415.1	40.5	0.21	0.30	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_018920185.1	34.2	0.19	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016181005.1	42.9	0.23	0.32	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_016187385.1	39.7	0.19	0.34	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.66
GCA_016187405.1	38.4	0.19	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.27
GCA_016198705.1	37.5	0.19	0.32	0.50	0	0	0	0	0	0	0	0	0	1	0	0	0	0	82.71
GCA_018304615.1	39.6	0.21	0.37	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_004297575.1	44.8	0.24	0.36	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_021161995.1	33.6	0.29	0.30	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.52
GCA_018920305.1	25.5	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.95
GCA_023256115.1	26.1	0.12	0.28	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.45
GCA_025058985.1	28.2	0.18	0.31	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.55
GCA_020832825.1	33.9	0.23	0.28	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.13
GCA_025057985.1	34.0	0.23	0.26	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_015522145.1	34.2	0.21	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.21
GCA_002688965.1	33.7	0.18	0.25	0.58	0	0	0	0	0	0	0	0	0	1	0	0	0	0	76.79
GCA_903825675.1	38.9	0.23	0.30	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.38
GCA_000806115.1	49.0	0.27	0.34	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_018304605.1	48.2	0.25	0.33	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.48
GCA_013331845.1	41.6	0.23	0.28	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_016180945.1	44.7	0.22	0.32	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_016180925.1	49.7	0.21	0.48	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_016187365.1	50.1	0.21	0.50	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.3
GCA_016184005.1	44.7	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_018304565.1	44.2	0.22	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_016187335.1	47.0	0.20	0.39	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_016198625.1	52.6	0.26	0.41	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.12
GCA_016193585.1	52.5	0.28	0.41	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_016191585.1	41.3	0.22	0.30	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.18
GCA_016198645.1	51.4	0.13	0.54	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.89
GCA_016198685.1	45.2	0.19	0.42	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_018304585.1	49.6	0.18	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.83
GCA_016202845.1	40.2	0.20	0.33	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.55
GCA_016202875.1	44.0	0.22	0.41	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.98
GCA_016187395.1	45.8	0.27	0.43	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.92
GCA_016213555.1	31.6	0.25	0.19	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.86
GCA_016219465.1	36.5	0.24	0.31	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.12
GCA_016219485.1	41.5	0.25	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.41
GCA_018304635.1	35.3	0.18	0.38	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.46
GCA_021157845.1	34.5	0.22	0.28	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_021163205.1	38.9	0.25	0.33	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.95
GCA_021158665.1	39.1	0.16	0.40	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.13
GCA_018920315.1	30.9	0.20	0.23	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.93
GCA_015522745.1	43.2	0.13	0.48	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_015523085.1	47.9	0.14	0.53	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.11
GCA_016177205.1	49.6	0.20	0.41	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.72
GCA_016180965.1	44.2	0.16	0.37	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_016195275.1	45.3	0.21	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.07
GCA_016202795.1	45.2	0.21	0.35	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_016202815.1	48.5	0.19	0.42	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_003663345.1	45.4	0.20	0.52	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.95
GCA_016198635.1	53.7	0.33	0.37	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.14
GCA_016432325.1	55.9	0.32	0.44	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_016219455.1	48.2	0.26	0.45	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.09
GCA_021162085.1	37.4	0.16	0.38	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_021160955.1	38.7	0.13	0.50	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_020355185.1	44.5	0.23	0.34	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.01
GCA_023133195.1	38.9	0.19	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_003550625.1	44.8	0.32	0.35	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_003553905.1	41.5	0.30	0.32	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_003554235.1	43.8	0.27	0.37	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.25
GCA_003554845.1	43.4	0.36	0.33	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_003555465.1	46.0	0.30	0.35	0.35	0	0	0	0	0	0	0	0	0	1	0	0	0	0	79.44
GCA_022257805.1	46.4	0.30	0.39	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87
GCA_016202865.1	39.1	0.28	0.24	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.6
GCA_016931255.1	46.9	0.21	0.46	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_020343635.1	49.5	0.24	0.44	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.03
GCA_021163005.1	49.5	0.21	0.48	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.1
GCA_016934325.1	54.1	0.24	0.60	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.02
GCA_016783545.1	35.9	0.23	0.22	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_016782405.1	44.9	0.23	0.42	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.85
GCA_020343575.1	42.9	0.22	0.32	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.66
GCA_016185435.1	47.1	0.27	0.46	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_016198605.1	52.9	0.30	0.40	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.86
GCA_016202745.1	52.0	0.29	0.41	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.65
GCA_016202785.1	57.7	0.34	0.44	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.49
GCA_016198585.1	63.2	0.27	0.56	0.17	0	0	0	0	0	0	0	0	0	1	0	0	0	0	75.39
GCA_016202725.1	63.2	0.23	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.52
GCA_017609225.1	41.6	0.21	0.32	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.15
GCA_017609145.1	44.9	0.23	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.57
GCA_018818465.1	35.9	0.19	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018816245.1	50.8	0.23	0.34	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_003663225.1	51.9	0.29	0.49	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.82
GCA_003663415.1	38.8	0.15	0.32	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_003663445.1	46.9	0.20	0.39	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.95
GCA_016867675.1	54.6	0.31	0.43	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.07
GCA_015520105.1	49.9	0.24	0.44	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.79
GCA_011772645.1	46.2	0.26	0.32	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.68
GCA_023128965.1	45.4	0.20	0.37	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_013151465.1	42.4	0.18	0.40	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.27
GCA_016932735.1	42.5	0.20	0.36	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_016932215.1	48.1	0.22	0.41	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.38
GCA_021162425.1	40.0	0.16	0.40	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_003663325.1	37.4	0.29	0.24	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.54
GCA_016932615.1	46.7	0.35	0.23	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_023659895.1	32.6	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_003663295.1	32.9	0.13	0.22	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.97
GCA_003663355.1	30.1	0.16	0.27	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_021163805.1	31.9	0.14	0.27	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_023134135.1	32.7	0.14	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.72
GCA_023659935.1	31.6	0.19	0.22	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.18
GCA_023659975.1	31.4	0.17	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.56
GCA_001873845.1	32.2	0.12	0.24	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.02
GCA_002083985.1	31.8	0.11	0.22	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.41
GCA_018260615.1	33.1	0.10	0.22	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.02
GCA_018260755.1	32.0	0.11	0.19	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.19
GCA_001742785.1	48.5	0.20	0.35	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.12
GCA_001723855.1	40.8	0.17	0.37	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.88
GCA_023252215.1	48.4	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.77
GCA_903930485.1	51.5	0.21	0.42	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.02
GCA_002254405.1	44.3	0.21	0.35	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.77
GCA_002254565.1	45.6	0.26	0.37	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.8

GCA_016931955.1	46.8	0.29	0.37	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.08
GCA_021731385.1	39.3	0.20	0.36	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.7
GCA_003663045.1	39.2	0.21	0.33	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.98
GCA_003663115.1	43.5	0.24	0.35	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.42
GCA_003663175.1	38.3	0.18	0.33	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.68
GCA_015523055.1	45.0	0.26	0.37	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.72
GCA_018897475.1	47.5	0.27	0.35	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.02
GCA_902384455.1	50.5	0.21	0.32	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.61
GCA_011380095.1	49.9	0.27	0.31	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.01
GCA_018815265.1	44.0	0.27	0.37	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.34
GCA_000402775.1	44.8	0.19	0.36	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.31
GCA_016867655.1	46.0	0.26	0.35	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.82
GCA_014729705.1	47.5	0.23	0.34	0.43	0	0	0	0	0	0	0	0	0	1	0	0	0	0	85.51
GCA_014727915.1	54.3	0.30	0.44	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.74
GCA_001723845.1	37.1	0.10	0.34	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.06
GCA_016935655.1	50.7	0.30	0.37	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.21
GCA_016840465.1	45.9	0.20	0.43	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.93
GCA_016840485.1	36.7	0.22	0.21	0.57	0	0	1	0	0	0	0	0	0	0	0	0	0	0	91.67
GCA_019056805.1	35.5	0.19	0.18	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_021158895.1	37.1	0.21	0.21	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.67
GCA_016839515.1	32.9	0.18	0.21	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.61
GCA_003144275.1	36.1	0.21	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.69
GCA_011364965.1	34.9	0.22	0.24	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_016839625.1	36.2	0.21	0.29	0.50	0	0	1	0	0	0	0	0	0	0	0	0	0	0	80.61
GCA_016839665.1	36.5	0.20	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.76
GCA_016839785.1	36.1	0.21	0.27	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.42
GCA_016839815.1	36.0	0.22	0.25	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_016840035.1	36.1	0.22	0.25	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.01
GCA_016840285.1	36.0	0.20	0.30	0.51	0	0	1	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_016840305.1	34.9	0.20	0.26	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_019057635.1	36.2	0.22	0.28	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.42
GCA_020348965.1	37.3	0.21	0.30	0.49	0	0	1	0	0	0	0	0	0	0	0	0	0	0	74.57
GCA_020351745.1	36.2	0.18	0.30	0.52	0	0	1	0	0	0	0	0	0	0	0	0	0	0	69.16
GCA_020353515.1	35.9	0.20	0.29	0.52	0	0	1	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_001940645.1	29.7	0.17	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_024276395.1	40.3	0.14	0.49	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.35
GCA_015520535.1	36.9	0.14	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.06
GCA_016840025.1	36.9	0.24	0.26	0.50	0	0	1	0	0	0	0	0	0	0	0	0	0	0	85.91
GCA_016839955.1	34.7	0.21	0.27	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_013166835.1	33.7	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_016839405.1	30.0	0.17	0.19	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_016840905.1	32.1	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.15
GCA_016840945.1	31.7	0.18	0.19	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_018238155.1	32.8	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_019056785.1	38.6	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_019058165.1	33.8	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.3
GCA_019058275.1	32.5	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_019894765.1	34.1	0.23	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_023128635.1	33.9	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.77
GCA_024276795.1	42.0	0.30	0.30	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.07
GCA_024280435.1	32.8	0.21	0.30	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.31
GCA_002726275.1	30.1	0.12	0.21	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_016839545.1	44.1	0.29	0.37	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.43
GCA_001940725.1	32.6	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_021399405.1	34.4	0.19	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_022574115.1	38.0	0.23	0.29	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.3
GCA_015522385.1	46.7	0.31	0.38	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.86
GCA_015523565.1	38.6	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_019057815.1	32.8	0.21	0.25	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_023705985.1	32.9	0.22	0.26	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_021513695.1	31.2	0.21	0.17	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_021513715.1	30.8	0.21	0.18	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_001940755.1	33.4	0.24	0.23	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.37
GCA_019057375.1	33.1	0.24	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_013166775.1	32.9	0.24	0.21	0.55	0	0	0	0	0	0	0	0	1	0	0	0	0	0	93.46
GCA_016839875.1	33.6	0.25	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.28
GCA_016839945.1	32.2	0.23	0.21	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.4
GCA_016839985.1	31.9	0.22	0.22	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016840095.1	33.2	0.26	0.22	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_018238545.1	34.0	0.21	0.26	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_019894795.1	33.8	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.22
GCA_021399345.1	33.5	0.24	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_021399395.1	34.3	0.26	0.22	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_023132955.1	33.2	0.24	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_023135215.1	33.4	0.23	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_023136245.1	32.9	0.23	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.67
GCA_023139025.1	33.4	0.24	0.23	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_023270155.1	33.5	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.51
GCA_023705905.1	33.7	0.23	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.56
GCA_023705945.1	34.6	0.23	0.24	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.47
GCA_016550395.1	43.0	0.26	0.24	0.50	0	0	0	0	0	0	0	0	1	0	0	0	0	0	78.04
GCA_016550405.1	44.5	0.30	0.25	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.46
GCA_016550425.1	44.5	0.29	0.25	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.67
GCA_016839365.1	45.9	0.31	0.26	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_016839805.1	43.8	0.28	0.25	0.47	0	0	0	0	0	0	0	0	1	0	0	0	0	0	94.86
GCA_016839995.1	45.2	0.31	0.26	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.47
GCA_016840185.1	45.3	0.30	0.25	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_016840595.1	44.5	0.30	0.24	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.93
GCA_016840405.1	44.7	0.29	0.24	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_016550415.1	43.2	0.32	0.25	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.5
GCA_016550485.1	49.0	0.38	0.26	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.33
GCA_016840065.1	46.9	0.39	0.26	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_016840135.1	47.1	0.37	0.27	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_021162905.1	34.5	0.20	0.25	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_019057675.1	48.1	0.27	0.29	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.13
GCA_019057715.1	47.5	0.25	0.31	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.65
GCA_019056875.1	40.8	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.02
GCA_019058495.1	46.3	0.36	0.39	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.48
GCA_004524545.1	35.7	0.19	0.20	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.55
GCA_016839385.1	34.2	0.20	0.20	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.49
GCA_016839865.1	35.3	0.20	0.22	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.29
GCA_016933055.1	35.3	0.18	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_014729055.1	34.4	0.19	0.19	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.08
GCA_001940655.1	45.1	0.18	0.30	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.45
GCA_018238965.1	38.4	0.19	0.20	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.15
GCA_021498095.1	31.0	0.14	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.93
GCF_008000775.1	31.2	0.15	0.17	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.74
GCA_019058015.1	29.4	0.13	0.14	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.74
GCA_019058135.1	29.2	0.14	0.15	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.36
GCA_016839425.1	33.6	0.13	0.20	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.03
GCA_016840695.1	35.5	0.15	0.20	0.65	0	0	0	0	0	0	0	0	0	1	0	0	0	0	63.73
GCA_016930515.1	35.1	0.13	0.20	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_019057355.1	32.5	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.87
GCA_016926735.1	26.2	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_019894715.1	26.8	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_005223125.1	29.9	0.15	0.15	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_013375485.1	29.9	0.15	0.16	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_016839585.1	29.2	0.14	0.13	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.46
GCA_016839635.1	29.6	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.79
GCA_016839655.1	30.2	0.16	0.14	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_016839705.1	31.4	0.17	0.15	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_016839845.1	33.4	0.18	0.15	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_016839915.1	29.9	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_016840085.1	29.5	0.15	0.14	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_019057775.1	31.4	0.17	0.16	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_019057865.1	29.1	0.14	0.14	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.88
GCA_019057975.1	30.2	0.17	0.16	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.51
GCA_019058245.1	29.0	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.52
GCA_019058365.1	29.5	0.14	0.15	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_019058425.1	29.8	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.41
GCA_019894875.1	31.6	0.17	0.15	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.33
GCA_019894975.1	31.7	0.17	0.14	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_020343655.1	29.5	0.15	0.13	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_020344955.1	29.7	0.14	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_004524515.1	30.4	0.14	0.14	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.21
GCA_019058445.1	31.0	0.14	0.13	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_019058515.1	33.5	0.19	0.16	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_004524385.1	30.5	0.14	0.13	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.23
GCA_004524535.1	30.4	0.14	0.13	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.09
GCA_019058295.1	30.8	0.13	0.13	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.52
GCA_004375715.1	32.3	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.7
GCA_004524725.1	32.1	0.15	0.15	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.94
GCA_005222975.1	31.5	0.15	0.12	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57

GCA_011364925.1	33.0	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_011364975.1	30.6	0.13	0.13	0.73	0	0	0	0	0	0	0	0	0	1	0	0	0	0	86.45
GCA_013375475.1	32.5	0.18	0.13	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_013375495.1	32.3	0.18	0.14	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_016839745.1	32.3	0.17	0.12	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_016839765.1	29.7	0.15	0.13	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_016840165.1	31.6	0.15	0.15	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_016840545.1	29.6	0.14	0.13	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.45
GCA_018238625.1	32.1	0.15	0.13	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_019057735.1	32.6	0.18	0.14	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_019057795.1	31.4	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_019894655.1	32.2	0.17	0.15	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.21
GCA_019894735.1	32.2	0.17	0.14	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.51
GCA_019894815.1	31.6	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.78
GCA_019894855.1	32.3	0.17	0.14	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.9
GCA_019894885.1	31.9	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.14
GCA_019894955.1	31.4	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_004524425.1	32.5	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.89
GCA_004524365.1	31.0	0.13	0.11	0.76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.54
GCA_008080735.1	33.6	0.16	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_008080765.1	33.2	0.17	0.16	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.19
GCA_014730165.1	30.9	0.16	0.16	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_014730295.1	33.4	0.17	0.17	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_016839555.1	29.6	0.13	0.12	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_014729315.1	33.6	0.17	0.18	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016839905.1	29.6	0.13	0.17	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.1
GCA_016932935.1	60.7	0.25	0.60	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.13
GCA_014729935.1	46.9	0.15	0.56	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.21
GCA_005191415.1	35.5	0.15	0.20	0.65	0	0	0	0	0	0	0	0	0	0	2	2	2	2	82.4
GCA_013375405.1	36.4	0.17	0.22	0.62	0	0	0	0	0	0	0	0	0	0	3	4	3	2	83.18
GCA_013375455.1	38.6	0.16	0.26	0.58	0	0	0	0	0	0	0	0	0	0	3	2	3	3	91.59
GCA_016840125.1	38.5	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	4	4	3	3	92.99
GCA_005191425.1	28.0	0.11	0.17	0.72	0	0	0	0	0	0	0	0	0	0	1	1	1	1	86.92
GCA_013375355.1	30.7	0.14	0.17	0.69	0	0	0	0	0	0	0	0	0	0	3	2	2	2	92.21
GCA_019058315.1	30.5	0.12	0.16	0.72	0	0	0	0	0	0	0	0	0	0	3	3	3	2	95.33
GCA_011365055.1	30.1	0.12	0.21	0.67	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.26
GCA_016839265.1	36.3	0.18	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.95
GCA_001940665.1	38.1	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_016294985.1	37.9	0.22	0.29	0.49	0	0	0	1	1	1	1	0	0	0	0	0	0	0	67.76
GCA_016840315.1	38.6	0.22	0.30	0.47	0	1	0	0	0	0	0	0	0	0	0	0	0	0	75.78
GCA_016840645.1	38.3	0.21	0.27	0.52	0	1	1	0	1	1	0	1	1	2	0	0	0	0	82.96
GCA_019057385.1	37.0	0.23	0.29	0.49	0	1	1	1	1	1	0	1	1	1	0	0	0	0	94.08
GCA_016840515.1	37.1	0.22	0.28	0.50	0	0	1	1	0	0	0	1	1	1	0	0	0	0	95.02
GCA_016292335.1	36.3	0.19	0.31	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.46
GCA_003662765.1	53.8	0.36	0.53	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_021498125.1	47.1	0.29	0.41	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_016839445.1	52.6	0.51	0.39	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_013388835.1	54.2	0.42	0.50	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_020348985.1	48.0	0.45	0.40	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.04
GCA_024276825.1	43.6	0.28	0.42	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.79
GCA_016840825.1	42.3	0.39	0.33	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.91
GCA_016841005.1	41.0	0.32	0.33	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_024275415.1	47.0	0.34	0.43	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_002825465.1	41.6	0.34	0.33	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_003345545.1	48.1	0.44	0.40	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_004524565.1	41.6	0.34	0.31	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_004524595.1	40.7	0.32	0.33	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_016839245.1	40.1	0.31	0.32	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.93
GCA_016839275.1	43.4	0.35	0.36	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_016840385.1	42.1	0.34	0.34	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.98
GCA_016933575.1	42.3	0.36	0.35	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_018238205.1	41.8	0.33	0.34	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.86
GCA_018238825.1	41.7	0.33	0.35	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_003345555.1	51.1	0.44	0.41	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_003345595.1	52.2	0.41	0.48	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.31
GCA_008080745.1	41.2	0.32	0.28	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_014728035.1	39.5	0.30	0.31	0.39	0	0	0	0	0	0	0	0	0	1	0	0	0	0	93.46
GCA_001563335.1	42.2	0.36	0.34	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.69
GCA_001940705.1	44.6	0.37	0.37	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.12
GCA_002825515.1	42.6	0.33	0.37	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_004376265.1	43.3	0.34	0.38	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_011364905.1	45.0	0.37	0.38	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.78
GCA_016839345.1	42.5	0.34	0.37	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_016840685.1	44.6	0.37	0.39	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_016840855.1	41.9	0.34	0.34	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_016840965.1	42.2	0.35	0.34	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_019057595.1	46.1	0.38	0.41	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.46
GCA_019894665.1	44.4	0.34	0.38	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_001563325.1	49.3	0.45	0.41	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_011364985.1	45.5	0.41	0.36	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.57
GCA_011365025.1	47.2	0.47	0.32	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_016839605.1	46.4	0.39	0.38	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.9
GCA_020355105.1	49.7	0.47	0.41	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.91
GCA_004524435.1	50.4	0.48	0.39	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.14
GCA_004524445.1	44.6	0.39	0.34	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_014730275.1	45.2	0.37	0.35	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.86
GCA_018335335.1	45.2	0.39	0.35	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.93
GCA_013138615.1	48.1	0.41	0.38	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.71
GCA_018238375.1	48.0	0.42	0.37	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_019057475.1	48.3	0.41	0.38	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_023134215.1	48.2	0.43	0.33	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.22
GCA_016840245.1	43.6	0.37	0.35	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.27
GCA_016840425.1	38.0	0.17	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_003551125.1	34.4	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_003553825.1	38.4	0.21	0.17	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_003558235.1	45.2	0.22	0.36	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_003660975.1	43.5	0.18	0.43	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_016177165.1	55.3	0.35	0.39	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018304505.1	47.1	0.20	0.37	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_024275665.1	38.8	0.07	0.51	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_024274695.1	51.4	0.14	0.61	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_021161465.1	44.0	0.24	0.39	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.81
GCA_021107635.1	39.3	0.18	0.35	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.56
GCA_023659865.1	42.3	0.20	0.41	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.89
GCA_016939415.1	55.4	0.15	0.63	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.83
GCA_021162685.1	39.6	0.23	0.44	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_015522845.1	52.1	0.26	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.95
GCA_023129115.1	56.0	0.26	0.45	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.79
GCA_024275655.1	43.0	0.25	0.40	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_015522495.1	40.3	0.24	0.39	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.07
GCA_003660865.1	41.2	0.20	0.39	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.36
GCA_017610525.1	42.9	0.20	0.40	0.40	0	0	0	0	0	0	0	0	0	1	0	0	0	0	71.96
GCA_013139905.1	32.8	0.13	0.27	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_023142905.1	37.2	0.13	0.27	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.3
GCA_002254415.1	28.0	0.09	0.17	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.81
GCA_003660905.1	36.4	0.15	0.27	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_023137195.1	35.3	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_013138765.1	36.4	0.14	0.40	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_013138805.1	40.3	0.19	0.48	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_019429125.1	34.0	0.16	0.36	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_023134675.1	39.1	0.19	0.45	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.61
GCA_019429005.1	29.8	0.12	0.24	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_013153555.1	33.1	0.16	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_015520895.1	31.5	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.15
GCA_015521505.1	31.3	0.18	0.32	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_017610545.1	42.8	0.22	0.35	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.66
GCA_023139785.1	41.8	0.23	0.34	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.07
GCA_018897155.1	40.6	0.15	0.32	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_002384675.1	43.7	0.19	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_015520605.1	44.3	0.14	0.51	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.47
GCA_003660555.1	43.2	0.28	0.47	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.52
GCA_003661465.1	50.1	0.22	0.50	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_012962055.1	50.5	0.28	0.48	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.54
GCA_001515185.1	50.5	0.27	0.39	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.87
GCA_004375695.1	51.8	0.28	0.41	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.8
GCA_023129675.1	53.4	0.28	0.42	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.71
GCA_020725055.1	56.3	0.31	0.45	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.08
GCA_020725895.1	53.4	0.23	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_014361095.1	51.9	0.24	0.46	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.08
GCA_001515205.2	54.8	0.24	0.53	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_021163965.1	53.6	0.32	0.42	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70
GCA_004347925.1	65.0	0.34	0.55	0.11	0	0	0	0	0	0	0	0	0	0	2	1	1	1	92.37
GCA_002010195.1	42.2	0.22	0.43	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35

GCA_002011215.1	39.5	0.18	0.44	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002011235.1	40.5	0.23	0.38	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.77
GCA_002494625.1	41.0	0.17	0.49	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.69
GCA_003662985.1	41.6	0.24	0.41	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.52
GCA_017656505.1	42.8	0.25	0.40	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000385565.1	43.2	0.20	0.44	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000025285.1	42.0	0.15	0.47	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.84
GCA_003663025.1	42.2	0.21	0.43	0.36	0	0	0	0	0	0	0	0	0	0	1	1	0	0	71.71
GCA_003663055.1	43.9	0.22	0.40	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.5
GCA_003978865.1	39.2	0.19	0.33	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.62
GCA_015520485.1	45.1	0.18	0.41	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35
GCF_000194625.1	47.0	0.21	0.44	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35
GCF_000008665.1	48.6	0.16	0.51	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_016757965.1	46.0	0.16	0.51	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002507545.1	44.3	0.16	0.49	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35
GCA_017656475.1	46.0	0.16	0.51	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.04
GCA_003662995.1	38.4	0.18	0.40	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_021163065.1	36.2	0.17	0.34	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.04
GCF_000025505.1	44.1	0.16	0.48	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_015520115.1	43.8	0.16	0.48	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.42
GCA_000789255.1	46.8	0.13	0.59	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.84
GCA_015163485.1	46.5	0.14	0.57	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.84
GCF_001006045.1	53.1	0.16	0.60	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002494725.1	44.5	0.13	0.62	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.16
GCA_015522195.1	43.6	0.12	0.62	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_015523645.1	41.4	0.18	0.54	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.95
GCA_002010045.1	39.8	0.17	0.42	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.69
GCA_002010215.1	44.8	0.18	0.50	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.77
GCA_002010285.1	42.3	0.17	0.47	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.92
GCA_015523665.1	33.9	0.15	0.37	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.24
GCA_015523335.1	45.1	0.19	0.43	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.04
GCA_004347865.1	45.9	0.23	0.51	0.27	0	0	0	0	0	0	0	0	0	1	1	1	1	1	97.6
GCA_011605865.1	41.7	0.18	0.51	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.54
GCA_025057895.1	37.1	0.17	0.48	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.62
GCA_025058735.1	35.9	0.17	0.45	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.37
GCA_025058955.1	40.1	0.17	0.46	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	1	84.02
GCA_025059545.1	40.2	0.19	0.45	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	1	92.96
GCA_002010305.1	40.2	0.16	0.43	0.41	0	0	0	0	0	0	0	0	1	2	2	2	2	2	99.84
GCA_015523685.1	44.2	0.15	0.61	0.24	0	0	0	0	0	0	0	0	0	2	2	2	2	0	95.6
GCA_002011165.1	41.2	0.10	0.57	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.08
GCA_014361165.1	46.7	0.10	0.71	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.53
GCA_003139855.1	51.8	0.29	0.40	0.32	0	0	0	0	0	0	0	0	0	1	1	1	1	1	95.92
GCA_003158275.1	51.5	0.28	0.40	0.32	0	0	0	0	0	0	0	0	0	0	2	0	1	1	74.16
GCA_003162175.1	52.2	0.28	0.40	0.32	0	0	0	0	0	0	0	0	0	1	1	1	1	1	94.58
GCA_003170935.1	48.7	0.26	0.35	0.39	0	0	0	0	0	0	0	0	0	1	1	1	1	1	90.03
GCA_015660915.1	51.0	0.29	0.40	0.32	0	0	0	0	0	0	0	0	0	1	1	1	1	1	96.57
GCA_015661395.1	52.0	0.28	0.40	0.32	0	0	0	0	0	0	0	0	0	1	1	1	1	1	96.41
GCF_000710615.1	57.8	0.24	0.42	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_900156425.1	57.0	0.24	0.42	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_020700235.1	56.1	0.25	0.43	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_000376445.1	61.8	0.22	0.51	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_001625445.1	60.2	0.21	0.53	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.69
GCA_003298465.1	63.0	0.28	0.53	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_020614375.1	62.1	0.24	0.52	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.87
GCF_020618475.1	57.7	0.25	0.48	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_021083305.1	59.2	0.23	0.50	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCA_024227995.1	67.9	0.29	0.59	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_004143485.2	64.6	0.27	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_004765805.1	67.3	0.26	0.60	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.23
GCF_008831545.1	61.5	0.27	0.47	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_003382685.1	65.9	0.27	0.55	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8
GCF_004765795.1	66.9	0.27	0.58	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_004087835.1	63.8	0.28	0.50	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_003369835.1	68.1	0.28	0.59	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_004765785.1	64.2	0.28	0.49	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_004765815.2	65.1	0.28	0.54	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_003023465.1	65.2	0.28	0.53	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.86
GCA_005239435.1	63.3	0.27	0.53	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_010747475.1	65.0	0.25	0.56	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.72
GCF_023238205.1	65.1	0.28	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_023238445.1	65.9	0.28	0.55	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.15
GCF_024138125.1	66.6	0.30	0.57	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_024138165.1	66.2	0.27	0.57	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.65
GCF_024218795.1	64.7	0.26	0.55	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_000196895.1	62.5	0.27	0.51	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.84
GCF_001593955.1	61.7	0.28	0.50	0.22	0	0	0	0	0	0	0	0	1	0	0	0	0	0	99.42
GCA_022561895.1	60.8	0.28	0.48	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.36
GCF_003697815.1	61.8	0.26	0.51	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.04
GCA_007128515.1	67.4	0.27	0.63	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.48
GCA_007129135.1	67.9	0.28	0.63	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.42
GCF_017094525.1	64.0	0.29	0.58	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.44
GCF_004799665.1	63.7	0.27	0.58	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_009741825.1	66.2	0.25	0.63	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.56
GCF_017094465.1	63.1	0.27	0.56	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.5
GCF_017094505.1	64.7	0.30	0.58	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.01
GCF_000336615.1	62.1	0.25	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.92
GCA_000336895.1	61.1	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.92
GCF_000223905.1	62.5	0.24	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_000336635.1	61.2	0.24	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_005406125.1	62.1	0.23	0.50	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.47
GCF_000011085.1	61.1	0.24	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_001280425.1	62.0	0.25	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.87
GCF_010119195.1	66.7	0.21	0.63	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_014647415.1	61.0	0.24	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_001485575.1	61.0	0.24	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_008729015.1	61.6	0.25	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_002844335.1	62.5	0.25	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_000337775.1	61.8	0.25	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_003862495.1	57.1	0.18	0.57	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.47
GCF_023115355.1	57.2	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.54
GCF_023276375.1	54.0	0.20	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.87
GCA_025041175.1	59.5	0.22	0.58	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.75
GCA_025041195.1	56.6	0.20	0.57	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.62
GCF_003058365.1	65.7	0.18	0.69	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.52
GCF_007421925.1	68.1	0.23	0.66	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_003020985.1	69.7	0.24	0.67	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.84
GCF_024298825.1	68.5	0.22	0.68	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8
GCF_024298885.1	67.9	0.21	0.67	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6
GCF_009791395.1	66.8	0.19	0.70	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCF_023699475.1	66.5	0.19	0.69	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_023074835.1	66.6	0.22	0.67	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCA_003021975.1	70.5	0.27	0.64	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.82
GCF_024227715.1	67.6	0.25	0.64	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_024228315.1	67.2	0.25	0.62	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_004681185.1	62.0	0.25	0.53	0.23	0	0	0	0	0	0	0	0	1	0	0	0	0	0	99.45
GCF_010119205.1	65.8	0.25	0.59	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.05
GCF_019599505.1	63.2	0.25	0.56	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.45
GCF_014647235.1	65.3	0.23	0.58	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCF_019599465.1	64.4	0.24	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_019599405.1	64.1	0.30	0.52	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCA_003020925.1	64.7	0.31	0.49	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.8
GCA_003021755.1	66.8	0.29	0.53	0.18	0	0	0	0	0	0	0	0	1	0	0	0	0	0	75.92
GCF_024218775.1	65.2	0.23	0.56	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_000379085.1	65.0	0.26	0.58	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_000023965.1	65.5	0.27	0.59	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_020405185.1	69.0	0.27	0.63	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCA_003021685.1	61.9	0.27	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.87
GCF_009617995.1	65.5	0.28	0.57	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_020217425.1	67.3	0.25	0.62	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_900114435.1	66.2	0.25	0.60	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_004944975.1	62.1	0.15	0.70	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.59
GCF_900880625.1	61.3	0.16	0.65	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_013839425.1	61.5	0.16	0.62	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.59
GCF_009690625.1	62.3	0.16	0.62	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.13
GCF_000470655.1	62.7	0.19	0.64	0.17	0	0	0	0	0	0	0	0	1	0	0	0	0	0	97.13
GCF_000023945.1	62.9	0.17	0.67	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.25
GCF_023028225.1	65.3	0.20	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_023028345.1	65.4	0.20	0.66	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_004118325.1	65.7	0.23	0.63	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.65
GCF_900110215.1	63.5	0.24	0.59	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_023698535.1	65.1	0.22	0.62	0.16	0	0	0	0	0	0	0	0	1	0	0	0	0	0	99.57
GCF_005049285.1	64.2	0.22	0.57	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_001989615.1	65.6	0.23	0.62	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5

GCF_009663395.1	65.1	0.29	0.47	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_009184545.1	64.3	0.30	0.46	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCA_003021175.1	66.7	0.23	0.58	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.37
GCA_003021785.1	65.1	0.28	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.47
GCA_003023185.1	67.1	0.24	0.57	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.68
GCF_024298865.1	66.8	0.28	0.56	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_024362405.1	66.6	0.27	0.55	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_000337455.1	67.7	0.20	0.67	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99
GCF_004698125.1	70.0	0.21	0.71	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_016065055.1	68.5	0.20	0.70	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_013415905.1	67.1	0.21	0.66	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_013415885.1	67.8	0.20	0.69	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_003730195.1	66.8	0.21	0.66	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.45
GCA_003023165.1	67.2	0.19	0.68	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.5
GCF_900100385.1	61.1	0.25	0.52	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.65
GCF_009831575.1	64.0	0.18	0.60	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCA_000416085.1	64.1	0.17	0.69	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.78
GCA_001564135.1	54.9	0.19	0.47	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.87
GCA_003021015.1	65.8	0.20	0.65	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.7
GCA_003021285.1	64.7	0.24	0.62	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.07
GCA_003021335.1	67.5	0.19	0.65	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.28
GCA_003022085.1	65.7	0.23	0.65	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.72
GCA_003022725.1	65.4	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.47
GCA_003022845.1	66.0	0.21	0.64	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.31
GCA_003551265.1	59.5	0.19	0.64	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.72
GCA_003551945.1	54.8	0.18	0.45	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.37
GCA_004015825.1	59.0	0.25	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.72
GCF_024300825.1	62.9	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_013391635.1	64.0	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_013391085.1	64.4	0.26	0.43	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.15
GCF_000591055.1	64.5	0.21	0.63	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_000026045.1	63.1	0.21	0.48	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.29
GCF_013391105.1	67.5	0.27	0.59	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.35
GCF_005239135.1	63.2	0.23	0.57	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.72
GCA_003020965.1	69.1	0.24	0.63	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.22
GCA_003021005.1	68.7	0.23	0.64	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.05
GCA_003021325.1	70.1	0.30	0.62	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.12
GCA_003021745.1	69.6	0.25	0.63	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.89
GCA_003022815.1	68.3	0.28	0.57	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.09
GCA_003022905.1	68.2	0.27	0.58	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.09
GCA_003022945.1	68.8	0.24	0.62	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.7
GCA_003023535.1	70.3	0.24	0.64	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.44
GCA_007121575.1	58.7	0.20	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.63
GCA_007122455.1	64.4	0.26	0.58	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.02
GCA_007135435.1	68.8	0.27	0.66	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.01
GCF_009741925.1	63.9	0.23	0.54	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8
GCF_013839515.1	64.5	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCA_018609665.1	71.4	0.25	0.66	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.82
GCF_024298905.1	66.9	0.28	0.58	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_024449025.1	62.7	0.24	0.58	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.98
GCA_003021305.1	67.1	0.17	0.69	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.47
GCA_003021105.1	68.3	0.28	0.60	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.6
GCA_003021655.1	69.0	0.19	0.71	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.25
GCA_003023785.1	68.3	0.18	0.72	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.13
GCA_003022005.1	70.4	0.29	0.65	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.81
GCA_009789175.1	61.9	0.25	0.52	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.57
GCF_009831455.1	68.7	0.23	0.66	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_003022745.1	67.1	0.26	0.62	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.6
GCA_003023485.1	68.0	0.26	0.64	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.24
GCA_018609945.1	67.3	0.26	0.61	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.96
GCF_024972755.1	63.6	0.19	0.62	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.38
GCF_001011115.1	62.8	0.19	0.61	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.23
GCF_000474235.1	67.4	0.30	0.56	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.47
GCF_014647455.2	67.9	0.30	0.50	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.15
GCF_014647155.1	67.2	0.25	0.55	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.28
GCF_014647115.1	68.7	0.27	0.55	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_009831555.1	66.8	0.25	0.57	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.19
GCF_001488575.1	66.6	0.33	0.47	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_900110535.1	67.9	0.30	0.55	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_021233415.1	68.6	0.30	0.53	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.06
GCF_021233435.1	64.8	0.32	0.44	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.86
GCF_008124605.1	66.5	0.28	0.50	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.42
GCF_000230955.2	66.4	0.30	0.54	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.65
GCF_001485535.1	66.0	0.33	0.46	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_009741975.1	68.2	0.33	0.49	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.4
GCF_011734195.1	67.9	0.33	0.48	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_021028995.1	63.8	0.31	0.43	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_021249345.1	67.3	0.31	0.54	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.23
GCF_021249405.1	66.2	0.29	0.55	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.58
GCF_021729015.1	68.6	0.31	0.55	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_014647475.1	66.9	0.24	0.48	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_001886955.1	63.6	0.23	0.57	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.09
GCA_018334775.1	59.5	0.16	0.53	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.15
GCF_020614395.1	67.5	0.39	0.35	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_007833275.1	66.2	0.36	0.38	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_000334895.1	66.0	0.23	0.65	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.51
GCF_000336675.1	65.4	0.26	0.58	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCF_000336695.1	63.8	0.23	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8
GCF_024508235.1	64.9	0.23	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.15
GCF_000336915.1	64.0	0.20	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.65
GCF_000336935.1	63.4	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.44
GCF_009900715.1	64.7	0.23	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_000755245.1	62.3	0.25	0.58	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.65
GCA_003021045.1	69.4	0.24	0.68	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.27
GCA_003021235.1	64.7	0.21	0.61	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_003021705.1	64.1	0.24	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.16
GCA_003021725.1	64.9	0.23	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.98
GCA_003022685.1	67.0	0.22	0.65	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.94
GCA_003022925.1	65.2	0.21	0.60	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.04
GCF_000336715.1	61.8	0.22	0.59	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.08
GCA_000496195.1	71.0	0.35	0.57	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCF_002952775.1	63.1	0.19	0.65	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_024972735.1	63.6	0.21	0.65	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.04
GCF_005543295.1	58.4	0.20	0.54	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.43
GCA_005239175.1	59.0	0.21	0.53	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.76
GCF_002844195.1	66.9	0.23	0.65	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.95
GCF_004116405.1	64.7	0.22	0.63	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_900129775.1	68.6	0.24	0.62	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.3
GCF_013401515.1	67.2	0.25	0.59	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_019823105.1	67.9	0.23	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.42
GCF_019880245.1	68.0	0.23	0.61	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.23
GCF_019880225.1	68.4	0.24	0.62	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.85
GCF_013402875.1	68.7	0.27	0.61	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_009831625.1	67.6	0.24	0.63	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.42
GCA_003020945.1	70.9	0.25	0.66	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.4
GCA_018609965.1	66.8	0.20	0.71	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.54
GCF_021431925.1	68.7	0.22	0.65	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.49
GCF_000495475.1	70.1	0.26	0.63	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.54
GCF_007655485.1	63.0	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.47
GCF_900107195.1	64.1	0.18	0.63	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_024464655.1	64.0	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.54
GCF_004799685.1	65.9	0.22	0.64	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.55
GCF_024464595.1	65.2	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.03
GCF_024494595.1	64.6	0.22	0.62	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.88
GCF_014212355.1	66.5	0.23	0.61	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_000739575.1	64.1	0.22	0.60	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.63
GCF_014646875.1	65.4	0.26	0.61	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.68
GCA_003665935.1	66.3	0.23	0.61	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_000337795.1	66.3	0.19	0.61	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.44
GCF_000336755.1	61.2	0.19	0.50	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_000336775.1	65.9	0.19	0.60	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.06
GCF_000336955.1	62.0	0.20	0.49	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_009674605.1	61.7	0.17	0.54	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.06
GCF_009674585.1	60.8	0.18	0.49	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.62
GCF_009674625.1	61.1	0.16	0.51	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99
GCF_001469875.2	65.7	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.44
GCF_001368915.1	66.3	0.18	0.62	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.25
GCF_000306765.2	60.3	0.19	0.48	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.25
GCF_000337815.1	61.8	0.17	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_000336815.1	65.7	0.18	0.60	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.06
GCF_001469865.1	60.9	0.18	0.52	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6
GCF_001482285.1	65.1	0.19	0.59	0.22	0	0	0	0	0	0	0	0	1	0	0	0	0	0	99.44
GCF_000337835.1	66.3	0.18	0.62	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.06

GCF_000025685.1	65.5	0.18	0.59	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_000172995.2	59.9	0.20	0.51	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.92
GCF_900115785.1	65.9	0.22	0.64	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_000337095.1	65.6	0.22	0.60	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.1
GCF_900112175.1	67.6	0.20	0.69	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_900110465.1	62.9	0.24	0.58	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_900103715.1	65.1	0.23	0.55	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_900114455.1	62.2	0.23	0.54	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_900109065.1	58.8	0.28	0.38	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_024494645.1	60.8	0.27	0.42	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.11
GCA_001563795.1	57.8	0.23	0.40	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_003554115.1	58.8	0.29	0.38	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.81
GCF_024178165.1	64.1	0.30	0.47	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_900115675.1	67.1	0.29	0.55	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.21
GCF_001307315.1	67.6	0.25	0.59	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.92
GCF_000739555.1	69.0	0.29	0.58	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.07
GCF_017874235.1	66.6	0.31	0.52	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.72
GCF_001282785.1	67.9	0.31	0.55	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.58
GCA_000224475.1	62.4	0.25	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.28
GCF_002025255.2	66.8	0.30	0.55	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.34
GCF_003605575.1	61.2	0.23	0.42	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_003605635.1	59.7	0.23	0.45	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.63
GCF_006861655.1	62.7	0.25	0.45	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCA_000496215.1	63.1	0.25	0.54	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85
GCF_006861665.1	61.8	0.24	0.45	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.05
GCF_001462205.1	68.3	0.26	0.60	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.54
GCF_900113245.1	65.0	0.18	0.63	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_900100875.1	65.7	0.18	0.60	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_900108505.1	64.5	0.22	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.41
GCF_900107205.1	65.5	0.24	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.11
GCF_002355635.1	66.0	0.23	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.22
GCF_003856835.1	65.7	0.29	0.50	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_000427685.1	65.0	0.29	0.53	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_024494725.1	65.2	0.25	0.57	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.95
GCF_003342675.1	66.0	0.28	0.54	0.18	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.68
GCF_024498175.1	67.1	0.25	0.62	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_003336245.1	66.2	0.28	0.55	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_023276355.1	64.6	0.27	0.52	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.44
GCF_023703775.1	68.0	0.29	0.59	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_023703795.1	65.3	0.24	0.61	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_900107665.1	65.1	0.26	0.50	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_003439925.1	65.3	0.22	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.29
GCF_001469955.1	62.5	0.21	0.54	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.24
GCF_020097815.1	64.5	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_020097835.1	64.1	0.23	0.58	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_020150815.1	63.8	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.23
GCA_000416005.1	50.7	0.18	0.56	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.22
GCF_000237865.1	47.7	0.16	0.48	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCA_000415965.1	49.4	0.17	0.50	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.51
GCA_000415985.1	48.0	0.19	0.46	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.78
GCF_001542905.1	68.0	0.23	0.65	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.92
GCF_000336995.1	67.2	0.23	0.58	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.16
GCF_017873815.1	64.5	0.22	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_004114995.1	66.3	0.24	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_900113615.1	67.4	0.24	0.65	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99
GCF_000336875.1	66.2	0.21	0.61	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.07
GCF_900182635.1	66.8	0.24	0.64	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_000337035.1	67.0	0.20	0.64	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_007671725.1	68.6	0.24	0.60	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.76
GCF_000337335.1	68.1	0.20	0.62	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_002114285.1	66.6	0.22	0.62	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.85
GCF_002252985.1	67.7	0.22	0.65	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCF_000739595.1	65.1	0.24	0.57	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.04
GCF_000337075.1	69.1	0.21	0.66	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_000337355.1	66.9	0.23	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.78
GCF_000022205.1	64.0	0.24	0.55	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.76
GCF_024494655.1	62.9	0.22	0.58	0.20	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.92
GCF_000337375.1	68.0	0.24	0.61	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_002727125.1	65.9	0.24	0.58	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.94
GCF_024494685.1	67.8	0.23	0.67	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.11
GCF_024494565.1	69.2	0.24	0.63	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_000337915.1	66.9	0.24	0.60	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.25
GCF_013267195.1	68.7	0.20	0.64	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_024494575.1	67.1	0.22	0.65	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_002286985.1	67.4	0.25	0.59	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.76
GCF_007671685.1	66.0	0.23	0.57	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_900111935.1	69.0	0.21	0.64	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_018228765.1	68.9	0.21	0.63	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.15
GCA_000496175.1	67.2	0.17	0.71	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.51
GCF_000746205.1	66.0	0.21	0.64	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_001261915.1	67.6	0.25	0.61	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8
GCA_001564205.1	64.5	0.22	0.59	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.48
GCF_002252755.1	67.6	0.23	0.61	0.16	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.8
GCA_003023405.1	67.7	0.20	0.66	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.52
GCF_003287355.1	66.1	0.24	0.64	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.61
GCA_003554605.1	65.7	0.19	0.59	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.94
GCF_003666015.1	66.5	0.22	0.60	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_003697845.1	66.1	0.24	0.63	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_003721435.2	67.7	0.23	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_003781945.1	66.5	0.25	0.57	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_003990725.2	66.6	0.20	0.57	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_004114375.1	65.9	0.22	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.22
GCF_005435165.1	67.4	0.22	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99
GCF_009742825.1	65.8	0.20	0.65	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.76
GCF_009806985.1	68.4	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.61
GCF_018623055.1	68.7	0.21	0.64	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99
GCF_000337415.1	68.0	0.19	0.66	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.68
GCF_017873555.1	68.0	0.21	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.85
GCF_002355655.1	68.6	0.22	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_900188065.1	62.9	0.18	0.62	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_900102375.1	68.3	0.21	0.62	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCA_000496235.1	59.1	0.13	0.70	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.17
GCF_023638035.1	51.5	0.25	0.32	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCA_001563965.1	62.2	0.20	0.45	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.26
GCF_007004735.1	66.1	0.16	0.70	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002906575.1	65.7	0.18	0.67	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.42
GCF_009176545.1	66.9	0.17	0.72	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.11
GCA_024229675.1	66.1	0.17	0.68	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.87
GCA_020567425.1	66.8	0.15	0.74	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.93
GCF_024296665.1	68.7	0.20	0.69	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.6
GCF_900103505.1	67.3	0.25	0.63	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_024495425.1	67.2	0.24	0.65	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_024464185.1	67.1	0.25	0.64	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_024609245.1	65.6	0.25	0.61	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_900112205.1	65.4	0.22	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.81
GCF_000226975.2	65.3	0.22	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.43
GCF_000337895.1	63.7	0.22	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.94
GCF_000455345.1	66.1	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.62
GCF_000455365.1	64.3	0.20	0.54	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.24
GCF_003610195.1	64.4	0.21	0.48	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000217715.1	65.2	0.22	0.48	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_020567525.1	68.0	0.17	0.70	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_011440375.1	68.1	0.21	0.67	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_900116205.1	61.5	0.23	0.52	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2
GCF_000517625.1	60.9	0.21	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000691505.1	60.8	0.22	0.52	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.74
GCF_017352155.2	65.2	0.22	0.57	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.95
GCF_013342145.1	65.7	0.21	0.56	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.54
GCF_003977755.1	64.5	0.21	0.54	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.62
GCF_000337495.1	65.2	0.21	0.56	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.17
GCF_000025325.1	64.3	0.22	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_023008545.1	63.1	0.23	0.60	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.93
GCF_000337515.1	64.5	0.17	0.59	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.65
GCF_024498195.1	65.0	0.19	0.66	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_023093535.1	66.8	0.16	0.68	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.67
GCF_000328525.1	64.3	0.20	0.59	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.25
GCA_007119345.1	68.6	0.17	0.72	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.06
GCA_007135505.1	64.5	0.20	0.63	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.46
GCF_024300625.1	63.1	0.17	0.62	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.59
GCA_022869805.1	64.2	0.23	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.81
GCF_023028105.1	65.0	0.21	0.59	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCF_023566055.1	65.1	0.22	0.60	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.43
GCF_017357405.1	63.4	0.22	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2

GCF_002156705.1	64.1	0.19	0.64	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCA_001563805.1	65.7	0.20	0.61	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.57
GCA_001563885.1	59.9	0.19	0.51	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.18
GCF_003430825.1	62.4	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_003841505.1	61.9	0.18	0.58	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_003841465.1	63.9	0.19	0.62	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_003841485.1	61.1	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35
GCF_008245225.1	62.5	0.20	0.56	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.92
GCF_000337535.1	62.0	0.22	0.50	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.42
GCF_000337555.1	62.4	0.22	0.51	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.11
GCF_000337135.1	60.4	0.24	0.50	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.74
GCF_000337575.1	61.7	0.24	0.50	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.17
GCF_000025625.1	61.1	0.24	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.17
GCF_001861355.1	61.5	0.25	0.50	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_000337595.1	61.5	0.22	0.51	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.04
GCF_023008585.1	63.7	0.24	0.60	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCF_000731985.1	64.6	0.22	0.53	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_020515625.1	64.3	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_002494345.1	63.9	0.21	0.55	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.92
GCF_000337175.1	63.7	0.21	0.53	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_013402815.2	60.1	0.20	0.53	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_004217335.1	60.7	0.21	0.49	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_900111485.1	61.0	0.22	0.49	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.11
GCF_000337475.1	61.8	0.21	0.49	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCA_000690595.2	65.1	0.23	0.56	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_000337615.1	63.7	0.22	0.53	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1
GCF_000230735.2	64.0	0.23	0.54	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.95
GCF_001953745.1	65.3	0.23	0.57	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_900110865.1	65.0	0.23	0.58	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.87
GCF_900110455.1	65.4	0.20	0.54	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_020405205.1	63.1	0.23	0.54	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.38
GCF_002572525.1	62.3	0.23	0.53	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35
GCF_005938085.1	61.5	0.21	0.51	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_013456555.2	61.5	0.23	0.51	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.19
GCF_019879105.1	61.1	0.22	0.52	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_020405225.1	62.1	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_024227435.1	63.0	0.20	0.58	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_024266705.1	60.9	0.21	0.58	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_024296685.1	65.5	0.22	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCA_000337115.1	65.4	0.22	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCF_000337195.1	64.0	0.22	0.52	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.24
GCF_005576615.1	63.4	0.21	0.53	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.54
GCF_000230715.2	62.2	0.24	0.53	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.62
GCF_900104065.1	62.9	0.26	0.49	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.57
GCF_024362525.1	65.5	0.23	0.58	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.93
GCF_000337675.1	64.4	0.28	0.51	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCF_000337695.1	64.4	0.28	0.53	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.92
GCF_000328685.1	64.7	0.30	0.52	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.73
GCF_008122205.1	63.2	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.93
GCA_003559215.1	64.8	0.29	0.51	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_023913515.1	63.4	0.23	0.54	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.33
GCF_002177135.1	60.2	0.22	0.42	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_011043775.1	58.9	0.21	0.43	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6
GCF_000337215.1	64.3	0.22	0.58	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_009392895.1	61.3	0.21	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.3
GCF_004799645.1	60.6	0.21	0.51	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_001971705.1	61.4	0.18	0.47	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.11
GCF_009834785.1	62.5	0.21	0.54	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.49
GCF_003670115.1	62.9	0.21	0.53	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.35
GCF_900108095.1	61.1	0.17	0.48	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.87
GCF_000337735.1	61.8	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.92
GCF_900100335.1	63.6	0.21	0.54	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_900156475.1	61.0	0.21	0.51	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.24
GCF_000383975.1	62.3	0.22	0.53	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.36
GCF_006543045.1	62.1	0.21	0.51	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.85
GCF_020177375.1	64.2	0.27	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.8
GCA_001564255.1	64.5	0.24	0.57	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_001564115.1	68.6	0.20	0.73	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.09
GCA_003552885.1	68.8	0.19	0.75	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.54
GCA_001564275.1	63.6	0.17	0.68	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.93
GCA_003552325.1	60.9	0.19	0.54	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.47
GCA_017357105.2	63.1	0.23	0.58	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.33
GCF_023973145.1	61.8	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.93
GCF_024138145.1	63.1	0.22	0.58	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2
GCF_024204665.1	63.0	0.22	0.58	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99
GCF_024298845.1	59.5	0.20	0.53	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.6
GCF_024362485.1	64.8	0.18	0.67	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.33
GCF_023638055.1	61.0	0.28	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_900215575.1	65.2	0.23	0.57	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_024494695.1	66.4	0.22	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCF_017094485.1	60.8	0.29	0.53	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCA_003021085.1	68.0	0.23	0.63	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.94
GCA_007122875.1	64.7	0.21	0.67	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.29
GCF_003675875.1	67.2	0.26	0.57	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.13
GCF_004785955.1	68.5	0.25	0.58	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCA_005954745.1	63.1	0.23	0.55	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_003675855.1	67.2	0.27	0.56	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_003023565.1	68.1	0.24	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.65
GCF_023204835.1	64.9	0.23	0.59	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.93
GCF_000403645.1	66.6	0.22	0.63	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.53
GCF_019693215.1	47.4	0.24	0.40	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.47
GCA_007123105.1	61.1	0.24	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.79
GCA_007118975.1	60.0	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.98
GCA_007118075.1	57.8	0.19	0.65	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.35
GCA_007118145.1	57.8	0.20	0.66	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.69
GCA_003022865.1	70.6	0.18	0.76	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_003023195.1	69.4	0.21	0.71	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.72
GCA_002503845.1	41.5	0.22	0.30	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.24
GCA_009889625.1	40.2	0.21	0.31	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.44
GCA_009889685.1	40.7	0.21	0.31	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.04
GCA_022450005.1	41.5	0.23	0.30	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.54
GCA_018609935.1	32.5	0.20	0.16	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.89
GCF_000063445.1	54.6	0.20	0.37	0.43	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	100
GCA_002067315.1	59.8	0.21	0.44	0.35	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	99.35
GCA_023436075.1	56.1	0.21	0.45	0.35	0	0	0	0	0	0	0	0	0	0	1	1	0	1	0	81.81
GCF_000251105.1	52.7	0.22	0.39	0.39	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	100
GCF_000011005.1	54.9	0.21	0.34	0.45	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	100
GCF_021023085.1	46.2	0.17	0.40	0.43	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	99.35
GCA_013329575.1	37.6	0.15	0.30	0.55	0	0	0	0	0	0	0	0	0	1	0	1	1	1	1	79.66
GCA_004212075.1	35.7	0.15	0.33	0.52	0	0	0	0	0	0	0	0	0	2	2	2	3	2	3	92.46
GCA_004212085.1	43.8	0.17	0.43	0.40	0	0	0	0	0	0	0	0	0	1	2	3	3	2	3	90.2
GCA_902158735.1	42.6	0.17	0.44	0.38	0	0	0	0	0	0	0	0	0	2	2	2	3	2	3	76.96
GCA_902158745.1	42.7	0.17	0.44	0.39	0	0	0	0	0	0	0	0	0	1	2	2	2	2	2	89.08
GCA_015660865.1	59.5	0.17	0.62	0.21	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	99.67
GCF_024170505.1	53.2	0.14	0.58	0.28	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	99.02
GCF_018132105.1	52.2	0.14	0.58	0.28	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	99.02
GCA_002496395.1	51.7	0.12	0.58	0.30	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	98.69
GCA_003838065.1	50.5	0.14	0.58	0.28	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	97.39
GCF_024170265.1	52.0	0.16	0.58	0.26	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	100
GCA_013329165.1	51.8	0.14	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	97.39
GCF_024372745.1	50.4	0.14	0.56	0.30	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	99.35
GCA_018883755.1	50.8	0.04	0.40	0.55	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	90.99
GCF_000015765.1	50.0	0.07	0.44	0.49	0	0	0	0	0	0	0	0	0	2	2	2	2	2	2	99.54
GCA_002287215.1	51.4	0.09	0.49	0.42	0	0	0	0	0	0	0	0	0	0	2	2	2	2	2	98.21
GCA_015063085.1	48.6	0.06	0.36	0.58	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	86.88
GCA_001940805.1	52.9	0.06	0.44	0.50	0	0	0	0	0	0	0	0	0	0	0	0	2	2	2	91.85
GCA_002498375.1	51.0	0.07	0.45	0.48	0	0	0	0	0	0	0	0	0	2	2	2	2	2	2	96.89
GCA_002506085.1	48.1	0.08	0.42	0.51	0	0	0	0	0	0	0	0	0	2	2	0	2	2	2	97.71
GCA_003315675.1	50.1	0.09	0.46	0.46	0	0	0	0	0	0	0	0	0	1	2	1	2	2	2	93.58
GCA_017387505.1	46.4	0.04	0.33	0.63	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	95.75
GCA_017399555.1	50.1	0.07	0.36	0.57	0	0	0	0	0	0	0	0	0	1	1	1	2	1	2	96.27
GCA_017408885.1	46.3	0.04	0.33	0.63	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	96.41
GCA_017555685.1	50.9	0.04	0.31	0.65	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	78.07
GCA_017622255.1	51.7	0.06	0.34	0.61	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	90.72
GCA_018065685.1	50.2	0.08	0.40	0.53	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	76.08
GCA_023396065.1	52.4	0.07	0.48	0.45	0	0	0	0	0	0	0	0	0	2	2	2	2	2	2	96.73
GCA_020854755.1	60.5	0.22	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	80
GCF_004102725.1	60.0	0.17	0.57	0.26	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	99.02
GCF_000304355.2	60.6	0.17	0.62	0.21	0	0	0	0	0	0	0	0	0	2	2	2	1	2	1	98.37
GCF_019669965.1	61.9	0.16	0.62	0.22	0	0	0	0	0	0	0	0	0	2	2	2	1	2	1	99.02
GCF_900095385.1	61.8	0.17	0.62	0.22	0	0	0	0	0	0	0	0	0	2	2	2	1	2	1	99.02
GCF_001602375.1	62.0	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	2	2	2	1	2	1	99.02
GCF_000015825.1	62.1	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	2	2	2	1	2	1	99.35

GCA_002503885.1	61.6	0.16	0.62	0.22	0	0	0	0	0	0	0	0	0	0	2	2	2	1	95.62
GCF_001017125.1	62.3	0.16	0.61	0.24	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.02
GCF_000691865.1	61.4	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	0	2	1	2	1	98.47
GCA_001896715.1	60.3	0.18	0.61	0.21	0	0	0	0	0	0	0	0	0	0	2	2	2	1	86.06
GCA_002497965.1	59.7	0.16	0.65	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	1	88.62
GCA_002498065.1	62.4	0.17	0.61	0.22	0	0	0	0	0	0	0	0	0	0	0	2	2	1	97.58
GCA_002499455.1	63.3	0.16	0.61	0.22	0	0	0	0	0	0	0	0	0	0	0	2	2	1	90.56
GCA_002501655.1	60.8	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	91.7
GCA_002506585.1	62.0	0.16	0.63	0.22	0	0	0	0	0	0	0	0	0	0	2	2	2	1	93.14
GCA_002508705.1	60.3	0.16	0.58	0.26	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.02
GCA_002839575.1	61.5	0.17	0.60	0.23	0	0	0	0	0	0	0	0	0	0	1	0	0	1	90.07
GCA_002839645.1	60.8	0.17	0.59	0.24	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.54
GCA_012510295.1	59.5	0.19	0.61	0.20	0	0	0	0	0	0	0	0	0	0	1	2	2	1	81.1
GCA_012510335.1	59.5	0.19	0.61	0.20	0	0	0	0	0	0	0	0	0	0	0	1	1	1	85.62
GCA_012511245.1	59.8	0.15	0.61	0.23	0	0	0	0	0	0	0	0	0	0	2	1	2	1	88.24
GCA_012521035.1	59.5	0.19	0.62	0.19	0	0	0	0	0	0	0	0	0	0	1	1	1	1	90.72
GCA_012797575.1	59.6	0.20	0.64	0.16	0	0	0	0	0	0	0	0	0	0	1	1	1	1	88.73
GCA_016841385.1	62.6	0.17	0.61	0.22	0	0	0	0	0	0	0	0	0	0	1	2	1	1	95.85
GCA_016841955.1	61.9	0.17	0.61	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.54
GCA_018433835.1	61.4	0.16	0.61	0.22	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.89
GCA_019136335.1	63.8	0.16	0.64	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	1	86.08
GCA_020696975.1	61.7	0.15	0.61	0.24	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.41
GCF_023195915.1	61.3	0.16	0.59	0.25	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.89
GCA_023230425.1	62.0	0.16	0.62	0.22	0	0	0	0	0	0	0	0	0	0	2	3	1	1	84.35
GCA_023393455.1	62.0	0.15	0.62	0.22	0	0	0	0	0	0	0	0	0	0	2	2	2	1	94.44
GCA_023457135.1	63.0	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	0	98.24
GCF_023702065.1	62.2	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.54
GCA_001512375.1	59.4	0.19	0.62	0.19	0	0	0	0	0	0	0	0	0	0	1	1	1	1	91.5
GCF_001571405.1	59.3	0.16	0.56	0.28	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.67
GCA_002503105.1	63.0	0.18	0.65	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	1	94.12
GCA_002503135.1	54.5	0.15	0.66	0.20	0	0	0	0	0	0	0	0	0	0	1	1	1	1	93.14
GCF_001571385.1	60.3	0.10	0.66	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_004297185.1	59.5	0.13	0.65	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.2
GCF_019633745.1	60.3	0.12	0.68	0.20	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.04
GCF_000275865.1	61.0	0.11	0.66	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.54
GCA_002498315.1	60.9	0.11	0.65	0.24	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCF_017875325.1	59.1	0.12	0.65	0.23	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.04
GCF_013377755.1	61.1	0.12	0.65	0.22	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.87
GCA_011104835.1	61.3	0.17	0.63	0.20	0	0	0	0	0	0	0	0	0	0	2	2	2	1	97.02
GCA_016841665.1	57.0	0.16	0.60	0.24	0	0	0	0	0	0	0	0	0	0	2	1	1	1	81.11
GCA_001412355.1	56.6	0.12	0.58	0.30	0	0	0	0	0	0	0	0	0	0	0	1	1	1	98.37
GCA_013415665.1	60.6	0.14	0.59	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	1	93.66
GCA_016926855.1	56.8	0.13	0.57	0.29	0	0	0	0	0	0	0	0	0	0	1	1	1	1	84.64
GCF_001315945.1	52.1	0.11	0.65	0.24	0	0	0	0	0	0	0	0	0	0	2	1	1	1	85.25
GCF_009914725.1	50.7	0.11	0.55	0.34	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.71
GCA_011045995.1	58.1	0.14	0.56	0.30	0	0	0	0	0	0	0	0	0	0	2	2	2	1	83.66
GCA_012523385.1	48.8	0.11	0.46	0.43	0	0	0	0	0	0	0	0	0	0	0	1	0	0	92.04
GCA_016841485.1	55.3	0.15	0.54	0.32	0	0	0	0	0	0	0	0	0	0	2	2	2	1	93.14
GCA_018687785.1	56.2	0.14	0.56	0.30	0	0	0	0	0	0	0	0	0	0	2	2	2	1	97.91
GCF_000784355.1	47.5	0.11	0.47	0.42	0	0	0	0	0	0	0	0	0	0	1	2	2	1	98.37
GCF_000147875.1	47.4	0.11	0.47	0.42	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.67
GCA_016926355.1	45.6	0.11	0.43	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.24
GCF_000711215.1	49.5	0.07	0.47	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.39
GCA_016937345.1	40.4	0.10	0.39	0.51	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.39
GCA_017412625.1	49.8	0.07	0.48	0.46	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.73
GCA_017553245.1	50.7	0.07	0.48	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCF_017875315.1	43.0	0.08	0.43	0.49	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCA_023396365.1	40.6	0.08	0.39	0.54	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.69
GCF_024662215.1	42.3	0.10	0.46	0.44	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_000243255.1	42.2	0.10	0.47	0.44	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_903819595.1	49.6	0.13	0.49	0.38	0	0	0	0	0	0	0	0	0	0	2	1	1	2	99.35
GCA_903828975.1	49.6	0.13	0.46	0.40	0	0	0	0	0	0	0	0	0	0	1	1	0	2	99.02
GCA_002067095.1	57.8	0.12	0.68	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	2	95.05
GCA_018263335.1	58.0	0.13	0.67	0.20	0	0	0	0	0	0	0	0	0	0	1	1	2	2	99.02
GCA_002506105.1	53.3	0.12	0.60	0.28	0	0	0	0	0	0	0	0	0	0	0	1	1	2	93.79
GCA_002509495.1	56.3	0.15	0.59	0.26	0	0	0	0	0	0	0	0	0	0	1	0	0	2	92.32
GCA_018262855.1	53.7	0.12	0.61	0.27	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.35
GCA_024518585.1	58.0	0.15	0.62	0.22	0	0	0	0	0	0	0	0	0	0	1	1	1	2	98.69
GCA_013331225.1	57.3	0.15	0.63	0.22	0	0	0	0	0	0	0	0	0	0	1	0	0	1	72.74
GCF_017873855.1	57.4	0.14	0.53	0.32	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCF_000017625.1	54.5	0.11	0.45	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.54
GCF_000327485.1	55.2	0.10	0.54	0.36	0	0	0	0	0	0	0	0	0	0	2	2	2	2	99.87
GCA_002067035.1	56.5	0.09	0.58	0.33	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCA_002495055.1	48.0	0.11	0.47	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	2	95
GCA_002495065.1	50.2	0.12	0.51	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	2	86.56
GCA_002502245.1	55.8	0.10	0.54	0.36	0	0	0	0	0	0	0	0	0	0	1	1	1	2	86.6
GCA_002502735.1	56.4	0.09	0.43	0.48	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.54
GCA_002508495.1	55.8	0.11	0.54	0.35	0	0	0	0	0	0	0	0	0	0	1	1	1	2	68.63
GCA_002835825.1	56.6	0.13	0.54	0.33	0	0	0	0	0	0	0	0	0	0	0	1	1	2	93.56
GCA_002839605.1	55.3	0.09	0.52	0.39	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCA_002839675.1	51.4	0.10	0.46	0.44	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCA_003136075.1	50.6	0.10	0.47	0.43	0	0	0	0	0	0	0	0	0	0	1	0	0	1	92.2
GCA_003141335.1	49.9	0.11	0.48	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	2	92.78
GCA_003154335.1	48.0	0.11	0.47	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	1	87.45
GCA_003157895.1	53.8	0.10	0.51	0.40	0	0	0	0	0	0	0	0	0	0	1	1	1	1	90.28
GCA_003170075.1	55.0	0.09	0.49	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.54
GCA_012798365.1	55.8	0.10	0.51	0.39	0	0	0	0	0	0	0	0	0	0	1	1	0	1	88.82
GCA_015660885.1	47.8	0.11	0.46	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.54
GCA_019695435.1	53.5	0.16	0.48	0.37	0	0	0	0	0	0	0	0	0	0	1	1	1	1	84.02
GCA_022710665.1	54.7	0.11	0.56	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	2	81.12
GCA_023227875.1	54.0	0.09	0.50	0.40	0	0	0	0	0	0	0	0	0	0	2	2	2	2	94.64
GCA_023228295.1	52.8	0.10	0.49	0.41	0	0	0	0	0	0	0	0	0	1	0	1	1	2	90.85
GCA_013331015.1	56.1	0.11	0.54	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	2	75.9
GCA_903832665.1	52.2	0.12	0.48	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	3	99.02
GCA_002067895.1	54.5	0.11	0.56	0.33	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCA_015660965.1	42.4	0.12	0.37	0.50	0	0	0	0	0	0	0	0	0	0	1	1	1	2	98.36
GCA_022711635.1	58.6	0.12	0.59	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	2	85.61
GCA_903900025.1	53.9	0.12	0.54	0.35	0	0	0	0	0	0	0	0	0	0	3	1	1	2	99.01
GCA_001412335.1	54.2	0.17	0.56	0.27	0	0	0	0	0	0	0	0	0	0	0	1	1	2	97.53
GCA_002509485.1	54.3	0.16	0.58	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	2	67.79
GCA_018432765.1	55.5	0.16	0.60	0.24	0	0	0	0	0	0	0	0	0	0	1	1	1	2	90.85
GCA_002503825.1	50.9	0.11	0.52	0.37	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCA_002068435.1	53.4	0.12	0.59	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	1	79.57
GCA_002499905.1	57.4	0.15	0.60	0.26	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCA_012516785.1	53.8	0.13	0.59	0.28	0	0	0	0	0	0	0	0	0	0	1	1	1	2	90.52
GCA_013415565.1	59.0	0.14	0.65	0.22	0	0	0	0	0	0	0	0	0	0	1	0	1	2	99.35
GCA_013415575.1	57.6	0.16	0.60	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	1	83.71
GCA_016699325.1	55.6	0.14	0.60	0.25	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.06
GCA_021371995.1	52.6	0.12	0.56	0.31	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.02
GCA_022710385.1	53.7	0.13	0.60	0.27	0	0	0	0	0	0	0	0	0	0	1	1	2	3	74.07
GCA_022841205.1	54.8	0.16	0.59	0.26	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.69
GCA_013331415.1	58.8	0.15	0.65	0.20	0	0	0	0	0	0	0	0	0	0	0	1	1	1	86.76
GCF_000021965.1	55.4	0.12	0.64	0.24	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.84
GCA_002495225.1	68.6	0.22	0.67	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	1	74.57
GCA_004332335.1	66.4	0.19	0.64	0.16	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.07
GCA_012728895.1	67.8	0.19	0.71	0.11	0	0	0	0	0	0	0	0	0	0	1	1	1	0	95.72
GCA_017883495.1	68.0	0.21	0.64	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.57
GCA_013331215.1	66.7	0.21	0.65	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.17
GCA_903926075.1	40.8	0.13	0.40	0.47	0	0	0	0	0	0	0	0	0	0	1	1	1	2	98.69
GCA_016926505.1	46.5	0.12	0.48	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.04
GCF_000013445.1	45.1	0.10	0.44	0.46	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.02
GCA_003251955.1	47.5	0.09	0.50	0.41	0	0	0	0	0	0	0	0	0	0	2	1	2	0	75.44
GCA_020216685.1	46.2	0.09	0.46	0.45	0	0	0	0	0	0	0	0	0	0	2	2	2	1	96.79
GCF_003173355.1	43.1	0.09	0.42	0.48	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.54
GCA_012520015.1	45.2	0.10	0.48	0.42	0	0	0	0	0	0	0	0	0	0	2	1	1	1	90.41
GCA_012729535.1	41.9	0.10	0.39	0.51	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.02
GCF_019263745.1	42.2	0.10	0.39	0.52	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.02
GCF_003173335.1	42.3	0.09	0.41	0.51	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.02
GCA_009779205.1	42.5	0.18	0.36	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	1	73.82
GCA_018263395.1	62.7	0.32	0.51	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.79
GCA_001914405.1	35.4	0.15	0.23	0.62	0	1	0	2	0	0	0	0	1	1	1	1	1	1	97.71
GCA_023016325.1	42.2	0.09	0.28	0.63	0	2	0	1	0	0	0	0	1	0	1	1	1	1	97.22
GCF_002153915.1	37.9	0.06	0.22	0.72	0	1	0	0	0	0	0	0	1	1	2	1	1	1	97.22
GCA_003034855.1	35.5	0.20	0.27	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.58
GCA_002010075.1	43.2	0.14	0.58	0.29	0	1	2	1	1	1	0	0	1	1	0	0	0	0	96.73
GCA_003661015.1	43.8	0.15	0.57	0.29	0	1	1	1	1	0	0	0	1	1	0	0	0	0	74.24
GCF_000711905.1	54.7	0.26	0.57	0.17	0	1	1	1	1	1	0	0	1	0	1	1	1	1	100
GCA_004193545.1	41.5	0.17	0.39	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	1	92.27
GCA_905067535.1	41.8	0.17	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	1	1	0	55.63
GCA_905067555.1	41.7	0.17	0.41	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	58.2
GCA_004212095.1	41.0	0.18	0.38	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	0	91.18
GCA_012910725.1	41.7	0.16	0.42	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	70.26
GCA_002254825.2	46.3	0.15	0.47	0.38	0	0	0	0	0	0	0	0	0	0	1	1	1	1	75.82

GCA_905171695.1	46.5	0.16	0.47	0.37	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.69
GCA_014859725.1	41.8	0.17	0.38	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.71
GCA_009649835.1	46.0	0.20	0.42	0.39	0	0	0	0	0	0	0	0	0	0	1	1	1	1	91.18
GCA_014237145.1	43.3	0.19	0.42	0.39	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.69
GCA_013330355.1	45.5	0.21	0.41	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.82
GCA_002926195.1	39.0	0.19	0.36	0.46	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.42
GCA_021108405.1	38.8	0.19	0.37	0.44	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.69
GCA_013374385.1	46.3	0.18	0.40	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	1	66.78
GCA_019429385.1	45.4	0.18	0.41	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_022353185.1	42.8	0.18	0.40	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.37
GCA_023136155.1	43.9	0.19	0.38	0.42	0	0	0	0	0	0	0	0	0	0	1	0	0	1	89.22
GCA_023544495.1	45.2	0.19	0.45	0.37	1	1	1	1	1	1	1	0	0	0	0	0	0	0	78.93
GCA_023544605.1	46.6	0.21	0.42	0.37	0	0	0	0	0	0	0	0	0	0	1	1	0	1	97.06
GCA_002503595.1	50.2	0.16	0.59	0.25	0	0	0	0	0	0	0	0	0	0	1	1	1	1	89.49
GCA_002506015.1	50.3	0.18	0.61	0.22	0	0	0	0	0	0	0	0	0	0	0	1	0	1	87.25
GCA_003194445.1	48.7	0.18	0.54	0.28	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.92
GCA_003601535.1	48.7	0.16	0.59	0.25	0	0	0	0	0	0	0	0	0	0	1	1	1	1	88.29
GCA_003661105.1	49.0	0.18	0.54	0.28	0	0	0	0	0	0	0	0	0	0	0	1	0	1	84.59
GCA_004211975.1	48.5	0.15	0.54	0.30	0	0	0	0	0	0	0	0	0	0	2	1	1	1	91.99
GCA_012961645.1	50.0	0.17	0.60	0.23	0	0	0	0	0	0	0	0	0	0	1	1	0	1	78.45
GCA_013572355.1	52.6	0.17	0.60	0.23	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.59
GCA_021159385.1	51.8	0.18	0.62	0.20	0	0	0	0	0	0	0	0	0	0	1	1	0	1	95.75
GCA_002839545.1	43.2	0.14	0.41	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.41
GCA_014859785.1	44.0	0.16	0.39	0.46	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.86
GCF_000685155.1	43.2	0.21	0.39	0.40	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.67
GCF_900196725.1	44.1	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	2	97.71
GCA_020724545.1	43.2	0.20	0.39	0.40	0	0	0	0	0	0	0	0	0	0	1	1	1	2	100
GCF_002487355.1	40.3	0.16	0.39	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.35
GCA_003104905.1	40.8	0.17	0.42	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.69
GCA_012026795.1	40.6	0.16	0.37	0.47	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_012026835.1	42.9	0.17	0.42	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.35
GCA_018899795.1	44.0	0.17	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	2	88.84
GCA_018900975.1	43.3	0.17	0.43	0.40	0	0	0	0	0	0	0	0	0	0	0	1	1	0	86.27
GCA_021409285.1	41.7	0.17	0.42	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	2	98.04
GCA_023249105.1	42.5	0.16	0.37	0.46	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.35
GCA_023249275.1	44.2	0.18	0.37	0.44	0	0	0	0	0	0	0	0	0	0	2	0	0	1	95.75
GCA_902384525.1	40.4	0.16	0.39	0.45	0	0	0	0	0	0	0	0	0	0	2	1	1	2	97.36
GCA_902386085.1	44.1	0.18	0.40	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	1	56.93
GCA_902386115.1	43.4	0.16	0.41	0.43	0	0	0	0	0	0	0	0	0	0	2	1	1	2	73.34
GCA_902386135.1	44.0	0.20	0.37	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	3	99.35
GCA_902386205.1	43.9	0.17	0.41	0.42	0	0	0	0	0	0	0	0	0	0	0	1	1	1	96.08
GCA_902386255.1	43.1	0.17	0.37	0.47	0	0	0	0	0	0	0	0	0	0	0	1	1	1	98.26
GCA_905339155.1	40.8	0.16	0.41	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	3	98.69
GCA_013331375.1	52.2	0.21	0.53	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.78
GCA_020793555.1	40.7	0.17	0.42	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	1	93.55
GCA_020793565.1	41.9	0.18	0.44	0.38	0	0	0	1	1	1	0	0	0	0	1	1	1	1	98.04
GCA_023544565.1	41.3	0.18	0.42	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	1	92.48
GCA_012329085.1	29.8	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	0	0	1	1	1	84.87
GCA_016926455.1	41.4	0.20	0.41	0.40	0	0	1	0	0	0	0	0	0	0	0	0	0	0	80.55
GCA_016935475.1	44.4	0.18	0.44	0.38	0	0	0	1	1	1	1	1	0	0	1	0	0	1	80.27
GCA_021106765.1	45.7	0.03	0.60	0.36	1	0	1	1	1	1	1	1	0	0	1	1	1	1	98.53
GCF_004363215.1	42.0	0.02	0.36	0.62	1	1	1	1	1	1	1	1	0	0	1	1	1	1	94.12
GCA_009776675.1	39.6	0.03	0.34	0.63	0	0	0	1	1	1	1	1	0	0	1	1	1	0	1	75.09
GCA_009783635.1	45.9	0.03	0.45	0.52	0	1	1	0	0	1	0	0	0	0	1	0	1	1	1	84.52
GCA_009784005.1	45.5	0.04	0.48	0.48	1	2	2	1	1	1	1	1	0	0	1	0	1	1	1	92.14
GCA_012518265.1	34.4	0.02	0.32	0.66	0	0	1	1	1	1	1	1	0	0	1	1	1	1	1	90.85
GCA_017613335.1	51.0	0.02	0.76	0.22	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	76.28
GCF_000013725.1	40.8	0.04	0.51	0.45	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	99.35
GCF_000765475.1	42.5	0.02	0.51	0.47	1	2	1	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_000970325.1	44.0	0.02	0.55	0.44	0	2	3	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_021184045.1	42.7	0.02	0.51	0.47	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_023684405.1	41.7	0.03	0.52	0.45	1	2	1	1	1	1	1	1	0	0	1	1	1	1	1	99.35
GCA_021108185.1	42.7	0.04	0.52	0.44	1	2	1	1	1	1	1	1	0	0	1	1	1	1	1	98.04
GCA_021108275.1	41.7	0.03	0.52	0.45	1	2	2	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_900774055.1	42.7	0.02	0.51	0.47	2	3	2	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_900111645.1	43.4	0.02	0.51	0.47	1	2	2	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_000196655.1	36.4	0.02	0.31	0.67	1	2	1	1	1	1	1	1	0	0	1	1	1	1	1	100
GCA_018609725.1	36.8	0.03	0.29	0.68	1	0	1	1	1	1	1	1	0	0	1	1	1	1	1	99.35
GCF_900215215.1	42.1	0.02	0.51	0.47	1	0	2	1	1	1	1	1	0	0	1	1	1	1	1	99.51
GCF_001889405.1	42.4	0.02	0.50	0.49	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.51
GCF_017874375.1	42.5	0.03	0.46	0.51	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.18
GCF_000025865.1	42.6	0.02	0.51	0.48	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.35
GCF_002761295.1	41.9	0.02	0.50	0.49	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.51
GCF_004137855.1	42.7	0.05	0.49	0.47	1	3	2	1	1	1	1	1	0	0	1	1	1	1	1	98.86
GCF_003722075.1	42.6	0.02	0.49	0.49	1	1	2	1	1	1	1	1	0	0	1	1	1	1	1	99.51
GCF_017873415.1	39.7	0.10	0.43	0.48	1	2	5	1	1	1	1	1	0	0	1	1	1	1	1	99.51
GCF_024500045.1	48.2	0.11	0.55	0.34	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_004745425.1	43.6	0.13	0.49	0.38	0	0	2	1	1	1	1	1	0	0	1	1	1	1	1	99.67
GCF_900114835.1	42.6	0.11	0.49	0.40	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_000306725.1	44.6	0.12	0.47	0.40	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_002243045.1	41.3	0.12	0.45	0.43	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.67
GCA_002501695.1	47.2	0.13	0.53	0.34	1	0	0	1	1	1	1	1	0	0	1	0	0	0	1	96.57
GCA_002507205.1	42.3	0.11	0.47	0.43	0	0	1	1	1	1	1	1	0	0	1	2	2	2	1	96.2
GCA_002508635.1	44.2	0.11	0.48	0.41	1	2	3	1	1	1	1	1	0	0	1	1	1	1	0	79.61
GCA_003565715.1	40.7	0.13	0.51	0.36	1	1	1	1	1	1	1	1	0	0	0	1	1	1	1	98.66
GCA_016278365.1	44.4	0.11	0.47	0.42	1	1	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_016278385.1	40.2	0.12	0.50	0.47	1	1	3	1	1	1	1	1	0	0	1	1	1	1	1	100
GCA_016932675.1	47.1	0.16	0.56	0.28	0	0	1	1	1	1	1	1	0	0	1	1	1	1	1	96.9
GCA_020055655.1	39.6	0.13	0.40	0.47	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	99.02
GCA_021767785.1	40.8	0.09	0.50	0.41	1	2	2	1	1	1	1	1	0	0	1	1	1	1	1	95.5
GCF_000504205.1	39.8	0.09	0.41	0.49	1	2	4	1	1	1	1	1	0	0	1	1	1	1	1	99.67
GCF_900100715.1	40.3	0.10	0.42	0.48	1	1	4	1	1	1	0	0	0	0	2	1	1	1	1	99.51
GCF_006546655.1	40.2	0.09	0.42	0.48	1	2	4	1	1	1	1	1	0	0	1	1	1	1	1	99.67
GCF_013388255.1	44.1	0.11	0.47	0.42	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000328665.1	41.9	0.09	0.48	0.42	1	2	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_001896725.1	42.3	0.10	0.51	0.39	1	0	2	1	1	1	1	1	0	0	1	1	1	1	1	99.18
GCA_002067265.1	41.0	0.09	0.46	0.45	1	0	1	0	0	0	0	0	0	0	1	1	1	1	0	71.41
GCA_002067275.1	44.3	0.10	0.54	0.37	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	92.97
GCA_002508425.1	41.1	0.10	0.46	0.44	1	1	1	0	1	1	1	1	0	0	1	1	0	0	1	95.26
GCA_014361205.1	38.1	0.10	0.44	0.47	0	1	0	0	0	0	0	0	0	0	0	1	1	1	1	99.67
GCA_020854785.1	43.6	0.13	0.51	0.37	0	0	0	1	1	1	0	1	0	0	1	1	1	1	1	76.38
GCA_024808815.1	34.3	0.06	0.39	0.56	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	99.67
GCA_007127385.1	40.5	0.05	0.51	0.44	1	1	1	0	1	1	0	0	0	0	0	0	0	0	1	81.81
GCF_000217995.1	39.2	0.06	0.48	0.46	1	1	4	1	1	1	1	1	0	0	1	1	1	1	1	99.35
GCF_000007345.1	42.7	0.06	0.46	0.48	2	3	2	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000970025.1	39.2	0.05	0.37	0.58	1	3	2	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000970305.1	39.1	0.05	0.37	0.58	1	3	3	1	1	1	1	1	0	0	1	1	1	1	1	99.18
GCF_000969985.1	39.2	0.06	0.39	0.56	1	3	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_023955635.1	40.1	0.11	0.39	0.50	1	3	0	0	1	1	1	1	0	0	1	1	1	2	1	93.46
GCF_001304615.2	41.3	0.05	0.42	0.54	2	2	0	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000970285.1	41.3	0.04	0.43	0.53	1	3	2	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_000970265.1	41.8	0.04	0.45	0.50	2	3	2	1	1	1	1	1	0	0	1	1	1	1	1	99.18
GCF_000970205.1	41.4	0.04	0.43	0.53	2	3	2	1	1	1	1	1	0	0	1	1	1	1	1	100
GCF_000970085.1	42.9	0.05	0.45	0.50	1	3	1	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000969965.1	41.7	0.06	0.44	0.50	2	4	2	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000979455.1	42.8	0.03	0.46	0.51	2	2	0	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_001714685.2	40.1	0.07	0.41	0.52	1	0	3	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_002496565.1	40.1	0.04	0.39	0.57	1	0	0	1	1	1	1	1	0	0	1	1	1	1	1	97.55
GCA_002499445.1	40.3	0.04	0.41	0.55	1	0	0	1	1	1	1	1	0	0	1	1	1	1	1	99.18
GCA_002505485.1	40.2	0.05	0.39	0.56	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	98.69
GCA_002509325.1	41.2	0.04	0.41	0.55	1	0	0	1	1	1	1	1	0	0	1	1	1	1	1	95.47
GCA_003157235.1	35.8	0.14	0.38	0.48	0	0	0	0	0	0	0	0	0	0	0	1	1	1	2	83.69
GCA_003164755.1	35.7	0.15	0.36	0.49	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	97.39
GCF_004099695.1	42.5	0.04	0.42	0.54	2	1	0	1	1	1	1	1	0	0	1	1	1	1	1	100
GCA_017883485.1	41.5	0.12	0.40	0.48	0	0	0	0	0	0	0	0	0	0	1	1	1	1	2	87.58
GCF_020804225.1	41.7	0.05	0.42	0.54	2	4	0	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_023399215.1	39.8	0.05	0.39	0.56	1	1	1	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_024280975.1	39.9	0.05	0.38	0.57	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	78.42
GCF_024372725.1	46.8	0.03	0.53	0.45	3	3	0	1	1	1	1	1	0	0	1	2	1	1	1	99.84
GCA_013331265.1	41.6	0.04	0.43	0.53	1	0	0	1	1	1	1	1	0	0	2	0	0	0	1	55.9
GCA_013331275.1	39.1	0.06	0.39	0.56	0	0	0	0	0	1	1	1	0	0	0	1	1	0	1	84.67
GCA_013330315.1	41.4	0.05	0.44	0.52	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	60.01
GCF_002287235.1	38.7	0.07	0.38	0.55	1	1	0	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000969885.1	41.2	0.04	0.41	0.55	2	3	1	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000969905.1	39.7	0.05	0.39	0.56	1	3	2	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCF_000970045.1	45.9	0.03	0.51	0.45	2	3	0	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_016841265.1	46.0	0.03	0.52	0.45	2	2	0	1	1	1	1	1	0	0	1	1	1	1	1	98.04
GCA_016841625.1	46.3	0.04	0.52	0.45	2	3	0	1	1	1	1	1	0	0	1	1	1	1	1	99.84
GCA_013329415.1	46.8	0.05	0.51	0.44	2	3	0	1	1	1	1	1	0	0	1	1	1	1	1	95.78
GCA_003162615.1	49.5	0.25	0.45	0.30	0	0	0	0	0	0	0	0	0	0	2	1	1	2	1	95.36
GCA_013415595.1	60.5	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	93.63
GCA_013178225.1	53.7	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	1	1	1	1	1	1	98.86
GCA_016927425.1	56.1	0.25	0.61	0.15	0	0	0	0	0	0	0	0	0	0	1	1	1	1	1	98.53

GCA_022865315.1	42.0	0.24	0.38	0.38	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.39
GCA_002502785.1	55.5	0.21	0.61	0.18	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.85
GCA_002506535.1	58.8	0.22	0.65	0.13	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.34
GCA_001509375.1	56.5	0.20	0.62	0.17	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_000235565.1	60.6	0.21	0.68	0.11	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_001602645.1	59.1	0.20	0.67	0.13	0	0	0	0	0	0	0	0	0	0	0	1	1	1	99.34
GCA_020844795.1	59.6	0.22	0.66	0.13	0	0	0	0	0	0	0	0	0	0	0	1	1	1	91.45
GCA_024649985.1	59.7	0.21	0.66	0.13	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.68
GCA_013329455.1	54.9	0.19	0.61	0.20	0	0	0	0	0	0	0	0	0	0	2	1	1	1	91.08
GCA_024518575.1	54.8	0.21	0.68	0.12	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.84
GCF_000014945.1	53.5	0.19	0.67	0.15	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_000204415.1	51.0	0.26	0.48	0.26	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.35
GCA_002067365.1	53.3	0.25	0.56	0.19	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.47
GCA_002067705.1	50.8	0.26	0.48	0.26	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.37
GCA_002067755.1	51.9	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.9
GCA_002256595.1	54.8	0.27	0.48	0.25	0	0	0	0	0	0	0	0	0	0	1	1	1	1	80.56
GCA_002505805.1	53.2	0.27	0.48	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_003857025.1	51.0	0.25	0.46	0.29	0	0	0	0	0	0	0	0	0	0	1	1	1	1	93.3
GCA_011391755.1	51.9	0.26	0.42	0.32	0	0	0	0	0	0	0	0	0	0	1	0	0	0	63.53
GCA_011620785.1	52.8	0.24	0.51	0.25	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.04
GCA_012798025.1	51.8	0.23	0.52	0.25	0	0	0	0	0	0	0	0	0	0	1	0	1	1	86.96
GCA_016706325.1	53.2	0.24	0.55	0.21	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.73
GCA_016927055.1	51.2	0.26	0.44	0.31	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.42
GCA_017994055.1	53.1	0.28	0.48	0.24	0	0	0	0	0	0	0	0	0	0	0	1	1	1	89.65
GCA_018052825.1	56.1	0.26	0.51	0.23	0	0	0	0	0	0	0	0	0	0	0	1	1	1	93.46
GCA_023229165.1	48.4	0.24	0.40	0.36	0	0	0	0	0	0	0	0	0	0	1	0	1	1	95.1
GCA_902385025.1	50.5	0.28	0.46	0.26	0	0	0	0	0	0	0	0	0	0	0	1	1	1	81.54
GCA_903871465.1	49.9	0.27	0.46	0.27	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.42
GCA_002067795.1	55.5	0.22	0.59	0.18	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.37
GCA_002506335.1	52.0	0.28	0.43	0.29	0	0	0	0	0	0	0	0	0	0	1	1	1	0	98.37
GCA_002501765.1	54.5	0.24	0.54	0.22	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.22
GCA_004212135.1	48.7	0.21	0.38	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	1	78.4
GCA_014859735.1	46.3	0.18	0.39	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	89.87
GCA_020725315.1	44.2	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	1	84.31
GCA_003194425.1	52.2	0.20	0.39	0.41	0	0	0	0	0	0	0	0	0	0	1	1	1	2	87.91
GCA_003194435.1	45.8	0.20	0.42	0.38	0	0	0	0	0	0	0	0	0	0	1	1	1	2	88.24
GCA_021159465.1	44.8	0.20	0.43	0.37	0	0	0	0	0	0	0	0	0	0	1	1	1	2	91.18
GCA_021159475.1	48.2	0.21	0.43	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	2	83.66
GCA_011049045.1	55.2	0.22	0.44	0.34	0	0	0	0	0	0	0	0	0	0	0	1	1	2	93.14
GCA_014061035.1	44.5	0.23	0.36	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	0	87.99
GCA_016649585.1	44.8	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	0	82.03
GCA_016928455.1	54.6	0.24	0.41	0.35	0	0	0	0	0	0	0	0	0	0	0	1	1	2	75.18
GCA_016930255.1	49.2	0.22	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	1	1	0	91.18
GCA_017883965.1	41.9	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	0	1	1	0	90.31
GCA_023659785.1	42.3	0.20	0.35	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	2	84.61
GCA_023131215.1	41.6	0.19	0.37	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	2	79.81
GCA_023659775.1	42.5	0.22	0.35	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	2	68.46
GCA_024699715.1	47.8	0.17	0.54	0.29	0	0	0	0	0	0	0	0	0	0	1	1	1	1	88.29
GCA_003336485.1	42.9	0.20	0.38	0.41	0	0	0	0	0	0	0	0	0	0	1	1	2	2	91.01
GCA_009903405.1	42.8	0.20	0.37	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	0	63.48
GCA_013139985.1	42.9	0.19	0.39	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	2	83.22
GCA_013180565.1	42.0	0.21	0.38	0.41	0	0	0	0	0	0	0	0	0	0	0	2	1	2	80.59
GCA_013180585.1	42.7	0.22	0.38	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	2	79.21
GCA_013374505.1	43.3	0.21	0.38	0.41	0	0	0	0	0	0	0	0	0	0	1	1	0	2	76.47
GCA_003160755.1	43.3	0.20	0.32	0.48	0	0	0	0	0	0	0	0	0	0	1	1	1	2	81.24
GCA_003601795.1	43.0	0.20	0.37	0.43	0	0	0	0	0	0	0	0	0	0	1	1	1	2	80.5
GCA_013180605.1	42.7	0.19	0.34	0.47	0	0	0	0	0	0	0	0	0	0	1	1	1	2	80.8
GCA_021161765.1	43.5	0.21	0.34	0.45	0	0	0	0	0	0	0	0	0	0	1	1	1	2	84.94
GCA_003661125.1	43.0	0.20	0.38	0.41	0	0	0	0	0	0	0	0	0	0	0	1	1	2	83.83
GCA_009618475.1	43.2	0.18	0.35	0.46	0	0	0	0	0	0	0	0	0	0	1	0	0	1	59.84
GCA_016782355.1	43.2	0.17	0.40	0.44	0	0	0	0	0	0	0	0	0	0	1	1	1	1	55.52
GCA_003661185.1	51.9	0.25	0.43	0.33	0	0	0	0	0	0	0	0	0	0	2	1	1	2	83.33
GCA_016207465.1	67.7	0.31	0.49	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.95
GCA_001766815.1	45.5	0.18	0.53	0.29	0	0	0	0	0	0	0	0	0	0	3	4	4	2	96.08
GCA_001766825.1	48.7	0.19	0.57	0.25	0	0	0	0	0	0	0	0	0	0	4	4	4	4	88.89
GCA_021129915.1	46.6	0.18	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.39
GCA_002495885.1	42.6	0.23	0.43	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.24
GCA_013415795.1	40.7	0.23	0.41	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_002789275.1	31.3	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.42
GCA_002897955.1	40.1	0.23	0.39	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_003229935.1	39.0	0.23	0.39	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_013152995.1	58.8	0.28	0.59	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.27
GCA_015521945.1	60.9	0.30	0.57	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_013152685.1	60.0	0.44	0.41	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_015521565.1	56.0	0.35	0.43	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_015521615.1	52.1	0.34	0.39	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_002011125.1	39.1	0.19	0.34	0.47	0	1	1	1	1	1	0	1	1	1	0	0	0	0	98.13
GCA_018830205.1	47.2	0.25	0.39	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.81
GCA_013152845.1	59.8	0.31	0.52	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.78
GCA_003695745.1	55.9	0.29	0.50	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.6
GCA_002923215.1	46.7	0.24	0.35	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.22
GCA_003230355.1	47.6	0.24	0.36	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.97
GCA_016207475.1	61.5	0.41	0.41	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.58
GCA_016212785.1	46.4	0.27	0.40	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_015520145.1	44.3	0.25	0.42	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_002779075.1	29.7	0.17	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.57
GCA_903916665.1	27.7	0.17	0.19	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.82
GCA_003559395.1	32.4	0.19	0.26	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.86
GCA_009392915.1	24.6	0.19	0.14	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.16
GCA_023230325.1	26.8	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.62
GCA_002779065.1	34.3	0.14	0.22	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81
GCA_002763225.1	30.9	0.10	0.31	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_017609625.1	32.7	0.14	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_018829335.1	32.3	0.10	0.32	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_024277355.1	28.0	0.08	0.24	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_017608995.1	40.2	0.22	0.30	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.9
GCA_021161055.1	42.7	0.28	0.35	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_021163505.1	39.8	0.23	0.31	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_017608575.1	38.3	0.13	0.43	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_002688035.1	41.3	0.26	0.28	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.69
GCA_017610245.1	44.8	0.26	0.35	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.25
GCA_017610205.1	37.7	0.16	0.30	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.49
GCA_017610265.1	40.1	0.18	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_017610335.1	37.4	0.16	0.31	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.42
GCA_017610485.1	46.0	0.24	0.37	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_017609945.1	46.8	0.24	0.34	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.28
GCA_017610175.1	44.8	0.17	0.35	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_016932355.1	46.2	0.25	0.35	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_017608725.1	43.8	0.20	0.36	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.97
GCA_016931555.1	41.2	0.19	0.32	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.26
GCA_020053055.1	38.5	0.12	0.30	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_000830275.1	43.1	0.20	0.39	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_016186855.1	40.4	0.14	0.42	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.89
GCA_016198165.1	46.5	0.11	0.51	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_000402355.1	47.4	0.13	0.55	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_002762975.1	37.3	0.13	0.33	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_005239615.1	52.3	0.17	0.59	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_016202305.1	51.9	0.16	0.64	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.93
GCA_013331625.1	48.8	0.16	0.53	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.18
GCA_902386385.1	49.9	0.14	0.56	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.92
GCA_002687735.1	35.3	0.15	0.32	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_024653865.1	47.9	0.15	0.41	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.93
GCA_024653905.1	35.0	0.13	0.33	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_002068885.1	30.2	0.08	0.19	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.34
GCA_012799645.1	30.1	0.08	0.14	0.78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_020717885.1	38.8	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_902385225.1	40.6	0.15	0.26	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_018651445.1	34.1	0.24	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.75
GCA_018691995.1	31.4	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.41
GCA_016187745.1	45.5	0.21	0.38	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.27
GCA_018304445.1	44.2	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.29
GCA_016205145.1	51.3	0.15	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_017610305.1	42.1	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_017609985.1	38.8	0.24	0.34	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_016218635.1	52.4	0.16	0.47	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81
GCA_016932875.1	29.7	0.04	0.33	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_021161405.1	38.8	0.27	0.31	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.46
GCA_018304465.1	47.9	0.12	0.39	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.84
GCA_018813975.1	39.5	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_013331925.1	42.9	0.17	0.43	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.81
GCA_018304425.1	58.4	0.21	0.49	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_016198125.1	48.1	0.13	0.43	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_016699555.1	51.0	0.24	0.36	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.13

GCA_016867455.1	45.5	0.20	0.27	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_020053155.1	46.9	0.23	0.34	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.19
GCA_013154145.1	58.9	0.19	0.54	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_015520865.1	49.7	0.24	0.43	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.6
GCA_013154035.1	52.3	0.21	0.50	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_015662385.1	55.1	0.25	0.46	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.76
GCA_015521515.1	44.0	0.22	0.42	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.27
GCA_017608775.1	37.0	0.32	0.23	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.45
GCA_016926295.1	40.1	0.27	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_021158055.1	42.1	0.11	0.44	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.23
GCA_013154095.1	45.7	0.28	0.34	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_024860865.1	36.5	0.24	0.28	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.81
GCA_003660605.1	36.2	0.18	0.42	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.69
GCA_021159325.1	37.7	0.16	0.47	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.03
GCA_023133315.1	37.5	0.18	0.39	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.89
GCA_001587575.1	34.5	0.19	0.22	0.58	0	0	0	0	0	0	0	0	0	1	1	1	2	0	90.98
GCA_001587595.1	33.5	0.20	0.23	0.58	0	0	0	0	0	0	0	0	0	1	1	1	2	0	86.02
GCA_001587675.1	34.1	0.19	0.22	0.59	0	0	0	0	0	0	0	0	0	1	1	1	1	0	85.02
GCA_001587715.1	35.4	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	1	1	1	2	0	85.27
GCA_003558335.1	33.8	0.20	0.24	0.56	0	0	0	0	0	0	0	0	0	1	1	1	1	0	85.27
GCA_012799835.1	33.8	0.19	0.23	0.57	0	0	0	0	0	0	0	0	0	0	1	1	1	0	90.77
GCA_013178285.1	34.5	0.19	0.22	0.60	0	0	0	0	0	0	0	0	0	1	1	1	2	0	93.87
GCA_020854815.1	35.2	0.20	0.25	0.55	0	0	0	0	0	0	0	0	0	1	1	1	2	0	93.87
GCA_023622545.1	34.9	0.19	0.21	0.60	0	0	0	0	0	0	0	0	0	0	1	1	2	0	71.66
GCA_013329085.1	35.5	0.19	0.25	0.55	0	0	0	0	0	0	0	0	0	2	2	1	1	0	74.56
GCA_016930445.1	48.9	0.28	0.46	0.26	0	0	0	0	0	0	0	0	0	1	0	0	1	0	76.73
GCA_020854925.1	58.3	0.31	0.42	0.28	0	0	0	0	0	0	0	0	0	1	1	1	0	0	80.87
GCA_004212155.1	55.2	0.22	0.53	0.26	0	0	0	0	0	0	0	0	0	1	1	1	1	0	85.55
GCA_011372835.1	55.8	0.25	0.52	0.23	0	0	0	0	0	0	0	0	0	1	0	0	0	0	66.34
GCA_018992565.1	46.7	0.29	0.49	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.26
GCA_018992685.1	46.7	0.30	0.48	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.29
GCF_000966265.1	54.3	0.15	0.66	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000725425.1	43.0	0.20	0.52	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_003663695.1	44.6	0.17	0.53	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.26
GCF_000195935.2	44.7	0.21	0.50	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214605.1	44.9	0.20	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000007305.1	40.8	0.20	0.46	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_000011105.1	41.9	0.19	0.47	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_001577775.1	44.6	0.19	0.50	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000211475.1	42.7	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000263735.1	42.3	0.21	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_003660485.1	45.0	0.21	0.50	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.04
GCF_000215995.1	51.6	0.17	0.61	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_024022995.1	43.3	0.19	0.51	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.51
GCF_024054535.1	43.0	0.19	0.52	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_020386975.1	44.1	0.22	0.52	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.01
GCF_000022545.1	40.2	0.17	0.49	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.51
GCF_001317345.1	39.3	0.19	0.46	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.51
GCF_001484685.1	44.6	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_001507935.1	43.5	0.20	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.53
GCA_003663525.1	40.3	0.17	0.49	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.88
GCA_003663535.1	40.3	0.17	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.88
GCF_012027425.1	39.7	0.18	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_021157445.1	42.5	0.21	0.49	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.16
GCF_023746595.1	39.4	0.19	0.47	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.51
GCF_000151105.2	41.7	0.15	0.53	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_000517445.1	40.3	0.15	0.52	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.55
GCA_015662175.1	43.7	0.17	0.51	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.11
GCF_012027325.1	41.2	0.16	0.55	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_017656495.1	40.3	0.15	0.52	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_002009975.1	38.1	0.20	0.45	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214465.1	54.7	0.15	0.66	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_904067545.1	54.6	0.14	0.67	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214365.1	56.4	0.14	0.67	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_001484195.1	54.3	0.14	0.67	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.77
GCF_000265525.1	55.8	0.15	0.68	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000769655.1	53.5	0.12	0.67	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000022365.1	53.6	0.12	0.67	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214385.1	51.7	0.13	0.66	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.03
GCF_000816105.1	52.9	0.12	0.67	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_900198835.1	54.6	0.13	0.69	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_006274605.1	54.9	0.13	0.68	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000009965.1	52.0	0.14	0.68	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000585495.1	54.8	0.13	0.68	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000018365.1	51.3	0.13	0.65	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.52
GCF_002214485.1	54.2	0.12	0.70	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_001592435.1	51.7	0.14	0.67	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_001647085.1	51.1	0.16	0.61	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214585.1	53.1	0.12	0.69	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214565.1	55.6	0.14	0.69	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214505.1	55.0	0.14	0.68	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_000151205.2	54.8	0.14	0.67	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000221185.1	56.1	0.12	0.71	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002214525.1	54.9	0.13	0.64	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_011050175.1	54.4	0.13	0.68	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.61
GCF_012027305.1	53.5	0.14	0.66	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027355.1	52.6	0.15	0.66	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027395.1	51.9	0.14	0.66	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027495.1	55.7	0.14	0.69	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027555.1	52.6	0.14	0.65	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027595.1	52.2	0.12	0.68	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027615.1	54.4	0.14	0.67	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027635.1	54.6	0.12	0.68	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_012027645.1	55.4	0.12	0.72	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCA_013153595.1	56.6	0.14	0.72	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.66
GCA_015520705.1	48.5	0.16	0.60	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.53
GCA_015521605.1	54.5	0.14	0.68	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.01
GCA_015522395.1	54.9	0.15	0.67	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.12
GCA_015523185.1	51.1	0.14	0.63	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.52
GCA_015523195.1	55.7	0.13	0.68	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.63
GCA_021160985.1	53.4	0.14	0.64	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.78
GCF_024707485.1	53.5	0.14	0.66	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_017873335.1	52.5	0.15	0.63	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.5
GCF_002214545.1	53.5	0.15	0.64	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000258515.1	54.5	0.12	0.69	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_902795935.1	27.3	0.11	0.13	0.77	0	0	0	0	0	0	0	0	0	1	1	1	1	1	92.01
GCA_020854915.1	26.1	0.16	0.15	0.69	0	0	0	0	0	0	0	0	0	1	1	1	1	1	100
GCA_002067325.1	40.7	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	2	2	2	0	0	97.99
GCA_002067565.1	36.6	0.16	0.25	0.59	0	0	0	0	0	0	0	0	0	0	1	0	0	0	75.04
GCA_002494495.1	37.6	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	1	1	1	0	0	97.56
GCA_002495625.1	40.5	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	2	2	2	2	0	99.94
GCA_002502855.1	40.2	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	1	1	1	0	0	96.98
GCA_003161815.1	33.3	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	1	1	1	0	73.93
GCA_003166335.1	32.4	0.12	0.18	0.70	0	0	0	0	0	0	0	0	0	1	1	1	2	0	100
GCA_011620845.1	41.2	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	1	1	1	0	0	98.07
GCA_015661405.1	31.2	0.11	0.18	0.72	0	0	0	0	0	0	0	0	0	1	1	1	1	0	99.73
GCA_017883605.1	38.7	0.18	0.25	0.57	0	0	0	0	0	0	0	0	0	1	1	1	1	0	94.13
GCA_018263005.1	36.2	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	1	1	0	0	94.4
GCA_021372715.1	35.5	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	1	0	0	2	0	96.29
GCF_000191585.1	35.8	0.13	0.24	0.63	0	0	0	0	0	0	0	0	0	2	2	2	2	0	99.2
GCF_000744455.1	32.6	0.14	0.20	0.67	0	0	0	0	0	0	0	0	0	1	1	1	1	0	98.4
GCA_003151535.1	32.5	0.16	0.19	0.65	0	0	0	0	0	0	0	0	2	2	1	1	2	0	94.89
GCA_003158115.1	32.1	0.15	0.19	0.66	0	0	0	0	0	0	0	0	0	0	1	0	2	0	95.73
GCA_003162115.1	33.9	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	2	1	0	1	0	91.22
GCA_003162655.1	34.9	0.16	0.27	0.58	0	0	0	0	0	0	0	0	0	0	2	0	1	0	82.7
GCA_003164415.1	32.4	0.15	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	2	0	75.6
GCA_009712615.1	39.8	0.14	0.31	0.55	0	0	0	0	0	0	0	0	0	2	2	2	2	0	94.13
GCA_023430285.1	36.5	0.14	0.25	0.61	0	0	0	0	0	0	0	0	0	1	1	1	2	0	83.4
GCA_024167805.1	35.3	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	2	2	2	1	0	98
GCF_017874455.1	38.1	0.14	0.34	0.52	0	0	0	0	0	0	0	0	0	1	1	1	1	0	100
GCF_900095295.1	38.5	0.13	0.35	0.53	0	0	0	0	0	0	0	0	0	1	1	1	1	0	99.73
GCF_000214725.1	35.7	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	1	1	1	2	0	99.73
GCA_002498385.1	38.2	0.13	0.31	0.56	0	0	0	0	0	0	0	0	0	2	2	2	1	0	98.4
GCF_002287175.1	33.2	0.14	0.17	0.68	0	0	0	0	0	0	0	0	0	2	2	2	2	0	99.2
GCA_002494885.1	33.1	0.14	0.19	0.66	0	0	0	0	0	0	0	0	0	1	1	1	2	0	98.4
GCA_002505765.1	33.8	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	1	1	1	2	0	99.2
GCA_002509665.1	33.0	0.15	0.20	0.66	0	0	0	0	0	0	0	0	0	1	1	1	2	0	80.93
GCA_016222945.1	32.6	0.13	0.17	0.70	0	0	0	0	0	0	0	0	0	2	2	2	1	0	99.2
GCA_023409695.1	33.0	0.15	0.16	0.69	0	0	0	0	0	0	0	0	0	1	2	1	1	0	89.67
GCA_023411115.1	33.5	0.16	0.17	0.67	0	0	0	0	0	0	0	0	0	1	1	0	2	0	99.2
GCA_023434825.1	31.6	0.14	0.15	0.71	0	0	0	0	0	0	0	0	0	3	1	2	3	0	95.29
GCA_023436175.1	32.6	0.14	0.18	0.68	0	0	0	0	0	0	0	0	0	2	1	1	2	0	90.11
GCF_000745485.1	33.2	0.14	0.16	0.69	0	0	0	0	0	0	0	0	0	2	2	2	2	0	99.2

GCF_023227715.1	33.4	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	2	2	2	2	99.2
GCF_001316325.1	41.2	0.15	0.33	0.52	0	0	0	0	0	0	0	0	0	0	3	3	3	1	91.82
GCF_000302455.1	38.0	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	2	2	2	2	98.93
GCF_017873625.1	37.8	0.15	0.23	0.61	0	0	0	0	0	0	0	0	0	0	2	2	2	2	98.93
GCA_000309865.1	38.6	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	2	2	2	2	96.53
GCA_000499765.1	39.7	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	2	2	2	2	98.13
GCA_002067065.1	38.1	0.15	0.23	0.62	0	0	0	0	0	0	0	0	0	0	1	2	1	2	95.73
GCA_002496805.1	36.3	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	2	2	2	2	92.04
GCA_003491305.1	41.4	0.17	0.22	0.61	0	0	0	0	0	0	0	0	0	0	2	2	2	2	100
GCA_012838205.1	36.5	0.16	0.22	0.61	0	0	0	0	0	0	0	0	0	0	2	2	2	2	97.6
GCA_013403005.1	38.1	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	2	2	2	2	99.2
GCA_016217785.1	39.0	0.15	0.22	0.63	0	0	0	0	0	0	0	0	0	0	2	2	2	2	98.93
GCA_020854975.1	37.9	0.14	0.23	0.62	0	0	0	0	0	0	0	0	0	0	1	1	1	2	94.93
GCA_020855015.1	38.1	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	1	1	1	1	89.39
GCF_002813695.1	39.4	0.17	0.23	0.61	0	0	0	0	0	0	0	0	0	0	2	2	2	2	98.93
GCF_003814835.1	30.0	0.21	0.16	0.63	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_900103415.1	36.5	0.24	0.19	0.57	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_001477655.1	31.8	0.19	0.16	0.65	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.2
GCA_015063005.1	33.2	0.22	0.17	0.61	0	0	0	0	0	0	0	0	0	0	1	1	1	0	89.31
GCF_001639275.1	27.7	0.19	0.15	0.66	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_000016525.1	31.0	0.20	0.16	0.65	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_023617305.1	30.3	0.19	0.14	0.67	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_001548675.1	34.2	0.25	0.17	0.58	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCA_002496065.1	34.8	0.24	0.23	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.88
GCA_015062935.1	34.2	0.23	0.17	0.61	0	0	0	0	0	0	0	0	0	0	0	1	1	1	97.6
GCA_015062985.1	35.0	0.23	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	1	90.54
GCA_017406825.1	36.9	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	1	96.65
GCA_017407115.1	33.8	0.21	0.20	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	1	89.6
GCA_017409525.1	34.9	0.23	0.19	0.57	0	0	0	0	0	0	0	0	0	0	2	2	2	1	97.6
GCA_017427765.1	33.7	0.25	0.17	0.58	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCA_017431965.1	33.8	0.22	0.18	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	1	95.81
GCA_017434525.1	34.5	0.24	0.21	0.55	0	0	0	0	0	0	0	0	0	0	1	1	0	1	97.2
GCA_017434555.1	32.3	0.17	0.17	0.66	0	0	0	0	0	0	0	0	0	1	0	1	0	1	98.76
GCA_017447225.1	34.3	0.23	0.18	0.59	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.54
GCA_017459665.1	34.3	0.24	0.20	0.56	0	0	0	0	0	0	0	0	0	0	1	1	1	0	84.35
GCA_017460025.1	33.4	0.20	0.20	0.60	0	0	0	0	0	0	0	0	0	0	1	2	2	1	86.06
GCA_017466685.1	33.1	0.21	0.19	0.60	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.09
GCA_017473945.1	34.4	0.24	0.19	0.57	0	0	0	0	0	0	0	0	0	0	2	2	2	1	95.23
GCA_017539065.1	33.8	0.25	0.17	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	1	97.64
GCA_017553445.1	34.1	0.23	0.18	0.58	0	0	0	0	0	0	0	0	0	0	2	2	1	1	93.66
GCA_017940815.1	35.9	0.24	0.18	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	1	98.4
GCA_021442885.1	28.4	0.20	0.12	0.67	0	0	0	0	0	0	0	0	0	0	1	1	1	0	92.4
GCA_022775905.1	31.5	0.22	0.15	0.63	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_024413395.1	28.5	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	1	0	0	0	1	88.32
GCA_024689425.1	32.3	0.22	0.18	0.59	0	0	0	0	0	0	0	0	0	0	0	1	0	1	98.13
GCA_900313645.1	36.1	0.25	0.18	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.1
GCA_900314615.1	34.1	0.21	0.18	0.61	0	0	0	0	0	0	0	0	0	0	0	1	0	1	99
GCA_900314695.1	32.7	0.23	0.17	0.60	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.4
GCA_900316895.1	36.5	0.27	0.20	0.53	0	0	0	0	0	0	0	0	0	0	1	0	0	1	94.4
GCA_900317865.1	31.6	0.18	0.19	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	1	92.53
GCA_900318035.1	35.1	0.25	0.18	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	1	92.39
GCA_902771225.1	30.8	0.19	0.17	0.64	0	0	0	0	0	0	0	0	0	0	2	3	2	1	100
GCA_900319985.1	33.9	0.25	0.18	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	1	88.73
GCA_900320515.1	36.9	0.27	0.20	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	1	87.73
GCA_900320955.1	32.6	0.22	0.19	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	1	86.42
GCA_900766745.1	32.7	0.23	0.15	0.61	0	0	0	0	0	0	0	0	0	1	1	1	1	1	97.6
GCA_900769095.1	31.5	0.24	0.13	0.63	0	0	0	0	0	0	0	0	0	0	0	1	1	1	95.33
GCA_902764015.1	40.5	0.31	0.24	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	1	89.95
GCA_902764455.1	32.6	0.22	0.16	0.62	0	0	0	0	0	0	0	0	0	0	1	1	2	1	96.41
GCA_902770715.1	34.4	0.23	0.18	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	1	98.93
GCA_902771435.1	35.4	0.25	0.19	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	1	93.33
GCA_902772665.1	33.6	0.21	0.24	0.55	0	0	0	0	0	0	0	0	0	0	0	1	0	0	81.76
GCA_902774605.1	39.0	0.25	0.22	0.53	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCA_902777885.1	32.8	0.20	0.18	0.62	0	0	0	0	0	0	0	0	0	0	1	2	1	1	80.62
GCA_902782595.1	35.2	0.23	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.5
GCA_902783085.1	29.4	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	0	1	1	1	1	81.15
GCA_902785855.1	29.0	0.19	0.14	0.68	0	0	0	0	0	0	0	0	0	0	2	1	1	1	97.81
GCA_902788255.1	35.7	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	1	100
GCA_902789505.1	35.1	0.23	0.21	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	1	92.87
GCA_902794475.1	35.9	0.25	0.22	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	1	80.49
GCA_902796575.1	32.3	0.18	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	1	82.16
GCA_902801725.1	34.5	0.25	0.19	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	1	96.8
GCA_904501935.1	33.3	0.24	0.17	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	1	88.15
GCA_934746965.1	28.3	0.18	0.13	0.69	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCF_003111625.1	36.9	0.26	0.19	0.55	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.4
GCA_015062905.1	37.0	0.27	0.21	0.53	0	0	0	0	0	0	0	0	0	0	1	1	1	1	92.05
GCA_015062915.1	37.0	0.26	0.18	0.57	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.8
GCA_015062925.1	29.8	0.15	0.16	0.69	0	0	0	0	0	0	0	0	0	0	0	1	0	1	83.28
GCF_003111605.1	29.9	0.19	0.10	0.71	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_000320505.1	29.0	0.22	0.09	0.68	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_002208625.1	24.4	0.20	0.06	0.73	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_900314605.1	25.9	0.17	0.10	0.73	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCA_905235195.1	26.2	0.18	0.09	0.74	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCF_000621965.1	24.2	0.17	0.08	0.75	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_002072215.1	25.4	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_019669925.1	25.6	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_001639285.1	26.8	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.6
GCA_003315655.1	25.3	0.18	0.17	0.65	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.6
GCA_009776495.1	27.0	0.18	0.19	0.63	0	0	0	0	0	0	0	0	0	0	0	1	1	1	72.98
GCA_009777005.1	25.5	0.17	0.19	0.64	0	0	0	0	0	0	0	0	0	0	0	1	1	1	85.6
GCA_009784145.1	25.5	0.15	0.17	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	1	73.76
GCF_020148105.1	25.7	0.15	0.13	0.72	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_001639295.1	25.7	0.14	0.13	0.73	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.6
GCF_001639265.1	27.0	0.17	0.15	0.68	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96
GCF_900114585.1	26.8	0.17	0.08	0.74	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCA_015063035.1	32.0	0.18	0.14	0.68	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.12
GCF_000024185.1	32.6	0.25	0.12	0.63	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.14
GCA_004553595.1	32.2	0.19	0.13	0.69	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCA_016291275.1	32.6	0.19	0.11	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	1	78.87
GCA_016838945.1	32.8	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.6
GCA_017404125.1	32.3	0.19	0.10	0.71	0	0	0	0	0	0	0	0	0	0	1	0	1	1	65.09
GCA_017410345.1	34.2	0.19	0.12	0.69	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.13
GCA_017432245.1	32.2	0.17	0.13	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	1	92.61
GCA_017646885.1	33.5	0.17	0.19	0.64	0	0	0	0	0	0	0	0	2	0	1	0	0	0	74.03
GCA_017652345.1	32.3	0.15	0.25	0.60	0	0	0	0	0	0	0	0	2	2	1	0	0	0	57.61
GCA_024409145.1	26.9	0.15	0.06	0.79	0	0	0	0	0	0	0	0	0	1	1	1	1	1	95.02
GCA_024409165.1	27.6	0.15	0.10	0.75	0	0	0	0	0	0	0	0	0	1	1	1	1	1	93.42
GCA_024409185.1	26.8	0.14	0.08	0.78	0	0	0	0	0	0	0	0	0	0	0	0	0	1	69.73
GCA_900314635.1	34.0	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	1	1	1	1	1	98.93
GCA_900321995.1	30.5	0.20	0.11	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.27
GCA_902769175.1	30.9	0.19	0.15	0.66	0	0	0	0	0	0	0	0	0	0	1	1	1	1	91.36
GCA_902774685.1	32.4	0.16	0.11	0.73	0	0	0	0	0	0	0	0	0	2	1	1	1	1	91.33
GCA_902784195.1	32.1	0.18	0.12	0.70	0	0	0	0	0	0	0	0	0	1	1	1	1	1	100
GCA_905235495.1	32.1	0.18	0.16	0.66	0	0	0	0	0	0	0	0	0	1	1	1	1	1	80.4
GCF_003149675.1	28.1	0.17	0.09	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	1	96
GCF_001729965.1	27.7	0.15	0.09	0.76	0	0	0	0	0	0	0	0	0	1	1	1	1	1	96.8
GCA_003266065.1	34.8	0.17	0.21	0.61	0	0	0	0	0	0	0	0	0	1	0	0	0	0	77.64
GCA_003266075.1	35.5	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	1	1	1	1	75.89
GCA_003266105.1	32.9	0.17	0.17	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	1	92.66
GCA_003266145.1	33.0	0.17	0.15	0.68	0	0	0	0	0	0	0	0	0	1	1	1	1	1	90.4
GCF_003268005.1	32.9	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	1	1	1	1	1	96.8
GCA_016282985.1	29.8	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	1	1	1	1	1	94.4
GCA_017430835.1	29.5	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	1	1	1	0	1	89.46
GCA_017431845.1	30.6	0.16	0.14	0.71	0	0	0	0	0	0	0	0	0	1	1	1	1	1	87.33
GCA_021199865.1	31.7	0.20	0.09	0.71	0	0	0	0	0	0	0	0	0	1	1	1	1	1	91.94
GCA_022768985.1	29.4	0.26	0.07	0.66	0	0	0	0	0	0	0	0	0	1	1	1	1	1	96.8
GCA_013330915.1	33.2	0.19	0.12	0.69	0	0	0	0	0	0	0	0	0	1	0	1	1	1	82.96
GCA_902782945.1	29.7	0.18	0.09	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	1	94.26
GCA_902797085.1	31.9	0.18	0.15	0.67	0	0	0	0	0	0	0	0	0	1	0	0	0	1	87.02
GCF_000012545.1	27.6	0.18	0.11	0.71	0	0	0	0	0	0	0	0	0	1	1	1	1	1	97.6
GCA_015062825.1	29.4	0.13	0.13	0.74	0	0	0	0	0	0	0	0	0	1	1	1	1	1	97.6
GCA_015062815.1	27.7	0.15	0.13	0.71	0	0	0	0	0	0	0	0	0	0	1	1	1	1	83.93
GCA_015062805.1	29.4	0.16	0.12	0.71	0	0	0	0	0	0	0	0	0	1	1	1	1	1	96
GCA_003491285.1	33.4	0.13	0.19	0.67	0	0	0	0	0	0	0	0	0	2	2	2	2	1	100
GCA_002509745.1	32.6	0.14	0.18	0.67	0	0	0	0	0	0	0	0	0	0	2	0	1	1	86.74
GCA_002839705.1	33.0	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	2	2	2	2	2	100
GCA_023249725.1	32.6	0.15	0.19	0.66	0	0	0	0	0	0	0	0	0	1	1	1	1	2	95.79
GCA_002495685.1	27.2	0.06	0.07	0.87	0	0	0	0	0	0	0	0	0	1	1	1	1	1	100
GCA_023440975.1	27.9	0.08	0.08	0.84	0	0	0	0	0	0	0	0	0	1	1	1	1	1	97.42
GCA_002504725.1	37.1	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	1	1	1	1	2	86.4
GCF_018141185.1	36.4	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	2	2	2	2	2	100
GCA_003558085.1	35.4	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	1	1	1	1	1	99.73
GCA_019084405.1	36.4	0.17	0.22	0.62	0	0	0	0	0	0	0	0	0	2	2	2	2	2	100

GCA_016874685.1	34.6	0.17	0.27	0.55	0	0	0	0	0	0	0	0	0	0	1	1	1	2	99.33
GCF_000166095.1	31.6	0.18	0.31	0.51	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCA_001507955.1	40.7	0.21	0.30	0.49	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.93
GCA_003584625.1	39.8	0.21	0.29	0.50	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_023167465.1	42.0	0.22	0.30	0.47	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCF_003264935.1	40.0	0.21	0.28	0.50	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.2
GCF_000145295.1	48.6	0.25	0.44	0.31	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_000828575.1	49.3	0.25	0.46	0.29	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_022014235.1	48.7	0.23	0.46	0.30	0	0	0	0	0	0	0	0	0	0	2	2	2	1	98.4
GCF_000008645.1	49.5	0.23	0.48	0.29	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_014889545.1	49.7	0.26	0.46	0.29	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCA_900095815.1	48.9	0.24	0.46	0.31	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_000092305.1	33.6	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.05
GCA_024278985.1	27.5	0.13	0.21	0.66	0	0	0	0	0	0	0	0	0	0	1	1	1	1	89.27
GCF_000371805.1	29.5	0.11	0.27	0.62	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.81
GCF_000739065.1	30.8	0.09	0.13	0.78	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCF_000023985.1	32.2	0.11	0.13	0.75	0	0	0	0	0	0	0	0	0	0	2	4	2	1	99.52
GCF_000091665.1	31.3	0.10	0.14	0.76	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCF_000025525.1	32.0	0.11	0.15	0.74	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCA_013153845.1	31.3	0.11	0.14	0.75	0	0	0	0	0	0	0	0	0	0	1	1	1	1	85.24
GCA_024490875.1	28.5	0.09	0.11	0.81	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.05
GCA_902827205.1	29.1	0.09	0.12	0.79	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.52
GCF_000024625.1	31.6	0.10	0.14	0.76	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCF_002945325.1	32.9	0.07	0.09	0.84	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.52
GCF_013760955.1	33.2	0.08	0.09	0.83	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.5
GCF_000016125.1	33.0	0.09	0.09	0.82	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.52
GCF_000017165.1	31.3	0.12	0.09	0.80	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.5
GCF_024807035.1	29.0	0.07	0.03	0.90	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.05
GCF_017875395.1	29.0	0.07	0.04	0.89	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.05
GCF_024807655.1	28.5	0.05	0.04	0.91	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.05
GCF_004310395.1	35.3	0.19	0.14	0.67	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.52
GCA_015662355.1	41.2	0.21	0.13	0.65	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.14
GCA_015661555.1	43.4	0.22	0.15	0.63	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.19
GCA_015663075.1	30.5	0.16	0.09	0.76	0	0	0	0	0	0	0	0	0	0	1	1	1	1	86.47
GCA_015661585.1	35.7	0.18	0.12	0.70	0	0	0	0	0	0	0	0	0	0	0	2	2	1	80.66
GCF_003351865.1	35.1	0.18	0.12	0.71	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.52
GCA_019561555.1	29.1	0.15	0.11	0.74	0	0	0	0	0	0	0	0	0	0	1	0	1	1	91.29
GCA_019561565.1	30.2	0.16	0.10	0.74	0	0	0	0	0	0	0	0	0	0	0	1	1	1	58.23
GCA_019561615.1	42.9	0.20	0.16	0.63	0	0	0	0	0	0	0	0	0	0	1	1	1	1	90.79
GCF_000017185.1	30.0	0.10	0.08	0.82	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.03
GCF_000179575.2	29.3	0.07	0.10	0.83	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.05
GCA_015523155.1	30.5	0.10	0.10	0.80	0	0	0	0	0	0	0	0	0	0	2	2	2	1	90.32
GCF_000376965.1	32.8	0.12	0.12	0.76	0	0	0	0	0	0	0	0	0	0	2	2	2	1	100
GCF_000243455.1	32.4	0.11	0.14	0.74	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCF_000214415.1	32.3	0.11	0.15	0.75	0	0	0	0	0	0	0	0	0	0	2	2	2	1	99.52
GCF_000007185.1	61.2	0.20	0.58	0.22	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.74
GCF_002201895.1	58.0	0.20	0.55	0.25	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.94
GCA_013154335.1	62.4	0.19	0.65	0.16	0	0	0	0	0	0	0	0	0	0	1	1	1	1	93.94
GCA_002778455.1	45.2	0.24	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.04
GCA_018304295.1	50.3	0.32	0.30	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_902384585.1	50.3	0.30	0.27	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.08
GCA_021813025.1	58.5	0.32	0.45	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.17
GCA_021814005.1	55.4	0.31	0.34	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.98
GCA_023248665.1	59.9	0.26	0.45	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.73
GCA_902384555.1	61.7	0.33	0.40	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.08
GCA_903923795.1	54.4	0.27	0.42	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.13
GCA_020056635.1	52.0	0.38	0.34	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_020056305.1	51.5	0.32	0.36	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_023248455.1	52.5	0.31	0.45	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.58
GCA_013331805.1	52.9	0.32	0.45	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.11
GCA_903892905.1	54.7	0.32	0.38	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.23
GCA_902386555.1	40.0	0.23	0.31	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.76
GCA_013425375.1	54.2	0.25	0.58	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.03
GCA_014730115.1	51.1	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.36
GCA_016212505.1	41.1	0.21	0.33	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_016212525.1	41.6	0.25	0.30	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.76
GCA_016926175.1	43.2	0.22	0.46	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.75
GCA_018812625.1	39.2	0.24	0.33	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.95
GCA_018812715.1	37.8	0.18	0.36	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.22
GCA_018813505.1	38.7	0.23	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.69
GCA_020052325.1	56.2	0.23	0.57	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.79
GCA_020053355.1	56.4	0.21	0.58	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.22
GCA_022627495.1	57.6	0.23	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.95
GCA_023248035.1	39.5	0.25	0.30	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.82
GCA_903835325.1	53.3	0.22	0.61	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.29
GCA_014727925.1	47.9	0.33	0.39	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_014727975.1	49.1	0.35	0.37	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_016932815.1	52.7	0.30	0.44	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.15
GCA_903828955.1	50.3	0.24	0.42	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_903835385.1	56.7	0.26	0.53	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.76
GCA_013425455.1	54.1	0.35	0.43	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.87
GCA_020052735.1	55.5	0.33	0.46	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.94
GCA_903920925.1	55.5	0.34	0.46	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.28
GCA_013425425.1	51.4	0.28	0.44	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.55
GCA_016180665.1	36.4	0.27	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.01
GCA_016935455.1	39.5	0.20	0.31	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.49
GCA_023129075.1	38.5	0.23	0.37	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.95
GCA_018304385.1	36.5	0.25	0.25	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.15
GCA_023247345.1	37.6	0.23	0.24	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_018813445.1	38.7	0.25	0.36	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.58
GCA_020726005.1	33.1	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.87
GCA_021823425.1	57.0	0.33	0.48	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_013331535.1	42.4	0.24	0.33	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.63
GCA_001871475.1	47.0	0.25	0.36	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.21
GCA_003694965.1	43.7	0.25	0.39	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_015522475.1	43.8	0.23	0.29	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_013153395.1	45.0	0.22	0.37	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.68
GCA_015520875.1	35.6	0.26	0.31	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.13
GCA_025058915.1	38.2	0.31	0.40	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_015523325.1	33.7	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_021163645.1	34.4	0.13	0.32	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.53
GCA_020854835.1	37.0	0.18	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.14
GCA_021158105.1	36.0	0.14	0.30	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_021163225.1	44.6	0.18	0.45	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_020854825.1	28.0	0.14	0.18	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.93
GCA_001871535.1	49.2	0.21	0.41	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81
GCA_021823945.1	52.1	0.31	0.39	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.75
GCA_016866895.1	48.0	0.35	0.32	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.82
GCA_003660965.1	47.6	0.33	0.44	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.4
GCA_902386535.1	57.6	0.40	0.41	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.28
GCA_902385155.1	57.2	0.16	0.65	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_020723065.1	42.1	0.13	0.35	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_903832205.1	50.6	0.27	0.30	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.83
GCA_020723045.1	47.2	0.24	0.34	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_024274875.1	41.4	0.19	0.33	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_903884505.1	56.8	0.31	0.46	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_903921825.1	58.5	0.38	0.41	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.86
GCA_013426015.1	48.5	0.30	0.47	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_013425335.1	47.7	0.32	0.45	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_013425405.1	47.1	0.32	0.44	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_902384795.1	49.7	0.34	0.27	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_016207225.1	40.4	0.31	0.30	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.12
GCA_016212395.1	47.3	0.17	0.35	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_021813385.1	51.2	0.32	0.39	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_902385515.1	54.9	0.24	0.58	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.51
GCA_023256495.1	29.9	0.18	0.30	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_023270015.1	44.6	0.32	0.39	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_023270055.1	45.6	0.25	0.43	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_023256515.1	37.6	0.25	0.32	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.3
GCA_021796295.1	48.3	0.34	0.39	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_021789155.1	44.2	0.19	0.45	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_021792095.1	56.5	0.41	0.44	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.75
GCA_021818925.1	53.4	0.42	0.42	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.53
GCA_021818995.1	54.2	0.41	0.41	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.41
GCA_021823435.1	53.2	0.40	0.42	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.83
GCA_021828295.1	55.1	0.43	0.40	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.45
GCA_023476545.1	53.4	0.36	0.46	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.27
GCA_021791725.1	48.7	0.21	0.46	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_021791245.1	43.3	0.22	0.43	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.61
GCA_021805625.1	47.7	0.31	0.42	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.35
GCA_021801765.1	45.5	0.26	0.48	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.14
GCA_021810455.1	39.2	0.16	0.43	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_021804095.1	41.3	0.21	0.40	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4

GCA_021829835.1	40.8	0.22	0.41	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.53
GCA_021845465.1	41.0	0.22	0.40	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.93
GCA_021846005.1	44.9	0.21	0.51	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.15
GCA_021804305.1	49.5	0.27	0.47	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.38
GCA_021792235.1	48.3	0.25	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_021802765.1	47.0	0.21	0.43	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_021803425.1	42.6	0.23	0.43	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_021803945.1	48.5	0.30	0.44	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_021848065.1	49.1	0.24	0.48	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.83
GCA_021851065.1	49.3	0.28	0.48	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_021851985.1	42.2	0.20	0.43	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.85
GCA_023379055.1	46.2	0.29	0.41	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.74
GCA_021803245.1	46.2	0.26	0.37	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.97
GCA_021848025.1	45.6	0.29	0.36	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_021801225.1	30.9	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.72
GCA_021803405.1	34.3	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.34
GCA_021817305.1	53.1	0.25	0.53	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_021821605.1	33.8	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.26
GCA_021848095.1	31.0	0.13	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_021850625.1	33.3	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_021850955.1	30.7	0.15	0.25	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.37
GCA_021852055.1	44.0	0.25	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.93
GCA_023485825.1	54.0	0.26	0.55	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.99
GCA_021797745.1	44.5	0.18	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_021812185.1	42.9	0.22	0.41	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.54
GCA_021827925.1	49.4	0.24	0.54	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.67
GCA_021790305.1	43.7	0.19	0.45	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.32
GCA_021817505.1	46.1	0.20	0.48	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_021850705.1	43.5	0.21	0.44	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.99
GCA_023487825.1	44.4	0.21	0.44	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.39
GCA_021785375.1	53.0	0.26	0.49	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.65
GCA_021791075.1	51.6	0.28	0.49	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.27
GCA_021796225.1	45.3	0.14	0.47	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.95
GCA_021797995.1	52.2	0.30	0.44	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_021804105.1	48.1	0.23	0.49	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.02
GCA_021810375.1	48.9	0.24	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_021817325.1	51.2	0.29	0.48	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.06
GCA_021817125.1	52.7	0.28	0.45	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.22
GCA_021811535.1	47.2	0.25	0.44	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.39
GCA_021835105.1	46.5	0.28	0.39	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.21
GCA_021850805.1	47.1	0.26	0.41	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.62
GCA_021809925.1	42.0	0.20	0.44	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_023379075.1	42.3	0.18	0.44	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.07
GCA_014874295.1	54.0	0.15	0.63	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.79
GCA_021787495.1	57.1	0.18	0.65	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.66
GCA_021654395.1	34.1	0.27	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.88
GCA_903858385.1	52.2	0.21	0.49	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.48
GCA_903884115.1	50.1	0.26	0.48	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_021792295.1	55.7	0.29	0.51	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.92
GCA_021801385.1	46.0	0.23	0.48	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.13
GCA_021850375.1	42.2	0.26	0.32	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.79
GCA_021792775.1	45.2	0.26	0.40	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_021801785.1	46.2	0.28	0.44	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.46
GCA_021816885.1	45.5	0.25	0.43	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_021817565.1	45.0	0.26	0.39	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.87
GCA_021789815.1	47.5	0.26	0.45	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_021791535.1	51.7	0.27	0.50	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_021791775.1	47.5	0.25	0.48	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_021799635.1	46.7	0.31	0.46	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.79
GCA_021801905.1	41.3	0.21	0.41	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_021806185.1	52.9	0.29	0.52	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.39
GCA_021810105.1	42.5	0.22	0.44	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_021819045.1	43.5	0.28	0.38	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.39
GCA_021828345.1	33.2	0.20	0.25	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.97
GCA_021828705.1	33.5	0.18	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.22
GCA_021851535.1	33.6	0.21	0.24	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.48
GCA_023485645.1	33.1	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.22
GCA_021792115.1	35.0	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.6
GCA_021800515.1	35.3	0.15	0.25	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.47
GCA_021848125.1	28.4	0.10	0.20	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_023474155.1	42.0	0.19	0.33	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75
GCA_021845575.1	37.5	0.16	0.38	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.69
GCA_021785605.1	50.9	0.23	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_021790455.1	50.0	0.22	0.45	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.83
GCA_021799475.1	46.6	0.18	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.82
GCA_021806095.1	29.3	0.09	0.20	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.28
GCA_021807115.1	55.6	0.32	0.51	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_021811605.1	51.8	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.28
GCA_021812025.1	49.7	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.81
GCA_021827605.1	49.8	0.23	0.46	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_023485505.1	46.1	0.18	0.45	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.27
GCA_021797895.1	50.9	0.22	0.55	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.38
GCA_021846635.1	49.6	0.22	0.50	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_023485545.1	49.9	0.23	0.52	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.34
GCA_021822165.1	51.3	0.28	0.51	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_021801355.1	48.3	0.20	0.52	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_021811435.1	51.9	0.24	0.55	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.07
GCA_021818545.1	48.2	0.18	0.50	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.54
GCA_021827995.1	56.1	0.30	0.54	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_021800135.1	47.8	0.24	0.50	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.45
GCA_021812105.1	49.4	0.27	0.49	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_021816645.1	49.7	0.23	0.50	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.3
GCA_021827955.1	46.6	0.21	0.47	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.83
GCA_021816895.1	46.4	0.29	0.38	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_021793035.1	48.7	0.24	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_021797575.1	48.8	0.20	0.58	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.27
GCA_021827525.1	49.2	0.21	0.56	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.16
GCA_023474385.1	49.4	0.24	0.53	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.61
GCA_021836925.1	53.8	0.22	0.54	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.08
GCA_023473425.1	48.1	0.19	0.53	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.13
GCA_021810685.1	55.1	0.25	0.57	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.36
GCA_021812205.1	54.8	0.27	0.56	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.32
GCA_021828155.1	53.2	0.25	0.52	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_023473665.1	52.9	0.21	0.54	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_021792395.1	42.9	0.21	0.42	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.72
GCA_021834785.1	42.8	0.21	0.44	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.72
GCA_023473255.1	42.8	0.20	0.43	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCF_002214165.1	39.4	0.10	0.46	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_021798935.1	35.4	0.09	0.43	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.8
GCA_021821445.1	29.1	0.08	0.32	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.16
GCF_016806735.1	45.8	0.16	0.50	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_021797495.1	45.0	0.16	0.48	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_021827665.1	48.1	0.17	0.54	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_021834865.1	45.9	0.15	0.49	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.45
GCA_023380795.1	46.8	0.16	0.53	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.56
GCA_023473395.1	46.1	0.13	0.52	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.68
GCA_023485295.1	46.4	0.23	0.43	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_009387755.1	47.3	0.31	0.38	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_023485745.1	47.5	0.31	0.38	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.42
GCA_021829015.1	52.8	0.23	0.55	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.23
GCA_013330215.1	50.0	0.31	0.37	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.92
GCA_902385045.1	32.5	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_903851445.1	54.6	0.31	0.38	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.77
GCA_903893865.1	53.2	0.13	0.48	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.42
GCA_021812145.1	39.7	0.12	0.43	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.38
GCA_023474775.1	38.6	0.12	0.46	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.26
GCA_016188965.1	58.0	0.17	0.51	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_016207165.1	56.4	0.21	0.46	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_016212375.1	52.9	0.17	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_016214445.1	51.6	0.26	0.48	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.25
GCA_016212465.1	46.2	0.19	0.46	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_023246885.1	39.6	0.20	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.88
GCA_023247085.1	39.8	0.18	0.22	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.33
GCA_902384935.1	57.5	0.24	0.48	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_002763345.1	59.2	0.24	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.92
GCA_002792915.1	59.8	0.23	0.53	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.83
GCA_002499405.1	54.6	0.14	0.53	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_016212475.1	42.2	0.22	0.37	0.41	0	0	0	0	0	0	0	0	1	0	0	0	0	0	89.17
GCA_018819225.1	50.5	0.21	0.37	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.42
GCA_005239845.1	54.7	0.26	0.35	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.96
GCA_013360305.1	39.0	0.17	0.31	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_018304285.1	52.5	0.17	0.50	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.91
GCA_013331595.1	49.6	0.23	0.43	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.02

