Title

Positional integration of lung adenocarcinoma susceptibility loci with primary human alveolar epithelial cell epigenomes

Journal

Epigenomics, 10(09)

ISSN

1750-1911

Authors

Yang, Chenchen

Stueve, Theresa Ryan

Yan, Chunli

et al.

Publication Date

2018-09-01

DOI

10.2217/epi-2018-0003

Peer reviewed

Positional Integration of Lung Adenocarcinoma Susceptibility Loci with Primary Human Alveolar Epithelial Cell Epigenomes

Chenchen Yang[1,2,3*], Theresa Ryan Stueve[1,2,3,4*], Chunli Yan[1,2,3], Suhn Kyong Rhie[1,2,3], Daniel J. Mullen[1,2,3], Jiao Luo[2,5], Beiyun Zhou[3,5,6], Zea Borok[2,3,5,6], Crystal N. Marconett[1,2,3], and Ite A. Offringa[1,2,3#]

1 Department of Surgery, **2** Department of Biochemistry & Molecular Medicine, **3** Norris Comprehensive Cancer Center, **4** Department of Preventive Medicine, **5** Division of Pulmonary and Critical Care and Sleep Medicine, Department of Medicine, **6** Hastings Center for Pulmonary Research, Keck School of Medicine, University of Southern California 90089, USA

[*] These authors contributed equally to this work

[#] Corresponding author: ilaird@usc.edu

Short title: Epigenetic environment of lung adenocarcinoma risk SNPs

Data deposition: Data is provided in GEO record GSE84273

Acknowledgements

H1648 and H522 cells were the kind gifts of the Dr. Eric Haura Laboratory. This work was supported by National Institute of Health (https://www.nih.gov/) grants R01 HL114094 (to IALO, ZB), R01 HL126877 and R01 HL112638 (to ZB), the Norris Comprehensive Cancer Center core grant (National Cancer Insttiture P30CA01408, supporting IALO), Department of Defense (http://cdmrp.army.mil/funding/lcrp) Concept Award W81XWH-14-1-0174-1 (to IALO), the Tobacco-Related Disease Research Program (award ID 500806, to IALO) and the California Community Foundation (http://www.calfund.org/) (to IALO, supporting CY and JL) and support from the Thomas G. Labrecque Foundation (https://tglfoundation.com/) (to IALO), the Whittier Foundation (to IALO), the Hastings Foundation (to ZB) and generous donations from Conya and Wallace Pembroke (to IALO). ZB is the Ralph Edgington Chair in Medicine and Hastings Professor of Medicine. TRS was supported by the National Institute of Health National Institute of Environmental Health Sciences (NIEHS,

NIH T32ES013678) and by the USC Provost's Postdoctoral Scholar Research Grant. DJM was supported by a University of Southern California Provost Fellowship and a Roy E. Thomas Foundation graduate scholarship. CNM was supported by American Cancer Society (https://www.cancer.org/research.html) /Canary Foundation (http://www.canaryfoundation.org/) postdoctoral fellowship # PFTED-10-207-01-SIED and later the Department of Surgery, Keck School of Medicine. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

Author Contributions

Conceptualization: CY (Chenchen Yang), TRS, CNM, IALO. Data curation: CY, CNM. Formal analysis: CY, TRS, DJM. Funding acquisition: CNM, TRS, BZ, ZB, IALO. Investigation: CY, TRS, CLY (Chunli Yang). Methodology: CY, TRS, CNM, SKR, DJM. Project administration: IALO. Resources: ZB, JL, BZ, IALO. Software: CY, SKR. Supervision: CNM, IALO. Validation: CY, TRS, CLY. Visualization: CY, TRS, DJM, IALO. Writing original draft: CY, TRS, IALO. Writing review & editing: All authors.

Abstract

Aim: To identify functional lung adenocarcinoma (LUAD) risk SNPs. **Materials & methods:** Eighteen validated LUAD risk SNPs ($p \leq 5x10^{-8}$) and 930 SNPs in high linkage disequilibrium ($r^2>0.5$) were integrated with epigenomic information from primary human alveolar epithelial cells. Enhancer-associated SNPs likely affecting transcription factor (TF) binding sites were predicted. Three SNPS were functionally investigated using luciferase assays, expression quantitative trait loci (eQTLs) and cancer-specific expression. **Results:** Forty-seven SNPs mapped to putative enhancers; eleven located to open chromatin. Of these, seven altered predicted TF binding motifs. Rs6942067 showed allele-specific luciferase expression and eQTL analysis indicate it influences expression of *DCBLD1*, a gene that encodes an unknown membrane protein and is overexpressed in LUAD. **Conclusions:** Integration of candidate LUAD risk SNPS with epigenomic marks from normal alveolar epithelium identified numerous candidate functional LUAD risk SNPs including rs6942067, which appears to affect *DCBLD1* expression.

Data deposition: Data are provided in GEO record GSE84273

Key words: SNP, lung adenocarcinoma, epigenomics, alveolar epithelial cells, enhancer, FAIRE, eQTL, rs6942067, *DCBLD1*

Introduction

Lung cancer is the leading cause of cancer death worldwide, and in the United States it is responsible for more deaths than breast, colorectal, and prostate cancer combined [1]. The most common histological subtype of lung cancer is lung adenocarcinoma (LUAD), accounting for over forty percent of new lung cancer cases. Never-smokers with lung cancer are more likely to have LUAD and to be women and persons of Asian descent [2, 3]. Though smoking is strongly implicated in lung cancer risk, it is estimated that half of all new cases arise in never smokers or smokers who quit many years ago [4]. Epidemiological studies indicate that in addition to environmental factors, LUAD susceptibility also has a significant genetic component [5-7].

To date, genome-wide association studies (GWAS) have uncovered 18 validated single nucleotide polymorphisms (SNPs) associated with LUAD risk ($p \leq 5x10^{-8}$), distributed over 12 chromosomal regions (Table 1). Causal links between these SNPs and lung health remain largely unknown. The principal challenges to understanding how SNPs confer susceptibility to LUAD are the same for all post-GWAS studies [8-11]. First, because GWAS SNPs are landmark or 'index' SNPs that serve as positional references for phenotypic associations, hundreds of SNPs in linkage disequilibrium (LD), could be the actual functional SNP. Secondly, the majority of all GWAS SNPs, including 17 of the 18 index LUAD SNPs (Table 1), reside outside of protein-coding regions of genes and are thus hypothesized to influence gene expression by disrupting regulatory elements that could be hundreds of kilobases away from their target genes. Consistent with this hypothesis, several groups have determined that the majority of causal or 'functional' noncoding SNPs are in fact concentrated in epigenomic features characteristic of enhancers of gene transcription [8-16]. Epigenomic features make up a layer of information that is superimposed onto the genome; this does not alter the genetic sequence but affects cell type-specific gene expression [17]. Epigenomic features include chemical modifications such as DNA methylation, regulatory RNAs, transcription factors, modified histones and genome-

organizing factors [17]. Epigenomic features characteristics of enhancers include regions of open chromatin (such as DNase I hypersensitive sites) which are accessible to DNA-binding proteins, histone 3 monomethylation at lysine 4 (H3K4me1, a mark for poised or active enhancers [18]) and histone 3 acetylation at lysine 27 (H3K27ac, a mark for active enhancers [19]). Identification of epigenetic marks disrupted by SNPs has allowed exciting progress to be made in post-GWAS investigations of genetic susceptibility to autoimmune disorders, Alzheimer's disease, diabetes, and cancers of the breast, prostate, and colon [10, 12-16, 20-22]. Importantly, in order to be relevant, the epigenomic features used for positional integration with candidate functional SNPs must be obtained from cell types pertinent to the disease at hand. In the case of LUAD, alveolar epithelial cells are highly relevant because LUAD arises in the peripheral lung.

Alveolar lung epithelium consists of two epithelial cell types: squamous type 1 (AT1) cells and cuboidal type 2 (AT2) cells. AT1 cells are considered terminally differentiated and mediate gas exchange. They are large delicate cells that form the interface between the air in the alveoli and the microcapillaries that surround the alveolar sacs are are the site for gas exchange [31]. AT1 cells make up 95% of the surface area of the alveoli, and could, therefore, be disproportionately impacted by inhaled toxicants such as those present in tobacco smoke or pollution. AT2 cells produce the surfactants required to prevent the collapse of alveoli upon expiration. In adult lung, they are the progenitors of AT1 cells in response to lung injury; AT2 cells can both self-renew and differentiate into AT1 cells, and this process can be replicated *in vitro* [32-35]. Given their proliferative capacity, AT2 cells are commonly implicated as the likely progenitors of LUAD [36-39]. However, because definitive data on the roles and interactions of AT1 and AT2 cells in LUAD initiation remain to be provided, we rationalized that both cell types (here collectively referred to as alveolar epithelial cells or AEC) should be investigated in LUAD risk studies. Here we use epigenomic data from purified primary human AT2 cells, *in vitro*-differentiated AT1-like cells, and LUAD cell lines for positional integration with LUAD risk SNPs, and apply a combination of bioinformatics and molecular approaches to identify candidate *functional* risk SNPs (outlined in flowchart Supplementary Fig 1).

Results & Discussion

Classification of SNPs associated with LUAD risk

We first carried out a literature review, collecting all SNPs reported to be significantly associated with LUAD risk. We filtered for genome-wide significance ($P<5x10^{-8}$) and for those SNPS that had been validated,

i.e. observed to be significant in more than one data set. We thus collected 18 validated GWAS index SNPs that had been significantly associated with LUAD risk (Table 1, Figure 1A). In agreement with the general observation that most GWAS SNPs are located in noncoding regions [9], 17 were found to be either intronic or intergenic, while the one, rs1051730, falls within an exon resulting in a synonymous mutation. We next obtained 930 SNPs in high linkage disequilibrium (LD; $r^2 \geq 0.5$) with the 18 index-SNPs using 1000 Genomes LD data [40] matched for the ethnicity of the population in which the index risk SNP was identified (Supplementary Table 1), and grouped these into functional classes for subsequent analysis (Supplementary Table 2). Of the 948 total index and LD SNPs, 583 were intronic, while 335 were intergenic. Only seven SNPs mapped to coding regions, including three missense mutations and four synonymous mutations. Seven SNPs were located in the 5' or 3' untranslated regions (UTRs), where microRNAs are most often targeted, and 16 in putative promoter regions (within 1000 bp to either side of the transcription start site or TSS).

Very little published data on the potential functionality of the 948 SNPs is available. Several SNPs in the 15q25.1 locus have been implicated as potential functional SNPs affecting expression of the cholinergic receptor, neuronal nicotinic alpha polypeptide-5 (CHRNA5), a protein involved in the nicotine response [41, 42]. Rs16969968 resides in the fifth exon of *CHRNA5* and changes an aspartic acid codon (GAT) into an asparagine codon (AAT) at amino acid 398 in the second intracellular loop. This makes the receptor less responsive to nicotine, thereby increasing nicotine dependence, heavy smoking, and potentially, lung cancer risk [43]. Rs55853698 and rs55781567, located in the 5'UTR of *CHRNA5*, have been reported to alter *CHRNA5* promoter activity [44].

To preliminarily evaluate whether the remaining two missense-causing SNPs (rs2076530 in *BTNL2* and rs9891146 in *C17orf58*) might alter protein function, we performed structure-activity predictions using PolyPhen2 and SIFT software. Neither of the missense mutations were predicted to be deleterious by either program (Supplementary Table 3), decreasing the likelihood that these SNPs might alter the function or structure of the proteins. To investigate whether the 7 SNPs in UTRs might affect miRNA targeting, we performed sequence-activity binding predictions using the miRNA target database TargetScanHuman. No allele for any UTR SNP was highlighted as a known microRNA target (Supplementary Table 4). As noted above, of the SNPs located in promoter regions, only the two CHRNA5 SNPs have been implicated in affecting promoter function (Supplementary Table 5).

In sum, except for several SNPs in the 15q25.1 locus, all loci appear to lack a biological mechanism explaining their association with increased LUAD risk. Because enhancers have been commonly implicated in risk SNP function [10, 12-16, 20-22], we explored whether one or more of the SNPs might influence risk by affecting AEC enhancers. To be thorough, we included all 948 SNPs in the investigation.

Identification of AEC enhancers

As a first step in generating AEC enhancer profiles, we purified AT2 cells from remnant human transplant lung. We used cells from a non-smoker to ensure optimally healthy cells, thereby limiting disease confounders. AT1 cells are too delicate to allow purification in sufficient numbers, necessitating derivation of AT1-like cells through *in vitro* differentiation over the course of 6 days as described [45] (Supplementary Figure 2A). At day 2 in culture, AT2 cells undergo dramatic changes in gene expression and epigenomic marks, and by days 4 and 6, they have transdifferentiated into cells that exhibit characteristics of native AT1 cells. We confirmed proper differentiation of the cells by Western blot analysis (Supplementary Figure 2B). We performed chromatin immunoprecipitation and subsequent DNA sequencing (ChIP-seq) using material from day 0 (D0; AT2 cells) and days 4 and 6 (D4, D6; AT1-like cells) using antibodies against enhancer marks H3K27ac and H3K4me1. In D0, D4, and D6 cells respectively, we identified 39,210, 44,976, and 43,743 H3K27ac peaks and 87,443, 76,292, and 75,490 H3K4me1 peaks (Supplementary Table 6; saturation plots are shown in Supplementary Figure 3A,B). Peak analysis revealed substantial overlap of peaks from different days (Supplementary Figure 4A,B).

In addition to ChIP-seq for enhancer marks, we also performed Formaldehyde-Assisted Isolation of Regulatory Elements-sequencing (FAIRE-seq [46]) on AECs from days 0, 4 and 6 in culture to identify nucleosome-depleted regions of the genome that are accessible to DNA-binding proteins (i.e. open chromatin, Supplementary Figure 3C). The D0 peaks were largely distinct from the D4/D6 peaks, while the latter showed substantial overlap (Supplementary Fig 4C). Plots of the tag density versus distance to the center of the FAIRE-seq peaks showed that FAIRE-seq signals were enriched in the center of FAIRE-seq peaks (nucleosome depletion), while as expected, signals for the histone modifications H3K27ac and H3K4me1 (on nucleosomes) were enriched in regions flanking FAIRE-seq peaks (Supplementary Figure 5).

Identification of SNPs present in enhancers

We next investigated which among the 948 candidate SNPs were located in AEC enhancer regions (i.e. were located in H3K27ac *and* H3K4me1 ChIP-seq peaks) in D0, D4, and/or D6 cells. We filtered out SNPs located on the extreme flanks of peaks by requiring that SNPs be significantly enriched in enhancer marks on both of the 0.5 kb flanking sides (Supplementary Figure 6). This yielded 47 AEC enhancer-associated SNPs that we classified as AT2 cell-specific (present only in D0 enhancers), AT1 cell-specific (present only in D4/6 enhancers) and general AEC enhancer SNPs (present in both AT1 and AT2 enhancers). Seven AT2-specific SNPs, 23 AT1-specific SNPs, and 17 AEC-specific SNPs were identified respectively (Table 2 and Figure 1B). Notably, none of the index-SNPs themselves were located in AEC, AT1 or AT2 cell enhancer elements. For 10 of the 18 index SNPs, including the two near the CHRNA5 region, we detected no AEC enhancer-associated LD SNPs. This could be because these SNPs do not function through enhancers (e.g. the previously identified missense and promoter *CHRNA5* SNPs), because they affect LUAD risk through effects on other cell types (such as immune cells, lung fibroblasts, etc.) or because their function is influenced by other factors such as smoking, which are not investigated here.

The 47 candidate AEC enhancer SNPs correspond to 8 of the 18 index GWAS LUAD risk SNPs (Table 2 and Figure 1B). The number of candidate SNPs per region varied from one or two to 22 SNPS on 6q22.1, in LD with index SNP rs9387478. The latter SNPs are located in the *DCBLD1* and *ROS1* gene region, which is also an intron of a putative fusion transcript between *GOPC* and *ROS1* and contains numerous active chromatin marks. Two SNPs in high LD with rs4488809 on chromosome 3q28 were found in general AEC enhancer marks located in the promoter region (-1000bp - +100bp from TSS) of TP63 (Supplementary Table 5), suggesting an enhancer close to a transcription start site. Such an enhancer may or may not affect the nearest gene [47]. In studies of risk enhancers, SNPs located in nucleosome-free, transcription factor (TF)-accessible regions of the regulatory element are the most promising candidates for functional follow-up [9]. We thus filtered the 47 candidate SNPs by whether they were located in FAIRE peaks, which resulted in 11 top candidates (Supplementary Figure 1B). To further evaluate these 11 SNPs, we assessed the likelihood that they would disrupt or create TF binding sites.

Identification of SNPs that affect transcription factor binding sites

We compiled motif positional weight matrixes (PWM) from ENCODE-motif [48], Factorbook [49] and HOCOMOCO [50] (Supplementary Figure 7). We removed TFs that are not expressed in AT1 and/or AT2 cells by excluding sites for TFs with low reads per kilobase per million (rpkm; set at rpkm≤3, from RNA-seq data [51]); binding sites for TFs that are not expressed in alveolar epithelium would not be expected to have any functional effects in these cells. Our analysis identified predicted transcription factor binding sites overlapping with 7 of the 11 candidate risk enhancer SNPs (Figure 1C, Table 3). Next, we searched publicly available ChIP-seq data from ENCODE [52] and GEO [53] for experimental evidence supporting binding of predicted TFs to the SNP regions. This approach is limited by the fact that publicly available ChIP-seq datasets such as those generated by the ENCODE consortium are restricted to the factors that have been examined to date. In this latter analysis, we included all ENCODE cell types, including but not limited to lung-relevant cell types such as A549 (a LUAD cell line), small airway epithelial cells (SAEC, normal primary cells from the more distal airways), IMR90 (a cell line derived from embryonic lung fibroblast), normal human lung fibroblasts (NHLF) and human pulmonary fibroblasts (HPF, obtained from a different source than NHLF). All of these cell types are distinct from AEC, and it is well recognized that enhancers vary considerably among cell types. However, if a predicted TF was reported to bind its target by ChIP-seq in any cell type, we took this as confirmation that the factor can actually bind to the predicted target in the context of a cellular environment. For 4 of the 7 SNPs, we found ChIP-seq data supporting binding of the TFs we had predicted. In addition, ChIP-seq data-based TF binding was noted for two SNP locations for which we had predicted no TF binding sites (rs2057314 and rs12602556, Table 3). This could happen when TFs bind in multi-protein complexes or bind indirectly to DNA. In the case of indirect binding, we assumed that an effect of the SNP would be less likely. We next focused on 3 SNPs for which predicted TF binding sites were supported by ChIP-based evidence (Figure 1C). These were: rs452384, corresponding to index SNP rs465498; and rs6942067 and rs9481728, corresponding to index SNP rs9387478.

Rs452384 lies in a putative general AEC enhancer in a central intron of the cleft lip and palate transmembrane protein 1-like (*CLPTM1L*) gene (Figure 2A). *CLPTM1L* was recently implicated in lung tumorigenesis [54] and encodes a membrane protein that leads to apoptosis when overexpressed in cisplatin-sensitive cells [55]. This SNP also resides in a strong DNase hypersensitive site in small airway epithelial cells

(SAECs, ENCODE data [48, 49]). Polymorphisms in *CLPTM1L* and the neighboring telomerase (*TERT*) gene have been reported to increase susceptibility to numerous cancers, including lung, pancreatic, and breast cancers [28, 56-59]. The reference (risk) allele of rs452384 forms a predicted site for NKX2-1 that is disrupted by the alternate allele (Table 3). Importantly, the ability of this TF to bind to this site is supported by ChIP-seq data in lung adenocarcinoma cell line H3122 (homozygous for the risk allele)[51] (Figure 2B,C). NKX2-1 plays a key role in driving lung epithelial tissue differentiation from endoderm [60, 61] and is one of the most significantly amplified genes in LUAD [53]. Interestingly, a binding site for the *MYC* proto-oncogene is predicted for the alternate rs452384 allele (Figure 2C). *MYC* is implicated in numerous cancers including LUAD [62-64] and has been ChIPed at rs452384 by the ENCODE Consortium in the MCF10A-Er-Src cell line (homozygous for the risk allele) [52].

Rs6942067 is located in the intergenic region between the *DCBLD1* (Discoidin, CUB and LCCL Domain-containing 1) and *ROS1* (ROS proto-oncogene 1, a receptor tyrosine kinase) genes (Figure 3). Rs6942067 is positioned in the center of a DNase hypersensitive region between two nucleosomes carrying H3K27ac and H3K4me1 marks and the reference (risk) A allele lies in a predicted binding site for E1A-binding protein P300 (EP300) that is disrupted by the alternate allele (Table 3). EP300 binding to this site has been observed by ChIP-seq in retinoic acid-treated neuroblastoma cell line SK-N-SH_RA (A/A genotype) (ENCODE data [52], Figure 3B,C). EP300 is a histone acetyltransferase that activates transcription via chromatin remodeling, and it has been implicated in a variety of cancers [65]. It is mutated and/or overexpressed in a low percentage of lung adenocarcinomas [66]. The alternate allele of rs6942067 forms a TF binding site for the thyroid hormone receptor alpha (THRA, Figure 3C), which is one of the several receptors for thyroid hormone known to be involved in lung development and alveolar cell function [67-69]. Notably, low levels of thyrotropin, a hormone that regulates thyroid hormone release, have been linked to an increased risk for prostate and lung cancer [70]. Like rs6942067, rs9481728 (located in the first intron of *DCBLD1*) carries enhancer histone marks and an EP300 site on the reference (risk) allele that is disrupted by the alternate allele (Figure 4, Table 3).

The epigenomic environment of the three SNPs, coupled with the presence of overlapping TF binding sites predicted to be affected by the SNP alleles, provided a strong rationale for functional analyses. This was further supported by the observation of active chromatin marks at the location of these three SNPs in LUAD cell lines [71] (Supplementary Figure 8-10). The first functional assay we carried out for the three candidate

functional SNPs was a luciferase assay, in which we cloned the PCR-amplified putative enhancer region and inserted it upstream of a minimal promoter in the luciferase gene reporter vector pGL4.26. The assay allows both alleles to be tested in the same genetic and cellular environment. We then tested whether the genomic segment containing either allele of the SNP would exhibit enhancer activity, and whether the alleles differed in the extent to which they could enhance expression.. Because immortalized human AEC are not available, we transfected each reporter construct into a LUAD cell line showing strong genomic H3K4me1 and H3K27ac peaks in the SNP region (based on publicly available H3K4me1 and H3K27ac ChIP-seq datasets for 26 lung cancer cell lines in DBTSS, http://dbtss.hgc.jp) [71]), reasoning that these cell lines would be enriched for TFs and coactivators required for enhancer activity at the locus of interest (Supplementary Figure 11)).

