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1 ***Functional Annotation of Bipolar Disorder 2 Risk Location Implicates***
2 ***Novel Susceptibility Genes***

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6 Short Title: Prioritization of BD2 GWAS Genes

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11 **Abstract**

12 *Introduction:* Bipolar 2 disorder (BD2) is an independent disease with specific familial aggregation,
13 significant functional impairment, specific treatment challenges and several distinctive clinical
14 features. However, unlike bipolar 1 disorder, studies investigating causal and functional genes are
15 lacking. **This study aims to identify and prioritize causal genetic variants and genes for BD2 by**
16 **analyzing brain-specific gene expression markers, to improve the understanding of its genetic**
17 **underpinnings and support advancements in diagnosis, treatment and prognosis.**

18 *Method:* We used FUMA, a genome wide association study (GWAS) annotation tool, to pinpoint
19 potential causal variants and genes from the largest BD2 GWAS data. Candidate causal variants most
20 likely affecting brain gene expression were prioritized using the following criteria: (1) variants
21 identified as eSNPs in any brain region within any brain expression quantitative trait loci (eQTL)
22 dataset; (2) variants annotated in the Regulome database with a score <5, indicating likely functional
23 localization; (3) the most common 15-core chromatin state across all cell types in the Roadmap
24 Epigenomics data being ≤7, reflecting an open chromatin state; (4) localization in genomic regions
25 with evidence of 3D chromatin interactions, as such interactions mediate genetic effects on gene
26 expression.

27 *Results:* We identified *AGRN*, *ORMDL3*, *SLC25A39*, *RUNDC3A*, *NOS2*, *C1orf159*, *RP11-5407.18*,
28 *RP11-465B22.3*, *RP11-5407.17* as candidate causal genes. These genes are associated with important
29 pathways such as synapse formation, mitochondrial and oxidative metabolism, intracellular
30 transport, neurotransmission and lipid metabolism-related pathways.

31 *Conclusion:* This study provides a guide for further experimental validation of functional variants,
32 BD2-associated genes and novel drug targets.

33 **Introduction**

34 Bipolar and related disorders are a group of illnesses characterised by biphasic mood episodes and
35 euthymia periods. This definition includes bipolar 1 (BD1), bipolar 2 (BD2), cyclothymia and other
36 forms of residual and atypical illness. BD2, previously defined as a 'mild form' of BD1 disorder, is a
37 distinct disease entity characterised by the presence of at least one hypomanic and one major
38 depressive episode [1]. BD2 differs from BD1 in many ways. Clinically, BD2 patients have a higher
39 number of mood episodes, a shorter mean episode duration and more persistent depression, but are
40 less likely to be hospitalised and less likely to have psychotic symptoms than BD1 patients [2].
41 Another study concluded that BD2 has less severe symptoms, shorter inter-episode duration and a
42 more chronic course than BD1 [3]. BD2 also has other distinctive features such as: older age of onset,
43 female predominance, higher seasonality and suicidality, family cumulation, more social problems
44 but less disability, cognitive impairment [2, 4] and lower heritability [5]. Importantly, longitudinal
45 studies have reported that BD2 is diagnostically stable and the percentage of patients who convert to
46 BD1 is low [6]. Despite these characteristics, BD2 is difficult to diagnose and treat. The main reason
47 for this is that hypomanic episodes, which do not typically cause loss of function and are much less
48 severe than mania, do not require hospital admission and are treated as major depressive disorder
49 [4]. This distinction has direct implications for the appropriate treatment and prognosis of BD2
50 patients.

51 Studies evaluating BD2, as a subgroup or separately, are lacking in BD studies, despite the many
52 features of BD2 that distinguish it from other mood disorders. A recent systematic review analysed
53 the relatively small number of candidate gene studies and genome wide association studies (GWAS)
54 investigating BD2 [7]. Candidate gene studies have reported genes related to monoaminergic system
55 (especially dopaminergic and serotonergic systems), calcium and cAMP signalling pathways, immune
56 system and neuroplasticity to be specific for BD2 [7]. GWAS and the polygenic risk scores (PRS)
57 calculated by linkage disequilibrium (LD) analysis from GWAS summary statistics data emphasize the
58 transdiagnostic genetic background. GWAS meta-analyses highlight that BD2 shares common genes
59 with both BD1 and schizophrenia (SCZ), while PRS analyses show a high genetic correlation of BD2
60 with unipolar depression (UD), and BD1 with SCZ [7, 8].

61 Most of the SNPs identified in GWASs are non-coding variants located in large genomic regions
62 containing multiple candidate genes and highly linked SNPs, and it is often challenging to identify
63 causal variants or genes [9]. Disease-causing variants can be GWAS index SNPs as well as those in LD

64 with the index SNP [10]. Several studies have shown that causative variants are located in regulatory
65 DNA elements, most frequently within enhancers [9]. These variants are usually expression
66 quantitative trait loci (eQTL) [11], which means that they affect disease risk by altering the function
67 of cell type-specific regulatory elements that can regulate gene expression through multiple
68 mechanisms, including modulation of chromatin accessibility, enhancer-promoter interaction, and
69 transcription factor (TF) binding [12]. Identification of causal variants and genes is essential for
70 understanding disease aetiology and guiding research for new drug targets [13]. To identify the most
71 likely causal variants and genes associated with BD2 in this study, we used FUMA [14], a GWAS
72 annotation tool that integrates multiple types of biological data, including SNP functional annotation,
73 brain eQTL, and chromatin interaction data.

74 **Method**

75 Characterization of genomic risk loci based on the largest BD2 GWAS

76 **The largest BD2 GWAS data we used in our study is a subset of a GWAS meta-analysis of 57 BD**
77 **cohorts collected in Europe, North America and Australia, totaling 41,917 individuals with BD**
78 **(cases) and 371,549 controls [8]. The BD sample in this meta-analysis consisted of BD1 (25,060**
79 **cases), BD2 (6,781 cases) and BD NOS (not otherwise specified) (10,076 cases). The included cases**
80 **met international consensus criteria for lifetime BD (DSM-IV, ICD-9 or ICD-10), as determined using**
81 **structured diagnostic interviews, clinician-administered checklists or medical record review. The**
82 **authors shared individual-level genotype and phenotype data for 52 cohorts (5 cohorts were**
83 **excluded) with Psychiatric Genomics Consortium (PGC). In PGC, these data are available as 3**
84 **different GWAS summary statistics files for all BD cases, BD1 cases only and BD2 cases only**
85 **([https://figshare.com/articles/dataset/PGC3_bipolar_disorder_GWAS_summary_statistics/](https://figshare.com/articles/dataset/PGC3_bipolar_disorder_GWAS_summary_statistics/14102594)**
86 **14102594**). We used FUMA (<https://fuma.ctglab.nl/>) to pinpoint potential causal variants and genes
87 from BD2 GWAS summary statistics (6,781 BD2 cases and 364,075 controls from PGC). The LD
88 structure was calculated based on the European population data from the 1000 Genomes Project.
89 FUMA facilitated the identification and annotation of genomic risk loci, enhancing our understanding
90 of the genetic underpinnings of BD2 susceptibility. Genomic risk loci were identified, and various
91 subsets of SNPs within these loci were categorized based on the following criteria:

92 **1.Independently Significant SNPs: These are SNPs with a p-value below 5×10^{-5} and are independent**
93 **from each other with $r^2 < 0.6$. While the conventional genome-wide significance threshold ($p < 5 \times$**
94 **10^{-8}) is commonly used in genomic studies, this approach is applied at the expense of the false-**
95 **negative rate [15]. Indeed, several studies have shown that a substantial portion of variants with**
96 **'sub-threshold' significance ($p < 5 \times 10^{-5}$) may still indicate actual disease risk loci [16, 17]. Wang et**

97 **al. examined SNPs associated with cardiac QT interval, finding that sub-threshold SNPs were**
98 **significantly present in predicted cardiac enhancers [18].**

99 **2.Candidate SNPs:** SNPs in LD with independently significant SNPs ($r^2 \geq 0.6$), having a minor allele
100 frequency (MAF) of at least 0.01, are considered candidate SNPs and are subjected to further
101 annotation.

102 **3.Independent Lead SNPs:** These are independent significant SNPs that are also independent from
103 each other with $r^2 < 0.1$.

104 **4.Genomic Risk Loci:** Genomic risk loci are defined by merging lead SNPs within a 250 kb window and
105 including all SNPs in LD ($r^2 \geq 0.6$) with any of the independent SNPs.

106 The candidate SNPs were subsequently annotated to determine their functional consequences on
107 gene function (including intergenic, downstream, upstream, 3' untranslated region, 5' untranslated
108 region, intronic, exonic, ncRNA_intronic, and ncRNA_exonic) based on Ensembl genes (build 85) using
109 the ANNOVAR tool.

110 Prioritization of BD2-related SNPs and genes using FUMA

111 Chromosomal position, reference and alternative alleles were paired for all SNPs in the 1000
112 Genomes Project Phase 3 analysis, and combined annotation-dependent depletion (CADD)
113 deleteriousness scores, Regulome database (RDB) scores (regulatory elements) and 15 core
114 chromatin states were queried. Brain eQTLs and Hi-C (high-throughput chromosome conformation
115 capture) data, illustrating the three-dimensional (3D) structure of chromatin and interactions, were
116 interrogated via the FUMA platform to assess the effects of all candidate SNPs on gene expression.
117 We prioritized candidate causal variants affecting gene expression in the brain using the following
118 criteria: (1) variants identified as eSNPs in any brain region according to GTEx V6, V7, V8, Braineac,
119 xQTLServer, CommonMind Consortium, PsychENCODE, Brainseq eQTL data; (2) variants annotated in
120 the RDB with a score < 5 , indicating potential involvement in functional regions affecting TF binding
121 and gene expression [19]; (3) variants located at loci with a chromatin state ≤ 7 based on the most
122 common 15-core chromatin states across brain tissues or cell types in Roadmap Epigenomics data, as
123 scores from 1 to 7 generally signify an open chromatin state [20], facilitating transcriptional
124 activation; and (4) genomic regions containing the variants with evidence of 3D chromatin
125 interactions, as such interactions mediate genetic effects on gene expression [21]. In addition,
126 disease-associated functional variants have been shown to be enriched in brain regions
127 (enhancer/promoter) defined by histone marks known to be associated with transcriptional

128 regulatory activity, such as H3K27ac, H3K4me1 and H3K4me3 [9]. We investigated which SNPs
129 mapped to the filtered candidate genes were enriched in these regions.

130 **Results**

131 Characterization of genomic risk loci

132 We used the FUMA platform for functional annotation of the latest and largest BD2 GWAS summary
133 statistics including 6,781 cases and 364,075 controls. Based on the BD2 GWAS summary statistics, 26
134 lead SNPs for BD2 and 788 candidate SNPs in LD with lead SNPs were identified among 31
135 independently significant SNPs at 26 genomic loci (shown in Table 1). Half of the candidate SNPs
136 were intronic variants, while almost half were intergenic and noncoding-RNA intronic variants,
137 meaning that most of these SNPs are located in non-coding genomic regions (shown in Fig. 1).

138 Prioritization of BD2-related eGenes

139 To find causal variants and genes among the candidate genes, we used the filtering strategy
140 described in the Methods section. Among all candidate SNPs (shown in Supplementary Table 1), we
141 selected variants with an RDB score less than 5 and the most common 15-core chromatin state being
142 not greater than 7 (shown in Supplementary Table 2). The variant list was then narrowed down by
143 selecting brain eQTLs among these variants. Finally, only variants showing chromatin interaction in
144 the brain Hi-C data were prioritised (shown in Supplementary Table 3). In addition, we checked
145 whether these variants were located in brain promoter or enhancer regions. Since a single eSNP can
146 be associated with the expression of multiple eGenes (and vice versa), we prioritised eGenes with the
147 most significant eQTL p-value and/or overlap in brain enhancer/promoter regions as likely functional
148 genes. As a result of this filtering strategy, we prioritised the genes that are located on chromosome
149 1 (*AGRN*, *C1orf159*, *RP11-5407.18*, *RP11-465B22.3*, *RP11-5407.17*) and chromosome 17 (*ORMDL3*,
150 *SLC25A39*, *RUNDC3A*, *NOS2*). All of the prioritised variants are intronic and three of them are located
151 within long non-coding genes. Of note, all prioritised genes are highly expressed in the emotion
152 regulatory regions of the brain (shown in Table 2).

153 **Discussion**

154 GWASs and candidate gene studies have identified some genetic variants associated with BD2, but
155 causal variants and genes have been largely undiscovered. In this study, we used the FUMA tool and
156 a prioritisation strategy to identify potential BD2 causal variants and genes, based on the most recent
157 and largest BD2 GWAS datas. We identified 788 candidate SNPs at 26 genomic risk loci. We found
158 that most of the candidate SNPs were located in non-coding regions. Similar to other psychiatric

159 disorders and complex diseases, SNPs identified in the BD2 GWAS are mostly located in regulatory
160 DNA regions [22].

161 We applied filters indicative of active transcription and open chromatin to distinguish causal and
162 functional variants among candidate genes, prioritising *AGRN*, *ORMDL3*, *SLC25A39*, *RUNDC3A*, *NOS2*,
163 *C1orf159*, *RP11-5407.18*, *RP11-465B22.3*, *RP11-5407.17*. ***AGRN***, the best known of these genes,
164 codes for a proteoglycan that is critical for the postsynaptic assembly of the neuromuscular junction
165 [23]. *AGRN* is also expressed in the brain [24]. A study reported that *AGRN* mutations impair the
166 proliferation of excitatory cells in the hippocampus and lead to depression-like behaviour [25]. *AGRN*
167 also induces dendritic filopodia and synapse formation in hippocampal neurons by acting on
168 glutamate receptors in the hippocampus through activation of RhoA GTPases [26]. Another study has
169 shown that *AGRN* regulates hippocampal neuronal excitability via Na⁺,K⁺-ATPase activity. It has been
170 reported that suppression of neuronal *AGRN* reverses manic-like behaviour [27]. Na⁺,K⁺-ATPase is
171 expressed in excitatory glutamatergic and inhibitory GABAergic neurons in the healthy brain and has
172 a higher GABAergic expression especially in the hippocampus [28]. Therefore, *AGRN*-Na⁺,K⁺-ATPase
173 interactions may predominate at synapses between excitatory and inhibitory neurons. Increased
174 glutamatergic, decreased GABAergic expression, upregulation of Na⁺,K⁺-ATPase genes and
175 associated hyperactive action potential firing and hyperexcitability phenotype have been shown in
176 dentate hippocampal cells of BD patients [29]. Therefore, we propose *AGRN* as likely to be one of the
177 genes contributing to BD pathology. ***ORMDL3*** encodes the protein 'ORMDL sphingolipid biosynthesis
178 regulator 3', which is a regulator of sphingolipid synthesis located in the endoplasmic reticulum and
179 inhibits serine palmitoyl transferase (SPT), the rate-limiting enzyme in sphingolipid biosynthesis [30].
180 Dysregulation of *ORMDL3* gene disrupts SPT inhibition and impairs the metabolism of ceramide, a
181 sphingolipid metabolite [31]. Ceramide is highly abundant in neural cell membranes and serves as a
182 precursor for complex sphingolipids that are important for brain homeostasis [32]. However, studies
183 indicate that ceramide accumulation promotes depression-like behaviors in mice, and these
184 behaviors can be rescued by certain antidepressants that reduce hippocampal ceramide levels, such
185 as amitriptyline and fluoxetine [33]. Ceramide accumulation has been found to have a negative effect
186 on cells by triggering apoptosis [34]. In lipidomic analysis, ceramides were found to be significantly
187 elevated in the plasma of UD and BD patients compared to healthy controls [35]. Ceramides were
188 also shown to be significantly elevated in the white matter of bipolar patients compared to control
189 levels [36]. However, the mechanism of ceramide increase in BD is not clear. Members of the
190 mitochondrial solute carrier (SLC) family 25 (SLC25) enable the transport of substances required for
191 biochemical pathways and cellular homeostasis across the inner mitochondrial membrane into the
192 mitochondria [37]. ***SLC25A39*** is involved in the first steps of heme biosynthesis [38] and in the

193 transport of cytosolic glutathione (GSH) into mitochondria. Loss of SLC25A39 has been shown to
194 reduce mitochondrial GSH levels and impair the activity of iron-sulphur cluster proteins. Many
195 reactions in mitochondria generate free oxygen radicals, commonly referred to as reactive oxygen
196 species (ROS), which cause cellular damage; GSH acts as an antioxidant, neutralising these harmful
197 molecules [39]. *SLC25A39* mutations have been reported to reduce the GSH levels in brain
198 mitochondria, leading to mitochondrial dysfunction, synaptic defects and neurodegeneration with
199 ROS accumulation [40]. Lam et al. reviewed the evidence on impairment of mitochondrial
200 morphology, distribution and dysfunction in BD patients [41]. In addition, increased oxidative stress,
201 characterised by increased ROS, is well known and documented in the pathogenesis of BD. Studies
202 have also shown that GSH levels in various brain regions are significantly lower in BD patients than in
203 controls [42]. ***RUNDC3A*** is expressed in the brain, in cells of neuroendocrine origin and in pancreatic
204 beta cells [43]. It is thought to function by interacting with the GTP-bound form of Rap2a, a member
205 of the Ras family, in the brain, and may play a role in vesicle formation, trafficking or function,
206 particularly at excitatory synapses [43, 44]. Extracellular vesicles are intricately involved in the
207 pathological mechanisms of BD and may serve as emerging biomarkers for clinical detection of BD
208 [45]. However, the exact role of *RUNDC3A* in BD pathology needs further clarification. Nitric oxide
209 (NO) is a reactive free radical that plays an important role as a messenger molecule in
210 neurotransmission, long-term memory enhancement in the brain [46, 47]. NO synthases (NOS) are
211 involved in NO synthesis from L-arginine and are encoded by *NOS1*, *NOS2* and *NOS3* genes [48]. It
212 has long been known that ***NOS2*** is expressed in neurons [49]. Higher plasma NO levels have been
213 shown in BD patients compared to healthy individuals [50, 51]. Also, pro-inflammatory and
214 regulatory cytokines are activated in BD patients, indicating the presence of low-grade inflammation
215 that can lead to central nervous system damage [52]. It is thought that this chronic inflammation
216 leads to iNOS (NOS2)-mediated production of large amounts of NO, which can lead to oxidative
217 stress, DNA and mitochondrial damage [53]. It has also been shown that depression and anxiety-like
218 behaviours are reduced and stress resilience is increased in *Nos2*-deficient mice [54]. Reduction of
219 *NOS2* levels and amelioration of mania-like behaviours of mania model in mice by lithium [55, 56]
220 and doxycycline [56], a potent anti-inflammatory agent, supports the link between *NOS2* and BD. The
221 ***C1orf159*** gene encodes a protein whose function has not been well-characterised. It is expressed
222 almost throughout the body and in all regions of the brain, and interacts with TFRC and TOMM6.
223 (<https://www.proteinatlas.org/ENSG00000131591-C1orf159>). *TFRC* encodes the transferrin (TF) cell
224 surface receptor required for cellular iron uptake by receptor-mediated endocytosis [57]. TF
225 receptors, particularly in neurons and oligodendrocytes, are required for iron uptake into these cells,
226 which is essential for several enzymatic reactions involved in cholesterol and phospholipid
227 production, mitochondrial activity and ATP synthesis [58]. It was shown that iron haemostasis,

228 mitochondrial activity, energy production and myelination were impaired when the TF receptor was
229 knocked out in oligodendrocyte cells [59]. Most mitochondrial proteins are synthesised in the cytosol
230 and transported into mitochondria by the TOM complexes [60]. Regular protein trafficking is
231 essential for mitochondrial function and TOMM6 ensures that the import receptors and the TOM
232 complex maintain a stable interaction [61]. In summary, disruptions in the interactions of C1orf159,
233 TFRC and TOMM6 may be associated with alterations in the pathways known to contribute to the
234 pathophysiology of BD, such as synaptic and mitochondrial dysfunction and iron homeostasis. The
235 other three genes (*RP11-5407.18*, *RP11-465B22.3*, *RP11-5407.17*) we prioritised code for long non-
236 coding RNAs (*lncRNAs*). There is now established evidence that lncRNAs play very important roles in
237 gene regulation, in particular by acting as enhancers or silencers, with cis or trans effects and high
238 tissue specificity. Moreover, they have been implicated in BD pathology [62]; our results provide
239 further evidence and pave the way for mechanistic studies to understand their contribution to the
240 pathophysiology of BD.

241 Our study is the first in the literature to systematically investigate candidate causal variants
242 associated with BD2 using the largest BD2 GWAS data. However, it has several limitations: First,
243 despite being the largest BD2 GWAS data in the literature, the sample size is still relatively small.
244 Therefore, some of our findings did not reach the commonly used statistical significance level in
245 many enrichment analyses. Larger GWAS data will allow us and others to uncover more candidate
246 genes and provide better information about the function and interaction of candidate genes with
247 integrative analyses. Another limitation is that although we used a comprehensive filtering strategy,
248 we could not include various epigenetic mechanisms, such as alternative splicing, DNA methylation
249 that affect gene functionality or expression in our analyses, as they are not available yet in FUMA.
250 Lastly, BD2, like many other psychiatric disorders, has highly heterogeneous clinical manifestations,
251 and likely heterogeneous genetic architecture. This may have prevented some candidate genes from
252 reaching significance in a relatively small sample set, such as the one used in this study.

253 **Conclusion**

254 We prioritised BD2 associated genes implicated in important pathways such as synapse formation
255 and neuronal excitation, mitochondria and oxidation metabolism, intracellular and extracellular
256 transport, lipid metabolism, GABA-glutamate neurotransmission. There is a need to experimentally
257 validate and elucidate the biological mechanisms of these potentially functional variants, and to
258 search for new drug targets.

259 **Statements**

260 **Statement of Ethics**

261 This study protocol was reviewed and approved by Izmir Biomedicine and Genome Center non-
262 interventional research ethics committee (IBG-GOEK), approval number 2024-033. Based on the
263 ethics committee decision, it was not necessary to obtain consent to participate statement.