GCA_001871495.1	50.6	0.18	0.42	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_013425325.1	53.7	0.27	0.43	0.30	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	81.31
GCA_016194335.1	57.3	0.28	0.46	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_016217775.1	49.6	0.22	0.29	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.98
GCA_020057405.1	55.8	0.30	0.30	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.14
GCA_021782355.1	33.4	0.18	0.14	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.09
GCA_001871595.1	54.8	0.39	0.29	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.8
GCA_015522865.1	38.2	0.24	0.28	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.63
GCA_003660925.1	48.9	0.18	0.52	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_017608385.1	31.8	0.13	0.33	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_017608045.1	29.4	0.08	0.22	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_017609105.1	29.6	0.07	0.22	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_003563585.1	30.5	0.14	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.34
GCA_007133845.1	29.9	0.11	0.26	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.2
GCA_021163365.1	32.0	0.14	0.30	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_015522785.1	37.3	0.19	0.27	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.41
GCA_021162365.1	36.5	0.19	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_024277205.1	32.1	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_000008085.1	31.6	0.22	0.21	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.13
GCA_020697515.1	32.2	0.24	0.23	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.99
GCF_023169545.1	24.6	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.66
GCA_003568775.1	32.2	0.21	0.20	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.62
GCA_001552015.1	24.2	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.07
GCA_000387965.1	24.3	0.15	0.19	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.52
GCF_003086415.1	24.5	0.16	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.67
GCA_002763115.1	31.2	0.11	0.13	0.76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_016211995.1	32.5	0.16	0.17	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_018303805.1	38.1	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.2
GCA_002763075.1	34.4	0.16	0.28	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.11
GCA_020724955.1	37.4	0.21	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.28
GCA_002690445.1	44.8	0.22	0.30	0.48	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	52.96
GCA_002688165.1	30.6	0.16	0.18	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.97
GCA_002688335.1	33.0	0.16	0.29	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.81
GCA_002688875.1	34.5	0.20	0.24	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.98
GCA_002686355.1	33.9	0.12	0.28	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.42
GCA_017609205.1	32.3	0.14	0.22	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.06
GCA_002688015.1	34.4	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.5
GCA_002686195.1	40.7	0.20	0.31	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.32
GCA_002687255.1	46.4	0.24	0.32	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.77
GCA_000405225.1	37.3	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.01
GCA_016866915.1	31.2	0.11	0.20	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.58
GCA_017610405.1	29.3	0.11	0.18	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.56
GCA_018303885.1	34.6	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.55
GCA_018821425.1	37.1	0.15	0.23	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.99
GCA_018829425.1	37.4	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.81
GCA_018830685.1	35.2	0.20	0.24	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.27
GCA_018830905.1	36.3	0.22	0.22	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.47
GCA_019428815.1	30.5	0.14	0.14	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.39
GCA_002897655.1	31.8	0.14	0.23	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.02
GCA_016784085.1	28.5	0.11	0.17	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.64
GCA_018304045.1	29.2	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.15
GCA_020056045.1	28.3	0.12	0.18	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.8
GCA_902385625.1	30.7	0.14	0.14	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.56
GCA_018303895.1	32.5	0.10	0.22	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.09
GCA_902385635.1	34.9	0.14	0.17	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.37
GCA_902385655.1	33.7	0.13	0.21	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.78
GCA_903828655.1	35.8	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.36
GCA_016867035.1	32.5	0.19	0.08	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.74
GCA_903866625.1	31.8	0.17	0.12	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.02
GCA_903873955.1	43.4	0.21	0.24	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.17
GCA_002792635.1	35.1	0.19	0.26	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.98
GCA_001872315.1	39.2	0.19	0.26	0.55	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	68.38
GCA_002254395.1	35.4	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.4
GCA_020430505.1	31.6	0.14	0.18	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_002762735.1	30.0	0.13	0.14	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_009992175.1	29.6	0.12	0.15	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.79
GCA_009992215.1	29.0	0.11	0.16	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.59
GCA_018303925.1	33.6	0.09	0.23	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_018830845.1	34.4	0.12	0.22	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.05
GCA_021799535.1	38.9	0.13	0.30	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_024654565.1	32.7	0.11	0.19	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.86
GCA_903831045.1	31.8	0.13	0.16	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_013329055.1	28.6	0.10	0.17	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_003694055.1	46.3	0.26	0.32	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.77
GCA_018221305.1	32.3	0.14	0.15	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.34
GCA_018657525.1	32.1	0.12	0.21	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_024278335.1	32.3	0.13	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.33
GCA_018651925.1	31.0	0.13	0.16	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.33
GCA_018651605.1	32.4	0.17	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.82
GCA_018653485.1	29.5	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.42
GCA_016181885.1	34.7	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.58
GCA_016181905.1	37.5	0.16	0.24	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.8
GCA_016188895.1	33.3	0.15	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.35
GCA_016188825.1	34.1	0.14	0.30	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.31
GCA_016186425.1	30.5	0.12	0.17	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.41
GCA_018304985.1	30.6	0.14	0.17	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.85
GCA_020724205.1	31.6	0.18	0.17	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.48
GCA_016186375.1	31.3	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.33
GCA_016186365.1	32.8	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.03
GCA_016181895.1	35.9	0.11	0.32	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.08
GCA_016204145.1	38.3	0.11	0.30	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.03
GCA_016234025.1	38.1	0.16	0.34	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.62
GCA_022561055.1	33.5	0.19	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.85
GCA_017610445.1	28.5	0.12	0.20	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.78
GCA_017609885.1	32.5	0.14	0.25	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.7
GCA_017609745.1	28.6	0.12	0.23	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.01
GCA_017609695.1	27.9	0.11	0.25	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.01
GCA_017609795.1	27.3	0.11	0.31	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.97
GCA_017609915.1	28.1	0.12	0.25	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.14
GCA_017609535.1	34.0	0.15	0.25	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.24
GCA_017609475.1	36.5	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_017609405.1	29.8	0.11	0.23	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_017609285.1	30.7	0.15	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.55
GCA_017609175.1	30.6	0.11	0.17	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_017609085.1	30.7	0.11	0.18	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.39
GCA_017609045.1	33.2	0.16	0.24	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.9
GCA_017608985.1	31.4	0.10	0.25	0.65	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	65.65
GCA_017609755.1	27.3	0.13	0.17	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.39
GCA_023144035.1	27.4	0.12	0.23	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.79
GCA_017608945.1	28.5	0.11	0.24	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.28
GCA_017608705.1	40.4	0.26	0.26	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.79
GCA_017608405.1	31.0	0.15	0.20	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.05
GCA_017608305.1	30.0	0.13	0.21	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.79
GCA_023139205.1	29.3	0.13	0.23	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.65
GCA_023137045.1	30.2	0.10	0.20	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.59
GCA_023133375.1	31.3	0.12	0.24	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.05
GCA_023132255.1	32.3	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.12
GCA_020053375.1	35.2	0.11	0.19	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.97
GCA_018304205.1	32.1	0.16	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.96
GCA_018304165.1	37.3	0.17	0.31	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.71
GCA_016234065.1	33.8	0.10	0.26	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.17
GCA_018304175.1	32.9	0.13	0.26	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_018304145.1	29.6	0.14	0.21	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.74
GCA_018304025.1	37.5	0.15	0.21	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.98
GCA_018303945.1	36.1	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.9
GCA_002688415.1	36.7	0.23	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.24
GCA_003693875.1	38.7	0.25	0.28	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.21
GCA_018303845.1	37.0	0.23	0.26	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68
GCA_018693315.1	39.7	0.25	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.72
GCA_018694115.1	38.0	0.21	0.20	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.99
GCA_018697035.1	38.4	0.24	0.26	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.11
GCA_018697295.1	34.8	0.19	0.17	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.11
GCA_018830525.1	35.5	0.19	0.21	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.34
GCA_018901375.1	39.1	0.25	0.32	0.43	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	57.49
GCA_021107855.1	38.4	0.22	0.26	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.31
GCA_022563455.1	33.3	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.51
GCA_023133415.1	36.9	0.20	0.28	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.52
GCA_023136775.1	32.8	0.16	0.22	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.18
GCA_023140635.1	35.8	0.17	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.31
GCA_023142835.1	33.6	0.17	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.03
GCA_023397215.1	24.9	0.08	0.10	0.82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.71
GCA_024654505.1	35.5	0.17	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.38
GCA_018303855.1	31.9	0.15	0.25	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.21

GCA_018303825.1	34.9	0.12	0.21	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.37
GCA_018303785.1	32.2	0.13	0.22	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.27
GCA_018304055.1	29.5	0.13	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.37
GCA_018303755.1	32.5	0.14	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.03
GCA_018901675.1	33.0	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.68
GCA_018901625.1	35.7	0.20	0.24	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.38
GCA_018898425.1	28.7	0.09	0.26	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.15
GCA_018897135.1	29.5	0.10	0.24	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.24
GCA_018818285.1	29.2	0.12	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.22
GCA_018816335.1	30.8	0.17	0.23	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_018816625.1	34.9	0.17	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.6
GCA_018815925.1	29.0	0.13	0.24	0.63	0	0	0	0	0	0	0	0	0	1	0	0	0	0	71.26
GCA_018830245.1	30.8	0.11	0.20	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.74
GCA_018221285.1	34.6	0.17	0.28	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.19
GCA_018825865.1	34.5	0.17	0.29	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.18
GCA_019659125.1	41.3	0.22	0.21	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.17
GCA_019662115.1	38.2	0.24	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.41
GCA_022709585.1	33.0	0.08	0.12	0.80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.86
GCA_000806015.1	30.1	0.11	0.24	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.01
GCA_016176815.1	30.9	0.11	0.22	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.48
GCA_001786395.1	35.6	0.16	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.44
GCA_001872185.1	31.6	0.17	0.19	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.8
GCA_018304325.1	28.9	0.16	0.16	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.9
GCA_002069705.1	29.4	0.10	0.17	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_022703705.1	29.5	0.08	0.12	0.80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.65
GCA_002689985.1	26.4	0.12	0.14	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.97
GCA_002731115.1	28.5	0.11	0.19	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.11
GCA_002763155.1	30.3	0.12	0.21	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.9
GCA_002763085.1	32.3	0.13	0.26	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.41
GCA_002763035.1	34.7	0.16	0.25	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.01
GCA_004195435.1	30.2	0.13	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.49
GCA_003554465.1	38.0	0.18	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.43
GCA_001786415.1	33.4	0.10	0.19	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.65
GCA_012798335.1	26.2	0.09	0.14	0.77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.26
GCA_021818475.1	33.5	0.10	0.20	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.68
GCA_023228065.1	30.0	0.12	0.23	0.65	0	0	0	0	0	0	0	0	0	1	0	0	0	0	71.57
GCA_023228245.1	46.5	0.18	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.88
GCA_023475035.1	33.6	0.12	0.19	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.12
GCA_902388025.1	33.4	0.10	0.18	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_009694755.1	31.6	0.12	0.22	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.03
GCA_016866935.1	33.0	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.81
GCA_018303995.1	33.1	0.15	0.25	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.84
GCA_009694725.1	42.3	0.13	0.18	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.24
GCA_016196285.1	42.3	0.20	0.29	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.58
GCA_016866955.1	38.7	0.14	0.15	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.24
GCA_002496015.1	40.8	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.5
GCA_018304105.1	38.9	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.43
GCA_018816205.1	40.5	0.18	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.04
GCA_018817405.1	37.3	0.17	0.28	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.51
GCA_018817905.1	37.9	0.18	0.29	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.67
GCA_002497285.1	34.3	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.58
GCA_016866975.1	38.8	0.18	0.30	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.19
GCA_016866995.1	32.6	0.11	0.23	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.88
GCA_015520065.1	34.6	0.16	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.85
GCA_014728745.1	32.0	0.10	0.15	0.75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.06
GCA_014728565.1	30.9	0.17	0.23	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.28
GCA_018829845.1	36.0	0.17	0.29	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.78
GCA_002780285.1	35.3	0.11	0.20	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.46
GCA_022572525.1	37.0	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.26
GCA_018829485.1	29.9	0.14	0.13	0.73	0	0	0	0	0	0	0	0	0	1	0	0	0	0	63.24
GCA_013331945.1	42.5	0.26	0.28	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.18
GCA_023511755.1	40.5	0.17	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.82
GCA_002254805.1	33.1	0.15	0.22	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.24
GCA_020343435.1	31.6	0.14	0.22	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.48
GCA_025058615.1	33.2	0.13	0.31	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.85
GCA_002499185.1	30.3	0.11	0.17	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.26
GCA_018304245.1	30.1	0.12	0.10	0.77	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.12
GCA_015121965.1	41.7	0.23	0.45	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.13
GCA_023269965.1	40.0	0.20	0.47	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.5
GCA_023261805.1	41.1	0.14	0.58	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.71
GCA_021791655.1	45.7	0.19	0.43	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.17
GCA_021800365.1	39.1	0.19	0.24	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.23
GCA_021818905.1	41.2	0.20	0.31	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.06
GCA_021852265.1	40.0	0.19	0.27	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.7
GCA_021802105.1	42.6	0.18	0.40	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.88
GCA_021850635.1	40.8	0.18	0.45	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.45
GCA_021818665.1	47.5	0.23	0.43	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.49
GCA_021807125.1	40.1	0.20	0.33	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.79
GCA_021836125.1	41.4	0.20	0.32	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.94
GCA_021810345.1	43.8	0.15	0.43	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.45
GCA_023380435.1	43.3	0.19	0.38	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.03
GCA_023380585.1	42.7	0.18	0.46	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.21
GCA_002502045.1	33.6	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.8
GCA_002503215.1	34.4	0.16	0.29	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.25
GCA_021794235.1	44.4	0.24	0.36	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.08
GCA_021796445.1	35.5	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.08
GCA_021797085.1	36.5	0.13	0.31	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.77
GCA_021798355.1	36.0	0.14	0.28	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.46
GCA_021799085.1	36.6	0.13	0.30	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.71
GCA_021802505.1	40.8	0.18	0.38	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.94
GCA_021807085.1	48.1	0.26	0.49	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.72
GCA_021811735.1	37.6	0.20	0.32	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.62
GCA_021817165.1	39.3	0.16	0.35	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.63
GCA_021834945.1	37.6	0.14	0.33	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.41
GCA_021846665.1	32.7	0.13	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.71
GCA_021851145.1	34.3	0.14	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.64
GCA_021852135.1	36.0	0.14	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.73
GCA_023378805.1	35.3	0.15	0.26	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.8
GCA_023378865.1	36.4	0.15	0.29	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.85
GCA_023380615.1	37.5	0.12	0.30	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.56
GCA_023488405.1	35.4	0.12	0.32	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.1
GCA_018221045.1	41.1	0.11	0.33	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_018220985.1	33.0	0.11	0.30	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.77
GCA_002763265.1	42.9	0.17	0.28	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_002688325.1	27.7	0.13	0.24	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.64
GCA_002687825.1	30.5	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.42
GCA_002688395.1	29.3	0.13	0.20	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.84
GCA_018302505.1	31.1	0.15	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_018831025.1	29.7	0.17	0.17	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.99
GCA_002687185.1	37.3	0.20	0.26	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.16
GCA_002687815.1	28.4	0.14	0.22	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_002688095.1	32.0	0.19	0.19	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.76
GCA_016181275.1	32.5	0.14	0.26	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_016188065.1	34.9	0.17	0.29	0.54	0	0	0	0	0	0	0	0	0	1	0	0	0	0	75.39
GCA_018302705.1	35.5	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_016784245.1	28.6	0.13	0.18	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.76
GCA_018692925.1	29.2	0.13	0.15	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_009691355.1	36.3	0.22	0.17	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.53
GCA_016235495.1	37.3	0.22	0.19	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_023245755.1	36.6	0.22	0.15	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.19
GCA_013331795.1	34.3	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_003694495.1	36.2	0.12	0.28	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_018653605.1	32.3	0.21	0.19	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_018656555.1	32.3	0.19	0.20	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_016211095.1	38.9	0.13	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.28
GCA_017608525.1	31.7	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_018302165.1	29.3	0.15	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.1
GCA_018302205.1	31.2	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.4
GCA_023245975.1	38.0	0.17	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_018896675.1	32.9	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018830945.1	41.1	0.19	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.7
GCA_013329215.1	44.6	0.21	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_000806155.1	29.7	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.29
GCA_016179945.1	29.3	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_018302765.1	30.2	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.54
GCA_023245565.1	25.7	0.12	0.16	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_016219825.1	39.6	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.73
GCA_018303515.1	29.3	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.64
GCA_018302545.1	28.8	0.16	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.74
GCA_018302235.1	27.9	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.77
GCA_018302105.1	27.7	0.15	0.21	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_023245385.1	37.0	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.59
GCA_002688355.1	27.6	0.15	0.14	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5

GCA_000830315.1	31.7	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.47
GCA_016181245.1	32.1	0.19	0.22	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.89
GCA_016203115.1	33.2	0.17	0.23	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.76
GCA_018303005.1	31.7	0.18	0.20	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_018303025.1	29.0	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_018302885.1	31.9	0.12	0.26	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.42
GCA_018302915.1	33.7	0.13	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.02
GCA_018302465.1	31.9	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_018302725.1	34.6	0.19	0.21	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.45
GCA_018302685.1	37.7	0.14	0.28	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.95
GCA_018819375.1	36.1	0.16	0.31	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.63
GCA_021107205.1	27.3	0.11	0.21	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.12
GCA_016181215.1	35.4	0.17	0.26	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.72
GCA_016188045.1	30.4	0.19	0.19	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_016185635.1	30.9	0.15	0.23	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_018302125.1	29.0	0.14	0.16	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_016185615.1	30.3	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.63
GCA_016185605.1	30.6	0.15	0.21	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.31
GCA_016185555.1	33.0	0.19	0.22	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.42
GCA_016203135.1	31.0	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_017609845.1	30.4	0.13	0.24	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.95
GCA_017609525.1	31.9	0.17	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_018303705.1	37.7	0.18	0.32	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.78
GCA_018303485.1	33.9	0.14	0.30	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.68
GCA_018303365.1	38.9	0.21	0.27	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.59
GCA_016203175.1	29.1	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_023246445.1	31.2	0.18	0.19	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.77
GCA_017609465.1	29.6	0.10	0.24	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_018302265.1	33.1	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.17
GCA_018816585.1	27.7	0.10	0.22	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.61
GCA_018303545.1	33.9	0.15	0.25	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_016185565.1	31.9	0.17	0.23	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.22
GCA_018302785.1	28.3	0.16	0.17	0.67	0	0	0	0	0	0	0	0	0	1	0	0	0	0	72.12
GCA_018302805.1	30.1	0.17	0.17	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_016432305.1	31.4	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_018302745.1	32.3	0.14	0.22	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.5
GCA_018302225.1	28.8	0.14	0.15	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_018671245.1	31.3	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_018652625.1	31.2	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_018652475.1	29.8	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_018663865.1	31.0	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_018693795.1	29.8	0.14	0.18	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_021107835.1	30.9	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_018829185.1	30.6	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.06
GCA_013824915.1	30.0	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.18
GCA_018302135.1	29.3	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_000402515.1	32.1	0.15	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.11
GCA_016845225.1	31.4	0.18	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_018655015.1	34.0	0.22	0.21	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_018658265.1	32.5	0.22	0.19	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.05
GCA_018658955.1	31.7	0.16	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_016177265.1	41.0	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.41
GCA_018302985.1	36.0	0.15	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_002505585.1	33.0	0.15	0.20	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_018894775.1	35.4	0.16	0.32	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.13
GCA_016866645.1	42.3	0.16	0.33	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.01
GCA_002779595.1	37.5	0.08	0.33	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.25
GCA_016931175.1	37.3	0.09	0.32	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_902385255.1	36.5	0.12	0.23	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_002686215.1	35.3	0.10	0.36	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.8
GCA_002725495.1	30.3	0.09	0.18	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.08
GCA_014239585.1	32.1	0.15	0.20	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_014240455.1	35.1	0.17	0.18	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_018698915.1	33.1	0.18	0.18	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_020343615.1	32.7	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_018652045.1	39.1	0.26	0.18	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_018692915.1	32.2	0.16	0.14	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_017609995.1	34.5	0.20	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.95
GCA_017608345.1	38.7	0.25	0.19	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_017608235.1	30.8	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.13
GCA_017608025.1	33.5	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_903864915.1	42.5	0.19	0.27	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_016182015.1	44.8	0.24	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_016204275.1	43.9	0.22	0.18	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_023245115.1	43.0	0.25	0.18	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.25
GCA_018304345.1	36.1	0.18	0.16	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.72
GCA_018304365.1	35.3	0.16	0.19	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.47
GCA_013331935.1	41.1	0.19	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_014728835.1	34.4	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.16
GCA_017608505.1	35.3	0.14	0.28	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.07
GCA_014729335.1	41.8	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.89
GCA_002779235.1	44.3	0.16	0.36	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_002762915.1	31.7	0.12	0.20	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.19
GCA_020854775.1	32.8	0.12	0.24	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_903891505.1	35.8	0.21	0.25	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.03
GCA_021735165.1	31.3	0.12	0.26	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_021736975.1	28.8	0.10	0.22	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_003560545.1	43.3	0.13	0.31	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_003562145.1	42.9	0.16	0.24	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.77
GCA_007131205.1	41.0	0.16	0.26	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_007116295.1	32.3	0.12	0.32	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.34
GCA_007117145.1	34.0	0.13	0.30	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.14
GCA_007117755.1	31.7	0.10	0.26	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.22
GCA_002762795.1	36.8	0.14	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_019323575.1	40.5	0.16	0.32	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.07
GCA_902385765.1	42.4	0.17	0.34	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.64
GCA_016203225.1	57.2	0.21	0.55	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_016203265.1	55.0	0.21	0.45	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.21
GCA_002687275.1	49.7	0.31	0.30	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.66
GCA_003694525.1	43.8	0.16	0.48	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.26
GCA_016188265.1	31.3	0.13	0.28	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016198725.1	40.9	0.15	0.37	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.93
GCA_016203345.1	48.9	0.20	0.47	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.37
GCA_016203445.1	37.1	0.19	0.41	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.99
GCA_016203425.1	39.4	0.13	0.36	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.43
GCA_016203395.1	38.9	0.17	0.35	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.79
GCA_016213425.1	32.0	0.14	0.31	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.07
GCA_016215315.1	32.4	0.15	0.30	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.89
GCA_017609645.1	32.2	0.09	0.27	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.07
GCA_020051845.1	52.8	0.23	0.60	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.81
GCA_018303245.1	44.4	0.17	0.36	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.49
GCA_018302815.1	45.2	0.17	0.45	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.94
GCA_023261345.1	40.3	0.17	0.33	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.43
GCA_023266895.1	40.9	0.18	0.38	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.74
GCA_019323255.1	43.8	0.21	0.33	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.5
GCA_003599055.1	51.5	0.18	0.43	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.09
GCA_016203305.1	44.8	0.25	0.38	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_014729505.1	43.8	0.21	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_014729555.1	39.8	0.16	0.32	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_019322895.1	39.2	0.14	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_019323015.1	38.5	0.16	0.29	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_019323135.1	36.2	0.13	0.27	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.51
GCA_019323555.1	39.8	0.17	0.26	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.08
GCA_014729195.1	35.4	0.13	0.28	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.4
GCA_016929895.1	34.1	0.14	0.26	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_019322995.1	32.2	0.13	0.24	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.67
GCA_003650585.1	43.8	0.20	0.32	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.72
GCA_903915225.1	45.5	0.23	0.36	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_017610005.1	34.0	0.16	0.29	0.55	0	0	0	0	0	0	0	0	0	1	0	0	0	0	78.74
GCA_005222965.1	30.2	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.62
GCA_023131705.1	34.0	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.36
GCA_003648985.1	36.9	0.18	0.30	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.76
GCA_003650545.1	36.2	0.18	0.30	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.48
GCA_002867475.1	31.0	0.13	0.26	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_018221135.1	36.9	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_018221175.1	36.1	0.16	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.51
GCA_023266675.1	34.3	0.15	0.22	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_016784165.1	30.5	0.13	0.23	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.8
GCA_019322735.1	32.1	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.8
GCA_023137655.1	29.6	0.12	0.18	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_903842985.1	41.4	0.18	0.32	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_903904885.1	42.5	0.15	0.39	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_903907555.1	40.1	0.15	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11

GCA_002762705.1	42.5	0.17	0.55	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.19
GCA_002762865.1	33.3	0.15	0.21	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_017609385.1	33.3	0.13	0.25	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_017610275.1	32.5	0.14	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.98
GCA_017610505.1	33.2	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018819345.1	33.1	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_018901315.1	33.5	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_018399355.1	33.1	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_003561825.1	42.0	0.22	0.31	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.52
GCA_002763335.1	46.7	0.28	0.40	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.61
GCA_001871415.1	57.1	0.25	0.60	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018657385.1	28.9	0.14	0.18	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_018661705.1	30.5	0.16	0.18	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.16
GCA_016192995.1	34.1	0.18	0.22	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_016205905.1	33.6	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.02
GCA_018303325.1	33.1	0.18	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_016219665.1	31.8	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_018303075.1	31.8	0.18	0.23	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_016214075.1	39.2	0.21	0.25	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_016215305.1	39.0	0.20	0.29	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.16
GCA_023267795.1	35.2	0.18	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.3
GCA_016935125.1	42.7	0.19	0.46	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_023898365.1	40.4	0.14	0.32	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_002685855.1	42.3	0.26	0.26	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.43
GCA_002686295.1	30.2	0.12	0.27	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_013202845.1	34.9	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_014384375.1	35.6	0.16	0.25	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCA_016784125.1	33.7	0.18	0.23	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_018812505.1	32.8	0.16	0.26	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.54
GCA_018819065.1	34.6	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_018817005.1	31.2	0.13	0.28	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_002687795.1	38.3	0.17	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.04
GCA_000830295.1	42.5	0.24	0.25	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_018657065.1	27.7	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_013335235.1	44.4	0.30	0.38	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.19
GCA_018671515.1	27.0	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_016928835.1	36.8	0.22	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_016935095.1	33.6	0.15	0.26	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_016934775.1	40.1	0.21	0.36	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_018815145.1	37.7	0.25	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_023701075.1	40.7	0.22	0.42	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.2
GCA_014729915.1	32.5	0.15	0.31	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_016784195.1	33.8	0.15	0.24	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.67
GCA_016784105.1	34.3	0.20	0.24	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.47
GCA_002686855.1	33.1	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_002688775.1	35.7	0.17	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_016177615.1	39.8	0.18	0.30	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.95
GCA_016181305.1	41.1	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.26
GCA_016185755.1	41.7	0.20	0.30	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.63
GCA_016185805.1	39.5	0.16	0.31	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.48
GCA_016185815.1	38.6	0.17	0.26	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.33
GCA_016185845.1	39.6	0.17	0.29	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.31
GCA_016185865.1	39.2	0.18	0.29	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.89
GCA_016185875.1	38.1	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.05
GCA_016185915.1	34.0	0.16	0.25	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.35
GCA_016185945.1	36.8	0.14	0.27	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.49
GCA_016187465.1	38.4	0.17	0.31	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.17
GCA_016188245.1	40.1	0.16	0.32	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.75
GCA_016192955.1	38.4	0.18	0.30	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.5
GCA_016192985.1	37.2	0.16	0.30	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.89
GCA_016211245.1	39.2	0.17	0.29	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.38
GCA_018303505.1	34.9	0.16	0.26	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.1
GCA_018303645.1	38.8	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.86
GCA_018303655.1	38.0	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.75
GCA_018303685.1	40.6	0.17	0.28	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.81
GCA_023259315.1	36.4	0.16	0.28	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.43
GCA_023266475.1	35.5	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.94
GCA_002688925.1	34.5	0.15	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.03
GCA_013330825.1	56.7	0.26	0.46	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_016181325.1	44.5	0.17	0.37	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.15
GCA_016180235.1	39.7	0.18	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.36
GCA_016184145.1	38.4	0.20	0.23	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_016185955.1	35.6	0.18	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.27
GCA_016187495.1	36.4	0.19	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.11
GCA_019323655.1	38.3	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.89
GCA_022564635.1	31.8	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.31
GCA_022565235.1	35.7	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.45
GCA_018303625.1	38.4	0.18	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_018303185.1	43.9	0.24	0.34	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_002763025.1	32.1	0.13	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.49
GCA_013204355.1	32.5	0.14	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.73
GCA_018655525.1	32.8	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_902529885.1	36.6	0.13	0.28	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.7
GCA_945861715.1	38.8	0.26	0.18	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_002792115.1	33.2	0.13	0.17	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_002688265.1	34.2	0.17	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_018670085.1	34.2	0.17	0.22	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_018697095.1	34.6	0.22	0.18	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_013331635.1	42.0	0.18	0.32	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.49
GCA_018221085.1	35.1	0.12	0.22	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_018696395.1	29.1	0.11	0.20	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_018657845.1	34.3	0.13	0.22	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_018657475.1	32.2	0.14	0.22	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_018664115.1	31.4	0.14	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_018670095.1	31.4	0.14	0.20	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.7
GCA_018696595.1	32.3	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_016181345.1	36.4	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.59
GCA_016181265.1	41.6	0.27	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.11
GCA_016203205.1	44.5	0.22	0.36	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.48
GCA_016203215.1	45.3	0.21	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.77
GCA_018302605.1	44.2	0.22	0.36	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_016179995.1	34.6	0.22	0.26	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.91
GCA_016179955.1	44.3	0.16	0.32	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.68
GCA_016188115.1	38.6	0.26	0.16	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_023265685.1	39.3	0.29	0.18	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_016188105.1	39.1	0.19	0.26	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_016185725.1	35.1	0.19	0.21	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_023259115.1	39.3	0.19	0.28	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_016185685.1	37.3	0.17	0.32	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.28
GCA_016185625.1	44.3	0.17	0.35	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_016213985.1	39.7	0.20	0.24	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.34
GCA_016214025.1	39.3	0.17	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_020053615.1	37.2	0.18	0.26	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.22
GCA_018303445.1	38.6	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_018303265.1	40.0	0.16	0.28	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.98
GCA_018303045.1	39.3	0.19	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_023265925.1	47.0	0.17	0.35	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_023266155.1	42.9	0.17	0.33	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.56
GCA_018812765.1	35.6	0.17	0.24	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_018812355.1	33.5	0.16	0.26	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_018824365.1	32.2	0.15	0.27	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_002687775.1	36.3	0.19	0.28	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.44
GCA_002762785.1	44.8	0.20	0.39	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.51
GCA_002762845.1	35.9	0.16	0.23	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_018676855.1	34.3	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_013331555.1	39.4	0.19	0.27	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.62
GCA_002686315.1	39.2	0.18	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.09
GCA_003695265.1	40.3	0.11	0.29	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_003695045.1	48.2	0.18	0.44	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.62
GCA_003694805.1	51.8	0.19	0.39	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.8
GCA_013152815.1	53.3	0.22	0.62	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.17
GCA_016926055.1	41.6	0.22	0.36	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.69
GCA_018221105.1	35.2	0.12	0.22	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.67
GCA_018646625.1	36.0	0.20	0.20	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.92
GCA_018675975.1	23.4	0.09	0.15	0.76	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.54
GCA_018653365.1	34.0	0.15	0.21	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_019323235.1	27.2	0.11	0.19	0.70	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_013202955.1	32.6	0.13	0.26	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.41
GCA_018303405.1	45.0	0.24	0.36	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_020637495.1	37.8	0.21	0.40	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_020637435.1	45.0	0.23	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.77
GCA_016180285.1	37.8	0.15	0.33	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.35
GCA_016180135.1	46.3	0.22	0.38	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.33

GCA_016180165.1	45.5	0.23	0.38	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.41
GCA_016188175.1	47.1	0.24	0.36	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.08
GCA_018813685.1	35.9	0.17	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.49
GCA_019322475.1	42.8	0.23	0.42	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.71
GCA_019323195.1	41.2	0.22	0.33	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.55
GCA_016188215.1	44.2	0.29	0.27	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_016187565.1	40.5	0.20	0.27	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_016203335.1	52.2	0.20	0.38	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.78
GCA_016211215.1	45.2	0.25	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.95
GCA_023255615.1	38.4	0.16	0.32	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_016211195.1	48.7	0.21	0.43	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.1
GCA_023264635.1	41.7	0.19	0.34	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_016219795.1	44.7	0.23	0.29	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.89
GCA_016219835.1	45.2	0.20	0.42	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_017610325.1	39.9	0.17	0.30	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_017608625.1	31.2	0.12	0.26	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_017609245.1	38.0	0.16	0.30	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_016928155.1	45.4	0.19	0.54	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_016928115.1	33.1	0.12	0.21	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.7
GCA_016935985.1	61.8	0.19	0.69	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_016938695.1	30.4	0.16	0.21	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_021162185.1	35.6	0.22	0.24	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.54
GCA_021161785.1	36.8	0.13	0.23	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_023144115.1	34.6	0.16	0.29	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_019322755.1	37.7	0.10	0.26	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.26
GCA_023132895.1	35.5	0.12	0.29	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_020052545.1	44.8	0.22	0.39	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.69
GCA_018303725.1	35.7	0.18	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.88
GCA_018303425.1	31.9	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.7
GCA_018303315.1	48.7	0.23	0.39	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.11
GCA_018303285.1	39.1	0.15	0.23	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_018303225.1	49.8	0.19	0.35	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.49
GCA_018303105.1	46.6	0.19	0.31	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.5
GCA_018263355.1	32.4	0.18	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_017608295.1	47.1	0.23	0.43	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_018302335.1	62.5	0.31	0.58	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.51
GCA_019323665.1	41.7	0.23	0.37	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.99
GCA_016211165.1	49.3	0.19	0.43	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.68
GCA_016932755.1	41.9	0.18	0.29	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_018303205.1	36.3	0.14	0.27	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.53
GCA_018302085.1	39.0	0.19	0.31	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_018816705.1	50.2	0.24	0.49	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_018813725.1	39.3	0.20	0.35	0.45	0	0	0	0	0	0	0	0	0	1	0	0	0	0	82.48
GCA_016929855.1	43.8	0.23	0.41	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.47
GCA_018825425.1	38.9	0.26	0.30	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.5
GCA_020057445.1	49.0	0.21	0.48	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.53
GCA_019323525.1	39.4	0.23	0.29	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_019323515.1	36.8	0.17	0.31	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.28
GCA_019322485.1	38.7	0.18	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_019322805.1	37.7	0.18	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_019322545.1	35.8	0.11	0.32	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.83
GCA_021734865.1	36.9	0.15	0.36	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_003564925.1	32.0	0.16	0.23	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.72
GCA_007117735.1	35.4	0.16	0.22	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.77
GCA_016926395.1	32.2	0.21	0.18	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.66
GCA_020430425.1	41.8	0.30	0.31	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.53
GCA_021734105.1	35.2	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	1	0	0	0	0	77.57
GCA_007116645.1	44.8	0.23	0.26	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_007117065.1	39.8	0.17	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.01
GCA_007128245.1	47.2	0.25	0.30	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_001595785.1	36.7	0.15	0.29	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_011372335.1	39.3	0.15	0.30	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.28
GCA_016930415.1	49.7	0.24	0.44	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_016932315.1	40.5	0.16	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_016933095.1	48.7	0.22	0.41	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_016935175.1	44.8	0.22	0.38	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_018819305.1	34.2	0.13	0.30	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.8
GCA_019322375.1	36.9	0.15	0.31	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_016935155.1	36.8	0.15	0.29	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_013331965.1	37.0	0.15	0.32	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.01
GCA_016180275.1	35.8	0.20	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.18
GCA_018302185.1	37.1	0.20	0.27	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.02
GCA_013331615.1	36.2	0.19	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.92
GCA_024206195.1	39.0	0.20	0.28	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_016180195.1	44.6	0.21	0.42	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.55
GCA_016180145.1	44.7	0.20	0.42	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.06
GCA_016188205.1	47.4	0.26	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.73
GCA_016192945.1	45.8	0.20	0.42	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.27
GCA_016192905.1	49.1	0.26	0.41	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.68
GCA_016211185.1	48.0	0.25	0.43	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.66
GCA_016935265.1	47.0	0.25	0.35	0.40	0	0	0	0	0	0	0	0	0	1	0	0	0	0	78.07
GCA_016180065.1	48.6	0.21	0.41	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75
GCA_016180085.1	48.7	0.23	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.22
GCA_016180105.1	49.4	0.26	0.38	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.87
GCA_016184345.1	48.2	0.21	0.36	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.07
GCA_016188145.1	47.8	0.23	0.36	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.61
GCA_016188155.1	47.9	0.25	0.34	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.34
GCA_016192915.1	47.7	0.22	0.36	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.44
GCA_023269295.1	47.5	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.32
GCA_013331515.1	50.4	0.20	0.48	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.28
GCA_002688315.1	36.8	0.17	0.28	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.21
GCA_016185705.1	46.5	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.75
GCA_018303115.1	44.6	0.21	0.37	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.87
GCA_003695435.1	41.2	0.17	0.36	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_018668595.1	29.9	0.11	0.22	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.51
GCA_018675335.1	30.3	0.08	0.16	0.75	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_013203345.1	39.9	0.17	0.43	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_016929255.1	51.1	0.20	0.56	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_018830225.1	50.0	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_019322385.1	45.6	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.77
GCA_020052935.1	49.2	0.22	0.43	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.74
GCA_016208715.1	46.9	0.19	0.38	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_016219765.1	46.5	0.20	0.39	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.69
GCA_013331125.1	48.0	0.18	0.54	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.11
GCA_013329175.1	48.4	0.28	0.42	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.07
GCA_011045925.1	41.9	0.18	0.35	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.17
GCA_002505945.1	37.6	0.19	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.25
GCA_002762985.1	44.4	0.19	0.50	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_016177315.1	45.0	0.22	0.32	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.26
GCA_016177345.1	44.1	0.17	0.33	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.82
GCA_016180035.1	49.3	0.17	0.45	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.29
GCA_016203375.1	44.7	0.17	0.27	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.28
GCA_013331695.1	43.0	0.21	0.28	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.21
GCA_014729495.1	42.8	0.15	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_018812465.1	40.8	0.16	0.48	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_002503705.1	59.6	0.22	0.56	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.45
GCA_003694385.1	57.0	0.24	0.44	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.84
GCA_014874255.1	61.7	0.26	0.56	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.71
GCA_018221165.1	49.8	0.27	0.35	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.14
GCA_002498125.1	56.2	0.29	0.48	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_018221245.1	45.5	0.26	0.39	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.5
GCA_023252315.1	67.0	0.41	0.51	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.67
GCA_013331575.1	54.8	0.25	0.53	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.6
GCA_023898345.1	36.6	0.21	0.23	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04
GCA_002506365.1	25.6	0.08	0.08	0.84	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.95
GCA_007117405.1	29.1	0.11	0.16	0.74	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.2
GCA_013215525.1	25.9	0.09	0.10	0.80	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_022565615.1	26.2	0.14	0.08	0.78	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.53
GCA_003599145.1	37.9	0.14	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.41
GCA_020057295.1	31.0	0.15	0.12	0.73	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.71
GCA_021813435.1	43.4	0.17	0.28	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_013330595.1	33.5	0.15	0.29	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_013329045.1	44.8	0.18	0.43	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.28
GCA_015522765.1	46.8	0.24	0.30	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.19
GCA_015520785.1	55.3	0.18	0.34	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.21
GCA_015519985.1	24.3	0.06	0.12	0.82	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_015520525.1	37.0	0.10	0.27	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018221205.1	42.3	0.19	0.37	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.98
GCA_018303575.1	53.4	0.22	0.44	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.15
GCA_018303125.1	41.4	0.23	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_014729995.1	40.7	0.21	0.35	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.55
GCA_023140175.1	34.7	0.18	0.30	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.68
GCA_014729345.1	46.9	0.22	0.52	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.04

GCA_018221125.1	34.8	0.16	0.24	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.38
GCA_019322435.1	35.5	0.17	0.22	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_020056025.1	38.0	0.15	0.33	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.36
GCA_019322455.1	30.5	0.13	0.20	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_019322815.1	32.4	0.14	0.24	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_019322535.1	31.5	0.12	0.23	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.78
GCA_014729675.1	36.2	0.17	0.35	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_014729145.1	34.3	0.15	0.26	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_014729015.1	54.8	0.18	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.23
GCA_016927245.1	57.1	0.17	0.57	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.84
GCA_019323355.1	40.9	0.22	0.25	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_023133595.1	38.1	0.19	0.27	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.97
GCA_019323415.1	40.8	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.49
GCA_014728875.1	42.5	0.21	0.30	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.51
GCA_019322855.1	39.9	0.21	0.26	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.07
GCA_019323495.1	40.7	0.22	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_017610385.1	32.4	0.18	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_018609855.1	44.9	0.21	0.33	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.68
GCA_022729315.1	56.1	0.21	0.41	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.94
GCA_022729255.1	38.8	0.20	0.43	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.37
GCA_022729275.1	38.1	0.20	0.42	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_022729285.1	38.1	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.53
GCA_022729335.1	41.2	0.23	0.37	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_022865265.1	50.5	0.18	0.53	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_022865215.1	52.4	0.31	0.48	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_022865275.1	43.9	0.45	0.26	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.77
GCA_001563875.1	42.6	0.31	0.24	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.17
GCA_001563905.1	41.0	0.24	0.19	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.61
GCA_001563915.1	39.4	0.23	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_001564035.1	43.2	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.25
GCA_001564145.1	40.1	0.17	0.26	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.21
GCA_022729235.1	48.5	0.33	0.33	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.14
GCA_013343275.1	46.9	0.33	0.24	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.6
GCF_009617975.1	43.2	0.23	0.28	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_001761425.1	46.4	0.29	0.29	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.77
GCA_000220375.1	43.6	0.29	0.33	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.39
GCA_022729355.1	44.8	0.23	0.32	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.27
GCA_000220355.1	56.2	0.36	0.47	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.58
GCA_001563995.1	42.2	0.26	0.29	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.99
GCA_014297435.1	44.3	0.29	0.25	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.14
GCA_003009795.1	42.6	0.26	0.33	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.97
GCA_003009815.1	43.5	0.28	0.31	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.56
GCA_020723935.1	63.1	0.41	0.45	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.62
GCA_018220955.1	42.1	0.27	0.34	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_018221005.1	42.3	0.21	0.36	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_018220935.1	35.7	0.20	0.24	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.1
GCA_018221025.1	39.8	0.22	0.31	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.43
GCA_011049195.1	52.5	0.16	0.53	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.36
GCA_015522095.1	58.1	0.21	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.48
GCA_003663565.1	40.7	0.18	0.42	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.11
GCA_003663585.1	41.7	0.26	0.36	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.46
GCA_003651105.1	47.2	0.28	0.50	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.07
GCA_021163455.1	42.2	0.21	0.46	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.47
GCA_021161865.1	41.4	0.22	0.33	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.67
GCA_021161685.1	41.2	0.24	0.42	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.55
GCA_003649745.1	36.1	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.18
GCA_021162485.1	35.2	0.22	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.2
GCA_003651045.1	34.8	0.14	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.36
GCA_003649845.1	34.5	0.25	0.26	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_003649715.1	37.7	0.19	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90
GCA_903877165.1	53.9	0.23	0.29	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.2
GCA_903930505.1	40.0	0.15	0.29	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.93
GCA_002254885.1	32.1	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.13
GCA_018334795.1	34.7	0.10	0.23	0.67	0	0	0	0	0	0	0	0	1	0	0	0	0	0	91.2
GCA_016932245.1	40.6	0.23	0.24	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.25
GCA_016936135.1	34.1	0.20	0.23	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.4
GCA_020343515.1	36.0	0.22	0.26	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.87
GCA_020350825.1	34.3	0.19	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.4
GCA_023140035.1	35.3	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.47
GCA_018824925.1	39.1	0.18	0.21	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.79
GCA_020054475.1	28.2	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.8
GCA_022848765.1	28.0	0.14	0.19	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_002900535.1	31.4	0.15	0.18	0.66	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.55
GCA_020341795.1	30.6	0.15	0.17	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.07
GCA_022866015.1	30.9	0.15	0.18	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.66
GCA_001595915.1	30.4	0.18	0.18	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.2
GCA_020054495.1	33.5	0.19	0.20	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.6
GCA_020350365.1	31.7	0.17	0.20	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.18
GCA_023128855.1	33.6	0.20	0.20	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.87
GCA_001595945.1	39.0	0.18	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.74
GCA_002496355.1	44.3	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.11
GCA_002506745.1	43.0	0.17	0.25	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.67
GCA_002900555.1	42.3	0.22	0.26	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.34
GCA_003942085.1	43.2	0.19	0.26	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_014894395.1	41.3	0.18	0.27	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94
GCA_016927555.1	49.3	0.21	0.26	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.86
GCA_016930995.1	42.3	0.19	0.25	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.2
GCA_017885605.1	41.9	0.17	0.26	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.47
GCA_902384685.1	38.5	0.18	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.67
GCA_002838935.1	53.7	0.21	0.45	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.8
GCA_016180755.1	67.5	0.46	0.42	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.08
GCA_020201445.1	70.5	0.33	0.59	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.22
GCA_023269235.1	68.5	0.33	0.52	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.87
GCA_019347820.1	65.8	0.32	0.62	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.52
GCA_011049295.1	61.1	0.34	0.39	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.47
GCA_008297795.1	43.8	0.18	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.47
GCA_021159125.1	43.6	0.19	0.42	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.4
GCA_003650975.1	50.0	0.19	0.50	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.39
GCA_011052825.1	33.8	0.13	0.41	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.4
GCA_014361195.1	34.8	0.17	0.36	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCA_014361245.1	34.8	0.14	0.37	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCA_021157745.1	38.5	0.16	0.42	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.74
GCA_021158865.1	34.2	0.13	0.38	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.6
GCA_021162305.1	36.4	0.15	0.41	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.8
GCA_021162815.1	39.5	0.13	0.44	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCA_021163175.1	38.2	0.16	0.43	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.87
GCA_021162065.1	45.4	0.18	0.49	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.07
GCA_002011355.1	37.9	0.15	0.39	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.48
GCA_021161135.1	39.2	0.18	0.37	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.4
GCA_024275755.1	37.0	0.17	0.37	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.8
GCA_008297865.1	35.8	0.17	0.35	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.94
GCA_002502685.1	39.1	0.21	0.24	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.99
GCA_013329495.1	42.9	0.26	0.38	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	1	82.93
GCA_002254765.1	54.2	0.23	0.56	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.88
GCA_021160765.1	49.1	0.22	0.48	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.47
GCA_002254385.1	53.8	0.18	0.73	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.48
GCA_016928095.1	52.3	0.18	0.71	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.8
GCA_016929175.1	53.2	0.19	0.69	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.81
GCA_023145185.1	52.4	0.25	0.57	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.67
GCA_020356005.1	43.0	0.22	0.32	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78
GCA_020696345.1	39.6	0.16	0.31	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_022615805.1	64.8	0.20	0.75	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.73
GCA_001875345.1	36.6	0.20	0.23	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_001875365.1	36.4	0.23	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	51.6
GCA_002497685.1	36.1	0.19	0.27	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.98
GCA_002506485.1	43.0	0.24	0.35	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_002718915.1	34.9	0.19	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66
GCA_002724775.1	36.9	0.20	0.25	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.36
GCA_014240055.1	36.1	0.21	0.26	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.38
GCA_014240255.1	35.4	0.19	0.25	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.6
GCA_015658585.1	43.6	0.23	0.39	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.37
GCA_016845825.1	37.2	0.20	0.25	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_022449785.1	37.0	0.18	0.29	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.6
GCA_902531985.1	36.6	0.20	0.26	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.4
GCA_902533295.1	36.3	0.21	0.27	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.07
GCA_902627615.1	36.7	0.19	0.24	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.22
GCA_001875425.1	37.5	0.20	0.28	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.71
GCA_002509225.1	37.2	0.19	0.28	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.76
GCA_002509165.1	64.9	0.28	0.52	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.25
GCA_002687355.1	56.4	0.28	0.49	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.8
GCA_002731655.1	63.7	0.26	0.55	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.6
GCA_002731905.1	57.9	0.28	0.50	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.13
GCA_003193815.1	65.4	0.25	0.55	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.04

GCA_022449705.1	64.0	0.31	0.52	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.13
GCA_002498205.1	34.3	0.13	0.32	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.88
GCA_002692465.1	34.7	0.14	0.31	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.4
GCA_002696315.1	34.5	0.14	0.30	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.33
GCA_002699515.1	33.7	0.14	0.30	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.33
GCA_002720095.2	35.3	0.20	0.30	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.2
GCA_002720275.1	34.7	0.15	0.30	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_002498185.1	44.9	0.11	0.68	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.09
GCA_002506705.1	45.3	0.09	0.71	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.21
GCA_002507425.1	41.9	0.17	0.52	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.22
GCA_002689345.1	42.8	0.09	0.68	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.2
GCA_002689565.1	42.3	0.11	0.53	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.74
GCA_002694245.1	42.8	0.13	0.59	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.13
GCA_002701145.1	43.6	0.09	0.70	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.13
GCA_002706615.1	41.4	0.10	0.61	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.13
GCA_002707335.2	40.5	0.13	0.56	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.78
GCA_002709705.1	44.0	0.10	0.67	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.33
GCA_002710015.1	41.8	0.18	0.54	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.94
GCA_002710205.1	43.9	0.12	0.62	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.05
GCA_002715725.1	42.6	0.12	0.56	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.96
GCA_002720115.1	43.0	0.13	0.55	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.93
GCA_002727515.1	41.4	0.12	0.59	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.6
GCA_002727695.1	44.6	0.12	0.67	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72
GCA_003602415.1	42.9	0.09	0.69	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.76
GCA_003602535.1	42.0	0.09	0.65	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.35
GCA_004195515.1	45.2	0.09	0.67	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.33
GCA_009936765.1	43.7	0.09	0.69	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.04
GCA_011522915.1	44.1	0.10	0.68	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.83
GCA_011525095.1	44.9	0.10	0.67	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.03
GCA_018650165.1	43.9	0.09	0.66	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.13
GCA_022452125.1	44.7	0.12	0.65	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.14
GCA_902563095.1	43.4	0.11	0.67	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.41
GCA_902605365.1	43.4	0.10	0.66	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.98
GCA_002699425.1	41.5	0.14	0.51	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.93
GCA_002719395.1	42.7	0.14	0.54	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.2
GCA_905181715.1	45.0	0.10	0.70	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.99
GCA_000246735.1	51.6	0.06	0.77	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.2
GCA_002170315.2	46.4	0.07	0.65	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.53
GCA_002172355.2	40.1	0.13	0.56	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.67
GCA_002495535.1	51.5	0.06	0.79	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.02
GCA_002495945.1	43.1	0.16	0.51	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.33
GCA_002496955.1	44.3	0.20	0.46	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.73
GCA_002499015.1	41.6	0.08	0.63	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_002499545.1	49.5	0.10	0.68	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.97
GCA_002499705.1	46.4	0.08	0.65	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.8
GCA_002502605.1	51.5	0.06	0.78	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.07
GCA_002505355.1	44.8	0.19	0.50	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.29
GCA_002506025.1	44.2	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.25
GCA_002506275.1	48.8	0.08	0.68	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.47
GCA_002687075.1	46.3	0.14	0.56	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.8
GCA_002697705.1	39.8	0.15	0.55	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.01
GCA_002702945.1	38.6	0.16	0.45	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.4
GCA_002726395.1	41.9	0.13	0.49	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.27
GCA_002727485.1	38.9	0.13	0.48	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.27
GCA_002729095.1	39.9	0.17	0.46	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.93
GCA_003602575.1	39.8	0.14	0.54	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.87
GCA_003602605.1	48.3	0.10	0.68	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.74
GCA_003602645.1	50.9	0.05	0.78	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.73
GCA_009887095.1	52.1	0.06	0.79	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.8
GCA_009887195.1	42.1	0.14	0.51	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.87
GCA_009937025.1	46.0	0.08	0.67	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84
GCA_009937205.1	41.5	0.08	0.64	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.2
GCA_011526375.1	43.2	0.16	0.49	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.06
GCA_012959845.1	41.8	0.09	0.64	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.4
GCA_018650105.1	41.2	0.08	0.64	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.39
GCA_018659375.1	41.8	0.14	0.51	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.73
GCA_018662825.1	44.8	0.08	0.65	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.6
GCA_018667575.1	41.0	0.15	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.6
GCA_018691345.1	48.6	0.10	0.67	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.64
GCA_018701175.1	48.6	0.09	0.69	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.49
GCA_022424925.1	49.7	0.11	0.67	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.8
GCA_022425585.1	42.1	0.13	0.53	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.54
GCA_022451835.1	39.7	0.14	0.50	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.79
GCA_024958795.1	40.5	0.08	0.64	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.4
GCA_013330285.1	50.5	0.08	0.74	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.49
GCA_013329865.1	45.0	0.20	0.50	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.49
GCA_013329925.1	41.6	0.13	0.51	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.55
GCA_902520595.1	46.0	0.09	0.62	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.76
GCA_905181785.1	52.2	0.06	0.79	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.67
GCA_905182125.1	51.2	0.05	0.79	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.8
GCA_905182185.1	42.4	0.10	0.64	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.27
GCA_905182635.1	46.5	0.07	0.68	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.8
GCA_905182715.1	46.3	0.07	0.70	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.81
GCA_905182725.1	46.4	0.07	0.70	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.22
GCA_013329355.1	44.8	0.18	0.50	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.55
GCA_013329255.1	52.1	0.06	0.78	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.47
GCA_013329295.1	39.5	0.13	0.52	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_002171315.2	44.5	0.12	0.63	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.88
GCA_002496635.1	44.6	0.12	0.64	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.23
GCA_002499195.1	45.7	0.14	0.67	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.93
GCA_002502215.1	48.4	0.13	0.66	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80
GCA_002698145.1	48.1	0.13	0.65	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.53
GCA_002706065.1	48.1	0.11	0.67	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.6
GCA_002719815.1	47.3	0.12	0.67	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.81
GCA_002722615.1	46.9	0.11	0.65	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.13
GCA_002726845.1	48.0	0.12	0.63	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.83
GCA_003602665.1	44.9	0.12	0.66	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.61
GCA_009887135.1	44.9	0.12	0.64	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.37
GCA_012270265.1	49.3	0.13	0.66	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.99
GCA_013911465.1	47.4	0.11	0.68	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.67
GCA_016777125.1	45.0	0.12	0.66	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.67
GCA_018623995.1	49.1	0.13	0.69	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.57
GCA_018645535.1	44.8	0.12	0.64	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.34
GCA_018666575.1	45.1	0.12	0.66	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.27
GCA_022425185.1	44.8	0.12	0.64	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.88
GCA_022451765.1	48.6	0.14	0.65	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.87
GCA_013330015.1	48.6	0.14	0.68	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.69
GCA_002496845.1	61.1	0.05	0.90	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_002694585.1	62.6	0.05	0.90	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.73
GCA_002722135.1	62.5	0.04	0.91	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.76
GCA_002723635.1	60.2	0.06	0.87	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.33
GCA_002731395.1	60.2	0.06	0.88	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.6
GCA_003602635.1	61.9	0.04	0.90	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.49
GCA_023254445.1	63.6	0.08	0.87	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.28
GCA_013330925.1	61.6	0.06	0.88	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.87
GCA_013330765.1	61.0	0.07	0.87	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.79
GCA_002718195.1	42.0	0.12	0.59	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.8
GCA_002505405.1	50.1	0.07	0.76	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.47
GCA_002494645.1	51.4	0.08	0.75	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.13
GCA_002495645.1	55.8	0.08	0.81	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.02
GCA_002497765.1	58.0	0.07	0.85	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.36
GCA_002502295.1	53.9	0.09	0.78	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.27
GCA_002689105.1	55.0	0.09	0.79	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.06
GCA_002694525.1	58.6	0.08	0.86	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.73
GCA_002704515.1	54.1	0.08	0.81	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.82
GCA_002714305.1	54.9	0.08	0.79	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.06
GCA_002722695.1	57.0	0.09	0.81	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.2
GCA_002725275.1	59.2	0.06	0.85	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.74
GCA_002726495.1	48.1	0.09	0.70	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.4
GCA_002728035.1	54.9	0.08	0.80	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.53
GCA_003602475.1	54.7	0.06	0.84	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.48
GCA_003602485.1	50.7	0.08	0.74	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.48
GCA_011524855.1	59.6	0.07	0.86	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.13
GCA_016778305.1	51.0	0.08	0.75	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.8
GCA_016779705.1	58.2	0.09	0.82	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.93
GCA_018662715.1	48.1	0.08	0.70	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.87
GCA_022426155.1	49.0	0.06	0.80	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.73
GCA_023254355.1	57.9	0.10	0.81	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.4
GCA_023254365.1	56.3	0.08	0.82	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.14
GCA_013330155.1	54.0	0.09	0.78	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.29
GCA_902625885.1	55.2	0.13	0.73	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.82
GCA_004195635.1	43.4	0.15	0.45	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.53
GCA_018649825.1	43.2	0.15	0.44	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.13

GCA_002505935.1	46.9	0.12	0.72	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.07
GCA_002719475.1	46.1	0.11	0.73	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.67
GCA_012959275.1	44.7	0.10	0.65	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.33
GCA_014240385.1	44.7	0.10	0.64	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.56
GCA_002503395.1	53.1	0.21	0.57	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.84
GCA_002715545.1	48.4	0.15	0.61	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.67
GCA_022447885.1	62.6	0.14	0.83	0.03	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.89
GCA_002170775.2	49.4	0.16	0.65	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.4
GCA_002495675.1	50.1	0.21	0.63	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.2
GCA_002497295.1	49.2	0.17	0.66	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.4
GCA_002499585.1	48.6	0.18	0.63	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72
GCA_002504845.1	49.5	0.16	0.65	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.2
GCA_002505455.1	49.8	0.17	0.67	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.4
GCA_002505695.1	49.7	0.21	0.62	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66
GCA_002507175.1	49.8	0.21	0.62	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.4
GCA_002712645.1	49.6	0.17	0.64	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.02
GCA_002717835.1	48.0	0.16	0.65	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.09
GCA_011523055.1	52.6	0.22	0.64	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84
GCA_002497905.1	48.5	0.07	0.73	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.27
GCA_002502625.1	39.6	0.14	0.48	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.51
GCA_002503045.1	40.4	0.14	0.49	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.94
GCA_002506875.1	48.7	0.08	0.72	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.67
GCA_002697105.1	40.0	0.14	0.48	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.13
GCA_002702985.1	39.8	0.15	0.48	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.64
GCA_002708015.1	39.8	0.15	0.47	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.27
GCA_002708695.1	39.5	0.16	0.44	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.67
GCA_002712285.1	46.4	0.08	0.68	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.69
GCA_002713585.1	48.8	0.08	0.72	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.73
GCA_002718215.1	41.5	0.15	0.50	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.02
GCA_002457555.1	45.8	0.13	0.63	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.73
GCA_002457595.1	43.6	0.10	0.62	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.4
GCA_002496905.1	45.5	0.13	0.64	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.28
GCA_002497025.1	45.1	0.12	0.64	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.51
GCA_002497895.1	52.3	0.08	0.80	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70
GCA_002498525.1	55.9	0.07	0.86	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.62
GCA_002498725.1	40.5	0.15	0.53	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.93
GCA_002502175.1	45.5	0.13	0.62	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.6
GCA_002502365.1	43.5	0.12	0.61	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.13
GCA_002685415.1	42.7	0.14	0.52	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.73
GCA_002708385.1	43.5	0.14	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.78
GCA_016845365.1	54.1	0.07	0.82	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86
GCA_022449345.1	48.1	0.12	0.69	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.8
GCA_022451235.1	45.3	0.13	0.63	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.6
GCA_023268715.1	45.4	0.13	0.60	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.4
GCA_013330385.1	44.5	0.12	0.64	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.99
GCA_013329905.1	52.8	0.09	0.77	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76
GCA_902560445.1	45.1	0.12	0.61	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.2
GCA_002494975.1	38.3	0.13	0.40	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.11
GCA_002495525.1	37.7	0.18	0.39	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.9
GCA_002497245.1	38.0	0.17	0.39	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.73
GCA_002498985.1	38.1	0.18	0.41	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.6
GCA_018654845.1	43.6	0.08	0.62	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.09
GCA_002504905.1	37.5	0.17	0.39	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.07
GCA_002685315.1	38.2	0.18	0.37	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.14
GCA_002686525.1	37.9	0.19	0.40	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.14
GCA_012960975.1	44.0	0.09	0.61	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.96
GCA_016777225.1	37.6	0.15	0.41	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.07
GCA_023700255.1	38.0	0.15	0.40	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.31
GCA_902511005.1	38.6	0.15	0.42	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.15
GCA_902514485.1	38.6	0.17	0.41	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.1
GCA_902593945.1	38.2	0.18	0.37	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.67
GCA_001628485.1	51.0	0.36	0.49	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.96
GCA_001629205.1	36.9	0.24	0.35	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.79
GCA_001629235.1	50.3	0.37	0.48	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.13
GCA_001629255.1	49.7	0.36	0.47	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.33
GCA_002172185.1	45.6	0.30	0.46	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.73
GCA_002172375.1	36.8	0.14	0.37	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.33
GCA_002457145.1	35.8	0.17	0.29	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.93
GCA_002457155.1	52.4	0.34	0.53	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.39
GCA_002496485.1	37.2	0.22	0.35	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.72
GCA_002503285.1	35.7	0.15	0.30	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.53
GCA_002506755.1	47.1	0.32	0.45	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.96
GCA_002683155.1	49.6	0.34	0.48	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.24
GCA_002697065.1	49.3	0.36	0.48	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.73
GCA_002712575.1	37.4	0.16	0.34	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.27
GCA_002713185.1	46.6	0.33	0.45	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.15
GCA_002716085.1	49.4	0.34	0.48	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.07
GCA_002718695.1	49.7	0.33	0.50	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.2
GCA_002719615.1	36.0	0.16	0.33	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.33
GCA_002720055.1	46.5	0.32	0.44	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.81
GCA_002722735.1	57.3	0.26	0.64	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.27
GCA_002723045.1	50.9	0.35	0.50	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.44
GCA_002725315.1	52.4	0.36	0.51	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.2
GCA_002728565.1	49.7	0.31	0.50	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.68
GCA_002731195.1	36.8	0.17	0.34	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.39
GCA_003602515.1	51.2	0.36	0.50	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.78
GCA_003602595.1	35.9	0.16	0.35	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.96
GCA_004195615.1	50.5	0.30	0.52	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86
GCA_014239955.1	51.6	0.32	0.52	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.38
GCA_022449945.1	52.5	0.38	0.50	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.18
GCA_023700245.1	35.9	0.15	0.31	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.73
GCA_902573015.1	49.9	0.35	0.48	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.72
GCA_902573085.1	50.2	0.33	0.51	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.67
GCA_902573115.1	47.9	0.27	0.50	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.92
GCA_902601345.1	50.5	0.36	0.49	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.41
GCA_902625325.1	50.4	0.36	0.48	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.8
GCA_905182515.1	36.7	0.13	0.33	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.67
GCA_002496725.1	46.8	0.30	0.49	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.41
GCA_002497985.1	51.7	0.30	0.57	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.47
GCA_002498925.1	51.4	0.32	0.54	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_002499325.1	46.7	0.31	0.50	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.27
GCA_002499345.1	46.8	0.30	0.49	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.62
GCA_002499865.1	46.5	0.32	0.49	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.82
GCA_002501605.1	47.5	0.33	0.49	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.33
GCA_002501805.1	47.0	0.31	0.50	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.93
GCA_002502095.1	46.8	0.32	0.49	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.16
GCA_002504435.1	52.4	0.32	0.54	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.93
GCA_002505775.1	47.7	0.32	0.49	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.13
GCA_002506825.1	46.9	0.30	0.48	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.61
GCA_002718995.2	51.7	0.31	0.53	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.4
GCA_002726275.1	52.2	0.29	0.56	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.2
GCA_002730095.1	47.7	0.33	0.51	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.58
GCA_002457195.1	48.1	0.14	0.62	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.26
GCA_002498455.1	49.0	0.17	0.59	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.54
GCA_002505685.1	48.4	0.17	0.60	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.6
GCA_002701965.1	47.5	0.16	0.57	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.45
GCA_002722595.1	44.7	0.18	0.56	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.16
GCA_002724815.1	49.5	0.16	0.60	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.51
GCA_022449845.1	51.9	0.14	0.68	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.97
GCA_002505495.1	56.8	0.18	0.74	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.37
GCA_002685895.1	45.0	0.12	0.60	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.33
GCA_002725475.1	42.1	0.14	0.52	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.43
GCA_002727675.1	39.6	0.14	0.46	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.69
GCA_012959435.1	44.2	0.11	0.60	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.12
GCA_012964335.1	44.5	0.11	0.61	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.12
GCA_014384685.1	43.8	0.13	0.58	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.9
GCA_016845345.1	44.2	0.10	0.59	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.36
GCA_018650285.1	43.6	0.08	0.61	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.56
GCA_003193925.1	60.8	0.21	0.72	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.67
GCA_022447095.1	57.9	0.25	0.66	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.96
GCA_002457605.1	53.6	0.24	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.35
GCA_002495735.1	55.9	0.26	0.60	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.73
GCA_002501885.1	48.4	0.26	0.52	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.36
GCA_002503055.1	49.2	0.26	0.54	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.16
GCA_002505325.1	54.1	0.24	0.59	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.75
GCA_022448665.1	59.2	0.23	0.69	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.56
GCA_002698225.1	51.4	0.27	0.57	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.27
GCA_002714745.1	51.3	0.28	0.51	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.07
GCA_002727275.1	50.2	0.26	0.54	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.56
GCA_004195715.1	55.5	0.24	0.61	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.56
GCA_014240285.1	55.8	0.26	0.62	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.62
GCA_019654055.1	59.6	0.30	0.60	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.4
GCA_016207515.1	62.3	0.29	0.60	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.27

GCA_020201485.1	72.0	0.28	0.66	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.22
GCA_021325135.1	71.6	0.26	0.67	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.62
GCA_003561665.1	61.8	0.27	0.47	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.54
GCA_003009755.1	69.3	0.26	0.67	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.16
GCA_020343715.1	64.2	0.45	0.48	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.74
GCA_023265395.1	67.2	0.42	0.52	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.27
GCA_016874675.1	66.3	0.27	0.65	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.27
GCF_000025665.1	39.2	0.14	0.41	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_015520565.1	39.1	0.13	0.40	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.13
GCA_015523135.1	38.5	0.12	0.39	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.01
GCA_013154005.1	47.0	0.10	0.47	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.16
GCA_015520985.1	54.5	0.14	0.63	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.41
GCA_015521465.1	41.7	0.12	0.45	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.16
GCA_015523125.1	44.9	0.11	0.50	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.58
GCA_015522955.1	42.5	0.13	0.45	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.13
GCA_021160945.1	40.8	0.15	0.45	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.7
GCA_021163705.1	41.7	0.15	0.47	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.16
GCA_015522935.1	40.3	0.11	0.47	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.03
GCA_015520975.1	43.6	0.12	0.52	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.19
GCA_002011395.1	57.6	0.15	0.67	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.61
GCA_002878135.1	41.0	0.17	0.53	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.39
GCA_009758405.1	35.7	0.13	0.41	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.58
GCA_023261755.1	32.6	0.11	0.38	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.39
GCA_023261745.1	35.7	0.08	0.51	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.26
GCA_003649915.1	44.0	0.23	0.47	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.2
GCA_003649695.1	55.1	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.16
GCA_020347705.1	44.0	0.23	0.38	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.33
GCA_020348445.1	41.8	0.22	0.36	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.2
GCA_020351895.1	41.9	0.24	0.37	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.4
GCA_020350865.1	49.7	0.29	0.45	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.3
GCA_021161085.1	58.5	0.31	0.54	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.45
GCA_024281315.1	49.1	0.18	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.8
GCA_013415695.1	51.4	0.22	0.65	0.13	0	0	0	0	0	0	0	0	0	1	1	1	1	1	98.39
GCA_020725985.1	58.9	0.27	0.66	0.07	0	0	0	0	0	0	0	0	0	1	1	0	0	0	91.98
GCA_014361295.1	46.0	0.17	0.56	0.28	0	0	0	0	0	0	0	0	1	1	1	1	1	1	98.39
GCA_024464195.1	44.3	0.16	0.56	0.28	0	0	0	0	0	0	0	0	1	1	1	1	0	0	88.41
GCA_001421185.1	62.1	0.18	0.68	0.14	0	0	2	1	1	1	0	0	1	0	2	1	1	1	96.61
GCA_001512965.1	58.8	0.16	0.70	0.13	0	0	1	0	0	0	0	0	0	1	1	1	1	1	98.06
GCA_002498285.1	62.0	0.25	0.61	0.14	0	0	0	0	0	0	0	0	1	1	1	1	1	0	84.72
GCA_002504525.1	60.8	0.17	0.70	0.13	0	0	2	1	1	1	0	0	1	1	1	1	1	1	95.04
GCA_012518185.1	42.0	0.15	0.47	0.38	0	0	1	1	1	1	0	0	1	0	0	0	0	1	94.35
GCA_012519255.1	53.5	0.18	0.58	0.24	0	1	2	1	1	1	0	0	1	0	1	1	0	1	97.58
GCF_000404225.1	41.3	0.05	0.49	0.45	1	1	2	1	1	1	0	0	1	0	1	1	1	1	98.79
GCA_905202485.1	42.7	0.05	0.50	0.45	0	1	2	1	1	1	0	0	1	0	1	1	1	1	97.98
GCA_905203995.1	44.8	0.04	0.46	0.50	0	0	0	0	0	0	0	0	0	0	1	1	1	1	95.16
GCA_944319735.1	41.0	0.06	0.49	0.45	0	0	2	1	1	1	0	0	1	0	1	1	1	1	98.79
GCF_000308215.1	60.5	0.11	0.72	0.17	0	1	4	2	3	2	0	0	2	1	1	1	1	1	98.39
GCA_002067635.1	58.8	0.23	0.63	0.14	0	0	2	1	1	1	0	0	1	0	1	0	1	2	73.4
GCA_002508545.1	62.7	0.22	0.65	0.13	1	1	1	1	1	1	0	0	0	1	1	1	1	1	97.31
GCA_012719175.1	57.1	0.19	0.64	0.17	0	0	1	2	2	2	0	0	2	1	1	1	1	1	95.16
GCA_016109435.1	62.1	0.21	0.68	0.12	0	0	2	1	1	1	0	0	1	0	1	1	1	1	94.35
GCA_018262895.1	58.4	0.21	0.65	0.15	1	1	1	1	1	1	0	0	1	1	1	1	1	1	96.77
GCA_022709105.1	60.2	0.24	0.63	0.13	0	0	1	0	0	0	0	0	0	0	1	2	2	0	83.9
GCA_012520845.1	60.7	0.04	0.81	0.15	0	0	0	1	1	1	0	0	1	0	1	1	1	1	97.98
GCA_012515075.1	59.9	0.03	0.83	0.14	0	0	2	1	1	1	0	0	1	0	1	1	1	1	89.44
GCA_024399155.1	38.1	0.13	0.37	0.49	0	0	0	0	0	0	0	0	0	0	1	1	1	1	77.15
GCA_024399215.1	39.6	0.21	0.37	0.42	0	0	0	0	0	0	0	0	0	0	1	0	0	0	73.12
GCA_024399275.1	39.7	0.23	0.38	0.40	0	0	0	0	0	0	0	0	0	0	1	1	1	1	89.92
GCA_023230065.1	42.1	0.02	0.60	0.38	0	1	2	1	1	1	0	0	1	0	2	1	2	1	94.35
GCA_006954405.1	47.6	0.04	0.82	0.15	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.18
GCA_017455785.1	50.8	0.07	0.79	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	1	85.64
GCA_002506905.1	51.5	0.02	0.78	0.20	0	1	2	1	1	1	0	0	1	0	1	1	1	1	98.69
GCA_012719315.1	62.7	0.04	0.88	0.08	0	0	2	1	1	1	0	0	1	0	1	0	1	1	90.19
GCA_019262145.1	43.7	0.01	0.73	0.26	0	1	1	1	1	1	0	0	1	0	1	1	1	1	99.6
GCF_000300255.2	55.6	0.02	0.84	0.13	0	1	2	1	1	1	0	0	1	1	1	1	1	1	98.39
GCA_000350305.1	58.3	0.02	0.90	0.08	0	2	2	1	1	1	0	0	1	0	1	1	1	1	97.98
GCF_001481295.1	60.4	0.07	0.83	0.10	0	2	2	1	0	1	0	0	1	0	0	2	0	1	93.73
GCA_001560915.1	54.0	0.02	0.85	0.13	0	1	2	1	1	1	0	0	1	0	1	1	1	1	97.18
GCA_002495325.1	58.1	0.02	0.82	0.16	0	1	2	1	1	1	0	0	1	0	1	1	1	1	96.37
GCA_002503545.1	60.1	0.03	0.87	0.10	0	1	2	0	1	1	0	0	1	1	1	0	1	1	88.38
GCA_015063225.1	59.2	0.02	0.90	0.08	0	1	0	1	1	1	0	0	1	1	1	1	1	1	93.95
GCA_024399175.1	57.9	0.04	0.85	0.11	0	1	2	1	1	1	0	0	1	0	0	0	0	1	80.87
GCA_024399195.1	53.7	0.06	0.76	0.19	0	0	0	1	1	1	0	0	1	1	1	1	1	1	88.07
GCA_024399225.1	53.1	0.03	0.77	0.20	0	0	0	1	1	1	0	0	1	0	1	1	1	0	65.68
GCA_902763685.1	56.2	0.03	0.86	0.12	0	2	1	1	1	1	0	0	1	0	1	1	1	1	93.15
GCA_902787415.1	59.4	0.04	0.88	0.08	0	1	2	1	1	1	0	0	1	0	1	1	1	0	92.88
GCA_009776625.1	61.6	0.08	0.80	0.12	0	2	1	1	0	1	0	0	1	0	2	2	2	1	88.04
GCA_009777615.1	52.3	0.02	0.74	0.24	0	1	2	0	1	1	0	0	1	0	1	1	1	1	97.98
GCA_009778275.1	53.0	0.02	0.74	0.24	0	1	0	0	0	0	0	0	0	0	1	1	1	0	74.46
GCA_009778575.1	52.1	0.03	0.73	0.24	0	2	1	1	1	1	0	0	1	0	1	1	1	1	93.82
GCA_009786295.1	50.3	0.03	0.71	0.26	0	1	0	0	0	0	0	0	0	0	1	1	1	1	77.9
GCA_023402275.1	46.9	0.01	0.73	0.26	0	2	2	1	1	1	0	0	1	1	1	1	1	1	95.97
GCF_000800805.1	49.2	0.02	0.67	0.31	0	0	2	1	1	1	0	0	1	0	1	1	1	1	97.85
GCA_003550345.1	62.6	0.15	0.77	0.08	0	0	0	0	0	0	0	0	0	0	1	1	1	1	87.5
GCA_003555025.1	62.0	0.15	0.76	0.08	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.58
GCA_003557905.1	54.9	0.15	0.73	0.13	0	1	1	1	1	1	0	0	1	0	1	1	0	0	89.69
GCA_003560875.1	56.7	0.16	0.72	0.12	0	0	0	0	0	0	0	0	0	0	1	1	0	1	86.5
GCA_007116915.1	53.9	0.16	0.70	0.13	0	0	1	0	0	0	0	0	0	0	0	0	0	1	70.88
GCA_007117455.1	55.6	0.13	0.80	0.07	0	1	1	0	1	1	0	0	1	1	0	0	0	0	65.97
GCA_001421175.1	54.6	0.11	0.72	0.17	0	0	0	0	0	0	0	0	0	0	1	1	2	1	94.09
GCA_002502965.1	54.3	0.11	0.73	0.15	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.18
GCA_002506255.1	53.1	0.13	0.69	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	1	61.16
GCA_012522645.1	54.5	0.14	0.70	0.16	0	0	0	0	0	0	0	0	0	0	1	1	1	1	93.15
GCA_015063185.1	50.8	0.05	0.78	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	1	85.89
GCA_015063195.1	45.3	0.05	0.61	0.34	0	0	0	0	0	0	0	0	0	0	0	1	0	1	91.53
GCA_016297775.1	54.3	0.02	0.87	0.11	0	0	0	0	0	0	0	0	0	0	1	1	1	1	91.13
GCA_017395275.1	57.4	0.08	0.77	0.15	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.02
GCA_017508065.1	51.8	0.07	0.76	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	1	93.15
GCA_944321505.1	61.8	0.09	0.84	0.08	0	0	0	0	0	0	0	0	0	0	1	1	1	1	96.37
GCA_001563305.1	55.5	0.03	0.89	0.08	0	3	2	1	1	1	0	0	1	1	1	1	1	1	96.37
GCA_002504405.1	59.4	0.02	0.89	0.09	0	0	1	1	1	1	0	0	0	0	1	1	1	1	97.98
GCA_002504495.1	59.0	0.13	0.76	0.11	0	1	0	1	1	1	0	0	1	0	1	1	1	0	82.12
GCA_002506175.1	51.1	0.02	0.86	0.11	0	2	0	1	1	1	0	0	0	1	0	0	0	0	81.94
GCA_002506425.1	58.1	0.08	0.83	0.09	0	1	1	1	1	1	0	0	1	1	1	1	1	1	89.8
GCA_009911715.1	59.5	0.02	0.90	0.08	0	1	2	1	1	1	0	0	1	0	1	1	1	1	98.79
GCA_006954465.1	58.2	0.10	0.82	0.08	0	1	3	1	0	1	0	0	1	1	1	0	1	1	81.12
GCA_015063125.1	53.5	0.03	0.86	0.11	0	3	1	1	1	1	0	0	1	1	1	1	1	1	97.18
GCA_015063135.1	59.7	0.16	0.71	0.13	0	1	2	1	1	1	0	0	1	0	1	1	1	1	89.19
GCA_015063165.1	57.2	0.07	0.82	0.11	0	1	2	1	1	1	0	0	1	1	1	1	1	1	97.18
GCA_015063235.1	51.4	0.04	0.86	0.10	0	1	1	1	1	1	0	0	0	1	0	0	0	1	81.26
GCA_015063245.1	54.1	0.02	0.89	0.09	0	0	2	1	1	1	0	0	0	1	1	1	1	1	95.1
GCA_015063285.1	51.5	0.03	0.85	0.12	0	0	2	1	1	1	0	0	0	0	1	1	1	1	95.56
GCA_016281925.1	57.8	0.10	0.77	0.13	0	0	2	0	1	1	0	0	1	1	0	0	0	1	82.43
GCA_016282555.1	54.7	0.06	0.72	0.21	0	1	2	1	0	1	0	0	0	0	1	1	0	1	82.85
GCA_016284295.1	56.1	0.04	0.87	0.09	0	0	1	1	1	1	0	0	0	1	1	1	1	1	93.15
GCA_016296195.1	56.2	0.04	0.86	0.10	0	1	0	1	0	1	0	0	1	0	1	0	0	2	86.69
GCA_017461225.1	61.6	0.03	0.89	0.08	0	0	2	1	1	1	0	0	1	0	1	1	1	1	95.7
GCA_017468935.1	53.2	0.04	0.85	0.10	0	0	1	1	1	1	0	0	1	1	1	1	1	1	95.56
GCA_017475875.1	58.4	0.11	0.79	0.11	0	2	1	1	1	1	0	0	1	1	2	1	1	1	81.18
GCA_017507885.1	56.6	0.03	0.85	0.11	0	0	2	1	1	1	0	0	0	0	1	1	1	1	89.78
GCA_017519045.1	60.3	0.13	0.75	0.12	0	1	2	1	1	1	0	0	1	1	0	1	1	1	92.88
GCA_017524805.1	55.3	0.07	0.80	0.13	0	1	2	1	1	1	0	0	1	1	1	1	1	1	97.98
GCA_017540825.1	60.0	0.15	0.73	0.12	0	1	2	1	1	1	0	0	1	1	1	1	1	1	91.94
GCA_017616575.1	60.4	0.26	0.59	0.15	0	0	1	1	1	1	0	0	0	0	0	1	1	1	66.49
GCA_017935945.1	54.1	0.02	0.88	0.10	0	1	2	1	1	1	0	0	1	0	1	1	1	1	96.37
GCA_900767505.1	56.0	0.04	0.89	0.08	0	0	2	0	0	0	0	0	1	0	0	0	0	1	89.46
GCA_905187815.1	59.8	0.03	0.88	0.08	0	0	1	1	1	1	0	0	1	1	1	1	1	1	98.52
GCA_934234005.1	46.3	0.02	0.70	0.28	0	1	2	1	1	1	0	0	1	0	1	1	1	1	87.38
GCA_934702355.1	55.3	0.01	0.90	0.08	0	1	2	1	1	1	0	0	1	0	1	1	1	1	98.79
GCA_944320485.1	60.7	0.04	0.88	0.08	0	2	2	2	1	1	0	0	1	0	1	1	1	1	87.88
GCA_944320495.1	61.6	0.06	0.85	0.08	0	2	2	0	1	1	0	0	1	0	1	0	1	1	92.02
GCA_944321985.1	57.4	0.05	0.85	0.10	0	3	2	1	1	1	0	0	1	0	1	1	1	1	85.1
GCA_944322255.1	60.9	0.01	0.91	0.08	0	0	1	1	1	1	0	0	1	1	1	1	1	1	96.33
GCA_945492685.1	57.2	0.05	0.85	0.10	0	0	1	1	1	1	0	0	1	0	1	0	0	0	69.37
GCA_013329105.1	48.6	0.14	0.58	0.28	0	0	0	0	0	0	0	0	0	0	0	1	1	1	74.25
GCA_002498365.1	55.5	0.02	0.80	0.18	0	3	2	0	1	1	0	0	1	0	1	1	1	1	97.18
GCA_002498605.1	47.0	0.02	0.69	0.29	0	1	1	1	1	1	0	0	1	0	1	1	1	0	93.15
GCA_002505345.1	55.2	0.02	0.81	0.17	0	3	2	0	1	1	0	0	1	0	1	1	1	1	97.98
GCA_002509405.1	54.9	0.03	0.80	0.17	0	2	2	0	1	1	0	0	1	0	0	1	1	1	93.15
GCA_011620825.1	54.2	0.05	0.75	0.21	0	0	2	0	1	1	0	0	1	0	1	1	1	1	74.67
GCA_009776695.1	52.6	0.08	0.73	0.19	0	0	0	0	1	0	0	0	0	0	1	1	1	1	86.69
GCA_009778265.1	51.9	0.06	0.74	0.20	0	0	2	1	2	1	0	0	1	0	0	0	0	0	59.49
GCA_009780575.1	49.7	0.06	0.74	0.20	0	1	2	1	1	1	0	0	1	0	1	1	1	1	94.76

GCA_009780795.1	53.5	0.09	0.73	0.18	0	0	1	0	1	0	0	0	0	0	1	1	1	1	89.47
GCA_009784745.1	46.5	0.07	0.70	0.23	0	0	2	0	1	1	0	0	1	0	1	1	1	1	91.74
GCA_003135935.1	53.6	0.21	0.60	0.19	0	0	0	0	0	0	0	0	0	0	1	1	1	0	94.23
GCA_003153895.1	54.0	0.22	0.59	0.19	0	0	0	0	0	0	0	0	0	0	2	0	1	0	89.71
GCA_016919565.1	58.2	0.25	0.62	0.14	0	0	0	0	0	0	0	0	0	0	1	1	1	1	66.88
GCA_016919625.1	57.3	0.14	0.69	0.16	0	0	0	0	0	0	0	0	0	0	1	1	1	1	87.1
GCA_002067865.1	57.0	0.13	0.69	0.18	0	0	1	1	1	1	0	0	1	0	1	1	1	1	99.19
GCA_013415865.1	52.3	0.10	0.73	0.18	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.39
GCA_021372315.1	56.5	0.12	0.71	0.17	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.58
GCA_002067045.1	62.1	0.19	0.69	0.11	0	0	0	0	0	0	0	0	0	0	0	1	0	0	84.06
GCA_002497075.1	57.9	0.16	0.67	0.17	0	0	0	0	0	0	0	0	0	0	0	1	0	1	98.39
GCA_004525545.1	55.4	0.16	0.63	0.21	0	0	1	1	1	2	0	0	1	1	1	1	1	1	95.97
GCA_012729095.1	59.7	0.18	0.70	0.12	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_016926075.1	61.1	0.20	0.71	0.09	0	0	0	0	0	0	0	0	0	0	1	1	1	1	72.85
GCA_021372335.1	63.0	0.20	0.69	0.12	0	0	2	1	1	1	0	0	1	1	1	1	1	1	95.97
GCA_013329565.1	59.4	0.18	0.67	0.16	0	0	0	0	0	0	0	0	0	0	1	1	1	1	87.61
GCA_019594055.1	49.8	0.22	0.58	0.20	0	0	0	0	0	0	0	0	0	0	0	1	0	0	91.2
GCA_007129655.1	43.3	0.19	0.47	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.8
GCA_019594305.1	45.2	0.20	0.49	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.87
GCA_018610025.1	48.1	0.23	0.52	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.39
GCA_003551675.1	43.9	0.20	0.55	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_003554965.1	42.7	0.17	0.56	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_003555395.1	44.5	0.18	0.60	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.8
GCA_018334755.1	45.7	0.20	0.54	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.4
GCA_018334835.1	41.5	0.19	0.53	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.6
GCA_019594195.1	42.5	0.19	0.59	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.07
GCA_003552585.1	42.6	0.17	0.53	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.73
GCA_003553085.1	46.6	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.2
GCA_003560595.1	43.2	0.20	0.50	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.96
GCA_007133925.1	50.0	0.20	0.60	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.53
GCA_019594025.1	44.5	0.18	0.46	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.28
GCA_019594235.1	39.6	0.15	0.47	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.04
GCA_003551065.1	41.0	0.18	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.6
GCA_005878375.1	66.3	0.32	0.60	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.98
GCA_016207545.1	66.9	0.34	0.55	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.8
GCA_017885655.1	59.2	0.37	0.54	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.2
GCA_022848825.1	57.1	0.46	0.45	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.08
GCA_022848865.1	57.1	0.42	0.48	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.93
GCA_023129265.1	56.0	0.43	0.48	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.94
GCA_023130895.1	56.4	0.43	0.48	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.87
GCA_023136265.1	56.9	0.43	0.48	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.93
GCA_022848835.1	57.7	0.42	0.45	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.36
GCA_022848785.1	64.6	0.43	0.43	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.47
GCA_005878915.1	64.9	0.36	0.54	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.16
GCA_005878955.1	67.8	0.37	0.55	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.36
GCA_020029475.1	67.9	0.39	0.54	0.07	0	0	0	0	0	0	0	0	1	0	0	0	0	0	96.76
GCA_001800745.1	68.0	0.27	0.67	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.47
GCA_001800825.1	69.3	0.24	0.71	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.67
GCA_005878325.1	64.6	0.30	0.61	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.19
GCA_005878385.1	63.3	0.27	0.62	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.98
GCA_005878415.1	66.1	0.28	0.63	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.74
GCA_005878485.1	64.3	0.29	0.61	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.45
GCA_005878515.1	64.1	0.28	0.63	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.13
GCA_005878525.1	63.9	0.27	0.63	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.81
GCA_005878615.1	65.0	0.28	0.64	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.71
GCA_005878635.1	64.6	0.30	0.62	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.55
GCA_005878665.1	64.1	0.28	0.62	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.6
GCA_005878985.1	64.2	0.28	0.63	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_005878995.1	64.4	0.27	0.61	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.33
GCA_005879015.1	63.8	0.29	0.61	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.19
GCA_005879045.1	64.1	0.28	0.62	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.46
GCA_005879065.1	63.8	0.26	0.64	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.6
GCA_021788795.1	69.0	0.29	0.66	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.42
GCA_013329855.1	67.7	0.28	0.66	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.76
GCA_023140195.1	51.5	0.40	0.45	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_004377185.1	50.2	0.40	0.46	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_020345725.1	49.5	0.44	0.42	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.73
GCA_016214785.1	58.2	0.28	0.51	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96
GCA_020696385.1	45.5	0.18	0.53	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_020697715.1	45.4	0.21	0.51	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.6
GCA_023135545.1	49.5	0.24	0.46	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.2
GCA_023137005.1	47.3	0.22	0.52	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.07
GCA_023136815.1	43.9	0.22	0.41	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.27
GCA_001595885.1	55.5	0.24	0.54	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.24
GCA_002496385.1	54.0	0.20	0.56	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.6
GCA_002499085.1	54.8	0.21	0.57	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.8
GCA_013791785.1	48.8	0.18	0.51	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.53
GCA_021796175.1	51.8	0.20	0.68	0.13	0	0	0	0	0	0	0	0	1	0	0	0	0	0	76.38
GCA_021806165.1	55.4	0.18	0.72	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.14
GCA_021811925.1	52.6	0.19	0.68	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93
GCA_021817225.1	52.6	0.18	0.71	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.94
GCA_019721035.1	50.9	0.15	0.71	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.01
GCA_019721075.1	49.6	0.14	0.68	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.14
GCA_021796895.1	51.6	0.15	0.72	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.87
GCA_019720975.1	50.1	0.15	0.72	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.01
GCA_001856825.1	44.3	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.13
GCA_014874235.1	45.7	0.26	0.52	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.82
GCA_021787125.1	46.2	0.28	0.50	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.28
GCA_021792255.1	44.1	0.25	0.50	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.97
GCA_021792355.1	43.7	0.23	0.48	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.97
GCA_021793855.1	43.7	0.27	0.47	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.85
GCA_021797855.1	46.3	0.24	0.51	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.06
GCA_021797915.1	44.2	0.24	0.50	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.55
GCA_021816725.1	44.3	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.27
GCA_021827945.1	44.3	0.25	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.67
GCA_021831005.1	45.0	0.25	0.50	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.94
GCA_023379555.1	43.7	0.23	0.51	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.66
GCA_023381415.1	46.6	0.26	0.51	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.53
GCA_017857235.1	35.9	0.15	0.39	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.58
GCA_023256475.1	38.0	0.16	0.42	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.58
GCA_023256615.1	37.2	0.13	0.43	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.95
GCA_021817415.1	43.2	0.23	0.50	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.74
GCF_001402945.1	34.0	0.10	0.24	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.37
GCA_016806715.1	44.4	0.20	0.49	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.02
GCA_021792655.1	46.1	0.21	0.54	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.96
GCA_021793945.1	45.7	0.20	0.52	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.01
GCA_023484805.1	46.7	0.21	0.54	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.98
GCF_900083515.1	37.3	0.16	0.42	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.33
GCA_021794355.1	39.5	0.18	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.52
GCA_021799315.1	39.6	0.18	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.98
GCA_021806345.1	38.1	0.19	0.42	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.93
GCA_021810575.1	39.4	0.17	0.46	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.88
GCA_021816385.1	40.0	0.16	0.49	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.36
GCA_021816745.1	41.6	0.10	0.48	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.83
GCA_021816965.1	40.5	0.14	0.53	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.75
GCA_021817255.1	40.8	0.16	0.43	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.07
GCA_021819225.1	40.2	0.17	0.46	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.77
GCA_021820405.1	39.6	0.17	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.98
GCA_021820525.1	39.7	0.13	0.46	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.37
GCA_021822985.1	41.8	0.16	0.55	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.31
GCA_021826765.1	41.5	0.14	0.55	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.59
GCA_021833045.1	37.5	0.16	0.43	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.65
GCA_021835265.1	36.9	0.18	0.41	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.09
GCA_023256455.1	39.8	0.13	0.46	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.22
GCA_023381355.1	42.4	0.17	0.51	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.34
GCA_023489425.1	38.2	0.16	0.44	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.05
GCF_000152265.2	36.5	0.12	0.29	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.74
GCF_002078355.1	36.5	0.11	0.28	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.47
GCA_002505185.1	37.1	0.13	0.33	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.07
GCA_021797025.1	36.6	0.13	0.33	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.69
GCA_021797225.1	36.4	0.14	0.30	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.97
GCA_021797295.1	37.6	0.14	0.33	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.94
GCA_021797385.1	37.5	0.12	0.33	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.23
GCA_021797555.1	29.9	0.08	0.24	0.69	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.74
GCA_021797735.1	32.8	0.11	0.26	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.74
GCA_021802165.1	37.0	0.13	0.31	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.27
GCA_021802205.1	36.5	0.12	0.33	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.41
GCA_021806235.1	32.7	0.11	0.26	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.92
GCA_021806295.1	39.0	0.12	0.32	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.74
GCA_021820565.1	38.5	0.11	0.35	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.32
GCA_021826795.1	36.7	0.12	0.32	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.29
GCA_021835185.1	37.3	0.12	0.32	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.78
GCA_021846695.1	37.3	0.13	0.29	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.99

GCA_000496135.1	38.5	0.16	0.43	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.72
GCA_021790415.1	37.8	0.19	0.41	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.74
GCA_021806355.1	41.0	0.18	0.48	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.36
GCA_021809755.1	37.4	0.17	0.41	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.96
GCA_021818675.1	38.3	0.15	0.45	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.36
GCA_021827885.1	40.7	0.20	0.47	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.48
GCA_021845325.1	37.4	0.17	0.42	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.59
GCA_000965745.1	46.4	0.20	0.52	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.94
GCA_014874365.1	44.4	0.19	0.48	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.39
GCA_021795055.1	48.6	0.20	0.56	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.38
GCA_021811635.1	48.6	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.75
GCA_021818715.1	48.5	0.19	0.59	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.33
GCA_023484105.1	44.5	0.18	0.58	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.33
GCA_021810045.1	42.7	0.17	0.47	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.94
GCA_021811505.1	44.2	0.18	0.51	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.57
GCA_021811525.1	45.3	0.18	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.69
GCA_021817455.1	45.3	0.18	0.47	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.13
GCA_021850545.1	46.0	0.18	0.45	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.31
GCA_021850745.1	45.5	0.19	0.51	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.95
GCA_021850835.1	45.8	0.19	0.47	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.57
GCA_023487765.1	46.0	0.18	0.51	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.22
GCA_023488885.1	43.7	0.18	0.46	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.65
GCA_023489435.1	45.6	0.17	0.46	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.33
GCA_021801305.1	43.7	0.16	0.55	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.73
GCA_021820245.1	42.2	0.17	0.52	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_021845155.1	43.0	0.17	0.53	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.18
GCA_021847855.1	42.4	0.18	0.49	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.01
GCA_021835025.1	33.1	0.10	0.31	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.15
GCA_021846395.1	33.5	0.10	0.32	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.97
GCA_021797955.1	38.1	0.17	0.42	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.27
GCA_021785735.1	44.4	0.18	0.50	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.59
GCA_021799755.1	44.4	0.18	0.53	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.28
GCA_021802055.1	48.7	0.22	0.54	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.87
GCA_021817735.1	48.0	0.25	0.54	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.43
GCA_021792045.1	41.0	0.18	0.44	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.32
GCA_021826925.1	40.9	0.19	0.43	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.3
GCA_021826835.1	37.5	0.18	0.41	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.24
GCA_023379355.1	43.9	0.16	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.31
GCA_021792595.1	48.7	0.20	0.59	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.33
GCA_021803655.1	48.2	0.19	0.58	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.28
GCA_023487205.1	49.5	0.23	0.56	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCF_900176435.1	36.0	0.10	0.30	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.59
GCA_021826785.1	34.4	0.11	0.26	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.76
GCF_001316105.1	56.4	0.23	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.61
GCF_000195915.1	46.0	0.14	0.64	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.52
GCF_003205235.1	44.0	0.14	0.62	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.55
GCA_008709555.1	46.8	0.11	0.69	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.74
GCA_023256435.1	44.1	0.13	0.64	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.33
GCF_000011185.1	39.9	0.17	0.38	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.97
GCA_002503205.1	42.6	0.16	0.52	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.46
GCA_021797265.1	45.7	0.15	0.57	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.51
GCA_021797525.1	42.4	0.15	0.50	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.01
GCA_021802365.1	43.4	0.13	0.54	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.28
GCA_021804185.1	44.0	0.16	0.56	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.67
GCA_023379825.1	44.0	0.15	0.57	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.85
GCA_002498845.1	46.5	0.14	0.60	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.79
GCA_021797355.1	46.0	0.17	0.57	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.02
GCA_021799185.1	45.5	0.14	0.58	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.55
GCA_021819605.1	47.4	0.14	0.61	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.67
GCA_023379345.1	48.1	0.17	0.59	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.22
GCA_002502705.1	41.3	0.17	0.48	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.79
GCA_021797055.1	41.5	0.18	0.49	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.58
GCA_021800105.1	44.1	0.22	0.50	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.97
GCA_021818765.1	44.4	0.21	0.49	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.31
GCA_021821635.1	44.7	0.19	0.53	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.07
GCA_021850505.1	42.0	0.17	0.49	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.62
GCA_023379845.1	44.4	0.21	0.50	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.78
GCA_015520045.1	44.5	0.19	0.52	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.58
GCA_023379435.1	42.8	0.20	0.55	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.96
GCA_011046235.1	54.5	0.25	0.61	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.07
GCA_001800675.1	57.0	0.30	0.61	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.8
GCA_001800815.1	56.4	0.31	0.59	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.8
GCA_016930135.1	59.2	0.32	0.63	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.69
GCA_018814355.1	56.1	0.30	0.61	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_020725925.1	60.4	0.32	0.62	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.2
GCA_022865445.1	55.7	0.35	0.57	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_021789945.1	60.9	0.33	0.62	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.2
GCA_020347565.1	59.6	0.24	0.69	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.4
GCA_020347645.1	54.0	0.29	0.62	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.01
GCA_020348345.1	55.7	0.25	0.66	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.07
GCA_020696365.1	57.7	0.28	0.64	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.47
GCA_020696395.1	58.0	0.28	0.66	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.47
GCA_022848805.1	57.8	0.29	0.63	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.4
GCA_013331315.1	60.3	0.30	0.64	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.79
GCA_011391345.1	60.6	0.27	0.67	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.63
GCA_018818785.1	53.5	0.22	0.69	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.27
GCA_013329135.1	60.2	0.30	0.62	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.67
GCA_023379385.1	35.8	0.16	0.35	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.27
GCA_021790425.1	67.4	0.33	0.60	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.47
GCA_021796385.1	61.6	0.31	0.57	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.27
GCA_021809545.1	64.5	0.30	0.57	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.2
GCA_021823345.1	64.6	0.32	0.54	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.07
GCA_021832495.1	61.5	0.31	0.57	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.06
GCA_021798195.1	68.7	0.22	0.74	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.67
GCA_021802125.1	69.1	0.33	0.63	0.05	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.27
GCA_021806135.1	68.9	0.22	0.71	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.27
GCA_021827405.1	69.8	0.23	0.70	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.47
GCA_021828085.1	70.2	0.33	0.61	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.37
GCA_021828665.1	72.5	0.30	0.62	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.58
GCA_022749845.1	68.5	0.52	0.38	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_022749995.1	69.1	0.53	0.36	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.6
GCA_022750125.1	68.3	0.49	0.39	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.74
GCA_022750455.1	67.1	0.33	0.55	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.74
GCA_022749815.1	65.6	0.35	0.52	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96
GCA_002495185.1	67.8	0.39	0.49	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.8
GCA_002503985.1	67.1	0.35	0.49	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98
GCA_013044425.1	67.3	0.37	0.51	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.36
GCA_013290345.1	68.4	0.39	0.53	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.84
GCA_021791335.1	70.2	0.33	0.57	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.6
GCA_021792485.1	68.1	0.40	0.49	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.08
GCA_021798415.1	70.8	0.43	0.49	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.87
GCA_021801925.1	72.9	0.36	0.56	0.08	0	0	0	0	0	0	0	0	0	1	0	0	0	0	92.4
GCA_021812305.1	72.1	0.41	0.52	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.47
GCA_021816865.1	70.9	0.43	0.50	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.07
GCA_021816955.1	69.9	0.34	0.55	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.39
GCA_021817245.1	69.7	0.38	0.53	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.27
GCA_021817605.1	70.2	0.44	0.48	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.47
GCA_021819135.1	69.5	0.36	0.55	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.07
GCA_021821785.1	70.2	0.36	0.52	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.27
GCA_021823085.1	67.8	0.37	0.53	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.27
GCA_021826525.1	67.7	0.39	0.50	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.74
GCA_021826685.1	67.3	0.39	0.47	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.67
GCA_021827545.1	69.0	0.37	0.54	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.81
GCA_021828195.1	67.2	0.37	0.53	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.07
GCA_021828715.1	72.0	0.39	0.53	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.01
GCA_021844945.1	67.2	0.39	0.48	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.67
GCA_021848165.1	71.2	0.38	0.49	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.69
GCA_022749835.1	68.5	0.44	0.47	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.67
GCA_022749895.1	68.7	0.41	0.47	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.36
GCA_022749905.1	68.4	0.46	0.44	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.25
GCA_022749935.1	67.6	0.44	0.45	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.67
GCA_022750055.1	67.5	0.41	0.50	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.67
GCA_022750115.1	69.0	0.44	0.47	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_022750155.1	68.4	0.39	0.53	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.68
GCA_022750195.1	68.1	0.39	0.49	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.87
GCA_022750205.1	68.1	0.41	0.47	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.97
GCA_022750295.1	69.6	0.38	0.48	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.07
GCA_022750335.1	67.0	0.42	0.46	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.17
GCA_022750355.1	66.6	0.42	0.45	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_022750375.1	67.8	0.38	0.49	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.42
GCA_022750415.1	68.7	0.40	0.46	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.14
GCA_022750435.1	69.5	0.39	0.48	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.58
GCA_015522885.1	47.8	0.15	0.51	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.87

GCA_024277315.1	48.4	0.19	0.53	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.87
GCA_024278375.1	48.1	0.19	0.48	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.6
GCA_002494765.1	48.2	0.27	0.42	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.53
GCA_002495235.1	53.2	0.23	0.60	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.03
GCA_011620765.1	44.3	0.24	0.47	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.82
GCA_001915065.1	53.3	0.46	0.34	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.92
GCA_001918745.1	51.8	0.46	0.31	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_001918765.1	51.9	0.48	0.31	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.88
GCA_001919285.1	52.1	0.46	0.33	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.23
GCA_002495485.1	54.1	0.47	0.36	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.28
GCA_005881615.1	51.9	0.46	0.33	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.41
GCA_005881695.1	52.2	0.45	0.32	0.22	0	0	0	0	0	0	0	0	0	1	0	0	0	0	88.79
GCA_005882895.1	52.0	0.48	0.32	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.55
GCA_005882905.1	53.4	0.47	0.35	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.69
GCA_005882955.1	51.9	0.42	0.35	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.43
GCA_005883075.1	52.0	0.45	0.31	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_005883085.1	52.0	0.46	0.32	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.05
GCA_005883695.1	52.0	0.46	0.32	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.43
GCA_005884195.1	51.9	0.47	0.30	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.51
GCA_005884605.1	51.8	0.44	0.32	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.29
GCA_005888635.1	52.0	0.44	0.35	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.15
GCA_005888745.1	51.7	0.44	0.33	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_005888755.1	52.0	0.46	0.31	0.23	0	0	0	0	0	0	0	0	0	1	0	0	0	0	93.46
GCA_021323395.1	51.9	0.46	0.33	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.06
GCA_005888675.1	50.7	0.43	0.31	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_005888695.1	50.8	0.42	0.33	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_005888735.1	53.1	0.46	0.34	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.86
GCA_018396775.1	32.5	0.10	0.18	0.72	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_018396815.1	30.9	0.10	0.20	0.71	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_018396725.1	52.8	0.29	0.36	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_001768965.1	50.8	0.37	0.40	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.26
GCA_003152955.1	50.0	0.32	0.44	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.38
GCA_023247835.1	51.1	0.36	0.38	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.01
GCA_022865625.1	52.5	0.43	0.44	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.63
GCA_022865705.1	49.1	0.43	0.41	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.72
GCA_018396565.1	46.0	0.26	0.44	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.55
GCA_018396915.1	45.5	0.25	0.46	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_018397035.1	51.9	0.41	0.45	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.24
GCA_001775955.1	37.7	0.23	0.31	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_007050885.1	41.8	0.26	0.32	0.42	0	0	0	0	0	0	0	0	0	2	0	0	0	0	91.98
GCA_023144075.1	37.4	0.25	0.33	0.42	0	0	0	0	0	0	0	0	0	1	0	0	0	0	77.88
GCA_001593865.1	51.1	0.38	0.27	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_021161255.1	50.0	0.38	0.27	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_018396755.1	41.4	0.30	0.27	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_018396535.1	41.0	0.49	0.22	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.93
GCA_025058595.1	44.0	0.49	0.22	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_018396395.1	47.4	0.37	0.26	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.6
GCA_001593855.1	50.5	0.27	0.29	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_003662305.1	50.9	0.27	0.29	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.45
GCA_003662485.1	51.9	0.32	0.25	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.75
GCA_003662515.1	51.2	0.24	0.30	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_002254975.1	33.1	0.20	0.13	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	58.41
GCA_003661965.1	39.1	0.34	0.16	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_002011035.1	51.9	0.27	0.36	0.37	0	1	2	1	1	1	0	0	1	1	0	0	0	0	100
GCA_002490245.1	47.4	0.26	0.28	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.88
GCA_003662645.1	51.1	0.29	0.37	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.63
GCA_001593925.1	52.7	0.27	0.38	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_001593935.1	51.9	0.28	0.37	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_001593845.1	53.9	0.28	0.42	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.81
GCA_003601695.1	42.7	0.29	0.27	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.57
GCA_003601725.1	44.8	0.25	0.34	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.96
GCA_003661975.1	45.6	0.29	0.33	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_021158305.1	43.5	0.29	0.28	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.52
GCA_021162225.1	44.2	0.29	0.31	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.31
GCA_018396405.1	42.7	0.28	0.24	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.79
GCA_018396435.1	42.8	0.26	0.28	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_018396555.1	42.9	0.27	0.29	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.92
GCA_018396635.1	44.5	0.30	0.25	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_018396655.1	43.5	0.31	0.24	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_018396795.1	41.2	0.25	0.27	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.45
GCA_018396975.1	46.0	0.38	0.21	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_018396995.1	43.6	0.30	0.24	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_025059045.1	44.8	0.30	0.33	0.37	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.13
GCA_003601835.1	46.8	0.28	0.32	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.19
GCA_018397055.1	42.3	0.25	0.27	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_018397065.1	41.4	0.22	0.26	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.43
GCA_015520475.1	44.1	0.25	0.33	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_003662715.1	41.6	0.25	0.29	0.46	0	0	1	1	0	0	0	1	1	1	0	0	0	0	75.68
GCA_001399805.1	47.1	0.28	0.32	0.40	0	0	0	0	0	0	0	0	0	0	1	1	1	0	91.59
GCA_001399795.1	44.2	0.27	0.32	0.41	0	0	0	0	0	0	0	0	0	1	1	1	1	1	93.77
GCA_003096235.1	41.7	0.24	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.47
GCA_003096255.1	43.5	0.26	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.03
GCA_004376385.1	43.3	0.26	0.28	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.84
GCA_016930555.1	42.8	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.53
GCA_020344315.1	43.9	0.28	0.30	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.87
GCA_024650005.1	38.1	0.19	0.23	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.29
GCA_020344715.1	46.3	0.37	0.38	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.05
GCA_020344435.1	47.8	0.36	0.40	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.7
GCA_020348365.1	47.6	0.34	0.38	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.23
GCA_020348945.1	43.7	0.26	0.34	0.40	0	0	0	1	0	0	0	1	1	0	0	0	0	0	83.18
GCA_020356305.1	46.1	0.34	0.35	0.31	0	0	0	1	1	0	0	0	1	1	0	0	0	0	76.18
GCA_023136395.1	39.3	0.22	0.25	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_014859755.1	45.2	0.29	0.33	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.34
GCA_020346825.1	44.3	0.35	0.33	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.06
GCA_004376295.1	43.2	0.29	0.33	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.82
GCA_020348865.1	45.5	0.39	0.37	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.32
GCA_020350305.1	43.9	0.31	0.32	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.26
GCA_020352535.1	47.1	0.41	0.34	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.27
GCA_020341775.1	45.9	0.34	0.34	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.82
GCA_020351305.1	41.6	0.30	0.31	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.03
GCA_020352645.1	45.6	0.36	0.38	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_020354575.1	41.6	0.31	0.30	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_019685575.1	45.6	0.26	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_020345645.1	47.4	0.29	0.36	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.75
GCA_023131555.1	47.0	0.30	0.41	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.29
GCA_023131225.1	42.6	0.31	0.27	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_004376645.1	44.6	0.35	0.31	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.69
GCA_002779555.1	47.4	0.34	0.34	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.31
GCA_022865455.1	47.2	0.35	0.36	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_018475625.1	47.7	0.23	0.31	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_001273385.1	32.4	0.21	0.19	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.79
GCA_016649625.1	33.9	0.21	0.21	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.11
GCA_022865885.1	46.0	0.35	0.38	0.28	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.07
GCA_018396705.1	43.2	0.27	0.24	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_018396875.1	46.0	0.32	0.25	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.39
GCA_025059195.1	45.8	0.27	0.26	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_025058315.1	44.8	0.32	0.28	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_019685655.1	41.8	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_023512225.1	42.2	0.24	0.29	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_018396935.1	41.7	0.25	0.28	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_020350385.1	44.2	0.27	0.28	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.78
GCA_019685555.1	43.6	0.27	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6
GCA_013388895.1	42.1	0.31	0.25	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_013388905.1	40.7	0.26	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_017883615.1	46.6	0.25	0.20	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.23
GCA_018396955.1	43.9	0.27	0.24	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_018396615.1	45.1	0.35	0.28	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.2
GCA_018396675.1	42.9	0.25	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.79
GCA_025057795.1	45.4	0.28	0.27	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_002010975.1	38.7	0.25	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.49
GCA_003601605.1	40.8	0.28	0.23	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.25
GCA_003133625.1	42.8	0.21	0.24	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_003141855.1	44.3	0.21	0.21	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_003151735.1	42.3	0.22	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_003164295.1	40.3	0.20	0.22	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6
GCA_003165195.1	42.9	0.23	0.24	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.72
GCA_003589585.1	44.9	0.25	0.20	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.79
GCA_009776805.1	35.6	0.18	0.20	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_009778385.1	39.3	0.17	0.19	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_009779045.1	38.1	0.16	0.16	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.19
GCA_009781395.1	39.0	0.16	0.16	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.26
GCA_009781675.1	43.4	0.23	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_009783705.1	43.3	0.21	0.20	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.6

GCA_009787175.1	38.9	0.20	0.18	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_009787585.1	37.8	0.18	0.17	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_012511995.1	39.9	0.22	0.21	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.92
GCA_012513715.1	37.7	0.21	0.20	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.55
GCA_012515445.1	47.0	0.26	0.16	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.2
GCA_023488835.1	44.5	0.23	0.20	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.93
GCA_023488905.1	47.5	0.26	0.20	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.53
GCA_903901015.1	45.8	0.22	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_003601785.1	43.5	0.24	0.29	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.44
GCA_003601875.1	37.3	0.17	0.24	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.87
GCA_001273335.1	44.0	0.24	0.33	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.54
GCA_007050895.1	43.3	0.25	0.29	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.33
GCA_016927015.1	45.9	0.25	0.28	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_016927895.1	45.2	0.23	0.27	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_004376975.1	41.9	0.29	0.31	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.88
GCA_014859805.1	42.1	0.27	0.31	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.51
GCA_013330975.1	45.2	0.37	0.36	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.35
GCA_002010925.1	41.9	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.28
GCA_002507245.1	40.9	0.25	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.35
GCA_003661945.1	46.7	0.29	0.26	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_009889605.1	42.2	0.25	0.27	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.13
GCA_021158125.1	40.3	0.27	0.22	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCA_009889585.1	47.4	0.22	0.33	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.88
GCA_003662535.1	54.0	0.37	0.30	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.25
GCA_002255025.1	58.8	0.23	0.54	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.83
GCA_011040545.1	54.9	0.49	0.28	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.71
GCA_020345945.1	45.7	0.36	0.35	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.66
GCA_020355125.1	40.2	0.26	0.23	0.51	0	0	0	1	0	1	0	0	1	1	0	0	0	0	84.84
GCA_023128135.1	38.2	0.21	0.31	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_018396415.1	42.8	0.26	0.28	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_001775995.1	48.1	0.35	0.39	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.11
GCA_001593875.1	61.8	0.34	0.45	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.9
GCA_021161045.1	55.8	0.32	0.39	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.19
GCA_003601775.1	58.4	0.30	0.42	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.42
GCA_003662205.1	62.9	0.41	0.43	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.86
GCA_016783455.1	57.5	0.39	0.39	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_020346605.1	58.1	0.39	0.43	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.44
GCA_020354065.1	57.0	0.37	0.44	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.39
GCA_002726865.1	48.4	0.30	0.35	0.36	0	0	0	0	0	0	0	0	0	1	0	0	0	0	92.99
GCA_016783485.1	58.2	0.37	0.43	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.9
GCA_018396695.1	43.3	0.27	0.33	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.99
GCA_018396515.1	52.3	0.31	0.37	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.56
GCA_018396865.1	50.8	0.29	0.36	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.86
GCA_001775965.1	61.2	0.46	0.34	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.13
GCA_013619005.1	53.8	0.39	0.22	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.64
GCA_014729945.1	43.3	0.28	0.18	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.85
GCA_014730055.1	41.9	0.27	0.22	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_016934355.1	57.5	0.45	0.28	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.51
GCA_018652685.1	51.4	0.37	0.21	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.12
GCA_020444005.1	45.9	0.33	0.20	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.5
GCA_020697635.1	59.3	0.45	0.29	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.99
GCA_001774245.1	51.8	0.36	0.29	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.58
GCA_016867505.1	35.7	0.15	0.20	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.96
GCA_016930055.1	32.9	0.13	0.19	0.68	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.41
GCA_017883585.1	56.9	0.39	0.30	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.58
GCA_013329615.1	58.9	0.42	0.28	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.6
GCA_011041895.1	40.9	0.29	0.26	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.58
GCA_017601265.1	58.3	0.34	0.46	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.47
GCA_002255045.1	42.1	0.27	0.36	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.75
GCA_011605715.1	36.2	0.27	0.23	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.89
GCA_017601145.1	34.7	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.35
GCA_017601245.1	41.5	0.29	0.30	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCA_011605725.1	46.4	0.33	0.32	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.26
GCA_017601225.1	47.5	0.34	0.32	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.38
GCA_017601345.1	43.2	0.29	0.30	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.26
GCA_017601395.1	47.5	0.32	0.35	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_025059435.1	41.5	0.26	0.31	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.19
GCA_021163045.1	35.1	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.66
GCA_024720975.1	40.2	0.34	0.29	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.21
GCA_003661385.1	52.8	0.49	0.32	0.18	0	0	0	0	0	0	0	0	0	1	0	0	0	0	90.65
GCA_011042755.1	57.1	0.28	0.57	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.51
GCF_000019605.1	49.0	0.19	0.55	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.39
GCA_003344655.1	56.7	0.23	0.64	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.25
GCA_020833055.1	48.6	0.18	0.56	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.45
GCA_023269865.1	44.1	0.19	0.51	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.24
GCF_003947435.1	42.9	0.20	0.48	0.32	0	0	0	0	0	0	0	0	0	0	1	1	1	1	93.93
GCA_015521385.1	56.9	0.23	0.63	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.65
GCA_015522685.1	41.8	0.23	0.41	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.45
GCA_021158805.1	45.1	0.31	0.37	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.3
GCA_003661265.1	46.9	0.28	0.39	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.72
GCA_003661365.1	43.6	0.27	0.39	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.75
GCA_003649185.1	37.2	0.20	0.32	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.24
GCA_003649145.1	43.6	0.32	0.31	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.6
GCA_003650625.1	44.5	0.30	0.37	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.96
GCA_025061245.1	35.4	0.24	0.25	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_011605825.1	36.7	0.21	0.32	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.7
GCA_020833005.1	38.1	0.20	0.32	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.66
GCA_025058215.1	31.7	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.18
GCA_025060975.1	36.7	0.21	0.33	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.73
GCA_003649085.1	42.7	0.28	0.29	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.42
GCA_021160575.1	50.7	0.46	0.31	0.23	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.12
GCA_015660995.1	49.9	0.28	0.42	0.30	0	0	0	0	0	0	0	0	0	0	1	1	1	1	100
GCA_025057955.1	34.3	0.20	0.34	0.46	0	0	1	0	0	0	0	0	0	0	2	2	2	1	100
GCA_001717005.1	58.2	0.24	0.57	0.18	0	1	0	1	1	1	1	0	1	1	0	1	1	1	90.34
GCA_001717025.1	55.4	0.24	0.57	0.19	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.07
GCA_024464205.1	53.4	0.20	0.59	0.21	0	0	0	0	0	0	0	0	0	0	1	2	2	1	90.98
GCA_001717015.1	55.8	0.24	0.56	0.20	0	0	0	0	0	0	0	0	0	0	1	1	1	1	91.59
GCA_014361455.1	53.7	0.24	0.53	0.24	0	0	0	0	0	0	0	0	0	0	2	2	2	1	92.52
GCA_004028775.1	54.5	0.23	0.58	0.18	0	0	1	0	0	0	0	0	0	0	1	1	1	1	100
GCA_016882195.1	54.3	0.28	0.44	0.28	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.07
GCA_004347955.1	50.3	0.26	0.51	0.23	0	0	0	0	0	0	0	0	0	0	1	1	1	1	90.19
GCA_014361445.1	46.9	0.21	0.45	0.34	0	0	0	0	0	0	0	0	0	0	1	1	1	1	99.07
GCA_004348015.1	28.5	0.16	0.28	0.56	0	0	1	0	0	0	0	0	0	0	1	1	1	1	98.13
GCA_020832905.1	27.4	0.13	0.25	0.61	0	0	1	0	0	0	0	0	0	0	1	1	1	1	100
GCA_003649615.1	49.1	0.31	0.30	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.46
GCA_003649565.1	42.2	0.25	0.30	0.46	0	0	0	0	0	0	0	0	0	0	1	0	0	1	76.84
GCA_003650865.1	51.4	0.37	0.32	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	1	89.71
GCA_004347965.1	43.5	0.29	0.30	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	97.18
GCA_011605835.1	54.5	0.29	0.42	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.6
GCA_025059375.1	44.5	0.26	0.33	0.42	0	0	0	0	0	0	0	0	0	0	1	1	1	1	98.53
GCA_025054515.1	52.4	0.27	0.42	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.86
GCA_025054795.1	53.2	0.35	0.40	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.39
GCA_025058435.1	52.9	0.23	0.46	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.39
GCA_000270325.1	51.6	0.30	0.38	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_002898355.1	52.6	0.41	0.35	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_015661775.1	48.5	0.32	0.24	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCA_015520425.1	51.1	0.39	0.26	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.66
GCA_000494185.1	54.9	0.43	0.32	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.87
GCA_002898395.1	51.4	0.39	0.33	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_009889515.1	52.3	0.37	0.33	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_025059595.1	53.7	0.36	0.36	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_025059745.1	54.0	0.28	0.51	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.75
GCA_000494145.1	61.4	0.17	0.74	0.09	0	0	0	0	0	0	0	0	0	1	0	0	0	0	82.65
GCA_025058055.1	57.0	0.20	0.67	0.13	0	0	0	0	0	0	0	0	0	1	0	0	0	0	87.3
GCA_025058175.1	61.8	0.18	0.71	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.14
GCA_025058225.1	58.9	0.19	0.68	0.12	0	0	0	0	0	0	0	0	0	1	0	0	0	0	79.29
GCA_021650775.1	54.8	0.36	0.33	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.01
GCA_023539395.1	38.4	0.34	0.24	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_023267855.1	37.5	0.31	0.23	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_023268155.1	40.7	0.34	0.27	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_000405685.1	37.9	0.31	0.25	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.55
GCA_023269855.1	38.6	0.29	0.27	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_025058515.1	37.8	0.30	0.24	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_023267975.1	47.5	0.29	0.32	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_025059205.1	45.3	0.25	0.32	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_023268355.1	45.0	0.27	0.31	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_003056285.1	51.3	0.34	0.37	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_023539445.1	46.2	0.26	0.34	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_023539495.1	51.7	0.33	0.36	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCA_021322375.2	52.0	0.36	0.33	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_023268255.1	53.7	0.34	0.35	0.30	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.06
GCA_002255105.1	51.5	0.29	0.41	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.28
GCA_003660635.1	47.4	0.23	0.36	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.02

GCA_021157985.1	53.8	0.25	0.37	0.37	0	0	0	0	0	0	0	0	0	1	0	0	0	0	69.66
GCA_021159365.1	45.5	0.24	0.36	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.15
GCA_021160205.1	48.5	0.24	0.37	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.22
GCA_021163925.1	49.8	0.26	0.41	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.54
GCA_025059415.1	51.2	0.26	0.39	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.78
GCF_013340765.1	62.1	0.25	0.65	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_009903775.1	66.8	0.38	0.49	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.26
GCA_023256385.1	59.6	0.26	0.63	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.65
GCA_015522695.1	54.5	0.37	0.43	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.63
GCA_021324115.1	49.2	0.22	0.53	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.63
GCA_021811935.1	63.7	0.35	0.56	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.04
GCA_021792955.1	47.6	0.27	0.41	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.24
GCA_021798095.1	47.5	0.27	0.40	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.67
GCA_002499005.1	49.0	0.25	0.39	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.14
GCA_002506605.1	36.7	0.15	0.33	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.74
GCA_009903795.1	37.8	0.15	0.36	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89
GCA_023256355.1	39.2	0.14	0.38	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.35
GCA_023256405.1	48.5	0.22	0.44	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.67
GCA_023381255.1	44.4	0.17	0.44	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.08
GCA_011043415.1	37.2	0.30	0.25	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_002011075.1	37.6	0.31	0.24	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_002011085.1	42.0	0.39	0.23	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCA_015523545.1	51.3	0.56	0.29	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.72
GCA_015523605.1	40.3	0.39	0.24	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.26
GCA_015661745.1	36.4	0.34	0.25	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.35
GCA_015522055.1	44.0	0.39	0.26	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.9
GCA_015523725.1	38.0	0.27	0.27	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.99
GCA_014361085.1	36.6	0.28	0.24	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_021162925.1	58.0	0.35	0.43	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.46
GCA_013288145.1	46.7	0.35	0.36	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.14
GCA_021325255.1	49.7	0.34	0.43	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.73
GCA_021792315.1	45.9	0.35	0.42	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.82
GCA_021806865.1	47.6	0.35	0.44	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.82
GCA_902812485.1	46.1	0.31	0.46	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_011605775.1	47.2	0.35	0.29	0.37	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.51
GCA_024256165.1	36.6	0.17	0.29	0.54	0	0	0	1	1	1	0	1	1	2	1	1	1	0	94.42
GCA_024256245.1	40.7	0.18	0.34	0.47	0	0	0	1	1	1	0	1	1	2	1	2	1	0	95.63
GCA_024256285.1	43.0	0.17	0.39	0.44	0	0	0	1	1	1	0	1	1	2	1	1	1	1	93.69
GCA_013388925.1	45.0	0.29	0.38	0.33	0	0	0	0	0	0	0	0	0	1	0	0	0	0	92.23
GCA_024256265.1	38.7	0.19	0.34	0.47	0	0	0	1	1	1	0	1	1	1	1	1	1	1	99.51
GCA_025058425.1	41.9	0.21	0.36	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_016190055.1	48.7	0.33	0.24	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.66
GCA_023379805.1	48.6	0.33	0.24	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_016184315.1	49.3	0.38	0.33	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_016206275.1	48.5	0.39	0.32	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.1
GCA_023266955.1	48.5	0.39	0.33	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.25
GCF_900248165.1	41.6	0.29	0.35	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_013538805.1	42.0	0.29	0.34	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_002898655.1	41.8	0.27	0.38	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.5
GCA_025054855.1	49.3	0.33	0.47	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_013538675.1	42.8	0.31	0.36	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.91
GCA_013538715.1	31.9	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.57
GCA_003724275.1	66.6	0.57	0.35	0.08	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.41
GCA_007570915.1	69.1	0.58	0.35	0.07	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.26
GCA_020027325.1	54.8	0.48	0.36	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.72
GCA_000200715.1	57.4	0.44	0.39	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_001443365.1	34.4	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_008974855.1	33.2	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.64
GCA_016276965.1	34.0	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.23
GCA_022573065.1	33.0	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.33
GCA_011055585.1	34.2	0.26	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.1
GCA_016838795.1	34.9	0.25	0.26	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.69
GCA_016838845.1	35.0	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_022564515.1	34.3	0.24	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_022574415.1	34.9	0.24	0.26	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.64
GCA_011773785.1	34.8	0.29	0.21	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_013867335.1	34.9	0.29	0.22	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.63
GCA_022562615.1	34.2	0.27	0.21	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.83
GCA_024644385.1	33.9	0.24	0.18	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.69
GCA_016200035.1	38.3	0.29	0.26	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.2
GCA_016838825.1	35.8	0.27	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_020027365.1	59.6	0.37	0.47	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.97
GCA_002781985.1	37.1	0.31	0.27	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.81
GCF_018128925.1	34.9	0.29	0.23	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_020431985.1	37.0	0.27	0.29	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCF_000220175.1	32.7	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_000204585.1	32.5	0.25	0.22	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_002737445.1	31.0	0.25	0.18	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_003569705.1	33.0	0.28	0.20	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_004297665.1	33.0	0.24	0.25	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.13
GCA_005798405.1	33.4	0.28	0.21	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_009697485.1	33.3	0.27	0.22	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.96
GCA_012030815.1	33.4	0.28	0.26	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.08
GCA_013140415.1	33.2	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.63
GCA_016234975.1	33.6	0.26	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.42
GCA_016844465.1	33.3	0.26	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.92
GCA_018334095.1	32.5	0.25	0.21	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_021414105.1	33.1	0.27	0.21	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.42
GCA_021414365.1	33.1	0.24	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_022758935.1	33.2	0.25	0.24	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.6
GCA_023264875.1	33.0	0.27	0.20	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_023265135.1	33.2	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCF_000812185.1	33.2	0.25	0.18	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_000402075.1	35.7	0.26	0.22	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.33
GCA_013390375.1	36.1	0.26	0.22	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.76
GCA_000746705.1	34.7	0.25	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.47
GCA_001510295.1	32.5	0.23	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.58
GCA_001627235.1	34.1	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.64
GCA_002698885.1	32.6	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.93
GCA_012964965.1	34.8	0.26	0.24	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.34
GCA_013390745.1	35.5	0.27	0.22	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.37
GCA_013390765.1	34.6	0.25	0.24	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.83
GCA_013390785.1	35.2	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.11
GCA_018263495.1	35.7	0.27	0.22	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.2
GCA_018647405.1	32.7	0.23	0.19	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.15
GCA_018691945.1	33.1	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.86
GCA_022450565.1	33.7	0.27	0.19	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.57
GCA_902511735.1	32.6	0.25	0.19	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.28
GCA_902512865.1	33.1	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.91
GCA_902552015.1	33.6	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.55
GCA_902566725.1	33.9	0.23	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.94
GCA_902578515.1	35.1	0.25	0.24	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.73
GCA_902590655.1	35.5	0.26	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.38
GCA_902606965.1	35.4	0.27	0.24	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.68
GCA_902608175.1	32.9	0.23	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	70.36
GCF_000956175.1	33.4	0.25	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002156965.1	31.4	0.22	0.18	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_013407145.1	33.0	0.26	0.20	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCF_000299365.1	34.2	0.26	0.24	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.66
GCA_022117465.1	30.4	0.22	0.17	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCF_000018465.1	34.2	0.27	0.23	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_013407165.1	33.1	0.26	0.19	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCF_000875775.1	33.8	0.26	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000242875.2	33.8	0.23	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.39
GCF_000299395.1	33.6	0.25	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_000746765.1	34.3	0.28	0.22	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.89
GCA_001437625.1	31.0	0.22	0.17	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_001510275.1	32.8	0.26	0.19	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCF_001541925.1	31.4	0.21	0.20	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_001543015.1	31.6	0.23	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002317795.1	31.4	0.23	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.85
GCA_002506665.1	41.2	0.34	0.30	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCA_003331425.1	31.2	0.22	0.17	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002730325.1	31.7	0.22	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.83
GCA_002788515.1	33.7	0.25	0.24	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.1
GCA_003702465.1	30.9	0.21	0.19	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_003702495.1	34.5	0.29	0.22	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95
GCA_003702525.1	34.5	0.30	0.21	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.72
GCA_003702545.1	34.9	0.31	0.22	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.26
GCA_003724285.1	53.0	0.42	0.38	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.81
GCA_003724325.1	47.9	0.40	0.36	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCF_006740685.1	33.8	0.28	0.21	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_007571135.1	41.9	0.29	0.33	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.35

GCA_007571225.1	49.9	0.31	0.42	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.02
GCA_008080815.1	32.6	0.27	0.21	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_013002265.1	33.9	0.27	0.23	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.47
GCA_013043295.1	33.3	0.27	0.20	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.34
GCA_013203245.1	33.7	0.24	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89
GCA_013215285.1	32.0	0.23	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_013390905.1	33.2	0.27	0.21	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_013867245.1	32.7	0.26	0.19	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_013911135.1	33.3	0.25	0.24	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.57
GCA_014075315.1	36.9	0.30	0.32	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCF_014078525.1	33.4	0.25	0.24	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_014384445.1	32.0	0.23	0.22	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.18
GCA_014384555.1	33.3	0.28	0.21	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.69
GCA_016125975.1	33.6	0.27	0.24	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_016784625.1	32.2	0.25	0.22	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	52.43
GCA_018263505.1	31.2	0.21	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.15
GCA_018657375.1	32.9	0.25	0.20	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.58
GCA_018668425.1	31.8	0.24	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.78
GCA_018674605.1	30.6	0.20	0.19	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.93
GCA_020431995.1	37.8	0.28	0.32	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.15
GCA_021268355.1	34.2	0.29	0.24	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_021296175.1	59.7	0.30	0.56	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCA_022564385.1	32.2	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.87
GCA_022565935.1	32.3	0.25	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.69
GCA_022573895.1	33.2	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_022823825.1	59.8	0.30	0.56	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.15
GCA_024276695.1	32.9	0.26	0.23	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_024644105.1	33.2	0.28	0.18	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_900620265.1	64.8	0.44	0.45	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_902514095.1	30.4	0.22	0.15	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.13
GCA_902514275.1	31.0	0.22	0.18	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.02
GCA_905479565.1	33.6	0.26	0.22	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.63
GCA_905612275.1	30.7	0.22	0.18	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	55.34
GCA_905612295.1	31.4	0.22	0.17	0.61	0	0	0	0	0	0	0	0	0	0	0	0	0	0	67.8
GCA_905612485.1	30.4	0.21	0.17	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.43
GCA_905616385.1	31.2	0.24	0.17	0.59	0	0	0	0	0	0	0	0	0	0	0	0	0	0	65.62
GCF_013407185.1	33.4	0.25	0.26	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_003175215.1	33.8	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_900167955.1	36.0	0.31	0.23	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.57
GCA_900065925.1	37.1	0.31	0.24	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCF_900177045.1	37.5	0.31	0.29	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCF_900143675.1	37.4	0.31	0.26	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_001917995.1	38.2	0.30	0.27	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.91
GCA_001920395.1	39.1	0.32	0.29	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.29
GCA_005877205.1	38.7	0.30	0.28	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.5
GCA_007280465.1	36.1	0.30	0.23	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.27
GCF_011319465.1	40.1	0.30	0.36	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.55
GCF_011319475.1	38.8	0.31	0.30	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.03
GCA_013288545.1	37.8	0.31	0.26	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.89
GCA_021323705.1	40.3	0.35	0.28	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_021325595.1	36.3	0.30	0.25	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_021325615.1	49.6	0.45	0.31	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.26
GCA_022545805.1	37.9	0.32	0.28	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.07
GCA_023252235.1	36.1	0.31	0.23	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.65
GCA_023252335.1	37.9	0.33	0.28	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCF_002787055.1	42.2	0.39	0.23	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.68
GCF_000685395.1	41.8	0.32	0.27	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCF_000955905.1	41.0	0.36	0.24	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002499525.1	38.2	0.33	0.24	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.91
GCA_004322465.1	42.6	0.33	0.28	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.76
GCA_005240025.1	44.3	0.31	0.32	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.91
GCA_010028495.1	40.1	0.33	0.25	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCF_013407275.1	41.3	0.32	0.26	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_016215465.1	39.9	0.30	0.26	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.85
GCA_016844685.1	38.5	0.31	0.27	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.85
GCA_016872015.1	41.3	0.39	0.22	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.01
GCA_016872055.1	41.3	0.36	0.22	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.71
GCA_021824845.1	41.3	0.34	0.26	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.76
GCA_023252015.1	39.4	0.31	0.26	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.72
GCA_900299125.1	36.4	0.31	0.24	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCF_000723185.1	42.2	0.36	0.27	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_003352285.1	35.5	0.30	0.20	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCF_014078545.1	35.8	0.29	0.21	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_005877305.1	35.7	0.27	0.23	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.64
GCA_007280335.1	35.5	0.26	0.21	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCA_013287585.1	35.4	0.27	0.23	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.61
GCA_016201435.1	35.5	0.27	0.24	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.61
GCA_023251295.1	35.4	0.26	0.26	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.05
GCA_023251795.1	37.6	0.21	0.27	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.85
GCA_013330055.1	35.9	0.25	0.27	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.6
GCA_016176745.1	36.1	0.30	0.24	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.44
GCA_016871975.1	37.0	0.33	0.21	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.13
GCA_009840065.1	46.5	0.33	0.36	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.6
GCA_009843815.1	45.0	0.28	0.35	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_016126025.1	61.2	0.43	0.42	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.63
GCA_021296165.1	61.7	0.43	0.43	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.78
GCA_011523285.1	29.6	0.14	0.27	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_020027255.1	30.4	0.14	0.29	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.01
GCA_019246625.1	35.8	0.27	0.27	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_021155845.1	33.8	0.25	0.26	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.71
GCA_021325295.1	44.3	0.35	0.35	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCF_007826885.1	34.0	0.24	0.25	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCF_900696045.1	34.1	0.27	0.25	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCF_001870125.1	33.9	0.25	0.25	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCF_000802205.1	34.1	0.26	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCF_008389435.1	33.4	0.24	0.24	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_009379865.1	33.5	0.25	0.26	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.86
GCA_013114705.1	34.3	0.25	0.25	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.94
GCA_013694585.1	33.6	0.24	0.26	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCA_013821245.1	34.1	0.22	0.23	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_016782225.1	34.6	0.23	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_016782315.1	34.6	0.24	0.25	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.22
GCA_002501855.1	38.9	0.28	0.30	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.29
GCA_933226995.1	39.6	0.27	0.31	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.94
GCA_009665115.1	39.3	0.29	0.30	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.71
GCF_009898475.1	38.9	0.29	0.30	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.2
GCA_003176995.1	38.9	0.28	0.31	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCF_000730285.1	50.1	0.37	0.32	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000303155.1	48.3	0.36	0.32	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002494895.1	49.7	0.43	0.34	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.72
GCA_002501845.1	49.1	0.35	0.33	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.49
GCA_013114715.1	48.2	0.35	0.32	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.23
GCA_013388945.1	54.5	0.41	0.36	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_021325075.1	49.5	0.38	0.30	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.78
GCA_022545875.1	48.9	0.44	0.30	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.3
GCA_023250885.1	51.5	0.38	0.31	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_023252395.1	50.5	0.37	0.32	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.8
GCF_000698785.1	52.7	0.37	0.33	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_013114725.1	30.8	0.17	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.12
GCA_005877075.1	34.3	0.24	0.28	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_005877345.1	35.1	0.25	0.27	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.5
GCA_014381105.1	36.0	0.30	0.28	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.92
GCA_014523495.1	34.2	0.25	0.28	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.6
GCA_014523525.1	35.0	0.24	0.28	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCA_014523595.1	35.4	0.26	0.29	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.43
GCA_021324715.1	35.6	0.26	0.26	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.32
GCA_022545895.1	37.8	0.28	0.31	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.05
GCA_023251115.1	35.9	0.25	0.28	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.54
GCA_014523485.1	28.8	0.16	0.19	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.16
GCA_014523515.1	28.1	0.18	0.19	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.78
GCA_014523685.1	38.3	0.33	0.26	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.04
GCA_009377575.1	38.7	0.31	0.31	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_014523625.1	38.9	0.31	0.32	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.45
GCA_014523665.1	38.9	0.31	0.31	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.9
GCA_014523695.1	39.0	0.31	0.32	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.17
GCA_002495315.1	46.0	0.39	0.34	0.27	0	0	0	0	0	0	0	0	1	0	0	0	0	0	91.91
GCA_003135575.1	58.4	0.41	0.44	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.89
GCA_003164815.1	59.5	0.42	0.47	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.03
GCA_021791695.1	59.6	0.42	0.46	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.6
GCA_021848045.1	64.7	0.47	0.47	0.06	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.75
GCA_902812495.1	44.1	0.30	0.41	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_016193005.1	53.9	0.40	0.43	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.32
GCA_005877185.1	57.5	0.39	0.46	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.81

GCA_005877225.1	56.7	0.38	0.43	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.97
GCA_005877365.1	57.0	0.39	0.44	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.49
GCA_002495205.1	61.7	0.51	0.40	0.09	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.23
GCA_014874415.1	59.4	0.43	0.43	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.31
GCA_016200025.1	60.5	0.50	0.39	0.12	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.12
GCA_016200045.1	58.6	0.43	0.44	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.51
GCA_016432545.1	60.3	0.45	0.42	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.57
GCA_021786335.1	59.3	0.40	0.47	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.21
GCA_021786575.1	58.5	0.38	0.46	0.15	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.59
GCA_021788415.1	63.0	0.47	0.43	0.10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	58.41
GCA_021796515.1	62.3	0.43	0.46	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.37
GCA_021800855.1	60.7	0.42	0.45	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.07
GCA_021807225.1	61.1	0.49	0.40	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.97
GCA_021811485.1	62.2	0.47	0.43	0.10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	53.96
GCA_021819035.1	61.6	0.43	0.46	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.98
GCA_021819105.1	63.2	0.48	0.42	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.84
GCA_021822995.1	60.0	0.45	0.42	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.98
GCA_021823325.1	61.0	0.47	0.41	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.38
GCA_021827865.1	62.5	0.45	0.46	0.10	0	0	0	0	0	0	0	0	0	1	0	0	0	0	97.57
GCA_021828185.1	60.4	0.44	0.45	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.25
GCA_021851265.1	60.5	0.42	0.47	0.11	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.61
GCA_002713325.1	36.1	0.22	0.28	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.33
GCA_022572285.1	46.3	0.36	0.35	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.61
GCA_016180375.1	45.8	0.38	0.29	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.83
GCA_013306035.1	32.6	0.24	0.22	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_002495905.1	32.0	0.23	0.21	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.08
GCA_002693165.1	32.0	0.19	0.22	0.58	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.3
GCA_002713205.1	31.1	0.17	0.19	0.64	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.07
GCA_013378385.1	34.0	0.23	0.25	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.09
GCA_022449325.1	33.3	0.24	0.21	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.86
GCA_016871995.1	44.9	0.37	0.28	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.06
GCA_024860875.1	45.2	0.37	0.28	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.29
GCA_003661605.2	50.8	0.46	0.25	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.1
GCA_021158265.1	38.2	0.31	0.21	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.62
GCA_002254745.1	37.2	0.31	0.19	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.57
GCA_015661855.1	36.5	0.34	0.16	0.50	0	0	0	0	0	0	0	0	0	1	0	0	0	0	88.53
GCA_003019595.1	43.8	0.23	0.37	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.59
GCA_003019535.1	49.8	0.34	0.36	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.07
GCA_902812505.1	49.1	0.35	0.35	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.59
GCA_021800035.1	51.6	0.35	0.45	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.22
GCA_021817005.1	51.6	0.35	0.45	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.49
GCA_023487445.1	53.1	0.37	0.43	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.65
GCA_002507085.1	53.4	0.21	0.51	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.4
GCA_011055275.1	51.0	0.26	0.46	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.83
GCA_023256295.1	54.3	0.26	0.57	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.98
GCA_023256375.1	44.1	0.19	0.38	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	69.16
GCF_000144915.1	57.2	0.22	0.51	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCA_000495735.1	59.2	0.29	0.47	0.24	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.05
GCA_002496425.1	56.2	0.27	0.50	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.08
GCF_003431325.1	57.8	0.26	0.49	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000591035.1	56.7	0.54	0.23	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.15
GCF_000011125.1	56.3	0.54	0.23	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.78
GCA_015521685.1	53.2	0.49	0.27	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.99
GCA_015523465.1	53.0	0.48	0.24	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.79
GCF_000317795.1	30.0	0.13	0.20	0.67	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCA_002506595.1	29.6	0.13	0.21	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.75
GCA_002877855.1	31.0	0.16	0.23	0.60	0	0	0	0	0	0	0	0	0	0	0	0	0	0	71.31
GCA_015522625.1	40.9	0.34	0.27	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93
GCA_015523575.1	39.9	0.34	0.25	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.25
GCA_023256325.1	30.9	0.14	0.23	0.63	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.84
GCA_020833325.1	47.8	0.43	0.25	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.31
GCA_025058835.1	57.3	0.39	0.38	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.78
GCA_013152575.1	49.8	0.39	0.23	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.33
GCA_015521085.1	54.2	0.52	0.23	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.47
GCA_015521175.1	53.7	0.48	0.20	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.93
GCA_015523485.1	48.2	0.38	0.23	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.96
GCA_015523445.1	54.5	0.56	0.21	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.62
GCA_015521705.1	52.3	0.47	0.28	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.77
GCA_015521205.1	45.9	0.29	0.25	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.57
GCA_015521095.1	44.3	0.40	0.20	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.3
GCA_015521115.1	53.3	0.44	0.23	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCA_015521185.1	57.2	0.54	0.24	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	72.57
GCA_015522635.1	41.6	0.26	0.28	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1
GCA_015522645.1	43.2	0.28	0.31	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1
GCA_015520195.1	44.6	0.35	0.25	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	57.28
GCA_003116855.1	45.6	0.45	0.28	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1
GCA_015521765.1	44.9	0.52	0.25	0.23	0	0	0	0	0	0	0	0	0	1	0	0	0	0	74.16
GCA_009903825.1	36.1	0.20	0.40	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.51
GCF_000513855.1	45.2	0.38	0.29	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000186365.1	53.1	0.44	0.36	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_002254665.1	34.4	0.32	0.19	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.81
GCA_013154205.1	43.5	0.31	0.27	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.48
GCA_015520735.1	43.9	0.29	0.29	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.26
GCA_021163115.1	38.5	0.35	0.19	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	68.99
GCA_021157925.1	36.2	0.22	0.24	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.64
GCA_021159785.1	36.5	0.23	0.28	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.73
GCA_025059075.1	40.7	0.31	0.27	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.84
GCA_003661825.1	43.6	0.51	0.19	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.96
GCF_000092465.1	36.8	0.26	0.21	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCF_000015945.1	35.7	0.24	0.22	0.53	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.73
GCF_000264495.1	55.6	0.43	0.38	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_009904025.1	50.2	0.37	0.36	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.44
GCA_022759365.1	51.9	0.39	0.37	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.84
GCA_023256015.1	57.0	0.45	0.39	0.16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.23
GCF_000092185.1	46.7	0.32	0.33	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCF_014962245.1	47.6	0.34	0.32	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCA_002495025.1	38.8	0.45	0.19	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.42
GCA_020832865.1	43.2	0.42	0.22	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.11
GCA_020833085.1	49.2	0.52	0.26	0.22	0	0	0	0	0	0	0	0	0	0	0	0	0	0	54.75
GCA_020833225.1	36.9	0.29	0.21	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.42
GCA_020833245.1	45.6	0.48	0.21	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.92
GCA_020833525.1	43.1	0.47	0.24	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	84.62
GCA_023269765.1	47.2	0.40	0.26	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.6
GCA_023269825.1	40.7	0.31	0.29	0.40	0	0	0	0	0	0	0	0	0	2	0	0	0	0	95.57
GCA_015522345.1	35.7	0.35	0.18	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.56
GCA_015521265.1	42.5	0.31	0.22	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.19
GCA_002899805.1	43.8	0.24	0.51	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.94
GCA_022759165.1	43.8	0.19	0.46	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.51
GCF_000258425.1	37.5	0.17	0.34	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.53
GCA_009904015.1	44.5	0.30	0.32	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.93
GCF_000017945.1	56.5	0.22	0.48	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCF_001481685.1	44.9	0.22	0.34	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCA_013154085.1	58.2	0.27	0.52	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.35
GCA_015521275.1	50.1	0.21	0.40	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	60.79
GCA_003661905.1	35.9	0.26	0.26	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.83
GCA_000145985.1	35.7	0.44	0.22	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_020832925.1	37.8	0.39	0.23	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.89
GCA_020833345.1	40.2	0.30	0.27	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.77
GCA_023269755.1	35.7	0.33	0.25	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.61
GCA_025058535.1	42.5	0.49	0.24	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.31
GCA_013154235.1	52.9	0.51	0.30	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	77.74
GCA_003661775.1	46.3	0.35	0.34	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	66.36
GCA_003661865.1	56.1	0.48	0.35	0.18	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.76
GCA_015662595.1	45.4	0.42	0.30	0.28	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.46
GCA_003661745.1	44.1	0.33	0.27	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.54
GCA_021158735.1	45.1	0.32	0.30	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	78.85
GCA_021163585.1	45.3	0.31	0.32	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.06
GCA_020833415.1	53.5	0.57	0.23	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.2
GCA_023255955.1	47.8	0.45	0.27	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.47
GCA_020832985.1	38.7	0.28	0.25	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.88
GCA_025058345.1	41.1	0.26	0.29	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.87
GCA_002255065.1	50.1	0.46	0.20	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.36
GCA_023255965.1	42.6	0.28	0.29	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.66
GCA_015523295.1	44.9	0.21	0.38	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.23
GCA_021160415.1	51.0	0.22	0.46	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.55
GCA_015521325.1	55.6	0.21	0.52	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.66
GCA_015521295.1	49.6	0.19	0.39	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	95.49
GCA_020833255.1	48.2	0.26	0.39	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.74
GCA_003056265.1	41.9	0.24	0.28	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.47
GCF_000015145.1	53.7	0.57	0.17	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.73
GCA_013153145.1	58.4	0.44	0.33	0.23	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.71
GCF_001412615.1	53.9	0.53	0.17	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.37
GCA_015661645.1	52.9	0.57	0.16	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.63

GCF_001462395.1	63.5	0.67	0.19	0.13	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1
GCF_000223395.1	54.9	0.40	0.30	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.05
GCA_015521195.1	60.7	0.51	0.29	0.19	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.07
GCA_003978665.1	53.4	0.47	0.24	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	63.52
GCA_013153105.1	65.5	0.62	0.24	0.14	0	0	0	0	0	0	0	0	0	1	0	0	0	0	76.55
GCA_013540595.1	48.3	0.41	0.23	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.46
GCA_015662475.1	44.4	0.44	0.24	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.68
GCA_015520245.1	68.4	0.57	0.34	0.10	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.3
GCA_000389735.1	51.7	0.16	0.54	0.29	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.4
GCF_003201835.2	31.9	0.19	0.28	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_009729015.1	34.2	0.17	0.31	0.52	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCF_000632495.1	35.6	0.21	0.31	0.48	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.4
GCA_003086435.1	34.0	0.16	0.29	0.55	0	0	0	0	0	0	0	0	0	0	0	0	0	0	64.54
GCF_009729545.1	34.4	0.17	0.30	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_002116695.1	30.6	0.15	0.28	0.57	0	0	0	0	0	0	0	0	0	1	0	0	0	0	100
GCF_021655615.1	35.1	0.17	0.30	0.53	0	0	0	0	0	0	0	0	0	1	0	0	0	0	98.81
GCF_003201765.2	31.1	0.15	0.27	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_022678445.1	48.9	0.25	0.38	0.38	0	0	0	0	0	0	0	0	0	1	0	0	0	0	100
GCA_000565255.1	47.0	0.24	0.37	0.38	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.88
GCA_019704295.1	39.6	0.24	0.32	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.21
GCF_000204925.1	42.0	0.21	0.39	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_003201675.2	43.7	0.22	0.42	0.36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCA_021654415.1	47.1	0.24	0.44	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCA_000016605.1	46.2	0.26	0.40	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_013343295.1	44.8	0.22	0.42	0.36	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.4
GCF_000243315.1	47.7	0.23	0.47	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_020886315.1	32.9	0.17	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000022485.1	35.3	0.21	0.30	0.50	0	0	0	0	0	0	0	0	0	2	0	0	0	0	99.4
GCF_019175345.1	35.4	0.20	0.30	0.50	0	0	0	0	0	0	0	0	0	2	0	0	0	0	99.4
GCF_900079115.1	35.8	0.21	0.29	0.51	0	0	0	0	0	0	0	0	0	2	0	0	0	0	100
GCF_001719125.1	34.8	0.19	0.30	0.52	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.4
GCF_009601705.1	34.7	0.19	0.29	0.51	0	0	0	0	0	0	0	0	0	2	0	0	0	0	100
GCF_009729035.1	37.6	0.18	0.35	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_019704315.1	40.1	0.20	0.33	0.47	0	0	0	0	0	0	0	0	0	1	0	0	0	0	99.4
GCA_003086555.1	38.0	0.18	0.33	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	74.68
GCF_003967175.1	51.1	0.26	0.49	0.25	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.62
GCA_017857195.1	47.7	0.23	0.45	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.63
GCF_000012285.1	36.7	0.18	0.34	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCA_000508305.1	36.3	0.18	0.33	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCF_001316045.1	38.6	0.24	0.32	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.21
GCA_002495845.1	43.1	0.19	0.44	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	56.55
GCF_008326425.1	42.4	0.21	0.41	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCF_009729055.1	32.7	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCA_012222305.1	32.6	0.16	0.28	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.4
GCF_000011205.1	32.8	0.18	0.28	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_015521735.1	38.6	0.34	0.19	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.21
GCA_015520265.1	59.0	0.49	0.30	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.1
GCA_000375685.1	32.0	0.18	0.26	0.56	0	0	0	0	0	0	0	0	0	0	0	0	0	0	73.65
GCA_017857595.1	30.0	0.15	0.23	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.38
GCA_021324265.1	36.6	0.23	0.31	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	96.32
GCA_000380705.1	28.7	0.12	0.23	0.65	0	0	0	0	0	0	0	0	0	0	0	0	0	0	88.24
GCA_015520395.1	52.8	0.42	0.29	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	85.05
GCA_003649665.1	40.2	0.29	0.28	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.46
GCA_021158375.1	38.7	0.28	0.26	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.78
GCA_021162845.1	47.1	0.29	0.33	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCA_003650925.1	44.5	0.40	0.36	0.24	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCA_003649445.1	38.6	0.31	0.22	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.79
GCA_003650815.1	40.2	0.34	0.22	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.99
GCA_003649515.1	43.7	0.36	0.26	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.82
GCA_003650785.1	39.2	0.39	0.24	0.37	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.18
GCA_003650675.1	42.1	0.27	0.28	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.79
GCA_003649235.1	39.9	0.29	0.25	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.66
GCA_021161825.1	38.1	0.29	0.20	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.38
GCA_003649225.1	40.2	0.36	0.20	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.69
GCA_002254595.1	42.6	0.28	0.15	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	61.54
GCA_003649495.1	58.1	0.41	0.37	0.21	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.9
GCF_014876775.1	53.9	0.46	0.28	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCA_002855745.1	56.7	0.39	0.34	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCF_000993805.1	47.9	0.33	0.29	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCA_021163245.1	32.9	0.22	0.20	0.57	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.85
GCA_023269735.1	67.8	0.43	0.43	0.14	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.79
GCA_025057995.1	47.4	0.31	0.28	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.18
GCF_000446015.1	46.5	0.38	0.22	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCF_000015225.1	57.6	0.45	0.28	0.27	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCA_020832965.1	50.0	0.34	0.34	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.49
GCA_020833575.1	61.5	0.49	0.37	0.14	0	0	0	0	0	0	0	0	0	1	0	0	0	0	86.15
GCA_003649205.1	43.2	0.43	0.27	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.53
GCF_000018305.1	43.1	0.19	0.28	0.53	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCF_001663375.1	48.5	0.26	0.29	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.06
GCA_002506515.1	42.3	0.20	0.26	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.9
GCA_023256255.1	42.8	0.24	0.26	0.51	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCA_002254895.1	34.2	0.29	0.23	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	53.99
GCA_013153275.1	43.8	0.37	0.32	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.65
GCA_013153895.1	38.2	0.30	0.30	0.40	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.28
GCA_013154355.1	38.7	0.36	0.30	0.35	0	0	0	0	0	0	0	0	0	0	0	0	0	0	76.8
GCA_001315925.1	53.1	0.25	0.45	0.30	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.33
GCA_001516585.1	46.8	0.22	0.37	0.41	0	0	0	0	0	0	0	0	0	0	0	0	0	0	97.43
GCA_002508315.1	53.7	0.23	0.46	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	83.22
GCA_023269935.1	43.5	0.21	0.32	0.47	0	0	0	0	0	0	0	0	0	0	0	0	0	0	50.18
GCF_001748385.1	49.1	0.19	0.37	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000148385.1	45.4	0.21	0.33	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCF_001316005.1	45.7	0.22	0.33	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.14
GCA_001316125.1	45.4	0.24	0.33	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.51
GCF_002506645.1	49.7	0.26	0.35	0.39	0	0	0	0	0	0	0	0	0	0	0	0	0	0	94.24
GCF_001315985.1	46.0	0.23	0.34	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.87
GCF_000190315.1	42.4	0.21	0.29	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_014646555.1	45.1	0.24	0.32	0.45	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCF_001316245.1	46.7	0.24	0.35	0.42	0	0	0	0	0	0	0	0	0	0	0	0	0	0	93.75
GCF_001316265.1	45.3	0.23	0.33	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.31
GCF_001316285.1	45.9	0.23	0.33	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	92.22
GCA_001516765.1	45.6	0.25	0.31	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	59.4
GCA_002496475.1	44.6	0.26	0.31	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.18
GCA_022014875.1	48.8	0.26	0.31	0.43	0	0	0	0	0	0	0	0	0	0	0	0	0	0	91.18
GCA_023256215.1	42.7	0.22	0.30	0.48	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.71
GCF_000007225.1	51.4	0.30	0.27	0.44	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000016385.1	55.1	0.39	0.29	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000015805.1	57.2	0.39	0.29	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000234805.1	57.0	0.40	0.31	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000015205.1	49.6	0.34	0.28	0.38	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000019805.1	59.9	0.43	0.31	0.26	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_000247545.1	55.1	0.39	0.29	0.33	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_001189275.1	58.3	0.35	0.33	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCA_009903905.1	57.8	0.35	0.34	0.31	0	0	0	0	0	0	0	0	0	0	0	0	0	0	81.56
GCA_020833025.1	62.6	0.42	0.41	0.17	0	0	0	0	0	0	0	0	0	0	0	0	0	0	98.16
GCA_020833205.1	55.8	0.35	0.33	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	62.13
GCA_022759345.1	56.2	0.36	0.33	0.32	0	0	0	0	0	0	0	0	0	0	0	0	0	0	80.02
GCA_000960885.1	58.0	0.38	0.28	0.34	0	0	0	0	0	0	0	0	0	0	0	0	0	0	99.26
GCF_002077075.2	60.9	0.41	0.39	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	75.06
GCA_002497345.1	58.9	0.36	0.37	0.27	0	0	0	0	0	0	0	0	0	1	0	0	0	0	66.91
GCF_000253055.1	55.1	0.34	0.37	0.29	0	0	0	0	0	0	0	0	0	0	0	0	0	0	100
GCF_000193375.1	59.7	0.41	0.35	0.24	0	0	0	0	0	0	0	0	0	2	0	0	0	0	100
GCA_015521775.1	60.5	0.40	0.41	0.20	0	0	0	0	0	0	0	0	0	0	0	0	0	0	86.03
GCA_014189685.1	37.9	0.17	0.21	0.62	0	0	0	0	0	0	0	0	0	0	0	0	0	0	90.65
GCA_002502135.1	39.5	0.19	0.27	0.54	0	0	0	0	0	0	0	0	0	0	0	0	0	0	79.91
GCA_002495465.1	42.1	0.22	0.31	0.46	0	0	0	0	0	0	0	0	0	0	0	0	0	0	82.55
GCA_002687935.1	41.0	0.20	0.30	0.50	0	0	0	0	0	0	0	0	0	0	0	0	0	0	89.72
GCA_014189675.1	41.8	0.22	0.30	0.49	0	0	0	0	0	0	0	0	0	0	0	0	0	0	87.23

Table S2.2. Distribution of pyrrolysine, methylamine methyltransferases, signatures of methane metabolism, and stop codon usage across all archaeal genomes available in GTDB r214.0. Genomes completeness is indicated by CheckM. Full genome and abbreviated genome ID's are indicated in accordance with GTDB accessions, and taxonomic information is designated per GTDB. Gene counts were determined using a custom script (see Methods), which iteratively searches profile Hidden Markov Models (pHMMs) and thresholds hits at an e-value of 1e-3 and the TC ("Trusted Cutoff") score cutoff indicated in the pHMM.

genome	TAG	total pyl proteins	average extension length	median extension length
GCA_019262145.1	0.01	26.0	120.4	79.0
GCA_023402275.1	0.01	27.0	171.5	141.0
GCA_944322255.1	0.01	49.0	200.9	107.0
GCA_934702355.1	0.01	24.0	174.4	82.0
GCF_000970325.1	0.02	43.0	203.2	150.0
GCF_001889405.1	0.02	48.0	170.6	115.5
GCA_015063225.1	0.02	41.0	239.6	143.0
GCF_021184045.1	0.02	62.0	216.2	152.5
GCA_000350305.1	0.02	37.0	189.8	171.0
GCF_002761295.1	0.02	49.0	149.1	129.0
GCA_002498605.1	0.02	23.0	100.7	65.0
GCA_009777615.1	0.02	40.0	264.0	148.0
GCA_002505345.1	0.02	30.0	120.6	107.5
GCF_000025865.1	0.02	53.0	218.4	153.0
GCA_002506905.1	0.02	36.0	131.4	90.0
GCA_009911715.1	0.02	42.0	172.4	130.5
GCF_000765475.1	0.02	60.0	216.4	114.0
GCA_023230065.1	0.02	44.0	152.5	94.0
GCF_000800805.1	0.02	45.0	181.4	37.0
GCF_900774055.1	0.02	59.0	181.7	120.0
GCA_017935945.1	0.02	57.0	140.6	121.0
GCA_015063245.1	0.02	40.0	204.1	131.0
GCF_004363215.1	0.02	35.0	186.1	121.0
GCA_002498365.1	0.02	39.0	205.3	164.0
GCA_002504405.1	0.02	43.0	159.4	99.0
GCF_003722075.1	0.02	58.0	157.3	99.0
GCA_002506175.1	0.02	50.0	191.0	162.0
GCA_001560915.1	0.02	49.0	180.7	106.0
GCA_934234005.1	0.02	49.0	192.2	114.0
GCF_000300255.2	0.02	45.0	158.0	136.0
GCF_000196655.1	0.02	70.0	187.2	133.5
GCF_900111645.1	0.02	68.0	203.9	113.5
GCA_002495325.1	0.02	42.0	135.1	96.5
GCA_012518265.1	0.02	40.0	172.6	151.0
GCF_900215215.1	0.02	62.0	153.8	114.5
GCA_902763685.1	0.03	52.0	161.3	135.0
GCA_009783635.1	0.03	29.0	153.8	131.0
GCA_015063125.1	0.03	56.0	171.7	116.0

GCF_017874375.1	0.03	72.0	175.5	111.5
GCA_002509405.1	0.03	46.0	157.9	129.0
GCA_015063285.1	0.03	70.0	158.2	125.0
GCF_024372725.1	0.03	131.0	130.1	39.0
GCA_017461225.1	0.03	46.0	184.2	127.5
GCA_021108275.1	0.03	100.0	137.5	73.0
GCA_018609725.1	0.03	81.0	89.4	46.0
GCA_016841265.1	0.03	126.0	124.8	47.5
GCA_001563305.1	0.03	51.0	264.6	163.0
GCF_000979455.1	0.03	126.0	109.3	45.5
GCA_021106765.1	0.03	66.0	118.5	47.5
GCA_002503545.1	0.03	63.0	204.2	151.0
GCF_023684405.1	0.03	100.0	171.3	111.0
GCF_000970045.1	0.03	156.0	155.9	64.5
GCA_905187815.1	0.03	72.0	143.2	85.0
GCA_012515075.1	0.03	37.0	140.1	71.0
GCA_009778575.1	0.03	63.0	173.9	120.0
GCA_017507885.1	0.03	70.0	158.5	122.5
GCA_016841625.1	0.04	162.0	115.3	37.0
GCA_009784005.1	0.04	60.0	176.0	129.0
GCF_004099695.1	0.04	140.0	109.1	28.5
GCA_015063235.1	0.04	74.0	188.2	117.0
GCA_002496565.1	0.04	153.0	112.7	39.0
GCF_000013725.1	0.04	105.0	116.6	68.0
GCA_016284295.1	0.04	86.0	153.1	87.0
GCA_012719315.1	0.04	67.0	128.4	92.0
GCA_012520845.1	0.04	65.0	116.3	84.0
GCA_002499445.1	0.04	132.0	107.6	27.0
GCA_002509325.1	0.04	126.0	118.6	34.0
GCA_902787415.1	0.04	108.0	150.6	118.0
GCA_016296195.1	0.04	125.0	144.2	111.0
GCA_024399175.1	0.04	91.0	171.4	154.0
GCF_000969885.1	0.04	138.0	89.4	28.5
GCA_017468935.1	0.04	91.0	131.7	95.0
GCA_944320485.1	0.04	102.0	175.2	113.0
GCF_000970265.1	0.04	174.0	116.4	42.5
GCA_021108185.1	0.04	103.0	119.9	63.0
GCF_000970205.1	0.04	201.0	124.5	40.0
GCF_000970285.1	0.04	221.0	94.0	29.0
GCF_004137855.1	0.05	104.0	81.9	30.5

GCA_905202485.1	0.05	102.0	85.6	27.0
GCA_023399215.1	0.05	197.0	99.8	25.0
GCF_001304615.2	0.05	154.0	83.6	23.0
GCA_013329415.1	0.05	196.0	147.2	70.0
GCF_020804225.1	0.05	216.0	91.5	32.0
GCF_000970085.1	0.05	259.0	80.0	30.0
GCA_944321985.1	0.05	129.0	166.6	137.0
GCF_000970305.1	0.05	222.0	80.1	21.5
GCA_007127385.1	0.05	71.0	75.5	18.0
GCA_002505485.1	0.05	211.0	96.0	34.0
GCF_000969905.1	0.05	230.0	85.1	30.5
GCF_000404225.1	0.05	115.0	101.2	16.0
GCF_000970025.1	0.05	237.0	102.4	33.0
GCF_000969965.1	0.06	230.0	125.6	44.5
GCF_000969985.1	0.06	268.0	85.2	29.0
GCA_944319735.1	0.06	116.0	75.1	19.5
GCF_000217995.1	0.06	126.0	73.7	17.0
GCA_009780575.1	0.06	78.0	64.9	28.5
GCF_000007345.1	0.06	296.0	94.3	34.0
GCF_024808815.1	0.06	123.0	61.4	13.0
GCA_013331275.1	0.06	255.0	82.9	37.0
GCA_024399195.1	0.06	178.0	188.8	135.0
GCA_016282555.1	0.06	97.0	142.2	91.0
GCA_944320495.1	0.06	162.0	168.2	99.0
GCA_001714685.2	0.07	284.0	84.5	25.0
GCA_017524805.1	0.07	136.0	167.0	116.5
GCA_015063165.1	0.07	151.0	184.0	117.0
GCF_001481295.1	0.07	175.0	106.3	58.0
GCF_002287235.1	0.07	326.0	72.5	25.0
GCA_009784745.1	0.07	97.0	87.3	34.0
GCA_002506425.1	0.08	146.0	156.4	104.0
GCA_009776695.1	0.08	109.0	90.5	31.0
GCA_009776625.1	0.08	112.0	165.3	119.5
GCF_023016325.1	0.09	127.0	72.0	21.0
GCA_009780795.1	0.09	120.0	96.6	37.0
GCA_021767785.1	0.09	198.0	36.1	11.0
GCF_000504205.1	0.09	267.0	53.4	16.0
GCF_006546655.1	0.09	268.0	56.5	15.0
GCF_000328665.1	0.09	266.0	59.9	19.0
GCA_002067275.1	0.10	207.0	75.9	20.0

GCF_017873415.1	0.10	272.0	53.1	14.0
GCA_002508425.1	0.10	243.0	70.9	17.0
GCA_001896725.1	0.10	225.0	74.3	18.0
GCA_006954465.1	0.10	273.0	134.8	103.0
GCA_016281925.1	0.10	208.0	125.9	93.0
GCF_900100715.1	0.10	306.0	69.8	16.5
GCA_017475875.1	0.11	213.0	135.1	110.0
GCA_002507205.1	0.11	248.0	51.2	14.0
GCA_023955635.1	0.11	557.0	50.7	20.0
GCF_013388255.1	0.11	289.0	56.6	19.0
GCF_000308215.1	0.11	288.0	104.7	39.5
GCA_016278365.1	0.11	312.0	62.8	17.0
GCF_900114835.1	0.11	330.0	66.1	17.0
GCF_024500045.1	0.11	304.0	71.4	20.0
GCF_002243045.1	0.12	356.0	70.1	17.5
GCA_016278385.1	0.12	361.0	58.4	18.0
GCA_000306725.1	0.12	364.0	66.8	18.0
GCF_004745425.1	0.13	320.0	54.8	17.0
GCA_002501695.1	0.13	298.0	69.2	19.0
GCA_003565715.1	0.13	258.0	54.6	19.0
GCA_002067865.1	0.13	272.0	89.4	28.5
GCA_002504495.1	0.13	265.0	134.7	94.0
GCA_017519045.1	0.13	305.0	162.0	112.0
GCA_020055655.1	0.13	320.0	55.8	13.0
GCA_002010075.1	0.14	222.0	168.1	147.5
GCA_003557905.1	0.15	201.0	103.7	41.0
GCA_012518185.1	0.15	245.0	55.7	16.0
GCA_017540825.1	0.15	328.0	179.4	125.0
GCA_001914405.1	0.15	340.0	66.9	23.0
GCA_015063135.1	0.16	341.0	174.1	112.0
GCA_016932675.1	0.16	313.0	75.8	23.0
GCA_004525545.1	0.16	251.0	76.2	32.0
GCA_002504525.1	0.17	376.0	101.4	41.0
GCA_024256165.1	0.17	243.0	38.6	13.0
GCA_024256285.1	0.17	312.0	69.3	18.5
GCA_001421185.1	0.18	434.0	97.3	48.0
GCA_020793565.1	0.18	427.0	56.1	21.0
GCA_012519255.1	0.18	364.0	101.9	36.0
GCA_016935475.1	0.18	317.0	48.4	17.0
GCA_024256245.1	0.18	269.0	54.2	16.0

GCA_002011125.1	0.19	407.0	50.2	16.0
GCA_024256265.1	0.19	552.0	49.3	14.0
GCA_012719175.1	0.19	443.0	73.1	28.0
GCA_021372335.1	0.20	290.0	108.4	54.0
GCA_016109435.1	0.21	427.0	107.5	45.0
GCA_018262895.1	0.21	429.0	86.6	34.0
GCA_016840645.1	0.21	1062.0	62.5	17.0
GCA_002508545.1	0.22	536.0	108.8	46.5
GCA_016840515.1	0.22	764.0	66.7	19.5
GCA_019057385.1	0.23	908.0	68.0	16.0
GCA_001717005.1	0.24	367.0	102.2	41.0
GCF_000711905.1	0.26	373.0	97.2	35.0
GCA_020348945.1	0.26	467.0	70.4	21.0
GCA_020355125.1	0.26	549.0	67.5	23.0
GCA_002011035.1	0.27	458.0	85.2	31.0

Table S2.3. Features of Pyl+ genomes and putative Pyl containing proteins. Total Pyl proteins were counted as the output of a custom script, which reassigned TAG to Pyl (see methods). Average and median extension lengths were calculated from the exension length per gene, which was determined as the difference (in number of amino acids) between an alternate stop (TGA or TAA) and the first instance of Pyl in a gene. TAG use is designation as a fraction (i.e. 1% = 0.01).