Functional analyses of rs452384 on chromosome 5p15.33

To functionally study rs452384 we used a 459-bp region from chr5:1330187-1331866 (hg19) containing either the reference (risk) allele (T) or the alternate allele (C) upstream of the minimal promoter in pGL4.26 and transfected these constructs into H1648 cells, which bear strong enhancer marks in this region (http://dbtss.hgc.jp)[71] (Supplementary Figure S11). Both constructs elicited 5~6-fold higher luciferase activity over background (empty pGL4.26), (Figure 5A), indicating an enhancer element is present. However, we did not observe significant differences in enhancer activity between the two alleles in H1648 cells. To ensure that we were not missing any key factors binding to adjacent sequences, we also studied a genomic fragment that had been expanded to the 5' and 3' end (as indicated in Supplementary Figure 12), but it did not show allele-specific activity either. We cannot exclude that differences in the TF profiles of AEC and H1648 might mask an allele-specific effect, or that specific environmental conditions (such as tobacco smoke exposure) might be required to reveal allele-specificity. Because this SNP had been highly ranked in a fine mapping study [72], we also examined the online eQTL database GTEx [73] for evidence of lung-specific expression quantitative loci (eQTLs), but detected no significant lung eQTL. We also looked for eQTLs in LUAD tissues (n=428) from TCGA, correcting for copy number variation and DNA methylation (the latter might affect gene expression in cancer), but detected no significant eQTLs either. The lack of an allele-specific difference in the luciferase assay as well as the lack of a detectable eQTL in lung tissue suggests that, despite its presence in a TF binding site in an AEC enhancer, this SNP may not be the functional SNP for index SNP rs465498. However, a limitation of GTEx and other available eQTL databases is that data is typically generated from whole tissue

samples and rarely from purified cell populations. Thus, any true cell type-specific allelic expression will be diluted by the presence of other cell types, such as lung fibroblasts, macrophages, or endothelial cells when 'lung eQTLs' are queried. In addition, we cannot exclude that a functional effect of this SNP may only be observable under certain developmental or environmental conditions. We do note that in GTEx, the risk allele was associated with higher expression of the adjacent telomerase reverse transcriptase (*TERT*) gene in esophageal tissue (P=3.9x10^{-9}, Figure 5B,D) and the cleft lip and palate transmembrane protein 1-like (*CLPTM1L*) gene in sun-exposed skin (P=2.1x10^{-7}, Figure 5D, E). Telomerase is a ribonucleoprotein polymerase that is part of the complex that maintains telomere ends by addition of the telomere repeat TTAGGG, and its overexpression is a key component of the transformation process in many malignant cancer types including lung cancer [26-28, 57, 59, 74, 75]. *TERT* has been repeatedly implicated in lung cancer, both through mutations and polymorphisms that lie in *TERT* and *CLPTM1L*. Indeed, *TERT* is significantly overexpressed in LUAD compared to non-tumor lung tissues in TCGA data, in which expression is very low (P=1.2x10^{-38}, Figure 5C). *CLPTM1L* is also elevated in LUAD (P=5.5x10^{-62}, Figure 5F) and was recently functionally implicated in lung cancer susceptibility and resistance to chemotherapy [76]. One possible problem in the ability to detect a *TERT* eQTL in lung tissue may be the very low expression levels of *TERT* in alveolar epithelium (RPKM of around 1 in AT2 cells (D=0) and absent in cells at D4 and D6), and the possibility that the SNP may only be functional under conditions that would promote cell proliferation, such as lung damage. Of note, rs452384 is located in DNase hypersensitive sites in small airway epithelial cells and numerous other cell types in the publicly available SNP annotation database HaploReg v4 [77].

Functional analyses of rs6942067 and rs9481728 on chromosome 6q22.1

To test for a functional role of rs6942067, we cloned an 836 bp region (chr6: 117785006-117785841, hg19) containing either the reference (risk) allele (A) or the alternate allele (G) into pGL4.26. Based on the presence of enhancer histone marks in the rs6942067 region [71], we performed reporter assays in LUAD cell line H1648 (Supplementary Figure 11B). In H1648 cells, luciferase activity over background was 6.8-fold and 3.5-fold over background for the A and G alleles respectively, indicating a 94% elevated enhancer activity for the reference allele (P=2.7x10^{-2}) (Figure 6A). We replicated these findings in H522 cells and observed that the

reference and alternate constructs respectively elicited 6.9-fold and 4.8-fold elevated activity over background, indicating a 45% stronger enhancer activity attributable to the reference (A) allele (P=8x10^{-3}) (Supplementary Figure 13).

Rs9481728 is located 30 kb downstream of rs6942067, in the first intron of *DCBLD1* (Figure 6D). We cloned a 912 bp region (chr6: 117817044-117817955, hg19**)** in pGL4.26 and transfected the DNA into H1648 LUAD cells, which also showed an enhancer peak on this SNP (Supplementary Figure 11C). However, we observed no activity over background (Supplementary Figure 14). While we cannot exclude that genomic interactions with more distant factors may be required for enhancer activity of this segment, given the activity observed using the region encompassing rs6942067, we pursued only rs6942067 further.

Examination of GTEx data for rs6942067 showed a strong genome-wide significant eQTL for *DCBLD1* in lung (Figure 6B). No other genes were found to be eQTLs associated with this SNP in lung or other tissues. To investigate more thoroughly, we also examined the flanking 1Mb window in the SNP region using TCGA LUAD samples. This was done using rs6930292, a SNP in high LD (r^2=1) as a surrogate, because SNP rs6942067 is not annotated in TCGA. We detected significant allele-specific expression of *DCBLD1* (p=0.041, corrected for the number of genes in the 1Mb window, Figure 6C). Surprisingly, in contrast to the luciferase-based assay, we detected lower expression of the reference (risk) allele, suggesting that in the genomic context, the reference allele might reduce, not enhance expression. However, we note that in GTEx, the risk allele is associated with higher DCBLD1 expression in blood cells but reduced expression in thyroid tissue (Figure 6E,F), supporting a complex role of the SNP in regulating gene expression. It is of interest that we predicted binding of THRA on the alternate allele (Figure 3C) and that this receptor can repress transcription in the absence of thyroid hormone and induce it in the presence of hormone [78]. Further investigations will be required to elucidate the role of rs6942067 and its TFs in LUAD risk.

The function of *DCBLD1* is currently unclear, making it difficult to predict how up- or down-regulation of this gene would affect lung cancer risk. The encoded protein is predicted to be membrane-associated. Its paralog NRP2, or VEGF165R2, is a transmembrane protein that interacts with vascular endothelial growth factor (VEGF) and is implicated in metastasis [79]. *DCBLD1* is significantly overexpressed in LUAD *vs.* non-tumor lung in TCGA data (P=1.7x10^{-23}, Figure 6G), and higher expression in LUAD is negatively associated with survival (Supplementary Figure 15). It is also possible that the enhancer at rs6942067 targets other

gene(s) that may not be detectable as an eQTL in the mix of lung cells analyzed in GTEx. rs6942067 lies between *DCBLD1* and *ROS1* (ROS proto-oncogene 1, a receptor tyrosine kinase)(Figure 6D). Translocations involving *ROS1* are known "driver" events in NSCLC; approximately 1% of lung tumors harbor ROS1 fusions [80]. It has been reported that the level of certain histone modifications influences the predisposition to chromosome translocations [81]. Thus, effects of this SNP on the epigenetic landscape and gene translocation might need to be considered.

Implications of our findings

In this study, we identified 47 AEC enhancer-associated SNPs from 948 LUAD candidate risk SNPs. To ensure we examined SNPs in true enhancers we focused on SNPs located in regions carrying *both* H3K4me1 and H3K27ac marks. However, it is possible that additional SNPs of interest are located in poised enhancers that are marked only with H3K4me1 and are activated by environmental stimuli such as exposure to tobacco smoke (the AECs used in this study were derived from a non-smoker). Of the 47 SNPs, we chose the 11 SNPs that were in FAIRE peaks for further study. In the future, it will be important to investigate SNPs in regulatory marks in AEC from smoker's lungs.

Our analyses do not provide strong evidence for a functional role of rs452384 on chromosome 5p15.33 in LUAD, despite recent fine mapping data in the *TERT/CLPTM1L* region which identified rs452384 as one of the top-ranked SNPs in the region [72]. How this SNP might function may require functional analyses using primary AEC or as yet unavailable immortalized AEC or a variety of environmental conditions such as exposure to tobacco smoke.

The reference (risk) allele of rs6942067 was associated with elevated enhancer activity in LUAD cell lines, but we detected an eQTL showing lower expression of *DCBLD1* in lung tissue carrying the reference allele. This emphasizes that luciferase assays may be helpful in detecting allele-specific activity but that the cell type or genomic context may affect the observed regulatory effects. The versatility of this SNP is supported by the differential *DCBLD1* eQTLs seen in different tissues (Figure 6B,E,F). EP300, which has been predicted to bind to the reference allele and was observed to do so in ChIP studies, is a histone acetyltransferase associated with gene activation. A lower activity of the reference allele might therefore be associated with competition of other factors with EP300 for binding. A role for *DCBLD1* in lung cancer is supported by its

increased expression in LUAD *vs.* non-tumor lung and by its negative association with survival. A recent study of non-smoking Asian women found that the association of rs9387478 (the index SNP for rs6942067) with LUAD was stronger in EGFR mutation-positive cases [82], suggesting that the environment, ethnicity and gender could all influence the manifestation of this genetic effect. Taken together, further studies into the function of *DCBLD1* in lung cancer are certainly warranted.

Our work emphasizes the importance of integrating epigenomes of purified disease-relevant cell types to elucidate the genetic basis for lung cancer risk. However, it also illustrates that focusing on disease-relevant cells may not be sufficient to identify functional SNPs for most index SNPs. In the case of lung cancer, one may require tobacco-exposed disease-relevant cells. Besides examining tobacco-smoke exposed cells and tissues, purification of other lung cell types will be required to investigate the role of SNPs in other histological subtypes of lung cancer [17]. A recent large-scale study of lung cancer susceptibility loci highlights the differences in genetic susceptibility between histological lung cancer subtypes [83]. Basal cells, which are airway epithelial cells that lie on the basement membrane and are thought to be involved in airway regeneration upon injury, are implicated as progenitors of squamous cell carcinoma [84,85]. Basal cells should be purified and epigenetically profiled in a similar fashion to the work described here. Further investigation of SNPs and their targets may ultimately yield more effective and personalized strategies for lung cancer risk assessment, prevention, and treatment.

Methods & Materials

Ethics statement

Remnant human transplant lung was obtained in compliance with Institutional Review Board-approved protocols for the use of human source material in research (HS-07-00660) and processed within 3 days of death.

Cell isolation, culture and quality control

Human AT2 cells were isolated from a de-identified non-smoker remnant transplant lung as described [45]. The subject in this study was a non-smoking male 62-year old male who died of cardiovascular disease. AT2 cells were plated and differentiated into AT1-like cells over the course of 6 days as described [45]. A549,

H1648, and H522 cells were cultured in RPMI 1640 w/L-glutamine (Lonza #12-702F, Walkersville, MD) supplemented with 10% fetal bovine serum and 100 units/mL of penicillin/streptomycin. All cell lines maintained by our laboratory are routinely tested and are negative for mycoplasma, and cell line identity was confirmed by DNA fingerprinting.

AEC RNA isolation, RNA-seq, protein isolation and Western blot analysis

RNA was obtained from day 0 (AT2), day 2 and day 4 (AT1-like) and day 6 (AT1-like) cells and sequenced. Briefly, total cell RNA was DNase I digested and then subjected to ribosomal RNA depletion with the Ribominus™ Eukaryote v2 kit (Life Technologies, # A15020, Grand Island, NY). Libraries were constructed with the TruSeq RNA Sample Prep Kit v2 (Illumina # RS-122-2001) and underwent Illumina HiSeq 2000 paired-end sequencing (2 x 50 bp) according to the manufacturer's instructions. Sequence reads were aligned to hg19 with TopHat2 v2.0.7 using default settings [86]. After mapping, data were further analyzed using Cufflinks [87] transcript assembly and quantification software (version 2.2.1) with default parameters and sequence bias detection and correction. Protein lysates obtained on days 0, 2, 4, and 6 were analyzed by Western blot to confirm proper *in vitro* differentiation, using antibodies specific for AT1 cells (anti-aquaporin 5 (AQP-005, Alomone Labs, Jerusalem, Israel) and anti-podoplanin (8.1.1, Santa Cruz Biotechnology, Santa Cruz, CA) and AT2 cells (anti-pro-surfactant protein C, AB3786, Millipore), with loading control anti-actin (AC-15 NB600-501, Novus Biologicals).

LUAD risk-associated SNPs collection

LUAD risk index SNPs were collected from published GWAS papers. A *P*-value cutoff of $\leq 5 \times 10^{-8}$ was applied for genome-wide significance. SNPs in high LD with LUAD index-SNPs ($r^2>0.5$) were retrieved using the online SNP annotation tool Haploreg v3, which calculates r^2 using data from the 1000 Genomes Project [40]. Because LD varies by ethnicity, this analysis was carried out taking into account the ethnicity of the population in which each index SNP was identified. Functional predictions for coding SNPs and miRNA targets were performed using ANNOVAR [88], which integrates data from PolyPhen-2 [89], SIFT [90] and TargetScan [91].

ChIP-seq and FAIRE-seq

Crosslinking and sonication for ChIP-seq and FAIRE-seq were performed using cells from day 0 (AT2), and cells from day 4 and day 6 (AT1-like) cells as described [45]. For ChIP-seq, chromatin was incubated with antibodies against H3K4me1 (Diagenode #pAb-037-050, Denville, NJ) and H3K27ac (Active Motif #39133, Carlsbad, CA) after sonication, and enrichment of AEC ChIP targets was confirmed by qPCR for each cell type. Libraries were created at the USC Epigenome Center and underwent Illumina GAII single-end sequencing as previously described. We used cutadapt-1.5 to filter low-quality reads. Remaining high-quality reads were aligned to reference human genome hg19 using bwa-0.7.7 with 2 mismatches allowed and mapping quality thresholds set to 20. Duplicate reads were removed with picard-tools-1.107. Peaks were called using SICER [92] (for FAIRE-seq, H3K27ac ChIP-seq, and H3K4me1 ChIP-seq respectively, window sizes of: 50bp, 100bp, 200bp; gap sizes of 50bp, 200bp and 200bp were used with an FDR cutoff =$1x10^{-4}$). Saturation plots (Supplementary Figure 3) were generated using the same peak calling methods on a proportion of reads. AEC ChIP-seq density plots (Supplementary Figure 5) were generated by running annotatePeaks.pl in HOMER [93].

For featured LUAD cell lines, raw FASTQ data for H3K27ac and H3K4me1 were downloaded from DBTSS (DataBase of Transcriptional Start Sites) database FTP (http://dbtss.hgc.jp) [71]. Quality control, alignment, duplicate removal, and peak calling were performed as described for AECs.

Identification of enhancer-associated SNPs

Candidate enhancer-associated SNPs were identified based on their position in both H3K27ac and H3K4me1 peaks in epigenomic data from day 0 (AT2), and/or day 4/day 6 (AT1-like). Candidate enhancer-associated SNPs that were significantly enriched (P<$1x10^{-3}$) for both H3K27ac and H3K4me1 signals were designated 'enhancer-associated SNPs' (AT1 or AT2-specific or general AEC enhancers). Enrichment analysis was performed in a 0.5 kb window flanking each SNP using the HOMER script getDifferentialPeaks and the R/Bioconductor packages rtracklayer and GenomicRanges (Supplementary Figure 6, https://www.bioconductor.org).

TF binding prediction

Sequences (±25 bp) around each AEC enhancer-associated SNPs containing ref/alt alleles were extracted using the R package "BSgenome.Hsapiens.UCSC.hg19". Motif positional weight matrixes (PWMs) compiled from ENCODE-motif [48], Factorbook [49] and HOCOMOCO [50] were downloaded and transformed into meme format. FIMO [95] was used to predict TF binding sites. We employed two approaches in TF motif identification. First, we used FIMO to predict TF motifs that overlap each SNP, with a significance threshold of P=1x10^{-4} based on Factorbook and HOCOMOCO motif databases. Secondly, we identified TFs with the potential to bind specific SNPs via integrating ENCODE/GEO TF ChIP-seq peaks over the locations of SNPs of interest. We then used FIMO to validate whether there are corresponding TF motifs formed/disrupted by the SNP, and set a less stringent threshold of P=1x10^{-3} for this step because binding predictions are supported by publicly-available ChIP-seq data for each factor at each SNP described and depicted in this manuscript. In addition, we checked the genotype of the SNP in available ChIP-seq data to determine whether the expected SNP allele forms the corresponding TF motif so that matched motif-TF events were identified. Furthermore, we limited all of our TFBS analyses to those cognate TFs with an AEC RPKM≥3, ensuring predicted TFs are expressed in AEC (Supplementary Figure 7).

Plasmid construction and luciferase enhancer assays

Putative enhancers spanning each SNP as well as the nearest DNAse HSS in A549 cells (ENCODE) were amplified by PCR from normal human male DNA (Promega #G1471, Madison, WI) using the primers listed in Supplementary Table 7. Amplicons were subcloned into the pGL4.26 luciferase plasmid (Promega, #E844A) upstream of a minimal promoter. The NEB Q5® Site-Directed Mutagenesis Kit (New England Biolabs #E0554S, Ipswich, MA) was used to change the allele under study. All constructs were verified by sequencing. All cell lines were transfected with the indicated constructs 48 hours prior to being harvested. A549 and H522 cells were transfected with Fugene HD (Promega #E2311) according to the manufacturer's instructions and H1648 cells were transfected with Lipofectamine® 3000 (ThermoFisher Scientific # L3000008, Waltham, MA). Luciferase assays were performed with the Dual-Luciferase Reporter Assay System (Promega # E1960) on the 96-well LUMIstar Omega Luminescence Microplate Reader (BMG LABTECH, Cary, NC) according to the manufacturer's instructions. All reported allele-specific enhancer activity represents the mean -/+ S.E.M. of three or more independent biological replicates assayed as technical triplicates.

eQTL tests

Tests in GTEx: eQTLs for rs452384 and rs6942067 were identified by directly searching the website of GTEx (The Genotype-Tissue Expression project) portal website [73].

Tests in TCGA: To identify eQTLs for rs6942067 in TCGA, we downloaded genomic information for 428 LUAD samples from the TCGA data portal website (https://tcga-data.nci.nih.gov/tcga/tcgaHome2.jsp). This included level-3 RNA-seq data, genotype, and methylation data. Expression data were log2 transformed ((log2(rsem+1)). Level-4 copy number variation (CNV) data were downloaded directly from the website (http://gdac.broadinstitute.org/runs/analyses__2014_01_15/data/LUAD/20140115/). For each gene, we calculated the methylation level as the mean beta value of all the CpGs within $\pm 1\text{kb}$ of the transcription start site (TSS). We used a multiple linear regression model to test the association between SNP genotype and gene expression, with adjustment for gene-level CNV and DNA methylation because CNV and DNA methylation might also influence gene expression. Since rs6942067 does not appear in the Affymetrix Genome-Wide Human SNP Array 6.0 platform (SNP 6.0), we chose rs6930292 (r^2 = 1, D' = 1 with rs6942067) as a surrogate for eQTL testing. For rs6942067, we performed eQTL analysis for rs6930292 against all genes within the flanking 1Mb region in the TCGA LUAD dataset. We also ruled out genes that are lowly expressed ((log2(rsem +1) <3). FDR was calculated using the Benjamini-Hochberg method, and the FDR cutoff was set at 0.05. Plots were generated using ggplot2 in R 3.1.1.

TCGA RNA expression analysis

Gene expression FPKM data (fragments per kilobase of transcript per million reads) from 521 LUAD tumor samples and 59 normal samples were downloaded using the TCGAbiolinks package (https://bioconductor.org/packages/release/bioc/html/TCGAbiolinks.html) and log2 transformed. Differential expression between tumor and normal tissue was assessed via Student's T-test. Plots were generated using ggplot2 in R 3.4.3.

AEC RNA expression analysis

RNA-seq was performed on the AEC sample for Day 0/2/4/6 respectively. Data were processed as described above in "AEC RNA isolation, RNA-seq, protein isolation and Western blot analysis**".** RPKMs were log2-transformed to represent the expression level.

TCGA Kaplan-Meier analysis

We used the TCGAanalyze_SurvivalKM function included in the TCGAbiolinks package. After removing duplicate tumor samples from the same subjects, we compared the survival of subjects in the highest tertile of *DCBLD1* expression (in FKPM) to subjects in the lowest tertile of expression. This resulted in a comparison of 161 subjects in the highest expression group to 161 subjects in the lowest expression group.

Data Visualization

The Integrative Genomics Viewer (IGV) 2.3.34 was used to visually inspect and graph all sequencing data [96]. All ChIP-seq QC plots were generated using R 3.1.1.

LEGENDS

Figure 1. Data generation and analysis flow chart. (A) 18 validated LUAD index SNPs with alleles indicated (the risk allele is colored red). (B) 47 AEC enhancer SNPs identified by integrating AEC ChIP-seq data, with alleles indicated (the inferred risk allele is colored red); presence in a FAIRE peak is marked as +. (C) SNP-affected TF binding motifs predicted in AEC enhancer SNPs in FAIRE peaks; those TFs whose binding is also supported by ChIP-seq evidence from publicly available datasets are colored red. SNPs for whom no TF biding motifs were predicted to be affected and no TF binding by ChIP has been reported are indicated by a gray box. (D) Luciferase enhancer assays for both alleles of regions containing rs452384 and rs6942067, tested in LUAD cell line H1648. (E) Potential eQTLs in lung tissues of the two investigated candidate AEC enhancer SNPs.

Figure 2. Epigenetic analysis of the rs452384 region. (A) Rs452384 is located in an intron of *CLPTM1L*. Histone enhancer marks and FAIRE peaks in the rs452384 region on day 0, 4 and 6 of AEC culture are indicated, and underneath each track, peaks called using SICER are marked. (B) ChIP-seq data for TF NKX2-1 from H3122 LUAD cells [51], which are homozygous for the reference (risk) T allele. (C) Predicted TF motifs for the sequences containing the reference (risk) and alternate alleles.

Figure 3. Epigenetic analysis of the rs6942067 region. (A) Rs6942067 is located in the intergenic region between gene *DCBLD1* and *ROS1*. Histone enhancer marks and FAIRE peaks in the rs6942067 region on day 0, 4 and 6 of AEC culture are indicated, and underneath each track, peaks called using SICER are marked. (B)

ChIP-seq data for TF EP300 from SK-N-SH neuroblastoma cells treated with retinoic acid [52], which are homozygous for the reference (risk) A allele. (C) Predicted TF motifs for the sequences containing the reference (risk) and alternate alleles.

Figure 4. Epigenetic analysis of the rs9481728 region. (A) Rs9481728 is located in an intron of *DCBLD1*. Histone enhancer marks and FAIRE peaks in the rs9481728 region on day 0, 4 and 6 of AEC culture are indicated, and underneath each track, peaks called using SICER are marked. (B) ChIP-seq data for TF EP300 from SK-N-SH neuroblastoma cells treated with retinoic acid [52], which are homozygous for the reference (risk) A allele. (C) Predicted TF motifs for the sequence containing the reference allele (no sites were predicted for the alternate allele).

Figure 5. Functional analyses for rs452384. (A) Enhancer luciferase assay performed in H1648 cells: relative luciferase signals were compared between cells transfected with the reference (T) or alternate (C) allele plasmids. (B) Association between rs452384 (T/C) and *TERT* expression in esophageal mucosa from the GTEx database. (C) Boxplot showing statistically significantly elevated expression of *TERT* in TCGA LUAD *vs.* non-tumor lung tissue. (D) Relative genomic positions of *TERT, CLPTM1L,* and SNP rs452384. (E) Association between rs452384 (T/C) and *CLPTM1L* expression in sun exposed skin from the GTEx database. (F) Boxplot showing statistically significantly elevated expression of *CLPTM1L* in TCGA LUAD *vs.* non-tumor lung tissue.