264 **Conflict of Interest Statement**

265 The authors have no conflicts of interest to declare.

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268 **Author Contributions**

269 Güneş Şayan Can: Writing-Original Draft, Writing-Review & Editing, Visualization, Methodology,
270 Investigation. Ebru Bakır: Methodology, Investigation, Resources. Yavuz Oktay: Conceptualization,
271 Writing-Review & Editing, Supervision

272 **Data Availability Statement**

273 The BD2 GWAS data used in this publication is from the Psychiatric Genomics Consortium. The data
274 that support the findings of this study are openly available in
275 [<https://pgc.unc.edu/for-researchers/download-results/>] at [http://doi.org/10.1038/s41588-021-](http://doi.org/10.1038/s41588-021-00857-4)
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426

427 **Figure Legends**

428 **Fig. 1.** Functional consequences of candidate SNPs on genes

429

Functional Annotation of Bipolar Disorder 2 Risk Location Implicates Novel Susceptibility Genes

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Abstract

Introduction: Bipolar 2 disorder (BD2) is an independent disease with specific familial aggregation, significant functional impairment, specific treatment challenges and several distinctive clinical features. However, unlike bipolar 1 disorder, studies investigating causal and functional genes are lacking. This study aims to identify and prioritize causal genetic variants and genes for BD2 by analyzing brain-specific gene expression markers, to improve the understanding of its genetic underpinnings and support advancements in diagnosis, treatment and prognosis.

Method: We used FUMA, a genome wide association study (GWAS) annotation tool, to pinpoint potential causal variants and genes from the largest BD2 GWAS data. Candidate causal variants most likely affecting brain gene expression were prioritized using the following criteria: (1) variants identified as eSNPs in any brain region within any brain expression quantitative trait loci (eQTL) dataset; (2) variants annotated in the Regulome database with a score <5, indicating likely functional localization; (3) the most common 15-core chromatin state across all cell types in the Roadmap Epigenomics data being ≤7, reflecting an open chromatin state; (4) localization in genomic regions with evidence of 3D chromatin interactions, as such interactions mediate genetic effects on gene expression.

Results: We identified AGRN, ORMDL3, SLC25A39, RUNDC3A, NOS2, C1orf159, RP11-5407.18, RP11-465B22.3, RP11-5407.17 as candidate causal genes. These genes are associated with important pathways such as synapse formation, mitochondrial and oxidative metabolism, intracellular transport, neurotransmission and lipid metabolism-related pathways.

Conclusion: This study provides a guide for further experimental validation of functional variants, BD2-associated genes and novel drug targets.

Introduction

Bipolar and related disorders are a group of illnesses characterised by biphasic mood episodes and euthymia periods. This definition includes bipolar 1 (BD1), bipolar 2 (BD2), cyclothymia and other forms of residual and atypical illness. BD2, previously defined as a 'mild form' of BD1 disorder, is a distinct disease entity characterised by the presence of at least one hypomanic and one major depressive episode [1]. BD2 differs from BD1 in many ways. Clinically, BD2 patients have a higher number of mood episodes, a shorter mean episode duration and more persistent depression, but are less likely to be hospitalised and less likely to have psychotic symptoms than BD1 patients [2]. Another study concluded that BD2 has less severe symptoms, shorter inter-episode duration and a more chronic course than BD1 [3]. BD2 also has other distinctive features such as: older age of onset, female predominance, higher seasonality and suicidality, family cumulation, more social problems but less disability, cognitive impairment [2, 4] and lower heritability [5]. Importantly, longitudinal studies have reported that BD2 is diagnostically stable and the percentage of patients who convert to BD1 is low [6]. Despite these characteristics, BD2 is difficult to diagnose and treat. The main reason for this is that hypomanic episodes, which do not typically cause loss of function and are much less severe than mania, do not require hospital admission and are treated as major depressive disorder [4]. This distinction has direct implications for the appropriate treatment and prognosis of BD2 patients.

Studies evaluating BD2, as a subgroup or separately, are lacking in BD studies, despite the many features of BD2 that distinguish it from other mood disorders. A recent systematic review analysed the relatively small number of candidate gene studies and genome wide association studies (GWAS) investigating BD2 [7]. Candidate gene studies have reported genes related to monoaminergic system (especially dopaminergic and serotonergic systems), calcium and cAMP signalling pathways, immune system and neuroplasticity to be specific for BD2 [7]. GWAS and the polygenic risk scores (PRS) calculated by linkage disequilibrium (LD) analysis from GWAS summary statistics data emphasize the transdiagnostic genetic background. GWAS meta-analyses highlight that BD2 shares common genes with both BD1 and schizophrenia (SCZ), while PRS analyses show a high genetic correlation of BD2 with unipolar depression (UD), and BD1 with SCZ [7, 8].

Most of the SNPs identified in GWASs are non-coding variants located in large genomic regions containing multiple candidate genes and highly linked SNPs, and it is often challenging to identify causal variants or genes [9]. Disease-causing variants can be GWAS index SNPs as well as those in LD

with the index SNP [10]. Several studies have shown that causative variants are located in regulatory DNA elements, most frequently within enhancers [9]. These variants are usually expression quantitative trait loci (eQTL) [11], which means that they affect disease risk by altering the function of cell type-specific regulatory elements that can regulate gene expression through multiple mechanisms, including modulation of chromatin accessibility, enhancer-promoter interaction, and transcription factor (TF) binding [12]. Identification of causal variants and genes is essential for understanding disease aetiology and guiding research for new drug targets [13]. To identify the most likely causal variants and genes associated with BD2 in this study, we used FUMA [14], a GWAS annotation tool that integrates multiple types of biological data, including SNP functional annotation, brain eQTL, and chromatin interaction data.

Method

Characterization of genomic risk loci based on the largest BD2 GWAS

The largest BD2 GWAS data we used in our study is a subset of a GWAS meta-analysis of 57 BD cohorts collected in Europe, North America and Australia, totaling 41,917 individuals with BD (cases) and 371,549 controls [8]. The BD sample in this meta-analysis consisted of BD1 (25,060 cases), BD2 (6,781 cases) and BD NOS (not otherwise specified) (10,076 cases). The included cases met international consensus criteria for lifetime BD (DSM-IV, ICD-9 or ICD-10), as determined using structured diagnostic interviews, clinician-administered checklists or medical record review. The authors shared individual-level genotype and phenotype data for 52 cohorts (5 cohorts were excluded) with Psychiatric Genomics Consortium (PGC). In PGC, these data are available as 3 different GWAS summary statistics files for all BD cases, BD1 cases only and BD2 cases only (https://figshare.com/articles/dataset/PGC3_bipolar_disorder_GWAS_summary_statistics/14102594). We used FUMA (<https://fuma.ctglab.nl/>) to pinpoint potential causal variants and genes from BD2 GWAS summary statistics (6,781 BD2 cases and 364,075 controls from PGC). The LD structure was calculated based on the European population data from the 1000 Genomes Project. FUMA facilitated the identification and annotation of genomic risk loci, enhancing our understanding of the genetic underpinnings of BD2 susceptibility. Genomic risk loci were identified, and various subsets of SNPs within these loci were categorized based on the following criteria:

1. Independently Significant SNPs: These are SNPs with a p-value below 5×10^{-5} and are independent from each other with $r^2 < 0.6$. While the conventional genome-wide significance threshold ($p < 5 \times 10^{-8}$) is commonly used in genomic studies, this approach is applied at the expense of the false-negative rate [15]. Indeed, several studies have shown that a substantial portion of variants with 'sub-threshold' significance ($p < 5 \times 10^{-5}$) may still indicate actual disease risk loci [16, 17]. Wang et al.

examined SNPs associated with cardiac QT interval, finding that sub-threshold SNPs were significantly present in predicted cardiac enhancers [18].

2.Candidate SNPs: SNPs in LD with independently significant SNPs ($r^2 \geq 0.6$), having a minor allele frequency (MAF) of at least 0.01, are considered candidate SNPs and are subjected to further annotation.

3.Independent Lead SNPs: These are independent significant SNPs that are also independent from each other with $r^2 < 0.1$.

4.Genomic Risk Loci: Genomic risk loci are defined by merging lead SNPs within a 250 kb window and including all SNPs in LD ($r^2 \geq 0.6$) with any of the independent SNPs.

The candidate SNPs were subsequently annotated to determine their functional consequences on gene function (including intergenic, downstream, upstream, 3' untranslated region, 5' untranslated region, intronic, exonic, ncRNA_intronic, and ncRNA_exonic) based on Ensembl genes (build 85) using the ANNOVAR tool.

Prioritization of BD2-related SNPs and genes using FUMA

Chromosomal position, reference and alternative alleles were paired for all SNPs in the 1000 Genomes Project Phase 3 analysis, and combined annotation-dependent depletion (CADD) deleteriousness scores, Regulome database (RDB) scores (regulatory elements) and 15 core chromatin states were queried. Brain eQTLs and Hi-C (high-throughput chromosome conformation capture) data, illustrating the three-dimensional (3D) structure of chromatin and interactions, were interrogated via the FUMA platform to assess the effects of all candidate SNPs on gene expression. We prioritized candidate causal variants affecting gene expression in the brain using the following criteria: (1) variants identified as eSNPs in any brain region according to GTEx V6, V7, V8, Braineac, xQTLServer, CommonMind Consortium, PsychENCODE, Brainseq eQTL data; (2) variants annotated in the RDB with a score < 5 , indicating potential involvement in functional regions affecting TF binding and gene expression [19]; (3) variants located at loci with a chromatin state ≤ 7 based on the most common 15-core chromatin states across brain tissues or cell types in Roadmap Epigenomics data, as scores from 1 to 7 generally signify an open chromatin state [20], facilitating transcriptional activation; and (4) genomic regions containing the variants with evidence of 3D chromatin interactions, as such interactions mediate genetic effects on gene expression [21]. In addition, disease-associated functional variants have been shown to be enriched in brain regions (enhancer/promoter) defined by histone marks known to be associated with transcriptional

regulatory activity, such as H3K27ac, H3K4me1 and H3K4me3 [9]. We investigated which SNPs mapped to the filtered candidate genes were enriched in these regions.

Results

Characterization of genomic risk loci

We used the FUMA platform for functional annotation of the latest and largest BD2 GWAS summary statistics including 6,781 cases and 364,075 controls. Based on the BD2 GWAS summary statistics, 26 lead SNPs for BD2 and 788 candidate SNPs in LD with lead SNPs were identified among 31 independently significant SNPs at 26 genomic loci (shown in Table 1). Half of the candidate SNPs were intronic variants, while almost half were intergenic and noncoding-RNA intronic variants, meaning that most of these SNPs are located in non-coding genomic regions (shown in Fig. 1).

Prioritization of BD2-related eGenes

To find causal variants and genes among the candidate genes, we used the filtering strategy described in the Methods section. Among all candidate SNPs (shown in Supplementary Table 1), we selected variants with an RDB score less than 5 and the most common 15-core chromatin state being not greater than 7 (shown in Supplementary Table 2). The variant list was then narrowed down by selecting brain eQTLs among these variants. Finally, only variants showing chromatin interaction in the brain Hi-C data were prioritised (shown in Supplementary Table 3). In addition, we checked whether these variants were located in brain promoter or enhancer regions. Since a single eSNP can be associated with the expression of multiple eGenes (and vice versa), we prioritised eGenes with the most significant eQTL p-value and/or overlap in brain enhancer/promoter regions as likely functional genes. As a result of this filtering strategy, we prioritised the genes that are located on chromosome 1 (*AGRN*, *C1orf159*, *RP11-5407.18*, *RP11-465B22.3*, *RP11-5407.17*) and chromosome 17 (*ORMDL3*, *SLC25A39*, *RUNDC3A*, *NOS2*). All of the prioritised variants are intronic and three of them are located within long non-coding genes. Of note, all prioritised genes are highly expressed in the emotion regulatory regions of the brain (shown in Table 2).

Discussion

GWASs and candidate gene studies have identified some genetic variants associated with BD2, but causal variants and genes have been largely undiscovered. In this study, we used the FUMA tool and a prioritisation strategy to identify potential BD2 causal variants and genes, based on the most recent and largest BD2 GWAS datas. We identified 788 candidate SNPs at 26 genomic risk loci. We found that most of the candidate SNPs were located in non-coding regions. Similar to other psychiatric

disorders and complex diseases, SNPs identified in the BD2 GWAS are mostly located in regulatory DNA regions [22].

We applied filters indicative of active transcription and open chromatin to distinguish causal and functional variants among candidate genes, prioritising *AGRN*, *ORMDL3*, *SLC25A39*, *RUNDC3A*, *NOS2*, *C1orf159*, *RP11-5407.18*, *RP11-465B22.3*, *RP11-5407.17*. ***AGRN***, the best known of these genes, codes for a proteoglycan that is critical for the postsynaptic assembly of the neuromuscular junction [23]. *AGRN* is also expressed in the brain [24]. A study reported that *AGRN* mutations impair the proliferation of excitatory cells in the hippocampus and lead to depression-like behaviour [25]. *AGRN* also induces dendritic filopodia and synapse formation in hippocampal neurons by acting on glutamate receptors in the hippocampus through activation of RhoA GTPases [26]. Another study has shown that *AGRN* regulates hippocampal neuronal excitability via Na⁺,K⁺-ATPase activity. It has been reported that suppression of neuronal *AGRN* reverses manic-like behaviour [27]. Na⁺,K⁺-ATPase is expressed in excitatory glutamatergic and inhibitory GABAergic neurons in the healthy brain and has a higher GABAergic expression especially in the hippocampus [28]. Therefore, *AGRN*-Na⁺,K⁺-ATPase interactions may predominate at synapses between excitatory and inhibitory neurons. Increased glutamatergic, decreased GABAergic expression, upregulation of Na⁺,K⁺-ATPase genes and associated hyperactive action potential firing and hyperexcitability phenotype have been shown in dentate hippocampal cells of BD patients [29]. Therefore, we propose *AGRN* as likely to be one of the genes contributing to BD pathology. ***ORMDL3*** encodes the protein 'ORMDL sphingolipid biosynthesis regulator 3', which is a regulator of sphingolipid synthesis located in the endoplasmic reticulum and inhibits serine palmitoyl transferase (SPT), the rate-limiting enzyme in sphingolipid biosynthesis [30]. Dysregulation of *ORMDL3* gene disrupts SPT inhibition and impairs the metabolism of ceramide, a sphingolipid metabolite [31]. Ceramide is highly abundant in neural cell membranes and serves as a precursor for complex sphingolipids that are important for brain homeostasis [32]. However, studies indicate that ceramide accumulation promotes depression-like behaviors in mice, and these behaviors can be rescued by certain antidepressants that reduce hippocampal ceramide levels, such as amitriptyline and fluoxetine [33]. Ceramide accumulation has been found to have a negative effect on cells by triggering apoptosis [34]. In lipidomic analysis, ceramides were found to be significantly elevated in the plasma of UD and BD patients compared to healthy controls [35]. Ceramides were also shown to be significantly elevated in the white matter of bipolar patients compared to control levels [36]. However, the mechanism of ceramide increase in BD is not clear. Members of the mitochondrial solute carrier (SLC) family 25 (SLC25) enable the transport of substances required for biochemical pathways and cellular homeostasis across the inner mitochondrial membrane into the mitochondria [37]. ***SLC25A39*** is involved in the first steps of heme biosynthesis [38] and in the

transport of cytosolic glutathione (GSH) into mitochondria. Loss of SLC25A39 has been shown to reduce mitochondrial GSH levels and impair the activity of iron-sulphur cluster proteins. Many reactions in mitochondria generate free oxygen radicals, commonly referred to as reactive oxygen species (ROS), which cause cellular damage; GSH acts as an antioxidant, neutralising these harmful molecules [39]. *SLC25A39* mutations have been reported to reduce the GSH levels in brain mitochondria, leading to mitochondrial dysfunction, synaptic defects and neurodegeneration with ROS accumulation [40]. Lam et al. reviewed the evidence on impairment of mitochondrial morphology, distribution and dysfunction in BD patients [41]. In addition, increased oxidative stress, characterised by increased ROS, is well known and documented in the pathogenesis of BD. Studies have also shown that GSH levels in various brain regions are significantly lower in BD patients than in controls [42]. ***RUNDC3A*** is expressed in the brain, in cells of neuroendocrine origin and in pancreatic beta cells [43]. It is thought to function by interacting with the GTP-bound form of Rap2a, a member of the Ras family, in the brain, and may play a role in vesicle formation, trafficking or function, particularly at excitatory synapses [43, 44]. Extracellular vesicles are intricately involved in the pathological mechanisms of BD and may serve as emerging biomarkers for clinical detection of BD [45]. However, the exact role of *RUNDC3A* in BD pathology needs further clarification. Nitric oxide (NO) is a reactive free radical that plays an important role as a messenger molecule in neurotransmission, long-term memory enhancement in the brain [46, 47]. NO synthases (NOS) are involved in NO synthesis from L-arginine and are encoded by *NOS1*, *NOS2* and *NOS3* genes [48]. It has long been known that ***NOS2*** is expressed in neurons [49]. Higher plasma NO levels have been shown in BD patients compared to healthy individuals [50, 51]. Also, pro-inflammatory and regulatory cytokines are activated in BD patients, indicating the presence of low-grade inflammation that can lead to central nervous system damage [52]. It is thought that this chronic inflammation leads to iNOS (NOS2)-mediated production of large amounts of NO, which can lead to oxidative stress, DNA and mitochondrial damage [53]. It has also been shown that depression and anxiety-like behaviours are reduced and stress resilience is increased in *Nos2*-deficient mice [54]. Reduction of *NOS2* levels and amelioration of mania-like behaviours of mania model in mice by lithium [55, 56] and doxycycline [56], a potent anti-inflammatory agent, supports the link between *NOS2* and BD. The ***C1orf159*** gene encodes a protein whose function has not been well-characterised. It is expressed almost throughout the body and in all regions of the brain, and interacts with TFRC and TOMM6. (<https://www.proteinatlas.org/ENSG00000131591-C1orf159>). *TFRC* encodes the transferrin (TF) cell surface receptor required for cellular iron uptake by receptor-mediated endocytosis [57]. TF receptors, particularly in neurons and oligodendrocytes, are required for iron uptake into these cells, which is essential for several enzymatic reactions involved in cholesterol and phospholipid production, mitochondrial activity and ATP synthesis [58]. It was shown that iron haemostasis,

mitochondrial activity, energy production and myelination were impaired when the TF receptor was knocked out in oligodendrocyte cells [59]. Most mitochondrial proteins are synthesised in the cytosol and transported into mitochondria by the TOM complexes [60]. Regular protein trafficking is essential for mitochondrial function and TOMM6 ensures that the import receptors and the TOM complex maintain a stable interaction [61]. In summary, disruptions in the interactions of C1orf159, TFRC and TOMM6 may be associated with alterations in the pathways known to contribute to the pathophysiology of BD, such as synaptic and mitochondrial dysfunction and iron homeostasis. The other three genes (*RP11-5407.18*, *RP11-465B22.3*, *RP11-5407.17*) we prioritised code for long non-coding RNAs (***lncRNAs***). There is now established evidence that lncRNAs play very important roles in gene regulation, in particular by acting as enhancers or silencers, with cis or trans effects and high tissue specificity. Moreover, they have been implicated in BD pathology [62]; our results provide further evidence and pave the way for mechanistic studies to understand their contribution to the pathophysiology of BD.

Our study is the first in the literature to systematically investigate candidate causal variants associated with BD2 using the largest BD2 GWAS data. However, it has several limitations: First, despite being the largest BD2 GWAS data in the literature, the sample size is still relatively small. Therefore, some of our findings did not reach the commonly used statistical significance level in many enrichment analyses. Larger GWAS data will allow us and others to uncover more candidate genes and provide better information about the function and interaction of candidate genes with integrative analyses. Another limitation is that although we used a comprehensive filtering strategy, we could not include various epigenetic mechanisms, such as alternative splicing, DNA methylation that affect gene functionality or expression in our analyses, as they are not available yet in FUMA. Lastly, BD2, like many other psychiatric disorders, has highly heterogeneous clinical manifestations, and likely heterogeneous genetic architecture. This may have prevented some candidate genes from reaching significance in a relatively small sample set, such as the one used in this study.

Conclusion

We prioritised BD2 associated genes implicated in important pathways such as synapse formation and neuronal excitation, mitochondria and oxidation metabolism, intracellular and extracellular transport, lipid metabolism, GABA-glutamate neurotransmission. There is a need to experimentally validate and elucidate the biological mechanisms of these potentially functional variants, and to search for new drug targets.

Statements

Statement of Ethics

This study protocol was reviewed and approved by Izmir Biomedicine and Genome Center non-interventional research ethics committee (IBG-GOEK), approval number 2024-033. Based on the ethics committee decision, it was not necessary to obtain consent to participate statement.

Conflict of Interest Statement

The authors have no conflicts of interest to declare.

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Author Contributions

Güneş Şayan Can: Writing-Original Draft, Writing-Review & Editing, Visualization, Methodology, Investigation. Ebru Bakır: Methodology, Investigation, Resources. Yavuz Oktay: Conceptualization, Writing-Review & Editing, Supervision

Data Availability Statement

The BD2 GWAS data used in this publication is from the Psychiatric Genomics Consortium. The data that support the findings of this study are openly available in [<https://pgc.unc.edu/for-researchers/download-results/>] at <http://doi.org/10.1038/s41588-021-00857-4>, reference number [8].