Predicted Mutations for Δ*pylBCD* (DDN121)				
Position	Mutation	Annotation	gene	Description
183,146	Δ2,853 bp		*[pylD]–[pylB]*	*[pylD], pylC, [pylB]*

Predicted Mutations for Δ*pylTS* (DDN146)				
Position	Mutation	Annotation	gene	Description
186,396	Δ1,490 bp		[MA_RS00825]	[MA_RS00825]
2,544,295	G→A	intergenic (-6/+190)	MA_RS28085 ← / ← MA_RS10665	hypothetical protein/MATE family efflux transporter

Table S2.4 Mutation predictions for CRISPR-edited genet deletion strains generated in this study. Mutations noted are specific to the knockout strains and omit mutations present in the parental background (WWM60). Predictions were generated using BreSeq run in default mode.

Growth rates for single Pyl Knockouts and native complements on a non-permissive (TMA) and permissive (MeOH) substrates			
		TMA	MeOH
Strain	Genotype	Average growth rate (h-1)	Average growth rate (h-1)
WWM60	parental strain	0.068 ± 0.001	0.084 ± 0.001
DDN038	WWM60/P*mcrB* (tetO4)::*uidA*	0.066 ± 0.005	0.075 ± 0.000
DDN146	Δ*pylTS*	n.g.	0.073 ± 0.004
DDN240	Δ*pylTS*/P*mcrB* (tetO1)::*uidA*	0.046 ± 0.001	0.074 ± 0.004
DDN121	Δ*pylBCD*	n.g.	0.072 ± 0.002
DDN184	Δ*pylBCD*/P*mcrB* (tetO1)::*uidA*	0.042 ± 0.002	0.073 ± 0.005

Growth rates for single Pyl Knockouts and Borrarchaeum weybense complements on a non-permissive (TMA) substrate		
		TMA
Strain	Genotype	Average growth rate (h-1)
DDN038	WWM60/P*mcrB* (tetO4)::*uidA*	0.070 ± 0.003
DDN146	Δ*pylTS*	n.g.
DDN318	Δ*pylTS*/P*mcrB* (tetO4)::*pylTS*$_{Bw}$	n.g.
DDN121	Δ*pylBCD*	n.g.
DDN319	Δ*pylBCD*/P*mcrB* (tetO4)::*pylBCD*$_{Bw}$	n.g.
DDN385	Δ*pylBCD*/P*mcrB* (tetO4)::*pylTSBCD*$_{Bw}$	n.g.

Growth rates for single Pyl Knockouts and ANME-3 complements on a non-permissive (TMA) substrate		
		TMA
Strain	Genotype	Average growth rate (h-1)
DDN038	WWM60/*PmcrB* (tetO4)::*uidA*	0.070 ± 0.003
DDN146	Δ*pylTS*	n.g.
DDN320	Δ*pylTS*/*PmcrB*(tetO4)::*pylT1S*$_{ANME-3}$	n.g.
DDN321	Δ*pylTS*/*PmcrB* (tetO4)::*pylT2S*$_{ANME-3}$	n.g.
DDN383	Δ*pylTS*/*PmcrB* (tetO4)::*pylT1S*$_{ANME-3Δ3bp}$	n.g.
DDN384	Δ*pylTS*/*PmcrB* (tetO4)::*pylT2S*$_{ANME-3Δ3bp}$	n.g.
DDN121	Δ*pylBCD*	n.g.
DDN322	Δ*pylBCD*/*PmcrB* (tetO4)::*pylTSBCD*$_{ANME-3}$	0.067 ± 0.004

Growth rates for point mutated methylamine MTases complements on a non-permissive (TMA) substrate		
		TMA
Strain	Genotype	Average growth rate (h-1)
DDN351	WWM60/*PmcrB* (tetO1)::*uidA*	0.051 ± 0.003
DDN121	Δ*pylBCD*	n.g.
DDN315	Δ*pylBCD*|*PmcrB*(tetO1)::*mttB1*$_{O334A}$	n.g.
DDN287	Δ*pylBCD*|*PmcrB*(tetO1)::*mttB1*$_{O334K}$	n.g.
DDN382	Δ*pylBCD*|*PmcrB*(tetO1)::*mttB1*$_{O334K}$C	n.g.

Table S2.5. Growth rates for mutant strains. All rates were calculated as the average of cultures grown in triplicate with the standard deviation designated as well. All strains were pre-grown on a permissive substrate (MeOH), before passaging to the experimental substrate (non-permissive, TMA; permissive, MeOH). n.g.: no growth, TMA: trimethylamine, MeOH: Methanol, MTase: methyltransferase.

genome	genus	species	TAG	stop identity	gene length (#AA)
GCA_020793555.1	g__DQIP01	s__DQIP01 sp020793555	17.0%	TGA	196
GCA_023544565.1	g__DQIP01	s__DQIP01 sp023544565	17.7%	TGA	202
GCA_020793565.1	g__DQIP01	s__DQIP01 sp020793565	17.7%	TGA	196
GCA_016926455.1	g__JAFGQV01	s__JAFGQV01 sp016926455	19.6%	TGA	196
GCA_021106765.1	g__JAIOTO01	s__JAIOTO01 sp021106765	3.2%	TGA	196
GCF_000970325.1	g__Methanococcoides	s__Methanococcoides methylutens_A	1.6%	TGA	197
GCF_021184045.1	g__Methanococcoides	s__Methanococcoides orientis	1.8%	TGA	197
GCF_000765475.1	g__Methanococcoides	s__Methanococcoides methylutens	2.0%	TGA	197
GCF_900774055.1	g__Methanococcoides	s__Methanococcoides sp900774055	2.0%	TGA	196
GCF_900111645.1	g__Methanococcoides	s__Methanococcoides vulcani	2.3%	TGA	197
GCA_021108275.1	g__Methanococcoides	s__Methanococcoides sp021108275	3.0%	TGA	197
GCF_023684405.1	g__Methanococcoides	s__Methanococcoides seepicolus	3.3%	TGA	197
GCF_000013725.1	g__Methanococcoides	s__Methanococcoides burtonii	3.8%	TGA	197
GCA_021108185.1	g__Methanococcoides	s__Methanococcoides sp021108185	4.4%	TGA	197
GCF_000196655.1	g__Methanohalobium	s__Methanohalobium evestigatum	2.3%	TAA	198
GCA_018609725.1	g__Methanohalobium	s__Methanohalobium sp018609725	3.1%	TAA	198
GCF_001889405.1	g__Methanohalophilus	s__Methanohalophilus halophilus	1.6%	TGA	196
GCF_002761295.1	g__Methanohalophilus	s__Methanohalophilus portucalensis	1.8%	TGA	198
GCF_000025865.1	g__Methanohalophilus	s__Methanohalophilus mahii	1.9%	TGA	198
GCF_003722075.1	g__Methanohalophilus	s__Methanohalophilus sp003722075	2.3%	TGA	196
GCF_900215215.1	g__Methanohalophilus	s__Methanohalophilus euhalobius	2.4%	TGA	196
GCF_017874375.1	g__Methanohalophilus	s__Methanohalophilus levihalophilus	2.8%	TGA	197
GCF_004137855.1	g__Methanohalophilus	s__Methanohalophilus profundi	4.5%	TGA	169
GCA_021767785.1	g__Methanolobus	s__Methanolobus sp021767785	9.1%	TGA	196
GCF_000504205.1	g__Methanolobus	s__Methanolobus tindarius	9.2%	TGA	196
GCF_006546655.1	g__Methanolobus	s__Methanolobus vulcani_A	9.3%	TGA	196
GCF_017873415.1	g__Methanolobus	s__Methanolobus bombayensis	9.9%	TGA	196
GCF_900100715.1	g__Methanolobus	s__Methanolobus vulcani	10.5%	TGA	196
GCA_002507205.1	g__Methanolobus	s__Methanolobus sp002507205	10.6%	TGA	196
GCF_013388255.1	g__Methanolobus	s__Methanolobus zinderi	11.0%	TGA	196
GCA_016278365.1	g__Methanolobus	s__Methanolobus sp016278365	11.1%	TGA	196
GCF_900114835.1	g__Methanolobus	s__Methanolobus profundi	11.2%	TGA	196
GCF_024500045.1	g__Methanolobus	s__Methanolobus chelungpuianus	11.3%	TGA	196
GCA_002508635.1	g__Methanolobus	s__Methanolobus sp002508635	11.5%	TGA	196
GCF_002243045.1	g__Methanolobus	s__Methanolobus psychrotolerans	11.5%	TGA	196
GCA_016278385.1	g__Methanolobus	s__Methanolobus sp016278385	12.3%	TGA	196

GCA_000306725.1	g__Methanolobus	s__Methanolobus psychrophilus	12.3%	TGA	196
GCF_004745425.1	g__Methanolobus	s__Methanolobus halotolerans	12.6%	TGA	196
GCA_002501695.1	g__Methanolobus	s__Methanolobus sp002501695	12.7%	TGA	196
GCA_003565715.1	g__Methanolobus	s__Methanolobus sp003565715	12.8%	TGA	196
GCA_020055655.1	g__Methanolobus	s__Methanolobus sp020055655	13.3%	TGA	196
GCA_016932675.1	g__Methanolobus	s__Methanolobus sp016932675	16.2%	TGA	196
GCA_002067265.1	g__Methanomethylovorans	s__Methanomethylovorans sp002067265	9.0%	TGA	196
GCF_000328665.1	g__Methanomethylovorans	s__Methanomethylovorans hollandica	9.5%	TGA	196
GCA_002067275.1	g__Methanomethylovorans	s__Methanomethylovorans sp002067275	9.5%	TGA	196
GCA_014361205.1	g__Methanomethylovorans	s__Methanomethylovorans sp014361205	9.7%	TGA	196
GCA_001896725.1	g__Methanomethylovorans	s__Methanomethylovorans sp001896725	9.9%	TGA	196
GCA_020854785.1	g__Methanomethylovorans	s__Methanomethylovorans sp020854785	12.8%	TGA	196
GCA_007127385.1	g__Methanosalsum	s__Methanosalsum sp007127385	5.1%	TGA	196
GCF_000217995.1	g__Methanosalsum	s__Methanosalsum zhilinae	5.7%	TGA	196
GCF_024808815.1	g__Methanosalsum	s__Methanosalsum natronophilum	5.8%	TGA	196
GCF_024372725.1	g__Methanosarcina	s__Methanosarcina sp024372725	3.0%	TGA	197
GCF_000979455.1	g__Methanosarcina	s__Methanosarcina sp000979455	3.2%	TGA	197
GCF_000970265.1	g__Methanosarcina	s__Methanosarcina lacustris	4.3%	TGA	197
GCF_000970285.1	g__Methanosarcina	s__Methanosarcina horonobensis	4.5%	TGA	197
GCF_020804225.1	g__Methanosarcina	s__Methanosarcina sp020804225	4.9%	TGA	197
GCF_000970085.1	g__Methanosarcina	s__Methanosarcina siciliae	4.9%	TAA	197
GCF_000969965.1	g__Methanosarcina	s__Methanosarcina sp000969965	5.6%	TGA	197
GCF_000007345.1	g__Methanosarcina	s__Methanosarcina acetivorans	5.7%	TAG	197
GCA_016841265.1	g__MTP4	s__MTP4 sp016841265	3.1%	TGA	198
GCF_000970045.1	g__MTP4	s__MTP4 sp000970045	3.3%	TGA	198
GCA_016841625.1	g__MTP4	s__MTP4 sp016841625	3.6%	TGA	198
GCA_013329415.1	g__MTP4	s__MTP4 sp9310u	4.7%	TGA	198

Table S2.6. Summary of stop codon use in *rnfA* from all genomes belonging to the family Methanosarcinaceae. Genus and species information was generated from GTDB r214.0 taxonomy metadata, and TAG usage was calculated as previously described. Stop codon identity is indicated by color, where TAA is given in yellow, TAG is given in orange, and TGA is given in gray. Gene length is indicated as amino acid sequence length.

locus	gene	WT_TMA.1	WT_TMA.2	WT_TMA.3	WT_MeOH.1	WT_MeOH.2	WT_MeOH.3	121_MeOH.1	121_MeOH.2	121_MeOH.3	146_MeOH.1	146_MeOH.2	146_MeOH.3
MA_RS00005	NA	4.78	5.12	4.83	5.33	5.13	5.24	5.10	5.55	5.98	5.33	4.90	5.12
MA_RS00010	putP	2.46	2.77	2.42	2.83	2.59	3.15	2.64	3.73	4.03	2.51	2.34	2.58
MA_RS00015	istB	0.05	0.03	0.04	0.03	0.01	0.02	0.04	0.05	0.07	0.02	0.02	0.03
MA_RS00020	istA	0.15	0.15	0.08	0.27	0.20	0.29	0.35	0.36	0.49	0.33	0.16	0.26
MA_RS00025	mfnA	4.83	5.06	5.15	5.40	5.04	5.36	5.22	5.59	5.86	5.69	5.16	5.26
MA_RS00030	NA	4.55	4.64	4.42	4.88	4.72	4.89	4.54	5.16	5.72	4.96	4.75	4.41
MA_RS00035	NA	4.58	4.65	4.82	4.90	4.84	4.84	4.77	5.32	5.51	4.86	4.49	4.91
MA_RS00040	NA	1.52	2.00	2.07	2.31	2.00	1.64	2.02	2.64	2.84	2.15	1.46	2.10
MA_RS00045	fhcD	6.78	6.91	6.82	7.42	6.97	7.22	7.22	7.63	7.92	7.27	7.00	6.99
MA_RS00050	NA	2.27	2.06	1.76	3.09	2.36	2.49	2.27	2.61	2.63	2.68	1.86	2.34
MA_RS00055	NA	2.36	2.58	2.51	3.12	2.79	2.98	2.72	3.72	3.91	2.81	2.93	2.60
MA_RS00060	NA	2.99	3.05	3.05	3.50	3.10	3.69	3.04	3.91	4.52	3.51	3.07	3.34
MA_RS00065	NA	1.61	1.61	1.71	1.97	1.77	1.86	2.20	2.53	2.60	1.95	1.89	1.84
MA_RS00070	NA	1.32	1.13	0.81	1.37	1.55	1.60	1.72	1.98	2.15	1.41	1.18	1.05
MA_RS00075	NA	1.27	1.63	0.52	1.48	1.09	0.76	2.20	2.39	1.09	1.59	1.42	1.33
MA_RS00090	NA	3.95	4.14	3.82	4.38	4.32	4.43	4.30	5.04	5.41	4.72	4.60	4.21
MA_RS00095	NA	3.78	3.96	4.01	4.45	3.99	4.17	4.11	4.99	5.20	3.95	3.85	3.88
MA_RS00100	NA	2.29	3.25	2.94	2.85	2.78	3.08	2.51	3.45	3.67	2.90	2.88	3.07
MA_RS00105	NA	1.69	1.60	1.60	2.02	1.94	1.52	1.63	2.39	2.11	1.44	1.61	1.66
MA_RS00110	NA	2.65	3.36	3.06	4.07	3.75	3.94	4.29	4.63	4.13	2.30	2.87	3.47
MA_RS00115	NA	3.28	3.42	3.38	4.33	3.98	4.34	4.50	5.01	4.94	3.50	3.79	3.91
MA_RS00120	NA	4.40	4.56	4.48	5.08	4.88	5.02	5.12	5.50	5.63	4.71	4.62	4.58
MA_RS00125	NA	3.37	3.92	3.61	4.10	3.62	3.94	3.64	4.46	4.46	3.39	3.69	3.71
MA_RS00130	NA	6.35	6.51	6.32	7.02	6.56	6.92	7.01	7.75	8.15	7.32	6.76	6.81
MA_RS00135	NA	0.20	0.32	0.51	0.52	0.42	0.35	0.64	0.80	1.09	0.48	0.44	0.44
MA_RS00145	NA	2.64	2.73	2.60	3.11	3.04	3.31	3.39	3.93	3.99	3.35	2.92	3.21
MA_RS00155	NA	2.48	2.44	2.78	2.59	2.03	2.39	2.91	3.30	2.91	2.68	2.19	2.45
MA_RS00160	porB	7.18	7.36	7.43	8.00	7.62	7.83	7.90	7.40	7.80	7.74	7.60	7.84
MA_RS00165	porA	7.90	8.23	8.04	8.93	8.35	8.71	8.65	8.78	9.14	8.88	8.52	8.63
MA_RS00170	porD	7.55	7.92	7.83	8.70	8.14	8.37	8.47	8.62	9.19	8.56	8.25	8.33
MA_RS00175	NA	8.01	8.18	8.15	8.91	8.38	8.56	8.87	8.79	9.13	8.93	8.37	8.55
MA_RS00180	dusB	3.09	3.25	3.15	3.19	3.14	3.12	3.50	3.73	4.33	3.69	3.57	3.47
MA_RS00185	NA	4.23	4.19	4.43	4.27	4.31	4.56	4.77	5.03	5.12	4.44	4.20	4.59
MA_RS00190	NA	3.64	3.66	3.65	4.07	3.85	4.17	4.00	4.56	4.75	3.67	3.73	4.01
MA_RS00195	NA	3.28	3.22	3.21	3.79	3.57	3.62	3.91	4.67	4.88	3.43	2.85	3.55
MA_RS00200	NA	2.75	3.14	2.90	3.34	3.21	3.32	3.34	4.18	4.33	3.01	3.23	3.46
MA_RS00205	twy1	3.88	4.05	4.05	4.23	4.30	4.38	4.26	4.48	4.83	4.34	4.31	4.27
MA_RS00210	NA	4.31	4.75	4.80	4.71	4.69	5.07	5.02	5.40	6.00	5.00	5.16	4.74
MA_RS00215	prf1	5.17	5.48	5.26	5.72	5.35	5.55	5.58	6.09	6.26	5.62	5.46	5.46
MA_RS00220	argS	4.98	5.36	5.16	5.57	5.13	5.44	5.35	5.80	6.04	5.45	5.24	5.30
MA_RS00230	NA	3.69	3.52	3.92	3.41	3.82	3.43	3.63	4.11	3.88	3.96	3.67	3.32
MA_RS00235	NA	2.86	3.09	2.88	3.15	2.92	3.13	3.37	3.28	3.42	3.24	3.03	3.19
MA_RS00240	NA	2.38	2.18	2.16	2.62	2.78	2.88	3.30	3.12	3.43	2.61	2.36	2.72
MA_RS00245	NA	1.34	0.95	0.77	1.21	0.83	1.82	1.49	1.49	1.06	1.12	1.05	1.60
MA_RS00250	NA	0.92	1.84	1.90	2.20	2.19	1.41	2.06	2.48	2.69	2.05	0.68	1.58
MA_RS00255	NA	2.41	2.38	2.62	2.65	2.50	2.73	2.80	3.26	3.13	2.50	2.50	2.67
MA_RS00260	NA	2.02	2.22	2.03	2.16	1.97	1.99	2.21	2.39	2.92	2.01	1.54	1.92
MA_RS00270	NA	3.25	3.30	3.29	3.77	3.53	3.47	3.81	4.00	4.11	4.06	3.60	3.28
MA_RS00275	NA	3.29	3.34	3.55	3.77	3.60	3.63	3.42	3.94	4.14	3.60	3.20	3.59
MA_RS00280	NA	2.32	2.34	2.27	3.03	2.66	2.95	2.77	4.10	3.83	2.53	2.66	2.63
MA_RS00285	#N/A	6.30	6.25	5.90	6.17	6.15	5.97	6.22	4.78	4.16	6.50	5.79	5.97
MA_RS00290	NA	8.38	8.44	8.46	8.56	8.47	8.59	8.61	9.13	9.37	8.59	8.34	8.37
MA_RS00295	NA	8.15	8.08	8.16	8.09	8.07	8.25	8.33	8.56	8.73	8.05	7.88	8.08
MA_RS00300	NA	7.99	8.00	8.08	8.25	8.09	8.22	8.27	8.72	9.03	8.18	8.06	8.08
MA_RS00305	NA	8.61	8.65	8.85	8.87	8.78	8.75	9.02	9.16	9.15	8.72	8.45	8.78
MA_RS00310	NA	1.39	1.48	1.09	1.54	1.75	1.24	1.73	2.04	1.93	1.67	1.48	1.74
MA_RS00315	NA	1.84	1.79	1.36	2.16	1.92	1.90	1.90	2.35	2.81	1.78	1.57	1.90
MA_RS00320	NA	3.79	3.82	3.29	3.62	4.00	3.99	3.93	4.30	3.84	3.96	3.63	3.87
MA_RS00325	NA	3.35	3.69	3.74	3.91	3.77	3.56	4.03	4.29	4.36	3.73	3.55	3.63
MA_RS00330	NA	3.99	4.43	4.19	4.47	4.42	4.59	4.48	4.58	4.97	4.34	4.13	4.39
MA_RS00335	NA	5.30	5.56	5.38	6.15	5.76	5.93	5.98	6.15	6.14	5.97	5.69	5.71
MA_RS00345	NA	4.38	4.68	4.81	4.95	4.50	4.78	4.73	5.50	5.27	5.29	4.68	4.60
MA_RS00350	NA	6.74	7.08	6.94	7.36	6.84	7.15	7.21	7.95	8.31	6.99	6.67	6.92
MA_RS00355	thiL	4.43	4.89	4.69	5.03	4.56	4.92	4.97	5.64	5.80	4.97	4.65	4.81
MA_RS00365	NA	3.88	4.44	3.94	4.74	4.22	4.60	4.63	4.87	5.30	4.58	4.52	4.60
MA_RS00370	mtlD	6.46	6.78	6.69	7.43	6.96	7.19	7.27	7.63	7.94	7.09	6.83	7.11
MA_RS00375	NA	6.45	6.72	6.82	7.27	7.02	7.15	7.21	7.72	8.08	7.20	6.61	7.04
MA_RS00380	radB	3.23	3.30	3.00	3.45	3.01	3.20	3.66	3.35	3.02	3.15	3.30	3.36
MA_RS00385	NA	5.13	5.36	5.09	5.64	5.32	5.60	5.41	5.70	5.99	5.39	5.25	5.18
MA_RS00390	NA	4.28	4.58	4.48	4.93	4.83	4.74	4.77	5.09	4.98	5.15	4.57	4.79
MA_RS00395	NA	6.13	6.21	6.40	6.41	6.23	6.40	6.23	7.10	7.52	6.61	6.37	6.15
MA_RS00400	NA	5.50	5.59	5.55	5.83	5.88	5.75	5.61	5.96	6.19	5.58	5.56	5.51
MA_RS00405	NA	1.65	1.63	1.96	1.97	1.75	1.96	1.82	2.50	2.81	1.91	1.52	1.50
MA_RS00415	NA	3.12	2.99	2.86	3.27	3.20	3.10	2.84	3.10	3.13	3.07	3.18	3.16
MA_RS00420	ppk1	5.46	5.66	5.60	6.12	5.80	6.03	5.90	6.28	6.50	6.15	5.76	5.88
MA_RS00425	NA	3.55	3.86	3.74	4.01	3.86	3.91	3.82	3.99	4.48	3.67	3.62	3.72
MA_RS00430	NA	2.51	2.59	2.66	2.76	2.92	2.89	2.91	3.22	3.40	2.61	2.65	2.90
MA_RS00435	NA	4.11	4.21	4.18	4.44	4.03	4.42	4.23	4.40	4.65	4.21	3.98	3.92
MA_RS00440	NA	9.56	9.80	9.69	10.46	10.01	10.22	10.52	10.62	11.18	9.64	10.08	10.22
MA_RS00445	dnaK	1.22	1.03	1.59	1.49	1.32	1.53	1.44	1.62	1.88	1.36	1.57	1.48
MA_RS00450	NA	2.65	2.73	2.58	3.11	2.56	3.09	2.59	3.58	3.76	2.89	2.61	2.66
MA_RS00455	NA	4.52	4.76	4.58	4.93	4.60	4.80	4.82	5.14	5.39	4.58	4.59	4.79
MA_RS00460	sepS	5.54	5.85	5.69	6.27	5.85	6.04	5.99	6.29	6.55	5.95	5.84	5.87
MA_RS00465	NA	2.06	2.54	2.34	2.42	2.38	2.62	2.95	2.41	2.35	2.30	2.42	2.76
MA_RS00470	NA	6.28	5.87	6.00	6.16	6.56	6.36	6.36	6.78	6.44	6.62	6.52	6.16
MA_RS00475	NA	4.02	4.08	3.98	4.56	4.43	4.52	4.59	4.88	4.89	4.29	4.38	4.14
MA_RS00485	NA	2.16	2.42	1.68	2.10	2.51	2.75	1.79	2.67	3.02	3.03	2.65	1.72
MA_RS00490	NA	0.34	0.38	0.26	0.70	0.59	0.67	0.36	0.78	1.04	0.46	0.27	0.38
MA_RS00495	NA	3.39	3.60	3.32	3.84	3.64	3.77	3.73	3.83	4.36	3.69	3.57	3.85
MA_RS00500	glyS	4.86	5.01	5.08	5.35	5.00	5.23	5.52	5.55	5.71	5.24	4.97	5.16
MA_RS00505	NA	2.51	2.60	2.87	2.75	2.63	2.60	3.00	3.05	3.24	2.62	2.77	2.29
MA_RS00510	NA	1.99	1.66	1.17	1.76	1.54	1.31	0.22	2.17	1.00	1.54	1.15	0.91
MA_RS00515	NA	0.64	0.33	0.00	0.61	0.44	1.12	0.21	1.70	0.45	0.70	0.37	0.68
MA_RS00525	NA	2.28	1.62	2.37	2.65	2.41	2.60	1.82	2.87	3.30	2.69	2.47	2.15
MA_RS00530	NA	2.25	2.12	2.40	2.85	2.57	1.78	1.87	3.46	3.49	2.08	2.64	2.33
MA_RS00535	NA	1.56	1.83	1.02	1.64	1.52	1.91	1.98	1.98	1.78	1.08	1.45	1.67
MA_RS00540	NA	1.19	0.28	0.40	1.38	0.77	0.30	2.03	1.37	0.28	1.11	0.85	0.75
MA_RS00545	NA	1.00	1.33	1.14	2.06	1.25	1.26	0.92	1.65	1.41	1.70	1.63	1.61
MA_RS00550	surE	4.21	4.32	4.44	4.79	4.56	4.63	4.70	4.88	5.02	4.64	4.63	4.42
MA_RS00555	moaA	5.36	5.80	5.62	6.03	5.69	6.07	6.01	6.14	6.39	6.07	5.84	6.03
MA_RS00560	NA	4.41	4.73	4.55	4.89	4.55	4.66	4.53	4.54	4.71	4.41	4.36	4.38
MA_RS00565	NA	5.15	5.50	5.25	5.47	5.21	5.57	5.53	6.16	6.22	5.38	5.28	5.28
MA_RS00570	NA	2.78	2.74	2.44	3.30	2.72	3.22	2.79	3.96	4.27	3.12	2.98	2.94
MA_RS00575	priL	4.87	4.92	4.74	5.23	5.02	5.15	5.12	5.28	5.63	4.91	5.09	5.16
MA_RS00580	NA	6.96	7.17	6.99	7.51	7.24	7.49	7.41	8.04	8.19	7.54	7.30	7.21
MA_RS00585	NA	4.90	5.05	5.14	5.51	5.15	5.31	5.62	6.35	6.68	5.27	5.14	5.56
MA_RS00590	NA	5.36	5.64	5.47	6.17	5.90	5.99	6.07	6.86	7.02	5.97	5.89	6.14
MA_RS00595	artA	4.29	4.34	4.36	4.52	4.22	4.42	4.23	4.68	5.05	4.58	4.31	4.27
MA_RS00600	NA	5.11	5.18	5.13	5.38	5.15	5.30	5.37	5.47	5.79	5.19	4.98	5.14
MA_RS00605	NA	3.44	3.76	3.46	4.07	3.88	3.84	3.56	4.27	4.35	3.29	3.50	3.53
MA_RS00610	NA	2.40	2.80	2.47	2.55	2.54	2.63	2.60	2.63	4.04	1.95	1.68	2.46
MA_RS00615	hisC	4.88	5.22	5.12	5.56	5.44	5.54	5.21	5.61	5.83	5.66	5.43	5.51
MA_RS00620	NA	5.20	5.42	5.33	5.80	5.49	5.76	5.59	5.82	5.94	5.72	5.40	5.57
MA_RS00630	NA	4.00	4.07	3.85	4.29	4.03	4.11	4.79	4.49	4.83	4.13	3.76	4.16
MA_RS00635	NA	4.08	4.42	4.73	4.68	4.31	4.46	4.54	5.00	5.13	4.69	4.31	4.65
MA_RS00640	NA	5.25	5.44	5.40	5.72	5.47	5.60	5.32	6.26	6.61	5.73	5.42	5.72
MA_RS00645	NA	4.15	4.28	4.37	4.55	4.35	4.42	4.54	5.33	5.72	4.61	4.35	4.56
MA_RS00650	NA	1.64	1.31	1.20	1.19	0.93	0.73	1.30	1.91	2.14	1.36	1.05	0.76
MA_RS00655	NA	3.02	3.56	3.27	3.86	3.52	3.76	3.57	3.55	3.86	3.53	3.59	3.32
MA_RS00665	NA	1.51	1.70	1.49	2.13	1.78	1.60	1.83	2.42	1.78	2.58	1.94	1.21
MA_RS00670	NA	2.10	2.33	2.19	2.72	2.31	2.50	2.45	3.35	3.53	2.69	2.54	2.55
MA_RS00675	NA	5.13	5.31	5.20	5.54	5.25	5.36	5.46	5.27	5.46	5.44	5.09	5.19
MA_RS00680	NA	5.13	5.54	5.44	5.55	5.37	5.36	5.63	5.47	5.74	5.41	5.27	5.51
MA_RS00685	purM	5.65	5.96	5.91	6.29	6.13	6.13	6.27	6.32	6.63	6.22	6.01	6.04
MA_RS00690	NA	5.78	6.06	5.91	6.41	6.06	6.29	6.21	6.37	6.67	6.38	6.02	6.11
MA_RS00695	NA	4.75	4.93	4.73	5.31	5.08	5.14	5.14	5.46	5.45	5.24	4.87	5.06
MA_RS00700	NA	5.42	5.33	5.50	5.52	5.19	5.58	5.99	6.50	6.13	5.33	5.11	4.98
MA_RS00705	NA	3.17	3.45	2.98	3.16	3.15	3.02	3.34	3.64	3.42	3.03	3.10	3.28
MA_RS00710	NA	3.30	3.27	3.27	3.84	3.04	3.56	3.58	3.68	3.48	3.34	3.21	3.10
MA_RS00715	NA	2.53	2.91	2.46	3.21	2.51	3.21	3.33	3.74	3.70	3.29	2.92	2.57
MA_RS00720	NA	4.08	3.73	3.67	4.12	3.94	4.14	4.22	4.55	4.38	4.69	4.10	4.13
MA_RS00725	NA	6.32	6.42	6.46	6.94	6.49	6.73	6.54	6.97	7.40	6.95	6.54	6.56
MA_RS00730	NA	6.36	6.62	6.54	7.09	6.71	6.95	6.70	6.95	7.22	6.85	6.66	6.63
MA_RS00735	NA	4.77	5.22	5.14	5.45	5.14	5.34	5.16	5.69	5.92	4.87	5.09	5.16
MA_RS00740	NA	5.55	5.74	5.27	2.71	2.85	2.68	3.28	4.68	4.57	3.90	3.34	2.77
MA_RS00745	NA	6.55	6.80	6.73	3.35	3.29	3.18	4.29	5.76	6.05	4.21	3.89	4.35
MA_RS00750	NA	6.64	6.96	6.75	2.41	2.36	2.55	4.14	4.80	5.04	3.36	3.81	4.17
MA_RS00765	NA	10.43	10.72	10.59	4.76	4.44	4.76	9.03	9.72	9.78	8.26	8.33	8.94
MA_RS00775	NA	9.40	9.54	9.55	6.83	6.50	6.68	8.80	9.69	9.66	8.13	8.02	8.53
MA_RS00780	NA	1.66	1.68	2.03	1.48	1.36	1.79	2.30	2.53	2.62	1.37	1.51	1.85
MA_RS00785	NA	1.73	1.85	1.47	2.29	1.84	2.07	2.25	2.74	3.31	2.03	1.59	1.50
MA_RS00790	NA	0.74	0.76	0.91	0.86	0.92	0.97	1.04	1.51	1.70	1.08	1.16	0.92

MA_RS00795	NA	5.25	5.59	5.41	5.09	4.76	5.05	5.08	5.65	5.86	5.12	4.71	4.92
MA_RS00805	NA	1.84	1.87	1.63	1.26	1.63	1.15	3.87	4.86	5.14	3.36	4.14	4.77
MA_RS00810	pyID	4.14	4.48	4.30	3.16	2.03	2.89	2.66	2.40	2.65	7.46	7.68	8.27
MA_RS00815	pyIC	4.99	5.23	5.23	3.72	3.33	3.52	0.00	0.00	0.00	8.69	8.78	9.28
MA_RS00820	pyIB	5.44	5.73	5.46	4.22	3.93	4.11	2.03	2.25	2.00	9.05	9.08	9.60
MA_RS00825	pyIS	5.22	5.44	5.39	5.03	4.58	4.67	7.28	7.91	7.91	5.13	4.81	5.07
MA_RS00835	NA	3.73	3.60	3.66	3.93	3.86	4.01	4.11	4.37	4.45	4.78	4.39	4.19
MA_RS00840	NA	3.00	3.27	3.39	3.60	3.45	3.40	3.42	4.01	3.77	3.59	3.66	3.46
MA_RS00845	NA	2.41	2.79	2.73	2.94	2.44	2.92	3.36	2.73	2.66	2.86	2.26	2.18
MA_RS00850	NA	2.52	2.98	2.24	3.15	3.03	2.85	3.55	3.06	3.42	2.64	2.80	2.96
MA_RS00855	NA	2.87	2.89	2.73	3.45	3.46	3.59	3.50	4.04	4.13	3.37	3.21	3.57
MA_RS00860	NA	2.81	3.17	3.08	2.77	2.70	2.55	2.83	3.58	3.80	2.95	2.23	2.85
MA_RS00865	NA	2.37	2.51	2.86	2.21	2.16	2.47	2.83	2.64	2.94	2.24	1.48	2.54
MA_RS00870	NA	3.71	3.97	3.87	3.66	3.41	3.75	3.34	4.18	4.11	3.30	3.32	3.52
MA_RS00875	NA	3.82	4.00	3.48	2.81	3.31	4.04	3.29	4.00	4.34	3.45	3.08	3.52
MA_RS00880	NA	4.20	4.46	4.20	4.70	4.56	4.60	4.62	4.41	4.61	4.29	4.13	4.53
MA_RS00885	NA	4.71	5.03	4.76	5.34	5.09	5.36	5.45	5.76	5.96	5.18	5.06	5.17
MA_RS00890	NA	2.77	2.56	1.72	2.14	2.13	3.02	3.62	3.67	2.80	2.83	2.88	2.07
MA_RS00900	NA	2.69	3.14	3.02	3.23	3.02	2.96	3.05	3.31	3.30	2.64	2.78	2.91
MA_RS00905	NA	1.51	1.59	1.99	2.01	2.32	1.83	2.06	2.28	2.32	1.75	1.02	1.85
MA_RS00910	NA	2.09	2.01	0.92	1.42	2.20	1.90	0.93	2.05	2.84	1.81	2.05	1.95
MA_RS00915	NA	1.44	1.26	1.53	1.92	1.66	1.62	1.58	1.82	1.86	1.65	1.56	1.20
MA_RS00920	NA	1.27	1.55	1.65	1.96	1.44	1.49	1.91	2.22	2.07	2.18	1.59	1.54
MA_RS00930	NA	5.53	5.84	5.64	6.14	5.87	6.07	5.94	5.90	6.05	6.03	5.85	5.86
MA_RS00935	NA	5.30	5.41	5.52	5.76	5.40	5.46	5.58	5.28	5.63	5.57	5.30	5.58
MA_RS00940	NA	1.96	2.36	2.45	2.72	2.20	2.49	2.73	3.12	3.36	2.88	2.00	2.30
MA_RS00945	NA	2.91	3.08	3.17	3.41	3.41	3.05	3.00	2.97	3.55	3.32	3.01	2.99
MA_RS00950	NA	3.80	3.92	3.63	4.16	3.97	4.09	4.00	4.50	4.66	4.15	3.97	4.03
MA_RS00955	NA	1.56	1.55	1.30	1.55	2.22	2.19	2.04	2.65	1.97	1.47	1.78	1.72
MA_RS00960	NA	1.95	1.79	2.25	2.41	2.18	2.43	1.74	3.30	3.26	2.66	2.46	2.43
MA_RS00965	NA	2.21	2.47	2.19	2.41	2.38	2.30	2.91	3.37	3.41	2.41	2.93	2.43
MA_RS00970	NA	2.71	2.55	2.53	2.95	2.71	2.83	2.81	3.24	3.56	3.32	3.16	3.33
MA_RS00975	NA	1.59	1.77	1.65	2.11	1.63	0.78	2.85	1.61	2.34	5.83	5.10	5.46
MA_RS00980	NA	1.59	1.84	1.49	2.25	1.79	1.94	1.82	2.26	3.10	5.07	4.95	4.95
MA_RS00985	NA	7.77	7.81	7.89	8.20	7.90	8.02	8.19	8.32	8.57	8.05	7.77	8.02
MA_RS00990	NA	7.48	7.79	7.54	8.03	7.80	8.00	8.00	8.17	8.27	8.17	7.76	7.84
MA_RS00995	NA	3.07	2.98	2.46	3.43	3.19	3.24	3.29	3.41	3.54	3.30	3.00	3.18
MA_RS01000	NA	3.00	2.97	2.45	3.31	2.81	3.16	2.96	3.33	3.60	3.48	2.97	3.18
MA_RS01005	NA	1.25	1.79	1.20	2.09	1.60	1.67	1.96	2.28	1.64	2.09	1.51	1.69
MA_RS01010	NA	3.35	3.37	3.04	3.71	3.72	3.39	3.64	4.09	4.17	3.82	3.50	3.22
MA_RS01020	NA	3.80	4.01	3.90	4.38	4.00	4.30	4.10	4.22	4.54	4.26	4.16	4.13
MA_RS01025	NA	3.00	3.40	3.23	3.49	3.45	3.55	3.33	3.88	4.36	3.57	3.26	3.75
MA_RS01030	NA	0.92	1.11	0.86	1.40	1.02	1.03	1.22	1.14	0.73	0.95	1.45	1.27
MA_RS01035	NA	3.03	2.58	2.65	2.51	3.14	3.30	2.71	3.77	3.86	3.13	3.33	2.93
MA_RS01040	NA	3.51	3.39	3.18	3.47	2.75	3.26	3.64	3.98	4.26	3.37	3.49	3.41
MA_RS01045	alaS	5.82	6.02	5.95	6.30	6.04	6.32	6.15	6.34	6.64	6.09	6.05	6.24
MA_RS01050	NA	3.17	3.43	2.91	3.88	3.26	3.69	3.61	4.05	4.36	4.05	3.62	3.43
MA_RS01055	NA	1.42	1.18	1.31	0.63	1.28	1.42	1.14	1.22	0.90	1.71	1.35	0.86
MA_RS01060	NA	0.70	0.72	1.50	0.34	1.24	1.07	1.39	1.29	1.33	1.30	1.05	1.02
MA_RS01065	NA	1.69	1.95	1.82	1.60	1.47	1.76	1.88	1.89	1.92	1.94	2.15	1.72
MA_RS01070	NA	3.78	4.02	4.07	4.13	3.99	4.08	4.12	5.05	5.37	3.94	3.78	3.96
MA_RS01075	NA	2.34	1.93	2.47	2.81	2.40	2.65	2.88	2.71	2.77	2.51	2.42	3.09
MA_RS01080	NA	6.53	6.71	6.68	7.22	6.80	7.11	7.19	7.44	7.71	7.46	6.87	6.95
MA_RS01085	NA	7.04	7.06	7.12	7.59	7.20	7.34	7.53	7.52	7.80	7.61	7.30	7.39
MA_RS01090	NA	3.43	3.56	3.46	3.74	3.55	3.81	3.81	4.44	4.63	3.59	3.52	3.60
MA_RS01095	NA	0.97	0.78	0.74	1.41	0.93	1.24	1.06	1.41	2.02	1.40	1.01	0.84
MA_RS01100	NA	0.60	0.47	0.38	0.83	0.57	0.66	0.48	0.96	0.80	0.75	0.43	0.43
MA_RS01105	NA	5.21	5.25	5.16	5.62	5.35	5.55	5.67	6.07	6.31	5.81	5.53	5.51
MA_RS01110	NA	4.30	4.31	4.42	4.91	4.71	4.78	4.76	5.54	5.69	5.01	4.49	4.69
MA_RS01115	truA	4.75	4.94	4.70	5.27	4.95	5.19	5.26	5.71	5.89	5.26	5.12	5.19
MA_RS01120	NA	2.77	2.84	3.10	3.38	3.19	3.25	3.46	3.31	3.16	2.94	2.77	3.34
MA_RS01125	NA	3.88	4.02	3.77	4.43	4.28	3.97	4.27	4.61	5.27	4.09	4.30	4.25
MA_RS01130	NA	3.61	3.97	3.94	4.35	3.84	4.33	4.13	4.69	5.20	3.61	3.80	4.07
MA_RS01135	map	4.66	4.78	4.77	5.27	4.90	5.04	5.25	5.37	5.59	4.91	4.69	4.98
MA_RS01140	NA	3.49	3.94	3.82	3.97	3.70	3.75	4.14	4.24	4.55	3.52	3.49	3.54
MA_RS01145	NA	0.73	0.95	1.09	1.56	1.31	1.22	1.68	1.63	1.32	1.47	1.44	1.33
MA_RS01150	#N/A	3.33	3.37	3.84	4.35	3.63	3.46	3.38	3.25	3.94	3.90	4.17	4.17
MA_RS01155	#N/A	4.42	4.47	5.13	3.88	4.52	4.39	4.85	2.00	1.63	3.95	4.36	4.55
MA_RS01160	NA	4.59	4.64	4.75	4.79	5.03	4.72	5.04	5.44	5.01	4.69	4.81	4.57
MA_RS01165	NA	6.47	6.73	6.66	7.44	7.07	7.25	7.25	7.65	7.80	7.12	6.79	7.02
MA_RS01170	hisG	6.30	6.48	6.41	6.93	6.59	6.74	6.86	7.43	7.61	7.00	6.67	6.81
MA_RS01175	hisA	5.62	5.78	5.85	6.12	5.94	6.17	6.40	6.17	6.56	6.15	5.96	6.10
MA_RS01180	hisB	5.16	5.63	5.46	5.89	5.69	5.88	5.95	6.33	6.84	6.10	5.89	5.71
MA_RS01185	NA	3.75	4.03	3.84	4.35	4.12	4.48	4.46	5.18	5.12	4.77	4.63	4.50
MA_RS01195	NA	1.11	1.30	1.58	1.64	1.34	1.57	1.62	2.61	2.83	1.55	1.50	1.90
MA_RS01200	NA	0.60	0.49	0.37	0.54	0.73	0.70	0.78	1.21	1.23	1.04	0.62	0.62
MA_RS01205	NA	2.16	2.17	2.43	2.72	2.18	2.25	2.54	3.02	2.76	2.29	2.19	2.12
MA_RS01215	NA	0.83	1.00	0.31	1.34	0.81	0.90	0.49	1.14	1.66	0.61	1.04	0.92
MA_RS01220	NA	1.21	1.30	0.97	1.28	1.48	0.99	1.56	1.80	1.70	1.42	1.53	1.49
MA_RS01225	NA	1.13	1.03	0.67	1.30	1.18	1.15	1.06	1.41	1.79	1.02	0.95	1.05
MA_RS01230	NA	3.22	3.44	3.48	3.71	3.27	3.24	3.32	4.19	4.34	3.83	3.21	3.51
MA_RS01240	NA	0.82	0.80	0.51	0.69	0.82	0.43	1.41	1.43	1.97	0.79	1.04	0.38
MA_RS01245	NA	0.69	0.86	1.03	0.78	1.39	1.53	1.05	1.77	1.84	1.32	1.09	1.44
MA_RS01250	NA	2.34	2.50	2.62	2.51	2.23	2.23	2.21	2.59	3.05	2.00	1.89	2.06
MA_RS01255	NA	3.12	3.24	3.26	3.42	3.02	3.21	2.97	3.77	4.03	2.98	2.65	2.72
MA_RS01260	NA	2.06	2.06	1.62	2.78	1.96	2.04	2.45	2.97	2.93	2.34	1.48	2.38
MA_RS01265	NA	3.79	4.10	3.82	4.00	3.64	4.10	4.03	4.34	4.62	4.11	4.06	3.81
MA_RS01270	NA	3.60	3.58	3.59	4.07	3.26	3.57	4.23	4.92	4.51	3.83	3.68	3.84
MA_RS01275	NA	2.60	2.91	2.96	3.31	3.46	3.69	3.81	3.78	4.05	3.81	3.09	3.20
MA_RS01280	NA	2.49	2.83	2.71	3.08	3.00	3.59	3.08	3.71	3.89	3.37	3.10	3.22
MA_RS01285	larE	3.81	3.92	3.83	4.45	3.92	4.30	4.13	4.36	4.85	4.10	3.90	4.12
MA_RS01290	glmM	4.61	4.61	4.60	5.05	4.73	4.91	5.06	5.32	5.39	4.89	4.63	4.60
MA_RS01295	NA	4.42	4.51	4.42	4.88	4.76	4.78	4.72	4.71	4.97	4.53	4.62	4.89
MA_RS01300	NA	4.52	4.64	4.67	5.10	4.80	5.01	4.79	4.96	5.21	4.90	4.68	4.89
MA_RS01305	NA	5.56	5.65	5.58	6.14	5.86	5.83	6.12	6.60	7.13	6.07	5.66	5.97
MA_RS01310	NA	5.27	5.41	5.28	5.81	5.41	5.52	5.65	5.68	5.93	5.59	5.41	5.56
MA_RS01315	NA	4.45	4.64	4.59	5.01	4.73	4.70	4.83	5.43	5.65	4.87	4.62	4.72
MA_RS01320	NA	4.21	4.40	4.33	5.23	4.75	5.01	5.15	5.65	5.75	5.04	4.75	4.71
MA_RS01325	NA	1.55	1.22	1.47	2.17	1.86	1.50	1.90	2.38	2.98	1.67	1.52	1.56
MA_RS01330	NA	5.20	5.40	5.15	5.86	5.35	5.71	5.67	6.20	6.44	5.75	5.41	5.52
MA_RS01335	acnA	5.34	5.67	5.46	5.97	5.71	5.77	5.85	5.88	6.08	5.66	5.49	5.72
MA_RS01340	NA	3.30	3.65	3.37	3.73	3.21	3.51	3.41	3.92	3.69	3.70	3.39	3.51
MA_RS01345	NA	3.09	3.10	2.97	3.22	3.43	3.26	3.16	3.62	3.77	3.16	3.41	2.87
MA_RS01350	NA	2.51	2.85	2.51	2.97	2.94	3.07	2.80	3.14	3.49	2.88	2.63	2.90
MA_RS01355	NA	3.36	3.64	3.30	3.88	3.58	3.89	3.93	4.19	4.58	3.70	3.55	3.74
MA_RS01360	NA	3.47	3.51	3.47	3.80	3.62	3.81	3.21	4.65	4.62	3.74	3.56	3.85
MA_RS01365	NA	2.89	2.83	3.10	3.32	2.98	3.30	2.91	3.39	3.52	2.98	2.78	2.74
MA_RS01370	tnpA	1.06	1.47	1.06	0.45	1.47	0.87	0.74	0.49	1.20	0.80	1.58	0.51
MA_RS01375	tnpB	4.71	4.57	4.89	5.35	4.99	5.19	5.10	6.00	6.31	5.48	5.07	5.02
MA_RS01380	NA	3.20	3.11	3.42	4.05	3.45	3.75	3.86	4.51	4.77	4.38	3.62	3.76
MA_RS01385	NA	1.41	1.17	1.43	1.54	1.76	1.17	0.98	1.58	1.51	1.11	1.33	1.38
MA_RS01390	thiC	2.00	2.18	1.80	2.56	2.50	2.67	2.29	2.76	2.70	2.52	2.47	2.12
MA_RS01395	NA	3.82	3.94	4.09	4.60	4.10	4.32	4.42	5.28	5.61	4.58	4.18	4.13
MA_RS01400	#N/A	2.04	0.46	0.00	1.84	1.65	0.17	1.65	2.48	1.59	2.67	0.16	2.52
MA_RS01405	NA	3.00	3.08	3.15	3.07	2.87	3.42	3.16	3.53	3.67	3.29	3.21	3.30
MA_RS01410	NA	3.34	3.56	3.13	3.70	3.39	4.01	3.61	3.86	4.06	4.17	3.82	3.78
MA_RS01415	NA	3.13	2.88	3.02	3.16	3.24	3.00	3.07	3.38	3.37	3.08	2.87	3.41
MA_RS01420	NA	3.50	3.80	3.67	3.98	3.92	4.04	4.09	4.18	4.01	4.02	3.80	3.79
MA_RS01425	NA	3.73	4.19	3.99	4.44	4.24	4.48	4.17	4.92	5.22	4.69	4.20	4.21
MA_RS01430	mtrH	8.20	8.65	8.45	8.99	8.62	8.92	8.78	9.11	9.43	8.12	8.47	8.67
MA_RS01435	mtrG	9.54	9.71	9.83	10.39	9.81	10.04	10.41	11.09	11.20	9.58	9.63	9.97
MA_RS01440	mtrF	8.37	8.75	8.59	9.21	8.74	8.94	9.18	9.69	9.99	8.31	8.52	8.80
MA_RS01445	mtrA	8.64	8.93	8.79	9.39	8.91	9.16	9.31	9.65	9.89	8.46	8.74	9.04
MA_RS01450	NA	8.32	8.71	8.48	9.24	8.68	8.99	8.86	9.14	9.58	8.30	8.50	8.71
MA_RS01455	mtrC	8.18	8.59	8.45	8.97	8.54	8.75	8.94	9.19	9.37	8.02	8.29	8.58
MA_RS01460	mtrD	8.25	8.65	8.38	9.14	8.54	8.91	8.80	9.45	9.89	8.29	8.48	8.70
MA_RS01465	mtrE	8.10	8.50	8.28	8.89	8.38	8.75	8.55	8.88	9.30	8.05	8.32	8.44
MA_RS01475	NA	3.53	3.93	3.77	3.92	3.53	3.92	3.96	4.46	4.29	4.02	3.86	4.08
MA_RS01480	NA	2.45	2.07	2.25	2.29	2.32	2.67	2.73	3.08	3.28	2.41	2.35	2.32
MA_RS01485	NA	5.06	5.32	5.08	5.26	4.82	5.16	4.99	5.58	5.87	5.39	5.10	5.20
MA_RS01490	wtpA	3.79	3.67	3.73	4.29	3.93	4.23	4.27	5.10	5.21	4.33	4.36	4.26
MA_RS01495	NA	2.24	2.04	2.18	2.62	2.39	2.92	2.03	2.84	3.19	2.86	2.79	2.77
MA_RS01500	NA	1.95	2.28	2.09	2.00	2.22	2.12	2.28	2.40	2.54	2.01	2.21	2.57
MA_RS01505	NA	3.96	3.93	4.02	4.24	4.14	3.95	4.01	4.40	4.50	4.18	4.20	3.73
MA_RS01510	NA	6.04	6.24	6.26	6.20	5.81	5.96	6.17	6.70	6.75	5.80	5.75	6.06
MA_RS01515	NA	4.90	5.10	4.97	4.84	4.57	4.90	5.29	5.42	5.47	4.67	4.41	4.98
MA_RS01520	NA	5.43	5.61	5.39	5.36	5.10	5.33	5.50	5.56	5.62	5.03	4.99	5.32
MA_RS01525	NA	3.57	3.60	3.61	3.61	3.50	3.62	3.86	4.11	4.37	3.90	3.79	3.91
MA_RS01530	NA	0.52	0.43	0.57	0.77	0.58	0.65	0.70	1.11	1.39	0.91	0.48	0.62
MA_RS01535	NA	4.28	4.33	4.13	4.67	4.44	4.54	4.64	4.98	4.78	4.37	4.14	4.39
MA_RS01540	NA	3.58	3.98	3.77	4.17	3.76	3.83	3.69	4.76	5.32	4.27	3.99	3.56
MA_RS01545	NA	4.69	5.02	4.81	5.12	5.11	5.15	5.14	6.12	5.94	5.63	4.88	5.06
MA_RS01550	NA	2.40	2.89	2.61	2.27	2.64	3.04	2.60	2.88	3.05	2.77	2.46	2.52

MA_RS01555	NA	2.29	2.30	3.16	2.38	2.85	2.61	3.04	2.24	2.79	2.70	2.46	2.87
MA_RS01560	NA	4.07	4.19	4.06	4.21	4.10	4.36	4.49	4.73	4.53	4.36	4.16	3.92
MA_RS01565	NA	0.89	1.02	1.03	1.21	1.38	1.23	1.48	1.49	1.34	1.35	0.85	1.45
MA_RS01570	NA	0.18	0.38	0.31	0.27	0.17	0.50	0.25	0.51	0.83	0.42	0.30	0.00
MA_RS01575	NA	1.00	1.45	1.38	1.19	1.36	1.22	1.12	1.16	1.31	0.80	1.14	1.49
MA_RS01580	NA	1.25	1.81	1.38	2.31	1.19	1.75	1.77	1.75	2.15	1.18	1.72	2.04
MA_RS01585	NA	1.11	1.27	1.45	1.71	1.36	1.46	1.17	1.11	1.50	1.36	1.36	1.61
MA_RS01590	NA	1.61	1.63	1.56	1.94	1.68	2.14	1.43	1.93	1.37	1.54	1.35	2.14
MA_RS01595	NA	0.77	1.10	0.63	1.89	1.47	1.86	1.72	1.50	1.52	1.14	1.63	1.56
MA_RS01600	NA	1.54	1.77	1.94	2.79	1.68	2.22	2.00	2.80	3.02	1.88	2.21	2.57
MA_RS01605	NA	0.54	1.10	1.49	1.79	0.88	2.35	1.96	1.76	1.34	1.01	1.28	2.14
MA_RS01620	NA	6.19	6.35	6.25	6.61	6.07	6.38	6.70	7.02	7.35	6.65	6.40	6.68
MA_RS01625	NA	5.76	6.02	5.82	6.24	5.73	6.12	6.27	6.54	7.08	6.04	6.04	6.39
MA_RS01630	NA	6.34	6.62	6.53	7.09	6.46	6.77	7.16	7.67	8.18	6.76	6.84	7.03
MA_RS01635	NA	5.76	5.95	6.09	6.35	6.01	6.15	6.73	6.55	6.70	5.92	6.13	6.41
MA_RS01640	NA	6.43	6.46	6.64	6.66	6.44	6.50	7.12	6.89	7.08	6.18	6.48	6.76
MA_RS01645	NA	6.28	6.54	6.45	6.87	6.45	6.69	6.96	6.83	6.95	6.42	6.61	6.85
MA_RS01650	NA	0.52	0.80	0.77	0.80	0.83	0.60	0.89	1.70	0.96	1.00	1.01	1.15
MA_RS01655	NA	3.66	3.88	3.73	3.82	3.53	3.79	3.78	4.28	4.47	4.02	3.42	3.51
MA_RS01660	NA	0.00	0.18	0.00	0.24	0.56	0.64	0.00	0.46	0.00	0.62	0.27	0.23
MA_RS01665	NA	2.57	2.45	2.13	2.84	2.64	2.74	2.76	3.22	3.59	2.79	2.77	2.24
MA_RS01670	NA	1.64	1.76	1.72	2.10	1.87	1.60	1.92	2.40	2.99	2.31	2.07	1.80
MA_RS01675	NA	1.22	1.51	1.70	1.54	1.68	1.36	1.97	2.43	2.69	2.03	1.39	1.67
MA_RS01680	purN	1.63	1.55	1.54	1.79	1.62	2.32	1.87	2.62	2.69	2.08	1.80	1.63
MA_RS01700	NA	2.52	2.95	3.18	3.38	2.45	2.70	3.55	3.93	4.00	2.58	2.73	3.23
MA_RS01705	NA	3.68	4.16	3.93	4.32	3.75	4.08	4.02	3.53	3.58	3.54	3.77	3.89
MA_RS01710	NA	4.94	5.12	5.21	5.66	5.21	5.51	5.61	5.63	5.85	5.11	5.14	5.42
MA_RS01715	NA	4.81	4.92	4.84	5.46	4.97	5.26	5.56	5.23	5.58	4.66	4.80	5.17
MA_RS01720	NA	5.11	5.36	5.19	5.83	5.33	5.60	5.55	5.41	5.89	5.17	5.49	5.43
MA_RS01725	modA	5.25	5.24	5.43	5.79	5.41	5.58	5.81	5.68	5.87	5.47	5.48	5.54
MA_RS01730	NA	3.60	3.90	3.76	4.07	3.82	4.20	4.17	4.65	4.91	4.13	3.76	3.80
MA_RS01735	NA	2.30	2.68	2.16	2.91	2.56	2.91	2.83	3.09	3.59	2.87	3.12	2.80
MA_RS01740	NA	1.86	2.42	2.45	2.46	1.92	2.29	2.92	2.48	2.88	2.65	2.34	2.56
MA_RS01745	NA	3.13	3.70	3.11	4.01	3.73	3.80	3.87	4.47	4.61	3.70	3.61	3.65
MA_RS01750	NA	2.54	3.01	3.17	3.56	3.25	3.52	3.23	3.65	3.69	3.22	3.22	3.27
MA_RS01755	NA	3.18	3.17	3.17	3.59	3.19	3.40	3.55	4.15	4.35	3.71	3.34	3.46
MA_RS01760	NA	2.93	3.29	2.57	3.62	3.03	3.49	3.24	3.51	3.58	3.41	3.33	3.46
MA_RS01765	NA	3.21	3.42	3.06	3.50	3.59	3.56	3.19	2.66	3.24	3.38	3.23	3.38
MA_RS01770	NA	4.85	5.03	4.98	5.29	5.13	5.39	4.98	5.38	5.60	5.49	5.31	5.24
MA_RS01775	NA	4.31	4.50	4.34	4.82	4.51	4.68	4.71	4.94	5.15	4.61	4.50	4.63
MA_RS01780	NA	6.77	7.13	6.97	7.21	6.72	7.05	7.05	7.45	7.81	6.98	6.74	6.92
MA_RS01785	NA	3.87	4.15	3.69	4.24	4.19	4.09	4.34	4.59	4.69	4.16	3.41	3.90
MA_RS01790	NA	3.43	3.56	3.38	3.59	3.60	3.53	3.84	4.35	4.56	3.67	3.29	3.52
MA_RS01795	NA	5.71	5.84	5.87	5.96	5.83	5.86	5.93	6.12	6.06	5.69	5.73	5.86
MA_RS01800	NA	5.48	5.82	5.63	5.86	5.63	5.83	5.73	5.62	5.82	5.55	5.57	5.67
MA_RS01805	NA	4.11	4.21	4.26	4.69	4.06	4.62	4.52	5.22	5.47	4.56	4.01	4.47
MA_RS01810	NA	2.70	2.77	3.02	2.82	2.81	2.55	3.44	3.26	3.28	2.77	2.77	3.18
MA_RS01815	NA	3.43	3.91	3.97	3.42	3.30	3.41	3.93	4.68	4.34	1.97	3.44	3.64
MA_RS01820	NA	3.54	4.12	3.98	3.64	3.41	3.63	4.52	5.88	5.62	2.44	3.50	4.05
MA_RS01825	NA	3.12	3.45	3.39	3.34	2.95	3.19	4.04	4.47	4.00	2.09	3.04	3.38
MA_RS01830	NA	1.67	1.55	1.63	1.88	1.74	2.11	2.04	2.34	2.60	1.95	1.86	1.86
MA_RS01840	NA	2.20	2.46	2.57	2.74	2.71	2.60	2.82	3.33	3.47	3.10	2.58	2.75
MA_RS01845	NA	0.20	0.19	0.27	0.38	0.25	0.35	0.33	0.46	0.76	0.26	0.30	0.33
MA_RS01850	NA	0.05	0.26	0.23	0.18	0.22	0.19	0.11	0.12	0.03	0.16	0.04	0.02
MA_RS01855	NA	1.11	1.05	0.97	1.42	0.90	1.43	1.12	1.97	2.30	1.28	1.58	1.37
MA_RS01860	#N/A	1.40	1.01	0.86	0.81	1.08	0.45	1.27	1.39	1.13	1.71	0.74	0.96
MA_RS01870	NA	0.80	0.64	0.28	0.97	0.96	0.96	1.34	0.62	1.54	0.88	0.36	0.80
MA_RS01875	NA	1.72	1.31	1.72	1.41	1.90	2.20	1.83	1.12	1.87	2.42	1.34	1.79
MA_RS01880	NA	1.50	2.30	1.73	1.17	1.83	2.15	2.26	1.02	0.68	1.99	1.21	2.07
MA_RS01885	NA	0.42	0.23	0.95	0.78	0.51	0.84	0.54	1.05	0.62	0.78	1.13	0.75
MA_RS01890	NA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.00	0.00	0.00
MA_RS01895	NA	0.87	1.07	1.10	1.40	1.39	1.26	0.93	1.38	1.50	1.46	0.44	1.13
MA_RS01900	NA	1.62	1.12	1.76	1.67	1.70	1.98	1.70	1.84	2.52	1.77	1.88	1.06
MA_RS01905	NA	1.29	1.15	1.09	1.85	1.63	1.37	1.79	1.41	2.20	1.98	1.23	1.58
MA_RS01910	NA	2.04	1.90	2.11	2.73	1.99	2.88	2.40	2.40	3.36	2.02	2.22	2.48
MA_RS01915	NA	2.63	2.70	3.00	3.03	2.96	2.89	2.27	3.32	3.72	2.97	2.42	2.46
MA_RS01920	NA	1.41	1.41	1.02	1.23	1.40	1.83	1.18	2.20	2.32	1.44	1.31	1.47
MA_RS01925	NA	2.31	2.32	2.39	2.68	2.62	2.75	2.74	2.91	3.51	3.29	2.71	2.50
MA_RS01930	NA	1.64	1.53	1.32	1.79	2.05	1.94	1.78	1.94	2.87	2.73	1.83	1.74
MA_RS01935	NA	2.72	2.65	2.66	2.72	3.02	2.81	2.81	3.39	3.17	3.43	2.51	2.86
MA_RS01940	NA	1.36	2.03	1.49	1.49	2.19	1.41	1.73	1.69	0.89	1.63	0.96	0.82
MA_RS01945	NA	2.70	3.09	3.24	3.21	3.23	3.09	2.91	3.35	3.01	2.48	2.52	2.04
MA_RS01950	pyrH	4.00	4.36	4.01	4.29	4.20	4.38	4.31	4.46	4.76	4.83	4.56	4.31
MA_RS01955	NA	2.84	3.09	3.12	3.39	2.94	3.03	2.98	4.01	4.18	2.99	2.97	2.87
MA_RS01960	NA	2.28	2.30	2.29	2.61	2.27	2.48	2.65	2.70	2.88	2.04	2.45	2.18
MA_RS01965	NA	1.81	1.49	2.05	2.85	1.00	2.03	2.55	2.89	3.16	2.48	2.05	2.12
MA_RS01970	NA	1.27	1.98	1.16	2.13	1.91	2.11	1.37	3.09	3.24	2.27	1.94	2.50
MA_RS01975	NA	2.53	2.79	2.79	2.89	2.63	3.02	2.55	2.95	2.83	2.76	2.37	3.16
MA_RS01980	NA	3.67	3.67	3.69	4.27	3.83	4.19	4.48	5.13	5.20	4.45	3.79	4.04
MA_RS01985	NA	2.99	3.37	3.09	3.69	3.18	3.52	3.27	3.71	3.79	3.51	3.10	3.16
MA_RS01990	NA	3.63	3.81	3.83	3.90	3.72	4.09	3.96	4.90	4.91	3.84	3.83	3.58
MA_RS02000	NA	4.53	4.78	4.55	5.23	4.91	5.33	5.25	5.85	5.82	4.93	4.96	5.22
MA_RS02005	tsaA	4.32	4.18	4.21	4.59	4.40	4.80	4.97	5.16	5.10	4.20	4.52	4.82
MA_RS02010	NA	0.99	0.97	1.24	1.24	1.34	1.45	1.13	1.60	1.69	1.12	1.21	1.34
MA_RS02015	cobN	1.46	1.55	1.37	1.90	1.69	1.87	1.71	1.70	1.60	1.73	1.82	1.91
MA_RS02025	cobN	1.95	2.28	2.18	2.31	2.09	2.30	2.65	3.08	2.85	1.96	2.00	2.37
MA_RS02030	NA	2.22	2.51	2.66	2.48	2.56	2.54	2.92	3.57	3.50	2.53	2.51	2.72
MA_RS02035	zupT	0.55	0.61	0.43	1.15	0.95	0.94	0.82	0.67	1.11	0.72	0.95	0.67
MA_RS02040	NA	0.43	0.43	0.49	0.56	0.34	0.67	0.40	1.14	0.95	0.71	0.46	0.51
MA_RS02045	NA	1.64	1.05	1.58	1.74	0.93	2.05	1.91	2.45	2.66	2.05	1.98	1.18
MA_RS02050	NA	1.01	1.76	1.53	1.11	1.18	1.71	1.99	2.39	3.09	2.00	1.70	1.08
MA_RS02055	NA	0.84	0.45	0.88	0.75	0.69	1.08	0.33	0.77	1.75	0.84	1.01	0.59
MA_RS02060	NA	0.21	0.42	0.33	0.32	0.62	0.97	0.79	1.13	0.40	0.23	0.00	0.00
MA_RS02065	NA	1.34	0.61	0.79	0.56	0.50	1.23	1.50	1.51	0.85	0.94	0.00	1.57
MA_RS02070	cbiQ	0.58	0.67	0.35	0.96	0.46	0.94	0.78	0.87	0.42	0.76	0.68	1.17
MA_RS02075	NA	0.51	0.94	0.85	0.72	1.00	0.74	1.19	1.13	1.25	0.70	0.45	0.75
MA_RS02085	NA	2.50	2.66	2.45	2.57	2.57	2.58	2.79	3.14	3.12	2.68	2.90	2.93
MA_RS02090	NA	0.34	0.61	0.00	0.87	0.58	0.00	0.00	0.41	0.00	0.36	0.12	0.00
MA_RS02095	NA	0.22	0.42	0.23	0.54	0.19	0.53	0.42	1.16	0.89	0.53	0.27	0.24
MA_RS02100	NA	1.48	1.61	1.44	1.91	1.72	1.78	1.67	2.47	2.49	1.83	1.57	1.99
MA_RS02105	NA	0.62	0.61	1.08	1.08	0.76	1.03	1.27	1.32	1.59	1.04	0.92	0.56
MA_RS02110	NA	1.12	0.47	0.55	1.19	0.23	1.30	0.43	1.34	1.55	1.10	1.77	0.76
MA_RS02115	NA	0.80	1.67	1.19	1.58	1.26	1.46	1.74	0.76	2.34	1.43	1.15	1.48
MA_RS02120	NA	1.89	2.28	2.15	2.33	1.92	2.24	1.88	2.89	3.13	2.28	2.18	1.91
MA_RS02125	NA	2.12	2.06	1.87	2.36	1.96	2.53	2.35	2.96	2.90	2.42	2.34	2.49
MA_RS02130	NA	1.65	1.83	1.71	2.49	2.24	2.34	2.32	2.80	3.17	2.07	1.93	2.32
MA_RS02135	NA	0.36	0.40	0.25	0.29	0.53	0.60	0.57	0.58	1.00	0.60	0.39	0.69
MA_RS02140	NA	1.02	0.89	0.67	1.14	1.29	1.50	0.84	1.85	1.83	1.36	1.44	1.20
MA_RS02145	NA	1.38	1.59	1.56	2.04	1.81	2.06	1.49	2.55	2.57	2.08	1.72	1.84
MA_RS02150	NA	1.99	2.49	2.50	2.50	2.40	2.73	2.63	2.91	3.23	3.03	2.63	2.63
MA_RS02155	NA	1.61	2.28	2.54	2.35	2.50	2.18	2.49	3.07	3.15	2.97	2.28	2.18
MA_RS02160	NA	1.71	1.93	1.43	2.13	1.86	2.02	1.87	2.28	2.81	2.42	1.89	2.02
MA_RS02165	NA	2.96	3.15	3.18	3.43	3.36	3.31	3.59	4.49	4.44	3.99	3.39	3.09
MA_RS02170	NA	0.82	0.80	1.45	0.65	0.65	0.44	1.16	1.08	1.82	0.81	0.74	1.01
MA_RS02175	NA	1.88	1.91	1.98	2.45	2.11	2.30	1.98	2.73	2.93	2.32	1.93	2.17
MA_RS02180	NA	1.81	1.94	2.11	2.26	2.50	2.42	2.52	2.72	3.51	2.20	1.29	2.22
MA_RS02185	NA	2.16	2.29	2.27	2.75	2.46	2.77	3.03	3.35	3.62	2.83	2.38	2.41
MA_RS02190	NA	0.51	0.48	0.46	0.66	0.87	0.54	0.42	0.00	1.05	0.38	0.24	0.19
MA_RS02195	NA	0.57	1.02	0.28	1.00	0.90	0.56	1.28	1.16	1.61	0.94	1.17	0.92
MA_RS02200	NA	0.58	0.61	0.87	0.63	0.68	1.27	0.58	1.48	1.83	1.00	1.19	1.27
MA_RS02205	NA	2.18	2.61	2.06	2.66	2.55	2.70	2.92	3.40	3.19	2.41	2.44	2.62
MA_RS02210	NA	1.61	1.24	1.03	1.71	1.60	1.39	1.24	1.54	2.15	1.67	1.58	1.65
MA_RS02220	NA	4.64	4.31	4.99	4.97	4.78	4.47	4.77	5.46	4.93	4.55	4.65	4.49
MA_RS02225	NA	3.02	3.36	3.20	2.89	3.24	3.58	3.86	4.00	4.46	3.41	3.32	3.25
MA_RS02230	NA	3.54	3.71	3.81	3.95	3.53	3.85	3.90	5.04	5.25	4.63	3.89	3.43
MA_RS02235	NA	0.43	0.29	0.86	0.26	0.83	0.71	0.36	0.62	0.19	1.04	0.43	0.50
MA_RS02240	NA	1.60	1.82	2.03	2.10	1.77	2.07	1.88	3.07	3.20	2.81	1.89	1.92
MA_RS02245	larB	4.27	4.54	4.51	4.77	4.50	4.65	4.79	5.04	5.21	4.46	4.32	4.54
MA_RS02250	larC	3.97	4.33	4.08	4.54	4.16	4.43	4.27	4.70	4.85	4.30	4.07	4.42
MA_RS02255	asd	5.15	5.44	5.39	5.55	5.41	5.55	5.62	5.53	5.55	5.35	5.47	5.56
MA_RS02260	NA	6.28	6.27	6.06	6.58	6.50	6.60	6.83	7.16	7.15	6.52	6.50	6.34
MA_RS02265	NA	4.06	4.22	4.18	4.96	4.61	4.54	4.68	5.05	5.16	5.08	4.53	4.82
MA_RS02270	NA	5.05	5.18	5.07	5.81	5.22	5.46	5.55	6.20	6.48	5.99	5.27	5.59
MA_RS02275	NA	1.67	2.62	1.84	2.37	2.59	2.57	2.76	2.84	3.46	2.57	2.30	2.45
MA_RS02285	NA	4.86	5.11	4.78	5.56	5.58	5.59	5.47	5.58	5.80	5.65	5.36	5.38
MA_RS02290	NA	3.20	3.37	3.34	3.82	3.64	3.65	4.16	4.22	4.62	4.14	3.52	3.70
MA_RS02295	#N/A	2.88	3.19	3.32	4.01	3.55	3.65	3.42	4.84	5.22	4.16	3.85	3.48
MA_RS02300	NA	5.58	5.65	5.53	6.00	5.81	5.95	6.00	6.11	6.20	6.17	5.76	5.69
MA_RS02305	NA	4.37	4.36	4.46	4.45	4.36	4.31	4.74	5.03	4.69	4.74	4.30	4.52
MA_RS02310	NA	3.87	4.21	3.97	4.52	4.00	4.38	4.15	4.80	4.99	4.38	4.07	4.28
MA_RS02315	NA	1.78	2.04	1.51	1.79	1.60	1.34	1.80	2.08	1.64	1.49	1.85	1.79
MA_RS02320	NA	1.45	1.12	0.86	1.36	0.86	0.97	0.89	1.65	2.11	1.03	0.99	0.99
MA_RS02325	NA	1.58	1.49	1.29	1.29	2.01	1.66	0.73	1.43	2.10	1.84	1.69	1.15

MA_RS02330	NA	2.39	2.52	1.62	2.24	2.00	2.39	2.05	3.43	2.95	2.39	1.66	2.16
MA_RS02340	NA	3.36	3.55	3.50	3.66	3.52	3.59	3.49	3.94	3.93	3.39	3.36	3.23
MA_RS02345	NA	1.32	1.75	1.88	1.71	1.54	1.24	0.52	1.47	1.81	1.77	1.38	1.49
MA_RS02350	msrB	2.51	2.87	2.30	3.26	2.34	2.76	1.97	2.89	3.38	2.64	2.19	2.17
MA_RS02360	NA	3.35	3.58	3.56	3.02	3.25	3.62	3.14	3.73	3.64	2.97	3.08	3.23
MA_RS02365	NA	2.96	2.89	2.73	3.11	3.12	2.85	2.95	3.44	3.35	2.93	2.86	2.93
MA_RS02370	NA	2.54	2.78	2.70	2.70	2.38	2.92	1.95	2.47	3.10	2.74	2.33	2.41
MA_RS02375	NA	2.16	2.13	2.35	2.19	2.20	2.27	2.34	2.82	2.56	2.34	2.18	2.46
MA_RS02380	mtaB	3.05	3.37	3.00	10.97	10.47	10.69	11.02	11.13	11.40	10.31	10.55	10.56
MA_RS02385	mtaC	2.26	2.68	2.60	11.24	10.77	10.92	11.38	11.71	12.05	10.62	10.74	10.86
MA_RS02395	NA	0.53	0.58	0.15	0.74	0.55	1.12	0.00	0.71	2.02	1.27	1.04	0.60
MA_RS02400	NA	3.71	3.83	3.73	5.64	5.24	5.42	5.73	6.05	6.20	5.53	5.34	5.19
MA_RS02405	NA	2.90	3.13	3.11	4.77	4.44	4.71	4.89	5.35	5.62	4.40	4.38	4.53
MA_RS02410	NA	2.01	2.28	2.05	2.31	1.99	2.20	2.36	2.54	2.75	2.20	2.40	2.36
MA_RS02415	NA	1.87	1.58	2.08	1.94	1.91	1.81	1.74	1.22	1.66	1.03	1.82	2.35
MA_RS02420	NA	3.99	3.81	3.90	3.79	4.05	3.96	4.55	4.10	3.93	3.85	3.77	3.52
MA_RS02425	NA	2.99	2.98	2.88	3.50	3.06	3.33	3.61	3.43	3.57	3.14	2.81	3.25
MA_RS02430	NA	1.23	1.22	1.52	1.28	1.65	1.25	1.48	1.59	1.66	1.31	1.21	1.09
MA_RS02440	NA	1.64	1.56	1.91	1.67	1.85	1.97	1.81	2.09	2.31	1.54	1.84	1.75
MA_RS02445	NA	1.56	1.53	1.56	1.55	1.36	1.65	1.67	1.93	2.58	1.99	1.90	2.27
MA_RS02450	NA	1.77	1.18	1.00	1.34	1.63	0.52	1.69	1.65	1.66	1.85	1.54	1.84
MA_RS02455	NA	2.26	2.74	2.44	3.11	2.80	3.05	2.95	3.55	4.10	3.38	3.05	3.01
MA_RS02465	NA	1.25	1.50	1.91	2.26	1.93	2.22	2.27	3.14	2.97	2.16	2.17	2.20
MA_RS02470	NA	1.92	2.09	1.93	2.19	2.16	2.37	2.19	2.46	2.87	2.37	2.32	2.19
MA_RS02475	NA	0.00	0.05	0.00	0.00	0.00	0.22	0.31	0.00	0.55	0.83	0.42	0.46
MA_RS02480	NA	2.00	1.90	1.81	2.07	2.56	2.39	2.62	3.06	2.65	2.84	2.20	1.83
MA_RS02485	NA	2.43	2.59	2.57	2.83	2.81	3.16	3.12	3.65	3.61	3.32	2.82	2.75
MA_RS02490	NA	1.63	1.89	1.88	2.21	2.33	2.72	2.07	2.98	3.51	2.01	2.29	1.60
MA_RS02495	NA	1.47	1.63	1.73	2.21	2.61	1.99	2.48	2.81	2.99	1.84	1.05	1.90
MA_RS02500	NA	2.70	2.86	3.21	3.29	3.17	3.51	2.97	3.73	3.90	3.51	2.86	3.35
MA_RS02505	NA	2.38	2.12	2.34	2.08	2.49	2.50	2.66	3.39	3.78	3.13	2.47	2.10
MA_RS02510	NA	2.26	2.06	2.65	2.67	2.14	2.40	2.86	3.18	3.66	2.69	1.82	2.47
MA_RS02520	NA	1.14	0.86	0.85	1.92	1.46	1.24	2.02	1.92	1.89	1.53	0.79	1.45
MA_RS02525	NA	4.13	4.53	4.64	4.86	4.60	4.69	4.81	5.45	5.74	4.95	4.44	4.49
MA_RS02530	NA	0.49	0.77	1.03	0.54	0.80	0.67	0.45	1.25	1.19	0.78	1.27	1.36
MA_RS02535	ygiD	2.43	2.15	2.26	2.38	2.04	2.15	2.57	2.74	2.90	2.56	2.43	2.15
MA_RS02540	NA	3.25	3.50	3.28	3.95	3.62	4.01	3.63	4.46	4.68	3.83	3.56	3.56
MA_RS02555	NA	3.23	3.44	3.27	3.94	3.64	3.82	3.97	4.24	4.57	4.21	3.80	4.02
MA_RS02560	NA	0.79	1.05	0.85	1.08	1.15	0.94	1.25	1.35	1.56	0.95	1.08	1.11
MA_RS02565	NA	1.98	2.17	2.03	2.53	1.92	2.70	0.82	1.82	1.86	1.75	1.02	1.45
MA_RS02570	NA	3.16	3.55	3.62	3.97	3.96	3.82	3.92	4.45	4.60	4.27	3.64	4.01
MA_RS02575	NA	2.10	1.91	1.49	2.19	2.02	1.99	2.55	2.11	2.93	2.31	1.52	1.32
MA_RS02585	NA	1.18	1.00	1.21	1.53	0.72	1.49	1.60	2.02	2.04	1.71	1.37	1.11
MA_RS02590	NA	1.75	1.64	1.93	2.06	1.91	1.88	2.31	2.23	2.85	2.56	2.01	2.20
MA_RS02595	NA	2.37	2.59	2.30	2.91	2.73	2.93	2.78	3.71	3.80	3.02	2.63	2.19
MA_RS02610	NA	2.35	2.50	2.23	2.60	2.35	2.58	2.46	3.51	3.79	2.42	2.01	1.92
MA_RS02620	NA	2.60	2.80	2.75	2.25	2.63	2.58	2.40	3.06	3.50	2.81	2.50	2.50
MA_RS02625	NA	2.61	2.61	2.79	2.53	2.35	2.46	2.30	3.24	3.34	2.85	2.51	2.31
MA_RS02630	NA	2.41	2.45	2.29	2.50	2.52	2.46	2.04	3.06	3.25	2.68	2.48	2.69
MA_RS02635	NA	2.10	1.95	2.13	2.10	2.13	2.07	1.74	2.26	3.06	2.22	2.33	1.77
MA_RS02640	NA	2.64	2.83	2.68	3.08	2.77	3.25	2.50	3.76	4.15	2.94	2.67	3.11
MA_RS02645	NA	4.29	4.49	4.47	4.62	4.51	4.90	4.80	5.72	6.18	5.00	4.72	4.79
MA_RS02650	NA	2.42	2.80	2.44	2.77	2.59	3.00	3.24	3.79	4.15	3.20	2.67	2.73
MA_RS02660	NA	1.55	1.78	1.73	1.59	1.78	2.01	1.85	3.13	2.76	2.03	1.53	2.13
MA_RS02665	NA	2.40	2.46	2.69	2.82	2.56	2.76	2.89	3.77	3.70	3.22	2.79	2.88
MA_RS02670	NA	1.22	1.46	0.82	1.60	1.84	0.79	1.64	2.31	2.13	1.50	1.28	1.58
MA_RS02680	NA	0.79	1.09	1.16	0.89	0.80	0.38	1.04	1.08	0.38	1.15	1.71	0.52
MA_RS02685	NA	2.57	2.55	2.44	2.33	2.42	2.31	2.68	2.78	3.09	2.48	2.73	2.82
MA_RS02690	NA	2.27	2.59	2.33	2.62	2.18	2.69	2.35	3.28	3.11	3.36	2.33	2.11
MA_RS02695	NA	2.49	2.70	2.43	3.12	3.29	3.06	2.56	3.59	3.63	3.38	2.67	2.42
MA_RS02700	NA	1.73	2.31	1.70	1.86	2.30	2.12	1.43	2.73	2.96	2.19	1.66	1.54
MA_RS02705	#N/A	0.97	0.92	1.38	0.00	1.07	0.90	0.80	0.00	0.00	0.00	0.00	0.69
MA_RS02710	NA	1.85	1.49	1.67	2.12	1.95	1.76	2.16	1.90	2.15	1.53	1.81	2.23
MA_RS02715	NA	3.79	3.93	3.92	4.40	4.34	4.46	4.60	4.58	4.99	4.29	3.87	4.21
MA_RS02720	NA	3.59	4.14	3.82	4.45	4.13	4.23	4.44	4.36	4.24	4.11	3.89	4.20
MA_RS02725	mutL	4.08	4.41	4.06	4.61	4.33	4.65	4.67	4.99	5.14	4.54	4.38	4.61
MA_RS02730	mutS	4.07	4.31	4.10	4.56	4.39	4.50	4.49	4.65	4.74	4.43	4.14	4.33
MA_RS02740	#N/A	2.96	3.41	2.63	2.83	3.37	2.76	2.91	2.21	2.27	3.35	2.48	3.13
MA_RS02745	NA	2.37	2.13	2.82	2.34	2.49	2.02	2.42	1.95	1.38	2.34	2.48	1.80
MA_RS02750	NA	2.74	3.05	3.02	3.11	2.80	3.04	3.41	3.38	3.44	3.09	3.12	3.05
MA_RS02760	NA	11.54	11.87	11.76	3.36	3.14	3.48	9.91	11.16	11.35	9.23	9.16	9.95
MA_RS02765	mttB	11.56	11.90	11.83	3.60	3.45	3.62	10.23	11.59	11.80	9.53	9.42	10.18
MA_RS02775	NA	11.73	12.06	12.04	3.28	3.25	3.42	10.39	11.43	11.68	9.53	9.49	10.36
MA_RS02780	NA	9.16	9.46	9.36	2.38	2.20	2.76	7.80	8.93	9.13	7.02	7.13	7.78
MA_RS02785	NA	10.11	10.43	10.37	3.29	3.01	3.08	8.97	10.47	10.67	8.28	8.25	8.84
MA_RS02790	mtbB	9.87	10.23	10.12	3.56	3.11	3.38	8.76	9.36	9.58	7.67	7.95	8.67
MA_RS02800	NA	3.23	3.29	3.18	3.13	3.08	2.88	2.95	3.81	3.83	3.03	2.52	2.95
MA_RS02805	lysS	4.57	4.94	4.76	5.56	5.35	5.46	4.96	4.92	5.45	5.14	4.85	4.98
MA_RS02810	NA	3.84	4.15	4.13	4.73	4.34	4.70	4.04	4.05	4.45	4.22	3.97	4.33
MA_RS02815	NA	4.60	4.73	4.38	4.32	4.66	4.73	4.67	5.68	5.68	5.27	4.63	4.44
MA_RS02820	NA	2.37	2.64	2.49	3.08	2.85	2.60	2.69	2.27	2.45	2.66	2.54	2.77
MA_RS02825	NA	3.02	3.13	3.24	3.80	3.67	3.71	3.54	3.54	3.75	3.68	3.35	3.61
MA_RS02830	NA	4.19	3.76	3.79	3.91	4.03	4.23	4.46	5.17	4.47	3.86	3.61	3.73
MA_RS02835	NA	3.61	4.06	3.84	4.77	4.03	4.55	4.48	5.21	5.00	4.29	4.09	4.11
MA_RS02840	hisF	4.28	4.47	4.46	4.94	4.64	4.95	4.66	4.79	4.76	4.60	4.25	4.42
MA_RS02845	NA	2.25	2.65	2.19	2.54	2.48	2.96	2.48	3.84	4.04	2.87	2.99	2.86
MA_RS02850	NA	3.14	3.32	3.50	3.89	3.60	3.89	3.59	3.87	4.06	3.52	3.38	3.40
MA_RS02855	NA	2.90	3.12	3.38	3.29	3.05	3.23	3.77	2.92	3.56	3.23	2.74	3.46
MA_RS02860	NA	3.14	3.48	3.23	3.90	3.33	3.33	3.70	3.97	4.48	3.72	3.07	3.51
MA_RS02870	NA	0.52	1.00	0.56	1.00	0.65	0.88	0.57	1.45	0.33	0.82	0.32	0.99
MA_RS02875	NA	4.39	4.62	4.47	5.32	4.82	4.98	5.16	5.27	5.38	5.31	4.59	4.95
MA_RS02880	ribB	4.54	4.47	4.33	5.33	4.90	5.18	5.37	5.55	5.52	5.56	4.82	4.89
MA_RS02885	NA	0.86	0.79	0.55	1.19	1.22	1.04	1.41	0.70	0.66	0.89	1.28	0.92
MA_RS02890	aroC	3.33	3.37	3.39	3.69	3.52	3.41	3.73	3.54	3.81	3.68	3.51	3.60
MA_RS02905	NA	1.25	1.30	1.59	1.75	1.62	1.99	1.80	1.99	2.16	1.68	1.67	1.57
MA_RS02915	NA	3.22	3.10	2.89	3.33	3.35	3.63	3.76	4.11	4.21	3.60	3.12	3.44
MA_RS02920	NA	3.11	3.23	3.34	3.39	3.32	3.48	3.77	4.47	4.78	3.17	3.36	3.31
MA_RS02925	NA	1.88	1.99	1.83	2.19	1.98	2.10	2.28	2.80	3.04	1.52	1.79	2.07
MA_RS02930	NA	1.14	1.30	0.87	1.43	1.56	1.53	1.18	1.82	2.13	0.76	1.01	0.98
MA_RS02935	NA	1.05	1.11	1.13	1.66	1.19	1.41	1.06	2.10	1.75	1.28	0.93	1.15
MA_RS02940	NA	1.55	1.59	2.19	2.27	1.73	1.99	2.19	2.19	2.84	1.82	1.24	1.72
MA_RS02945	NA	2.04	2.27	2.10	2.76	2.36	2.79	2.74	3.15	3.67	2.55	2.11	2.42
MA_RS02950	NA	1.32	1.55	1.65	1.87	1.90	2.08	1.69	2.48	2.77	1.86	1.68	1.86
MA_RS02955	NA	1.95	2.04	2.55	1.83	1.96	2.45	2.51	2.53	2.80	2.23	1.89	1.89
MA_RS02960	NA	1.58	1.42	1.39	1.84	1.79	1.74	2.02	2.21	2.14	1.77	1.56	1.43
MA_RS02965	NA	1.37	1.22	1.34	1.63	1.43	1.65	1.49	2.46	2.60	1.37	1.58	1.75
MA_RS02970	NA	1.34	1.39	1.74	1.72	1.88	1.63	1.87	2.56	2.59	1.67	1.64	1.86
MA_RS02975	NA	1.79	1.83	1.71	2.17	2.22	2.22	2.23	2.54	2.66	2.37	2.12	1.85
MA_RS02980	NA	1.82	2.08	1.99	2.28	2.06	1.83	1.96	2.88	3.32	2.18	1.51	1.98
MA_RS02990	NA	0.32	1.20	0.67	0.21	0.92	1.05	0.15	1.49	1.10	0.75	1.27	1.43
MA_RS03000	NA	0.76	1.69	1.62	1.63	1.43	1.74	1.19	2.16	2.06	1.30	1.11	1.23
MA_RS03005	NA	1.66	1.31	1.94	2.06	1.83	2.23	0.84	2.20	2.18	2.08	2.18	1.07
MA_RS03010	ahbD	5.03	5.23	5.29	5.51	5.37	5.62	5.39	5.57	5.70	5.51	5.37	5.38
MA_RS03015	ahbA	4.79	4.82	4.71	5.28	5.00	5.13	5.06	5.60	5.52	5.19	4.83	5.01
MA_RS03020	ahbB	4.31	4.30	4.21	4.65	4.47	4.38	3.95	4.74	5.00	4.31	4.37	4.56
MA_RS03025	NA	3.97	4.25	4.08	4.32	4.08	4.24	4.28	4.08	4.13	4.05	4.11	3.87
MA_RS03030	hemA	4.87	4.96	4.90	5.39	5.11	5.13	5.22	5.28	5.51	5.04	4.96	5.07
MA_RS03035	hemB	4.91	5.07	5.01	5.49	5.20	5.40	5.39	5.90	5.92	5.26	5.26	5.14
MA_RS03040	NA	0.87	0.84	0.97	1.15	1.01	0.88	1.03	1.49	1.82	1.30	1.26	0.85
MA_RS03050	hemL	5.25	5.49	5.36	5.87	5.40	5.77	5.50	5.43	5.60	5.63	5.46	5.57
MA_RS03055	hemC	5.50	5.80	5.56	5.99	5.66	5.81	5.90	5.48	5.64	5.64	5.60	5.74
MA_RS03060	NA	4.71	4.95	4.93	5.00	4.94	5.04	4.93	4.23	4.47	4.35	4.77	4.72
MA_RS03065	NA	4.46	4.69	4.81	4.95	4.77	4.98	4.82	4.84	5.34	4.59	4.69	4.81
MA_RS03070	NA	4.46	4.79	4.71	4.86	4.55	4.55	4.90	5.14	5.17	4.61	4.38	4.75
MA_RS03075	NA	3.36	3.84	3.81	3.73	3.68	3.68	3.79	4.39	4.49	3.99	3.23	3.40
MA_RS03080	NA	5.29	5.55	5.40	5.78	5.45	5.55	5.68	5.78	5.80	5.50	5.28	5.53
MA_RS03085	NA	2.62	2.95	2.90	2.86	2.90	3.19	3.37	3.27	2.87	2.94	3.08	2.96
MA_RS03095	NA	5.11	5.36	5.19	5.64	5.36	5.48	5.39	5.63	5.74	5.47	5.27	5.47
MA_RS03100	NA	4.09	4.42	4.13	4.68	4.48	4.44	4.37	4.24	4.55	4.27	4.24	4.51
MA_RS03105	serA	7.15	7.47	7.29	7.80	7.48	7.74	7.48	7.85	8.15	7.64	7.41	7.53
MA_RS03110	NA	4.61	5.00	4.94	5.28	4.96	5.24	5.05	5.15	5.66	4.81	4.97	4.95
MA_RS03115	NA	3.07	3.24	3.37	3.75	3.59	3.66	3.65	4.00	4.43	3.48	3.43	3.62
MA_RS03125	NA	8.59	8.75	8.65	9.17	8.68	8.89	9.08	9.75	9.86	9.21	8.80	8.94
MA_RS03130	NA	8.09	8.24	8.13	8.57	8.19	8.33	8.81	8.97	8.81	8.58	8.25	8.44
MA_RS03135	NA	8.31	8.67	8.47	8.84	8.54	8.84	8.59	8.84	9.01	8.78	8.55	8.74
MA_RS03140	NA	7.66	7.99	7.68	8.41	7.94	8.27	8.03	8.62	9.00	8.44	7.99	8.11
MA_RS03145	#N/A	7.64	7.94	7.81	8.37	7.95	8.09	7.90	7.84	8.36	7.98	7.83	8.00
MA_RS03150	NA	7.97	7.99	8.05	8.52	8.03	8.35	8.58	9.33	9.40	8.67	8.21	8.19
MA_RS03155	rpsB	8.66	9.00	8.86	9.38	8.90	9.21	9.10	9.66	10.10	9.41	9.01	9.07
MA_RS03160	NA	6.89	7.13	6.96	7.37	7.01	7.24	7.40	7.39	7.50	7.16	7.14	7.29
MA_RS03165	NA	4.03	4.23	4.57	4.61	4.28	4.62	4.83	5.18	5.55	4.74	4.27	4.45
MA_RS03170	NA	4.65	4.63	4.58	4.99	4.76	4.50	4.92	5.39	5.38	4.77	4.79	4.78
MA_RS03175	fni	4.85	5.06	5.03	5.33	5.06	4.95	5.06	4.93	5.06	4.82	4.89	5.15

MA_RS03180	NA	5.73	5.89	5.87	6.34	5.98	6.13	6.21	6.58	6.73	6.28	5.84	6.05
MA_RS03185	NA	5.21	5.34	5.08	5.61	5.39	5.42	5.33	5.54	5.56	5.60	5.23	5.34
MA_RS03190	NA	1.18	1.52	1.22	1.20	1.80	1.47	0.62	1.87	2.68	0.55	1.40	1.55
MA_RS03195	ppdK	7.85	8.12	8.02	8.45	8.03	8.25	8.34	8.67	8.97	7.94	7.97	8.16
MA_RS03200	NA	6.66	6.82	6.85	6.99	6.86	6.87	6.68	7.34	7.47	7.11	6.66	6.68
MA_RS03205	NA	5.61	5.81	5.76	6.28	5.91	6.16	6.16	6.82	6.86	6.45	5.82	6.05
MA_RS03210	NA	3.10	3.22	3.41	3.40	3.27	3.11	3.28	3.83	3.71	3.53	3.50	3.27
MA_RS03220	NA	3.56	3.50	3.60	4.11	3.55	4.01	3.95	4.52	4.26	4.63	3.99	4.26
MA_RS03225	#N/A	2.07	1.50	2.35	1.74	2.77	1.97	2.73	0.75	1.38	2.58	1.48	2.77
MA_RS03230	NA	1.70	2.05	2.19	2.22	2.48	2.23	2.07	2.93	3.23	2.48	2.18	1.91
MA_RS03235	NA	2.03	2.15	1.72	2.18	2.19	2.58	2.37	1.97	2.32	2.26	2.40	2.28
MA_RS03240	NA	1.66	2.14	1.39	2.09	2.28	2.09	2.38	2.61	2.75	2.33	1.60	1.67
MA_RS03245	NA	4.48	4.80	4.82	4.82	4.79	4.88	4.95	5.11	5.16	4.91	4.93	4.64
MA_RS03250	NA	1.68	1.67	2.21	2.02	2.22	1.80	1.97	2.10	2.50	1.97	1.63	1.81
MA_RS03255	NA	1.87	1.70	1.98	2.02	1.59	2.04	1.99	1.94	1.63	1.83	1.56	1.59
MA_RS03260	NA	1.37	1.46	1.72	1.67	1.35	1.62	1.47	2.21	2.35	1.45	1.54	1.15
MA_RS03265	NA	2.21	2.35	2.31	2.46	2.37	2.79	2.48	3.22	3.56	1.81	2.30	1.92
MA_RS03270	NA	3.74	4.01	4.12	4.31	4.07	4.24	4.32	4.64	4.77	4.46	4.03	4.04
MA_RS03275	NA	2.34	2.30	2.18	2.12	2.75	2.73	2.31	3.32	3.13	2.82	2.35	2.53
MA_RS03280	NA	2.51	2.91	2.98	2.99	3.18	3.49	2.72	3.41	3.27	3.32	2.81	3.17
MA_RS03285	NA	2.14	2.39	1.82	2.53	2.27	2.40	2.54	2.86	2.76	2.71	2.29	2.81
MA_RS03295	NA	1.54	1.65	1.45	2.08	1.70	2.08	2.72	2.62	2.97	1.62	1.81	1.85
MA_RS03300	NA	1.49	1.49	1.25	1.96	1.65	1.99	1.99	2.15	1.97	1.35	1.50	1.69
MA_RS03305	NA	3.38	3.67	3.41	4.33	6.42	4.47	4.33	4.66	5.23	4.44	4.59	4.56
MA_RS03310	NA	4.60	4.59	4.31	4.97	4.98	5.37	4.55	5.15	5.63	5.21	5.35	5.32
MA_RS03315	groES	8.27	8.47	8.37	9.27	9.02	9.15	9.37	8.86	9.17	9.01	8.88	9.19
MA_RS03320	groL	8.05	8.12	8.07	8.99	8.68	8.81	9.01	8.77	9.05	8.98	8.79	9.05
MA_RS03325	NA	3.29	3.55	3.54	3.93	3.23	3.77	3.64	4.13	4.57	3.97	3.67	3.70
MA_RS03330	NA	2.37	2.51	2.38	2.42	2.42	2.45	3.26	2.76	3.11	2.27	2.54	2.47
MA_RS03335	NA	1.99	1.88	1.27	2.31	2.26	2.27	2.01	2.84	2.79	2.43	2.13	1.91
MA_RS03340	NA	4.65	4.71	4.72	5.08	4.78	4.89	4.98	5.12	5.26	4.97	4.76	4.84
MA_RS03345	NA	2.99	3.60	3.68	3.65	3.11	3.38	3.72	3.95	4.33	3.27	3.57	3.76
MA_RS03355	NA	1.08	1.02	1.46	1.96	1.72	1.82	1.97	2.09	2.24	1.99	0.88	1.36
MA_RS03360	NA	5.54	5.74	5.82	5.85	5.68	5.73	6.19	6.06	5.61	5.78	5.42	5.45
MA_RS03365	NA	1.45	1.15	1.25	1.61	1.65	1.29	0.97	2.56	2.47	2.16	1.19	1.55
MA_RS03375	#N/A	4.61	5.11	4.29	5.12	5.31	5.04	4.55	3.63	3.65	4.41	4.53	5.01
MA_RS03380	NA	4.39	4.84	4.76	5.04	4.71	4.91	4.98	5.17	5.57	4.88	4.63	5.05
MA_RS03385	NA	6.06	6.46	6.50	6.82	6.53	6.74	6.90	7.27	7.47	6.85	6.40	6.76
MA_RS03390	NA	7.88	8.12	8.06	8.59	8.26	8.36	8.38	8.60	8.88	8.56	8.26	8.53
MA_RS03395	NA	8.20	8.51	8.26	9.29	8.66	8.99	8.97	9.58	9.96	9.56	8.88	9.07
MA_RS03400	NA	7.81	8.03	8.04	8.62	8.18	8.32	8.68	8.67	8.85	8.77	8.37	8.46
MA_RS03405	NA	4.70	5.01	4.86	5.17	5.11	5.46	4.89	5.61	5.78	5.15	4.82	4.98
MA_RS03410	prlS	3.22	3.49	3.51	3.73	3.51	3.77	3.74	3.91	3.81	3.54	3.43	3.51
MA_RS03415	NA	1.38	1.58	1.50	1.76	1.43	1.41	2.03	2.05	2.56	1.85	1.79	1.59
MA_RS03420	NA	0.97	1.86	1.53	1.95	2.13	2.22	1.69	2.90	2.90	2.23	1.58	2.13
MA_RS03425	NA	3.71	4.03	3.76	4.26	3.93	3.97	4.02	4.05	4.29	4.17	3.75	3.94
MA_RS03430	NA	3.74	3.74	3.94	4.01	3.94	3.92	3.98	3.57	3.81	3.74	3.60	3.65
MA_RS03435	NA	0.85	1.16	1.53	2.04	1.59	1.72	1.52	2.04	2.14	1.30	1.71	1.88
MA_RS03440	NA	3.52	3.89	3.66	3.93	3.93	4.01	3.74	3.99	4.39	4.06	3.73	3.81
MA_RS03445	NA	4.59	4.87	4.62	5.12	5.01	5.03	5.39	5.42	5.27	4.88	4.85	4.88
MA_RS03450	thpR	4.00	4.08	4.36	4.38	4.17	4.40	3.78	3.59	3.60	3.80	3.87	4.14
MA_RS03455	NA	3.45	3.72	3.41	4.04	3.89	3.63	3.81	4.30	4.11	3.71	3.34	3.62
MA_RS03460	NA	5.82	6.06	5.77	6.63	6.17	6.55	6.14	6.88	7.31	6.38	6.27	6.33
MA_RS03465	NA	5.65	5.91	5.82	6.46	6.16	6.27	6.10	6.74	7.11	6.04	5.96	6.26
MA_RS03470	NA	5.50	5.71	5.40	6.17	5.80	6.18	5.71	6.29	6.82	5.64	5.93	5.98
MA_RS03475	NA	5.63	5.83	5.70	6.53	6.05	6.53	6.10	7.07	7.30	6.13	6.25	6.20
MA_RS03480	NA	5.78	6.10	5.83	6.52	6.27	6.57	6.12	7.04	7.44	6.07	6.17	6.16
MA_RS03485	NA	5.45	5.85	5.33	6.27	5.91	6.24	5.88	6.76	7.12	5.86	5.78	6.13
MA_RS03490	NA	5.19	5.47	5.19	5.87	5.55	5.73	5.16	5.30	5.80	4.98	5.25	5.44
MA_RS03495	NA	5.05	5.46	5.00	5.95	5.53	5.99	5.20	6.08	6.34	5.41	5.39	5.47
MA_RS03500	NA	1.93	2.19	1.97	2.63	1.98	2.35	2.60	2.98	3.47	2.73	1.94	2.24
MA_RS03505	NA	1.50	1.76	1.53	1.87	2.02	1.85	1.74	1.83	2.60	1.99	1.49	1.65
MA_RS03510	NA	2.43	2.45	2.19	2.68	2.50	2.68	2.09	3.38	2.97	2.61	2.78	2.45
MA_RS03515	NA	5.38	5.55	5.77	5.89	5.60	5.71	5.67	5.97	6.32	5.69	5.43	5.44
MA_RS03520	NA	4.29	4.79	4.57	4.94	4.49	4.72	4.51	4.85	5.05	4.83	4.69	4.60
MA_RS03525	NA	6.26	6.20	6.15	6.51	6.22	6.49	6.48	7.51	7.29	6.95	6.57	6.32
MA_RS03530	NA	3.98	4.03	3.69	3.49	3.72	4.09	3.92	3.93	4.17	4.14	3.95	3.47
MA_RS03535	NA	4.29	4.36	4.29	4.43	4.32	4.25	4.37	4.26	4.61	3.96	3.91	4.20
MA_RS03540	oadA	5.88	6.20	6.02	6.76	6.21	6.45	6.62	6.53	6.85	6.46	6.22	6.27
MA_RS03545	NA	6.04	6.32	6.20	6.78	6.35	6.53	6.77	6.65	7.02	6.46	6.24	6.46
MA_RS03550	NA	5.55	5.94	5.77	6.45	5.95	6.18	6.41	6.67	6.71	6.20	5.94	6.08
MA_RS03555	NA	3.38	3.39	2.93	3.55	3.44	3.52	3.90	3.88	3.81	3.49	2.92	3.53
MA_RS03560	NA	4.29	4.35	4.26	4.81	4.34	4.61	5.08	5.40	5.57	4.76	4.26	4.78
MA_RS03565	NA	4.08	4.49	4.32	4.84	4.28	4.34	4.93	5.25	5.40	4.60	4.43	4.63
MA_RS03570	NA	3.95	3.92	3.96	4.27	3.98	4.33	4.39	4.33	4.60	4.06	4.11	4.24
MA_RS03575	NA	3.62	3.93	3.93	4.27	4.15	4.25	4.33	4.89	5.14	4.36	4.10	4.21
MA_RS03580	NA	3.39	3.46	3.52	3.92	3.58	3.98	4.00	4.37	4.63	3.80	3.59	4.07
MA_RS03585	NA	2.90	3.09	2.40	3.27	3.09	3.32	3.33	3.97	4.16	3.29	3.16	2.97
MA_RS03590	NA	4.44	4.44	4.45	4.72	4.64	4.55	4.89	4.91	4.66	4.41	4.38	4.47
MA_RS03595	NA	5.63	5.55	5.69	5.74	5.51	5.68	5.83	5.69	5.65	4.97	4.93	5.33
MA_RS03600	NA	7.45	7.77	7.70	8.37	7.99	8.21	8.02	8.27	8.57	8.14	7.88	7.92
MA_RS03605	NA	7.38	7.68	7.56	8.35	7.95	8.11	8.05	8.40	8.77	8.16	7.87	7.94
MA_RS03610	NA	4.30	4.26	4.43	4.71	4.72	4.77	4.71	4.60	4.54	4.84	4.67	4.65
MA_RS03615	NA	2.71	2.57	2.50	2.98	2.65	3.06	2.90	3.78	3.26	2.93	2.41	3.00
MA_RS03620	NA	1.30	1.18	1.07	1.27	1.33	1.31	1.41	1.73	1.61	0.83	1.00	1.10
MA_RS03625	NA	1.98	1.70	1.89	2.14	1.71	1.52	1.69	2.04	2.41	1.85	1.94	1.94
MA_RS03630	NA	6.91	7.12	7.04	7.50	7.08	7.34	7.18	7.83	8.07	7.43	7.06	7.08
MA_RS03635	NA	6.03	6.38	6.28	6.51	6.23	6.36	6.42	6.07	6.16	5.97	6.08	6.24
MA_RS03640	NA	4.61	4.81	4.67	5.09	4.60	4.98	4.70	5.50	5.68	4.72	4.85	4.89
MA_RS03645	NA	2.93	2.92	2.14	3.26	3.31	3.40	2.98	3.02	3.43	3.45	3.16	2.90
MA_RS03650	NA	0.91	1.07	0.76	0.73	1.19	0.95	0.99	1.61	1.33	1.21	0.97	1.00
MA_RS03655	NA	0.37	0.54	0.77	0.59	0.58	0.33	0.33	0.43	0.77	0.51	0.27	0.48
MA_RS03660	NA	0.36	0.82	0.73	1.35	0.68	1.09	0.65	1.01	1.37	0.74	0.69	1.24
MA_RS03665	NA	1.95	2.18	2.09	2.58	2.02	2.53	1.83	2.84	2.81	2.22	2.31	2.25
MA_RS03670	NA	1.68	1.82	1.52	2.22	1.70	2.26	1.57	2.21	2.32	1.93	1.66	1.85
MA_RS03675	NA	0.00	0.41	0.00	0.00	0.00	0.00	0.00	1.19	0.00	0.49	0.74	0.41
MA_RS03680	NA	0.95	0.95	0.96	1.21	0.90	1.29	0.85	0.87	1.49	1.25	0.37	1.04
MA_RS03685	NA	2.67	2.84	2.66	2.70	2.42	2.74	2.91	3.60	3.27	3.54	3.11	2.90
MA_RS03690	NA	0.49	0.46	0.71	0.74	0.57	0.28	0.47	0.68	1.06	0.87	0.61	0.62
MA_RS03695	NA	1.21	0.87	0.37	0.94	0.63	1.27	0.73	1.15	1.61	1.39	0.47	1.06
MA_RS03700	NA	1.78	2.25	1.81	2.54	2.47	2.32	2.25	3.13	2.86	2.42	1.96	1.53
MA_RS03705	NA	4.36	4.72	4.68	4.75	4.35	4.75	4.71	4.84	5.11	4.67	4.59	4.75
MA_RS03710	NA	4.61	4.86	4.70	4.92	4.68	4.78	4.77	4.92	5.30	4.59	4.50	4.78
MA_RS03715	NA	3.50	3.55	3.28	4.28	3.64	4.01	4.02	4.66	4.13	4.22	3.91	3.96
MA_RS03720	#N/A	3.72	3.15	3.16	4.14	4.54	3.97	3.92	3.89	4.24	4.69	3.90	3.50
MA_RS03725	NA	4.52	4.67	4.60	4.60	4.73	4.97	4.77	4.79	4.97	4.83	4.55	4.82
MA_RS03730	NA	3.94	4.44	4.16	4.35	4.20	4.52	4.67	5.20	5.09	4.79	4.06	4.72
MA_RS03735	NA	5.12	5.33	5.06	5.55	5.37	5.84	5.44	5.64	5.64	5.46	5.26	5.48
MA_RS03740	cofD	4.60	4.78	4.52	5.10	4.86	5.05	4.87	5.25	5.34	5.23	4.75	4.81
MA_RS03745	NA	3.77	4.15	4.15	4.19	3.99	4.39	4.17	4.91	5.42	3.91	4.19	4.27
MA_RS03755	#N/A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS03760	dph2	2.94	3.09	2.93	3.61	3.58	3.75	3.48	3.60	3.86	3.99	3.42	3.66
MA_RS03765	NA	4.01	4.05	4.34	4.57	4.49	4.36	4.63	4.78	5.33	4.69	4.48	4.48
MA_RS03770	NA	6.65	6.89	6.80	7.11	6.86	6.98	7.00	7.08	7.33	6.85	6.68	6.89
MA_RS03775	NA	5.80	5.97	5.97	6.31	5.91	6.22	6.10	6.53	7.02	6.22	5.99	6.12
MA_RS03780	psiS	4.15	4.25	4.07	4.66	4.58	4.51	4.66	4.82	5.14	4.49	4.36	4.54
MA_RS03785	NA	2.29	1.52	1.35	2.43	2.58	2.34	2.64	3.14	2.88	1.93	2.75	2.49
MA_RS03790	NA	4.24	4.38	3.95	4.74	4.72	4.64	4.52	5.64	5.69	4.73	4.99	4.99
MA_RS03795	NA	3.67	3.97	3.61	4.10	3.78	4.15	3.83	4.14	3.77	3.77	4.12	3.69
MA_RS03800	lysA	5.39	5.83	5.53	6.26	5.87	6.15	6.04	6.32	6.63	6.24	5.81	5.95
MA_RS03805	polX	1.87	1.94	1.66	2.20	2.07	2.12	1.85	2.38	2.56	2.13	1.94	2.24
MA_RS03810	NA	0.68	1.15	1.12	1.42	1.08	1.59	1.27	1.79	1.85	0.97	1.06	1.31
MA_RS03815	#N/A	3.19	3.33	3.29	3.25	3.46	3.38	3.05	3.80	4.01	3.29	3.39	2.65
MA_RS03820	NA	2.16	1.41	1.86	2.16	2.37	1.85	1.40	3.16	3.04	2.54	1.69	1.82
MA_RS03825	NA	0.11	0.58	0.11	0.79	0.50	0.32	1.16	0.91	0.39	0.28	1.18	0.31
MA_RS03830	NA	0.91	0.95	0.64	0.71	0.69	1.06	1.20	1.01	1.76	1.26	1.17	0.96
MA_RS03840	#N/A	1.66	1.80	1.67	1.82	1.21	1.67	1.28	1.83	1.83	1.91	1.52	2.06
MA_RS03845	NA	1.07	1.19	1.02	1.30	1.54	1.01	1.42	1.57	2.33	1.84	1.13	1.57
MA_RS03850	NA	2.92	2.76	2.48	3.02	3.07	3.15	3.08	3.25	3.79	3.47	2.91	2.68
MA_RS03855	NA	0.86	1.14	0.65	1.58	1.51	1.58	1.26	1.86	1.82	1.79	1.76	1.03
MA_RS03870	NA	1.28	1.23	1.08	1.06	1.13	1.85	1.51	1.31	1.48	1.41	1.23	1.56
MA_RS03875	NA	1.02	0.92	0.40	0.82	1.08	0.85	0.90	0.93	0.92	1.13	1.09	1.23
MA_RS03880	#N/A	2.00	2.33	2.11	3.38	2.82	2.74	2.80	3.27	3.32	2.76	2.82	2.36
MA_RS03885	NA	1.81	2.06	1.77	2.61	1.70	2.45	2.59	2.45	2.32	2.31	2.57	2.22
MA_RS03890	NA	1.06	1.57	1.37	1.86	1.51	1.29	2.13	1.70	2.15	1.50	1.29	1.51
MA_RS03895	NA	0.68	0.43	0.60	0.17	0.25	0.22	0.39	0.76	0.85	0.65	1.08	0.46
MA_RS03900	NA	2.22	2.22	2.19	2.41	2.34	2.35	2.04	2.65	2.77	2.55	1.87	2.32
MA_RS03905	NA	3.03	3.40	3.40	3.45	3.43	3.52	3.19	3.94	4.29	2.83	3.16	3.29
MA_RS03910	NA	0.83	1.28	1.26	1.50	1.54	1.60	2.22	1.04	1.59	1.66	1.30	1.31
MA_RS03915	cysS	3.71	4.09	3.64	4.26	4.00	4.07	4.25	4.48	4.89	4.08	4.04	4.17
MA_RS03920	NA	3.70	3.88	3.85	4.34	3.93	3.95	4.20	4.59	4.65	4.22	3.78	3.83
MA_RS03925	NA	0.60	0.40	1.49	0.76	1.44	0.91	0.16	1.14	1.84	0.92	1.27	1.02
MA_RS03930	NA	4.40	4.53	4.57	5.03	4.61	4.61	4.63	5.13	5.22	4.60	4.53	4.53