Figure 6. Functional analyses for rs6942067. (A) Enhancer luciferase assay performed in H1648 cells (459bp fragment, Figure S11B); relative luciferase signals were compared between cells transfected with either the reference (A) or alternate (G) allele plasmids. (B) Association between rs6942067 (A/G) and *DCBLD1* expression in lung from the GTEx database. (C) Association between rs6942067 and *DCBLD1* expression in LUAD tumors from the TCGA database. (D) Relative genomic positions of *DCBLD1* and SNP rs6942067. (E, F) The association between rs6942067 (A/G) and *DCBLD1* expression in blood cells (E) and thyroid (F) from the GTEx database. (G) Boxplot showing statistically significantly elevated expression of *DCBLD1* in TCGA LUAD *vs.* non-tumor lung tissue.

Supporting information

Supplementary Figure 1. Flow chart of bioinformatic and experimental analyses.

Supplementary Figure 2. *In vitro* differentiation of primary alveolar epithelial cells (A) Schematic of *in vitro* differentiation of AT2 to AT1-like cells and isolation of RNA and epigenomic materials. (B) Western blot to confirm AT2 cell to AT1-like cell differentiation. Lysates from day 0, 2, 4 and 6 in culture were probed by Western blot with antibodies for beta-actin (loading control), aquaporin 5 (AQP5), an AT1 cell protein involved in water homeostasis, podoplanin (PDPN), an AT1 cell membrane glycoprotein of unknown function, and surfactant protein C (SFTPC), an AT2 cell marker which is not expressed in AT1 cells.

Supplementary Figure 3. Saturation plots of ChIP-seq on AEC. Plots of peak number *vs*. reads number or relative reads number of (A) H3K27ac ChIP-seq, (B) H3K4me1 ChIP-seq, and (C) FAIRE-seq.

Supplementary Figure 4. Venn diagram of ChIP-seq peaks. Comparison of AEC ChIP-seq peaks between D0, D4 and D6 for (A) H3K27Ac, (B) H3K4me1 and (C) FAIRE.

Supplementary Figure 5. Relative ChIP-seq tag density around FAIRE peaks of AEC. D0 (A), D4 (B) and D6 (C).

Supplementary Figure 6. Process for identification of strong candidate functional SNPs located internally in enhancer histone marked regions. (A) We chose SNPs that lie in both H3K4me1 peaks and H3K27ac peaks as candidate enhancer-associated SNPs. In this example, SNP-2 and SNP-3 would be selected as candidate enhancer-associated SNPs. (B) To rule out low-confidence candidate enhancer-associated SNPs, we tested the enrichment of H3K4me1 and H3K27ac signals around the SNP (±500bp) versus ChIP-seq input signals. As an example, SNP2 but not SNP3 would be ruled out of the enhancer-associated SNP list.

Supplementary Figure 7. Process for identification of TFs that may be binding to the SNP regions.

Supplementary Figure 8. Epigenetic landscape around rs452384. From top to bottom are indicated: RefSeq genes (if present), FAIRE peaks in AEC at days 0, 4, 6 in culture, DNase hypersensitivity peaks in A549 cells (ENCODE data [48, 49], H3K27ac peaks (indicating active enhancers) in AEC at days 0, 4, 6 in culture, H3K4me1 peaks (indicating poised or active enhancers) in AEC at days 0, 4, 6 in culture, H3K27ac peaks in several LUAD cell lines (data from DBTSS [71]). Called peaks are underlined.

Supplementary Figure 9. Epigenetic landscape around rs6942067. From top to bottom are indicated: RefSeq genes (if present), FAIRE peaks in AEC at days 0, 4, 6 in culture, DNase hypersensitivity peaks in A549 cells (ENCODE data [48, 49], H3K27ac peaks (indicating active enhancers) in AEC at days 0, 4, 6 in

culture, H3K4me1 peaks (indicating poised or active enhancers) in AEC at days 0, 4, 6 in culture, H3K27ac peaks in several LUAD cell lines (data from DBTSS [71]). Called peaks are underlined.

Supplementary Figure 10. Epigenetic landscape around rs9481728. From top to bottom are indicated: RefSeq genes (if present), FAIRE peaks in AEC at days 0, 4, 6 in culture, DNase hypersensitivity peaks in A549 cells (ENCODE data [48, 49], H3K27ac peaks (indicating active enhancers) in AEC at days 0, 4, 6 in culture, H3K4me1 peaks (indicating poised or active enhancers) in AEC at days 0, 4, 6 in culture, H3K27ac peaks in several LUAD cell lines (data from DBTSS [71]). Called peaks are underlined.

Supplementary Figure 11. Histone enhancer marked areas containing the four top candidate SNPs in LUAD cell lines showing regions cloned for functional assays. Data is from the DBTSS database [71]. (A) Histone modifications in H1648 cells for rs452384 and the enhancer region cloned. (B) Histone modifications in H1648 for rs6942067 and the enhancer region cloned. (C) Histone modifications in H1648 cells for rs9481728 and the enhancer region cloned. (D) Histone modifications in A549 cells for rs11364096 and the enhancer region cloned.

Supplementary Figure 12. Histone enhancer marked areas in LUAD cell lines showing alternate region cloned for functional assay. As in Supplementary Figure 11A, but longer fragment around rs452384.

Supplementary Figure 13. Enhancer luciferase assay of rs6942067 in H522 cells. Relative luciferase signals were compared between clones with either reference (A) allele or alternative (G) allele.

Supplementary Figure 14. Enhancer luciferase assay of rs9481728 in H1648 cells. Relative luciferase signals were compared between clones with either reference (A) allele or alternative (G) allele.

Supplementary Figure 15. Kaplan Meier survival analysis of LUAD patients from TCGA using FPKM data. 161 subjects in the highest tertile of *DCBLD1* expression (in FKPM) were compared to 161 subjects in the lowest tertile of expression.

Supplementary Table 1. List of 930 LD SNPs. The table is based on data from HaploReg (v3, [40]) ordered by chromosome and position in the genome and includes the original index SNPs, which have been indicated in bold. Columns indicate, from left to right, SNP ID, chromosome number, position (based on GRCh37/hg19), reference and alternate alleles, LD indicators r2 and D, input (index) SNP, population tested ASN=Asian,

EUR=European, population related to index SNP information, presence of Biofeatures in HaploReg, number of biofeatures, the nature of observed biofeatures.

Supplementary Table 2. Annotation of LUAD risk-associated SNPs

Supplementary Table 3. Functional prediction of LUAD risk-associated SNPs located in exons

Supplementary Table 4. Functional prediction of LUAD risk-associated SNPs located in UTRs

Supplementary Table 5. SNPs located in promoter regions

Supplementary Table 6. ChIP-seq and FAIRE-seq statistics

Supplementary Table 7. Cloning primers for pGL4.26/ luciferase reporter gene constructs

Summary Points

- Integration of 948 candidate LUAD risk-associated SNPs with alveolar epithelial cell epigenomic information identified 47 SNPs in putative enhancer regions, marking them as candidate functional SNPS of increased interest.
- Focusing specifically on the 11 of the 47 SNPs that were located in open DNA as indicated by FAIRE analyses, 7 were predicted to disrupt transcription factor binding sites.
- Genomic fragments containing rs452384 showed increased luciferase activity over background (reporter vector lacking a genomic fragment), suggesting the region contains an enhancer, but no allele specific activity or lung eQTLs were detected.
- A genomic fragment carrying rs6942067 showed increased expression of the risk allele when examined in a luciferase reporter assay, indicating presence of an enhancer and the potential of the SNP to affect gene expression.
- eQTL of *DCBLD1* was observed in GTEx for rs6942067 in lung as well as thyroid, with higher expression of the alternate allele, while blood showed eQTL of *DCBLD1* with higher expression of the reference allele, suggesting the role of this SNP is likely complex.

- TCGA LUAD data showed increased *DCBLD1* expression in cells containing homozygous alternate alleles, and *DCBLD1* is significantly overexpressed in LUAD tumor *vs.* non-tumor lung in TCGA, supporting a possible role of this gene in LUAD development or progression.

References

1. Jemal A, Bray F, Center MM, Ferlay J, Ward E, Forman D. Global cancer statistics. *CA Cancer J. Clin.* 61(2), 69-90 (2011).
2. Toh CK, Lim WT. Lung cancer in never-smokers. *J. Clin. Pathol.* 60(4), 337-40 (2007).
3. Sun S, Schiller JH, Gazdar AF. Lung cancer in never smokers--a different disease. *Nat. Rev. Cancer.* 7(10), 778-90 (2007).
4. American Cancer Society. Cancer Facts & Figures 2015 (2015).
www.cancer.org/research/cancerfactsstatistics/cancerfactsfigures2015/index
5. Brennan P, Hainaut P, Boffetta P. Genetics of lung-cancer susceptibility. *Lancet Oncol.* 12(4), 399-408 (2011).
6. Lan Q, Hsiung CA, Matsuo K *et al.* Genome-wide association analysis identifies new lung cancer susceptibility loci in never-smoking women in Asia. *Nat Genet.* 44(12), 1330-5 (2012).
7. Li Y, Sheu CC, Ye Y *et al.* Genetic variants and risk of lung cancer in never smokers: a genome-wide association study. *Lancet Oncol.* 11(4), 321-30 (2010).
8. Coetzee SG, Rhie SK, Berman BP, Coetzee GA, Noushmehr H. FunciSNP: an R/bioconductor tool integrating functional non-coding data sets with genetic association studies to identify candidate regulatory SNPs. *Nucleic Acids Res.* 40(18), e139 (2012).
9. Tak YG, Farnham PJ. Making sense of GWAS: using epigenomics and genome engineering to understand the functional relevance of SNPs in non-coding regions of the human genome. *Epigenetics Chromatin.* 8, 57 (2015).

**** A thorough review about the utility of epigenomic information to identify functional risk SNPS.**

10. Schaub MA, Boyle AP, Kundaje A, Batzoglou S, Snyder M. Linking disease associations with regulatory information in the human genome. *Genome Res.* 22(9), 1748-59 (2012).
11. Freedman ML, Monteiro AN, Gayther SA *et al.* Principles for the post-GWAS functional characterization of cancer risk loci. *Nat. Genet.* 43(6), 513-8 (2011).
12. Farh KK, Marson A, Zhu J *et al.* Genetic and epigenetic fine mapping of causal autoimmune disease variants. *Nature.* 518(7539), 337-43 (2015).
13. Maurano MT, Haugen E, Sandstrom R *et al.* Large-scale identification of sequence variants influencing human transcription factor occupancy in vivo. *Nat. Genet.* 47(12), 1393-401 (2015).

*** An great example or large scale functional analysis of SNPs to identify functional variants implicated in TF binding.**

14. Hazelett DJ, Rhie SK, Gaddis M *et al.* Comprehensive functional annotation of 77 prostate cancer risk loci. PLoS Genet. 10(1), e1004102 (2014).
15. Rhie SK, Coetzee SG, Noushmehr H *et al.* Comprehensive functional annotation of seventy-one breast cancer risk Loci. PLoS One. 8(5), e63925 (2013).
16. Yao L, Tak YG, Berman BP, Farnham PJ. Functional annotation of colon cancer risk SNPs. *Nat. Commun.* 5, 5114 (2014).
17. Stueve TR, Marconett CN, Zhou B *et al.* The importance of detailed epigenomic profiling of different cell types within organs. *Epigenomics* 8(6), 817-829 (2016).

*** A manuscript emphasizing the importance and applications of obtaining epigenomes from many different cell types.**

18. Heintzman ND, Stuart RK, Hon G *et al.* Distinct and predictive chromatin signatures of transcriptional promoters and enhancers in the human genome. *Nat. Genet.* 39(3), 311-8 (2007).
19. Heintzman ND, Hon GC, Hawkins RD *et al.* Histone modifications at human enhancers reflect global cell-type-specific gene expression. *Nature.* 459(7243), 108-12 (2009).
20. Akhtar-Zaidi B, Cowper-Sal-lari R, Corradin O *et al.* Epigenomic enhancer profiling defines a signature of colon cancer. *Science.* 336(6082), 736-9 (2012).
21. Pasquali L, Gaulton KJ, Rodríguez-Seguí SA *et al.* Pancreatic islet enhancer clusters enriched in type 2 diabetes risk-associated variants. *Nat. Genet.* 46(2), 136-43 (2014).
22. Gjoneska E, Pfenning AR, Mathys H *et al.* Conserved epigenomic signals in mice and humans reveal immune basis of Alzheimer's disease. *Nature.* 518(7539), 365-9 (2015).
23. Wang Y, McKay JD, Rafnar T *et al.* Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. *Nat Genet.* 46(7), 736-41 (2014).
24. Shiraishi K, Kunitoh H, Daigo Y *et al.* A genome-wide association study identifies two new susceptibility loci for lung adenocarcinoma in the Japanese population. *Nat. Genet.* 44(8), 900-3 (2012).

25. Miki D, Kubo M, Takahashi A *et al.* Variation in TP63 is associated with lung adenocarcinoma susceptibility in Japanese and Korean populations. *Nat. Genet.* 42(10), 893-6 (2010).
26. Hsiung CA, Lan Q, Hong YC *et al.* The 5p15.33 locus is associated with risk of lung adenocarcinoma in never-smoking females in Asia. *PLoS Genet.* 6(8), e1001051 (2010).
27. Landi MT, Chatterjee N, Yu K *et al.* A genome-wide association study of lung cancer identifies a region of chromosome 5p15 associated with risk for adenocarcinoma. *Am. J. Hum. Genet.* 85(5), 679-91 (2009).
28. Hu Z, Wu C, Shi Y *et al.* A genome-wide association study identifies two new lung cancer susceptibility loci at 13q12.12 and 22q12.2 in Han Chinese. *Nat. Genet.* 43(8), 792-6 (2011).
29. Dong J, Hu Z, Wu C *et al.* Association analyses identify multiple new lung cancer susceptibility loci and their interactions with smoking in the Chinese population. *Nat. Genet.* 44(8), 895-9 (2012).
30. Wang Z, Seow WJ, Shiraishi K *et al.* Meta-analysis of genome-wide association studies identifies multiple lung cancer susceptibility loci in never-smoking Asian women. *Hum. Mol. Genet.* 25(3), 620-9 (2016).
31. Dobbs LG, Johnson MD, Vanderbilt J, Allen L, Gonzalez R. The great big alveolar TI cell: evolving concepts and paradigms. *Cell. Physiol. Biochem*. 25(1), 55-62 (2010).
32. Rackley CR, Stripp BR. Building and maintaining the epithelium of the lung. J. Clin. Invest. 122(8), 2724-30 (2012).

**** A review that provides a clear overview of cell types within the lung, information that is required when considering progenitors of lung cancer**

33. Wang J, Edeen K, Manzer R *et al.* Differentiated human alveolar epithelial cells and reversibility of their phenotype in vitro. *Am. J. Respir. Cell Mol. Biol.* 36(6), 661-8 (2007).
34. Ballard PL, Lee JW, Fang X *et al.* Regulated gene expression in cultured type II cells of adult human lung. *Am. J. Physiol. Lung Cell Mol. Physiol.* 299(1), L36-50 (2010).
35. Danto SI, Shannon JM, Borok Z, Zabski SM, Crandall ED. Reversible transdifferentiation of alveolar epithelial cells. *Am. J. Respir. Cell Mol. Biol.* 12(5), 497-502 (1995).
36. Desai TJ, Brownfield DG, Krasnow MA. Alveolar progenitor and stem cells in lung development, renewal and cancer. *Nature.* 507(7491), 190-4 (2014).

*** A discussion of the alveolar compartment of the lung and its contribution to lung cancer development.**

37. Xu X, Rock JR, Lu Y *et al.* Evidence for type II cells as cells of origin of K-Ras-induced distal lung adenocarcinoma. *Proc. Natl. Acad. Sci. USA.* 109(13), 4910-5 (2012).
38. Lin C, Song H, Huang C *et al.* Alveolar type II cells possess the capability of initiating lung tumor development. *PLoS One.* 7(12), e53817 (2012).
39. Mainardi S, Mijimolle N, Francoz S, Vicente-Dueñas C, Sánchez-García I, Barbacid M. Identification of cancer initiating cells in K-Ras driven lung adenocarcinoma. *Proc. Natl. Acad. Sci. USA.* 111(1), 255-60 (2014).
40. Khurana E, Fu Y, Colonna V *et al.* Integrative annotation of variants from 1092 humans: application to cancer genomics. *Science.* 342(6154), 1235587 (2013).
41. Falvella FS, Galvan A, Frullanti E *et al.* Transcription deregulation at the 15q25 locus in association with lung adenocarcinoma risk. *Clin. Cancer Res.* 15(5), 1837-42 (2009).
42. Nguyen JD, Lamontagne M, Couture C *et al*. Susceptibility loci for lung cancer are associated with mRNA levels of nearby genes in the lung. Carcinogenesis. 35(12), 2653–9 (2014).
43. Improgo MR, Scofield MD, Tapper AR, Gardner PD. The nicotinic acetylcholine receptor CHRNA5/A3/B4 gene cluster: dual role in nicotine addiction and lung cancer. *Prog. Neurobiol.* 92(2), 212-26 (2010).
44. Doyle GA, Wang MJ, Chou AD *et al.* In vitro and ex vivo analysis of CHRNA3 and CHRNA5 haplotype expression. *PLoS One.* 6(8), e23373 (2011).
45. Marconett CN, Zhou B, Rieger ME *et al.* Integrated transcriptomic and epigenomic analysis of primary human lung epithelial cell differentiation. *PLoS Genet.* 9(6), e1003513 (2013).
46. Giresi PG, Kim J, McDaniell RM, Iyer VR, Lieb JD. FAIRE (Formaldehyde-Assisted Isolation of Regulatory Elements) isolates active regulatory elements from human chromatin. *Genome Res.* 17(6), 877-85 (2007).
47. Sanyal A, Lajoie BR, Jain G, Dekker J. The long-range interaction landscape of gene promoters. *Nature.* 489(7414), 109-13 (2012).

*** A manuscript providing information on long range interactions between regulatory elements such as enhancers and their target genes.**

48. Kheradpour P, Kellis M. Systematic discovery and characterization of regulatory motifs in ENCODE TF binding experiments. *Nucleic Acids Res.* 42(5), 2976-87 (2014).

49. Wang J, Zhuang J, Iyer S *et al.* Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. *Nucleic Acids Res.* 41(Database issue), D171-6 (2013).
50. Kulakovskiy IV, Medvedeva YA, Schaefer U *et al.* HOCOMOCO: a comprehensive collection of human transcription factor binding sites models. *Nucleic Acids Res.* 41(Database issue), D195-202 (2013).
51. Marconett CN, Zhou B, Siegmund KD, Borok Z, Laird-Offringa IA. Transcriptomic Profiling of Primary Alveolar Epithelial Cell Differentiation in Human and Rat. *Genom Data.* 2, 105-9 (2014).
52. Bernstein BE, Birney E, Dunham I, Green ED, Gunter C, Snyder M. An integrated encyclopedia of DNA elements in the human genome. *Nature.* 489(7414), 57-74 (2012).
**** A solid primer on ENCODE, which provides and important resource of public epigenomic data.**
53. Watanabe H, Francis JM, Woo MS *et al.* Integrated cistromic and expression analysis of amplified NKX2-1 in lung adenocarcinoma identifies LMO3 as a functional transcriptional target. *Genes Dev.* 27(2), 197-210 (2013).
54. James MA, Vikis HG, Tate E, Rymaszewski AL, You M. CRR9/CLPTM1L regulates cell survival signaling and is required for Ras transformation and lung tumorigenesis. *Cancer Res.* 74(4):1116-27 (2014).
55. James MA, Wen W, Wang Y *et al.* Functional characterization of CLPTM1L as a lung cancer risk candidate gene in the 5p15.33 locus. *PLoS One.* 7(6), e36116 (2012).
56. Wang Z, Zhu B, Zhang M *et al.* Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. *Hum. Mol. Genet*. 23(24), 6616-33 (2014).
57. Chen XF, Cai S, Chen QG *et al.* Multiple variants of TERT and CLPTM1L constitute risk factors for lung adenocarcinoma. *Genet. Mol. Res.* 11(1), 370-8 (2012).
58. Timofeeva MN, Hung RJ, Rafnar T *et al.* Influence of common genetic variation on lung cancer risk: meta-analysis of 14 900 cases and 29 485 controls. *Hum. Mol. Genet.* 21(22), 4980-95 (2012).
59. Mocellin S, Verdi D, Pooley KA *et al.* Telomerase reverse transcriptase locus polymorphisms and cancer risk: a field synopsis and meta-analysis. *J. Natl. Cancer Inst.* 104(11), 840-54 (2012).
60. Minoo P. Transcriptional regulation of lung development: emergence of specificity. *Respir. Res.* 1(2), 109-15 (2000).
61. Herriges M, Morrisey EE. Lung development: orchestrating the generation and regeneration of a complex organ. *Development.* 141(3), 502-13 (2014).
62. Dang CV. c-Myc target genes involved in cell growth, apoptosis, and metabolism. *Mol. Cell. Biol.* 19(1), 1-11 (1999).
63. Seo AN, Yang JM, Kim H *et al.* Clinicopathologic and prognostic significance of c-MYC copy number gain in lung adenocarcinomas. *Br. J. Cancer.* 110(11), 2688-99 (2014).
64. Iwakawa R, Kohno T, Kato M *et al.* MYC amplification as a prognostic marker of early-stage lung adenocarcinoma identified by whole genome copy number analysis. *Clin. Cancer Res.* 17(6), 1481-9 (2011).
65. Iyer NG, Ozdag H, Caldas C. p300/CBP and cancer. *Oncogene.* 23(24), 4225-31 (2004).
66. Kan Z, Jaiswal BS, Stinson J *et al.* Diverse somatic mutation patterns and pathway alterations in human cancers. *Nature.* 466(7308), 869-73 (2010).
67. Rajatapiti P, Kester MH, de Krijger RR, Rottier R, Visser TJ, Tibboel D. Expression of glucocorticoid, retinoid, and thyroid hormone receptors during human lung development. *J. Clin. Endocrinol. Metab.* 90(7), 4309-14 (2005).
68. Kolla V, Gonzales LW, Gonzales J *et al.* Thyroid transcription factor in differentiating type II cells: regulation, isoforms, and target genes. *Am. J. Respir. Cell Mol. Biol.* 36(2), 213-25 (2007).
69. Hume R, Richard K, Kaptein E, Stanley EL, Visser TJ, Coughtrie MW. Thyroid hormone metabolism and the developing human lung. *Biol. Neonate.* 80 Suppl 1, 18-21 (2001).
70. Hellevik AI, Asvold BO, Bjøro T, Romundstad PR, Nilsen TI, Vatten LJ. Thyroid function and cancer risk: a prospective population study. *Cancer Epidemiol. Biomarkers Prev.* 18(2), 570-4 (2009).
71. Suzuki A, Wakaguri H, Yamashita R *et al.* DBTSS as an integrative platform for transcriptome, epigenome and genome sequence variation data. *Nucleic Acids Res.* 43(Database issue), D87-91 (2015).
*** Description of DBTSS, a great resouce for epigenomic information on lung cancer cell lines.**
72. Kachuri L, Amos CI, McKay JD *et al.* Fine mapping of chromosome 5p15.33 based on a targeted deep sequencing and high density genotyping identifies novel lung cancer susceptibility loci. *Carcinogenesis.* 37(1), 96-105 (2016).
73. Consortium G. The Genotype-Tissue Expression (GTEx) project. *Nat. Genet.* 45(6), 580-5 (2013).
**** Description of the Genotype-Tissue Expression (GTEx) project, a public resource to identify eQTLs.**