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Figure Legends

Fig. 1. Functional consequences of candidate SNPs on genes

Figure 1. Functional consequences of candidates SNPs on genes

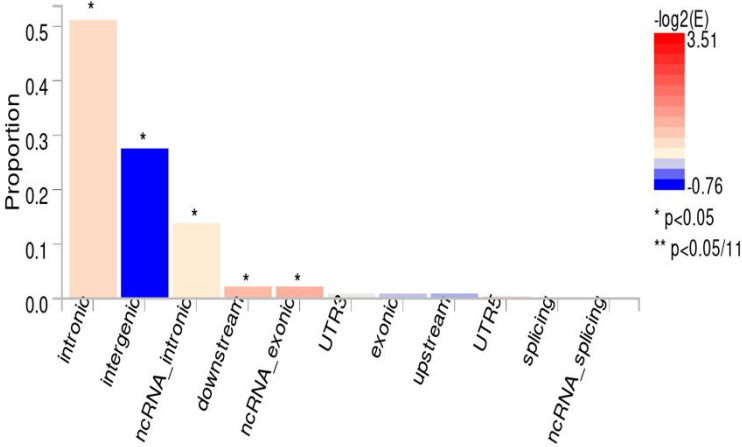


Table 1. Summary results of genome-wide analysis of Bipolar Disorders 2 based on FUMA

Index	Number
Genomic risk loci	26
Lead SNPs	26
Independently significant SNPs	31
Candidate SNPs	788
Candidate GWAS tagged SNPs	647
Mapped genes	50

Table 2. Nine Prioritized eGenes

UniqID	RsID	Function	RDB	CommonChrState	eQTL gene	eQTL pvalue	Brain eQTL tissue	Regulation type	Brain Ci tissue
1:960409:C:G	rs4970392	intronic	4	7	C1orf159	3,28E-02	Cerebellum	enhancer	Yes
1:956852:C:T	rs9777931	intronic	4	2	AGRN	0.000109	Temporal cortex	promoter-enhancer	Yes
1:960409:C:G	rs4970392	intronic	4	7	RP11-465B22.3	3,28E-02	Anterior_cingulate_cortex	enhancer	Yes
1:959169:C:G	rs3845292	intronic	3a	7	RP11-54O7.17	1,14E-09	Brain_Caudate_nucleus	enhancer	Yes
1:960409:C:G	rs4970392	intronic	4	7	RP11-54O7.18	1,49E+00	Prefrontal and temporal cortex	enhancer	Yes
17:26216397:A:G	rs7220420	intronic	2b	5	NOS2	3,91E-32	Brain_Nucleus_accumbens		Yes
17:37843550:C:T	rs2517954	intronic	4	5	ORMDL3	1,72E-01	Prefrontal and temporal cortex		Yes
17:42155838:A:G	rs9913925	intronic	2b	4	SLC25A39	1,75E-01	Dorsolateral prefrontal cortex	enhancer	Yes
17:42155838:A:G	rs9913925	intronic	2b	4	RUNDC3A	0.049	Postmortem brain data	enhancer	Yes

*uniqID: Chromosome:position:allels, rsID : ID of the lead SNPs, RDB: Regulome database, commonChrState: the most common 15-core chromatin state across all tissues, eQTL: Expression quantitative trait loci, Ci: Chromatine Interactions, RDB ranking: *2b* TF binding + any motif + Footprint + chromatin accessibility peak, *3a* TF binding + any motif + chromatin accessibility peak, *4* TF binding + chromatin accessibility peak

CADD	Combined Annotation Dependent Depletion
chr	chromosome
ciMapFilt	chromatin interaction mapping filter
commonChrState	the most common 15-core chromatin state across 127 tissue/cell types
db	database
dist	distance
eqtlMapFilt	eQTL mapping filter
func	functional consequence
gwasP	GWAS <i>P</i> value
IndSigSNP	independent significant SNP
MAF	minor allele frequency
minChrState	the minimum 15-core chromatin state across 127 tissue/cell type
or	odds ratio
pos	position
posMapFilt	position mapping filter
RDB	RegulomeDB score
RiskIncAllele	risk increasing allele

uniqID	rsID	chr	pos	non_effect	effect_allele	MAF	gwasP	beta	se
1:933790:	rs9442392	1	933790	A	G	0.4056	0.00027960	0.07950410	0.0219
1:935222:	rs2298214	1	935222	A	C	0.4105	NA	NA	NA
1:936111:(rs	1936360	1	936111	T	C	0.4095	0.00044890	0.07680360	0.0219
1:943968:(rs	1330331	1	943968	T	C	0.4334	0.00029790	0.07749790	0.0214
1:950113: rs	1402582	1	950113	G	GAAGT	0.4344	NA	NA	NA
1:950677:(rs	9331223	1	950677	C	T	0.4284	0.00030810	0.07780320	0.0216
1:951283:(rs	9442363	1	951283	T	C	0.4304	NA	NA	NA
1:951295:(rs	9442388	1	951295	T	C	0.4304	NA	NA	NA
1:952428:	rs9442611	1	952428	A	G	0.4384	0.00013320	0.08229860	0.0215
1:953952:	rs9442612	1	953952	A	G	0.4394	0.00014940	0.08180110	0.0216
1:954777:	rs6176629	1	954777	A	C	0.4404	0.00013710	0.08229860	0.0216
1:956852:(rs	9777931	1	956852	T	C	0.4473	7.32E-02	0.08590240	0.0217
1:959155:	rs3845291	1	959155	A	G	0.4602	0.00017030	0.08350440	0.0222
1:959169:(rs	3845292	1	959169	C	G	0.4503	0.00015280	0.08299830	0.0219
1:959231:	rs4039721	1	959231	A	G	0.492	0.00012380	0.08690220	0.0226
1:960409:(rs	4970392	1	960409	C	G	0.4404	8.78E-03	0.09709940	0.0219
1:962606:	rs4970393	1	962606	A	G	0.4274	3.08E-02	0.09140250	0.0219
1:962891:(rs	4970394	1	962891	T	C	0.4294	2.73E-02	0.09180400	0.0219
1:965009:	rs7157658	1	965009	G	A	0.4205	NA	NA	NA
1:965480:(rs	6263804	1	965480	C	CAT	0.4344	NA	NA	NA
1:965876: rs	3702709	1	965876	CGT	C	0.4722	NA	NA	NA
1:965876:(rs	1112034	1	965876	C	T	0.1461	NA	NA	NA
1:966391: rs	1382061	1	966391	A	ATG	0.4274	NA	NA	NA
1:967658:(rs	4970349	1	967658	T	C	0.4344	1.31E-02	0.09530100	0.0219
1:970215:(rs	9442364	1	970215	C	G	0.4264	4.86E-02	0.08879810	0.0219
1:972180:	rs4970350	1	972180	A	G	0.4254	5.78E-02	0.08790090	0.0219
1:978603:(rs	3588118	1	978603	C	CCT	0.4513	NA	NA	NA
1:984302:(rs	9442391	1	984302	C	T	0.4364	3.88E-03	0.09999910	0.0216
1:985266:(rs	2275813	1	985266	T	C	0.4543	5.53e-06	0.09970050	0.0219
1:985446:(rs	2275812	1	985446	G	T	0.4911	NA	NA	NA
1:992819:	rs9331226	1	992819	A	G	0.4284	0.00017060	0.08490160	0.0226
1:993360:	rs1330324	1	993360	A	C	0.4354	7.39E-02	0.08490160	0.0214
1:995481:(rs	9442393	1	995481	G	T	0.4374	NA	NA	NA
1:998582:(rs	3813194	1	998582	C	G	0.4443	0.000132	0.08139560	0.0213
1:1004389rs	1383737	1	1004389	TC	T	0.4324	NA	NA	NA
1:1004957rs	4073176	1	1004957	A	G	0.4245	0.00039630	0.07520020	0.0212
1:1004980rs	4073177	1	1004980	A	G	0.4245	0.000399	0.07520020	0.0212
1:1006223rs	9442394	1	1006223	A	G	0.4254	0.000504	0.07390080	0.0212
1:1007432rs	4333796	1	1007432	A	G	0.4384	0.00068260	0.07209730	0.0212
1:1009234rs	9442366	1	1009234	C	T	0.4384	0.00099290	0.07000160	0.0212
1:1010717rs	9442368	1	1010717	T	C	0.4334	0.002703	0.06369750	0.0212
1:1011087rs	6056165	1	1011087	C	CG	0.4354	NA	NA	NA
1:1014836rs	1240160	1	1014836	G	A	0.4493	0.001336	0.06849940	0.0214
1:1014864rs	1241104	1	1014864	A	T	0.4473	0.001643	0.06730340	0.0214
1:1015126rs	3602749	1	1015126	G	A	0.4443	0.003114	0.06649900	0.0225
1:1015257rs	9442369	1	1015257	G	A	0.4443	0.001794	0.06660200	0.0213
1:1015551rs	9442370	1	1015551	T	C	0.4592	0.00093980	0.07129680	0.0215

1:1017170rs3766193	1	1017170 G	C	0.4493	0.001487	0.06760250.0213
1:1017197rs3766192	1	1017197 T	C	0.4513	0.00106	0.06979650.0213
1:1018144rs9442395	1	1018144 C	T	0.4414	0.002115	0.06489780.0211
1:1018562rs9442371	1	1018562 T	C	0.4414	0.002337	0.06429780.0211
1:1018704rs9442372	1	1018704 G	A	0.4404	0.002271	0.06440100.0211
1:1019180rs9442396	1	1019180 C	T	0.4334	0.00287	0.06320010.0212
1:1022037rs6701114	1	1022037 T	C	0.4414	0.005343	0.06000320.0215
1:2455095rs1162077	1	2.46E+08 A	G	0.01889	4.11E-03	-0.479004 0.104
1:2455159rs1148874	1	2.46E+08 A	C	0.02286	2.56E-02	-0.433201 0.1029
3:4238754rs247412	3	42387540 G	T	0.3827	2.40E-03	-0.099698 0.0211
3:4239238rs33511	3	42392381 A	G	0.3837	2.41E-03	-0.099499 0.0211
3:4239747rs247416	3	42397470 T	C	0.3837	2.06E-03	-0.100096 0.0211
3:4240687rs26353	3	42406870 G	T	0.3956	0.0001147	-0.079996 0.0207
4:2992449rs1400191	4	29924495 A	T	0.0159	NA	NA NA
4:2992462rs6179455	4	29924629 A	G	0.0159	8.99E-02	-0.350806 0.0896
4:2992503rs6179455	4	29925037 G	A	0.0159	0.001217	-0.308102 0.0953
4:2992640rs1382439	4	29926402 T	G	0.0159	0.001328	-0.305696 0.0952
4:2992729rs1508654	4	29927297 C	T	0.0159	0.001314	-0.305995 0.0952
4:2992880rs6179455	4	29928801 C	T	0.0159	0.001295	-0.306402 0.0952
4:2992884rs6179586	4	29928841 G	A	0.0159	0.00119	-0.308102 0.0951
4:2992975rs1688251	4	29929753 C	A	0.0159	0.001314	-0.305398 0.095
4:2993024rs6179586	4	29930249 T	G	0.0159	0.001249	-0.307000 0.0951
4:2993064rs6179586	4	29930640 T	A	0.0159	0.001246	-0.307095 0.0951
4:2993197rs4339167	4	29931976 A	C	0.0159	0.001216	-0.307694 0.0951
4:2993473rs2000637	4	29934735 A	AAAG	0.0159	NA	NA NA
4:2993570rs6854433	4	29935701 G	A	0.0159	0.001104	-0.310800 0.0953
4:2993612rs7696810	4	29936124 C	A	0.0159	0.001175	-0.308606 0.0951
4:2994067rs6179586	4	29940671 G	A	0.01789	1.47E-02	-0.370295 0.0855
4:2994279rs6179586	4	29942796 A	G	0.01789	6.3e-06	-0.386206 0.0855
4:2994578rs6179586	4	29945788 T	C	0.01789	1.97E-02	-0.373603 0.0875
4:2995071rs6107526	4	29950719 A	G	0.01789	1.14E-02	-0.374402 0.0853
4:2995611rs7584392	4	29956117 C	T	0.01789	2.00E-02	-0.373196 0.0875
4:2995973rs7911284	4	29959736 C	T	0.01789	2.13e-05	-0.367504 0.0865
4:2996195rs6179586	4	29961957 C	G	0.01789	2.27E-02	-0.366696 0.0865
4:29963004:2996300	4	29963005 G	A	0.09046	NA	NA NA
4:29963004:2996300	4	29963005 G	C	0.01789	NA	NA NA
4:2996377rs6179587	4	29963775 A	G	0.01889	1.29E-02	-0.373893 0.0857
4:2996484rs7380843	4	29964841 C	T	0.01889	1.13e-05	-0.377694 0.086
4:2996500rs6179587	4	29965009 A	T	0.01889	1.16E-02	-0.377300 0.086
4:2996924rs5932120	4	29969243 G	A	0.01988	1.35e-05	-0.374199 0.086
4:2997074rs5720400	4	29970745 T	A	0.01889	1.5e-05	-0.372601 0.0861
4:2997150rs7683956	4	29971504 G	A	0.01889	1.58E-02	-0.371600 0.0861
4:2997205rs6179592	4	29972055 G	C	0.01889	1.61E-02	-0.371194 0.0861
4:2997281rs6179592	4	29972810 C	G	0.01889	1.63E-02	-0.370904 0.0861
4:2997403rs5857164	4	29974034 CAT	C	0.01889	NA	NA NA
4:2997447rs6179592	4	29974471 T	C	0.01789	2.01E-02	-0.373995 0.0877
4:2997809rs6179593	4	29978099 A	G	0.01889	1.72E-02	-0.369904 0.0861
4:2998225rs5681677	4	29982255 A	G	0.01889	1.32E-02	-0.375406 0.0862

4:2998272rs7380860	4 29982728 G	C	0.01889	1.34E-02	-0.375100	0.0861
4:2998535rs6179593	4 29985353 T	C	0.01889	1.42E-02	-0.373704	0.0861
4:2998604rs6179593	4 29986043 A	C	0.02386	1.64e-07	-0.403197	0.077
4:2999527rs6179286	4 29995273 T	A	0.01889	6.1e-05	-0.334005	0.0833
4:2999569rs7380864	4 29995690 G	A	0.02386	2.27E-04	-0.394302	0.0762
4:2999671rs6179286	4 29996714 C	T	0.01889	5.61E-02	-0.335095	0.0832
4:3000052rs6179291	4 30000524 T	C	0.01889	6.55E-02	-0.332302	0.0833
4:30000924:3000092	4 30000922 C	A	0.01889	NA	NA	NA
4:30000924:3000092	4 30000922 C	T	0.05169	NA	NA	NA
4:3000324rs7380864	4 30003242 A	C	0.01889	6.38E-02	-0.333097	0.0833
4:3000395rs3691680	4 30003953 GTT	G	0.01988	NA	NA	NA
4:3000902rs6179291	4 30009020 G	C	0.01789	7.90E-02	-0.329699	0.0835
4:3001105rs4414915	4 30011056 C	T	0.01789	0.000127	-0.321500	0.0839
4:3001111rs4388047	4 30011115 A	G	0.01789	0.0001211	-0.322397	0.0839
4:3001276rs6179291	4 30012766 C	A	0.01789	0.0001226	-0.322397	0.0839
4:3001511rs6179292	4 30015118 C	A	0.01789	0.0001319	-0.321197	0.084
4:3001573rs6179292	4 30015739 A	C	0.01789	0.0001298	-0.321500	0.084
4:3001927rs5915414	4 30019271 G	C	0.01789	0.0001489	-0.319103	0.0841
4:3002528rs6840115	4 30025287 C	T	0.01789	0.01535	-0.244099	0.1007
4:3003267rs5862541	4 30032678 T	A	0.01789	0.01681	-0.241205	0.1009
4:3003286rs7662949	4 30032869 G	A	0.01789	0.01606	-0.243001	0.1009
5:1039189rs6759760	5 1.04E+08 T	G	0.1441	1.29E-03	-0.136197	0.0281
5:1040724rs3584192	5 1.04E+08 C	T	0.162	9.37E-03	-0.117905	0.0266
5:1684031rs6237725	5 1.68E+08 C	T	0.05368	3.39E-02	-0.178397	0.043
5:1684034rs7551191	5 1.68E+08 G	A	0.05268	4.17E-02	-0.177501	0.0433
5:1684038rs6237725	5 1.68E+08 T	C	0.05268	4.24E-02	-0.177202	0.0433
5:1684041rs6237725	5 1.68E+08 T	C	0.05268	4.28E-02	-0.177095	0.0433
5:16840425:1684042	5 1.68E+08 C	T	0.000994	NA	NA	NA
5:16840425:1684042	5 1.68E+08 C	G	0.05268	NA	NA	NA
5:1684042rs6237725	5 1.68E+08 T	G	0.05268	3.96E-02	-0.177895	0.0433
5:1684044rs6237725	5 1.68E+08 C	T	0.05268	4.00E-02	-0.177799	0.0433
5:1684049rs1195279	5 1.68E+08 G	A	0.05268	4.40E-02	-0.176796	0.0433
5:1684053rs1137733	5 1.68E+08 T	C	0.05268	4.32E-02	-0.176999	0.0433
5:1684068rs5928203	5 1.68E+08 A	G	0.05268	4.34E-02	-0.176999	0.0433
5:1684077rs1195551	5 1.68E+08 C	A	0.05268	4.54E-02	-0.176403	0.0433
5:1684085rs6237858	5 1.68E+08 T	C	0.05268	3.84E-02	-0.178098	0.0433
5:1684094rs6237858	5 1.68E+08 A	G	0.05268	3.8e-05	-0.178194	0.0432
5:1684120rs6237859	5 1.68E+08 T	C	0.05268	3.22E-02	-0.179605	0.0432
5:1684121rs6237859	5 1.68E+08 A	G	0.05268	3.19E-02	-0.179700	0.0432
5:1684122rs6237859	5 1.68E+08 A	G	0.05368	2.72E-02	-0.180395	0.043
5:1684135rs5992283	5 1.68E+08 G	A	0.05268	NA	NA	NA
5:1684136rs1149146	5 1.68E+08 G	T	0.05268	NA	NA	NA
5:1684136rs1154572	5 1.68E+08 G	C	0.05268	3.51E-02	-0.180000	0.0435
5:1684136rs1162213	5 1.68E+08 T	A	0.05268	3.46E-02	-0.180096	0.0435
5:1684136rs1155853	5 1.68E+08 A	G	0.05268	2.93E-02	-0.180599	0.0432
5:1684139rs6237860	5 1.68E+08 T	C	0.05368	3.20E-02	-0.179796	0.0432
5:1684139rs6237860	5 1.68E+08 T	C	0.05467	3.75E-02	-0.178002	0.0432
5:1684140rs6237860	5 1.68E+08 A	G	0.05368	3.02E-02	-0.180203	0.0432

5:1684145rs6057324	5	1.68E+08	T	C	0.05368	2.98E-02	-0.180299	0.0432
5:1684147rs6237860	5	1.68E+08	T	C	0.05368	3.42E-02	-0.178803	0.0432
5:1684156rs6237861	5	1.68E+08	G	C	0.05368	2.97E-02	-0.180299	0.0432
5:1684157rs1459833	5	1.68E+08	C	CCT	0.05368	NA	NA	NA
5:1684158rs6237861	5	1.68E+08	T	C	0.05368	2.83E-02	-0.180694	0.0432
5:1684159rs8006212	5	1.68E+08	T	C	0.05368	2.93E-02	-0.180395	0.0432
5:1684161rs6237861	5	1.68E+08	T	A	0.05368	2.97E-02	-0.180299	0.0432
5:1684163rs6237861	5	1.68E+08	A	C	0.05368	2.78E-02	-0.180898	0.0432
5:1684165rs6237861	5	1.68E+08	A	G	0.05368	2.88E-02	-0.180503	0.0432
5:1684169rs6237861	5	1.68E+08	C	T	0.05368	2.64E-02	-0.181401	0.0432
5:1684176rs6237861	5	1.68E+08	A	G	0.05368	2.63E-02	-0.181401	0.0431
5:1684182rs5702716	5	1.68E+08	C	T	0.05467	2.07E-02	-0.183105	0.043
5:1684184rs6065058	5	1.68E+08	A	G	0.05467	2.05e-05	-0.183201	0.043
5:1684188rs1218950	5	1.68E+08	G	A	0.05467	2.02E-02	-0.183298	0.043
5:1684188rs1218792	5	1.68E+08	A	G	0.05467	2.02E-02	-0.183298	0.043
5:1684192rs6237861	5	1.68E+08	C	A	0.05467	2.12E-02	-0.182697	0.043
5:1684195rs6237862	5	1.68E+08	T	C	0.0497	9.79E-02	-0.191802	0.0492
5:1684200rs6237862	5	1.68E+08	C	G	0.0507	8.60E-02	-0.193002	0.0491
5:1684201rs3797714	5	1.68E+08	C	T	0.0497	7.28E-02	-0.194896	0.0491
5:1684202rs6237862	5	1.68E+08	A	G	0.0497	6.86E-02	-0.195601	0.0491
5:1684205rs1150275	5	1.68E+08	A	C	0.0497	6.84E-02	-0.195601	0.0491
5:1684211rs1157425	5	1.68E+08	A	G	0.0497	6.83E-02	-0.195601	0.0491
5:1684212rs6237862	5	1.68E+08	A	G	0.0497	6.85E-02	-0.195504	0.0491
5:1684214rs1412156	5	1.68E+08	G	A	0.0497	0.0002093	-0.193002	0.0521
5:1684219rs6237862	5	1.68E+08	A	C	0.0497	8.32E-02	-0.193402	0.0491
5:1684228rs6237862	5	1.68E+08	G	A	0.04871	8.71E-02	-0.192796	0.0491
5:1684239rs7580591	5	1.68E+08	A	C	0.04871	7.92E-02	-0.193803	0.0491
5:1684241rs1144795	5	1.68E+08	A	G	0.04871	8.1e-05	-0.193596	0.0491
5:1684246rs6237862	5	1.68E+08	A	G	0.04871	6.37e-05	-0.196197	0.0491
5:1684247rs7994007	5	1.68E+08	T	C	0.04871	NA	NA	NA
5:1684248rs7748425	5	1.68E+08	C	T	0.04871	NA	NA	NA
5:1684249rs6237862	5	1.68E+08	T	C	0.04871	6.40E-02	-0.196197	0.0491
5:1684250rs1160833	5	1.68E+08	G	C	0.04871	7.74E-02	-0.194203	0.0491
5:1684256rs6237862	5	1.68E+08	T	C	0.04871	7.98E-02	-0.193803	0.0491
5:1684256rs6237863	5	1.68E+08	C	T	0.04871	7.64E-02	-0.194301	0.0491
5:1684257rs7575039	5	1.68E+08	G	C	0.04871	0.001356	-0.193196	0.0603
5:1684257rs7597381	5	1.68E+08	T	A	0.04871	0.001233	-0.195200	0.0604
5:1684258rs1135958	5	1.68E+08	C	T	0.04871	8.09E-02	-0.193693	0.0491
5:1684259rs1129211	5	1.68E+08	A	G	0.04871	NA	NA	NA
5:1684261rs1428023	5	1.68E+08	G	GGT	0.04871	NA	NA	NA
5:168426 rs5505826	5	1.68E+08	CCATAAGCC		0.0497	NA	NA	NA
5:1684264rs1484392	5	1.68E+08	C	T	0.04871	NA	NA	NA
5:1684266rs6237863	5	1.68E+08	C	T	0.04871	7.61E-02	-0.194398	0.0491
5:1684269rs6237863	5	1.68E+08	A	G	0.04871	8.07E-02	-0.193693	0.0491
5:1684300rs6237863	5	1.68E+08	C	T	0.0497	5.21E-02	-0.197804	0.0489
5:1684303rs1005530	5	1.68E+08	C	T	0.06859	6.53E-02	-0.166798	0.0418
5:1684304rs1006245	5	1.68E+08	G	A	0.06859	6.47E-02	-0.166905	0.0418
5:1684308rs6237863	5	1.68E+08	T	C	0.0497	4.98E-02	-0.198304	0.0489