MA_RS03935	NA	2.07	2.67	2.08	2.45	2.22	2.64	2.59	2.96	3.11	3.09	3.02	2.85
MA_RS03940	NA	0.42	0.32	1.04	0.18	0.38	0.76	0.74	0.63	0.52	0.64	0.19	0.47
MA_RS03945	NA	0.48	0.91	0.73	0.73	0.57	0.78	0.37	0.77	0.71	1.34	0.26	1.04
MA_RS03955	NA	2.60	2.65	1.94	2.99	2.86	2.92	2.49	3.28	3.40	2.77	2.86	3.09
MA_RS03960	NA	3.58	3.61	3.73	4.11	3.92	4.16	3.82	4.25	4.68	3.95	3.84	4.00
MA_RS03965	NA	1.77	1.94	1.95	2.26	1.99	2.18	2.53	2.40	2.99	2.08	2.13	2.28
MA_RS03975	lysS	3.84	4.29	4.26	4.56	4.29	4.43	4.59	4.89	5.12	4.86	4.35	4.53
MA_RS03980	NA	1.13	1.33	1.36	1.69	1.41	1.44	1.02	1.16	1.69	1.34	1.27	1.27
MA_RS03985	NA	2.85	2.99	3.07	3.13	2.95	3.18	3.10	2.88	3.33	2.97	2.77	2.90
MA_RS03990	NA	2.66	2.72	2.73	2.96	2.69	3.00	2.88	3.94	4.24	2.94	2.79	2.78
MA_RS03995	NA	1.09	1.39	1.10	1.25	0.43	1.17	0.74	1.30	1.06	1.08	1.11	1.22
MA_RS04000	NA	1.19	1.10	1.63	1.19	0.69	1.91	1.28	1.55	1.85	1.20	1.44	0.78
MA_RS04005	NA	0.88	0.72	1.26	0.68	0.79	0.85	0.63	0.62	1.81	0.94	0.90	0.74
MA_RS04010	NA	1.27	1.69	1.33	1.70	1.42	1.45	1.60	2.44	2.47	1.55	1.54	2.14
MA_RS04015	NA	1.51	1.72	1.16	2.22	0.98	2.02	1.60	2.23	2.51	1.31	0.69	1.56
MA_RS04020	NA	1.63	1.48	1.59	1.59	1.27	1.78	1.25	1.89	1.54	1.03	1.64	1.50
MA_RS04025	NA	0.39	0.38	0.07	0.77	0.41	0.43	0.42	0.74	1.04	0.52	0.76	0.43
MA_RS04030	NA	0.81	0.98	0.56	0.55	1.18	1.46	1.22	1.33	1.41	1.16	1.51	1.18
MA_RS04035	#N/A	1.20	0.68	0.84	0.40	1.65	1.54	0.59	1.92	1.96	1.48	1.37	1.12
MA_RS04040	NA	1.79	1.84	1.93	2.13	1.56	1.90	1.74	2.46	2.60	2.41	2.14	2.08
MA_RS04045	NA	1.63	1.59	1.82	2.02	1.67	1.49	2.05	1.50	1.52	1.01	1.54	1.51
MA_RS04050	NA	1.45	1.58	0.97	1.77	2.09	1.71	1.99	2.92	2.61	1.72	1.70	1.66
MA_RS04055	NA	0.56	0.54	0.91	1.15	0.77	0.87	0.97	0.88	0.68	0.51	0.90	0.73
MA_RS04060	NA	3.69	3.91	3.62	4.00	3.69	4.13	4.08	5.33	5.25	4.56	4.35	4.40
MA_RS04070	NA	3.47	3.71	3.60	3.71	3.56	3.65	3.76	4.34	4.64	2.87	3.47	3.67
MA_RS04075	NA	2.72	2.53	2.43	3.07	3.01	3.04	3.10	3.63	3.80	2.43	3.16	3.26
MA_RS04080	mtaA	3.12	3.15	2.89	3.18	3.14	3.10	2.96	3.12	3.27	3.07	3.20	3.00
MA_RS04085	NA	2.49	2.70	2.44	2.73	2.52	2.53	2.62	2.67	3.31	2.53	2.42	2.75
MA_RS04090	NA	3.27	3.12	3.09	3.61	3.33	3.65	3.65	3.91	3.88	3.79	3.06	3.47
MA_RS04095	NA	3.21	3.48	3.22	3.67	3.53	3.60	3.66	4.05	4.38	3.56	3.00	3.45
MA_RS04100	NA	5.04	5.09	5.20	5.55	5.26	5.37	5.68	5.94	5.80	5.56	5.06	5.17
MA_RS04105	NA	2.29	2.15	1.78	2.29	2.49	2.38	2.81	2.61	2.61	2.22	1.56	2.00
MA_RS04115	NA	0.61	0.23	0.37	0.90	0.53	0.44	0.45	1.63	0.81	0.44	0.54	0.89
MA_RS04120	NA	0.36	0.28	0.00	0.52	0.73	0.59	0.18	0.78	0.20	0.31	0.56	0.91
MA_RS04125	NA	3.34	3.35	3.18	3.58	3.20	3.53	3.22	3.11	3.58	3.31	3.54	3.54
MA_RS04130	NA	1.25	1.50	1.31	1.86	2.04	1.60	1.58	2.25	2.11	1.57	1.92	1.46
MA_RS04135	NA	1.53	1.47	1.26	1.77	1.65	1.93	1.58	2.34	2.55	1.15	1.26	1.37
MA_RS04140	NA	1.73	1.81	1.62	2.19	1.97	2.00	1.63	2.35	2.15	1.61	1.21	1.44
MA_RS04145	NA	1.92	2.02	2.44	2.65	2.10	2.25	1.95	2.66	2.89	1.85	1.50	1.88
MA_RS04150	NA	0.97	1.75	1.66	1.75	1.58	1.65	1.60	2.15	2.07	1.78	1.27	1.46
MA_RS04155	NA	1.23	1.73	1.19	2.27	1.16	1.50	1.49	2.82	2.65	2.03	2.15	1.60
MA_RS04160	NA	0.84	0.65	0.67	0.75	0.45	0.97	0.71	1.01	0.45	0.86	0.00	0.85
MA_RS04165	NA	1.15	1.19	1.03	1.18	1.07	1.26	0.81	0.73	1.19	1.30	1.46	0.97
MA_RS04170	NA	0.69	0.93	0.65	0.57	0.71	0.93	0.65	0.87	1.64	1.02	0.98	0.97
MA_RS04175	NA	1.62	1.97	1.79	2.32	1.29	1.58	1.84	2.57	2.42	2.17	1.98	2.03
MA_RS04180	NA	3.07	2.87	2.87	3.12	2.89	2.85	2.73	3.32	3.31	2.53	2.75	2.72
MA_RS04185	NA	2.46	2.52	2.45	2.60	2.66	2.64	2.62	2.94	2.97	2.87	2.80	2.63
MA_RS04190	NA	1.79	1.96	2.23	2.20	1.71	2.03	2.55	2.94	2.20	2.33	1.72	2.12
MA_RS04195	NA	0.77	1.09	0.35	0.12	0.83	0.51	0.52	0.96	0.61	0.98	0.00	1.49
MA_RS04200	NA	3.48	3.78	3.56	4.17	3.85	4.08	3.75	4.24	4.57	4.20	3.92	4.01
MA_RS04205	NA	3.52	3.92	3.57	4.23	4.19	4.18	4.08	4.46	4.81	3.70	3.97	4.00
MA_RS04210	NA	4.15	4.44	4.24	4.60	4.53	4.53	4.64	4.62	5.09	4.22	4.16	4.50
MA_RS04215	NA	3.54	3.45	3.52	4.00	3.67	3.80	3.88	4.01	4.47	3.67	3.28	3.75
MA_RS04220	NA	2.38	2.51	2.06	2.08	3.21	2.78	2.89	1.48	2.11	1.79	1.62	2.05
MA_RS04225	NA	4.17	4.23	3.67	4.18	4.00	4.12	4.64	3.57	3.65	3.82	3.61	4.01
MA_RS04230	NA	2.60	2.33	2.42	2.36	2.46	2.82	3.01	3.29	3.34	2.54	2.24	2.52
MA_RS04235	NA	2.53	2.38	1.89	2.79	2.99	3.23	3.07	3.66	3.80	3.32	2.78	3.31
MA_RS04240	NA	3.18	3.57	3.48	3.90	3.62	3.86	3.96	4.44	4.69	4.00	3.52	3.80
MA_RS04245	NA	4.80	4.86	4.98	5.30	5.00	5.21	5.44	5.89	5.83	5.28	4.73	5.06
MA_RS04250	NA	5.31	5.66	5.53	6.12	5.71	5.98	6.11	6.30	6.71	6.21	5.66	6.02
MA_RS04255	NA	4.70	5.06	4.88	5.28	5.11	5.36	5.33	5.65	5.89	5.43	5.22	5.30
MA_RS04260	NA	5.23	5.41	5.25	5.46	5.42	5.61	6.01	6.02	5.91	5.93	5.49	5.65
MA_RS04265	mdh	4.36	4.61	4.63	4.90	4.77	4.79	4.73	4.88	4.97	5.20	4.64	4.81
MA_RS04270	NA	3.52	3.81	3.82	4.20	3.79	3.90	3.91	4.26	4.42	3.87	3.69	3.80
MA_RS04275	NA	5.08	5.31	5.18	5.08	4.95	5.20	4.90	5.04	5.16	4.71	4.98	4.83
MA_RS04285	NA	4.39	4.72	4.93	5.14	4.83	5.01	5.01	5.94	6.07	5.34	4.94	4.87
MA_RS04290	NA	4.24	4.35	4.25	4.71	4.51	4.73	4.43	4.89	5.24	4.36	4.44	4.67
MA_RS04295	NA	3.72	4.04	4.07	4.44	4.00	4.59	4.48	5.06	5.26	4.83	4.35	4.22
MA_RS04300	NA	4.80	4.95	5.11	5.10	4.84	5.12	5.49	6.27	5.90	5.47	5.13	5.06
MA_RS04305	NA	3.67	3.84	3.93	4.21	4.20	4.28	4.21	3.94	4.47	3.95	3.92	4.33
MA_RS04310	NA	4.62	4.53	4.54	5.00	4.91	4.81	5.45	5.05	4.46	5.12	4.81	4.94
MA_RS04320	slmA	11.52	11.86	11.67	12.12	11.53	11.86	11.94	12.44	12.72	11.98	11.61	11.66
MA_RS04325	NA	6.48	6.72	6.65	7.04	6.65	6.95	6.76	7.45	7.67	7.20	6.77	6.77
MA_RS04330	NA	0.91	1.56	1.59	2.30	1.87	2.08	2.30	3.46	3.26	2.29	1.85	2.22
MA_RS04335	NA	5.92	6.07	6.06	6.44	6.36	6.38	6.30	6.59	6.56	6.32	5.82	6.22
MA_RS04340	NA	6.40	6.85	6.72	7.19	6.92	7.07	6.73	7.04	7.34	7.14	6.58	6.88
MA_RS04345	NA	6.31	6.78	6.53	7.03	6.82	6.93	6.60	6.92	7.05	7.00	6.45	6.73
MA_RS04350	NA	5.33	5.81	5.68	5.92	5.83	5.85	5.60	5.71	5.83	5.91	5.34	5.53
MA_RS04355	#N/A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS04360	NA	1.83	1.63	1.70	2.22	2.09	2.22	2.60	2.95	2.99	2.00	1.82	1.90
MA_RS04365	NA	0.14	0.08	0.23	0.20	0.29	0.23	0.45	0.45	0.45	0.25	0.18	0.28
MA_RS04370	NA	0.57	0.56	0.30	0.60	0.36	0.55	0.49	0.63	1.18	0.43	0.63	0.49
MA_RS04375	NA	0.96	0.60	0.90	0.09	0.24	0.75	0.85	0.70	1.54	0.81	0.59	0.75
MA_RS04380	NA	2.69	3.13	3.48	3.81	3.46	4.15	3.41	4.11	4.04	2.97	3.61	4.23
MA_RS04385	NA	3.14	3.75	3.75	4.26	3.93	3.92	4.13	4.80	4.47	3.33	4.06	4.41
MA_RS04390	NA	2.84	3.23	3.41	3.85	3.42	4.18	3.25	3.63	3.53	3.07	4.00	4.17
MA_RS04395	NA	1.76	2.35	2.58	2.60	2.53	3.22	2.47	2.92	2.93	1.96	2.32	3.46
MA_RS04400	NA	1.42	1.56	1.85	2.11	1.84	2.05	2.33	2.40	2.20	1.50	1.82	2.51
MA_RS04405	NA	1.48	1.14	1.77	1.79	1.64	1.64	1.85	2.20	1.66	1.00	1.10	1.84
MA_RS04410	NA	1.39	1.69	1.18	1.75	1.59	1.36	1.60	1.99	2.16	1.00	1.48	1.66
MA_RS04415	NA	3.65	3.61	3.81	3.92	3.68	3.66	3.73	4.12	4.39	3.67	3.43	3.38
MA_RS04420	NA	2.35	2.24	2.57	0.73	0.83	1.61	1.80	2.04	2.24	2.17	2.56	2.96
MA_RS04425	NA	3.50	3.47	3.59	1.00	1.11	1.39	2.67	3.45	3.14	2.38	3.37	3.95
MA_RS04440	NA	1.83	1.95	1.94	2.17	1.90	2.86	2.53	2.40	2.96	2.63	2.42	2.48
MA_RS04445	NA	1.06	1.44	1.07	2.00	1.59	1.67	2.02	2.05	2.04	1.27	1.67	1.30
MA_RS04450	NA	1.84	1.65	1.15	1.60	1.93	1.41	1.52	1.91	2.78	1.83	1.62	1.67
MA_RS04455	mtaA	3.53	3.86	3.65	4.00	3.60	4.00	3.52	3.47	3.56	3.37	2.87	3.65
MA_RS04460	NA	1.73	1.89	1.85	2.08	1.94	2.22	3.17	3.45	3.63	2.40	2.53	2.64
MA_RS04465	NA	1.64	1.80	1.52	2.23	1.89	2.20	4.17	4.44	4.15	3.12	3.29	3.77
MA_RS04470	NA	0.98	1.04	1.08	0.92	0.86	0.95	5.04	5.23	5.30	3.85	3.69	4.32
MA_RS04475	NA	1.26	1.29	1.20	1.56	1.42	1.65	7.60	8.13	8.07	6.71	6.36	6.75
MA_RS04480	NA	2.01	2.15	1.95	1.67	1.54	1.46	1.26	1.82	2.20	1.73	1.58	1.67
MA_RS04485	NA	1.67	1.75	1.06	1.38	2.05	1.28	1.70	2.30	2.38	1.83	1.73	1.44
MA_RS04490	NA	3.99	4.30	4.23	4.71	4.22	4.68	2.47	3.05	3.45	2.81	2.25	2.66
MA_RS04495	NA	4.67	4.98	4.76	5.23	4.83	5.04	4.04	4.26	4.42	3.79	3.51	3.88
MA_RS04510	NA	5.11	5.28	5.05	5.93	5.41	5.78	5.68	6.09	6.48	5.78	5.44	5.55
MA_RS04515	NA	1.63	1.95	2.01	2.26	1.96	2.79	2.09	2.39	2.42	1.60	1.52	2.26
MA_RS04520	NA	2.05	2.73	2.57	2.72	2.70	2.90	2.68	2.73	2.94	2.22	2.79	2.94
MA_RS04525	NA	1.94	2.20	2.17	2.47	2.21	2.41	2.20	2.62	2.24	1.83	1.97	2.32
MA_RS04530	NA	1.66	2.06	1.90	2.39	2.21	2.64	2.37	2.84	2.61	2.01	2.39	2.57
MA_RS04535	NA	1.66	1.77	1.78	2.43	1.93	2.81	2.05	2.44	2.33	1.65	2.25	2.65
MA_RS04540	cobN	1.90	2.26	2.52	3.00	2.75	3.24	2.72	2.97	3.09	2.13	2.76	3.48
MA_RS04545	NA	2.03	2.17	2.70	3.26	2.72	3.19	3.03	3.41	3.06	1.90	2.98	3.66
MA_RS04550	NA	1.41	1.72	2.24	2.64	2.39	2.84	2.53	2.69	2.64	1.67	3.01	3.20
MA_RS04555	NA	1.36	1.61	2.25	2.41	2.05	2.56	2.49	2.74	2.32	1.55	1.85	2.70
MA_RS04560	NA	0.79	1.07	1.42	1.83	1.68	1.76	1.59	1.53	1.60	0.80	1.37	2.52
MA_RS04565	NA	1.16	1.37	1.95	2.03	2.05	2.18	1.89	2.45	1.80	1.29	1.87	2.76
MA_RS04570	NA	1.12	1.27	0.82	1.73	1.92	1.30	1.96	2.26	2.50	1.66	1.66	1.76
MA_RS04575	NA	1.30	1.53	1.87	1.78	1.79	1.53	1.84	2.10	2.10	2.03	1.28	1.49
MA_RS04580	NA	1.51	1.63	1.92	1.99	2.27	2.05	2.36	2.53	2.27	2.21	1.92	2.20
MA_RS04585	NA	1.42	1.83	1.61	1.82	2.05	2.14	2.27	2.37	2.89	1.69	1.82	2.15
MA_RS04590	NA	1.64	1.54	2.07	2.59	1.84	1.96	2.11	2.88	2.62	2.45	2.14	1.96
MA_RS04595	cobN	3.04	3.36	3.24	3.63	3.33	3.43	3.48	3.58	3.73	3.11	3.06	3.35
MA_RS04600	NA	2.66	3.04	2.82	3.26	2.85	2.92	3.11	3.45	3.61	3.12	2.77	3.10
MA_RS04605	NA	1.52	1.68	1.79	2.15	1.69	2.48	1.76	2.48	2.82	2.38	2.07	1.80
MA_RS04610	NA	4.70	4.77	4.73	4.96	4.75	4.94	4.92	5.10	5.30	4.69	4.70	4.75
MA_RS04615	NA	0.10	0.27	0.00	0.19	0.20	0.20	0.78	0.19	0.48	0.00	0.42	0.49
MA_RS04620	NA	5.56	5.89	5.43	4.74	4.58	6.04	3.48	5.04	7.06	5.70	4.08	4.70
MA_RS04625	pstC	3.32	3.95	3.46	3.09	2.73	3.96	1.47	2.52	4.43	2.93	2.67	2.68
MA_RS04630	pstA	2.33	2.71	2.71	2.06	1.48	3.06	1.24	1.73	3.34	1.92	1.66	1.74
MA_RS04635	pstB	2.44	2.61	2.28	1.76	1.70	2.27	0.87	2.34	3.72	2.12	1.63	2.09
MA_RS04640	phoU	2.36	2.80	1.96	1.86	2.07	2.54	2.10	2.45	3.30	2.37	2.05	2.38
MA_RS04645	NA	3.68	3.87	3.98	4.35	4.09	4.24	4.11	4.44	4.51	4.04	3.94	3.81
MA_RS04650	NA	4.75	5.03	4.91	5.41	5.05	5.36	5.41	5.69	6.18	5.50	5.17	5.37
MA_RS04655	NA	4.53	4.99	4.86	5.29	5.07	5.23	5.48	5.94	6.22	5.34	4.83	5.27
MA_RS04660	eif1A	4.12	4.34	4.46	4.34	4.07	4.66	5.13	4.69	4.77	4.25	4.29	4.87
MA_RS04665	#N/A	15.34	15.13	15.36	14.95	15.38	15.06	15.32	14.34	14.12	15.05	15.31	15.27
MA_RS04670	#N/A	16.23	16.24	16.20	16.21	16.20	16.24	16.14	16.22	16.16	16.21	16.20	16.18
MA_RS04675	#N/A	5.55	5.50	5.69	5.81	5.95	6.14	5.68	6.22	6.06	5.88	5.97	5.75
MA_RS04680	NA	1.78	0.00	2.98	0.00	2.73	2.90	2.91	2.48	3.87	1.80	2.69	0.35
MA_RS04685	NA	6.80	7.14	6.96	7.59	7.29	7.41	7.64	8.34	8.51	7.46	7.03	7.31
MA_RS04690	NA	7.01	7.25	7.14	7.51	7.28	7.41	7.61	8.08	8.08	7.56	7.28	7.32
MA_RS04695	NA	4.97	5.39	5.44	5.76	5.21	5.60	5.73	6.26	6.49	5.67	5.52	5.44

MA_RS04700	NA	3.27	2.94	3.89	3.36	3.50	3.88	3.76	3.98	4.32	3.14	4.00	3.10
MA_RS04710	hisI	1.69	1.52	2.25	2.05	2.34	2.68	2.90	2.94	3.37	2.54	3.30	2.33
MA_RS04715	NA	3.33	3.37	3.53	3.89	3.76	4.08	3.97	4.32	4.63	3.96	4.11	3.89
MA_RS04720	NA	0.75	0.95	1.67	1.34	1.42	2.40	2.46	1.75	2.65	0.51	2.92	1.67
MA_RS04725	NA	0.74	0.20	0.56	0.90	1.26	1.99	2.42	1.85	2.57	1.00	2.75	1.29
MA_RS04730	NA	0.83	1.26	1.35	1.77	1.69	2.19	2.72	1.97	2.85	1.69	3.04	0.70
MA_RS04735	hisH	3.99	4.34	3.91	4.16	4.22	4.83	4.50	4.60	4.77	4.59	4.70	3.99
MA_RS04740	NA	4.40	4.65	4.64	5.03	4.77	5.03	5.10	4.97	5.20	4.95	5.12	4.96
MA_RS04745	NA	5.54	5.73	5.70	6.27	5.72	6.11	6.11	6.32	6.58	5.49	5.72	5.78
MA_RS04750	NA	6.16	6.55	6.22	7.02	6.45	6.74	6.97	7.52	7.62	6.77	6.44	6.45
MA_RS04755	NA	4.51	4.67	4.68	4.87	4.75	4.95	5.12	5.29	5.50	4.89	4.86	4.81
MA_RS04760	NA	2.34	1.93	2.27	2.15	1.89	3.05	3.22	2.96	2.92	2.04	3.44	2.90
MA_RS04765	NA	5.53	5.72	5.54	5.84	5.70	5.79	5.82	5.61	5.53	5.85	5.53	5.62
MA_RS04770	NA	3.78	3.87	4.11	4.27	4.08	4.47	4.45	4.37	4.28	4.17	4.17	4.07
MA_RS04775	NA	4.02	4.28	3.98	4.93	4.48	4.91	5.30	5.32	5.43	5.39	4.96	4.86
MA_RS04780	NA	4.24	4.57	4.19	4.54	4.53	4.69	5.00	5.22	4.94	4.15	4.63	4.28
MA_RS04785	NA	7.92	8.13	8.01	8.39	8.19	8.34	8.29	8.91	8.94	8.61	8.37	8.23
MA_RS04790	NA	7.77	7.96	7.86	8.21	7.93	8.30	8.09	8.60	8.67	8.34	8.08	8.08
MA_RS04795	NA	6.55	6.91	6.77	7.21	6.81	7.00	7.00	7.54	7.84	7.00	6.95	6.95
MA_RS04800	NA	4.05	4.47	3.91	4.24	4.03	4.66	4.44	4.99	5.34	4.27	4.67	4.00
MA_RS04805	NA	3.56	3.66	3.87	4.34	4.20	4.37	4.45	4.66	4.95	5.03	4.64	4.24
MA_RS04810	NA	0.92	0.96	0.68	0.63	1.28	2.06	2.31	1.82	1.19	0.92	2.94	1.05
MA_RS04815	NA	0.45	0.59	0.74	1.48	1.56	2.21	2.39	1.04	1.29	1.01	2.86	1.07
MA_RS04820	NA	1.98	1.62	1.56	2.36	2.01	2.72	2.83	2.03	2.61	1.72	3.35	1.80
MA_RS04830	mtlB	1.65	2.01	2.16	2.79	2.45	3.14	3.00	2.62	2.86	2.38	3.35	2.21
MA_RS04840	mtlB	1.54	2.02	1.79	2.25	2.01	2.77	2.91	1.60	2.25	1.83	3.16	1.74
MA_RS04845	NA	1.45	1.58	2.00	2.18	1.58	2.82	3.14	1.84	1.92	2.00	3.28	1.81
MA_RS04850	NA	1.79	2.13	1.77	1.83	1.74	3.20	2.94	2.55	1.99	0.85	3.02	2.69
MA_RS04855	NA	3.71	4.05	4.09	4.23	4.11	4.60	4.54	5.14	5.46	4.49	4.31	4.39
MA_RS04860	NA	5.41	5.72	5.48	6.00	5.73	5.88	6.00	6.17	6.45	5.73	5.74	5.79
MA_RS04865	NA	4.09	4.26	4.14	4.60	4.54	4.55	4.94	4.93	5.15	4.70	4.81	4.50
MA_RS04870	NA	4.73	4.93	4.50	5.23	4.88	5.05	5.22	5.62	6.00	4.96	5.16	5.01
MA_RS04875	cobS	4.41	4.41	4.55	4.57	4.25	4.69	4.58	4.22	4.47	4.07	4.61	4.43
MA_RS04880	cobZ	4.56	4.62	4.57	4.65	4.54	4.77	5.00	4.49	4.85	4.37	4.72	4.69
MA_RS04890	NA	4.31	4.50	4.38	4.57	4.32	4.63	4.87	5.34	5.67	4.50	4.77	4.63
MA_RS04895	cobD	4.93	5.16	5.19	5.10	4.76	5.18	5.43	5.76	6.09	5.15	5.28	5.21
MA_RS04900	hisS	4.51	4.63	4.43	4.78	4.47	4.82	4.62	5.04	5.09	4.89	4.88	4.55
MA_RS04905	NA	2.64	2.81	2.71	2.89	2.88	3.58	3.45	3.46	3.81	3.16	3.76	2.89
MA_RS04915	#N/A	2.45	2.12	2.48	2.31	2.88	3.01	3.06	1.84	2.29	2.32	3.44	2.10
MA_RS04920	NA	2.10	1.30	1.82	1.50	1.73	2.65	2.82	1.64	2.35	1.60	3.17	1.78
MA_RS04925	NA	0.99	0.85	0.51	1.03	0.78	2.30	2.70	1.09	0.87	0.56	3.00	0.56
MA_RS04930	NA	0.50	0.65	0.55	0.51	0.59	2.19	2.40	1.12	0.87	0.29	2.87	1.02
MA_RS04935	NA	7.94	7.95	7.93	8.32	8.17	8.29	8.23	8.69	9.10	8.34	8.11	8.05
MA_RS04940	NA	2.98	2.80	3.26	3.63	2.92	3.99	3.49	4.12	3.58	3.15	3.85	3.46
MA_RS04945	NA	3.33	3.72	3.99	3.87	3.76	4.38	3.98	4.07	4.16	3.26	4.25	4.17
MA_RS04950	NA	3.62	4.08	4.41	4.63	4.07	4.94	4.52	5.04	4.91	3.62	4.68	4.89
MA_RS04955	NA	1.65	1.49	1.73	2.01	1.82	2.63	2.86	2.20	1.96	1.96	3.17	1.57
MA_RS04960	NA	2.12	2.53	2.46	2.54	2.29	3.06	3.32	3.26	3.32	2.37	3.32	2.45
MA_RS04965	nadC	3.17	3.53	3.41	3.64	3.34	3.39	4.05	3.48	3.50	3.28	3.75	3.37
MA_RS04970	queD	1.10	0.69	0.38	1.08	1.31	2.40	2.54	1.26	0.85	0.92	2.85	1.06
MA_RS04980	NA	4.77	4.94	4.89	4.71	4.79	5.11	5.02	5.21	5.37	4.95	5.14	5.01
MA_RS04985	nadA	4.98	5.19	5.18	5.45	5.23	5.56	5.35	5.42	5.80	5.67	5.44	5.37
MA_RS04995	NA	2.77	2.94	2.83	2.87	3.30	3.69	3.49	3.19	3.47	3.16	3.86	3.05
MA_RS05000	NA	3.58	3.72	3.57	4.06	3.65	4.29	4.23	4.27	4.53	3.95	3.99	3.93
MA_RS05005	NA	3.34	3.62	3.49	3.91	3.69	4.00	4.16	4.34	4.09	3.45	3.84	3.52
MA_RS05015	NA	3.62	3.65	3.83	3.70	3.36	3.67	4.03	4.62	4.19	3.95	3.97	3.55
MA_RS05020	NA	2.05	1.71	2.19	1.98	2.28	2.99	3.04	2.02	2.27	2.40	3.22	1.64
MA_RS05025	NA	0.73	0.72	0.73	1.19	0.66	2.41	2.24	1.34	1.11	1.32	2.97	1.13
MA_RS05040	NA	4.72	4.64	4.52	4.78	4.63	4.84	4.78	4.39	4.80	4.59	4.82	4.67
MA_RS05045	pyrF	4.41	4.90	4.64	5.07	4.76	5.29	5.10	4.87	5.40	4.96	5.02	5.05
MA_RS05055	NA	2.71	2.44	2.39	2.47	2.83	3.47	3.43	3.29	2.57	3.18	3.58	2.69
MA_RS05060	katG	4.15	4.60	4.22	4.72	4.62	5.01	4.58	4.48	4.70	4.24	4.73	4.36
MA_RS05065	NA	3.95	4.12	4.21	4.57	4.36	4.53	4.99	4.94	5.31	4.26	4.53	3.93
MA_RS05070	NA	0.21	0.29	0.43	0.26	0.36	2.03	2.25	0.59	0.98	0.29	2.80	0.38
MA_RS05075	NA	0.30	0.16	0.00	0.00	0.23	2.04	2.21	0.35	0.00	0.31	2.81	0.00
MA_RS05080	frhA	3.29	3.64	3.40	3.85	3.38	3.88	3.94	2.97	3.16	3.09	4.05	3.27
MA_RS05085	frhD	2.77	3.25	2.59	3.17	3.08	3.79	3.53	2.91	3.01	2.90	4.08	3.39
MA_RS05090	frhG	3.43	3.66	3.27	3.54	3.75	3.95	3.69	3.37	3.26	3.18	4.09	3.78
MA_RS05095	frhB	2.78	3.00	2.56	3.09	3.13	3.58	3.73	3.44	3.06	3.08	3.69	3.30
MA_RS05100	NA	2.96	2.88	2.88	2.93	3.01	3.69	3.73	4.30	4.58	3.34	3.95	3.01
MA_RS05105	NA	2.99	3.13	3.08	2.80	2.52	3.59	3.42	3.97	3.97	3.41	3.79	2.67
MA_RS05110	NA	2.19	1.96	1.97	2.16	2.34	3.33	3.43	2.61	2.94	2.17	3.60	2.37
MA_RS05115	NA	1.82	2.41	2.00	1.75	2.78	2.67	3.39	2.78	2.79	1.91	3.68	2.49
MA_RS05120	NA	1.91	2.18	1.05	1.61	1.41	2.24	2.58	2.22	1.81	1.46	3.28	1.70
MA_RS05125	NA	1.95	1.88	1.39	2.48	1.58	2.49	2.66	2.46	2.52	2.40	3.18	2.05
MA_RS05130	NA	0.90	0.17	1.04	1.09	1.07	2.33	2.52	1.43	1.99	1.15	2.95	1.40
MA_RS05140	NA	0.41	0.59	0.28	0.82	0.50	2.14	2.39	1.19	1.23	0.78	2.85	0.58
MA_RS05145	NA	1.17	1.62	1.28	1.57	1.61	2.48	2.62	1.68	2.16	1.40	3.04	1.00
MA_RS05150	#N/A	0.00	0.53	0.30	0.53	1.00	1.75	2.17	1.41	0.98	0.87	2.77	0.23
MA_RS05155	NA	0.69	0.61	0.89	0.63	0.53	2.31	2.36	1.74	1.49	1.05	3.01	1.03
MA_RS05160	NA	1.27	1.39	1.15	1.49	1.37	2.35	2.80	2.23	2.35	1.80	2.81	0.87
MA_RS05165	NA	2.19	2.22	2.44	2.57	2.39	2.83	3.05	3.28	2.93	2.88	3.32	2.45
MA_RS05170	NA	1.51	1.30	1.32	1.66	1.31	2.53	2.78	2.26	2.37	2.03	3.01	2.08
MA_RS05175	NA	1.48	1.10	1.67	1.80	1.10	2.54	2.76	1.81	1.90	1.80	2.91	2.00
MA_RS05180	#N/A	2.55	2.51	2.67	3.12	2.91	3.24	3.31	3.47	3.53	3.33	3.66	2.83
MA_RS05185	NA	1.34	1.32	1.62	1.56	1.84	2.63	2.51	1.28	1.50	1.93	3.17	1.91
MA_RS05190	NA	1.76	2.06	1.31	2.11	2.21	2.99	2.97	1.80	1.90	1.89	3.42	2.71
MA_RS05195	NA	2.75	2.93	2.93	3.33	2.98	3.35	3.79	4.07	3.98	3.12	3.67	3.22
MA_RS05200	NA	2.09	2.35	2.52	2.61	2.49	3.01	3.07	3.56	3.32	2.68	3.44	2.18
MA_RS05205	#N/A	2.13	2.01	1.86	2.19	1.97	2.81	3.12	2.88	3.27	2.29	3.48	2.34
MA_RS05210	NA	2.36	2.55	2.43	2.70	2.79	3.25	3.62	3.53	3.90	3.07	3.75	2.55
MA_RS05225	furnC	1.88	2.31	1.71	2.47	2.23	3.09	3.03	2.55	2.80	2.65	3.50	2.14
MA_RS05230	NA	2.37	2.55	1.81	3.01	2.28	3.15	3.21	2.63	3.02	2.30	3.59	2.75
MA_RS05240	NA	3.06	3.23	3.29	3.52	3.39	3.88	3.73	3.27	3.44	3.67	4.04	3.65
MA_RS05250	NA	1.35	1.35	1.33	1.67	1.43	2.42	2.66	1.86	2.42	1.98	3.29	1.81
MA_RS05255	NA	2.68	3.22	2.44	3.52	2.79	3.50	3.48	3.82	3.87	2.83	3.67	2.57
MA_RS05260	NA	2.80	3.12	2.82	3.48	2.95	3.53	3.61	3.73	3.94	3.12	3.64	3.11
MA_RS05265	cydB	1.91	2.16	2.56	2.67	2.42	3.24	3.00	2.41	2.55	2.35	3.30	2.09
MA_RS05270	prf1	2.21	2.68	2.68	2.66	2.14	3.26	3.33	3.46	3.89	2.76	3.51	2.61
MA_RS05275	tnpB	2.38	2.46	2.60	3.08	2.88	3.29	3.34	3.75	3.93	3.02	3.80	2.79
MA_RS05280	tnpA	0.19	0.48	0.09	0.64	0.28	2.15	2.26	0.76	0.80	0.50	0.00	0.53
MA_RS05285	acsC	6.63	6.92	6.75	8.06	7.66	7.96	7.80	8.02	8.59	8.22	7.61	7.61
MA_RS05290	cdhD	6.47	6.80	6.63	7.94	7.54	7.83	7.72	7.85	8.30	8.03	7.42	7.49
MA_RS05295	NA	7.05	7.25	7.30	8.38	8.06	8.24	8.31	8.17	8.60	8.35	7.83	8.05
MA_RS05300	cdhC	6.73	6.96	6.86	8.04	7.64	7.88	7.78	8.18	8.70	7.89	7.38	7.58
MA_RS05305	cdhB	6.80	7.13	7.08	8.08	7.70	7.91	7.89	8.61	9.11	7.82	7.40	7.57
MA_RS05310	cdhA	6.18	6.59	6.40	7.40	7.06	7.22	7.09	7.60	8.00	6.94	6.63	6.83
MA_RS05320	#N/A	3.64	4.01	3.89	4.07	3.80	4.20	4.45	4.77	4.89	3.99	4.26	3.78
MA_RS05325	NA	2.96	3.05	3.14	3.53	3.46	3.91	3.66	4.03	3.80	3.87	3.94	3.35
MA_RS05330	NA	1.65	1.49	1.86	2.05	1.84	2.98	2.80	1.87	2.21	1.95	3.24	1.50
MA_RS05335	NA	2.15	2.50	2.48	2.55	1.95	3.12	3.09	2.34	2.63	2.42	3.31	2.25
MA_RS05340	NA	2.46	2.52	2.42	2.76	2.96	3.45	3.48	3.16	2.64	2.79	3.68	2.65
MA_RS05345	iorA	5.06	5.42	5.21	5.66	5.22	5.63	5.42	5.70	5.93	5.45	5.42	5.33
MA_RS05350	NA	5.24	5.50	5.42	5.68	5.38	5.58	5.65	5.55	5.88	5.40	5.49	5.43
MA_RS05355	NA	0.42	0.53	0.26	0.61	0.11	2.02	2.30	0.68	1.16	0.92	2.83	0.92
MA_RS05360	NA	4.85	5.12	5.18	5.36	5.39	5.59	5.23	6.18	6.21	5.42	5.22	5.29
MA_RS05365	NA	3.86	4.12	4.03	4.14	4.05	4.50	4.17	4.58	5.16	3.97	4.26	4.11
MA_RS05370	NA	3.99	4.00	4.10	4.33	4.21	4.61	4.47	5.22	5.93	4.12	4.39	4.34
MA_RS05375	nadE	3.76	4.02	4.06	4.35	4.32	4.63	4.44	5.17	5.25	4.20	4.39	4.06
MA_RS05380	NA	4.47	4.78	4.70	5.08	4.83	5.22	4.98	5.83	6.03	5.20	4.89	4.99
MA_RS05385	NA	3.61	3.60	4.07	4.21	3.62	4.12	4.22	4.51	4.89	4.00	4.13	4.19
MA_RS05390	NA	4.35	4.47	4.51	4.58	4.39	4.69	4.75	5.25	5.46	4.62	4.66	4.25
MA_RS05395	NA	1.65	1.78	1.62	2.00	2.06	2.96	3.04	3.01	3.11	2.18	3.26	2.20
MA_RS05410	NA	0.13	0.21	0.38	0.42	0.34	2.03	2.30	0.61	0.81	0.37	2.79	0.42
MA_RS05430	NA	3.46	3.41	3.62	3.96	3.68	4.05	4.38	4.40	4.62	3.96	4.13	3.48
MA_RS05435	NA	0.54	0.57	0.33	0.97	0.99	2.23	2.38	1.32	1.68	0.89	2.77	0.81
MA_RS05440	NA	2.45	2.57	2.57	2.84	2.76	3.38	3.37	3.25	3.49	2.88	3.58	2.80
MA_RS05450	NA	0.32	0.21	0.23	0.63	0.38	2.09	2.27	0.50	1.16	0.87	2.90	0.37
MA_RS05465	NA	0.82	1.77	0.92	0.79	0.81	2.55	2.60	1.77	1.56	1.57	2.90	0.90
MA_RS05470	istB	0.11	0.02	0.02	0.06	0.01	2.00	2.16	0.18	0.21	0.10	2.73	0.06
MA_RS05475	istA	0.58	0.73	0.83	0.61	0.76	2.23	2.34	1.07	1.21	0.96	2.81	0.50
MA_RS05480	NA	1.82	1.79	1.69	1.51	2.01	2.69	2.94	2.52	2.60	1.84	3.18	1.85
MA_RS05485	NA	3.25	3.49	3.58	3.60	3.61	4.01	4.22	4.64	4.92	4.14	4.14	3.53
MA_RS05490	NA	2.29	2.55	2.24	2.75	2.78	3.14	3.30	3.83	4.26	3.11	3.61	2.70
MA_RS05495	NA	1.20	1.41	1.31	1.85	1.68	2.69	2.89	2.19	2.34	1.62	3.06	1.32
MA_RS05500	NA	0.38	0.37	0.32	0.56	0.43	2.06	2.32	0.89	0.91	0.61	2.84	0.58
MA_RS05505	istA	0.50	0.58	0.32	0.58	0.58	2.19	2.29	0.87	1.03	0.75	2.85	0.73
MA_RS05510	istB	0.38	0.56	0.62	0.72	0.35	2.12	2.40	1.34	1.79	0.85	2.82	1.02
MA_RS05515	NA	1.09	1.23	1.49	1.14	1.54	2.35	2.78	2.02	1.96	1.15	3.05	1.48
MA_RS05520	NA	2.49	2.58	2.36	2.89	2.58	3.27	3.46	3.42	3.68	3.06	3.42	2.61
MA_RS05525	NA	1.83	2.02	1.73	2.45	2.39	2.97	3.24	3.05	3.05	2.32	3.29	2.15
MA_RS05530	NA	2.80	2.88	3.05	2.99	2.87	3.54	3.54	4.06	4.58	3.33	3.96	2.99
MA_RS05535	NA	2.93	3.00	3.01	3.33	3.08	3.60	3.91	3.83	4.46	3.20	3.92	3.18

MA_R505540	NA	2.06	2.27	2.30	2.47	2.41	3.07	3.14	3.00	3.29	2.04	3.31	2.07
MA_R505545	NA	2.37	2.55	2.45	3.13	2.49	3.15	3.79	4.04	4.21	2.19	3.55	2.53
MA_R505550	NA	2.37	2.31	2.45	3.19	2.72	3.44	3.53	4.04	4.23	2.71	3.71	2.79
MA_R505555	NA	2.48	2.59	2.73	3.41	3.16	3.64	3.74	4.09	4.09	2.50	3.71	3.01
MA_R505570	NA	4.42	4.75	4.74	5.23	4.96	5.33	5.21	5.83	6.04	5.13	5.00	5.06
MA_R505575	NA	3.28	3.35	3.43	3.79	3.83	3.98	4.11	4.78	5.03	3.45	3.92	3.33
MA_R505580	NA	0.20	0.92	0.00	0.29	0.07	2.04	2.25	0.12	0.72	0.61	0.00	0.42
MA_R505585	NA	0.66	0.48	0.44	0.55	0.57	2.09	2.30	0.42	0.00	0.19	0.00	0.35
MA_R505595	rpl3p	7.68	8.06	7.94	8.32	8.03	8.12	8.33	8.48	8.64	7.95	7.93	8.10
MA_R505600	rpl4p	8.33	8.58	8.55	8.95	8.56	8.70	8.93	9.13	9.39	8.50	8.44	8.72
MA_R505605	NA	7.97	8.30	8.20	8.78	8.20	8.54	8.70	9.49	9.84	8.53	8.21	8.55
MA_R505610	NA	8.34	8.58	8.60	8.99	8.51	8.70	8.84	9.19	9.58	8.61	8.46	8.76
MA_R505615	NA	8.60	8.87	8.84	9.12	8.78	8.93	9.03	9.27	9.68	8.69	8.61	8.93
MA_R505620	NA	8.36	8.78	8.69	9.13	8.70	8.93	9.06	9.47	9.74	8.84	8.64	8.92
MA_R505625	NA	7.99	8.33	8.37	8.62	8.25	8.51	8.55	8.73	9.01	8.31	8.21	8.48
MA_R505630	rpmC	8.27	8.57	8.62	8.95	8.40	8.73	8.74	8.47	9.10	8.45	8.42	8.66
MA_R505635	NA	9.02	9.18	9.22	9.67	9.21	9.46	9.56	9.43	9.79	9.23	9.08	9.42
MA_R505640	NA	8.49	8.81	8.85	9.20	8.77	8.94	9.16	9.24	9.67	8.72	8.48	9.00
MA_R505645	rpl14p	7.57	7.84	7.87	8.14	7.87	8.02	8.32	8.14	8.43	7.73	7.56	7.95
MA_R505650	rplX	8.48	8.65	8.77	9.08	8.71	8.70	9.26	9.41	9.57	8.78	8.56	8.92
MA_R505655	NA	8.29	8.57	8.54	8.91	8.46	8.75	8.89	9.14	9.48	8.56	8.33	8.61
MA_R505660	NA	8.01	8.34	8.35	8.62	8.22	8.45	8.62	8.67	8.94	8.22	8.01	8.34
MA_R505665	NA	8.40	8.51	8.72	8.83	8.54	8.59	9.15	9.12	9.19	8.49	8.24	8.75
MA_R505670	NA	8.50	8.69	8.73	9.00	8.62	8.75	8.98	9.04	9.25	8.46	8.50	8.87
MA_R505675	rplGp	8.14	8.46	8.39	8.77	8.37	8.70	8.78	8.92	9.35	8.45	8.39	8.52
MA_R505680	NA	7.62	8.05	7.84	8.31	7.91	8.25	8.12	8.59	8.94	8.05	7.92	8.07
MA_R505685	NA	7.89	8.12	8.12	8.51	8.13	8.29	8.89	8.68	8.89	8.15	8.03	8.30
MA_R505690	NA	8.44	8.76	8.75	8.87	8.66	8.83	8.92	8.56	8.90	8.38	8.39	8.72
MA_R505695	NA	8.34	8.70	8.70	8.92	8.54	8.84	8.90	9.13	9.58	8.63	8.48	8.72
MA_R505700	NA	8.55	8.75	8.84	8.96	8.69	8.83	8.97	9.00	9.39	8.55	8.45	8.86
MA_R505705	NA	7.46	7.73	7.66	7.93	7.61	7.86	8.08	8.00	8.20	7.49	7.51	7.76
MA_R505710	secY	7.05	7.43	7.24	7.65	7.28	7.57	7.40	7.72	8.09	7.20	7.29	7.34
MA_R505715	NA	7.22	7.42	7.37	7.74	7.35	7.59	7.60	7.46	7.82	7.11	7.23	7.36
MA_R505720	NA	2.37	2.87	2.64	3.01	2.52	3.39	3.38	3.32	3.60	3.30	3.54	2.12
MA_R505725	NA	1.62	1.54	1.55	2.26	1.59	2.68	2.94	2.59	2.28	2.29	3.20	1.28
MA_R505730	NA	1.01	1.48	1.37	1.64	1.72	2.53	2.61	1.45	0.97	1.55	3.14	2.14
MA_R505735	NA	1.31	1.84	1.00	2.02	0.46	2.39	2.52	1.63	2.61	1.82	2.88	1.35
MA_R505740	NA	3.24	3.29	3.28	3.56	3.20	3.70	4.11	4.09	4.23	3.26	4.00	3.19
MA_R505745	NA	5.97	6.15	6.18	6.42	6.25	6.45	6.38	6.89	7.13	6.64	6.43	6.36
MA_R505750	NA	5.93	5.88	5.89	6.32	6.09	6.17	6.26	6.58	6.53	6.11	6.24	6.05
MA_R505755	NA	4.50	4.71	4.18	4.68	4.48	4.83	4.87	4.57	4.54	4.34	4.64	4.80
MA_R505760	#N/A	3.65	4.03	3.69	3.75	3.13	3.68	3.34	0.11	0.12	2.58	3.94	2.54
MA_R505765	NA	2.65	2.59	2.84	3.17	2.71	3.51	3.47	3.51	4.06	3.19	3.76	3.04
MA_R505770	NA	1.85	2.08	1.60	2.23	2.32	3.00	2.99	2.63	3.14	2.00	3.25	2.29
MA_R505775	NA	7.95	8.24	8.12	8.49	8.10	8.34	8.43	8.75	8.90	8.30	8.17	8.24
MA_R505780	NA	8.03	8.41	8.28	8.78	8.26	8.55	8.55	8.98	9.39	8.66	8.34	8.46
MA_R505785	NA	8.29	8.61	8.58	8.70	8.42	8.54	8.70	8.08	8.29	8.26	8.28	8.64
MA_R505790	NA	7.14	7.51	7.25	7.82	7.37	7.69	7.56	8.07	8.38	7.69	7.54	7.56
MA_R505795	NA	0.46	0.30	0.23	0.21	0.18	2.09	0.50	0.41	0.80	0.73	0.37	0.66
MA_R505800	NA	1.20	1.58	1.38	1.56	1.23	2.62	1.05	1.90	2.37	1.83	1.53	1.38
MA_R505810	NA	0.02	0.01	0.00	0.02	0.02	1.97	0.07	0.12	0.13	0.09	0.06	0.01
MA_R505815	#N/A	5.20	5.54	5.48	4.98	5.39	5.29	5.45	5.37	6.18	5.43	5.43	5.32
MA_R505820	#N/A	2.96	3.20	2.82	3.25	3.35	3.48	3.03	3.57	4.01	3.18	2.73	2.74
MA_R505825	NA	1.46	1.47	1.18	1.57	1.61	2.61	1.68	2.11	2.44	1.29	1.13	1.59
MA_R505830	NA	1.97	2.24	2.19	2.47	2.37	3.05	2.55	2.55	3.01	2.70	2.39	2.60
MA_R505835	NA	2.41	2.85	2.76	2.92	2.95	3.49	3.02	3.23	3.59	3.23	2.89	3.16
MA_R505840	NA	2.27	2.09	2.09	2.31	2.16	2.97	2.56	2.74	3.10	2.19	2.41	2.15
MA_R505845	NA	1.10	1.28	1.52	1.51	1.55	2.42	1.05	1.19	1.85	1.00	1.56	1.48
MA_R505850	NA	1.05	1.25	1.74	1.49	1.02	2.52	2.14	1.95	1.78	1.53	1.76	1.51
MA_R505855	NA	2.98	3.35	3.26	3.17	3.07	3.89	3.08	3.50	3.95	3.97	3.08	2.97
MA_R505860	NA	0.09	0.02	0.03	0.07	0.07	1.98	0.16	0.25	0.20	0.12	0.15	0.02
MA_R505870	NA	1.92	2.15	2.01	2.63	2.11	3.13	2.58	3.31	3.46	2.80	2.39	2.75
MA_R505875	NA	1.67	1.90	1.88	2.62	2.19	2.91	2.26	2.81	2.76	1.93	2.18	2.49
MA_R505880	NA	0.49	0.44	0.54	0.60	0.70	2.20	0.47	1.06	1.16	0.77	0.30	0.72
MA_R505885	NA	0.71	0.91	1.17	1.22	0.83	2.43	1.05	1.78	1.80	1.17	1.43	1.62
MA_R505890	NA	1.84	2.09	2.07	2.23	2.34	2.93	2.01	2.76	3.02	2.56	2.38	2.24
MA_R505895	NA	1.40	1.39	1.64	1.68	1.88	2.76	1.66	2.24	2.58	1.89	0.87	1.63
MA_R505900	NA	1.71	1.79	1.21	1.71	1.48	2.86	2.30	2.83	2.79	1.85	1.67	1.93
MA_R505905	NA	1.85	2.00	2.32	2.20	2.20	2.65	2.47	2.83	2.64	1.75	1.59	2.41
MA_R505910	NA	3.05	2.86	3.16	3.01	3.38	3.41	2.94	4.07	3.79	3.55	2.64	3.08
MA_R505915	hypE	4.10	4.27	4.12	4.53	4.25	4.81	4.77	4.76	4.50	4.68	4.09	4.50
MA_R505920	hypB	4.12	4.58	4.31	4.93	4.93	5.09	5.00	5.31	5.50	5.30	4.63	4.94
MA_R505925	hypA	3.23	3.60	3.38	3.86	3.55	3.93	3.80	4.41	4.44	3.76	3.67	3.21
MA_R505930	hypD	3.48	3.88	3.76	4.11	4.05	4.27	4.15	4.41	4.70	3.90	3.84	4.02
MA_R505935	hypC	4.18	4.30	4.41	4.62	4.23	4.41	4.53	4.37	5.04	4.45	3.73	4.36
MA_R505945	NA	6.58	6.77	6.68	7.09	6.68	6.92	6.81	7.26	7.58	6.32	6.47	6.57
MA_R505950	NA	6.62	6.95	6.83	7.14	6.78	7.02	6.88	7.16	7.45	6.32	6.62	6.78
MA_R505955	NA	5.71	5.96	5.80	6.06	5.80	6.17	5.91	5.95	6.35	5.16	5.67	5.78
MA_R505960	NA	5.02	5.06	5.12	5.30	4.95	5.26	5.31	5.34	5.74	4.42	4.97	5.07
MA_R505965	NA	2.83	2.76	2.92	3.36	3.22	3.66	3.68	3.71	3.62	3.52	3.48	3.48
MA_R505970	NA	2.66	2.96	2.92	3.59	3.11	3.39	3.22	4.01	4.08	3.24	2.97	3.36
MA_R505975	NA	2.64	2.96	2.77	3.29	2.94	3.21	3.00	3.16	3.44	2.74	2.89	2.91
MA_R505980	NA	2.45	2.64	2.06	2.77	2.27	3.07	2.49	3.44	3.57	1.99	2.45	2.45
MA_R505985	NA	0.89	1.19	0.91	1.59	1.28	1.49	1.12	1.75	2.16	1.42	0.98	1.33
MA_R505990	NA	3.11	3.26	3.06	3.34	3.59	3.84	3.65	4.15	4.63	3.79	3.58	3.42
MA_R505995	NA	2.61	3.17	3.10	3.25	2.74	2.87	2.87	3.48	3.34	3.45	3.18	2.78
MA_R506000	glpX	4.49	4.75	4.61	4.78	4.74	4.81	4.90	4.81	5.07	4.81	4.67	4.73
MA_R506005	NA	3.31	3.73	3.44	3.85	3.47	3.84	3.70	3.85	4.27	3.49	3.77	3.86
MA_R506015	NA	0.62	0.67	0.56	0.70	0.46	0.57	0.66	0.85	0.81	0.62	0.57	0.70
MA_R506020	NA	1.52	1.69	1.91	2.41	1.88	1.80	1.86	2.39	2.85	1.83	1.57	1.74
MA_R506025	NA	4.47	4.82	4.49	4.82	4.61	4.93	4.88	5.40	5.15	4.83	4.66	4.32
MA_R506030	NA	2.24	2.25	2.59	2.72	2.59	2.32	2.69	2.73	3.66	2.45	2.99	2.35
MA_R506035	NA	0.14	0.83	0.48	0.00	0.60	0.71	0.45	0.82	0.61	0.78	0.69	1.25
MA_R506045	NA	0.47	0.60	0.59	0.64	0.88	0.73	1.07	1.38	1.99	0.71	0.90	0.53
MA_R506050	NA	1.47	1.67	1.41	1.88	2.10	2.04	1.68	2.14	2.57	1.71	1.09	1.43
MA_R506055	NA	5.24	5.41	5.34	5.86	5.52	5.68	5.70	6.11	6.40	5.65	5.44	5.65
MA_R506060	NA	3.88	4.17	4.00	4.41	4.30	4.50	4.55	4.71	4.95	4.35	3.99	4.36
MA_R506065	NA	3.15	3.25	3.51	3.62	3.71	3.86	3.90	4.30	4.49	3.81	3.60	3.86
MA_R506070	NA	4.97	5.22	5.12	5.38	5.07	5.10	5.27	4.95	4.95	4.88	4.83	4.98
MA_R506075	NA	5.32	5.30	5.30	5.76	5.53	5.67	5.66	5.98	6.20	6.10	5.69	5.51
MA_R506080	moaC	3.57	3.65	3.46	3.69	3.54	3.75	3.90	3.42	3.53	3.45	3.15	3.50
MA_R506085	NA	1.86	2.24	1.94	1.60	1.35	2.19	1.73	2.89	3.27	2.28	1.61	2.41
MA_R506090	NA	2.59	2.70	2.79	2.80	2.63	2.94	2.81	2.91	3.11	2.72	2.36	2.73
MA_R506095	NA	4.98	5.15	5.02	5.40	5.18	5.36	5.17	5.37	5.71	5.18	5.10	5.18
MA_R506100	NA	4.92	5.27	5.20	5.72	5.30	5.57	5.61	6.14	6.48	5.06	5.15	5.43
MA_R506105	gmd	6.37	6.58	6.45	7.11	6.60	6.91	7.04	7.62	7.97	6.85	6.58	6.85
MA_R506110	gmd	5.89	6.08	5.97	6.71	6.25	6.49	6.69	7.30	7.43	6.52	6.21	6.41
MA_R506115	NA	4.42	4.64	4.70	4.88	4.63	4.83	4.92	5.71	5.99	4.96	4.69	4.89
MA_R506120	NA	3.47	3.50	3.58	3.97	3.55	4.04	4.20	5.04	5.39	4.06	3.88	3.97
MA_R506125	NA	3.06	2.93	3.12	3.48	3.09	3.60	3.57	4.14	4.40	3.00	3.22	3.00
MA_R506135	NA	2.74	3.02	3.05	3.43	3.18	3.42	3.41	4.37	4.58	2.72	3.07	3.20
MA_R506140	NA	2.49	3.07	2.85	3.17	3.03	3.07	3.35	4.00	4.32	2.39	2.67	2.93
MA_R506145	NA	3.20	3.22	3.29	3.59	3.12	3.40	3.70	4.80	5.13	3.44	3.34	3.33
MA_R506150	NA	3.41	3.48	3.79	3.47	3.34	3.60	3.69	4.72	4.84	3.65	3.43	3.46
MA_R506155	NA	2.86	3.12	2.95	3.31	3.09	3.50	3.42	4.09	4.74	3.00	3.26	3.27
MA_R506160	NA	4.14	4.22	4.42	4.40	4.31	4.38	4.57	5.17	5.56	4.50	4.21	4.16
MA_R506165	NA	4.42	4.79	4.41	5.08	4.69	5.14	5.18	5.80	6.09	5.31	4.68	4.87
MA_R506170	NA	2.56	2.76	2.49	2.64	2.40	2.54	2.76	3.30	3.31	2.16	2.41	2.61
MA_R506175	NA	4.24	4.38	4.51	4.69	4.44	4.47	4.55	5.22	5.33	4.70	4.31	4.47
MA_R506185	wrbA	4.05	4.33	4.07	4.28	4.45	4.42	4.49	4.74	4.50	4.09	4.36	4.22
MA_R506190	NA	4.25	4.55	4.39	4.70	4.55	4.72	4.57	4.60	4.89	4.59	4.45	4.65
MA_R506195	NA	3.28	3.38	3.53	3.86	3.88	4.09	3.57	4.37	4.16	3.92	3.97	3.57
MA_R506200	NA	3.66	3.97	3.74	4.04	3.69	4.07	4.09	4.68	4.85	4.21	3.77	3.95
MA_R506205	NA	3.08	3.10	2.96	3.34	3.08	3.22	3.26	3.79	4.37	3.55	3.12	3.15
MA_R506210	NA	2.40	2.77	2.56	2.75	2.64	2.83	2.44	2.93	2.97	2.66	2.53	2.71
MA_R506215	NA	1.61	1.89	1.65	1.66	1.64	1.95	1.72	1.95	2.10	2.09	2.09	1.81
MA_R506220	NA	2.43	2.37	2.48	2.63	2.05	2.65	2.23	2.74	2.88	2.20	2.14	2.18
MA_R506225	NA	1.26	1.13	1.21	1.35	0.76	1.41	0.57	1.46	1.88	1.41	1.00	1.21
MA_R506230	NA	0.74	0.71	0.34	1.16	0.45	1.21	0.87	1.10	2.10	0.88	0.64	0.85
MA_R506235	NA	0.68	0.45	0.00	0.60	0.47	1.00	0.55	1.04	1.14	0.93	0.55	0.89
MA_R506245	NA	1.08	0.98	0.63	1.05	1.18	0.79	0.53	1.10	1.27	1.31	0.91	0.86
MA_R506250	#N/A	0.36	0.01	0.63	0.23	0.31	0.14	0.10	0.22	0.32	0.30	0.30	0.00
MA_R506255	NA	1.78	1.48	1.33	0.90	1.15	1.75	1.52	2.55	1.69	1.64	1.09	1.82
MA_R506260	anfO	1.03	0.69	0.74	1.08	1.22	1.03	1.10	1.77	1.84	1.58	0.99	0.98
MA_R506265	NA	1.63	1.79	1.27	1.69	1.63	1.95	1.91	2.24	2.42	2.17	2.00	1.82
MA_R506270	nifH	0.97	1.58	1.29	1.60	1.80	1.46	1.48	2.08	1.96	1.83	1.59	1.34
MA_R506275	NA	1.35	1.68	1.71	1.34	1.59	1.77	1.33	2.18	2.44	2.20	1.38	1.39
MA_R506280	anfO	2.00	2.55	2.66	2.65	2.04	2.59	2.47	3.10	3.46	2.75	2.67	2.41
MA_R506285	anfK	3.79	4.01	4.09	4.47	4.13	4.28	4.25	5.07	5.34	4.60	4.00	4.37
MA_R506290	anfG	3.29	3.70	3.49	3.74	3.67	4.14	3.74	3.96	3.63	3.78	3.78	3.92
MA_R506295	anfD	3.34	3.36	3.47	3.96	3.67	3.83	4.03	4.52	4.61	4.09	3.61	3.97
MA_R506300	NA	3.22	3.20	2.86	3.85	3.30	3.66	3.69	4.00	4.10	3.44	3.23	3.29
MA_R506305	NA	1.93	1.75	1.92	2.33	2.62	2.69	2.17	2.71	3.24	2.03	2.10	1.60

MA_RS06310	nifH	0.51	0.71	0.83	0.91	1.04	0.86	0.73	1.17	1.37	1.08	0.91	1.07
MA_RS06315	NA	0.65	0.75	0.04	0.61	0.81	0.52	1.29	1.73	1.21	0.66	1.58	0.77
MA_RS06320	NA	0.87	0.79	0.65	0.76	1.62	0.78	1.52	1.56	2.11	1.10	1.00	1.05
MA_RS06325	vnfD	1.95	1.66	2.11	2.53	2.10	2.38	2.45	2.88	3.25	2.69	2.08	2.35
MA_RS06330	vnfG	1.92	2.11	2.39	3.12	1.99	2.50	2.63	3.35	3.91	3.08	2.29	2.28
MA_RS06335	vnfK	1.86	2.01	1.73	2.32	1.86	2.53	2.35	2.51	3.22	2.14	1.84	2.43
MA_RS06340	NA	1.97	2.07	2.17	2.65	2.29	2.63	2.53	2.24	2.98	2.20	2.40	2.56
MA_RS06345	NA	1.56	1.68	1.88	1.76	2.08	2.13	1.62	2.42	2.62	1.92	1.54	2.04
MA_RS06350	NA	1.03	1.31	0.77	1.53	1.46	1.57	1.35	2.04	2.11	0.98	1.15	1.64
MA_RS06355	NA	1.33	1.23	1.54	1.60	1.45	1.86	1.41	1.91	2.25	1.63	1.23	1.53
MA_RS06360	hscB	2.06	1.81	1.92	2.42	2.25	2.05	1.88	2.53	2.98	2.68	1.61	1.93
MA_RS06365	NA	3.04	3.10	3.16	3.42	3.22	3.38	3.06	3.93	4.51	3.74	3.58	3.31
MA_RS06370	NA	2.27	2.52	2.43	3.35	2.66	2.94	3.16	3.53	4.05	3.29	2.88	3.09
MA_RS06375	NA	2.45	2.61	2.88	3.13	2.80	2.93	2.79	3.71	3.98	3.27	2.45	3.03
MA_RS06380	NA	2.46	2.08	2.34	3.03	2.71	3.16	3.08	3.49	3.71	2.82	2.53	3.06
MA_RS06385	NA	2.55	2.88	2.63	3.22	2.87	2.94	3.00	3.44	4.01	3.15	2.89	2.91
MA_RS06390	NA	2.24	2.55	2.24	2.78	2.66	2.84	2.97	3.25	3.69	2.56	2.36	2.58
MA_RS06395	NA	1.99	2.07	1.98	2.51	2.09	2.55	2.69	3.09	3.46	3.05	2.46	2.73
MA_RS06400	NA	1.54	1.58	1.23	1.87	1.22	1.88	1.77	2.41	2.67	2.01	2.03	1.82
MA_RS06405	NA	0.90	1.31	1.16	1.44	1.62	1.07	1.18	1.57	1.65	1.06	1.13	1.41
MA_RS06410	NA	0.85	0.62	0.58	1.46	1.25	1.45	0.88	1.28	1.55	1.09	0.70	0.70
MA_RS06415	NA	0.34	0.46	0.33	0.75	0.96	0.74	0.77	0.29	0.81	0.35	0.79	0.62
MA_RS06420	NA	2.69	2.87	2.82	3.11	3.07	3.06	3.21	3.36	3.84	3.12	2.84	2.89
MA_RS06425	modB	3.27	3.51	3.32	3.86	3.17	3.69	3.67	3.48	4.18	3.52	3.37	3.53
MA_RS06430	modA	3.69	3.81	3.86	4.42	3.94	4.25	4.28	4.64	4.95	4.35	3.91	4.01
MA_RS06435	NA	5.23	5.41	5.41	5.69	5.65	5.89	5.71	6.43	6.25	5.39	5.37	5.03
MA_RS06440	NA	3.87	3.99	3.91	4.06	4.07	4.18	3.84	4.87	4.91	3.99	3.61	3.49
MA_RS06445	NA	0.63	0.77	0.91	1.09	1.17	1.27	1.21	1.39	1.34	0.84	0.73	0.92
MA_RS06455	NA	1.43	1.69	1.72	1.90	1.87	1.98	1.80	2.91	3.05	1.93	1.89	1.76
MA_RS06460	NA	1.28	0.85	0.78	1.11	0.93	1.15	1.72	1.85	1.76	0.94	1.15	0.81
MA_RS06465	NA	1.74	1.58	1.52	2.08	1.66	2.18	1.92	2.32	2.00	1.45	2.20	1.90
MA_RS06470	NA	1.52	1.72	2.07	2.18	1.70	2.02	1.58	2.29	2.04	1.63	1.84	1.73
MA_RS06475	NA	1.77	1.89	2.38	2.15	2.02	2.06	2.11	2.69	2.71	1.99	2.53	2.21
MA_RS06480	NA	2.24	2.52	2.58	3.03	2.42	2.79	2.84	2.76	3.41	2.28	2.42	3.07
MA_RS06485	NA	2.42	2.75	3.18	3.34	2.67	3.05	3.01	3.37	3.71	2.84	2.64	3.15
MA_RS06490	NA	3.51	3.94	3.84	4.22	3.89	4.23	3.79	4.77	4.88	4.02	3.88	4.17
MA_RS06495	NA	1.26	1.15	1.12	1.51	1.28	1.42	1.14	1.27	1.84	1.18	1.37	1.26
MA_RS06500	NA	1.18	0.73	1.06	1.42	1.18	1.60	0.48	1.54	1.55	1.08	1.43	1.07
MA_RS06505	NA	0.40	0.30	0.39	1.26	0.83	0.88	0.24	0.86	1.24	0.30	0.50	0.83
MA_RS06510	rpsJ	8.27	8.65	8.49	9.00	8.59	8.91	8.66	9.36	9.94	8.86	8.55	8.77
MA_RS06515	tuf	9.78	10.09	9.99	10.59	10.08	10.35	10.46	10.80	11.15	10.47	10.11	10.26
MA_RS06520	NA	8.27	8.60	8.53	8.99	8.60	8.79	8.90	9.01	9.32	8.44	8.39	8.73
MA_RS06525	NA	8.09	8.34	8.41	8.88	8.41	8.64	8.74	9.36	9.86	8.65	8.27	8.54
MA_RS06530	NA	7.68	7.97	7.96	8.45	7.97	8.30	8.38	8.70	9.11	8.01	7.83	8.11
MA_RS06535	NA	7.45	7.68	7.61	8.10	7.65	7.89	8.13	8.74	9.00	7.96	7.56	7.82
MA_RS06540	NA	7.43	7.62	7.69	7.85	7.57	7.64	7.95	8.05	8.25	7.41	7.32	7.62
MA_RS06545	rpoA2	5.67	6.14	5.95	6.75	6.26	6.47	6.60	6.87	7.23	6.56	6.25	6.45
MA_RS06550	NA	6.57	6.87	6.79	7.43	7.04	7.22	7.33	7.53	7.83	7.19	7.01	7.25
MA_RS06555	rpoB	6.58	6.84	6.73	7.36	6.99	7.17	7.22	7.63	7.85	7.26	6.96	7.21
MA_RS06560	NA	6.38	6.63	6.47	7.24	6.80	7.07	7.19	7.41	7.45	7.22	6.81	7.04
MA_RS06565	NA	3.63	3.54	3.70	4.37	4.04	3.62	4.92	5.04	5.05	4.44	4.10	3.86
MA_RS06570	#N/A	5.63	5.87	5.98	5.87	5.98	5.60	6.41	2.10	3.41	4.91	5.52	5.93
MA_RS06580	NA	2.28	2.39	2.22	2.87	2.46	2.67	2.64	3.37	3.57	2.29	2.36	2.68
MA_RS06585	NA	2.62	3.15	2.48	3.37	3.05	3.19	3.11	4.20	4.63	3.30	2.87	2.86
MA_RS06590	NA	2.09	2.23	2.04	2.52	2.40	2.21	2.37	3.01	3.60	2.58	1.83	2.08
MA_RS06595	NA	2.19	2.39	2.19	2.63	2.52	2.67	2.87	3.35	3.63	2.28	2.22	2.61
MA_RS06600	NA	3.63	4.05	3.73	4.58	4.21	4.57	4.25	4.89	5.32	4.46	4.18	4.27
MA_RS06605	NA	2.96	3.21	3.01	3.84	3.52	3.80	3.40	4.04	4.12	3.52	3.61	3.85
MA_RS06610	NA	2.11	2.27	2.30	2.78	2.87	2.76	2.56	3.39	3.90	2.48	2.83	2.55
MA_RS06615	NA	1.81	2.03	2.07	2.40	1.89	2.31	2.44	2.91	3.14	2.29	1.78	2.25
MA_RS06620	NA	5.45	5.63	5.51	6.16	5.83	5.99	6.24	6.32	6.47	5.88	5.59	5.89
MA_RS06625	NA	5.17	5.49	5.43	5.81	5.45	5.74	5.91	6.06	6.31	5.63	5.39	5.66
MA_RS06630	NA	3.95	4.32	4.23	4.68	4.38	4.54	4.50	4.70	5.16	4.46	4.44	4.59
MA_RS06635	NA	4.48	4.75	4.78	4.96	4.86	4.84	4.77	5.18	5.40	5.11	4.68	4.97
MA_RS06640	NA	4.40	4.57	4.57	4.94	4.69	4.86	4.80	5.06	5.52	5.04	4.69	4.89
MA_RS06645	coxBC	4.74	4.88	4.99	5.18	4.96	5.05	5.05	4.85	5.19	4.96	4.81	5.05
MA_RS06650	NA	2.45	2.68	2.47	2.91	2.87	2.95	2.76	2.73	2.95	2.76	2.20	2.94
MA_RS06655	NA	2.41	2.59	2.39	2.67	2.56	2.56	2.79	3.37	3.43	3.07	2.80	2.67
MA_RS06660	NA	1.89	1.11	1.30	1.37	1.50	1.20	1.42	2.56	2.50	1.23	1.19	1.17
MA_RS06665	NA	4.01	4.22	3.96	4.24	4.38	4.29	4.21	5.28	5.40	4.30	4.18	4.30
MA_RS06670	NA	2.84	2.75	3.17	2.87	2.78	2.90	2.87	4.44	4.29	2.47	2.90	2.49
MA_RS06675	NA	2.20	2.41	2.43	2.69	2.64	2.56	2.71	3.64	4.20	2.69	2.49	2.81
MA_RS06680	NA	1.08	1.45	1.56	1.10	1.58	1.49	1.59	2.17	1.95	1.16	1.50	1.39
MA_RS06685	NA	3.43	3.74	3.67	3.61	3.84	3.89	3.99	4.34	4.36	4.01	3.92	3.86
MA_RS06690	NA	3.96	4.07	4.07	4.22	3.98	4.01	4.22	4.07	4.00	4.03	3.89	4.02
MA_RS06695	NA	1.75	1.73	1.77	1.97	1.87	1.89	2.20	2.55	2.60	2.13	2.07	1.71
MA_RS06700	NA	2.08	1.72	1.79	2.40	2.14	2.42	2.01	2.05	3.00	2.56	1.83	2.05
MA_RS06710	NA	0.92	1.04	0.95	1.31	1.06	1.49	1.10	1.61	1.34	1.38	0.93	1.06
MA_RS06720	NA	3.69	4.15	3.91	4.14	4.02	4.12	4.30	4.01	4.39	4.05	3.22	3.41
MA_RS06725	NA	3.66	3.98	3.67	3.95	3.88	4.31	3.85	5.05	4.97	4.20	3.70	3.85
MA_RS06735	NA	0.72	0.78	0.66	0.93	0.47	0.88	0.32	0.90	1.37	0.59	0.81	0.50
MA_RS06740	tadA	0.97	0.91	0.87	1.03	1.01	1.42	1.17	1.20	1.68	1.05	1.06	1.43
MA_RS06750	NA	3.51	3.62	3.46	3.88	3.52	3.78	3.87	4.53	5.06	3.64	3.50	3.67
MA_RS06755	NA	3.57	3.76	3.89	3.78	3.59	3.58	4.48	4.28	4.36	3.39	3.36	3.40
MA_RS06760	NA	0.84	0.49	0.50	1.01	0.81	0.78	0.68	1.21	1.01	1.00	0.81	0.47
MA_RS06765	NA	0.79	0.69	0.34	0.50	0.40	0.65	0.86	0.72	0.91	0.31	0.93	0.66
MA_RS06775	NA	3.91	3.96	3.96	4.61	4.30	4.47	4.46	4.96	5.01	4.59	4.26	4.54
MA_RS06780	NA	3.06	3.23	3.04	3.50	3.07	3.24	3.16	3.13	3.39	3.19	3.24	3.01
MA_RS06785	coo5	2.01	2.43	2.59	2.60	2.37	2.39	2.18	2.28	2.67	2.17	2.05	2.41
MA_RS06790	NA	4.98	5.16	5.11	5.61	5.23	5.61	5.49	6.31	6.65	5.76	5.41	5.42
MA_RS06795	larA	3.14	3.18	3.11	3.52	3.24	3.56	3.60	3.41	3.46	3.66	3.19	3.17
MA_RS06800	larA	3.97	4.25	4.33	4.63	4.29	4.47	4.52	4.36	4.63	4.64	4.38	4.39
MA_RS06815	NA	6.09	6.31	6.23	6.28	6.04	6.35	6.03	6.31	6.58	5.75	5.94	5.95
MA_RS06820	NA	0.52	0.19	0.78	0.68	0.63	0.86	0.99	0.82	0.87	0.84	0.94	0.93
MA_RS06825	gatD	4.76	4.99	4.82	5.30	4.99	5.31	5.17	5.82	6.13	5.52	4.90	5.20
MA_RS06830	argH	4.40	4.71	4.44	4.98	4.57	4.83	4.73	5.17	5.53	4.89	4.71	4.79
MA_RS06835	NA	0.91	1.14	1.22	0.90	1.44	1.03	1.47	1.52	1.63	1.61	0.59	1.24
MA_RS06840	NA	1.97	1.95	1.52	1.80	1.42	1.92	1.87	2.66	2.97	1.69	1.51	1.86
MA_RS06845	NA	2.21	2.32	2.39	2.71	2.31	2.26	2.71	3.10	3.46	2.77	2.75	2.28
MA_RS06850	NA	2.44	2.40	2.30	2.79	2.79	2.82	2.99	3.36	3.54	3.05	2.50	2.90
MA_RS06865	NA	0.96	1.13	1.69	0.75	1.10	0.71	0.80	1.23	0.73	0.99	1.37	0.17
MA_RS06870	NA	1.84	2.10	1.73	2.25	1.89	2.23	1.78	2.52	2.62	2.09	2.18	2.39
MA_RS06875	NA	2.97	3.05	2.97	3.32	3.04	3.11	3.24	3.72	3.66	2.99	3.04	3.19
MA_RS06880	NA	1.59	1.76	1.54	1.23	2.36	1.23	2.00	2.24	2.20	1.63	0.59	1.64
MA_RS06885	NA	0.43	0.30	0.51	1.14	0.74	0.55	1.17	1.17	1.01	0.59	1.01	0.76
MA_RS06890	NA	1.68	2.31	2.20	2.65	2.01	2.14	2.02	2.85	2.91	2.26	2.03	1.95
MA_RS06895	NA	0.12	0.34	0.65	1.51	0.79	0.29	1.34	1.99	0.98	0.44	1.26	0.51
MA_RS06905	NA	0.60	0.64	0.52	0.88	0.66	0.92	0.88	0.97	1.05	0.83	0.43	0.82
MA_RS06915	NA	0.40	0.61	0.22	0.72	0.99	1.04	0.94	0.71	0.41	0.81	0.00	1.04
MA_RS06920	NA	1.02	0.91	1.00	1.59	1.37	1.50	0.86	1.81	1.74	1.12	0.85	0.80
MA_RS06925	NA	0.40	0.67	0.98	0.75	0.41	0.85	0.38	0.00	1.10	1.27	0.28	0.00
MA_RS06940	NA	4.03	4.17	4.37	4.33	4.49	4.16	4.09	3.96	4.50	4.18	4.37	4.13
MA_RS06945	NA	2.42	2.68	2.67	3.09	2.66	3.08	1.90	3.13	2.40	1.62	2.21	2.59
MA_RS06950	NA	1.16	1.01	1.02	0.85	0.77	1.13	1.43	1.58	1.21	0.85	0.39	0.76
MA_RS06955	NA	1.42	1.70	1.83	1.64	2.02	2.14	1.66	2.30	2.88	2.26	2.34	1.59
MA_RS06960	NA	4.24	4.47	4.41	4.84	4.64	4.82	4.66	4.70	4.94	4.30	4.46	4.68
MA_RS06965	NA	3.34	3.35	3.29	3.74	3.99	4.12	3.86	4.53	5.00	3.70	3.75	4.09
MA_RS06970	NA	2.15	2.44	2.44	2.81	2.12	2.48	2.62	2.85	3.26	2.37	2.37	2.72
MA_RS06975	NA	0.44	0.62	0.73	0.89	0.79	0.97	0.63	0.97	0.78	0.58	0.89	0.55
MA_RS06980	NA	0.93	0.61	0.56	1.05	0.64	0.77	0.59	0.97	1.28	0.98	0.49	0.92
MA_RS06985	NA	0.59	0.51	0.00	0.56	0.67	0.00	1.20	0.86	0.65	0.84	0.61	0.28
MA_RS06990	NA	0.78	0.87	0.39	1.10	0.58	0.83	0.44	0.53	0.84	1.04	1.05	0.69
MA_RS06995	NA	0.84	0.84	0.22	0.95	0.89	0.81	0.78	1.12	0.97	1.17	0.00	1.58
MA_RS07000	NA	5.69	5.98	6.13	5.83	6.13	6.02	6.23	5.55	5.78	5.96	5.88	5.87
MA_RS07005	NA	4.72	5.14	5.04	4.39	4.87	5.24	5.51	5.39	5.00	5.17	5.13	5.18
MA_RS07010	eif1A	3.80	3.44	4.21	3.46	3.79	4.24	5.02	4.91	4.84	3.59	4.24	4.68
MA_RS07015	NA	0.63	1.54	1.07	1.12	1.69	1.60	1.96	2.14	2.89	2.00	1.63	2.02
MA_RS07020	NA	0.00	0.00	0.50	0.00	0.63	0.00	0.33	0.29	0.35	0.53	0.00	0.00
MA_RS07025	NA	6.32	6.16	6.21	5.97	6.34	6.18	6.48	7.02	5.99	6.40	6.33	5.92
MA_RS07030	eif1A	1.29	1.63	1.38	1.56	1.46	1.19	1.44	2.88	2.69	1.90	1.50	1.73
MA_RS07040	NA	3.68	3.96	3.65	4.13	3.74	4.18	3.91	4.43	4.73	3.95	3.58	3.82
MA_RS07045	NA	1.77	2.06	1.80	2.20	2.16	2.29	2.26	2.14	2.27	1.90	1.96	2.04
MA_RS07055	NA	0.63	0.96	0.28	0.87	1.13	1.18	1.29	1.41	1.18	1.26	1.43	1.75
MA_RS07065	NA	2.25	2.10	1.80	2.07	2.13	2.06	1.99	2.48	2.14	1.92	2.21	2.12
MA_RS07070	NA	2.58	2.59	2.56	3.00	2.95	3.01	3.03	3.24	3.45	2.96	2.90	2.90
MA_RS07075	NA	4.43	4.64	4.44	5.10	4.68	5.02	4.93	5.44	5.59	4.96	4.62	4.86
MA_RS07080	NA	2.32	2.27	2.61	2.70	2.42	3.01	3.19	3.22	2.14	2.14	2.12	2.58
MA_RS07085	NA	4.21	4.61	4.38	4.50	4.12	4.29	4.44	5.14	5.30	4.51	4.05	4.34
MA_RS07090	NA	2.42	2.02	2.11	2.07	1.95	2.23	2.26	2.80	2.77	2.03	1.72	1.39
MA_RS07100	NA	4.69	4.43	4.43	4.90	4.43	4.69	5.29	5.39	4.82	4.67	4.67	4.51
MA_RS07105	trxB	4.92	4.90	4.97	5.25	5.10	5.10	5.34	5.38	5.09	4.84	4.74	4.83
MA_RS07110	NA	4.72	4.80	4.92	5.47	4.97	5.35	5.33	5.00	5.18	5.05	4.49	4.44
MA_RS07115	dphS	4.19	4.41	4.21	4.64	4.42	4.60	4.56	4.79	5.33	4.45	4.36	4.49

MA_RS07120	NA	3.98	4.32	4.19	4.93	4.33	4.63	4.50	4.66	5.10	4.53	4.38	4.72
MA_RS07125	NA	4.50	4.55	4.67	5.06	4.63	4.96	5.09	5.57	5.82	5.36	4.98	5.01
MA_RS07130	NA	4.10	4.46	4.11	4.78	4.60	4.93	4.72	5.10	5.26	4.88	4.68	4.77
MA_RS07135	NA	4.51	4.66	4.63	5.39	5.10	5.12	4.94	4.81	5.32	4.93	5.02	5.07
MA_RS07140	NA	4.47	4.65	4.13	4.88	4.46	4.48	4.83	5.07	5.09	5.00	4.34	4.48
MA_RS07145	NA	5.49	5.70	5.89	6.13	5.58	5.75	6.40	6.94	6.82	6.25	5.75	5.91
MA_RS07150	NA	4.78	4.66	4.77	5.11	4.63	4.92	5.20	5.03	5.11	4.97	4.34	4.64
MA_RS07155	NA	0.20	0.35	0.16	0.36	0.24	0.24	0.25	0.45	0.41	0.38	0.14	0.28
MA_RS07160	NA	4.01	4.00	3.99	4.30	3.97	4.30	3.99	4.31	4.76	4.39	4.18	4.04
MA_RS07165	NA	5.96	6.33	6.04	6.76	6.38	6.54	6.46	7.15	7.42	6.89	6.35	6.46
MA_RS07170	NA	5.94	6.46	6.22	6.83	6.44	6.63	6.72	6.91	7.22	6.84	6.33	6.65
MA_RS07175	NA	4.66	4.77	4.67	5.11	5.06	5.08	5.23	5.55	5.61	5.37	4.78	5.25
MA_RS07180	hslB	6.06	6.32	6.16	6.80	6.19	6.47	6.62	7.38	7.53	6.69	6.27	6.54
MA_RS07185	NA	5.92	6.29	5.92	6.62	6.15	6.54	6.30	6.86	7.22	6.47	6.27	6.27
MA_RS07190	#N/A	0.16	0.54	0.49	0.45	0.15	0.15	0.64	0.55	0.65	0.24	0.34	0.93
MA_RS07195	NA	0.62	0.52	0.32	0.56	0.00	0.38	0.03	0.72	0.96	0.37	0.48	0.27
MA_RS07200	NA	2.49	2.87	2.36	2.90	2.65	3.08	2.61	3.03	3.36	2.72	2.56	2.95
MA_RS07205	NA	5.45	5.55	5.52	5.90	5.75	5.88	5.99	6.52	6.66	6.36	5.87	6.05
MA_RS07210	NA	5.07	5.47	5.32	5.71	5.28	5.48	5.85	6.08	6.14	5.55	5.24	5.27
MA_RS07215	hisE	3.83	4.07	3.83	4.52	3.90	4.45	4.20	4.87	5.24	3.82	4.37	3.82
MA_RS07220	NA	6.12	6.28	6.42	6.58	6.26	6.47	6.32	6.38	6.46	6.54	6.27	6.24
MA_RS07225	NA	1.36	1.17	1.14	1.50	2.38	1.97	2.31	1.75	2.03	1.41	1.39	1.63
MA_RS07230	nlkR	2.56	2.35	2.11	2.99	2.46	2.47	2.38	3.64	3.53	3.27	3.44	3.14
MA_RS07235	NA	4.24	4.60	4.37	4.84	4.50	4.72	4.43	5.25	5.28	5.26	4.62	4.35
MA_RS07240	NA	0.99	1.23	1.46	1.38	1.70	1.75	1.76	1.61	1.83	1.54	1.65	1.97
MA_RS07245	NA	1.61	1.33	2.38	2.36	1.26	2.04	2.28	2.36	2.61	1.75	1.87	2.28
MA_RS07255	NA	4.76	4.86	4.69	5.08	4.81	4.93	4.94	5.33	5.61	4.67	4.59	4.80
MA_RS07260	NA	1.15	0.95	1.00	1.19	0.94	1.39	1.08	1.58	1.11	1.69	1.40	0.28
MA_RS07270	NA	0.16	0.22	0.18	0.13	0.26	0.29	0.08	0.22	0.00	0.21	0.00	0.00
MA_RS07275	NA	0.00	0.09	0.16	0.29	0.22	0.00	0.86	0.00	0.20	0.35	0.00	0.11
MA_RS07280	NA	1.99	1.92	1.91	2.36	1.52	2.06	1.75	1.84	2.24	1.46	1.40	1.60
MA_RS07285	NA	1.92	2.32	2.10	2.42	2.24	2.92	3.07	3.16	2.98	2.31	2.45	2.79
MA_RS07290	NA	1.30	1.43	0.78	0.90	1.13	0.72	2.09	1.53	1.43	1.49	1.52	1.16
MA_RS07295	NA	1.86	2.33	1.98	2.92	2.82	2.11	2.65	2.95	3.50	2.62	1.93	2.00
MA_RS07300	NA	1.90	1.90	1.90	1.94	1.71	2.00	2.30	2.15	2.61	2.37	1.39	2.17
MA_RS07305	NA	5.06	5.25	5.18	5.47	5.20	5.44	5.41	5.69	5.90	5.49	5.16	5.26
MA_RS07310	mtnP	4.40	4.60	4.66	4.90	4.66	4.77	4.59	5.67	5.80	5.22	4.91	4.84
MA_RS07315	NA	0.60	1.05	0.80	0.78	1.13	0.93	0.32	0.14	0.75	0.54	0.52	0.29
MA_RS07320	NA	4.34	4.79	4.56	4.90	4.64	4.72	4.63	4.97	5.07	4.87	4.64	4.81
MA_RS07325	NA	5.01	5.16	5.07	5.44	5.34	5.44	5.23	6.02	5.90	5.75	5.33	5.32
MA_RS07330	NA	5.07	4.89	5.23	5.66	5.14	5.41	6.02	5.90	5.68	5.43	5.25	5.16
MA_RS07335	NA	5.38	5.26	5.49	5.58	5.42	5.43	5.77	5.99	5.99	5.55	5.41	5.45
MA_RS07340	#N/A	3.67	3.76	3.35	2.72	3.10	3.84	3.26	2.04	2.51	2.76	3.24	3.01
MA_RS07345	#N/A	3.00	2.52	2.50	1.68	2.33	2.46	2.40	0.45	0.59	1.98	2.29	1.34
MA_RS07350	NA	1.84	1.57	2.00	1.85	1.83	1.78	2.02	1.64	1.54	1.61	1.53	2.30
MA_RS07355	NA	4.92	5.20	5.05	5.32	4.82	4.92	4.76	5.53	5.92	4.74	4.89	5.27
MA_RS07360	NA	4.49	4.87	4.83	4.94	4.46	4.73	4.76	5.10	5.16	3.79	4.27	4.63
MA_RS07365	NA	3.66	4.22	3.52	4.08	3.60	4.03	3.61	4.39	4.34	3.18	3.33	3.63
MA_RS07375	NA	1.82	1.39	1.82	1.37	1.42	1.50	1.87	1.67	1.12	0.62	1.42	1.51
MA_RS07380	NA	5.40	5.73	5.50	6.14	5.83	6.06	6.02	6.57	6.80	6.63	5.85	5.98
MA_RS07385	NA	6.04	6.29	6.15	6.83	6.50	6.67	6.57	7.00	7.39	7.21	6.53	6.57
MA_RS07390	NA	6.04	6.37	6.22	6.95	6.45	6.70	6.69	7.16	7.46	7.44	6.52	6.55
MA_RS07395	NA	2.98	2.89	3.03	3.00	2.74	2.87	2.67	3.25	3.59	3.07	2.84	2.68
MA_RS07405	NA	1.94	2.00	1.35	2.30	1.78	2.35	1.83	2.14	2.38	1.92	1.74	1.46
MA_RS07410	NA	0.62	0.60	0.31	1.00	1.02	1.26	0.77	1.33	1.39	0.86	0.84	0.89
MA_RS07415	NA	3.22	3.27	2.77	3.26	3.37	3.17	2.95	3.14	3.41	3.24	3.28	3.26
MA_RS07420	NA	3.15	3.43	3.07	3.67	3.59	4.04	3.35	4.13	4.30	3.73	3.44	3.61
MA_RS07425	NA	3.39	3.86	3.85	4.31	3.76	4.15	3.71	4.92	5.14	3.94	3.82	4.00
MA_RS07430	msrA	3.08	2.96	2.68	3.39	2.63	3.43	3.64	3.81	4.07	3.23	3.14	2.97
MA_RS07435	NA	3.77	3.95	3.84	3.95	3.75	3.76	3.77	4.38	4.07	3.68	3.79	3.69
MA_RS07440	NA	5.56	5.54	5.78	5.75	5.78	5.54	6.05	7.12	7.46	6.25	5.50	5.66
MA_RS07445	NA	1.39	1.93	1.70	1.98	1.83	1.69	1.55	2.30	2.19	1.91	2.02	1.60
MA_RS07450	NA	2.36	2.69	2.72	3.01	2.88	3.07	3.07	4.09	4.27	3.27	2.92	3.04
MA_RS07455	NA	4.05	4.18	4.12	4.84	4.33	4.63	4.62	5.12	5.45	4.86	4.30	4.44
MA_RS07460	NA	3.73	3.97	3.83	4.52	3.88	4.31	4.08	4.60	5.05	4.16	4.04	4.22
MA_RS07465	NA	4.84	4.74	4.98	5.13	4.88	4.97	5.03	5.25	5.37	5.17	4.98	4.85
MA_RS07480	nudC	3.07	3.54	3.30	3.35	3.17	3.42	3.27	3.66	3.68	3.41	3.05	3.33
MA_RS07485	NA	2.74	3.03	2.89	3.31	2.78	3.49	3.20	2.88	3.18	2.94	3.56	3.09
MA_RS07490	rsmA	3.19	3.63	3.33	3.67	3.27	3.81	3.55	4.09	4.36	3.59	3.75	3.63
MA_RS07495	NA	6.02	6.25	6.18	6.64	6.39	6.43	6.45	6.87	6.97	6.51	6.12	6.35
MA_RS07500	NA	6.75	6.97	6.99	7.45	7.04	7.26	7.59	7.86	8.01	7.25	6.75	6.92
MA_RS07505	NA	6.23	6.52	6.45	6.71	6.57	6.66	6.66	6.84	6.92	6.86	6.38	6.56
MA_RS07510	NA	5.09	5.37	5.13	5.52	5.13	5.47	5.52	5.42	5.46	5.44	5.23	5.39
MA_RS07515	tmrY	3.89	3.97	3.71	3.90	3.67	3.89	4.00	3.08	3.31	3.79	3.93	3.92
MA_RS07520	NA	4.33	4.35	4.15	4.85	4.51	4.76	4.80	4.57	4.53	4.50	4.40	4.54
MA_RS07525	NA	3.41	3.86	3.64	4.14	3.79	4.20	3.95	4.61	4.76	3.94	3.92	3.86
MA_RS07530	NA	1.79	1.88	1.21	1.20	1.70	1.99	2.89	2.64	2.65	1.70	1.81	1.81
MA_RS07535	NA	1.21	1.15	1.35	0.74	1.37	1.06	2.00	1.41	2.36	1.07	1.19	1.37
MA_RS07540	NA	6.90	7.31	7.04	7.43	7.11	7.28	7.16	7.52	7.39	7.67	7.02	7.03
MA_RS07545	NA	0.68	0.60	0.09	0.35	0.53	1.01	0.66	0.41	0.44	0.94	0.86	1.03
MA_RS07550	NA	3.94	4.11	4.03	3.94	4.07	4.15	4.07	4.02	4.04	3.84	3.82	4.02
MA_RS07555	NA	5.23	5.46	5.51	5.82	5.39	5.57	6.20	6.41	6.28	5.86	5.51	5.87
MA_RS07560	NA	4.41	4.98	4.76	5.05	4.75	4.91	5.25	5.45	5.62	5.27	4.73	5.02
MA_RS07565	NA	4.15	4.34	4.33	4.43	4.04	4.56	4.50	5.11	5.06	4.91	4.30	4.41
MA_RS07575	NA	5.02	5.27	5.23	5.63	5.08	5.38	5.57	5.76	6.09	5.38	5.01	5.31
MA_RS07580	NA	3.96	3.94	3.22	3.72	3.81	4.00	4.29	4.46	3.82	4.18	3.86	4.05
MA_RS07585	NA	3.11	3.51	3.85	3.36	3.44	3.52	3.52	3.93	4.27	3.19	3.07	3.50
MA_RS07595	NA	2.72	2.71	3.29	3.00	2.58	3.03	3.33	3.65	3.76	2.99	2.90	2.77
MA_RS07605	thiI	3.20	3.42	3.45	3.87	3.57	3.83	3.61	4.27	4.46	3.88	3.36	3.61
MA_RS07610	NA	2.00	1.79	1.36	1.29	2.27	2.15	1.86	2.93	1.71	1.73	1.88	1.55
MA_RS07615	NA	1.93	1.51	1.64	2.09	1.91	1.77	1.74	2.42	2.09	1.91	1.49	1.80
MA_RS07620	NA	5.23	5.52	5.34	5.69	5.23	5.58	5.72	6.21	5.99	5.54	5.14	5.35
MA_RS07625	NA	2.37	2.63	2.42	2.98	2.60	2.70	2.69	3.05	3.26	2.58	2.45	2.74
MA_RS07630	#N/A	4.23	4.33	4.44	4.37	3.96	4.16	4.31	4.62	3.74	4.22	4.25	4.35
MA_RS07635	NA	6.36	6.43	6.34	6.60	6.39	6.64	6.73	7.04	7.16	7.02	6.71	6.37
MA_RS07640	NA	6.32	6.35	6.43	6.61	6.64	6.41	7.08	7.30	6.81	6.88	6.26	6.33
MA_RS07645	NA	3.02	3.33	3.77	4.13	3.65	3.76	3.85	4.09	4.27	3.56	3.33	3.92
MA_RS07650	NA	4.37	4.48	4.39	4.83	4.63	4.71	4.76	4.62	4.97	4.59	4.34	4.68
MA_RS07655	NA	3.56	3.91	3.52	4.33	3.73	4.19	4.37	4.19	4.68	4.24	3.92	4.17
MA_RS07660	NA	3.95	3.72	4.06	3.86	4.01	3.46	3.63	3.80	3.55	3.63	3.11	3.60
MA_RS07665	grpE	6.07	6.18	6.32	6.94	6.71	6.77	7.38	6.80	7.42	6.27	6.80	6.96
MA_RS07670	dnaK	8.44	8.56	8.46	9.41	8.99	9.23	9.43	9.52	10.16	8.92	9.24	9.39
MA_RS07675	dnaJ	6.74	6.72	6.79	7.49	7.16	7.33	7.57	7.60	8.28	6.93	7.24	7.58
MA_RS07680	trkA	3.67	3.91	4.11	3.76	3.67	3.69	4.02	4.32	4.34	3.99	3.59	3.90
MA_RS07685	NA	2.48	2.87	2.90	2.80	2.72	2.87	2.44	3.10	3.30	2.79	2.83	2.69
MA_RS07695	trkA	4.13	4.30	4.43	4.64	4.39	4.66	4.55	4.65	4.81	4.28	4.30	4.26
MA_RS07700	NA	3.08	3.30	3.36	3.56	3.19	3.60	3.65	3.78	4.25	3.05	3.37	3.14
MA_RS07705	NA	5.46	5.62	5.52	5.80	5.64	5.78	5.90	6.22	6.30	5.73	5.58	5.68
MA_RS07710	NA	5.68	6.00	5.78	6.13	5.84	6.08	6.39	6.70	6.98	5.86	5.71	6.16
MA_RS07715	NA	4.23	4.53	4.27	4.95	4.59	4.76	4.61	5.57	5.73	4.64	4.66	4.90
MA_RS07720	NA	4.47	4.42	4.49	4.79	4.39	4.58	5.01	5.53	5.74	4.68	4.59	4.69
MA_RS07725	cofC	4.64	4.90	4.55	5.15	4.87	5.30	5.10	5.47	5.75	4.65	4.84	5.17
MA_RS07730	cofH	5.75	6.07	5.91	6.37	6.03	6.21	6.25	6.54	6.93	5.66	5.93	6.15
MA_RS07735	cofH	5.80	5.95	5.78	6.12	5.81	6.10	6.08	6.04	6.33	5.46	5.81	5.93
MA_RS07740	cofG	5.55	5.76	5.68	6.20	5.96	5.98	6.00	5.98	6.31	5.14	5.66	5.85
MA_RS07745	NA	5.12	5.36	5.28	5.73	5.45	5.61	5.54	5.83	6.19	5.17	5.28	5.53
MA_RS07750	NA	4.38	4.53	4.16	4.63	4.62	4.71	4.67	4.82	4.65	4.45	4.27	4.48
MA_RS07760	fpoA	6.96	7.15	7.06	7.89	7.40	7.71	7.50	8.22	8.66	7.87	7.23	7.50
MA_RS07765	fpoB	7.79	7.99	7.90	8.50	8.07	8.25	8.30	8.26	8.62	8.09	7.91	8.21
MA_RS07770	fpoC	6.93	7.20	6.79	7.69	7.29	7.57	7.43	8.27	8.45	7.47	7.11	7.22
MA_RS07775	fpoD	7.46	7.71	7.55	8.17	7.74	7.96	7.96	8.17	8.46	7.65	7.67	7.84
MA_RS07780	fpoH	7.36	7.62	7.52	7.94	7.54	7.83	7.61	7.42	7.72	6.94	7.51	7.60
MA_RS07785	fpoI	7.03	7.35	7.02	7.90	7.31	7.68	7.38	7.74	8.35	7.01	7.27	7.47
MA_RS07790	#N/A	6.16	6.44	6.35	6.61	6.12	6.56	6.19	6.41	7.02	5.51	6.09	6.14
MA_RS07795	#N/A	7.04	7.37	7.14	7.54	7.18	7.63	7.20	7.44	7.96	6.58	7.13	7.27
MA_RS07800	fpoK	6.86	7.12	7.03	7.40	7.07	7.34	7.06	7.38	7.90	6.32	6.84	7.18
MA_RS07805	fpoL	7.03	7.28	7.07	7.65	7.17	7.57	7.34	8.06	8.36	6.53	7.13	7.23
MA_RS07810	fpoM	7.43	7.65	7.47	7.94	7.53	7.85	7.77	7.96	8.33	6.64	7.33	7.51
MA_RS07815	fpoN	6.95	7.31	6.96	7.60	7.15	7.47	7.29	7.57	7.95	6.27	7.06	7.23
MA_RS07820	NA	7.44	7.68	7.31	7.86	7.60	7.70	7.80	8.20	8.46	6.60	7.26	7.55
MA_RS07845	NA	1.44	1.16	0.58	1.03	1.76	0.82	1.70	2.33	2.03	1.62	1.19	1.45
MA_RS07850	NA	1.83	1.73	2.16	1.67	2.01	1.47	1.33	2.37	2.48	1.73	2.09	1.57
MA_RS07855	NA	0.97	0.60	0.70	1.35	0.97	1.15	0.72	1.23	1.51	1.07	0.84	1.05
MA_RS07860	NA	2.07	2.78	2.20	3.14	2.85	2.28	3.05	3.80	3.95	3.22	2.61	2.42
MA_RS07865	NA	1.45	1.51	1.98	2.51	1.83	1.14	2.06	2.54	2.85	2.36	1.59	1.43
MA_RS07880	NA	3.21	3.30	3.40	3.51	3.58	3.53	3.87	4.29	4.29	3.31	3.01	3.28
MA_RS07885	NA	1.57	2.03	1.85	2.41	2.20	2.40	1.96	2.55	2.58	1.83	2.23	2.04
MA_RS07890	NA	0.90	0.69	0.57	0.94	1.08	0.81	1.16	0.90	1.09	0.98	0.56	0.76
MA_RS07895	NA	2.30	2.43	2.24	2.20	2.09	1.78	2.50	2.46	2.46	2.24	2.32	2.06
MA_RS07900	rplT4ae	8.60	8.86	8.73	9.22	8.74	8.97	9.13	9.70	9.92	9.10	8.73	8.80
MA_RS07905	NA	8.35	8.57	8.51	8.85	8.52	8.73	9.03	9.50	9.81	8.88	8.58	8.54
MA_RS07910	NA	8.03	8.44	8.30	8.58	8.21	8.46	8.32	8.06	8.48	7.93	8.10	8.21
MA_RS07915	ndk	8.31	8.61	8.53	8.76	8.45	8.61	8.48	8.21	8.59	8.14	8.28	8.43

MA_RS07920	infB	7.42	7.74	7.60	8.00	7.59	7.83	7.84	8.14	8.37	7.58	7.47	7.70
MA_RS07925	NA	6.39	6.71	6.56	6.89	6.61	6.72	7.11	7.02	7.10	6.56	6.40	6.65
MA_RS07930	#N/A	2.01	2.10	2.44	2.24	2.44	2.83	2.80	3.55	3.78	2.92	2.39	2.68
MA_RS07935	NA	2.02	2.62	1.85	2.51	1.98	2.80	2.92	3.34	3.60	2.44	2.90	2.53
MA_RS07940	NA	2.09	2.07	2.15	2.20	2.42	2.74	2.43	2.60	2.93	2.33	2.20	2.25
MA_RS07945	NA	2.14	2.37	2.27	2.73	2.66	2.86	2.63	3.25	3.60	2.63	2.50	2.48
MA_RS07955	NA	2.50	2.63	2.55	2.73	2.48	2.66	2.50	3.36	3.84	2.66	2.20	2.62
MA_RS07960	NA	3.02	2.74	3.38	3.20	2.61	2.88	3.02	3.91	3.31	3.18	2.97	2.98
MA_RS07965	istB	0.05	0.03	0.02	0.09	0.07	0.03	0.00	0.09	0.09	0.09	0.00	0.10
MA_RS07970	istA	0.74	0.71	0.74	1.01	0.90	1.05	0.84	1.02	1.17	1.08	0.69	0.80
MA_RS07980	NA	2.01	1.98	2.04	2.50	2.13	2.89	2.23	3.13	3.49	2.58	2.35	2.24
MA_RS07985	NA	1.55	1.68	2.04	2.11	2.13	1.81	1.87	2.15	2.77	1.45	1.86	2.02
MA_RS07990	NA	1.31	1.54	1.46	1.89	1.60	1.82	2.03	2.29	2.31	1.36	1.52	1.90
MA_RS07995	NA	1.74	2.07	1.43	2.29	1.77	2.36	1.40	2.94	3.27	2.07	1.85	2.39
MA_RS08000	NA	2.08	2.20	1.97	2.17	2.55	2.78	2.26	2.80	3.37	2.31	2.32	2.20
MA_RS08005	NA	2.45	2.55	2.56	3.12	2.56	2.89	3.18	3.82	3.99	3.23	2.91	2.92
MA_RS08010	#N/A	0.58	0.30	0.36	0.60	0.31	0.29	0.13	0.44	0.77	0.46	0.46	0.47
MA_RS08015	NA	1.59	1.73	1.70	1.99	1.65	1.81	1.94	2.65	3.03	1.54	1.79	1.83
MA_RS08020	NA	1.30	1.92	1.88	2.12	2.00	2.13	2.14	2.67	3.19	1.66	1.73	2.11
MA_RS08025	NA	1.17	1.23	0.94	1.44	1.12	1.03	0.66	1.79	2.41	0.92	1.00	0.84
MA_RS08030	NA	1.99	2.20	1.94	1.96	2.38	2.49	2.38	3.21	3.50	2.30	2.18	2.23
MA_RS08035	NA	2.17	2.43	2.10	2.16	2.23	2.59	2.63	3.10	3.43	2.88	2.34	2.42
MA_RS08040	NA	1.18	1.59	1.80	1.72	1.52	1.70	1.94	2.43	2.51	1.90	1.43	2.02
MA_RS08045	#N/A	0.95	0.96	0.42	1.06	0.84	0.92	0.70	1.23	1.01	1.70	1.08	1.30
MA_RS08050	NA	2.79	3.28	3.00	3.74	3.14	3.48	3.31	4.23	4.70	3.68	3.23	3.20
MA_RS08055	NA	4.26	4.51	4.40	4.83	4.78	4.85	4.88	5.36	5.50	4.75	4.47	4.50
MA_RS08060	NA	5.36	5.75	5.41	5.75	5.41	5.66	5.26	6.63	7.03	5.70	5.64	5.48
MA_RS08065	NA	3.45	3.44	3.17	3.16	3.82	3.77	4.17	3.62	3.35	3.12	3.07	3.38
MA_RS08070	NA	1.65	1.94	1.76	2.15	2.13	2.01	2.34	2.60	2.76	2.05	1.78	2.00
MA_RS08085	NA	1.03	1.13	0.93	1.36	1.39	1.37	1.72	1.62	2.15	1.49	1.11	1.42
MA_RS08090	NA	0.58	0.45	0.00	0.27	0.21	0.75	0.38	0.78	0.00	0.34	0.40	0.82
MA_RS08095	NA	0.41	1.38	0.60	1.25	0.98	1.08	0.91	1.27	2.33	1.00	0.35	1.29
MA_RS08100	NA	0.81	1.09	1.17	1.10	1.26	1.21	1.25	1.85	1.61	1.33	1.35	0.98
MA_RS08105	NA	0.13	0.00	0.00	0.44	0.15	0.79	0.97	0.46	1.28	0.00	0.00	0.00
MA_RS08110	NA	1.15	0.85	1.41	1.56	0.81	1.34	1.31	2.75	3.12	1.39	1.20	1.42
MA_RS08115	NA	3.19	3.25	3.30	3.28	3.36	3.35	3.33	4.55	4.70	4.02	3.58	3.45
MA_RS08125	NA	1.83	2.15	1.76	1.79	1.78	1.58	1.77	2.73	2.93	2.05	2.09	1.68
MA_RS08130	NA	1.39	0.92	1.66	0.64	1.07	1.15	1.49	1.87	1.68	1.13	1.72	0.95
MA_RS08135	NA	1.24	1.51	1.53	1.91	1.35	1.52	1.35	2.60	2.93	1.56	1.43	1.26
MA_RS08140	pdxT	4.19	4.22	4.39	4.71	4.35	4.51	4.58	4.48	4.55	4.05	4.23	4.71
MA_RS08145	pdxS	5.64	5.79	5.59	5.85	5.87	5.86	5.92	5.62	5.69	5.75	5.66	5.84
MA_RS08150	NA	3.97	4.12	4.15	4.55	4.20	4.71	4.54	5.13	5.42	4.32	4.08	4.20
MA_RS08155	NA	1.67	1.92	1.75	1.94	1.72	1.77	2.01	2.21	2.48	2.16	1.86	2.28
MA_RS08160	NA	2.19	2.41	2.00	2.29	2.16	2.10	2.33	1.83	2.56	1.67	2.32	1.95
MA_RS08165	NA	2.33	2.46	2.50	3.01	2.99	2.98	2.52	2.87	2.70	2.98	2.81	2.87
MA_RS08170	NA	0.46	0.56	0.20	0.75	0.59	0.44	0.97	0.54	0.29	0.77	0.30	0.20
MA_RS08175	NA	1.62	1.83	1.58	1.88	1.96	2.12	1.99	2.06	2.12	2.16	1.54	1.78
MA_RS08180	NA	3.16	3.14	3.25	3.08	3.08	3.20	3.02	3.71	3.99	2.60	2.65	2.82
MA_RS08185	NA	0.54	0.75	0.00	0.71	1.11	0.78	0.91	0.95	1.09	1.04	0.80	0.00
MA_RS08190	NA	2.73	2.94	2.97	2.92	2.85	3.15	2.77	3.27	3.69	3.17	2.55	2.92
MA_RS08195	NA	1.92	1.94	1.76	1.69	2.14	2.16	2.38	2.62	2.09	2.34	1.69	1.93
MA_RS08200	istB	0.39	0.21	0.28	0.27	0.27	0.22	0.29	0.49	0.59	0.40	0.19	0.31
MA_RS08205	istA	0.47	0.79	0.83	0.74	0.71	0.74	0.76	0.89	1.21	0.82	0.56	0.50
MA_RS08210	NA	0.47	0.25	0.16	0.26	0.37	0.28	0.59	0.48	0.61	0.52	0.55	0.27
MA_RS08215	NA	2.58	2.64	2.62	2.96	2.70	2.81	2.90	3.42	3.24	2.71	2.62	2.76
MA_RS08220	NA	1.63	1.49	1.69	1.91	1.76	1.82	1.81	2.42	2.65	2.00	1.82	1.78
MA_RS08230	gyrA	4.33	4.65	4.48	4.90	4.56	4.83	4.81	5.11	5.45	4.57	4.60	4.77
MA_RS08235	gyrB	4.44	4.70	4.64	5.03	4.65	4.88	4.80	4.90	5.30	4.58	4.65	4.76
MA_RS08240	NA	4.04	4.44	4.16	4.58	4.24	4.44	4.61	4.50	4.75	4.30	4.33	4.56
MA_RS08245	NA	4.43	4.71	4.74	4.95	4.61	4.81	4.98	4.90	5.03	4.67	4.55	4.72
MA_RS08250	NA	3.27	2.99	3.65	3.51	3.49	3.19	3.44	4.05	3.66	3.32	3.42	3.57
MA_RS08255	NA	2.37	2.60	2.41	2.70	2.60	2.59	3.50	4.07	4.19	2.33	2.69	2.98
MA_RS08260	NA	3.68	3.96	3.81	4.35	3.90	4.39	4.37	5.16	5.59	4.30	4.13	4.16
MA_RS08265	NA	4.25	4.62	4.29	4.70	4.55	4.89	4.75	5.30	5.48	4.55	4.32	4.57
MA_RS08275	NA	3.12	3.06	2.89	3.60	3.48	3.41	3.74	3.66	4.14	4.10	3.55	3.58
MA_RS08285	NA	1.58	0.67	0.26	1.31	1.14	1.48	1.40	2.13	2.74	1.86	0.75	1.86
MA_RS08295	NA	3.18	3.42	2.90	3.72	3.43	3.66	3.38	4.43	4.82	3.85	3.50	3.27
MA_RS08300	NA	2.43	2.67	2.53	2.94	2.44	2.75	2.70	3.69	3.78	2.81	2.66	2.68
MA_RS08305	NA	1.39	1.36	0.89	0.82	0.62	0.66	1.96	2.19	1.56	1.09	0.76	1.14
MA_RS08310	NA	1.64	1.66	0.99	1.52	1.31	1.66	1.70	2.02	1.50	1.73	1.28	1.41
MA_RS08315	NA	3.11	2.35	2.88	2.92	3.14	3.46	3.62	4.24	2.32	3.85	2.63	2.99
MA_RS08325	NA	0.74	1.07	0.08	0.00	0.86	0.07	0.90	0.45	0.30	0.45	0.91	1.37
MA_RS08330	NA	2.51	2.95	2.83	3.07	2.34	3.04	3.16	3.78	4.06	3.01	2.67	2.65
MA_RS08335	NA	2.74	3.05	3.17	3.41	3.09	3.34	3.07	4.04	4.29	3.64	3.20	3.03
MA_RS08340	NA	4.63	4.90	4.78	5.13	4.78	4.91	5.03	4.91	5.36	4.95	4.64	4.81
MA_RS08345	NA	1.48	1.66	1.71	1.18	1.42	1.74	1.73	2.56	2.24	1.82	1.35	1.19
MA_RS08350	NA	0.80	1.08	1.08	1.52	0.81	0.83	1.22	1.79	1.46	0.50	1.02	1.35
MA_RS08355	NA	1.33	1.29	1.52	0.96	1.05	1.69	2.26	2.60	2.95	2.06	1.46	2.18
MA_RS08365	thrC	5.62	5.90	5.75	6.12	5.84	5.96	5.96	6.06	6.41	5.97	5.65	5.87
MA_RS08370	leuS	5.64	5.96	5.76	6.31	5.90	6.23	6.07	6.35	6.72	6.14	5.98	6.09
MA_RS08380	NA	4.19	4.51	4.40	4.65	4.38	4.55	4.48	4.68	4.87	4.37	4.12	4.41
MA_RS08385	NA	0.97	1.16	1.08	0.78	0.84	0.69	2.00	1.15	1.26	1.45	1.28	0.74
MA_RS08390	mtaA	3.60	3.62	3.46	3.99	3.80	3.77	3.59	4.18	4.01	3.64	3.50	3.52
MA_RS08395	mtaB	4.28	4.89	4.72	5.43	4.97	5.43	4.86	5.85	6.14	4.78	4.46	4.77
MA_RS08400	mtaC	4.20	4.64	4.55	5.26	4.71	5.19	5.15	5.44	5.86	4.46	4.25	4.57
MA_RS08405	#N/A	15.36	15.15	15.38	14.96	15.40	15.07	15.33	14.34	14.12	15.06	15.32	15.34
MA_RS08410	#N/A	4.09	4.42	4.28	4.25	4.25	4.01	4.23	3.71	4.09	4.19	4.61	4.54
MA_RS08415	#N/A	16.25	16.27	16.23	16.23	16.22	16.27	16.17	16.24	16.17	16.24	16.23	16.20
MA_RS08420	#N/A	5.28	5.45	5.55	5.65	5.66	5.92	5.64	6.10	5.93	5.88	5.92	5.74
MA_RS08425	NA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	3.60	0.00	0.00	0.00
MA_RS08435	NA	0.00	0.73	0.00	0.00	0.63	0.72	0.70	0.96	1.32	0.84	0.76	1.28
MA_RS08440	NA	0.43	0.68	2.29	0.42	1.48	0.00	0.94	0.29	0.99	0.24	0.29	0.44
MA_RS08450	NA	2.51	2.58	3.13	2.85	2.62	2.77	2.92	3.42	3.52	3.28	2.94	2.84
MA_RS08455	NA	1.56	1.65	2.75	1.98	1.91	1.77	2.37	2.56	2.93	2.15	1.86	1.88
MA_RS08460	NA	1.52	1.77	2.69	2.24	2.09	2.03	2.33	2.82	2.76	2.03	1.95	1.96
MA_RS08465	NA	1.59	1.79	2.64	2.01	1.83	2.19	1.97	2.24	2.44	2.10	1.93	2.07
MA_RS08470	NA	2.63	2.66	3.20	3.17	2.96	3.44	2.79	3.03	3.27	2.87	2.79	2.97
MA_RS08475	NA	2.68	2.77	3.22	3.13	2.72	3.22	2.82	3.10	3.34	2.91	2.96	2.89
MA_RS08480	NA	2.08	2.28	3.11	2.49	2.12	2.54	2.13	2.85	3.37	2.57	2.12	2.44
MA_RS08485	NA	2.02	1.54	2.57	2.09	2.06	2.25	2.21	2.63	2.58	1.64	1.64	2.20
MA_RS08490	NA	0.83	1.63	2.62	1.64	0.94	0.81	1.27	1.72	1.74	1.21	0.98	1.25
MA_RS08495	NA	5.15	5.39	5.39	5.52	5.28	5.42	5.34	5.49	5.80	5.40	5.07	5.21
MA_RS08500	NA	1.12	1.16	2.64	1.27	1.00	1.13	1.32	1.87	2.13	1.44	1.03	1.30
MA_RS08510	NA	2.57	2.87	3.44	3.10	3.03	3.36	3.17	3.48	3.69	3.21	2.95	3.00
MA_RS08515	NA	2.71	3.11	3.68	3.39	3.08	3.21	3.56	4.27	4.51	3.40	3.07	3.26
MA_RS08520	NA	1.36	1.74	2.69	1.93	1.46	1.96	1.31	2.75	2.25	1.85	2.23	1.42
MA_RS08525	NA	1.33	1.66	2.90	1.85	1.54	1.79	1.78	2.73	2.33	1.80	1.57	1.37
MA_RS08530	NA	2.17	2.19	3.07	2.52	2.39	2.35	2.69	3.08	3.53	2.67	2.40	2.36
MA_RS08535	NA	2.62	2.88	3.48	3.46	3.17	3.32	3.25	3.95	4.25	3.69	3.05	3.38
MA_RS08540	NA	1.29	1.89	2.90	1.70	1.48	1.22	2.34	2.13	2.59	1.65	1.10	1.12
MA_RS08545	NA	0.82	1.27	2.43	1.02	1.52	1.60	1.14	2.17	2.09	1.69	1.73	1.24
MA_RS08560	NA	2.02	2.08	2.80	2.03	2.14	1.99	2.19	2.31	1.44	2.03	1.53	2.15
MA_RS08565	NA	2.65	2.62	3.02	2.92	2.79	2.70	2.80	2.61	2.88	2.73	2.54	2.62
MA_RS08570	NA	4.26	4.33	4.32	4.43	4.32	4.46	4.15	4.99	5.08	4.33	4.29	4.20
MA_RS08575	NA	2.20	2.49	3.26	3.20	2.56	2.69	2.60	3.22	3.13	2.36	2.66	2.40
MA_RS08580	NA	2.81	3.25	3.50	3.19	3.16	3.33	3.05	3.40	3.69	3.20	2.99	2.87
MA_RS08585	NA	4.09	4.19	4.16	4.72	4.21	4.56	4.32	5.15	5.38	4.77	4.39	4.30
MA_RS08590	NA	2.77	3.16	3.56	3.61	3.14	3.38	3.02	3.39	3.78	3.08	3.05	3.00
MA_RS08595	NA	3.39	3.18	3.82	3.63	2.74	3.35	3.59	3.82	3.87	3.38	3.25	3.83
MA_RS08600	NA	3.31	3.70	4.06	3.30	3.75	3.61	3.88	4.52	4.30	3.05	3.51	3.57
MA_RS08610	NA	4.03	4.29	4.52	4.07	4.15	4.12	4.91	4.67	4.33	4.34	4.08	4.26
MA_RS08620	NA	2.88	3.24	3.72	3.56	2.99	2.88	3.31	4.25	4.10	3.99	3.42	3.37
MA_RS08630	NA	0.44	0.00	2.24	0.80	0.00	0.60	0.20	0.31	0.31	1.06	0.61	0.54
MA_RS08635	NA	1.15	1.42	2.65	1.37	0.95	1.42	1.33	1.21	1.46	0.86	1.21	1.14
MA_RS08640	NA	5.31	5.41	5.56	5.34	4.87	5.10	5.22	6.07	5.95	4.88	4.74	4.75
MA_RS08645	NA	1.99	2.42	3.12	2.26	2.69	2.31	2.15	1.95	2.54	2.25	2.27	1.96
MA_RS08650	NA	4.52	4.67	4.76	4.89	4.45	4.81	5.03	5.16	5.10	4.56	4.49	4.53
MA_RS08655	NA	2.74	3.20	3.74	3.51	2.60	3.12	3.55	3.96	3.51	3.15	2.90	3.01
MA_RS08660	NA	2.72	2.71	3.03	3.07	2.83	3.03	3.43	3.57	4.00	3.00	2.39	3.01
MA_RS08665	NA	5.45	5.74	5.56	5.84	5.56	5.62	5.30	6.11	5.89	5.63	5.27	5.28
MA_RS08670	eno	6.81	7.06	7.04	7.44	7.09	7.25	7.29	7.86	8.13	7.53	7.02	7.21
MA_RS08680	NA	3.29	3.13	3.41	3.43	3.27	3.50	3.49	3.92	3.91	3.81	3.04	3.42
MA_RS08685	NA	2.77	2.87	3.62	2.99	2.79	3.21	3.20	3.09	3.36	3.00	2.94	2.93
MA_RS08690	NA	4.84	4.96	5.06	5.36	4.90	5.23	5.27	5.58	5.72	5.25	4.93	5.01
MA_RS08695	NA	2.07	2.31	2.81	2.06	2.07	2.12	2.10	2.33	2.68	1.88	1.86	2.03
MA_RS08700	NA	2.01	2.05	2.94	2.42	2.05	2.24	2.44	2.90	2.97	1.67	1.91	2.24
MA_RS08705	NA	1.70	2.44	3.35	2.14	2.37	2.74	2.61	3.44	3.18	2.37	2.81	2.67
MA_RS08710	NA	0.83	0.76	2.56	1.10	0.58	1.07	0.85	1.62	1.72	0.71	0.71	1.05
MA_RS08715	NA	7.11	7.21	7.26	7.76	7.46	7.60	7.85	8.15	8.46	7.59	7.51	7.63
MA_RS08725	rpiA	5.32	5.51	5.55	5.60	5.45	5.55	5.69	5.68	5.96	5.29	5.34	5.67
MA_RS08730	aspS	6.12	6.43	6.40	6.83	6.35	6.65	6.63	7.09	7.42	6.77	6.37	6.50
MA_RS08735	NA	1.19	0.98	3.10	1.29	1.69	1.33	2.11	1.89	1.54	1.30	1.57	1.56
MA_RS08740	NA	3.30	3.32	3.89	3.28	3.12	3.52	3.14	3.50	3.49	3.56	3.46	2.89

MA_RS08745	NA	3.54	3.55	3.93	4.07	3.96	4.27	3.69	4.38	4.85	4.54	4.15	4.33
MA_RS08760	NA	1.68	0.47	2.58	2.19	1.39	1.66	1.56	1.87	1.78	1.68	1.93	1.38
MA_RS08765	NA	2.06	2.57	3.14	2.94	2.65	2.69	2.96	3.02	3.12	2.38	2.65	2.35
MA_RS08770	NA	2.60	2.78	3.18	2.71	2.60	2.99	2.58	3.49	3.02	2.92	2.44	2.49
MA_RS08775	NA	3.11	3.21	3.63	3.75	3.27	3.50	3.41	3.86	4.13	3.47	3.27	3.33
MA_RS08790	NA	1.83	2.73	3.07	2.21	1.61	2.38	2.36	3.16	2.90	2.64	1.98	1.99
MA_RS08795	NA	2.42	2.01	3.44	2.24	2.51	2.53	2.44	2.83	3.41	3.15	2.17	2.27
MA_RS08805	NA	2.00	1.59	2.73	2.49	2.62	2.39	3.04	3.21	3.35	2.83	2.31	2.49
MA_RS08810	NA	1.36	1.69	2.70	1.26	1.70	1.57	1.48	2.57	2.61	2.01	1.53	1.29
MA_RS08815	NA	1.00	0.86	2.66	1.66	1.42	1.50	1.28	2.47	2.21	0.86	1.61	1.15
MA_RS08825	NA	0.63	1.20	2.42	1.10	0.83	0.87	1.09	1.59	0.56	1.36	0.92	1.11
MA_RS08830	NA	1.04	0.93	2.26	1.63	0.98	0.71	0.66	2.27	2.61	1.67	1.67	0.93
MA_RS08835	NA	1.65	0.89	2.21	1.42	0.80	0.59	1.25	1.64	1.93	1.25	1.46	1.04
MA_RS08840	NA	1.12	0.77	2.63	1.17	0.81	1.00	1.87	1.35	2.14	1.41	1.51	1.47
MA_RS08845	NA	2.00	1.82	2.61	1.90	2.12	1.97	2.54	2.07	2.67	2.65	1.89	2.63
MA_RS08850	NA	0.63	0.58	2.31	0.85	1.04	0.98	1.11	1.25	1.29	1.26	0.89	0.80
MA_RS08855	NA	3.43	3.62	3.67	3.70	3.30	3.78	3.46	4.29	4.86	3.74	3.85	3.96
MA_RS08860	NA	2.48	2.23	2.89	2.63	2.67	2.78	2.47	2.66	2.35	2.59	2.38	2.32
MA_RS08865	NA	3.08	3.23	3.50	3.50	3.40	3.37	3.04	3.76	3.88	3.22	2.93	3.39
MA_RS08870	NA	2.16	2.22	3.16	2.77	2.45	2.28	2.81	2.52	2.63	2.31	2.22	2.17
MA_RS08875	mch	6.66	6.98	6.79	7.37	7.09	7.35	7.00	7.47	7.63	7.13	6.97	7.06
MA_RS08880	NA	3.21	3.36	3.47	3.46	3.37	3.26	3.45	3.75	4.27	3.45	3.21	2.79
MA_RS08885	NA	0.35	0.00	2.20	0.46	0.34	0.32	0.48	0.19	0.77	0.31	0.61	0.00
MA_RS08890	NA	5.77	6.12	6.04	6.37	5.96	6.18	6.38	6.23	6.44	6.15	6.00	6.12
MA_RS08895	NA	2.88	2.81	3.11	3.06	2.93	3.22	2.55	3.11	3.99	2.82	2.48	2.64
MA_RS08900	NA	5.56	5.87	5.86	5.72	5.75	5.80	5.41	5.26	5.29	5.34	5.32	5.57
MA_RS08905	NA	1.51	1.71	2.62	1.61	1.37	1.56	1.60	1.06	1.57	1.92	1.63	1.69
MA_RS08910	NA	2.71	2.87	3.41	2.43	2.52	2.61	2.72	2.60	2.09	2.43	1.84	2.15
MA_RS08915	NA	2.21	2.26	2.94	2.64	2.37	2.33	2.59	2.85	2.72	2.40	2.22	2.23
MA_RS08920	NA	2.20	2.49	3.20	2.80	2.72	2.20	2.84	2.64	3.05	2.14	2.24	2.46
MA_RS08925	NA	2.56	2.46	3.27	2.88	2.56	2.77	2.53	2.98	2.44	2.63	2.62	2.60
MA_RS08930	corA	2.22	2.33	3.00	2.43	2.23	2.24	2.35	2.76	2.67	2.66	2.49	2.42
MA_RS08935	NA	2.18	2.19	2.63	2.28	1.98	2.48	2.32	3.11	3.37	2.10	2.02	2.14
MA_RS08940	NA	2.52	2.87	3.49	3.51	3.26	3.53	3.07	4.19	4.46	3.30	3.03	3.52
MA_RS08950	NA	4.31	4.59	4.58	4.99	4.62	4.77	4.86	5.47	5.58	4.88	4.66	4.75
MA_RS08960	NA	5.03	5.40	5.37	5.43	5.19	5.32	5.40	5.75	5.94	5.05	5.25	5.27
MA_RS08965	NA	4.94	5.43	5.30	5.35	4.98	5.27	5.17	5.61	5.87	4.97	5.16	5.19
MA_RS08970	iotA	5.14	5.49	5.37	5.37	5.14	5.33	5.31	5.32	5.51	5.00	5.11	5.20
MA_RS08975	NA	0.30	0.85	2.31	0.98	0.81	0.68	0.72	0.99	1.07	0.90	1.12	0.88
MA_RS08980	NA	1.61	1.34	2.43	1.41	1.87	2.08	1.50	1.13	2.00	1.85	1.49	1.71
MA_RS08985	NA	1.03	1.19	2.45	1.67	1.42	1.47	1.13	2.07	1.93	1.35	1.60	1.54
MA_RS08990	NA	1.49	1.61	2.51	1.91	1.90	1.92	1.90	2.38	2.51	1.75	1.43	1.86
MA_RS08995	NA	1.53	1.59	2.52	2.56	2.06	1.45	2.38	1.28	2.97	2.39	1.44	1.40
MA_RS09000	NA	1.70	1.84	2.88	2.31	1.51	1.93	1.68	2.39	2.80	1.97	1.73	1.76
MA_RS09005	NA	0.70	0.96	2.33	0.57	1.27	0.57	1.20	1.85	0.00	0.42	1.80	1.90
MA_RS09010	NA	3.29	3.79	3.96	3.82	3.60	3.69	3.48	3.76	3.80	3.65	3.32	3.50
MA_RS09015	NA	2.37	2.76	2.70	2.29	2.48	2.12	2.66	2.25	2.53	2.79	2.03	1.95
MA_RS09025	NA	1.46	1.65	2.62	2.10	1.84	1.96	2.01	2.50	2.77	1.83	1.48	1.73
MA_RS09030	NA	0.88	0.78	2.47	0.77	0.80	0.93	0.78	1.22	1.11	0.91	0.86	0.79
MA_RS09035	NA	2.69	2.89	3.36	3.08	3.06	3.27	2.56	3.59	3.48	3.81	3.50	2.97
MA_RS09040	NA	4.41	4.54	4.60	4.09	4.62	4.57	4.43	4.45	4.46	4.77	4.53	4.48
MA_RS09045	NA	2.28	2.36	3.15	2.85	2.10	2.53	2.60	2.86	2.91	2.62	2.17	2.79
MA_RS09050	NA	0.69	0.61	2.43	1.01	0.66	1.02	0.70	1.21	0.86	0.88	0.97	1.05
MA_RS09055	NA	0.71	0.64	2.45	1.22	1.25	1.54	1.00	1.32	1.17	0.88	1.06	0.77
MA_RS09060	NA	1.19	1.51	2.72	2.11	1.67	1.94	1.71	1.22	1.86	1.89	1.25	1.61
MA_RS09065	NA	0.88	1.11	2.36	1.60	1.31	1.39	1.17	1.00	0.60	1.23	1.23	1.18
MA_RS09070	NA	0.52	0.67	2.31	0.93	0.82	0.79	0.78	0.88	0.83	0.57	1.02	0.90
MA_RS09075	NA	0.75	0.53	2.48	0.77	0.47	0.13	0.54	0.30	0.35	0.84	0.94	0.77
MA_RS09080	NA	0.69	0.70	2.25	0.94	0.76	0.82	0.75	1.29	1.01	1.04	1.04	0.89
MA_RS09085	NA	0.92	0.99	2.36	1.16	1.43	1.38	1.57	1.78	1.76	1.42	1.48	1.51
MA_RS09090	NA	0.45	0.59	2.48	0.95	1.00	1.12	1.37	1.53	1.30	0.86	0.13	1.23
MA_RS09095	NA	1.87	2.14	3.01	1.95	2.19	2.06	2.37	2.81	2.89	2.06	2.16	1.92
MA_RS09100	NA	2.18	2.44	3.06	2.64	2.65	2.74	2.35	3.23	3.43	2.95	2.70	2.58
MA_RS09105	NA	2.27	2.51	3.10	2.74	2.49	2.62	2.52	3.37	3.72	2.89	2.35	2.54
MA_RS09120	NA	1.88	1.98	2.89	2.56	2.31	2.53	2.58	2.99	3.32	2.51	2.28	2.53
MA_RS09130	NA	0.45	0.29	0.00	0.15	0.33	0.43	0.18	0.39	0.34	0.63	0.00	0.46
MA_RS09135	NA	2.71	2.90	3.29	3.04	2.99	3.42	2.98	3.53	3.75	3.16	3.04	3.06
MA_RS09140	NA	0.75	0.74	2.39	0.64	0.77	0.57	0.63	1.00	1.02	0.84	0.72	0.92
MA_RS09145	NA	0.87	0.64	2.37	1.21	0.59	1.04	1.07	1.34	1.37	1.00	0.70	0.85
MA_RS09160	nikR	0.33	0.39	2.31	0.00	0.55	0.61	0.53	0.44	0.16	0.45	0.55	1.08
MA_RS09170	NA	1.53	1.59	2.53	2.09	1.33	1.87	1.65	2.11	2.62	1.47	1.66	1.92
MA_RS09185	NA	2.42	2.52	3.28	2.87	2.64	2.85	2.80	3.09	3.53	2.97	2.70	2.88
MA_RS09195	NA	0.49	0.83	2.40	0.99	0.74	0.88	0.99	0.91	1.73	1.22	0.47	1.06
MA_RS09200	NA	1.79	1.89	2.92	1.82	2.11	2.10	1.69	2.56	2.79	2.54	2.06	1.70
MA_RS09205	NA	2.38	2.17	3.37	2.88	2.95	3.02	2.71	3.43	3.78	3.38	2.79	2.85
MA_RS09215	NA	1.98	2.06	3.03	2.22	2.14	2.50	2.03	2.86	3.38	3.08	2.61	2.63
MA_RS09220	NA	2.90	3.18	3.29	3.35	3.34	3.12	3.22	3.95	4.22	3.55	2.82	2.74
MA_RS09225	NA	6.50	6.66	6.55	7.10	6.84	6.94	7.34	7.48	7.62	7.19	7.00	6.82
MA_RS09230	rnpA2	6.77	6.96	6.83	7.19	6.86	7.16	7.32	7.65	7.97	7.10	6.91	7.04
MA_RS09235	rnpA1	6.08	6.32	6.32	6.67	6.33	6.56	6.76	7.06	7.33	6.34	6.21	6.53
MA_RS09240	rnpA	6.95	7.27	7.20	7.59	7.21	7.50	7.44	8.09	8.50	7.43	7.15	7.27
MA_RS09245	NA	6.85	7.13	7.10	7.45	7.16	7.27	7.29	7.75	8.12	7.27	6.90	7.25
MA_RS09250	psmA	6.65	6.78	6.89	7.09	6.76	6.83	7.18	7.22	7.39	6.99	6.64	6.88
MA_RS09255	NA	4.58	4.83	4.97	5.16	4.52	5.19	4.99	5.43	6.14	4.84	4.87	5.03
MA_RS09260	NA	5.54	5.89	5.85	5.94	5.85	6.24	5.90	6.09	6.48	5.67	5.84	6.01
MA_RS09265	NA	6.59	6.68	6.69	7.09	6.77	6.88	7.00	7.42	7.77	6.88	6.70	6.94
MA_RS09270	NA	8.41	8.41	8.49	8.56	8.56	8.43	8.76	8.89	8.76	9.05	8.53	8.54
MA_RS09275	NA	1.68	1.40	2.72	1.58	0.99	1.27	1.58	1.61	2.31	1.24	1.38	1.51
MA_RS09280	tnpB	2.47	2.48	2.99	2.93	2.73	2.93	2.83	4.12	4.19	3.16	2.89	2.74
MA_RS09285	NA	0.59	0.56	2.36	0.54	0.58	0.84	0.62	1.12	0.95	0.73	0.50	0.47
MA_RS09300	NA	4.35	4.64	4.79	4.70	4.66	4.72	4.76	4.73	5.01	4.55	4.53	4.85
MA_RS09305	thiC	4.49	4.85	4.98	4.95	4.93	4.97	5.05	4.65	4.79	5.08	4.81	5.06
MA_RS09310	NA	3.35	3.54	3.96	4.01	3.82	3.84	3.53	4.26	4.39	4.10	3.57	3.78
MA_RS09315	NA	2.83	2.77	3.28	2.81	2.88	3.13	2.71	3.60	3.41	3.24	2.90	3.04
MA_RS09320	NA	1.27	1.43	2.35	1.81	1.02	1.67	1.33	1.56	1.91	1.25	1.37	0.66
MA_RS09330	NA	3.41	3.56	3.80	3.67	3.45	3.56	3.40	3.79	4.06	3.19	3.19	3.40
MA_RS09335	NA	2.31	2.60	2.85	2.45	2.65	2.05	2.38	1.67	2.47	2.25	2.29	2.88
MA_RS09340	NA	3.43	3.38	3.83	3.24	3.32	3.49	3.48	3.64	3.96	3.23	2.89	3.04
MA_RS09345	NA	2.63	2.46	3.24	2.70	2.62	2.64	2.66	3.13	3.19	2.56	2.22	2.55
MA_RS09350	NA	1.56	1.97	2.57	2.33	2.08	2.31	2.02	2.32	2.29	1.80	1.41	1.49
MA_RS09355	NA	2.40	2.48	3.08	2.05	2.86	2.92	2.61	3.20	2.97	2.49	2.18	2.15
MA_RS09360	NA	2.09	2.20	3.09	2.38	2.45	2.53	2.31	2.74	2.88	2.20	1.51	2.29
MA_RS09365	NA	2.07	1.71	3.06	2.24	1.83	2.13	2.17	2.48	2.10	1.79	2.02	1.94
MA_RS09370	ilvD	6.16	6.27	6.31	6.66	6.42	6.61	6.47	6.46	6.70	6.45	6.31	6.46
MA_RS09375	NA	2.49	2.48	3.31	2.16	2.74	2.20	2.91	3.19	2.28	2.36	0.98	2.10
MA_RS09380	mtrH	3.73	3.79	4.22	4.29	3.97	3.95	3.80	4.55	4.77	4.00	3.97	4.07
MA_RS09385	NA	4.44	4.68	4.72	4.89	4.66	4.96	4.87	4.97	4.76	4.57	4.77	4.73
MA_RS09390	mbiX	4.37	4.55	4.74	4.59	4.35	4.53	4.70	4.71	4.78	4.66	4.20	4.44
MA_RS09395	NA	0.69	0.22	2.48	1.04	0.93	0.58	1.05	0.58	1.32	0.01	0.65	1.09
MA_RS09400	NA	0.79	0.76	2.44	1.05	1.48	1.30	1.88	1.67	1.48	1.41	0.96	1.72
MA_RS09405	NA	0.44	0.00	0.00	0.68	0.40	1.52	0.43	0.85	0.74	0.00	0.00	0.51
MA_RS09410	NA	0.50	0.82	2.27	0.43	0.61	0.55	0.59	1.43	0.84	0.99	0.68	1.04
MA_RS09415	NA	3.95	3.93	4.28	4.17	3.93	4.26	4.38	4.90	5.03	4.24	4.08	4.10
MA_RS09425	#N/A	1.93	1.27	3.49	2.13	2.22	1.23	2.85	3.17	2.40	3.35	2.06	2.07
MA_RS09430	NA	2.92	2.55	3.36	2.92	2.90	3.28	3.06	4.13	3.94	3.66	2.00	2.88
MA_RS09435	NA	1.13	1.28	2.38	1.29	1.33	1.22	1.91	1.51	1.05	1.21	1.25	0.64
MA_RS09440	NA	2.86	3.26	3.68	3.46	3.33	3.30	3.26	3.82	3.70	3.17	3.11	3.34
MA_RS09445	NA	0.20	0.34	2.23	0.28	0.35	0.37	0.39	0.44	0.66	0.33	0.21	0.23
MA_RS09450	NA	3.81	3.99	4.44	4.62	4.52	4.45	4.35	4.57	4.53	4.45	3.95	4.17
MA_RS09455	NA	6.22	6.45	6.62	7.04	6.69	6.90	7.02	7.42	7.58	6.97	6.48	6.80
MA_RS09460	rlbC	6.40	6.59	6.54	7.00	6.72	6.89	6.92	7.25	7.36	6.90	6.59	6.82
MA_RS09465	rlbH	5.68	5.96	5.90	6.41	6.23	6.36	6.40	6.83	6.70	6.30	6.10	6.31
MA_RS09470	NA	6.24	6.57	6.45	6.96	6.70	6.91	6.89	7.17	7.35	6.75	6.60	6.84
MA_RS09475	NA	4.79	4.59	4.69	5.32	4.86	5.44	5.07	5.84	5.97	5.45	5.22	5.05
MA_RS09480	NA	5.02	5.15	5.34	5.81	5.40	5.84	5.33	5.77	6.60	5.55	5.17	5.31
MA_RS09485	NA	4.54	4.63	5.10	5.33	4.86	5.37	5.07	5.60	6.22	5.09	4.74	5.00
MA_RS09490	NA	1.17	1.48	2.42	1.69	1.47	1.71	1.14	2.03	2.40	1.64	1.55	1.22
MA_RS09495	NA	1.90	1.87	3.00	1.79	1.61	2.24	1.78	2.25	2.31	1.91	1.67	1.74
MA_RS09500	NA	2.44	2.28	2.95	2.63	2.13	1.68	2.63	3.55	3.88	2.60	2.56	2.54
MA_RS09505	NA	4.47	4.97	4.82	4.86	4.32	4.92	4.88	5.53	5.78	4.24	4.31	4.20
MA_RS09510	NA	0.52	0.16	2.30	0.52	0.72	0.92	1.03	1.15	1.35	0.76	0.88	1.06
MA_RS09515	NA	0.15	0.18	2.19	0.27	0.11	0.19	0.09	0.31	0.57	0.30	0.24	0.14
MA_RS09520	#N/A	0.00	0.00	2.66	0.18	0.58	1.20	0.08	0.12	0.38	0.38	0.40	0.65
MA_RS09525	NA	0.85	0.54	2.41	0.61	0.84	0.85	0.96	1.38	1.54	1.08	0.59	0.63
MA_RS09530	NA	5.19	5.20	5.42	5.31	5.37	5.64	5.86	6.77	6.75	6.34	5.77	5.57
MA_RS09535	NA	1.79	2.01	3.16	2.57	2.14	2.27	2.61	3.06	3.11	3.16	3.03	2.85
MA_RS09545	NA	2.60	2.78	3.59	2.86	2.74	2.97	2.97	4.28	4.55	2.93	2.78	2.65
MA_RS09550	NA	2.20	2.54	3.17	2.87	2.43	2.49	2.71	3.33	3.61	3.06	2.21	2.18
MA_RS09555	NA	2.91	2.97	3.35	2.44	2.47	2.50	2.05	3.09	3.54	2.51	2.57	2.17
MA_RS09565	NA	0.88	0.74	2.47	0.60	1.02	0.91	1.04	0.67	0.97	1.15	0.60	1.38
MA_RS09570	NA	1.39	1.62	2.85	1.68	1.20	1.72	1.38	1.96	2.22	1.34	1.76	1.57
MA_RS09575	NA	0.00	0.90	2.41	0.69	0.34	0.00	0.42	0.00	1.08	0.00	0.82	0.76
MA_RS09580	NA	1.54	1.71	2.77	1.84	1.86	2.15	2.11	2.66	2.92	1.91	1.87	1.84

MA_RS09585	NA	1.64	1.84	2.41	2.01	1.04	1.99	1.70	2.16	2.44	1.91	1.98	1.41
MA_RS09590	NA	2.58	2.90	3.41	3.43	2.88	3.00	3.13	3.61	3.88	2.79	2.72	2.81
MA_RS09600	NA	1.53	1.58	2.79	1.75	2.04	1.84	1.36	1.92	2.22	1.67	1.46	1.76
MA_RS09605	NA	1.53	1.07	2.67	1.21	1.51	1.79	1.61	1.25	2.02	1.71	1.29	1.32
MA_RS09625	NA	0.17	0.00	0.00	0.00	0.00	0.47	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS09630	NA	0.20	0.43	2.22	0.28	0.28	0.61	0.13	0.30	0.19	0.47	0.16	0.10
MA_RS09635	NA	0.89	1.25	2.25	1.45	1.18	0.75	0.53	0.62	1.61	1.43	1.07	1.05
MA_RS09640	NA	0.87	0.98	2.52	1.21	0.97	1.19	0.62	0.87	1.08	0.93	0.21	0.76
MA_RS09645	NA	0.23	0.59	2.37	0.91	0.66	0.69	0.46	0.89	1.31	0.97	0.85	0.83
MA_RS09650	NA	0.71	0.71	2.33	0.76	0.61	1.05	0.30	0.95	1.24	0.97	0.49	0.49
MA_RS09655	NA	0.31	0.18	2.38	0.57	0.17	0.42	0.00	0.34	0.70	0.35	0.40	0.14
MA_RS09665	NA	1.89	2.26	2.55	2.11	1.74	1.56	2.22	2.81	3.76	2.05	2.59	1.75
MA_RS09670	NA	2.09	2.47	3.02	2.11	2.89	2.37	2.85	3.28	3.24	2.53	2.38	2.66
MA_RS09675	NA	2.06	2.45	3.13	2.79	1.85	2.51	2.41	3.27	3.72	2.95	1.90	2.59
MA_RS09680	NA	3.10	3.45	3.77	3.73	3.55	4.08	3.55	4.25	4.44	4.02	3.52	3.75
MA_RS09685	NA	3.43	3.60	3.87	3.80	3.73	3.84	3.99	4.17	4.62	4.20	3.85	3.74
MA_RS09690	NA	1.97	1.51	2.69	1.51	1.52	1.70	2.14	1.36	1.52	1.72	1.51	1.39
MA_RS09695	NA	2.39	2.89	3.11	2.93	2.80	3.05	2.44	3.16	3.38	3.02	2.89	2.54
MA_RS09700	NA	2.29	2.46	3.30	2.77	2.55	2.85	2.73	3.06	3.13	2.70	2.56	3.00
MA_RS09705	NA	2.17	2.84	3.22	2.98	2.75	2.76	2.87	4.01	3.77	3.52	3.03	2.75
MA_RS09710	NA	3.68	3.80	4.16	4.20	3.89	4.24	4.22	4.71	5.35	4.11	4.16	4.61
MA_RS09715	lon	6.29	6.31	6.21	7.22	6.77	6.97	7.28	7.37	8.32	6.24	7.15	7.41
MA_RS09720	NA	5.28	4.86	5.49	5.76	5.56	5.72	6.28	6.15	6.86	4.75	5.66	5.99
MA_RS09725	NA	1.63	1.44	2.71	1.81	1.54	1.68	1.81	2.39	2.57	1.91	1.61	1.71
MA_RS09730	NA	1.45	1.44	2.50	1.81	1.83	1.80	1.72	2.59	2.05	1.78	1.34	1.44
MA_RS09740	NA	0.59	1.28	2.21	1.00	1.50	0.80	0.55	1.02	1.27	0.99	0.88	1.28
MA_RS09745	NA	1.69	2.15	2.70	2.01	2.16	2.04	2.32	2.22	2.56	2.55	1.94	2.12
MA_RS09750	NA	2.60	1.91	2.79	1.76	2.18	2.50	1.80	2.73	2.34	2.85	2.11	2.71
MA_RS09755	NA	2.75	3.18	3.68	3.67	3.04	3.31	3.27	3.98	4.36	3.56	2.98	3.10
MA_RS09765	NA	1.25	2.22	2.74	2.25	1.06	1.56	1.66	1.51	1.32	2.31	1.67	1.83
MA_RS09770	NA	3.09	3.36	3.58	3.52	3.53	3.42	3.85	3.63	3.83	3.47	3.37	3.52
MA_RS09775	gigP	2.76	3.13	3.59	3.19	2.93	3.08	3.33	3.62	3.83	3.20	2.54	3.17
MA_RS09780	NA	0.74	0.73	2.27	1.62	1.48	1.19	1.40	1.74	1.15	2.34	1.24	1.28
MA_RS09785	NA	1.01	2.16	3.04	2.15	1.92	0.84	2.80	1.54	0.95	2.37	2.08	1.92
MA_RS09790	NA	2.36	2.54	2.92	2.77	1.94	2.21	2.37	2.66	2.49	2.68	2.47	2.45
MA_RS09795	NA	3.84	3.93	4.15	4.22	3.78	3.99	4.22	4.44	4.84	3.87	3.73	3.75
MA_RS09810	NA	0.10	0.48	2.28	0.63	0.47	0.92	0.70	0.96	1.36	0.74	0.41	0.55
MA_RS09815	istA	1.77	1.89	2.73	1.79	1.72	1.91	1.51	2.47	2.47	2.05	1.87	1.71
MA_RS09820	istB	2.37	2.40	3.04	2.72	2.59	2.72	2.68	3.51	3.58	3.03	2.65	2.54
MA_RS09825	NA	0.14	0.21	2.35	0.37	0.48	0.63	0.35	0.59	1.06	0.44	0.28	0.11
MA_RS09830	NA	0.78	1.03	2.32	0.83	1.25	1.03	1.07	2.04	1.71	1.22	1.50	0.87
MA_RS09835	NA	2.92	3.52	3.62	3.80	3.41	3.61	3.61	4.43	4.78	3.74	3.54	3.83
MA_RS09840	NA	3.72	3.95	4.03	4.15	3.78	3.66	4.11	4.88	5.23	4.35	3.63	3.77
MA_RS09845	NA	0.92	0.51	2.45	0.92	0.29	1.23	0.88	1.26	1.44	0.32	0.63	0.32
MA_RS09850	NA	0.58	0.79	2.52	1.36	0.86	0.99	0.80	1.32	1.73	1.21	0.73	1.21
MA_RS09855	NA	0.59	0.59	2.37	0.98	0.88	0.98	1.05	1.17	1.33	0.97	0.95	0.47
MA_RS09860	NA	1.10	1.42	2.59	1.38	1.10	1.55	1.53	2.15	2.77	1.45	1.15	1.03
MA_RS09870	NA	3.35	3.52	3.91	3.77	3.32	3.61	3.50	4.29	4.69	3.75	3.35	3.54
MA_RS09875	NA	3.11	3.12	3.57	3.27	2.86	3.15	3.28	4.07	4.49	3.60	2.46	2.59
MA_RS09880	NA	1.67	1.62	2.63	1.80	1.58	1.65	1.85	2.36	3.08	2.09	1.88	1.71
MA_RS09885	NA	0.24	0.20	2.19	0.26	0.21	0.17	0.22	0.36	0.40	0.17	0.30	0.18
MA_RS09890	NA	0.42	0.16	2.33	0.50	0.41	0.58	0.34	0.68	0.98	0.15	0.34	0.14
MA_RS09895	NA	0.36	0.44	2.23	0.73	0.77	0.67	0.27	0.66	0.42	0.72	0.86	0.41
MA_RS09900	NA	1.48	2.02	2.92	2.07	1.72	2.28	1.11	3.45	3.48	2.76	2.56	1.88
MA_RS09905	NA	0.19	0.18	2.18	0.18	0.22	0.13	0.14	0.30	0.35	0.19	0.26	0.14
MA_RS09910	NA	1.64	1.95	2.81	2.01	1.92	1.67	2.18	2.41	2.53	1.87	1.55	1.73
MA_RS09915	NA	2.22	2.40	2.87	2.59	2.62	2.64	2.38	2.82	2.88	2.52	2.53	2.14
MA_RS09920	NA	1.55	1.59	2.74	2.35	1.70	2.25	1.80	2.37	2.67	1.88	1.61	1.91
MA_RS09925	NA	2.73	3.06	3.30	3.34	3.03	3.30	3.22	3.78	4.11	2.79	2.88	2.99
MA_RS09940	NA	0.58	0.73	2.36	0.65	0.99	0.90	0.17	0.72	1.10	0.61	0.57	0.55
MA_RS09945	NA	6.66	6.74	6.86	7.17	6.88	7.03	7.13	7.66	7.44	7.41	6.89	6.62
MA_RS09950	NA	2.00	2.60	3.05	2.66	1.88	2.33	2.17	2.62	3.30	2.69	1.91	2.14
MA_RS09955	NA	2.03	2.70	2.91	2.09	2.68	2.79	2.47	3.24	3.81	2.55	2.34	2.31
MA_RS09960	NA	1.11	1.09	2.28	1.33	1.05	1.24	1.44	1.70	1.80	1.21	1.19	1.00
MA_RS09965	NA	0.88	0.83	2.26	1.00	0.62	1.17	0.78	1.00	1.27	1.17	0.88	0.97
MA_RS09970	NA	0.36	0.67	2.39	0.71	0.71	0.94	0.85	1.24	1.27	0.81	0.92	0.90
MA_RS09975	NA	0.65	0.62	2.42	0.78	0.69	0.82	0.95	1.52	0.93	0.36	0.96	0.80
MA_RS09980	NA	0.98	1.25	2.53	1.13	1.15	1.49	1.54	1.42	1.56	1.57	1.03	1.18
MA_RS09985	NA	0.63	0.91	2.45	0.50	0.49	0.58	0.50	1.12	0.59	0.73	0.95	0.91
MA_RS09990	NA	0.40	0.35	2.22	0.71	0.70	0.61	0.64	0.38	0.77	0.54	0.45	0.19
MA_RS09995	NA	1.71	1.15	2.28	1.27	0.55	1.23	1.09	2.79	3.00	1.11	1.12	1.50
MA_RS10005	NA	3.09	3.36	3.71	3.46	3.26	3.35	3.41	3.94	4.25	3.54	3.10	3.37
MA_RS10015	NA	3.24	3.34	3.83	3.56	3.45	3.79	3.86	3.89	4.51	3.66	3.11	3.39
MA_RS10020	NA	4.06	4.35	4.66	4.70	4.52	4.69	4.94	5.73	6.12	5.14	4.65	4.84
MA_RS10025	NA	2.91	3.39	3.71	3.80	3.44	3.68	3.39	4.57	4.76	4.05	3.65	4.09
MA_RS10030	NA	1.97	1.69	2.83	1.85	2.26	2.49	1.59	2.71	2.43	2.29	1.96	2.09
MA_RS10035	NA	4.00	3.94	4.30	4.18	4.18	4.34	3.89	4.43	3.77	4.48	4.16	3.77
MA_RS10040	NA	3.92	4.22	4.28	4.00	3.75	4.02	4.01	5.03	4.98	4.23	4.14	3.75
MA_RS10045	NA	1.85	2.11	1.89	1.72	1.50	1.98	2.15	2.71	3.28	2.42	2.35	2.04
MA_RS10050	NA	0.97	0.82	0.54	1.00	1.06	1.32	1.22	1.46	1.51	1.25	0.67	1.25
MA_RS10055	NA	0.25	0.19	0.22	0.38	0.36	0.34	0.42	0.57	0.60	0.39	0.36	0.14
MA_RS10060	cas10	0.34	0.30	0.23	0.56	0.16	0.45	0.14	0.35	0.80	0.51	0.40	0.47
MA_RS10065	csm2	0.60	0.46	0.68	0.77	0.38	1.26	0.81	1.61	1.68	0.87	0.46	0.30
MA_RS10070	csm3	1.75	1.47	1.58	1.83	1.23	1.44	1.51	2.28	2.25	1.99	1.42	1.78
MA_RS10075	csm4	1.73	1.66	1.81	2.32	2.09	2.16	1.85	2.70	3.16	2.38	2.21	2.34
MA_RS10080	csm5	1.28	1.21	1.50	1.44	1.26	1.52	1.55	2.31	2.72	1.70	1.19	1.96
MA_RS10090	NA	3.47	3.51	3.25	3.93	3.68	3.73	3.75	4.69	4.95	3.99	3.81	3.66
MA_RS10095	NA	0.29	0.00	0.06	0.00	0.00	0.92	0.11	0.48	0.51	0.79	0.00	0.05
MA_RS10105	NA	1.69	1.51	1.46	3.06	2.07	1.83	2.61	2.85	3.30	2.81	1.68	2.08
MA_RS10110	NA	1.25	1.00	0.92	0.36	0.33	0.17	1.41	2.08	0.96	1.89	0.41	1.16
MA_RS10115	NA	1.61	1.98	1.96	1.92	1.20	1.79	2.41	1.93	2.22	0.84	1.76	2.21
MA_RS10120	NA	2.47	2.62	2.33	2.78	2.66	3.05	2.75	3.19	3.20	2.99	2.48	2.89
MA_RS10125	NA	2.34	2.09	2.74	1.65	2.47	1.55	2.27	1.68	2.77	2.72	1.52	2.80
MA_RS10130	NA	3.03	3.06	2.69	3.47	3.34	3.25	3.50	3.72	3.56	3.37	3.35	3.41
MA_RS10135	NA	1.03	1.31	0.89	1.35	1.45	1.73	1.16	1.62	1.14	1.33	1.31	1.69
MA_RS10140	NA	1.20	1.51	1.23	1.91	1.41	1.60	1.85	2.05	2.32	1.78	1.93	1.71
MA_RS10145	NA	2.31	2.49	2.69	3.15	2.69	2.85	2.90	3.30	3.44	2.80	2.31	2.56
MA_RS10150	NA	2.59	2.78	3.02	3.30	3.17	3.13	3.04	3.40	3.52	3.14	2.91	3.16
MA_RS10155	NA	2.51	2.90	2.76	2.92	2.97	2.84	3.34	3.08	3.57	2.65	3.07	2.96
MA_RS10160	NA	3.04	3.38	3.09	3.56	3.31	3.56	3.42	4.23	4.46	3.71	3.40	3.26
MA_RS10165	NA	1.52	1.69	1.46	1.81	1.71	1.83	1.95	2.51	2.32	2.04	1.98	1.87
MA_RS10170	NA	1.21	1.72	1.17	2.18	1.62	1.73	1.85	1.89	2.48	1.65	1.58	1.45
MA_RS10175	NA	2.95	2.70	2.86	2.40	3.16	2.81	3.05	3.27	3.31	3.22	2.78	2.79
MA_RS10180	NA	4.28	4.43	4.33	4.75	4.45	4.60	4.54	5.62	5.79	5.29	4.38	4.80
MA_RS10185	NA	1.57	1.94	2.05	2.33	2.09	2.58	1.87	2.70	2.92	2.73	2.55	2.22
MA_RS10190	NA	1.39	1.54	1.79	1.93	1.77	1.59	1.94	2.49	1.93	2.53	1.76	1.73
MA_RS10195	pheT	5.04	5.24	5.04	5.67	5.28	5.52	5.38	6.09	6.28	6.01	5.28	5.43
MA_RS10200	NA	0.43	0.34	0.19	0.60	0.26	0.21	0.16	0.47	0.53	0.59	0.48	0.47
MA_RS10205	NA	2.56	2.81	2.40	3.16	3.15	3.24	3.02	3.02	3.11	3.21	2.96	3.33
MA_RS10210	mhB	3.45	3.61	3.61	4.07	3.43	3.53	3.77	4.45	5.09	4.09	3.81	3.94
MA_RS10220	NA	1.19	1.34	1.53	1.83	1.62	1.74	1.83	2.90	3.04	2.13	1.97	2.08
MA_RS10225	NA	1.20	1.63	1.67	1.63	2.05	1.75	1.67	1.80	1.95	1.63	1.28	1.69
MA_RS10230	purQ	5.82	5.97	5.86	6.55	6.19	6.33	6.27	6.54	6.63	6.48	6.03	6.09
MA_RS10235	purS	6.50	6.58	6.58	7.20	6.86	6.94	7.37	7.44	7.89	7.14	6.77	6.71
MA_RS10240	NA	2.39	3.33	2.86	2.41	3.26	2.66	2.48	3.42	3.30	2.86	2.49	2.86
MA_RS10245	NA	3.16	3.56	3.48	3.82	3.62	3.68	3.78	4.11	4.50	4.29	3.72	4.01
MA_RS10250	NA	2.53	3.25	2.61	3.20	2.89	2.97	3.48	3.06	2.91	3.31	2.60	3.06
MA_RS10255	NA	2.55	2.36	2.19	2.56	2.31	2.40	2.54	2.18	2.03	2.12	2.19	2.54
MA_RS10260	dacB	1.11	1.42	1.13	1.33	1.14	1.42	1.37	1.65	1.93	1.42	1.05	1.33
MA_RS10265	NA	1.73	2.07	2.19	2.31	2.30	2.40	2.37	2.95	2.74	2.40	2.27	2.12
MA_RS10270	NA	2.12	1.94	1.70	2.69	2.56	2.51	2.58	3.08	3.47	2.14	1.96	2.34
MA_RS10275	NA	2.36	2.56	1.98	2.67	2.47	2.82	2.49	3.48	3.41	2.73	2.38	2.50
MA_RS10280	NA	1.51	1.60	1.98	1.72	1.82	1.43	1.74	2.03	1.57	1.58	1.49	1.53
MA_RS10285	NA	4.86	5.01	4.79	5.23	4.95	5.00	5.10	5.47	5.55	5.57	5.24	5.17
MA_RS10290	NA	3.64	3.80	3.66	4.20	3.83	3.91	3.66	4.49	4.45	3.98	3.67	3.80
MA_RS10295	NA	2.81	2.88	3.05	2.94	2.89	3.09	3.27	3.29	2.86	3.19	2.78	3.19
MA_RS10300	NA	2.47	2.57	2.11	3.14	2.88	2.69	2.45	2.55	2.90	2.74	2.68	3.02
MA_RS10305	NA	3.40	3.73	3.47	3.95	3.87	3.86	4.35	3.84	3.81	3.67	3.92	4.06
MA_RS10310	radC	1.75	2.17	1.90	2.61	2.70	2.14	2.41	2.45	3.33	2.13	1.97	2.35
MA_RS10315	NA	2.35	2.74	2.93	3.22	2.72	2.73	2.85	3.61	3.65	3.37	2.67	2.85
MA_RS10320	NA	5.43	5.62	5.47	6.06	5.84	5.92	5.72	5.93	6.28	6.14	5.68	5.88
MA_RS10325	NA	4.58	4.79	4.75	5.29	4.94	5.24	5.05	5.40	5.62	5.23	4.94	5.01
MA_RS10330	NA	0.00	0.00	0.23	0.16	0.65	0.48	0.00	0.21	0.00	0.33	0.23	0.00
MA_RS10335	NA	0.66	0.36	0.58	0.99	1.24	1.16	0.86	1.51	1.30	1.58	1.24	0.59
MA_RS10340	NA	0.48	0.57	0.62	0.33	0.39	0.60	0.40	1.20	1.22	0.79	0.56	0.92
MA_RS10345	NA	1.50	1.78	1.56	1.95	1.77	2.15	1.82	2.49	2.66	1.96	1.74	1.72
MA_RS10350	NA	1.86	1.76	2.37	2.75	2.15	2.47	2.60	3.00	2.96	2.53	2.20	2.19
MA_RS10360	NA	3.55	3.79	3.57	4.08	3.64	3.90	3.92	4.38	4.39	3.79	3.59	3.64
MA_RS10375	NA	0.94	0.47	0.00	0.87	1.24	0.95	0.72	1.24	1.64	0.62	0.76	0.24
MA_RS10380	NA	1.04	0.86	0.84	0.95	1.15	1.82	0.78	1.23	0.92	1.12	0.47	1.10
MA_RS10385	NA	0.77	1.17	0.30	0.81	1.07	1.23	1.40	1.40	1.33	1.01	1.00	1.57
MA_RS10390	NA	2.98	3.02	2.94	3.23	3.06	3.04	3.35	3.48	4.07	3.73	2.98	3.41
MA_RS10400	NA	0.95	0.50	0.85	1.38	1.27	1.39	1.33	1.23	1.85	1.51	1.27	0.89