74. Ma X, Gong R, Wang R *et al.* Recurrent TERT promoter mutations in non-small cell lung cancers. *Lung Cancer.* 86(3), 369-73 (2014).
75. Calado RT. Telomeres in lung diseases. *Prog. Mol. Biol. Transl. Sci.* 125, 173-83 (2014).
76. James MA, Wen W, Wang Y, *et al.* Functional characterization of CLPTM1L as a lung cancer risk candidate gene in the 5p15.33 locus. *PLOS One* 7(6), e36116 (2012).
77. Ward LD, Kellis M. HaploReg v4: systematic mining of putative causal variants, cell types, regulators and target genes for human complex traits and disease. *Nucleic Acids Res.* 44(D1), D877-81 (2016).
**** Description of HaploReg, a key resource to carry our data mining on candidate risk variants.**
78. Astapova I. Role of co-regulators in metabolic and transcriptional actions of thyroid hormone. *J. Mol. Endocrinol.* 56(3), 73-97 (2016).
79. Caunt M, Mak J, Liang WC *et al.* Blocking neuropilin-2 function inhibits tumor cell metastasis. *Cancer Cell.* 13(4), 331-42 (2008).
80. Takeuchi K, Soda M, Togashi Y *et al.* RET, ROS1 and ALK fusions in lung cancer. *Nat. Med.* 18(3), 378-81 (2012).
81. Burman B, Zhang ZZ, Pegoraro G, Lieb JD, Misteli T. Histone modifications predispose genome regions to breakage and translocation. *Genes Dev.* 29(13), 1393-402 (2015).
82. Seow WJ, Matsuko K, Hsiung CA *et al.* Association between GWAS-identified lung adenocarcinoma susceptibility loci and EGFR mutations in never-smoking Asian women, and comparison with findings from Western populations. *Hum. Mol. Genet.* 26(2), 454-465 (2017).
83. McKay JD, Hung RJ, Han Y *et al.* Large-scale association analysis identifies new lung cancer susceptibility loci and heterogeneity in genetic susceptibility across histologial subtypes. Nature Genet. 49(7), 1126-1132 (2017).
*** A recent large analysis showing SNPS exhibit differental risk based lung cancer histological subtype.**
84. Sutherland KD, Berns A. Cell of origin of lung cancer. *Mol. Oncol.* 4(5), 397-403 (2010).
85. Van de Laar E, Clifford M, Hasenoeder S *et al.* Cell surface marker profiling of human tracheal basal cells reveals distinct subpopulations, identifies MST1/MSP as a mitogenic signal, and identifies new biomarkers for lung squamous cell carcinomas. *Respir. Res.* 15, 160 (2014).
86. Kim D, Pertea G, Trapnell C, Pimentel H, Kelley R, Salzberg SL. TopHat2: accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biol.* 14(4), R36 (2013).
87. Trapnell C, Williams BA, Pertea G *et al.* Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. *Nat. Biotechnol.* 28(5), 511-5 (2010).
88. San Lucas FA, Wang G, Scheet P, Peng B. Integrated annotation and analysis of genetic variants from next-generation sequencing studies with variant tools. *Bioinformatics.* 28(3), 421-2 (2012).
89. Adzhubei I, Jordan DM, Sunyaev SR. Predicting functional effect of human missense mutations using PolyPhen-2. Curr Protoc Hum Genet. Chapter 7, Unit7.20 (2013).
90. Ng PC, Henikoff S. SIFT: Predicting amino acid changes that affect protein function. *Nucleic Acids Res.* 31(13), 3812-4 (2003).
91. Friedman RC, Farh KK, Burge CB, Bartel DP. Most mammalian mRNAs are conserved targets of microRNAs. *Genome Res.* 19(1), 92-105 (2009).
92. Zang C, Schones DE, Zeng C, Cui K, Zhao K, Peng W. A clustering approach for identification of enriched domains from histone modification ChIP-Seq data. *Bioinformatics.* 25(15), 1952-8 (2009).
93. Heinz S, Benner C, Spann N *et al.* Simple combinations of lineage-determining transcription factors prime cis-regulatory elements required for macrophage and B cell identities. *Mol Cell.* 38(4), 576-89 (2010).
94. Zhang Y, Liu T, Meyer CA *et al.* Model-based analysis of ChIP-Seq (MACS). *Genome Biol.* 9(9), R137 (2008).
95. Charles E. Grant TLB, and William Stafford Noble. FIMO: Scanning for occurrences of a given motif. *Bioinformatics.* 27(7), 1017–1018 (2011).
96. Thorvaldsdóttir H, Robinson JT, Mesirov JP. Integrative Genomics Viewer (IGV): high-performance genomics data visualization and exploration. *Brief Bioinform.* 14(2), 178-92 (2013).

Table 1. Lung adenocarcinoma-associated risk index SNPs, listed by chromosome

Chr	Position (hg19)	Genes	SNPs	Population	Annotation	P values in GWAS [ref]
3	189356261	*TP63*	rs4488809	Asian	Intron	4.2×10^{-25} [28]
3	189357602	*TP63*	rs13314271	European	Intron	7.22×10^{-10} [23]
3	189383183	*TP63*	rs10937405	Asian	Intron	7×10^{-17} [24] 7×10^{-12} [25]
5	1286516	*TERT*	rs2736100	Asian, European	Intron	2.50×10^{-32} [24] 4×10^{-27} [6] 2.60×10^{-20} [26] 3×10^{-11} [25] 3.74×10^{-14} [27]
5	1287194	*TERT*	rs2853677	Asian	Intron	3×10^{-40} [24]
5	1325803	*CLPTM1L*	rs465498	Asian	Intron	1.20×10^{-13} [28]
5	146644115	*STK32A*	rs2895680	Asian	Intron	3.22×10^{-11} [29]
6	32368087	*BTNL2*	rs3817963	Asian	Intron	3×10^{-10} [24]
6	32433167	*HLA class II*	rs2395185	Asian	Intergenic	9.47×10^{-10} [6]
6	41493412	*FOXP4*	rs7741164	Asian	Intron	1.22×10^{-12} [30]
6	117786180	*ROS1, DCBLD1*	rs9387478	Asian	Intergenic	1.55×10^{-9} [6]
9	22160087	*CDKN2B-AS1*	rs72658409	Asian	Intergenic	1.94×10^{-9} [30]
10	114498476	*VTI1A*	rs7086803	Asian	Intron	1.19×10^{-11} [6]
12	52349071	*ACVR1B*	rs11610143	Asian	Intron	2.25×10^{-9} [30]
13	24293859	*MIPEP*	rs753955	Asian	Intergenic	3.90×10^{-10} [28]
15	78806023	*HYKK (AGPHD1)*	rs8034191	European	Intron	1.46×10^{-15} [27]
15	78894339	*CHRNA3*	rs1051730	European	Exon: Synonymous	7.10×10^{-19} [27]
17	65898809	*BPTF*	rs7216064	Asian	Intron	7×10^{-11} [24]

Note: To be included in our study, LUAD risk must have been specifically mentioned as affected by the SNP and the reported p-value must be $p \leq 5 \times 10^{-8}$. Chr: Chromosome; Position (hg19): Based on human genome 19 numbering; Genes: gene or nearest gene (if the SNP is not in a gene body) using Human Genome Organization name. GWAS: genome-wide association study.

Table 2. Enhancer-associated SNPs in lung adenocarcinoma, listed by chromosome

rsID	Chr	Pos (hg19)	Ref	Alt	r^2 **	D' **	Index SNP_ Population***	AEC_Type	Nearest Gene	Annotation	FAIRE-seq Peak
rs7631358	chr3	189348411	**G**	A	0.75	-0.94	rs4488809_ASN	AT1_specific	*TP63*	Intergenic	
rs76937731	chr3	189348968	**GCTCCA**	G	0.61	-0.92	rs4488809_ASN	AT1_specific	*TP63*	Intergenic	
rs380145	chr5	1328897	**C**	T	0.62	0.95	rs465498_ASN	AT1_specific	*CLPTM1L*	Intron	
rs452932	chr5	1330253	**T**	C	0.92	0.99	rs465498_ASN	AT1_specific	*CLPTM1L*	Intron	
rs452384	chr5	1330840	**T**	C	0.92	0.99	rs465498_ASN	AEC_specific	*CLPTM1L*	Intron	+
rs370348	chr5	1331219	**A**	G	0.89	0.95	rs465498_ASN	AT2_specific	*CLPTM1L*	Intron	
rs2447853	chr5	1333077	**A**	G	0.66	0.88	rs465498_ASN	AT1_specific	*CLPTM1L*	Intron	
rs31489	chr5	1342714	**C**	A	0.9	0.97	rs465498_ASN	AT1_specific	*CLPTM1L*	Intron	
rs31490	chr5	1344458	**G**	A	0.9	0.97	rs465498_ASN	AT2_specific	*CLPTM1L*	Intron	
rs31037	chr5	146615785	**T**	G	0.66	0.84	rs2895680_ASN	AT1_specific	*STK32A*	Intron	
rs9381074	chr6	41505196	T	**A**	0.7	0.86	rs7741164_ASN	AEC_specific	*FOXP4*	Intron	
rs9401006	chr6	117732924	**T**	C	0.63	0.8	rs9387478_ASN	AT1_specific	*ROS1*	Intron	
rs9385012	chr6	117733191	**T**	C	0.64	0.81	rs9387478_ASN	AT1_specific	*ROS1*	Intron	
rs9401007	chr6	117733275	**G**	A	0.64	0.81	rs9387478_ASN	AT1_specific	*ROS1*	Intron	
rs9385013	chr6	117733452	**C**	T	0.64	0.81	rs9387478_ASN	AT1_specific	*ROS1*	Intron	
rs1407185	chr6	117733650	**A**	T	0.61	0.82	rs9387478_ASN	AEC_specific	*ROS1*	Intron	
rs1407184	chr6	117733717	**G**	A	0.71	0.93	rs9387478_ASN	AEC_specific	*ROS1*	Intron	
rs1321816	chr6	117734533	**T**	C	0.66	0.84	rs9387478_ASN	AT1_specific	*ROS1*	Intron	
rs3777981	chr6	117735255	**A**	C	0.67	0.84	rs9387478_ASN	AEC_specific	*ROS1*	Intron	
rs2243	chr6	117737390	**G**	A	0.72	0.94	rs9387478_ASN	AEC_specific	*ROS1*	Intron	
rs9374658	chr6	117741495	**T**	G	0.73	0.94	rs9387478_ASN	AEC_specific	*ROS1*	Intron	
rs4945584	chr6	117750980	**T**	C	0.83	0.98	rs9387478_ASN	AT1_specific	*ROS1*	Intergenic	+
rs9372480	chr6	117760579	**C**	T	0.86	0.98	rs9387478_ASN	AT2_specific	*ROS1*	Intergenic	
rs4946254	chr6	117765313	**G**	A	0.87	0.97	rs9387478_ASN	AT2_specific	*ROS1*	Intergenic	
rs6941337	chr6	117768448	**A**	G	0.89	0.98	rs9387478_ASN	AEC_specific	*ROS1*	Intergenic	
rs6937083	chr6	117785308	**A**	T	1	1	rs9387478_ASN	AT1_specific	*DCBLD1*	Intergenic	
rs6942067	chr6	117785696	**A**	G	0.54	1	rs9387478_ASN	AT1_specific	*DCBLD1*	Intergenic	+
rs9320604	chr6	117816045	**G**	A	0.76	0.93	rs9387478_ASN	AT1_specific	*DCBLD1*	Intron	
rs4946259	chr6	117816093	**A**	G	0.56	0.95	rs9387478_ASN	AT1_specific	*DCBLD1*	Intron	
rs9481728	chr6	117817165	**C**	T	0.76	0.93	rs9387478_ASN	AEC_specific	*DCBLD1*	Intron	+
rs929057	chr6	117818911	**T**	A	0.76	0.93	rs9387478_ASN	AEC_specific	*DCBLD1*	Intron	+
rs929058	chr6	117819198	**A**	G	0.67	0.93	rs9387478_ASN	AEC_specific	*DCBLD1*	Intron	+
rs2057314	chr6	117819357	**A**	G	0.76	0.93	rs9387478_ASN	AEC_specific	*DCBLD1*	Intron	+
rs11364096	chr10	114502022	TG	**T**	1	1	rs7086803_ASN	AEC_specific	*VTI1A*	Intron	+
rs12217440	chr10	114502218	G	**A**	1	1	rs7086803_ASN	AT2_specific	*VTI1A*	Intron	
rs7094841	chr10	114502411	T	**C**	1	1	rs7086803_ASN	AEC_specific	*VTI1A*	Intron	
rs78223856	chr10	114527225	C	**T**	0.63	0.88	rs7086803_ASN	AT1_specific	*VTI1A*	Intron	+

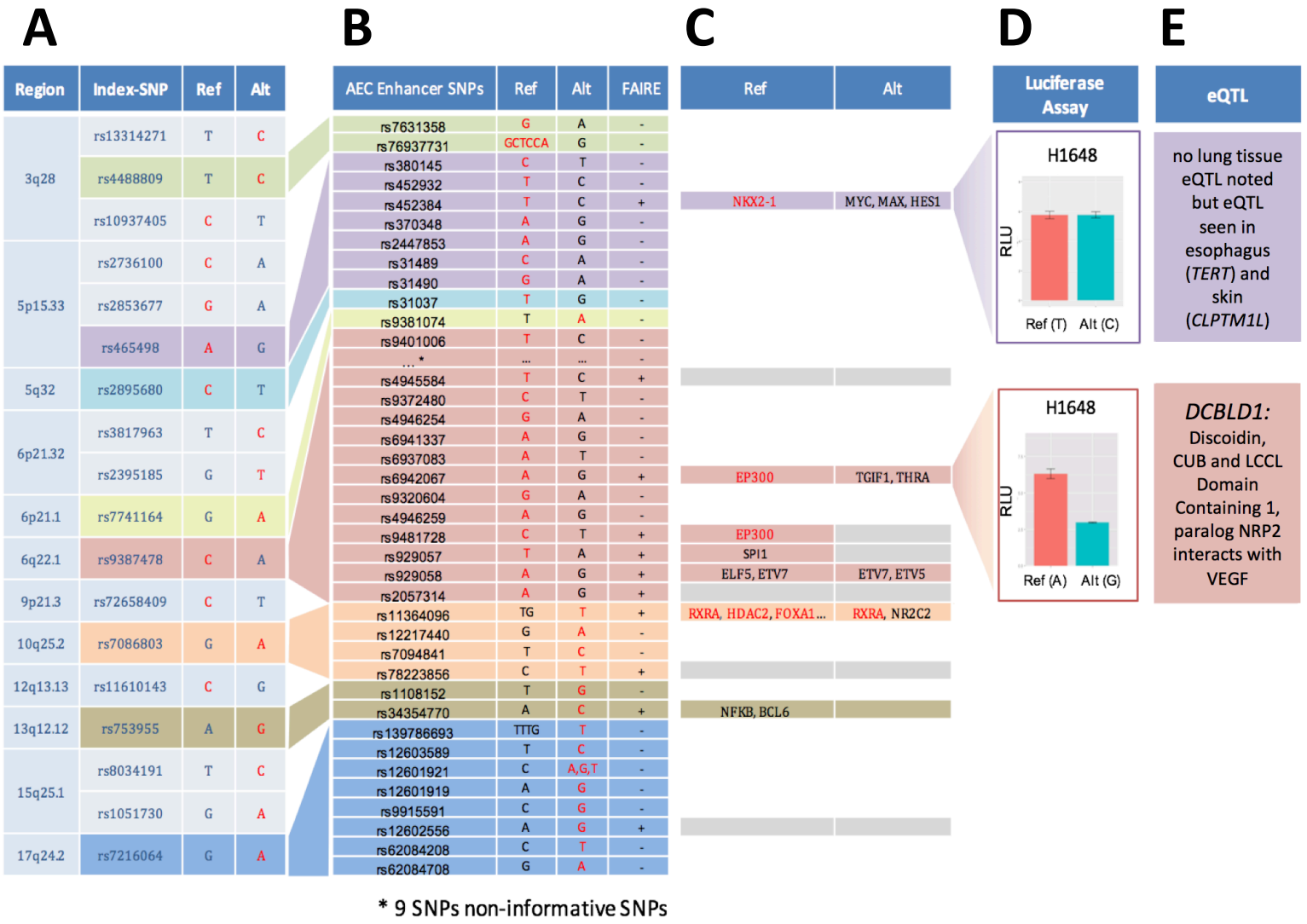
rs1108152	chr13	24312446	T	**G**	0.65	0.92	rs753955_ASN	AT1_specific	*MIPEP*	Intron	
rs34354770	chr13	24327618	A	**C**	0.59	0.88	rs753955_ASN	AEC_specific	*MIPEP*	Intron	+
rs139786693	chr17	65825228	TTTG	**T**	0.75	0.9	rs7216064_ASN	AT1_specific	*BPTF*	Intron	
rs12603589	chr17	65825248	T	**C**	0.8	0.91	rs7216064_ASN	AT1_specific	*BPTF*	Intron	+
rs12601921	chr17	65825354	C	**A,G,T**	0.72	0.92	rs7216064_ASN	AT1_specific	*BPTF*	Intron	
rs12601919	chr17	65825374	A	**G**	0.73	0.92	rs7216064_ASN	AT2_specific	*BPTF*	Intron	
rs9915591	chr17	65826090	C	**G**	0.81	0.92	rs7216064_ASN	AEC_specific	*BPTF*	Intron	
rs12602556	chr17	65826861	A	**G**	0.81	0.92	rs7216064_ASN	AEC_specific	*BPTF*	Intron	
rs62084208	chr17	65827443	C	**T**	0.81	0.92	rs7216064_ASN	AT1_specific	*BPTF*	Intron	
rs62084708	chr17	66049707	G	**A**	0.51	0.73	rs7216064_ASN	AT2_specific	*KPNA2*	Intergenic	

Chr: Chromosome; Position (hg19): Based on human genome 19 numbering; Ref: Reference allele (risk alleles indicated in bold); Alt: alternate allele (risk alleles indicated in bold); r2 and D': linkage disequilibrium information based on the population in which risk was identified for each SNP; ASN: Asian; AEC: alveolar epithelial cell; AT1: alveolar type 1 cell; AT2: alveolar type 2 cell; Nearest Gene: gene or nearest gene (if the SNP is not in a gene body) using Human Genome Organization name. GWAS: genome-wide association study. FAIRE-seq: formaldehyde-assisted identification of regulatory elements-sequencing.

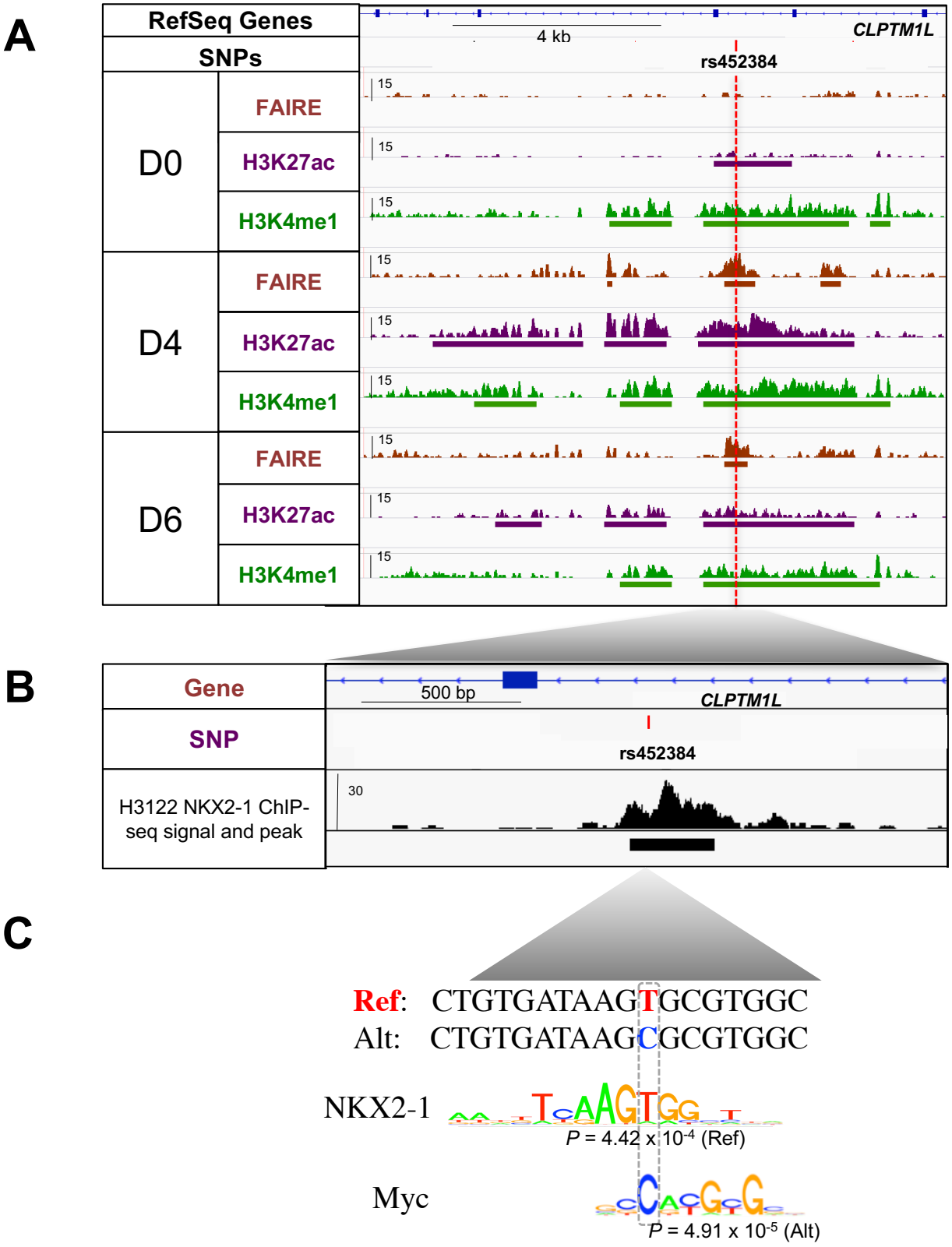
Table 3. Transcription factor binding motif prediction for AEC enhancer SNPs in FAIRE-seq peaks