5:1684320rs7515092	5	1.68E+08	C	T	0.0497	5.34E-02	-0.197500	0.0489
5:1684321rs1995036	5	1.68E+08	A	AT	0.0497	NA	NA	NA
5:1684322rs6237863	5	1.68E+08	C	T	0.0497	5.42E-02	-0.197402	0.0489
5:1684325rs6237863	5	1.68E+08	G	A	0.0497	5.47E-02	-0.197305	0.0489
5:1684326rs6237863	5	1.68E+08	C	T	0.0497	5.44E-02	-0.197402	0.0489
5:1684330rs6237946	5	1.68E+08	C	A	0.0497	6.72E-02	-0.195102	0.0489
5:1684331rs1215271	5	1.68E+08	C	T	0.0507	5.73E-02	-0.196903	0.0489
5:1684332rs1215272	5	1.68E+08	A	T	0.0497	5.78E-02	-0.196805	0.0489
5:1684332rs1215353	5	1.68E+08	A	C	0.0497	5.69E-02	-0.196903	0.0489
5:1684334rs1215272	5	1.68E+08	C	T	0.0497	6.70E-02	-0.195102	0.0489
5:1684337rs1163905	5	1.68E+08	T	C	0.0497	6.73e-05	-0.195102	0.0489
5:1684338rs1485480	5	1.68E+08	CAG	C	0.0497	NA	NA	NA
5:1684339rs1153481	5	1.68E+08	T	C	0.0497	7.16E-02	-0.194398	0.0489
5:1684342rs1475526	5	1.68E+08	A	AT	0.0497	NA	NA	NA
5:1684343rs6237946	5	1.68E+08	T	C	0.0497	6.87E-02	-0.194896	0.049
5:1684344rs6237946	5	1.68E+08	T	G	0.0497	6.66e-05	-0.195200	0.0489
5:1684345rs6237946	5	1.68E+08	C	A	0.0497	6.66E-02	-0.195200	0.049
5:1684353rs1773428	5	1.68E+08	G	A	0.1759	0.0006672	-0.086604	0.0255
5:1684356rs6237946	5	1.68E+08	T	C	0.0497	0.0002589	-0.189805	0.052
5:1684356rs5588411	5	1.68E+08	G	GTT	0.0497	NA	NA	NA
5:1684356rs7542223	5	1.68E+08	G	T	0.000994	NA	NA	NA
5:1684357rs1004554	5	1.68E+08	A	G	0.1759	0.0006713	-0.086495	0.0254
5:1684358rs1004551	5	1.68E+08	T	C	0.1759	0.0007061	-0.086102	0.0254
5:1684360rs7482501	5	1.68E+08	A	AT	0.06759	NA	NA	NA
5:1684362rs8000416	5	1.68E+08	G	A	0.0497	6.99E-02	-0.194398	0.0489
5:1684364rs6237946	5	1.68E+08	G	A	0.162	3.32E-02	-0.107696	0.0259
5:1684366rs6237946	5	1.68E+08	T	A	0.0497	4.6e-05	-0.199402	0.0489
5:1684367rs1003813	5	1.68E+08	C	T	0.161	3.88E-02	-0.107095	0.026
5:1684368rs1003814	5	1.68E+08	C	T	0.161	5.07E-02	-0.105404	0.026
5:1684376rs6237947	5	1.68E+08	T	C	0.16	4.58E-02	-0.106405	0.0261
5:1684384rs1195564	5	1.68E+08	T	A	0.06759	9.33E-02	-0.163001	0.0417
5:1684390rs1004238	5	1.68E+08	G	A	0.0497	6.43e-05	-0.195394	0.0489
5:1684427rs7569685	5	1.68E+08	C	A	0.1769	2.50E-02	-0.105905	0.0251
5:1684443rs6237947	5	1.68E+08	G	A	0.04672	2.98E-02	-0.204199	0.0489
5:1684456rs2278391	5	1.68E+08	A	G	0.16	1.31E-02	-0.113403	0.026
5:1684486rs6237947	5	1.68E+08	A	G	0.04672	3.27E-02	-0.203402	0.049
5:1684488rs9968663	5	1.68E+08	T	C	0.06561	7.52E-02	-0.165299	0.0417
5:1684489rs1130247	5	1.68E+08	G	GA	0.06561	NA	NA	NA
5:1684491rs2278390	5	1.68E+08	T	C	0.1759	3.31E-02	-0.104505	0.0252
5:1684494rs6237947	5	1.68E+08	T	C	0.06561	9.35e-05	-0.162801	0.0417
5:1684497rs7851013	5	1.68E+08	G	C	0.04672	5.11E-02	-0.198097	0.0489
5:1684497rs7802563	5	1.68E+08	C	G	0.0666	9.30E-02	-0.162895	0.0417
5:1684499rs7891402	5	1.68E+08	A	T	0.04771	5.75E-02	-0.195795	0.0487
5:1684506rs6237947	5	1.68E+08	G	T	0.04672	4.15E-02	-0.200294	0.0489
5:1684525rs6237947	5	1.68E+08	G	A	0.06561	6.69E-02	-0.166101	0.0417
5:1684529rs6237947	5	1.68E+08	A	G	0.04672	2.79E-02	-0.205303	0.049
5:1684530rs1432904	5	1.68E+08	C	A	0.06759	6.62E-02	-0.166302	0.0417
5:1684531rs1432902	5	1.68E+08	A	C	0.06561	7.63E-02	-0.165004	0.0417

5:1684534rs2862288	5	1.68E+08	G	A	0.06561	7.66E-02	-0.165004	0.0417
5:1684535rs7244816	5	1.68E+08	CA	C	0.06561	NA	NA	NA
5:1684537rs1195398	5	1.68E+08	A	C	0.06561	0.0001582	-0.165004	0.0437
5:1684541rs1196055	5	1.68E+08	T	A	0.06561	7.52E-02	-0.165204	0.0417
5:1684549rs2879135	5	1.68E+08	G	A	0.1759	2.44E-02	-0.106105	0.0251
5:1684555rs6237948	5	1.68E+08	G	A	0.04672	2.69E-02	-0.205794	0.049
5:1684571rs1432900	5	1.68E+08	A	G	0.04374	3.22E-02	-0.204002	0.0491
5:1684572rs1335546	5	1.68E+08	G	A	0.04771	2.61E-02	-0.205794	0.0489
5:1684584rs6237948	5	1.68E+08	A	G	0.04871	2.32e-06	-0.220297	0.0466
5:1684591rs891961	5	1.68E+08	C	G	0.04871	1.41E-03	-0.221295	0.0459
5:1684591rs891960	5	1.68E+08	T	A	0.04871	1.41E-03	-0.221295	0.0459
5:1684592rs7447181	5	1.68E+08	T	C	0.04871	1.37E-03	-0.221594	0.0459
5:1684592rs1335466	5	1.68E+08	C	T	0.04871	1.40E-03	-0.221395	0.0459
5:1684594rs1864984	5	1.68E+08	A	G	0.04871	1.12E-03	-0.223506	0.0459
5:1684595rs3752034	5	1.68E+08	AT	A	0.09543	NA	NA	NA
5:1684595rs5681511	5	1.68E+08	AT	ATTTTT	0.0497	NA	NA	NA
5:1684596rs2014354	5	1.68E+08	TCG	T	0.0497	NA	NA	NA
5:1684596rs3903092	5	1.68E+08	C	T	0.04175	NA	NA	NA
5:1684598rs6237948	5	1.68E+08	G	C	0.04871	1.17e-06	-0.223106	0.0459
5:1684601rs6237948	5	1.68E+08	C	T	0.04871	1.37e-06	-0.221694	0.0459
5:1684601rs6237948	5	1.68E+08	G	A	0.04871	1.94E-03	-0.222094	0.0467
5:1684601rs1429814	5	1.68E+08	TTTTG	T	0.0497	NA	NA	NA
5:1684607rs7706724	5	1.68E+08	T	C	0.04871	1.48E-03	-0.220896	0.0459
5:1684607rs7706730	5	1.68E+08	T	C	0.1441	8.75E-05	-0.145696	0.0272
5:1684607rs7706743	5	1.68E+08	A	C	0.04871	1.51E-03	-0.220696	0.0459
5:1684609rs1446342	5	1.68E+08	T	C	0.04871	8.23E-04	-0.226800	0.046
5:1684626rs2857221	5	1.68E+08	A	G	0.0497	NA	NA	NA
5:1684636rs5723223	5	1.68E+08	AT	A	0.1282	NA	NA	NA
5:1684650rs3214608	5	1.68E+08	GT	G	0.0497	NA	NA	NA
5:1684657rs1134187	5	1.68E+08	T	TG	0.1461	NA	NA	NA
5:1684657rs6237948	5	1.68E+08	T	A	0.1461	NA	NA	NA
5:1684663rs2016851	5	1.68E+08	GTT	G	0.1511	NA	NA	NA
5:1684664rs7716628	5	1.68E+08	C	T	0.1461	8.36E-05	-0.146101	0.0273
5:1684665rs7720655	5	1.68E+08	G	T	0.1292	3.01E-05	-0.156501	0.0282
5:1684704rs6237948	5	1.68E+08	A	G	0.0497	2.74E-03	-0.219898	0.0469
5:1684744rs6237948	5	1.68E+08	T	G	0.04871	6.05E-04	-0.232802	0.0467
5:1684767rs6237952	5	1.68E+08	G	T	0.0497	3.48E-04	-0.237597	0.0466
5:1684821rs2007962	5	1.68E+08	T	TG	0.0497	NA	NA	NA
5:1684827rs6237952	5	1.68E+08	T	C	0.04175	7.75E-04	-0.255305	0.0517
7:2817352rs702815	7	28173522	T	C	0.2584	0.009935	0.05530220	0.0215
7:2817426rs1062796	7	28174268	TAC	T	0.2584	NA	NA	NA
7:2817495rs849136	7	28174957	G	A	0.2584	0.01041	0.05489520	0.0214
7:2817529rs849137	7	28175290	G	A	0.2584	0.01043	0.05489520	0.0214
7:2818081rs1133294	7	28180818	G	GA	0.2624	NA	NA	NA
7:2818234rs860263	7	28182346	G	A	0.2624	0.005012	0.05940030	0.0212
7:2818509rs849141	7	28185091	G	A	0.2555	0.003819	0.06160290	0.0213
7:2818647rs849143	7	28186473	T	G	0.2624	0.002565	0.06700420	0.0222
7:2818908rs1029534	7	28189083	G	T	0.2684	0.003856	0.06110450	0.0212

7:2818994rs1708299	7 28189946 G	A	0.2684	0.004032	0.06089750.0212
7:2820207rs506154	7 28202079 C	T	0.2614	0.003022	0.06330330.0213
7:2820314rs537124	7 28203142 T	C	0.2614	0.003325	0.06249580.0213
7:2820530rs552707	7 28205303 C	T	0.2624	0.002912	0.06380070.0214
7:2820730rs481806	7 28207300 T	G	0.2624	0.003342	0.06259910.0213
7:2821066rs520161	7 28210660 C	T	0.2793	0.002703	0.06420400.0214
7:2821282rs508347	7 28212824 C	T	0.2793	0.003369	0.06190380.0211
7:2821461rs1022675	7 28214614 C	A	0.3211	6.31E-04	0.12479830.0251
7:7897205rs1450729	7 78972055 T	TTTTA	0.2594	NA	NA NA
7:7897238rs6665067	7 78972380 C	T	0.2604	1.86E-04	0.11879580.0228
7:7897286rs5662607	7 78972864 TAA	TAA	0.4006	NA	NA NA
7:7897286rs2007791	7 78972864 TAA	T	0.2565	NA	NA NA
7:7897425rs1715230	7 78974253 G	T	0.2604	1.38E-04	0.11989630.0228
7:7897441rs7315604	7 78974412 T	C	0.2604	1.26E-04	0.12659740.024
7:7897441rs7315604	7 78974416 T	A	0.2604	1.56E-04	0.12569820.024
7:7897449rs1406151	7 78974494 A	G	0.2604	1.35E-04	0.11989630.0227
7:7897481rs6651026	7 78974810 G	A	0.2604	1.48E-04	0.11949710.0227
7:7897482rs1715230	7 78974827 G	A	0.2604	1.22E-04	0.12040180.0227
7:7897568rs1715231	7 78975689 T	C	0.2614	1.37E-04	0.11979870.0227
7:7897589rs6081966	7 78975892 C	T	0.2604	1.58E-04	0.11920420.0227
7:7897589rs5585334	7 78975893 T	A	0.2604	1.57E-04	0.11930180.0227
7:7897606rs1715232	7 78976064 A	G	0.2604	1.31E-04	0.12000270.0227
7:7897609rs1715232	7 78976096 C	A	0.2604	1.32E-04	0.12000270.0227
7:7897621rs1715233	7 78976212 C	A	0.2614	1.34E-04	0.11989630.0227
7:7897634rs1715233	7 78976347 G	A	0.2624	1.36E-04	0.11989630.0227
7:7897636rs1715233	7 78976368 T	C	0.2624	1.56e-07	0.11939950.0228
7:7897645rs1715233	7 78976455 A	T	0.2624	1.13E-04	0.12080070.0228
7:7897648rs1715233	7 78976485 T	A	0.2624	9.78E-05	0.12140310.0228
7:7897653rs7315607	7 78976538 A	G	0.2614	1.35e-07	0.11989630.0227
7:7897740rs1715234	7 78977401 G	A	0.2604	1.59E-04	0.11930180.0228
7:7897766rs1715234	7 78977666 C	T	0.2614	1.35E-04	0.11989630.0227
7:7897772rs1715235	7 78977721 C	T	0.2614	1.35E-04	0.11979870.0227
7:7897775rs1715236	7 78977754 T	C	0.2614	1.35E-04	0.11979870.0227
7:7897796rs7804381	7 78977963 T	A	0.2614	1.33E-04	0.11989630.0227
7:7897800rs7808267	7 78978006 A	T	0.2614	1.33E-04	0.11989630.0227
7:7897815rs7804560	7 78978150 C	A	0.2604	1.34E-04	0.11989630.0227
7:7901815rs1132188	7 79018159 TAA	T	0.2793	NA	NA NA
7:7903402rs727390	7 79034026 A	G	0.2674	6.62E-05	0.11930180.0221
8:5867736rs1009627	8 58677362 G	A	0.0666	2.83E-03	-0.193305 0.0413
8:5868314rs9942783	8 58683140 T	C	0.06958	5.43E-03	-0.185101 0.0407
9:3699803rs1179009	9 36998031 T	C	0.1372	0.0002607	-0.100704 0.0276
9:3700370rs6253370	9 37003704 C	T	0.1034	NA	NA NA
9:3700385rs6253371	9 37003857 T	G	0.1034	1.32E-03	-0.144401 0.0298
9:3701650rs5717218	9 37016502 C	G	0.1034	2.43E-03	-0.140297 0.0298
9:3702051rs6253371	9 37020516 A	G	0.1034	1.59E-03	-0.142600 0.0297
9:3703031rs5726823	9 37030316 A	C	0.1093	1.75E-04	-0.152498 0.0292
9:3703075rs6253371	9 37030751 A	C	0.1044	1.54E-03	-0.143397 0.0298
9:3703107rs3739440	9 37031074 T	C	0.1093	2.29E-04	-0.151404 0.0293

9:3704582rs4483247	9 37045825 G	A	0.1441	2.73E-03 -0.121094 0.0258
9:3705161rs1097317	9 37051615 C	G	0.1431	8.10E-03 -0.115803 0.026
9:3705208rs1097317	9 37052080 T	C	0.1431	1.14E-02 -0.113605 0.0259
9:3705224rs1097317	9 37052244 G	C	0.1431	1.22E-02 -0.113202 0.0259
9:3705245rs6253373	9 37052451 C	T	0.1431	NA NA NA
9:3705245rs1457493	9 37052454 A	AGGAGGT	0.1431	NA NA NA
9:3705334rs1097317	9 37053346 C	G	0.1431	7.96E-03 -0.115702 0.0259
9:3705506rs1097317	9 37055065 G	C	0.1431	8.33E-03 -0.115399 0.0259
9:3705510rs1097317	9 37055109 G	A	0.1431	8.44E-03 -0.115298 0.0259
9:3705571rs1097317	9 37055710 G	A	0.1431	9.31e-06 -0.114804 0.0259
9:3705637rs1097317	9 37056373 A	G	0.1441	8.16E-03 -0.115399 0.0259
9:3707661rs6253374	9 37076618 T	A	0.1481	1.45E-02 -0.110596 0.0255
9:3707817rs1443796	9 37078175 AT	A	0.1481	NA NA NA
9:3707818rs7896837	9 37078184 T	A	0.1481	NA NA NA
9:3707890rs6253374	9 37078909 T	C	0.1481	1.42E-02 -0.110696 0.0255
9:3708094rs1097319	9 37080941 G	A	0.1471	NA NA NA
9:3708094rs1097319	9 37080944 G	A	0.1471	1.92E-02 -0.109402 0.0256
9:3708233rs1097319	9 37082333 G	A	0.1471	1.95E-02 -0.109301 0.0256
9:3708240rs1097319	9 37082403 G	A	0.1471	1.95E-02 -0.109301 0.0256
9:3708272rs1128372	9 37082726 A	G	0.1471	1.95E-02 -0.109301 0.0256
9:3708830rs2021510	9 37088308 CT	C	0.1849	NA NA NA
9:3709101rs1237706	9 37091018 T	C	0.1471	2.07E-02 -0.108799 0.0256
9:3709550rs6777757	9 37095504 A	G	0.1471	2.17E-02 -0.108498 0.0255
9:3709830rs6253566	9 37098306 G	C	0.1471	2.26e-05 -0.108197 0.0255
9:3709933rs1097320	9 37099335 A	G	0.1421	1.22e-05 -0.113202 0.0259
9:3710052rs1097320	9 37100525 T	G	0.1471	2.30E-02 -0.109803 0.0259
9:3710423rs1097320	9 37104234 G	A	0.1471	2.29E-02 -0.107997 0.0255
9:3710637rs6253567	9 37106370 A	T	0.1471	7.36E-02 -0.105805 0.0267
9:3710644rs6253567	9 37106442 C	T	0.1471	2.27E-02 -0.107997 0.0255
9:3710675rs1097321	9 37106754 T	C	0.1471	2.42E-02 -0.107596 0.0255
9:3711381rs1097321	9 37113815 C	G	0.1471	2.58E-02 -0.107095 0.0255
9:3711584rs1498418	9 37115849 CAAATAAA	C	0.1501	NA NA NA
9:3712174rs1097322	9 37121745 G	A	0.1471	NA NA NA
9:3712178rs1097322	9 37121785 A	T	0.1471	NA NA NA
9:3712183rs1097322	9 37121837 C	T	0.1471	2.54E-02 -0.106895 0.0254
9:3712591rs1237680	9 37125911 T	C	0.1481	4.19E-02 -0.103795 0.0253
9:3712798rs1097322	9 37127983 A	C	0.1471	2.58E-02 -0.106694 0.0253
9:3713246rs6098223	9 37132463 T	C	0.1481	2.66E-02 -0.106305 0.0253
9:3713285rs5640153	9 37132859 A	G	0.1471	2.56E-02 -0.106594 0.0253
9:3713340rs1426239	9 37133406 CT	C	0.1481	NA NA NA
9:3713401rs5795165	9 37134011 A	G	0.1491	2.77E-02 -0.106105 0.0253
9:3713437rs6253570	9 37134370 C	G	0.1421	1.29e-05 -0.112004 0.0257
9:3713965rs1097322	9 37139650 A	G	0.1481	4.20E-02 -0.103595 0.0253
9:3713989rs1097322	9 37139899 A	G	0.1491	2.73E-02 -0.106205 0.0253
9:3714017rs2068020	9 37140170 A	G	0.1471	2.67E-02 -0.106305 0.0253
9:3715098rs1097323	9 37150985 A	G	0.1471	0.0001053 -0.102896 0.0265
9:3715125rs1097323	9 37151252 T	C	0.1471	3.22E-02 -0.105404 0.0254
9:3715134rs1748696	9 37151342 G	C	0.1471	3.22E-02 -0.105404 0.0254

9:3715146rs1748698	9 37151468 G	A	0.1471	3.27e-05	-0.105304	0.0254
9:3715238rs1081451	9 37152389 A	G	0.1521	4.05E-02	-0.103096	0.0251
9:3715903rs1409469	9 37159032 CTGTT	C	0.1471	NA	NA	NA
9:3716640rs1238036	9 37166400 C	T	0.1461	3.64E-02	-0.104605	0.0253
9:3717180rs1097324	9 37171808 C	T	0.1461	3.69E-02	-0.104605	0.0253
9:3717554rs6253571	9 37175547 T	C	0.1461	3.56E-02	-0.104805	0.0254
9:3717576rs1081451	9 37175765 C	T	0.1511	4.68e-05	-0.102198	0.0251
9:3717605rs5617104	9 37176051 TTTTG	TTTTGTTT(0.000994	NA	NA	NA	NA
9:3717605rs1445571	9 37176051 TTTTG	T	0.1501	NA	NA	NA
9:3717792rs1097324	9 37177924 G	A	0.1461	3.14E-02	-0.105604	0.0254
9:3718258rs6253571	9 37182580 G	C	0.1471	0.0001219	-0.101899	0.0265
9:3718265rs6253571	9 37182655 A	G	0.1471	3.03E-02	-0.105304	0.0252
9:3718463rs5691615	9 37184633 T	C	0.1471	3.69E-02	-0.104605	0.0253
9:3718478rs5831984	9 37184780 G	A	0.1471	3.79E-02	-0.104405	0.0254
9:3719215rs1097324	9 37192156 A	G	0.1461	3.7e-05	-0.104605	0.0254
9:3719298rs1097324	9 37192988 C	A	0.1461	4.27E-02	-0.103695	0.0253
9:3719817rs1097325	9 37198176 C	T	0.1461	3.95E-02	-0.104094	0.0253
9:3720296rs5608394	9 37202969 T	C	0.1471	3.40E-02	-0.105005	0.0253
9:37205689:3720568	9 37205689 A	AT	0.1461	NA	NA	NA
9:3720610rs6070363	9 37206109 T	G	0.1461	3.94e-05	-0.104094	0.0253
9:3720726rs4526442	9 37207269 T	C	0.1461	NA	NA	NA
9:3721905rs1097325	9 37219050 T	A	0.1461	3.25E-02	-0.105204	0.0253
9:3722315rs5461445	9 37223151 T	TA	0.1461	NA	NA	NA
9:3722386rs2029646	9 37223862 G	A	0.1511	4.44E-02	-0.102398	0.0251
9:3722446rs1097325	9 37224460 C	T	0.1461	3.27E-02	-0.105104	0.0253
9:3722892rs2005157	9 37228927 GGTTCAACG	G	0.1461	NA	NA	NA
9:3723222rs1097326	9 37232221 A	G	0.1461	3.17E-02	-0.105504	0.0253
9:3723640rs2015015	9 37236409 A	AT	0.1481	NA	NA	NA
9:3723796rs6163741	9 37237963 T	C	0.1461	3.04E-02	-0.105705	0.0254
9:3724048rs6253572	9 37240488 C	T	0.1451	3.41E-02	-0.104905	0.0253
9:3724250rs1097326	9 37242504 C	T	0.1461	3.42E-02	-0.104905	0.0253
9:3724270rs495304	9 37242704 A	T	0.1511	4.25E-02	-0.102697	0.0251
9:3724983rs1097326	9 37249831 C	T	0.1461	3.26E-02	-0.105304	0.0253
9:3725469rs1097326	9 37254694 G	T	0.1461	3.31E-02	-0.105204	0.0253
9:3725561rs6714462	9 37255616 A	T	0.1461	3.20E-02	-0.105404	0.0253
9:3725728rs1097327	9 37257282 C	T	0.1461	3.33E-02	-0.105204	0.0253
9:3725911rs1097327	9 37259118 C	T	0.1471	5.08E-02	-0.102597	0.0253
9:3725923rs1097327	9 37259236 G	A	0.1471	3.47E-02	-0.104905	0.0253
9:3725967rs4304407	9 37259678 G	A	0.1461	3.02E-02	-0.105805	0.0254
9:3726822rs1097328	9 37268221 T	C	0.1461	4.05E-02	-0.104305	0.0254
9:3727178rs6253379	9 37271781 A	G	0.1471	3.47E-02	-0.105104	0.0254
9:3727423rs5823560	9 37274236 TC	T	0.1471	NA	NA	NA
9:3727790rs1097328	9 37277902 C	A	0.1461	3.47E-02	-0.105005	0.0254
9:3728017rs1097328	9 37280173 A	G	0.1461	3.34E-02	-0.105304	0.0254
9:3728283rs1097328	9 37282830 G	A	0.1451	NA	NA	NA
9:3728334rs6253379	9 37283343 C	T	0.1461	3.33E-02	-0.105304	0.0254
9:3728893rs5826524	9 37288938 A	C	0.1461	3.36E-02	-0.105304	0.0254
9:3728993rs1097328	9 37289932 C	A	0.1412	2.06e-05	-0.109301	0.0257