MA_RS10405	NA	3.18	3.19	3.59	3.97	2.97	3.61	3.22	4.22	4.36	3.38	3.43	3.29
MA_RS10410	NA	1.43	1.55	1.78	2.07	1.55	1.49	1.81	1.86	2.52	1.84	1.17	1.64
MA_RS10415	glgX	1.70	1.87	1.77	1.98	1.74	2.01	2.09	2.37	2.51	1.99	1.78	2.00
MA_RS10420	NA	1.73	1.86	2.01	2.14	2.08	2.31	2.10	2.29	2.73	2.17	2.08	1.98
MA_RS10425	NA	1.75	2.00	1.68	2.46	2.13	2.35	2.51	2.50	2.64	2.10	1.88	2.03
MA_RS10430	NA	3.94	4.05	3.93	3.98	3.95	3.89	3.88	3.34	3.48	3.62	3.85	3.71
MA_RS10435	NA	4.09	4.18	4.07	4.29	4.16	4.36	4.55	4.73	4.65	4.62	4.49	4.26
MA_RS10440	NA	2.91	3.38	3.45	3.77	3.16	3.37	2.97	3.91	3.94	3.64	3.31	3.85
MA_RS10450	NA	1.77	1.81	1.74	2.38	2.04	2.28	2.52	2.84	3.22	2.09	2.01	1.92
MA_RS10455	NA	3.05	3.30	3.52	3.30	2.82	3.38	3.25	3.92	4.03	3.80	3.54	3.46
MA_RS10460	NA	2.50	2.21	2.47	2.43	2.49	2.68	2.28	2.41	2.65	2.57	2.48	2.43
MA_RS10465	NA	1.56	1.74	1.59	1.51	1.51	1.38	1.98	1.96	2.31	1.71	1.70	1.49
MA_RS10470	NA	2.14	1.79	1.43	1.89	1.56	2.39	2.65	1.31	2.34	1.87	1.46	1.93
MA_RS10475	NA	1.36	1.49	0.38	1.71	2.04	1.33	1.91	2.05	1.91	1.86	1.45	1.04
MA_RS10480	NA	1.29	1.33	1.50	1.45	1.23	1.34	1.55	1.67	1.38	1.25	1.17	1.29
MA_RS10485	alaXM	3.01	3.22	3.06	3.43	3.54	3.12	3.45	3.62	3.63	3.47	3.29	2.88
MA_RS10490	#N/A	2.70	2.60	1.92	2.78	2.89	2.92	2.86	3.41	3.83	2.93	2.77	2.22
MA_RS10495	NA	0.38	0.60	0.32	0.71	0.40	0.73	0.73	1.09	1.19	0.71	0.79	0.55
MA_RS10505	NA	3.39	3.62	3.54	4.04	3.81	3.88	4.14	4.40	4.51	4.25	3.83	3.75
MA_RS10510	NA	0.01	0.04	0.08	0.08	0.08	0.04	0.09	0.18	0.26	0.09	0.04	0.07
MA_RS10515	NA	1.46	1.86	1.75	1.85	1.43	2.00	1.26	2.48	2.53	2.19	1.91	1.31
MA_RS10520	NA	0.31	0.65	0.31	0.36	0.44	0.48	0.75	0.73	1.13	0.80	0.39	0.15
MA_RS10525	NA	3.54	3.32	3.14	3.00	3.26	3.09	3.23	4.09	4.52	3.41	2.94	2.63
MA_RS10535	NA	3.08	3.03	3.15	3.05	2.92	2.97	3.67	4.46	4.84	3.59	3.07	2.94
MA_RS10540	NA	1.36	1.09	1.08	1.33	1.48	1.97	2.25	2.67	2.71	1.70	1.44	1.59
MA_RS10545	istA	1.54	1.51	1.68	1.58	1.51	1.59	1.34	1.96	2.33	1.73	1.57	1.44
MA_RS10550	istB	2.42	2.49	2.32	2.78	2.65	2.80	2.75	3.61	3.69	3.10	2.69	2.63
MA_RS10555	NA	2.49	2.31	2.53	2.66	2.32	2.85	3.04	3.52	3.67	2.74	2.26	2.49
MA_RS10560	NA	1.03	1.62	1.54	1.24	0.55	1.59	1.39	1.12	1.71	1.20	0.63	1.78
MA_RS10565	NA	0.27	0.77	0.39	0.81	0.50	0.30	0.87	0.35	0.13	1.14	0.43	0.54
MA_RS10570	NA	3.79	4.11	3.97	3.85	3.61	3.96	3.89	4.04	4.03	3.63	3.89	3.95
MA_RS10575	NA	2.76	3.15	2.76	2.84	2.98	2.87	2.96	2.95	3.09	2.25	2.42	3.01
MA_RS10580	NA	0.66	0.70	0.04	0.48	0.68	0.28	0.00	0.50	1.68	0.75	0.66	0.51
MA_RS10585	NA	2.32	2.25	2.05	2.46	2.30	2.55	2.21	2.80	2.24	2.48	2.23	2.05
MA_RS10595	NA	2.60	3.00	2.26	2.90	3.24	2.88	3.00	4.11	4.12	3.82	2.93	2.87
MA_RS10600	NA	1.22	1.30	1.07	1.09	1.02	1.54	1.70	1.71	2.15	2.03	1.21	1.69
MA_RS10605	NA	3.38	3.23	3.32	3.98	3.80	3.75	3.47	4.49	4.92	3.97	3.88	3.76
MA_RS10610	NA	2.95	2.63	2.84	3.00	2.35	2.61	2.22	3.72	3.60	3.22	3.31	2.51
MA_RS10615	NA	2.18	2.39	2.01	2.30	2.26	2.26	1.87	2.43	3.13	2.53	3.04	2.57
MA_RS10625	NA	2.16	1.85	2.50	2.45	2.72	2.19	2.32	3.26	3.15	2.37	2.70	1.99
MA_RS10640	NA	2.06	2.12	1.97	2.42	2.48	2.48	2.56	3.67	3.92	2.53	1.93	2.24
MA_RS10645	NA	2.05	2.30	2.35	2.37	2.05	2.48	2.53	2.92	3.29	2.37	2.26	2.36
MA_RS10650	NA	4.05	4.44	4.38	4.53	4.34	4.45	4.51	4.70	4.45	5.06	4.66	4.52
MA_RS10655	NA	3.05	3.33	3.58	3.51	3.06	3.38	3.49	3.45	3.12	3.42	3.53	3.70
MA_RS10660	NA	1.99	2.18	1.68	2.59	2.15	2.42	2.34	1.96	2.31	1.89	1.17	2.08
MA_RS10665	NA	2.22	2.30	2.43	2.59	2.38	2.69	2.46	2.84	2.84	2.86	2.61	2.60
MA_RS10670	NA	2.74	2.58	2.73	2.66	2.59	2.64	2.61	3.16	2.82	2.67	2.40	2.80
MA_RS10675	NA	1.39	1.40	1.74	1.62	1.41	1.71	1.88	1.87	2.13	1.27	1.41	1.61
MA_RS10680	NA	0.72	1.21	0.46	2.06	1.03	0.84	1.15	1.38	1.79	1.54	0.78	0.98
MA_RS10690	NA	4.08	3.95	4.15	4.24	3.86	4.22	4.31	5.08	5.25	4.72	4.11	4.15
MA_RS10695	NA	0.97	1.02	1.09	1.30	1.57	1.41	1.10	1.72	2.00	1.62	1.72	1.52
MA_RS10700	NA	2.24	2.22	2.51	2.85	2.51	2.79	2.80	2.72	2.37	2.21	2.26	2.04
MA_RS10705	NA	3.28	3.54	3.56	3.76	3.60	3.78	3.69	4.10	4.08	4.02	3.48	3.53
MA_RS10710	NA	4.08	4.05	3.85	4.32	3.85	3.83	3.74	4.54	3.71	4.02	3.64	3.55
MA_RS10720	NA	1.23	0.95	1.35	1.73	0.87	1.24	0.17	1.36	1.50	1.38	0.80	1.53
MA_RS10725	NA	1.48	1.39	2.49	2.08	1.76	2.43	1.86	2.35	2.89	2.41	1.61	2.35
MA_RS10730	NA	2.75	3.16	2.89	3.02	3.09	3.31	3.37	3.50	3.16	3.46	3.04	3.35
MA_RS10735	NA	0.03	0.00	0.55	0.00	0.00	0.00	0.19	0.00	0.99	0.28	0.36	0.00
MA_RS10740	NA	0.63	0.54	0.02	0.47	0.39	0.28	0.27	0.78	0.76	0.62	0.82	0.23
MA_RS10745	NA	0.53	0.38	0.42	0.00	0.00	0.34	0.77	0.54	0.00	0.47	0.39	0.71
MA_RS10750	NA	0.03	0.53	0.00	0.00	0.38	0.73	0.00	1.11	0.00	0.00	0.00	1.11
MA_RS10755	NA	0.06	0.14	0.17	0.13	0.18	0.14	0.52	0.16	0.39	0.50	0.00	0.19
MA_RS10760	NA	1.21	1.14	1.82	1.11	1.18	0.77	1.28	1.65	1.59	1.79	1.63	0.98
MA_RS10765	NA	1.47	1.52	1.64	1.68	1.51	1.25	1.63	2.29	1.92	1.66	1.49	1.66
MA_RS10770	NA	0.75	0.90	0.72	0.68	0.77	0.79	0.63	0.72	1.08	0.56	0.81	0.82
MA_RS10775	NA	2.04	2.24	2.22	2.96	2.47	2.73	2.79	3.26	3.60	3.09	2.76	2.74
MA_RS10785	NA	4.00	4.34	3.95	4.24	3.96	4.16	4.16	4.39	4.67	4.21	3.93	3.97
MA_RS10790	NA	3.22	3.59	3.64	3.64	3.41	3.38	3.67	3.41	3.47	3.50	3.33	3.36
MA_RS10795	NA	4.59	4.68	4.68	4.77	4.72	4.79	4.78	4.82	4.97	4.79	4.53	4.58
MA_RS10800	istB	0.08	0.10	0.13	0.30	0.27	0.18	0.22	0.39	0.50	0.24	0.16	0.08
MA_RS10805	istA	0.11	0.20	0.18	0.28	0.39	0.17	0.30	0.46	0.36	0.30	0.31	0.19
MA_RS10810	NA	0.51	1.00	0.61	0.61	0.70	1.07	0.61	1.07	1.13	1.08	0.73	0.97
MA_RS10815	NA	2.21	2.33	2.27	2.35	2.12	2.46	2.64	3.24	3.36	2.56	2.20	2.42
MA_RS10820	NA	0.52	0.39	0.51	0.79	0.62	0.69	0.79	1.01	1.26	0.84	0.66	0.54
MA_RS10825	NA	1.40	1.75	2.03	1.58	1.72	1.75	2.00	2.36	2.71	1.84	1.40	2.05
MA_RS10830	NA	1.95	2.12	2.26	2.41	2.37	2.61	2.24	3.09	3.47	2.67	2.24	2.62
MA_RS10835	NA	0.56	0.23	0.00	0.26	1.03	0.15	0.60	1.15	0.38	0.88	0.96	0.50
MA_RS10840	NA	0.32	0.34	0.48	0.38	0.28	0.37	0.39	0.73	0.91	0.55	0.28	0.35
MA_RS10845	NA	0.49	0.76	0.61	0.70	0.55	0.68	0.75	0.84	0.72	0.86	0.61	0.59
MA_RS10850	NA	0.79	0.83	1.29	1.21	1.30	1.63	1.31	1.60	1.77	2.08	1.03	1.46
MA_RS10860	NA	1.79	2.18	2.02	2.35	2.09	2.38	2.05	2.72	3.36	2.03	2.14	1.71
MA_RS10865	NA	2.63	2.76	2.42	3.04	2.77	2.98	2.92	3.32	3.21	2.84	2.09	2.82
MA_RS10870	NA	1.51	1.97	1.77	2.28	1.75	2.27	2.14	2.89	2.92	2.66	1.75	1.80
MA_RS10875	NA	0.03	0.57	0.18	0.00	0.35	0.46	0.00	0.93	1.18	0.26	0.00	0.28
MA_RS10880	NA	0.00	0.06	0.00	0.00	0.08	0.16	0.13	0.28	0.29	0.25	0.10	0.00
MA_RS10885	NA	0.62	0.86	0.63	1.26	1.08	1.12	0.75	1.42	2.09	1.00	1.12	0.90
MA_RS10890	NA	3.76	4.04	3.98	4.35	4.09	4.17	4.22	4.84	5.02	4.23	3.63	4.17
MA_RS10895	NA	3.34	3.65	3.56	4.17	3.92	4.09	3.90	4.57	4.71	4.36	3.82	3.93
MA_RS10900	NA	1.10	1.06	1.25	1.51	1.17	1.60	1.39	1.89	2.12	1.63	1.15	1.20
MA_RS10905	NA	1.16	0.81	1.29	1.33	1.02	1.62	1.21	2.20	1.41	1.43	1.30	1.26
MA_RS10910	NA	1.10	0.87	0.23	1.88	0.87	1.15	1.32	2.29	1.95	0.92	1.46	1.03
MA_RS10920	NA	0.08	0.32	0.19	0.43	0.33	0.13	0.37	0.65	0.81	0.51	0.08	0.32
MA_RS10925	NA	0.18	0.19	0.30	0.34	0.29	0.25	0.28	0.53	0.58	0.50	0.28	0.26
MA_RS10930	NA	1.47	0.75	0.00	1.20	0.79	1.00	1.53	2.16	1.99	1.21	0.68	0.89
MA_RS10935	NA	2.10	2.24	2.24	2.68	2.23	2.44	2.41	2.60	2.95	2.31	2.28	2.46
MA_RS10940	NA	0.97	1.11	1.38	1.17	1.02	1.21	0.86	1.34	2.40	0.86	0.80	1.17
MA_RS10945	NA	2.16	1.84	2.16	2.11	2.25	2.10	1.95	2.69	3.53	2.40	2.21	2.01
MA_RS10950	NA	3.74	3.93	3.82	4.13	4.04	4.12	4.14	4.33	4.36	3.90	3.62	3.90
MA_RS10955	NA	4.13	4.45	4.12	4.73	4.26	4.58	4.63	5.28	5.34	4.86	4.28	4.47
MA_RS10960	htpX	4.53	4.82	4.81	5.10	4.80	4.94	4.71	5.00	5.39	4.70	4.50	4.89
MA_RS10965	NA	2.53	3.19	3.25	3.13	3.02	3.13	3.84	2.70	2.96	2.49	2.99	3.02
MA_RS10970	NA	4.33	4.67	4.22	4.68	4.34	4.74	4.80	4.94	5.22	4.72	4.56	4.65
MA_RS10975	NA	3.17	3.33	2.88	3.23	3.12	3.44	3.21	3.82	4.32	3.44	2.99	2.72
MA_RS10980	NA	1.96	1.95	1.61	1.89	1.65	1.90	2.41	3.10	2.74	2.35	2.02	2.03
MA_RS10985	NA	2.94	3.09	2.97	3.33	3.02	3.29	3.44	3.59	3.91	3.24	2.97	3.34
MA_RS10995	NA	2.10	2.62	2.49	2.74	2.58	2.90	2.84	3.52	4.22	2.54	2.69	2.73
MA_RS11000	NA	2.78	2.86	3.02	3.12	3.01	3.02	3.35	4.09	4.21	2.87	2.86	2.87
MA_RS11010	NA	1.94	2.15	2.24	2.37	2.16	2.56	2.21	3.26	3.37	2.05	1.73	2.48
MA_RS11015	NA	2.76	2.95	2.86	3.17	3.01	3.00	3.11	3.74	3.84	2.96	2.71	3.10
MA_RS11030	NA	0.87	0.78	0.80	0.83	0.42	1.16	1.52	1.78	1.18	0.76	1.11	0.00
MA_RS11035	NA	1.17	1.79	1.32	1.27	1.65	1.72	1.83	2.35	2.39	2.09	1.56	1.70
MA_RS11040	NA	0.16	0.39	0.62	0.00	0.00	0.41	0.00	0.00	0.94	0.46	0.75	0.44
MA_RS11045	NA	0.20	0.28	0.00	0.61	0.00	0.21	0.00	0.29	0.00	0.00	0.47	0.00
MA_RS11060	NA	1.41	0.99	1.02	1.62	1.39	1.20	2.01	2.71	2.27	2.17	1.33	1.78
MA_RS11065	NA	1.64	1.22	1.76	1.72	1.25	2.00	2.54	2.06	2.61	1.55	0.99	1.34
MA_RS11070	NA	2.21	1.98	2.57	1.79	1.93	2.51	2.29	2.39	2.67	2.39	2.32	1.77
MA_RS11075	NA	0.47	0.39	1.11	1.23	1.13	1.33	0.34	0.35	1.32	1.36	1.19	1.36
MA_RS11080	NA	2.53	1.95	2.52	2.88	2.96	2.90	2.68	3.76	3.38	3.28	2.47	3.13
MA_RS11085	NA	2.70	2.98	2.69	3.32	3.43	3.47	3.48	3.85	4.13	3.41	3.29	3.58
MA_RS11090	NA	2.51	2.82	2.59	2.83	2.79	3.17	3.50	4.08	3.79	3.41	2.87	2.52
MA_RS11095	NA	3.26	3.88	3.94	3.86	3.96	4.14	4.05	4.42	4.55	4.45	3.97	4.05
MA_RS11100	NA	3.00	3.26	2.90	3.40	3.40	3.23	3.29	4.26	4.21	3.90	3.08	3.29
MA_RS11105	NA	1.93	2.23	1.35	2.24	1.87	1.74	1.93	2.89	2.67	1.93	2.40	1.46
MA_RS11110	NA	3.44	3.44	3.20	3.59	3.43	3.46	3.52	4.93	5.29	3.89	3.40	3.41
MA_RS11115	NA	2.58	2.94	2.69	2.48	2.34	2.66	2.54	3.51	4.07	2.45	2.48	2.32
MA_RS11120	NA	1.55	1.84	1.60	1.54	1.73	1.98	1.82	2.59	2.90	1.21	1.65	1.83
MA_RS11125	NA	5.41	5.64	5.52	6.19	5.65	5.96	5.94	6.26	6.38	5.86	5.75	5.64
MA_RS11130	carB	5.45	5.77	5.63	6.15	5.85	6.06	5.97	6.05	6.47	5.92	5.80	5.94
MA_RS11135	carA	6.22	6.36	6.28	6.76	6.53	6.57	6.80	6.96	7.19	6.80	6.49	6.77
MA_RS11140	NA	4.71	4.83	4.75	5.22	4.97	5.14	5.24	5.13	5.23	4.74	4.89	5.04
MA_RS11145	NA	4.07	4.35	4.16	4.85	4.45	4.70	4.68	5.37	5.74	4.33	4.22	4.33
MA_RS11150	NA	4.79	4.89	4.89	5.55	5.47	5.65	5.48	5.98	6.28	4.75	4.98	5.09
MA_RS11155	NA	1.16	1.51	1.14	1.63	1.62	1.58	1.50	2.21	2.07	1.40	1.32	1.77
MA_RS11160	NA	0.85	1.02	0.74	1.66	1.00	1.45	1.22	1.62	1.88	1.19	1.29	0.98
MA_RS11165	NA	0.72	1.09	1.16	1.31	1.13	1.16	1.57	1.95	1.21	1.56	1.22	0.99
MA_RS11170	NA	0.66	0.92	0.90	1.10	0.86	0.86	0.85	0.60	1.16	0.67	0.60	0.73
MA_RS11175	NA	1.52	1.87	1.52	1.80	1.18	1.38	2.18	1.79	1.72	1.51	1.20	1.62
MA_RS11180	NA	2.73	2.55	2.53	2.91	3.03	3.37	3.25	3.31	3.57	2.91	2.62	3.00
MA_RS11185	NA	2.57	2.90	2.58	3.81	3.30	3.73	3.81	4.63	4.78	4.09	3.20	3.39
MA_RS11195	NA	2.26	2.48	2.91	3.06	2.75	3.36	3.18	3.14	3.29	2.28	2.94	3.41
MA_RS11205	NA	0.31	1.21	0.91	1.81	1.00	1.00	1.26	0.61	2.26	1.26	1.17	1.22
MA_RS11210	NA	3.11	3.20	3.35	3.87	3.55	3.04	3.61	4.77	4.72	4.14	3.70	3.28
MA_RS11230	NA	0.18	0.00	1.03	0.00	0.05	0.00	0.32	0.00	0.34	0.00	0.00	0.45

MA_RS11235	mtaA	2.13	2.29	2.66	2.27	2.15	2.51	2.24	2.42	2.49	2.48	2.41	2.38
MA_RS11240	NA	1.32	1.74	1.20	1.42	1.44	1.75	1.91	2.95	2.95	1.56	1.35	1.26
MA_RS11245	NA	1.26	2.16	1.89	2.22	2.22	2.43	2.18	3.09	2.76	2.51	2.56	2.12
MA_RS11255	NA	1.25	1.14	1.39	1.91	1.31	1.67	1.42	2.32	1.80	1.99	1.67	1.38
MA_RS11260	NA	0.63	0.08	0.67	0.42	0.15	0.73	0.58	1.02	1.39	0.52	0.76	0.69
MA_RS11265	NA	0.46	1.07	0.89	1.06	0.73	0.98	0.42	1.58	1.62	0.89	1.45	0.27
MA_RS11270	NA	1.22	1.02	0.21	1.29	0.70	1.30	1.11	1.51	2.43	1.55	1.08	1.51
MA_RS11275	NA	1.68	1.48	1.26	1.58	1.69	1.93	1.10	2.36	2.48	1.61	1.49	1.56
MA_RS11280	NA	1.54	1.84	1.76	1.61	1.80	2.19	1.12	2.49	2.71	2.31	1.97	1.88
MA_RS11285	NA	1.17	1.65	1.97	1.61	1.69	1.85	1.77	2.72	3.41	1.58	1.53	1.61
MA_RS11290	NA	0.97	1.42	1.21	1.27	1.63	1.39	1.16	2.32	2.48	1.45	1.33	1.03
MA_RS11295	NA	1.16	1.08	1.05	1.70	0.92	1.54	1.51	2.66	2.50	1.20	1.16	0.91
MA_RS11300	NA	2.27	2.43	2.44	2.66	2.38	2.59	2.72	3.30	3.86	2.71	2.29	2.50
MA_RS11305	NA	2.89	3.11	2.99	3.13	3.12	3.12	3.22	4.34	4.49	3.19	3.19	2.80
MA_RS11310	NA	2.07	2.21	2.39	2.39	2.08	2.39	2.79	3.58	3.84	2.35	2.61	2.28
MA_RS11315	NA	1.92	1.75	1.82	2.54	2.19	2.25	2.34	3.04	3.68	2.44	2.27	2.11
MA_RS11320	NA	1.43	1.38	1.63	1.60	1.05	1.23	2.09	2.69	3.11	1.56	1.65	1.30
MA_RS11325	NA	2.59	2.76	3.10	2.65	2.66	2.63	3.41	3.90	4.20	2.93	2.80	2.97
MA_RS11330	rfbD	2.58	2.85	2.76	3.00	2.95	2.57	3.50	3.55	3.70	3.09	2.58	2.86
MA_RS11335	NA	0.70	1.22	1.11	0.99	1.03	1.32	0.86	1.68	1.65	1.11	0.72	0.92
MA_RS11340	rfbB	1.60	1.63	1.82	1.55	1.96	1.59	1.82	2.47	2.89	2.00	1.63	1.39
MA_RS11345	NA	0.00	0.00	0.00	0.20	0.00	0.04	0.00	0.05	0.16	0.11	0.00	0.00
MA_RS11350	NA	1.74	1.71	1.74	2.01	1.87	1.87	2.16	2.45	2.53	2.10	1.99	1.67
MA_RS11355	NA	0.55	0.61	0.71	0.89	0.58	0.82	0.79	0.63	0.68	0.79	0.71	0.41
MA_RS11360	NA	1.22	2.00	1.77	1.94	1.67	1.93	1.43	2.24	2.29	2.45	1.41	1.97
MA_RS11365	NA	2.13	2.43	2.40	2.36	2.32	2.59	2.71	3.25	3.02	2.58	2.90	2.55
MA_RS11375	NA	3.43	3.40	3.57	2.86	2.81	2.82	3.18	3.71	3.68	3.05	3.17	3.19
MA_RS11380	NA	2.88	3.09	3.23	2.52	2.47	2.46	2.48	2.92	3.14	2.60	2.65	2.96
MA_RS11390	NA	2.00	2.19	2.16	2.20	1.88	1.95	1.89	2.23	2.73	1.77	1.61	2.12
MA_RS11395	NA	0.52	0.55	0.38	0.62	1.01	0.63	0.39	0.92	2.15	0.80	1.13	0.63
MA_RS11400	NA	2.36	2.48	2.62	2.76	2.74	2.91	2.54	3.10	3.04	2.38	2.55	2.64
MA_RS11405	NA	3.12	3.45	3.43	3.61	3.40	3.69	3.23	3.67	3.98	3.35	3.32	3.47
MA_RS11410	istB	0.24	0.18	0.25	0.62	0.36	0.46	0.47	0.65	0.98	0.57	0.31	0.26
MA_RS11415	istA	0.48	0.49	0.46	0.79	0.76	0.79	0.61	1.03	0.96	0.89	0.74	0.61
MA_RS11420	NA	0.89	1.20	1.40	1.61	0.89	1.48	1.31	1.88	2.32	1.07	1.33	1.57
MA_RS11425	NA	1.92	2.43	1.94	2.75	1.96	2.71	2.59	3.69	3.81	2.35	2.67	2.34
MA_RS11430	NA	1.79	1.91	0.50	2.36	1.96	2.35	2.13	2.87	2.99	2.48	1.79	2.29
MA_RS11435	NA	2.12	1.90	1.45	2.13	1.98	2.59	2.62	3.23	3.52	2.42	1.38	1.90
MA_RS11440	NA	2.00	2.08	2.15	2.21	1.58	1.70	3.04	2.36	3.00	1.55	1.69	2.07
MA_RS11445	NA	1.99	2.12	2.23	2.12	1.99	2.22	2.07	2.42	2.79	1.95	1.78	2.27
MA_RS11450	NA	2.93	3.41	3.20	3.19	3.19	3.45	3.25	2.82	3.07	2.93	2.84	2.95
MA_RS11455	NA	3.16	3.17	3.07	3.24	3.42	3.64	3.26	4.06	4.17	3.32	2.94	3.03
MA_RS11460	NA	2.36	2.05	2.59	2.24	2.10	2.47	2.28	1.82	2.53	2.14	1.72	1.44
MA_RS11465	NA	3.07	3.00	2.57	2.18	2.40	2.35	2.37	3.22	2.46	1.61	2.02	1.58
MA_RS11475	NA	1.09	1.62	1.26	1.84	1.72	1.48	2.29	2.73	3.07	2.15	1.37	1.36
MA_RS11480	NA	0.77	1.23	0.87	0.50	0.88	0.45	0.92	1.83	1.95	1.36	0.79	1.16
MA_RS11490	NA	2.79	2.86	2.73	3.21	3.05	3.36	2.98	3.43	3.83	2.96	3.06	2.98
MA_RS11500	NA	2.04	1.96	2.33	2.09	1.51	2.13	1.77	2.29	1.76	1.42	1.54	1.33
MA_RS11505	NA	0.84	1.07	1.42	1.31	1.19	1.33	1.46	1.59	1.79	1.03	0.95	1.13
MA_RS11510	NA	0.54	0.41	0.30	0.61	0.53	0.90	0.03	1.23	0.94	1.20	0.78	0.40
MA_RS11515	NA	1.54	1.62	1.41	1.81	1.45	1.50	2.28	2.35	1.65	0.99	1.14	1.16
MA_RS11520	NA	3.23	3.42	3.21	3.61	3.48	3.65	3.09	3.45	3.16	2.99	2.91	3.12
MA_RS11525	NA	1.76	1.85	0.57	1.14	1.63	1.56	1.69	2.00	1.85	2.16	1.47	1.79
MA_RS11530	NA	0.38	0.21	0.71	0.33	0.31	0.07	0.51	0.40	0.33	0.44	0.34	0.23
MA_RS11535	NA	2.76	3.14	3.10	3.63	3.07	3.44	3.56	4.21	4.52	3.86	3.29	3.28
MA_RS11540	NA	3.39	3.56	3.60	3.54	3.81	3.63	3.54	4.65	4.77	3.66	3.89	3.53
MA_RS11550	NA	2.03	2.09	1.99	1.98	1.37	1.60	2.18	2.78	3.08	2.24	1.76	1.43
MA_RS11565	NA	1.68	1.83	1.57	2.57	2.50	2.54	2.18	2.99	3.06	2.42	1.67	2.05
MA_RS11570	NA	2.23	2.33	2.38	2.50	2.40	2.35	2.51	3.18	3.63	2.14	1.68	1.76
MA_RS11575	NA	2.24	2.37	2.29	2.53	2.60	2.70	3.38	3.42	2.97	2.71	2.54	2.42
MA_RS11580	NA	1.24	0.48	1.32	1.91	1.01	1.45	1.47	2.30	1.43	1.42	1.79	0.95
MA_RS11585	NA	1.29	1.22	1.41	1.44	1.46	1.33	1.67	2.04	2.23	1.32	1.28	1.71
MA_RS11590	NA	0.10	0.00	0.00	0.00	0.21	0.00	0.00	0.00	0.66	0.00	0.00	0.10
MA_RS11600	NA	0.28	1.08	0.44	0.00	0.25	0.35	0.43	0.35	0.77	0.00	0.00	0.08
MA_RS11605	NA	4.41	4.66	4.68	5.15	4.79	4.92	4.86	5.22	5.53	4.96	4.65	4.57
MA_RS11610	NA	1.07	0.82	1.56	1.20	1.23	1.31	1.18	1.96	1.91	1.69	1.27	1.41
MA_RS11615	NA	0.58	0.55	0.86	0.76	0.40	1.08	1.32	1.54	1.32	0.69	0.47	0.00
MA_RS11625	NA	1.08	0.96	0.94	1.12	1.15	1.68	1.17	1.88	2.26	1.13	1.48	0.90
MA_RS11630	NA	0.12	0.09	0.19	0.07	0.10	0.04	0.14	0.14	0.16	0.18	0.07	0.06
MA_RS11635	NA	1.47	1.79	1.69	1.33	2.10	1.62	2.03	1.94	2.05	1.20	1.89	1.51
MA_RS11640	NA	5.34	5.61	5.53	5.88	5.61	5.84	5.63	6.16	6.36	5.76	5.37	5.48
MA_RS11645	NA	0.17	0.55	0.00	0.30	1.26	0.69	0.40	1.37	0.84	0.27	0.52	0.40
MA_RS11650	NA	1.59	0.86	1.41	1.12	1.24	1.38	1.52	2.01	2.10	1.35	1.29	1.07
MA_RS11655	NA	0.89	0.74	1.18	1.10	1.50	1.56	1.71	2.61	2.24	1.49	1.55	1.30
MA_RS11660	NA	1.51	2.02	2.16	2.16	2.00	1.75	1.67	2.45	2.73	1.72	1.60	1.48
MA_RS11665	NA	2.63	2.80	2.88	3.23	2.97	2.53	3.21	3.60	4.13	3.56	2.82	2.48
MA_RS11670	NA	3.54	3.83	3.36	3.77	3.64	3.97	3.57	3.82	3.65	3.69	3.36	3.67
MA_RS11675	NA	1.26	0.79	1.64	2.04	0.88	1.61	2.09	0.97	1.92	1.28	1.40	1.51
MA_RS11680	NA	0.91	0.98	1.51	1.15	1.19	1.66	1.37	1.59	1.34	0.91	0.87	0.92
MA_RS11685	#N/A	0.45	0.00	0.22	0.48	0.55	0.67	0.20	0.55	0.63	0.61	0.44	0.49
MA_RS11695	NA	3.54	3.81	3.43	3.54	3.49	3.94	3.83	3.66	3.94	3.25	3.09	3.41
MA_RS11705	NA	1.68	1.82	2.34	1.34	1.10	1.13	1.39	1.86	1.64	0.95	1.01	0.71
MA_RS11710	NA	1.22	1.09	0.90	0.85	0.97	1.17	1.11	1.54	1.67	0.78	0.72	0.86
MA_RS11715	NA	5.30	5.49	5.47	6.16	5.58	5.82	6.33	6.86	7.30	5.91	5.34	5.46
MA_RS11720	NA	0.63	0.65	0.99	0.90	0.61	0.79	1.03	1.15	1.00	0.80	0.56	0.30
MA_RS11725	NA	2.03	2.26	2.45	2.22	2.16	2.53	2.67	2.73	3.03	1.99	1.87	1.88
MA_RS11730	NA	2.83	3.04	3.04	3.07	2.96	2.41	3.04	3.17	3.03	2.78	2.60	2.27
MA_RS11740	NA	0.32	0.67	0.78	1.54	0.73	1.83	1.15	1.49	1.29	0.63	1.62	1.05
MA_RS11745	NA	0.19	0.19	0.33	0.22	0.15	0.09	0.10	0.05	0.15	0.20	0.10	0.11
MA_RS11750	#N/A	1.37	0.81	0.93	1.32	1.25	1.23	1.37	1.98	1.83	1.01	0.67	1.64
MA_RS11760	NA	2.51	2.71	2.18	3.10	2.05	2.75	2.12	3.32	3.14	2.31	2.31	2.38
MA_RS11765	NA	1.94	2.22	2.12	2.39	1.89	2.35	2.59	2.90	3.09	1.82	1.65	1.92
MA_RS11770	NA	1.08	1.95	1.79	0.99	1.23	2.16	0.65	0.89	1.55	1.29	0.58	0.87
MA_RS11775	NA	1.52	1.96	1.52	2.05	1.64	1.84	1.87	2.76	2.53	1.93	1.91	1.66
MA_RS11780	NA	1.64	1.74	1.88	1.64	1.75	0.91	1.51	1.50	2.09	1.63	1.55	0.75
MA_RS11785	NA	2.17	2.16	2.37	2.78	2.35	2.81	2.23	2.88	3.29	2.08	1.50	2.03
MA_RS11790	NA	4.20	4.51	4.35	4.47	4.36	4.43	4.48	4.90	5.05	3.53	3.50	4.04
MA_RS11795	NA	4.81	5.08	5.03	5.21	4.86	5.14	5.23	5.68	6.06	4.55	4.31	4.45
MA_RS11800	NA	5.21	5.47	5.34	5.43	5.18	5.34	5.45	5.68	5.86	4.78	4.71	4.88
MA_RS11805	NA	1.35	1.89	1.99	2.58	1.91	2.17	2.73	1.90	2.82	1.72	1.55	1.98
MA_RS11810	NA	2.23	2.11	1.61	2.93	1.99	1.96	2.78	2.67	2.68	1.92	2.29	1.66
MA_RS11815	NA	0.53	1.04	1.18	1.34	0.77	1.08	1.11	0.78	1.50	0.69	0.14	1.21
MA_RS11820	NA	0.58	1.25	0.32	1.20	0.74	1.38	1.37	1.61	1.77	0.67	0.88	0.75
MA_RS11825	modA	2.74	3.11	2.99	3.55	3.18	3.30	3.12	3.74	4.05	3.25	3.01	3.31
MA_RS11830	modB	3.15	3.29	3.18	3.67	3.02	3.61	3.51	3.11	3.64	3.23	3.12	3.43
MA_RS11835	NA	2.27	2.45	2.44	2.85	2.65	2.59	2.95	3.16	3.33	2.71	2.33	2.66
MA_RS11850	NA	1.62	1.29	1.20	2.48	1.82	1.37	1.73	2.12	2.43	1.87	1.46	1.47
MA_RS11855	NA	0.11	0.18	0.00	0.67	0.80	0.58	0.39	0.56	1.60	0.30	0.36	0.47
MA_RS11860	NA	2.93	3.13	3.11	3.31	3.00	3.46	2.98	3.18	2.93	2.96	2.74	2.63
MA_RS11865	NA	2.08	2.18	2.33	2.55	2.17	2.74	2.12	2.64	2.88	1.95	1.82	2.07
MA_RS11870	NA	0.00	0.85	0.82	0.00	0.00	0.00	0.86	0.17	0.00	0.00	0.00	0.28
MA_RS11875	NA	0.43	0.00	0.00	0.00	0.48	0.00	0.00	0.38	0.28	0.00	0.00	0.00
MA_RS11880	NA	3.58	3.57	3.55	4.32	3.73	4.34	3.92	4.98	4.97	3.70	3.45	3.02
MA_RS11885	NA	2.21	2.25	2.15	2.23	2.47	2.58	1.87	2.18	2.59	1.59	1.64	1.25
MA_RS11890	#N/A	1.27	1.69	1.23	1.32	1.37	1.21	1.51	1.95	0.74	1.20	0.74	0.47
MA_RS11895	NA	1.69	1.48	1.79	2.05	1.54	1.81	1.98	2.03	1.96	1.87	1.24	1.73
MA_RS11905	NA	2.48	2.59	2.70	3.00	2.90	3.23	3.28	3.40	3.42	2.67	2.76	2.64
MA_RS11910	NA	0.53	1.24	0.78	0.56	0.51	1.50	0.68	0.00	0.38	0.99	0.33	0.57
MA_RS11915	NA	1.25	1.37	1.43	1.51	1.50	1.77	1.29	1.87	1.95	1.36	1.19	1.16
MA_RS11920	NA	3.55	3.59	3.45	3.81	3.72	3.86	3.31	3.80	3.56	3.34	3.05	2.57
MA_RS11925	NA	0.21	0.73	0.00	1.39	0.50	0.49	0.37	1.86	1.39	1.60	1.73	0.31
MA_RS11930	NA	1.27	1.92	1.62	1.47	2.09	1.64	1.91	1.69	1.85	1.25	1.42	1.58
MA_RS11935	NA	3.47	3.61	3.31	3.60	3.53	2.95	3.91	3.12	2.56	2.21	2.87	2.79
MA_RS11940	NA	4.29	4.30	3.99	4.35	4.09	4.36	4.17	5.23	4.96	3.66	3.79	3.71
MA_RS11945	NA	2.63	2.88	2.83	3.00	2.81	2.85	2.85	3.04	3.12	2.49	2.49	2.52
MA_RS11950	NA	1.83	2.05	1.99	2.30	2.16	2.47	2.21	2.91	3.11	2.38	1.82	1.86
MA_RS11960	NA	1.05	0.90	1.30	0.85	1.27	1.06	0.56	1.59	1.88	0.99	1.10	0.58
MA_RS11965	NA	4.16	4.38	4.24	4.48	4.15	4.45	4.34	4.40	4.67	3.65	3.83	3.62
MA_RS11975	NA	0.12	0.00	0.73	0.00	0.00	0.40	0.36	0.81	0.73	1.39	0.00	0.26
MA_RS11985	NA	2.54	2.76	3.00	2.92	2.67	2.89	2.74	2.82	3.34	2.40	2.30	2.50
MA_RS11990	NA	1.12	1.01	0.91	1.22	1.02	1.21	0.82	1.74	1.60	0.67	0.34	1.12
MA_RS11995	NA	1.02	1.43	1.59	1.38	1.42	1.37	1.36	2.19	2.40	1.47	1.16	0.97
MA_RS12000	ade	3.43	3.61	3.47	3.86	3.78	3.85	3.77	3.89	4.21	3.20	2.92	2.96
MA_RS12005	NA	3.79	3.86	3.44	3.34	3.68	3.93	4.23	4.49	4.58	3.21	2.72	2.73
MA_RS12010	NA	1.31	0.74	1.39	1.15	0.85	0.85	1.53	0.88	1.17	1.14	0.97	0.51
MA_RS12015	NA	0.29	0.32	0.55	0.81	0.27	0.35	0.00	1.73	1.13	0.25	0.87	0.42
MA_RS12020	NA	1.56	1.72	1.74	2.11	1.90	2.05	2.08	2.28	2.18	2.07	1.54	1.73
MA_RS12025	NA	2.28	2.72	2.62	3.59	2.81	2.63	3.35	3.50	3.29	3.11	2.68	2.52
MA_RS12035	NA	3.74	3.96	3.99	4.25	4.20	4.13	4.14	4.45	4.29	3.74	3.56	3.58
MA_RS12040	NA	2.94	3.19	3.32	3.33	2.99	3.08	3.42	3.84	4.16	2.76	2.29	2.64
MA_RS12045	NA	1.64	1.93	1.43	2.11	1.85	2.09	2.01	2.71	3.10	1.53	1.26	1.67
MA_RS12050	NA	2.16	2.56	2.74	2.97	2.51	2.74	2.48	4.04	3.38	2.83	1.77	2.45
MA_RS12055	NA	3.38	3.39	3.61	4.05	3.86	4.00	3.83	4.30	4.58	3.81	3.22	3.30

MA_RS12060	NA	1.49	1.63	1.65	1.46	2.04	1.81	1.96	2.45	1.58	0.99	1.62	1.14
MA_RS12065	NA	3.55	3.82	3.87	4.01	3.89	4.01	3.81	4.06	4.28	3.75	3.47	3.38
MA_RS12070	NA	0.99	1.00	1.70	1.64	0.85	2.02	0.19	2.55	2.12	1.95	1.21	1.63
MA_RS12075	NA	1.49	1.45	1.54	1.84	1.70	1.85	1.27	2.15	1.92	1.12	0.96	1.41
MA_RS12085	NA	2.13	2.39	2.73	2.82	2.86	2.91	2.25	3.07	3.02	2.19	2.05	2.28
MA_RS12090	NA	2.06	2.55	2.62	2.86	2.09	2.66	2.65	3.14	3.44	2.15	2.53	2.67
MA_RS12095	NA	2.25	2.38	1.39	2.45	2.02	2.35	2.35	2.75	2.96	2.20	1.94	1.91
MA_RS12100	NA	1.16	1.96	2.13	1.66	1.75	1.88	2.57	2.66	2.47	1.47	1.63	1.87
MA_RS12110	NA	0.97	1.39	1.00	1.48	1.31	1.31	1.31	1.87	2.25	0.95	0.94	0.96
MA_RS12115	NA	0.72	0.87	1.01	1.41	1.13	1.66	1.29	1.56	1.89	1.19	0.73	0.88
MA_RS12125	NA	2.14	2.40	2.83	2.72	2.54	2.76	2.78	3.40	3.17	2.65	2.14	2.27
MA_RS12130	NA	1.62	2.22	1.79	2.75	1.98	2.78	2.24	2.97	3.34	1.85	1.76	2.00
MA_RS12135	NA	1.56	1.53	1.16	1.97	1.77	1.91	1.62	1.77	2.33	1.95	1.28	1.28
MA_RS12140	NA	1.60	2.07	1.53	2.29	2.11	2.14	2.02	2.94	3.23	2.23	2.00	2.29
MA_RS12145	NA	1.16	1.45	1.02	1.48	1.20	0.90	1.92	1.43	2.35	1.40	1.62	1.50
MA_RS12150	NA	1.79	1.54	1.19	2.08	1.85	1.80	1.96	2.48	2.72	1.34	1.53	1.66
MA_RS12155	NA	3.08	3.16	3.12	3.33	3.27	3.46	3.35	3.74	3.82	3.22	2.99	2.88
MA_RS12160	NA	3.15	3.50	3.42	3.38	3.08	3.29	2.64	3.97	4.55	3.42	2.87	2.93
MA_RS12165	NA	2.53	2.81	2.77	3.61	3.26	3.48	3.57	4.56	4.75	3.80	3.17	2.99
MA_RS12170	NA	3.07	3.35	3.25	3.01	2.87	3.30	2.88	3.65	4.11	2.84	2.69	2.91
MA_RS12175	NA	3.58	3.89	3.74	3.84	3.61	3.44	3.21	4.14	4.60	3.14	2.85	3.38
MA_RS12180	NA	3.42	3.76	3.57	3.92	3.69	3.91	3.99	4.44	4.74	3.72	3.46	3.61
MA_RS12185	NA	0.96	1.47	1.32	0.84	0.91	1.29	1.18	1.33	1.87	1.35	0.65	0.89
MA_RS12195	NA	1.26	1.08	1.09	1.13	1.29	1.19	1.40	1.79	1.15	1.30	0.75	1.05
MA_RS12200	NA	2.95	3.09	2.70	3.21	2.83	3.15	3.11	4.20	4.44	2.99	2.79	2.79
MA_RS12205	NA	0.92	0.53	0.56	0.59	0.50	1.13	0.96	1.88	1.74	1.53	1.37	1.25
MA_RS12210	NA	1.63	2.04	1.90	1.38	2.12	2.54	2.59	3.39	2.94	2.37	2.25	1.98
MA_RS12215	NA	1.47	1.45	1.52	1.44	1.31	1.39	1.84	2.68	2.78	1.86	1.59	1.88
MA_RS12225	NA	1.89	1.82	1.83	2.26	2.33	2.48	2.17	2.90	3.08	2.47	1.64	2.13
MA_RS12230	#N/A	0.68	0.64	1.14	1.35	1.14	1.22	1.51	1.34	1.55	1.37	0.65	0.70
MA_RS12235	NA	0.22	0.29	0.00	0.70	0.13	0.47	0.26	0.48	1.08	0.15	0.23	0.72
MA_RS12240	NA	0.48	0.99	0.60	0.78	0.62	0.40	1.29	0.75	0.87	0.98	0.32	0.70
MA_RS12245	NA	4.52	4.78	4.66	4.80	4.56	4.81	4.70	4.90	5.16	4.71	4.52	4.80
MA_RS12250	NA	5.39	5.64	5.56	5.74	5.44	5.77	5.64	5.73	5.98	5.73	5.55	5.81
MA_RS12255	brxL	3.67	3.80	3.65	4.30	3.84	4.19	4.08	4.45	4.55	4.16	3.79	3.89
MA_RS12260	pglZ	3.36	3.69	3.60	4.02	3.68	3.98	3.90	4.56	4.96	4.26	3.75	3.82
MA_RS12265	NA	1.14	1.26	1.34	1.65	1.17	0.97	1.22	1.79	1.71	1.21	0.86	1.36
MA_RS12270	NA	3.46	3.53	3.62	3.75	3.48	3.90	3.67	4.70	3.94	4.15	3.32	3.52
MA_RS12280	NA	2.02	2.21	1.91	2.59	2.43	2.61	2.41	2.68	3.09	1.85	2.19	2.15
MA_RS12285	NA	1.79	2.06	1.81	2.77	2.48	2.37	2.34	2.86	3.10	2.36	2.19	2.41
MA_RS12290	NA	2.50	2.52	2.28	2.69	2.43	2.86	2.79	3.17	3.26	2.76	2.64	2.63
MA_RS12295	NA	1.96	2.31	2.40	2.42	2.17	2.41	2.81	3.51	3.85	2.22	2.12	2.14
MA_RS12300	pglX	3.26	3.48	3.44	3.73	3.48	3.69	3.49	4.39	4.69	3.07	3.11	3.49
MA_RS12305	brxC	3.44	3.61	3.66	3.86	3.44	3.84	3.75	4.34	4.70	3.67	3.30	3.63
MA_RS12310	NA	2.58	2.52	2.19	3.11	2.08	2.62	2.78	3.27	3.83	2.68	2.81	2.66
MA_RS12315	#N/A	2.08	2.19	2.02	2.29	1.49	2.34	1.17	2.53	1.42	1.45	1.51	2.00
MA_RS12320	NA	3.75	3.90	3.79	4.13	3.98	4.17	3.82	4.58	4.82	4.06	3.68	3.60
MA_RS12325	NA	2.15	2.34	2.30	3.00	2.28	2.65	2.11	3.05	3.55	2.76	1.87	2.84
MA_RS12335	NA	0.25	0.21	0.23	0.06	0.13	0.14	0.18	0.28	0.40	0.14	0.34	0.18
MA_RS12340	NA	0.12	0.00	0.68	0.00	0.00	0.59	0.00	0.12	0.00	0.78	0.00	0.20
MA_RS12345	NA	2.33	2.10	1.85	2.46	2.31	1.98	2.14	2.54	2.96	2.15	2.34	2.08
MA_RS12350	NA	1.88	2.00	1.97	2.55	2.34	2.48	2.38	3.05	3.43	2.24	2.14	2.80
MA_RS12355	NA	2.53	2.38	2.41	2.94	2.82	2.78	2.77	2.99	3.43	2.53	2.43	2.43
MA_RS12360	NA	1.64	1.94	2.10	2.34	1.90	2.39	2.50	2.79	3.25	2.12	2.09	2.19
MA_RS12365	NA	0.86	0.86	0.97	1.10	0.87	0.72	0.56	1.16	1.54	1.03	0.76	1.07
MA_RS12370	#N/A	0.63	0.64	0.62	0.74	0.39	0.73	0.56	0.55	0.43	0.31	0.63	1.02
MA_RS12375	NA	0.50	0.51	0.32	0.46	0.53	0.48	0.72	0.54	1.54	0.91	0.72	0.23
MA_RS12380	NA	1.04	1.05	1.51	0.71	1.75	1.72	1.99	1.38	1.92	1.19	0.90	1.84
MA_RS12385	#N/A	5.02	5.09	5.04	5.03	5.04	4.73	5.36	3.81	3.74	5.33	5.23	4.43
MA_RS12390	NA	5.31	5.50	5.48	5.82	5.62	5.56	5.76	6.25	6.33	5.90	5.64	5.67
MA_RS12395	NA	6.33	6.69	6.66	7.10	6.76	6.97	6.82	8.14	8.37	7.59	6.95	6.70
MA_RS12400	NA	3.96	4.02	3.99	4.05	4.16	3.78	4.08	4.92	4.77	4.58	4.08	3.80
MA_RS12405	pap	3.99	4.07	4.01	4.39	4.05	4.42	4.27	4.82	5.05	4.06	3.90	4.06
MA_RS12410	NA	0.60	0.73	0.59	0.40	0.71	0.67	0.72	1.07	1.16	0.75	0.70	0.62
MA_RS12415	NA	1.90	2.10	1.51	2.48	1.86	1.68	1.66	2.19	2.43	1.96	1.38	1.93
MA_RS12420	NA	0.92	1.05	0.59	0.81	1.09	1.39	0.66	0.47	1.37	1.19	1.12	0.66
MA_RS12425	NA	0.83	0.36	1.46	1.80	1.51	1.20	1.71	1.92	2.43	1.38	1.34	2.08
MA_RS12430	NA	1.83	1.88	0.77	1.90	2.02	1.75	2.11	3.02	2.85	2.20	1.47	2.05
MA_RS12435	#N/A	2.78	2.56	2.89	2.75	2.61	3.08	2.72	2.21	3.30	3.25	3.22	2.93
MA_RS12445	NA	1.47	1.80	1.46	2.18	1.63	2.03	2.54	3.18	3.14	2.42	2.17	2.53
MA_RS12455	NA	3.51	3.61	3.57	3.62	3.80	3.56	4.02	4.19	4.40	3.88	3.28	3.92
MA_RS12460	NA	1.94	1.93	1.10	1.66	2.15	1.39	1.95	1.73	1.36	1.82	1.79	1.37
MA_RS12470	NA	2.76	3.15	3.02	3.35	3.38	3.06	3.50	3.37	3.48	3.35	2.97	3.19
MA_RS12475	NA	2.29	2.65	2.59	2.83	2.70	2.90	2.74	3.05	3.58	2.76	2.38	2.87
MA_RS12485	NA	2.65	2.48	2.34	2.70	2.72	2.63	2.90	3.63	4.03	3.09	2.77	2.84
MA_RS12490	NA	1.00	0.95	0.78	0.98	1.56	1.42	1.24	1.56	1.27	1.08	1.17	0.83
MA_RS12495	NA	1.25	1.07	1.82	1.75	1.73	1.74	1.98	1.26	1.54	1.65	2.27	1.73
MA_RS12500	NA	0.40	0.65	0.11	1.21	0.61	0.71	0.00	0.66	1.05	0.61	0.33	0.23
MA_RS12505	NA	1.41	1.76	1.67	1.60	1.50	1.85	1.48	1.79	2.16	1.43	1.36	1.29
MA_RS12510	NA	2.60	2.53	2.84	2.86	2.38	2.87	2.76	3.34	2.99	2.92	2.58	2.49
MA_RS12515	NA	0.62	0.27	0.00	0.19	0.06	0.20	0.77	0.51	0.56	1.32	0.78	0.35
MA_RS12520	NA	2.56	2.86	2.59	2.65	2.40	2.66	2.57	3.00	2.96	2.44	2.45	2.47
MA_RS12525	NA	3.37	3.46	3.56	3.47	3.26	3.31	3.46	3.51	4.00	3.39	3.35	3.07
MA_RS12530	NA	2.81	3.33	2.95	3.16	3.26	3.23	3.13	3.20	3.53	3.01	3.06	3.14
MA_RS12535	NA	0.92	1.25	0.83	1.32	0.77	1.81	1.08	1.91	2.19	1.32	1.03	1.36
MA_RS12540	NA	1.79	1.85	1.55	2.13	1.81	2.66	1.85	2.46	3.26	2.62	2.02	2.03
MA_RS12545	NA	1.64	1.70	1.87	2.09	1.79	2.34	2.02	2.34	2.73	2.19	1.84	1.81
MA_RS12550	NA	1.46	1.57	1.72	2.00	1.66	1.69	1.80	2.09	2.14	1.81	1.83	1.82
MA_RS12555	NA	0.54	0.46	0.57	1.11	0.60	0.42	0.89	1.77	1.90	1.77	1.81	1.27
MA_RS12560	NA	1.58	1.73	0.88	1.57	1.69	1.64	2.18	2.77	2.35	2.47	1.88	2.40
MA_RS12565	NA	1.73	2.15	1.39	2.00	2.14	2.22	2.65	3.22	3.26	2.60	2.27	1.94
MA_RS12570	NA	1.91	1.74	1.92	1.61	1.86	1.84	2.03	1.73	2.00	1.82	1.42	2.18
MA_RS12575	NA	2.74	3.10	2.60	3.29	3.04	3.17	3.30	3.39	3.39	3.11	2.87	2.86
MA_RS12580	NA	0.38	0.49	0.32	0.00	0.00	0.18	1.15	0.56	0.56	0.33	0.31	0.24
MA_RS12585	mtbB	0.72	1.22	1.20	0.24	0.58	0.77	1.01	1.06	1.25	0.91	0.54	0.61
MA_RS12595	NA	0.48	0.64	0.79	0.53	0.45	0.83	0.68	0.95	0.93	1.06	0.89	0.83
MA_RS12600	NA	3.81	3.77	3.76	3.93	3.75	4.17	3.77	4.15	4.35	3.70	3.82	3.71
MA_RS12605	NA	0.51	0.55	0.00	0.00	0.25	0.98	1.01	0.36	0.81	1.21	0.32	0.30
MA_RS12610	NA	3.91	4.12	4.25	3.96	3.91	4.17	4.51	4.37	4.41	4.06	3.66	4.04
MA_RS12620	NA	3.70	4.32	4.24	4.41	4.03	4.26	4.12	4.90	5.01	4.17	3.98	4.31
MA_RS12625	ilvS	6.18	6.46	6.31	6.69	6.32	6.54	6.53	6.61	6.87	6.40	6.23	6.40
MA_RS12630	NA	2.38	2.50	2.18	2.80	2.82	2.87	2.94	3.26	3.30	2.25	2.60	2.53
MA_RS12635	NA	1.04	0.87	1.18	0.84	1.45	1.50	1.17	1.49	1.76	1.26	1.15	1.51
MA_RS12640	NA	1.78	2.08	2.01	2.09	1.70	2.53	1.88	2.19	2.52	1.88	2.02	1.97
MA_RS12645	NA	2.17	2.03	1.92	2.74	2.07	2.62	1.93	3.31	3.14	2.10	1.97	2.10
MA_RS12650	NA	1.79	1.63	1.59	1.92	0.87	1.37	1.32	1.55	1.82	1.33	1.60	1.75
MA_RS12655	NA	1.73	1.85	1.90	1.98	1.62	2.25	2.00	2.27	2.23	1.93	1.55	1.89
MA_RS12660	NA	1.51	1.59	1.10	1.69	1.15	2.23	1.54	2.40	3.15	2.38	1.99	1.85
MA_RS12665	NA	1.12	1.85	1.22	2.06	2.43	2.54	2.46	2.20	2.85	1.75	1.88	2.32
MA_RS12670	NA	2.14	2.20	2.72	2.34	2.69	2.52	2.52	2.98	2.65	1.63	2.24	2.65
MA_RS12675	atpD	2.50	2.74	2.71	3.27	2.67	3.02	2.99	3.06	3.24	2.24	2.71	2.62
MA_RS12680	NA	1.03	1.32	0.63	0.21	1.62	1.16	0.61	2.18	2.34	1.43	0.92	1.34
MA_RS12685	NA	1.69	0.87	0.87	1.05	1.54	1.87	1.47	1.82	2.26	1.57	1.23	1.52
MA_RS12690	#N/A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS12695	NA	4.44	4.63	4.68	4.75	4.54	4.57	4.47	5.03	5.60	4.81	4.27	4.40
MA_RS12700	NA	3.31	3.89	3.87	4.19	3.58	4.21	3.87	4.44	4.99	4.12	3.81	3.96
MA_RS12705	NA	0.51	0.19	0.37	0.59	0.38	0.29	0.41	0.26	0.52	0.42	0.18	0.00
MA_RS12710	NA	1.59	1.58	2.24	1.48	1.40	1.98	2.17	2.93	2.90	1.93	2.62	1.99
MA_RS12715	NA	2.51	2.84	2.67	2.90	2.78	2.78	3.10	3.22	3.05	2.71	2.38	2.65
MA_RS12725	NA	4.29	4.51	4.46	4.69	4.52	4.71	4.67	4.92	5.07	4.52	4.38	4.47
MA_RS12730	NA	1.29	0.68	0.99	1.24	1.63	1.89	1.17	2.19	1.74	1.81	1.99	0.90
MA_RS12735	#N/A	0.38	0.65	0.00	0.09	0.00	0.00	0.00	1.20	0.84	0.09	0.00	1.09
MA_RS12740	NA	1.41	1.08	1.58	1.28	1.02	1.04	1.41	0.88	1.39	0.73	1.07	1.28
MA_RS12745	NA	1.71	1.60	1.53	2.01	1.90	2.49	1.97	2.60	2.71	2.23	2.08	1.76
MA_RS12750	NA	1.34	0.67	0.56	1.53	1.58	1.46	1.15	1.51	1.91	1.06	0.87	0.91
MA_RS12755	NA	1.95	2.40	2.54	2.52	2.24	2.11	2.01	2.79	2.59	2.19	1.85	2.26
MA_RS12760	NA	2.61	2.89	2.71	2.95	2.70	3.02	3.19	3.25	3.67	2.96	2.94	2.77
MA_RS12765	NA	2.93	3.15	3.14	3.43	3.24	3.44	3.51	3.99	4.20	3.62	3.35	3.46
MA_RS12770	NA	3.98	4.45	4.03	4.67	4.17	4.56	4.73	4.99	5.39	4.58	4.38	4.09
MA_RS12780	NA	1.17	1.23	1.18	1.47	1.01	1.25	1.31	1.75	2.15	1.34	1.18	1.28
MA_RS12785	NA	1.05	1.34	1.47	1.60	1.54	1.65	1.34	1.99	2.15	1.57	1.37	1.56
MA_RS12795	NA	1.87	1.76	1.69	1.75	1.93	1.83	2.00	2.37	2.50	2.28	1.90	2.36
MA_RS12800	NA	1.41	1.64	1.78	2.24	2.07	2.15	1.94	2.48	3.00	2.23	2.22	2.05
MA_RS12805	NA	2.29	2.37	2.05	3.03	2.55	2.82	2.38	2.76	3.35	2.77	2.50	2.49
MA_RS12810	NA	1.55	2.20	2.10	2.20	2.14	2.60	2.52	3.15	3.55	2.64	2.42	2.63
MA_RS12815	NA	0.83	1.14	1.13	1.92	1.37	1.68	2.07	2.24	2.78	2.30	1.93	1.47
MA_RS12825	NA	1.55	1.74	1.04	1.19	0.57	1.18	2.26	1.37	2.57	1.62	1.25	1.52
MA_RS12830	NA	0.52	0.53	0.62	0.42	0.50	0.42	0.57	0.54	0.74	0.96	0.35	0.30
MA_RS12835	NA	0.54	0.30	0.12	0.76	0.28	0.00	0.28	0.53	0.43	0.24	0.15	0.19
MA_RS12840	NA	0.51	0.72	0.58	0.81	0.22	0.83	0.45	0.91	0.53	0.49	0.76	0.53
MA_RS12850	NA	2.05	2.10	1.75	2.39	2.21	2.51	2.24	2.18	2.19	2.36	2.47	2.49
MA_RS12855	NA	2.25	2.23	2.32	2.63	2.47	2.74	2.93	2.71	2.83	2.79	2.71	2.90
MA_RS12860	NA	0.20	0.40	0.00	0.47	0.41	0.98	0.44	0.99	0.55	0.61	0.35	0.62

MA_RS12865	NA	0.19	0.02	0.00	0.23	0.10	0.24	0.08	0.38	0.25	0.49	0.13	0.61
MA_RS12870	NA	1.60	1.60	1.72	1.98	1.95	2.26	2.14	2.80	2.94	2.42	2.36	1.98
MA_RS12880	NA	1.47	1.80	1.54	1.85	1.76	2.13	1.85	2.54	2.43	2.15	1.52	1.49
MA_RS12885	NA	1.21	1.14	1.23	1.79	1.27	1.59	1.40	1.80	2.15	1.71	1.47	1.52
MA_RS12890	NA	3.08	3.02	2.64	3.34	3.39	3.49	3.27	3.45	3.25	3.33	3.29	3.52
MA_RS12895	NA	1.91	1.95	2.11	2.59	2.16	2.54	2.09	2.34	2.75	2.51	2.38	2.83
MA_RS12900	NA	1.57	1.85	2.21	1.98	2.08	2.29	2.21	2.39	2.61	2.86	1.97	2.12
MA_RS12905	NA	2.60	2.99	2.63	3.36	2.98	3.07	3.09	3.25	3.64	3.50	3.33	3.16
MA_RS12910	NA	0.77	0.74	1.06	1.37	0.82	1.69	1.56	1.25	1.11	1.14	1.25	1.26
MA_RS12915	NA	1.76	1.46	1.86	2.23	1.71	1.97	1.69	1.66	2.02	2.26	2.16	1.88
MA_RS12920	NA	2.06	2.27	2.24	2.24	1.74	2.53	2.22	2.05	1.97	2.29	2.35	2.64
MA_RS12925	NA	1.58	1.61	1.58	2.02	1.33	1.83	1.83	1.83	1.92	2.20	2.15	2.11
MA_RS12935	NA	1.36	1.34	0.36	0.30	0.95	1.02	0.74	1.50	0.67	1.01	1.06	1.24
MA_RS12940	NA	1.64	1.45	1.15	1.89	1.87	1.28	1.89	2.55	2.26	1.70	1.99	1.64
MA_RS12945	NA	1.18	0.97	1.24	0.96	1.01	0.55	0.79	1.69	1.71	1.24	1.32	1.18
MA_RS12950	NA	0.46	0.38	0.57	0.47	0.57	0.15	0.60	0.67	0.00	0.50	0.66	0.70
MA_RS12955	NA	0.41	0.77	0.78	0.36	0.71	0.81	0.63	1.10	0.79	0.41	0.42	0.43
MA_RS12965	NA	2.37	1.89	1.86	2.51	2.32	2.45	2.15	3.56	3.50	2.93	2.58	2.22
MA_RS12970	NA	0.74	0.73	0.70	0.70	0.55	1.12	0.79	1.78	1.47	0.82	0.74	0.89
MA_RS12975	NA	3.97	4.27	4.09	4.70	4.27	4.48	4.74	5.33	5.66	5.00	4.22	4.49
MA_RS12980	NA	3.55	3.56	3.95	4.18	3.81	4.07	3.89	4.01	4.50	4.06	3.83	4.06
MA_RS12985	NA	3.05	3.04	3.00	3.59	3.13	3.70	3.19	3.13	3.48	3.50	3.27	3.32
MA_RS12990	NA	2.71	3.05	3.29	3.46	3.16	3.21	3.38	3.28	3.77	3.34	3.01	3.10
MA_RS12995	NA	1.61	1.37	1.64	1.97	1.36	1.72	1.73	2.25	2.47	1.18	1.53	1.78
MA_RS13000	NA	1.56	1.81	1.11	1.52	1.67	2.08	1.79	2.43	2.97	1.72	1.25	1.70
MA_RS13005	NA	1.92	2.04	1.75	2.57	2.29	2.45	2.08	2.46	2.37	2.09	2.15	2.45
MA_RS13010	NA	1.72	2.11	1.81	1.79	1.75	2.21	1.21	2.02	2.83	2.02	1.71	1.74
MA_RS13015	NA	0.89	1.16	1.15	1.18	1.32	1.55	1.30	1.59	1.49	1.33	1.31	1.42
MA_RS13020	NA	0.84	1.31	1.61	1.12	0.58	1.13	1.10	1.87	1.05	1.43	1.32	1.19
MA_RS13025	NA	0.86	0.51	0.66	0.59	0.93	1.47	1.77	0.96	0.38	1.16	1.84	0.69
MA_RS13030	NA	1.07	1.23	1.39	1.61	1.27	1.44	1.42	1.65	1.85	1.47	1.86	1.61
MA_RS13035	NA	1.00	1.12	1.23	1.35	1.13	1.19	1.15	1.71	1.75	1.36	1.19	1.09
MA_RS13040	NA	3.15	3.33	3.25	3.70	3.38	3.13	3.43	3.56	4.14	4.02	3.49	3.76
MA_RS13045	NA	1.94	1.99	2.24	1.92	1.79	2.00	2.49	1.54	1.94	1.87	1.44	1.76
MA_RS13050	NA	5.67	5.92	5.88	6.28	5.86	6.16	6.25	6.34	6.56	6.39	5.98	6.21
MA_RS13055	#N/A	0.87	0.82	0.94	1.06	0.75	1.16	0.96	0.99	1.30	1.72	1.15	1.20
MA_RS13060	NA	3.12	3.43	3.01	3.86	3.36	3.32	3.39	3.91	4.10	4.01	3.15	3.42
MA_RS13065	NA	4.17	4.41	4.36	4.43	4.12	4.45	4.69	4.65	4.83	4.25	4.29	4.29
MA_RS13070	NA	3.70	3.83	3.50	3.99	3.69	3.89	3.95	4.59	4.82	4.23	3.87	3.96
MA_RS13075	NA	0.55	0.56	0.75	0.85	0.55	0.46	0.91	0.91	1.35	0.70	0.77	0.74
MA_RS13080	#N/A	0.45	0.30	0.57	0.74	0.55	0.46	0.37	1.17	1.43	0.67	0.20	0.84
MA_RS13085	NA	2.68	2.85	2.90	3.08	2.94	3.10	3.13	2.97	3.22	2.80	2.59	3.07
MA_RS13090	NA	4.23	4.23	4.36	4.46	4.32	4.26	4.47	4.90	4.93	4.64	4.26	4.30
MA_RS13095	NA	3.35	3.64	3.72	3.87	3.60	3.49	3.49	4.43	4.91	4.25	3.52	3.42
MA_RS13100	NA	4.36	4.43	4.40	4.62	4.57	4.52	4.29	4.62	4.69	4.82	4.43	4.37
MA_RS13105	NA	3.12	3.36	2.95	3.63	3.32	3.80	3.52	4.63	4.57	4.12	3.69	3.62
MA_RS13115	#N/A	0.41	0.02	0.25	0.18	0.00	0.59	0.23	0.31	0.30	0.72	0.23	0.00
MA_RS13120	NA	1.19	1.35	0.97	0.99	1.03	1.20	1.36	1.94	1.70	1.64	1.06	1.41
MA_RS13125	NA	0.28	0.13	0.44	0.72	0.60	0.27	0.22	0.57	0.52	0.63	0.58	0.34
MA_RS13130	NA	0.63	0.80	0.61	0.78	0.83	0.61	0.80	1.12	1.45	0.77	0.68	0.68
MA_RS13135	NA	1.06	1.13	1.73	1.04	0.94	1.59	1.81	2.67	1.90	1.81	1.39	1.44
MA_RS13145	NA	1.92	1.25	1.27	1.50	1.37	1.85	1.53	2.53	2.46	2.04	1.26	1.83
MA_RS13150	NA	1.37	1.51	1.43	1.45	1.81	1.76	1.41	2.37	2.40	1.98	1.57	2.26
MA_RS13155	NA	1.92	1.74	1.66	1.90	2.32	1.95	2.09	3.30	3.53	2.93	2.24	2.31
MA_RS13160	NA	1.35	1.40	1.49	2.14	1.56	1.41	1.45	2.17	2.76	1.51	1.50	1.48
MA_RS13165	NA	1.65	1.42	0.66	1.39	1.44	1.38	1.36	2.09	2.04	1.17	1.26	0.64
MA_RS13170	NA	1.74	1.82	1.73	1.85	1.97	2.06	1.84	2.01	2.04	1.78	1.84	1.94
MA_RS13175	pncB	4.11	4.29	4.04	4.48	4.02	4.09	4.50	4.85	5.31	4.17	4.07	4.23
MA_RS13180	NA	3.05	3.39	3.44	2.99	2.94	3.14	3.14	3.80	4.13	3.04	3.07	3.59
MA_RS13185	NA	1.97	2.25	1.96	2.17	1.98	2.29	2.01	2.72	3.29	2.07	1.93	2.07
MA_RS13190	NA	2.10	2.04	2.48	2.87	2.80	2.92	2.83	3.20	2.71	3.40	2.23	2.24
MA_RS13195	NA	0.33	0.11	0.80	0.95	0.40	0.65	0.62	1.28	1.34	0.75	1.11	0.28
MA_RS13200	NA	0.68	0.48	0.56	0.93	0.72	0.85	0.84	1.21	1.41	1.02	0.75	0.66
MA_RS13205	#N/A	0.91	0.50	0.25	0.44	0.43	0.80	1.35	1.05	0.93	0.09	0.66	0.98
MA_RS13210	NA	2.60	3.01	2.51	3.15	2.72	2.78	3.01	3.39	3.37	2.98	2.62	2.72
MA_RS13215	NA	4.09	4.35	4.03	4.44	4.16	4.28	4.10	4.76	4.82	4.67	4.37	4.29
MA_RS13220	NA	2.10	1.96	1.45	2.13	1.82	2.12	2.09	2.22	1.82	2.11	2.26	2.11
MA_RS13225	NA	1.48	1.87	1.48	2.36	1.90	1.73	1.73	2.63	1.82	2.17	2.01	1.46
MA_RS13230	NA	2.20	2.46	2.20	2.70	2.64	3.02	2.59	3.13	3.94	3.08	2.79	2.61
MA_RS13235	NA	5.52	5.74	5.61	5.98	5.79	5.92	6.08	6.66	6.60	6.25	5.76	5.84
MA_RS13240	NA	5.21	5.50	5.25	5.86	5.46	5.85	5.68	6.44	6.64	6.02	5.55	5.67
MA_RS13245	NA	0.48	0.48	0.91	0.69	0.43	0.62	1.45	2.25	2.33	1.65	1.95	1.75
MA_RS13250	NA	1.23	1.72	0.84	1.89	1.36	1.47	1.33	1.42	1.57	1.90	1.33	1.38
MA_RS13255	NA	2.24	2.56	2.16	3.02	2.47	2.69	2.83	3.08	3.33	2.76	2.47	2.56
MA_RS13260	NA	1.97	2.20	2.37	2.51	1.99	2.49	2.38	2.74	2.55	2.99	2.19	2.27
MA_RS13265	NA	1.54	1.67	1.93	1.47	1.37	1.84	1.66	1.88	2.34	2.11	1.23	1.50
MA_RS13270	NA	1.77	1.87	2.06	2.38	2.11	2.48	2.50	2.42	2.46	2.47	2.13	1.99
MA_RS13275	NA	2.01	2.00	2.32	2.28	2.18	1.98	1.93	2.08	3.00	1.81	1.97	1.87
MA_RS13280	NA	3.78	3.83	3.99	3.86	3.53	3.68	3.66	4.95	4.95	3.81	3.46	3.53
MA_RS13285	NA	4.34	4.54	4.50	4.64	4.38	4.66	4.68	5.21	5.53	4.51	4.32	4.43
MA_RS13290	NA	1.02	1.02	1.30	1.44	1.03	1.30	1.67	2.53	2.39	1.92	1.40	1.62
MA_RS13295	NA	4.38	4.65	4.34	4.98	4.58	4.95	5.31	5.81	5.88	5.02	4.77	4.63
MA_RS13300	NA	5.28	5.51	5.29	5.97	5.55	5.89	5.73	6.51	6.67	5.99	5.68	5.51
MA_RS13305	NA	3.28	3.39	3.28	3.85	3.36	3.77	3.30	4.11	4.31	3.66	3.34	3.22
MA_RS13310	NA	4.56	4.45	4.45	4.79	4.82	4.95	5.05	5.65	5.59	5.18	4.75	4.56
MA_RS13315	NA	5.43	5.57	5.57	3.14	3.44	3.01	5.52	6.46	6.32	5.59	5.40	5.49
MA_RS13325	NA	2.99	2.87	2.62	3.02	3.22	3.21	3.32	3.63	3.59	3.26	2.91	2.99
MA_RS13335	NA	2.93	2.66	2.76	3.22	2.99	3.13	3.50	3.33	3.65	3.16	3.00	3.30
MA_RS13340	NA	2.29	2.47	2.30	3.05	2.69	2.93	2.95	3.13	3.42	3.00	2.66	2.53
MA_RS13345	NA	3.73	4.08	3.80	4.22	4.04	4.13	4.09	4.92	5.15	4.44	4.12	3.88
MA_RS13350	NA	0.84	0.91	1.24	0.95	1.18	1.13	1.03	1.86	2.04	1.34	1.30	1.05
MA_RS13355	NA	3.26	3.20	3.21	3.50	3.55	3.70	3.65	4.08	4.22	3.74	3.52	3.45
MA_RS13365	NA	2.32	2.28	2.11	2.78	2.45	2.94	2.51	2.79	3.43	2.70	2.46	2.68
MA_RS13370	engB	3.10	3.39	2.97	3.68	3.38	3.71	4.00	4.30	4.37	3.68	3.70	3.96
MA_RS13375	NA	4.50	4.81	4.71	5.04	4.65	4.93	4.79	5.28	5.59	4.84	4.59	4.76
MA_RS13380	NA	4.98	5.23	5.14	5.63	5.26	5.43	5.39	5.99	6.32	5.63	5.18	5.36
MA_RS13385	NA	5.18	5.28	5.17	5.74	5.41	5.74	5.97	6.41	6.70	6.04	5.52	5.54
MA_RS13390	NA	4.18	4.29	4.52	4.32	4.05	4.38	4.45	4.68	4.78	4.41	4.19	4.32
MA_RS13395	NA	3.91	4.22	4.04	4.47	4.10	4.30	4.50	5.30	5.57	4.74	3.86	4.25
MA_RS13400	NA	4.13	3.72	4.33	4.30	4.37	3.89	4.03	4.48	4.44	4.16	3.65	3.74
MA_RS13405	NA	0.61	0.72	0.41	1.20	0.91	0.84	1.11	1.53	0.95	0.99	0.67	1.21
MA_RS13410	NA	0.56	0.56	0.45	0.52	0.51	0.50	0.17	0.68	0.81	0.45	0.64	0.42
MA_RS13415	istB	0.03	0.09	0.00	0.16	0.00	0.14	0.05	0.25	0.35	0.02	0.00	0.07
MA_RS13420	istA	0.18	0.20	0.28	0.43	0.43	0.35	0.30	0.53	0.52	0.49	0.35	0.21
MA_RS13430	NA	0.30	0.84	0.83	0.69	0.62	0.29	0.83	0.86	0.35	0.84	0.39	1.02
MA_RS13435	NA	1.86	1.82	1.71	1.79	1.75	1.76	2.08	2.93	2.83	2.15	1.51	2.03
MA_RS13440	NA	0.57	0.34	0.49	0.61	0.15	0.22	0.25	0.99	0.00	1.27	0.24	0.62
MA_RS13445	NA	1.08	1.29	1.13	1.52	1.40	1.43	1.62	1.77	2.01	1.28	1.38	1.54
MA_RS13450	NA	0.46	0.75	1.75	1.23	0.65	0.83	1.19	0.89	0.52	0.82	0.54	1.57
MA_RS13455	NA	0.56	1.02	0.72	0.72	1.07	1.07	1.40	1.67	1.27	0.93	0.88	0.99
MA_RS13460	NA	1.28	1.18	1.48	1.58	1.57	1.57	1.37	1.91	2.28	1.81	1.32	1.68
MA_RS13465	NA	0.06	0.17	0.51	0.00	0.24	0.64	0.00	0.50	0.88	0.68	0.26	0.71
MA_RS13470	NA	0.56	0.24	0.00	0.04	1.18	0.45	0.00	0.08	0.24	0.36	0.00	0.70
MA_RS13475	NA	0.62	0.30	0.01	0.37	0.54	0.29	0.00	0.96	1.12	0.35	0.34	0.63
MA_RS13480	NA	0.32	0.55	0.34	0.73	0.43	0.78	0.49	1.16	0.86	0.79	0.68	0.56
MA_RS13485	NA	0.72	0.30	0.74	0.39	0.22	1.17	0.27	1.31	1.33	0.87	0.93	0.72
MA_RS13490	NA	0.45	0.18	0.17	0.14	0.85	0.72	0.23	1.04	0.95	0.46	0.05	0.51
MA_RS13495	NA	0.03	0.26	0.18	0.01	0.42	0.01	0.00	0.00	0.00	0.26	0.77	0.14
MA_RS13500	NA	0.52	0.65	0.00	0.64	0.47	0.51	0.32	1.23	0.65	0.64	0.53	0.87
MA_RS13505	NA	0.77	0.27	0.29	0.57	0.55	1.11	0.92	1.30	1.14	0.81	0.27	0.90
MA_RS13515	NA	1.15	0.99	1.22	1.62	1.36	1.74	1.74	0.78	1.05	2.39	1.33	1.53
MA_RS13520	NA	0.12	0.37	0.45	0.00	0.00	0.52	0.67	0.23	0.07	0.22	0.12	0.10
MA_RS13525	#N/A	0.77	0.86	1.08	1.82	1.30	1.54	1.76	1.66	1.75	1.80	1.33	1.48
MA_RS13530	NA	3.49	3.49	3.12	3.96	3.56	3.87	3.58	4.24	4.89	4.30	3.80	3.70
MA_RS13535	NA	1.30	1.25	0.98	1.32	1.30	1.34	1.56	2.38	2.37	1.64	1.33	1.12
MA_RS13540	NA	1.59	1.67	1.72	1.73	1.75	1.78	1.71	3.04	2.92	2.05	1.82	1.69
MA_RS13545	NA	4.76	4.66	4.90	4.86	4.88	4.78	4.48	5.17	5.42	5.07	4.71	4.59
MA_RS13550	NA	4.23	4.23	4.23	4.45	4.22	4.25	4.62	5.54	5.80	4.27	4.27	4.08
MA_RS13555	NA	2.57	2.95	2.98	2.94	2.75	2.98	2.75	3.85	3.60	2.99	2.88	2.80
MA_RS13560	NA	0.27	0.28	0.25	0.35	0.32	0.29	0.47	0.43	0.70	0.54	0.12	0.54
MA_RS13565	NA	0.00	0.21	0.67	0.34	0.12	0.46	0.25	0.00	0.30	0.15	0.15	0.23
MA_RS13570	NA	0.59	0.45	0.00	0.11	0.37	0.58	0.26	0.26	0.20	0.00	0.34	0.31
MA_RS13575	NA	0.00	0.00	0.37	0.23	0.23	0.70	0.42	0.00	1.11	0.24	0.00	0.28
MA_RS13580	NA	0.00	0.51	0.62	0.40	0.39	0.63	0.40	0.00	0.44	0.58	0.00	0.00
MA_RS13585	NA	0.03	0.00	0.00	0.59	0.76	0.00	0.33	0.33	0.00	0.04	0.32	0.00
MA_RS13590	NA	0.00	0.50	0.00	1.09	0.00	0.44	0.63	0.00	0.00	0.49	0.70	0.00
MA_RS13595	NA	3.46	3.00	3.32	2.74	3.39	3.34	3.83	4.53	4.57	3.46	3.75	3.49
MA_RS13600	NA	3.14	2.49	2.54	2.64	2.79	2.92	2.97	4.08	4.04	3.26	3.37	2.83
MA_RS13605	NA	0.20	1.08	0.00	0.66	1.33	1.22	0.35	1.52	2.01	1.22	0.52	1.17
MA_RS13615	NA	0.42	0.57	0.17	0.32	0.76	0.79	0.50	0.98	1.18	0.62	0.53	0.25
MA_RS13625	NA	6.51	6.59	6.49	6.67	6.39	6.49	6.57	7.01	6.83	6.40	6.27	6.46
MA_RS13630	NA	1.17	0.85	0.64	0.56	1.55	1.96	2.18	1.42	1.46	0.93	1.83	1.80
MA_RS13635	NA	0.72	1.28	0.73	0.95	1.29	1.59	1.82	2.09	1.43	1.87	1.53	1.98

MA_RS13640	NA	1.27	1.55	0.83	1.54	1.68	1.39	1.58	1.25	2.22	1.81	1.50	1.25
MA_RS13645	NA	0.46	0.58	0.49	1.21	0.60	0.62	0.89	1.58	0.82	0.64	1.19	0.97
MA_RS13650	NA	0.50	0.24	1.02	0.71	0.67	1.63	1.17	1.12	0.89	0.90	0.61	0.65
MA_RS13655	NA	0.56	0.81	0.97	1.47	0.93	1.06	1.36	1.48	1.40	1.44	1.47	1.13
MA_RS13660	NA	3.45	2.79	3.17	3.59	3.20	3.39	3.86	3.77	3.37	3.72	3.51	3.53
MA_RS13665	NA	1.56	1.86	1.96	1.66	2.11	2.16	1.71	2.90	3.03	2.54	1.91	1.93
MA_RS13670	#N/A	1.35	1.33	1.40	1.19	1.30	1.74	1.85	2.57	2.29	1.33	1.46	1.68
MA_RS13675	NA	0.72	0.66	0.89	0.69	0.50	0.93	0.61	1.56	1.30	0.94	0.67	0.84
MA_RS13680	NA	1.20	0.59	0.61	0.84	0.52	1.31	0.35	0.98	0.80	0.52	1.03	0.50
MA_RS13685	NA	5.33	5.52	5.56	5.55	5.42	5.43	5.75	6.48	6.36	5.70	5.34	5.32
MA_RS13690	NA	1.19	1.16	1.31	1.50	1.42	1.32	1.36	1.39	1.80	1.48	1.39	1.23
MA_RS13695	NA	1.49	1.55	1.74	1.61	1.78	1.81	2.13	2.05	2.27	2.02	1.92	1.80
MA_RS13700	NA	1.83	2.30	1.93	2.55	2.54	2.46	2.41	2.39	2.74	2.09	2.01	2.12
MA_RS13705	NA	1.38	1.90	1.89	1.78	1.83	2.38	1.58	2.07	1.91	1.79	1.06	1.61
MA_RS13710	NA	0.85	1.11	1.30	1.19	1.36	1.32	1.27	1.26	1.50	0.25	0.51	0.74
MA_RS13715	NA	0.63	0.79	0.56	0.67	0.50	0.83	1.23	1.42	1.22	0.64	0.95	0.94
MA_RS13720	NA	0.15	0.13	0.10	0.13	0.11	0.16	0.15	0.21	0.24	0.11	0.14	0.17
MA_RS13725	NA	0.72	0.85	0.74	0.93	0.84	0.90	0.73	1.43	1.33	1.17	0.57	1.00
MA_RS13730	NA	2.08	1.61	2.25	2.11	2.16	1.68	1.81	1.64	2.16	1.56	1.20	2.30
MA_RS13740	NA	0.93	0.64	0.73	0.85	1.02	1.07	0.24	0.41	0.69	1.36	0.58	0.77
MA_RS13745	NA	0.21	0.78	0.37	0.13	0.35	0.90	0.85	0.61	0.28	0.75	0.53	0.00
MA_RS13750	NA	0.74	0.46	0.20	0.36	0.39	0.00	0.46	0.59	0.98	0.31	0.00	0.00
MA_RS13755	NA	0.00	0.18	0.32	0.00	0.00	0.00	0.23	0.30	0.32	0.16	0.00	0.13
MA_RS13765	NA	0.96	1.62	1.50	1.56	1.83	1.47	1.43	2.14	1.44	1.64	1.75	1.27
MA_RS13770	NA	1.56	1.79	1.81	1.87	1.73	1.98	1.54	1.70	1.94	1.94	1.87	1.98
MA_RS13775	NA	1.08	1.22	0.91	1.66	1.57	1.50	1.51	1.45	1.74	1.31	1.62	1.60
MA_RS13780	NA	0.48	0.45	0.41	1.25	1.05	1.15	0.93	0.72	1.15	0.61	1.27	1.10
MA_RS13785	NA	1.40	1.75	1.69	2.45	2.20	2.39	1.87	2.88	2.47	2.49	1.75	2.01
MA_RS13795	NA	0.90	0.93	1.10	1.11	1.46	1.31	0.98	1.57	1.76	1.42	1.51	1.46
MA_RS13800	NA	0.91	1.10	0.97	1.12	1.11	1.13	0.97	1.22	1.49	1.20	0.99	0.99
MA_RS13805	NA	0.78	0.82	1.05	1.53	1.66	1.46	1.69	1.27	1.66	1.44	1.08	1.46
MA_RS13810	NA	3.23	3.29	3.50	3.73	3.63	3.91	3.61	4.10	4.52	4.05	3.39	3.81
MA_RS13815	NA	4.02	4.05	4.11	4.47	4.25	4.16	4.40	4.17	4.17	4.23	4.04	4.21
MA_RS13820	NA	1.60	1.38	1.89	1.84	1.78	2.04	1.89	2.30	3.03	1.72	1.89	1.48
MA_RS13825	NA	2.24	2.35	2.56	2.69	2.81	2.82	2.94	2.42	3.28	1.95	2.31	1.91
MA_RS13840	NA	0.57	1.10	0.78	0.84	0.97	0.74	0.43	0.96	1.46	0.79	0.83	0.92
MA_RS13845	NA	0.00	0.00	0.00	0.00	0.87	0.00	0.00	0.00	1.18	0.77	0.00	0.98
MA_RS13850	NA	0.08	0.45	0.00	0.53	0.81	0.44	0.11	0.24	0.98	0.00	0.27	0.23
MA_RS13855	NA	1.53	1.10	1.12	1.38	0.37	1.48	1.77	2.34	0.85	1.21	1.41	1.62
MA_RS13860	NA	0.79	0.89	1.48	0.89	1.01	0.65	0.00	1.50	1.32	1.08	1.82	1.13
MA_RS13875	NA	0.46	1.05	1.20	1.23	0.89	1.23	1.25	1.22	0.92	1.01	0.76	0.87
MA_RS13880	#N/A	0.30	0.13	0.50	0.36	0.16	0.23	0.36	0.47	0.18	0.64	0.00	0.27
MA_RS13885	NA	2.78	3.12	3.01	3.30	2.88	3.11	3.28	3.94	3.80	2.94	2.73	2.74
MA_RS13890	NA	3.42	2.85	3.11	3.71	3.16	3.51	3.37	4.17	4.18	3.33	3.32	3.22
MA_RS13895	glnM	1.58	1.77	1.92	2.34	1.98	2.41	2.29	2.64	2.53	2.14	1.86	2.21
MA_RS13900	NA	1.16	1.21	1.09	1.93	1.69	1.21	1.62	1.93	2.15	1.78	1.53	1.33
MA_RS13905	ppsA	2.17	2.13	2.05	2.33	2.07	2.37	2.28	2.64	2.74	2.08	1.96	2.24
MA_RS13920	pgk	2.20	2.58	2.23	3.08	2.33	2.70	2.77	3.18	3.62	3.06	2.58	2.42
MA_RS13925	NA	1.27	1.37	1.60	1.43	1.27	1.35	1.66	1.96	2.14	1.70	1.19	1.44
MA_RS13930	gpmI	1.41	1.56	1.35	1.98	1.77	1.83	1.83	2.09	2.27	2.06	1.78	1.94
MA_RS13935	NA	0.27	0.44	0.22	0.65	0.25	0.12	1.11	0.31	0.88	0.54	0.85	0.50
MA_RS13940	NA	2.73	3.07	2.82	3.19	2.99	3.24	2.91	3.17	3.35	3.20	3.04	3.21
MA_RS13950	NA	3.63	3.70	3.50	4.14	3.96	4.27	4.36	4.84	4.51	4.49	3.98	4.26
MA_RS13955	NA	2.59	2.83	2.73	3.10	2.74	2.94	2.99	3.23	3.88	2.75	2.70	2.87
MA_RS13960	NA	0.49	1.09	0.34	0.91	1.48	0.65	0.37	0.74	0.91	1.00	1.10	0.64
MA_RS13965	NA	1.40	1.33	1.18	1.46	1.30	1.81	1.54	2.20	2.40	1.69	1.82	1.84
MA_RS13970	NA	3.24	3.44	3.32	3.75	3.55	3.63	3.66	4.33	4.62	3.86	3.62	3.59
MA_RS13975	NA	1.79	2.19	1.95	2.41	2.21	2.34	2.23	3.28	3.11	2.50	1.91	2.23
MA_RS13985	NA	0.16	0.63	0.34	0.24	0.43	0.47	0.44	1.37	1.15	0.27	0.15	0.00
MA_RS13995	NA	1.03	1.02	1.53	1.67	1.37	1.27	1.59	2.17	2.23	1.44	1.65	1.32
MA_RS14000	NA	1.81	2.29	2.35	2.82	2.50	2.66	2.81	3.69	3.15	2.70	2.23	2.88
MA_RS14010	NA	0.23	0.00	0.25	0.00	0.28	0.31	0.00	0.33	0.24	0.18	0.00	0.52
MA_RS14015	NA	1.04	0.95	0.87	1.53	1.07	1.64	0.92	1.31	1.82	1.43	1.60	1.67
MA_RS14020	NA	0.92	0.52	0.22	0.59	1.05	1.00	1.08	0.92	1.53	1.11	0.82	1.07
MA_RS14025	NA	1.66	1.30	1.07	1.85	1.17	1.34	1.89	1.67	1.97	1.87	1.42	1.13
MA_RS14030	NA	1.18	1.59	1.68	2.16	2.43	2.50	2.64	2.06	2.30	2.48	1.48	2.32
MA_RS14035	NA	0.72	0.77	0.57	0.84	1.12	0.91	1.15	1.34	1.13	0.97	0.88	1.18
MA_RS14040	NA	1.76	1.61	1.30	2.19	1.85	1.85	1.94	2.35	2.62	1.75	1.46	1.90
MA_RS14045	NA	1.24	1.27	1.42	1.54	1.04	1.51	0.94	1.12	1.71	1.36	0.85	1.16
MA_RS14050	NA	0.70	1.02	1.02	1.08	1.00	0.96	1.47	1.13	0.70	0.86	0.50	0.62
MA_RS14060	ppcA	4.41	4.45	4.38	5.57	4.99	5.30	5.74	4.74	5.13	5.86	5.25	5.19
MA_RS14070	NA	1.78	1.37	1.69	2.10	2.09	1.81	1.38	2.36	2.47	1.94	1.64	1.35
MA_RS14075	NA	0.23	1.56	1.20	0.40	1.50	0.81	1.99	2.11	3.00	0.53	1.06	0.66
MA_RS14080	NA	3.06	3.14	3.14	3.41	3.20	3.22	3.44	3.58	3.75	3.52	3.32	3.39
MA_RS14085	NA	1.04	1.29	1.05	1.40	1.58	1.11	1.06	1.33	1.82	1.44	0.66	1.11
MA_RS14095	NA	0.17	0.15	0.02	0.14	0.17	0.38	0.47	0.47	0.60	0.31	0.43	0.38
MA_RS14100	mprF	1.51	1.65	1.66	1.87	1.91	1.93	1.94	2.46	2.33	1.75	1.69	1.67
MA_RS14105	NA	2.25	2.38	2.43	2.12	2.32	2.93	2.67	2.87	3.02	2.45	2.29	2.27
MA_RS14120	NA	1.10	0.93	1.09	0.73	1.07	1.15	1.16	2.12	2.24	1.46	0.88	0.73
MA_RS14125	NA	0.71	0.00	0.06	0.63	0.54	1.13	1.20	0.32	0.11	0.83	1.44	0.41
MA_RS14130	NA	1.53	2.02	1.73	2.25	1.87	1.89	1.70	2.69	3.01	2.38	2.01	1.78
MA_RS14135	NA	0.34	0.37	0.15	0.36	0.27	0.65	0.48	0.56	0.28	0.28	0.35	0.67
MA_RS14155	NA	2.99	2.94	2.87	3.28	2.87	3.56	2.57	3.67	4.27	3.46	3.13	2.44
MA_RS14160	NA	1.31	1.50	1.85	1.81	2.10	2.40	1.86	2.41	2.38	1.92	1.70	1.62
MA_RS14165	NA	1.71	1.91	1.98	2.17	2.05	1.97	2.01	2.86	3.17	2.42	2.06	1.94
MA_RS14170	NA	2.90	3.06	3.25	3.35	3.26	3.02	3.21	3.14	4.16	3.44	2.97	3.13
MA_RS14175	NA	2.06	1.98	1.93	2.17	2.12	1.82	1.29	2.74	2.64	2.68	1.81	1.80
MA_RS14180	NA	3.60	3.58	3.93	4.32	3.89	4.07	4.21	4.87	5.29	4.23	3.94	3.81
MA_RS14185	NA	3.05	3.36	3.29	3.73	3.32	3.68	3.65	4.54	4.81	3.17	3.07	3.44
MA_RS14190	NA	2.23	2.20	2.39	2.21	2.17	2.52	2.57	3.26	3.71	1.72	2.02	2.05
MA_RS14195	NA	2.16	2.13	2.26	2.56	2.25	2.41	2.13	3.50	3.78	2.12	2.28	2.00
MA_RS14200	NA	0.63	1.05	0.68	0.50	0.86	0.46	0.69	0.81	1.88	0.25	0.95	0.99
MA_RS14205	NA	7.43	7.73	7.70	7.88	7.65	7.86	7.90	8.02	8.33	7.39	7.48	7.72
MA_RS14210	NA	7.96	8.27	8.06	8.52	8.17	8.39	8.35	8.43	8.65	8.11	7.92	8.20
MA_RS14215	nadA	6.17	6.53	6.57	6.78	6.39	6.68	6.97	7.44	7.90	6.60	6.42	6.76
MA_RS14220	nifU	7.64	7.94	7.78	8.35	7.79	8.06	8.44	9.13	9.43	8.30	7.79	8.24
MA_RS14225	nifS	7.57	7.80	7.82	8.13	7.76	7.89	8.41	8.52	8.66	7.99	7.56	7.94
MA_RS14230	NA	2.19	2.38	2.92	1.95	2.28	2.31	2.33	2.10	1.86	2.34	2.43	2.36
MA_RS14235	cysK	7.19	7.40	7.41	7.59	7.26	7.47	7.74	7.81	7.89	7.58	7.19	7.44
MA_RS14240	#N/A	6.61	6.91	6.76	7.01	6.73	6.89	7.01	7.32	7.53	6.90	6.64	6.88
MA_RS14245	thiE	2.43	2.43	2.20	3.31	2.60	3.02	2.99	3.73	4.24	3.22	2.96	3.10
MA_RS14250	thiM	2.83	2.99	2.92	3.41	3.10	3.45	3.34	3.66	3.98	3.66	3.10	3.47
MA_RS14255	NA	1.79	1.91	2.21	2.54	2.36	2.51	2.53	3.38	3.27	2.58	2.07	2.64
MA_RS14260	NA	0.47	0.46	0.62	0.52	0.42	0.65	0.44	1.12	0.99	0.68	0.37	0.51
MA_RS14265	NA	0.43	0.51	0.38	0.73	0.67	0.76	0.74	1.23	1.09	0.54	1.15	0.93
MA_RS14270	NA	0.99	1.15	0.59	1.35	1.13	1.10	0.88	1.66	1.82	1.38	1.10	0.95
MA_RS14275	NA	4.45	4.74	4.69	5.08	4.82	5.03	5.01	5.42	5.59	5.22	4.75	4.87
MA_RS14280	NA	0.41	0.63	0.57	0.85	0.61	0.79	0.50	1.13	1.25	0.75	0.76	0.51
MA_RS14285	NA	2.73	2.57	2.31	2.39	2.75	2.49	2.68	2.73	2.74	2.62	1.88	2.38
MA_RS14290	NA	3.47	3.71	3.48	3.88	3.68	3.91	3.80	4.77	5.39	4.09	3.82	3.51
MA_RS14295	NA	3.81	4.15	3.85	4.38	4.07	4.38	4.35	5.15	5.56	4.53	4.22	4.30
MA_RS14310	NA	0.26	0.39	0.30	0.11	0.43	0.30	0.17	0.62	0.33	0.32	0.28	0.18
MA_RS14330	NA	0.63	0.37	0.43	0.47	0.64	0.44	0.60	1.27	1.67	0.85	0.00	0.47
MA_RS14335	#N/A	0.29	0.94	0.99	0.95	0.14	0.73	2.26	1.97	0.86	0.73	1.47	0.50
MA_RS14345	istA	0.52	0.50	0.29	0.56	0.60	0.75	0.61	0.88	0.92	0.72	0.68	0.62
MA_RS14350	istB	0.40	0.59	0.46	0.61	0.21	0.66	0.53	0.86	1.21	0.57	0.58	0.49
MA_RS14355	NA	3.03	3.07	3.72	3.34	2.76	2.75	3.36	3.86	4.18	3.68	3.45	3.21
MA_RS14360	NA	1.64	1.72	1.63	2.23	1.90	2.18	2.34	2.75	3.11	1.98	1.91	1.85
MA_RS14365	NA	3.06	3.44	3.25	3.52	3.15	3.31	2.99	4.06	4.31	3.84	3.47	3.50
MA_RS14370	NA	4.00	4.38	4.11	4.58	4.18	4.52	4.39	4.45	4.60	4.45	4.50	4.43
MA_RS14375	NA	0.72	0.79	0.79	1.85	1.57	1.52	0.49	1.27	1.98	1.89	1.19	0.55
MA_RS14380	NA	2.24	2.80	1.88	2.92	2.47	2.57	2.72	2.41	2.68	2.94	2.50	2.42
MA_RS14385	NA	2.37	2.53	2.76	3.02	2.52	2.85	2.34	3.34	3.62	2.94	2.49	3.01
MA_RS14390	NA	2.69	2.73	2.95	2.53	2.40	2.71	1.55	1.92	2.16	1.96	1.96	1.54
MA_RS14400	NA	0.14	0.13	0.37	0.35	0.27	0.28	0.44	0.37	0.59	0.22	0.37	0.18
MA_RS14410	NA	2.77	2.58	2.86	3.02	2.76	3.20	2.83	3.94	4.50	3.52	3.01	2.92
MA_RS14415	NA	0.28	0.16	0.00	1.07	0.57	0.00	0.00	0.28	0.74	1.43	1.12	0.30
MA_RS14420	NA	0.23	0.32	0.79	1.34	0.33	0.97	0.64	0.67	1.17	0.69	0.00	0.63
MA_RS14425	NA	0.80	0.25	0.30	1.25	0.88	0.68	1.69	1.89	0.85	0.80	1.56	0.52
MA_RS14430	#N/A	2.52	2.64	2.81	3.33	2.77	3.21	2.74	4.02	4.10	3.25	2.49	2.75
MA_RS14435	NA	2.15	2.44	2.14	2.86	2.56	2.86	2.77	2.80	3.20	2.91	2.52	2.76
MA_RS14455	NA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.04	0.13	0.00	0.00
MA_RS14465	NA	2.00	2.58	2.25	2.79	2.30	2.95	2.79	3.38	3.33	2.64	2.18	2.52
MA_RS14470	NA	0.33	0.52	0.39	0.73	0.41	0.64	0.37	0.93	0.96	0.54	0.63	0.37
MA_RS14475	NA	2.47	2.46	2.67	3.16	2.83	3.04	2.98	3.10	3.64	3.19	2.24	2.76
MA_RS14480	NA	1.93	2.12	1.76	2.57	2.07	1.78	2.39	2.57	3.07	2.12	1.84	2.12
MA_RS14490	NA	2.07	2.21	2.35	2.61	2.38	2.73	2.74	2.76	3.53	2.54	2.39	2.49
MA_RS14500	NA	1.24	0.90	0.56	1.31	1.64	1.39	1.59	1.90	2.27	0.97	1.30	1.62
MA_RS14515	NA	3.63	3.74	3.77	3.95	3.69	3.94	4.31	4.56	4.64	4.12	3.74	3.83
MA_RS14520	NA	0.74	0.45	0.89	0.99	0.53	0.96	0.30	1.14	0.80	0.64	0.57	0.61
MA_RS14525	NA	0.73	0.67	0.86	0.87	0.81	1.17	1.34	1.56	1.08	1.25	0.76	0.64
MA_RS14530	NA	0.78	0.88	0.60	0.62	0.81	0.27	1.13	1.14	0.86	1.25	1.13	1.00
MA_RS14535	NA	0.37	0.64	0.35	0.89	0.83	1.06	1.17	1.54	1.41	0.91	0.81	0.76

MA_RS14540	NA	1.38	1.53	1.68	2.01	1.55	2.06	1.88	2.40	2.63	2.08	1.53	1.73
MA_RS14550	NA	0.67	0.56	0.12	1.13	1.00	1.22	0.70	0.82	1.32	1.11	1.00	0.57
MA_RS14555	NA	0.42	0.25	0.79	0.68	0.41	0.70	0.32	0.98	1.09	0.56	0.88	0.85
MA_RS14560	NA	0.76	1.07	0.23	0.67	0.87	0.88	1.01	0.76	1.13	0.96	0.92	0.63
MA_RS14565	NA	2.06	2.11	1.70	1.86	1.71	2.14	2.69	3.14	2.41	2.62	2.45	1.94
MA_RS14570	NA	4.51	4.85	4.62	4.93	4.46	4.61	4.68	5.54	5.87	4.86	4.35	4.41
MA_RS14590	NA	2.16	2.41	2.40	3.23	3.09	2.85	3.46	3.48	3.38	3.10	3.57	2.41
MA_RS14595	NA	2.78	2.81	2.38	3.02	2.88	3.29	3.48	3.63	3.50	3.08	3.49	2.97
MA_RS14605	NA	2.76	2.94	3.10	2.96	3.47	3.33	3.48	4.03	3.82	3.36	2.89	3.01
MA_RS14610	NA	3.75	3.63	3.00	3.66	3.24	3.62	3.92	4.75	4.88	4.13	3.65	3.46
MA_RS14615	NA	2.38	2.52	2.62	2.55	2.60	2.79	3.35	3.17	3.20	2.77	2.43	2.46
MA_RS14640	NA	1.15	1.53	1.58	1.26	1.48	1.15	1.71	2.69	2.18	1.56	1.48	1.41
MA_RS14645	ltrA	2.83	2.86	2.76	3.40	2.90	3.29	3.04	3.81	4.14	3.30	3.02	3.16
MA_RS14665	NA	1.93	1.31	1.46	2.20	0.90	1.35	1.89	1.95	2.16	1.66	1.67	1.56
MA_RS14670	NA	1.99	1.21	1.38	1.64	1.76	1.14	0.88	2.51	2.64	1.04	1.62	1.34
MA_RS14675	NA	1.53	1.80	2.08	1.37	1.72	2.17	1.52	2.70	2.30	1.43	2.07	0.81
MA_RS14680	NA	1.13	1.89	1.34	1.84	2.30	1.56	1.45	2.55	2.48	0.95	1.74	1.52
MA_RS14685	NA	1.09	0.77	2.75	2.11	0.71	2.74	2.85	2.75	2.63	1.49	1.57	1.58
MA_RS14690	NA	1.06	1.18	1.14	1.62	0.88	1.65	1.49	2.04	2.26	1.02	1.25	0.97
MA_RS14695	NA	0.51	1.18	0.00	0.99	0.26	0.41	0.49	1.54	1.11	0.44	1.20	0.28
MA_RS14700	NA	1.32	0.96	0.84	1.18	0.85	1.45	1.50	2.14	2.08	1.85	1.53	0.70
MA_RS14705	NA	0.78	0.83	0.96	1.01	1.04	0.95	1.05	1.68	1.88	1.09	1.20	1.03
MA_RS14710	NA	0.17	0.74	0.00	0.00	0.00	0.28	1.63	0.79	1.33	0.61	0.00	0.00
MA_RS14715	NA	0.77	0.68	0.35	1.01	0.68	0.75	0.55	1.26	1.31	1.30	1.01	0.71
MA_RS14720	NA	0.00	0.47	0.00	0.00	0.26	0.51	0.33	0.14	0.00	0.00	0.33	0.27
MA_RS14725	NA	0.26	0.08	0.23	0.44	0.17	0.12	0.11	0.52	0.64	0.74	0.31	0.33
MA_RS14730	NA	0.69	1.04	1.11	0.82	1.08	0.68	1.05	1.20	1.60	1.34	0.75	1.14
MA_RS14735	NA	0.62	0.67	0.63	0.61	0.92	1.09	0.96	1.17	1.66	1.04	0.51	0.43
MA_RS14745	#N/A	3.23	3.65	3.33	3.65	3.60	2.77	3.15	3.05	3.30	3.76	3.19	3.14
MA_RS14750	NA	6.48	6.72	6.59	6.96	6.76	6.85	6.97	7.02	7.15	6.77	6.68	6.76
MA_RS14755	nlkR	3.23	3.31	3.68	3.47	3.49	3.60	4.07	4.29	4.41	3.52	3.48	3.66
MA_RS14760	NA	3.61	3.69	3.36	3.92	3.51	3.82	4.07	4.54	4.89	3.85	3.51	3.95
MA_RS14765	NA	4.06	4.45	4.03	4.38	4.24	4.41	4.68	5.59	5.78	4.63	4.22	4.35
MA_RS14770	NA	0.89	0.74	1.39	1.32	1.22	1.30	1.02	1.81	1.85	1.65	1.22	1.32
MA_RS14775	NA	0.65	0.32	1.08	0.61	0.34	0.60	0.00	0.62	1.34	0.69	0.00	0.00
MA_RS14780	NA	2.75	2.32	2.55	2.98	3.00	2.58	3.33	3.67	3.03	2.76	2.19	2.51
MA_RS14785	NA	2.41	2.44	2.19	2.38	2.29	2.49	2.86	3.46	3.62	2.66	2.38	2.33
MA_RS14790	istB	0.42	0.25	0.26	0.31	0.25	0.28	0.32	0.72	0.69	0.39	0.19	0.39
MA_RS14795	istA	0.50	0.27	0.43	0.51	0.73	0.70	0.60	0.67	0.83	0.69	0.43	0.49
MA_RS14800	NA	0.32	0.20	0.23	0.54	0.25	0.27	0.37	0.48	1.03	0.76	1.00	0.30
MA_RS14805	NA	1.79	1.92	2.15	1.49	1.68	0.99	1.92	2.53	2.59	2.37	1.74	1.72
MA_RS14810	NA	2.47	2.78	2.63	2.76	2.71	2.71	2.89	3.16	2.98	2.42	2.19	2.15
MA_RS14815	NA	4.93	5.28	5.18	5.51	5.10	5.40	5.24	5.95	6.24	5.25	5.04	5.13
MA_RS14820	NA	3.19	3.46	3.27	3.83	3.62	3.68	3.99	4.43	4.55	3.92	3.55	3.54
MA_RS14830	NA	3.44	3.53	3.52	3.78	3.49	3.72	3.50	3.86	4.10	3.63	3.16	3.75
MA_RS14840	NA	0.97	1.13	1.12	1.14	1.05	1.39	1.23	1.89	2.12	1.36	1.31	1.14
MA_RS14845	NA	1.63	1.62	1.88	0.95	1.97	2.18	1.18	2.18	1.99	1.99	1.61	1.61
MA_RS14850	NA	1.29	1.43	0.95	1.30	1.67	1.15	1.44	1.91	1.82	1.27	1.51	1.38
MA_RS14860	NA	1.29	1.15	0.83	1.14	1.10	1.49	1.13	1.53	2.03	1.34	0.90	1.15
MA_RS14865	NA	2.01	2.10	2.17	2.23	2.24	2.28	1.80	2.41	2.46	2.14	2.32	1.97
MA_RS14870	NA	0.96	1.66	0.94	1.82	1.60	1.77	0.97	2.21	2.29	1.38	1.84	1.69
MA_RS14875	NA	2.02	2.23	2.21	2.57	2.35	2.51	2.59	3.39	3.54	2.76	2.40	2.61
MA_RS14880	NA	1.15	1.41	1.16	1.66	1.94	1.89	1.47	1.51	1.98	1.51	1.39	1.62
MA_RS14885	NA	3.73	4.10	3.74	3.99	3.96	4.14	4.00	4.07	4.41	3.90	3.81	4.05
MA_RS14890	NA	2.49	2.71	2.62	2.74	2.62	2.97	2.94	3.42	3.27	2.49	2.72	2.49
MA_RS14895	NA	2.21	2.79	2.02	2.36	2.51	2.79	2.52	2.33	2.77	2.44	1.95	2.76
MA_RS14900	NA	1.94	2.02	1.80	2.19	2.27	1.81	2.15	2.61	3.02	2.04	1.45	2.16
MA_RS14905	NA	2.31	2.37	2.46	2.56	2.21	2.42	2.58	3.22	3.21	2.59	2.29	2.31
MA_RS14910	NA	1.68	2.05	1.62	2.41	2.03	2.07	2.11	2.62	2.98	1.77	1.53	2.14
MA_RS14915	NA	1.13	1.35	1.31	1.17	1.14	1.26	1.58	1.84	2.19	1.23	1.34	1.29
MA_RS14920	NA	1.16	1.26	1.20	1.56	1.51	1.73	1.53	2.00	2.10	1.66	1.65	1.25
MA_RS14930	NA	1.04	0.55	0.00	1.04	1.42	1.22	2.16	1.56	1.94	1.31	0.22	1.15
MA_RS14935	NA	3.06	3.09	3.09	3.35	2.85	3.32	3.21	3.38	3.62	3.01	2.91	2.94
MA_RS14940	NA	3.19	3.13	3.12	3.36	3.13	3.24	3.54	3.86	3.96	3.39	2.98	3.19
MA_RS14950	NA	0.94	0.55	0.00	0.22	0.71	0.23	0.69	0.00	0.00	0.70	0.00	0.46
MA_RS14955	NA	1.98	2.13	1.87	2.37	2.06	2.17	2.39	2.36	2.33	1.91	2.35	2.17
MA_RS14960	#N/A	5.30	5.29	4.96	4.21	5.09	4.27	5.39	2.06	2.30	3.34	4.64	5.10
MA_RS14970	NA	4.09	3.88	4.01	4.19	3.99	4.33	4.52	4.14	4.02	4.30	4.44	4.35
MA_RS14975	NA	1.21	1.03	0.95	1.96	1.50	1.16	1.38	2.43	2.92	1.81	1.59	1.26
MA_RS14980	NA	1.98	1.64	1.59	1.64	1.62	2.55	2.14	2.52	2.63	1.70	1.94	2.24
MA_RS14985	NA	0.79	1.35	0.52	0.86	0.82	0.96	0.68	1.17	1.60	1.02	0.23	0.93
MA_RS14990	NA	0.81	1.18	1.22	0.97	0.35	0.46	0.20	0.99	1.42	0.68	0.00	0.47
MA_RS14995	NA	0.34	0.00	0.00	1.58	0.00	0.62	0.00	0.00	0.48	1.08	0.00	0.00
MA_RS15000	NA	4.23	4.36	4.32	4.54	4.21	4.19	4.14	3.64	3.54	3.93	4.15	4.14
MA_RS15005	NA	1.13	1.36	1.57	1.66	1.61	1.69	1.70	2.48	2.89	2.10	1.63	1.39
MA_RS15010	NA	1.70	1.81	1.97	2.00	2.01	2.12	1.97	2.39	2.59	1.60	2.13	1.97
MA_RS15015	NA	1.80	1.94	2.17	1.61	1.67	1.95	2.40	2.02	2.20	1.64	1.85	1.88
MA_RS15020	NA	4.64	4.56	4.55	4.90	4.58	4.97	4.93	5.95	6.23	5.01	4.98	4.73
MA_RS15025	gatE	4.90	5.04	4.96	5.27	5.00	5.21	5.35	5.62	5.66	5.09	4.88	5.16
MA_RS15030	NA	1.88	1.38	1.74	1.97	1.94	1.83	1.51	1.71	2.20	1.96	1.63	1.36
MA_RS15035	#N/A	0.51	0.77	0.00	1.06	1.23	1.88	0.98	1.07	1.92	1.57	1.05	0.90
MA_RS15040	NA	1.49	2.21	2.11	2.31	2.11	2.26	2.36	2.19	2.30	2.06	2.04	1.85
MA_RS15045	NA	1.14	1.13	1.42	1.69	1.75	1.11	1.35	1.42	1.34	0.84	1.05	1.56
MA_RS15050	NA	3.49	3.82	3.58	4.06	4.01	4.07	4.21	4.37	4.54	4.14	3.90	4.21
MA_RS15055	hdrA2	4.00	4.35	4.18	4.74	4.44	4.61	4.44	4.76	4.94	4.71	4.40	4.59
MA_RS15060	NA	1.86	1.98	1.95	1.38	1.26	2.35	1.41	3.10	3.71	2.54	0.62	1.85
MA_RS15065	NA	4.95	4.94	4.67	5.16	5.04	5.08	5.00	5.58	5.33	4.98	4.61	4.57
MA_RS15070	NA	1.29	1.26	1.42	1.62	1.15	1.61	1.53	1.67	2.70	1.75	1.52	1.34
MA_RS15075	NA	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.31	0.00	0.00	0.00	0.34
MA_RS15080	NA	3.70	3.87	3.79	4.17	4.21	4.20	4.32	4.88	5.08	4.35	4.31	4.01
MA_RS15085	NA	2.93	2.45	2.23	2.76	2.56	3.02	3.16	2.76	2.93	2.51	2.00	2.92
MA_RS15095	NA	4.74	5.00	4.92	5.10	4.99	5.17	4.69	4.97	5.11	4.50	4.68	4.71
MA_RS15100	NA	4.85	5.16	4.81	5.26	5.05	5.31	4.93	5.56	5.85	5.07	4.96	5.10
MA_RS15105	NA	4.70	4.94	4.62	5.13	4.84	5.23	4.92	5.69	6.21	5.08	4.81	5.14
MA_RS15110	NA	1.14	1.36	0.83	0.89	1.25	1.03	1.08	1.38	1.98	0.79	0.74	1.05
MA_RS15115	NA	1.16	1.14	0.55	0.66	1.58	1.31	0.87	1.15	1.01	1.38	1.56	1.45
MA_RS15120	NA	0.68	0.49	0.62	0.76	1.31	1.06	1.50	1.13	1.65	1.44	0.72	0.37
MA_RS15125	NA	1.56	1.25	1.93	1.87	2.17	2.02	1.84	1.85	2.47	2.31	2.07	1.61
MA_RS15130	NA	1.27	1.20	1.59	1.87	1.24	1.56	1.98	1.51	1.66	1.66	1.32	1.95
MA_RS15135	NA	2.26	2.69	2.41	3.15	2.82	2.71	3.01	3.65	4.10	3.16	2.65	2.95
MA_RS15140	NA	1.03	1.13	1.27	1.42	1.55	1.56	1.59	1.96	1.96	1.63	1.24	1.52
MA_RS15150	NA	4.36	4.50	4.49	4.62	4.42	4.60	4.55	4.68	4.97	4.27	4.26	4.51
MA_RS15155	NA	4.08	4.33	4.39	4.44	4.18	4.35	4.40	4.64	4.57	4.27	3.82	4.28
MA_RS15160	NA	2.69	2.77	2.76	3.19	2.80	3.06	2.97	3.65	3.82	2.81	2.70	3.02
MA_RS15165	NA	0.91	1.62	0.79	2.05	1.94	0.28	0.80	1.62	1.66	1.17	1.44	1.30
MA_RS15170	NA	2.16	2.46	2.32	2.51	2.53	2.61	2.55	2.84	3.05	2.45	2.42	2.23
MA_RS15175	NA	3.51	3.69	3.52	3.94	3.82	3.95	3.75	3.84	3.87	3.88	3.81	3.68
MA_RS15180	NA	3.86	3.92	4.06	4.22	4.10	4.21	4.19	4.15	4.34	4.17	4.05	4.03
MA_RS15185	NA	4.03	4.39	4.24	4.38	4.05	4.23	4.20	4.80	5.01	3.82	3.71	3.96
MA_RS15190	NA	5.83	6.11	6.08	6.19	5.85	6.11	6.06	6.33	6.58	5.84	5.82	5.88
MA_RS15195	NA	4.62	4.69	4.57	4.80	4.68	4.85	4.66	5.16	5.56	4.57	4.49	4.72
MA_RS15200	NA	1.12	0.87	0.94	1.35	1.15	1.15	1.36	2.06	1.89	1.50	0.87	1.47
MA_RS15205	NA	1.35	1.49	0.93	1.36	1.69	1.76	1.16	2.13	2.38	1.31	1.80	1.44
MA_RS15210	NA	0.94	0.55	0.27	0.83	1.28	1.44	1.42	1.75	1.66	0.64	1.36	0.86
MA_RS15220	NA	1.66	2.12	2.00	2.24	2.21	2.33	2.38	1.97	2.36	2.01	2.11	1.76
MA_RS15225	NA	1.02	1.17	0.98	1.09	1.00	1.17	0.99	1.65	1.59	1.64	0.82	1.26
MA_RS15235	NA	1.76	2.34	1.90	2.34	1.72	2.25	1.90	3.15	3.02	3.08	2.48	2.25
MA_RS15240	NA	0.53	0.60	0.75	0.97	0.71	0.99	0.68	1.36	1.30	0.69	0.87	0.76
MA_RS15245	NA	1.18	1.39	0.96	1.55	1.36	1.34	1.55	1.82	1.62	1.48	1.00	1.56
MA_RS15250	NA	6.08	6.29	6.20	6.87	6.48	6.75	6.54	6.62	6.99	6.84	6.42	6.59
MA_RS15255	NA	6.30	6.59	6.36	7.21	6.78	6.99	7.03	7.32	7.80	7.21	6.82	6.94
MA_RS15260	NA	5.83	5.84	5.78	6.54	6.21	6.29	6.63	6.62	6.65	6.33	5.91	6.20
MA_RS15265	NA	5.64	5.83	5.84	6.46	6.08	6.35	6.39	6.61	7.06	6.64	6.16	6.39
MA_RS15270	NA	5.68	5.97	6.02	6.82	6.25	6.32	6.55	6.66	7.33	6.83	6.17	6.36
MA_RS15275	NA	3.76	4.07	3.94	4.13	3.78	4.08	4.31	4.89	5.26	3.89	3.79	3.98
MA_RS15280	NA	1.95	1.97	2.13	2.45	1.76	2.36	2.67	2.70	2.56	2.26	2.12	2.06
MA_RS15285	NA	1.50	1.70	1.57	1.67	1.29	1.83	1.43	1.37	1.99	1.69	1.45	1.81
MA_RS15290	NA	2.96	2.90	2.54	3.20	3.09	3.11	3.33	3.39	2.86	3.02	3.08	2.56
MA_RS15295	NA	2.03	2.46	2.79	2.50	2.29	1.97	3.51	3.36	3.54	2.02	2.79	2.25
MA_RS15300	NA	1.92	2.47	2.48	2.41	2.16	2.71	2.15	3.12	3.28	2.68	2.47	2.15
MA_RS15305	NA	3.98	3.99	3.65	4.21	3.75	4.15	3.74	4.75	4.57	4.11	3.77	3.76
MA_RS15310	NA	3.15	2.99	2.65	3.05	3.26	3.24	2.95	3.61	3.76	3.51	2.93	3.07
MA_RS15315	NA	3.42	3.33	3.46	3.74	3.40	3.60	3.36	3.72	4.03	3.42	3.03	3.01
MA_RS15320	#N/A	1.55	1.78	1.97	2.26	2.02	1.82	1.72	2.80	2.82	2.57	2.01	2.11
MA_RS15325	NA	0.17	0.00	0.38	1.11	0.65	0.54	0.88	0.00	2.11	0.00	0.00	0.47
MA_RS15330	NA	0.17	0.22	0.13	0.12	0.20	0.29	0.06	0.26	0.30	0.10	0.26	0.09
MA_RS15335	NA	0.58	1.48	1.31	2.14	2.77	1.80	1.69	1.98	1.52	1.61	2.30	1.08
MA_RS15340	NA	0.28	0.21	0.64	0.42	0.00	0.43	0.17	0.27	0.28	0.02	0.27	0.11
MA_RS15345	NA	2.58	2.77	2.70	3.15	2.93	3.09	3.10	3.79	3.93	3.21	2.94	3.07
MA_RS15350	NA	0.86	0.53	0.64	0.95	0.94	1.09	0.00	1.37	1.01	1.02	1.15	1.41
MA_RS15355	NA	3.34	3.54	3.34	3.93	3.46	3.68	3.82	4.17	4.20	3.81	3.65	3.61
MA_RS15365	NA	5.90	6.15	5.98	5.80	5.49	6.00	5.43	6.29	6.26	5.21	5.25	5.46
MA_RS15370	NA	6.17	6.41	6.33	5.68	5.69	5.90	5.40	6.03	6.18	5.07	5.39	5.41

MA_RS15375	NA	2.67	2.37	2.61	3.36	2.53	2.95	3.50	3.32	3.23	2.90	2.80	2.43
MA_RS15390	NA	1.92	2.04	2.17	2.55	2.22	2.62	2.53	3.28	3.56	2.62	2.38	2.38
MA_RS15395	NA	0.38	0.40	0.31	0.42	0.27	0.44	0.36	0.58	0.51	0.25	0.27	0.31
MA_RS15400	NA	0.56	0.36	0.86	0.64	0.30	0.36	1.10	1.40	1.14	1.24	0.68	0.74
MA_RS15405	NA	2.00	2.27	2.16	2.87	2.37	2.78	2.75	2.86	3.48	3.19	2.50	2.71
MA_RS15425	#N/A	0.60	0.62	0.23	1.05	0.82	0.52	0.42	0.40	0.14	0.82	0.71	0.34
MA_RS15430	NA	0.58	0.93	0.58	0.85	0.66	0.79	0.91	1.42	1.47	0.68	0.49	0.72
MA_RS15435	NA	2.36	2.45	2.43	3.08	2.37	2.71	2.62	3.29	3.34	2.72	2.35	2.36
MA_RS15455	NA	3.86	3.63	3.80	3.79	3.77	3.76	3.48	4.54	4.86	4.27	3.79	3.67
MA_RS15460	NA	2.63	2.87	2.91	2.74	2.53	3.05	2.74	3.61	2.83	3.06	2.77	2.99
MA_RS15465	NA	2.97	2.90	3.13	3.42	3.23	3.29	3.84	3.26	3.18	2.33	3.37	3.24
MA_RS15470	NA	2.68	2.96	2.83	3.00	2.96	2.74	2.64	3.29	3.36	2.93	2.68	3.29
MA_RS15475	NA	1.32	1.15	1.61	1.53	1.59	1.42	1.68	1.33	1.64	1.62	1.42	1.70
MA_RS15480	NA	1.70	1.86	1.75	2.69	2.22	2.15	2.29	2.14	2.37	2.07	2.00	1.96
MA_RS15485	NA	0.00	0.00	0.00	0.00	0.37	0.15	0.00	0.62	0.07	0.35	0.12	0.00
MA_RS15500	NA	1.13	1.24	0.96	1.38	1.61	1.20	1.61	1.80	1.75	1.58	1.31	1.63
MA_RS15505	NA	1.81	1.62	1.34	2.16	1.88	1.90	1.98	2.39	2.66	1.81	1.55	1.92
MA_RS15510	NA	7.29	7.67	7.53	8.02	7.42	7.80	7.90	8.67	8.87	7.82	7.47	7.58
MA_RS15520	NA	3.11	3.37	3.28	3.56	3.22	3.47	3.45	3.65	4.10	3.45	2.66	2.75
MA_RS15525	NA	2.38	2.58	2.39	2.73	2.27	2.80	2.42	3.25	3.53	2.57	2.43	2.35
MA_RS15530	NA	2.51	2.79	2.83	3.10	2.64	3.22	2.50	3.44	3.17	2.97	2.68	2.74
MA_RS15535	NA	4.63	4.39	4.21	3.35	3.77	3.11	4.67	4.10	3.18	3.00	3.37	3.13
MA_RS15540	NA	0.67	0.58	0.65	0.72	0.74	0.55	0.94	1.38	1.26	0.71	0.65	0.77
MA_RS15545	NA	2.41	2.52	2.40	2.87	2.38	2.88	2.76	3.03	3.23	2.88	1.72	2.69
MA_RS15550	NA	1.92	1.85	2.52	2.33	2.05	2.61	2.49	3.65	3.63	2.54	2.27	2.53
MA_RS15555	NA	5.08	5.23	5.42	5.47	5.15	5.45	5.36	5.72	5.93	5.05	5.07	5.10
MA_RS15560	NA	2.34	2.48	1.96	1.63	2.50	2.31	2.26	2.11	2.66	2.07	2.22	1.71
MA_RS15570	NA	4.20	4.49	4.44	4.08	3.51	3.72	3.97	4.55	4.56	4.54	4.10	4.01
MA_RS15585	NA	0.87	1.26	0.90	0.65	1.14	1.93	1.61	1.87	1.56	2.14	0.84	2.07
MA_RS15590	NA	0.78	1.90	1.43	1.46	1.53	1.53	1.88	2.47	2.41	1.11	1.43	0.83
MA_RS15595	NA	1.58	1.94	1.90	1.91	1.48	1.49	2.01	2.50	2.43	1.43	1.08	1.74
MA_RS15600	NA	1.25	1.52	1.72	1.40	1.78	1.78	1.56	1.89	2.28	1.24	1.61	1.30
MA_RS15605	NA	0.70	1.05	1.12	1.35	1.20	1.25	1.23	2.50	2.67	1.59	1.19	1.02
MA_RS15615	NA	0.00	0.15	0.00	0.20	0.00	0.00	0.00	0.01	1.08	0.00	0.00	0.00
MA_RS15620	NA	0.48	0.53	0.00	0.26	0.00	0.00	0.91	0.68	0.47	0.59	0.00	0.30
MA_RS15625	NA	1.81	2.08	1.98	2.13	1.65	2.41	2.31	2.97	3.50	2.36	2.16	2.30
MA_RS15630	NA	3.20	3.53	3.22	3.76	3.44	3.58	3.46	4.55	4.65	4.03	3.93	3.44
MA_RS15635	NA	2.28	2.77	2.61	2.93	2.70	2.52	2.76	3.76	4.20	3.20	2.72	2.80
MA_RS15640	NA	3.01	2.99	3.32	3.58	3.37	3.31	3.32	3.59	3.78	3.67	3.34	3.21
MA_RS15645	NA	3.27	3.59	3.54	3.95	3.75	3.93	4.05	4.93	5.07	4.13	3.75	3.91
MA_RS15650	NA	2.42	2.04	2.14	1.94	2.56	2.27	2.20	3.17	3.55	2.78	2.77	2.32
MA_RS15655	NA	4.13	4.05	3.94	4.31	4.27	3.99	4.43	4.78	4.95	4.41	3.89	4.27
MA_RS15660	NA	3.87	3.97	3.67	4.32	4.12	3.89	4.23	4.47	4.36	3.62	3.78	3.85
MA_RS15665	trpE	4.56	4.72	4.62	4.78	4.55	4.73	4.85	4.82	4.98	3.66	4.25	4.22
MA_RS15670	NA	4.86	5.04	4.86	5.23	4.98	5.08	5.11	5.32	5.70	3.79	4.53	4.63
MA_RS15675	trpD	4.45	4.75	4.58	4.73	4.52	4.55	4.86	4.35	4.25	3.29	3.64	4.34
MA_RS15680	trpA	3.54	3.98	3.88	3.89	3.74	4.02	4.14	3.50	3.15	2.87	3.22	3.40
MA_RS15685	trpB	4.00	4.29	4.23	4.37	3.98	4.18	4.38	4.00	3.71	2.97	3.46	3.83
MA_RS15690	NA	4.46	4.71	4.72	4.72	4.60	4.65	4.83	4.84	5.29	4.12	4.47	5.00
MA_RS15695	NA	0.51	1.06	0.47	0.76	1.42	0.26	1.30	0.42	1.80	0.56	1.17	1.15
MA_RS15700	NA	1.25	1.66	1.32	1.88	1.72	1.79	1.79	2.17	2.20	0.96	1.34	1.97
MA_RS15705	NA	0.76	0.66	0.44	0.64	1.05	1.15	0.42	0.00	0.62	0.44	0.74	1.22
MA_RS15710	NA	2.76	2.13	2.85	2.19	3.09	2.80	2.84	3.51	2.88	3.15	2.86	2.51
MA_RS15715	NA	3.19	2.67	2.61	2.89	2.80	3.24	2.76	3.93	3.22	3.73	3.09	3.09
MA_RS15720	NA	0.92	1.01	1.10	1.13	1.22	1.04	0.53	0.86	1.85	1.08	0.53	0.80
MA_RS15730	NA	3.36	3.40	3.56	3.59	3.33	4.00	4.01	3.73	3.72	3.62	3.03	2.97
MA_RS15745	fae	6.72	6.94	6.93	7.16	6.70	6.92	6.98	7.35	7.70	7.38	6.75	6.89
MA_RS15750	NA	4.05	4.46	4.42	4.54	3.97	4.45	4.38	5.14	5.60	4.92	4.13	4.52
MA_RS15755	NA	2.63	3.12	3.19	2.91	2.72	2.94	3.13	4.29	4.39	3.40	2.72	3.21
MA_RS15760	NA	4.50	4.63	4.46	4.85	4.33	4.84	4.64	5.40	5.68	4.71	4.52	4.79
MA_RS15765	NA	4.92	5.13	5.05	5.47	5.19	5.14	5.25	5.57	5.59	5.07	5.11	5.28
MA_RS15770	NA	5.19	5.41	5.21	5.75	5.35	5.87	5.61	6.76	6.93	6.14	5.64	5.66
MA_RS15775	NA	5.18	5.43	5.31	5.82	5.56	5.62	5.72	6.16	6.32	5.98	5.44	5.71
MA_RS15780	NA	5.92	6.25	5.94	6.70	6.22	6.58	6.34	7.32	7.37	6.76	6.24	6.32
MA_RS15785	NA	5.96	6.11	6.06	6.33	6.15	6.29	6.27	6.29	6.40	5.93	6.01	6.18
MA_RS15790	NA	3.60	3.92	3.44	4.25	3.94	4.14	4.09	4.69	5.06	4.07	4.01	4.02
MA_RS15795	NA	3.60	3.44	3.37	3.80	3.61	3.39	3.57	4.16	4.05	3.92	3.19	3.87
MA_RS15800	NA	5.25	5.50	5.35	6.13	5.82	6.08	5.79	6.41	6.83	6.13	5.85	5.97
MA_RS15805	NA	5.51	5.67	5.58	6.14	5.84	6.06	5.86	6.33	6.65	6.05	5.89	5.94
MA_RS15810	NA	3.46	3.68	3.75	4.07	3.87	3.91	3.96	3.90	4.14	3.73	3.63	3.91
MA_RS15815	NA	3.25	3.32	3.32	3.48	3.39	3.74	3.43	4.35	4.07	3.84	3.36	3.30
MA_RS15820	NA	5.55	5.77	5.76	6.00	5.49	5.67	5.88	6.27	6.38	5.65	5.38	5.54
MA_RS15825	glmS	5.45	5.82	5.71	6.06	5.55	5.78	5.98	6.23	6.46	5.87	5.49	5.68
MA_RS15830	glmM	4.96	5.21	5.19	5.65	5.06	5.30	5.37	5.57	5.81	5.27	4.99	5.16
MA_RS15835	NA	4.26	4.57	4.32	4.70	4.38	4.51	4.96	4.83	5.17	4.32	4.43	4.78
MA_RS15840	NA	4.86	4.96	5.01	5.14	5.27	5.32	5.28	5.57	5.46	5.59	4.60	4.92
MA_RS15845	NA	0.16	0.81	0.20	0.00	0.65	0.64	0.28	0.98	0.55	0.88	0.00	0.00
MA_RS15855	NA	4.38	3.88	4.16	4.37	3.93	4.02	4.31	3.86	4.63	4.33	4.22	3.64
MA_RS15860	NA	4.36	3.97	4.16	4.13	4.04	4.18	4.46	4.81	5.20	4.52	4.55	3.78
MA_RS15865	NA	4.63	4.90	4.83	5.01	4.90	5.06	4.98	5.23	5.60	4.98	4.85	5.07
MA_RS15870	NA	4.96	4.83	4.74	5.26	5.30	5.01	5.48	6.13	5.93	5.57	5.05	5.28
MA_RS15875	mz	3.24	3.28	3.22	3.44	3.27	3.52	3.51	3.49	3.47	3.52	3.32	3.43
MA_RS15880	NA	0.52	0.38	0.61	0.43	0.51	0.60	0.39	0.89	0.59	0.46	0.71	0.93
MA_RS15885	cobA	4.29	4.42	4.35	5.01	4.62	4.54	5.09	4.91	5.01	4.79	4.36	4.58
MA_RS15890	NA	4.01	4.26	4.25	4.43	3.97	4.09	4.70	4.40	4.59	4.12	4.01	4.45
MA_RS15895	ahbC	5.05	5.52	5.26	5.72	5.29	5.60	5.28	5.52	5.74	5.51	5.32	5.41
MA_RS15900	NA	2.27	2.03	1.20	2.56	2.49	2.54	3.05	3.21	4.04	2.22	2.35	2.32
MA_RS15905	NA	1.65	1.56	1.03	2.05	1.78	1.88	2.05	2.29	2.71	2.03	1.92	1.86
MA_RS15910	NA	1.46	1.85	0.98	1.72	1.23	1.35	2.06	2.02	2.54	1.68	1.52	1.68
MA_RS15915	NA	3.24	3.36	3.57	3.71	3.56	3.65	3.78	4.21	4.72	3.91	3.46	3.61
MA_RS15920	NA	4.56	4.71	4.74	4.61	4.57	4.71	5.00	5.32	5.59	4.81	4.50	4.67
MA_RS15925	NA	3.77	4.13	3.85	4.05	4.02	4.40	4.21	4.58	4.71	3.77	3.34	4.31
MA_RS15930	NA	1.18	0.92	1.28	1.49	1.32	1.15	1.08	1.78	1.74	1.50	1.14	1.46
MA_RS15935	NA	0.91	0.34	0.45	0.87	0.14	0.46	0.65	0.49	0.68	1.20	0.80	0.98
MA_RS15940	NA	0.66	0.42	0.42	0.99	0.90	0.84	0.70	0.90	0.99	0.82	0.65	1.31
MA_RS15945	NA	0.62	1.14	1.00	0.97	0.94	0.63	0.91	1.01	0.67	0.88	0.97	0.76
MA_RS15950	NA	1.01	1.51	1.39	1.79	1.65	1.50	1.45	1.72	1.72	1.79	0.96	1.57
MA_RS15955	NA	1.17	1.32	0.75	1.61	1.62	1.56	1.67	1.46	1.74	2.12	1.70	2.00
MA_RS15960	NA	1.05	0.81	1.09	1.26	1.34	0.56	1.07	1.45	1.10	0.98	1.13	1.18
MA_RS15965	NA	1.35	0.92	0.71	0.86	0.53	1.51	1.28	1.12	2.15	0.62	1.29	0.76
MA_RS15970	NA	5.92	6.18	6.09	6.55	6.13	6.45	6.30	6.58	6.85	6.64	6.28	6.23
MA_RS15975	NA	0.82	1.24	1.26	1.15	1.46	1.90	0.92	1.93	2.23	1.28	1.10	1.65
MA_RS15980	flaJ	0.90	0.87	1.14	1.12	0.95	1.22	1.41	1.47	1.55	1.21	0.77	1.13
MA_RS15985	NA	1.66	1.61	1.42	2.09	1.47	1.79	1.95	1.87	2.65	2.08	1.64	1.86
MA_RS15990	NA	0.94	1.09	0.71	0.76	0.93	0.74	1.40	1.64	1.29	0.61	0.59	0.56
MA_RS15995	NA	0.71	0.93	1.02	0.63	0.13	1.20	1.23	1.92	1.98	0.59	0.94	1.28
MA_RS16000	NA	1.09	0.96	0.70	1.09	0.81	1.38	1.44	2.15	1.38	1.10	1.13	0.81
MA_RS16005	NA	0.64	0.78	1.18	0.76	1.38	0.90	1.47	1.01	1.28	1.06	1.01	0.50
MA_RS16010	NA	1.72	1.76	1.26	2.03	0.94	1.48	1.32	2.03	1.83	1.42	1.56	1.69
MA_RS16015	NA	0.67	0.68	0.79	0.81	1.05	0.98	0.87	1.29	0.94	0.95	0.91	0.45
MA_RS16020	NA	1.65	2.02	1.71	1.99	2.17	2.50	2.11	2.90	2.85	1.95	1.98	1.88
MA_RS16025	NA	1.29	1.80	1.43	1.58	1.91	1.66	1.57	2.45	2.34	2.11	1.36	1.13
MA_RS16030	NA	2.28	1.87	2.48	2.28	2.30	2.33	2.47	3.53	3.31	2.37	2.26	2.38
MA_RS16035	NA	1.49	1.81	1.57	2.04	1.95	2.29	1.90	2.57	2.83	1.84	1.89	2.19
MA_RS16040	NA	2.05	1.34	2.06	2.11	2.29	1.97	1.85	2.08	2.65	1.84	1.45	1.74
MA_RS16045	NA	1.92	1.89	2.21	2.80	2.34	2.32	1.86	3.30	3.52	1.94	1.69	2.16
MA_RS16050	NA	1.63	1.35	1.61	2.00	1.76	2.15	2.24	2.39	2.84	1.87	1.80	2.00
MA_RS16055	NA	1.57	1.69	1.98	2.17	1.79	2.48	2.14	3.08	3.36	1.98	2.19	2.16
MA_RS16060	NA	2.17	2.36	2.43	2.68	2.58	2.68	2.47	3.25	3.55	3.01	2.59	2.61
MA_RS16065	NA	4.92	5.02	4.50	5.35	5.18	5.11	5.79	6.32	5.83	5.59	5.26	5.18
MA_RS16070	hmgA	4.38	4.61	4.59	4.92	4.65	4.60	4.72	5.09	5.26	4.62	4.37	4.70
MA_RS16075	NA	2.03	2.43	2.15	2.64	2.02	2.68	2.40	3.37	2.92	2.49	2.11	2.69
MA_RS16080	NA	4.24	4.42	4.39	4.60	4.29	4.55	4.56	4.84	5.12	4.00	4.22	4.28
MA_RS16085	NA	3.39	3.96	3.57	3.99	3.57	4.00	3.80	4.03	4.22	3.51	3.55	3.74
MA_RS16090	NA	0.00	0.00	0.44	0.00	0.34	0.19	0.00	0.73	0.44	0.00	0.11	0.00
MA_RS16095	NA	0.26	0.33	0.37	0.77	0.41	0.75	0.33	0.60	0.50	0.94	0.48	0.28
MA_RS16100	NA	0.62	0.16	0.72	0.85	0.67	0.69	0.89	1.08	0.80	0.03	0.12	0.79
MA_RS16105	NA	0.46	0.15	0.50	0.20	0.17	0.58	0.55	0.35	0.81	0.37	0.43	0.98
MA_RS16110	NA	0.57	0.85	0.68	1.47	0.88	0.78	0.63	0.73	1.39	0.60	0.99	1.21
MA_RS16115	NA	0.63	0.89	0.30	1.16	0.99	1.39	1.09	1.75	1.81	1.04	1.12	1.34
MA_RS16120	flaJ	0.85	1.11	0.63	1.11	0.84	0.72	0.49	1.08	1.73	0.95	0.74	1.33
MA_RS16125	NA	0.61	0.84	0.82	1.36	1.01	0.98	1.38	1.26	1.41	1.57	1.23	1.15
MA_RS16135	hacA	4.05	4.05	4.07	4.33	4.17	4.17	4.55	4.53	4.57	4.42	4.09	4.24
MA_RS16140	NA	1.71	2.16	2.08	2.34	2.25	2.36	1.80	2.37	3.05	2.11	2.13	1.67
MA_RS16145	NA	1.56	1.87	1.92	1.76	1.87	2.10	2.17	2.41	2.58	2.13	1.74	2.10
MA_RS16155	NA	2.16	2.26	2.21	2.67	2.41	2.66	2.49	3.10	3.25	2.40	2.49	2.35
MA_RS16160	NA	1.68	2.00	1.87	1.97	1.74	2.00	1.73	2.38	2.76	2.68	2.55	2.02
MA_RS16165	NA	1.02	1.69	0.93	1.61	1.25	1.61	1.60	2.75	2.38	1.51	2.01	2.31
MA_RS16170	NA	1.90	1.97	1.72	2.18	1.98	1.98	1.74	2.40	2.38	2.29	1.95	2.09
MA_RS16180	NA	2.24	2.31	2.11	2.64	2.68	3.22	2.31	3.21	3.03	2.51	2.48	2.47
MA_RS16185	NA	2.42	2.93	2.53	2.89	2.42	2.95	2.65	3.55	3.61	3.32	2.74	2.43
MA_RS16190	pstC	1.82	1.90	1.60	2.11	1.60	2.28	1.76	2.07	2.27	2.21	1.69	1.90
MA_RS16195	pstA	0.74	0.78	0.94	1.26	0.98	0.94	0.86	0.72	0.68	0.72	0.63	0.61