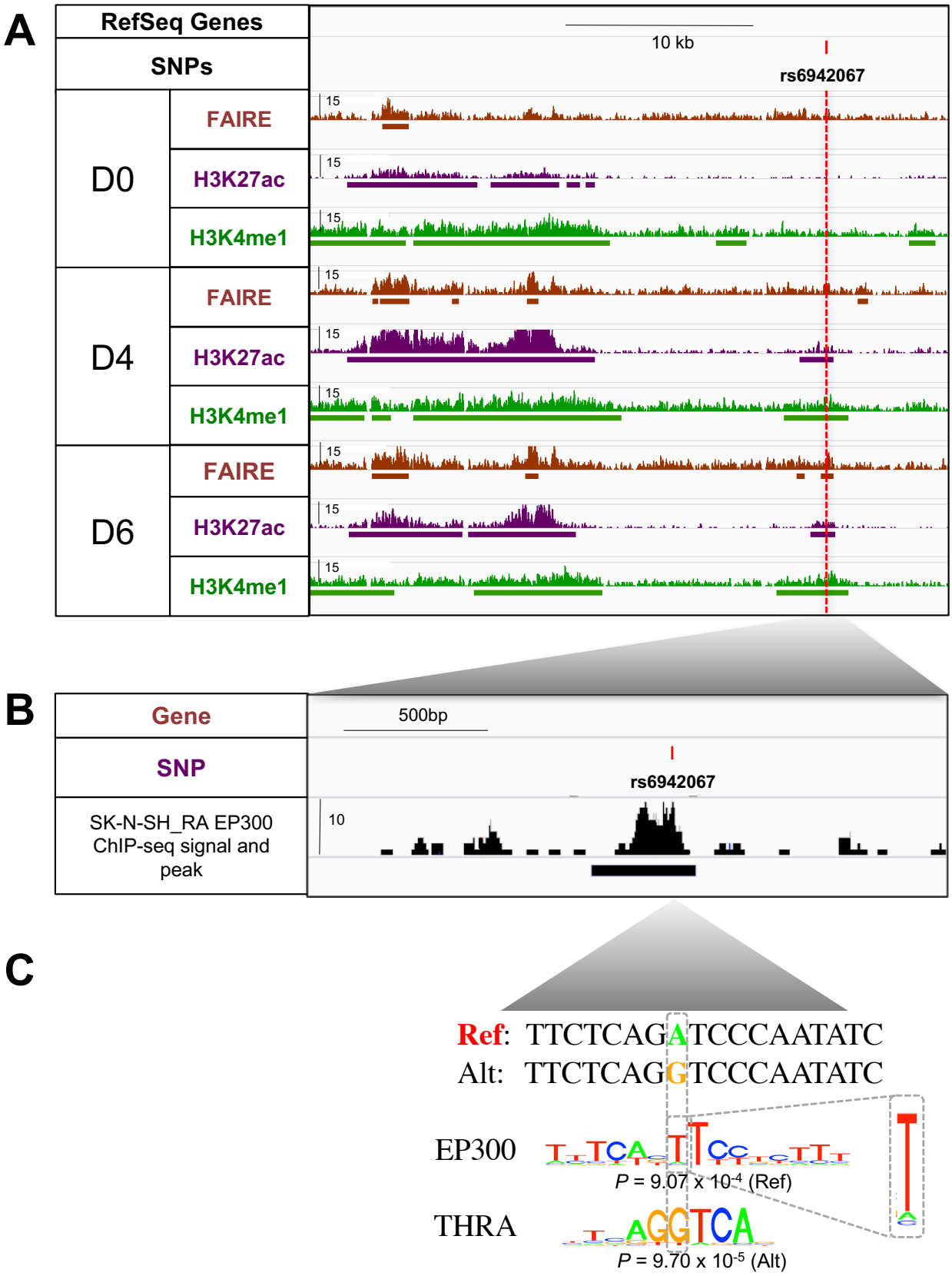
rsID	Ref	Alt	ChIP-seq TF Binding		
			Hom Ref	Het	Hom Alt
rs452384	**NKX2-1**	MYC, MAX, HES1	**NKX2-1**, MYC, FOS		
rs6942067	**EP300**	TGIF1, THRA	POLR2A, **EP300**	POLR2A, FOSL2, GATA2, JUN, FOS	JUND
rs9481728	**EP300**		POLR2A, **EP300**	GATA2, FOS, MAFK	
rs929057	SPI1				
rs929058	ELF5, ETV7	ETV7, ETV5			
rs2057314			PolR2A	PolR2A, TCF7L2, TCF12, SPI1, FOS	NFIC, SPI1
rs11364096	**RXRA, HDAC2, SP1, FOXA**, NR1H2, PPARG	RXRA, NR2C2	**RXRA, HDAC2, SP1, FOXA1,** FOXA2, EP300, CEBPB, GATA2, TCF7L2, NFIC, ZNF217, ESR1, MYBL2, POLR2A, ARID3A, STAT1, STAT3, FOS, HNF4G, NKX2-1		
rs34354770	NFKB, BCL6		FOXA2		
rs12602556				RBBP5, EGR1	

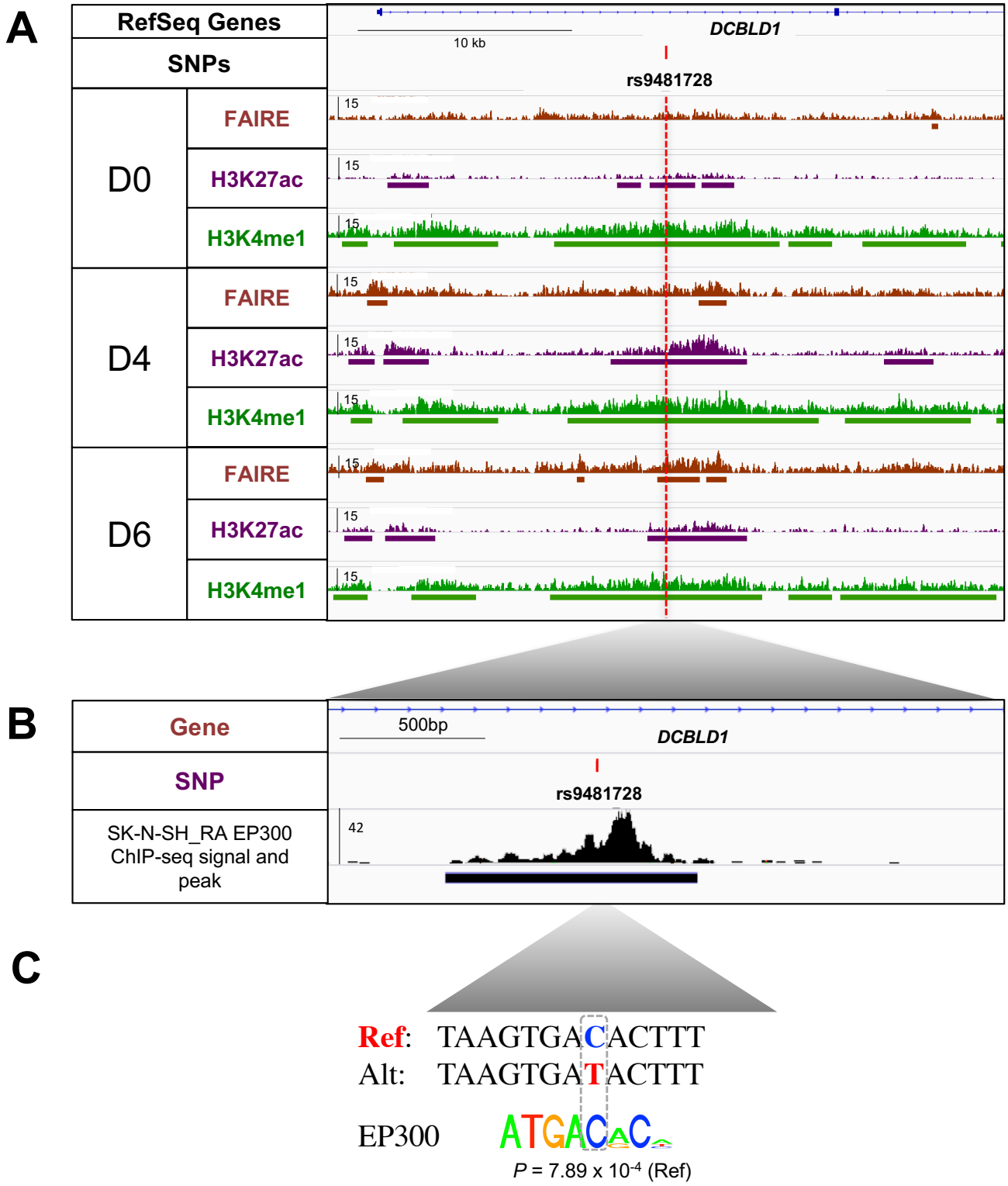
Note: Two of the 11 SNPs in FAIRE peaks (rs4945584 and rs78223856) showed no predicted TF motifs or evidence of ChIP-seq TF binding and are not listed. AEC: alveolar epithelial cell ; FAIRE-seq: formaldehyde-assisted identification of regulatory elements-sequencing; Ref: Reference allele (transcription factors (TFs) indicated in **bold** were both predicted *and* detected by ChIP-seq); Alt: alternate allele (transcription factors (TFs) indicated in **bold** were both predicted *and* detected by ChIP-seq); Hom Ref: ChIP-seq experiment carried out with cells containing a homozygous reference allele; Het: ChIP-seq experiment carried out with cells containing heterozygous alleles; Hom Alt: ChIP-seq experiment carried out with cells containing a homozygous alternate allele.

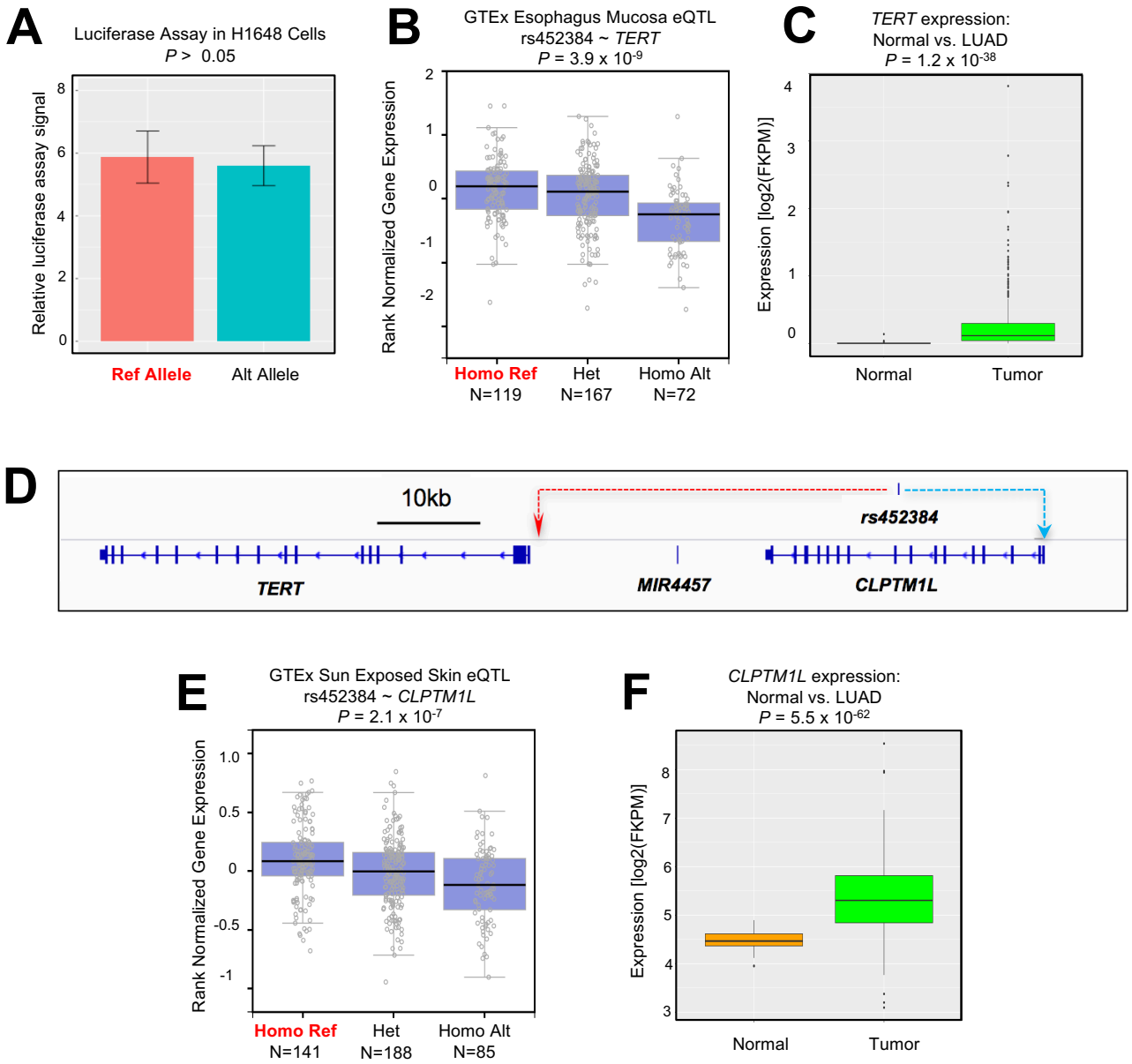


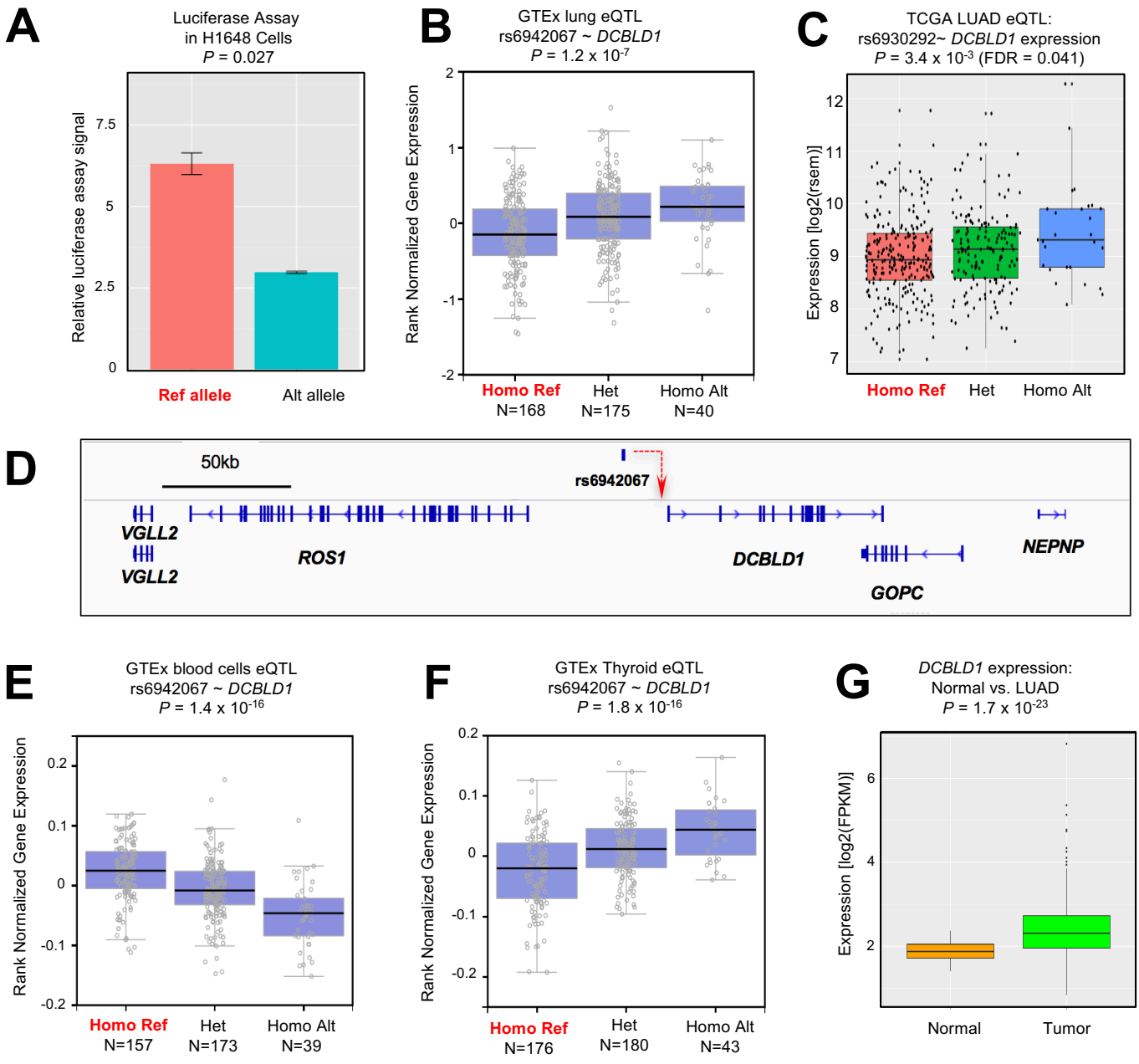
* 9 SNPs non-informative SNPs


A
RefSeq Genes
SNPs
D0
FAIRE
H3K27ac
H3K4me1
D4
FAIRE
H3K27ac
H3K4me1
D6
FAIRE
H3K27ac
H3K4me1
4 kb
CLPTM1L
rs452384
15
B
Gene
SNP
H3122 NKX2-1 ChIP-seq signal and peak
500 bp
CLPTM1L
rs452384
30
C
Ref: CTGTGATAAGTGCGTGGC
Alt: CTGTGATAAGCGCGTGGC
NKX2-1
P = 4.42 x 10-4 (Ref)
Myc
P = 4.91 x 10-5 (Alt)


A
RefSeq Genes
SNPs
D0
FAIRE
H3K27ac
H3K4me1
D4
FAIRE
H3K27ac
H3K4me1
D6
FAIRE
H3K27ac
H3K4me1
10 kb
rs6942067
15
B
Gene
SNP
SK-N-SH_RA EP300 ChIP-seq signal and peak
500bp
rs6942067
10
C
Ref: TTCTCAGATCCCAATATC
Alt: TTCTCAGGTCCCAATATC
EP300
P = 9.07 x 10-4 (Ref)
THRA
P = 9.70 x 10-5 (Alt)


A
RefSeq Genes
SNPs
DCBLD1
10 kb
rs9481728
D0
FAIRE
H3K27ac
H3K4me1
D4
FAIRE
H3K27ac
H3K4me1
D6
FAIRE
H3K27ac
H3K4me1
15
B
Gene
SNP
SK-N-SH_RA EP300 ChIP-seq signal and peak
500bp
DCBLD1
rs9481728
42
C
Ref: TAAGTGACACTTT
Alt: TAAGTGATACTTT
EP300
P = 7.89 x 10-4 (Ref)


A
Luciferase Assay in H1648 Cells
P > 0.05
Relative luciferase assay signal
Ref Allele
Alt Allele
B
GTEx Esophagus Mucosa eQTL
rs452384 ~ TERT
P = 3.9 x 10-9
Rank Normalized Gene Expression
Homo Ref
N=119
Het
N=167
Homo Alt
N=72
C
TERT expression:
Normal vs. LUAD
P = 1.2 x 10-38
Expression [log2(FKPM)]
Normal
Tumor
D
10kb
rs452384
TERT
MIR4457
CLPTM1L
E
GTEx Sun Exposed Skin eQTL
rs452384 ~ CLPTM1L
P = 2.1 x 10-7
Rank Normalized Gene Expression
Homo Ref
N=141
Het
N=188
Homo Alt
N=85
F
CLPTM1L expression:
Normal vs. LUAD
P = 5.5 x 10-62
Expression [log2(FKPM)]
Normal
Tumor


A
Luciferase Assay
in H1648 Cells
P = 0.027
Relative luciferase assay signal
7.5
5
2.5
0
Ref allele
Alt allele
B
GTEx lung eQTL
rs6942067 ~ DCBLD1
P = 1.2 x 10-7
Rank Normalized Gene Expression
2
1
0
-1
-2
Homo Ref
N=168
Het
N=175
Homo Alt
N=40
C
TCGA LUAD eQTL:
rs6930292~ DCBLD1 expression
P = 3.4 x 10-3 (FDR = 0.041)
Expression [log2(rsem)]
12
11
10
9
8
7
Homo Ref
Het
Homo Alt
D
50kb
rs6942067
VGLL2
VGLL2
ROS1
DCBLD1
GOPC
NEPNP
E
GTEx blood cells eQTL
rs6942067 ~ DCBLD1
P = 1.4 x 10-16
Rank Normalized Gene Expression
0.2
0.1
0
-0.1
-0.2
Homo Ref
N=157
Het
N=173
Homo Alt
N=39
F
GTEx Thyroid eQTL
rs6942067 ~ DCBLD1
P = 1.8 x 10-16
Rank Normalized Gene Expression
0.2
0.1
0
-0.1
-0.2
Homo Ref
N=176
Het
N=180
Homo Alt
N=43
G
DCBLD1 expression:
Normal vs. LUAD
P = 1.7 x 10-23
Expression [log2(FPKM)]
6
4
2
Normal
Tumor

rsID	chr	pos	ref	alt	r2	D.	Input_SNP	Population	IndexSNP_Info	Biofeature_Overlap	Biofeature_Overlap_Num	Biofeature_Overlap_Names
rs73188250	chr3	189301627	C	T	0.6,0.52	0.79,0.83	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs3922955	chr3	189302969	A	G	0.61,0.52	0.81,0.83	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs17443378	chr3	189303627	C	G	0.61,0.52	0.81,0.83	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs9849804	chr3	189303679	C	T	0.51	-0.92	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs6444389	chr3	189323685	T	G	0.58	0.93	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs1920288	chr3	189325289	A	G	0.57	0.92	rs13314271	EUR	rs13314271_EUR	TRUE	2	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs9822622	chr3	189326046	A	G	0.53	0.94	rs13314271	EUR	rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs73194153	chr3	189327230	G	A	0.52	-0.93	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs4687073	chr3	189327405	A	C	0.52	-0.94	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9882796	chr3	189330551	G	A	0.61	0.94	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs9812901	chr3	189331804	C	T	0.59	0.88	rs10937405	ASN	rs10937405_ASN	FALSE	0	NA
rs56260952	chr3	189334966	A	G	0.64,0.59	0.85,0.92	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs9825172	chr3	189335242	T	A	0.77,0.63	0.9,0.97	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs9881000	chr3	189335606	C	A	0.65,0.59	0.85,0.92	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs36108040	chr3	189335844	A	G	0.82,0.95	0.91,0.98	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs10937395	chr3	189336370	G	A	0.59	-0.89	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs4687076	chr3	189336473	T	C	0.6	0.89	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs35149393	chr3	189337394	C	T	0.6	-0.89	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs28632188	chr3	189337839	G	A	0.78,0.64	0.9,0.98	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs200520205	chr3	189338304	AAC	A	0.51	0.82	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs61298448	chr3	189338305	AC	A	0.56	0.88	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs34566957	chr3	189339311	T	G	0.6,0.6	-0.89,-0.95	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs142098434	chr3	189339377	C	CAT	0.61	0.9	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs9827043	chr3	189339497	G	T	0.56	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9864559	chr3	189339649	A	G	0.61	0.9	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs16864652	chr3	189340147	G	A	0.61	-0.9	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs7622692	chr3	189340241	C	G	0.56	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs71308969	chr3	189340886	G	A	0.61	-0.9	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs10937396	chr3	189341297	G	A	0.67,0.6	-0.87,-0.92	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs9332461	chr3	189341790	G	A	0.8,0.65	0.9,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs7643161	chr3	189342639	T	C	0.73	0.94	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs4398410	chr3	189344011	C	T	0.81,0.65	0.9,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs17444539	chr3	189344126	T	A	0.55	0.93	rs10937405	ASN	rs10937405_ASN	FALSE	0	NA
rs6790258	chr3	189344149	C	T	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs9830151	chr3	189345114	G	A	0.73	0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs34829136	chr3	189345366	G	A	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs35135349	chr3	189345380	A	G	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs34429293	chr3	189345519	G	T	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs34505637	chr3	189345631	G	A	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs71308970	chr3	189345904	C	A	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs6797409	chr3	189346522	C	A	0.62	-0.92	rs4488809	ASN	rs4488809_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9835951	chr3	189346567	C	T	0.8,0.65	0.9,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs6800124	chr3	189346815	C	G	0.62	-0.92	rs4488809	ASN	rs4488809_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs35139818	chr3	189346959	C	G	0.73	-0.93	rs4488809	ASN	rs4488809_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7631358	chr3	189348411	G	A	0.75	-0.94	rs4488809	ASN	rs4488809_ASN	TRUE	6	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs76937731	chr3	189348968	GCTCCA	G	0.61	-0.92	rs4488809	ASN	rs4488809_ASN	TRUE	5	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs13064999	chr3	189349501	G	A	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs13087793	chr3	189349742	T	C	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs34234442	chr3	189349846	GA	G	0.63	-0.93	rs4488809	ASN	rs4488809_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11928222	chr3	189350265	T	G	0.76	-0.95	rs4488809	ASN	rs4488809_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs36021505	chr3	189350483	G	A	0.65	-0.94	rs4488809	ASN	rs4488809_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs35837956	chr3	189350641	T	G	0.65	-0.94	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island
rs35867177	chr3	189350687	A	G	0.65	-0.94	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island
rs12107970	chr3	189353098	G	A	0.69	-1	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs12107966	chr3	189353186	C	T	0.69	-1	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs12374182	chr3	189354008	G	A	0.69	-1	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA

rs55779747	chr3	189354127	A	C	0.99,0.99	1,0.99	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs34951828	chr3	189354655	T	C	0.69	-1	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs11720249	chr3	189354741	C	T	0.59	-0.99	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs4396880	chr3	189356221	G	A	0.92,0.66	0.96,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs4488809	**chr3**	**189356261**	**T**	**C**	**1,0.98**	**1,0.99**	**rs4488809,rs13314271**	**ASN,EUR**	**rs4488809_ASN,rs13314271_EUR**	**FALSE**	**0**	**NA**
rs4381914	chr3	189356598	A	G	0.91,0.66	0.96,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs4396881	chr3	189356665	G	A	0.91,0.66	0.96,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs4327365	chr3	189356675	T	C	0.92,0.66	0.96,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs7636839	chr3	189356941	A	G	0.99,0.99	1,0.99	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs13080835	chr3	189357199	G	T	0.99,1	1,1	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs13314271	**chr3**	**189357602**	**T**	**C**	**0.99,1**	**1,1**	**rs4488809,rs13314271**	**ASN,EUR**	**rs4488809_ASN,rs13314271_EUR**	**FALSE**	**0**	**NA**
rs12696594	chr3	189357616	A	G	0.98,1	1,1	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs13325621	chr3	189358698	C	T	0.95,0.66	0.98,1	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs12107251	chr3	189358862	A	G	0.66	-0.96	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island
rs55862124	chr3	189359836	T	C	0.97,0.99	0.99,0.99	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs12107025	chr3	189359903	T	A	0.66	-0.97	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs7619517	chr3	189360235	T	C	0.97,0.99	0.99,0.99	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs7629983	chr3	189360406	A	G	0.97,0.98	0.99,0.99	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs13084874	chr3	189361400	T	C	0.97,0.98	0.99,0.99	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs6766775	chr3	189361939	C	G	0.66	-0.97	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs9837544	chr3	189362620	T	C	0.95,0.58	0.98,0.89	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs36092415	chr3	189362968	G	A	0.67	-0.98	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs9842008	chr3	189363001	T	C	0.85	0.97	rs10937405	ASN	rs10937405_ASN	FALSE	0	NA
rs9827354	chr3	189363999	C	T	0.54	0.84	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9827487	chr3	189364094	C	A	0.52	0.81	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9827991	chr3	189364424	C	T	0.54	0.85	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs1920235	chr3	189365424	A	G	0.67	0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs4687080	chr3	189365491	G	A	0.66	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs4687081	chr3	189365570	G	A	0.66	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9811174	chr3	189366595	G	A	0.8	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9811214	chr3	189366763	C	T	0.8	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs6807954	chr3	189366979	A	T	0.55	0.86	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs6808068	chr3	189367116	A	G	0.56	0.86	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs28612247	chr3	189367352	C	A	0.67	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs17504410	chr3	189367551	C	T	0.67	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs8179917	chr3	189368097	C	A	0.55	0.86	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9821164	chr3	189368255	G	A	0.8	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs4426661	chr3	189368357	T	A	0.8	-0.98	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs6772378	chr3	189368648	G	A	0.55	0.86	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs12330526	chr3	189368962	T	C	0.51	-0.8	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9826717	chr3	189369390	G	A	0.51	-0.8	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs12330765	chr3	189369843	A	T	0.51	-0.8	rs13314271	EUR	rs13314271_EUR	TRUE	1	CTCF_D0_2013_3_MB1B2B3_fdr1e2_MACS2_peaks
rs9869716	chr3	189370705	A	G	0.54	0.85	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs1920271	chr3	189370780	G	A	0.5	-0.79	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs1881992	chr3	189371811	G	T	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs9847400	chr3	189372997	G	T	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs13082542	chr3	189373303	T	C	0.65	-0.96	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs1920248	chr3	189373991	T	A	1,0.65	1,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs34729753	chr3	189376046	A	G	0.65	-0.96	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs4362700	chr3	189376305	A	G	1,0.65	1,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs9835487	chr3	189376356	C	T	1,0.65	1,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs13095135	chr3	189377530	A	C	0.65	-0.96	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs6809573	chr3	189378218	A	G	0.64	-0.95	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs1920272	chr3	189378556	A	G	0.94,0.96	0.98,0.98	rs4488809,rs13314271	ASN,EUR	rs4488809_ASN,rs13314271_EUR	FALSE	0	NA
rs13321778	chr3	189379290	C	G	0.57	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs1920273	chr3	189379493	G	A	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs1920274	chr3	189379524	A	G	0.57	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs73194199	chr3	189380470	C	A	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs73195959	chr3	189380483	G	A	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	FALSE	0	NA
rs73195961	chr3	189380563	G	A	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs73195962	chr3	189380707	G	T	0.67	-0.97	rs13314271	EUR	rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs62291707	chr3	189381256	G	A	1,0.66	1,0.99	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs10937404	chr3	189382083	G	A	0.57	-0.97	rs13314271	EUR	rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs6774934	chr3	189382257	A	G	0.65	-0.96	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs9816619	chr3	189382904	T	C	0.75	0.96	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs10937405	**chr3**	**189383183**	**C**	**T**	**1,0.5**	**1,0.8**	**rs10937405,rs13314271**	**ASN,EUR**	**rs10937405_ASN,rs13314271_EUR**	**TRUE**	**1**	**FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island**
rs4600802	chr3	189383430	C	T	0.75	0.96	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs2378507	chr3	189383538	A	G	1,0.63	1,0.97	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs2378508	chr3	189383780	T	C	0.75	0.96	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs9985415	chr3	189385947	C	T	0.99,0.64	1,0.98	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs74422675	chr3	189386155	CTA	C	0.65	-0.96	rs4488809	ASN	rs4488809_ASN	TRUE	1	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island
rs4011816	chr3	189388865	C	G	1,0.63	1,0.97	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs3954248	chr3	189389076	G	T	0.98	1	rs10937405	ASN	rs10937405_ASN	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island

rs138906960	chr3	189390410	AAAGG	A	0.55,0.66,0.65	0.96,0.94,0.93	rs10937405,rs4488809,rs133142	ASN,ASN,EUR	rs10937405_ASN,rs4488809_ASN,rs133142	FALSE	0	NA
rs6794898	chr3	189390700	G	C	1,0.63	1,0.97	rs10937405,rs13314271	ASN,EUR	rs10937405_ASN,rs13314271_EUR	FALSE	0	NA
rs13067268	chr3	189392029	A	G	0.64	-0.95	rs4488809	ASN	rs4488809_ASN	FALSE	0	NA
rs10054203	chr5	1279964	G	C	0.58	-0.78	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs7734992	chr5	1280128	T	C	0.62	-0.82	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs4975538	chr5	1280830	G	C	0.65	-0.88	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs34002450	chr5	1280940	GAGCCCACC	G	0.62	-0.89	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs7726159	chr5	1282319	C	A	0.81	-0.97	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs7725218	chr5	1282414	G	A	0.81,0.5	-0.97,-0.95	rs2736100,rs2736100	ASN,EUR	rs2736100_ASN,rs2736100_EUR	FALSE	0	NA
rs7713218	chr5	1283312	A	G	0.52,0.91,0.5	0.81,0.96,0.71	rs2853677,rs2736100,rs273610	ASN,ASN,EUR	rs2853677_ASN,rs2736100_ASN,rs2736100	FALSE	0	NA
rs7717443	chr5	1283486	T	C	0.78	0.9	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs4449583	chr5	1284135	C	T	0.79	-0.97	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs10866498	chr5	1285162	C	T	0.8	0.93	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs7705526	chr5	1285974	C	A	0.82	-0.95	rs2736100	ASN	rs2736100_ASN	FALSE	0	NA
rs2736100	**chr5**	**1286516**	**C**	**A**	**0.53,1,1**	**0.83,1,1**	**rs2853677,rs2736100,rs273610**	**ASN,ASN,EUR**	**rs2853677_ASN,rs2736100_ASN,rs2736100**	**TRUE**	**1**	**CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks**
rs2853677	**chr5**	**1287194**	**G**	**A**	**1,0.53**	**1,0.83**	**rs2853677,rs2736100**	**ASN,ASN**	**rs2853677_ASN,rs2736100_ASN**	**FALSE**	**0**	**NA**
rs2736099	chr5	1287340	A	G	0.66,0.52	0.91,0.74	rs2853677,rs2736100	ASN,ASN	rs2853677_ASN,rs2736100_ASN	FALSE	0	NA
rs2736102	chr5	1302144	T	C	0.72	-0.85	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs2853666	chr5	1302914	G	A	0.7	-0.85	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs2735945	chr5	1303901	T	C	0.79	-0.9	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs4404721	chr5	1306165	T	C	0.81	-0.91	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs4530805	chr5	1306331	T	C	0.79	-0.9	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs7446461	chr5	1306521	G	C	0.53	0.86	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs11133727	chr5	1306765	C	G	0.79	-0.9	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs201770763	chr5	1307434	T	TTA	0.74	-0.87	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs4635969	chr5	1308552	G	A	0.56	0.9	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs61574973	chr5	1309168	T	C	0.83	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs60622800	chr5	1309904	G	A	0.83	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs6554758	chr5	1310152	G	A	0.83	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs6866294	chr5	1311693	T	C	0.84	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs6866783	chr5	1312020	T	C	0.84	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs35953391	chr5	1312329	C	T	0.58	0.91	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs13356727	chr5	1312457	G	A	0.84	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs13355267	chr5	1312935	T	C	0.83	-0.91	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs36115365	chr5	1313242	G	C	0.58	0.91	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs28379291	chr5	1313701	A	G	0.84	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs10078017	chr5	1314009	C	T	0.84	-0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs4975615	chr5	1315343	G	A	0.84	-0.92	rs465498	ASN	rs465498_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4975616	chr5	1315660	G	A	0.84	-0.92	rs465498	ASN	rs465498_ASN	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs13170453	chr5	1317481	A	G	0.6	0.95	rs465498	ASN	rs465498_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs3816659	chr5	1317820	A	G	0.88	-0.95	rs465498	ASN	rs465498_ASN	TRUE	2	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs451360	chr5	1319680	C	A	0.64	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs421629	chr5	1320136	G	A	0.94	0.99	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs380286	chr5	1320247	G	A	0.8	1	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs381949	chr5	1322468	G	A	0.92	0.97	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs13178866	chr5	1323212	C	T	0.95	1	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs414965	chr5	1324121	G	A	0.95	1	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs421284	chr5	1325590	T	C	1	1	rs465498	ASN	rs465498_ASN	TRUE	1	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island
rs466502	chr5	1325767	A	G	1	1	rs465498	ASN	rs465498_ASN	TRUE	1	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island
rs465498	**chr5**	**1325803**	**A**	**G**	**1**	**1**	**rs465498**	**ASN**	**rs465498_ASN**	**TRUE**	**2**	**H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island**
rs11133729	chr5	1327101	C	G	0.95	1	rs465498	ASN	rs465498_ASN	TRUE	1	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island
rs383009	chr5	1327851	C	T	0.89	1	rs465498	ASN	rs465498_ASN	TRUE	1	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island
rs380145	chr5	1328897	C	T	0.62	0.95	rs465498	ASN	rs465498_ASN	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs452932	chr5	1330253	T	C	0.92	0.99	rs465498	ASN	rs465498_ASN	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island

rs452384	chr5	1330840	T	C	0.92	0.99	rs465498	ASN	rs465498_ASN	TRUE	8	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs370348	chr5	1331219	A	G	0.89	0.95	rs465498	ASN	rs465498_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs2447853	chr5	1333077	A	G	0.66	0.88	rs465498	ASN	rs465498_ASN	TRUE	6	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs397640	chr5	1334729	C	T	0.53	1	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs3030832	chr5	1335385	CTG	C	0.63	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs200350933	chr5	1335390	TGG	T	0.62	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs457130	chr5	1336178	A	T	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs467095	chr5	1336221	T	C	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs455433	chr5	1336243	A	G	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs460073	chr5	1336459	T	C	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs462608	chr5	1336626	T	A	0.9	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs456366	chr5	1337070	T	C	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs459961	chr5	1337106	T	A	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs31484	chr5	1337906	A	T	0.89	0.96	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs42269	chr5	1339985	C	A	0.83	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs31487	chr5	1341101	G	C	0.9	0.97	rs465498	ASN	rs465498_ASN	TRUE	1	H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs111986123	chr5	1342157	A	G	0.89	0.96	rs465498	ASN	rs465498_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs31489	chr5	1342714	C	A	0.9	0.97	rs465498	ASN	rs465498_ASN	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs31490	chr5	1344458	G	A	0.9	0.97	rs465498	ASN	rs465498_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs27996	chr5	1345474	A	G	0.88	0.95	rs465498	ASN	rs465498_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs27071	chr5	1346081	T	C	0.6	0.95	rs465498	ASN	rs465498_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs27070	chr5	1346303	G	C	0.88	0.96	rs465498	ASN	rs465498_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs27069	chr5	1347128	C	T	0.88	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs27068	chr5	1347239	C	T	0.59	0.93	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37011	chr5	1348798	A	T	0.86	0.94	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37010	chr5	1349535	A	G	0.84	0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37009	chr5	1350339	C	T	0.85	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs40182	chr5	1350397	G	A	0.83	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37008	chr5	1351538	G	A	0.85	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37007	chr5	1352372	G	C	0.88	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs57516180	chr5	1354022	GCTGGA	G	0.85	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs40181	chr5	1354462	G	T	0.88	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37006	chr5	1355058	C	T	0.88	0.95	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37005	chr5	1356450	C	T	0.82	0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37004	chr5	1356684	C	T	0.57	0.93	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37003	chr5	1356771	A	C	0.82	0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA
rs37002	chr5	1356944	C	T	0.82	0.92	rs465498	ASN	rs465498_ASN	FALSE	0	NA

rs31036	chr5	146615260	C	A	0.67	0.84	rs2895680	ASN	rs2895680_ASN	TRUE	8	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs31037	chr5	146615785	T	G	0.66	0.84	rs2895680	ASN	rs2895680_ASN	TRUE	7	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs4705137	chr5	146622239	C	T	0.71	0.85	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs1368283	chr5	146623961	T	A	0.71	0.85	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs7736308	chr5	146624907	C	A	0.71	0.85	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs1978705	chr5	146627598	T	C	0.77	0.88	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs10875620	chr5	146630321	T	C	0.77	0.88	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs4705030	chr5	146630724	G	C	0.8	0.91	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs11167971	chr5	146632594	C	T	0.8	0.91	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs11167973	chr5	146634669	T	C	0.85	0.92	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs9687343	chr5	146635568	T	C	0.85	0.93	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs9687216	chr5	146635761	A	G	0.85	0.92	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs11167981	chr5	146637156	A	G	0.87	0.95	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs6890102	chr5	146641615	T	C	1	1	rs2895680	ASN	rs2895680_ASN	TRUE	1	H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1155945	chr5	146642457	C	T	1	1	rs2895680	ASN	rs2895680_ASN	FALSE	0	NA
rs6869912	chr5	146642859	G	A	0.64	1	rs2895680	ASN	rs2895680_ASN	TRUE	1	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs2895680	**chr5**	**146644115**	**C**	**T**	**1**	**1**	**rs2895680**	**ASN**	**rs2895680_ASN**	**FALSE**	**0**	**NA**
rs199581114	chr5	146644672	ATC	A	0.59	0.98	rs2895680	ASN	rs2895680_ASN	TRUE	1	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island
rs6868578	chr5	146647271	C	G	0.6	0.88	rs2895680	ASN	rs2895680_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs9268434	chr6	32346452	A	T	0.57	0.91	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs9268458	chr6	32350384	C	A	0.81	0.9	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs4373382	chr6	32350868	A	C	0.57	0.91	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs9268460	chr6	32351283	T	C	0.58	0.91	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs4424066	chr6	32354428	A	G	0.66	0.98	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs9268472	chr6	32355605	G	A	0.66	0.98	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs9268473	chr6	32355683	A	G	0.61	0.91	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs9268476	chr6	32358942	T	A	0.64	0.92	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs3817973	chr6	32361111	C	T	0.66	0.98	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs2076533	chr6	32363527	C	T	0.66	0.98	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs2076530	chr6	32363816	T	C	0.57	0.98	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs2076529	chr6	32363955	T	C	0.66	0.98	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs3817966	chr6	32367847	T	C	0.99	1	rs3817963	ASN	rs3817963_ASN	FALSE	0	NA
rs3817963	**chr6**	**32368087**	**T**	**C**	**1**	**1**	**rs3817963**	**ASN**	**rs3817963_ASN**	**FALSE**	**0**	**NA**
rs9268833	chr6	32428062	C	T	0.91	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268834	chr6	32428079	C	A	0.91	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs147642819	chr6	32428097	T	TG	0.5	0.91	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268835	chr6	32428115	G	A	0.92	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268838	chr6	32428715	G	A	0.92	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268839	chr6	32428772	A	G	0.79	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268846	chr6	32429245	C	G	0.86	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268849	chr6	32429327	C	T	0.96	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268853	chr6	32429643	T	C	0.96	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268858	chr6	32429758	T	C	0.95	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268860	chr6	32429825	C	T	0.96	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268864	chr6	32430326	T	A	0.97	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs7747529	chr6	32431124	G	A	0.97	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268884	chr6	32431640	T	A	0.95	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs58667488	chr6	32431785	A	C	0.55	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268889	chr6	32431886	A	G	0.95	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268905	chr6	32432077	G	C	0.98	0.99	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268906	chr6	32432181	A	G	0.98	0.99	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268923	chr6	32432835	C	T	1	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs2395185	**chr6**	**32433167**	**G**	**T**	**1**	**1**	**rs2395185**	**ASN**	**rs2395185_ASN**	**FALSE**	**0**	**NA**
rs2395186	chr6	32433192	C	G	1	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs2894257	chr6	32433276	G	A,C,T	0.62	0.95	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268944	chr6	32433654	T	C	0.54	0.96	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268947	chr6	32433741	G	A	0.78	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268949	chr6	32433798	C	T	0.78	0.99	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268951	chr6	32433907	G	A	0.75	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268954	chr6	32434011	G	A	0.78	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA

rs9268960	chr6	32434130	T	C	0.73	0.87	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268961	chr6	32434135	G	A	0.72	0.87	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268963	chr6	32434149	C	T	0.72	0.87	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268965	chr6	32434240	G	A	0.97	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268969	chr6	32434349	C	T	1	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9268970	chr6	32434361	C	A	1	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9391781	chr6	32434850	G	C	1	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs4947340	chr6	32435338	C	T	0.71	0.95	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28654725	chr6	32435542	A	G	0.74	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895224	chr6	32435556	A	G	0.67	1	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895225	chr6	32435684	T	C	0.64	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs77701583	chr6	32435699	C	T	0.62	0.84	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs77244909	chr6	32436240	A	C	0.93	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs76914018	chr6	32436250	A	T	0.93	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895234	chr6	32437050	A	G	0.86	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895235	chr6	32437160	T	A	0.78	0.9	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9405038	chr6	32437614	G	T	0.9	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9368725	chr6	32438159	C	T	0.91	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9380306	chr6	32438298	A	G	0.89	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9368726	chr6	32438542	T	C	0.95	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9405108	chr6	32438648	C	T	0.95	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9391877	chr6	32438867	G	T	0.92	0.96	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9405109	chr6	32439029	T	C	0.92	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9405110	chr6	32439108	A	C	0.9	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9405040	chr6	32439393	A	C	0.82	0.97	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9286790	chr6	32439828	G	A	0.88	0.98	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9348886	chr6	32441008	C	T	0.87	0.94	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs12215261	chr6	32441150	C	A,G,T	0.86	0.93	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs12215313	chr6	32441276	C	T	0.76	0.92	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs13211921	chr6	32442836	T	G	0.63	0.86	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9391879	chr6	32443172	C	T	0.61	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9378264	chr6	32443451	G	A	0.61	0.86	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895241	chr6	32443665	T	C	0.5	0.7	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895242	chr6	32443666	G	C	0.51	0.72	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28732242	chr6	32444078	G	A	0.57	0.84	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28732244	chr6	32444096	C	T	0.57	0.78	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs12194148	chr6	32444198	G	T	0.62	0.87	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs12207473	chr6	32444330	A	C	0.61	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs12195582	chr6	32444544	C	T	0.55	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895251	chr6	32444708	T	A,G	0.51	0.72	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs113660101	chr6	32444733	TG	T	0.6	0.84	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895255	chr6	32445079	C	T	0.59	0.83	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895257	chr6	32445114	A	G	0.56	0.8	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895258	chr6	32445117	C	T	0.56	0.8	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28895261	chr6	32445306	G	A	0.56	0.79	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9405112	chr6	32445600	G	A	0.73	0.86	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9378212	chr6	32445691	C	T	0.59	0.86	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17209866	chr6	32445992	G	A	0.6	0.86	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17209873	chr6	32446010	T	C	0.55	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17209887	chr6	32446051	A	C	0.6	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203514	chr6	32446071	C	G	0.6	0.85	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17209907	chr6	32446261	C	T	0.6	0.78	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203549	chr6	32446307	T	C	0.5	0.74	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs139916710	chr6	32446425	GAAT	G	0.55	0.76	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203563	chr6	32446459	G	A,C,T	0.57	0.79	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17209950	chr6	32446588	G	A	0.71	0.84	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203570	chr6	32446674	A	T	0.5	0.71	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203612	chr6	32446853	A	T	0.55	0.81	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203619	chr6	32446922	T	C	0.58	0.81	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203626	chr6	32446994	G	A,T	0.5	0.73	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs17203636	chr6	32447014	G	A	0.56	0.82	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs29001652	chr6	32447111	A	G	0.57	0.83	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs29001478	chr6	32447162	G	A	0.55	0.81	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs29001620	chr6	32447216	A	T	0.57	0.83	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs28732246	chr6	32447219	G	A	0.57	0.83	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs29001568	chr6	32447341	G	A	0.57	0.83	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs35007143	chr6	32447518	T	A	0.5	0.72	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs4994859	chr6	32447715	A	G	0.52	0.76	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs4994855	chr6	32447873	A	G	0.55	0.81	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs4994854	chr6	32447900	T	C	0.54	0.79	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9394098	chr6	32449138	C	T	0.54	0.79	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9394099	chr6	32449160	G	T	0.5	0.73	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs9394100	chr6	32449188	G	A	0.5	0.81	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA

rs9394101	chr6	32449198	A	G	0.5	0.8	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs5018660	chr6	32449293	A	G	0.51	0.76	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs1964995	chr6	32449411	T	C	0.51	0.75	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs5020946	chr6	32450089	G	T	0.54	0.78	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs138473995	chr6	32451678	TC	T	0.57	0.76	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs71565331	chr6	32451693	T	C	0.55	0.75	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs62405565	chr6	32452281	C	G,T	0.59	0.77	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs71565340	chr6	32452506	C	T	0.57	0.76	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs34036879	chr6	32453336	G	T	0.56	0.79	rs2395185	ASN	rs2395185_ASN	FALSE	0	NA
rs2894439	chr6	41480093	G	A	0.53	0.84	rs7741164	ASN	rs7741164_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2496644	chr6	41482745	A	C	0.84	-0.95	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs181350472	chr6	41483123	A	G	0.83	0.94	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs9367106	chr6	41483390	G	C	0.79	0.9	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs9367107	chr6	41483450	G	A	0.86	0.95	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs12660421	chr6	41488378	G	A	0.95	0.98	rs7741164	ASN	rs7741164_ASN	TRUE	1	H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2495237	chr6	41488749	G	A	0.66	-0.97	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs1977358	chr6	41489854	T	C	0.89	-0.96	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs1977357	chr6	41490052	G	A	0.95	-0.98	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs41435745	chr6	41490382	G	C	0.95	0.98	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2495239	chr6	41490488	A	G	0.66	-0.97	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2495240	chr6	41491139	G	A	0.66	-0.97	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs7741164	**chr6**	**41493412**	**G**	**A**	**1**	**1**	**rs7741164**	**ASN**	**rs7741164_ASN**	**FALSE**	**0**	**NA**
rs4236076	chr6	41493703	A	G	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2477845	chr6	41494058	T	C	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2496655	chr6	41494367	A	G	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2495241	chr6	41494572	A	G	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2495242	chr6	41494849	A	G	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2495243	chr6	41495291	G	A	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs2495244	chr6	41495339	A	G	0.7	-1	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs1853837	chr6	41497035	C	A	0.94	0.99	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs55889968	chr6	41501225	A	G	0.7	0.86	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs12175265	chr6	41501834	G	A	0.7	0.86	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs1886814	chr6	41502683	A	C	0.68	0.85	rs7741164	ASN	rs7741164_ASN	FALSE	0	NA
rs4714474	chr6	41503561	G	A	0.7	0.86	rs7741164	ASN	rs7741164_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9381074	chr6	41505196	T	A	0.7	0.86	rs7741164	ASN	rs7741164_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs1321802	chr6	117725912	G	C	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	5	CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs3798390	chr6	117726553	C	T	0.61	0.79	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs7770923	chr6	117726980	C	A	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7771211	chr6	117727025	G	A	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7770814	chr6	117727056	A	G	0.7	0.91	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7771271	chr6	117727236	C	A	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7771437	chr6	117727313	C	T	0.57	0.79	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7772046	chr6	117727485	G	A	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7771637	chr6	117727491	A	G	0.59	0.78	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs765515	chr6	117727922	T	A,C	0.7	0.91	rs9387478	ASN	rs9387478_ASN	TRUE	2	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7776244	chr6	117727949	C	A	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	2	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs765516	chr6	117728118	C	T	0.62	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9489149	chr6	117729429	C	G	0.51	0.75	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs9489150	chr6	117730358	C	A	0.56	0.75	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs2273602	chr6	117730592	G	A	0.58	0.77	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs78716460	chr6	117731128	T	A	0.56	0.76	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1321800	chr6	117731129	C	T	0.55	0.77	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1321799	chr6	117731177	G	T	0.6	0.79	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island

rs1321798	chr6	117731192	A	G	0.6	0.79	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs3798393	chr6	117731968	G	C	0.59	0.79	rs9387478	ASN	rs9387478_ASN	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs3798394	chr6	117732362	A	T	0.6	0.79	rs9387478	ASN	rs9387478_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs9401006	chr6	117732924	T	C	0.63	0.8	rs9387478	ASN	rs9387478_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs9385012	chr6	117733191	T	C	0.64	0.81	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs9401007	chr6	117733275	G	A	0.64	0.81	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs9385013	chr6	117733452	C	T	0.64	0.81	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs1407185	chr6	117733650	A	T	0.61	0.82	rs9387478	ASN	rs9387478_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs1407184	chr6	117733717	G	A	0.71	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs1321816	chr6	117734533	T	C	0.66	0.84	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs3777981	chr6	117735255	A	C	0.67	0.84	rs9387478	ASN	rs9387478_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs2243	chr6	117737390	G	A	0.72	0.94	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island

rs9374658	chr6	117741495	T	G	0.73	0.94	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1853148	chr6	117750200	A	G	0.83	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs4945584	chr6	117750980	T	C	0.83	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	5	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs9372480	chr6	117760579	C	T	0.86	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4946254	chr6	117765313	G	A	0.87	0.97	rs9387478	ASN	rs9387478_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs6941337	chr6	117768448	A	G	0.89	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	7	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs9374662	chr6	117777804	G	A	0.99	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs13192511	chr6	117778381	C	T	0.51	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs9489199	chr6	117779546	G	T	0.51	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs2180811	chr6	117780158	T	A	0.99	1	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9481719	chr6	117780894	C	T	0.51	1	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4946256	chr6	117781276	T	C	0.99	1	rs9387478	ASN	rs9387478_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs6941824	chr6	117782356	T	C	0.51	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs9374663	chr6	117782634	A	G	0.99	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs6930292	chr6	117783770	G	T	0.54	1	rs9387478	ASN	rs9387478_ASN	TRUE	3	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs6910338	chr6	117783991	T	C	0.51	1	rs9387478	ASN	rs9387478_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs717970	chr6	117784418	A	C	0.54	1	rs9387478	ASN	rs9387478_ASN	TRUE	4	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs717969	chr6	117784567	G	T	0.54	1	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs6937083	chr6	117785308	A	T	1	1	rs9387478	ASN	rs9387478_ASN	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs6942067	chr6	117785696	A	G	0.54	1	rs9387478	ASN	rs9387478_ASN	TRUE	6	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9387478	**chr6**	**117786180**	**C**	**A**	**1**	**1**	**rs9387478**	**ASN**	**rs9387478_ASN**	**TRUE**	**2**	**H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island**
rs7739294	chr6	117786542	C	T	0.51	1	rs9387478	ASN	rs9387478_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1407182	chr6	117787124	C	T	0.54	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs1407181	chr6	117787151	T	G	0.54	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs7749229	chr6	117787897	C	T	0.51	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs13212002	chr6	117788146	A	G	0.54	1	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs34882116	chr6	117789497	G	C	0.99	0.99	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs1853147	chr6	117789587	A	C	0.53	0.99	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs1853146	chr6	117789811	T	A	0.51	0.96	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA

rs12528785	chr6	117791595	C	T	0.75	0.98	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs2883418	chr6	117791751	T	C	0.79	0.97	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs9387479	chr6	117792612	T	C	0.77	0.98	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs199734544	chr6	117793245	A	ATCC	0.71	0.98	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs112910733	chr6	117793246	T	TCCTG	0.7	0.98	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs6940922	chr6	117798204	C	T	0.79	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2354346	chr6	117798509	T	C	0.79	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4946258	chr6	117803538	C	T	0.72	0.95	rs9387478	ASN	rs9387478_ASN	TRUE	7	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs34431655	chr6	117803676	C	G	0.74	0.98	rs9387478	ASN	rs9387478_ASN	TRUE	4	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs6911915	chr6	117809031	T	C	0.7	0.94	rs9387478	ASN	rs9387478_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs2105907	chr6	117809225	A	G	0.7	0.94	rs9387478	ASN	rs9387478_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs9387481	chr6	117810822	T	C	0.74	0.92	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs9489213	chr6	117811706	A	T	0.76	0.93	rs9387478	ASN	rs9387478_ASN	FALSE	0	NA
rs12527127	chr6	117813269	G	C	0.75	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	4	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4945586	chr6	117815020	T	A	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9320604	chr6	117816045	G	A	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4946259	chr6	117816093	A	G	0.56	0.95	rs9387478	ASN	rs9387478_ASN	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9481728	chr6	117817165	C	T	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	7	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs929057	chr6	117818911	T	A	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	8	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs929058	chr6	117819198	A	G	0.67	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	9	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island

rs2057314	chr6	117819357	A	G	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	9	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs9688361	chr6	117821888	T	G	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs10683954	chr6	117822150	C	CTG	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs4946260	chr6	117822993	C	T	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs10782186	chr6	117823508	T	C	0.76	0.93	rs9387478	ASN	rs9387478_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs72693685	chr9	22143371	T	A	0.57	0.81	rs72658409	ASN	rs72658409_ASN	TRUE	2	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7853656	chr9	22144530	T	G	0.58	0.81	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs10965256	chr9	22151465	G	A	0.58	0.81	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs10965258	chr9	22153663	A	G	0.68	0.83	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs72658409	**chr9**	**22160087**	**C**	**T**	**1**	**1**	**rs72658409**	**ASN**	**rs72658409_ASN**	**TRUE**	**3**	**H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island**
rs10965267	chr9	22161828	T	G	1	1	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs10965270	chr9	22163090	G	A,C	1	1	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs861190	chr9	22166917	G	A	0.94	-0.98	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs828580	chr9	22168464	T	A	0.62	-0.89	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs10965274	chr9	22169978	C	T	0.62	0.89	rs72658409	ASN	rs72658409_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1981047	chr9	22173499	T	G	0.62	0.89	rs72658409	ASN	rs72658409_ASN	FALSE	0	NA
rs7899937	chr10	114450632	C	T	0.6	0.92	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7917140	chr10	114451006	T	C	0.59	0.92	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs148008143	chr10	114453238	G	A	0.8	0.92	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196059	chr10	114453368	C	A	0.6	0.92	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196060	chr10	114454166	C	T	0.55	0.88	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196061	chr10	114454170	C	T	0.56	0.89	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs60562286	chr10	114454187	T	A	0.81	0.93	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs6585171	chr10	114455505	C	G	0.6	0.94	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs6585172	chr10	114455816	G	T	0.61	0.94	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs150032814	chr10	114459501	C	T	0.81	0.93	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs146935756	chr10	114459753	C	T	0.81	0.94	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196063	chr10	114460013	A	C	0.81	0.94	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs58693092	chr10	114463096	G	A	0.83	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs79007922	chr10	114465429	T	A	0.83	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs3802554	chr10	114465770	C	T	0.63	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7898046	chr10	114465821	G	A	0.63	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7897837	chr10	114465872	A	G	0.63	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7077338	chr10	114466502	G	A	0.63	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs61228232	chr10	114467124	G	A	0.83	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7906312	chr10	114467517	C	A	0.63	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7911081	chr10	114468819	C	T	0.62	0.94	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7896810	chr10	114469091	T	C	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7896815	chr10	114469101	T	A	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7091778	chr10	114469514	G	A	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs10885373	chr10	114469529	G	A	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7919503	chr10	114470504	A	G	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196070	chr10	114471565	C	G	0.56	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs146945846	chr10	114473224	CATT	C	0.87	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7090942	chr10	114474934	G	A	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196072	chr10	114476466	T	C	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs963460	chr10	114481070	G	A	0.65	0.95	rs7086803	ASN	rs7086803_ASN	TRUE	4	CTCF_D0_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island
rs7922476	chr10	114482213	G	A	0.51	0.79	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs6585180	chr10	114482501	A	G	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs61570109	chr10	114484689	CT	C	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs10885377	chr10	114485063	T	G	0.65	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7088796	chr10	114486621	G	A	0.66	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7088860	chr10	114486867	A	G	0.88	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA

rs12265047	chr10	114487925	G	A	0.89	-0.96	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196080	chr10	114492578	T	A	0.94	0.97	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7915752	chr10	114492742	C	G	0.7	0.96	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs2419812	chr10	114492835	G	T	0.94	0.97	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs1885281	chr10	114492898	A	G	0.94	0.97	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs75295815	chr10	114493066	A	C	0.94	0.97	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs1885282	chr10	114493097	C	T	0.94	0.97	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs112342409	chr10	114493532	A	G	0.76	0.96	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7920475	chr10	114493880	G	A	0.96	0.98	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs10885380	chr10	114494296	G	A	0.96	0.98	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs34486819	chr10	114495868	G	A	0.6	0.94	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs41292624	chr10	114496717	G	A	0.99	1	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7086803	**chr10**	**114498476**	**G**	**A**	**1**	**1**	**rs7086803**	**ASN**	**rs7086803_ASN**	**FALSE**	**0**	**NA**
rs7916100	chr10	114500118	G	A	1	1	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7916159	chr10	114500377	A	G	1	1	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs6585182	chr10	114500402	A	G	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7096588	chr10	114500851	A	C	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs7075510	chr10	114501509	C	T	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	6	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7075671	chr10	114501685	A	G	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	7	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11364096	chr10	114502022	TG	T	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	7	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12217440	chr10	114502218	G	A	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7094841	chr10	114502411	T	C	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7085406	chr10	114503496	G	C	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7086477	chr10	114504405	C	T	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7090269	chr10	114504533	G	A	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7090171	chr10	114504597	C	A	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11196086	chr10	114505098	C	T	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs11196087	chr10	114506406	T	C	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7070850	chr10	114507596	G	C	0.52	1	rs7086803	ASN	rs7086803_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11196088	chr10	114507733	G	A	1	1	rs7086803	ASN	rs7086803_ASN	TRUE	2	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11196089	chr10	114509290	T	C	0.98	1	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs75514019	chr10	114515219	G	A	0.9	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs17130045	chr10	114515330	C	T	0.9	0.95	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs7073675	chr10	114520515	G	T	0.75	0.91	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196096	chr10	114525358	G	A	0.63	0.88	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs12217233	chr10	114525553	G	T	0.63	0.88	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA

rs78223856	chr10	114527225	C	T	0.63	0.88	rs7086803	ASN	rs7086803_ASN	TRUE	7	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11196100	chr10	114530518	C	G	0.59	0.83	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs59967370	chr10	114530941	C	A	0.59	0.83	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196101	chr10	114531094	T	C	0.59	0.83	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs6585187	chr10	114531711	C	A	0.59	0.83	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs79272970	chr10	114535302	A	G	0.6	0.84	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196106	chr10	114542699	T	C	0.56	0.82	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs11196107	chr10	114544657	A	G	0.54	0.79	rs7086803	ASN	rs7086803_ASN	FALSE	0	NA
rs10783484	chr12	52331681	C	T	0.67	0.92	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs61914027	chr12	52343231	C	A	0.93	0.98	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs58617820	chr12	52343370	T	C	0.9	0.96	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs61914028	chr12	52343480	G	A	0.92	0.97	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs4761839	chr12	52346983	G	A	0.98	0.99	rs11610143	ASN	rs11610143_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7962469	chr12	52348259	A	G	0.85	-1	rs11610143	ASN	rs11610143_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11610143	**chr12**	**52349071**	**C**	**G**	**1**	**1**	**rs11610143**	**ASN**	**rs11610143_ASN**	**TRUE**	**3**	**H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island**
rs11612312	chr12	52349088	T	C	1	1	rs11610143	ASN	rs11610143_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs79583832	chr12	52352239	CA	C	1	1	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs61914045	chr12	52352301	G	A	1	1	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs813469	chr12	52352449	G	A	0.82	0.98	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs813470	chr12	52352745	G	A	0.85	1	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs772222	chr12	52356892	A	G	0.71	0.94	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs771997	chr12	52358168	G	A	0.76	0.94	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs771998	chr12	52358195	T	C	0.75	0.94	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs10876222	chr12	52362479	T	A	0.76	0.94	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs10783486	chr12	52362786	G	A	0.76	0.94	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs11169970	chr12	52368428	G	A	0.84	0.93	rs11610143	ASN	rs11610143_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2242106	chr12	52369300	C	T	0.76	0.94	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs3214829	chr12	52369955	A	AA,AG	0.76	0.94	rs11610143	ASN	rs11610143_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11169971	chr12	52371341	T	A	0.76	0.94	rs11610143	ASN	rs11610143_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs34437092	chr12	52379238	A	G	0.83	0.92	rs11610143	ASN	rs11610143_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs2252518	chr12	52381026	C	A	0.76	0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs2252526	chr12	52381230	G	T	0.75	0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs4761841	chr12	52383227	G	C	0.86	-0.94	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs4761842	chr12	52383229	G	C	0.8	-0.92	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs2453069	chr12	52383641	C	T	0.75	-0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs7301802	chr12	52384353	G	A	0.74	0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs2641530	chr12	52384811	C	T	0.74	-0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs4762039	chr12	52387337	G	A	0.76	0.93	rs11610143	ASN	rs11610143_ASN	TRUE	2	CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2854464	chr12	52388891	A	G	0.71	0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs2359997	chr12	52391833	C	T	0.76	0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs877869	chr12	52392200	G	A	0.76	0.93	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs11169975	chr12	52394974	C	G	0.63	0.88	rs11610143	ASN	rs11610143_ASN	FALSE	0	NA
rs1104905	chr13	24278349	C	T	0.58	0.84	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs57766297	chr13	24284374	A	G	0.84	0.97	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs9580740	chr13	24286322	A	T	0.89	0.98	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs2147662	chr13	24288993	G	A	0.75	0.99	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs2861539	chr13	24289783	A	G	0.88	0.98	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs12867512	chr13	24289849	G	A	0.88	0.99	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs11617518	chr13	24290267	C	T	0.88	0.99	rs753955	ASN	rs753955_ASN	TRUE	3	CTCF_D0_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks
rs9580741	chr13	24290621	T	C	0.88	0.99	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs745068	chr13	24291878	T	G	0.88	0.99	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs745069	chr13	24291972	T	C	0.96	0.99	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs753955	**chr13**	**24293859**	**A**	**G**	**1**	**1**	**rs753955**	**ASN**	**rs753955_ASN**	**TRUE**	**1**	**H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island**

rs753954	chr13	24294105	G	A	0.98	1	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs753953	chr13	24294158	C	T	0.98	1	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs12867179	chr13	24294903	C	T	0.97	1	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs7993131	chr13	24297153	A	C	0.75	-0.93	rs753955	ASN	rs753955_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7999422	chr13	24297905	T	C	0.69	-0.94	rs753955	ASN	rs753955_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs6490821	chr13	24298343	G	A	0.69	-0.94	rs753955	ASN	rs753955_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7337010	chr13	24298485	A	C	0.68	-0.93	rs753955	ASN	rs753955_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9507149	chr13	24299435	T	C	0.69	-0.94	rs753955	ASN	rs753955_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2861538	chr13	24302284	G	A	0.66	0.93	rs753955	ASN	rs753955_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1108152	chr13	24312446	T	G	0.65	0.92	rs753955	ASN	rs753955_ASN	TRUE	6	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs17421051	chr13	24323383	C	T	0.61	0.89	rs753955	ASN	rs753955_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7330379	chr13	24325156	A	G	0.6	0.89	rs753955	ASN	rs753955_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs17336602	chr13	24326052	G	C	0.6	0.89	rs753955	ASN	rs753955_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4770489	chr13	24326754	A	G	0.6	0.89	rs753955	ASN	rs753955_ASN	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs34354770	chr13	24327618	A	C	0.59	0.88	rs753955	ASN	rs753955_ASN	TRUE	8	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs1886531	chr13	24333884	C	T	0.53	0.82	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs12428143	chr13	24339825	A	G	0.52	0.82	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs35572228	chr13	24341296	A	T	0.5	0.79	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs7332361	chr13	24343336	C	G	0.5	0.79	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs61946408	chr13	24344585	G	A	0.5	0.79	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs7318823	chr13	24348330	C	T	0.5	0.79	rs753955	ASN	rs753955_ASN	FALSE	0	NA
rs200422183	chr15	78719501	A	AT	0.51	0.74	rs8034191	EUR	rs8034191_EUR	FALSE	0	NA
rs72736802	chr15	78719501	A	T	0.51	0.72	rs8034191	EUR	rs8034191_EUR	FALSE	0	NA
rs72738704	chr15	78719832	G	C	0.55,0.63	0.76,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs951985	chr15	78720923	T	G	0.52	0.79	rs8034191	EUR	rs8034191_EUR	FALSE	0	NA
rs1394371	chr15	78724469	C	T	0.5	0.81	rs8034191	EUR	rs8034191_EUR	FALSE	0	NA
rs17483548	chr15	78730313	G	A	0.57,0.66	0.76,0.82	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	9	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs17405217	chr15	78731149	C	T	0.57,0.66	0.76,0.82	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	7	CTCF_D0_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs17483686	chr15	78733390	A	T	0.55,0.64	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs17483721	chr15	78733731	T	C	0.55,0.64	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island

rs139043337	chr15	78734588	ATTAC	A	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs55983731	chr15	78735269	C	T	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs72738718	chr15	78735438	G	C	0.55,0.63	0.76,0.79	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2089162	chr15	78739763	A	G	0.55,0.64	0.76,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs2938670	chr15	78740688	T	G	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2656052	chr15	78740932	A	C	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2568494	chr15	78740964	G	A	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7181486	chr15	78741618	T	C	0.55,0.64	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs17483929	chr15	78742376	G	A	0.55,0.64	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs56219465	chr15	78742579	A	G	0.55,0.64	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2656065	chr15	78750549	G	A	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs72738732	chr15	78752188	C	G	0.57,0.66	0.76,0.82	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs2009746	chr15	78754102	A	G	0.55,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs17484235	chr15	78761414	C	G	0.57,0.66	0.76,0.82	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs72738736	chr15	78765122	G	T	0.56,0.63	0.77,0.8	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs1504550	chr15	78766250	A	G	0.57,0.66	0.76,0.82	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs17484524	chr15	78772676	A	G	0.58,0.67	0.77,0.83	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs11858836	chr15	78783277	G	A	0.59,0.67	0.77,0.84	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs200776054	chr15	78801393	A	AC	0.7,0.86	0.88,1	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs11852372	chr15	78801394	A	C	0.73,0.9	0.87,0.99	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	2	H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs9788721	chr15	78802869	C	T	0.75,0.92	-0.91,-0.98	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs8034191	**chr15**	**78806023**	**T**	**C**	**0.82,1**	**0.93,1**	**rs1051730,rs8034191**	**EUR,EUR**	**rs1051730_EUR,rs8034191_EUR**	**FALSE**	**0**	**NA**
rs34684276	chr15	78813155	G	A	0.6,0.72	0.82,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs10519203	chr15	78814046	G	A	0.82,0.99	-0.94,-1	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs8031948	chr15	78816057	G	T	0.84,0.98	0.94,0.99	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs8042849	chr15	78817929	C	T	0.62,0.72	-0.94,-0.99	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs931794	chr15	78826180	G	A	0.84,0.97	-0.95,-0.99	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs72738786	chr15	78828086	G	T	0.85,0.96	0.94,0.98	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs58365910	chr15	78849034	T	C	0.87,0.92	0.95,0.97	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs72740955	chr15	78849779	C	T	0.88,0.93	0.95,0.97	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs2036527	chr15	78851615	G	A	0.88,0.92	0.96,0.97	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs55853698	chr15	78857939	T	G	0.88,0.92	0.95,0.97	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	3	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs55781567	chr15	78857986	C	G	0.89,0.92	0.96,0.97	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	3	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs11633958	chr15	78862064	C	T	0.95,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs7172118	chr15	78862453	C	A	0.97,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs17486195	chr15	78865197	A	G	0.97,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs140330585	chr15	78866445	G	A	0.95,0.83	0.98,0.94	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs17486278	chr15	78867482	A	C	0.97,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs72740964	chr15	78868636	G	A	0.96,0.85	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs7180002	chr15	78873993	A	T	0.97,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs200776369	chr15	78874842	AG	A	0.91,0.81	0.99,0.96	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs56390833	chr15	78877381	C	A	0.95,0.83	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs951266	chr15	78878541	G	A	0.97,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs16969968	chr15	78882925	G	A	0.98,0.84	0.99,0.95	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs8192482	chr15	78886198	C	T	0.99,0.83	1,0.94	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs4887067	chr15	78886947	G	A	0.99,0.83	1,0.94	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs1051730	**chr15**	**78894339**	**G**	**A**	**1,0.82**	**1,0.93**	**rs1051730,rs8034191**	**EUR,EUR**	**rs1051730_EUR,rs8034191_EUR**	**FALSE**	**0**	**NA**
rs1317286	chr15	78896129	A	G	0.99,0.82	1,0.92	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs12914385	chr15	78898723	C	T	0.84,0.68	1,0.88	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA

rs55676755	chr15	78898932	C	G	1,0.82	1,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs56077333	chr15	78899003	C	A	0.89,0.73	1,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs141518190	chr15	78900647	A	G	0.82,0.68	1,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs147499554	chr15	78900650	C	T	0.82,0.68	1,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs138544659	chr15	78900701	T	G	0.79,0.65	1,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs147144681	chr15	78900908	C	T	0.86,0.71	1,0.94	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs114205691	chr15	78901113	C	T	1,0.82	1,0.93	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs146009840	chr15	78906177	A	T	0.99,0.83	1,0.94	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs8040868	chr15	78911181	T	C	0.81,0.65	1,0.87	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	TRUE	1	CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks
rs4243084	chr15	78911672	G	C	0.98,0.8	0.99,0.91	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs149959208	chr15	78912710	T	TGCGCGGGC	0.9,0.74	0.97,0.9	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs71448806	chr15	78913353	CGCGGGCGG	C	0.62,0.5	0.89,0.78	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs8039449	chr15	78914534	C	T	0.83,0.76	0.98,0.91	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs10851907	chr15	78915864	G	A	0.72,0.64	0.98,0.9	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs55958997	chr15	78915872	C	A	0.82,0.75	0.96,0.9	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs2869548	chr15	78922638	G	A	0.82,0.73	0.95,0.88	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs17487223	chr15	78923987	C	T	0.83,0.75	0.95,0.88	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs72743158	chr15	78926445	T	C	0.75,0.67	0.91,0.84	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs67426328	chr15	78934318	C	G	0.59,0.54	0.82,0.76	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs55988292	chr15	78936168	A	G	0.6,0.55	0.83,0.77	rs1051730,rs8034191	EUR,EUR	rs1051730_EUR,rs8034191_EUR	FALSE	0	NA
rs3936134	chr17	65814382	C	G	0.54	0.82	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs929580	chr17	65815463	T	C	0.54	0.82	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs72631329	chr17	65818374	T	C	0.54	0.82	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs77103901	chr17	65822573	CAG	C	0.71	0.87	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs139786693	chr17	65825228	TTTG	T	0.75	0.9	rs7216064	ASN	rs7216064_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12603589	chr17	65825248	T	C	0.8	0.91	rs7216064	ASN	rs7216064_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12601921	chr17	65825354	C	A,G,T	0.72	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12601919	chr17	65825374	A	G	0.73	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs9915591	chr17	65826090	C	G	0.81	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	6	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12602556	chr17	65826861	A	G	0.81	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	7	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs62084208	chr17	65827443	C	T	0.81	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	4	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs202105424	chr17	65828368	AT	A	0.74	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2080090	chr17	65828371	T	A	0.62	0.87	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs62084210	chr17	65828710	A	G	0.81	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island

rs12449312	chr17	65829358	A	C	0.82	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs7223643	chr17	65830282	A	G	0.82	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1976052	chr17	65830578	C	T	0.82	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7209675	chr17	65831258	A	T	0.82	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs200597847	chr17	65831740	AG	A	0.72	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs75873575	chr17	65831741	GT	G	0.8	0.9	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7218014	chr17	65832016	T	C,G	0.73	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs7221651	chr17	65832390	G	A	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12452511	chr17	65832576	A	G	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	4	FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1976053	chr17	65833002	C	G	0.8	0.91	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1976054	chr17	65833224	T	G	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7208909	chr17	65833546	T	C	0.74	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2052187	chr17	65834737	T	C	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11079705	chr17	65835452	A	T	0.73	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11079706	chr17	65835470	G	T	0.82	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs11079707	chr17	65835617	G	A	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs80135947	chr17	65836001	A	C	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs141331058	chr17	65836574	CTTG	C	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs6504542	chr17	65836642	T	C	0.79	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs8082512	chr17	65837059	T	C	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1599859	chr17	65837193	C	G	0.83	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs1966410	chr17	65837215	T	C	0.83	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs58551145	chr17	65837235	A	G	0.83	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs6504543	chr17	65837659	T	C	0.82	0.91	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8067892	chr17	65837983	A	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8074078	chr17	65838743	T	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs8073510	chr17	65839210	A	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12450363	chr17	65840108	T	C	0.8	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084212	chr17	65840244	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs112222385	chr17	65840524	T	C	0.68	0.92	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs200529597	chr17	65840808	CG	C	0.64	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11871285	chr17	65840809	G	T	0.69	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11868959	chr17	65840810	T	C	0.69	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs2365466	chr17	65841129	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs2365467	chr17	65841284	TA	T,TT,TTT	0.82	0.91	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs2365468	chr17	65841318	C	T	0.82	0.91	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084213	chr17	65842016	A	G	0.82	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7223930	chr17	65842186	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs7224923	chr17	65842265	T	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs62084214	chr17	65843325	C	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs8081517	chr17	65845697	A	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs8081856	chr17	65845918	A	G	0.79	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084234	chr17	65847060	A	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island

rs7212293	chr17	65847325	A	G	0.83	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs78452260	chr17	65848522	G	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	4	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs4791048	chr17	65848994	G	A	0.82	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	4	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs2086744	chr17	65849275	C	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	4	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island
rs2046323	chr17	65849927	T	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs4791046	chr17	65851973	G	A	0.83	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs4790908	chr17	65852907	T	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11079709	chr17	65853363	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084235	chr17	65853437	C	T	0.84	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12450072	chr17	65853517	C	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs74541577	chr17	65853651	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs74561219	chr17	65853759	T	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs55931203	chr17	65854602	C	T	0.69	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs62084237	chr17	65854807	G	A	0.6	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs28609796	chr17	65855104	T	A	0.54	0.91	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs62084238	chr17	65856573	T	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2128792	chr17	65857177	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs2365764	chr17	65857714	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084240	chr17	65859233	C	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs75352663	chr17	65860059	AT	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs60432293	chr17	65860407	T	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs59950564	chr17	65860859	A	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs8077872	chr17	65861059	G	T	0.83	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs34739687	chr17	65862114	TA	T	0.79	0.91	rs7216064	ASN	rs7216064_ASN	TRUE	5	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4790905	chr17	65863350	C	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs34872586	chr17	65863466	T	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs58141639	chr17	65864902	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs61067468	chr17	65866035	G	A	0.83	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084245	chr17	65867129	C	T	0.79	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084246	chr17	65867911	G	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9912084	chr17	65868035	A	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9912770	chr17	65868233	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11869819	chr17	65868669	A	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs55939964	chr17	65869297	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs12602912	chr17	65870073	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12450907	chr17	65870644	T	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9890629	chr17	65871559	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12451707	chr17	65871598	G	A	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4569324	chr17	65872750	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084247	chr17	65872903	C	T	0.77	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs112651248	chr17	65872935	AAG	A	0.8	0.91	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9915108	chr17	65874463	T	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9913471	chr17	65874495	C	T	0.79	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084248	chr17	65874541	C	T	0.83	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12451511	chr17	65874861	T	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084249	chr17	65874998	A	G	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs200215613	chr17	65875266	TTTTC	T	0.7	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11867517	chr17	65875326	C	T	0.85	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA

rs11867537	chr17	65875492	A	G	0.81	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11867618	chr17	65875587	G	A	0.83	0.94	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs35243555	chr17	65876477	G	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs58122682	chr17	65876915	T	C	0.85	0.94	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs201859733	chr17	65877610	T	TG	0.67	0.92	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs8074644	chr17	65878217	G	C	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084251	chr17	65878736	G	A	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9892803	chr17	65879243	T	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs140912776	chr17	65879572	TA	T	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084252	chr17	65879578	G	C	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9897982	chr17	65879592	G	T	0.85	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs201512564	chr17	65880256	T	TTC	0.72	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs199697046	chr17	65880257	T	TC	0.73	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs6504545	chr17	65880367	A	G	0.75	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs6504546	chr17	65880385	A	C	0.77	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7213292	chr17	65880443	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs3935969	chr17	65881959	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4318247	chr17	65882172	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	2	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs75360723	chr17	65882542	A	AT	0.87	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	2	FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs8082661	chr17	65884701	G	A	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7208663	chr17	65885171	T	C	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs75231441	chr17	65885485	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12452823	chr17	65885783	G	A	0.87	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11079710	chr17	65885911	C	T	0.73	0.91	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs6504548	chr17	65886048	T	C	0.85	0.93	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8079291	chr17	65887622	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs8079754	chr17	65887896	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	4	CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs6504549	chr17	65888784	A	G	0.85	0.93	rs7216064	ASN	rs7216064_ASN	TRUE	2	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs11653507	chr17	65892064	T	A	0.5	-0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs59640213	chr17	65892280	G	A	0.59	0.81	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs60856912	chr17	65892343	G	T	0.79	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs61676547	chr17	65892507	G	C	0.71	0.97	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs56148300	chr17	65892752	T	C	0.98	1	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs3206817	chr17	65892834	A	G	1	1	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs56404791	chr17	65893019	T	G	0.98	1	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs145606454	chr17	65893289	AC	A	0.99	1	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island
rs6504550	chr17	65894542	A	G	0.83	1	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7216064	**chr17**	**65898809**	**G**	**A**	**1**	**1**	**rs7216064**	**ASN**	**rs7216064_ASN**	**FALSE**	**0**	**NA**
rs8065906	chr17	65902645	G	A	0.93	0.99	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs6504551	chr17	65903326	T	G	0.83	1	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs202228218	chr17	65906928	AT	A	0.84	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12602655	chr17	65909442	A	G	0.9	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8072225	chr17	65912960	A	G	0.94	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs55896768	chr17	65913358	T	C	0.94	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12600941	chr17	65918807	A	G	0.9	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62085991	chr17	65920508	G	A	0.89	0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4790981	chr17	65921834	A	G	0.92	0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62085992	chr17	65923083	T	A	0.89	0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62085993	chr17	65923152	T	C	0.95	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs73338706	chr17	65926604	T	C	0.92	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4271626	chr17	65930133	G	A	0.95	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4791300	chr17	65930772	A	G	0.94	0.98	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs4791299	chr17	65930937	A	G	0.87	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs56393562	chr17	65933918	C	T	0.95	0.98	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs5821447	chr17	65936179	TATTAA	T	0.93	0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8071463	chr17	65938655	G	A	0.92	-0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12451721	chr17	65939075	G	A	0.86	0.95	rs7216064	ASN	rs7216064_ASN	TRUE	2	CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks
rs6504555	chr17	65940727	A	G	0.88	-0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11870068	chr17	65944515	A	C	0.91	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7223357	chr17	65945536	C	G	0.92	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7223813	chr17	65945840	A	G	0.9	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12449442	chr17	65947640	G	A	0.88	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11867401	chr17	65947970	G	A	0.91	-0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9907491	chr17	65949993	G	A	0.91	-0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs71142114	chr17	65950290	GT	G	0.91	-0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4790974	chr17	65951107	A	T	0.91	-0.97	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA

rs4790973	chr17	65951133	C	T	0.91	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs77706698	chr17	65953348	G	A	0.83	0.95	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs12601759	chr17	65955284	A	G	0.92	0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs139709271	chr17	65955758	T	TCCTCCAGCC	0.64	0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9899520	chr17	65957568	A	G	0.8	-0.96	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs59956089	chr17	65960854	T	C	0.55	0.84	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs60626066	chr17	65961233	G	A	0.53	0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs10445361	chr17	65962238	T	G	0.82	0.91	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs77596502	chr17	65964170	TAGG	T	0.73	0.88	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086042	chr17	65967443	C	T	0.62	-0.88	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086043	chr17	65968003	A	G	0.78	0.9	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086044	chr17	65970837	G	T	0.77	0.88	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086045	chr17	65973731	G	A	0.74	0.87	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs147446457	chr17	65974419	TA	T	0.51	0.74	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4791212	chr17	65975385	C	T	0.73	0.87	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7210027	chr17	65977053	C	T	0.77	-0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4790941	chr17	65977132	G	A	0.77	0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs11656743	chr17	65980289	G	A	0.77	-0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086046	chr17	65982943	C	T	0.77	0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs75772932	chr17	65984537	G	A	0.72	0.87	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs5821444	chr17	65987509	TTAA	T	0.75	-0.89	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs9891146	chr17	65988049	T	C	0.61	-0.87	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7502307	chr17	65989961	C	G	0.65	0.81	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs113985803	chr17	65989971	G	A	0.71	-0.86	rs7216064	ASN	rs7216064_ASN	TRUE	1	H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs56305452	chr17	65990500	C	A	0.73	-0.87	rs7216064	ASN	rs7216064_ASN	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs56315139	chr17	65990571	C	G	0.59	-0.86	rs7216064	ASN	rs7216064_ASN	TRUE	5	H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs62086884	chr17	65994400	G	C	0.59	0.81	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs4791295	chr17	65997317	G	A	0.64	0.82	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs28855509	chr17	65998167	T	C	0.6	0.82	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs74564337	chr17	65999567	C	T	0.65	0.81	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs6504568	chr17	65999648	C	T	0.6	-0.78	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs75756093	chr17	66000578	TAGTC	T	0.63	0.81	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086889	chr17	66000603	C	T	0.64	0.81	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8081714	chr17	66001130	A	G	0.64	-0.81	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs78186330	chr17	66004715	G	A	0.6	0.78	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs201874160	chr17	66007548	TTTTG	T	0.52	0.78	rs7216064	ASN	rs7216064_ASN	TRUE	4	CTCF_D0_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D4_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,CTCF_D6_2013_3_MB1B2B3_fdr1e2_MACS2_peaks,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island
rs62086897	chr17	66008044	A	C	0.59	0.79	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086898	chr17	66009120	A	G	0.54	0.78	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086899	chr17	66009134	C	T	0.54	0.78	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086903	chr17	66016006	T	C	0.61	0.79	rs7216064	ASN	rs7216064_ASN	TRUE	4	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs62086904	chr17	66016096	C	T	0.58	0.78	rs7216064	ASN	rs7216064_ASN	TRUE	4	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs62086906	chr17	66019926	T	C	0.57	0.78	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086907	chr17	66021167	A	G	0.56	0.77	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62086908	chr17	66021214	G	C	0.56	0.77	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7405987	chr17	66021394	A	G	0.56	0.77	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs8076753	chr17	66022841	G	A	0.56	0.77	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs79778350	chr17	66023786	C	T	0.54	0.77	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084669	chr17	66024170	A	G	0.56	0.77	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs35229997	chr17	66029590	T	G	0.54	0.76	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7226002	chr17	66030835	T	C	0.54	0.76	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs62084681	chr17	66030992	G	A	0.54	0.76	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island

rs62084682	chr17	66031521	G	C	0.54	0.76	rs7216064	ASN	rs7216064_ASN	TRUE	4	FAIRE_D0_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D4_2013_3_MB1B2-W50-G50-FDR0.01-island,FAIRE_D6_2013_3_MB1B2-W50-G50-FDR0.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs7214119	chr17	66032298	G	A	0.53	0.75	rs7216064	ASN	rs7216064_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K9ac_D0_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D4_2013_3_MB1B2B3-W200-G200-FDR.01-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs8075764	chr17	66033109	C	A	0.54	0.76	rs7216064	ASN	rs7216064_ASN	TRUE	3	H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D4_2013_3_B1-W200-G200-FDR1e-04-island,H3K9ac_D6_2013_3_MB1B2-W200-G200-FDR.01-island
rs146286181	chr17	66035128	CTA	C	0.53	0.75	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084689	chr17	66035289	T	C	0.53	0.75	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084692	chr17	66035844	C	T	0.52	0.75	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084694	chr17	66037594	G	T	0.53	0.75	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084697	chr17	66038556	G	A	0.53	0.75	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084703	chr17	66043384	C	T	0.52	0.74	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs74354868	chr17	66045831	G	A	0.5	0.74	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7503050	chr17	66048462	G	T	0.52	0.74	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs7503810	chr17	66049531	G	A,C	0.51	0.73	rs7216064	ASN	rs7216064_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs62084708	chr17	66049707	G	A	0.51	0.73	rs7216064	ASN	rs7216064_ASN	TRUE	5	H3K27ac_D0_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D4_2013_3_B1-W100-G200-FDR1e-04-island,H3K27ac_D6_2013_3_B1-W100-G200-FDR1e-04-island,H3K4me1_D0_2013_3_MB1B2B3-W200-G200-FDR1e-04-island,H3K4me1_D6_2013_3_MB1B2B3-W200-G200-FDR1e-04-island
rs35040337	chr17	66056682	A	G	0.51	0.73	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs74976757	chr17	66060906	G	T	0.5	0.73	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs62084740	chr17	66061184	C	T	0.51	0.73	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs74900486	chr17	66062873	C	T	0.51	0.73	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA
rs75544834	chr17	66066438	T	C	0.5	0.72	rs7216064	ASN	rs7216064_ASN	FALSE	0	NA

Supplementary Table 2. Annotation of LUAD risk-associated SNPs

Region	Number
Intron	583
Intergenic region	335
Promoter region	16
5' or 3' UTR	7
Exon – Synonymous	4
Exon – Missense	3
Exon – Nonsense	0
Total	948

Supplementary Table 3. Functional prediction of LUAD risk-associated SNPs located in exons

rsID	IndexSNP-Population-r^2*	Gene	SIFT score	SIFT pred	Polyphen HDIV score	Polyphen HDIV pred	Polyphen HVAR score	Polyphen HVAR pred
rs2076530	rs3817963-ASN-0.57	BTNL2	NA	NA	0	Benign	0	Benign
rs9891146	rs7216064-ASN-0.61	C17orf58	1	Tolerated	0	Benign	0	Benign
rs16969968	rs1051730-EUR-0.98	CHRNA5	0.18	Tolerated	0.045	Benign	0.011	Benign

*ASN: Asian, EUR: European

Supplementary Table 4. Functional prediction of LUAD risk-associated SNPs located in UTRs

rsID	InputSNP-Population-r^2*	Region	Gene	targetScanS
rs11656743	rs7216064-ASN-0.77	UTR3	BPTF	None
rs8192482	rs1051730-EUR-0.99	UTR3	CHRNA5	None
rs4887067	rs1051730-EUR-0.99	UTR3	CHRNA5	None
rs55853698	rs1051730-EUR-0.88	UTR5	CHRNA5	None
rs55781567	rs1051730-EUR-0.89	UTR5	CHRNA5	None
rs71448806	rs1051730-EUR-0.62	UTR5	CHRNA3	None
rs2854464	rs11610143-ASN-0.71	UTR3	ACVR1B	None

*ASN: Asian, EUR: European

Table S5. SNPs located in promoter regions

rsID	chr	Pos (hg19)	index SNP-population-r^2*	D'	gene	Direction	Distance from TSS (basepairs)**
rs7631358	chr3	189348411	rs4488809-ASN-0.75	-0.94	TP63	5'	803
rs76937731	chr3	189348968	rs4488809-ASN-0.61	-0.92	TP63	5'	246
rs60622800	chr5	1309904	rs465498-ASN-0.83	-0.92	MIR4457	5	411
rs6554758	chr5	1310152	rs465498-ASN-0.83	-0.92	MIR4457	5	659
rs27996	chr5	1345474	rs465498-ASN-0.88	0.95	CLPTM1L	5	471
rs4946258	chr6	117803538	rs9387478-ASN-0.72	0.95	DCBLD1	5	280
rs34431655	chr6	117803676	rs9387478-ASN-0.74	0.98	DCBLD1	5	142
rs17483548	chr15	78730313	rs8034191-EUR-0.66	0.82	IREB2	5	203
rs8039449	chr15	78914534	rs1051730-EUR-0.83	0.98	CHRNA3	5	896
rs67426328	chr15	78934318	rs1051730-EUR-0.59	0.82	CHRNB4	5	730
rs7502307	chr17	65989961	rs7216064-ASN-0.65	0.81	C17orf58	5	195
rs113985803	chr17	65989971	rs7216064-ASN-0.71	-0.86	C17orf58	5	205
rs56305452	chr17	65990500	rs7216064-ASN-0.73	-0.87	C17orf58	5	734
rs56315139	chr17	65990571	rs7216064-ASN-0.59	-0.86	C17orf58	5	805
rs62084681	chr17	66030992	rs7216064-ASN-0.54	0.76	KPNA2	5	854
rs62084682	chr17	66031521	rs7216064-ASN-0.54	0.76	KPNA2	5	325

*ASN: Asian, EUR: European; ** TSS= transcription start site

Supplementary Table 6. ChIP-seq and FAIRE-seq statistics

	FAIRE			H3K27ac			H3K4me1		
	D0	D4	D6	D0	D4	D6	D0	D4	D6
# reads (Raw)	123,608,859	125,035,637	139,654,375	116,753,350	72,563,956	52,203,734	143,424,035	123,706,480	99,326,714
# reads (QC)	123,568,043	124,998,560	139,618,662	116,676,688	72,535,483	52,185,120	126,980,095	123,667,091	93,075,899
% High Quality Reads	99.97%	99.97%	99.97%	99.93%	99.96%	99.96%	88.53%	99.97%	93.71%
# reads (Aligned)	83,307,530	86,831,534	102,285,869	43,490,305	56,340,155	43,145,070	80,895,482	91,934,330	69,183,936
% Aligned Reads	67.42%	69.47%	73.26%	37.27%	77.67%	82.68%	63.71%	74.34%	74.33%
# reads (RemDup)	77,901,295	79,059,239	96,003,349	10,038,246	30,166,166	13,803,476	65,431,882	89,228,395	62,078,258
% Unique Reads	93.51%	91.05%	93.86%	23.08%	53.54%	31.99%	80.88%	97.06%	89.73%
# Peaks	80,845	89,177	95,117	39,210	44,976	43,743	87,443	76,292	75,490

Supplementary Table 7. Cloning primers for pGL4.26/ luciferase reporter gene constructs

SNP, construct length, & (hg19 genomic coordinates)	Forward	Reverse
rs452384, 1680 bp in *CLPTM1L* (chr5:1330187-1331866)	5'- AAATATGGTACCCCACCCGAACACGCATTTCCT -3'	5'- TAATAAGCTAGCCTCACTGGAGCCTGCGGTAG-3'
rs452384, 459 bp in *CLPTM1L* (chr5:1330613-1331071)	5'—AAATATGGTACCCAGGTACTCCCCAGTCCACG-3'	5'— TAATAACTCGAGCGTGTTCTGCGTTGTTGTCTCC-3'
rs6942067, 836 bp in *DCBLD1*/*GOPC* (chr6:117785006-117785841)	5'- AAATATGGTACCCCCTATGTGTCAATCACCTCCC -3'	5'- TAATAACTCGAGGACTTCAGCTTCTGGGAAGATG -3'
rs9481728, 912 bp in *DCBLD1* (chr6:117817044-117817955)	5'- AAATATGGTACCTCTTTGGACACTGATGGAAGTA-3'	5'- TAATAACTCGAGGGTTGTGCCTACTGAAGTGATTT3'

sequence that participates in PCR reaction underlined; additional sequence= restriction enzyme sites.
Lower case = base subject to mutagenesis