9:3729103rs6253380	9 37291034 C	T	0.1461	3.90E-02	-0.104405	0.0254
9:3729307rs6253380	9 37293079 G	A	0.1461	4.14E-02	-0.104094	0.0254
9:3729362rs3802420	9 37293627 C	T	0.1471	4.11E-02	-0.104094	0.0254
9:3729565rs1097329	9 37295658 A	G	0.1471	3.84E-02	-0.104505	0.0254
9:3730373rs1133800	9 37303730 A	G	0.1461	4.19E-02	-0.104094	0.0254
9:3733103rs1097330	9 37331037 A	G	0.1461	4.12E-02	-0.104194	0.0254
9:3733160rs1237821	9 37331605 G	T	0.1461	3.92e-05	-0.104505	0.0254
9:3733391rs5984943	9 37333910 T	C	0.1461	4.18E-02	-0.104194	0.0254
9:3734452rs1097330	9 37344529 T	C	0.1332	0.0001313	-0.101501	0.0265
9:3734580rs7273778	9 37345800 A	G	0.1461	3.63E-02	-0.105005	0.0254
9:3736081rs5612171	9 37360811 T	G	0.1471	3.07E-02	-0.106105	0.0254
9:3736131rs1097330	9 37361314 T	C	0.1481	3.34E-02	-0.105604	0.0254
9:3736178rs7273779	9 37361785 G	A	0.1481	3.16E-02	-0.106005	0.0255
9:3737517rs5612880	9 37375178 C	A	0.1451	0.0001445	-0.103096	0.0271
9:3737746rs6253380	9 37377466 C	T	0.1431	4.01E-02	-0.106594	0.026
9:3737778rs2006273	9 37377786 AAAAAAA/A		0.172	NA	NA	NA
9:3739041rs5775740	9 37390411 G	A	0.1491	3.34E-02	-0.107395	0.0259
9:3739415rs7876059	9 37394150 C	T	0.17	0.0009417	-0.084197	0.0254
9:3739437rs7860922	9 37394373 C	G	0.17	0.000961	-0.084001	0.0254
9:3740639rs7047872	9 37406391 C	T	0.171	0.00136	-0.080895	0.0253
10:725352rs1159487	10 72535250 G	A	0.4503	3.44E-02	0.08250120	0.0199
10:725359rs1222147	10 72535922 A	C	0.336	5.91e-07	0.10599830	0.0212
10:725366rs7088513	10 72536697 T	C	0.2714	7.72E-02	0.08920060	0.0226
10:725372rs6682768	10 72537260 AC	A	0.339	NA	NA	NA
10:725387rs1277634	10 72538798 A	C	0.2694	0.00023350	0.08260250	0.0225
10:811715rs3997799	10 81171576 C	T	0.05368	0.0002941	-0.159300	0.044
10:811719rs7747926	10 81171965 C	A	0.05368	0.0002514	-0.161096	0.044
10:811721rs1145555	10 81172133 A	G	0.05368	0.0003012	-0.158901	0.044
10:811742rs7758456	10 81174291 C	A	0.05666	0.0001506	-0.161801	0.0427
10:811769rs1100296	10 81176954 T	C	0.06163	0.002784	-0.133794	0.0447
10:811769rs1100296	10 81176966 G	A	0.06163	NA	NA	NA
10:811783rs731095	10 81178376 G	A	0.05368	0.0002244	-0.162201	0.044
10:811783rs731094	10 81178378 A	G	0.05368	0.0002243	-0.162295	0.044
10:811787rs5652952	10 81178725 CG	C	0.05368	NA	NA	NA
10:811787rs731093	10 81178739 A	G	0.05368	0.0002074	-0.163095	0.044
10:811855rs7677188	10 81185534 A	G	0.05567	1.64E-03	-0.200404	0.0418
10:127107rs7965105	10 1.27E+08 G	T	0.0497	0.0006292	-0.150404	0.044
10:127107rs7798321	10 1.27E+08 C	T	0.0497	0.0006284	-0.150299	0.044
10:127107rs7416123	10 1.27E+08 A	T	0.0497	0.0006284	-0.150299	0.044
10:127109rs1235491	10 1.27E+08 C	T	0.04771	0.001086	-0.145696	0.0446
10:127111rs1235806	10 1.27E+08 T	C	0.04771	0.001157	-0.144702	0.0445
10:127112rs1124446	10 1.27E+08 G	T	0.04771	0.001174	-0.144401	0.0445
10:127113rs5500645	10 1.27E+08 A	ATGTG	0.0497	NA	NA	NA
10:12711310:127113	10 1.27E+08 C	CGTGTGT	0.000994	NA	NA	NA
10:127113rs7761145	10 1.27E+08 C	T	0.0497	NA	NA	NA
10:127114rs7416125	10 1.27E+08 G	A	0.0497	0.001322	-0.140297	0.0437
10:12711510:127115	10 1.27E+08 A	G	0.04871	NA	NA	NA
10:127120rs1124447	10 1.27E+08 G	A	0.04771	0.00162	-0.139802	0.0443

10:127125rs7694809	10	1.27E+08	T	C	0.04771	0.001673	-0.139503	0.0444
10:127127rs1124448	10	1.27E+08	A	G	0.04771	0.002159	-0.136300	0.0444
10:127128rs7951834	10	1.27E+08	G	A	0.0507	0.002391	-0.134503	0.0443
10:127129rs2016843	10	1.27E+08	A	AAAC	0.04871	NA	NA	NA
10:127130rs1124448	10	1.27E+08	A	G	0.04871	0.001843	-0.138101	0.0443
10:127130rs5715244	10	1.27E+08	CGTGTT	CGTGTTGT	0.0497	NA	NA	NA
10:127133rs1124449	10	1.27E+08	T	C	0.0497	0.003357	-0.129402	0.0441
10:127134rs7416128	10	1.27E+08	A	G	0.04871	0.002234	-0.134697	0.0441
10:127134rs7086669	10	1.27E+08	T	C	0.0497	0.001453	-0.142001	0.0446
10:127134rs7086670	10	1.27E+08	T	C	0.0497	0.001315	-0.143200	0.0446
10:127135rs7997140	10	1.27E+08	C	G	0.0497	0.002587	-0.133497	0.0443
10:127136rs1124449	10	1.27E+08	T	A	0.0497	0.002648	-0.133097	0.0443
10:127137rs1124449	10	1.27E+08	C	T	0.0497	0.009444	-0.121399	0.0468
10:127138rs1124449	10	1.27E+08	C	T	0.0497	0.002755	-0.132594	0.0443
10:127138rs1477005	10	1.27E+08	CT	C	0.0507	NA	NA	NA
10:127140rs1235550	10	1.27E+08	T	C	0.0497	0.003055	-0.131305	0.0443
10:127141rs1235554	10	1.27E+08	G	C	0.0497	0.003046	-0.131396	0.0443
10:127143rs1463875	10	1.27E+08	AAAT	A	0.04871	NA	NA	NA
10:127144rs1124450	10	1.27E+08	G	C	0.04771	0.001425	-0.142704	0.0448
10:127144rs1124450	10	1.27E+08	T	C	0.04771	0.001365	-0.143304	0.0448
10:127146rs1124450	10	1.27E+08	A	G	0.05368	0.0001401	-0.155403	0.0408
10:127153rs7711994	10	1.27E+08	T	C	0.05268	8.55E-02	-0.160403	0.0408
10:127153rs1489418	10	1.27E+08	A	AT	0.05268	NA	NA	NA
10:127155rs7537024	10	1.27E+08	C	T	0.05268	7.71E-02	-0.161401	0.0408
10:127155rs1124450	10	1.27E+08	G	A	0.05268	7.62E-02	-0.161495	0.0408
10:127156rs7852101	10	1.27E+08	C	G	0.05567	5.72E-02	-0.162801	0.0405
10:127158rs1124450	10	1.27E+08	C	T	0.05567	4.92E-02	-0.164202	0.0404
10:127160rs1124451	10	1.27E+08	C	T	0.05567	4.91E-02	-0.164202	0.0404
10:127160rs1124451	10	1.27E+08	T	C	0.05567	4.85E-02	-0.164296	0.0404
10:127161rs1124451	10	1.27E+08	A	G	0.05567	4.79e-05	-0.164403	0.0404
10:127164rs7463722	10	1.27E+08	A	G	0.05567	5.21E-02	-0.163295	0.0404
10:127167rs7462097	10	1.27E+08	A	G	0.05567	5.07E-02	-0.163696	0.0404
10:12716810:127168	10	1.27E+08	C	G	0.05567	0.0002142	-0.157203	0.0425
10:127168rs7780298	10	1.27E+08	G	A	0.05567	4.08E-02	-0.166196	0.0405
10:127171rs1124451	10	1.27E+08	T	C	0.06064	1.09E-03	-0.186498	0.0382
10:127172rs1235925	10	1.27E+08	C	G	0.05567	4.05E-02	-0.166397	0.0405
10:127173rs1090138	10	1.27E+08	A	G	0.05467	3.97E-02	-0.166597	0.0405
10:127174rs1235976	10	1.27E+08	C	G	0.05467	3.85E-02	-0.166905	0.0406
10:127181rs7540936	10	1.27E+08	C	T	0.05467	3.67E-02	-0.168205	0.0408
10:130121rs1225472	10	1.3E+08	T	C	0.06163	0.0008669	-0.142404	0.0428
10:130132rs5902616	10	1.3E+08	TG	T	0.05865	NA	NA	NA
10:130145rs1241530	10	1.3E+08	C	T	0.05765	3.11E-03	-0.207897	0.0446
10:130147rs1506051	10	1.3E+08	AT	A	0.06064	NA	NA	NA
10:130148rs1101617	10	1.3E+08	A	G	0.05765	4.11E-03	-0.205303	0.0446
10:130149rs1857386	10	1.3E+08	A	G	0.05964	3.91e-06	-0.203904	0.0442
10:130149rs2105393	10	1.3E+08	A	G	0.05865	3.30E-03	-0.205401	0.0442
10:130150rs2892323	10	1.3E+08	G	A	0.05964	3.83E-03	-0.204101	0.0442
10:130150rs7922418	10	1.3E+08	A	T	0.05964	3.91E-03	-0.203904	0.0442

10:130150rs1936423	10	1.3E+08	G	T	0.05964	3.99E-03	-0.203696	0.0442
10:130150rs2185976	10	1.3E+08	C	A	0.05964	4.05E-03	-0.203500	0.0442
10:130151rs4626991	10	1.3E+08	T	C	0.05964	4.09E-03	-0.203500	0.0442
10:130151rs5788915	10	1.3E+08	AT	A	0.05964	NA	NA	NA
10:130151rs4529820	10	1.3E+08	C	T	0.05964	4.16E-03	-0.203304	0.0442
10:130151rs1225447	10	1.3E+08	A	C	0.05964	4.25E-03	-0.203095	0.0442
10:130152rs1226374	10	1.3E+08	C	T	0.05964	4.30E-03	-0.202997	0.0442
10:130152rs5727462	10	1.3E+08	G	A	0.05964	4.31E-03	-0.202997	0.0442
10:130152rs5566833	10	1.3E+08	G	A	0.06064	NA	NA	NA
10:130153rs1419239	10	1.3E+08	T	C	0.05865	3.81E-03	-0.204199	0.0442
10:130154rs7284922	10	1.3E+08	G	A	0.05964	4.52E-03	-0.202605	0.0442
10:130154rs6186303	10	1.3E+08	G	A	0.05964	4.53E-03	-0.202605	0.0442
10:130154rs4415667	10	1.3E+08	C	T	0.05964	4.67E-03	-0.202397	0.0442
10:130154rs2387612	10	1.3E+08	G	A	0.05964	4.65E-03	-0.202397	0.0442
10:130155rs2014384	10	1.3E+08	T	TG	0.05964	NA	NA	NA
10:130155rs6045013	10	1.3E+08	G	T	0.05964	4.77e-06	-0.202201	0.0442
10:130155rs5568114	10	1.3E+08	T	C	0.05964	4.41E-03	-0.202899	0.0442
10:130155rs5787725	10	1.3E+08	G	A	0.05964	4.82E-03	-0.202201	0.0442
10:130156rs1383271	10	1.3E+08	C	CTAAT	0.05964	NA	NA	NA
10:130156rs6186418	10	1.3E+08	C	T	0.05865	4.20E-03	-0.203500	0.0442
10:130156rs6186418	10	1.3E+08	T	C	0.06064	4.74E-03	-0.202299	0.0442
10:130156rs5509644	10	1.3E+08	T	TA	0.05666	NA	NA	NA
10:130156rs1225390	10	1.3E+08	T	C	0.05865	4.09E-03	-0.203794	0.0442
10:130157rs1225412	10	1.3E+08	A	C	0.05865	4.17E-03	-0.203598	0.0442
10:130173rs1101619	10	1.3E+08	T	C	0.05567	4.64E-02	-0.193693	0.0476
11:642027rs606063	11	64202729	C	T	0.4115	7.46E-03	-0.088099	0.0197
11:642050rs534874	11	64205021	A	G	0.4115	7.68E-03	-0.088099	0.0197
11:642063rs3589552	11	64206362	AT	A	0.4115	NA	NA	NA
11:642078rs670837	11	64207893	A	G	0.4115	7.89E-03	-0.088000	0.0197
11:642144rs1089750	11	64214474	T	C	0.3072	2.69e-06	-0.099897	0.0213
12:643326rs7969898	12	64332644	A	G	0.09841	3.85E-03	0.14189870	0.0307
12:704695rs698128	12	70469557	T	A	0.3459	2.47E-02	0.08580140	0.0203
12:704737rs3109876	12	70473776	T	C	0.3241	3.91e-06	0.09630050	0.0209
12:704738rs3098307	12	70473854	A	G	0.3241	3.08E-02	0.09110130	0.0219
12:704744rs3772187	12	70474488	CT	C	0.3449	NA	NA	NA
12:704748rs3098308	12	70474888	G	A	0.338	NA	NA	NA
12:704750rs3108487	12	70475049	A	G	0.3241	3.98E-03	0.09620060	0.0209
12:704754rs2118432	12	70475462	T	G	0.3241	3.90E-03	0.09630050	0.0209
12:704764rs2870885	12	70476440	C	G	0.3241	5.66E-03	0.09460080	0.0208
12:704769rs3103885	12	70476954	T	C	0.3241	3.80E-03	0.09640040	0.0209
12:704818rs3125805	12	70481828	G	T	0.3221	NA	NA	NA
12:704818rs3098315	12	70481895	T	A	0.2913	NA	NA	NA
12:704823rs3098316	12	70482343	G	C	0.325	NA	NA	NA
12:704823rs3103889	12	70482361	A	G	0.4175	NA	NA	NA
12:704827rs3103890	12	70482717	G	A	0.3201	NA	NA	NA
12:704827rs3103892	12	70482728	C	T	0.4036	NA	NA	NA
12:704836rs3125806	12	70483627	C	T	0.326	NA	NA	NA
12:704862rs2870884	12	70486240	T	C	0.4105	0.00217	0.06360370	0.0207

12:704934rs1590049	12 70493406 A	G	0.325	7.04E-03	0.09359960.0208
12:704946rs1236638	12 70494623 T	C	0.3141	9.19E-03	0.09269760.0209
12:705394rs7958131	12 70539420 A	T	0.3161	1.93e-05	0.08920060.0209
12:705483rs1117811	12 70548333 C	G	0.3161	1.92E-02	0.08920060.0209
12:705496rs7296734	12 70549632 A	G	0.3151	2.04E-02	0.08889870.0209
12:705541rs1242225	12 70554135 A	C	0.3161	1.98E-02	0.08899930.0209
12:705616rs2870883	12 70561697 C	T	0.3181	1.81E-02	0.08940180.0209
12:705648rs1087910	12 70564816 A	G	0.2555	0.00131	0.07089630.0221
12:705648rs1087910	12 70564817 A	G	0.2555	0.001198	0.07099880.0219
12:705673rs1127035	12 70567362 TC	T	0.3241	NA	NA NA
12:705678rs1232014	12 70567876 A	G	0.2555	0.001252	0.07080320.0219
12:705682rs1232036	12 70568238 T	G	0.2555	0.001225	0.07089630.0219
12:705724rs7297924	12 70572408 A	C	0.3231	7.31E-02	0.08639780.0218
12:705738rs1236836	12 70573896 G	A	0.2555	NA	NA NA
12:705742rs1087910	12 70574254 A	C	0.2555	0.001313	0.07040250.0219
12:705747rs1406013	12 70574781 C	T	0.2555	0.001239	0.07080320.0219
12:705799rs6581925	12 70579967 G	A	0.2555	0.001203	0.07099880.0219
12:705817rs5798971	12 70581793 TA	T	0.2555	NA	NA NA
12:706005rs1117813	12 70600595 A	G	0.2555	0.001376	0.07019740.0219
12:706029rs1149563	12 70602966 T	C	0.2555	0.001364	0.07019740.0219
12:706030rs1149563	12 70603050 G	C	0.2555	0.001409	0.07000160.0219
12:706070rs7312236	12 70607067 C	T	0.2555	0.001428	0.06989910.0219
12:706073rs1087911	12 70607371 A	T	0.2555	0.001432	0.06989910.0219
12:706163rs2068688	12 70616330 T	C	0.2555	0.001382	0.07010420.0219
12:706169rs1161427	12 70616913 C	T	0.3161	2.41e-05	0.08800170.0208
12:706224rs1722612	12 70622424 C	T	0.2555	0.0012	0.07099880.0219
12:706229rs1087911	12 70622991 T	G	0.2555	0.001269	0.07070070.0219
12:706230rs1087911	12 70623090 G	A	0.2555	0.001194	0.07110130.0219
12:706238rs7980088	12 70623855 T	C	0.2555	0.001201	0.07099880.0219
12:706263rs1044458	12 70626392 C	T	0.2555	0.001179	0.07110130.0219
12:706270rs1087911	12 70627084 A	G	0.2555	0.00121	0.07099880.0219
12:706323rs1242316	12 70632340 C	T	0.2555	NA	NA NA
12:706331rs6192990	12 70633113 C	T	0.2555	0.001112	0.07150170.0219
13:732415rs7321284	13 73241598 A	G	0.02485	6.16E-02	0.37670200.094
13:733129rs7321500	13 73312961 C	T	0.02584	2.43E-03	0.43260020.0918
13:734446rs7321875	13 73444688 A	G	0.02386	0.00012590.37530130.0979	
13:734794rs1463301	13 73479484 A	G	0.01988	0.03753	0.24510070.1178
13:734962rs3749680	13 73496289 A	AT	0.01988	NA	NA NA
13:735681rs7321879	13 73568140 G	C	0.02485	3.82E-02	0.36289850.0881
14:334933rs1959171	14 33493380 G	A	0.3569	NA	NA NA
14:334948rs1959172	14 33494808 C	T	0.3817	0.001219	-0.068696 0.0213
14:334949rs1959173	14 33494971 T	A	0.3618	0.0004908	-0.074195 0.0213
14:334961rs1709993	14 33496159 T	C	0.3191	4.67E-02	-0.087400 0.0215
14:334979rs1013078	14 33497971 G	A	0.3658	0.0001096	-0.082002 0.0212
14:335101rs8014371	14 33510133 C	A	0.3519	9.02E-02	-0.083696 0.0214
14:335104rs1013607	14 33510444 T	G	0.3658	0.0002372	-0.078696 0.0214
14:335111rs1013885	14 33511102 T	C	0.2763	1.36E-02	-0.099002 0.0228
14:335137rs1953445	14 33513730 A	G	0.335	4.32E-03	-0.103894 0.0226