MA_RS16200	NA	0.97	0.87	0.68	1.09	0.91	1.25	1.07	1.11	1.64	0.55	1.07	0.79
MA_RS16205	NA	0.63	0.73	0.81	1.21	0.78	1.16	0.99	1.06	1.47	0.94	1.31	0.40
MA_RS16210	NA	0.84	1.19	1.09	1.41	1.08	0.99	1.14	1.53	1.82	1.07	1.34	1.27
MA_RS16215	NA	4.97	5.19	4.98	4.87	4.87	5.14	4.66	5.44	5.40	4.96	4.61	4.83
MA_RS16220	NA	1.78	2.25	1.76	1.60	1.88	1.59	1.08	1.98	2.61	1.45	1.57	1.53
MA_RS16230	NA	0.89	0.48	0.61	1.13	0.94	1.29	0.76	1.67	1.70	0.96	0.71	0.28
MA_RS16240	NA	1.99	1.90	2.41	1.96	1.62	1.85	1.39	1.80	2.71	1.32	1.95	1.77
MA_RS16245	NA	2.81	2.82	2.76	2.75	2.45	2.62	2.38	3.41	3.96	2.68	2.28	2.24
MA_RS16250	NA	0.71	0.19	0.09	1.35	0.78	0.30	0.62	0.35	0.84	1.06	0.37	0.49
MA_RS16255	NA	0.37	0.60	0.33	1.38	0.83	0.80	0.58	1.99	2.08	1.03	0.87	1.07
MA_RS16260	NA	3.16	3.16	3.07	3.50	3.41	3.34	3.74	3.79	3.64	3.17	3.29	3.59
MA_RS16265	NA	1.48	1.25	1.50	1.27	1.51	1.44	1.69	2.04	2.78	2.01	1.75	1.41
MA_RS16270	NA	0.00	0.11	0.00	0.00	0.36	0.00	0.31	0.26	0.36	0.00	0.00	0.00
MA_RS16275	NA	0.48	0.48	0.29	0.00	0.59	0.69	0.36	0.65	0.97	0.67	0.00	0.22
MA_RS16285	NA	1.82	1.78	2.09	1.65	1.82	2.29	3.02	2.75	2.74	2.03	1.68	1.59
MA_RS16290	NA	1.13	1.31	1.40	1.58	0.98	1.71	1.83	1.99	1.90	1.76	1.67	1.37
MA_RS16295	NA	0.20	0.15	0.27	0.28	0.32	0.25	0.30	0.49	0.53	0.40	0.37	0.16
MA_RS16300	NA	1.38	1.19	1.08	1.49	1.29	1.71	1.12	2.40	1.89	1.93	0.97	0.96
MA_RS16305	NA	1.80	1.75	2.16	2.10	1.94	2.24	2.19	2.89	2.86	2.49	2.05	2.07
MA_RS16310	NA	1.06	1.37	1.53	1.33	0.99	1.12	0.91	2.16	2.22	1.36	1.22	1.28
MA_RS16315	NA	1.74	2.04	1.76	2.37	2.21	2.05	2.08	2.97	2.87	2.59	2.07	2.09
MA_RS16320	NA	2.88	2.84	3.30	3.34	2.96	3.07	3.11	4.12	4.35	2.99	2.49	2.80
MA_RS16325	NA	2.10	1.92	1.92	2.12	2.25	2.15	2.09	3.44	3.78	2.64	2.14	2.34
MA_RS16330	istB	0.29	0.12	0.13	0.48	0.51	0.44	0.24	0.56	0.65	0.33	0.28	0.42
MA_RS16335	istA	0.37	0.32	0.38	0.35	0.53	0.35	0.54	0.52	0.41	0.41	0.38	0.38
MA_RS16340	NA	0.68	0.25	0.71	0.79	0.43	1.19	0.84	1.42	0.98	0.71	1.01	0.48
MA_RS16345	NA	1.85	1.97	2.18	3.27	2.30	3.17	2.97	3.05	3.29	2.67	2.19	2.65
MA_RS16350	NA	2.62	3.02	2.58	3.77	3.36	3.59	3.26	3.67	3.81	3.25	3.27	3.04
MA_RS16355	NA	2.29	2.67	2.57	3.59	3.23	3.21	3.48	3.60	3.67	3.31	3.05	3.14
MA_RS16360	NA	5.42	5.42	5.40	5.62	5.41	5.46	5.76	5.72	6.07	5.74	5.16	5.54
MA_RS16370	NA	5.50	5.24	5.49	5.56	5.59	5.37	5.83	6.38	6.00	5.93	5.33	5.47
MA_RS16375	#N/A	4.57	4.26	4.18	4.49	4.62	4.44	4.66	3.55	4.12	4.89	4.49	4.55
MA_RS16380	#N/A	4.62	4.39	4.47	4.92	4.95	4.78	4.93	4.59	4.86	5.54	4.80	4.96
MA_RS16385	#N/A	2.19	2.29	1.52	2.87	2.58	2.32	2.65	2.54	1.52	2.71	2.51	1.56
MA_RS16390	NA	2.35	2.22	2.38	2.31	2.28	2.36	2.08	3.08	3.27	1.94	1.70	1.80
MA_RS16400	NA	0.54	0.27	0.46	1.02	0.73	0.38	0.90	1.13	1.56	0.88	1.06	0.41
MA_RS16405	NA	1.91	2.07	1.85	1.88	1.96	2.18	2.55	2.38	2.07	1.58	1.87	2.18
MA_RS16410	NA	3.99	3.92	3.65	4.04	3.64	4.05	4.80	3.85	3.77	3.68	2.92	4.09
MA_RS16415	NA	3.58	3.94	3.70	4.03	4.29	4.04	4.30	4.45	4.61	3.95	3.49	4.09
MA_RS16420	NA	3.55	3.82	3.68	3.97	3.84	3.96	4.11	4.57	4.45	3.68	3.49	4.07
MA_RS16425	NA	3.28	3.50	3.43	3.92	3.61	3.52	3.96	4.18	4.18	3.64	3.25	3.82
MA_RS16430	NA	5.52	5.72	5.63	5.91	5.60	5.88	5.90	6.41	6.38	6.05	5.65	5.73
MA_RS16435	NA	4.17	4.24	4.03	4.00	3.96	4.10	4.09	4.45	4.43	3.95	4.02	4.03
MA_RS16440	NA	1.89	1.50	2.08	2.43	2.32	2.16	1.06	2.56	2.74	1.82	1.76	1.79
MA_RS16450	NA	4.31	4.71	4.44	4.89	4.70	4.76	4.71	5.04	5.27	4.42	4.56	4.62
MA_RS16455	NA	5.05	5.29	5.06	5.45	5.19	5.42	5.48	5.38	5.57	4.95	5.14	5.30
MA_RS16460	NA	4.58	4.88	4.72	5.24	4.88	5.00	5.24	5.76	5.92	4.93	4.99	5.00
MA_RS16465	NA	5.69	5.79	5.75	6.09	5.71	5.92	5.94	6.12	6.30	5.75	5.82	5.92
MA_RS16470	NA	5.06	5.26	5.17	5.43	5.03	5.47	5.24	5.75	6.03	5.50	5.17	5.26
MA_RS16475	pheA	3.19	3.53	3.55	3.47	3.59	3.45	3.77	3.43	3.71	3.28	3.24	3.19
MA_RS16480	NA	1.42	1.20	1.17	1.61	1.35	1.60	1.50	2.32	2.13	1.57	1.43	1.72
MA_RS16485	NA	2.66	2.78	3.13	2.91	2.71	2.86	3.31	3.39	2.51	2.55	2.45	2.36
MA_RS16490	NA	3.02	2.85	3.07	3.32	3.35	3.35	3.31	3.84	3.91	3.48	3.25	3.46
MA_RS16495	NA	3.64	3.97	3.89	4.03	3.71	3.99	3.98	4.95	5.15	3.88	3.84	4.16
MA_RS16500	NA	2.34	2.29	2.15	2.53	2.51	2.72	2.84	3.91	4.09	2.83	2.55	2.90
MA_RS16505	NA	0.97	0.46	0.96	0.81	1.34	0.87	1.02	1.67	1.47	1.49	1.35	1.07
MA_RS16510	NA	1.02	0.83	0.96	0.78	0.84	0.80	1.46	1.03	0.83	0.48	1.40	0.60
MA_RS16515	NA	0.33	0.23	0.16	0.27	0.20	0.33	0.36	0.44	0.55	0.25	0.20	0.21
MA_RS16520	NA	2.22	2.97	2.27	3.21	2.98	2.76	3.38	2.70	2.83	2.89	2.86	2.75
MA_RS16525	NA	3.19	3.49	3.49	3.91	3.64	3.57	3.69	4.16	4.41	4.10	3.62	3.54
MA_RS16530	NA	3.65	3.51	3.79	4.20	3.67	4.08	3.84	4.18	4.66	4.27	4.10	3.83
MA_RS16535	NA	4.38	4.26	4.05	4.67	4.55	4.56	4.88	4.45	4.53	4.35	4.19	4.71
MA_RS16545	NA	3.84	4.17	3.90	4.64	4.36	4.20	4.53	4.47	4.59	4.40	4.52	4.30
MA_RS16550	NA	3.76	3.94	4.23	4.51	4.15	3.96	4.40	4.81	5.24	4.15	4.24	3.90
MA_RS16555	NA	2.80	2.82	2.60	2.61	2.55	2.78	3.11	3.01	2.64	1.91	2.23	2.37
MA_RS16560	NA	2.16	2.15	2.15	2.29	2.21	2.57	2.26	2.62	2.58	2.50	1.93	2.07
MA_RS16565	NA	2.44	2.40	2.50	2.59	2.52	2.56	2.83	2.97	2.44	2.68	2.39	2.23
MA_RS16570	NA	1.17	1.42	1.19	1.53	1.52	1.23	1.43	1.43	1.31	1.80	1.22	1.61
MA_RS16575	NA	2.86	3.08	3.06	3.15	3.16	3.11	2.93	3.47	3.38	2.75	2.85	2.76
MA_RS16580	NA	3.08	3.36	3.50	3.52	3.53	3.64	3.57	3.67	3.79	3.16	3.06	3.38
MA_RS16585	NA	3.22	3.24	3.09	3.18	3.23	3.37	3.42	3.34	3.36	3.09	3.00	3.48
MA_RS16590	NA	1.95	2.10	1.93	2.22	2.01	2.37	2.50	2.94	3.11	2.37	2.32	2.51
MA_RS16595	NA	2.00	1.32	2.12	1.44	1.58	1.90	1.89	0.91	1.91	1.43	0.88	1.43
MA_RS16605	NA	0.79	0.62	0.41	0.88	1.11	0.54	0.58	0.99	0.73	0.56	0.46	0.86
MA_RS16610	NA	0.32	0.44	0.00	0.30	0.25	0.72	0.26	0.69	0.86	0.19	0.00	0.54
MA_RS16615	NA	1.13	1.21	1.26	1.48	1.54	1.72	1.71	1.81	1.97	1.38	1.58	1.29
MA_RS16620	NA	1.40	1.49	1.58	1.34	0.90	1.55	1.37	1.46	1.49	1.52	1.21	1.34
MA_RS16625	NA	1.55	1.67	1.47	2.00	1.51	1.92	1.54	2.31	2.64	1.23	0.73	1.42
MA_RS16630	NA	1.92	2.15	2.39	1.72	1.82	1.93	2.18	2.72	3.58	1.47	1.35	2.04
MA_RS16635	NA	2.62	2.88	3.08	3.19	2.52	3.03	2.61	3.50	3.92	2.58	2.64	2.60
MA_RS16640	NA	3.27	3.84	3.23	3.76	3.24	3.65	3.58	3.85	4.02	3.78	3.70	3.01
MA_RS16655	NA	5.47	5.82	5.75	6.28	5.82	6.12	6.16	7.01	7.18	6.42	5.90	5.99
MA_RS16660	#N/A	4.91	5.31	4.92	5.62	5.16	5.47	5.86	6.59	6.75	5.96	5.17	5.54
MA_RS16665	NA	3.10	3.29	3.27	3.68	3.32	3.40	3.56	3.82	3.96	3.35	3.39	3.50
MA_RS16670	NA	1.33	1.65	0.12	1.40	1.16	0.95	1.96	2.31	1.41	0.58	0.94	0.66
MA_RS16680	NA	0.71	0.93	0.00	0.75	0.99	1.35	0.26	1.42	1.17	1.14	1.32	0.67
MA_RS16685	purF	6.62	6.85	6.79	7.04	6.84	7.00	7.05	7.31	7.55	6.86	6.79	6.81
MA_RS16690	NA	6.39	6.26	6.38	6.64	6.26	6.50	7.09	7.13	7.44	6.73	6.37	6.54
MA_RS16700	thiD	2.42	2.47	2.61	2.61	2.58	2.53	2.66	2.74	2.62	2.98	2.50	2.87
MA_RS16705	NA	5.04	5.21	5.23	5.68	5.30	5.51	5.55	5.84	6.03	5.36	5.25	5.56
MA_RS16710	NA	1.88	1.90	2.19	2.38	2.42	2.27	2.39	3.44	3.58	2.41	2.30	1.91
MA_RS16715	NA	3.87	3.76	4.23	4.31	4.12	3.92	4.23	4.62	4.57	4.40	3.86	4.01
MA_RS16720	hisD	4.09	4.18	4.14	4.48	4.29	4.42	4.61	4.84	4.85	4.69	4.18	4.22
MA_RS16725	NA	3.48	3.63	3.52	3.93	3.70	3.85	3.72	4.10	4.29	3.71	3.73	3.83
MA_RS16730	NA	3.36	3.71	3.43	3.95	3.71	3.92	3.70	3.78	4.21	3.64	3.63	3.75
MA_RS16735	NA	4.73	5.06	4.94	5.44	5.20	5.16	5.22	5.96	6.22	5.78	5.09	5.23
MA_RS16740	NA	5.03	5.26	4.89	5.36	5.24	5.50	5.46	5.35	5.30	5.39	5.33	5.50
MA_RS16745	NA	2.16	2.61	2.18	2.41	2.19	2.28	2.59	2.95	2.86	2.24	2.37	2.83
MA_RS16750	NA	2.34	2.37	2.39	2.52	2.64	2.43	2.39	3.30	2.94	2.61	2.62	2.38
MA_RS16760	NA	0.28	0.40	0.38	0.27	0.52	0.51	0.38	0.56	0.52	0.45	0.43	0.21
MA_RS16765	NA	2.93	3.15	2.76	3.35	3.49	3.56	3.17	4.10	4.08	3.51	3.53	3.02
MA_RS16770	trsA	6.03	6.16	5.97	5.92	6.01	6.11	6.11	6.39	5.69	5.97	5.86	5.77
MA_RS16775	NA	2.28	2.10	1.84	2.54	2.13	2.66	2.25	2.95	3.39	2.68	1.91	2.07
MA_RS16785	NA	1.58	1.98	1.70	1.79	2.15	2.44	2.04	2.53	3.14	2.21	2.03	2.21
MA_RS16790	NA	1.84	1.83	1.72	2.05	2.07	1.87	1.57	2.51	2.50	2.18	2.15	1.83
MA_RS16795	#N/A	1.27	0.76	0.65	1.13	1.20	1.16	0.64	2.41	1.05	0.52	0.50	0.64
MA_RS16800	NA	1.36	1.78	1.75	1.90	1.33	1.86	1.33	2.31	1.99	1.93	1.44	1.81
MA_RS16820	NA	0.48	0.44	0.36	0.41	0.01	0.19	0.79	0.33	0.89	0.05	0.43	0.81
MA_RS16825	NA	0.00	0.00	0.27	0.20	0.00	0.00	0.03	0.37	0.00	0.00	0.73	0.28
MA_RS16830	NA	0.68	0.90	0.79	0.63	0.00	0.82	0.00	0.30	0.16	0.46	0.00	0.80
MA_RS16835	NA	0.10	0.37	0.69	0.30	0.32	0.23	0.00	0.19	0.00	0.00	0.00	0.30
MA_RS16840	NA	0.33	0.16	0.30	0.00	0.00	0.62	0.27	1.05	0.83	0.83	0.34	0.22
MA_RS16845	NA	0.48	0.31	0.13	0.43	0.34	0.14	0.35	0.41	0.93	0.00	0.11	0.13
MA_RS16850	NA	0.00	0.83	0.00	0.18	0.18	0.35	0.42	0.10	0.68	0.64	0.40	0.19
MA_RS16860	NA	0.90	0.77	0.78	0.91	0.69	1.04	0.20	0.28	0.95	1.15	0.00	0.85
MA_RS16865	NA	0.92	0.47	0.62	1.34	0.94	1.04	1.30	1.43	1.95	0.99	0.98	0.99
MA_RS16870	NA	0.64	0.82	0.70	0.94	0.59	1.01	0.69	1.26	1.39	0.86	1.24	0.64
MA_RS16875	NA	0.29	0.29	0.39	0.32	0.00	0.00	0.21	0.61	0.67	1.02	0.97	0.25
MA_RS16880	NA	0.24	0.13	0.00	0.70	0.69	0.22	0.24	0.79	0.43	0.40	0.26	0.00
MA_RS16885	NA	2.58	3.50	3.43	3.67	3.29	3.54	3.77	3.79	4.13	3.76	3.39	2.88
MA_RS16890	NA	1.01	1.08	0.63	0.75	1.72	0.84	0.80	1.49	1.31	1.89	1.27	1.20
MA_RS16895	NA	2.58	2.54	2.29	2.50	3.02	2.28	2.60	2.95	2.92	2.74	2.06	2.33
MA_RS16900	NA	0.81	0.90	0.71	0.00	0.73	0.44	0.88	0.72	0.91	0.88	0.68	0.29
MA_RS16905	NA	3.63	3.37	3.40	3.63	3.61	3.68	3.77	4.32	3.95	3.51	3.62	3.41
MA_RS16915	NA	1.05	1.78	2.01	1.79	1.77	1.99	2.29	1.56	1.63	1.89	1.35	1.83
MA_RS16920	NA	4.69	4.85	4.67	5.14	4.84	4.78	5.28	5.55	5.48	4.92	4.63	4.86
MA_RS16925	NA	2.00	2.57	2.31	2.41	2.10	2.31	2.31	2.83	2.69	2.60	2.20	2.16
MA_RS16930	NA	3.76	3.35	3.80	3.76	4.14	3.31	3.97	4.27	4.27	3.65	3.43	3.24
MA_RS16935	NA	1.58	1.76	1.37	0.98	1.91	1.74	1.59	2.29	2.74	2.18	1.41	2.24
MA_RS16940	NA	2.67	2.77	2.57	3.03	2.89	3.21	3.07	3.39	3.71	3.02	2.75	2.83
MA_RS16945	NA	4.17	4.37	4.23	4.63	4.32	4.59	4.44	4.74	5.21	4.34	4.12	4.00
MA_RS16950	NA	0.26	0.40	0.73	0.00	1.45	0.21	0.23	1.09	1.66	0.58	0.00	0.00
MA_RS16955	NA	4.12	4.48	4.26	4.40	4.03	4.24	4.73	5.07	5.24	4.61	4.38	4.54
MA_RS16965	ala	3.67	3.91	3.70	3.65	3.73	3.79	3.78	4.40	4.27	3.80	3.43	3.48
MA_RS16970	NA	3.83	4.00	3.94	4.31	4.34	4.27	4.13	4.51	4.21	4.20	4.16	4.08
MA_RS16975	NA	4.22	4.27	4.25	4.31	4.24	4.35	4.22	4.18	4.55	4.27	4.14	4.14
MA_RS16980	NA	2.94	2.52	2.12	2.35	2.60	2.74	3.07	3.57	3.05	3.11	3.54	2.98
MA_RS16985	NA	2.37	2.70	2.23	2.89	1.59	1.98	2.19	3.22	3.53	2.37	2.43	2.11
MA_RS16990	NA	2.37	2.49	2.49	2.74	2.68	3.10	3.04	3.47	3.85	3.08	2.56	2.81
MA_RS17000	NA	1.60	2.40	1.78	2.24	2.34	2.72	2.58	3.37	3.46	2.92	2.55	2.23
MA_RS17005	NA	0.88	0.79	1.43	1.22	0.53	1.28	0.78	1.08	1.09	1.12	0.44	1.38
MA_RS17010	NA	7.10	7.46	7.33	7.39	6.93	7.34	7.21	7.77	7.97	7.31	6.90	7.09
MA_RS17015	fxsA	4.74	4.86	4.97	4.64	5.03	4.75	4.80	4.81	4.59	4.59	4.79	4.95

MA_RS17020	NA	3.63	4.00	3.99	4.33	3.95	4.13	4.39	5.01	5.35	4.53	4.15	4.27
MA_RS17025	NA	3.69	4.08	3.78	4.14	4.12	4.23	4.09	4.90	5.29	4.66	3.97	3.97
MA_RS17030	nifS	2.59	2.28	2.73	2.51	2.39	2.86	2.68	3.01	3.18	2.69	2.21	2.41
MA_RS17035	nifU	0.88	2.07	1.14	1.30	1.94	1.75	1.78	1.54	2.51	1.17	1.25	1.87
MA_RS17045	NA	1.88	1.97	2.22	2.44	2.01	2.17	2.21	3.37	3.85	2.53	1.81	2.25
MA_RS17050	mptN	2.92	3.05	3.05	3.29	2.90	3.04	3.16	2.39	2.92	3.06	2.63	2.91
MA_RS17060	pth2	4.76	4.86	4.86	5.24	4.44	4.97	5.31	5.62	5.78	5.12	4.93	4.85
MA_RS17065	NA	4.34	4.71	4.47	4.94	4.56	4.89	4.82	5.24	5.54	5.11	4.67	4.70
MA_RS17070	truD	3.28	3.50	3.18	3.86	3.39	3.66	3.73	3.92	4.17	3.75	3.57	3.61
MA_RS17090	NA	0.82	0.77	0.55	0.72	0.93	0.25	1.20	0.89	0.98	0.85	0.62	0.86
MA_RS17095	NA	0.36	0.08	0.50	0.28	0.00	0.66	0.48	0.61	0.64	0.15	0.34	0.00
MA_RS17100	NA	0.71	0.49	0.28	0.66	0.40	0.17	0.74	1.64	0.25	0.60	0.27	0.38
MA_RS17105	NA	2.19	2.21	2.69	2.91	2.75	2.59	2.81	3.37	3.18	2.92	2.69	2.16
MA_RS17110	pyrG	5.53	5.73	5.53	6.07	5.82	6.00	6.02	6.50	6.64	5.93	5.67	5.93
MA_RS17115	NA	4.43	4.55	4.65	4.80	4.78	4.96	4.68	4.81	4.92	4.79	4.59	4.67
MA_RS17120	NA	4.26	4.46	4.53	4.71	4.40	5.06	4.92	5.00	5.12	5.12	4.20	4.71
MA_RS17125	cosS	3.35	3.63	3.76	4.01	3.85	4.12	3.89	4.30	4.47	3.95	3.80	3.89
MA_RS17130	NA	3.00	3.32	3.39	3.56	3.30	3.64	3.28	3.61	4.16	3.48	3.62	3.38
MA_RS17135	NA	3.40	3.28	3.15	3.76	3.26	3.46	3.47	3.62	3.78	3.58	2.88	3.48
MA_RS17140	NA	1.85	2.00	2.06	2.51	2.28	1.93	2.18	2.30	2.80	1.89	1.88	1.94
MA_RS17145	NA	0.83	0.88	0.52	0.84	0.91	0.81	1.14	0.93	0.92	1.57	1.07	1.15
MA_RS17150	NA	5.44	5.91	5.68	6.20	5.70	6.02	6.00	6.29	6.77	5.41	5.52	5.88
MA_RS17155	NA	5.73	6.11	5.93	6.30	5.98	6.17	6.33	6.60	6.92	5.86	5.98	6.16
MA_RS17160	lonB	7.20	7.48	7.31	7.84	7.37	7.69	7.63	7.81	8.09	7.70	7.41	7.48
MA_RS17165	NA	3.30	3.42	3.30	3.66	3.58	3.53	3.58	4.03	3.94	3.77	3.47	3.49
MA_RS17170	NA	2.72	2.76	2.69	3.00	3.22	2.88	2.70	3.32	3.43	3.22	2.62	2.52
MA_RS17175	NA	1.79	1.95	1.83	1.63	1.60	2.01	1.81	1.93	2.03	1.63	1.20	1.66
MA_RS17185	NA	2.45	2.62	2.61	2.46	2.44	2.73	2.35	3.67	4.32	2.84	2.54	2.56
MA_RS17190	NA	4.07	3.68	3.83	4.20	3.48	3.77	4.25	4.20	3.22	4.04	3.71	3.48
MA_RS17195	NA	3.61	4.04	3.85	4.09	4.00	3.72	3.47	4.46	4.49	3.90	3.94	3.89
MA_RS17200	NA	2.32	2.72	2.90	3.55	3.04	3.62	3.43	3.15	3.51	3.02	3.07	3.22
MA_RS17205	comE	2.55	2.82	2.79	3.42	2.96	3.49	3.11	3.27	3.55	3.12	2.90	3.27
MA_RS17210	NA	3.11	3.33	3.04	3.61	3.34	3.77	3.19	3.69	3.87	3.12	3.34	3.49
MA_RS17215	#N/A	3.30	3.49	3.02	2.49	3.83	2.56	4.30	3.43	2.92	3.42	3.49	2.99
MA_RS17220	#N/A	4.41	3.95	4.33	3.78	4.10	4.32	4.09	3.23	3.32	3.72	3.95	4.40
MA_RS17225	#N/A	4.35	3.83	4.15	4.24	4.24	4.32	4.22	4.23	4.00	4.39	4.17	4.32
MA_RS17230	#N/A	3.16	3.33	3.77	2.32	2.77	2.94	3.02	1.48	2.53	2.62	2.74	2.75
MA_RS17235	#N/A	1.11	1.61	1.31	0.73	1.05	0.94	1.48	0.64	0.30	0.36	0.53	0.34
MA_RS17240	#N/A	1.36	2.26	0.57	0.82	0.96	1.18	0.00	1.62	0.00	1.60	1.10	0.77
MA_RS17245	NA	5.23	5.06	5.06	5.66	5.67	5.09	6.38	6.27	5.96	5.92	5.36	5.48
MA_RS17250	NA	3.13	3.21	2.84	3.45	3.66	3.46	3.53	3.98	4.00	3.43	3.21	2.66
MA_RS17255	NA	3.89	3.84	4.01	5.06	4.78	4.81	4.34	5.04	5.35	4.58	4.26	3.98
MA_RS17260	ccsA	2.62	2.96	2.75	3.25	3.23	3.46	3.05	3.42	3.75	2.41	3.00	2.96
MA_RS17265	NA	3.52	3.58	3.45	4.20	3.88	3.86	3.61	4.27	4.33	3.59	3.74	3.69
MA_RS17270	NA	4.28	4.32	4.53	5.14	4.64	4.95	4.61	4.71	5.02	4.98	4.68	4.96
MA_RS17275	pyrE	3.95	4.63	4.20	4.82	4.46	4.62	4.70	4.69	4.63	4.76	4.28	4.76
MA_RS17280	NA	3.76	3.47	3.82	4.46	4.11	3.65	3.88	4.75	4.99	3.97	3.39	3.83
MA_RS17285	purD	5.24	5.43	5.43	5.72	5.43	5.64	5.83	5.60	5.85	5.44	5.37	5.54
MA_RS17290	argF	5.59	5.92	5.68	6.23	5.88	6.10	6.02	6.04	6.13	5.83	5.71	5.96
MA_RS17295	#N/A	1.66	1.20	1.04	2.02	1.87	1.82	2.18	1.96	1.73	2.05	1.61	1.39
MA_RS17310	NA	2.89	3.13	3.07	3.53	3.33	3.38	3.45	3.94	4.21	3.53	3.27	3.17
MA_RS17315	NA	0.85	1.20	1.17	1.19	1.14	1.47	1.38	1.37	1.44	1.01	1.12	1.23
MA_RS17320	NA	1.40	1.53	1.36	1.98	1.36	2.02	1.88	2.85	2.95	1.82	1.82	1.81
MA_RS17325	NA	3.80	3.98	3.96	4.23	4.15	4.19	4.24	4.87	4.97	4.41	3.95	3.98
MA_RS17335	NA	2.26	2.12	1.51	2.73	1.67	2.52	1.87	2.93	2.73	2.85	2.29	2.16
MA_RS17340	NA	2.61	2.64	2.69	2.99	3.27	2.85	3.25	3.11	3.06	2.90	3.35	3.01
MA_RS17350	NA	2.01	2.05	2.27	2.22	2.44	2.44	1.41	2.60	2.38	1.90	2.13	2.35
MA_RS17355	uvrB	3.42	3.78	3.86	4.33	3.91	4.23	4.10	4.34	4.61	4.43	4.02	4.28
MA_RS17360	uvrC	3.75	4.04	3.95	4.83	4.50	4.78	4.50	5.15	5.44	4.91	4.35	4.53
MA_RS17365	uvrA	4.24	4.62	4.30	5.22	4.87	5.05	5.13	5.29	5.53	5.07	4.75	5.08
MA_RS17370	istA	0.49	0.44	0.27	0.61	0.53	0.77	0.50	0.85	0.88	0.71	0.65	0.60
MA_RS17375	istB	0.42	0.37	0.61	0.78	0.31	0.61	0.49	1.02	1.58	0.85	0.49	0.63
MA_RS17380	NA	2.40	2.59	2.82	2.43	2.64	2.80	2.70	3.65	3.91	2.90	2.51	2.58
MA_RS17385	NA	1.45	1.28	1.58	1.56	1.55	1.03	1.42	2.33	1.55	1.43	1.34	1.68
MA_RS17390	NA	0.66	0.17	0.85	0.00	0.29	0.02	0.50	1.52	0.31	1.05	0.54	0.12
MA_RS17395	NA	1.39	1.53	1.41	1.99	1.61	1.56	1.56	1.78	2.28	2.05	1.62	1.46
MA_RS17400	NA	1.89	1.96	2.05	2.25	2.02	2.15	2.02	2.72	2.88	1.89	2.04	1.96
MA_RS17405	NA	2.12	1.91	2.16	2.38	2.55	2.35	2.30	2.94	2.95	1.90	2.00	2.02
MA_RS17410	NA	2.81	2.62	3.19	4.23	3.84	3.96	3.82	4.66	4.66	4.02	3.44	3.22
MA_RS17415	NA	0.50	0.84	0.39	0.56	0.32	0.50	0.04	0.31	0.09	0.07	0.66	0.33
MA_RS17420	NA	0.50	0.81	0.43	0.84	0.53	0.69	1.02	1.65	1.16	1.30	0.42	0.95
MA_RS17425	NA	1.32	1.36	1.53	1.45	1.32	1.45	1.60	1.98	2.18	1.80	1.23	1.41
MA_RS17430	NA	2.17	2.15	2.51	2.71	2.41	2.44	3.05	3.63	3.50	3.40	3.10	2.72
MA_RS17435	NA	1.89	2.02	1.82	2.45	1.92	2.63	2.49	2.90	3.25	2.77	2.72	2.38
MA_RS17440	NA	2.39	1.89	1.66	3.08	3.06	2.50	2.51	3.01	2.78	3.39	3.22	3.13
MA_RS17445	NA	6.04	6.31	6.16	6.60	6.14	6.51	6.49	7.01	7.20	7.11	6.42	6.52
MA_RS17450	NA	4.27	4.66	4.46	4.63	4.46	4.62	4.91	5.55	5.61	4.56	4.26	4.43
MA_RS17455	NA	5.30	5.56	5.38	5.62	5.26	5.55	5.66	6.06	6.18	5.37	5.23	5.29
MA_RS17460	NA	7.19	7.42	7.34	7.67	7.34	7.49	7.42	7.68	7.89	7.41	7.16	7.28
MA_RS17465	NA	2.77	2.96	3.08	3.20	2.91	2.95	3.28	3.73	3.83	2.99	2.64	3.20
MA_RS17470	NA	3.86	3.86	4.12	4.45	4.35	4.32	4.53	5.09	5.33	4.92	4.41	4.22
MA_RS17475	NA	1.99	2.15	2.12	2.12	1.89	2.23	2.28	3.11	3.35	2.57	1.70	2.24
MA_RS17480	NA	1.64	1.65	1.92	2.31	2.25	1.93	1.88	2.55	2.50	2.34	1.77	1.94
MA_RS17490	NA	0.90	0.70	1.25	1.24	1.35	1.15	1.83	1.47	1.93	1.24	0.48	1.20
MA_RS17500	NA	0.09	0.33	0.27	0.25	0.25	0.28	0.00	0.07	0.62	0.00	0.25	0.00
MA_RS17505	istB	0.30	0.11	0.12	0.33	0.44	0.45	0.28	0.66	0.56	0.37	0.24	0.45
MA_RS17510	istA	0.50	0.32	0.43	0.59	0.58	0.50	0.62	0.73	0.72	0.53	0.48	0.55
MA_RS17520	NA	2.09	1.92	1.66	2.20	2.30	2.12	2.48	2.32	2.63	2.34	2.11	1.86
MA_RS17525	NA	2.47	2.67	2.56	3.28	3.05	3.00	3.16	3.52	3.32	2.79	3.21	3.04
MA_RS17530	NA	1.79	2.33	2.10	2.67	1.93	1.91	2.42	2.71	2.82	2.74	2.26	2.08
MA_RS17535	NA	1.25	1.71	1.36	2.02	1.82	1.61	1.95	1.71	2.13	1.97	1.58	2.05
MA_RS17540	NA	1.71	1.20	2.32	0.90	1.70	2.70	1.81	2.84	2.18	1.84	1.78	1.57
MA_RS17545	NA	3.14	3.56	3.46	4.09	3.47	4.14	4.03	4.66	4.98	3.92	3.64	3.58
MA_RS17550	tnpB	4.72	4.58	4.91	5.36	5.01	5.22	5.13	6.00	6.31	5.48	5.08	5.04
MA_RS17555	tnpA	0.93	0.67	0.52	0.57	0.54	1.05	0.65	0.54	0.84	0.71	0.93	1.03
MA_RS17560	NA	0.71	0.96	1.23	1.11	1.11	0.90	1.27	1.54	1.19	1.12	1.23	0.89
MA_RS17565	NA	2.11	2.38	2.22	2.04	1.41	1.75	2.18	1.96	2.29	1.76	1.76	1.67
MA_RS17570	NA	1.54	1.16	1.12	0.88	1.47	1.40	1.47	1.47	1.10	0.96	1.43	0.39
MA_RS17580	NA	3.17	3.27	3.11	3.54	3.17	3.48	3.28	4.45	4.27	3.61	3.37	3.42
MA_RS17590	NA	2.26	2.36	2.19	2.34	2.27	2.43	2.45	3.41	3.80	2.85	2.09	2.34
MA_RS17595	arfO	3.73	3.69	3.35	3.55	3.59	3.75	4.01	3.89	3.71	3.49	3.54	3.58
MA_RS17605	ilvD	4.03	4.30	4.16	4.54	4.26	4.38	4.58	4.58	4.81	4.48	4.46	4.58
MA_RS17620	NA	0.25	0.26	0.47	0.26	0.80	1.03	0.99	1.51	0.00	1.39	0.49	0.33
MA_RS17625	NA	0.40	0.52	0.44	0.32	0.24	0.19	0.57	0.35	0.56	0.94	0.35	0.76
MA_RS17630	NA	4.24	4.32	4.42	4.15	4.24	4.62	4.66	4.70	4.29	4.14	4.43	4.55
MA_RS17635	NA	1.37	1.63	1.54	1.70	1.58	1.47	1.16	1.80	1.92	1.11	0.92	1.14
MA_RS17640	NA	0.79	1.16	0.79	1.23	1.08	1.67	0.96	1.12	1.36	1.08	0.70	0.94
MA_RS17645	NA	2.65	2.69	2.37	2.76	2.75	3.12	2.97	3.15	3.21	2.79	2.65	2.49
MA_RS17650	NA	8.10	8.54	8.45	8.49	8.16	8.43	8.34	9.02	9.18	6.91	7.60	7.96
MA_RS17655	NA	1.31	1.16	0.95	1.53	1.23	1.71	2.05	1.57	1.62	2.02	1.76	1.22
MA_RS17665	NA	0.16	0.14	0.00	0.03	0.00	0.00	0.00	0.05	0.22	0.28	0.03	0.14
MA_RS17675	NA	5.55	5.74	5.68	6.19	5.81	6.08	6.03	6.55	7.01	6.33	5.81	6.01
MA_RS17680	NA	1.71	2.04	1.31	2.22	2.09	2.38	1.89	2.57	2.53	2.38	1.81	1.75
MA_RS17685	NA	3.90	4.08	4.15	4.47	3.94	3.93	4.30	5.10	5.35	4.65	3.96	4.22
MA_RS17690	NA	1.57	1.64	1.80	1.91	1.89	1.89	1.84	1.98	2.00	1.54	1.59	1.73
MA_RS17695	NA	1.52	1.33	1.56	0.58	0.91	1.65	0.91	1.56	1.84	1.73	1.05	1.70
MA_RS17700	NA	2.43	2.24	2.02	2.50	2.21	2.26	2.85	3.27	3.91	2.89	1.57	2.13
MA_RS17705	NA	0.75	0.85	0.37	1.49	0.93	1.27	0.99	1.54	1.12	1.62	0.70	0.84
MA_RS17710	NA	1.40	1.23	1.62	1.51	1.80	2.06	0.52	2.67	2.42	1.87	1.75	1.47
MA_RS17720	NA	3.25	3.37	3.24	3.57	3.34	3.77	3.47	4.08	4.31	3.69	3.59	3.58
MA_RS17725	NA	1.99	1.86	2.16	1.85	2.47	2.52	2.27	2.88	3.44	2.38	2.03	2.17
MA_RS17730	NA	3.34	3.45	3.24	3.72	3.29	3.69	3.42	4.30	4.53	4.14	3.58	3.87
MA_RS17735	NA	2.80	3.23	2.87	3.16	3.12	3.44	2.64	3.19	3.51	3.29	2.93	3.26
MA_RS17745	NA	1.15	1.14	1.14	1.14	0.79	1.05	1.13	1.22	1.68	0.99	1.06	0.98
MA_RS17750	NA	1.45	1.63	1.20	1.74	1.69	1.71	1.68	1.89	2.06	1.87	1.48	1.19
MA_RS17755	NA	2.91	3.24	2.93	3.55	3.28	3.27	3.32	3.22	3.18	3.10	2.65	2.72
MA_RS17760	NA	1.97	2.55	2.21	2.37	2.28	2.60	2.48	3.08	2.84	2.97	2.92	2.67
MA_RS17765	NA	1.00	1.56	1.09	1.21	1.55	2.15	1.50	1.90	2.52	2.05	1.44	1.77
MA_RS17770	NA	2.28	2.99	1.92	3.26	2.90	2.73	3.26	4.15	4.11	3.67	3.00	3.24
MA_RS17775	NA	2.96	3.37	2.98	3.44	3.49	3.52	3.75	3.62	3.76	3.82	3.42	3.64
MA_RS17780	NA	0.61	0.80	0.55	0.91	0.69	0.74	1.00	1.15	1.52	1.13	0.95	0.91
MA_RS17785	NA	4.26	4.27	4.50	4.28	4.61	4.28	4.45	4.77	4.05	4.24	4.19	3.97
MA_RS17790	NA	2.35	1.70	1.44	1.57	1.90	2.14	1.72	1.91	2.29	1.59	1.56	1.62
MA_RS17795	ppsA	4.07	4.26	4.07	4.20	3.93	4.22	4.23	4.55	4.68	3.71	3.76	3.75
MA_RS17800	NA	4.67	4.59	5.07	4.45	4.29	4.71	4.45	5.40	6.04	4.55	4.64	4.20
MA_RS17805	NA	3.81	4.14	4.07	4.52	4.07	4.42	4.32	4.78	5.00	4.02	4.01	4.30
MA_RS17810	NA	3.53	3.40	3.68	3.69	3.87	3.89	3.77	4.46	4.39	3.97	3.95	3.80
MA_RS17815	NA	2.58	2.52	2.86	1.64	2.24	2.22	2.15	2.51	2.53	2.05	2.40	2.16
MA_RS17825	NA	0.84	1.02	1.39	1.16	1.08	1.18	1.18	1.93	2.49	1.47	1.07	1.28
MA_RS17830	NA	2.16	2.39	2.53	2.31	1.44	1.31	2.13	2.62	2.96	2.19	2.21	2.39
MA_RS17835	NA	2.26	2.51	2.52	2.46	2.13	2.51	2.89	2.95	2.57	2.41	2.36	2.30
MA_RS17840	NA	8.24	8.37	8.40	8.24	7.95	8.12	8.33	8.37	8.62	8.05	8.02	8.05
MA_RS17845	NA	3.66	3.98	3.72	4.30	3.78	4.07	4.38	4.55	4.81	4.29	3.86	3.88

MA_R17850	NA	2.01	2.49	2.26	2.49	2.39	2.27	2.70	3.24	3.94	2.91	2.18	2.61
MA_R17855	NA	2.90	2.96	3.02	3.12	3.00	3.16	3.33	3.04	3.00	2.82	2.73	3.15
MA_R17860	NA	3.35	3.83	3.62	4.02	3.77	3.77	4.47	4.94	4.23	3.83	3.37	3.44
MA_R17870	NA	0.85	0.74	0.73	0.86	1.21	0.87	1.27	1.60	1.62	1.05	1.40	1.29
MA_R17875	NA	2.87	2.99	3.23	3.20	2.76	2.87	3.09	3.52	3.97	3.35	2.94	3.19
MA_R17880	NA	3.24	3.30	3.10	3.73	3.32	3.68	3.41	3.86	3.82	2.99	2.59	3.15
MA_R17885	NA	3.02	3.32	3.30	3.42	2.94	3.13	3.29	3.80	3.80	2.87	2.37	2.63
MA_R17890	NA	1.55	1.81	1.93	1.70	2.00	2.12	2.20	2.10	2.20	1.79	1.84	1.38
MA_R17895	NA	1.09	1.01	0.84	0.90	1.06	0.94	0.44	1.23	0.82	0.91	0.43	0.66
MA_R17900	NA	1.83	1.72	1.84	2.00	2.02	1.97	1.90	2.20	2.40	2.09	2.03	2.21
MA_R17905	NA	3.05	3.05	3.76	3.42	3.50	3.26	4.04	2.47	3.79	3.06	2.58	3.27
MA_R17910	NA	4.32	4.56	4.49	4.85	4.61	4.84	4.87	5.03	5.34	5.00	4.49	4.68
MA_R17915	istB	0.56	0.36	0.34	0.41	0.32	0.39	0.45	0.88	0.86	0.52	0.39	0.48
MA_R17920	istA	0.93	0.78	1.09	1.10	1.13	1.31	1.04	1.38	1.46	1.14	0.77	0.95
MA_R17925	#N/A	1.43	2.85	1.74	2.31	1.52	1.75	1.40	1.95	0.73	1.47	2.14	1.23
MA_R17935	NA	0.53	0.88	1.16	1.47	0.91	1.01	1.19	0.96	1.49	1.07	0.87	0.90
MA_R17940	NA	5.73	5.85	5.88	5.83	5.67	5.83	5.82	6.05	5.90	5.80	5.84	5.62
MA_R17945	NA	4.34	4.62	4.87	4.66	4.34	4.70	4.52	4.55	4.30	4.88	4.59	4.52
MA_R17950	NA	4.18	4.15	4.11	4.62	4.65	4.41	4.82	4.71	4.88	4.86	4.53	4.80
MA_R17955	NA	3.24	3.67	3.55	3.85	3.82	4.25	4.06	4.32	4.66	4.25	3.96	4.15
MA_R17960	NA	2.35	2.41	2.08	2.45	2.17	1.74	2.37	2.00	2.39	1.42	2.53	1.74
MA_R17975	NA	0.66	1.15	0.42	0.72	0.67	0.87	0.93	1.07	1.16	0.80	0.83	1.19
MA_R17980	NA	1.60	0.91	1.60	1.41	1.66	1.32	1.49	2.37	2.37	1.52	1.69	1.36
MA_R17985	NA	0.36	0.53	0.00	1.02	0.28	0.77	0.00	0.81	1.51	0.22	0.00	0.47
MA_R17990	rsgA	2.29	2.49	1.98	2.15	2.18	2.39	2.47	2.42	2.43	2.15	1.97	2.19
MA_R17995	NA	5.21	5.33	5.51	4.70	4.67	4.62	4.83	4.52	4.55	4.55	4.47	4.67
MA_R18000	NA	0.45	0.65	0.66	0.50	0.28	0.00	0.37	0.50	0.77	0.23	0.85	0.52
MA_R18005	amrS	1.57	2.18	1.69	1.93	1.97	2.39	1.82	2.51	2.70	2.03	1.56	1.76
MA_R18010	NA	1.88	1.60	1.86	1.61	1.76	2.10	2.42	2.40	2.03	1.66	1.80	2.23
MA_R18015	NA	1.46	1.32	1.95	2.06	2.09	1.74	2.50	2.37	1.87	1.61	1.76	2.20
MA_R18020	NA	1.52	1.89	1.91	1.97	1.79	2.28	1.93	1.90	1.67	1.45	1.43	2.24
MA_R18025	NA	0.62	1.15	0.92	1.39	0.87	1.28	1.21	1.12	1.22	1.00	1.37	1.13
MA_R18030	NA	0.45	0.88	0.68	0.51	0.53	0.86	0.79	1.20	0.89	0.64	0.23	0.65
MA_R18035	NA	1.70	1.96	0.70	1.15	0.99	2.24	0.97	2.66	2.74	2.69	2.03	1.99
MA_R18040	NA	1.79	1.65	1.82	2.26	1.58	2.11	2.31	2.20	2.66	1.96	1.79	2.10
MA_R18045	NA	2.26	2.49	2.41	2.69	2.40	2.73	2.61	3.21	3.13	2.55	2.40	2.67
MA_R18050	NA	1.25	1.74	1.84	2.11	1.77	1.78	1.73	2.63	2.99	1.73	1.48	2.13
MA_R18055	nikD	0.87	1.83	1.21	1.18	0.95	1.19	1.51	1.70	1.72	1.49	1.53	1.60
MA_R18060	nikC	0.90	1.43	1.74	1.85	1.87	1.86	2.45	2.09	2.82	2.14	1.75	2.10
MA_R18065	NA	1.60	1.21	1.47	1.83	1.76	2.07	1.77	2.33	2.55	1.68	1.84	1.82
MA_R18070	NA	1.44	2.16	2.25	2.37	1.58	2.47	2.34	3.09	2.80	2.38	2.13	2.26
MA_R18075	NA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04	0.14	0.00	0.00
MA_R18080	NA	1.32	1.57	1.39	1.48	1.36	2.05	1.23	1.42	1.51	1.01	1.08	1.83
MA_R18085	NA	1.83	1.89	1.50	1.52	1.89	2.07	1.79	1.80	1.69	1.76	1.86	2.26
MA_R18090	nikC	0.87	1.13	1.18	1.06	1.08	1.20	0.61	1.47	0.98	0.86	1.08	1.36
MA_R18095	NA	0.26	0.43	1.09	0.82	0.48	0.76	0.46	1.32	0.59	0.46	0.31	0.47
MA_R18100	NA	0.46	0.36	0.54	1.08	0.36	0.56	0.19	0.00	0.61	0.42	0.36	0.84
MA_R18105	NA	0.51	0.76	0.70	0.94	1.34	1.06	0.76	1.09	1.07	0.46	0.60	0.84
MA_R18110	NA	2.99	2.61	2.71	2.95	2.64	2.58	2.98	3.81	3.56	2.41	3.02	2.42
MA_R18115	NA	3.41	3.56	3.57	3.93	3.87	3.81	3.81	4.10	4.34	3.40	3.45	3.73
MA_R18120	NA	2.65	2.70	2.43	2.84	2.95	2.86	3.10	3.63	3.41	2.75	2.90	2.79
MA_R18125	NA	3.07	2.91	2.30	3.16	3.30	3.49	3.50	3.31	3.34	3.16	3.19	3.23
MA_R18130	NA	0.92	0.87	0.36	0.85	0.57	0.96	1.07	1.30	0.77	1.19	0.94	1.33
MA_R18150	NA	1.41	1.33	1.15	1.79	1.87	1.38	1.91	1.88	1.79	1.75	1.70	1.79
MA_R18155	NA	1.80	1.76	1.85	2.29	1.80	1.94	2.35	2.64	3.05	2.05	2.21	2.12
MA_R18160	NA	1.53	1.78	2.01	2.18	2.12	2.20	2.27	2.55	3.00	2.05	1.77	1.91
MA_R18165	NA	0.87	1.26	1.08	1.65	0.35	0.36	1.65	0.83	1.16	1.96	0.92	1.22
MA_R18170	NA	0.76	0.58	0.95	1.50	1.00	1.29	1.50	0.87	0.75	0.62	1.14	0.76
MA_R18175	feoB	0.62	0.81	0.85	1.10	0.70	1.07	1.09	1.10	1.40	0.93	1.05	0.77
MA_R18180	NA	0.73	0.26	0.50	0.55	1.36	0.00	0.98	0.00	1.06	0.40	1.07	0.00
MA_R18185	NA	0.36	0.29	0.00	0.00	0.39	0.00	1.64	0.82	0.88	0.55	0.00	0.00
MA_R18190	NA	0.38	0.62	0.19	0.86	0.18	0.35	0.00	0.79	0.39	0.00	0.00	1.03
MA_R18195	NA	1.55	1.22	1.49	1.67	1.40	1.68	1.52	1.83	2.52	1.33	1.50	1.39
MA_R18200	amrS	3.19	3.65	3.27	3.55	3.57	3.31	3.24	3.84	4.01	3.67	3.24	3.26
MA_R18210	NA	3.44	3.41	3.70	4.30	3.88	4.28	4.02	4.49	4.70	4.30	4.04	3.79
MA_R18215	NA	4.96	5.26	5.10	5.66	5.27	5.30	5.54	5.93	6.03	5.75	5.05	5.22
MA_R18220	NA	4.08	4.16	4.08	4.30	4.20	4.31	4.80	4.63	4.76	4.55	4.15	4.27
MA_R18225	tatC	3.32	3.41	3.42	3.84	3.15	3.52	3.58	3.63	3.85	3.61	3.42	3.68
MA_R18230	tatC	3.16	3.65	3.47	3.89	3.65	4.07	3.78	4.40	4.38	4.16	3.66	3.93
MA_R18240	NA	4.96	5.17	5.05	5.40	5.08	5.34	5.22	5.52	5.63	4.78	4.97	5.10
MA_R18245	NA	1.78	1.86	1.96	2.27	1.82	2.17	1.99	2.71	3.70	2.76	1.53	2.27
MA_R18250	NA	2.56	2.63	2.44	2.70	2.52	2.31	2.82	3.21	3.81	3.35	2.65	2.62
MA_R18255	NA	2.56	2.50	2.58	3.26	3.08	3.02	2.66	3.57	3.89	3.45	2.85	2.94
MA_R18260	NA	0.13	0.07	0.14	0.09	0.07	0.15	0.13	0.13	0.27	0.27	0.08	0.09
MA_R18265	NA	0.78	0.73	0.42	0.04	0.43	0.29	0.06	1.53	1.70	0.63	0.32	0.46
MA_R18270	NA	1.34	1.51	1.67	1.19	1.05	1.48	1.31	1.92	2.54	1.61	1.21	1.06
MA_R18275	NA	1.87	2.35	1.92	2.35	2.35	2.41	2.50	2.47	2.62	2.30	2.10	2.35
MA_R18280	NA	6.00	6.21	6.16	5.76	5.54	5.65	6.26	6.80	6.68	5.86	5.83	5.79
MA_R18285	NA	5.79	6.10	6.07	4.73	4.71	4.54	5.54	6.09	6.01	4.78	4.85	5.32
MA_R18290	NA	3.90	4.20	4.10	3.51	3.34	3.66	4.14	4.25	4.35	3.85	3.73	4.03
MA_R18295	NA	2.94	2.89	3.32	3.56	3.35	3.74	3.60	4.66	4.03	4.48	3.72	3.77
MA_R18300	NA	2.35	2.53	2.18	2.84	2.70	2.24	3.13	2.90	3.17	3.12	2.43	2.78
MA_R18305	NA	1.65	1.49	1.79	1.57	2.00	1.55	1.89	2.67	2.09	2.53	1.79	1.75
MA_R18310	NA	2.24	2.49	2.62	3.20	2.76	3.10	3.01	3.56	3.96	3.32	2.94	3.05
MA_R18320	NA	2.74	2.64	2.10	2.53	2.84	2.47	3.05	3.15	3.29	2.94	2.62	2.81
MA_R18325	istB	0.35	0.20	0.14	0.25	0.11	0.30	0.32	0.37	0.45	0.18	0.11	0.27
MA_R18330	istA	0.75	0.50	0.79	0.90	0.87	1.07	1.02	1.21	1.19	0.83	0.78	0.79
MA_R18340	NA	3.02	3.23	3.46	3.57	3.14	3.64	3.41	4.15	4.53	4.07	3.11	3.37
MA_R18345	NA	1.19	0.74	1.31	1.39	1.46	1.04	1.02	1.30	1.65	1.37	0.68	0.48
MA_R18355	cofE	3.80	3.66	3.81	3.73	3.89	3.68	3.88	3.93	3.89	4.44	4.15	4.11
MA_R18360	NA	1.33	1.88	1.30	1.96	2.15	2.17	1.76	2.48	2.72	2.21	1.98	1.80
MA_R18370	NA	4.24	4.35	4.51	4.33	4.52	4.52	4.34	4.66	4.76	4.62	4.32	4.24
MA_R18375	NA	3.21	3.35	3.24	3.86	3.70	3.74	3.52	3.76	4.08	3.45	3.15	3.46
MA_R18380	folP	3.67	3.71	3.85	4.11	3.86	4.16	4.33	4.22	4.59	4.11	3.85	3.99
MA_R18390	NA	6.08	6.32	6.29	6.72	6.40	6.53	6.64	6.55	6.96	6.52	6.23	6.57
MA_R18395	glyA	5.77	5.98	5.91	6.42	6.12	6.30	6.27	6.49	6.68	6.25	6.10	6.24
MA_R18400	purN	4.70	4.95	5.04	5.41	5.13	5.39	5.70	5.94	6.29	5.71	5.31	5.41
MA_R18405	NA	0.73	0.41	0.48	0.89	0.69	0.40	0.08	0.68	1.42	1.67	0.80	1.11
MA_R18410	NA	5.37	5.46	5.44	5.80	5.71	5.81	5.64	6.22	6.51	5.94	5.47	5.66
MA_R18415	NA	4.33	4.56	4.43	4.67	4.58	4.80	4.68	4.90	4.99	4.92	4.76	4.71
MA_R18420	NA	3.81	4.10	3.88	4.66	4.22	4.56	4.31	4.36	4.71	4.23	4.24	4.17
MA_R18425	NA	5.33	5.67	5.67	5.85	5.61	5.72	5.95	5.89	5.98	5.71	5.50	5.80
MA_R18430	NA	6.86	7.02	6.91	7.45	7.15	7.21	7.33	8.04	8.27	7.89	7.09	7.22
MA_R18440	NA	2.67	2.75	3.02	2.55	2.37	2.68	1.56	1.92	2.17	1.95	1.95	1.50
MA_R18445	NA	2.27	2.38	2.20	2.67	2.26	2.64	3.10	3.25	3.75	2.92	2.58	2.50
MA_R18450	NA	1.42	1.83	1.76	2.04	1.82	2.10	2.45	2.29	2.71	2.26	2.01	1.84
MA_R18455	NA	1.73	1.32	1.41	1.42	0.94	1.75	1.31	1.70	1.50	1.47	1.32	0.92
MA_R18460	NA	1.62	1.60	1.35	1.91	1.49	2.03	1.50	2.69	3.21	2.31	1.42	1.92
MA_R18465	NA	1.68	1.48	1.69	1.81	1.18	1.81	1.91	2.37	3.04	1.49	1.32	2.29
MA_R18470	NA	2.35	2.18	2.63	2.55	2.52	2.45	2.43	2.97	3.31	2.37	1.88	2.65
MA_R18475	NA	1.32	1.98	1.48	1.49	1.87	2.13	1.56	2.45	2.00	2.33	1.47	1.91
MA_R18480	NA	1.61	1.82	1.55	2.14	1.82	2.02	1.85	2.62	3.27	2.17	1.64	1.64
MA_R18485	NA	1.04	0.85	0.42	0.68	0.79	0.96	1.06	1.48	2.02	0.91	0.58	1.25
MA_R18490	NA	0.36	1.29	0.74	1.11	0.25	1.20	0.07	1.27	2.15	0.66	0.83	0.97
MA_R18495	NA	2.18	2.52	2.38	2.77	2.57	2.30	2.79	3.40	3.67	2.54	2.52	2.65
MA_R18500	NA	2.12	2.35	2.19	2.81	2.46	2.55	2.62	3.11	3.56	2.52	2.43	2.72
MA_R18510	NA	2.33	2.76	2.81	3.35	3.18	3.36	3.01	3.66	4.26	3.20	3.28	3.20
MA_R18515	radA	5.91	6.18	6.06	6.76	6.59	6.64	6.44	6.66	6.86	6.76	6.55	6.64
MA_R18520	NA	2.53	2.71	2.82	3.06	2.62	3.17	3.32	3.86	3.78	3.74	2.88	3.04
MA_R18525	NA	3.83	4.00	3.26	4.22	3.68	3.87	4.01	4.94	4.47	4.41	3.90	3.50
MA_R18530	NA	2.98	3.14	3.38	3.29	3.12	3.04	3.08	3.33	3.64	3.08	3.19	2.90
MA_R18535	NA	1.93	2.06	1.75	1.86	2.25	2.13	2.17	2.47	2.16	2.24	1.68	1.75
MA_R18540	NA	1.76	1.24	1.42	1.36	0.93	1.38	1.56	1.56	2.57	1.85	1.97	0.81
MA_R18545	NA	3.80	3.81	3.85	4.21	4.06	4.16	4.14	3.92	4.29	3.79	4.05	3.94
MA_R18550	cbiQ	4.41	4.50	4.41	4.79	4.42	4.60	4.52	5.08	5.15	4.61	4.75	4.61
MA_R18555	NA	3.15	2.86	2.90	2.40	2.49	2.78	3.25	3.72	3.32	2.63	2.24	2.89
MA_R18560	NA	2.99	3.31	3.22	2.77	2.26	2.76	3.35	3.76	3.48	2.68	2.86	2.90
MA_R18565	NA	0.87	1.32	1.36	1.38	1.46	1.92	1.47	1.61	0.82	1.50	2.09	1.40
MA_R18570	NA	6.33	6.66	6.44	6.96	6.51	6.76	6.67	7.25	7.41	6.35	6.25	6.38
MA_R18575	NA	1.08	1.16	1.67	1.78	1.55	1.57	1.12	1.96	2.27	1.69	1.21	1.40
MA_R18585	cca	4.18	4.43	4.27	4.73	4.50	4.72	4.46	4.58	4.65	4.91	4.44	4.62
MA_R18590	NA	1.69	1.87	1.89	2.22	1.83	2.29	2.18	2.82	3.25	2.15	1.70	1.93
MA_R18595	NA	4.01	4.35	4.32	4.81	4.26	4.66	4.46	5.01	5.35	4.08	4.20	4.48
MA_R18600	NA	4.36	4.57	4.44	4.93	4.62	4.82	4.76	4.96	5.07	4.31	4.51	4.67
MA_R18605	pfkC	4.65	4.94	4.84	5.31	4.93	5.13	4.87	5.28	5.38	4.79	4.73	4.82
MA_R18610	argJ	5.00	5.19	5.13	5.61	5.22	5.40	5.43	5.32	5.75	5.50	5.08	5.28
MA_R18615	NA	5.25	5.35	5.39	6.04	5.56	5.61	5.88	6.42	6.69	6.01	5.33	5.69
MA_R18620	argC	4.35	4.67	4.50	4.96	4.71	4.91	4.94	5.07	5.39	5.08	4.72	4.80
MA_R18625	#N/A	1.62	2.05	1.92	2.48	2.33	1.85	2.54	2.36	2.18	1.77	0.96	1.48
MA_R18630	NA	2.58	3.09	3.10	3.33	3.02	3.00	2.77	3.36	3.76	2.76	2.70	2.37
MA_R18635	NA	2.43	2.83	2.83	2.73	3.23	2.51	3.18	2.82	3.01	2.40	2.01	2.43
MA_R18640	NA	2.49	2.53	2.49	2.56	2.73	3.06	2.79	3.55	3.37	2.75	2.71	2.94
MA_R18650	NA	1.24	1.44	1.68	1.74	1.67	1.87	1.81	2.78	2.67	2.09	1.62	1.59

MA_RS18655	NA	3.39	3.39	3.65	3.87	3.89	3.80	4.04	4.26	4.34	3.97	3.47	3.65
MA_RS18660	NA	1.61	1.96	1.45	2.04	2.18	2.03	2.31	2.71	2.72	1.90	1.77	2.27
MA_RS18670	NA	1.57	1.79	1.74	1.88	1.07	1.41	2.15	3.48	2.74	2.32	1.00	2.34
MA_RS18675	NA	0.36	0.76	0.00	0.69	0.56	1.06	0.59	0.64	0.49	0.34	0.25	0.45
MA_RS18680	NA	0.85	0.52	0.00	0.00	0.98	0.63	1.24	0.66	1.51	0.75	0.48	0.00
MA_RS18685	NA	1.81	1.94	2.31	2.13	2.15	2.26	2.47	2.60	3.56	2.25	2.03	2.69
MA_RS18690	NA	2.96	3.20	3.23	3.70	3.13	3.45	3.63	4.38	4.65	3.64	3.08	3.63
MA_RS18695	NA	3.12	3.29	3.44	3.93	3.51	3.61	3.81	4.60	5.15	4.07	3.35	3.63
MA_RS18700	NA	2.90	3.25	3.18	3.73	3.64	3.61	3.49	3.68	4.21	3.82	3.38	3.72
MA_RS18705	NA	2.64	2.61	2.79	2.71	2.81	2.63	3.21	3.87	4.07	2.98	2.78	2.61
MA_RS18710	#N/A	2.38	2.25	2.99	2.86	2.11	2.38	2.23	1.92	2.31	2.17	2.39	2.40
MA_RS18715	NA	0.59	0.28	0.00	0.70	0.21	0.00	1.12	0.38	0.23	0.00	0.22	0.78
MA_RS18720	NA	0.08	0.24	0.13	0.33	0.85	0.40	0.65	0.80	0.37	0.51	0.22	0.00
MA_RS18725	NA	5.53	4.87	5.03	6.47	6.13	6.68	6.88	6.74	7.76	4.65	6.21	6.76
MA_RS18730	NA	1.37	1.70	1.92	2.13	1.74	1.89	2.00	2.09	2.05	2.06	2.04	1.86
MA_RS18735	NA	4.07	4.61	4.47	4.97	4.26	4.76	4.77	4.65	4.51	4.44	4.33	4.44
MA_RS18740	pgk	5.02	5.31	5.26	5.64	5.18	5.54	5.55	6.14	6.40	5.62	5.38	5.36
MA_RS18745	NA	2.42	3.13	2.90	3.27	2.59	3.17	3.05	3.78	3.54	3.03	2.87	2.67
MA_RS18750	NA	2.77	2.77	2.44	2.97	2.85	2.52	2.77	3.89	3.44	2.98	2.94	2.05
MA_RS18755	NA	2.93	3.26	2.58	3.44	2.97	3.17	3.22	4.14	4.34	2.81	2.72	3.03
MA_RS18760	NA	2.25	2.14	2.45	3.26	2.95	2.51	3.01	3.45	2.95	2.70	2.79	2.87
MA_RS18770	NA	2.43	2.62	2.49	2.79	2.44	2.81	2.89	3.58	3.65	2.55	2.24	2.65
MA_RS18775	NA	1.91	2.27	2.25	2.41	2.17	2.63	2.58	2.68	2.92	1.87	2.04	1.98
MA_RS18780	NA	2.62	2.78	2.80	3.15	3.12	2.73	2.89	3.58	3.27	2.82	2.35	2.84
MA_RS18785	NA	2.66	2.70	2.53	2.89	2.77	2.59	2.82	3.11	2.99	2.30	2.40	2.49
MA_RS18790	NA	2.12	2.39	1.82	2.39	2.21	2.35	2.33	1.94	2.51	2.15	2.38	2.15
MA_RS18795	NA	2.28	2.79	2.90	2.71	3.01	2.97	3.20	3.43	3.21	2.66	3.19	3.05
MA_RS18800	NA	2.68	2.99	2.93	3.38	3.07	3.03	3.14	3.30	3.80	3.30	2.83	3.05
MA_RS18805	NA	7.07	7.42	7.16	7.89	7.41	7.66	7.56	8.14	8.38	7.77	7.32	7.39
MA_RS18810	pta	6.77	7.16	6.98	7.60	7.04	7.36	7.33	7.96	8.33	7.56	7.03	7.03
MA_RS18815	NA	3.34	3.56	4.09	3.87	3.34	3.74	3.98	4.15	4.75	4.06	3.74	4.16
MA_RS18820	NA	4.33	4.69	4.51	4.89	4.88	5.00	4.73	4.86	5.26	4.93	4.90	4.85
MA_RS18825	NA	2.61	3.26	2.72	3.41	3.13	3.24	3.04	4.10	4.08	2.80	2.58	2.99
MA_RS18830	NA	2.37	2.73	2.68	2.90	2.51	2.89	2.46	2.56	3.24	2.05	2.70	2.63
MA_RS18835	NA	2.06	2.44	2.19	2.61	2.56	2.56	2.77	2.92	3.25	2.30	2.16	2.50
MA_RS18840	mtaA	2.06	2.41	2.04	2.72	2.59	2.24	2.49	2.99	2.93	2.18	2.43	2.32
MA_RS18845	NA	1.32	1.39	1.19	1.35	1.51	1.72	1.54	2.22	1.60	1.47	1.29	1.27
MA_RS18850	NA	0.69	0.35	0.49	0.97	0.94	1.09	1.06	1.26	1.73	1.29	1.00	0.83
MA_RS18860	NA	2.00	1.28	0.86	1.71	1.26	1.70	1.49	1.69	2.07	1.49	1.22	1.04
MA_RS18865	NA	0.46	0.30	0.26	0.53	0.47	0.48	0.35	0.56	0.82	0.86	0.45	0.75
MA_RS18870	NA	6.61	6.37	6.55	6.60	6.68	6.47	6.61	6.44	6.47	5.98	6.42	6.22
MA_RS18880	NA	2.82	2.77	2.80	2.84	2.78	2.67	3.00	2.67	3.17	2.84	2.34	2.37
MA_RS18885	hlfX	3.11	3.45	3.29	3.40	3.31	3.49	3.58	3.68	3.77	3.31	3.29	3.40
MA_RS18890	NA	3.98	3.81	3.97	4.07	4.11	3.89	4.18	4.47	4.19	3.82	4.09	4.23
MA_RS18895	endA	3.67	4.02	3.88	4.07	3.82	4.10	3.88	3.94	4.08	3.73	3.82	3.93
MA_RS18905	cfbB	4.97	5.29	5.30	5.47	5.16	5.32	5.39	5.19	5.47	5.03	5.11	5.31
MA_RS18910	cfbC	4.83	5.13	5.05	5.34	4.94	5.33	5.22	5.34	5.74	5.14	4.98	5.14
MA_RS18915	cfbD	4.41	4.76	4.41	4.93	4.64	4.97	4.92	5.03	5.21	4.85	4.53	4.80
MA_RS18920	cfbE	5.36	5.70	5.63	6.04	5.78	6.00	5.83	5.93	6.12	5.70	5.84	5.95
MA_RS18925	cfbA	6.63	6.93	6.74	7.33	6.98	7.31	7.05	7.73	7.86	7.38	7.31	7.27
MA_RS18930	NA	2.06	2.48	2.39	2.47	2.30	2.55	2.85	3.08	3.31	2.43	2.66	2.67
MA_RS18935	NA	1.46	1.81	2.27	1.43	2.47	1.94	1.95	2.73	2.74	1.83	1.30	1.59
MA_RS18940	NA	2.30	2.59	2.47	2.48	1.98	2.68	2.21	3.68	3.18	2.60	2.35	2.46
MA_RS18945	NA	3.75	3.87	3.69	4.17	3.62	3.81	3.84	3.60	4.36	3.70	3.07	3.50
MA_RS18950	NA	3.28	3.17	3.46	3.27	3.45	3.43	3.50	2.83	3.29	3.17	3.44	3.04
MA_RS18955	NA	3.00	2.66	2.82	3.33	2.88	2.85	3.62	4.01	3.92	3.25	2.91	2.70
MA_RS18960	NA	3.95	4.07	4.12	3.30	3.60	3.11	3.07	3.95	3.56	3.65	3.51	3.53
MA_RS18965	NA	1.59	2.02	1.69	1.68	1.75	1.85	1.91	2.09	1.94	1.56	1.49	2.14
MA_RS18970	NA	0.99	1.39	1.11	1.35	1.15	1.40	1.78	2.18	2.16	1.39	1.26	1.38
MA_RS18975	NA	2.10	2.38	2.36	2.66	2.36	2.33	2.99	3.19	3.77	2.66	2.71	2.58
MA_RS18980	NA	2.21	2.30	2.01	2.44	2.37	2.39	2.23	3.07	3.01	1.70	2.34	2.67
MA_RS18985	NA	1.95	2.15	1.84	2.10	1.97	2.25	2.00	2.76	3.17	2.00	1.86	2.22
MA_RS18990	NA	4.45	4.42	4.72	4.70	4.34	4.20	4.87	5.57	5.17	4.51	4.33	4.56
MA_RS18995	#N/A	0.30	0.51	0.52	0.31	0.83	0.25	0.65	1.38	0.84	0.78	0.97	0.57
MA_RS19000	NA	2.24	2.30	2.96	2.74	2.49	3.39	2.94	3.79	4.31	3.19	2.61	2.97
MA_RS19005	hrA	1.68	2.01	1.91	2.21	1.97	2.14	1.70	2.61	3.08	2.59	2.20	2.06
MA_RS19010	NA	0.32	0.48	0.39	0.60	0.41	0.67	0.38	0.87	0.96	0.54	0.60	0.37
MA_RS19020	NA	0.94	1.61	1.93	0.54	0.83	1.22	1.40	1.88	1.47	0.03	0.67	1.17
MA_RS19025	NA	0.94	1.13	1.17	1.18	1.14	1.44	1.33	1.81	1.91	1.51	0.66	1.25
MA_RS19035	NA	0.20	0.58	0.37	0.53	0.37	0.31	0.70	1.43	0.69	0.40	0.87	0.48
MA_RS19040	NA	0.89	0.82	0.91	1.30	1.46	1.41	1.56	0.83	1.79	1.02	0.78	1.24
MA_RS19055	NA	0.85	0.94	0.87	1.06	1.29	1.23	0.88	1.33	1.80	1.17	0.89	0.71
MA_RS19060	NA	1.30	0.55	0.28	0.72	0.69	1.02	1.00	1.20	2.52	0.00	0.61	0.58
MA_RS19065	NA	2.06	2.10	1.80	2.58	2.37	2.47	2.81	2.90	3.05	2.63	2.17	2.33
MA_RS19070	NA	3.01	2.94	3.03	3.32	3.39	3.27	3.46	3.45	3.57	3.05	3.13	3.40
MA_RS19075	NA	2.29	2.66	2.08	3.02	2.61	2.65	2.97	3.27	3.20	3.12	2.93	2.90
MA_RS19080	NA	1.76	1.86	1.50	1.81	1.82	1.83	1.58	1.84	2.29	1.89	1.69	1.50
MA_RS19085	NA	1.60	1.95	1.56	1.57	2.09	1.80	2.36	2.60	2.29	2.26	1.54	2.12
MA_RS19100	NA	0.10	0.38	0.00	0.00	0.00	0.00	0.00	0.22	0.00	0.19	0.00	0.00
MA_RS19105	NA	1.12	0.77	0.91	1.30	1.01	1.27	1.26	1.83	2.08	1.10	0.98	1.14
MA_RS19110	cas5b	2.27	2.43	2.30	2.72	3.18	2.99	2.54	3.22	3.76	2.64	2.34	2.70
MA_RS19115	cas7i	2.57	2.71	2.29	3.13	3.01	3.12	2.95	3.64	3.65	3.06	2.83	3.09
MA_RS19120	cas8a1	2.42	2.56	2.03	2.88	2.75	2.88	2.56	3.14	3.51	2.53	2.36	2.42
MA_RS19125	cas2	1.92	1.92	1.96	2.37	1.45	2.04	2.39	3.32	3.68	1.35	1.94	1.81
MA_RS19130	cas1b	1.40	1.26	1.21	1.76	1.53	1.49	1.58	2.09	2.01	1.35	1.31	1.06
MA_RS19135	cas4	1.13	0.94	1.49	0.99	1.14	1.82	0.90	2.01	2.37	1.40	1.58	0.74
MA_RS19140	cas6	1.20	1.33	1.44	1.43	1.51	0.85	1.68	2.28	1.72	1.42	1.14	1.10
MA_RS19145	NA	3.12	3.16	3.17	3.70	3.43	3.78	3.96	3.81	3.98	3.49	3.17	3.73
MA_RS19150	NA	2.46	2.75	2.64	2.76	2.51	3.11	2.45	2.78	3.28	2.56	1.95	2.89
MA_RS19155	NA	1.39	1.39	1.12	1.32	1.95	1.74	1.46	2.29	2.47	1.31	1.91	1.79
MA_RS19160	NA	4.90	5.09	5.07	5.37	5.15	5.35	5.07	5.21	5.44	5.53	5.36	5.33
MA_RS19165	NA	2.83	3.14	2.73	3.28	3.18	3.48	3.19	3.24	3.58	3.50	3.31	3.59
MA_RS19170	NA	1.61	1.70	1.42	1.37	1.71	1.84	1.15	1.44	1.07	1.15	1.94	1.70
MA_RS19175	NA	4.01	4.12	4.18	4.23	4.14	4.26	4.15	4.09	4.21	3.59	3.63	4.12
MA_RS19180	NA	3.29	3.77	3.53	3.81	3.27	3.70	3.40	3.74	3.97	3.24	3.32	3.36
MA_RS19185	NA	4.89	5.00	4.91	5.22	5.06	5.08	5.48	5.97	6.01	4.99	4.85	5.17
MA_RS19190	NA	2.88	2.87	2.94	3.41	3.01	3.52	3.69	4.14	4.29	3.60	3.22	3.37
MA_RS19195	NA	5.14	5.38	5.44	5.71	5.37	5.51	5.48	5.90	6.30	5.80	5.20	5.37
MA_RS19200	NA	4.81	4.92	5.10	5.55	5.28	5.18	5.69	6.14	6.29	5.44	5.08	5.18
MA_RS19205	NA	3.96	4.07	3.90	4.43	4.09	4.15	3.89	4.13	4.63	3.97	3.97	4.21
MA_RS19210	NA	5.28	5.41	5.39	5.88	5.71	5.90	5.64	6.26	6.49	5.94	5.81	5.82
MA_RS19215	NA	4.46	4.86	4.57	4.97	4.88	5.01	4.95	5.02	5.42	4.88	4.72	5.06
MA_RS19220	NA	5.40	5.77	5.60	5.95	5.96	6.01	5.78	5.94	6.34	5.86	5.65	5.89
MA_RS19225	NA	6.62	6.86	6.71	7.25	6.90	7.13	7.15	7.27	7.52	7.01	6.77	6.93
MA_RS19230	NA	6.97	7.20	7.22	7.68	7.18	7.40	7.52	7.53	7.81	7.33	7.09	7.36
MA_RS19235	NA	6.17	6.41	6.38	6.79	6.53	6.72	7.10	7.05	7.33	6.76	6.34	6.72
MA_RS19240	NA	6.11	6.12	6.19	6.57	6.17	6.60	6.45	6.31	6.71	6.27	6.12	6.33
MA_RS19245	NA	7.80	7.97	7.91	8.24	8.02	8.07	8.22	8.62	8.84	8.48	7.92	8.03
MA_RS19250	NA	7.93	8.19	8.06	8.32	8.12	8.33	8.24	9.02	9.21	8.78	8.22	8.28
MA_RS19255	NA	6.54	6.99	6.83	7.07	6.97	7.10	6.81	7.11	7.69	7.20	6.93	7.09
MA_RS19260	NA	0.92	1.28	1.71	2.14	1.61	0.95	2.14	0.84	1.35	1.11	0.17	1.20
MA_RS19285	NA	1.76	1.50	1.23	1.78	1.43	1.54	2.20	2.72	2.55	2.11	2.11	1.50
MA_RS19290	NA	2.03	1.99	2.36	2.07	2.23	2.36	2.08	2.88	3.27	2.69	2.24	1.83
MA_RS19295	NA	2.72	2.99	2.54	3.24	2.85	3.40	3.04	4.15	4.42	3.65	3.11	3.22
MA_RS19300	NA	1.87	2.02	1.96	2.10	2.21	2.18	1.87	2.06	2.01	1.93	2.05	1.94
MA_RS19305	NA	4.04	4.01	4.10	4.46	4.42	4.59	4.38	4.30	4.28	4.56	4.28	4.39
MA_RS19310	NA	5.05	5.19	5.00	5.41	5.07	5.50	5.46	5.48	5.64	5.70	5.20	5.44
MA_RS19315	NA	2.95	3.14	3.11	3.43	3.06	3.39	3.25	3.74	3.95	3.27	2.63	2.89
MA_RS19320	NA	0.37	0.34	0.27	0.88	0.90	0.73	0.13	0.42	0.73	0.26	1.06	0.95
MA_RS19325	NA	2.37	1.99	2.69	2.63	2.75	2.88	2.42	3.10	3.05	2.66	2.65	2.78
MA_RS19330	NA	3.22	3.30	3.12	3.50	3.84	4.07	3.39	4.92	5.01	3.72	3.47	3.69
MA_RS19335	NA	3.01	3.00	3.05	3.41	3.23	3.53	3.49	3.51	3.75	3.71	3.36	3.46
MA_RS19340	#N/A	0.38	0.39	0.36	0.48	0.67	1.27	0.57	0.81	1.79	1.10	0.83	1.15
MA_RS19350	NA	1.89	2.27	2.07	2.23	2.15	1.75	1.85	1.98	2.57	1.86	1.93	1.81
MA_RS19355	NA	2.65	2.90	2.91	3.26	2.89	3.13	2.99	3.62	3.78	3.21	3.19	3.17
MA_RS19360	nadE	3.47	3.44	3.67	3.46	3.59	3.61	3.57	3.41	3.68	3.15	3.22	3.80
MA_RS19365	NA	2.57	3.22	3.05	3.45	2.91	3.21	3.02	3.43	4.26	3.32	2.80	3.00
MA_RS19370	NA	3.03	3.33	3.39	3.67	3.22	3.36	2.99	3.58	3.97	3.17	3.05	3.29
MA_RS19375	NA	3.48	3.62	3.84	3.68	3.48	3.55	3.05	3.45	4.51	3.44	3.38	3.52
MA_RS19380	NA	2.14	1.97	2.12	2.14	1.72	2.22	2.39	3.12	3.47	2.48	2.24	2.27
MA_RS19385	tnpB	3.12	3.09	3.25	3.71	3.72	3.59	3.59	4.14	4.25	4.07	3.79	3.76
MA_RS19390	tnpA	0.71	0.59	0.61	1.43	0.46	0.84	0.00	1.49	1.52	0.53	0.46	1.22
MA_RS19395	NA	4.19	4.35	4.91	4.06	4.33	4.28	4.60	5.02	5.37	4.71	4.61	4.53
MA_RS19400	uppS	5.66	5.85	5.86	5.84	5.54	5.73	6.00	6.25	6.03	5.75	5.60	5.62
MA_RS19415	NA	2.26	2.65	2.15	2.69	2.45	2.69	2.50	2.83	3.17	1.94	2.08	2.46
MA_RS19420	NA	2.52	2.63	2.08	3.43	2.65	3.13	3.35	3.65	3.68	2.15	2.64	2.68
MA_RS19425	NA	2.21	2.49	2.48	2.90	2.25	2.77	2.82	2.75	3.74	2.21	2.46	1.82
MA_RS19430	NA	0.40	0.73	1.44	0.95	0.88	0.70	0.86	0.58	1.87	1.10	1.10	1.15
MA_RS19435	NA	3.13	3.28	3.18	3.38	2.92	3.09	3.26	3.83	4.01	3.56	3.40	3.36
MA_RS19440	NA	6.54	6.87	6.65	7.09	6.84	7.16	6.80	7.26	7.56	6.84	6.87	7.04
MA_RS19445	fpoF	8.82	8.99	8.79	9.49	9.08	9.29	9.33	10.00	10.08	9.23	9.04	9.21
MA_RS19450	mer	9.15	9.39	9.22	9.82	9.43	9.69	9.54	10.02	10.24	9.39	9.47	9.53
MA_RS19455	NA	1.18	0.48	0.86	1.08	1.85	1.69	1.39	1.27	1.53	1.31	1.36	1.46

MA_RS19460	NA	4.89	5.23	5.28	5.70	5.21	5.28	6.07	6.86	6.72	5.60	5.01	5.35
MA_RS19465	NA	5.73	6.17	6.05	6.59	6.26	6.24	6.48	6.85	7.08	6.05	5.52	6.15
MA_RS19470	NA	4.88	5.12	5.11	5.40	5.26	5.48	5.94	6.06	5.84	5.00	4.87	5.14
MA_RS19475	NA	4.93	5.30	5.37	5.69	5.22	5.64	5.91	6.47	6.24	5.74	5.25	5.27
MA_RS19480	NA	6.15	6.38	6.36	6.49	6.34	6.49	6.66	5.84	6.18	5.79	5.86	6.31
MA_RS19485	NA	4.83	5.21	5.09	5.40	5.18	5.27	5.36	5.55	5.69	4.94	4.86	5.04
MA_RS19490	NA	3.51	3.53	3.78	4.17	3.85	4.22	4.22	4.57	4.75	3.93	3.37	3.79
MA_RS19495	afpA	3.99	4.11	3.92	4.51	4.29	4.33	4.49	5.00	5.22	4.66	4.39	4.34
MA_RS19500	NA	4.66	4.99	4.73	5.20	5.04	4.97	5.21	5.95	5.86	4.84	4.59	5.02
MA_RS19505	NA	4.44	4.81	4.63	5.08	4.71	5.06	4.73	5.28	5.75	4.80	4.57	4.87
MA_RS19510	NA	3.62	3.93	3.70	4.06	3.95	4.30	3.91	3.85	4.37	3.19	3.56	4.15
MA_RS19515	NA	2.27	2.29	2.17	2.95	2.55	2.85	3.01	3.40	3.76	2.64	2.51	2.42
MA_RS19520	NA	1.53	2.36	1.47	2.38	2.11	2.20	2.31	1.91	1.87	2.01	1.93	1.85
MA_RS19525	NA	0.72	0.64	0.99	1.29	1.22	0.77	0.20	1.30	1.40	1.21	0.66	0.90
MA_RS19530	NA	2.77	3.35	3.19	3.22	3.21	3.32	3.47	3.82	3.57	3.66	3.34	3.60
MA_RS19535	NA	2.85	3.10	2.62	3.25	2.74	3.33	3.07	3.90	4.05	3.60	2.89	3.36
MA_RS19540	NA	3.48	3.43	3.44	3.85	3.67	3.85	3.80	4.08	4.69	4.19	3.89	4.14
MA_RS19545	hscB	4.03	3.87	3.97	4.66	4.18	4.23	4.63	4.31	4.27	4.67	4.33	4.54
MA_RS19550	NA	4.83	4.97	4.97	5.29	4.94	5.24	5.16	5.73	5.95	4.89	4.94	5.08
MA_RS19555	NA	4.13	4.28	4.28	4.23	3.93	3.97	3.79	4.51	4.72	3.81	3.90	3.77
MA_RS19560	NA	1.99	2.16	2.29	2.39	2.06	2.38	2.29	2.74	2.90	1.81	1.99	2.18
MA_RS19565	NA	2.77	2.99	2.83	3.31	2.89	2.92	2.71	3.62	3.81	2.87	2.99	2.69
MA_RS19570	NA	2.55	2.72	2.64	3.04	2.92	2.91	3.28	3.83	4.08	2.82	2.80	2.77
MA_RS19575	NA	3.87	4.02	4.13	4.22	4.07	4.44	4.42	5.43	5.57	4.49	4.27	4.15
MA_RS19580	NA	2.88	2.89	2.77	2.97	2.62	3.11	3.16	3.82	4.18	3.45	3.08	2.75
MA_RS19585	istA	2.21	2.25	2.30	2.21	2.09	2.30	1.96	2.79	3.04	2.46	2.15	2.02
MA_RS19590	istB	2.35	2.39	2.28	2.73	2.57	2.71	2.66	3.51	3.57	2.98	2.63	2.53
MA_RS19595	NA	0.39	0.29	0.35	0.26	0.29	0.33	0.23	0.40	0.52	0.24	0.39	0.20
MA_RS19600	NA	0.13	0.68	0.84	0.36	0.78	0.00	1.44	1.10	1.39	0.82	0.63	0.97
MA_RS19605	NA	1.51	1.34	1.68	1.80	1.42	1.94	1.59	2.30	2.63	1.68	1.44	1.51
MA_RS19610	NA	2.10	2.21	2.48	2.05	2.04	1.78	2.40	3.67	3.99	2.52	2.29	2.16
MA_RS19620	NA	3.82	4.13	4.10	4.45	4.01	4.21	4.43	5.41	5.74	4.55	4.43	4.33
MA_RS19625	NA	3.57	3.58	3.43	3.97	3.85	3.70	4.19	4.73	4.88	3.53	3.77	3.86
MA_RS19630	NA	1.69	1.61	1.59	2.14	1.81	1.84	2.11	2.80	3.33	2.03	2.19	1.72
MA_RS19635	NA	0.86	1.05	0.95	1.22	0.93	1.10	1.02	1.72	2.24	1.73	0.95	1.03
MA_RS19640	NA	1.39	1.25	1.29	1.58	1.47	1.83	0.93	2.24	2.13	2.03	1.94	1.16
MA_RS19645	NA	1.55	1.68	1.73	1.65	1.68	1.84	2.01	2.41	2.72	2.01	1.59	1.61
MA_RS19650	NA	0.18	0.16	0.17	0.13	0.00	0.23	0.04	0.09	0.17	0.49	0.47	0.00
MA_RS19665	NA	2.52	2.64	2.74	3.36	2.61	3.01	3.18	3.37	4.05	2.72	2.67	2.73
MA_RS19670	NA	3.15	3.18	3.29	3.58	3.16	2.90	3.51	4.16	4.29	3.21	2.41	3.23
MA_RS19675	rfbD	3.88	3.87	3.57	3.66	3.60	3.80	3.72	4.42	4.59	3.47	3.07	3.77
MA_RS19680	rfbB	3.88	4.15	4.04	4.44	4.22	4.49	3.95	4.99	5.53	3.89	4.03	4.18
MA_RS19685	rfbC	4.00	4.18	3.89	4.31	4.00	4.21	4.22	5.02	5.24	3.52	3.76	3.90
MA_RS19690	NA	4.36	4.39	4.30	4.64	4.24	4.56	4.62	5.18	5.28	4.39	4.23	4.36
MA_RS19695	NA	2.25	2.59	2.08	2.59	2.60	2.87	2.69	3.25	3.50	2.31	2.45	2.63
MA_RS19700	arsM	2.78	2.83	2.83	3.15	2.55	2.80	3.48	3.49	3.93	3.18	3.02	2.68
MA_RS19705	NA	3.13	3.40	3.26	3.77	3.28	3.74	3.77	4.58	3.69	3.83	3.88	3.90
MA_RS19710	NA	1.74	2.70	2.00	1.90	2.26	1.73	2.15	2.34	2.03	1.99	2.15	1.90
MA_RS19715	NA	5.06	5.38	5.28	5.72	5.11	5.33	5.91	5.79	5.98	5.51	5.12	5.33
MA_RS19720	gltA	5.10	5.48	5.23	5.71	5.32	5.64	5.64	5.91	6.16	5.70	5.34	5.52
MA_RS19725	NA	1.59	1.76	2.05	2.03	1.94	1.81	1.88	2.42	3.19	2.30	2.14	2.48
MA_RS19730	#N/A	2.07	1.71	1.83	2.32	2.25	0.46	1.24	1.76	0.79	1.69	2.54	1.61
MA_RS19735	NA	3.92	4.28	3.92	4.38	4.59	4.15	4.40	4.61	5.24	4.71	4.29	4.19
MA_RS19745	ilvC	7.19	7.51	7.38	7.86	7.53	7.69	7.76	7.64	7.97	8.11	7.60	7.75
MA_RS19750	ilvN	7.96	8.05	8.17	8.45	8.19	8.24	8.52	8.41	8.64	9.22	8.26	8.67
MA_RS19755	NA	7.81	8.09	7.96	8.59	8.14	8.35	8.29	8.57	8.98	9.34	8.40	8.55
MA_RS19760	NA	7.23	7.50	7.38	7.89	7.48	7.63	7.62	7.95	8.33	8.41	7.57	7.71
MA_RS19765	NA	1.57	1.31	1.41	1.80	1.67	1.83	2.08	2.30	1.82	2.04	1.36	1.70
MA_RS19770	NA	1.37	1.09	1.47	0.58	0.89	1.50	1.03	1.26	1.89	1.36	1.30	1.30
MA_RS19775	NA	0.31	0.60	0.64	0.39	0.46	0.50	0.35	0.74	0.83	0.88	0.55	0.87
MA_RS19780	NA	0.17	0.48	0.73	0.09	0.00	0.00	0.33	1.29	0.91	0.00	0.30	0.00
MA_RS19785	NA	0.50	0.82	0.48	1.07	0.91	0.82	1.07	0.95	1.21	0.87	0.86	0.52
MA_RS19790	NA	0.61	0.65	0.78	1.19	1.42	0.49	1.43	1.59	1.51	1.21	0.68	0.46
MA_RS19795	NA	0.93	0.81	0.91	0.92	0.94	0.84	1.15	1.37	1.43	1.02	0.89	1.08
MA_RS19800	NA	0.59	0.50	0.36	1.04	0.81	1.15	0.63	0.97	0.91	0.27	0.79	0.18
MA_RS19805	NA	1.26	0.55	1.56	1.40	1.06	1.41	1.13	2.03	1.69	1.99	0.78	0.89
MA_RS19810	NA	0.94	0.81	0.61	1.40	1.48	1.29	1.07	1.92	1.01	1.18	0.94	0.97
MA_RS19815	NA	0.85	0.00	0.79	0.49	0.81	0.46	0.79	0.00	0.59	1.14	0.49	0.21
MA_RS19820	NA	0.30	0.38	0.95	0.15	0.40	0.20	0.19	0.20	1.12	0.08	0.00	0.26
MA_RS19830	NA	0.60	0.29	0.44	1.39	0.50	0.00	0.86	1.04	1.01	0.84	0.77	0.32
MA_RS19835	NA	0.73	0.59	1.47	1.53	0.48	0.46	1.17	1.10	1.12	1.39	1.04	1.13
MA_RS19840	NA	0.57	0.43	0.61	1.27	1.07	1.42	0.62	0.71	1.55	0.86	0.85	0.83
MA_RS19845	NA	0.34	0.10	0.65	1.32	0.71	0.68	0.60	0.78	2.16	0.58	0.12	1.13
MA_RS19850	NA	0.81	0.65	0.45	0.99	0.40	0.54	0.84	0.32	1.27	0.71	0.42	1.26
MA_RS19855	NA	0.31	0.57	0.27	1.05	0.23	1.01	1.28	1.09	2.16	0.86	0.71	0.57
MA_RS19860	NA	0.55	1.06	0.45	0.67	0.97	1.09	0.94	0.99	1.70	0.93	0.84	1.16
MA_RS19865	NA	0.56	1.28	1.29	1.19	0.93	1.40	0.96	1.17	1.64	1.06	0.42	0.92
MA_RS19870	NA	0.71	0.12	0.88	0.94	1.57	1.00	1.55	0.91	1.68	1.38	0.77	0.47
MA_RS19875	NA	0.47	0.17	1.66	1.62	0.67	1.22	1.08	1.39	1.86	1.49	0.92	0.42
MA_RS19880	NA	0.50	1.03	0.95	1.37	1.05	1.33	1.74	1.44	2.07	1.56	1.36	1.29
MA_RS19885	NA	0.68	0.52	0.99	0.79	0.23	1.39	0.81	1.00	1.50	1.01	1.21	0.92
MA_RS19890	NA	0.20	0.86	1.12	0.87	0.70	1.00	0.43	0.94	2.41	1.48	1.02	1.18
MA_RS19895	NA	0.11	0.23	0.00	0.30	0.29	1.01	0.53	0.00	0.22	0.01	0.67	0.78
MA_RS19900	NA	2.38	2.44	2.30	3.07	2.72	3.02	3.17	3.57	3.89	2.75	2.67	2.55
MA_RS19910	NA	0.02	0.48	0.74	0.29	0.23	0.43	0.27	0.62	0.52	0.16	0.36	0.08
MA_RS19915	NA	1.87	2.13	1.76	2.21	1.33	2.58	2.10	2.85	2.97	2.13	2.21	1.83
MA_RS19920	NA	1.05	1.26	1.18	1.42	1.03	1.09	1.58	1.92	1.91	1.49	1.39	1.44
MA_RS19925	NA	1.17	0.92	1.01	1.16	0.32	1.27	1.34	1.41	2.12	1.29	0.87	1.28
MA_RS19930	NA	0.91	1.23	0.79	1.19	1.03	1.45	1.18	1.63	2.66	1.32	0.97	0.99
MA_RS19935	tetL	1.48	1.40	1.86	1.51	1.76	1.86	1.68	2.06	1.87	1.87	1.44	2.02
MA_RS19940	NA	0.84	1.48	0.37	1.15	1.42	1.33	1.36	2.07	2.83	1.98	1.39	1.43
MA_RS19945	NA	0.43	0.52	0.40	0.32	0.56	0.68	0.33	1.31	1.12	0.79	0.76	0.54
MA_RS19950	NA	2.40	2.31	2.37	2.82	2.76	2.87	2.89	2.94	3.09	2.79	2.61	2.72
MA_RS19955	NA	1.18	0.53	0.66	0.61	0.78	1.23	1.21	2.02	1.85	0.50	0.57	1.49
MA_RS19960	NA	0.37	0.24	0.72	0.30	0.17	1.30	0.21	0.19	1.35	0.16	0.86	0.30
MA_RS19965	NA	0.53	1.29	1.28	1.61	1.50	1.98	1.98	1.68	1.86	1.11	1.09	1.73
MA_RS19970	NA	0.55	0.64	0.60	0.83	1.10	1.04	0.85	1.02	0.24	1.19	0.90	0.93
MA_RS19975	NA	1.02	1.06	1.71	1.45	1.35	1.61	1.14	1.79	1.54	1.21	1.20	1.27
MA_RS19980	NA	0.84	1.06	0.70	0.61	1.47	0.87	1.43	0.82	1.11	0.68	0.48	1.53
MA_RS19985	NA	0.41	0.72	0.32	0.63	1.09	1.24	0.79	0.38	1.84	1.12	1.30	0.32
MA_RS19990	NA	1.44	1.09	0.39	1.81	1.30	1.40	1.02	1.50	0.98	0.64	1.04	1.35
MA_RS19995	#N/A	0.00	0.00	0.00	0.20	0.70	0.00	0.00	0.13	0.00	0.00	0.17	0.00
MA_RS20000	NA	0.05	0.94	0.59	1.25	1.25	1.13	0.52	0.94	0.15	0.75	1.22	0.80
MA_RS20005	NA	0.00	1.44	0.96	0.98	0.32	1.68	0.90	0.32	1.13	0.72	0.08	0.60
MA_RS20010	NA	0.00	0.33	0.54	1.15	1.00	0.16	0.30	1.00	1.49	0.12	0.99	0.21
MA_RS20015	NA	0.84	0.20	0.65	0.75	0.68	0.52	0.29	0.40	0.87	0.46	0.00	0.27
MA_RS20025	NA	1.91	1.86	1.78	2.01	1.63	1.21	1.75	2.02	2.98	1.89	1.80	1.78
MA_RS20030	NA	2.03	2.31	2.18	2.43	2.18	2.78	2.33	3.26	3.56	2.66	2.74	2.47
MA_RS20035	NA	0.21	0.29	0.42	0.32	0.35	0.39	0.16	0.70	0.46	0.30	0.29	0.35
MA_RS20060	NA	2.68	2.75	2.68	2.40	2.56	2.75	1.88	2.77	3.22	3.11	2.37	2.46
MA_RS20065	NA	3.42	3.63	3.24	3.63	3.23	3.59	3.60	4.44	4.60	3.59	3.18	3.08
MA_RS20075	NA	5.08	5.13	5.33	5.32	5.13	5.32	5.38	5.61	5.77	5.21	4.88	4.98
MA_RS20080	NA	7.02	7.05	7.26	7.54	7.35	7.42	7.59	8.55	8.65	7.72	7.28	7.25
MA_RS20085	NA	5.32	5.49	5.46	5.79	5.55	5.82	5.94	6.60	6.83	5.75	5.67	5.65
MA_RS20090	NA	2.68	2.77	3.01	2.54	2.40	2.68	1.55	1.92	2.17	1.96	1.91	1.51
MA_RS20100	NA	5.21	5.49	5.43	5.62	5.44	5.56	5.87	5.90	6.20	5.54	5.27	5.47
MA_RS20105	NA	4.77	5.07	4.87	5.46	5.22	5.42	5.32	6.22	6.52	5.19	4.98	5.35
MA_RS20110	NA	3.91	4.03	3.84	4.51	4.09	4.33	4.89	5.30	4.88	4.49	4.21	4.66
MA_RS20115	NA	4.12	4.50	4.21	4.78	4.59	4.78	4.43	5.27	5.55	4.79	4.74	4.62
MA_RS20120	NA	5.75	6.13	5.96	6.27	6.13	6.42	6.14	6.65	6.69	6.28	6.08	6.17
MA_RS20125	NA	2.07	2.20	2.16	1.74	2.45	2.43	2.24	2.65	3.13	2.28	1.80	2.49
MA_RS20130	NA	3.12	3.05	3.05	3.18	3.35	3.27	3.27	3.81	4.41	3.08	3.25	3.44
MA_RS20135	cdhA	6.84	7.08	6.89	8.51	7.94	8.30	8.04	8.04	8.84	8.89	8.16	8.14
MA_RS20140	cdhB	7.66	7.83	7.70	9.31	8.70	9.08	9.11	9.25	9.93	9.82	8.97	8.97
MA_RS20145	cdhC	7.42	7.69	7.53	9.05	8.55	8.80	8.75	8.67	9.31	9.35	8.63	8.72
MA_RS20150	NA	7.19	7.39	7.39	8.54	8.21	8.40	8.50	8.31	8.75	8.55	8.00	8.24
MA_RS20155	cdhD	6.54	6.87	6.69	8.03	7.62	7.89	7.78	7.89	8.37	8.13	7.48	7.61
MA_RS20160	acsC	6.87	7.15	7.00	8.33	7.92	8.20	8.05	8.19	8.77	8.50	7.85	7.90
MA_RS20165	NA	0.89	0.87	0.65	0.93	1.11	0.81	1.12	1.39	1.35	1.08	1.06	1.07
MA_RS20170	NA	0.38	0.37	0.19	0.43	0.26	0.49	0.22	0.41	0.89	0.34	0.66	0.22
MA_RS20175	NA	2.68	2.51	2.71	3.06	2.61	2.82	3.07	3.47	3.47	2.96	2.55	2.99
MA_RS20180	NA	5.15	5.35	5.38	5.67	5.53	5.60	5.89	6.25	6.36	5.70	5.43	5.70
MA_RS20185	NA	4.74	4.95	4.70	5.39	5.07	5.25	5.18	5.53	5.90	5.33	5.14	5.06
MA_RS20190	NA	4.83	5.24	5.08	5.34	5.07	5.40	5.30	5.85	6.08	5.48	5.19	5.37
MA_RS20195	NA	4.75	4.83	4.66	5.39	5.04	5.14	5.42	5.51	5.87	5.05	4.98	5.26
MA_RS20200	psmB	7.27	7.43	7.35	7.68	7.44	7.59	7.44	8.28	8.52	7.77	7.46	7.47
MA_RS20205	NA	5.94	6.35	6.27	6.77	6.32	6.51	6.42	6.98	7.24	6.18	6.18	6.39
MA_RS20210	NA	3.54	3.62	3.47	3.84	3.61	3.74	3.40	3.73	4.23	3.42	3.12	3.58
MA_RS20215	ftsZ	6.86	7.17	7.07	7.32	7.01	7.21	7.25	7.56	7.50	7.14	6.87	7.07
MA_RS20220	NA	3.55	3.71	3.61	4.02	3.65	4.07	3.97	4.37	4.71	3.89	3.88	3.93
MA_RS20225	NA	3.56	3.80	4.24	4.31	3.70	4.15	4.11	5.04	5.06	4.51	3.63	3.93
MA_RS20230	NA	6.75	7.05	6.86	7.43	6.88	7.21	7.08	7.58	8.01	7.17	6.97	6.92
MA_RS20235	NA	4.63	4.79	4.58	4.87	4.85	4.94	4.71	4.60	4.86	5.32	4.81	5.01

MA_RS20240	NA	2.77	2.98	2.62	3.12	2.97	3.06	2.97	3.51	3.63	3.38	2.71	3.23
MA_RS20245	NA	2.90	3.10	2.96	3.25	3.24	3.19	3.32	3.47	3.54	3.13	3.03	3.18
MA_RS20250	NA	4.04	3.93	3.99	4.62	4.37	4.31	4.36	4.80	5.17	4.18	4.16	4.22
MA_RS20255	sepF	6.36	6.45	6.45	6.96	6.56	6.51	7.33	7.75	7.88	7.03	6.56	6.71
MA_RS20260	NA	5.72	6.06	5.97	6.29	5.93	6.25	6.27	6.65	6.78	6.28	5.92	6.06
MA_RS20265	proS	5.20	5.38	5.27	5.73	5.45	5.70	5.68	5.86	6.13	5.70	5.50	5.59
MA_RS20275	NA	5.05	5.17	5.10	5.05	4.70	4.86	5.29	5.49	5.82	5.13	5.10	5.38
MA_RS20285	#N/A	3.08	2.69	2.62	3.22	3.19	1.96	2.77	2.10	2.63	3.59	2.69	2.79
MA_RS20290	#N/A	4.93	4.55	4.55	4.83	5.39	4.74	5.32	2.06	2.86	3.75	4.56	4.72
MA_RS20295	#N/A	2.23	1.84	2.14	2.01	1.41	0.75	1.28	0.73	0.78	0.92	1.72	0.53
MA_RS20300	NA	6.02	6.25	6.13	6.65	6.25	6.52	6.54	6.58	6.88	6.11	6.00	6.29
MA_RS20305	pyk	5.58	6.01	5.75	6.36	5.90	6.16	6.19	6.60	6.93	5.97	5.73	5.99
MA_RS20310	NA	6.81	6.97	6.90	7.38	7.01	7.21	7.42	8.05	8.20	7.50	7.08	7.11
MA_RS20315	NA	3.12	3.26	3.58	3.15	2.78	3.73	3.75	3.80	4.72	3.69	2.99	3.39
MA_RS20320	NA	1.66	0.39	1.31	0.75	0.87	1.99	1.47	1.46	1.57	1.07	0.39	1.20
MA_RS20325	NA	3.25	3.28	3.38	3.76	3.33	3.76	3.77	3.62	3.88	3.78	3.63	3.54
MA_RS20330	nifH	1.34	2.05	2.43	2.41	2.03	2.17	2.46	3.07	3.03	1.83	1.83	1.65
MA_RS20335	NA	1.41	1.95	2.61	2.44	1.61	2.34	3.02	2.59	2.35	1.72	1.56	1.55
MA_RS20340	NA	2.19	2.63	2.09	3.10	2.41	2.85	3.11	3.46	4.00	3.56	2.63	2.69
MA_RS20345	nifD	2.15	2.67	2.52	2.74	2.50	2.81	2.84	2.88	3.25	2.56	2.21	2.72
MA_RS20350	nifK	3.34	3.43	3.40	3.70	3.51	3.67	3.48	3.68	3.93	3.57	3.45	3.49
MA_RS20355	nifE	1.84	2.05	2.42	2.52	2.00	2.43	2.28	2.40	2.89	2.69	1.99	2.20
MA_RS20360	NA	2.21	2.60	2.34	2.81	2.70	3.11	2.61	2.69	3.16	3.26	2.76	2.89
MA_RS20365	modB	1.51	1.69	1.50	1.56	1.85	1.33	1.75	1.95	2.52	2.38	1.85	2.11
MA_RS20370	NA	1.29	1.38	1.35	1.43	1.22	1.45	1.89	1.69	2.28	1.59	1.29	1.43
MA_RS20375	NA	0.48	0.00	0.00	0.26	0.19	0.00	0.00	0.72	0.34	0.04	0.00	0.49
MA_RS20380	NA	0.49	0.68	0.36	0.98	0.81	1.70	0.76	1.77	0.81	1.24	0.61	0.93
MA_RS20385	NA	0.98	1.22	1.46	1.43	1.28	1.26	1.42	1.75	2.12	1.49	1.19	1.56
MA_RS20390	NA	0.78	1.17	0.53	1.12	0.78	1.79	1.13	1.57	2.11	1.54	0.91	1.06
MA_RS20395	NA	0.78	1.22	1.50	1.30	1.18	1.58	1.53	1.16	1.47	1.31	1.25	1.51
MA_RS20400	NA	0.92	1.06	1.06	1.62	1.01	1.27	1.03	1.54	1.24	1.05	0.84	0.88
MA_RS20405	NA	1.46	1.43	1.38	1.74	1.78	1.61	1.55	1.69	2.16	1.89	1.51	1.24
MA_RS20410	NA	0.39	0.79	0.00	0.88	0.50	0.68	0.39	0.85	1.15	0.81	0.00	0.45
MA_RS20415	NA	1.51	1.45	1.60	1.27	1.33	1.98	1.46	1.49	1.87	1.46	1.77	1.37
MA_RS20420	NA	2.16	2.72	2.18	1.85	2.05	2.60	2.79	3.05	3.72	2.90	2.50	3.15
MA_RS20425	NA	2.20	1.95	2.17	2.33	2.36	2.52	2.15	2.81	3.43	2.71	2.48	2.67
MA_RS20435	NA	1.23	1.31	1.47	1.43	1.48	1.76	1.52	1.71	2.01	1.90	1.71	1.77
MA_RS20440	NA	3.65	3.79	3.49	4.03	4.00	3.99	4.02	4.56	4.42	3.94	3.64	3.53
MA_RS20445	NA	6.66	6.93	6.82	7.26	6.84	6.86	7.14	7.59	6.88	5.70	6.26	6.64
MA_RS20450	NA	4.97	5.32	5.21	5.56	5.21	5.38	5.25	5.38	5.35	4.01	4.82	5.04
MA_RS20455	NA	3.91	4.34	4.26	3.96	3.86	4.22	3.97	4.80	4.28	2.52	3.10	3.32
MA_RS20460	NA	0.71	1.15	1.31	0.42	0.66	0.83	1.16	1.32	1.75	1.37	0.91	1.39
MA_RS20465	NA	0.62	0.48	0.71	1.10	0.97	0.94	0.70	1.13	1.03	0.92	0.53	0.98
MA_RS20470	NA	1.22	1.60	0.98	1.87	1.48	1.62	1.61	2.31	2.06	1.88	1.69	1.77
MA_RS20475	NA	0.65	0.76	0.47	0.83	0.75	0.99	1.01	0.79	1.55	0.78	0.87	1.11
MA_RS20480	NA	2.05	2.88	2.73	2.96	2.22	1.97	2.46	3.31	3.21	2.52	2.64	3.04
MA_RS20485	NA	0.74	1.09	1.32	1.42	1.37	1.58	1.38	1.87	1.81	1.53	1.60	1.71
MA_RS20490	NA	1.65	1.29	1.00	2.16	1.87	1.49	1.62	1.64	1.87	1.77	1.48	1.92
MA_RS20495	NA	1.37	1.66	1.68	2.30	2.06	1.72	1.92	2.86	2.53	2.80	2.37	2.04
MA_RS20500	NA	1.37	1.69	1.49	1.74	1.87	1.83	1.92	1.61	2.43	1.85	1.83	1.51
MA_RS20505	tusB	1.40	1.21	1.47	1.32	1.31	2.12	1.79	2.19	2.25	2.45	0.34	1.90
MA_RS20510	NA	1.68	1.18	1.48	1.86	1.74	1.85	1.16	2.01	1.83	1.25	0.57	1.49
MA_RS20520	#N/A	3.93	4.24	4.38	4.69	4.13	4.64	4.33	4.91	4.98	3.96	4.39	4.60
MA_RS20525	NA	4.22	4.45	4.51	4.76	4.48	4.86	4.51	5.06	4.97	4.15	4.26	4.69
MA_RS20530	NA	4.09	4.24	4.56	4.52	4.07	4.62	4.20	5.02	4.80	3.91	4.06	4.49
MA_RS20535	crcB	2.15	1.96	2.18	2.70	2.21	2.58	2.94	3.91	3.73	2.38	2.53	2.05
MA_RS20540	NA	2.26	2.44	2.11	2.79	1.81	2.81	3.11	3.48	3.40	2.78	2.44	2.97
MA_RS20545	NA	2.06	2.12	1.52	2.30	2.11	2.54	2.15	2.41	2.40	1.99	1.98	1.83
MA_RS20550	NA	2.60	2.03	2.62	2.64	2.88	2.16	2.98	3.38	2.80	2.96	2.19	2.63
MA_RS20555	NA	3.29	2.95	2.80	3.92	3.38	3.71	3.48	3.95	4.04	3.59	3.26	3.19
MA_RS20560	NA	1.84	1.40	2.13	1.05	1.64	2.49	1.67	1.70	2.14	1.46	1.61	1.71
MA_RS20565	NA	1.17	1.57	1.63	1.98	2.05	2.06	1.60	1.94	2.15	1.98	1.61	1.68
MA_RS20570	NA	0.99	0.97	1.18	1.66	1.43	1.88	1.69	0.96	1.40	2.07	1.49	1.97
MA_RS20575	NA	2.36	2.14	2.85	2.67	1.82	2.85	2.68	3.40	3.12	2.84	2.26	2.50
MA_RS20580	NA	1.12	1.46	1.80	1.56	1.34	1.41	1.78	1.74	1.94	1.72	1.74	1.71
MA_RS20585	arsB	0.74	0.86	0.70	0.85	0.91	1.02	0.75	1.26	1.08	0.61	0.64	0.83
MA_RS20590	NA	0.50	0.45	0.35	0.28	0.27	0.71	0.24	0.80	1.07	0.80	0.34	1.08
MA_RS20595	NA	2.54	2.59	2.08	2.10	2.13	2.44	1.65	2.75	3.19	2.38	1.84	2.14
MA_RS20600	NA	3.11	3.50	3.67	3.72	3.25	3.68	3.41	3.81	3.39	3.81	3.04	3.26
MA_RS20605	NA	2.41	2.40	2.72	2.49	2.44	2.67	2.41	3.33	3.14	2.81	2.27	2.67
MA_RS20610	NA	1.94	2.25	2.32	2.08	1.95	1.98	1.38	3.10	2.28	1.57	0.93	1.11
MA_RS20615	NA	1.28	2.04	1.75	1.87	2.15	1.54	2.18	2.00	2.97	1.84	2.32	1.94
MA_RS20620	NA	2.05	2.00	1.00	2.03	2.05	2.37	2.45	2.93	2.59	2.08	1.13	1.31
MA_RS20625	NA	3.36	3.56	3.03	3.75	3.82	3.83	3.73	4.14	4.07	3.96	3.48	3.66
MA_RS20630	NA	2.56	2.42	2.08	2.70	2.64	2.81	2.64	2.92	2.97	2.82	2.14	3.07
MA_RS20635	NA	5.47	5.80	5.69	6.22	5.84	6.09	6.27	6.68	7.06	6.48	6.11	6.28
MA_RS20645	NA	2.59	2.78	2.78	3.30	3.22	2.94	3.52	3.19	3.56	2.77	2.28	2.60
MA_RS20650	NA	2.29	2.31	2.15	2.48	2.44	2.80	2.66	3.06	3.45	2.41	2.40	2.46
MA_RS20655	NA	1.80	1.88	1.82	2.31	2.23	2.31	2.16	3.07	2.82	2.23	1.82	2.16
MA_RS20665	NA	3.63	3.83	3.62	3.96	3.72	4.02	3.92	4.74	4.89	4.20	3.56	3.75
MA_RS20670	NA	3.55	3.71	3.82	4.26	4.07	4.18	4.14	4.77	4.81	4.31	3.94	4.12
MA_RS20675	NA	4.92	5.13	5.15	5.44	5.11	5.28	5.38	6.00	6.10	5.23	4.76	5.10
MA_RS20680	NA	1.34	1.27	1.30	1.92	1.46	1.36	1.53	1.47	1.86	1.77	1.36	1.10
MA_RS20685	NA	3.30	3.33	3.36	3.71	3.54	3.56	3.71	4.23	4.31	3.46	3.43	3.48
MA_RS20690	NA	2.10	2.52	2.02	2.65	2.64	2.69	2.43	2.66	3.17	2.51	2.16	3.05
MA_RS20695	NA	5.20	5.37	5.28	5.60	5.43	5.60	5.55	5.84	5.93	5.44	5.19	5.29
MA_RS20700	NA	1.60	1.21	1.04	1.43	1.86	2.04	1.49	1.87	2.14	1.48	1.73	1.66
MA_RS20705	NA	7.02	7.19	7.15	7.39	7.19	7.32	7.26	7.68	7.59	7.55	7.11	7.14
MA_RS20710	NA	7.04	7.03	6.99	7.36	7.18	7.39	7.48	7.85	8.09	7.57	6.98	7.30
MA_RS20715	purB	4.77	5.08	4.98	5.48	5.11	5.52	5.33	5.67	6.01	5.65	5.22	5.21
MA_RS20725	NA	3.86	4.05	3.91	4.32	4.16	4.32	4.42	4.49	4.84	4.20	3.75	4.29
MA_RS20730	#N/A	1.81	2.44	0.00	0.54	1.61	0.00	2.00	1.87	0.00	2.07	1.69	2.08
MA_RS20735	NA	1.16	1.16	0.94	1.38	1.01	1.11	1.15	1.78	1.30	1.11	1.12	1.06
MA_RS20740	tadA	2.43	2.69	2.76	2.92	2.78	2.84	2.78	3.30	3.72	2.79	2.48	2.69
MA_RS20745	NA	1.98	2.33	2.44	2.43	2.26	2.35	2.39	2.84	2.97	2.05	2.15	2.47
MA_RS20750	NA	3.45	3.91	3.44	4.18	3.88	4.14	4.04	4.19	4.90	4.19	4.00	4.13
MA_RS20755	ablB	6.18	6.41	6.20	6.65	6.47	6.62	6.58	6.92	7.13	6.46	6.29	6.57
MA_RS20760	ablA	6.17	6.43	6.19	6.76	6.50	6.65	6.64	6.59	6.88	6.34	6.32	6.61
MA_RS20765	NA	0.34	0.39	1.02	0.00	0.00	0.71	0.00	0.62	0.41	0.00	0.14	0.00
MA_RS20770	NA	1.84	1.92	1.87	2.03	1.55	1.56	1.70	1.69	1.88	1.37	1.53	1.38
MA_RS20775	NA	1.59	1.65	2.04	2.24	2.03	1.92	2.21	2.59	2.41	2.91	1.96	2.06
MA_RS20780	NA	1.95	1.75	1.26	2.34	1.66	2.31	1.84	2.10	2.12	1.74	1.77	1.80
MA_RS20785	NA	5.13	4.85	4.94	5.40	5.52	5.49	5.81	5.63	5.41	5.37	5.15	5.24
MA_RS20790	NA	4.44	4.57	4.61	5.32	5.20	5.06	4.72	5.34	5.84	5.04	4.42	4.80
MA_RS20795	speB	4.44	4.45	4.41	4.93	4.54	4.65	4.88	5.08	5.21	4.56	4.59	4.64
MA_RS20800	NA	6.28	6.32	6.41	6.62	6.38	6.48	6.87	7.19	7.40	6.89	6.53	6.64
MA_RS20805	NA	2.69	2.54	2.40	2.72	2.80	2.61	2.94	3.64	4.01	3.11	2.85	2.85
MA_RS20810	NA	3.57	3.67	3.63	4.04	3.83	4.04	3.68	4.17	4.06	3.84	3.68	3.73
MA_RS20815	NA	2.97	2.92	3.32	3.53	3.28	2.89	3.23	4.05	3.85	2.86	2.78	3.30
MA_RS20820	NA	2.58	2.50	2.14	2.99	2.56	3.01	2.60	3.22	3.06	3.08	2.50	2.44
MA_RS20825	NA	4.42	4.68	4.67	4.67	4.54	4.44	4.70	5.21	5.80	4.59	4.42	4.43
MA_RS20830	NA	5.30	5.53	5.28	5.81	5.62	5.65	5.71	6.21	6.47	5.47	5.34	5.56
MA_RS20835	NA	5.34	5.54	5.40	5.79	5.30	5.68	5.62	6.18	6.31	5.33	5.37	5.71
MA_RS20840	NA	5.92	6.15	6.12	6.37	6.08	6.24	6.25	6.42	6.78	5.99	5.87	6.14
MA_RS20845	NA	5.64	5.82	5.78	6.23	5.93	6.16	6.06	6.30	6.47	5.71	5.72	5.87
MA_RS20850	NA	5.07	5.46	5.25	5.64	5.13	5.52	5.82	5.50	5.75	5.40	5.01	5.38
MA_RS20855	NA	5.23	5.46	5.41	5.62	5.28	5.51	5.85	6.00	6.32	5.40	5.20	5.50
MA_RS20860	atwA	5.60	5.99	5.87	6.22	5.90	6.08	6.13	6.79	7.05	6.09	5.60	5.89
MA_RS20865	NA	3.05	3.27	3.23	3.42	3.46	3.55	3.31	4.07	4.11	3.37	3.05	3.30
MA_RS20870	NA	3.99	3.94	3.90	4.48	4.01	4.52	4.22	4.39	4.51	4.34	4.03	3.73
MA_RS20875	NA	4.90	4.89	4.87	4.96	4.79	4.69	4.84	5.46	5.20	5.40	4.91	4.65
MA_RS20880	NA	3.56	3.72	3.27	3.66	3.94	3.89	3.92	4.95	4.69	4.46	4.30	3.94
MA_RS20890	fen	3.36	3.56	3.48	3.70	3.54	3.56	3.61	4.06	4.24	3.48	3.15	3.56
MA_RS20895	NA	2.50	2.70	2.77	2.64	2.48	3.03	2.76	2.63	3.20	2.50	2.70	2.69
MA_RS20900	NA	2.91	2.99	3.18	3.12	3.24	3.44	3.29	3.01	3.17	3.13	2.86	2.94
MA_RS20905	gpmI	4.37	4.51	4.19	4.87	4.67	4.83	4.81	4.91	4.98	4.63	4.28	4.42
MA_RS20910	NA	2.08	2.32	1.79	2.70	2.51	3.06	2.22	2.40	2.73	2.18	2.43	2.16
MA_RS20915	NA	0.59	1.54	1.47	1.13	0.62	1.59	1.37	0.69	1.44	0.62	1.69	1.18
MA_RS20920	NA	5.67	5.88	5.71	5.68	5.31	5.52	5.62	6.22	6.28	5.22	5.22	5.25
MA_RS20925	NA	5.33	5.51	5.52	5.91	5.56	5.91	5.83	6.44	6.82	5.85	5.21	5.77
MA_RS20930	purH	6.46	6.73	6.58	7.28	6.89	7.19	7.03	7.46	7.76	7.29	6.95	7.07
MA_RS20935	NA	1.20	1.65	1.39	1.51	1.50	1.80	1.64	2.05	2.10	1.91	1.49	1.86
MA_RS20940	nth	3.14	3.12	3.02	3.74	3.43	3.61	3.37	4.12	4.09	3.73	3.61	3.37
MA_RS20945	NA	4.29	4.65	4.58	4.67	4.51	4.83	4.84	5.60	5.47	4.51	4.70	5.28
MA_RS20950	cbiM	3.98	4.25	4.15	4.30	4.06	4.41	4.61	5.20	4.95	4.18	4.37	4.63
MA_RS20955	NA	0.78	0.41	0.65	1.11	0.38	0.63	0.46	1.25	0.87	0.51	1.18	0.53
MA_RS20960	NA	2.66	2.96	2.27	3.12	3.47	2.94	2.24	3.54	4.09	3.71	2.41	2.34
MA_RS20965	NA	2.08	2.30	2.32	2.67	2.87	3.02	2.37	2.81	3.65	3.18	2.54	1.94
MA_RS20970	cbiQ	2.94	3.34	3.46	3.69	3.31	3.71	3.44	4.16	4.56	3.33	3.29	3.35
MA_RS20975	NA	4.09	4.46	4.33	4.96	4.60	4.91	4.57	5.32	5.42	4.75	4.48	4.59
MA_RS20985	NA	1.91	2.42	2.27	2.92	2.85	2.55	2.12	3.19	3.30	2.61	2.22	2.34
MA_RS20990	cbiQ	0.85	1.40	0.81	1.19	1.34	1.39	1.23	2.21	1.92	1.64	1.50	1.86
MA_RS20995	cbiM	0.74	0.72	0.43	1.10	1.43	1.24	1.02	0.69	1.10	0.74	0.41	1.12

MA_RS21010	NA	1.89	1.93	1.98	2.39	2.27	2.37	2.67	3.30	3.63	2.69	2.20	2.41
MA_RS21015	dinB	1.59	1.58	1.45	1.67	1.66	1.77	1.58	1.97	1.61	1.71	1.20	1.52
MA_RS21020	NA	2.48	2.22	2.26	3.26	2.52	2.45	3.26	3.02	1.93	2.55	2.84	2.31
MA_RS21030	NA	3.83	4.01	3.86	4.35	4.26	4.34	4.20	4.11	4.34	4.42	4.17	4.41
MA_RS21035	NA	0.12	0.26	0.00	0.85	0.00	0.00	0.22	0.62	0.22	0.25	0.00	0.56
MA_RS21040	NA	0.33	0.71	0.00	0.42	0.00	0.26	0.46	1.60	1.92	1.01	0.00	1.00
MA_RS21045	NA	0.87	1.18	0.63	1.04	1.60	1.42	1.86	1.84	1.76	1.98	0.77	1.81
MA_RS21050	NA	1.56	1.99	1.98	2.28	2.03	2.30	2.10	2.53	3.17	2.20	2.25	2.27
MA_RS21055	NA	1.49	1.63	1.41	1.77	1.42	1.74	1.55	2.24	2.48	1.71	1.75	1.32
MA_RS21065	NA	2.13	2.23	2.16	2.59	2.63	2.66	2.82	3.46	3.82	2.58	2.71	2.32
MA_RS21070	NA	1.52	1.87	1.62	1.17	1.25	1.73	1.45	2.38	2.58	1.09	1.51	1.33
MA_RS21075	NA	1.50	1.96	2.06	2.03	1.76	2.50	1.82	3.00	2.84	1.77	1.99	1.64
MA_RS21080	NA	2.44	2.36	1.91	2.92	2.81	2.83	2.54	3.26	3.25	2.31	2.65	2.61
MA_RS21085	NA	1.50	2.02	1.75	2.49	1.94	2.06	1.89	2.61	2.44	1.89	1.64	1.75
MA_RS21090	NA	6.21	6.51	6.40	6.25	6.33	6.43	5.99	6.59	7.07	5.50	5.82	6.13
MA_RS21095	NA	6.85	7.12	6.91	7.03	6.81	7.00	6.65	7.11	7.41	5.97	6.46	6.71
MA_RS21100	NA	7.22	7.54	7.44	7.24	7.12	7.33	7.13	7.09	7.41	6.03	6.65	7.04
MA_RS21105	NA	5.93	6.45	6.28	6.31	6.03	6.37	5.82	6.88	7.01	5.36	5.70	5.92
MA_RS21110	cyaB	4.80	5.08	5.03	5.07	4.63	4.88	4.66	5.08	5.19	3.70	4.42	4.79
MA_RS21115	NA	3.49	3.95	3.91	4.19	3.83	4.02	3.96	4.84	5.17	4.02	3.88	4.10
MA_RS21120	metG	5.73	6.04	5.86	6.33	5.94	6.16	6.17	6.44	6.64	6.10	5.92	6.00
MA_RS21125	sppA	4.80	5.06	4.87	5.16	4.95	5.09	5.08	5.36	5.64	5.33	4.86	5.15
MA_RS21130	serS	5.96	6.22	5.97	6.80	6.37	6.56	6.47	6.67	6.94	6.82	6.37	6.50
MA_RS21140	NA	4.33	4.59	4.49	4.60	4.60	4.84	4.68	5.19	5.29	4.30	4.38	4.43
MA_RS21145	NA	4.64	4.95	4.79	5.27	4.88	5.15	5.27	6.13	6.43	5.04	4.81	5.05
MA_RS21150	NA	5.07	5.28	5.08	5.69	5.29	5.47	5.46	6.03	6.26	5.26	5.15	5.42
MA_RS21155	NA	5.51	5.69	5.48	6.12	5.76	6.04	6.03	6.60	6.81	5.73	5.83	5.89
MA_RS21165	purL	5.41	5.63	5.41	5.90	5.51	5.71	5.60	5.62	5.97	5.67	5.39	5.53
MA_RS21170	NA	1.43	1.55	1.65	2.01	1.74	1.96	1.96	2.82	2.93	2.18	1.73	1.95
MA_RS21175	NA	1.97	1.42	1.09	1.27	1.08	1.42	1.85	1.43	2.16	1.88	1.76	0.61
MA_RS21180	ycIH	6.78	6.90	6.93	7.05	6.99	6.87	7.28	7.88	8.18	7.48	7.16	7.03
MA_RS21185	NA	5.55	5.65	5.54	6.00	5.62	5.77	5.70	6.42	6.60	6.00	5.63	5.86
MA_RS21190	NA	3.18	3.62	3.08	4.02	3.65	3.96	3.71	4.17	4.57	4.04	4.00	3.72
MA_RS21195	NA	0.71	0.96	0.65	1.16	1.36	0.98	1.75	1.64	1.38	1.15	1.27	1.25
MA_RS21200	NA	6.10	6.19	6.16	6.54	6.25	6.44	6.50	7.13	7.20	6.72	6.19	6.25
MA_RS21205	NA	5.11	5.36	5.34	5.60	5.31	5.61	5.50	6.04	6.19	5.64	5.34	5.53
MA_RS21210	NA	4.03	4.13	4.37	4.49	4.01	4.55	4.32	4.87	5.12	4.39	4.33	4.47
MA_RS21215	NA	0.37	0.55	0.35	0.69	0.83	0.95	0.87	0.69	1.47	0.57	0.45	0.59
MA_RS21220	NA	2.88	2.87	2.69	3.43	3.56	2.86	2.62	4.46	4.32	4.06	3.38	2.71
MA_RS21225	NA	1.85	1.70	2.50	1.20	1.75	2.11	1.82	1.94	2.76	2.00	1.41	1.93
MA_RS21230	NA	3.87	3.97	3.69	4.22	3.90	3.88	4.40	4.67	5.01	3.90	3.57	3.16
MA_RS21235	NA	0.23	0.16	0.17	0.05	0.20	0.21	0.63	0.64	0.38	0.29	0.44	0.11
MA_RS21240	NA	1.88	2.59	2.68	2.87	2.47	2.67	2.63	3.38	3.56	3.04	2.68	2.16
MA_RS21245	NA	0.83	0.81	0.87	0.65	1.09	1.09	0.97	1.78	1.92	1.31	0.96	0.77
MA_RS21250	NA	1.88	1.42	1.65	1.69	1.91	0.78	1.96	1.25	1.44	1.33	0.79	1.51
MA_RS21260	ftsA	1.66	1.89	1.75	2.06	2.01	1.74	1.81	1.70	2.04	1.94	1.81	1.66
MA_RS21265	nlkR	7.24	7.18	7.31	7.49	7.52	7.47	7.53	7.87	7.55	7.47	7.47	7.32
MA_RS21270	NA	3.41	3.41	3.28	3.74	3.67	4.03	3.78	4.45	4.68	4.36	3.93	3.70
MA_RS21275	NA	3.96	4.15	4.27	4.51	4.25	4.54	4.35	4.70	4.83	4.08	4.01	4.23
MA_RS21280	NA	1.60	1.81	1.91	2.25	1.95	2.18	1.95	2.35	2.95	1.47	1.61	1.80
MA_RS21285	NA	3.39	3.64	3.62	3.81	3.64	3.70	3.78	3.80	3.79	3.79	3.15	3.63
MA_RS21290	NA	3.84	4.08	3.51	4.17	4.23	4.14	3.93	5.02	5.12	4.24	4.11	4.59
MA_RS21295	NA	2.73	3.12	3.02	3.46	3.13	3.22	3.08	3.83	3.92	3.08	2.86	3.02
MA_RS21300	NA	3.50	3.79	3.58	3.85	3.82	3.93	3.89	4.37	4.29	3.57	3.86	3.69
MA_RS21305	NA	1.39	1.49	1.36	1.40	1.60	1.80	1.71	2.52	2.81	1.60	1.54	1.80
MA_RS21310	NA	2.94	3.06	3.04	3.16	3.24	3.61	3.20	4.17	3.94	3.15	2.98	3.04
MA_RS21320	NA	3.10	3.53	3.26	3.67	3.32	3.52	3.34	3.95	4.09	3.38	3.49	3.52
MA_RS21325	NA	3.92	4.11	3.92	4.11	3.93	4.17	4.12	4.46	4.53	4.34	4.12	3.80
MA_RS21330	NA	4.09	4.04	3.98	4.37	4.44	4.20	4.37	4.30	4.27	4.05	4.11	4.25
MA_RS21335	crcB	4.08	4.07	3.96	3.99	4.30	4.28	4.44	4.02	4.81	4.06	4.38	4.34
MA_RS21340	crcB	3.32	3.38	3.23	3.28	3.22	3.36	2.83	3.87	3.95	3.21	3.22	3.52
MA_RS21345	NA	3.06	3.33	3.25	3.50	3.10	4.07	3.54	4.08	3.94	3.79	3.74	3.80
MA_RS21355	NA	3.18	3.15	2.93	3.35	3.14	3.27	3.62	4.04	3.91	3.18	3.24	3.58
MA_RS21360	NA	5.59	5.75	5.71	6.27	5.93	5.94	6.41	6.36	6.70	6.43	5.99	5.95
MA_RS21365	NA	6.02	6.08	6.01	6.56	6.27	6.48	6.87	6.96	7.11	6.73	6.29	6.42
MA_RS21370	NA	5.84	5.96	5.91	6.52	6.29	6.46	6.60	6.69	6.96	6.90	6.52	6.59
MA_RS21375	NA	2.62	2.73	2.49	2.95	2.95	2.92	2.46	4.03	4.24	3.08	2.68	2.55
MA_RS21380	NA	2.41	2.54	2.27	2.96	3.10	2.65	3.71	3.61	3.75	3.00	1.63	2.65
MA_RS21385	NA	5.99	6.32	6.18	6.52	6.41	6.43	6.54	7.08	7.31	6.54	6.26	6.09
MA_RS21395	NA	4.26	4.42	4.36	4.76	4.54	4.59	4.66	5.31	5.59	4.84	4.37	4.62
MA_RS21400	proB	4.85	5.22	5.14	5.52	5.14	5.38	5.43	5.59	6.05	5.77	5.30	5.46
MA_RS21405	proC	5.07	5.45	4.97	5.80	5.48	5.58	5.55	5.46	5.81	5.87	5.55	5.54
MA_RS21410	NA	6.69	6.88	6.66	7.05	6.70	6.96	6.84	7.62	7.75	6.49	6.51	6.60
MA_RS21415	NA	1.11	0.88	1.09	1.33	1.03	1.39	1.12	1.88	1.71	0.73	1.20	1.09
MA_RS21420	NA	0.85	0.82	0.75	1.02	0.87	1.33	0.81	0.72	1.11	0.70	0.98	0.65
MA_RS21425	NA	2.80	1.94	2.45	2.85	2.68	3.23	2.51	3.14	3.58	2.53	2.23	2.75
MA_RS21440	ftsY	4.60	4.85	4.62	5.41	5.11	5.24	5.24	5.49	5.82	5.06	4.80	5.14
MA_RS21445	pfdA	6.25	6.40	6.39	6.90	6.59	6.77	6.95	7.22	7.64	6.86	6.36	6.60
MA_RS21450	rpl18a	6.85	7.16	7.12	7.60	7.41	7.56	8.02	8.01	8.28	7.62	7.29	7.49
MA_RS21455	NA	7.79	8.02	7.86	8.60	8.12	8.45	8.48	8.90	9.10	8.70	8.23	8.30
MA_RS21460	NA	7.46	7.80	7.56	8.22	7.88	8.19	8.24	8.37	8.39	8.21	7.77	8.06
MA_RS21465	NA	7.08	7.39	7.20	8.09	7.66	7.90	7.98	8.73	8.94	8.43	7.66	7.86
MA_RS21470	NA	7.98	8.12	8.16	8.65	8.31	8.47	8.63	9.20	9.39	8.84	8.45	8.61
MA_RS21475	NA	8.28	8.51	8.44	9.16	8.83	9.04	9.17	9.56	9.84	9.49	8.84	9.01
MA_RS21480	NA	5.42	5.58	5.54	6.00	5.77	5.95	6.07	5.98	6.42	5.97	5.66	5.85
MA_RS21485	NA	2.30	2.48	2.03	2.91	2.77	2.40	2.62	3.61	3.09	2.41	2.73	2.33
MA_RS21490	NA	3.54	3.48	3.56	3.77	3.37	4.04	3.29	4.49	4.20	3.57	2.93	2.97
MA_RS21495	NA	3.84	4.00	3.94	4.30	3.84	4.15	4.33	4.61	5.00	4.53	4.01	4.07
MA_RS21500	NA	0.30	0.48	0.40	0.36	0.38	0.48	0.41	0.61	0.94	0.49	0.33	0.32
MA_RS21505	NA	1.50	1.61	1.52	2.29	1.91	2.08	2.25	2.30	2.45	2.09	2.34	2.12
MA_RS21510	#N/A	2.66	2.08	1.85	1.74	2.66	2.14	2.37	1.52	2.43	1.81	2.53	2.27
MA_RS21515	NA	1.06	0.48	1.32	0.69	0.92	0.70	0.55	2.04	1.92	1.61	0.47	0.39
MA_RS21520	NA	3.67	3.55	3.50	3.90	3.55	4.00	3.71	4.23	4.26	3.92	3.48	2.98
MA_RS21525	NA	2.72	3.28	2.98	3.20	3.39	3.21	3.32	4.46	4.92	3.75	2.72	3.07
MA_RS21530	NA	1.14	1.38	1.30	1.00	1.54	0.94	1.33	1.93	2.18	1.59	1.40	1.46
MA_RS21535	NA	0.97	1.49	0.51	0.78	1.28	1.55	0.26	0.88	1.76	1.54	0.62	0.21
MA_RS21540	NA	1.69	1.42	1.89	1.75	2.03	1.73	1.49	2.46	2.32	1.67	1.85	1.76
MA_RS21545	NA	1.33	2.09	1.59	1.99	1.64	1.98	1.59	0.95	2.52	1.25	1.86	1.62
MA_RS21550	NA	2.26	2.36	2.19	2.45	2.56	2.88	2.53	3.68	3.81	2.94	2.53	2.30
MA_RS21555	istA	2.00	1.93	1.94	2.01	1.80	2.10	1.77	2.25	2.40	1.95	1.80	1.74
MA_RS21560	istB	1.34	1.44	1.37	1.69	1.52	1.66	1.63	2.37	2.44	1.94	1.60	1.59
MA_RS21570	NA	2.66	3.11	2.95	2.93	2.57	2.85	2.28	3.18	3.44	2.56	2.42	2.32
MA_RS21575	NA	0.74	0.41	0.43	0.69	0.87	0.85	0.79	1.27	1.39	0.84	0.82	0.58
MA_RS21580	NA	1.00	1.18	1.14	1.10	1.25	1.47	0.93	1.53	1.84	1.31	1.12	1.77
MA_RS21585	NA	1.07	1.42	1.37	1.56	1.12	2.05	0.87	2.05	1.67	1.45	1.53	0.74
MA_RS21590	NA	1.78	1.89	1.42	2.13	1.84	1.51	1.94	1.74	2.26	2.24	2.13	2.03
MA_RS21595	NA	0.47	0.41	1.02	0.91	0.98	0.82	1.17	0.57	0.90	0.83	1.12	1.22
MA_RS21605	NA	0.00	0.00	0.00	0.00	0.12	0.00	0.00	0.00	0.00	0.00	0.00	0.37
MA_RS21610	NA	0.12	0.09	0.00	0.35	0.63	0.65	0.00	0.26	0.00	0.14	0.11	0.19
MA_RS21615	NA	0.97	0.89	1.29	0.93	1.26	0.62	1.59	1.81	1.87	1.17	1.19	1.47
MA_RS21620	NA	3.46	3.49	3.57	4.07	3.38	3.83	3.97	4.41	4.54	3.59	3.46	3.39
MA_RS21625	NA	1.57	2.27	2.51	2.20	2.34	1.55	1.96	2.05	2.16	1.39	2.11	1.43
MA_RS21630	NA	2.40	2.29	2.33	2.81	2.63	2.86	2.49	2.69	3.04	2.48	2.45	2.75
MA_RS21635	NA	0.96	1.27	1.40	1.41	0.80	1.42	0.93	1.46	1.70	1.24	1.27	1.15
MA_RS21640	#N/A	1.74	0.81	1.34	0.51	0.07	1.87	1.37	1.26	1.43	0.74	1.22	1.27
MA_RS21645	#N/A	2.24	2.00	1.08	1.17	0.00	2.04	2.20	0.00	0.00	2.41	1.28	2.70
MA_RS21650	NA	5.40	5.46	5.35	5.77	5.62	5.60	5.79	6.38	6.66	5.97	5.54	5.72
MA_RS21655	NA	5.02	5.24	5.12	5.73	5.32	5.57	5.48	6.08	6.22	5.73	5.32	5.62
MA_RS21660	NA	4.42	4.73	4.63	5.09	4.75	5.09	4.96	5.43	5.66	4.97	4.79	5.03
MA_RS21665	ahaH	9.02	9.34	9.25	9.86	9.38	9.68	9.55	10.41	10.91	9.56	9.22	9.44
MA_RS21670	NA	8.81	9.13	9.01	9.58	9.09	9.39	9.19	9.90	10.26	9.12	8.97	9.19
MA_RS21675	NA	7.84	7.94	7.84	8.12	7.95	8.01	7.96	7.75	7.64	7.32	7.48	7.93
MA_RS21680	NA	8.78	8.99	9.03	9.48	9.03	9.31	9.40	10.19	10.52	9.01	8.83	9.13
MA_RS21685	NA	8.45	8.86	8.68	9.18	8.75	9.05	8.88	9.51	9.91	8.57	8.59	8.84
MA_RS21690	NA	9.30	9.54	9.44	9.96	9.52	9.78	9.99	10.84	11.09	9.57	9.40	9.65
MA_RS21695	NA	8.94	9.25	9.13	9.61	9.21	9.44	9.47	9.99	10.27	9.04	9.02	9.33
MA_RS21700	NA	8.78	9.15	9.03	9.55	9.12	9.39	9.35	9.96	10.29	8.97	8.95	9.19
MA_RS21705	NA	8.70	9.02	9.00	9.31	9.02	9.16	9.32	9.88	10.23	8.77	8.70	9.07
MA_RS21710	hypF	0.56	0.75	0.86	0.98	0.92	0.62	0.87	1.19	1.11	1.04	1.40	0.97
MA_RS21715	NA	3.26	3.21	2.97	3.52	3.08	3.44	3.50	4.37	3.74	3.56	3.42	3.27
MA_RS21720	NA	4.13	4.25	4.25	4.38	4.12	4.07	4.71	4.88	4.81	4.14	3.78	4.12
MA_RS21735	NA	4.98	4.69	4.53	1.37	1.92	2.21	1.63	2.54	2.86	2.22	2.24	2.56
MA_RS21740	NA	5.36	5.18	4.98	2.44	2.40	1.90	2.80	3.02	3.23	3.12	2.80	3.02
MA_RS21745	NA	4.43	4.39	3.81	1.00	1.55	1.07	1.02	1.29	1.64	1.79	1.48	1.77
MA_RS21750	NA	3.81	3.98	3.73	4.06	3.82	4.33	3.93	4.59	4.86	4.31	4.13	4.06
MA_RS21755	NA	4.64	4.79	4.71	4.88	4.67	4.98	4.64	5.39	5.83	4.98	4.98	4.62
MA_RS21760	NA	6.50	6.48	6.72	6.64	6.68	6.96	6.70	7.72	7.98	7.22	6.88	6.52
MA_RS21765	NA	1.51	1.48	2.07	1.39	1.58	1.91	1.85	1.83	1.57	1.86	1.04	1.92
MA_RS21770	NA	1.31	1.96	1.53	1.66	1.89	1.71	2.14	1.56	1.73	1.98	1.70	1.85
MA_RS21775	NA	2.12	2.12	2.10	2.43	1.85	2.39	2.31	3.01	2.83	2.39	2.02	1.71
MA_RS21780	NA	2.72	2.58	2.30	2.95	2.69	3.07	3.62	3.34	3.13	2.78	2.52	2.66
MA_RS21785	NA	0.87	1.17	0.88	0.85	1.08	1.21	1.10	1.18	1.74	1.24	0.73	1.15
MA_RS21790	NA	3.80	3.99	3.81	4.47	4.07	4.26	4.52	4.97	5.29	4.27	4.25	4.49

MA_RS21795	NA	5.08	5.27	5.46	5.66	5.21	5.36	5.97	5.85	5.86	5.20	5.37	5.77
MA_RS21800	NA	3.72	4.02	3.86	4.57	4.14	4.41	4.62	5.18	5.02	4.31	4.69	4.42
MA_RS21805	NA	1.41	1.60	1.65	2.17	1.68	2.12	1.84	2.18	2.35	2.26	1.97	1.64
MA_RS21810	NA	2.80	3.13	3.21	3.16	3.33	3.52	3.55	3.84	4.19	3.42	3.30	3.31
MA_RS21815	NA	2.66	2.85	3.02	3.28	2.84	3.07	3.15	3.97	4.00	3.32	2.89	2.90
MA_RS21820	#N/A	0.20	0.83	0.53	0.75	0.83	0.70	0.97	0.55	1.54	0.59	0.39	0.57
MA_RS21825	ltrA	2.82	2.85	2.73	3.40	2.89	3.27	3.01	3.80	4.14	3.28	3.00	3.15
MA_RS21830	NA	2.08	2.28	2.10	2.79	2.43	2.55	2.58	2.84	3.33	2.93	2.77	2.72
MA_RS21835	NA	1.84	2.28	2.36	3.19	2.39	2.87	2.68	3.20	3.54	2.83	2.48	2.66
MA_RS21840	istA	0.72	1.03	0.56	0.86	0.87	1.15	0.83	0.74	1.39	0.97	1.26	0.86
MA_RS21850	NA	1.43	1.25	1.20	1.65	0.75	1.12	1.78	2.07	2.42	1.49	1.55	1.07
MA_RS21860	#N/A	1.22	1.80	1.66	0.48	0.45	0.00	0.75	0.75	1.75	1.24	1.58	1.46
MA_RS21865	NA	4.96	5.30	5.31	5.75	5.42	5.75	5.68	5.92	5.99	5.68	5.58	5.24
MA_RS21870	NA	5.38	5.36	5.57	5.62	5.57	5.39	5.43	5.77	5.92	5.66	5.37	5.55
MA_RS21880	NA	3.28	3.71	3.45	3.82	3.96	3.86	3.81	4.40	3.90	3.28	3.57	3.40
MA_RS21885	NA	4.92	4.93	4.78	4.73	4.68	4.91	5.21	5.63	5.38	4.89	4.72	4.77
MA_RS21890	NA	3.33	3.38	3.41	3.82	3.63	3.77	4.08	4.05	4.13	3.64	3.30	3.52
MA_RS21895	NA	6.19	6.11	6.17	6.12	6.36	6.35	6.40	6.58	6.24	6.84	6.19	6.13
MA_RS21900	nifB	5.64	5.90	5.79	6.69	6.28	6.47	6.59	6.71	6.96	6.89	6.27	6.40
MA_RS21905	queD	4.24	4.15	4.04	5.30	4.91	4.82	5.22	4.67	5.23	5.67	4.99	5.08
MA_RS21910	NA	4.67	4.91	4.67	6.06	5.42	5.85	5.93	5.71	6.21	6.62	5.89	5.82
MA_RS21915	NA	5.07	5.23	5.09	6.24	5.76	5.89	6.09	5.82	6.44	6.73	6.07	6.06
MA_RS21920	queC	4.39	4.49	4.24	5.67	5.22	5.36	5.27	5.32	5.89	6.41	5.32	5.34
MA_RS21925	NA	3.35	3.57	3.62	3.31	3.38	3.05	3.55	3.56	2.83	3.34	3.23	2.93
MA_RS21930	NA	1.11	1.17	1.10	1.76	1.59	1.02	1.67	1.84	1.62	1.19	0.84	1.25
MA_RS21935	NA	2.42	2.63	2.99	2.58	2.80	2.59	2.41	2.36	2.62	2.22	2.43	2.77
MA_RS21940	NA	3.29	3.71	3.62	4.05	3.83	3.95	3.84	3.95	4.13	3.68	3.69	3.93
MA_RS21945	NA	3.13	3.23	3.22	3.38	3.38	3.44	3.57	3.95	3.78	3.33	2.56	3.24
MA_RS21950	NA	2.61	3.41	2.68	3.29	2.75	3.45	3.38	3.77	4.16	3.16	2.99	3.48
MA_RS21955	NA	1.00	0.79	1.18	1.03	1.14	1.57	0.85	1.38	1.69	1.28	1.31	0.97
MA_RS21960	NA	3.49	3.77	3.80	3.92	3.91	4.01	4.32	4.37	4.65	3.94	3.61	3.69
MA_RS21965	NA	4.24	4.42	4.22	4.74	4.40	4.29	4.88	5.00	4.73	4.82	3.79	4.21
MA_RS21970	NA	3.13	3.25	3.50	3.41	3.11	3.17	3.41	3.78	3.45	3.82	3.07	3.29
MA_RS21975	NA	1.44	1.44	1.48	1.92	1.34	1.83	2.11	2.59	2.91	1.91	1.60	1.93
MA_RS21985	NA	1.02	1.58	1.05	1.04	1.74	1.31	1.46	1.63	1.13	2.17	1.73	1.40
MA_RS21990	NA	2.98	3.42	2.89	3.07	3.53	3.54	3.10	3.74	3.64	3.49	3.27	3.15
MA_RS21995	NA	2.79	2.95	2.60	3.12	2.56	3.03	2.72	3.86	4.33	3.35	2.99	2.52
MA_RS22000	NA	2.12	2.28	2.79	3.27	3.42	2.82	3.11	3.90	3.34	3.24	2.98	2.72
MA_RS22005	NA	0.56	1.11	1.01	0.58	1.11	1.74	0.27	0.27	0.72	0.54	1.00	1.57
MA_RS22015	glnA	5.56	5.97	5.81	6.13	5.69	6.01	5.95	6.56	7.09	5.45	5.38	5.61
MA_RS22025	NA	6.69	6.94	6.88	7.23	6.92	7.15	7.09	7.21	7.72	6.19	6.66	6.96
MA_RS22030	NA	6.88	7.20	7.03	7.57	7.26	7.49	7.29	7.63	7.93	6.47	7.05	7.28
MA_RS22035	NA	7.00	7.27	7.22	7.60	7.35	7.42	7.75	7.98	8.04	6.53	6.98	7.39
MA_RS22040	NA	6.87	7.16	7.06	7.54	7.22	7.48	7.41	7.64	7.85	6.55	7.00	7.31
MA_RS22045	NA	1.86	2.31	1.60	2.71	1.88	2.21	2.64	3.23	2.93	2.45	2.45	2.48
MA_RS22050	NA	2.07	2.07	2.37	2.33	2.37	2.56	2.41	2.90	3.36	2.28	1.84	2.23
MA_RS22055	NA	1.82	1.80	1.31	1.60	1.32	1.23	1.87	2.62	2.02	1.78	2.02	1.32
MA_RS22070	NA	1.05	1.20	0.99	1.08	1.11	1.07	0.95	1.67	1.10	1.15	0.91	1.11
MA_RS22075	NA	2.80	3.17	2.93	3.32	3.13	3.28	3.20	3.88	4.05	3.40	3.29	3.10
MA_RS22080	NA	2.28	2.71	2.05	3.19	2.52	2.72	2.85	3.82	3.98	2.78	2.35	2.83
MA_RS22090	NA	1.37	1.22	1.35	1.98	1.40	1.90	1.90	2.65	2.91	2.19	1.55	2.00
MA_RS22095	NA	2.73	2.78	3.01	2.98	2.83	3.26	3.13	3.87	3.41	3.39	2.76	2.92
MA_RS22100	NA	3.21	3.33	3.34	3.68	3.26	3.47	3.83	3.80	4.16	3.53	3.35	3.47
MA_RS22105	NA	0.63	0.80	0.60	1.02	1.17	1.30	0.54	1.66	1.93	1.48	1.04	1.21
MA_RS22110	NA	0.32	0.37	0.52	0.65	0.56	0.38	0.56	0.81	0.94	1.02	0.74	0.45
MA_RS22115	npdG	4.51	4.92	4.46	5.17	4.64	4.74	5.03	5.69	5.79	5.06	4.85	4.72
MA_RS22120	hdrC	4.69	4.96	4.80	5.04	4.86	4.93	5.15	5.26	5.18	5.06	4.54	4.92
MA_RS22125	hdrB	4.43	4.75	4.71	5.13	4.75	5.00	4.85	5.42	5.61	4.87	4.69	4.87
MA_RS22130	NA	3.29	3.72	3.48	4.14	3.64	3.95	3.85	4.26	4.85	3.94	3.61	3.88
MA_RS22135	NA	3.30	3.25	3.63	3.56	3.20	3.48	3.32	3.76	4.05	3.50	3.04	2.99
MA_RS22140	NA	4.50	4.62	4.63	4.78	4.82	4.71	4.66	5.29	5.11	4.41	4.47	4.49
MA_RS22145	NA	3.47	3.64	3.76	3.64	3.74	3.62	3.60	3.51	3.67	2.74	2.84	2.89
MA_RS22150	NA	3.55	4.13	4.16	4.10	4.21	4.02	3.81	4.17	4.01	2.86	2.86	3.18
MA_RS22155	NA	4.62	4.79	5.07	4.86	4.98	4.64	4.71	5.28	4.71	4.49	4.09	4.24
MA_RS22160	NA	4.05	4.46	4.26	4.24	4.17	3.76	3.95	4.85	4.39	3.10	2.78	3.25
MA_RS22165	NA	4.89	4.92	5.01	5.40	5.15	4.95	5.75	5.08	4.60	4.92	4.76	4.87
MA_RS22170	NA	6.20	6.48	6.32	6.73	6.51	6.55	6.62	6.51	6.57	6.39	6.07	6.16
MA_RS22175	NA	1.63	1.70	1.63	2.65	2.10	2.41	2.17	2.87	3.10	2.00	2.42	2.56
MA_RS22180	NA	2.01	2.39	1.88	2.70	2.48	2.84	2.39	3.24	3.10	2.52	2.80	2.22
MA_RS22185	NA	2.27	2.58	2.12	2.56	2.61	2.57	2.69	2.51	2.72	2.30	2.15	2.21
MA_RS22190	NA	1.65	1.44	1.93	1.58	1.69	2.15	1.84	2.19	2.29	1.39	1.29	1.97
MA_RS22195	NA	1.28	1.74	2.22	1.84	1.50	1.54	1.92	1.62	1.92	1.71	1.60	1.86
MA_RS22200	NA	1.41	1.05	1.94	1.18	1.30	1.97	0.73	1.70	1.53	1.23	1.54	1.30
MA_RS22205	NA	0.88	0.92	1.16	0.85	0.76	1.21	1.27	1.22	1.98	1.28	1.27	1.44
MA_RS22210	NA	5.81	5.84	5.67	6.33	5.78	6.25	6.10	6.79	7.00	6.52	6.04	5.98
MA_RS22215	NA	4.60	5.02	5.06	5.13	5.02	5.11	5.24	5.55	5.58	5.31	5.10	5.13
MA_RS22220	NA	3.65	4.00	3.73	4.16	3.90	4.29	4.15	5.01	5.12	4.33	4.10	3.86
MA_RS22225	NA	4.33	4.63	4.48	4.85	4.82	4.87	4.77	5.61	5.44	5.01	4.78	4.65
MA_RS22230	NA	5.43	5.84	5.65	6.10	5.62	5.95	5.93	6.26	6.44	5.82	5.81	5.93
MA_RS22235	cobJ	5.55	5.83	5.84	5.97	5.78	5.74	6.02	5.95	6.46	5.71	5.68	5.96
MA_RS22240	NA	5.23	5.80	5.67	5.98	5.54	5.75	5.95	5.99	6.14	5.48	5.63	5.93
MA_RS22245	NA	5.62	5.97	5.75	6.33	5.71	5.89	6.12	6.91	7.29	6.31	6.02	6.24
MA_RS22250	NA	5.82	6.10	5.93	6.37	5.98	6.14	6.29	6.72	7.00	6.15	5.95	6.38
MA_RS22255	NA	5.64	5.87	5.68	6.29	5.89	6.05	6.09	6.74	7.20	6.15	5.81	5.96
MA_RS22260	cbiT	4.16	4.38	4.56	4.36	4.04	4.00	4.29	4.87	5.64	4.73	4.29	4.53
MA_RS22265	NA	4.03	4.26	4.27	5.16	4.76	5.03	5.06	5.83	6.04	5.19	4.70	4.87
MA_RS22270	NA	6.90	7.08	7.04	7.52	7.16	7.51	7.43	7.65	7.89	7.64	7.34	7.30
MA_RS22275	NA	3.53	3.65	3.65	4.01	3.72	3.70	3.99	3.94	3.76	3.54	3.65	3.62
MA_RS22280	NA	5.76	5.66	5.81	6.05	5.81	5.84	5.95	6.55	6.37	6.39	5.92	5.80
MA_RS22285	NA	6.21	6.42	6.36	6.86	6.53	6.66	6.53	7.23	7.44	6.70	6.48	6.48
MA_RS22290	NA	1.73	1.85	2.14	2.12	2.05	1.96	2.38	1.86	1.73	2.11	1.71	1.83
MA_RS22295	NA	2.18	2.50	2.63	2.46	2.02	2.69	2.54	2.38	1.20	1.72	1.83	2.22
MA_RS22300	ftsZ	6.75	6.98	6.90	7.19	6.92	7.11	7.14	7.07	7.31	6.89	6.76	6.90
MA_RS22305	NA	7.72	8.10	8.05	8.36	8.04	8.31	8.21	8.88	9.21	8.46	8.16	8.20
MA_RS22310	NA	7.68	7.95	7.85	8.21	7.91	8.17	8.20	8.54	8.87	8.25	7.83	7.99
MA_RS22315	NA	8.54	8.63	8.69	9.11	8.91	8.94	9.22	9.28	9.46	8.83	8.67	9.01
MA_RS22320	NA	9.36	9.65	9.46	10.06	9.66	9.90	9.88	10.36	10.78	9.92	9.63	9.82
MA_RS22325	NA	9.61	9.88	9.78	10.27	9.81	10.08	10.18	10.53	10.78	10.01	9.79	9.96
MA_RS22330	rpl12p	9.12	9.31	8.67	9.54	9.23	9.49	8.94	9.93	10.31	9.44	9.27	9.45
MA_RS22335	NA	1.83	1.89	1.79	2.06	1.98	2.13	1.76	2.28	2.27	2.39	2.06	1.96
MA_RS22340	NA	2.26	2.87	2.94	3.21	2.79	3.13	3.17	3.55	3.85	2.98	2.58	3.01
MA_RS22345	NA	2.32	2.75	2.76	2.54	2.72	3.07	3.31	3.29	3.30	3.70	3.14	3.01
MA_RS22350	NA	0.00	0.29	0.00	0.21	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS22355	#N/A	1.18	0.95	0.87	0.75	0.91	1.17	0.96	1.69	1.06	0.66	1.40	0.81
MA_RS22360	NA	2.99	3.06	2.78	2.79	2.79	2.79	2.65	3.51	3.24	2.94	2.47	2.74
MA_RS22365	NA	2.46	2.77	2.73	3.20	2.80	3.22	3.05	3.63	3.87	3.28	3.16	3.10
MA_RS22370	NA	2.90	3.20	2.91	3.48	3.26	3.46	3.26	3.32	3.55	3.44	3.45	3.32
MA_RS22385	NA	2.03	2.37	2.34	2.55	2.33	2.70	2.46	2.60	2.92	2.67	2.43	2.60
MA_RS22390	NA	1.91	2.06	2.13	2.32	2.09	2.10	2.00	2.95	2.63	1.91	2.21	2.35
MA_RS22395	NA	2.70	2.89	2.64	3.14	2.94	3.19	3.12	3.31	3.68	2.96	2.92	2.98
MA_RS22400	NA	2.83	3.12	2.94	3.51	3.30	3.50	3.22	3.61	3.96	3.48	3.43	3.46
MA_RS22410	NA	0.50	0.28	0.69	0.61	0.00	0.59	0.40	1.04	0.88	0.09	0.60	0.18
MA_RS22415	NA	0.79	1.22	0.99	1.29	1.44	1.25	1.28	1.88	2.18	1.27	1.53	1.27
MA_RS22420	NA	0.92	0.96	1.27	1.02	1.09	1.24	0.98	1.44	1.78	1.07	1.11	1.17
MA_RS22425	NA	1.52	1.83	1.72	2.04	2.10	1.93	1.87	2.07	2.42	2.03	1.98	2.06
MA_RS22440	NA	1.74	2.04	2.00	2.57	1.94	2.50	1.99	2.08	2.50	1.91	2.24	2.04
MA_RS22445	NA	2.86	3.23	2.97	3.63	3.18	3.55	3.34	3.84	4.21	3.54	3.35	3.46
MA_RS22455	NA	2.22	2.44	2.28	2.67	2.57	2.43	2.61	2.90	3.13	2.78	2.81	2.61
MA_RS22465	NA	3.47	3.65	3.57	3.82	3.94	3.89	3.71	4.24	4.45	4.13	3.95	3.83
MA_RS22470	NA	2.56	2.09	2.24	2.26	1.91	1.40	1.54	3.17	3.42	2.65	1.75	1.57
MA_RS22480	NA	3.30	3.57	3.50	3.85	3.53	3.68	3.86	4.00	4.26	3.71	3.55	3.70
MA_RS22485	NA	4.05	4.24	4.28	4.72	4.24	4.48	4.59	5.27	5.61	4.49	4.37	4.38
MA_RS22490	NA	0.53	0.77	0.90	0.19	0.87	0.62	1.00	1.22	1.38	0.66	0.50	0.46
MA_RS22500	NA	2.20	2.33	2.31	2.49	2.53	2.54	2.67	2.74	2.92	2.47	2.46	2.59
MA_RS22510	NA	1.68	1.96	1.86	2.32	2.18	2.38	2.17	2.49	2.89	2.25	2.18	2.19
MA_RS22520	NA	3.04	3.38	3.28	3.70	3.36	3.65	3.51	3.96	4.35	3.63	3.41	3.60
MA_RS22530	NA	1.21	1.27	1.60	1.93	1.97	1.91	1.87	2.16	2.43	2.10	2.05	1.90
MA_RS22540	NA	0.70	0.89	0.77	0.26	0.93	1.11	0.00	0.33	0.34	0.91	0.26	0.71
MA_RS22545	NA	2.39	2.31	2.46	2.16	2.26	2.16	2.29	2.51	2.54	2.39	2.30	2.39
MA_RS22550	NA	1.87	1.79	1.89	2.01	2.26	1.95	1.91	2.07	2.23	1.92	1.91	1.94
MA_RS22555	NA	2.62	2.80	2.39	3.30	3.02	3.01	2.88	3.36	3.28	2.94	2.36	2.86
MA_RS22565	NA	1.99	2.30	2.06	2.28	2.20	2.63	2.62	2.99	3.31	2.54	2.46	2.50
MA_RS22570	NA	2.70	2.91	2.91	3.09	2.76	3.10	3.43	3.46	3.64	2.60	2.82	3.11
MA_RS22575	NA	1.94	1.80	1.61	2.17	1.92	1.94	2.36	2.18	1.98	1.83	1.59	1.92
MA_RS22585	NA	2.80	2.52	2.49	2.81	2.87	3.01	2.92	3.14	2.53	2.89	3.14	1.95
MA_RS22590	NA	4.05	4.19	4.02	4.84	4.57	4.88	4.65	4.85	5.21	3.97	4.15	4.51
MA_RS22595	NA	3.77	4.06	4.05	4.61	4.49	4.82	4.70	5.02	5.38	4.16	3.97	4.37
MA_RS22600	NA	4.13	4.48	4.33	4.97	4.61	4.93	5.03	5.64	5.75	4.51	4.31	4.66
MA_RS22605	NA	3.64	3.80	3.44	4.04	3.94	4.13	4.36	4.13	4.40	3.52	3.62	3.78
MA_RS22610	thiC	8.29	8.43	8.22	8.30	7.61	8.12	8.78	9.13	9.95	8.86	9.00	9.12
MA_RS22615	aglJ	5.24	5.30	5.25	5.55	5.34	5.54	5.75	6.14	6.22	5.85	5.27	5.33
MA_RS22620	NA	6.20	6.30	6.23	6.54	6.21	6.51	6.34	6.81	7.16	6.89	6.45	6.35
MA_RS22625	scpB	3.16	3.29	3.11	3.51	3.33	3.41	3.29	3.45	3.78	3.25	3.03	3.43

MA_RS22630	NA	4.03	4.32	4.28	4.26	4.15	4.28	4.23	4.69	4.93	3.99	3.99	4.23
MA_RS22635	smc	4.59	4.77	4.69	4.88	4.64	4.74	4.93	5.24	5.43	4.41	4.35	4.67
MA_RS22640	NA	4.88	5.16	4.97	5.45	5.06	5.23	5.22	5.49	5.55	5.15	4.86	5.14
MA_RS22650	NA	6.27	6.21	6.14	6.69	6.76	6.64	7.29	7.60	7.63	7.34	6.68	6.55
MA_RS22660	feoB	3.40	3.61	3.29	3.80	3.62	3.95	3.53	3.59	3.76	3.22	3.18	3.49
MA_RS22665	NA	3.37	3.76	3.71	3.89	3.71	3.61	3.57	3.79	3.80	3.76	3.36	3.81
MA_RS22670	NA	4.70	4.95	5.15	5.32	5.40	5.25	4.99	5.47	5.39	5.47	5.19	5.19
MA_RS22675	#N/A	4.53	3.83	4.01	4.14	4.21	3.22	4.32	2.69	2.13	3.22	3.61	4.05
MA_RS22685	NA	2.38	2.47	2.55	2.61	2.49	3.24	2.31	2.35	2.96	2.85	2.80	2.86
MA_RS22690	NA	3.67	3.87	3.96	4.05	3.92	4.08	3.96	4.06	4.44	4.22	3.71	3.97
MA_RS22695	NA	2.96	3.05	2.89	3.46	3.16	3.13	3.25	3.43	3.63	3.26	3.35	3.47
MA_RS22700	NA	1.80	2.08	1.45	1.97	1.90	2.37	1.89	2.85	3.08	2.48	2.04	2.32
MA_RS22705	NA	4.50	4.89	4.39	4.06	3.91	3.89	3.78	4.20	5.08	4.50	4.11	4.11
MA_RS22710	NA	4.17	4.49	4.30	4.29	3.70	3.90	3.92	4.44	4.65	4.06	3.74	3.94
MA_RS22715	NA	4.06	4.40	4.26	4.31	3.73	3.85	4.06	4.25	4.65	3.82	3.33	4.03
MA_RS22720	NA	1.76	1.57	1.70	2.07	2.06	1.46	1.21	2.47	2.55	2.15	1.46	2.03
MA_RS22730	#N/A	2.26	3.36	2.80	2.35	3.08	2.33	2.82	0.71	1.10	1.56	2.09	1.84
MA_RS22735	ilvE	5.94	5.98	5.97	6.24	6.04	6.15	6.10	6.46	6.56	6.07	5.85	5.98
MA_RS22740	NA	4.66	4.75	4.69	5.08	4.83	4.89	4.90	4.54	4.38	4.57	4.62	4.74
MA_RS22745	NA	4.91	5.13	5.11	5.27	5.14	5.30	5.48	5.73	5.59	5.39	5.18	5.22
MA_RS22750	NA	1.97	2.02	2.01	2.21	2.29	2.63	2.35	2.60	2.66	2.29	2.20	2.23
MA_RS22755	#N/A	1.25	1.03	1.23	1.53	1.11	1.70	1.36	1.57	1.11	1.83	1.15	1.47
MA_RS22760	NA	1.27	0.94	1.17	0.85	0.00	0.00	0.58	0.81	0.83	1.47	0.00	1.04
MA_RS22765	NA	2.11	2.21	2.22	1.95	1.85	2.01	1.71	1.99	2.91	1.40	1.85	1.46
MA_RS22770	NA	2.32	2.85	2.55	2.73	2.58	2.71	3.04	2.93	3.04	2.59	2.76	2.69
MA_RS22780	#N/A	0.94	0.00	0.00	0.00	0.70	0.00	0.00	0.00	1.37	0.00	0.00	1.40
MA_RS22785	#N/A	1.88	1.83	1.69	2.39	1.85	2.55	2.15	3.16	3.88	2.70	2.07	2.49
MA_RS22790	NA	1.38	1.75	1.77	2.30	1.53	2.44	1.99	3.20	3.47	1.57	1.88	1.48
MA_RS22795	NA	2.39	2.82	2.54	2.96	2.68	3.02	2.69	3.80	3.98	3.12	3.28	2.71
MA_RS22800	NA	1.83	2.05	1.95	2.24	2.18	2.31	2.51	3.19	3.42	2.40	2.26	2.16
MA_RS22805	NA	0.86	1.12	1.45	1.65	1.24	1.02	1.40	1.77	1.95	1.06	0.77	1.40
MA_RS22810	NA	0.17	0.43	0.84	0.59	0.56	0.42	0.91	0.94	1.46	0.61	0.31	0.87
MA_RS22815	NA	2.50	2.43	2.78	3.04	2.83	2.93	2.97	3.36	3.18	2.83	2.41	2.84
MA_RS22820	NA	0.94	1.32	1.13	1.44	1.36	1.63	1.65	1.80	2.23	1.32	1.08	1.43
MA_RS22825	NA	1.03	1.06	1.27	1.73	1.04	1.35	1.72	1.49	1.72	1.21	1.14	1.14
MA_RS22830	NA	2.18	2.60	2.61	2.38	2.42	2.65	2.42	2.69	3.17	2.06	1.96	2.30
MA_RS22835	NA	3.41	3.46	3.39	3.44	3.45	3.43	3.42	3.80	3.64	3.43	3.36	3.49
MA_RS22840	NA	2.01	1.99	1.90	2.58	2.28	2.20	2.42	3.04	2.97	2.08	2.09	1.63
MA_RS22845	NA	2.86	3.02	2.89	2.99	2.79	3.15	2.69	3.05	3.07	2.40	2.92	2.89
MA_RS22850	NA	1.89	2.49	2.13	2.28	2.12	2.06	1.48	2.48	2.67	1.37	1.42	1.97
MA_RS22855	NA	1.65	2.08	2.23	1.97	1.49	1.78	1.82	2.07	2.03	1.00	1.77	1.80
MA_RS22860	NA	2.09	2.35	1.78	2.05	1.81	1.77	1.96	2.73	2.43	1.57	1.54	2.32
MA_RS22865	NA	1.46	1.65	1.66	1.91	1.57	1.60	1.70	1.64	2.14	1.11	1.40	1.61
MA_RS22870	NA	1.28	1.29	0.94	1.35	0.80	1.43	1.23	0.65	1.49	0.50	0.58	1.74
MA_RS22875	NA	1.58	1.24	1.67	1.65	1.49	1.68	1.82	1.85	2.27	1.13	1.38	1.31
MA_RS22880	NA	4.09	4.22	4.03	4.82	4.35	4.54	4.48	5.14	5.45	4.47	4.32	4.46
MA_RS22885	NA	4.80	4.93	4.85	5.13	4.90	5.20	5.13	5.55	5.58	5.33	5.22	4.96
MA_RS22890	NA	1.53	1.63	1.52	1.59	1.64	1.92	1.55	1.83	2.04	1.48	1.70	1.75
MA_RS22895	NA	3.29	3.57	3.57	3.91	3.59	3.88	3.73	4.22	4.33	3.30	3.43	3.54
MA_RS22900	mtaA	9.13	9.48	9.28	10.54	10.09	10.34	10.28	10.69	10.94	10.05	10.05	10.07
MA_RS22905	NA	5.27	5.38	5.33	6.31	6.03	6.25	6.26	6.55	6.94	5.67	5.63	5.90
MA_RS22910	NA	2.12	2.24	2.36	2.83	2.72	2.94	2.98	3.63	3.66	2.74	2.58	2.62
MA_RS22915	NA	4.77	4.87	4.74	5.11	4.69	5.20	5.10	5.68	5.79	5.15	4.62	4.89
MA_RS22920	NA	4.68	4.86	4.56	5.05	4.79	4.98	4.95	5.72	5.68	5.31	4.94	4.81
MA_RS22925	NA	1.73	2.62	2.46	2.14	2.13	2.38	2.95	5.86	3.30	3.26	7.20	8.19
MA_RS22930	NA	1.33	1.55	1.97	2.14	1.32	1.40	2.17	4.72	3.22	2.09	4.86	5.94
MA_RS22935	NA	2.86	3.19	3.13	3.62	3.38	3.43	3.77	4.38	3.94	3.60	4.52	5.68
MA_RS22945	NA	2.31	2.54	2.09	2.93	2.77	2.83	2.42	3.69	3.45	2.96	3.68	4.51
MA_RS22955	mtaC	2.97	2.87	3.10	9.82	9.05	9.34	8.02	5.62	5.97	7.49	6.82	5.79
MA_RS22960	mtaB	2.88	3.20	2.90	9.69	8.87	9.26	7.65	5.58	6.16	7.41	6.68	5.59
MA_RS22965	NA	1.67	1.93	1.50	8.30	7.38	7.92	6.55	4.49	4.81	6.05	5.38	4.32
MA_RS22970	NA	0.33	0.40	0.63	3.57	2.92	3.24	2.55	0.94	1.33	1.90	1.67	1.57
MA_RS22975	NA	3.14	3.33	3.12	3.99	3.65	3.83	3.61	3.70	3.75	3.55	3.20	3.49
MA_RS22980	NA	5.70	5.98	5.83	6.36	6.09	6.26	6.25	6.78	6.90	6.46	6.11	6.17
MA_RS22985	NA	4.76	5.06	5.05	5.50	5.13	5.45	5.58	6.26	6.68	5.78	5.35	5.49
MA_RS22990	NA	4.88	5.06	5.14	5.18	4.79	5.09	5.22	5.99	6.26	5.49	4.92	5.26
MA_RS22995	cdhA	5.30	5.52	5.37	7.00	6.46	6.79	6.60	6.29	7.02	7.54	6.77	6.68
MA_RS23000	NA	1.75	1.77	1.74	1.39	2.31	2.42	1.87	2.75	2.38	2.22	1.88	2.28
MA_RS23005	#N/A	3.30	3.17	1.74	3.58	3.37	3.30	3.83	3.98	2.60	4.25	4.28	3.28
MA_RS23010	NA	4.41	4.58	4.72	4.80	4.60	4.85	4.69	4.97	5.03	4.83	4.47	4.72
MA_RS23015	NA	4.47	4.51	4.64	5.10	4.87	5.10	4.95	5.49	5.86	5.00	4.40	4.66
MA_RS23020	NA	3.23	3.57	3.55	3.67	3.49	3.51	3.02	3.57	3.89	3.27	3.25	3.31
MA_RS23025	NA	5.89	6.12	6.03	6.33	6.14	6.31	6.28	6.69	6.85	6.22	6.02	6.20
MA_RS23030	NA	4.20	4.33	4.58	4.87	4.52	5.02	4.35	5.50	5.54	4.62	4.51	4.63
MA_RS23035	NA	5.09	5.34	5.24	5.70	5.21	5.46	5.76	5.50	5.76	5.33	5.04	5.40
MA_RS23040	NA	4.60	4.66	4.37	5.23	4.75	4.88	5.34	5.49	5.60	4.92	4.63	4.80
MA_RS23045	NA	3.18	3.36	3.20	3.87	3.24	4.16	3.48	4.28	5.06	3.62	3.13	3.35
MA_RS23050	NA	2.74	3.01	3.11	3.37	2.67	3.20	3.24	3.19	3.58	3.20	2.35	3.02
MA_RS23055	NA	3.60	3.98	3.81	4.56	4.23	4.40	4.42	4.23	4.61	4.09	4.02	4.21
MA_RS23060	NA	4.49	4.47	4.66	4.71	4.50	4.58	4.87	5.49	5.55	4.75	4.26	4.33
MA_RS23065	NA	8.55	8.77	8.67	9.46	9.00	9.17	9.44	9.64	10.02	8.76	9.05	9.18
MA_RS23070	NA	4.39	4.54	4.58	5.18	4.74	5.21	4.89	5.36	5.41	5.19	4.89	4.78
MA_RS23075	NA	4.54	4.84	4.81	5.25	5.00	5.13	5.13	5.34	5.26	5.03	4.77	4.99
MA_RS23080	NA	3.76	3.82	3.87	4.37	3.94	3.90	4.26	3.70	3.92	3.76	3.70	3.67
MA_RS23085	NA	3.71	3.90	3.89	4.05	3.87	4.33	4.15	4.63	4.94	3.74	3.62	3.90
MA_RS23090	NA	3.25	3.35	3.34	3.26	3.42	3.22	3.55	4.07	4.05	3.08	3.15	3.27
MA_RS23095	tgtA	4.96	5.12	4.98	5.18	5.03	5.10	5.15	5.14	5.23	5.19	5.08	5.18
MA_RS23100	NA	4.39	4.58	4.62	4.99	4.63	4.64	4.62	4.87	5.03	4.82	4.67	4.62
MA_RS23105	NA	3.78	3.87	3.83	4.42	4.14	4.13	4.52	4.52	4.87	4.13	3.78	4.40
MA_RS23110	NA	3.34	3.59	3.21	4.09	3.73	3.98	3.82	4.23	4.69	3.79	3.62	3.90
MA_RS23115	NA	1.85	1.96	1.85	2.32	2.10	2.26	2.49	2.50	2.89	2.44	2.37	2.04
MA_RS23120	NA	2.42	2.59	2.54	2.88	2.69	2.87	2.84	3.18	3.52	2.90	2.68	2.86
MA_RS23125	NA	0.35	0.27	0.00	0.15	0.48	0.91	0.17	0.83	0.86	0.00	0.47	0.30
MA_RS23130	NA	0.37	0.60	0.47	0.92	0.38	0.45	0.56	0.34	0.82	0.53	0.24	0.78
MA_RS23135	NA	0.38	0.00	0.18	0.16	0.29	0.25	0.10	0.20	0.15	0.07	0.00	0.61
MA_RS23140	NA	7.52	7.74	7.59	8.05	7.68	7.94	8.20	8.68	8.72	7.82	7.61	7.77
MA_RS23145	serB	7.46	7.68	7.63	8.02	7.69	7.95	8.04	8.55	8.79	7.83	7.62	7.78
MA_RS23150	NA	9.68	9.87	9.74	10.42	10.01	10.23	10.21	10.58	10.88	10.07	9.89	9.94
MA_RS23155	NA	4.33	4.58	4.48	4.60	4.58	4.27	4.30	4.65	4.89	4.77	4.40	4.53
MA_RS23160	NA	3.08	3.32	3.26	3.30	3.51	3.64	3.34	3.87	4.03	3.51	2.93	3.26
MA_RS23165	tmk	2.45	2.64	2.68	3.01	2.84	2.65	2.57	2.93	3.20	3.04	2.46	2.69
MA_RS23170	NA	3.15	3.34	3.32	3.77	3.79	3.78	3.94	3.93	4.36	3.82	3.53	3.13
MA_RS23175	NA	3.83	3.80	4.06	4.32	4.08	4.21	4.13	4.37	4.25	3.95	3.89	4.00
MA_RS23180	NA	6.43	6.56	6.43	6.90	6.54	6.76	6.95	7.18	7.10	6.70	6.34	6.61
MA_RS23185	NA	4.80	4.94	4.75	5.15	5.00	5.00	4.92	5.12	5.27	4.70	4.70	4.78
MA_RS23190	NA	3.85	4.34	3.95	4.43	4.21	4.48	4.37	5.02	5.37	4.29	4.40	4.26
MA_RS23195	NA	1.63	1.54	1.38	1.58	1.78	1.95	0.98	1.59	2.03	1.35	1.50	1.63
MA_RS23205	NA	4.29	4.43	4.41	5.22	4.59	5.03	4.98	5.61	6.07	5.16	4.72	4.84
MA_RS23210	NA	3.59	3.97	3.81	4.04	3.92	3.93	4.32	4.54	4.62	3.87	3.53	3.74
MA_RS23215	NA	1.18	1.31	1.03	1.61	1.30	1.64	1.48	1.95	2.49	1.65	1.81	2.10
MA_RS23220	NA	2.39	2.76	2.65	3.18	2.90	2.97	2.68	3.17	3.49	2.33	2.64	2.34
MA_RS23225	NA	1.35	1.96	1.62	1.48	2.74	1.86	1.98	3.41	2.86	2.65	1.25	1.83
MA_RS23230	NA	2.33	2.52	2.13	2.85	2.64	3.17	2.43	3.12	3.36	2.78	2.49	2.83
MA_RS23235	NA	2.19	2.07	2.27	2.57	1.90	2.48	2.33	3.24	3.35	2.47	2.29	2.37
MA_RS23240	NA	3.08	3.53	2.87	4.02	3.70	3.89	3.88	4.96	5.31	4.19	4.13	3.98
MA_RS23245	NA	1.17	1.87	1.47	2.29	2.08	2.51	2.17	1.37	2.30	2.35	2.27	1.91
MA_RS23250	NA	1.85	2.16	1.93	2.27	2.29	1.95	2.35	2.46	2.63	2.16	2.13	1.85
MA_RS23255	NA	1.92	2.08	2.30	2.42	2.47	2.63	2.27	3.14	3.18	2.65	2.45	2.68
MA_RS23260	NA	1.60	1.74	1.94	1.66	1.60	1.85	2.00	2.28	2.37	1.95	1.65	1.55
MA_RS23265	NA	1.34	1.27	1.42	0.94	1.13	1.22	1.23	1.45	1.63	1.00	0.69	1.25
MA_RS23270	NA	3.77	3.51	3.89	3.57	3.23	3.89	3.44	4.44	4.27	3.96	3.83	3.43
MA_RS23275	NA	5.27	5.54	5.28	5.70	5.30	5.64	5.55	6.07	6.21	5.55	5.30	5.27
MA_RS23280	NA	3.83	4.49	4.13	4.51	3.98	4.51	4.79	5.69	6.03	4.54	4.16	4.39
MA_RS23285	galU	5.29	5.53	5.45	5.98	5.80	5.85	5.78	6.40	6.80	6.01	5.58	5.56
MA_RS23290	NA	5.67	5.92	5.79	6.18	5.75	6.01	6.18	6.74	6.97	6.18	5.93	6.09
MA_RS23295	NA	3.53	3.87	3.72	4.35	3.75	4.18	4.22	5.05	5.28	4.17	3.84	3.91
MA_RS23305	NA	1.36	1.05	1.47	1.53	1.33	1.33	1.58	1.65	1.93	1.43	1.27	1.43
MA_RS23310	NA	4.31	4.59	4.43	4.80	4.72	4.98	4.54	5.28	5.46	5.25	4.72	4.86
MA_RS23315	NA	2.50	2.55	2.95	2.57	2.66	2.96	2.29	3.13	3.10	2.21	2.19	2.34
MA_RS23320	NA	2.06	1.78	2.56	2.20	1.90	2.15	2.24	2.43	3.15	1.92	2.02	1.91
MA_RS23330	NA	2.12	2.45	2.24	2.16	2.29	2.87	2.32	2.96	2.60	2.62	2.28	2.32
MA_RS23335	NA	5.49	5.51	5.43	6.14	5.73	5.83	6.20	5.87	6.41	6.12	5.54	5.87
MA_RS23340	NA	7.49	7.65	7.67	8.29	7.83	7.95	8.42	9.08	9.33	8.39	7.75	8.01
MA_RS23345	dapA	7.36	7.63	7.44	8.07	7.67	7.92	7.95	8.03	8.24	8.07	7.69	7.79
MA_RS23350	dapB	6.95	7.32	7.22	7.82	7.31	7.56	7.62	8.20	8.54	7.79	7.37	7.41
MA_RS23355	NA	1.94	1.66	0.83	1.80	1.76	2.14	1.24	2.12	2.30	0.98	1.15	2.04
MA_RS23360	NA	1.48	1.85	1.75	1.78	1.96	1.89	1.25	2.69	2.66	1.75	1.21	2.44
MA_RS23365	NA	2.06	2.41	2.03	2.57	2.68	1.91	2.17	2.54	2.58	1.64	2.08	2.84
MA_RS23370	NA	2.87	2.81	2.82	2.78	2.70	3.06	2.86	3.42	2.94	2.77	2.40	2.70
MA_RS23375	NA	1.87	1.81	1.78	1.45	1.48	2.38	2.38	1.50	2.99	1.72	0.90	1.77
MA_RS23380	NA	2.36	2.57	2.51	3.24	2.83	3.30	2.80	3.19	3.70	2.82	3.08	2.95
MA_RS23385	NA	2.21	2.32	2.34	2.63	2.50	2.69	2.70	3.03	3.43	2.37	2.30	2.35
MA_RS23390	NA	0.39	0.42	0.00	0.72	0.70	1.03	0.45	1.21	1.38	1.13	0.00	0.49

MA_RS23395	NA	1.80	2.15	2.10	2.47	2.27	2.35	2.56	3.41	3.51	2.58	2.26	2.48
MA_RS23400	NA	2.36	2.68	2.63	1.87	2.24	2.17	2.32	2.98	3.27	2.26	2.15	1.93
MA_RS23405	NA	2.84	3.18	3.17	3.83	3.47	3.89	3.36	3.98	4.11	3.49	3.12	3.34
MA_RS23410	NA	3.10	2.95	2.99	3.64	3.05	3.35	3.11	4.22	4.64	3.30	2.88	3.15
MA_RS23415	NA	1.96	2.11	1.57	2.58	2.08	2.01	2.24	3.17	3.28	2.08	1.94	2.37
MA_RS23420	NA	1.26	1.93	1.37	1.38	1.71	1.95	2.01	2.64	2.75	1.08	1.87	1.66
MA_RS23425	NA	1.19	1.57	0.91	1.48	1.38	1.59	1.55	2.71	2.58	1.03	0.00	1.36
MA_RS23430	NA	0.88	1.30	0.85	1.41	1.29	1.10	1.26	1.24	2.17	0.93	1.11	0.73
MA_RS23435	NA	1.26	1.51	1.78	1.44	1.19	1.48	1.64	1.08	1.88	0.78	0.77	0.75
MA_RS23440	NA	0.84	0.98	0.67	1.09	1.32	1.26	0.84	1.93	2.13	1.26	0.59	1.05
MA_RS23445	NA	0.96	0.73	0.95	0.77	1.20	0.67	1.34	1.72	1.30	1.17	0.87	0.69
MA_RS23450	NA	1.40	1.34	1.55	1.75	1.34	1.65	1.00	2.13	2.10	1.51	1.81	1.60
MA_RS23455	NA	1.36	1.55	1.54	1.86	1.47	1.90	1.94	2.37	2.67	2.12	0.99	2.20
MA_RS23460	NA	1.16	1.46	1.24	1.98	1.61	1.51	1.36	1.93	2.52	1.61	1.16	1.69
MA_RS23465	NA	0.95	1.08	0.51	1.49	1.43	1.03	0.90	2.02	1.90	1.21	1.53	1.23
MA_RS23470	NA	0.94	0.77	1.33	1.25	1.18	1.09	0.89	2.20	1.71	1.34	1.09	1.00
MA_RS23475	NA	4.20	4.19	4.21	4.69	4.36	4.67	4.67	5.15	5.21	4.52	4.15	4.40
MA_RS23480	pyrI	4.80	4.92	4.86	5.37	4.91	5.31	5.03	5.51	5.94	4.92	4.85	5.05
MA_RS23485	pyrB	5.45	5.62	5.65	5.76	5.67	5.78	5.68	5.93	6.13	5.56	5.44	5.65
MA_RS23490	NA	1.53	2.31	2.00	1.86	1.63	2.08	2.17	1.64	1.89	1.61	1.79	2.23
MA_RS23495	NA	3.90	4.04	4.13	4.29	4.06	4.34	4.48	4.60	4.82	4.06	3.80	4.24
MA_RS23500	NA	1.59	1.81	2.06	2.28	2.22	2.18	2.08	1.84	2.45	2.03	1.93	1.89
MA_RS23505	#N/A	0.00	0.25	0.00	0.38	0.00	0.25	0.50	0.00	0.16	0.00	0.00	0.00
MA_RS23510	NA	1.06	1.06	1.15	1.43	1.36	1.72	1.30	1.30	1.10	1.28	1.47	1.34
MA_RS23515	mcrQ	4.29	4.58	4.43	4.86	4.63	4.92	4.87	5.21	5.38	4.70	4.80	4.82
MA_RS23525	NA	0.65	0.81	0.47	0.59	0.49	1.13	0.98	1.76	1.04	0.73	1.12	0.84
MA_RS23530	guaA	4.73	4.80	4.82	5.12	4.84	5.10	5.20	5.11	5.25	5.16	4.81	4.79
MA_RS23535	NA	4.31	4.47	4.43	5.08	4.58	4.74	5.39	5.73	5.84	5.36	4.65	4.85
MA_RS23540	NA	4.95	5.23	5.06	5.66	5.22	5.38	5.39	5.72	6.09	5.79	5.22	5.32
MA_RS23545	NA	3.93	4.05	4.05	4.56	4.14	4.30	4.12	4.54	4.68	4.43	4.28	4.21
MA_RS23550	argB	4.44	4.31	4.51	4.59	4.50	4.41	4.61	4.78	4.48	4.77	4.46	4.55
MA_RS23555	NA	5.45	5.23	5.36	5.42	5.57	5.45	5.71	5.48	5.30	5.37	5.05	5.30
MA_RS23560	mptA	6.39	6.60	6.45	6.98	6.55	6.81	6.80	7.56	7.78	6.88	6.65	6.66
MA_RS23565	NA	3.21	2.91	2.44	3.63	3.65	3.10	3.83	3.60	3.70	3.05	3.16	3.28
MA_RS23570	NA	4.55	4.65	4.74	5.10	4.85	5.01	5.20	5.53	5.90	5.11	4.71	4.89
MA_RS23575	NA	3.42	3.40	3.37	3.92	3.65	3.68	3.86	3.98	4.04	3.49	3.56	3.63
MA_RS23580	NA	0.41	0.69	0.11	1.17	0.61	0.93	0.93	1.22	0.50	0.61	0.20	0.97
MA_RS23585	gatC	5.28	5.17	5.34	6.03	5.36	5.51	6.20	5.90	6.53	5.57	5.33	5.37
MA_RS23590	gatA	5.56	5.85	5.78	6.13	5.76	5.99	6.01	6.18	6.40	5.81	5.69	5.90
MA_RS23595	gatB	5.78	6.03	6.02	6.36	6.08	6.20	6.14	6.37	6.69	5.97	5.84	5.97
MA_RS23600	NA	4.21	4.42	4.18	4.64	4.43	4.81	4.54	4.99	4.98	4.65	4.64	4.52
MA_RS23605	NA	3.56	3.77	3.82	3.95	3.67	3.82	3.75	4.24	4.09	3.80	3.31	3.67
MA_RS23615	istB	0.46	0.40	0.31	0.34	0.33	0.33	0.48	0.79	0.73	0.63	0.34	0.41
MA_RS23620	istA	0.69	0.61	0.89	0.82	0.86	0.95	0.83	1.13	1.30	0.95	0.60	0.79
MA_RS23625	NA	0.90	0.80	0.83	0.86	0.65	1.10	1.09	1.21	1.12	1.15	1.07	1.11
MA_RS23630	NA	0.40	0.47	0.89	0.86	0.65	0.47	1.00	0.36	0.68	0.61	1.09	0.34
MA_RS23635	NA	1.10	0.75	0.79	0.76	1.26	1.28	1.36	1.21	1.97	1.33	1.20	1.13
MA_RS23640	NA	1.25	1.21	1.28	1.31	1.12	1.52	1.64	1.51	1.79	1.30	1.98	1.68
MA_RS23645	NA	1.22	0.82	1.20	1.36	1.00	1.55	1.50	1.45	1.88	1.41	1.59	1.39
MA_RS23650	NA	1.49	1.58	1.13	2.02	1.47	1.72	1.75	1.88	2.34	1.44	2.24	2.02
MA_RS23655	NA	1.90	1.89	1.73	2.12	2.04	1.99	1.68	1.99	1.87	1.95	2.06	1.88
MA_RS23660	NA	1.24	1.38	1.11	1.29	1.45	0.93	1.13	1.56	1.83	1.19	0.74	0.82
MA_RS23670	NA	1.60	1.60	1.92	1.95	1.98	2.01	2.17	2.08	1.84	1.87	1.80	1.54
MA_RS23675	NA	2.01	2.01	1.96	2.37	2.23	2.62	2.45	2.96	3.14	2.57	2.39	1.90
MA_RS23680	htpX	7.99	8.06	8.02	8.34	8.03	8.22	8.15	7.83	8.03	8.59	8.09	8.07
MA_RS23685	NA	4.62	4.79	4.73	4.94	4.76	5.00	5.04	5.02	5.29	5.06	4.63	4.96
MA_RS23690	aroA	4.31	4.73	4.53	4.92	4.45	4.76	4.93	5.18	5.30	4.77	4.66	4.83
MA_RS23695	NA	1.61	2.24	1.55	2.38	1.90	1.74	2.11	2.44	2.13	2.03	1.89	2.05
MA_RS23700	mcrA	10.34	10.75	10.62	11.02	10.59	10.88	10.81	11.17	11.57	10.55	10.51	10.75
MA_RS23705	mcrG	10.54	10.87	10.76	11.18	10.77	11.04	11.18	11.52	11.84	10.79	10.65	10.94
MA_RS23710	mcrC	11.56	11.80	11.84	12.21	11.76	11.96	12.26	12.62	12.87	11.70	11.59	11.96
MA_RS23715	mcrD	10.91	11.37	11.22	11.59	11.24	11.52	11.40	11.46	11.73	10.85	11.05	11.34
MA_RS23720	mcrB	10.55	10.94	10.84	11.26	10.83	11.11	11.14	11.61	11.89	10.90	10.85	10.99
MA_RS23725	mmp10	4.77	4.96	4.97	5.46	5.07	5.47	5.25	5.87	6.14	5.00	5.22	5.44
MA_RS23730	NA	4.05	4.19	4.10	4.48	4.29	4.36	4.54	4.49	4.60	4.06	4.01	4.24
MA_RS23735	NA	5.51	5.38	5.35	5.70	5.45	5.74	5.57	5.44	6.20	5.28	5.39	5.40
MA_RS23740	NA	4.82	4.97	4.88	5.17	5.12	5.21	4.86	4.63	4.93	4.78	4.81	5.10
MA_RS23745	rbcL	5.12	5.29	5.12	5.63	5.39	5.52	5.31	5.36	5.60	5.23	5.20	5.25
MA_RS23750	NA	1.51	1.96	1.73	2.19	2.11	2.08	1.94	2.11	2.41	1.92	2.02	2.08
MA_RS23755	NA	0.81	1.13	1.07	0.72	1.19	1.32	1.10	0.74	1.27	0.96	1.46	1.22
MA_RS23765	NA	1.20	1.47	1.47	1.43	1.72	1.85	1.98	2.26	2.11	1.90	2.05	2.09
MA_RS23770	mtaA	2.39	2.75	2.37	2.73	2.92	2.62	2.65	2.63	2.64	2.46	2.34	2.39
MA_RS23775	NA	1.66	1.67	1.62	2.41	2.19	2.38	2.62	2.78	3.16	2.45	1.78	2.25
MA_RS23780	NA	1.66	1.95	1.72	1.99	1.65	2.07	1.99	2.62	2.73	2.08	2.13	2.10
MA_RS23785	NA	1.05	1.29	1.56	1.44	1.66	1.26	1.82	2.51	2.53	1.96	1.64	2.01
MA_RS23790	NA	0.88	0.95	0.71	1.49	1.18	1.52	1.33	2.09	1.98	1.63	2.32	2.42
MA_RS23795	NA	0.79	0.82	1.11	1.37	1.07	1.64	1.07	0.88	0.72	1.19	0.98	0.49
MA_RS23800	NA	0.19	0.21	0.65	0.45	0.40	0.00	0.71	1.02	0.36	0.48	0.34	1.00
MA_RS23805	mnhG	4.87	4.88	5.25	5.63	5.30	5.71	5.62	6.18	6.69	5.24	5.36	5.17
MA_RS23810	NA	4.56	4.71	4.55	5.20	4.64	5.34	4.91	5.97	6.41	4.93	5.04	4.99
MA_RS23815	NA	5.37	5.56	5.54	6.23	5.71	6.14	5.85	6.81	7.21	5.37	5.56	5.70
MA_RS23820	NA	5.19	5.52	5.34	5.98	5.51	5.95	5.47	6.12	6.45	5.10	5.51	5.50
MA_RS23825	NA	4.79	5.12	4.89	5.56	5.03	5.28	5.11	5.74	6.32	4.53	5.11	5.18
MA_RS23830	NA	5.45	5.83	5.63	6.09	5.79	5.81	6.00	6.27	6.76	5.54	5.68	5.72
MA_RS23835	NA	5.15	5.52	5.32	5.89	5.54	5.78	5.46	6.05	6.40	5.34	5.56	5.58
MA_RS23845	NA	5.78	5.86	5.61	6.46	6.08	6.39	6.54	6.70	7.52	6.04	6.16	6.38
MA_RS23850	NA	6.04	5.84	6.10	6.72	6.39	6.60	7.07	7.35	8.07	6.12	6.58	6.77
MA_RS23855	NA	6.02	6.11	5.88	6.92	6.62	6.81	6.93	6.92	7.77	5.69	6.63	7.04
MA_RS23860	NA	6.59	6.44	6.41	7.26	6.86	6.99	7.40	7.33	8.24	6.32	6.98	7.21
MA_RS23865	NA	3.09	3.27	3.48	3.29	3.11	3.33	3.56	3.98	4.24	3.06	3.07	3.21
MA_RS23870	NA	2.32	2.43	2.35	2.47	2.39	2.55	2.34	3.56	3.85	2.74	2.65	1.82
MA_RS23885	NA	3.02	3.12	2.54	3.30	3.21	3.37	2.95	3.81	3.97	3.51	3.10	2.95
MA_RS23895	NA	3.91	4.03	3.93	4.17	4.18	4.36	3.75	4.24	4.68	4.29	3.92	4.06
MA_RS23900	NA	2.54	2.85	2.93	3.29	2.66	2.93	3.10	3.30	4.13	3.14	2.71	2.98
MA_RS23905	NA	1.49	1.81	0.93	2.56	1.67	1.92	2.32	2.50	3.78	1.82	2.19	2.34
MA_RS23910	NA	0.23	0.48	0.18	1.07	0.60	0.00	0.58	0.00	0.97	0.97	0.29	0.22
MA_RS23915	NA	3.14	3.14	3.15	3.54	3.66	3.83	3.66	4.25	3.85	3.59	3.31	3.18
MA_RS23920	#N/A	2.66	3.00	3.15	2.55	3.03	2.87	2.80	3.58	3.81	3.25	2.81	3.35
MA_RS23925	#N/A	4.19	4.28	3.92	4.58	4.80	3.97	4.60	5.05	3.68	4.73	4.48	4.72
MA_RS23930	#N/A	3.27	2.94	2.99	3.34	3.57	3.27	3.47	3.66	3.09	3.76	3.20	3.29
MA_RS23935	NA	5.09	5.27	5.19	5.60	5.23	5.34	5.70	5.87	5.93	5.60	5.26	5.39
MA_RS23955	NA	5.04	4.97	4.98	5.51	5.18	5.49	5.40	5.40	5.30	5.65	5.41	5.33
MA_RS23960	NA	5.46	5.73	5.70	6.14	5.97	6.00	6.08	5.97	6.00	5.78	5.76	5.94
MA_RS23965	NA	5.01	5.30	5.11	5.48	5.25	5.51	5.76	5.52	5.65	5.38	5.09	5.50
MA_RS23970	aroD	5.30	5.72	5.44	5.92	5.84	5.87	5.87	6.24	6.14	5.66	5.65	5.91
MA_RS23975	NA	4.37	4.66	4.53	4.86	4.64	4.88	4.95	4.81	4.98	4.28	4.46	4.79
MA_RS23980	NA	3.86	4.27	4.04	4.41	4.15	4.62	4.36	4.41	4.69	3.88	3.70	4.45
MA_RS23985	NA	3.07	3.20	3.24	3.52	3.14	3.43	3.62	4.00	4.19	3.25	3.06	2.98
MA_RS23990	NA	2.45	3.01	3.09	3.22	3.02	3.58	3.29	4.07	3.91	1.99	3.01	3.56
MA_RS23995	NA	3.04	3.22	3.39	3.47	3.26	3.76	3.64	3.77	3.73	2.16	2.99	3.72
MA_RS24000	NA	3.13	3.28	3.75	3.38	3.30	3.68	3.39	3.79	3.63	2.52	3.26	3.53
MA_RS24005	NA	3.49	3.78	4.22	4.03	3.91	4.26	4.09	4.13	3.99	2.95	3.72	4.43
MA_RS24010	NA	4.34	4.76	5.05	5.15	4.75	5.26	4.98	5.56	5.23	4.02	4.93	5.37
MA_RS24015	NA	4.24	4.76	5.00	4.88	4.70	5.29	4.75	5.59	5.41	4.11	4.89	5.17
MA_RS24025	NA	2.21	2.57	2.30	2.66	2.27	2.57	2.66	3.20	2.95	2.43	2.47	2.27
MA_RS24030	NA	0.99	1.12	1.00	1.02	1.26	1.63	1.49	1.65	1.56	0.97	1.34	1.12
MA_RS24035	NA	1.47	2.28	2.10	1.94	2.14	2.51	2.56	2.60	2.87	2.00	2.17	2.46
MA_RS24040	tpiA	5.81	6.01	5.91	6.42	6.09	6.25	6.25	6.35	6.66	6.21	6.04	6.21
MA_RS24045	NA	6.98	7.32	7.18	7.72	7.27	7.51	7.59	7.55	7.93	7.71	7.49	7.44
MA_RS24050	NA	3.26	3.27	3.27	3.73	3.42	3.29	3.65	3.48	4.00	3.30	3.04	3.44
MA_RS24055	#N/A	2.28	2.14	0.61	2.05	1.57	1.40	2.12	0.00	0.47	0.70	2.05	1.65
MA_RS24060	NA	2.99	3.17	3.28	3.52	3.02	3.31	3.18	3.91	3.66	3.60	2.28	3.05
MA_RS24065	NA	1.21	1.44	1.35	1.61	1.35	1.72	1.69	2.27	2.45	1.61	1.49	1.92
MA_RS24070	#N/A	5.69	5.90	5.46	6.16	6.15	6.33	5.79	6.18	6.01	6.16	6.00	5.86
MA_RS24075	#N/A	16.32	16.32	16.29	16.30	16.29	16.30	16.22	16.26	16.21	16.30	16.30	16.27
MA_RS24080	#N/A	15.36	15.15	15.38	14.96	15.41	15.07	15.34	14.30	14.13	15.03	15.32	15.30
MA_RS24085	NA	7.62	7.81	7.85	8.41	8.10	8.14	8.42	8.62	8.77	7.60	7.71	7.91
MA_RS24090	NA	3.87	4.67	4.42	5.09	4.84	4.91	5.04	5.14	5.70	4.68	4.22	4.83
MA_RS24095	NA	4.23	4.52	4.46	5.11	4.62	4.88	4.86	5.52	5.81	4.92	4.36	4.79
MA_RS24100	NA	2.99	3.30	3.08	3.85	3.60	3.39	3.48	3.75	4.16	3.52	3.02	3.68
MA_RS24110	NA	0.47	1.58	0.85	1.64	2.16	1.65	0.89	1.01	1.15	1.69	0.45	1.40
MA_RS24115	NA	1.61	1.98	1.70	2.35	2.71	2.18	2.06	2.11	2.37	2.76	1.72	2.27
MA_RS24120	NA	1.51	1.70	0.58	2.03	2.40	2.14	2.17	2.05	2.20	2.24	1.05	1.73
MA_RS24125	NA	3.63	3.55	3.45	3.73	3.89	4.16	3.47	4.60	4.52	3.96	3.36	3.75
MA_RS24130	NA	2.92	3.02	2.96	3.08	3.41	3.27	3.39	3.21	3.36	3.40	3.28	2.74
MA_RS24135	NA	0.34	0.74	0.65	0.47	0.78	1.29	0.65	0.91	0.78	0.75	0.39	0.33
MA_RS24140	lnrA	1.86	2.13	2.18	2.63	2.21	2.95	2.25	3.02	3.44	2.56	2.23	2.49
MA_RS24145	NA	1.85	2.05	1.96	2.19	2.09	2.67	2.23	3.12	3.63	2.55	2.17	2.16
MA_RS24150	NA	1.72	2.09	1.57	2.34	2.11	2.74	1.93	2.96	3.70	2.59	2.10	2.16
MA_RS24155	NA	3.45	3.27	3.60	4.02	3.76	3.96	4.29	4.75	4.54	3.92	3.33	3.53
MA_RS24160	NA	3.88	4.20	3.87	4.53	4.20	4.43	4.34	4.05	4.59	4.12	4.31	4.26
MA_RS24165	NA	4.28	4.50	4.48	4.84	4.79	4.82	4.67	4.73	4.83	4.84	4.69	4.62
MA_RS24170	arcS	4.27	4.68	4.54	4.87	4.56	4.81	4.63	4.49	4.87	4.61	4.66	4.67

MA_RS24175	rimI	4.00	3.99	4.09	4.46	4.05	4.52	4.59	4.83	4.81	4.40	3.94	4.28
MA_RS24180	NA	3.92	4.11	4.16	4.35	4.68	4.61	4.51	5.36	4.84	4.63	4.32	4.00
MA_RS24185	dnaG	5.44	5.63	5.58	5.94	5.72	5.77	5.69	6.02	6.26	5.86	5.66	5.78
MA_RS24190	NA	2.09	2.21	2.13	2.40	2.14	2.53	2.65	2.56	2.41	2.23	2.03	2.15
MA_RS24195	rtcA	2.15	2.37	2.25	2.13	2.49	2.59	2.61	2.63	2.73	2.27	2.48	2.69
MA_RS24200	NA	4.00	4.19	3.55	4.36	3.83	4.11	4.13	4.40	4.59	4.12	3.80	3.33
MA_RS24205	NA	2.50	2.88	2.73	2.19	2.46	2.55	2.81	3.29	2.88	1.73	2.04	2.59
MA_RS24210	NA	1.59	1.76	1.63	2.01	1.75	1.66	2.53	3.00	3.14	1.70	1.86	1.88
MA_RS24215	NA	0.89	1.06	0.87	1.53	1.21	0.88	1.52	0.66	1.05	0.85	0.86	1.57
MA_RS24220	NA	2.38	2.62	2.53	2.89	2.65	2.91	2.67	3.15	3.30	2.99	2.91	2.77
MA_RS24225	NA	1.63	1.66	1.87	2.04	1.96	1.96	2.23	2.22	2.23	2.01	1.31	2.25
MA_RS24230	NA	3.13	3.32	3.40	3.91	3.62	3.83	3.93	4.17	4.10	3.68	3.30	3.59
MA_RS24240	NA	3.84	4.22	4.08	4.36	4.01	4.06	4.39	4.65	4.63	3.97	3.54	4.17
MA_RS24245	NA	3.54	3.76	4.04	3.97	3.77	4.07	4.25	4.06	4.28	3.76	3.38	4.17
MA_RS24250	NA	5.76	6.02	5.88	7.05	6.52	6.77	6.78	6.67	7.35	7.37	6.51	6.56
MA_RS24255	NA	7.23	7.48	7.46	8.19	7.72	7.96	7.97	8.25	8.79	8.75	7.76	7.89
MA_RS24260	NA	7.05	7.33	7.18	7.98	7.52	7.76	7.59	7.92	8.27	8.60	7.59	7.74
MA_RS24265	NA	4.98	5.16	5.11	5.20	5.09	5.18	5.35	5.53	5.27	4.90	4.86	4.99
MA_RS24270	NA	2.44	2.82	2.67	2.56	2.79	2.75	2.59	2.99	2.89	2.59	2.43	2.49
MA_RS24275	NA	4.26	4.41	4.30	4.79	4.45	4.50	4.66	4.87	4.89	4.74	4.26	4.46
MA_RS24280	NA	3.74	4.09	3.96	4.20	4.24	4.44	4.36	4.81	4.96	4.42	4.37	4.26
MA_RS24285	NA	1.19	1.18	0.97	2.01	1.86	1.58	1.68	2.10	2.36	1.70	1.72	1.77
MA_RS24295	NA	3.89	4.07	4.12	4.43	4.11	4.15	4.34	4.46	4.53	4.37	4.10	4.26
MA_RS24300	NA	4.51	4.83	4.54	4.85	4.83	4.77	4.71	5.12	5.51	4.94	4.77	4.76
MA_RS24305	fliE	4.38	4.41	4.59	5.06	4.68	4.80	4.99	5.44	5.92	4.99	4.43	4.53
MA_RS24315	NA	1.39	1.53	0.99	1.87	1.68	1.57	1.78	2.65	2.37	1.39	1.49	1.66
MA_RS24320	NA	1.84	1.46	2.14	1.99	2.36	1.71	2.48	3.07	4.06	2.76	2.49	3.15
MA_RS24325	NA	1.63	1.92	1.76	2.04	1.93	1.99	1.79	2.72	2.98	2.32	1.73	1.62
MA_RS24330	NA	2.05	2.10	2.30	2.60	2.21	2.86	2.66	3.04	3.44	2.60	2.26	2.45
MA_RS24335	NA	1.01	0.98	1.33	1.27	1.70	1.32	1.42	1.99	1.77	1.68	0.88	0.81
MA_RS24340	#N/A	3.37	3.63	3.56	3.64	3.34	3.69	3.97	4.73	3.95	4.21	3.57	3.67
MA_RS24345	#N/A	0.29	0.58	0.00	0.82	0.41	0.45	0.89	1.19	1.62	0.83	0.00	1.03
MA_RS24350	NA	2.13	2.34	2.07	2.60	2.22	2.66	2.51	3.29	3.55	2.90	2.38	2.49
MA_RS24355	NA	1.39	1.36	1.35	1.77	1.30	1.87	1.10	2.09	2.34	1.31	1.09	1.38
MA_RS24380	NA	2.63	3.11	2.96	3.58	3.12	3.67	3.65	4.48	4.76	3.55	3.85	3.28
MA_RS24390	NA	2.12	2.29	2.13	2.48	2.37	3.08	3.07	2.79	2.84	2.41	3.31	2.35
MA_RS24395	NA	2.49	2.88	2.90	3.18	2.65	3.77	3.51	4.02	4.12	3.44	3.73	2.77
MA_RS24400	NA	1.43	1.18	1.23	1.73	1.56	2.57	1.24	2.17	2.21	1.80	1.40	1.58
MA_RS24405	NA	3.27	3.25	3.56	3.67	3.58	3.85	3.55	4.48	4.66	3.30	3.50	3.68
MA_RS24415	NA	0.72	0.47	0.61	0.67	0.71	0.89	0.19	0.79	1.04	0.73	0.36	0.64
MA_RS24425	NA	0.90	0.09	0.41	0.69	1.08	1.03	1.08	1.71	1.53	0.43	0.60	0.35
MA_RS24430	NA	1.55	1.35	1.53	1.97	1.65	1.70	1.59	2.15	2.38	1.61	1.91	1.77
MA_RS24435	NA	1.82	2.03	2.34	2.42	2.20	2.73	2.45	3.20	3.80	2.66	2.47	2.62
MA_RS24440	NA	1.95	2.04	1.94	2.19	2.14	2.23	2.36	2.84	3.14	2.42	2.01	2.15
MA_RS24445	NA	1.59	1.87	2.01	2.02	1.71	1.90	1.97	1.65	1.94	1.65	1.63	1.46
MA_RS24450	NA	1.43	1.74	0.94	1.63	0.95	1.11	1.27	1.85	0.94	1.41	0.90	1.24
MA_RS24455	NA	0.30	0.53	2.19	0.54	0.53	0.18	0.26	0.80	0.37	0.29	0.49	0.17
MA_RS24460	NA	2.18	2.53	3.06	2.62	2.57	2.26	2.32	3.38	3.68	2.63	2.23	2.28
MA_RS24465	NA	2.33	2.80	3.47	3.03	2.96	2.83	3.21	3.96	4.20	3.13	2.92	3.03
MA_RS24470	NA	0.64	1.12	2.45	1.01	0.70	0.84	0.69	1.49	1.43	1.36	1.02	0.29
MA_RS24475	NA	2.36	2.66	3.18	2.96	2.50	3.07	2.86	3.44	3.44	3.07	2.91	2.74
MA_RS24485	NA	2.81	2.84	3.33	2.91	2.57	2.88	3.93	3.33	3.97	3.77	3.19	3.06
MA_RS24490	NA	1.78	1.74	2.73	2.23	1.99	1.71	2.90	2.77	2.86	3.37	1.49	2.42
MA_RS24495	NA	1.73	1.76	2.85	2.15	1.95	2.23	2.34	2.33	2.32	1.97	1.65	2.03
MA_RS24500	NA	1.86	1.72	2.66	2.16	2.26	2.04	2.16	3.22	3.41	2.38	2.03	1.92
MA_RS24510	NA	1.70	1.29	2.77	2.26	2.03	1.70	1.50	2.19	2.35	2.38	2.15	1.79
MA_RS24515	NA	2.33	2.56	3.32	2.55	2.46	2.57	2.97	3.69	3.49	3.02	2.87	2.86
MA_RS24520	NA	1.44	1.87	1.85	1.82	1.67	2.20	1.88	3.08	3.24	2.13	1.96	1.76
MA_RS24525	NA	3.00	3.01	2.87	3.33	3.28	3.22	3.60	3.87	4.29	3.38	3.09	3.19
MA_RS24535	NA	1.24	1.35	1.23	1.70	1.65	1.71	1.63	1.79	1.91	1.56	1.47	1.51
MA_RS24540	NA	1.23	0.80	1.68	1.19	1.59	0.87	1.28	1.73	2.15	1.50	1.35	1.27
MA_RS24545	NA	1.39	1.53	1.00	1.74	2.08	1.86	2.09	2.39	3.04	1.80	2.32	2.18
MA_RS24550	NA	0.17	0.00	0.00	0.00	0.00	0.00	0.00	0.31	0.00	0.48	0.56	0.00
MA_RS24555	NA	2.50	2.82	2.51	3.10	2.70	2.96	2.80	2.92	3.33	3.00	2.74	3.06
MA_RS24560	NA	3.77	4.21	4.08	4.23	3.82	4.06	4.49	5.29	5.56	4.54	4.18	4.04
MA_RS24565	NA	2.01	1.81	1.91	2.46	2.25	2.20	2.57	2.60	2.83	2.60	2.12	2.30
MA_RS24570	NA	2.81	2.83	2.93	3.00	2.16	3.05	2.61	3.79	3.37	2.62	2.74	2.99
MA_RS24585	NA	0.55	0.31	0.83	1.04	0.77	1.04	1.17	1.23	1.37	0.90	0.76	0.59
MA_RS24590	NA	2.69	2.88	2.72	3.11	2.77	2.97	3.01	3.58	3.67	2.70	2.33	2.63
MA_RS24595	NA	2.36	2.38	2.17	2.85	2.62	2.95	2.77	3.20	3.29	2.41	2.37	2.09
MA_RS24605	NA	3.07	3.16	3.11	3.31	3.20	3.27	3.14	3.76	3.72	3.22	3.07	3.32
MA_RS24610	NA	0.79	0.79	0.90	0.78	0.81	0.93	1.00	1.34	1.36	1.01	0.76	0.85
MA_RS24635	NA	0.11	0.33	0.00	0.75	0.23	0.25	0.26	0.53	0.30	0.31	0.53	0.62
MA_RS24645	#N/A	1.47	1.47	1.67	1.36	1.42	1.86	1.31	1.92	2.19	1.90	1.29	1.66
MA_RS24650	NA	1.87	2.25	1.75	2.42	2.11	2.28	2.14	3.13	3.45	2.25	2.01	2.43
MA_RS24655	NA	2.43	2.47	2.62	3.14	2.66	3.30	2.75	3.74	4.48	3.27	2.98	2.74
MA_RS24670	#N/A	1.92	2.32	2.12	2.35	2.33	1.98	2.15	2.85	3.05	2.67	2.19	2.27
MA_RS24675	NA	1.80	2.08	1.95	2.50	2.12	2.17	2.56	2.79	2.99	2.60	2.31	2.18
MA_RS24710	NA	0.12	0.42	0.13	0.67	0.59	0.38	0.59	1.13	1.05	0.73	0.49	0.52
MA_RS24715	NA	0.17	0.00	0.64	0.47	0.33	0.97	0.00	0.94	1.17	0.96	1.11	1.06
MA_RS24730	NA	0.82	1.11	1.07	1.14	1.04	1.16	1.11	1.56	1.85	1.04	0.88	1.20
MA_RS24735	NA	0.68	0.66	0.75	0.84	0.57	0.81	1.03	1.09	1.19	0.43	0.64	0.74
MA_RS24745	NA	0.76	0.84	0.84	1.08	0.74	1.01	0.80	1.35	1.91	1.12	0.88	0.88
MA_RS24750	NA	2.44	2.89	2.42	2.92	2.79	3.00	2.95	3.92	4.12	3.31	2.54	2.72
MA_RS24755	NA	2.62	2.93	2.57	3.01	2.88	3.22	2.83	3.51	3.81	3.03	2.99	2.93
MA_RS24765	NA	1.33	1.49	1.56	1.99	1.55	1.73	1.85	2.11	2.35	1.79	1.67	1.56
MA_RS24770	NA	2.11	2.34	2.14	2.54	2.42	2.65	2.51	2.87	3.07	2.61	2.57	2.55
MA_RS24775	NA	1.37	1.32	0.82	1.55	1.17	1.66	1.72	2.22	2.42	2.04	1.18	1.74
MA_RS24790	NA	2.42	2.75	2.69	2.81	2.63	3.09	2.85	3.47	3.63	2.92	2.42	2.68
MA_RS24800	NA	1.12	1.66	1.47	1.45	1.12	0.98	1.33	2.10	1.78	1.74	1.96	1.03
MA_RS24805	NA	4.67	4.93	4.85	4.87	4.72	4.84	4.95	5.33	5.54	4.85	4.55	4.78
MA_RS24810	NA	3.26	3.39	3.25	3.72	3.39	3.68	3.93	4.57	4.88	3.52	3.49	3.63
MA_RS24815	NA	0.43	0.76	0.79	0.88	0.57	0.87	0.69	0.77	0.97	0.89	0.65	0.83
MA_RS24820	NA	3.06	3.03	3.06	2.96	2.83	3.11	2.96	3.64	4.10	2.82	2.83	2.74
MA_RS24830	NA	1.97	2.57	2.20	2.58	2.43	2.72	2.72	3.09	3.17	2.56	2.29	2.69
MA_RS24845	NA	2.87	3.13	2.82	3.38	3.14	3.41	3.14	3.65	3.89	3.47	3.26	3.29
MA_RS24850	NA	1.22	1.39	1.38	1.18	1.46	1.41	1.70	1.89	2.59	1.55	1.39	1.27
MA_RS24855	#N/A	1.49	1.99	2.13	2.11	2.06	1.98	1.94	2.91	2.77	1.52	2.47	2.37
MA_RS24870	NA	0.00	0.09	0.00	0.00	0.00	0.00	0.00	0.52	0.57	0.00	0.00	0.00
MA_RS24875	NA	0.40	0.09	0.32	0.00	0.23	0.25	0.00	0.00	0.31	0.00	0.00	0.00
MA_RS24880	NA	1.58	1.91	1.93	1.55	1.35	1.45	1.43	2.39	2.68	1.80	1.48	1.89
MA_RS24890	NA	3.40	3.54	3.34	3.90	3.85	3.82	3.45	4.38	4.56	4.06	3.52	3.51
MA_RS24895	#N/A	10.01	9.85	9.86	9.93	10.05	9.84	10.08	10.23	9.84	10.20	9.99	9.90
MA_RS24915	NA	10.01	10.37	10.21	4.48	4.42	4.58	9.04	10.03	10.01	8.24	8.25	8.85
MA_RS24920	NA	3.85	3.96	4.15	3.71	3.36	3.75	3.58	4.15	4.39	3.47	3.38	3.89
MA_RS24925	NA	2.88	3.39	3.15	3.48	3.10	3.57	3.25	4.02	4.17	3.85	3.48	3.40
MA_RS24930	NA	2.39	2.54	2.79	2.27	2.83	2.07	2.90	3.07	2.43	2.57	1.97	3.09
MA_RS24935	NA	2.23	2.26	2.38	2.73	2.36	2.46	2.75	3.43	3.62	3.07	2.65	2.67
MA_RS24945	NA	0.81	0.84	1.37	0.96	0.53	0.17	0.90	1.01	1.17	0.94	1.19	1.97
MA_RS24950	NA	0.00	0.31	0.48	0.35	0.00	0.14	0.00	0.45	0.47	0.37	0.16	0.20
MA_RS24955	#N/A	1.69	2.22	0.57	1.31	1.79	2.28	2.42	3.01	3.22	2.36	2.30	1.62
MA_RS24965	NA	1.66	0.59	0.54	0.85	1.36	1.22	1.98	2.45	1.16	1.33	1.97	1.64
MA_RS24975	NA	0.46	0.13	0.36	0.24	0.00	0.40	0.00	0.00	0.30	0.65	0.13	0.38
MA_RS24980	NA	1.80	1.52	2.94	1.91	2.04	2.86	1.73	2.74	3.63	2.53	1.86	2.34
MA_RS24985	#N/A	1.36	1.55	1.34	1.54	2.04	1.78	2.48	2.50	1.91	1.27	2.23	1.17
MA_RS24990	#N/A	0.89	0.96	0.00	0.88	0.83	0.75	0.85	1.35	2.24	0.91	0.76	0.74
MA_RS24995	#N/A	2.57	1.88	1.84	2.36	3.02	3.10	3.21	2.10	2.90	2.44	2.20	3.13
MA_RS25000	NA	2.75	2.94	2.84	3.44	3.08	3.30	3.44	3.65	4.00	3.31	2.86	3.15
MA_RS25010	NA	3.23	3.27	2.98	3.61	3.31	3.46	3.43	4.01	4.13	3.59	2.93	3.42
MA_RS25015	NA	6.83	6.94	7.25	7.20	6.91	7.11	7.21	6.48	6.74	6.96	6.85	7.17
MA_RS25020	NA	0.21	0.84	0.79	0.55	0.32	0.60	0.38	2.03	1.97	0.95	0.05	0.83
MA_RS25025	#N/A	3.07	3.17	2.99	3.62	3.84	3.86	3.99	4.47	4.13	4.36	3.82	3.56
MA_RS25030	NA	1.68	2.04	1.89	2.37	2.27	2.43	2.10	2.40	2.85	2.34	2.19	2.38
MA_RS25035	#N/A	1.34	2.08	1.92	2.28	1.72	1.34	1.48	2.53	2.80	2.17	2.19	2.01
MA_RS25040	#N/A	1.70	1.67	1.83	1.91	1.97	2.74	1.67	1.87	2.95	1.82	2.31	1.65
MA_RS25050	#N/A	1.92	2.02	2.03	2.22	2.11	2.17	2.18	2.58	2.85	2.27	2.55	2.04
MA_RS25060	#N/A	1.36	1.13	0.74	1.86	1.82	1.51	0.44	1.81	1.71	2.50	1.35	1.84
MA_RS25065	#N/A	1.92	2.49	2.15	2.30	2.44	2.58	2.63	2.91	2.06	2.72	2.00	1.93
MA_RS25070	#N/A	2.27	1.97	1.17	2.32	2.35	2.34	2.77	2.82	2.86	2.50	2.28	1.75
MA_RS25075	#N/A	1.33	1.65	2.01	1.69	1.71	2.18	1.85	2.35	2.05	2.19	1.92	1.95
MA_RS25080	NA	0.28	0.63	2.37	0.83	0.77	0.00	2.24	1.43	2.83	0.66	2.83	1.32
MA_RS25085	NA	3.93	4.11	3.71	3.39	3.99	4.16	4.30	4.85	4.38	4.39	4.31	4.16
MA_RS25090	NA	2.38	2.71	2.80	2.80	2.52	3.24	3.41	3.39	3.64	2.74	3.46	2.73
MA_RS25095	NA	2.02	1.93	2.03	2.25	2.08	3.01	2.99	2.26	2.49	2.30	3.42	2.05
MA_RS25100	#N/A	1.09	0.99	1.54	0.97	2.07	2.49	2.51	2.34	1.75	1.17	2.91	1.26
MA_RS25110	NA	1.73	1.87	1.91	2.18	2.03	3.01	2.85	2.82	2.85	2.29	3.19	1.84
MA_RS25115	NA	0.52	0.28	0.00	0.20	0.64	2.13	2.35	1.47	1.85	0.69	2.80	0.68
MA_RS25120	NA	0.80	0.82	0.76	1.22	0.97	2.44	2.48	1.13	1.36	1.22	2.99	1.09
MA_RS25125	#N/A	1.06	1.24	1.08	1.85	1.97	2.75	2.64	2.70	3.26	2.02	3.15	1.94
MA_RS25130	#N/A	0.68	0.84	0.73	1.35	0.40	2.29	2.33	1.81	0.88	1.55	2.91	0.00
MA_RS25135	NA	0.86	1.07	0.67	1.02	1.36	2.26	2.41	2.49	1.52	1.14	3.08	1.13
MA_RS25140	NA	1.37	1.36	1.33	1.49	1.30	2.53	2.68	2.30	2.35	1.57	3.06	1.36
MA_RS25165	NA	1.02	0.92	1.06	1.60	1.75	1.47	1.76	2.32	2.71	1.55	1.59	1.52

MA_RS25175	NA	0.69	1.12	1.54	0.22	0.70	1.01	0.22	1.02	0.54	0.99	0.84	0.42
MA_RS25180	NA	0.78	0.54	0.77	0.60	0.49	1.67	1.10	0.89	0.95	0.97	0.40	0.31
MA_RS25185	NA	0.65	0.63	0.60	0.43	0.49	0.83	0.78	0.81	0.42	0.17	0.43	1.20
MA_RS25190	NA	3.22	2.86	2.81	3.06	3.35	3.76	3.14	3.66	2.90	2.96	2.87	3.22
MA_RS25195	NA	0.44	1.00	1.25	0.61	0.57	0.84	0.91	1.05	1.55	0.88	0.29	0.81
MA_RS25200	NA	1.90	1.93	1.83	2.26	2.01	2.39	1.92	2.75	3.11	2.35	2.08	2.08
MA_RS25205	NA	0.57	0.79	1.26	0.84	0.86	1.68	0.26	1.42	1.51	1.02	0.48	0.59
MA_RS25210	NA	1.63	1.83	1.98	1.62	2.11	2.35	1.22	2.56	2.62	2.02	2.10	1.88
MA_RS25215	#N/A	1.19	1.57	1.57	1.04	0.64	1.71	1.06	2.11	1.97	1.09	1.17	1.51
MA_RS25220	NA	1.22	1.89	1.64	1.59	1.21	2.22	2.01	2.87	3.12	1.90	1.83	1.99
MA_RS25225	NA	0.44	0.14	0.00	0.00	0.33	0.20	0.82	0.40	0.37	0.35	0.00	0.00
MA_RS25230	#N/A	1.60	1.59	2.72	1.73	1.73	1.57	2.02	1.86	2.32	1.91	1.51	1.88
MA_RS25235	NA	1.72	1.31	2.68	2.12	1.45	1.83	2.12	2.44	2.82	1.72	1.83	1.51
MA_RS25240	NA	0.53	0.88	2.27	1.11	0.78	1.08	1.34	1.66	2.05	1.17	1.02	0.60
MA_RS25245	NA	1.87	2.03	2.93	2.63	2.52	2.25	2.65	2.31	2.51	2.06	2.26	2.33
MA_RS25255	NA	1.47	1.52	2.79	1.57	1.65	1.61	1.80	2.57	2.41	2.15	1.61	1.64
MA_RS25260	#N/A	0.99	1.50	2.51	1.41	1.48	1.62	1.68	1.84	2.14	1.34	1.14	1.61
MA_RS25265	#N/A	2.71	3.14	3.44	3.14	3.23	3.08	3.16	2.93	3.30	2.93	2.87	2.86
MA_RS25270	#N/A	3.27	3.35	3.73	3.32	3.07	3.78	3.28	3.61	3.66	3.56	3.01	3.44
MA_RS25275	#N/A	1.76	1.88	3.04	2.30	2.38	2.18	1.73	2.36	2.69	2.62	2.13	2.15
MA_RS25280	#N/A	1.00	1.24	2.22	1.65	0.63	0.67	0.00	0.89	0.27	0.30	0.66	1.57
MA_RS25285	#N/A	1.15	1.26	2.37	1.28	1.03	0.88	1.10	0.97	1.41	0.72	1.08	1.08
MA_RS25290	#N/A	2.27	2.13	2.53	2.13	2.26	2.47	2.21	1.96	1.63	1.12	2.33	2.53
MA_RS25305	#N/A	2.05	2.16	2.80	2.66	2.85	2.65	2.77	3.35	2.73	2.86	2.66	2.88
MA_RS25310	#N/A	1.17	1.17	2.55	1.44	1.33	1.30	1.28	1.58	1.38	1.17	1.61	1.70
MA_RS25325	#N/A	1.10	1.43	2.58	1.64	1.59	1.42	2.06	2.41	2.36	1.78	1.68	1.38
MA_RS25330	#N/A	1.27	1.11	2.58	1.55	1.35	1.83	0.90	2.03	1.71	1.68	0.99	0.90
MA_RS25350	#N/A	0.52	0.00	0.00	1.08	0.00	0.00	0.71	0.21	0.00	0.21	0.00	0.12
MA_RS25355	#N/A	1.15	1.68	2.46	1.68	1.75	1.72	1.89	2.11	2.27	1.69	1.92	1.91
MA_RS25365	#N/A	1.46	1.64	2.51	2.05	1.81	2.11	1.63	2.24	2.64	2.02	1.79	1.76
MA_RS25370	#N/A	1.12	1.17	2.63	1.60	1.45	1.57	1.41	1.42	1.07	1.16	1.01	1.50
MA_RS25375	NA	7.10	7.46	7.22	7.85	7.52	7.80	7.88	8.30	8.50	8.00	7.57	7.67
MA_RS25380	tnpA	0.34	0.06	2.18	0.57	0.02	0.03	0.00	0.07	0.03	0.01	0.01	0.00
MA_RS25385	NA	1.06	0.68	2.43	1.00	1.12	1.10	1.03	1.27	1.69	1.26	0.85	0.95
MA_RS25400	eIF1A	0.76	0.60	2.43	1.43	0.61	1.91	0.97	1.94	2.28	1.72	0.97	1.31
MA_RS25405	NA	1.45	0.33	2.57	1.67	0.00	1.14	0.33	0.98	2.02	1.23	0.00	1.12
MA_RS25415	NA	1.42	1.20	2.65	2.11	1.73	1.90	2.29	2.94	3.43	1.98	2.04	1.59
MA_RS25425	#N/A	0.50	0.20	2.31	0.36	0.68	0.60	0.30	0.54	0.53	0.57	0.46	0.26
MA_RS25430	#N/A	1.03	1.80	2.82	2.52	1.66	0.29	1.72	1.58	2.04	1.53	1.51	1.10
MA_RS25435	NA	1.15	1.50	2.48	1.08	1.79	2.14	1.17	2.51	2.94	1.73	1.15	1.73
MA_RS25440	#N/A	1.21	1.65	1.01	1.77	0.78	0.98	1.75	2.50	2.18	1.89	0.99	0.89
MA_RS25445	#N/A	3.80	3.89	4.05	4.09	3.87	4.13	4.31	5.46	5.58	4.23	4.02	4.09
MA_RS25450	#N/A	2.02	2.26	2.56	1.90	1.89	2.13	1.59	2.25	2.76	1.83	1.97	1.41
MA_RS25465	#N/A	1.71	1.38	2.16	2.36	1.40	2.56	1.83	3.15	3.27	2.96	1.59	1.90
MA_RS25470	NA	1.43	1.51	1.00	0.38	1.28	1.81	1.17	2.01	1.57	1.86	0.54	1.10
MA_RS25475	NA	1.64	1.87	1.98	2.27	2.11	2.17	2.20	2.86	3.15	2.04	1.59	1.97
MA_RS25480	NA	1.93	1.91	1.93	2.11	2.03	2.14	2.31	2.66	2.76	2.15	2.27	1.50
MA_RS25490	NA	0.03	0.12	0.00	0.00	0.35	0.43	0.00	0.54	0.87	0.30	0.65	0.88
MA_RS25495	NA	1.79	1.51	2.48	1.61	1.81	2.35	1.75	2.41	3.18	1.78	1.93	1.43
MA_RS25505	NA	0.80	2.30	1.42	1.78	2.26	1.99	1.90	2.53	2.46	1.62	1.49	1.44
MA_RS25510	NA	2.47	2.72	2.74	2.93	2.70	2.82	3.01	3.85	3.96	2.52	2.67	2.38
MA_RS25535	NA	2.73	2.72	2.83	2.72	2.49	2.94	3.03	3.79	3.07	2.66	2.77	2.68
MA_RS25545	NA	0.35	0.38	0.89	0.44	0.38	0.00	0.36	0.00	0.00	0.00	0.65	0.27
MA_RS25550	NA	2.03	2.27	2.16	2.85	2.63	2.59	2.90	2.74	3.23	2.68	2.42	2.36
MA_RS25565	NA	0.30	0.28	0.50	0.70	0.40	0.51	0.58	0.66	0.66	0.97	0.61	0.44
MA_RS25570	#N/A	1.21	1.15	1.05	0.84	1.15	1.02	0.91	1.54	2.00	1.66	1.14	1.04
MA_RS25575	NA	0.63	0.64	0.37	0.73	0.41	0.58	0.82	1.12	1.06	0.88	0.58	0.64
MA_RS25580	NA	0.50	0.52	0.60	0.65	0.62	0.61	0.60	0.97	1.22	0.84	0.63	0.49
MA_RS25590	#N/A	0.41	0.28	0.00	0.41	0.82	0.72	0.41	1.11	0.47	0.00	0.00	0.26
MA_RS25595	NA	0.13	0.34	0.00	0.98	0.33	0.69	0.00	0.41	1.21	0.82	1.46	0.37
MA_RS25600	#N/A	1.23	1.27	1.18	1.47	1.44	1.61	1.38	1.50	1.64	1.57	1.47	1.19
MA_RS25605	NA	2.40	2.22	2.42	2.82	2.35	2.58	3.06	3.58	3.81	3.11	2.58	2.53
MA_RS25610	NA	1.06	0.97	1.08	1.28	1.04	1.05	1.10	1.30	1.74	1.61	1.25	0.94
MA_RS25615	#N/A	1.59	1.40	1.31	1.79	1.55	1.78	1.87	2.37	2.65	1.95	1.86	1.87
MA_RS25620	NA	0.26	0.15	0.19	0.55	0.63	0.02	0.62	1.27	0.91	0.14	0.56	0.32
MA_RS25625	#N/A	0.53	0.59	0.41	0.78	0.68	0.43	0.91	1.21	0.93	0.66	0.25	0.68
MA_RS25630	NA	3.01	3.46	3.20	3.49	3.37	3.11	3.22	3.78	4.14	3.72	3.40	3.19
MA_RS25635	NA	1.67	1.51	1.55	2.45	1.75	2.07	2.19	1.72	2.26	1.39	2.39	2.16
MA_RS25640	NA	1.42	1.76	1.95	1.99	1.67	2.02	2.06	2.78	2.71	2.46	1.89	1.77
MA_RS25645	NA	1.61	1.85	1.76	2.11	1.94	1.98	2.15	3.14	2.93	2.69	2.07	1.93
MA_RS25650	NA	0.29	0.37	0.00	0.00	0.12	0.51	0.55	0.91	0.19	0.66	0.86	0.19
MA_RS25655	NA	0.18	0.14	0.12	0.15	0.10	0.18	0.05	0.24	0.16	0.13	0.24	0.08
MA_RS25660	#N/A	1.09	1.52	1.04	1.91	1.24	2.06	1.34	2.00	2.38	1.82	1.55	1.62
MA_RS25665	NA	1.29	1.11	0.96	1.38	1.28	1.20	1.40	1.89	2.08	1.63	1.37	1.15
MA_RS25670	NA	1.48	1.42	0.42	0.96	0.73	1.44	0.82	2.25	2.05	1.96	1.18	1.48
MA_RS25675	#N/A	1.23	1.45	1.49	2.17	1.72	1.72	2.13	1.78	2.42	1.86	1.12	1.52
MA_RS25680	NA	2.35	2.43	2.02	2.79	2.54	2.63	2.95	3.66	3.62	3.00	2.64	2.48
MA_RS25685	NA	0.42	0.73	0.92	0.58	0.23	0.10	0.41	0.82	0.44	0.50	0.11	0.30
MA_RS25690	#N/A	0.31	0.17	0.36	0.00	0.24	0.00	0.00	0.00	0.00	0.00	0.00	0.37
MA_RS25695	NA	1.20	1.06	0.90	1.44	1.19	1.19	1.30	1.79	2.02	1.51	1.24	1.11
MA_RS25700	#N/A	0.62	0.69	0.62	1.11	1.36	0.98	1.09	0.85	1.34	0.89	0.53	0.86
MA_RS25715	#N/A	1.41	0.23	2.02	1.16	1.47	1.02	2.03	1.98	1.78	0.71	0.45	1.60
MA_RS25720	#N/A	0.49	0.67	1.20	0.90	0.84	0.94	0.64	1.52	1.99	1.20	1.40	0.55
MA_RS25725	#N/A	0.20	0.72	0.85	0.52	0.62	1.02	0.86	1.29	1.13	0.70	1.11	0.74
MA_RS25730	NA	1.19	1.59	1.66	1.53	1.67	1.48	1.50	2.76	2.25	1.90	1.60	1.26
MA_RS25735	NA	1.45	1.12	1.49	1.58	1.80	1.72	1.61	2.40	2.28	1.86	1.48	1.45
MA_RS25745	#N/A	1.37	1.02	1.44	1.17	1.49	1.26	1.60	1.74	2.20	1.67	1.54	1.14
MA_RS25755	#N/A	1.14	1.17	1.40	1.56	1.35	1.68	1.28	1.87	1.65	1.70	1.13	1.16
MA_RS25760	NA	2.38	2.46	2.61	3.00	2.68	2.63	3.22	3.86	3.97	3.31	2.93	2.70
MA_RS25765	#N/A	3.97	3.18	2.88	2.97	3.53	3.34	3.58	3.60	3.25	2.82	2.91	3.65
MA_RS25770	#N/A	0.00	0.00	0.00	0.67	0.36	0.80	0.00	0.00	0.48	0.00	0.75	0.00
MA_RS25775	#N/A	1.44	1.35	0.80	1.62	1.86	1.65	2.00	2.12	2.33	1.27	1.35	1.92
MA_RS25780	NA	7.44	7.73	7.80	7.99	7.68	7.74	8.31	8.79	8.97	8.13	7.96	7.79
MA_RS25785	NA	0.75	0.63	0.50	1.08	1.01	1.30	0.92	1.41	1.22	1.11	1.17	0.56
MA_RS25790	NA	2.38	2.59	2.58	2.89	2.78	2.85	3.24	3.82	3.94	3.22	2.92	2.83
MA_RS25795	tnpA	1.23	0.99	0.85	0.83	1.25	0.88	1.34	1.35	1.05	0.90	0.92	0.93
MA_RS25800	#N/A	1.50	1.69	1.41	1.89	1.84	2.03	2.02	2.35	2.65	2.07	1.53	1.81
MA_RS25805	NA	1.24	1.33	1.33	1.62	1.97	1.78	2.04	2.73	2.25	1.26	1.65	1.46
MA_RS25815	NA	1.13	1.07	0.13	0.94	1.13	1.51	1.07	1.94	1.70	1.40	0.58	1.30
MA_RS25820	NA	1.77	1.97	2.24	2.38	2.41	1.81	2.60	2.07	1.62	2.64	1.92	1.87
MA_RS25825	NA	0.93	0.92	0.35	0.85	0.93	0.74	0.60	2.05	0.00	0.28	0.00	0.50
MA_RS25830	NA	0.90	1.06	0.85	1.06	1.26	1.01	1.45	1.36	1.78	1.23	0.67	1.12
MA_RS25835	NA	1.38	1.63	1.77	1.90	1.58	1.96	1.85	2.29	2.57	1.85	1.74	1.67
MA_RS25840	NA	1.81	1.88	1.90	2.14	2.02	2.25	2.26	3.00	3.40	2.58	2.20	2.17
MA_RS25845	#N/A	0.59	0.65	0.78	0.69	0.61	0.77	0.54	1.09	1.09	0.77	0.53	0.53
MA_RS25855	NA	1.23	0.77	0.00	0.00	1.14	0.00	1.18	0.00	1.21	0.58	0.00	1.00
MA_RS25860	NA	0.74	0.00	0.00	0.00	0.00	0.00	0.57	0.72	1.15	0.42	0.00	0.97
MA_RS25865	NA	0.72	1.35	1.12	1.04	1.35	1.56	1.17	1.95	1.47	2.10	0.78	1.21
MA_RS25870	NA	3.28	3.54	3.36	3.89	3.11	3.67	3.56	4.56	4.64	4.46	3.29	3.87
MA_RS25875	NA	1.06	0.47	0.85	0.14	0.39	1.14	0.80	1.33	1.35	0.58	0.25	0.42
MA_RS25880	NA	2.55	2.47	2.90	2.57	2.77	2.54	2.80	2.65	2.70	2.41	2.33	2.65
MA_RS25885	NA	1.07	1.19	1.18	1.15	1.16	1.50	1.87	2.05	2.39	1.57	1.51	1.18
MA_RS25890	NA	1.59	2.00	1.85	2.34	2.03	2.03	2.25	3.16	3.33	2.49	1.97	2.20
MA_RS25895	NA	1.21	1.25	1.05	1.59	0.90	1.42	1.59	1.44	1.66	1.79	1.45	1.00
MA_RS25900	NA	0.46	1.05	1.20	1.68	1.13	1.52	1.63	1.39	2.29	1.53	0.99	1.26
MA_RS25905	NA	1.09	1.77	1.05	1.54	1.67	1.74	1.04	1.88	2.07	2.03	1.57	1.07
MA_RS25920	#N/A	1.23	1.48	1.27	1.75	1.67	1.87	1.79	2.29	2.35	1.75	1.39	2.00
MA_RS25930	#N/A	2.79	2.49	2.21	3.41	2.66	2.95	3.01	2.89	3.57	3.05	2.67	2.99
MA_RS25945	#N/A	1.09	1.50	0.72	1.20	1.29	1.86	1.71	2.00	1.34	1.51	1.50	1.45
MA_RS25960	#N/A	1.77	1.62	1.27	2.34	1.63	2.08	1.73	1.96	2.57	1.67	1.86	2.38
MA_RS25970	#N/A	2.90	3.12	2.73	3.45	3.01	3.34	3.13	3.69	4.16	3.62	3.21	3.15
MA_RS25980	#N/A	2.00	1.52	2.62	2.86	2.43	3.31	2.70	2.98	3.63	3.35	1.99	2.85
MA_RS25985	#N/A	2.25	2.72	2.53	3.19	2.77	3.09	3.21	3.22	2.93	3.02	2.75	3.13
MA_RS25990	#N/A	2.54	2.77	2.34	3.09	2.51	2.69	2.78	2.95	3.34	3.06	3.01	2.88
MA_RS26005	#N/A	0.55	0.20	0.31	0.61	0.64	0.59	0.81	1.05	1.67	0.95	0.61	0.70
MA_RS26010	NA	0.39	0.73	0.00	0.00	0.30	0.78	0.36	0.21	0.70	0.58	0.19	0.00
MA_RS26015	NA	0.91	0.78	0.97	1.40	0.73	1.11	1.70	1.34	1.59	1.20	1.65	0.91
MA_RS26020	NA	1.58	2.03	1.73	1.97	1.89	1.88	2.33	2.94	2.90	2.34	2.31	1.85
MA_RS26025	#N/A	0.51	0.62	0.00	0.24	0.64	0.74	0.55	1.11	1.71	0.74	0.54	0.68
MA_RS26030	#N/A	1.37	1.50	2.50	1.98	1.27	2.02	1.80	2.62	2.82	1.85	2.56	1.85
MA_RS26040	#N/A	2.16	2.70	2.75	2.97	2.47	3.21	2.88	2.75	3.24	2.61	2.42	2.88
MA_RS26045	#N/A	7.27	7.40	7.40	7.14	7.37	7.43	7.55	6.99	7.15	7.30	7.30	7.70
MA_RS26050	#N/A	0.34	0.79	0.15	0.40	0.54	0.68	1.35	1.67	1.06	0.99	0.89	0.59
MA_RS26065	NA	1.92	2.21	2.17	2.72	2.28	2.52	2.77	3.45	3.88	2.70	2.42	2.47
MA_RS26070	NA	7.68	7.76	7.68	8.32	8.18	8.00	8.75	8.44	8.59	8.36	7.95	8.37
MA_RS26075	#N/A	3.60	4.22	3.94	3.92	4.36	3.95	4.28	5.27	5.32	4.49	4.06	4.12
MA_RS26080	#N/A	1.24	1.39	1.10	1.21	1.37	1.60	0.84	2.04	2.24	1.14	1.88	1.10
MA_RS26090	NA	1.44	1.34	1.32	1.88	1.64	1.83	1.95	2.68	2.81	2.17	1.68	1.55
MA_RS26095	NA	1.82	2.12	1.67	2.43	2.31	2.39	1.38	3.13	3.57	2.11	2.28	2.64
MA_RS26100	#N/A	3.30	3.74	4.08	4.11	3.40	3.75	3.78	4.25	4.39	3.79	3.60	3.37
MA_RS26105	NA	2.57	3.24	2.11	3.60	2.95	3.33	3.28	3.98	4.54	4.35	3.85	3.48
MA_RS26120	NA	2.15	2.30	2.14	2.66	2.38	2.73	2.49	2.96	3.21	2.70	2.58	2.50
MA_RS26125	NA	0.79	0.60	0.75	0.00	0.38	0.52	0.00	1.50	0.78	0.63	0.59	0.51

MA_RS26130	#N/A	0.69	0.36	0.55	0.23	0.21	0.75	0.19	1.10	1.83	0.75	1.01	1.17
MA_RS26140	NA	1.90	2.28	2.34	3.12	2.11	2.00	2.23	3.43	3.61	3.27	2.51	2.87
MA_RS26145	#N/A	0.58	0.76	1.07	0.97	0.45	0.65	0.27	1.61	1.04	0.92	0.55	0.74
MA_RS26150	#N/A	1.04	1.34	0.97	1.34	1.23	1.69	1.23	2.19	1.70	1.96	1.67	1.19
MA_RS26155	#N/A	1.18	1.62	1.73	1.68	1.89	1.81	1.49	2.39	2.45	2.08	1.80	1.52
MA_RS26165	#N/A	2.13	2.25	2.39	2.60	2.52	2.56	2.34	2.66	3.01	2.63	2.42	2.35
MA_RS26170	#N/A	1.48	1.58	0.86	2.32	2.19	2.18	2.08	2.03	3.10	1.98	1.72	2.21
MA_RS26175	#N/A	2.12	2.20	1.79	2.54	1.89	2.38	2.02	2.98	2.97	2.50	2.41	2.51
MA_RS26205	#N/A	2.25	2.65	2.65	2.97	2.65	2.94	2.68	3.13	3.82	2.87	2.82	2.79
MA_RS26210	#N/A	2.16	2.13	2.10	2.43	2.11	2.78	2.34	2.78	3.27	2.64	2.21	2.51
MA_RS26225	#N/A	1.75	2.26	2.20	2.40	2.40	2.46	2.29	2.53	3.17	2.00	1.69	1.69
MA_RS26235	NA	2.74	2.78	3.58	3.29	2.65	3.36	3.39	4.23	4.50	3.38	3.04	2.96
MA_RS26245	NA	0.20	0.14	0.31	0.58	0.00	0.41	0.00	0.00	0.75	0.00	0.00	0.00
MA_RS26250	NA	0.20	0.21	0.20	0.38	0.15	0.31	0.51	0.20	0.29	0.43	0.00	0.00
MA_RS26255	#N/A	1.49	1.76	1.76	2.32	1.49	2.12	2.05	2.50	3.26	2.07	1.81	1.45
MA_RS26265	#N/A	2.33	2.50	2.20	1.57	1.67	2.37	2.23	3.12	2.85	2.67	2.36	2.82
MA_RS26270	NA	3.94	4.35	4.12	3.67	3.49	3.61	4.32	3.95	4.17	4.26	3.92	3.97
MA_RS26275	#N/A	1.84	2.10	1.72	2.28	2.15	2.12	2.01	2.29	2.85	2.49	2.23	2.48
MA_RS26290	NA	1.55	0.21	0.03	1.10	1.12	0.93	1.89	1.84	1.99	0.41	1.10	1.89
MA_RS26295	#N/A	0.93	0.97	1.12	1.20	1.37	1.50	1.38	1.48	1.62	1.36	1.30	1.23
MA_RS26300	#N/A	1.13	0.61	0.92	1.65	1.44	1.09	1.15	2.13	0.78	1.69	1.46	1.10
MA_RS26310	#N/A	1.67	1.29	1.40	1.97	1.65	1.92	1.66	2.38	2.26	2.30	1.39	1.67
MA_RS26315	#N/A	0.44	0.71	0.66	0.90	1.26	0.73	1.21	1.38	1.79	0.59	1.35	1.68
MA_RS26320	#N/A	1.38	0.60	0.61	1.30	0.16	0.90	1.14	1.07	1.33	0.58	0.38	0.85
MA_RS26340	#N/A	2.16	2.33	2.31	3.04	3.00	2.62	2.84	3.50	2.64	2.67	2.64	2.53
MA_RS26345	#N/A	2.67	3.15	2.68	2.95	3.17	3.09	2.90	2.80	2.77	2.68	2.77	3.16
MA_RS26355	NA	3.85	4.23	4.35	4.23	3.82	4.12	4.65	5.04	5.38	4.42	3.90	4.35
MA_RS26360	NA	3.44	3.44	2.76	3.66	3.08	3.11	3.72	3.37	3.47	3.45	2.62	3.79
MA_RS26365	NA	0.48	0.41	0.65	1.04	0.85	0.67	0.77	1.17	1.42	1.63	0.19	0.10
MA_RS26370	NA	2.23	2.02	0.00	2.85	2.63	2.47	2.70	2.82	3.62	3.35	3.08	2.15
MA_RS26375	#N/A	9.41	9.68	9.68	3.62	3.45	3.48	8.28	8.49	8.67	7.13	7.49	7.90
MA_RS26380	NA	3.00	3.65	3.32	2.94	2.29	2.26	2.74	2.83	3.07	2.93	2.65	2.88
MA_RS26385	NA	0.86	1.21	1.30	0.63	0.65	0.99	1.15	2.65	2.65	0.75	1.32	1.16
MA_RS26395	#N/A	1.40	1.45	1.62	2.47	1.46	1.78	2.02	1.80	2.96	2.24	1.31	1.33
MA_RS26400	NA	0.27	0.38	0.00	0.88	0.61	0.46	0.00	0.63	0.51	0.41	0.00	0.35
MA_RS26405	#N/A	0.50	0.38	0.88	0.00	0.97	0.00	1.07	1.58	1.78	0.00	0.00	0.00
MA_RS26410	#N/A	0.91	0.90	1.19	0.67	0.81	1.11	0.68	0.09	0.78	0.91	0.48	1.32
MA_RS26415	NA	0.86	1.02	1.45	0.95	1.46	1.05	1.51	1.47	1.60	0.97	1.49	0.93
MA_RS26425	NA	0.00	0.18	0.00	0.00	0.29	0.00	0.00	0.00	0.72	0.00	0.00	0.00
MA_RS26430	NA	0.27	0.00	0.00	0.00	0.00	0.36	0.57	0.00	0.00	0.22	0.74	0.00
MA_RS26440	NA	2.66	3.51	3.32	3.42	3.22	3.22	3.43	4.17	3.74	3.70	3.05	3.18
MA_RS26445	NA	3.37	3.34	3.72	3.79	3.90	3.82	4.00	4.23	4.59	3.44	3.70	3.63
MA_RS26450	NA	0.46	0.26	0.00	0.14	0.20	0.00	0.17	0.57	0.49	0.29	0.39	0.46
MA_RS26455	NA	1.95	1.82	1.80	2.20	1.58	1.71	1.35	2.04	1.58	1.86	1.77	1.32
MA_RS26460	NA	2.64	2.41	3.00	2.78	2.72	2.93	3.03	3.82	4.22	2.58	2.91	3.41
MA_RS26465	NA	4.33	4.16	4.64	4.60	4.35	4.42	4.59	5.61	6.17	5.04	4.51	4.67
MA_RS26470	NA	1.98	1.83	2.08	2.64	1.87	2.82	2.38	2.15	2.52	2.10	1.19	2.41
MA_RS26475	NA	0.33	0.06	0.62	0.00	0.00	0.27	0.31	0.00	0.00	0.00	0.00	0.00
MA_RS26480	#N/A	6.94	6.96	6.75	7.06	0.00	7.14	0.00	7.33	0.00	7.37	7.07	7.22
MA_RS26485	NA	2.11	2.19	2.72	1.96	2.51	2.06	2.05	3.51	3.46	3.05	2.55	1.88
MA_RS26490	NA	0.63	1.00	0.68	0.31	1.61	1.35	0.94	1.64	1.45	2.13	0.63	1.24
MA_RS26495	#N/A	1.41	1.50	1.99	1.79	1.68	2.25	1.68	2.07	2.86	2.51	2.13	2.17
MA_RS26500	NA	1.02	1.80	1.31	1.14	1.92	1.55	1.34	1.95	2.23	2.56	1.34	1.10
MA_RS26505	NA	0.25	0.00	0.48	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS26515	NA	0.26	1.21	1.20	1.20	1.51	1.40	1.56	2.02	1.25	0.97	1.27	0.96
MA_RS26520	#N/A	0.24	0.00	0.00	0.60	0.00	0.00	1.17	0.57	0.54	0.92	1.47	0.62
MA_RS26525	NA	2.98	1.91	1.88	2.56	2.64	2.89	2.70	2.67	2.62	2.20	2.51	2.70
MA_RS26530	NA	1.90	1.43	1.76	1.30	1.70	1.30	1.78	1.08	0.00	1.17	1.97	1.78
MA_RS26535	NA	2.63	2.55	2.76	2.93	3.05	3.30	3.11	3.26	2.76	2.35	3.06	3.41
MA_RS26540	#N/A	2.37	2.57	3.13	3.41	3.12	3.59	3.03	3.61	3.52	3.86	3.23	3.63
MA_RS26545	#N/A	3.33	3.90	3.62	4.12	3.83	3.92	3.78	4.32	4.50	4.18	3.94	3.86
MA_RS26550	#N/A	3.95	4.11	3.89	4.27	3.97	4.27	4.16	5.06	4.90	4.39	4.28	4.11
MA_RS26555	NA	2.49	2.77	2.98	3.10	2.81	3.73	3.39	3.16	4.12	3.46	3.99	2.69
MA_RS26560	#N/A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.79	0.00	0.00
MA_RS26565	#N/A	1.90	2.41	2.11	2.11	1.83	2.54	2.85	3.47	3.28	1.61	3.47	1.91
MA_RS26570	NA	0.70	2.18	0.95	0.68	1.66	2.25	2.41	1.72	2.08	0.83	2.74	1.56
MA_RS26575	NA	0.69	1.56	1.28	0.41	0.67	2.42	2.45	1.55	1.61	1.23	2.90	1.07
MA_RS26580	#N/A	1.82	2.00	1.56	1.72	2.17	2.75	3.19	2.49	2.16	1.08	3.10	1.99
MA_RS26585	NA	0.45	0.55	0.00	0.64	0.00	0.00	0.35	1.12	1.62	0.43	0.63	0.49
MA_RS26590	NA	1.80	2.29	1.47	0.56	2.08	3.08	1.57	2.52	2.98	1.86	1.98	0.97
MA_RS26595	#N/A	0.00	0.69	0.00	0.24	0.91	1.37	0.00	1.38	1.37	0.00	0.00	0.94
MA_RS26600	NA	0.15	0.31	1.22	0.00	0.81	0.76	1.35	2.12	0.58	0.23	1.13	1.41
MA_RS26610	NA	0.19	0.00	1.31	0.00	0.00	0.13	0.15	0.00	0.00	0.00	0.00	0.45
MA_RS26615	NA	0.19	0.27	1.36	0.08	0.40	0.68	0.49	0.92	1.01	0.31	0.00	0.00
MA_RS26620	#N/A	3.37	3.47	3.32	4.00	3.54	4.22	4.03	4.61	4.72	3.70	3.65	3.88
MA_RS26625	#N/A	3.12	3.76	3.39	3.90	3.31	4.27	3.97	4.13	4.77	2.93	3.54	3.64
MA_RS26630	#N/A	0.74	1.18	0.94	1.75	1.01	0.74	1.83	1.70	1.52	0.96	1.53	2.34
MA_RS26635	NA	2.11	2.10	2.24	2.45	1.83	1.98	2.17	3.20	3.28	2.42	2.50	2.11
MA_RS26640	NA	1.89	1.91	1.66	1.90	2.53	2.30	1.29	2.39	2.87	2.55	1.54	2.21
MA_RS26645	#N/A	0.97	1.25	1.17	1.83	1.00	1.36	1.45	2.38	1.80	1.37	1.45	0.92
MA_RS26650	#N/A	1.70	1.74	1.18	1.85	0.35	1.90	0.38	0.00	2.01	2.36	1.69	1.84
MA_RS26655	NA	0.59	1.61	1.24	1.02	1.51	1.23	0.95	0.39	2.06	1.23	0.43	0.95
MA_RS26660	NA	1.58	2.23	1.38	1.95	2.23	2.17	2.27	2.81	3.10	2.30	1.43	1.64
MA_RS26665	#N/A	1.25	1.09	1.28	1.10	1.54	1.34	1.57	1.71	1.77	1.61	1.29	0.84
MA_RS26670	NA	0.38	0.00	0.00	0.85	0.07	0.00	0.08	0.86	0.84	0.00	0.00	0.11
MA_RS26675	NA	0.45	0.87	0.47	0.20	0.54	0.70	1.18	0.42	0.00	0.34	0.85	0.37
MA_RS26680	NA	0.70	1.26	1.34	1.01	1.25	1.31	1.99	1.80	1.95	1.51	1.08	2.14
MA_RS26685	NA	8.58	8.48	8.37	8.36	8.26	8.39	8.40	8.42	8.51	8.72	8.52	8.53
MA_RS26690	NA	1.94	1.88	1.13	1.58	2.26	1.09	2.77	3.21	3.61	1.57	1.92	2.50
MA_RS26695	NA	1.09	1.58	1.58	1.98	1.72	1.54	0.76	2.41	3.28	2.33	1.44	2.29
MA_RS26700	NA	0.29	0.89	1.17	0.94	0.31	0.60	0.39	0.67	1.57	0.23	0.91	1.20
MA_RS26705	NA	1.12	1.31	2.40	1.38	1.36	1.25	1.57	1.27	1.28	1.35	1.26	0.63
MA_RS26710	NA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.47	0.00	0.00
MA_RS26715	NA	0.56	0.86	2.33	1.33	1.66	0.59	0.55	2.07	1.07	1.75	1.18	1.30
MA_RS26720	NA	0.23	1.01	2.14	0.48	0.78	0.40	1.23	1.55	0.98	0.81	0.54	1.03
MA_RS26725	#N/A	1.55	1.55	2.70	2.35	1.74	2.19	1.68	2.45	2.81	2.17	2.01	1.84
MA_RS26730	#N/A	2.28	2.24	2.94	2.51	2.29	2.47	2.51	2.98	3.33	2.88	2.61	2.44
MA_RS26735	#N/A	0.65	1.12	2.33	1.39	0.94	1.06	0.20	0.95	1.28	1.05	1.11	1.31
MA_RS26740	#N/A	1.75	2.03	2.68	2.36	2.41	2.31	2.03	2.47	2.77	2.76	2.24	2.11
MA_RS26745	#N/A	1.24	1.82	2.59	1.60	1.62	1.88	1.78	2.35	2.51	1.78	1.74	1.64
MA_RS26750	#N/A	1.23	1.30	2.31	1.63	1.73	1.01	1.40	1.79	1.68	1.90	1.67	1.31
MA_RS26755	#N/A	1.02	1.34	2.92	1.79	1.75	1.71	1.32	2.31	2.41	1.79	2.25	1.74
MA_RS26760	#N/A	1.74	2.43	3.10	2.37	2.14	2.20	1.65	2.60	3.13	2.50	2.97	2.68
MA_RS26765	#N/A	1.79	2.17	2.86	2.65	2.33	2.51	2.43	2.90	3.04	2.56	2.20	2.17
MA_RS26770	#N/A	1.14	1.42	2.62	2.14	1.52	1.57	1.65	1.66	1.55	1.43	1.60	1.70
MA_RS26775	NA	0.54	0.32	2.38	1.46	0.89	1.59	0.40	1.24	1.40	0.58	0.17	0.56
MA_RS26780	NA	1.26	0.42	2.26	1.04	1.51	0.00	0.75	0.66	0.40	0.69	1.34	1.22
MA_RS26785	NA	3.22	3.29	3.56	3.30	3.83	3.69	4.21	2.04	2.40	3.61	3.84	3.93
MA_RS26790	NA	0.48	0.12	2.28	0.13	0.42	0.22	0.68	0.48	0.87	0.58	0.21	0.25
MA_RS26795	NA	0.45	0.35	2.41	0.00	0.44	0.83	1.12	1.38	1.34	1.02	0.00	0.00
MA_RS26805	NA	2.61	2.69	3.03	2.86	2.96	2.79	3.15	3.54	3.10	2.44	2.98	3.49
MA_RS26810	NA	0.54	0.00	0.00	0.46	0.00	0.57	0.76	0.15	0.39	1.02	1.10	0.04
MA_RS26815	NA	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.04
MA_RS26820	NA	1.10	1.34	2.41	1.00	1.37	1.44	1.65	1.13	1.70	1.83	0.59	1.16
MA_RS26825	NA	2.06	2.45	2.73	2.63	2.52	3.26	3.33	3.03	3.67	2.11	1.08	2.93
MA_RS26830	#N/A	0.39	1.89	0.00	0.89	0.70	1.25	0.00	1.17	1.61	0.52	0.00	1.09
MA_RS26835	NA	3.65	3.16	3.52	4.00	3.64	3.38	3.87	4.70	4.62	4.28	3.07	3.38
MA_RS26840	NA	2.86	3.01	3.00	2.79	2.83	2.60	3.26	3.10	4.43	2.93	3.28	2.22
MA_RS26845	#N/A	3.25	3.10	2.58	3.59	3.15	3.40	3.49	3.87	4.15	3.61	3.29	3.27
MA_RS26850	NA	0.61	0.15	0.00	0.55	0.33	0.83	0.69	1.58	0.87	0.96	0.55	1.63
MA_RS26855	#N/A	0.34	1.18	0.77	1.83	1.25	0.82	0.32	1.34	0.56	0.92	0.23	0.41
MA_RS26860	NA	0.68	1.05	0.71	0.60	1.16	1.05	1.48	1.38	1.58	1.03	0.82	0.48
MA_RS26865	NA	2.02	1.96	2.23	2.23	2.53	2.52	2.29	1.93	1.77	1.92	1.65	0.44
MA_RS26875	NA	1.42	1.37	2.43	1.56	1.34	2.18	1.27	1.34	1.69	1.16	1.83	1.16
MA_RS26880	NA	0.00	0.20	0.00	0.48	0.63	0.08	0.59	0.00	0.00	0.40	0.77	0.73
MA_RS26885	NA	0.19	0.48	1.06	0.90	0.79	0.61	0.76	1.62	1.41	0.70	0.34	1.06
MA_RS26890	NA	1.33	1.08	0.70	0.85	0.34	0.75	1.38	1.43	2.09	0.56	0.67	0.77
MA_RS26895	NA	0.78	0.40	1.05	0.65	0.37	0.43	0.65	0.60	0.67	0.63	0.52	0.64
MA_RS26900	#N/A	2.22	1.73	1.07	1.80	2.01	2.79	2.86	3.44	2.97	2.22	2.50	2.20
MA_RS26905	NA	1.67	1.90	1.57	1.85	2.02	2.31	2.38	2.96	0.85	2.98	2.07	2.39
MA_RS26910	NA	1.66	1.29	1.77	2.17	1.50	1.71	1.42	1.97	2.06	1.42	1.70	1.22
MA_RS26915	NA	1.02	0.38	1.26	0.99	1.03	1.35	0.87	0.00	0.36	0.28	0.34	0.70
MA_RS26920	NA	0.00	0.30	0.06	0.23	0.00	0.00	0.88	0.39	0.70	0.00	0.74	0.32
MA_RS26925	NA	0.18	0.00	0.00	0.00	0.38	0.00	0.37	1.06	0.00	0.00	0.38	0.00
MA_RS26930	NA	0.48	0.61	0.83	0.76	0.45	0.00	0.44	0.37	0.64	1.12	0.61	0.20
MA_RS26935	NA	1.31	0.41	1.39	0.65	1.74	0.40	1.49	1.51	1.24	1.39	1.53	1.31
MA_RS26940	#N/A	0.43	0.52	0.95	0.93	0.11	0.57	0.43	0.42	1.21	1.16	0.58	0.63
MA_RS26945	#N/A	0.85	0.76	1.00	0.71	1.13	1.42	1.41	1.04	2.00	1.21	1.13	0.28
MA_RS26950	NA	1.79	1.69	1.21	2.01	0.52	2.00	1.37	2.74	2.38	0.64	0.78	0.62
MA_RS26955	NA	0.40	0.29	0.00	0.74	0.89	0.31	0.00	0.37	1.06	0.33	0.00	0.83
MA_RS26960	NA	0.43	0.45	0.57	0.57	0.30	0.55	1.36	0.00	0.72	1.16	0.00	0.77
MA_RS26965	NA	1.17	1.05	1.31	1.56	1.74	1.22	1.83	1.88	1.75	0.18	1.11	1.42
MA_RS26970	#N/A	5.20	5.23	5.12	5.70	5.14	5.26	5.61	6.72	6.83	5.39	5.15	4.34

MA_RS26975	NA	0.38	0.00	1.22	0.32	0.33	0.36	0.50	0.50	0.49	0.00	0.00	0.00
MA_RS26980	NA	1.80	1.82	1.69	1.82	2.06	2.17	3.67	1.53	0.42	1.86	1.45	0.97
MA_RS26985	#N/A	3.71	3.92	3.94	4.12	3.73	4.44	4.68	4.59	4.79	3.98	3.57	3.17
MA_RS26990	NA	0.77	1.39	0.96	1.79	1.88	1.89	0.24	2.41	1.76	1.41	1.55	1.70
MA_RS26995	NA	1.15	1.27	1.16	0.85	1.22	1.56	1.27	1.76	2.71	1.14	1.73	1.44
MA_RS27000	NA	4.88	4.99	5.03	3.82	4.39	4.02	4.22	3.99	3.91	4.49	4.02	3.72
MA_RS27005	#N/A	1.79	1.96	1.94	2.31	1.81	1.89	2.20	2.67	2.78	2.30	2.10	1.67
MA_RS27010	NA	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.27	0.00	0.00	0.44	0.00
MA_RS27015	NA	1.02	0.60	0.36	0.97	0.00	0.36	0.52	0.74	1.63	0.69	0.00	0.76
MA_RS27020	#N/A	1.26	1.31	1.78	1.61	1.49	1.49	2.18	1.95	1.49	1.40	1.26	1.71
MA_RS27025	NA	2.21	0.97	1.56	0.94	0.09	0.67	1.22	0.82	1.34	1.50	1.19	1.52
MA_RS27030	NA	3.85	3.73	3.32	3.10	3.95	3.88	4.29	4.52	3.04	3.29	3.06	3.13
MA_RS27035	NA	1.01	1.13	0.76	0.00	0.93	0.43	0.68	0.99	1.84	0.64	1.19	0.73
MA_RS27045	#N/A	0.31	0.34	0.54	0.00	1.03	0.03	0.55	0.93	0.00	0.40	0.00	0.43
MA_RS27050	NA	0.00	0.15	0.00	0.00	0.00	0.32	0.00	0.40	0.00	0.04	0.00	0.50
MA_RS27055	#N/A	0.03	0.00	0.00	0.05	0.00	0.00	0.00	0.28	0.26	0.35	0.07	0.18
MA_RS27060	NA	0.00	0.00	0.00	0.00	0.00	0.35	0.82	0.00	0.00	0.41	0.00	0.00
MA_RS27070	NA	0.34	0.39	0.00	0.00	0.86	0.30	0.00	0.00	0.00	0.72	0.34	0.00
MA_RS27075	NA	0.03	0.29	0.05	0.89	0.39	0.61	0.41	0.44	0.00	0.00	0.00	0.00
MA_RS27080	NA	0.20	0.22	0.39	0.03	0.00	0.00	0.00	0.67	0.00	0.00	0.00	0.00
MA_RS27085	NA	0.63	0.00	0.47	0.64	1.07	0.00	0.00	0.51	0.00	0.00	0.00	0.00
MA_RS27090	NA	1.56	0.72	0.31	1.63	1.08	1.17	0.49	1.93	1.45	1.84	1.63	1.54
MA_RS27095	NA	0.53	1.18	1.34	0.87	0.71	1.41	0.00	1.87	1.94	1.36	1.16	1.62
MA_RS27100	NA	0.19	0.00	0.00	0.29	0.28	0.00	0.00	0.35	0.60	0.73	0.10	0.00
MA_RS27105	NA	0.43	1.28	0.22	1.24	0.84	1.42	0.25	0.00	0.00	0.00	0.74	1.84
MA_RS27110	NA	1.23	1.00	2.29	2.40	1.94	1.82	1.30	1.07	1.26	1.10	1.68	1.99
MA_RS27120	NA	0.21	0.86	0.42	0.32	0.34	1.23	0.77	0.73	1.01	1.23	0.39	1.32
MA_RS27125	NA	0.52	0.80	0.94	0.95	0.17	0.79	0.65	1.63	0.57	1.30	0.73	0.22
MA_RS27130	NA	0.00	0.00	0.00	1.47	0.00	1.15	0.00	0.17	0.32	0.60	0.16	0.00
MA_RS27135	NA	0.76	0.56	1.03	0.54	0.22	0.11	0.47	0.00	0.40	0.66	0.64	0.74
MA_RS27140	NA	0.00	0.08	0.00	0.47	0.25	0.12	0.70	0.14	0.07	0.33	0.86	0.26
MA_RS27145	NA	3.03	2.55	2.80	2.92	2.88	2.72	2.90	3.04	4.22	2.76	2.52	3.41
MA_RS27150	#N/A	5.94	5.81	5.92	5.84	5.72	5.95	5.99	5.91	6.25	5.98	5.80	5.98
MA_RS27155	NA	0.43	0.50	0.03	0.63	0.49	0.87	1.31	0.30	2.46	1.13	0.03	0.97
MA_RS27160	#N/A	0.44	0.47	0.52	0.99	1.34	1.31	0.84	1.06	1.46	0.91	0.68	1.43
MA_RS27165	NA	0.63	0.17	0.40	0.82	0.40	0.80	0.78	0.68	0.91	0.99	0.78	0.41
MA_RS27170	NA	1.55	1.79	1.60	2.28	1.81	2.72	1.92	2.99	3.09	2.18	1.41	1.21
MA_RS27180	NA	0.00	0.25	0.00	0.07	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS27185	#N/A	1.19	1.09	1.47	1.37	1.31	1.68	1.12	1.79	1.77	1.45	1.07	1.55
MA_RS27190	#N/A	1.00	1.06	1.23	1.48	1.16	1.43	1.36	1.83	1.26	1.39	1.05	1.32
MA_RS27195	#N/A	0.88	1.52	1.46	1.92	1.64	1.67	1.41	1.55	1.72	1.55	1.93	1.58
MA_RS27200	#N/A	2.18	1.78	2.29	2.27	2.31	2.22	2.25	2.86	3.29	2.44	1.97	2.25
MA_RS27205	#N/A	1.64	1.84	1.48	2.15	1.76	2.19	1.93	2.33	2.68	2.24	1.91	2.00
MA_RS27210	NA	1.30	1.17	1.33	1.23	1.36	1.14	1.22	2.02	2.09	1.92	1.59	1.67
MA_RS27215	NA	2.23	1.92	2.44	2.08	2.22	2.19	1.79	2.52	3.29	2.40	2.15	2.09
MA_RS27225	NA	0.56	0.53	0.00	0.53	0.00	0.00	0.37	0.09	0.43	1.04	0.00	0.00
MA_RS27230	#N/A	1.41	0.98	2.16	1.29	1.91	1.99	1.08	1.64	2.29	2.00	1.51	1.73
MA_RS27235	NA	0.49	0.48	0.00	0.64	0.57	0.47	1.29	1.10	2.02	1.60	0.81	0.83
MA_RS27240	NA	0.70	0.62	0.75	0.72	0.84	1.01	0.67	1.53	1.61	1.50	0.90	0.78
MA_RS27245	NA	1.63	1.67	2.12	2.20	2.13	2.24	1.24	2.59	2.64	2.10	2.40	1.01
MA_RS27250	NA	0.41	1.23	0.97	1.00	1.41	0.33	0.85	0.00	0.00	0.54	1.73	1.44
MA_RS27260	NA	3.42	3.43	3.54	3.70	3.61	3.74	3.95	3.81	3.38	3.57	3.72	3.69
MA_RS27270	NA	0.57	0.37	0.00	0.69	0.00	0.68	0.00	1.20	0.90	0.28	0.00	0.27
MA_RS27275	NA	0.67	0.74	0.49	0.82	0.52	0.34	0.00	0.37	0.00	0.00	0.00	0.03
MA_RS27285	NA	0.40	0.00	0.52	0.00	0.78	0.00	0.69	0.39	0.45	0.00	0.69	0.42
MA_RS27290	#N/A	0.41	0.30	0.58	0.47	0.29	0.29	0.97	1.32	1.24	0.33	0.27	0.40
MA_RS27295	#N/A	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.36	0.00	0.00	0.43	0.00
MA_RS27300	NA	0.92	1.18	1.59	1.36	1.59	1.49	1.81	2.21	2.96	1.59	1.50	1.77
MA_RS27305	NA	0.16	0.08	0.00	0.09	0.60	0.36	0.42	0.42	0.00	0.37	0.33	0.50
MA_RS27310	NA	0.88	0.91	1.58	1.47	1.63	1.52	0.97	1.85	2.73	1.32	0.60	1.44
MA_RS27315	NA	1.60	1.71	1.95	0.61	1.33	1.62	0.87	2.08	2.28	1.76	1.02	1.13
MA_RS27320	#N/A	1.48	0.78	0.78	1.55	1.83	1.22	1.65	1.60	1.33	1.64	0.86	1.06
MA_RS27325	NA	1.36	0.79	0.10	0.68	0.88	1.70	1.67	2.23	2.25	1.29	1.62	1.58
MA_RS27330	#N/A	2.65	3.04	3.05	3.17	2.80	3.10	3.03	3.51	3.72	2.76	2.72	2.68
MA_RS27335	#N/A	3.54	3.59	3.70	3.74	3.49	3.67	3.65	4.01	4.21	3.51	3.12	3.23
MA_RS27340	#N/A	1.26	1.73	2.16	1.49	2.18	2.21	1.23	2.09	1.81	2.32	1.44	1.61
MA_RS27345	NA	0.51	0.59	0.65	0.98	1.07	0.83	0.83	1.28	1.61	0.62	0.00	1.05
MA_RS27350	NA	0.29	0.20	0.00	0.00	0.00	0.00	0.39	0.00	0.00	0.73	0.00	0.31
MA_RS27355	NA	1.96	1.87	2.13	1.57	2.40	1.93	2.11	1.72	1.91	2.21	1.87	1.92
MA_RS27360	NA	0.41	0.72	0.00	0.36	1.10	0.44	0.62	1.30	0.00	0.33	0.00	0.51
MA_RS27365	#N/A	1.19	1.87	1.45	1.88	2.32	1.85	2.92	2.18	2.25	1.98	1.06	1.77
MA_RS27370	NA	1.26	0.98	0.66	1.38	1.06	1.71	1.12	1.50	1.95	1.77	0.82	0.78
MA_RS27375	NA	0.11	0.00	0.34	0.09	0.21	0.03	0.30	0.11	0.84	0.00	0.79	0.06
MA_RS27380	NA	0.85	1.70	2.50	2.39	2.64	1.38	3.07	3.79	2.98	3.17	3.40	1.58
MA_RS27385	NA	1.04	0.76	1.10	1.20	0.67	0.97	1.01	1.02	0.94	0.79	1.14	1.00
MA_RS27390	NA	3.87	3.62	4.07	4.12	3.79	4.29	4.73	5.03	4.90	4.61	4.00	4.27
MA_RS27395	NA	1.29	0.47	1.44	1.01	1.34	0.80	0.91	2.20	2.01	1.46	0.73	0.49
MA_RS27400	#N/A	4.06	4.13	4.32	3.58	3.90	4.11	3.88	4.67	5.51	4.28	3.96	3.28
MA_RS27405	NA	2.70	3.10	2.68	2.81	2.55	2.79	2.70	3.47	3.45	2.96	3.00	2.29
MA_RS27410	NA	0.98	1.25	0.32	1.87	1.01	0.65	1.17	1.92	2.17	1.12	1.27	0.86
MA_RS27415	NA	0.85	0.34	0.16	0.42	0.74	0.00	0.00	0.11	0.00	0.00	0.77	0.23
MA_RS27420	NA	0.00	0.00	0.00	0.31	0.36	0.00	0.18	0.00	0.40	0.00	0.00	0.25
MA_RS27425	NA	3.17	2.66	2.94	3.26	3.03	2.62	3.62	3.30	3.96	2.40	2.70	3.43
MA_RS27430	NA	2.36	2.81	2.03	2.51	2.52	1.85	0.00	2.50	3.58	3.19	2.53	2.63
MA_RS27435	NA	3.63	3.98	3.83	4.20	3.65	4.16	4.26	4.60	5.02	4.50	4.21	4.27
MA_RS27440	NA	0.77	1.00	1.14	1.16	0.00	1.47	0.00	2.14	1.33	1.06	1.61	0.65
MA_RS27445	NA	0.83	1.34	0.74	0.63	0.00	0.87	0.80	0.08	0.00	0.39	0.44	0.00
MA_RS27450	NA	0.03	0.55	0.00	0.00	0.00	0.00	0.31	0.00	0.00	0.00	0.00	1.41
MA_RS27455	NA	0.41	1.00	0.38	0.95	0.42	1.16	0.86	0.74	1.15	0.57	0.51	0.81
MA_RS27460	NA	0.97	1.85	1.05	1.80	1.57	1.13	1.09	2.65	1.75	2.01	1.33	1.19
MA_RS27465	#N/A	2.31	2.38	2.90	2.12	2.08	2.11	2.62	2.73	2.59	1.92	1.93	2.47
MA_RS27470	#N/A	0.90	1.10	0.50	1.69	1.56	0.89	0.86	2.16	1.79	1.92	0.88	1.49
MA_RS27475	NA	0.17	0.26	0.00	0.00	0.00	0.00	0.20	0.00	0.49	0.13	0.00	0.00
MA_RS27480	#N/A	0.50	0.39	0.53	0.34	0.50	0.94	0.71	0.63	1.76	1.83	0.99	1.07
MA_RS27490	#N/A	1.67	2.23	1.62	2.05	1.96	2.96	1.75	2.24	2.60	2.80	1.68	2.18
MA_RS27495	#N/A	2.53	2.64	2.41	2.93	2.45	2.95	2.71	3.13	2.44	2.54	2.78	2.45
MA_RS27500	#N/A	2.52	2.40	2.23	3.15	2.66	3.04	2.46	2.63	2.39	2.60	2.80	3.02
MA_RS27505	#N/A	0.73	0.56	0.45	0.43	1.00	1.32	1.03	1.32	1.21	1.03	1.10	0.55
MA_RS27510	#N/A	2.76	2.34	2.73	3.30	2.28	3.23	2.76	2.22	2.94	3.03	3.22	3.22
MA_RS27515	#N/A	2.88	3.10	2.82	3.34	3.25	3.41	3.15	3.55	4.24	3.51	3.38	3.39
MA_RS27520	#N/A	3.00	3.29	3.35	3.74	3.49	3.75	3.62	3.98	4.10	3.63	3.60	3.66
MA_RS27525	#N/A	2.95	3.30	3.22	3.72	3.11	3.76	3.43	4.34	4.57	3.83	3.45	3.45
MA_RS27535	NA	4.67	4.30	4.26	5.27	5.10	5.06	5.57	5.69	5.89	5.34	5.24	5.50
MA_RS27540	NA	0.00	1.08	0.30	1.35	0.00	1.25	0.40	2.17	1.62	1.10	0.99	1.17
MA_RS27550	NA	1.88	1.62	1.85	1.62	1.64	2.06	1.51	1.64	1.53	1.93	1.85	1.92
MA_RS27555	NA	0.00	1.20	0.00	1.02	0.17	0.63	0.00	0.00	0.00	0.36	0.00	0.55
MA_RS27560	NA	0.22	0.24	0.00	0.33	0.39	0.00	0.68	0.00	1.42	0.77	0.90	0.00
MA_RS27565	NA	0.54	0.20	0.68	0.51	0.54	0.83	0.62	0.52	0.69	1.12	0.60	0.89
MA_RS27570	NA	0.90	1.39	0.00	0.64	0.97	1.35	0.98	1.31	1.15	0.60	0.80	1.33
MA_RS27575	NA	0.54	0.42	0.00	0.56	0.00	0.32	0.37	0.25	0.51	0.51	0.00	0.00
MA_RS27580	NA	0.00	0.70	0.60	0.00	0.29	0.62	1.00	0.00	0.00	0.43	0.00	0.00
MA_RS27585	NA	0.00	0.00	0.00	0.57	0.98	0.55	0.65	1.33	1.19	0.58	0.00	0.57
MA_RS27590	#N/A	1.90	1.81	1.26	2.53	1.65	1.95	1.83	2.60	3.80	2.18	1.90	1.95
MA_RS27595	NA	1.08	1.91	1.61	1.01	1.73	2.44	1.32	2.35	1.47	1.78	2.06	1.08
MA_RS27600	NA	1.04	0.40	1.10	1.36	2.19	0.83	0.73	0.88	1.35	1.37	0.00	0.81
MA_RS27605	NA	0.00	0.00	0.00	0.88	0.44	0.19	0.00	0.00	0.00	0.00	0.00	0.00
MA_RS27610	#N/A	1.18	0.62	1.10	1.50	0.01	0.12	0.71	0.49	1.03	0.77	0.84	1.34
MA_RS27615	NA	0.48	0.53	0.69	0.33	0.00	0.00	0.56	0.89	0.39	0.91	0.00	0.44
MA_RS27620	NA	0.68	0.43	0.95	0.51	0.70	1.30	0.64	2.15	1.52	1.06	0.60	0.89
MA_RS27625	NA	1.63	1.40	1.59	2.35	2.51	2.42	1.53	1.85	2.09	2.29	1.86	1.92
MA_RS27635	NA	4.40	4.89	4.63	4.89	4.88	5.45	5.52	5.62	4.82	5.97	5.34	5.27
MA_RS27640	NA	1.65	2.53	1.45	1.16	1.92	2.16	2.34	2.21	3.49	2.77	2.19	1.66
MA_RS27645	NA	7.11	7.04	6.77	7.35	7.65	7.54	7.73	8.97	7.64	8.50	7.74	7.51
MA_RS27650	NA	3.41	3.38	3.57	3.49	3.80	3.61	3.94	4.19	4.47	4.16	3.87	3.74
MA_RS27655	#N/A	0.04	0.16	0.00	0.44	0.31	0.43	0.37	0.88	0.78	0.15	0.28	0.24
MA_RS27660	NA	0.24	0.21	0.28	0.00	0.16	0.75	0.31	1.09	1.25	0.53	0.45	0.19
MA_RS27665	NA	2.88	2.68	2.72	3.13	2.89	2.78	3.03	3.35	3.74	3.51	2.98	2.62
MA_RS27670	NA	2.23	1.92	2.39	2.08	2.22	2.19	1.79	2.47	3.27	2.40	2.15	2.09
MA_RS27675	NA	0.90	0.82	0.85	0.50	0.57	0.94	0.87	0.15	0.71	0.93	0.98	1.60
MA_RS27680	NA	0.20	0.28	0.00	0.28	0.20	0.22	0.46	0.13	0.93	0.90	0.09	0.00
MA_RS27685	NA	1.20	2.32	2.23	1.99	2.17	2.33	2.56	2.05	3.03	1.62	2.34	2.22
MA_RS27690	#N/A	1.52	1.49	2.08	1.44	1.83	2.41	1.50	2.87	2.42	1.16	1.00	2.15
MA_RS27695	NA	0.97	0.25	1.05	0.75	0.48	1.30	1.35	1.61	1.26	0.96	0.00	0.69
MA_RS27700	NA	0.43	0.00	0.00	0.00	0.00	1.12	0.51	0.28	0.00	0.31	0.00	0.70
MA_RS27705	NA	0.32	0.73	0.58	0.81	0.42	0.00	0.62	1.47	0.64	1.03	0.58	0.26
MA_RS27710	#N/A	1.57	1.60	1.80	1.80	1.66	2.04	1.62	1.67	2.56	2.11	2.04	1.65
MA_RS27715	#N/A	3.28	3.98	3.39	4.07	4.04	4.00	3.75	4.25	4.16	3.92	3.94	3.76
MA_RS27720	#N/A	2.81	3.15	3.20	3.44	3.47	3.60	2.97	3.06	3.65	3.17	2.91	3.03
MA_RS27725	#N/A	2.84	2.69	2.86	3.11	3.14	3.28	2.87	3.25	3.36	2.91	2.82	2.86
MA_RS27730	NA	0.34	0.00	0.45	0.56	1.13	0.17	0.00	0.18	0.97	0.31	1.26	0.65
MA_RS27735	#N/A	2.46	2.07	2.30	2.69	2.71	2.90	2.20	2.60	3.17	2.95	2.85	2.72
MA_RS27740	NA	1.20	0.75	0.00	0.94	1.12	1.05	0.55	0.67	1.96	0.31	0.04	0.75
MA_RS27745	NA	0.87	0.87	1.58	1.47	0.96	0.50	2.20	0.71	2.66	0.46	1.21	1.44