14:335142rs8017417	14 33514270 A	C	0.336	3.78E-02	-0.089399	0.0217
14:335266rs1014781	14 33526641 G	A	0.3579	0.0006098	-0.075596	0.0221
14:426733rs7267430	14 42673369 A	G	0.3002	2.58E-04	0.11679580	0.0227
16:729447rs7507080	16 72944759 C	T	0.008946	5.20E-04	-0.589598	0.1175
16:818937rs1164241	16 81893720 C	G	0.4821	1.84E-03	0.09460080	0.0198
17:261818rs2108952	17 26181865 T	C	0.2515	0.002725	0.06500090	0.0217
17:261845rs1139020	17 26184545 AG	A	0.2515	NA	NA	NA
17:261854rs7211592	17 26185418 T	G	0.2515	0.001816	0.06769600	0.0217
17:261862rs4796147	17 26186288 G	A	0.2505	0.002222	0.06639610	0.0217
17:261875rs986993	17 26187576 G	A	0.2515	0.002123	0.06669550	0.0217
17:261941rs7220473	17 26194116 C	T	0.2535	0.001236	0.07000160	0.0217
17:261983rs4796172	17 26198381 G	A	0.2425	0.00046040	0.07689620	0.022
17:262040rs1986311	17 26204098 G	T	0.2545	0.005699	0.06130200	0.0222
17:262064rs3751972	17 26206414 A	C	0.2425	0.001821	0.06939540	0.0222
17:262068rs4796206	17 26206896 C	G	0.3032	8.92E-03	0.09329900	0.021
17:262118rs5819824	17 26211855 GA	G	0.4046	NA	NA	NA
17:262136rs1131928	17 26213679 A	AT	0.2475	NA	NA	NA
17:262147rs1996283	17 26214737 AGG	A	0.328	NA	NA	NA
17:262160rs7224724	17 26216090 C	T	0.3022	6.53E-03	0.09440060	0.0209
17:262163rs9903233	17 26216356 A	G	0.3022	6.95E-03	0.09309860	0.0207
17:262163rs7220420	17 26216397 G	A	0.2435	0.001408	0.07010420	0.022
17:262167rs4796222	17 26216786 G	A	0.2435	0.001428	0.07000160	0.022
17:262203rs4063521	17 26220355 T	G	0.3032	1.08E-02	0.09110130	0.0207
17:262225rs2079714	17 26222520 A	G	0.2445	0.002205	0.06730340	0.022
17:262228rs4796228	17 26222810 A	G	0.3042	1.08E-02	0.09110130	0.0207
17:262228rs1069527	17 26222886 ATTTGT	A	0.2445	NA	NA	NA
17:262255rs1034895	17 26225558 C	G	0.2823	0.00337	0.06270240	0.0214
17:262304rs8078361	17 26230480 T	C	0.2475	0.00231	0.06700420	0.022
17:262307rs4796234	17 26230795 G	C	0.3032	6.74E-03	0.09319880	0.0207
17:262329rs2191058	17 26232917 C	T	0.2465	0.002154	0.06749970	0.022
17:262352rs7212926	17 26235226 C	T	0.3032	5.93E-03	0.09379990	0.0207
17:262356rs3471532	17 26235633 TG	T	0.2465	NA	NA	NA
17:262391rs3559103	17 26239169 A	AT	0.2584	NA	NA	NA
17:262404rs4795142	17 26240411 A	G	0.2465	0.001956	0.06820050	0.022
17:262414rs7218395	17 26241477 A	G	0.3042	3.88E-03	0.09550100	0.0207
17:262422rs1294825	17 26242263 A	G	0.4324	2.39E-03	0.09759840	0.0207
17:262427rs1165769	17 26242726 G	C	0.2455	0.00375	0.06410090	0.0221
17:262427rs9630740	17 26242756 G	C	0.2445	0.003459	0.06470100	0.0221
17:262450rs1165742	17 26245037 A	T	0.3022	9.21E-03	0.09229650	0.0208
17:262488rs3057246	17 26248808 ATTATTTA'A	A	0.2962	NA	NA	NA
17:262489rs2108949	17 26248922 T	G	0.3012	9.73E-03	0.09219620	0.0208
17:262501rs1157502	17 26250109 T	G	0.2465	0.002602	0.06660200	0.0221
17:262507rs1108038	17 26250721 G	A	0.2435	0.002553	0.06679840	0.0221
17:262511rs9646434	17 26251158 G	C	0.2435	0.004513	0.06320010	0.0223
17:262528rs1165761	17 26252856 C	T	0.2416	0.005686	0.06169690	0.0223
17:262534rs8082467	17 26253468 A	G	0.2445	0.006369	0.06080340	0.0223
17:377802rs3395356	17 37780296 T	A	0.2903	0.002714	0.06420400	0.0214
17:378102rs881844	17 37810218 G	C	0.332	0.00333	0.06000320	0.0204

17:378138rs1186928	17 37813856 C	G	0.326	0.003072	0.06059630.0205
17:378140rs1877031	17 37814080 A	G	0.327	0.002879	0.06100100.0205
17:378158rs1165878	17 37815899 A	G	0.326	0.002181	0.06259910.0204
17:378174rs2271308	17 37817482 C	T	0.2793	0.001977	0.06700420.0217
17:378214rs931992	17 37821435 T	G	0.326	0.002004	0.06320010.0205
17:378223rs1053651	17 37822311 C	A	0.2783	0.001838	0.06749970.0217
17:378243rs3764351	17 37824339 A	G	0.34	0.002954	0.06080340.0205
17:378271rs407307	17 37827163 G	A	0.332	0.000273	0.07559900.0208
17:378280rs14050	17 37828072 T	C	0.3141	0.00025650.07699800.0211	
17:378284rs2952151	17 37828496 C	T	0.3141	0.00022560.07770150.0211	
17:378287rs2941503	17 37828745 G	A	0.3141	0.00021860.07789570.0211	
17:378287rs907087	17 37828787 A	G	0.3111	0.00027330.07670170.0211	
17:378291rs2247862	17 37829129 G	A	0.3111	0.00034970.07530220.0211	
17:378295rs903504	17 37829570 G	C	0.3241	0.00025420.07580290.0207	
17:378295rs903503	17 37829571 A	C	0.3241	0.00026250.07570090.0207	
17:378296rs903502	17 37829604 T	C	0.3241	0.00026880.07549700.0207	
17:378304rs2934956	17 37830447 A	T	0.3241	0.00025060.07580290.0207	
17:378309rs2941504	17 37830900 G	A	0.3101	0.000362	0.07509810.021
17:378310rs1565922	17 37831035 G	A	0.3131	0.000362	0.07499610.021
17:378312rs1379071	17 37831297 C	CCCCA	0.3231	NA	NA NA
17:378313rs1055897	17 37831304 G	C	0.325	NA	NA NA
17:378316rs1565920	17 37831613 A	G	0.3201	0.00019920.07709990.0207	
17:378320rs1495102	17 37832093 C	T	0.3052	0.00031550.07599760.0211	
17:378321rs1495101	17 37832103 A	C	0.3052	0.000313	0.07599760.0211
17:378322rs1495100	17 37832279 T	C	0.3211	0.00045230.07589560.0216	
17:378323rs2934953	17 37832315 A	T	0.3052	0.00030670.07609950.0211	
17:378323rs2934952	17 37832366 A	G	0.3052	0.00030490.07609950.0211	
17:378327rs2941505	17 37832704 G	A	0.3191	0.00051830.07509810.0216	
17:378327rs2952152	17 37832735 C	T	0.3181	0.00022970.07639600.0207	
17:378330rs2941506	17 37833035 G	A	0.3191	0.00022870.07649790.0207	
17:378333rs2934951	17 37833328 G	A	0.3181	0.00022570.07649790.0208	
17:378335rs907088	17 37833567 C	G	0.325	0.00052730.07120370.0205	
17:378336rs907089	17 37833600 A	G	0.3241	0.00054060.07110130.0206	
17:378336rs907090	17 37833632 C	T	0.3241	0.00053980.07110130.0205	
17:378338rs9675194	17 37833805 C	T	0.325	0.00051490.07139930.0205	
17:378338rs2313171	17 37833842 C	T	0.3241	0.00049740.07150170.0205	
17:378343rs732084	17 37834357 C	A	0.3231	0.00045920.07200430.0205	
17:378343rs732083	17 37834367 A	G	0.332	0.00050730.07129680.0205	
17:378345rs1215029	17 37834541 C	T	0.325	0.00044540.07219970.0205	
17:378347rs1215060	17 37834715 A	G	0.328	0.00036740.07310170.0205	
17:378349rs8077172	17 37834977 T	G	0.325	0.00044730.07209730.0205	
17:378349rs8078228	17 37834998 T	C	0.325	0.000447	0.07209730.0205
17:378352rs1018246	17 37835240 T	C	0.325	0.00044920.07209730.0206	
17:378357rs1107891	17 37835755 C	T	0.325	0.00046510.07190190.0206	
17:378362rs1476278	17 37836243 T	C	0.328	0.000387	0.07289720.0205
17:378363rs9303274	17 37836353 C	T	0.328	0.00037540.07299950.0205	
17:378365rs1294098	17 37836581 A	G	0.328	0.00039330.07280420.0205	
17:378383rs2517952	17 37838301 G	A	0.3062	0.00025350.07720170.0211	

17:378387rs2517957	17 37838716 A	G	0.328	0.00036570.07320390.0205
17:378387rs2517958	17 37838751 A	G	0.328	0.00038690.07289720.0205
17:378394rs903501	17 37839493 C	T	0.3121	0.00063190.07139930.0209
17:378412rs2517953	17 37841211 C	G	0.335	1.82E-02 0.08719550.0203
17:378435rs2517954	17 37843550 C	T	0.3191	3.53E-02 0.08539750.0206
17:378436rs2517955	17 37843681 T	C	0.335	1.92E-02 0.08700300.0204
17:378438rs2517956	17 37843859 A	G	0.3191	3.60E-02 0.08529650.0206
17:378465rs2517959	17 37846512 T	A	0.3191	NA NA NA
17:378465rs2517960	17 37846521 C	T	0.335	1.79E-02 0.08729630.0204
17:378477rs5578857	17 37847799 TA	T	0.326	NA NA NA
17:378486rs2904765	17 37848675 G	T	0.326	NA NA NA
17:378486rs2904766	17 37848677 G	A	0.3201	NA NA NA
17:378505rs5571737	17 37850569 T	C	0.3151	NA NA NA
17:378505rs2904768	17 37850571 T	C	0.3151	NA NA NA
17:378530rs2643194	17 37853048 T	C	0.3091	1.03E-02 0.09219620.0209
17:378530rs2517951	17 37853097 T	C	0.326	6.97E-03 0.09269760.0206
17:378531rs2643195	17 37853118 G	A	0.3101	9.36E-03 0.09249710.0209
17:378545rs2934971	17 37854507 T	G	0.3101	6.76E-02 0.08719550.0219
17:378586rs1565923	17 37858678 G	A	0.3101	8.75E-03 0.09309860.0209
17:378617rs2952155	17 37861718 C	T	0.2505	0.00010840.08749790.0226
17:378660rs1810132	17 37866005 T	C	0.3111	4.91E-03 0.09570100.0209
17:378687rs4252627	17 37868715 T	C	0.334	4.77e-06 0.09450070.0207
17:378703rs2934967	17 37870378 A	G	0.3101	6.01E-03 0.09500100.021
17:378768rs2952156	17 37876835 G	A	0.3101	3.61E-03 0.09729910.021
17:378774rs2952157	17 37877412 A	G	0.3111	3.38E-03 0.09749860.021
17:378774rs1165399	17 37877447 G	C	0.335	3.3e-06 0.09630050.0207
17:378790rs2088126	17 37879030 G	A	0.3101	4.13E-03 0.09670010.021
17:378797rs903506	17 37879762 A	G	0.328	2.05e-06 0.09839630.0207
17:378805rs5474545	17 37880525 ATTTTTTTTA	A	0.336	NA NA NA
17:378840rs1058808	17 37884037 G	C	0.327	2.20E-03 0.09819690.0208
17:378892rs5296999	17 37889241 C	CT	0.3052	NA NA NA
17:378934rs4795393	17 37893484 T	C	0.3658	5.37E-02 0.08180110.0203
17:379037rs2941520	17 37903730 T	C	0.2962	3.99E-02 -0.087204 0.0212
17:420564rs2700836	17 42056480 T	C	0.04274	0.00094310.13879620.042
17:420579rs2631288	17 42057937 G	C	0.03976	0.00035910.15380200.0431
17:420612rs1731892	17 42061213 G	C	0.04076	0.00046170.15040080.043
17:420625rs2046534	17 42062562 A	G	0.03579	0.00026480.15709770.0431
17:420652rs1642595	17 42065227 A	G	0.07455	4.36e-06 0.14649570.0319
17:420652rs1642594	17 42065275 A	G	0.07455	4.33E-03 0.14649570.0319
17:420654rs1731885	17 42065468 G	C	0.07356	NA NA NA
17:420664rs7759392	17 42066435 ATTT	A	0.03579	NA NA NA
17:420670rs2019189	17 42067036 C	T	0.03479	0.00034040.15369910.0429
17:420731rs7215801	17 42073103 A	G	0.0666	5.19E-03 0.14740220.0324
17:420759rs6503486	17 42075980 C	T	0.02485	0.007273 0.14530300.0541
17:420762rs5779300	17 42076286 C	A	0.0328	3.22E-03 0.19660240.0422
17:420772rs408943	17 42077282 G	C	0.0328	2.86E-02 0.17819630.0426
17:420781rs378922	17 42078115 G	T	0.0328	1.92E-02 0.18169630.0425
17:420791rs3412951	17 42079136 AG	A	0.0328	NA NA NA

17:420838rs228770	17 42083840 C	T	0.0328	2.2e-05	0.18030280.0425
17:420843rs228772	17 42084377 A	G	0.0328	5.74E-04	0.22759760.0455
17:420851rs228773	17 42085150 C	T	0.0328	1.98E-02	0.18129600.0425
17:420853rs170639	17 42085352 C	G	0.0328	2.27E-02	0.17990190.0425
17:420861rs640631	17 42086180 T	C	0.0328	1.21E-02	0.18520070.0423
17:420875rs228775	17 42087501 T	C	0.0328	NA	NA NA
17:420882rs228776	17 42088253 C	T	0.0328	2.07E-02	0.18070350.0425
17:420883rs2001952	17 42088390 A	AAAG	0.0328	NA	NA NA
17:420888rs12889	17 42088853 A	G	0.0328	2.36E-02	0.17950090.0425
17:421071rs3457546	17 42107113 T	C	0.03181	2.59E-02	-0.178397 0.0424
17:421199rs3750547	17 42119971 CGCCCAGCC		0.03777	NA	NA NA
17:421271rs6662669	17 42127126 A	G	0.03181	2.90E-02	-0.178002 0.0426
17:421333rs2631292	17 42133398 G	A	0.0328	3.72e-05	0.17549830.0426
17:421338rs664610	17 42133817 C	T	0.0328	3.74E-02	0.17549830.0426
17:421350rs4793073	17 42135095 C	A	0.0328	3.71e-05	0.17559900.0426
17:421350rs4793074	17 42135096 C	T	0.0328	3.73E-02	0.17559900.0426
17:421558rs9913925	17 42155838 A	G	0.1262	2.82E-03	-0.131499 0.0281
20:512167rs5321792	20 51216707 C	CACACACA	0.0507	NA	NA NA
20:512718rs1403743	20 51271816 T	C	0.06262	0.003396	-0.112698 0.0385
20:51272820:512728	20 51272802 C	G	0.06262	2.24E-03	-0.132800 0.0281
20:51272820:512728	20 51272802 T	G	0.1441	0.008186	-0.099798 0.0378

r2	IndSigSNP	GenomicL	nearestGe dist	func	CADD	RDB	minChrStac	commonCl
0.623097	rs9442391	1	RP11-5407	358 upstream:	2,385		5	1 13
0.631368	rs9442391	1	HES4	0 exonic	0.567	NA		1 1
0.616333	rs9442391	1	HES4	558 upstream	4,685	NA		1 11
0.61916	rs9442391	1	RP11-5407	358 upstream	1,439		5	5 14
0.638239	rs9442391	1	ISG15	192 downstrea	0.709	NA		1 7
0.623737	rs9442391	1	ISG15	756 downstrea	0.27		6	1 5
0.63023	rs9442391	1	ISG15	1362 intergenic	0.179		6	5 5
0.63023	rs9442391	1	ISG15	1374 intergenic	2,953		5	5 5
0.663626	rs9442391	1	ISG15	2507 intergenic	2,939		6	5 5
0.670057	rs9442391	1	AGRN	1550 intergenic	3,903		5	5 5
0.666382	rs9442391	1	AGRN	725 upstream	4,289		4	1 2
0.65504	rs9442391	1	AGRN	0 intronic	Nov-81		4	1 2
0.684308	rs9442391	1	AGRN	0 intronic	3,623		6	2 7
0.713069	rs9442391	1	AGRN	0 intronic	0.069	3a		2 7
0.627829	rs9442391	1	AGRN	0 intronic	0.643	NA		2 7
0.824816	rs9442391	1	AGRN	0 intronic	3,401		4	1 7
0.829443	rs9442391	1	AGRN	0 intronic	2,728		6	4 5
0.859851	rs9442391	1	AGRN	0 intronic	1,105		6	4 5
0.804321	rs9442391	1	AGRN	0 intronic	1,112		5	4 5
0.85999	rs9442391	1	AGRN	0 intronic	6,159	NA		5 5
0.609754	rs9442391	1	AGRN	0 NA	2,564	NA		5 14
0.609754	rs9442391	1	AGRN	0 intronic	0.088		5	5 14
0.82151	rs9442391	1	AGRN	0 intronic	5,648	NA		5 14
0.85358	rs9442391	1	AGRN	0 intronic	1,041		5	2 7
0.825514	rs9442391	1	AGRN	0 intronic	3,991		7	1 13
0.828869	rs9442391	1	AGRN	0 intronic	2,159	3a		4 14
0.814553	rs9442391	1	AGRN	0 intronic	Feb-64	NA		3 5
	1 rs9442391	1	AGRN	0 exonic	Mar-13		4	4 5
0.908038	rs9442391	1	AGRN	0 intronic	1,392	NA		4 5
0.611356	rs9442391	1	AGRN	0 intronic	7,789	NA		4 5
0.900384	rs9442391	1	AGRN:RP1	1322:1322 intergenic	9,929		5	5 14
0.896385	rs9442391	1	RP11-465E	1753 intergenic	14.23		5	5 13
0.83127	rs9442391	1	RP11-465E	0 ncRNA_int	4,864	2b		1 12
0.780067	rs9442391	1	RP11-465E	0:00 ncRNA_ex	0.712		5	2 13
0.702129	rs9442391	1	RP11-465E	0 ncRNA_int	1,189	NA		1 1
0.741201	rs9442391	1	RP11-465E	221 downstrea	9,789		5	1 2
0.741201	rs9442391	1	RP11-465E	244 downstrea	4,945		5	1 2
0.737318	rs9442391	1	RNF223	122 downstrea	0.279		4	1 14
0.704721	rs9442391	1	RNF223	0 exonic	0.225		5	3 14
0.710177	rs9442391	1	RNF223	0 intronic	4,197	2b		1 14
0.713372	rs9442391	1	RNF223	1029 intergenic	6,602		5	5 14
0.709305	rs9442391	1	RNF223	1399 intergenic	9,331	NA		5 14
0.689107	rs9442391	1	C1orf159	2361 intergenic	3,649		5	1 2
0.683278	rs9442391	1	C1orf159	2333 intergenic	5,935		5	1 2
0.674746	rs9442391	1	C1orf159	2071 intergenic	9,615	NA		1 2
0.674746	rs9442391	1	C1orf159	1940 intergenic	7,918		5	1 2
0.609069	rs9442391	1	C1orf159	1646 intergenic	23-Mar		5	1 2

0.669858	rs9442391	1 C1orf159	27 downstrea	Apr-55	5	4	5
0.664187	rs9442391	1 C1orf159	0 downstrea	26-Mar NA		4	5
0.683074	rs9442391	1 C1orf159	0 UTR3	1,347	4	3	5
0.683074	rs9442391	1 C1orf159	0 intronic	24-Jan	5	4	5
0.686723	rs9442391	1 C1orf159	0 intronic	3,467	5	4	15
0.706735	rs9442391	1 C1orf159	0 intronic	26-Apr	5	3	15
0.632375	rs9442391	1 C1orf159	0 intronic	3,921	4	3	15
	1 rs1162077	2 KIF26B	0 intronic	0.17	6	5	15
0.81926	rs1162077	2 KIF26B	0 intronic	0.712	6	5	15
0.995552	rs247416	3 EIF4BP4	3680 intergenic	0.728 3a		1	15
0.991142	rs247416	3 EIF4BP4	8521 intergenic	2,867	7	1	15
	1 rs247416	3 EIF4BP4	13610 intergenic	2,323	7	5	15
0.616669	rs247416	3 EIF4BP4	23010 intergenic	0.377	7	5	15
0.655715	rs6179593	4 RP11-390C	15081 intergenic	1,363	6	9	15
0.655715	rs6179593	4 RP11-390C	15215 intergenic	0.812	7	9	15
0.655715	rs6179593	4 RP11-390C	15623 intergenic	0.166	6	9	15
0.655715	rs6179593	4 RP11-390C	16988 intergenic	0.372	7	9	15
0.655715	rs6179593	4 RP11-390C	17883 intergenic	0.955	7	9	15
0.655715	rs6179593	4 RP11-390C	19387 intergenic	0.296	6	9	15
0.655715	rs6179593	4 RP11-390C	19427 intergenic	0.245	6	9	15
0.655715	rs6179593	4 RP11-390C	20339 intergenic	0.824 2b		9	15
0.655715	rs6179593	4 RP11-390C	20835 intergenic	0.718	7	9	15
0.655715	rs6179593	4 RP11-390C	21226 intergenic	1,199	7	9	15
0.655715	rs6179593	4 RP11-390C	22562 intergenic	1,498	6	9	15
0.655715	rs6179593	4 RP11-390C	25321 intergenic	1,989 NA		9	15
0.655715	rs6179593	4 RP11-390C	26287 intergenic	4,168	7	9	15
0.655715	rs6179593	4 RP11-390C	26710 intergenic	2,562	6	9	15
0.740722	rs6179593	4 RPS3AP17	23594 intergenic	2,224	6	9	15
0.740722	rs6179593	4 RPS3AP17	21469 intergenic	0.314	7	9	15
0.740722	rs6179593	4 RPS3AP17	18477 intergenic	0.66	5	9	15
0.740722	rs6179593	4 RPS3AP17	13546 intergenic	Feb-18	5	9	15
0.740722	rs6179593	4 RPS3AP17	8148 intergenic	5,658	7	9	15
0.740722	rs6179593	4 RPS3AP17	4529 intergenic	7,391	6	15	15
0.740722	rs6179593	4 RPS3AP17	2308 intergenic	0.723	7	9	15
0.740722	rs6179593	4 RPS3AP17	1260 intergenic	1,905	7	9	15
0.740722	rs6179593	4 RPS3AP17	1260 NA	1,314 NA		9	15
0.783488	rs6179593	4 RPS3AP17	490 downstrea	1,686	6	9	15
0.783488	rs6179593	4 RPS3AP17	0 ncRNA_exi	6,583	7	9	15
0.783488	rs6179593	4 RPS3AP17	0 ncRNA_exi	1,735	6	9	15
0.741926	rs6179593	4 RPS3AP17	3862 intergenic	2,469	6	9	15
0.783488	rs6179593	4 RPS3AP17	5364 intergenic	Apr-98	6	9	15
0.783488	rs6179593	4 RPS3AP17	6123 intergenic	1,344	6	9	15
0.783488	rs6179593	4 RPS3AP17	6674 intergenic	8,562	6	9	15
0.783488	rs6179593	4 RPS3AP17	7429 intergenic	0.064	5	9	15
0.783488	rs6179593	4 RPS3AP17	8653 intergenic	3,179 NA		9	15
0.740722	rs6179593	4 RPS3AP17	9090 intergenic	2,856	6	9	15
0.783488	rs6179593	4 RPS3AP17	12718 intergenic	0.636	7	9	15
0.783488	rs6179593	4 RPS3AP17	16874 intergenic	0.513	6	9	15

0.783488	rs6179593	4 RPS3AP17	17347 intergenic	0.063	7	9	15
0.783488	rs6179593	4 RPS3AP17	19972 intergenic	0.377	5	9	15
	1 rs6179593	4 RPS3AP17	20662 intergenic	0.958	6	9	15
0.783488	rs6179593	4 RP11-174E	13299 intergenic	6,623	7	9	15
	1 rs6179593	4 RP11-174E	12882 intergenic	1,293	6	9	15
0.783488	rs6179593	4 RP11-174E	11858 intergenic	3,905	6	9	15
0.783488	rs6179593	4 RP11-174E	8048 intergenic	Mar-89	6	9	15
0.783488	rs6179593	4 RP11-174E	7650 intergenic	1,762	7	9	15
0.783488	rs6179593	4 RP11-174E	7650 NA	1,298 NA		9	15
0.783488	rs6179593	4 RP11-174E	5330 intergenic	3,801	7	9	15
0.741926	rs6179593	4 RP11-174E	4619 intergenic	0.707 NA		9	15
0.740722	rs6179593	4 RP11-174E	0 ncRNA_int	0.55	6	9	15
0.740722	rs6179593	4 RP11-174E	1117 intergenic	1,146	6	9	15
0.740722	rs6179593	4 RP11-174E	1176 intergenic	0.577	7	9	15
0.740722	rs6179593	4 RP11-174E	2827 intergenic	5,636	6	9	15
0.740722	rs6179593	4 RP11-174E	5179 intergenic	2,534	6	9	15
0.740722	rs6179593	4 RP11-174E	5800 intergenic	0.051	6	9	15
0.740722	rs6179593	4 RP11-174E	9332 intergenic	0.538	7	9	15
0.740722	rs6179593	4 RP11-174E	15348 intergenic	0.597	6	9	15
0.740722	rs6179593	4 RP11-174E	22739 intergenic	4,312	5	9	15
0.740722	rs6179593	4 RP11-174E	22930 intergenic	2,743	6	9	15
	1 rs6759760	5 RP11-6N13	0 ncRNA_int	2,713	7	5	15
0.74876	rs6759760	5 RP11-6N13	0 ncRNA_int	3,891 3a		15	15
0.662327	rs6237952	6 SLIT3	0 intronic	Apr-39	5	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	2,412	4	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	19.25	4	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	5,313	7	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.005 NA		5	14
0.675155	rs6237952	6 SLIT3	0 NA	0.008 NA		5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.305	7	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	1,556	7	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.303	7	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.118	4	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	Oct-64	7	5	15
0.675155	rs6237952	6 SLIT3	0 intronic	0.158	7	5	15
0.675155	rs6237952	6 SLIT3	0 intronic	5,042	7	5	15
0.675155	rs6237952	6 SLIT3	0 intronic	1,451	6	5	15
0.675155	rs6237952	6 SLIT3	0 intronic	0.012	7	5	15
0.675155	rs6237952	6 SLIT3	0 intronic	0.406	7	5	15
0.662327	rs6237952	6 SLIT3	0 intronic	0.347	7	5	15
0.675155	rs6237952	6 SLIT3	0 intronic	0.05	7	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.035	5	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.503	5	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.017	5	5	14
0.675155	rs6237952	6 SLIT3	0 intronic	0.914	5	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	0.197	6	5	14
0.656253	rs6237952	6 SLIT3	0 intronic	0.004	6	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	0.496	6	5	14

0.662327	rs6237952	6 SLIT3	0 intronic	Jan-41	5	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	15-Jun	4	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	0.508	7	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	2,429 NA		5	14
0.662327	rs6237952	6 SLIT3	0 intronic	0.004	5	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	9,302	5	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	0.576	7	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	2,107	7	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	1,468	7	5	14
0.662327	rs6237952	6 SLIT3	0 intronic	Oct-32 2b		5	14
0.662327	rs6237952	6 SLIT3	0 intronic	Jan-33	6	5	14
0.680122	rs6237952	6 SLIT3	0 intronic	5,381 3a		5	14
0.680122	rs6237952	6 SLIT3	0 intronic	Jul-49 2b		5	14
0.680122	rs6237952	6 SLIT3	0 intronic	1,878	5	5	14
0.680122	rs6237952	6 SLIT3	0 intronic	0.344	5	5	14
0.680122	rs6237952	6 SLIT3	0 intronic	5,238	5	5	15
0.71639	rs6237952	6 SLIT3	0 intronic	1,252	6	5	15
0.702162	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,511	4	2	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	8,544 NA		2	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,051	5	2	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	2,225	5	5	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_exi	1,778	5	5	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	3,923	5	5	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	2,922	5	5	15
0.71639	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,457	5	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	5,389	5	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.531	5	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	2,001	6	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	5,383	7	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	3,436	7	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.739	7	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	1,111	7	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.577	5	4	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.87	6	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.118	7	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.526	6	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	1,072	6	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.114	6	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	1,427	7	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	0.375 NA		5	15
0.71639	rs6237952	6 SLIT3	0 intronic	4,072 NA		5	15
0.731136	rs6237952	6 SLIT3	0 intronic	1,436	6	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	2,002	5	5	15
0.731136	rs6237952	6 SLIT3	0 intronic	1,121	6	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.097	5	5	15
0.639453	rs6237952	6 SLIT3	0 intronic	4,078	5	5	15
0.639453	rs6237952	6 SLIT3	0 intronic	0.213	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	3,524	4	5	15

0.888334	rs6237952	6 SLIT3	0 intronic	0.206	6	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	2,166 NA		5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.436	7	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	1,815	7	1	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.121	7	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	1,634	7	5	15
0.871093	rs6237952	6 SLIT3	0 intronic	1,502	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.592	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.638	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.894	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.948	7	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.839 NA		5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.037	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	1,019 NA		5	15
0.888334	rs6237952	6 SLIT3	0 intronic	2,973	4	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	1,899 2b		2	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.813 3a		2	15
0.604017	rs7720655	6 SLIT3	0 intronic	2,787	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.05	6	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	0.712 NA		5	15
0.888334	rs6237952	6 SLIT3	0 NA	0.499	6	5	15
0.604017	rs7720655	6 SLIT3	0 intronic	May-59 3a		5	15
0.604017	rs7720655	6 SLIT3	0 intronic	Jan-62 3a		5	15
0.649362	rs6237952	6 SLIT3	0 intronic	0.416 NA		5	15
0.888334	rs6237952	6 SLIT3	0 intronic	1,147	4	2	15
0.677575	rs7720655	6 SLIT3	0 intronic	May-36	4	2	15
0.888334	rs6237952	6 SLIT3	0 intronic	3,102	4	2	15
0.669608	rs7720655	6 SLIT3	0 intronic	3,034	5	2	15
0.669608	rs7720655	6 SLIT3	0 intronic	1,275	7	5	15
0.661689	rs7720655	6 SLIT3	0 intronic	1,578	6	5	15
0.649362	rs6237952	6 SLIT3	0 intronic	0.164	5	5	15
0.888334	rs6237952	6 SLIT3	0 intronic	3,449	6	5	15
0.61275	rs7720655	6 SLIT3:CTB-	0:00 ncRNA_int	Mar-99	6	5	15
0.943966	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	5,471	7	5	15
0.684172	rs7720655	6 SLIT3:CTB-	0:00 ncRNA_ex0.171	NA		5	15
0.943966	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,367	7	5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	6,066	6	5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	3,873 NA		5	15
0.61716	rs7720655	6 SLIT3:CTB-	0:00 ncRNA_ex0.196	NA		5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,532	6	5	15
0.943966	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,296	6	5	15
0.687702	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_ex	1,971	6	5	15
0.924735	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int0.356		5	5	15
0.943966	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_ex	1,768	7	4	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,392	7	5	15
0.943966	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	7,788	5	5	15
0.677145	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	2,348 NA		5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	Oct-18 NA		5	15

0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_exi	1,219	6	5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_exi	8,631 NA		5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,202	6	5	15
0.670008	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	Dec-47	7	5	15
0.622477	rs7720655	6 SLIT3:CTB-	0:00 ncRNA_int	17.89	5	2	15
0.943966	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	3,004	7	5	15
0.888298	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	8,562 NA		2	15
0.924735	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	4,606	5	2	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.015	7	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	4,486	5	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	7,652	5	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.057	5	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	4,761	5	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.94 NA		5	15
0.962641	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.644 NA		5	15
0.962641	rs6237952	6 SLIT3:CTB-	0:00 NA	NA NA		5	15
0.962641	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.074 NA		5	15
0.743854	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.213 NA		5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.456	7	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.113	6	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.134	7	5	15
0.962641	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	1,292 NA		5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	2,409	6	5	15
0.838212	rs7720655	6 SLIT3:CTB-	0:00 ncRNA_int	2,403	7	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.707	7	5	15
0.981184	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	0.829	7	5	15
1	rs6237952	6 SLIT3:CTB-	0:00 ncRNA_int	Jan-73	7	5	15
0.95744	rs7720655	6 SLIT3:CTB-	0:00 ncRNA_int	1,847 NA		5	15
1	rs6237952	6 SLIT3	0 intronic	0.668 NA		5	15
0.855128	rs7720655	6 SLIT3	0 intronic	3-Jul NA		5	15
0.855128	rs7720655	6 SLIT3	0 intronic	5,661	7	5	15
0.790671	rs7720655	6 SLIT3	0 intronic	0.832 NA		5	15
0.855128	rs7720655	6 SLIT3	0 intronic	3,138	6	5	15
1	rs7720655	6 SLIT3	0 intronic	0.225	7	5	15
1	rs6237952	6 SLIT3	0 intronic	1,552	6	4	15
0.981184	rs6237952	6 SLIT3	0 intronic	7,531	7	5	15
1	rs6237952	6 SLIT3	0 intronic	8,897	7	5	15
1	rs6237952	6 SLIT3	0 intronic	0.372 NA		5	15
0.851588	rs6237952	6 SLIT3	0 intronic	2,013	6	5	15
0.683395	rs1022675	7 JAZF1	0 intronic	1,109	4	5	5
0.683395	rs1022675	7 JAZF1	0 intronic	0.713 NA		5	5
0.683395	rs1022675	7 JAZF1	0 intronic	8,683	4	5	5
0.683395	rs1022675	7 JAZF1	0 intronic	15-Jun NA		4	5
0.713367	rs1022675	7 JAZF1	0 intronic	9,291 NA		5	15
0.713367	rs1022675	7 JAZF1	0 intronic	0.15	4	4	15
0.744817	rs1022675	7 JAZF1	0 intronic	7,048 3a		4	15
0.713367	rs1022675	7 JAZF1	0 intronic	1,091	6	4	5
0.737392	rs1022675	7 JAZF1	0 intronic	Dec-82	6	2	15

0.737392	rs1022675	7 JAZF1	0 intronic	8,185 NA		4	15
0.76861	rs1022675	7 JAZF1	0 intronic	0.107	7	4	5
0.76861	rs1022675	7 JAZF1	0 intronic	4,416	7	4	5
0.771419	rs1022675	7 JAZF1	0 intronic	1,352	5	2	15
0.771419	rs1022675	7 JAZF1	0 intronic	1,466	7	4	5
0.713607	rs1022675	7 JAZF1	0 intronic	Apr-36	6	4	5
0.713607	rs1022675	7 JAZF1	0 intronic	Nov-92	5	4	5
	1 rs1022675	7 JAZF1	0 intronic	15	5	5	5
0.825681	rs727390	8 MAGI2	0 intronic	0.985 NA		5	15
0.831234	rs727390	8 MAGI2	0 intronic	0.82	7	5	15
0.850309	rs727390	8 MAGI2	0 intronic	NA NA		5	15
0.850309	rs727390	8 MAGI2	0 intronic	0.488 NA		5	15
0.831234	rs727390	8 MAGI2	0 intronic	3,988	7	5	15
0.831234	rs727390	8 MAGI2	0 intronic	1,486	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	2,786	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	Mar-77 NA		5	15
0.831234	rs727390	8 MAGI2	0 intronic	2,594	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	2,101	7	5	15
0.826203	rs727390	8 MAGI2	0 intronic	0.4	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	5,449	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	4,882	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	3,442	7	5	15
0.831234	rs727390	8 MAGI2	0 intronic	2,049	6	5	15
0.827072	rs727390	8 MAGI2	0 intronic	6,515	7	5	15
0.823025	rs727390	8 MAGI2	0 intronic	6,726	5	5	15
0.823025	rs727390	8 MAGI2	0 intronic	6,748	5	5	15
0.823025	rs727390	8 MAGI2	0 intronic	7,221	6	5	15
0.823025	rs727390	8 MAGI2	0 intronic	5,845	6	5	15
0.827072	rs727390	8 MAGI2	0 intronic	1,954	6	5	15
0.831234	rs727390	8 MAGI2	0 intronic	9,535	6	5	15
0.827072	rs727390	8 MAGI2	0 intronic	2,959	5	5	15
0.827072	rs727390	8 MAGI2	0 intronic	0.305	6	5	15
0.827072	rs727390	8 MAGI2	0 intronic	5,369	7	5	15
0.827072	rs727390	8 MAGI2	0 intronic	Nov-67	7	5	15
0.827072	rs727390	8 MAGI2	0 intronic	Sep-64	7	5	15
0.831234	rs727390	8 MAGI2	0 intronic	17-Nov	5	5	15
0.797508	rs727390	8 MAGI2	0 intronic	2,169 NA		5	15
	1 rs727390	8 MAGI2	0 intronic	0.614	7	5	15
	1 rs1009627	9 RP11-388C	0 ncRNA_int	1,192	6	14	15
0.95508	rs1009627	9 RP11-388C	0 ncRNA_int	0.06	5	9	15
0.633056	rs5726823	10 PAX5	0 intronic	Nov-51	5	3	14
0.916196	rs5726823	10 PAX5:RP11	0:00 ncRNA_int	0.961	7	2	13
0.916196	rs5726823	10 PAX5:RP11	0:00 ncRNA_int	2,543	6	2	13
0.916196	rs5726823	10 PAX5	0 intronic	16-Jul	7	4	14
0.916196	rs5726823	10 PAX5	0 intronic	Apr-58	5	3	13
	1 rs5726823	10 PAX5	0 intronic	6,342 3a		1	12
0.947433	rs5726823	10 PAX5	0 intronic	2,068 3a		2	13
	1 rs5726823	10 PAX5	0 intronic	2,752	5	2	13

1	rs4483247	10 RP11-297E	1006 intergenic	0.007	7	5	14
0.991905	rs4483247	10 RP11-297E	4380 intergenic	0.124	6	5	14
0.991905	rs4483247	10 RP11-297E	4845 intergenic	0.93	6	5	14
0.991905	rs4483247	10 RP11-297E	5009 intergenic	3,326	5	5	14
0.991905	rs4483247	10 RP11-297E	5216 intergenic	1,038	6	5	14
0.991905	rs4483247	10 RP11-297E	5219 intergenic	1,883 NA		5	14
0.991905	rs4483247	10 RP11-297E	6111 intergenic	0.604	6	5	14
0.975775	rs4483247	10 RP11-297E	7830 intergenic	4,537	5	5	13
0.991905	rs4483247	10 RP11-297E	7874 intergenic	4,203	5	5	13
0.991905	rs4483247	10 RP11-297E	8475 intergenic	4,185	7	5	14
1	rs4483247	10 RP11-297E	9138 intergenic	13 2b		5	14
0.938249	rs4483247	10 RP11-465N	828 upstream	7,136	5	5	14
0.938249	rs4483247	10 RP11-220I	634 downstrea	0.04 NA		5	14
0.938249	rs4483247	10 RP11-220I	625 downstrea	0.148	6	5	14
0.938249	rs4483247	10 RP11-220I	0 ncRNA_ex	0.261	7	1	14
0.930295	rs4483247	10 RP11-220I	0 ncRNA_ex	4,591	6	1	1
0.930295	rs4483247	10 RP11-220I	0 ncRNA_ex	4,931	7	1	1
0.930295	rs4483247	10 RP11-220I	0 ncRNA_int	6,648	5	1	5
0.930295	rs4483247	10 RP11-220I	0 ncRNA_int	5,776	5	1	5
0.930295	rs4483247	10 RP11-220I	0 ncRNA_int	13-Sep	5	1	5
0.708767	rs4483247	10 RP11-220I	0 ncRNA_ex	0.162 NA		4	5
0.930295	rs4483247	10 RP11-220I	619 downstrea	0.138	7	5	5
0.930295	rs4483247	10 RP11-220I	5105 intergenic	1,701	6	5	15
0.930295	rs4483247	10 RP11-220I	7907 intergenic	1,756	7	5	15
0.96776	rs4483247	10 RP11-220I	8936 intergenic	0.437	7	5	15
0.930295	rs4483247	10 RP11-220I	10126 intergenic	13.86 2b		5	15
0.930295	rs4483247	10 RP11-220I	8310 intergenic	4,964	6	5	15
0.930295	rs4483247	10 RP11-220I	6174 intergenic	2,763	5	5	15
0.930295	rs4483247	10 RP11-220I	6102 intergenic	0.878	5	5	15
0.930295	rs4483247	10 RP11-220I	5790 intergenic	3,177	7	5	15
0.930295	rs4483247	10 RP11-220I	0 ncRNA_int	1,668	7	5	15
0.909591	rs4483247	10 RP11-220I	361 upstream	0.611 NA		5	15
0.930295	rs4483247	10 ZCCHC7	0 intronic	0.784	5	1	1
0.930295	rs4483247	10 ZCCHC7	0 intronic	0.231	5	1	1
0.930295	rs4483247	10 ZCCHC7	0 intronic	0.371	5	1	2
0.938249	rs4483247	10 ZCCHC7	0 intronic	2,761	7	2	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	2,801	6	3	5
0.938249	rs4483247	10 ZCCHC7	0 intronic	1,418	5	4	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	4,504	6	4	5
0.938249	rs4483247	10 ZCCHC7	0 intronic	0.835 NA		4	5
0.930892	rs4483247	10 ZCCHC7	0 intronic	0.089	7	4	5
0.96776	rs4483247	10 ZCCHC7	0 intronic	8,774	5	4	5
0.938249	rs4483247	10 ZCCHC7	0 intronic	2,242	5	1	5
0.930892	rs4483247	10 ZCCHC7	0 intronic	13-May	5	1	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	3,424	6	1	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	2,779	7	5	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	2-Aug	7	5	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	1,221	7	5	5

0.930295	rs4483247	10 ZCCHC7	0 intronic	Oct-55	6	5	5
0.895595	rs4483247	10 ZCCHC7	0 intronic	1,204	6	4	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	19.34 NA		4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	3,465	6	5	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	5,471	6	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	4,801	6	4	5
0.902553	rs4483247	10 ZCCHC7	0 intronic	3,657	6	4	5
0.908476	rs4483247	10 ZCCHC7	0 intronic	NA NA		4	5
0.908476	rs4483247	10 ZCCHC7	0 intronic	1,733 NA		4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	3,975	6	5	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	0.685	6	4	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	2-Aug	7	4	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	3,994	7	4	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	1,834	5	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	6,677	7	2	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	20-Jan	4	2	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	5,898 3a		2	5
0.930295	rs4483247	10 ZCCHC7	0 intronic	0.495	5	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	5,433 NA		4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	0.375	5	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	Nov-76	5	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	3,762	5	2	15
0.906204	rs4483247	10 ZCCHC7	0 intronic	Jan-48 NA		5	15
0.902553	rs4483247	10 ZCCHC7	0 intronic	1,191	5	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	Dec-21	6	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	0.79 NA		5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	1,442	5	5	15
0.922937	rs4483247	10 ZCCHC7	0 intronic	9,769 NA		5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	1-Jan	6	3	15
0.914511	rs4483247	10 ZCCHC7	0 intronic	4,825	6	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	Dec-63	5	5	15
0.902553	rs4483247	10 ZCCHC7	0 intronic	14.53	5	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	10-Feb	7	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	3,483	7	4	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	3,613	5	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	12-Mar	5	5	15
0.930295	rs4483247	10 ZCCHC7	0 intronic	1,176	7	5	15
0.930295	rs4483247	10 ZCCHC7	0 intronic	2,184	7	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	0.509	7	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	8,291	7	4	15
0.930295	rs4483247	10 ZCCHC7	0 intronic	7,816	4	5	15
0.930295	rs4483247	10 ZCCHC7	0 intronic	6,844 NA		5	15
0.907152	rs4483247	10 ZCCHC7	0 intronic	2,787	6	4	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	1,285	5	5	15
0.91364	rs4483247	10 ZCCHC7	0 intronic	0.233	7	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	7,462	7	2	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	6,722	5	3	15
0.959788	rs4483247	10 ZCCHC7	0 intronic	4,347	4	2	15