MA_RS27750	NA	0.99	0.54	1.19	1.15	0.63	1.64	0.44	0.91	0.95	0.27	0.19	1.08
MA_RS27760	NA	2.08	1.96	3.01	1.74	1.99	1.87	2.46	2.81	2.60	0.34	0.96	1.47
MA_RS27765	NA	8.40	8.40	8.39	8.68	8.62	8.63	8.53	7.72	7.99	7.81	8.11	8.38
MA_RS27770	NA	1.30	1.23	1.31	1.79	1.17	2.08	1.55	1.41	2.97	2.28	1.81	2.21
MA_RS27775	NA	0.87	1.23	0.74	2.59	1.27	2.22	1.31	1.93	1.96	1.53	1.15	1.97
MA_RS27780	NA	2.29	2.19	1.72	2.11	1.93	2.14	1.97	2.67	3.38	2.81	1.59	1.97
MA_RS27785	NA	1.76	0.95	0.90	1.93	1.29	1.55	0.84	3.27	2.18	1.87	1.43	0.80
MA_RS27790	NA	3.82	4.13	3.60	4.33	3.53	4.12	3.93	4.64	4.32	4.73	4.34	3.95
MA_RS27795	NA	0.37	0.64	0.00	0.31	0.00	0.42	0.64	0.72	1.09	0.39	0.96	0.13
MA_RS27800	NA	5.29	5.00	5.26	5.70	5.61	5.33	5.98	6.40	7.46	5.09	5.62	5.69
MA_RS27805	NA	2.34	2.90	2.51	2.85	3.30	3.66	3.12	3.49	4.91	3.63	2.94	2.92
MA_RS27810	#N/A	2.31	2.30	2.42	2.13	2.81	2.52	1.89	2.66	2.59	2.17	2.46	2.51
MA_RS27815	#N/A	0.56	0.96	0.83	1.17	1.20	1.32	0.87	1.51	1.50	1.37	0.98	0.96
MA_RS27820	#N/A	1.10	1.71	1.91	1.77	1.42	2.48	2.10	0.76	1.15	2.15	2.42	1.46
MA_RS27825	NA	2.23	1.95	2.44	2.08	2.28	2.53	1.79	2.52	3.29	2.40	2.15	2.16
MA_RS27830	NA	1.18	0.40	1.28	1.21	0.35	0.55	0.45	0.81	2.59	1.21	1.52	1.16
MA_RS27835	#N/A	2.16	2.16	1.95	3.01	2.14	2.99	2.43	2.41	4.02	3.79	2.77	2.22
MA_RS27845	NA	1.19	1.24	1.49	1.92	1.00	0.31	2.10	1.57	2.98	2.23	1.78	1.63
MA_RS27850	#N/A	0.26	0.25	0.00	0.00	0.48	0.00	0.00	0.84	0.00	0.00	0.19	0.03
MA_RS27855	NA	5.64	5.59	5.70	5.70	6.03	5.86	5.44	6.60	5.92	6.40	5.89	5.85
MA_RS27875	NA	0.65	0.02	2.47	0.30	1.50	1.88	2.14	1.72	2.56	0.30	2.56	1.45
MA_RS27880	NA	0.12	1.24	0.43	0.78	1.51	2.05	2.33	0.41	1.80	1.49	2.69	0.42
MA_RS27905	NA	0.41	0.80	1.03	1.04	1.07	0.71	1.30	0.28	1.17	0.48	0.64	0.78
MA_RS27910	#N/A	1.71	1.67	1.88	2.38	1.93	1.83	2.07	2.52	3.10	2.75	1.88	2.41
MA_RS27915	NA	3.28	3.39	3.23	3.75	3.37	3.94	3.81	4.45	4.59	3.25	3.38	3.67
MA_RS27920	#N/A	0.08	0.20	0.33	0.00	0.34	0.29	0.32	0.33	0.18	1.17	0.08	0.03
MA_RS27925	#N/A	0.58	1.22	1.19	0.23	0.94	0.48	0.08	0.45	1.19	0.31	1.67	0.36
MA_RS27930	#N/A	1.05	2.06	0.89	1.92	1.60	1.84	2.22	2.21	2.32	1.46	1.65	0.84
MA_RS27935	#N/A	1.31	1.63	1.35	1.70	2.29	1.69	1.23	1.85	2.64	1.80	2.03	1.77
MA_RS27940	#N/A	0.32	0.92	0.00	1.05	0.20	1.23	0.54	1.56	0.63	0.87	0.48	0.40
MA_RS27945	#N/A	2.02	2.13	2.15	2.49	2.72	2.53	2.45	2.91	3.36	2.44	2.04	2.44
MA_RS27950	#N/A	1.13	0.14	1.37	0.54	0.71	1.43	1.67	1.99	2.65	0.73	1.97	1.57
MA_RS27955	#N/A	0.00	0.20	0.00	0.54	0.00	0.00	0.00	0.00	0.00	0.28	0.36	0.00
MA_RS27965	#N/A	0.85	0.34	0.00	0.64	1.16	1.32	0.95	1.57	2.48	1.39	0.66	0.47
MA_RS27970	NA	3.35	3.15	3.55	4.52	4.30	3.90	4.15	5.05	4.55	3.58	3.46	3.35
MA_RS27975	NA	2.17	2.16	2.08	2.19	2.52	2.48	2.66	3.10	3.02	2.80	2.59	2.56
MA_RS27980	#N/A	0.00	0.82	0.00	0.82	0.43	0.00	0.00	0.00	0.62	0.85	0.00	0.00
MA_RS27985	#N/A	2.50	1.94	2.96	2.66	2.22	2.91	3.39	2.47	2.95	2.19	2.44	1.80
MA_RS27990	#N/A	6.59	6.84	7.09	7.55	6.93	7.00	7.68	8.37	8.57	8.47	7.21	7.50
MA_RS27995	NA	0.52	0.21	1.06	1.25	1.07	0.55	1.20	0.24	0.88	0.76	0.00	0.67
MA_RS28000	#N/A	1.26	0.83	1.52	1.33	2.10	1.01	0.93	1.51	1.54	0.89	1.11	1.07
MA_RS28005	NA	2.11	2.47	2.40	2.26	2.15	2.33	2.83	1.94	2.52	2.54	2.31	2.72
MA_RS28010	#N/A	1.56	0.45	2.47	2.38	1.73	2.23	1.13	2.11	2.72	2.17	1.71	1.39
MA_RS28015	#N/A	1.24	1.02	1.86	1.77	0.59	1.03	0.77	0.00	1.68	1.28	1.66	1.88
MA_RS28020	NA	3.04	2.56	2.57	3.42	2.90	3.80	4.45	4.63	4.18	3.84	3.25	3.80
MA_RS28025	#N/A	1.54	1.73	1.84	2.67	2.54	2.14	2.09	3.35	2.19	2.79	2.16	2.12
MA_RS28030	#N/A	0.56	1.07	1.44	1.34	1.22	0.87	1.59	2.76	2.29	1.44	1.16	1.29
MA_RS28035	#N/A	0.47	0.65	0.00	0.69	0.00	0.00	0.45	0.62	0.03	0.00	0.36	0.49
MA_RS28040	NA	9.65	10.06	9.92	2.35	2.49	3.42	8.18	9.18	9.48	7.40	7.59	8.19
MA_RS28045	NA	1.85	2.60	2.14	1.86	2.22	2.91	3.10	2.65	2.83	3.09	3.32	2.27
MA_RS28050	#N/A	3.72	4.04	3.94	4.84	4.24	4.74	5.01	5.36	5.89	4.27	4.66	4.44
MA_RS28055	#N/A	4.08	4.25	4.24	4.86	4.56	5.07	4.84	5.30	5.72	4.58	4.69	4.42
MA_RS28060	NA	0.73	0.36	0.73	0.42	0.54	1.97	0.00	0.52	0.41	0.00	2.74	0.00
MA_RS28065	#N/A	3.21	3.68	2.89	3.03	3.25	3.52	3.40	4.40	4.34	3.43	3.28	3.59
MA_RS28070	#N/A	1.88	2.02	1.78	2.26	1.93	2.20	2.73	2.78	3.39	2.03	1.95	2.20
MA_RS28075	NA	6.92	6.91	7.00	6.86	6.80	7.03	7.35	7.96	7.41	7.17	6.65	6.72
MA_RS28080	NA	3.52	2.63	3.85	2.64	2.49	2.16	2.83	3.46	2.72	3.21	2.41	2.37
MA_RS28085	NA	0.54	0.69	1.67	1.80	0.96	1.79	1.79	0.69	2.17	1.62	1.16	1.53
MA_RS28090	NA	5.66	5.80	5.57	5.48	5.26	5.28	5.20	5.72	5.32	5.24	4.92	5.19
MA_RS28095	NA	1.28	1.28	1.05	2.16	0.00	0.53	2.08	2.06	1.56	0.86	1.81	1.36
MA_RS28100	NA	1.94	1.58	2.65	2.03	1.57	1.78	2.00	2.15	2.08	0.74	1.51	1.55
MA_RS28105	#N/A	5.92	6.55	6.35	6.60	6.35	6.57	6.66	7.32	7.50	6.02	6.08	6.38
MA_RS28110	NA	2.16	1.52	3.20	2.70	2.98	2.96	3.90	3.58	3.71	3.42	3.29	2.66
MA_RS28115	NA	0.30	0.34	0.41	0.39	0.33	0.38	0.32	0.52	0.45	0.34	0.33	0.37
MA_RS28120	NA	0.30	0.42	0.20	0.35	0.24	0.25	0.21	0.60	0.55	0.44	0.12	0.13
MA_RS28125	#N/A	2.85	3.10	3.10	3.77	3.20	3.55	3.30	4.12	4.58	3.84	3.45	3.48
MA_RS28130	#N/A	3.05	3.50	2.93	3.53	3.09	3.46	3.28	3.82	3.95	3.34	3.31	3.25

Table S2.7. RNA-Seq Raw data. DESeq2 results for all pairwise comparisons made in the analysis of RNA-Seq data. log2(FPKM) values are in a separate table, where DDN121 refers to ΔpylBCD and DDN146 refers to ΔpylTS. WT refers to the parental strain of all knockouts, WWM60; substrate is indicated following each strain in the comparison. All results represent values derived from cultures grown in triplicate. For each gene, the log2 fold change, p-value, and q-value are indicated in the corresponding column. TMA: trimethylamine, MeOH: Methanol.

genome	pyl+	TAG	TGA	TAA	gc	tax	checkM	genome size (Mb)	aRF1	prfB	prfA	eRF1_d1	eRF1_d2	eRF1_d3
GCA_016926815.1	0	0.19	0.42	0.38	38.52352	d__Archaea;p__Aenigmarchaeota;c__Aenigmarchaeota;o__Aenigmarchaeota;f__JACPZ201;g__JACPZ201;s__JACPZ201;s__JACPZ201 sp016926815	91.12	0.946672	1	0	0	0	0	0
GCA_016931255.1	0	0.21	0.46	0.34	46.85193	d__Archaea;p__Aenigmarchaeota;c__Aenigmarchaeota;o__Aenigmarchaeota;f__OM2P011;f__JAFGSV01;g__JAFGFG01;s__JAFGFG01 sp016931255	90.06	0.929379	1	0	0	1	0	0
GCA_029129865.1	0	0.2	0.37	0.43	45.41549	d__Archaea;p__Aenigmarchaeota;c__Aenigmarchaeota;o__Aenigmarchaeota;f__OM2P011;f__OM2P011;g__CS3-C152;s__CS3-C152 sp029129865	96.19	1.034484	1	0	0	0	0	0
GCA_001873845.1	0	0.12	0.24	0.64	32.19057	d__Archaea;p__Altiarchaeota;c__Altiarchaeia;o__Altiarchaeales;f__Altiarchaeaceae;g__Altiarchaeum;s__Altiarchaeum hamiconexum	95.02	1.660967	1	0	0	1	0	0
GCA_018809615.1	0	0.1	0.22	0.68	33.55408	d__Archaea;p__Altiarchaeota;c__Altiarchaeia;o__Altiarchaeales;f__Altiarchaeaceae;g__Altiarchaeum;s__Altiarchaeum sp002941105	95.02	2.227023	1	0	0	1	0	0
GCA_018897475.1	0	0.27	0.35	0.37	47.53299	d__Archaea;p__Altiarchaeota;c__Altiarchaeia;o__MC4;f__OM2M01;g__WALD01;s__WALD01 sp018897475	95.02	1.41422	1	0	0	0	0	0
GCA_902884455.1	0	0.21	0.32	0.48	50.50229	d__Archaea;p__Altiarchaeota;c__Altiarchaeia;o__MC4;f__SCGC-AAA252-I15;g__CABMKB01;s__CABMKB01 sp902384455	92.81	2.815149	1	0	0	0	0	1
GCA_014727915.1	0	0.13	0.44	0.26	54.31416	d__Archaea;p__Altiarchaeota;c__Altiarchaeia;o__MC4;f__SCGC-AAA252-I15;g__WJMO01;s__WJMO01 sp014727915	91.74	1.803974	1	0	0	0	0	0
GCA_016840465.1	0	0.2	0.43	0.37	45.94799	d__Archaea;p__Asgardarchaeota;c__Baldrarchaeia;o__Baldrarchaeales;f__Baldrarchaeaceae;g__Baldrarchaeum;s__Baldrarchaeum yapensis	93.93	2.267786	1	0	0	0	0	0
GCA_016840465.1	0	0.21	0.36	0.43	46.58671	d__Archaea;p__Asgardarchaeota;c__Baldrarchaeota;o__Baldrarchaeota;f__DXJG01;g__DXJG01;s__DXJG01 sp016840465	91.67	3.207774	1	0	0	0	0	0
GCA_019058805.1	0	0.19	0.18	0.62	35.47826	d__Archaea;p__Asgardarchaeota;c__Baldrarchaeota;o__Baldrarchaeota;f__DXJG01;g__DXJG01;s__DXJG01 sp019058805	95.33	1.922513	1	0	0	0	0	0
GCA_016935155.1	0	0.21	0.16	0.63	32.92619	d__Archaea;p__Asgardarchaeota;c__Hodarchaeia;o__Hodarchaeales;f__Hodarchaeaceae;g__Hodarchaeum;s__Hodarchaeum mangrovi	93.61	4.000209	1	0	0	0	0	0
GCA_003144275.1	0	0.21	0.26	0.51	36.14008	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__Hodarchaeales;f__Hodarchaeaceae;g__Hodarchaeum;s__Hodarchaeum sp003144275	93.69	3.94826	1	0	0	0	0	0
GCA_016840265.1	0	0.2	0.3	0.51	36.00286	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__Hodarchaeales;f__Hodarchaeaceae;g__Hodarchaeum;s__Hodarchaeum sp016840265	96.19	4.660121	1	0	0	0	0	0
GCA_019657635.1	0	0.22	0.28	0.5	36.17389	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__Hodarchaeales;f__Hodarchaeaceae;g__Hodarchaeum;s__Hodarchaeum sp019657635	90.42	3.186535	1	0	0	0	0	0
GCA_020353515.1	0	0.2	0.29	0.52	35.87585	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__Hodarchaeales;f__Hodarchaeaceae;g__Hodarchaeum;s__Hodarchaeum sp020353515	92.99	4.943498	1	0	0	0	0	0
GCA_001940645.1	0	0.17	0.21	0.62	29.72057	d__Archaea;p__Asgardarchaeota;c__Hodarchaeota;o__LC-30-37;f__LC-30-37;g__LC-30-37;s__LC-30-37 sp001940645	91.59	3.694828	1	0	0	0	0	0
GCA_013166835.1	0	0.23	0.22	0.55	33.72157	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABLTE01;f__JABLTE01;g__JABLTE01;s__JABLTE01 sp013166835	96.19	3.557906	1	0	0	0	0	0
GCA_018238135.1	0	0.22	0.23	0.55	32.78855	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABLTE01;f__JABLTE01;g__JABLTE01;s__JABLTE01 sp018238135	94.39	4.076992	1	0	0	0	0	0
GCA_019058165.1	0	0.23	0.22	0.55	33.77406	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABLTE01;f__JABLTE01;g__JABLTE01;s__JABLTE01 sp019058165	91.3	3.357971	1	0	0	0	0	0
GCA_019058275.1	0	0.22	0.23	0.55	32.45534	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABLTE01;f__JABLTE01;g__JABLTE01;s__JABLTE01 sp019058275	95.33	4.121334	1	0	0	0	0	0
GCA_019894765.1	0	0.22	0.2	0.57	34.11923	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABLTE01;f__JABLTE01;g__JABLTE01;s__JABLTE01 sp019894765	91.59	3.365315	1	0	0	0	0	0
GCA_024280435.1	0	0.21	0.3	0.49	32.8227	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABAED01;f__Kariarchaeaceae;g__JAURDD01;s__JAURDD01 sp024280435	93.31	4.0328	1	0	0	0	0	0
GCA_015221565.1	0	0.19	0.38	0.43	38.5818	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__Kariarchaeaceae;g__WJAX01;s__WJAX01 sp015221565	91.12	3.571168	1	0	0	0	0	0
GCA_019057815.1	0	0.21	0.25	0.54	32.75497	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA601;g__18H4-34;s__18H4-34 sp019057815	95.33	3.735735	1	0	0	0	0	1
GCA_023170595.1	0	0.22	0.26	0.51	32.93303	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA601;g__18H4-34;s__18H4-34 sp023170595	91.12	3.621764	1	0	0	0	0	1
GCA_021513695.1	0	0.21	0.17	0.62	31.23889	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA601;g__PR6;s__PR6 sp021513695	93.46	3.081793	1	0	0	0	0	1
GCA_021513715.1	0	0.21	0.18	0.61	30.84529	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA601;g__PR6;s__PR6 sp021513715	95.33	3.326783	1	0	0	0	0	1
GCA_019657375.1	0	0.24	0.23	0.53	33.69389	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp019657375	94.39	3.468451	1	0	0	1	0	0
GCA_013166775.1	0	0.24	0.21	0.55	32.91157	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp013166775	93.46	3.947693	1	0	0	1	0	0
GCA_016840235.1	0	0.22	0.23	0.55	33.23389	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp016840235	92.52	3.444035	1	0	0	1	0	0
GCA_018238545.1	0	0.21	0.26	0.53	34.00528	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp018238545	94.39	3.828557	1	0	0	1	0	0
GCA_019894765.1	0	0.22	0.23	0.55	33.90079	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp019894765	93.22	3.067769	1	0	0	1	0	0
GCA_021339345.1	0	0.24	0.25	0.52	33.48577	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp021339345	91.59	3.265656	1	0	0	1	0	0
GCA_021399355.1	0	0.26	0.22	0.53	34.28852	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp021399355	92.52	2.816154	1	0	0	1	0	0
GCA_021135955.1	0	0.24	0.24	0.52	33.2033	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp021135955	92.52	3.583978	1	0	0	1	0	0
GCA_021135215.1	0	0.23	0.21	0.56	33.42339	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp021135215	92.52	2.886057	1	0	0	1	0	0
GCA_023705575.1	0	0.25	0.25	0.52	33.69772	d__Archaea;p__Asgardarchaeota;c__Heimdallarchaeota;o__JABA601;f__JABA603;g__JABA603;s__JABA603 sp023705575	91.59	3.741597	0	0	0	1	0	0
GCA_016650425.1	0	0.29	0.25	0.46	44.54219	d__Archaea;p__Asgardarchaeota;c__Hermodarchaeota;o__Hermodarchaeales;f__Hermodarchaeaceae;g__Hermodarchaeum;s__Hermodarchaeum sp016650425	92.67	3.764229	1	0	1	1	1	1
GCA_016935245.1	0	0.31	0.26	0.43	45.68432	d__Archaea;p__Asgardarchaeota;c__Hermodarchaeota;o__Hermodarchaeales;f__Hermodarchaeaceae;g__Hermodarchaeum;s__Hermodarchaeum sp016935245	91.12	2.225222	1	0	0	1	1	1
GCA_016839805.1	0	0.25	0.25	0.47	43.84106	d__Archaea;p__Asgardarchaeota;c__Hermodarchaeota;o__Hermodarchaeales;f__Hermodarchaeaceae;g__Hermodarchaeum;s__Hermodarchaeum sp016839805	94.86	2.309456	1	0	0	1	1	1
GCA_016840405.1	0	0.29	0.24	0.47	44.68796	d__Archaea;p__Asgardarchaeota;c__Hermodarchaeota;o__Hermodarchaeales;f__Hermodarchaeaceae;g__Hermodarchaeum;s__Hermodarchaeum yapensis	92.99	2.706021	1	0	0	1	1	1
GCA_019058875.1	0	0.23	0.23	0.55	40.78194	d__Archaea;p__Asgardarchaeota;c__Jordarchaeia;o__Jordarchaeales;f__Jordarchaeaceae;g__Jordarchaeum;s__Jordarchaeum madagascariense	95.02	3.677542	1	0	0	0	0	0
GCA_019058495.1	0	0.36	0.39	0.25	46.29998	d__Archaea;p__Asgardarchaeota;c__LC30;o__LC30;f__LC30;g__LC30;s__LC30 sp019058495	95.48	2.88186	1	0	0	0	0	0
GCA_016833355.1	0	0.18	0.21	0.61	35.32187	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__AMAR8-1;g__AMAR8-1;s__AMAR8-1 sp016933055	94.39	3.780324	1	0	0	0	0	1
GCA_021498095.1	0	0.14	0.18	0.67	31.01657	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__MK-D1;g__Promethoarchaeum;s__Promethoarchaeum sp021498095	93.93	4.361485	1	0	0	0	0	1
GCA_026007775.1	0	0.19	0.17	0.68	31.17307	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__MK-D1;g__Promethoarchaeum;s__Promethoarchaeum syntrophicum	91.74	4.427197	1	0	0	0	0	0
GCA_019058015.1	0	0.13	0.14	0.73	29.38997	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__6H3-1;s__6H3-1 sp019058015	91.74	3.841278	0	0	0	0	0	0
GCA_016928735.1	0	0.15	0.14	0.71	26.22777	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__JAFGOM01;s__JAFGOM01 sp016928735	90.65	3.880097	0	0	0	0	0	0
GCA_019053365.1	0	0.15	0.71	29.52976	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__Loki-b32;s__Loki-b32 sp019053365	91.59	4.730379	1	0	0	0	0	0
GCA_019057795.1	0	0.15	0.14	0.71	31.35511	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__SOKP01;s__SOKP01 sp019057795	94.39	4.954151	1	0	0	0	0	0
GCA_014730195.1	0	0.16	0.16	0.68	30.03451	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__TEKIR-8;s__TEKIR-8 sp014730195	92.52	4.6324	1	1	0	0	0	0
GCA_014730295.1	0	0.17	0.17	0.65	33.40959	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__TEKIR-8;s__TEKIR-8 sp014730295	94.39	5.144361	1	0	0	0	0	0
GCA_016356555.1	0	0.13	0.12	0.74	29.56994	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__CR-4;f__SOKP01;g__TEKIR-8;s__TEKIR-8 sp016356555	92.52	5.244429	0	0	0	0	0	0
GCA_013375455.1	0	0.19	0.26	0.58	38.63243	d__Archaea;p__Asgardarchaeota;c__Helarchaeales;f__HEL-GB-Ag;g__JABXJT01;s__JABXJT01 sp013375455	91.59	5.355224	1	0	0	0	0	0
GCA_016840125.1	0	0.18	0.23	0.59	38.45775	d__Archaea;p__Asgardarchaeota;c__Helarchaeales;f__HEL-GB-Ag;g__JABXJT01;s__JABXJT01 sp016840125	92.99	5.09224	1	0	0	0	0	0
GCA_013375355.1	0	0.14	0.17	0.69	30.72541	d__Archaea;p__Asgardarchaeota;c__Helarchaeales;f__JABXJV01;g__JABXJV01;s__JABXJV01 sp013375355	92.21	4.55051	1	0	0	0	0	0
GCA_019058315.1	0	0.12	0.16	0.72	30.49287	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__Helarchaeales;f__JABXJV01;g__JABXJV01;s__JABXJV01 sp019058315	95.33	5.794824	1	0	0	0	0	0
GCA_013360055.1	0	0.12	0.21	0.67	30.05586	d__Archaea;p__Asgardarchaeota;c__Lokiarchaeia;o__Helarchaeales;f__RODO01;g__RODO01;s__RODO01 sp013360055	96.26	4.677338	1	0	0	0	0	0
GCA_016839265.1	0	0.18	0.21	0.61	36.28318	d__Archaea;p__Asgardarchaeota;c__Odinarchaeia;o__Odinarchaeales;f__Odinarchaeaceae;g__Odinarchaeum;s__Odinarchaeum sp016839265	95.95	1.350507	1	0	0	0	0	0
GCA_021006805.1	0	0.18	0.26	0.56	38.0544	d__Archaea;p__Asgardarchaeota;c__Odinarchaeia;o__Odinarchaeales;f__Odinarchaeaceae;g__Odinarchaeum;s__Odinarchaeum sp021006805	96.26	1.46071	1	0	0	0	0	0
GCA_002610075.1	1	0.14	0.58	0.29	43.19986	d__Archaea;p__Halobacteriota;c__Methanosarcinia;o__Methanosarcinales;f__Methermicoccaceae;g__JdFR-19;s__JdFR-19 sp002610075	96.73	1.288683	1	0	0	0	0	0
GCA_016840515.1	0	0.22	0.28	0.5	37.09205	d__Archaea;p__Thermoproteota;c__Bilwiarchaeia;o__Bilwiarchaeales;f__Bilwiarchaeaceae;g__Bilwiarchaeum;s__Bilwiarchaeum yapensis	95.03	3.633074	1	0	0	0	0	0
GCA_021498125.1	0	0.2	0.41	0.37	47.07953	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__BdS-09;s__BdS-09 sp021498125	95.33	3.114145	1	0	0	0	0	0
GCA_013388835.1	0	0.43	0.5	0.08	54.18395	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__JACABL01;s__JACABL01 sp013388835	94.39	3.013036	1	0	0	0	0	0
GCA_024278825.1	0	0.28	0.42	0.3	43.57658	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__JAJRWD01;s__JAJRWD01 sp024278825	95.79	2.935212	1	0	0	0	0	0
GCA_024275415.1	0	0.34	0.43	0.23	46.97701	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP5-2226;s__MP5-2226 sp024275415	94.39	3.525578	0	0	0	0	0	1
GCA_002525465.1	0	0.34	0.33	0.33	41.61138	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp002525465	92.06	3.51187	0	0	0	1	0	0
GCA_004524565.1	0	0.34	0.31	0.35	41.58473	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp004524565	96.19	3.132667	0	0	0	0	0	0
GCA_004524555.1	0	0.32	0.33	0.35	40.65413	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp004524555	92.99	4.171535	0	0	0	0	0	0
GCA_016839545.1	0	0.32	0.37	0.31	40.14386	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp016839545	93.93	3.418532	0	0	0	0	0	0
GCA_016839275.1	0	0.35	0.36	0.29	43.37825	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp016839275	91.59	2.577824	0	0	0	0	0	0
GCA_016840385.1	0	0.34	0.32	0.32	42.08686	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp016840385	91.98	3.875586	0	0	0	0	0	0
GCA_018238205.1	0	0.33	0.34	0.33	41.76666	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp018238205	94.86	3.574248	0	0	0	0	0	0
GCA_018238825.1	0	0.33	0.35	0.33	41.67559	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__MP8T-1;s__MP8T-1 sp018238825	92.06	2.77924	0	0	0	0	0	0
GCA_008080745.1	0	0.32	0.26	0.4	41.22754	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SHM001;s__SHM001 sp008080745	92.99	3.161981	0	0	0	0	0	0
GCA_014728635.1	0	0.31	0.39	0.39	54.5262	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SHM001;s__SHM001 sp014728635	93.46	4.338587	1	0	0	0	0	0
GCA_001940705.1	0	0.37	0.37	0.26	44.57872	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SMTZ1-45;s__SMTZ1-45 sp001940705	90.12	2.855654	1	0	0	0	0	0
GCA_002825515.1	0	0.33	0.37	0.29	42.58848	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SMTZ1-45;s__SMTZ1-45 sp002825515	90.19	3.487971	0	0	0	1	0	0
GCA_004372265.1	0	0.34	0.38	0.28	43.33388	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SMTZ1-45;s__SMTZ1-45 sp004372265	90.65	3.037202	0	0	0	1	0	0
GCA_016840685.1	0	0.37	0.39	0.24	44.63438	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SMTZ1-45;s__SMTZ1-45 sp016840685	94.39	3.228751	0	0	0	0	0	0
GCA_001563325.1	0	0.41	0.41	0.18	49.23154	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__SMTZ1-83;s__SMTZ1-83 sp001563325	90.19	3.263924	0	0	0	0	1	1
GCA_004524445.1	0	0.38	0.34	0.27	44.5829	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__TEKIR-14;s__TEKIR-14 sp004524445	96.19	2.792701	0	0	0	0	0	0
GCA_014730275.1	0	0.35	0.27	0.37	45.21353	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__WJL01;s__WJL01 sp014730275	94.86	3.64338	0	0	0	0	0	0
GCA_018335335.1	0	0.38	0.35	0.26	45.17346	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__WJL01;s__WJL01 sp018335335	93.93	2.444246	0	0	0	0	0	0
GCA_018238375.1	0	0.42	0.37	0.21	47.99809	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__WTCK01;s__WTCK01 sp018238375	92.06	2.508877	0	0	0	0	0	0
GCA_019057475.1	0	0.41	0.38	0.2	48.27154	d__Archaea;p__Thermoproteota;c__Thermoarchaeia;f__Thermoarchaeales;f__Thermoarchaeaceae;g__WTCK01;s__WTCK01 sp019057475	92.99	3.339253	0	0	0	0	0	0
GCA_016840425.1	0	0.17	0.21	0.61	38.01333	d__Archaea;p__Thermoproteota;c__Wukongarchaeia;o__Wukongarchaeales;f__Wukongarchaeaceae;g__Wukongarchaeum;s__Wukongarchaeum yapensis	92.52	2.156567	0	0	0	0	0	0
GCA_021161465.1	0	0.24	0.29	0.38	44.64333	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__B1Sed10-29;f__WALL01;f__JAGHAM01;g__WALL01 sp021161465	90.81	0.970726	1	0	0	0	0	0
GCA_021162685.1	0	0.23	0.44	0.33	39.63731	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__B1Sed10-29;f__WALL01;f__WALL01;g__JAGGYF01;s__JAGGYF01 sp021162685	98.13	1.113673	1	0	0	0	0	1
GCA_021291555.1	0	0.19	0.45	0.29	55.97003	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__B1Sed10-29;f__WALL01;f__WALL01;g__WALL01;s__WALL01 sp021291555	95.79	1.247464	1	0	0	1	0	0
GCA_021137195.1	0	0.26	0.26	0.48	35.33898	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__B1Sed10-29;f__Ex4484-52;g__Ex4484-52;s__Ex4484-52 sp021137195	90.19	1.419684	1	0	0	1	0	0
GCA_018897155.1	0	0.15	0.32	0.52	40.5773	d__Archaea;p__Thermoplasmatota;c__Thermoplasmata;o__Ex4484-52;o__Ex4484-52;f__LFW-46;g__LFW-46;s__LFW-46 sp018897155	92.06	1.426221	1	0	0	0	0	0
GCA_014361055.1	0	0.24	0.46	0.3	51.9886	d__Archaea;p__Hadarchaeota;c__Hadarchaeia;o__Hadarchaeales;f__Hadarchaeaceae;g__Hadarchaeum;s__Hadarchaeum sp014361055	94.08	1.190365	0	0	0	0	0	0
GCA_009437925.1	0	0.34	0.55	0.11	65.01622	d__Archaea;p__Hadarchaeota;c__Hadarchaeia;o__Hadarchaeales;f__WYZLMO6;g__WYZLMO6;s__WYZLMO6 sp009437925	92.37	1.241441	1	0	0	0	0	0
GCA_020110195.1	0	0.43	0.34	0.22	42.2145	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archaeoglobus sp020110195	90.35	1.966558	1	0	0	0	0	0
GCA_020211215.1	0	0.18	0.44	0.37	39.49442	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archaeoglobus;s__Archaeoglobus sp020211215	100	2.701738	1	0	0	0	0	0
GCA_020494625.1	0	0.39	0.38	0.23	40.4574	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archaeoglobus;s__Archaeoglobus sp020494625	94.77	2.360045	1	0	0	0	0	0
GCA_017656505.1	0	0.25	0.4	0.36	42.75582	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archaeoglobus;s__Archaeoglobus sp017656505	100	2.524591	1	0	0	0	0	0
GCA_002885585.1	0	0.22	0.44	0.34	42.23389	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archaeoglobus sp002885585	100	2.676231	1	0	0	0	0	0
GCA_000025285.1	0	0.15	0.47	0.38	42.00456	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archaeoglobus;s__Archaeoglobus B.s.; Archaeoglobus_B.profundus	99.84	1.563423	1	0	0	0	0	0
GCA_016520485.1	0	0.18	0.41	0.41	45.0746	d__Archaea;p__Halobacteriota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__Archaeoglobus;s__Archa

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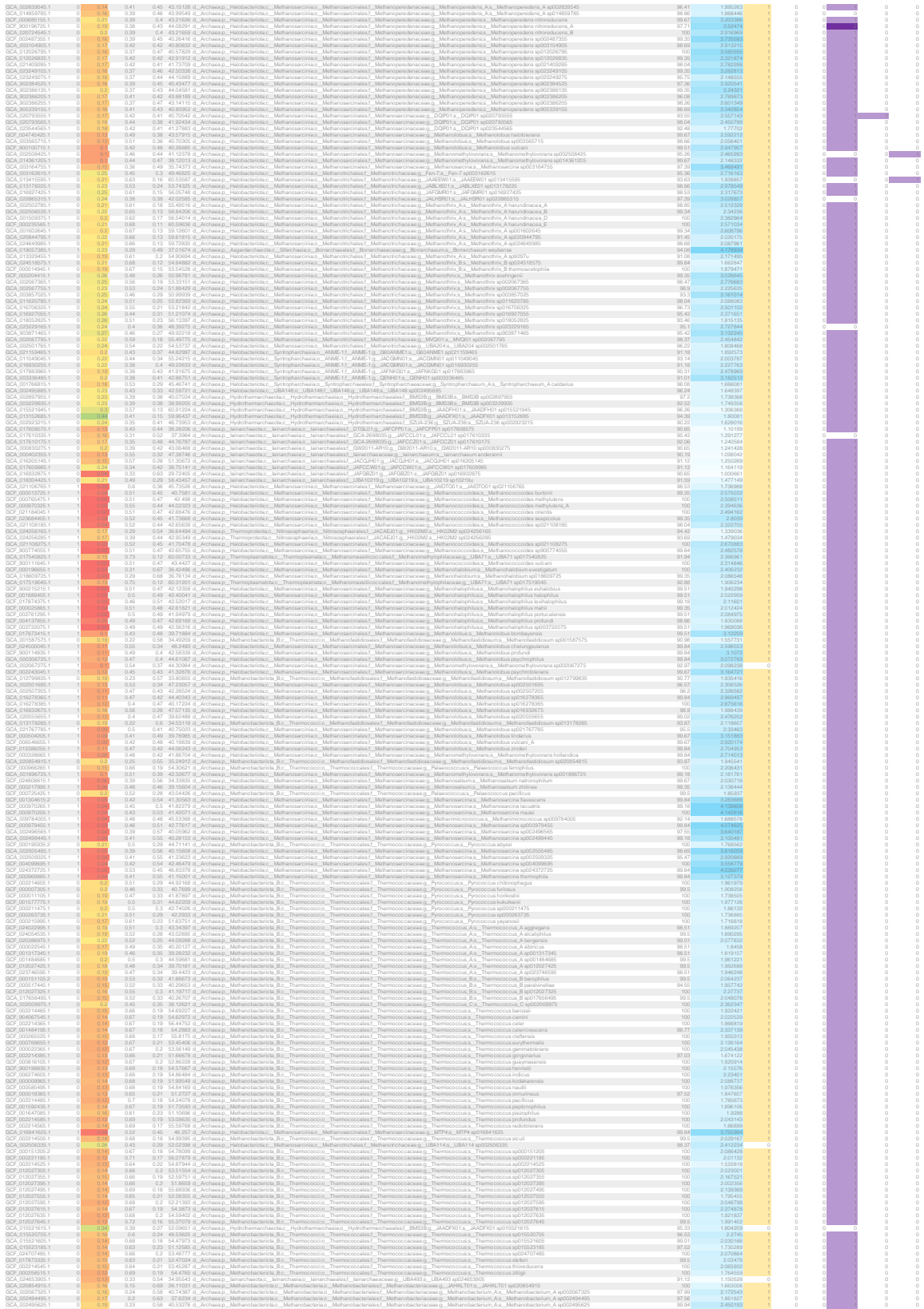
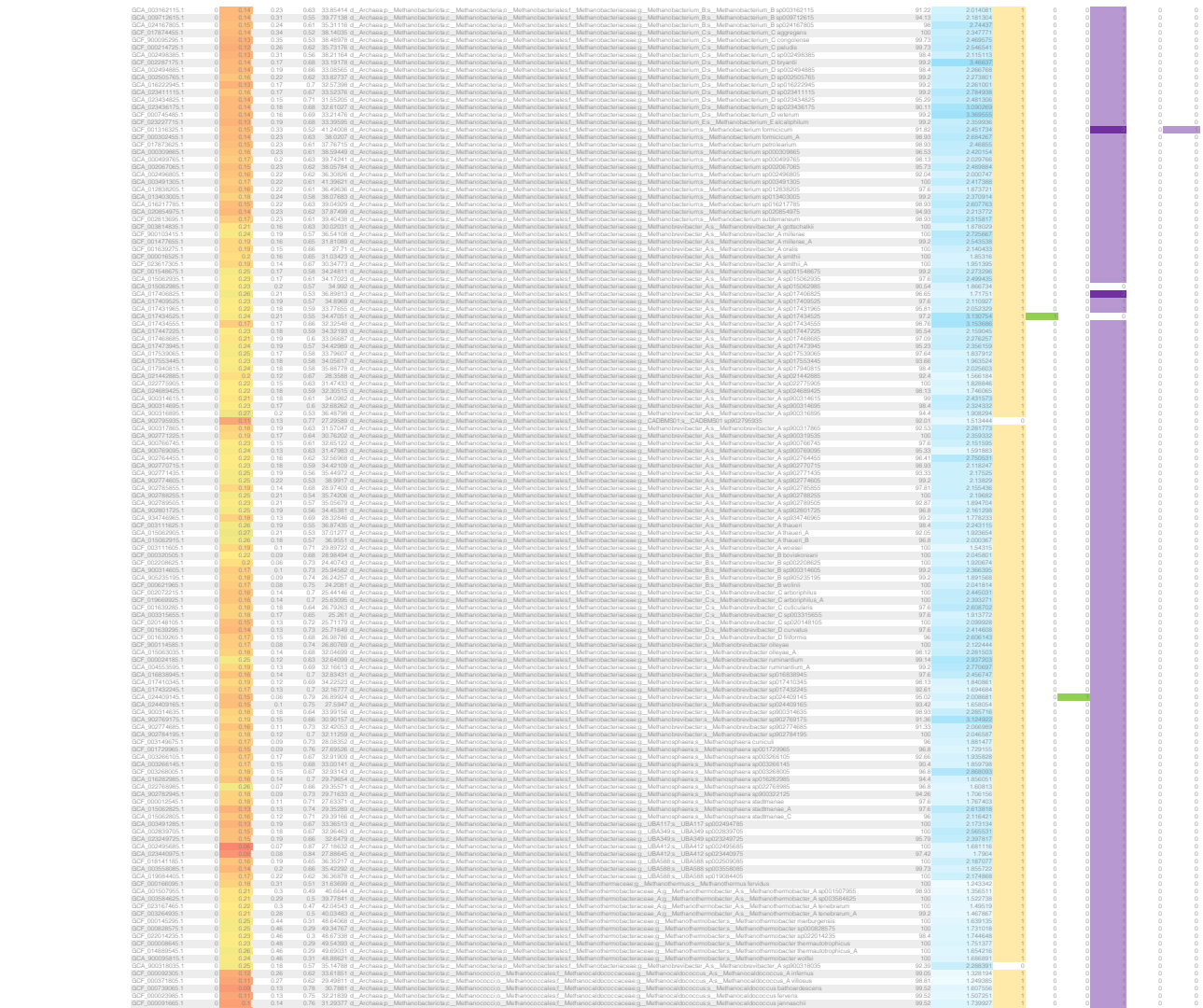
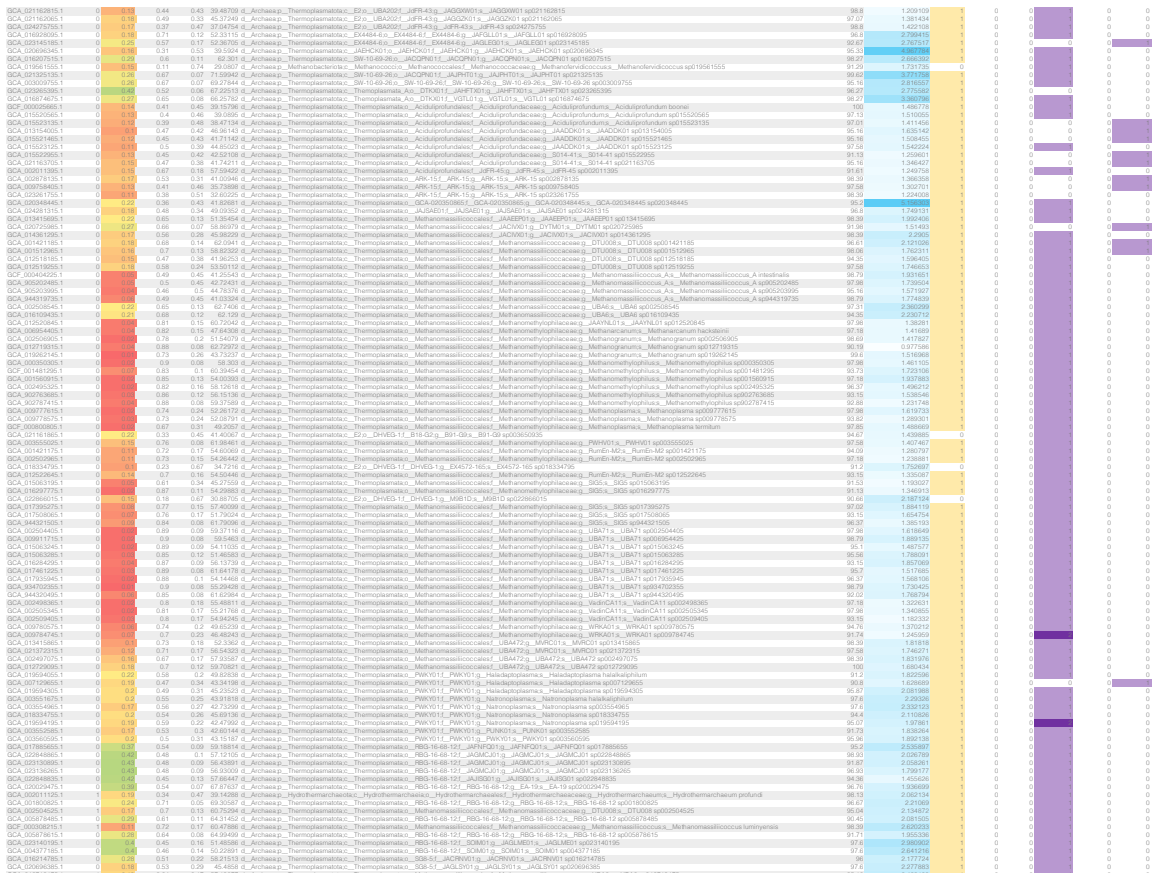
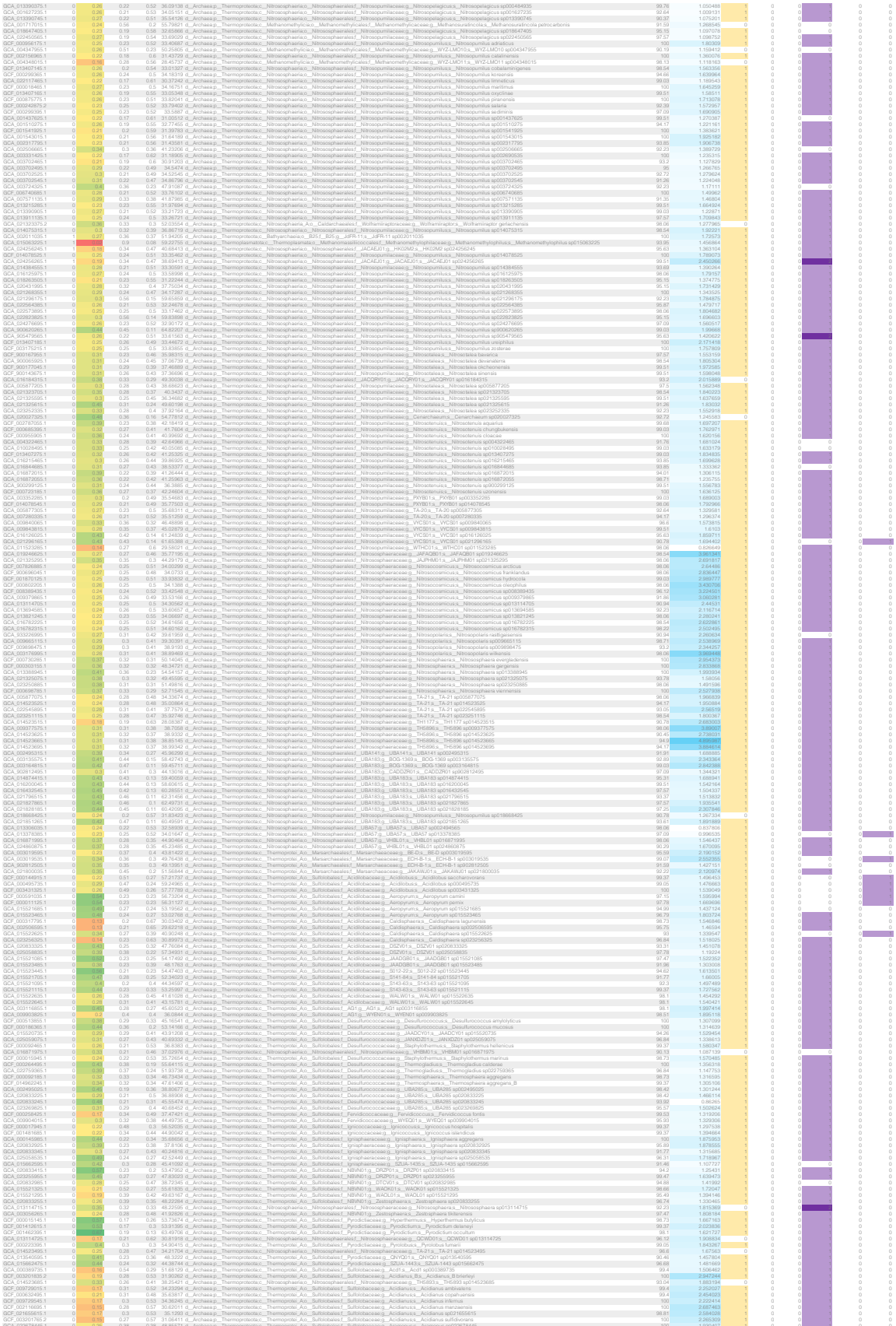
GCF_023028105.1	0	0.21	0.59	0.2	64.9546	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__JALIQP01;s__JALIQP01 sp023028105	99.44	4.75036	1		0	0			0	0
GCF_023566055.1	0	0.22	0.6	0.18	65.08571	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__JALIQP01;s__JALIQP01 sp023566055	99.43	4.59454	1		0	0			0	0
GCF_002156705.1	0	0.19	0.64	0.17	64.10829	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrarchaeobacuturnis;__Natrarchaeobaculum aegyptiacum	99.53	3.930546	1		0	0			0	0
GCF_003403825.1	0	0.18	0.23	62.36402	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrarchaeobacuturnis;__Natrarchaeobaculum sulfurireducens	99.13	3.769253	1		0	0			0	0
GCF_003841505.1	0	0.18	0.58	0.24	61.9359	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrarchaeobiusis;__Natrarchaeobius chlorinivoraris	99.49	4.556498	1		0	0			0	0
GCF_003841465.1	0	0.19	0.62	0.19	63.86336	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrarchaeobiusis;__Natrarchaeobius chitinivorans	99.3	4.61448	1		0	0			0	0
GCF_003841485.1	0	0.21	0.57	0.22	61.13398	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrarchaeobiusis;__Natrarchaeobius halalkaliphilus	99.35	3.511219	1		0	0			0	0
GCF_008245225.1	0	0.2	0.58	0.24	62.51998	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrarchaeobiusis;__Natrarchaeobius swarujaae	99.92	4.301488	1		0	0			0	0
GCF_000337535.1	0	0.22	0.26	61.99454	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrialba;__Natrialba aegyptia	99.42	4.618382	1		0	0			0	0
GCF_000337555.1	0	0.22	0.51	0.27	62.38896	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrialba;__Natrialba asiatica	99.11	4.404172	1		0	0			0	0
GCF_000337135.1	0	0.24	0.5	0.27	61.41757	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrialba;__Natrialba chahannaoensis	99.74	4.930274	1		0	0			0	0
GCF_000337595.1	0	0.22	0.51	0.27	61.52122	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natrialbaceae;g__Natrialba;__Natrialba taiwanensis	99.04	4.635192	1		0	0			0	0
GCF_003208585.1	0	0.24	0.6	0.16	63.66540	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronolumina;__Natribaculum breve	99.53	4.332918	1		0	0			0	0
GCF_000731985.1	0	0.22	0.53	0.25	64.55832	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas altunensis	99.57	3.774135	1		0	0			0	0
GCF_002494345.1	0	0.21	0.55	0.24	63.86658	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas ejinorensis	99.50	4.476324	1		0	0			0	0
GCF_000337175.1	0	0.21	0.53	0.26	63.72259	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas gelri	99.3	4.023662	1		0	0			0	0
GCF_013402815.2	0	0.2	0.53	0.27	60.13554	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas halophilum	99.49	4.942592	1		0	0			0	0
GCF_000337335.1	0	0.21	0.49	0.29	60.72564	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas hispanicum	98.8	4.256502	1		0	0			0	0
GCF_900111485.1	0	0.22	0.49	0.29	61.04068	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas hispanicum_A	99.11	3.96348	1		0	0			0	0
GCF_000337375.1	0	0.21	0.49	0.3	61.72938	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas limicola	99.19	3.522721	1		0	0			0	0
GCF_000690595.2	0	0.23	0.56	0.21	65.11208	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas mahii	99.57	3.794337	1		0	0			0	0
GCF_000337615.1	0	0.22	0.53	0.25	63.71963	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas pallidum	98.1	3.915614	1		0	0			0	0
GCF_002250735.2	0	0.23	0.54	0.23	63.99113	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas pellirubrum	99.36	4.3541	1		0	0			0	0
GCF_001953745.1	0	0.23	0.57	0.2	65.25405	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas saccharevirus	99.3	3.990616	1		0	0			0	0
GCF_900110845.1	0	0.23	0.58	0.19	64.07983	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas salina	99.67	4.857017	1		0	0			0	0
GCF_900110455.1	0	0.2	0.54	0.26	65.44825	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas saltfodinae	98.73	4.272165	1		0	0			0	0
GCF_004455255.1	0	0.23	0.54	0.23	63.14298	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas salinaciti	99.38	4.704329	1		0	0			0	0
GCF_005938085.1	0	0.21	0.51	0.27	61.49332	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas sp005938085	99.57	4.263024	1		0	0			0	0
GCF_019879155.1	0	0.22	0.52	0.26	61.12237	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas sp019879155	99.57	3.978458	1		0	0			0	0
GCF_024227435.1	0	0.2	0.58	0.22	63.02158	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas sp024227435	98.92	4.771126	1		0	0			0	0
GCF_024266705.1	0	0.21	0.58	0.22	60.93316	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas sp024266705	99.57	5.443524	1		0	0			0	0
GCF_000337515.1	0	0.22	0.56	0.22	65.39880	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas thermoalcaliphilum	99.8	3.652575	1		0	0			0	0
GCF_000337195.1	0	0.22	0.52	0.27	63.95689	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronomonas;__Natronomonas versiforme	99.24	4.190799	1		0	0			0	0
GCF_000337635.2	0	0.21	0.53	0.23	62.23552	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronobacteriumts;__Natronobacterium gregoryi	99.62	3.785275	1		0	0			0	0
GCF_900104065.1	0	0.24	0.49	0.25	62.87148	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronobacteriumts;__Natronobacterium tacoconense	99.57	4.009868	1		0	0			0	0
GCF_004362525.1	0	0.22	0.19	65.49409	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronobiforma;__Natronobiforma sp004362525	98.93	3.9861	1		0	0			0	0
GCF_000337675.1	0	0.28	0.51	0.21	64.36264	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronococcus;__Natronococcus amylolyticus	98.53	4.416521	1		0	0			0	0
GCF_000337695.1	0	0.26	0.53	0.19	64.41111	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronococcus;__Natronococcus jeotgali	99.92	4.496181	1		0	0			0	0
GCF_000329685.1	0	0.22	0.52	0.18	64.66365	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronococcus;__Natronococcus occultus	99.73	4.314176	1		0	0			0	0
GCF_003559915.1	0	0.29	0.51	0.2	64.78823	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronococcus;__Natronococcus sp003559915	98.73	3.941209	1		0	0			0	0
GCF_001777135.1	0	0.22	0.49	0.29	60.20160	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronolimnobius;__Natronolimnobius baerhuensis	99.92	3.914121	1		0	0			0	0
GCF_003928895.1	0	0.21	0.51	0.29	61.33523	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum albiense	99.3	4.348483	1		0	0			0	0
GCF_004799645.1	0	0.21	0.51	0.28	60.61379	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum bangense	100	4.382412	1		0	0			0	0
GCF_001971735.1	0	0.21	0.47	0.36	61.35258	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum daqingense	99.11	3.635796	1		0	0			0	0
GCF_003670115.1	0	0.21	0.53	0.26	62.87346	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum halophilum	99.35	4.865879	1		0	0			0	0
GCF_900108085.1	0	0.17	0.48	0.36	61.10585	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum sediminis	99.67	3.782543	1		0	0			0	0
GCF_003337735.1	0	0.2	0.5	0.3	61.77978	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum sulfidifaciens	98.92	3.460268	1		0	0			0	0
GCF_900156475.1	0	0.21	0.51	0.28	60.95051	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Natronorubrum;__Natronorubrum thiocyanatum	99.24	4.200319	1		0	0			0	0
GCF_006543045.1	0	0.21	0.51	0.28	62.0991	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Salinadaptatus;__Salinadaptatus halalkaliphilus	98.85	4.521581	1		0	0			0	0
GCF_000177375.1	0	0.22	0.19	64.19503	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Salinisaeta;__Salinisaeta trapezicolorata	97.8	4.533468	1		0	0			0	0
GCF_015642475.1	0	0.68	0.15	43.59505	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Tc-B-R11a;__Tc-B-R11 sp015642475	94.93	3.164622	0		0	0			0	0
GCF_017357105.2	0	0.23	0.58	0.2	63.05772	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Tc-B-R11a;__Tc-B-R11 sp017357105	99.33	4.235152	1		0	0			0	0
GCF_023973145.1	0	0.22	0.58	0.19	61.79580	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Tc-B-R11a;__Tc-B-R11 sp023973145	98.93	3.53067	1		0	0			0	0
GCF_024138145.1	0	0.22	0.58	0.2	63.1064	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Tc-B-R11a;__Tc-B-R11 sp024138145	99.2	3.854603	1		0	0			0	0
GCF_024204665.1	0	0.22	0.58	0.2	62.95790	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Tc-B-R11a;__Tc-B-R11 sp024204665	99	4.531219	1		0	0			0	0
GCF_024298845.1	0	0.2	0.53	0.27	59.49046	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Halobacteriales;f__Tc-B-R11a;__Tc-B-R11 sp024298845	99.6	4.217547	1		0	0			0	0
GCF_023638555.1	0	0.28	0.54	0.19	60.36457	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Natronoarchaeum;__Natronoarchaeum aerophilus	99.13	3.289722	1		0	0			0	0
GCF_902215575.1	0	0.23	0.57	0.22	65.15962	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Natronoarchaeum;__Natronoarchaeum philippinense	98.73	3.164179	1		0	0			0	0
GCF_024494695.1	0	0.22	0.6	0.17	66.35012	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Natronoarchaeum;__Natronoarchaeum rubrum	98.13	4.032584	1		0	0			0	0
GCF_017099485.1	0	0.22	0.53	0.19	60.7887	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Natronoarchaeum;__Natronoarchaeum sulfidigenes	99.53	3.041127	1		0	0			0	0
GCF_003621085.1	0	0.23	0.63	0.14	68.02298	d__Archaea;p__Halobacteriota;c__Halobacteria;o__PXRD1;g__PXRD1;s__PXRD1 sp003021085	92.94	3.385703	1		0	0			0	0
GCF_004785855.1	0	0.25	0.58	0.16	68.45282	d__Archaea;p__Halobacteriota;c__Halobacteria;o__QS-9-68-17;g__Halostella;s__Halostella litorea	98.73	3.752525	1		0	0			0	0
GCF_003675855.1	0	0.27	0.56	0.17	67.23465	d__Archaea;p__Halobacteriota;c__Halobacteria;o__QS-9-68-17;g__Halostella;s__Halostella salina	99.07	3.735525	1		0	0			0	0
GCF_023049835.1	0	0.23	0.59	0.18	64.93859	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Salinarchaeum;__Salinarchaeum lemnariae	96.93	3.169627	1		0	0			0	0
GCF_003403645.1	0	0.22	0.63	0.15	66.58590	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Salinarchaeum;__Salinarchaeum sp000403645	97.53	3.25526	1		0	0			0	0
GCF_019693215.1	0	0.24	0.4	0.37	47.36201	d__Archaea;p__Halobacteriota;c__Halobacteria;o__Salinarchaeaceae;g__Salinarchaeum;s__Salinarchaeum sp019693215	96.47	2.656678	0		0	0			0	0
GCF_001187075.1	0	0.19	0.65	0.16	57.77580	d__Archaea;p__Halobacteriota;c__Halobacteria;o__SKSH10;g__SKSH10;s__SKSH10 sp001187075	96.35	1.630711	0		0	0			0	0
GCF_018609935.1	0	0.02	0.16	0.84	39.50613	d__Archaea;p__Halobacteriota;c__JAHENH01;g__JAHENH01;s__JAHENH01 sp018609935	91.89	2.259503	0		0	0			0	0
GCF_000634445.1	0	0.22	0.37	0.43	54.60295	d__Archaea;p__Methanocellales;c__Methanocellales;o__Methanocellales;f__Methanocellaceae;g__Methanocella;s__Methanocella_A arvoryzae	100	3.179858	1		0	0			0	0
GCF_002667315.1	0	0.21	0.44	0.35	59.82792	d__Archaea;p__Methanocellales;c__Methanocellales;o__Methanocellales;f__Methanocellaceae;g__Methanocella;s__Methanocella_A sp002667315	99.35	3.24377	1		0	0			0	0
GCF_000251155.1	0	0.22	0.39	0.39	52.7452	d__Archaea;p__Methanocellales;c__Methanocellales;o__Methanocellales;f__Methanocellaceae;g__Methanocella;s__Methanocella conradii	100	2.37844	1		0	0			0	0
GCF_002611505.1	0	0.22	0.34	0.45	54.91988	d__Archaea;p__Methanocellales;c__Methanocellales;o__Methanocellales;f__Methanocellaceae;g__Methanocella;s__Methanocella paludicola	100	2.957635	1		0	0			0	0
GCF_021023085.1	0	0.17	0.4	0.43	46.19146	d__Archaea;p__Methanocellales;c__Methanocellales;o__Methanocellales;f__Methanocellaceae;g__PGCK01;s__PGCK01 sp021023085	99.35	3.193569	1		0	0			0	0
GCF_004212075.1	0	0.18	0.33	0.52	35.88813	d__Archaea;p__Methanopirales;c__Methanopirales;o__Methanopirales;f__Methanopiralaceae;g__Methanopirus;s__Methanopirus thermophilum	92.46	1.257141	0		0	0			0	0
GCF_004212085.1	0	0.17	0.43	0.4	43.80132	d__Archaea;p__Methanopirales;c__Methanopirales;o__Methanopirales;f__Methanopiralaceae;g__Methanoliviera;s__Methanoliviera hydrocarbonicum	90.2	1.664055	0		0	0			0	0
GCF_018645885.1	0	0.17	0.62	0.21	59.93083	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__JACTUA01;s__JACTUA01 sp015925685	99.67	1.935927	1		0	0			0	0
GCF_024170555.1	0	0.18	0.58	0.28	53.15874	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus alkaliphilus	99.02	2.087147	0		0	0			0	0
GCF_018132105.1	0	0.18	0.58	0.26	52.23332	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus chunghsingensis	99.02	2.134545	0		0	0			0	0
GCF_002496395.1	0	0.18	0.58	0.3	51.69759	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus sp002496395	98.69	2.074195	0		0	0			0	0
GCF_003838865.1	0	0.18	0.58	0.28	50.54514	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus sp003838865	97.39	1.687998	0		0	0			0	0
GCF_024170265.1	0	0.18	0.58	0.26	52.5327	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus sp003838185	100	1.957917	0		0	0			0	0
GCF_013229165.1	0	0.14	0.57	0.28	51.80348	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus sp9912u	97.39	1.932401	0		0	0			0	0
GCF_024127435.1	0	0.18	0.56	0.3	52.40495	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocalculus;s__Methanocalculus taiwanensis	99.35	2.342624	0		0	0			0	0
GCF_018883755.1	0.04	0.4	0.55	0.05	50.75233	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum fasciculiplumum	99.99	1.251241	0		0	0			0	0
GCF_000337635.1	0.02	0.44	0.49	0.05	50.02659	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum labreanum	99.54	1.804962	0		0	0			0	0
GCF_002287215.1	0	0.49	0.42	0.09	51.42847	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum parvum	98.21	1.709133	0		0	0			0	0
GCF_001940805.1	0.08	0.44	0.5	52.90058	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp001940805	91.85	1.965334	0		0	0			0	0
GCF_002498375.1	0.07	0.45	0.48	51.03151	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp002498375	96.89	1.561804	0		0	0			0	0
GCF_002506085.1	0.08	0.42	0.51	48.0801	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp002506085	97.71	1.810882	0		0	0			0	0
GCF_003159375.1	0.08	0.46	0.46	50.10588	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp003159375	93.58	1.697106	0		0	0			0	0
GCF_017387505.1	0.09	0.33	0.63	46.42593	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp017387505	95.75	1.425001	0		0	0			0	0
GCF_017399555.1	0.09	0.36	0.57	50.6767	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp017399555	96.27	2.024668	0		0	0			0	0
GCF_017408885.1	0.09	0.33	0.63	46.269	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp017408885	96.41	1.553516	0		0	0			0	0
GCF_017622255.1	0.09	0.34	0.61	51.71943	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp017622255	90.72	1.501372	0		0	0			0	0
GCF_023390245.1	0.07	0.48	0.45	52.42963	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum sp023390245	96.73	2.079429	0		0	0			0	0
GCF_004102725.1	0.17	0.57	0.26	59.97287	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum_A;s__Methanocorpusculum_A taiwanensis	99.02	2.75072	0		0	0			0	0
GCF_000304355.2	0.17	0.62	0.21	60.64004	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanocorpusculaceae;g__Methanocorpusculum;s__Methanocorpusculum;s__Methanocorpusculum labreanum	96.37	2.789774	0		0	0			0	0
GCF_019689965.1	0.17	0.62	0.22	61.86006	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus chikugoensis	99.02	2.622259	0		0	0			0	0
GCF_900095385.1	0.17	0.62	0.22	61.83677	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus chikugoensis_A	99.02	2.649157	0		0	0			0	0
GCF_901603375.1	0.16	0.61	0.23	62.94151	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus horonobensis	99.02	2.446106	0		0	0			0	0
GCF_000015825.1	0.16	0.61	0.23	62.06304	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus marisnigri	99.35	2.478101	0		0	0			0	0
GCF_002503885.1	0.16	0.62	0.22	61.57728	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus marisnigri_B	95.62	2.550543	0		0	0			0	0
GCF_001617125.1	0.16	0.61	0.24	62.32986	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sediminis	99.02	2.489717	0		0	0			0	0
GCF_003691485.1	0.16	0.61	0.23	61.44414	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp003691485	98.47	2.542944	0		0	0			0	0
GCF_002498065.1	0.16	0.61	0.22	62.35391	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp002498065	97.58	2.4687	0		0	0			0	0
GCF_002499455.1	0.16	0.61	0.22	63.32967	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp002499455	96.58	2.336968	0		0	0			0	0
GCF_002506585.1	0.16	0.63	0.22	61.96228	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp002506585	93.14	2.72109	0		0	0			0	0
GCF_002508705.1	0.16	0.58	0.26	60.27917	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp002508705	99.02	2.901776	0		0	0			0	0
GCF_002835575.1	0.16	0.6	0.23	61.51495	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp002835575	90.07	2.547219	0		0	0			0	0
GCF_002839645.1	0.17	0.59	0.24	60.82783	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp002839645	99.54	2.792193	0		0	0			0	0
GCF_015251055.1	0.17	0.62	0.19	59.46264	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp015251055	90.72	2.242624	0		0	0			0	0
GCF_016841385.1	0.17	0.61	0.22	62.6212	d__Archaea;p__Methanomicrobia;o__Methanomicrobiales;f__Methanoculleaceae;g__Methanoculleus;s__Methanoculleus sp016841385	95.85	2.168266	0		0	0	







GCA_002503985.1	0	0.25	0.49	0.15	67.13701	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp002503985	98	1.767809	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_013290045.1	0	0.39	0.53	0.08	68.3833	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp013290045	91.84	2.227652	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021791335.1	0	0.33	0.57	0.1	70.2323	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021791335	95.6	1.407422	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021801985.1	0	0.36	0.56	0.08	72.86069	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021801985	92.4	1.571138	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021816955.1	0	0.34	0.55	0.11	69.85608	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021816955	91.39	1.421469	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_023256615.1	0	0.18	0.43	0.39	37.1855	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__Thermoplasmatales;f__GCA-001896425;g__JAGDXD01;s__JAGDXD01 sp023256615	93.95	1.215608	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021817245.1	0	0.36	0.53	0.1	69.73347	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021817245	96.27	2.313694	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021817605.1	0	0.44	0.48	0.08	70.15049	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021817605	97.45	1.746815	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021819135.1	0	0.36	0.55	0.09	69.5353	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021819135	95.07	2.201446	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021821785.1	0	0.36	0.52	0.12	70.20094	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021821785	94.27	1.685664	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021826165.1	0	0.39	0.47	0.13	67.23252	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021826165	96.67	1.398163	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021828195.1	0	0.37	0.53	0.1	67.19623	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp021828195	97.07	1.62351	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022749005.1	0	0.46	0.45	0.11	67.60200	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022749005	92.67	1.785925	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022750005.1	0	0.41	0.5	0.09	67.5231	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022750005	94.67	1.518393	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022750115.1	0	0.48	0.47	0.09	69.02259	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022750115	97.2	2.11925	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022750155.1	0	0.39	0.53	0.08	68.45379	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022750155	97.88	1.127927	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022750195.1	0	0.39	0.49	0.12	68.08844	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022750195	97.87	2.448124	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022750245.1	0	0.38	0.48	0.14	69.5885	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022750245	97.07	2.036516	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022750415.1	0	0.46	0.46	0.14	68.74966	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__UBA184;f__UBA184;g__UBA184;s__UBA184 sp022750415	96.14	2.00081	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_024278375.1	0	0.19	0.48	0.33	48.05331	d__Archaea;p__Thermoplasmatota;c__UBA186;o__UBA186;f__UBA186;g__WAL001;s__WAL001 sp024278375	93.6	1.419201	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_002494765.1	0	0.27	0.42	0.31	48.177	d__Archaea;p__Thermoplasmatota;c__UBA186;o__UBA186;f__UBA186;g__UBA186;s__UBA186 sp002494765	92.53	1.815647	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_001918765.1	0	0.31	0.22	51.80435	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__40CM-2-53-6 sp001918765	91.12	1.775681	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_005884195.1	0	0.47	0.3	0.23	51.91448	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__40CM-2-53-6 sp005884195	90.51	1.924307	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_005888635.1	0	0.44	0.35	0.21	51.95131	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__40CM-2-53-6 sp005888635	95.15	2.179949	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_005885745.1	0	0.44	0.33	0.23	51.71139	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__40CM-2-53-6 sp005885745	96.73	2.195209	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021806355.1	0	0.18	0.48	0.34	40.96666	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__Thermoplasmatales;f__Thermoplasmatalaceae;g__GCA-000496135;s__GCA-000496135 sp021806355	91.36	1.751171	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021823985.1	0	0.31	0.23	51.97554	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__40CM-2-53-6 sp021823985	94.46	2.014444	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021823995.1	0	0.46	0.33	0.21	51.8883	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__40CM-2-53-6 sp021823995	92.06	2.006564	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_005835745.1	0	0.46	0.34	0.2	53.06604	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;g__40CM-2-53-6;s__BA-19;s__BA-19 sp005835745	94.86	2.390752	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396775.1	0	0.3	0.18	0.72	32.45403	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;f__DTDX01;g__DTDX01;s__DTDX01 sp018396775	97.2	1.33087	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396815.1	0	0.13	0.2	0.71	30.94106	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;f__DTDX01;g__DTDX01;s__DTDX01 sp018396815	98.13	1.485783	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396925.1	0	0.28	0.36	0.36	32.83309	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;f__DTDB01;g__DTDB01;s__DTDB01 sp018396925	96.26	1.753657	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022865625.1	0	0.43	0.43	0.13	52.49652	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;f__FEH-987;g__JALHTB01;s__JALHTB01 sp022865625	94.63	2.013659	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022867705.1	0	0.41	0.41	0.16	49.14162	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;f__JALHTB01;g__JALHTB01;s__JALHTB01 sp022867705	92.72	1.927407	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396915.1	0	0.25	0.46	0.3	45.4924	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__40CM-2-53-6;f__RBG-13-38-0;g__DTMT01;s__DTMT01 sp018396915	97.3	1.630699	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_001939865.1	0	0.38	0.27	0.35	51.069	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B24;f__B24;g__B24;s__B24 sp001939865	96.73	1.731599	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021161255.1	0	0.38	0.27	0.36	49.99173	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B24;f__B24;g__B24;s__B24 sp021161255	96.73	1.673789	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396755.1	0	0.3	0.27	0.44	41.42706	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B24;f__B24;g__DTBU01;s__DTBU01 sp018396755	98.06	1.993321	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018363035.1	0	0.22	0.22	0.29	41.03342	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B24;f__DRYS01;g__DRYS01;s__DRYS01 sp018363035	93.93	1.414552	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_025058595.1	0	0.39	0.22	0.28	44.02555	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B24;f__DRYS01;g__DRYS01;s__DRYS01 sp025058595	97.2	1.449623	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021799185.1	0	0.46	0.28	0.47	47.34483	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B24-0;g__B24-0;s__B24-0 sp021799185	96.88	1.34717	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_001593925.1	0	0.27	0.38	0.36	52.68061	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__B26-1;s__B26-1 sp001593925	90.65	1.348101	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021803655.1	0	0.19	0.58	0.23	45.1533	d__Archaea;p__Thermoplasmatota;c__Thermoplasmatota;o__Thermoplasmatales;f__Thermoplasmatalaceae;g__JAMDBT01;s__JAMDBT01 sp021803655	90.28	1.648631	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_001593935.1	0	0.37	0.35	0.28	51.91762	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__B26-1;s__B26-1 sp001593935	92.39	1.690193	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021158305.1	0	0.29	0.28	0.43	43.46714	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__B63;s__B63 sp021158305	92.52	1.634124	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396455.1	0	0.28	0.24	0.49	42.65188	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__DTE001;s__DTE001 sp018396455	95.79	1.489207	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396635.1	0	0.3	0.25	0.44	44.4524	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__DTE001;s__DTE001 sp018396635	98.13	1.451033	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396695.1	0	0.3	0.24	0.46	45.6191	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__DTE001;s__DTE001 sp018396695	97.07	1.461834	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_025059045.1	0	0.3	0.33	0.37	44.76713	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__JANXEA01;s__JANXEA01 sp025059045	98.13	1.424858	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_015329475.1	0	0.25	0.33	0.42	44.06592	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__WAQA01;s__WAQA01 sp015329475	95.19	1.634867	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_013996265.1	0	0.28	0.32	0.4	47.03311	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__BA1;g__BA1;s__BA1 sp013996265	91.59	1.931714	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_001399795.1	0	0.27	0.32	0.41	44.20231	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__B26-1;g__BA2;s__BA2 sp001399795	93.77	1.455689	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_012465005.1	0	0.23	0.23	0.58	38.15346	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__BA1;g__BR4-1;s__BR4-1 sp012465005	96.29	2.152501	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_004376295.1	0	0.39	0.33	0.28	43.22675	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__BA1;g__SOJ201;s__SOJ201 sp004376295	97.82	1.88986	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_021799185.1	0	0.58	0.58	0.29	45.408	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__Thermoplasmatales;f__Thermoplasmatalaceae;g__UBA509;s__UBA509 sp021799185	90.55	1.681583	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_020341775.1	0	0.34	0.34	0.31	45.85949	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__SOJ201;g__GCA-020341775;s__GCA-020341775 sp020341775	90.82	1.921102	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_011046225.1	0	0.25	0.61	0.14	54.45737	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__DTMM01;g__DSA001;s__DSA001 sp011046225	91.07	1.567555	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_020351305.1	0	0.31	0.4	0.29	41.58634	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__SOJ201;g__GCA-020351305;s__GCA-020351305 sp020351305	96.03	1.870377	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_020354575.1	0	0.31	0.3	0.39	41.58735	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__SOJ201;g__GCA-020354575;s__GCA-020354575 sp020354575	95.33	1.838111	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_019865555.1	0	0.26	0.23	0.51	45.55340	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__SOJ201;g__JABFQD01;s__JABFQD01 sp019865555	98.13	1.529616	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_023131555.1	0	0.3	0.41	0.3	47.02323	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__SOJ201;g__JAGLZJ01;s__JAGLZJ01 sp023131555	90.29	1.122796	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_023131255.1	0	0.31	0.27	0.41	42.58418	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__SOJ201;g__JAGLZN01;s__JAGLZN01 sp023131255	92.06	1.916045	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022779555.1	0	0.34	0.32	0.32	47.44235	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__20-14-0-80-47-9;s__20-14-0-80-47-9 sp022779555	90.31	1.429808	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022865455.1	0	0.36	0.36	0.29	47.22136	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__20-14-0-80-47-9;s__20-14-0-80-47-9 sp022865455	95.33	2.014782	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018475625.1	0	0.31	0.31	0.46	47.71298	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__ACD2MB-2;s__ACD2MB-2 sp018475625	90.07	2.477615	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_022865885.1	0	0.35	0.38	0.28	46.02887	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__DRUK01;s__DRUK01 sp022865885	90.07	2.840721	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018306705.1	0	0.27	0.24	0.48	43.23232	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__DRVP01;s__DRVP01 sp018306705	90.07	1.726761	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_025059195.1	0	0.27	0.26	0.47	45.8098	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__DRVP01;s__DRVP01 sp025059195	96.26	1.370041	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_019845455.1	0	0.25	0.25	0.5	41.62710	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__DSLH01;s__DSLH01 sp019845455	98.13	1.514441	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_023512225.1	0	0.24	0.29	0.47	42.24664	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__DSLH01;s__DSLH01 sp023512225	96.26	1.980323	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_019685555.1	0	0.27	0.23	0.51	43.63297	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__JABFQN01;s__JABFQN01 sp019685555	98.6	1.463178	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_013388965.1	0	0.29	0.51	0.21	40.72989	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__JACAEB01;s__JACAEB01 sp013388965	90.65	1.501575	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_018396615.1	0	0.35	0.26	0.37	45.08577	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__JAGTOT01;s__JAGTOT01 sp018396615	90.2	1.643261	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
GCA_025057795.1	0	0.27	0.24	0.44	45.36302	d__Archaea;p__Thermoprotei;o__Bathyarchaeia;f__B26-1;f__UBA233;g__JANXEP01;s__JANXEP01 sp025057795	98.13	1.90205	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0



GCA_019704295.1	0	0.24	0.32	0.43	39.56805	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__HS-7;s__HS-7 sp019704295	98.21	2.151177	1	0	0			0	0
GCF_000204925.1	0	0.21	0.39	0.4	41.99456	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Metallosphaera;s__Metallosphaera cuprina	100	1.840348	1	0	0			0	0
GCF_003201675.2	0	0.22	0.42	0.36	43.73313	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Metallosphaera;s__Metallosphaera hakonensis	99.4	2.544115	1	0	0			0	0
GCA_021854415.1	0	0.24	0.44	0.32	47.19384	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Metallosphaera;s__Metallosphaera javensis	99.4	2.464819	1	0	0			0	0
GCA_021800855.1	0	0.45	0.13	60.74208	d__Archaea;p__Thermoproteota;c__Nitrososphaeria;o__Nitrososphaerales;f__UBA183;g__UBA183;s__UBA183 sp021800855	92.07	1.446049	0	0	0			0	0	
GCF_000016855.1	0	0.26	0.4	0.33	46.22533	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Metallosphaera;s__Metallosphaera sedula	100	2.191517	1	0	0			0	0
GCF_013343295.1	0	0.22	0.42	0.36	44.79973	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Metallosphaera;s__Metallosphaera tengchongensis	99.4	2.176897	1	0	0			0	0
GCF_000243315.1	0	0.47	0.3	47.74426	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Metallosphaera;s__Metallosphaera yellowstonensis	100	2.817452	1	0	0			0	0	
GCF_002686315.1	0	0.17	0.26	0.56	32.90411	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Saccharolobus;s__Saccharolobus caldissimus	100	3.075795	1	0	0			0	0
GCF_000022485.1	0	0.21	0.3	0.5	35.3054	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Saccharolobus;s__Saccharolobus islandicus	99.4	2.85441	1	0	0			0	0
GCF_019175345.1	0	0.2	0.3	0.5	35.36243	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Saccharolobus;s__Saccharolobus shibatae	99.4	2.916875	1	0	0			0	0
GCF_900079115.1	0	0.21	0.29	0.51	35.83502	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Saccharolobus;s__Saccharolobus solfataricus	100	3.034024	1	0	0			0	0
GCF_011719125.1	0	0.19	0.3	0.52	34.77225	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Saccharolobus;s__Saccharolobus sp011719125	99.4	2.688317	1	0	0			0	0
GCF_009601705.1	0	0.19	0.29	0.51	34.7413	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Saccharolobus;s__Saccharolobus sp009601705	100	2.543529	1	0	0			0	0
GCF_009729035.1	0	0.18	0.35	0.47	37.61344	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sygolobus;s__Sygolobus azoricus	100	1.987069	1	0	0			0	0
GCF_019704315.1	0	0.2	0.33	0.47	40.14356	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sygolobus;s__Sygolobus caldivivus	99.4	2.35841	1	0	0			0	0
GCF_003967175.1	0	0.26	0.49	0.25	51.14502	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sulfodicoccus;s__Sulfodicoccus acidiphilus	97.62	2.353189	1	0	0			0	0
GCA_018757195.1	0	0.21	0.45	0.33	47.71133	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sulfodicoccus sp017757195	96.63	1.781932	1	0	0			0	0
GCF_000012285.1	0	0.18	0.34	0.48	36.70759	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sulfolobus;s__Sulfolobus acidocaldarius	99.4	2.225959	1	0	0			0	0
GCA_009508355.1	0	0.18	0.33	0.49	36.30204	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sulfolobus;s__Sulfolobus acidocaldarius_A	99.4	2.06192	1	0	0			0	0
GCF_001316045.1	0	0.24	0.32	0.45	38.61303	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sulfuracidifex;s__Sulfuracidifex metallicus	93.21	2.214633	1	0	0			0	0
GCF_008326455.1	0	0.21	0.41	0.38	42.99097	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfolobaceae;g__Sulfuracidifex;s__Sulfuracidifex tepidarius	99.4	2.560765	1	0	0			0	0
GCF_003729055.1	0	0.18	0.28	0.54	32.74511	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfurisphaera;g__Sulfurisphaera chwakunensis	99.4	2.803915	1	0	0			0	0
GCA_012222305.1	0	0.16	0.28	0.56	32.64372	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfurisphaera;g__Sulfurisphaera sp012222305	99.4	2.789526	1	0	0			0	0
GCF_000011205.1	0	0.18	0.28	0.54	32.76572	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__Sulfurisphaera;g__Sulfurisphaera tokodaii	100	2.694756	1	0	0			0	0
GCA_015521735.1	0	0.34	0.19	0.47	38.62812	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__WANQ01;g__WANQ01;s__WANQ01 sp015521735	98.21	2.033788	1	0	0			0	0
GCA_015520365.1	0	0.46	0.3	0.21	58.36353	d__Archaea;p__Thermoproteota;c__Thermoprotei_Ao_Sulfolobales;f__WAZQ01;g__WAZQ01;s__WAZQ01 sp015520365	98.1	1.730613	0	0	0			0	0
GCA_017857595.1	0	0.15	0.23	0.62	30.00675	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Geoarchaeales;f__Geoarchaeaceae;g__AAA261-N23;s__AAA261-N23 sp017857595	93.38	1.472322	1	0	0			0	0
GCA_021324265.1	0	0.23	0.31	0.46	36.62444	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Geoarchaeales;f__Geoarchaeaceae;g__DSFC01;s__DSFC01 sp021324265	96.32	1.449046	0	0	0			0	0
GCF_011628645.1	0	0.29	0.33	0.38	47.65391	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__JAGDGK01;f__JAGDGK01;g__JAGDGK01;s__JAGDGK01 sp011628645	99.26	2.184699	1	0	0			0	0
GCA_003650925.1	0	0.43	0.36	0.24	44.50111	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__OMSL011;f__OMSL011;g__B12-G16;s__B12-G16 sp003650925	99.26	2.143158	1	0	0			0	0
GCA_003649445.1	0	0.31	0.22	0.47	38.60492	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__B15-G9;g__B15-G9;s__B15-G9 sp003649445	97.79	3.543876	1	0	0			0	0
GCA_003650785.1	0	0.39	0.24	0.37	39.15385	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__B20-G17;g__B20-G17;s__B20-G17 sp003650785	91.18	1.448026	1	0	0			0	0
GCA_003650675.1	0	0.27	0.28	0.45	42.12482	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__B67-G16;g__B67-G16;s__B67-G16 sp003650675	97.79	2.565063	1	0	0			0	0
GCA_021161825.1	0	0.29	0.2	0.51	38.13123	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__B69-G16;g__B69-G16;s__B69-G16 sp021161825	93.38	1.667877	1	0	0			0	0
GCF_014876775.1	0	0.46	0.28	0.26	53.86131	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__Infimifilum;s__Infimifilum lucidum	98.53	1.625346	1	0	0			0	0
GCA_002855745.1	0	0.36	0.34	0.27	56.70198	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__Infimifilum;s__Infimifilum sp002855745	99.26	1.851421	1	0	0			0	0
GCF_000993805.1	0	0.33	0.29	0.38	47.94012	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__Infimifilum;s__Infimifilum uzonense	98.53	1.611988	1	0	0			0	0
GCF_001163245.1	0	0.22	0.2	0.57	32.93762	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__JAGOB01;s__JAGOB01 sp021163245	94.85	1.947278	1	0	0			0	0
GCA_023269735.1	0	0.43	0.14	0.42	67.77219	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__JANXEW01;s__JANXEW01 sp023269735	97.79	1.502755	1	0	0			0	0
GCF_025257695.1	0	0.31	0.28	0.41	47.37968	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__JAXVEW01;s__JAXVEW01 sp025257695	91.18	1.807962	1	0	0			0	0
GCF_000446015.1	0	0.38	0.22	0.4	46.50626	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__Thermofilum;s__Thermofilum B adornatum	99.26	1.750259	1	0	0			0	0
GCF_000015225.1	0	0.45	0.28	0.27	57.64614	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__Thermofilum;s__Thermofilum B pendens	98.53	1.813393	1	0	0			0	0
GCA_008232965.1	0	0.34	0.34	0.32	49.86935	d__Archaea;p__Thermoproteota;c__Thermoplasmata;f__Thermoflexales;g__Thermofilum;s__Thermofilum B sp008232965	94.49	1.958423	1	0	0			0	0
GCA_003649025.1	0	0.43	0.27	0.3	43.24523	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__B15-G16;g__B15-G16;s__B15-G16 sp003649025	98.53	2.066741	1	0	0			0	0
GCF_000016355.1	0	0.19	0.28	0.53	43.09584	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Caldivirga;s__Caldivirga maquilingensis	99.26	2.077567	1	0	0			0	0
GCF_001663375.1	0	0.26	0.29	0.45	48.46561	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Caldivirga;s__Caldivirga sp001663375	97.06	2.260471	1	0	0			0	0
GCA_002556515.1	0	0.2	0.26	0.54	42.30368	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Caldivirga;s__Caldivirga sp002556515	98.9	1.855853	1	0	0			0	0
GCA_023256255.1	0	0.24	0.26	0.51	42.8483	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Caldivirga;s__Caldivirga sp023256255	99.26	2.067412	1	0	0			0	0
GCA_013153375.1	0	0.37	0.32	0.32	43.75312	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__JAADER01;s__JAADER01 sp013153375	92.65	1.396224	0	0	0			0	0
GCA_013153895.1	0	0.3	0.3	0.4	38.18422	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__JAADER01;s__JAADER01 sp013153895	92.26	1.756476	1	0	0			0	0
GCA_001516585.1	0	0.22	0.37	0.41	46.82643	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Thermocladium;s__Thermocladium sp001516585	97.43	1.87695	1	0	0			0	0
GCF_001746385.1	0	0.19	0.37	0.44	49.07525	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta B thermophila	100	2.022504	1	0	0			0	0
GCF_001148385.1	0	0.21	0.33	0.46	45.42771	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta distributa	99.26	2.374137	1	0	0			0	0
GCF_001516055.1	0	0.22	0.33	0.46	45.74899	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta distributa_B	93.14	2.076046	1	0	0			0	0
GCF_000446015.1	0	0.38	0.22	0.4	46.50626	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta distributa_D	94.24	1.427541	0	0	0			0	0
GCF_000015225.1	0	0.21	0.29	0.49	42.367	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta moutnovskia	98.53	2.298985	0	0	0			0	0
GCF_014646555.1	0	0.34	0.32	0.32	45.12965	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta souniana	99.26	2.424395	0	0	0			0	0
GCF_001316245.1	0	0.24	0.35	0.42	46.72659	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta sp001316245	93.75	2.443876	1	0	0			0	0
GCF_001316285.1	0	0.21	0.33	0.44	45.27505	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta sp001316285	91.31	2.240042	1	0	0			0	0
GCA_002496475.1	0	0.26	0.31	0.43	44.56936	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta sp002496475	91.18	1.60163	1	0	0			0	0
GCA_022814875.1	0	0.26	0.31	0.43	48.78456	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermocladiaceae;g__Vulcanisaeta;s__Vulcanisaeta sp022814875	91.18	1.29862	1	0	0			0	0
GCF_000007225.1	0	0.3	0.27	0.44	51.36252	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum aerophilum	100	2.322243	1	0	0			0	0
GCF_000016385.1	0	0.38	0.29	0.32	55.05088	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum arsenaticum	100	2.121576	1	0	0			0	0
GCF_000015865.1	0	0.38	0.29	0.32	57.15083	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum calidifontis	100	2.030313	1	0	0			0	0
GCF_000234805.1	0	0.4	0.31	0.29	56.96681	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum ferrireducens	100	2.467972	1	0	0			0	0
GCF_000015255.1	0	0.34	0.28	0.38	49.55905	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum islandicum	100	1.626402	1	0	0			0	0
GCF_000019805.1	0	0.43	0.31	0.26	59.91062	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum neutrophilum	100	1.769823	1	0	0			0	0
GCF_000247545.1	0	0.38	0.29	0.33	55.051	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum oguniense	100	2.45292	1	0	0			0	0
GCA_001189275.1	0	0.35	0.33	0.32	58.30844	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum sp001189275	100	1.993257	1	0	0			0	0
GCA_020833025.1	0	0.42	0.41	0.17	62.63341	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Pyrobaculum;s__Pyrobaculum sp020833025	96.16	1.557389	1	0	0			0	0
GCF_000860885.1	0	0.38	0.28	0.34	57.95114	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Thermoproteus;s__Thermoproteus sp000860885	99.26	1.691324	1	0	0			0	0
GCF_000253055.1	0	0.34	0.37	0.29	55.12626	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Thermoproteus;s__Thermoproteus tenax	100	1.841542	1	0	0			0	0
GCF_001193375.1	0	0.41	0.35	0.24	59.85208	d__Archaea;p__Thermoproteota;c__Thermoprotei;o__Thermoproteales;f__Thermoproteaceae;g__Thermoproteus;s__Thermoproteus uzonensis	100	1.936063	1	0	0			0	0
GCA_014189685.1	0	0.17	0.21	0.62	37.91406	d__Archaea;p__Undinarchaeota;c__Undinarchaeota;o__Naiadarchaeales;f__Naiadarchaeaceae;g__Naiadarchaeum;s__Naiadarchaeum limnaeum	90.65	0.993883	1	0	0			0	0
GCF_000007345.1	1	0.74	0.46	0.48	42.66269	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina acetivorans	99.84	4.7	2	0	0			0	0
GCF_000970225.1	1	0.93	0.37	0.58	39.19433	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina barkeri	99.84	4.574907	2	0	0			0	0
GCF_000970305.1	1	0.94	0.37	0.58	39.08061	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina barkeri_A	99.78	4.582045	2	0	0			0	0
GCF_000969965.1	1	0.94	0.39	0.56	39.24956	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina barkeri_B	99.84	4.907186	2	0	0			0	0
GCF_000970285.1	1	0.94	0.43	0.53	41.31105	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina horonobensis	100	5.018607	2	0	0			0	0
GCF_000970285.1	1	0.93	0.45	0.5	42.94041	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina siciliae	99.84	5.017354	2	0	0			0	0
GCF_000969965.1	1	0.94	0.44	0.5	41.69249	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina sp000969965	99.84	4.137337	2	0	0			0	0
GCA_001714685.2	1	0.93	0.41	0.52	40.10305	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina sp001714685	99.84	4.231043	2	0	0			0	0
GCF_002804225.1	1	0.93	0.42	0.54	41.87192	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina sp002804225	99.84	4.596082	2	0	0			0	0
GCA_003399215.1	1	0.93	0.39	0.56	39.77191	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina sp003399215	99.84	4.212543	2	0	0			0	0
GCF_002287235.1	1	0.93	0.38	0.55	38.74885	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina spelaei	99.84	5.08888	2	0	0			0	0
GCF_003969905.1	1	0.93	0.39	0.56	39.71283	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__Methanosarcinaceae;g__Methanosarcina;s__Methanosarcina vacuolata	99.84	4.563869	2	0	0			0	0
GCF_000970045.1	1	0.94	0.51	0.45	45.93023	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__MTP4;s__MTP4 sp000970045	99.84	4.211401	2	0	0			0	0
GCA_016841265.1	1	0.93	0.52	0.45	46.0019	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__MTP4;s__MTP4 sp016841265	98.04	3.653553	2	0	0			0	0
GCA_013329415.1	1	0.94	0.51	0.44	46.79442	d__Archaea;p__Euryarchaeota;c__Methanosarcinia;o__Methanosarcinales;f__MTP4;s__MTP4 sp013310u	95.78	3.852524	2	0	0			0	0
GCA_025059545.1	0	0.19	0.45	0.36	40.19441	d__Archaea;p__Euryarchaeota;c__Archaeoglobi;o__Archaeoglobales;f__Archaeoglobaceae;g__WYZ-LMO2;s__WYZ-LMO2 sp025059545	92.96	1.490003	1	0	0			0	0
GCF_900156455.1	0	0.24	0.42	0.34	56.99158	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Haladaptatus;s__Haladaptatus litoreus	100	4.671103	2	0	0			0	0
GCF_020700235.1	0	0.25	0.43	0.33	56.05389	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Haladaptatus;s__Haladaptatus paucihalophilus	99.5	5.031324	2	0	0			0	0
GCF_000376445.1	0	0.22	0.51	0.26	61.76638	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Haladaptatus;s__Haladaptatus pallidirubidus	99.08	4.31754	2	0	0			0	0
GCF_000614375.1	0	0.24	0.52	0.24	62.12104	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Haladaptatus;s__Haladaptatus sp000614375	98.67	5.035238	2	0	0			0	0
GCF_020618475.1	0	0.25	0.48	0.27	57.89464	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Haladaptatus;s__Haladaptatus sp020618475	99.5	5.0	2	0	0			0	0
GCF_004765795.1	0	0.27	0.58	0.16	66.91856	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halorubrum;s__Halorubrum marinum	99.93	3.783529	2	0	0			0	0
GCF_004765785.1	0	0.28	0.49	0.22	64.17554	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halorubrum;s__Halorubrum ruber	99.93	4.318307	2	0	0			0	0
GCF_005239435.1	0	0.27	0.53	0.19	63.28816	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halorussus;s__Halorussus sp005239435	99.5	5.154658	2	0	0			0	0
GCF_010747475.1	0	0.25	0.56	0.19	64.95204	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halorussus;s__Halorussus sp010747475	97.72	4.408935	2	0	0			0	0
GCF_023238445.1	0	0.28	0.55	0.18	65.87766	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halorussus;s__Halorussus sp023238445	99.15	3.668365	2	0	0			0	0
GCF_024816735.1	0	0.26	0.55	0.18	64.74921	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halorussus;s__Halorussus sp024816735	99.5	4.739434	2	0	0			0	0
GCA_025041175.1	0	0.22	0.58	0.2	59.48487	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halocatenus;s__Halocatena sp025041175	98.75	5.099388	2	0	0			0	0
GCF_009730285.1	0	0.19	0.7	0.11	66.79962	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halomarina;s__Halomarina oriensis	98.53	4.060107	2	0	0			0	0
GCF_023074835.1	0	0.22	0.67	0.11	66.62455	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halomarina;s__Halomarina salina	99.08	4.461942	2	0	0			0	0
GCF_020405185.1	0	0.27	0.63	0.11	68.95351	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Haloferacaceae;g__Halomicrobium;s__Halomicrobium salinisoli	99.13	3.984467	2	0	0			0	0
GCF_020217425.1	0	0.22	0.62	0.12	67.31347	d__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__

Table S2.8. Distribution of the archaeal release factor (aRF1), the bacterial release factors (prfA & prfB), and all three domains of the eukaryotic release factors (eRF1_d1, eRF1_d2, eRF1_d3). Genomes were designated as Pyl+ or Pyl- was determined using the definitions described in the methods and is represented as a 0 for those Pyl- genomes and 1 for those Pyl+ genomes. Genome size was included from GTDB r214.0 metadata.

Readthrough to Truncation Ratio
(Pyl supply/Pyl demand)MeOH/(Pyl supply/Pyl demand)TMA

Rep	Readthrough:Truncation TMA	Readthrough:Truncation MeOH	RT:T Ratios MeOH/TMA
Rep 1	0.006	0.013	2.00
Rep 2	0.006	0.011	1.77
Rep 3	0.006	0.010	1.86
		average	1.88

Supply Ratio*Demand Ratio>1 (for MeOH v. TMA)
(Pyl supplyMeOH/Pyl supplyTMA)*(Pyl demandTMA/Pyl demandMeOH)>1

Rep	Supply Ratio	Demand Ratio	>1 ?
Rep 1	0.753	2.652	2.00
Rep 2	0.450	3.926	1.77
Rep 3	0.578	3.211	1.86
		average	1.87

Table S2.10. Fold change ratios and untransformed values for Pyl supply/Pyl demand, or the ratio of extension to truncation on trimethylamine and methanol. Values were calculated from FPKM data generated in our RNA-Seq study, as the [max(pylBCD)]/[ΣUAG-transcripts]. Under the model presented in the text, we can rearrange the equation such that the Supply/Demand Ratios between the two substrates can be represented by the following inequality: (Pyl supply MeOH/Pyl supply TMA)*(Pyl demand TMA/Pyl demand MeOH)>1. These calculations are shown in the second table. Since the values shown in the second table come from a rearrangement of the equations used in the first, the final column values are equivalent. All FPKM values are in Table S8; please note that those are log2(FPKM) values, here we use untransformed FPKM.

Gene	Accession	Description
atwA	TIGR03269.1	methyl co-enzyme M redcutase system, component A2
mcrA	TIGR03256.1	methyl co-enzyme m reductase, subunit alpha
mtmB	PF05369.16	Monomethylamine methyltransferase MtmB
mtbB	TIGR02368.1	[dimethylamine--corrinoid protein] Co-methyltransferase
mttB	TIGR02369.1	[trimethylamine--corrinoid protein] Co-methyltransferase
pylB	TIGR03910.1	methyl-ornithine synthase
pylC	TIGR03909.1	3-methylornithine L-lysine ligase
pylD	TIGR03911.1	3-methylornithyl-N6-L-lysine dehydrogenase
pylS	NF007083.1	pyrrolysine--tRNA(Pyl) ligase
pylSn	TIGR03912.1	pyrrolysine--tRNA(Pyl) ligase, N-terminal region or small subunit
pylSc	TIGR02367.1	pyrrolysine--tRNA(Pyl) ligase, C-terminal region or large subunit
aRF-1	TIGR03676.1	peptide chain release factor aRF-1
eRF1_1	PF03463.20	eRF1 domain 1
eRF1_2	PF03464.20	eRF1 domain 2
eRF1_3	PF03465.20	eRF1 domain 3
prfA	TIGR00019.1	peptide chain release factor 1
prfB	TIGR00020.2	peptide chain release factor 2
rnfA	NF041835.1	Rnf electron transport complex subunit RnfA

Table S2.10. Table of all HMM accessions used in the generation of presence/absence information in the duration of this study.

Name	Primer Sequence	Description
KS142	GAAGTTTAAACCTGCAGG**GAATTACACGATCACTAATTTT**	forward primer to amplify *mtaBC1* promoter with 5' overhang to pDN201 *AscI*
KS143	TCAGGTCATCATCAGACAAT**ACATGTGCTTACAGCATAATTAG**	reverse primer to amplify *mtaBC1* promoter with 3' overhang contianing sgRNA pylB (N-term)
KS144	ATTGTCTGATGATGACCTGA**GTTTTAGAGCTAGAAATAGC**	forward primer to amplify cas9 scaffold+linker from pDN241 with 5' overhang to pylB sgRNA (N-term)
KS145	TGGAAATTGCGCAGGGGATT**TTCGTTTTCTCTTTTTAGGTG**	reverse primer to amplify cas9 scaffold+linker from pDN241 with 3' overhang to pylB sgRNA (C-term)
KS146	AATCCCCTGCGCAATTTCCA**GTTTTAGAGCTAGAAATAGC**	foward primer to amplify cas9 scaffold + *mtaBC1* terminator from pDN241 with 5' overhang to pylD sgRNA (C-term)
KS147	AGCGGCCGCGATCGCCGG**TACATGAGGGCTGAAAAGCCG**	reverse primer to amplify cas9 scaffold + *mtaBC1* terminator from pDN241 with 3' overhang to pDN201 *AscI*
KS148	GCCTTTTTTTTTCGAAGTT**TGCTCTCCCGGAGAAAAAAAGAC**	forward primer to amplify upstream region for pyl HR repair template with 5' overhang to pDN201 *PmeI*
KS149	CCGTACTTTTCTTGAAGCT**TGAAAGCCTTCAATTATTTTCTCTCCG**	reverse primer to amplify upstream region for pyl HR repair template with 3' overhang to downstream
KS150	GAAAATAATTGAAGGCTTTCA**AGCTTCAAGAAAAGTACGGAGTG**	forward primer to amplify downstream region for pyl HR repair template with 5' overhang to upstream
KS151	GTAATTCCCTGCAGGTTTTGTT**TGTCCTTTTTCCAAAATGA**	reverse primer to amplify downstream region for pyl HR repair template with 3' overhang to pDN201 *PmeI*
KS152	AATAAATTAAGGAGGAAATTCA**TTGATCAAAAAAATGGCAACCGA**	forward primer to amplify pyl for complementation with 5' overhang to pJK029A *NdeI/HindIII*
KS153	CATTATACGAAGTTATCAAGA**TTACAGGATAGAATACAGCATGGA**	reverse primer to amplify pyl for complementation with 3' overhang to pJK029A *NdeI/HindIII*
KS156	GGAATCTAACCCGGCTGAAC**ACATGTGCTTACAGC**	reverse primer to amplify mtaBC1 promoter with 3' overhang contianing sgRNA **pylT** (N-term)
KS157	GTTCAGCCGGGTTAGATTCC**GTTTTAGAGCTAGAAATAG**	forward primer to amplify cas9 scaffold+linker from pDN241 with 5' overhang to **pylT** sgRNA (N-term)
KS158	TAAAACGAAACCGGCTCCTATCCAGGTTCGTT**TTCTCTTTTTAGGTG**	reverse primer to amplify cas9 scaffold+linker from pDN241 with 3' overhang to **pylT** sgRNA (N-term)
KS159	CGAACCTGGATAGGAGCCGGTTTC**GTTTTAGAGCTAGAAATAG**	forward primer to amplify cas9 scaffold+linker from pDN241 with 5' overhang to **pylS** sgRNA (N-term) -- use with KS142
KS160	GCCTTTTTTTTTCGAAGTTT**GGTTTCGAATGGCTCTCTTCC**	forward primer to amplify HR *upstream* for **pylTS KO plasmid** with 5' extension to PmeI cut
KS161	GCGTTCAAG**GGATTTAGAGTCCATTCGATCT**	reverse primer to amplify HR *upstream* for **pylTS KO** with 3' extension to HR downstream
KS162	TCTAAATCC**CTTGAACGCCTGCTGAAAGT**	forward primer to amplify HR *downstream* for **pylTS KO** with 5' extension to HR upstream
KS163	GTAATTCCCTGCAGGTTT**CAGGGACTTGATTGTTGACTCA**	reverse primer to amplify HR *downstream* for **pylTS KO** with 3' extension to PmeI cut
KS170	AATAAATTAAGGAGGAAATTCA**TTGATCAAAAAAATGGCAACCGA**	forward primer to amplify *pylBCD* for overexpression, 5' extension to pJK27A NdeI
KS171	CATTATACGAAGTTATCAAGA**TTACAGGATAGAATACAGCATGGA**	reverse primer to amplify *pylBCD* for overexpression, 3' extension to pJK27A HindIII
KS172	AGATCGAATGGACTCTAAATCC**AGCTTCAAGAAAAGTACGGAGTG**	forward primer to amplify *pylBCD* for overexpression with 5' overhang to the *pylTS* upstream template
KS173	CACTCCGTACTTTTCTTGAAGCT**GGATTTAGAGTCCATTCGATCT**	reverse primer to amplify *pylTS* for overexpression with 3' overhang to the *pylBCD* downstream template

KS174	ACAATCAAGTCCCTGAGGG	sequencing primer for *pylBCD* complement in pJK27A; binds in *pylB*
KS175	AGTCATAGGAGACGGGAC	sequencing primer for *pylBCD* complement in pJK27A; binds in *pylC*
KS176	AACCAGCCCTGCACA	sequencing primer for *pylBCD* complement in pJK27A; binds in *pylD*
KS184	GGTCCCAGAGTTCGGTAT	forward primer for REAL diagnostic of *pylBCD* -- 4.6 kb if WT; 1.8kb if KO
KS185	CCTGAAGCGGATCTATGC	reverse primer for REAL diagnostic of *pylBCD* -- 4.6 kb if WT; 1.8kb if KO
KS186	TGAGGCAGGAACGTCATA	forward primer for REAL diagnostic of *pylTS* -- 3.6kb if WT; 2.1kb if KO
KS187	GGGATTTGCCAGTCAACT	reverse primer for REAL diagnostic of *pylTS* -- 3.6kb if WT; 2.1kb if KO
KS188	CTG CAA TAC ACT TTC TTG TCC	Fw primer to amplify repA gene in pC2A (Primer designed and used by Nayak_2016_PNAS, for detail see, Fig. S2 (B))
KS189	TCA TCC ACT TTG AAG GGA GAA G	Rw primer to amplify repA gene in pC2A (Primer designed and used by Nayak_2016_PNAS, for detail see, Fig. S2 (B))
KS220	CTTCGGTCGGAGCCAT	Fw primer to sequence *hpt*
KS221	GCACGACCCCATGAATG	Rv primer to sequence *hpt*
KS263	AGCCACGCAGGAATAGTA	F primer to confirm ΔmsrF/ΔrdmS in WWM380 and WWM977
KS264	TGAGGGTCAGTGTGTCTC	R primer to confirm ΔmsrF/ΔrdmS in WWM380 and WWM977
KS272	AATAAATTAAGGAGGAAATTCA**ATGGCAAAAAATAATGCA**	F primer to amplify mttB1 with overhang to pJK27A
KS273	CGGGATCTTTGCATCAGActt**GGTGCCTGCCACGAAT**	R primer to amplify mttB1 with overhang to C terminus (and point mutation O>K)
KS274	ATTCGTGGCAGGCACCaag**TCTGATGCAAAGATCCCG**	F primer to amplify mttB1 with overhang to N temrinus (and point mutation O>K)
KS275	CATTATACGAAGTTATCAAGAT**TACATGCCTCTGAAG**	R primer to amplify mttB1 with overhang to pJK27A
KS276	CGGGATCTTTGCATCAGAtgc**GGTGCCTGCCACGAAT**	R primer to amplify mttB1 with overhang to N terminus (and point mutation O>A)
KS277	ATTCGTGGCAGGCACCgca**TCTGATGCAAAGATCCCG**	F primer to amplify mttB1 with overhang to C terminus (and point mutation O>A)
KS284	AAAAGTGTTGTAAAGCGCCTCA	Sequencing primer for pKS108 (ANME-3 pylBCD)
KS285	ATTGGTGGGGGCTAATGTGA	Sequencing primer for pKS106 (B. weybense pylBCD)
KS286	TTTGTCGAAGGACTTGCGGT	Sequencing primer for pKS106 (B. weybense pylBCD)
KS289	CATTATACGAAGTTATCAAGATTAGAGTAAGA**CTGCTCTTACCTTGCTGAC**	R primer to add mttC1 to mttB1O334K construct
KS290	CTCTAAATCCGTTCAGCCGAGTTGAATTCCCGGGGTTTCC**ACCATGTTTCTGAATCCCGG**	F primer to add pylT1S with 3 bp deletion part 1
KS291	TCAGAAATCAGATCATGTTGATCGAATGGA**CTCTAAATCCGTTCAGCCGA**	F primer to add pylT1S with 3 bp deletion part 2

KS292	AATAAATTAAGGAGGAAATTCAGAAATCAGA**TCATGTTGATCGAATGGACT**	F primer to add pylT1S with 3 bp deletion part 3 -- with overhang to pJK29A
KS293	AGTCGGGTTAATTTCCCTTGGTTTCCA**CCATGTTTCTGAATCCCGG**	F primer to add pylT2S with 3 bp deletion part 1
KS294	TCATATTGATCGAATGGACTCTAAATCTGTTT**AGTCGGGTTAATTTCCCTTG**	F primer to add pylT2S with 3 bp deletion part 2
KS295	AATAAATTAAGGAGGAAATTCAGACATCAGA**TCATATTGATCGAATGGACT**	F primer to add pylT2S with 3 bp deletion part 3 -- with overhang to pJK29A
KS296	CATTATACGAAGTTATCAAGA**TCAAAGGTTAGTGCTGATCC**	R primer to add pylS from ANME-3 to the pylT deletions
KS297	ATAGGAGTGATTCCTTCAAATGGAAAGT**TTTTTCAGCTCCTTTGAATC**	F primer to amplify pylBCD (Bw) for insertion with pylTS in pJK29A
KS298	CATTATACGAAGTTATCAAGAT**TAAAATGTGGCATCTAAAGC**	R primer to amplify pylBCD (Bw) for insertion with pylTS in pJK29A
KS299	AATAAATTAAGGAGGAAATTCA**GGAGGCCGGTCGGAAAG**	F primer to amplify pylTS (Bw) for insertion with pylBCD in pJK29A
KS300	TTGAAGGAATCACTCCTATCT**AGATATCTAATCGCCATCCG**	R primer to amplify pylTS (Bw) for insertion with pylBCD in pJK29A
KS301	AGTGGGAATTGAACGACTG	Sequencing primer for pKS120 pylTSBCD Bw in pJK29A
KS302	AATAAATTAAGGAGGAAATTCAA**TGGCAGAATCTCTATTTACA**	F primer to amplify *rnfA* for insertion in pJK29A
KS303	CGTCCTTGTAGTCCCCGCCACC**CTCAAGCGGAATCACCCC**	R primer to amplify *rnfA* for insertion in pJK29A (first 1x flag addition)
KS304	TTAGATGTCG**TCGTCCTTGTAGTCCCCGC**	R primer to amplify *rnfA* for insertion in pJK29A (second 1x flag addition)
KS305	CATTATACGAAGTTATCAAGA**TTAGATGTCGTCGTCCTTGT**	R primer to amplify *rnfA* for insertion in pJK29A with overlap to pJK29A and TAG>TAA stop mutation
KS306	TATAGAGTTTATGAGCACACGC**CTCAAGCGGAATCACCCC**	R primer to amplify *rnfA* part 1 with TAG>GCG (ala) internal to long form
KS307	GGTGATTCCGCTTGAGGCGT**GTGCTCATAAACTCTATAGC**	F primer to amplify *rnfA* part 2 with with TAG>GCG (ala) internal to long form
KS308	GTCCTTGTAGTCCCCGCCACC**AAGACCTTGGAAGCAATGA**	R primer to add 1xflag to long form *rnfA*
KS309	CGTCCTTGTAGTCCCCGCCACC**CTCAAGCGGAATCACCCC**	R primer to add 1x flag to ambiguous form *rnfA* #1
KS310	CACTACCCGCCACCGATGTCGT**CGTCCTTGTAGTCCCCGC**	R primer to add 1x flag to ambiguous form *rnfA #2*
KS311	ACGACGACATCGGTGGCGGG**TAGTGTGCTCATAAACTCTA**	F primer to amplify second part of ambiguous form *rnfA*
KS312	CATTATACGAAGTTATCAAGA**TTAAAGACCTTGGAAGCAAT**	R primer to insert ambiguous form *rnfA* into pJK29A

Table S2.11. Table of all primers and gblocks used in this study. For all primers containing overhangs for gibson assembly, the bolded text indicates the primer binding site. Primers containing sgRNA's for primers have the sgRNA sequence in red text. gblocks are indicated using the following name designation: gBlock_KSx, where x indicates the number.

Plasmid	Description	Source
pAMG40	Vector for fosmid retrofitting that contains pC2A and λattB	(106)
pJK027A	Vector with *PmcrB(tetO1)* promoter fusion to *uidA* that contains ϕC31-attB and λattP	(106)
pJK029A	Vector with *PmcrB(tetO4)* promoter fusion to *uidA* that contains ϕC31-attB and λattP	(106)
pDN201	pJK027A-derived plasmid with *PmcrB(tetO1)* promoter fusion to Spy cas9	(61)
pDPG10	Cointegrate of pAMG40 and pJK029A	(131)
pKS11	Cointegrate of pAMG40 and pJK027A	(114)
pKS32	contains two sgRNA's targeting pylB-pylD to make pyl biosynthesis KO	This study
pKS34	HR template to delete pylB-pylD, made by linearizing pKS32 with *PmeI*	This study
pKS35	cointegrate of pKS34 with pAMG40 made with BP Clonase II MM	This study
pKS36	pJK27A with PmcrB(tetO1) driving expression of *pylBCD* to complement the pyl KO	This study
pKS37	cointegrate of pKS36 with pAMG40 made with BP Clonase II MM	This study
pKS42	derivative of pDN201 with dual sgRNA's targeting *pylTS* at AscI site	This study
pKS43	derivative of pKS42 with HR Template for truncated *pylTS* (in frame) at PmeI site	This study
pKS44	cointegrate of pKS43 with pAMG40 made with BP Clonase II MM	This study
pKS66	derivative of pJK27A with *pylTS* under control of PmcrB(tetO1)	This study
pKS67	cointegrate of pKS66 and pAMG40	This study
pKS74	derivative of pJK29A with N-terminally 1xFLAG tagged *rdmS* WT under control of PmcrB(tetO4)	This study
pKS75	cointegrate of pKS74 and pAMG40	This study
pKS98	derivative of pJK27A with mttB1O334K under control of PmcrB(tetO1)	This study
pKS99	cointegrate of pKS98 and pAMG40	This study
pKS100	derivative of pJK27A with mttB1O334A under control of PmcrB(tetO1)	This study
pKS101	cointegrate of pKS100 and pAMG40	This study
pKS104	deritvative of pJK29A with pylTS from B. weybense under control of PmcrB(tetO4)	This study
pKS105	cointegrate of pKS104 and pAMG40	This study
pKS106	deritvative of pJK29A with pylBCD from B. weybense under control of PmcrB(tetO4)	This study
pKS107	cointegrate of pKS106 and pAMG40	This study
pKS108	deritvative of pJK29A with pylT**1**S from ANME3 S7 under control of PmcrB(tetO4)	This study

pKS109	cointegrate of pKS108 and pAMG40	This study
pKS110	deritvative of pJK29A with pylT**2**S from ANME3 S7 under control of PmcrB(tetO4)	This study
pKS111	cointegrate of pKS110 and pAMG40	This study
pKS112	deritvative of pJK29A with pylBCD from ANME3 S7 under control of PmcrB(tetO4)	This study
pKS113	cointegrate of pKS112 and pAMG40	This study
pKS114	deritvative of pJK27A with mttCB1 from M. acetivorans under control of PmcrB(tetO1)	This study
pKS115	cointegrate of pKS1114 and pAMG40	This study
pKS116	derivative of pJK29A with ANME pylT1S Δ3bp under control of PmcrB(tetO4)	This study
pKS117	cointegrate of pKS116 and pAMG40	This study
pKS118	derivative of pJK29A with ANME pylT2S Δ3bp under control of PmcrB(tetO4)	This study
pKS119	cointegrate of pKS118 and pAMG40	This study
pKS120	derivative of pJK29A with Bw pylBCD under control of PmcrB(tetO4)	This study
pKS121	cointegrate of pKS120 and pAMG40	This study
pKS122	derivative of pJK29A with rnfA-1xFLAG (TAG>TGA) -- short form control	This study
pKS123	cointegrate of pKS122 and pAMG40	This study
pKS124	derivative of pJK29A with rnfA-1xFLAG (TAG>GCG(ala)) -- long form control	This study
pKS125	cointegrate of pKS124 and pAMG40	This study
pKS126	derivative of pJK29A with rnfA-1xFLAG-TAG-extension -- experimental form	This study
pKS127	cointegrate of pKS126 and pAMG40	This study

Table S2.12. Table of all plasmids and their descriptions used in this study.

Strain	Genotype	Ref
WWM60	*M. acetivorans delta hpt:: PmcrB-tetR*	(106)
WWM977	*M. acetivorans Δhpt:: PmcrB-tetR ΔrdmS*	(129)
DDN038	*M. acetivorans Δhpt:: PmcrB-tetR/pDPG010 [PmcrB(tetO4)-uidA]*	(131)
DDN121	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD*	this study
DDN146	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS*	this study
DDN184	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS37* [PmcrB(tetO1)-*pylBCD*]	this study
DDN228	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS75* [PmcrB(tetO4)-1xFLAG-*rdmS*]	this study
DDN229	*M. acetivorans Δhpt::PmcrB-tetR*/pKS75 [PmcrB(tetO4)-1xFLAG-rdmS]	this study
DDN240	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS/pKS67* [PmcrB(tetO4)-*pylTS*]	this study
DDN287	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS99* [PmcrB(tetO1)-*mttB1O334K*]	this study
DDN315	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS99* [PmcrB(tetO1)-*mttB1O334A*]	this study
DDN318	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS/pKS105* [PmcrB(tetO4)-*pylTSBw*]	this study
DDN319	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS107* [PmcrB(tetO4)-*pylBCDBw*]	this study
DDN320	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS/pKS109* [PmcrB(tetO4)-*pylT1Sanme3*]	this study
DDN321	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS/pKS111* [PmcrB(tetO4)-*pylT2Sanme3*]	this study
DDN322	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS113* [PmcrB(tetO4)-*pylBCDanme3*]	this study
DDN351	*M. acetivorans Δhpt:: PmcrB-tetR/pKS11 [PmcrB(tetO1)-uidA*]	this study
DDN382	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS115* [PmcrB(tetO1)-*mttB1O334KC1*]	this study
DDN383	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS/pKS117* [PmcrB(tetO4)-*pylT1Δ3bpSanme3*]	this study
DDN384	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylTS/pKS119* [PmcrB(tetO4)-*pylT2Δ3bpSanme3*]	this study
DDN385	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS121* [PmcrB(tetO4)-*pylTSBCDBw*]	this study

Table S2.13. Table of all Methanosarcina acetivorans strains and their descriptions used in this study. *Bw* refers to complements derived from *Borrarcheaum weybense*, anme3 refers to complements derived from ANME-3 bin S7.

Appendix C. Supplementary information for Chapter 3

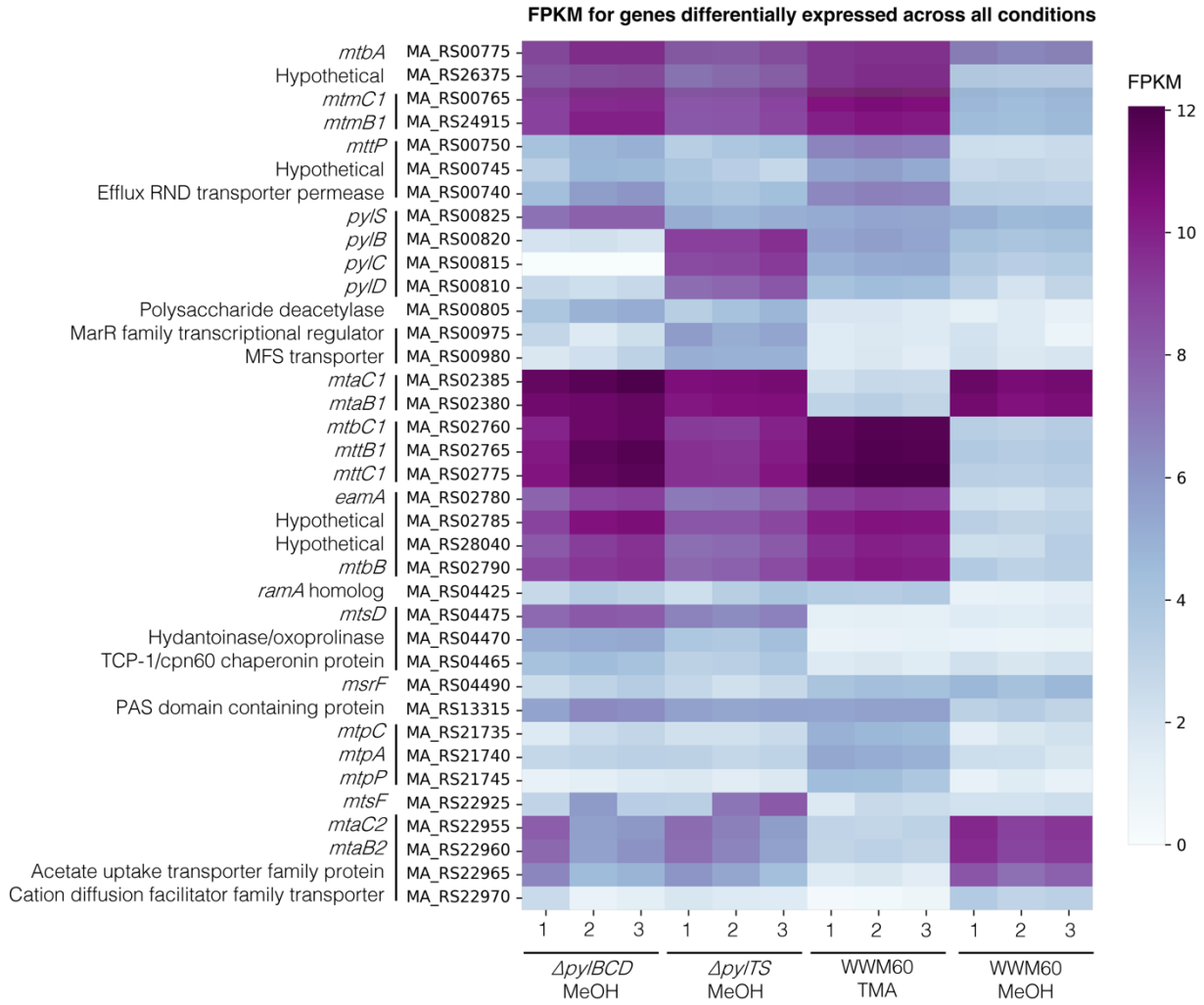


Fig S3.1. FPKM values for all genes differentially expressed in any pairwise comparison between Δ*pylBCD* (MeOH), Δ*pylTS* (MeOH), and WWM60 (MeOH and TMA). Color intensity is reflective of the $\log_2$FPKM values as indicated by the scale on the right side of the heatmap.

accession	annotation	protein_length	pyl_position	extension_length
GCF_000007345.1_0012	Chemotaxis protein methyltransferase	386	382	4
GCF_000007345.1_0083	hypothetical protein	440	17	423
GCF_000007345.1_0100	hypothetical protein	107	49	58
GCF_000007345.1_0125	hypothetical protein	124	82	42
GCF_000007345.1_0144	hypothetical protein	459	201	258
GCF_000007345.1_0149	hypothetical protein	436	434	2
GCF_000007345.1_0156	[FeFe] hydrogenase maturase subunit HydE	368	346	22
GCF_000007345.1_0174	Putative S-adenosyl-L-methionine-dependent methyltransferase	321	288	33
GCF_000007345.1_0183	hypothetical protein	214	5	209
GCF_000007345.1_0203	hypothetical protein	171	9	162
GCF_000007345.1_0242	Type IV secretion system protein PtlH	574	5	569
GCF_000007345.1_0271	hypothetical protein	397	21	376
GCF_000007345.1_0324	hypothetical protein	347	336	11
GCF_000007345.1_0361	Fatty acid metabolism regulator protein	122	95	27
GCF_000007345.1_0362	hypothetical protein	239	237	2
GCF_000007345.1_0364	hypothetical protein	132	13	119
GCF_000007345.1_0366	hypothetical protein	66	29	37
GCF_000007345.1_0371	Fatty acid metabolism regulator protein	202	192	10
GCF_000007345.1_0383	putative ABC transporter ATP-binding protein YknY	274	259	15
GCF_000007345.1_0385	Methylthioribose-1-phosphate isomerase	311	307	4
GCF_000007345.1_0393	hypothetical protein	123	86	37
GCF_000007345.1_0397	hypothetical protein	436	434	2
GCF_000007345.1_0405	putative cation efflux system protein	58	2	56
GCF_000007345.1_0412	hypothetical protein	124	28	96
GCF_000007345.1_0420	hypothetical protein	381	173	208
GCF_000007345.1_0421	hypothetical protein	201	198	3
GCF_000007345.1_0424	hypothetical protein	529	219	310
GCF_000007345.1_0447	hypothetical protein	301	228	73
GCF_000007345.1_0452	hypothetical protein	64	34	30
GCF_000007345.1_0456	hypothetical protein	70	48	22
GCF_000007345.1_0474	hypothetical protein	339	330	9
GCF_000007345.1_0504	hypothetical protein	106	75	31
GCF_000007345.1_0527	hypothetical protein	51	2	49
GCF_000007345.1_0534	Glycine betaine methyltransferase	496	333	163
GCF_000007345.1_0539	hypothetical protein	468	355	113
GCF_000007345.1_0573	hypothetical protein	158	1	157
GCF_000007345.1_0623	hypothetical protein	327	322	5
GCF_000007345.1_0625	hypothetical protein	234	220	14
GCF_000007345.1_0642	hypothetical protein	79	1	78
GCF_000007345.1_0664	Electron transport complex subunit RsxA	225	196	29
GCF_000007345.1_0733	hypothetical protein	94	44	50
GCF_000007345.1_0766	N-substituted formamide deformylase	587	549	38
GCF_000007345.1_0775	Lipase 1	320	78	242
GCF_000007345.1_0780	hypothetical protein	115	7	108
GCF_000007345.1_0820	hypothetical protein	244	141	103
GCF_000007345.1_0842	hypothetical protein	72	51	21
GCF_000007345.1_0858	Uroporphyrinogen decarboxylase	355	90	265
GCF_000007345.1_0866	Alkaline phosphatase synthesis sensor protein PhoR	976	215	761
GCF_000007345.1_0882	Glutathione transport system permease protein GsiC	307	251	56
GCF_000007345.1_0931	Glycine betaine methyltransferase	496	333	163
GCF_000007345.1_0932	hypothetical protein	469	355	114
GCF_000007345.1_0940	Cobalamin biosynthesis protein CobD	327	319	8
GCF_000007345.1_0944	hypothetical protein	217	21	196
GCF_000007345.1_0971	hypothetical protein	47	35	12
GCF_000007345.1_0983	tRNA(fMet)-specific endonuclease VapC	116	114	2
GCF_000007345.1_1003	Fumarate hydratase class II	545	433	112
GCF_000007345.1_1005	putative NAD-dependent oxidoreductase	82	62	20
GCF_000007345.1_1011	hypothetical protein	422	415	7
GCF_000007345.1_1020	hypothetical protein	206	170	36
GCF_000007345.1_1037	hypothetical protein	336	30	306
GCF_000007345.1_1065	hypothetical protein	354	346	8
GCF_000007345.1_1070	hypothetical protein	213	173	40
GCF_000007345.1_1116	GTP 3',8-cyclase 1	512	509	3
GCF_000007345.1_1161	hypothetical protein	181	170	11
GCF_000007345.1_1178	D-inositol 3-phosphate glycosyltransferase	376	356	20
GCF_000007345.1_1183	D-inositol-3-phosphate glycosyltransferase	399	388	11
GCF_000007345.1_1190	hypothetical protein	53	38	15
GCF_000007345.1_1199	hypothetical protein	494	439	55
GCF_000007345.1_1208	hypothetical protein	147	129	18
GCF_000007345.1_1258	hypothetical protein	69	48	21
GCF_000007345.1_1277	hypothetical protein	118	105	13
GCF_000007345.1_1279	putative sensor histidine kinase pdtaS	1360	1355	5
GCF_000007345.1_1290	hypothetical protein	180	26	154
GCF_000007345.1_1300	hypothetical protein	102	80	22
GCF_000007345.1_1303	hypothetical protein	53	1	52
GCF_000007345.1_1309	hypothetical protein	445	438	7
GCF_000007345.1_1331	hypothetical protein	92	86	6
GCF_000007345.1_1332	hypothetical protein	259	243	16
GCF_000007345.1_1343	putative HTH-type transcriptional regulator YybR	147	113	34
GCF_000007345.1_1354	hypothetical protein	77	44	33
GCF_000007345.1_1357	hypothetical protein	90	16	74
GCF_000007345.1_1369	Phosphoglycolate phosphatase	308	14	294
GCF_000007345.1_1403	hypothetical protein	107	95	12
GCF_000007345.1_1429	hypothetical protein	478	94	384
GCF_000007345.1_1469	hypothetical protein	177	49	128

Table S3.1. Summary of all predicted UAG-containing proteins in *Methanosarcina acetivorans*. Accession number for Prokka annotated GTDB genes is designated alongside the putative predicted function. Protein length refers to the complete length assuming UAG readthrough, Pyl position refers to the amino acid sequence at which the UAG codon is located, and the extension length refers to the length of amino acid sequence that UAG readthrough would produce.

Position	Mutation	Annotation	Gene	Description
1,024,737	2745 bp→GC	pseudogene (89-2833/2928 nt)	*MA_RS04495* ←	PAS domain-containing protein
1,977,510	G→A	intergenic (-92/+277)	*MA_RS08545* ← / ← *MA_RS25240*	NUDIX domain-containing protein/IS1 family transposase
3,638,877	G→A	Y525Y (TAC→TAT)	*MA_RS15265* ←	AMP-binding protein
5,078,585	G→A	M1M (ATG→ATA) †	*hypF* →	carbamoyltransferase HypF

Table S3.2. Mutation predictions for CRISPR-edited gene deletion strains generated in this study. Mutations noted are specific to WWM977, the Δ*rdmS* strain. Predictions were generated using BreSeq run in default mode.

new_locus	annotation	log2_fold_change	p_value	q_value
MA_RS04495	GAF domain-containing protein	5.06560067	0	1.00E-300
MA_RS23765	cobalamin-dependent protein	5.138592874	3.72E-295	9.16E-292
MA_RS23785	hydantoinase/oxoprolinase family protein	2.545426891	4.31E-56	4.24E-53
MA_RS04060	hypothetical protein	2.659649255	8.51E-54	5.28E-51
MA_RS23790	hydantoinase/oxoprolinase family protein	3.098981086	8.58E-54	5.28E-51
MA_RS26375	#N/A	-2.711919332	6.95E-49	3.80E-46
MA_RS18725	Hsp20/alpha crystallin family protein	-3.022931845	1.80E-48	8.07E-46
MA_RS16380	#N/A	2.603813149	1.55E-31	2.64E-29
MA_RS03375	#N/A	2.874889706	2.43E-24	1.90E-22
MA_RS23755	hypothetical protein	4.569129567	7.23E-24	5.48E-22
MA_RS14785	transposase	-2.689437368	2.07E-19	9.50E-18
MA_RS14000	hypothetical protein	-3.332603307	8.30E-19	3.38E-17
MA_RS22150	ATP-binding protein	3.279534847	8.55E-18	3.09E-16
MA_RS22145	4Fe-4S binding protein	3.207115427	3.41E-15	9.59E-14
MA_RS10055	IS481-like element ISMac4 family transposase	3.037173153	1.11E-13	2.53E-12
MA_RS22160	NifB/NifX family molybdenum-iron cluster-bindingprotein	3.030515433	1.30E-13	2.92E-12
MA_RS04355	#N/A	8.615171353	6.87E-13	1.36E-11
MA_RS11355	IS481-like element ISMac4 family transposase	2.756061189	1.36E-10	1.93E-09
MA_RS22675	#N/A	2.551690636	1.79E-10	2.48E-09
MA_RS22930	hypothetical protein	3.560545691	4.92E-10	6.30E-09
MA_RS22925	cobalamin-dependent protein	4.870419879	5.88E-10	7.37E-09
MA_RS25025	#N/A	-3.232824752	7.80E-10	9.56E-09
MA_RS15535	hypothetical protein	-2.946304408	8.55E-10	1.04E-08
MA_RS02740	#N/A	2.791862023	1.68E-09	1.96E-08
MA_RS15395	IS481-like element ISMac4 family transposase	2.663093004	2.89E-09	3.24E-08
MA_RS05760	#N/A	4.192355904	3.22E-07	2.55E-06
MA_RS17230	#N/A	2.510064838	5.43E-07	4.14E-06
MA_RS07155	IS481-like element ISMac4 family transposase	3.025190942	6.28E-07	4.74E-06
MA_RS05860	IS481-like element ISMac4 family transposase	3.56666052	1.25E-06	8.87E-06
MA_RS08200	IS21-like element ISMac3 family helper ATPase IstB	2.692718924	1.31E-06	9.26E-06
MA_RS07345	#N/A	3.067103237	2.05E-06	1.39E-05
MA_RS05810	IS481-like element ISMac4 family transposase	3.918005284	2.85E-06	1.88E-05
MA_RS00280	type II toxin-antitoxin system ParD family antitoxin	-2.705268461	4.24E-06	2.72E-05
MA_RS04155	carboxymuconolactone decarboxylase family protein	-2.559515625	8.62E-06	5.20E-05
MA_RS07965	IS21-like element ISMac3 family helper ATPase IstB	5.067149894	1.29E-05	7.47E-05
MA_RS27465	#N/A	-3.148794258	1.94E-05	0.00010712
MA_RS24055	#N/A	3.262098722	2.18E-05	0.0001193
MA_RS10400	hypothetical protein	-6.729448628	2.85E-05	0.00015229
MA_RS02045	hypothetical protein	-3.03038045	5.96E-05	0.0002961
MA_RS23225	hypothetical protein	-2.641660767	0.00012468	0.0005727
MA_RS15210	RimK/LysX family protein	-2.656871093	0.000388	0.00157892
MA_RS25280	#N/A	3.009827088	0.00065708	0.00252368
MA_RS27695	hypothetical protein	-5.654842159	0.00073489	0.00277927
MA_RS20295	#N/A	2.954563017	0.0007466	0.00281705
MA_RS07270	VWA domain-containing protein	3.995120563	0.00088417	0.00325872
MA_RS22760	hypothetical protein	2.611112687	0.00123647	0.00438644
MA_RS22540	hypothetical protein	2.850708784	0.00325169	0.01040371
MA_RS27250	hypothetical protein	3.445993588	0.00398781	0.0124357
MA_RS07315	hypothetical protein	2.502791988	0.00538319	0.01617255
MA_RS06250	#N/A	2.878920405	0.00688605	0.02009895
MA_RS01660	hypothetical protein	3.248832096	0.00750452	0.02164749
MA_RS19455	hypothetical protein	-4.065097238	0.00982623	0.02710607
MA_RS20010	hypothetical protein	-3.683965352	0.01673384	0.04245101
MA_RS27570	hypothetical protein	-3.177052572	0.03255508	0.07483716
MA_RS11855	MscL family protein	-2.507999294	0.04250211	0.09367967
MA_RS27955	#N/A	3.596233845	0.05255115	0.11115201
MA_RS27070	hypothetical protein	3.245418671	0.05467589	0.1142232
MA_RS17985	hypothetical protein	-3.752409018	0.05605477	0.11660908
MA_RS27450	hypothetical protein	2.890835281	0.05857278	0.12049231
MA_RS02705	#N/A	3.001016034	0.06180075	0.12579864
MA_RS13495	hypothetical protein	3.32256361	0.06591447	0.13242059
MA_RS27045	#N/A	-3.466458397	0.07547689	0.14806701
MA_RS11045	hypothetical protein	2.606467973	0.09059714	0.17157704
MA_RS12690	#N/A	3.517371654	0.09209099	0.17373794
MA_RS27555	hypothetical protein	2.995921365	0.16538886	0.27956566
MA_RS02475	hypothetical protein	-3.621216061	0.20213523	0.32740588
MA_RS20765	hypothetical protein	-2.583259988	0.22563257	0.35632289
MA_RS27420	hypothetical protein	-3.102554165	0.26289395	0.39854982
MA_RS26560	#N/A	4.213663322	0.28218161	0.42156015
MA_RS27050	hypothetical protein	-2.960232128	0.46451762	0.60929269

Table S3.3 DESeq2 information for all genes differentially expressed between DDN121 (Δ*pylBCD*) v. DDN202 (Δ*pylBCD+PmcrB(tetO4)-rdmS$_{O216K}$*). Locus ID, annotation, $\log_2$fold-change in expression, and statistical significance (p-value and q-value) are indicated.

Name	Primer Sequence	Description
KS224	ATGGACTACAAGGACGACGACATCG GTGGCGGG**AAAAAGTTCGATATAA ATCTT**	Fw primer to amplify rdmS with O216K mutation and N-terminal 1xFLAG
KS225	GTCAGGACCCGGTACTC**CTTGGTGC ATTCTTCATACCC**	Rv primer to amplify rdmS with O216K mutation with overhang at 3' end to second half of rdmS
KS226	GGGTATGAAGAATGCACC**AAGGAGT ACCGGGTCCTGAC**	Fw primer to amplify rdmS with O216K mutation with overhang at 5' end to second half of rdmS
KS227	CATTATACGAAGTTATCAAGA**TCAAG ACTCTATTTGATTCATGC**	Rv primer to amplify rdmS with O216K mutation with overhang at 3' end to pJK29A
KS228	CATTATACGAAGTTATCAAGA**TCAGG TCTTCTCTAATTCG**	Rv primer to amplify rdmS O216K + msrF with overhang at 3' end to pJK29A
KS229	AATAAATTAAGGAGGAAATTCA**ATGG ACTACAAGGACGAC**	Fw primer to amplify rdmS with O216K mutation, N-terminal 1xFLAG with overhang at 5' end to pJK29A
KS230	AATAAATTAAGGAGGAAATTCA**ATGA AAAAGTTCGATATAAATCTT**	Fw primer to amplify rdmS with O216K mutation
KS231	TCCCTACTGGACTGA	Sequencing primer for RdmS constructs
KS232	GTGGCAGCTCATCCAGA	Sequencing primer for RdmS constructs
KS238	GACCGACGGGATTGAGAT	Sequencing primer for RdmS constructs
KS239	TCAGATGTCGTCGTCCTTGTAGTCC CCGCCACCAG**ACTCTATTTGATTCA TGC**	Rv primer to amplify rdmS with C-terminal linker & FLAG
KS240	ATGTGGTCACATCCTCAGTTTGAAAA AGGTGGCGGG**AAAAAGTTCGATAT AAATCTT**	Fw primer to amplify rdmS with N-terminal Strep and linker
KS241	CATTATACGAAGTTATCAAGA**TCAGA TGTCGTCGTCCTT**	Rv primer to amplify rdmS C term FLAG with overhang to pJK29A
KS242	AATAAATTAAGGAGGAAATTCA**ATGT GGTCACATCCTCAG**	Fw primer to amplify rdmS with N term Strep with overhang to pJK29A
KS266	CATTATACGAAGTTATCAAGA**AAGG GGCAGGCTTTCG**	R primer to amplify signal region of rdmS with overhang (3' with TGA stop + pJK29A)
KS267	CATTATACGAAGTTATCAAGA**TCAGG TGCATTCTTCATACCC**	R primer to amplify Pyl truncated rdmS with overhange (3' with TGA stop + pJK29A)
KS268	AATAAATTAAGGAGGAAATTCA**ATGA GGGTTGACTACGG**	F primer to amplify HTPase region of rdmS with overhang (5' to pJK29A)
KS269	CATTATACGAAGTTATCAAGA**TCAAG ACTCTATTTGATT**	R primer to amplify HTPase region of rdmS with overhang (3' to pJK29A)
KS270	CATTATACGAAGTTATCAAGA**TCAAA GGGGCAGGCTTTCG**	R primer to amplify signal region of rdmS with overhang (3' with TGA stop + pJK29A) ***WITH STOP CODON***
KS271	ATGGACTACAAGGACGACGACATCG GTGGCGGG**AGGGTTGACTACGG**	F primer to amplify HTPase region of rdmS with overhang containing 1X FLAG and linker

Table S3.4 Primer table for all primers used in generating strains and plasmids in Chapter 3. Bolded regions are the primer annealing sites.

Plasmid Name	Construction Details	Reference
pAMG40	Vector for fosmid retrofitting that contains pC2A and λattB	(106)
pJK029A	Vector with *PmcrB(tetO4)* promoter fusion to *uidA* that contains ϕC31-attB and λattP	(106)
pDPG10	Cointegrate of pAMG40 and pJK029A	(131)
pKS72	derivative of pJK29A with *rdmS* O216K under control of PmcrB(tetO4)	This Study
pKS73	cointegrate of pKS72 and pAMG40	This Study
pKS76	derivative of pJK29A with untagged *rdmS* WT under control of PmcrB(tetO4)	This Study
pKS77	cointegrate of pKS76 and pAMG40	This Study
pKS82	derivative of pJK29A with rdmS signal domains under control of PmcrB(tetO4)	This Study
pKS83	cointegrate of pKS82 and pAMG40	This Study
pKS84	derivative of pJK29A with rdmS HTPase domain under control of PmcrB(tetO4)	This Study
pKS85	cointegrate of pKS84 and pAMG40	This Study
pKS86	derivative of pJK29A with rdmS prematurely truncated at Pyl under control of PmcrB(tetO4)	This Study
pKS87	cointegrate of pKS86 and pAMG40	This Study

Table S3.5. Table of all plasmids used in Chapter 3.

Strain	Genotype	Ref
WWM60	*M. acetivorans delta hpt:: PmcrB-tetR*	(106)
WWM977	*M. acetivorans Δhpt:: PmcrB-tetR ΔrdmS*	(129)
DDN038	*M. acetivorans Δhpt:: PmcrB-tetR/pDPG010 [PmcrB(tetO4)-uidA]*	(131)
DDN121	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD*	this study
DDN202	*M. acetivorans Δhpt:: PmcrB-tetR, ΔpylBCD/pKS73* [PmcrB(tetO4)-$rdmS_{O216K}$]	this study
DDN238	*M. acetivorans Δhpt:: PmcrB-tetR, ΔrdmS/pKS73* [PmcrB(tetO4)-$rdmS_{O216K}$]	this study
DDN239	*M. acetivorans Δhpt:: PmcrB-tetR, ΔrdmS/pKS73* [PmcrB(tetO4)-$rdmS_{WT}$]	this study
DDN246	*M. acetivorans Δhpt:: PmcrB-tetR, ΔrdmS/pKS73* [PmcrB(tetO4)-$rdmS_{signal}$]	this study
DDN247	*M. acetivorans Δhpt:: PmcrB-tetR, ΔrdmS/pKS73* [PmcrB(tetO4)-$rdmS_{atpase}$]	this study
DDN238	*M. acetivorans Δhpt:: PmcrB-tetR, ΔrdmS/pKS73* [PmcrB(tetO4)-$rdmS_{truncation}$]	this study

Table S3.6. Table of all strains used in Chapter 3.