0.922382	rs4483247	10 ZCCHC7	0 intronic	7,527 3a		1	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	1,177	5	2	15
0.916032	rs4483247	10 ZCCHC7	0 intronic	4,248 NA		2	15
0.930295	rs4483247	10 ZCCHC7	0 intronic	1,882	4	2	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	1,855	5	4	5
0.922382	rs4483247	10 ZCCHC7	0 intronic	16.49 3a		5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	4,258	7	5	15
0.922382	rs4483247	10 ZCCHC7	0 intronic	1,766	7	5	15
0.821919	rs4483247	10 ZCCHC7	0 intronic	4,495	7	4	15
0.89099	rs4483247	10 ZCCHC7	0 intronic	0.016	6	4	15
0.915024	rs4483247	10 ZCCHC7	2664 intergenic	May-51	5	4	15
0.922937	rs4483247	10 ZCCHC7	3167 intergenic	0.002	6	4	15
0.922937	rs4483247	10 ZCCHC7	3638 intergenic	2,152	4	5	15
0.883165	rs4483247	10 RP11-397C	7996 intergenic	6,969	4	2	15
0.88273	rs4483247	10 RP11-397C	5708 intergenic	4,089	5	5	15
0.735034	rs4483247	10 RP11-397C	5388 intergenic	1,234 NA		5	15
0.742725	rs4483247	10 RP11-397C	5979 intergenic	3,393	4	5	15
0.622868	rs4483247	10 RP11-397C	9718 intergenic	6,358	7	5	15
0.622868	rs4483247	10 RP11-397C	9941 intergenic	2,776	5	5	15
0.618067	rs4483247	10 GRHPR	16271 intergenic	4,685 2a		2	15
0.624602	rs1222147	11 TBATA	0 intronic	3,079	5	5	15
	1 rs1222147	11 TBATA	0 intronic	2,166	5	5	15
0.704047	rs1222147	11 TBATA	0 intronic	1,262	4	5	15
0.987212	rs1222147	11 TBATA	0 intronic	0.435 NA		1	15
0.689858	rs1222147	11 TBATA	0 intronic	2,978	5	1	15
0.81381	rs7677188	12 ZCCHC24	0 intronic	0.916 NA		2	15
0.81381	rs7677188	12 ZCCHC24	0 intronic	7,082	5	2	7
0.81381	rs7677188	12 ZCCHC24	0 intronic	2,278 3a		2	15
0.766343	rs7677188	12 ZCCHC24	0 intronic	3,251 2b		4	15
0.814688	rs7677188	12 ZCCHC24	0 intronic	0.402	5	2	15
0.814688	rs7677188	12 ZCCHC24	0 intronic	4,728	5	2	15
0.81381	rs7677188	12 ZCCHC24	0 intronic	4,787	5	2	15
0.81381	rs7677188	12 ZCCHC24	0 intronic	Feb-51	5	2	15
0.81381	rs7677188	12 ZCCHC24	0 intronic	0.398 NA		4	15
0.81381	rs7677188	12 ZCCHC24	0 intronic	13.67 NA		4	15
	1 rs7677188	12 ZCCHC24	0 intronic	0.79	7	1	15
0.630851	rs1124451	13 RPS27P18	54925 intergenic	3,797	6	9	15
0.630851	rs1124451	13 RPS27P18	54824 intergenic	0.473	6	9	15
0.630851	rs1124451	13 RPS27P18	54662 intergenic	0.319	6	9	15
0.659665	rs1124451	13 RPS27P18	52874 intergenic	0.794	7	9	15
0.659665	rs1124451	13 RPS27P18	50390 intergenic	Jan-53	6	9	15
0.659665	rs1124451	13 RPS27P18	49508 intergenic	1,379	6	9	15
0.630851	rs1124451	13 RPS27P18	49069 intergenic	2,891 NA		7	15
0.630851	rs1124451	13 RPS27P18	49068 intergenic	7,551 NA		7	15
0.630851	rs1124451	13 RPS27P18	49068 NA	3,444	6	7	15
0.630851	rs1124451	13 RPS27P18	47429 intergenic	0.428	6	9	15
0.644986	rs1124451	13 RPS27P18	47184 intergenic	0.696	6	9	15
0.659665	rs1124451	13 RPS27P18	41607 intergenic	3,795	7	9	15

0.659665	rs1124451	13 RPS27P18	36727 intergenic	0.286	7	13	15
0.659665	rs1124451	13 RPS27P18	34563 intergenic	0.822	6	9	15
0.679486	rs1124451	13 RPS27P18	33419 intergenic	0.446	6	14	15
0.708608	rs1124451	13 RPS27P18	32506 intergenic	0.927	NA	7	15
0.708608	rs1124451	13 RPS27P18	31944 intergenic	0.446	5	5	15
0.693787	rs1124451	13 RPS27P18	31798 intergenic	NA	NA	5	15
0.693787	rs1124451	13 RPS27P18	28868 intergenic	1,746	7	5	15
0.708608	rs1124451	13 RPS27P18	28159 intergenic	1,209	6	5	15
0.724322	rs1124451	13 RPS27P18	27942 intergenic	1,115	7	5	15
0.724322	rs1124451	13 RPS27P18	27940 intergenic	4,595	7	5	15
0.724322	rs1124451	13 RPS27P18	26388 intergenic	0.287	6	5	15
0.724322	rs1124451	13 RPS27P18	25809 intergenic	4,245	6	5	15
0.724322	rs1124451	13 RPS27P18	24372 intergenic	4,748	6	5	15
0.724322	rs1124451	13 RPS27P18	24026 intergenic	Mar-31	7	5	15
0.709472	rs1124451	13 RPS27P18	23365 intergenic	0.338	NA	5	15
0.724322	rs1124451	13 RPS27P18	21271 intergenic	3,179	7	5	15
0.724322	rs1124451	13 RPS27P18	20998 intergenic	0.665	7	5	15
0.739712	rs1124451	13 RPS27P18	18279 intergenic	17.97	NA	5	15
0.755674	rs1124451	13 RPS27P18	17278 intergenic	Dec-49	5	2	15
0.755674	rs1124451	13 RPS27P18	17271 intergenic	Nov-14	5	2	15
0.851583	rs1124451	13 RPS27P18	16136 intergenic	0.576	7	5	15
0.868135	rs1124451	13 RPS27P18	8844 intergenic	1,402	6	5	15
0.868135	rs1124451	13 RPS27P18	8715 intergenic	1,121	NA	5	15
0.868135	rs1124451	13 RPS27P18	6988 intergenic	0.593	7	5	15
0.868135	rs1124451	13 RPS27P18	6549 intergenic	15-Mar	7	5	15
0.917038	rs1124451	13 RPS27P18	5399 intergenic	1,279	5	1	15
0.917038	rs1124451	13 RPS27P18	3371 intergenic	0.312	6	5	15
0.917038	rs1124451	13 RPS27P18	2112 intergenic	0.349	7	5	15
0.917038	rs1124451	13 RPS27P18	1275 intergenic	0.594	4	7	15
0.917038	rs1124451	13 RPS27P18	959 downstrea	3,155	5	7	15
0.917038	rs1124451	13 RPS27P18	2371 intergenic	6,587	6	5	14
0.917038	rs1124451	13 RPS27P18	5331 intergenic	0.674	2a	5	15
0.917038	rs1124451	13 RPS27P18	5738 intergenic	0.603	7	5	15
0.917038	rs1124451	13 RPS27P18	5787 intergenic	1,144	6	5	15
1	rs1124451	13 RPS27P18	8905 intergenic	3,349	5	2	15
0.917038	rs1124451	13 RPS27P18	10118 intergenic	1-May	3a	5	15
0.900665	rs1124451	13 RPS27P18	11068 intergenic	0.138	6	5	15
0.900665	rs1124451	13 RPS27P18	11906 intergenic	5,872	6	5	15
0.900665	rs1124451	13 RPS27P18	19124 intergenic	Feb-33	5	5	15
0.843384	rs1241530	14 RP11-264E	3471 intergenic	0.607	4	5	15
0.916763	rs1241530	14 RP11-264E	13903 intergenic	0.08	NA	9	15
1	rs1241530	14 RP11-264E	26881 intergenic	4,536	7	9	15
0.951624	rs1241530	14 RP11-264E	28802 intergenic	1,189	NA	14	15
1	rs1241530	14 RP11-264E	29766 intergenic	3,378	7	13	15
0.967274	rs1241530	14 RP11-264E	31080 intergenic	7,437	5	9	15
0.983392	rs1241530	14 RP11-264E	31372 intergenic	3,312	5	9	15
0.967274	rs1241530	14 RP11-264E	31678 intergenic	3,098	7	9	15
0.967274	rs1241530	14 RP11-264E	31694 intergenic	6,128	7	9	15

0.967274	rs1241530	14 RP11-264E	31840 intergenic	8,598	7	9	15
0.967274	rs1241530	14 RP11-264E	32413 intergenic	0.556	6	9	15
0.967274	rs1241530	14 RP11-264E	32540 intergenic	6,815	6	9	15
0.967274	rs1241530	14 RP11-264E	32719 intergenic	0.708 NA		9	15
0.967274	rs1241530	14 RP11-264E	32816 intergenic	4,812	6	9	15
0.967274	rs1241530	14 RP11-264E	33163 intergenic	13.33	6	7	15
0.967274	rs1241530	14 RP11-264E	33527 intergenic	2,837	6	7	15
0.967274	rs1241530	14 RP11-264E	33770 intergenic	Feb-78	7	7	15
0.951624	rs1241530	14 RP11-264E	34450 intergenic	0.513	7	7	15
0.983392	rs1241530	14 RP11-264E	35155 intergenic	0.759 NA		5	15
0.967274	rs1241530	14 RP11-264E	35647 intergenic	0.188	7	5	15
0.967274	rs1241530	14 RP11-264E	35871 intergenic	2,937	7	1	15
0.967274	rs1241530	14 RP11-264E	36334 intergenic	2,921	6	9	15
0.967274	rs1241530	14 RP11-264E	36456 intergenic	1,667	6	9	15
0.967274	rs1241530	14 RP11-264E	36647 intergenic	1,263 NA		9	15
0.967274	rs1241530	14 RP11-264E	37149 intergenic	2,582	6	9	15
0.967274	rs1241530	14 RP11-264E	37334 intergenic	2,152	7	9	15
0.967274	rs1241530	14 RP11-264E	37402 intergenic	Apr-34	6	9	15
0.967274	rs1241530	14 RP11-264E	37541 intergenic	9,263 NA		9	15
0.983392	rs1241530	14 RP11-264E	37616 intergenic	3,906	6	9	15
0.951624	rs1241530	14 RP11-264E	38144 intergenic	0.071	7	9	15
0.853167	rs1241530	14 RP11-264E	38156 intergenic	0.757 NA		9	15
0.983392	rs1241530	14 RP11-264E	38215 intergenic	4,689	7	9	15
0.983392	rs1241530	14 RP11-264E	38522 intergenic	2,858	6	1	15
0.769686	rs1241530	14 RP11-264E	55019 intergenic	0.058	6	5	15
0.604343	rs1089750	15 AP003774.	2586 intergenic	1,486	5	5	14
0.604343	rs1089750	15 AP003774.	4878 intergenic	0.014	5	5	14
0.604343	rs1089750	15 AP003774.	6219 intergenic	0.03 NA		5	14
0.604343	rs1089750	15 AP003774.	7750 intergenic	0.698	5	5	14
1	rs1089750	15 AP003774.	2071 intergenic	5,076	6	5	14
1	rs7969898	16 SRGAP1	0 intronic	1,672	6	4	15
0.896306	rs3103885	17 RP11-611E	0 ncRNA_int	1,366	7	5	15
1	rs3103885	17 RP11-611E	0 ncRNA_int	0.858 NA		5	15
1	rs3103885	17 RP11-611E	0 ncRNA_int	0.853	6	5	15
0.86177	rs3103885	17 RP11-611E	0 ncRNA_int	0.687 NA		5	15
0.933132	rs3103885	17 RP11-611E	0 ncRNA_int	0.983	6	5	15
1	rs3103885	17 RP11-611E	0 ncRNA_int	3,946	6	5	15
1	rs3103885	17 RP11-611E	0 ncRNA_int	3,144	6	5	15
1	rs3103885	17 RP11-611E	0 ncRNA_int	7-May	7	5	15
1	rs3103885	17 RP11-611E	0 ncRNA_int	0.705	7	5	15
0.982556	rs3103885	17 RP11-611E	0 ncRNA_int	1,497	6	5	15
0.815358	rs3103885	17 RP11-611E	0 ncRNA_int	2,838	6	5	15
0.986997	rs3103885	17 RP11-611E	0 ncRNA_int	0.443	7	5	15
0.691943	rs3103885	17 RP11-611E	0 ncRNA_int	1,106	6	5	15
0.917108	rs3103885	17 RP11-611E	0 ncRNA_int	0.876	7	5	15
0.655879	rs3103885	17 RP11-611E	0 ncRNA_int	0.791	7	5	15
0.991345	rs3103885	17 RP11-611E	0 ncRNA_int	0.64	7	5	15
0.710563	rs3103885	17 RP11-611E	0 ncRNA_int	0.801 NA		5	15

0.986927	rs3103885	17 RP11-611E	0 ncRNA_int	Aug-72 NA		5	15
0.939762	rs3103885	17 RP11-611E	0 ncRNA_int	3,063	7	5	15
0.897231	rs3103885	17 RP11-611E	0 ncRNA_int	6,757	5	14	15
0.897231	rs3103885	17 RP11-611E	0 ncRNA_int	11-Aug	5	7	9
0.89323	rs3103885	17 RP11-611E	0 ncRNA_int	0.219	7	8	9
0.897231	rs3103885	17 RP11-611E	0 ncRNA_int	13.35	7	5	15
0.888529	rs3103885	17 RP11-611E	0 ncRNA_int	2,742 NA		5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	3,697	7	14	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	4,245	7	14	15
0.865565	rs3103885	17 RP11-611E	0 ncRNA_int	1,402 NA		14	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	0.798	6	14	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	1,282	6	14	15
0.869143	rs3103885	17 RP11-611E	0 ncRNA_int	0.188	7	1	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	1,281 3a		1	15
0.689332	rs3103885	17 RP11-611E	0:00 ncRNA_exi	Mar-53	7	1	15
0.689332	rs3103885	17 RP11-611E	0:00 ncRNA_int	0.275	7	1	15
0.689332	rs3103885	17 RP11-611E	0:00 ncRNA_int	3,678	6	5	15
0.689332	rs3103885	17 RP11-611E	0:00 ncRNA_int	1,247 NA		5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	0.795	7	9	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	9,837	7	9	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	1,925	7	9	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	9,749	6	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	3,872	5	1	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	0.057	6	5	15
0.897231	rs3103885	17 RP11-611E	0 ncRNA_int	7,114	7	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	7-Apr	6	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	1,735	6	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	3,975	6	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	2,957	6	4	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	6,942	6	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	2,372	5	5	15
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	0.542	6	4	5
0.689332	rs3103885	17 RP11-611E	0 ncRNA_int	11-Sep	6	4	5
0.962563	rs7321500	18 RPL21P11C	36232 intergenic	3-Sep	6	14	15
	1 rs7321500	18 BORA	0 intronic	4,012	7	4	5
0.925282	rs7321500	18 PIBF1	0 intronic	7,557	7	4	5
0.777696	rs7321500	18 PIBF1	0 intronic	4,847	6	4	5
0.777696	rs7321500	18 PIBF1	0 intronic	0.542 NA		4	5
0.962563	rs7321500	18 PIBF1	0 intronic	1,586	7	5	5
0.794216	rs1953445	19 NPAS3	0 intronic	0.145	6	5	15
0.813836	rs1953445	19 NPAS3	0 intronic	5,443	7	5	15
0.871757	rs1953445	19 NPAS3	0 intronic	2,514	6	5	15
0.918584	rs1953445	19 NPAS3	0 intronic	Dec-66	5	5	15
0.865338	rs1953445	19 NPAS3	0 intronic	1,777	7	5	15
0.812498	rs1953445	19 NPAS3	0 intronic	3,018	5	5	15
0.764793	rs1953445	19 NPAS3	0 intronic	Jan-45	6	4	15
0.727598	rs1953445	19 NPAS3	0 intronic	1,942	5	5	15
	1 rs1953445	19 NPAS3	0 intronic	Jan-84	6	4	15

0.995358	rs1953445	19 NPAS3	0 intronic	0.538	7	5	15
0.689416	rs1953445	19 NPAS3	0 intronic	2,242	7	4	15
	1 rs7267430	20 RP11-313C	55564 intergenic	8,956	6	9	15
	1 rs7507080	21 ZFH3	0 intronic	0.909 3a		5	15
	1 rs1164241	22 PLCG2	0 intronic	3,177	6	4	15
0.611248	rs7218395	23 RP1-66C13	0 intronic	5,725	7	5	15
0.611248	rs7218395	23 RP1-66C13	0 intronic	4,321 NA		5	15
0.611248	rs7218395	23 RP1-66C13	0 intronic	0.851	7	5	15
0.615833	rs7218395	23 RP1-66C13	0 intronic	9,945	5	5	15
0.611248	rs7218395	23 RP1-66C13	0 intronic	2,139	7	5	15
0.603448	rs7218395	23 RP1-66C13	0 intronic	6,153	5	5	15
0.676283	rs7218395	23 RP1-66C13	0 intronic	3,954	5	5	15
0.679889	rs7218395	23 RP1-66C13	0:00 ncRNA_int	0.234 NA		4	15
0.756974	rs7218395	23 RP1-66C13	0:00:00 ncRNA_ex	0.382	5	4	15
0.959871	rs7218395	23 RP1-66C13	0:00:00 ncRNA_ex	4,139	5	5	15
0.638512	rs7218395	23 RP1-66C13	0:00 intronic	1,576 NA		5	5
0.766122	rs7218395	23 RP1-66C13	0:00 intronic	0.422 NA		5	5
0.877151	rs7218395	23 RP1-66C13	0:00 intronic	0.566 NA		5	5
0.973199	rs7218395	23 RP1-66C13	0:00 intronic	6,021	4	2	5
0.973199	rs7218395	23 RP1-66C13	0:00 intronic	0.565	4	5	5
0.752624	rs7218395	23 RP1-66C13	0:00 intronic	0.077 2b		5	5
0.752624	rs7218395	23 RP1-66C13	0:00 intronic	2,959	7	4	5
0.977732	rs7218395	23 RP1-66C13	0:00 UTR5	14-Aug 2b		1	1
0.764345	rs7218395	23 LYRM9	741 intergenic	15.75	6	2	14
0.955648	rs7218395	23 LYRM9	1031 intergenic	Oct-82	5	2	14
0.764345	rs7218395	23 LYRM9	1107 intergenic	14.91 NA		2	14
0.629048	rs7218395	23 LYRM9	3779 intergenic	12-Aug	5	5	14
0.774634	rs7218395	23 LYRM9	8701 intergenic	0.145	7	5	14
0.995509	rs7218395	23 LYRM9	9016 intergenic	0.161	7	5	14
0.770891	rs7218395	23 LYRM9	11138 intergenic	0.934	4	2	14
0.995509	rs7218395	23 LYRM9	13447 intergenic	2,415 3a		5	15
0.770891	rs7218395	23 LYRM9	13854 intergenic	3,117 NA		5	15
0.7295	rs7218395	23 LYRM9	17390 intergenic	3,389 NA		5	15
0.770891	rs7218395	23 RP11-218F	16162 intergenic	2,596	7	5	15
	1 rs7218395	23 RP11-218F	15096 intergenic	5,048	5	5	15
	1 rs1294825	23 RP11-218F	14310 intergenic	0.008	7	5	15
0.758182	rs7218395	23 RP11-218F	13847 intergenic	0.186 3a		2	15
0.763492	rs7218395	23 RP11-218F	13817 intergenic	Jul-39	4	2	15
0.991033	rs7218395	23 RP11-218F	11536 intergenic	1,299	7	5	15
0.820786	rs7218395	23 RP11-218F	7765 intergenic	0.483 NA		5	15
0.986571	rs7218395	23 RP11-218F	7651 intergenic	2,486	7	5	15
0.771343	rs7218395	23 RP11-218F	6464 intergenic	2,106	6	5	15
0.760645	rs7218395	23 RP11-218F	5852 intergenic	0.543	7	5	15
0.760222	rs7218395	23 RP11-218F	5415 intergenic	0.67	5	5	15
0.753333	rs7218395	23 RP11-218F	3717 intergenic	1,069	5	5	15
0.755357	rs7218395	23 RP11-218F	3105 intergenic	0.437	7	5	15
0.611583	rs903506	24 AC087491.	1529 intergenic	0.831	4	5	14
0.695709	rs903506	24 STARD3	0 intronic	4,856 2b		2	5

0.717135	rs903506	24 STARD3	0 intronic	3,669	5	4	5
0.714059	rs903506	24 STARD3	0 exonic	23-Jan NA		3	4
0.717135	rs903506	24 STARD3	0 intronic	May-21	4	2	4
0.638086	rs903506	24 STARD3	0 intronic	6,299 NA		2	4
0.717135	rs903506	24 TCAP	0 UTR5	3,558 2b		1	5
0.635016	rs903506	24 TCAP	0 exonic	15-Jul	4	1	7
0.726426	rs903506	24 PNMT	0 intronic	5,182 NA		1	10
0.856208	rs903506	24 PGAP3	211 downstrea	6,732 2b		2	13
0.828601	rs903506	24 PGAP3	0 UTR3	9,075 NA		5	14
0.828601	rs903506	24 PGAP3	0 UTR3	3,808 2b		2	7
0.828601	rs903506	24 PGAP3	0 UTR3	1,933	4	2	5
0.815947	rs903506	24 PGAP3	0 UTR3	5,518 2b		2	5
0.815947	rs903506	24 PGAP3	0 intronic	5,042 NA		5	5
0.871908	rs903506	24 PGAP3	0 intronic	May-27	5	5	5
0.871908	rs903506	24 PGAP3	0 intronic	0.735 NA		5	5
0.871908	rs903506	24 PGAP3	0 intronic	Oct-89 NA		5	5
0.871908	rs903506	24 PGAP3	0 intronic	2,618	5	4	5
0.819962	rs903506	24 PGAP3	0 exonic	16.51	4	2	5
0.832619	rs903506	24 PGAP3	0 intronic	3,558 NA		2	5
0.903743	rs903506	24 PGAP3	0 intronic	17.97 NA		2	7
0.894031	rs903506	24 PGAP3	0 intronic	15-Feb	4	2	7
0.899342	rs903506	24 PGAP3	0 intronic	6,673 NA		2	7
0.835231	rs903506	24 PGAP3	0 intronic	0.419 NA		2	7
0.835231	rs903506	24 PGAP3	0 intronic	4,101 NA		2	7
0.903631	rs903506	24 PGAP3	0 intronic	4,395 NA		2	7
0.835231	rs903506	24 PGAP3	0 intronic	4,901	5	2	7
0.835231	rs903506	24 PGAP3	0 intronic	7,614 NA		2	7
0.894611	rs903506	24 PGAP3	0 intronic	0.924 3a		2	7
0.890365	rs903506	24 PGAP3	0 intronic	8,336	4	2	7
0.894611	rs903506	24 PGAP3	0 intronic	8,419 3a		2	7
0.890365	rs903506	24 PGAP3	0 intronic	4,723 NA		2	7
0.868578	rs903506	24 PGAP3	0 intronic	3,164	5	2	7
0.864368	rs903506	24 PGAP3	0 intronic	6,234	5	2	7
0.864368	rs903506	24 PGAP3	0 intronic	5,932	5	2	5
0.868578	rs903506	24 PGAP3	0 intronic	5,338	4	2	7
0.864368	rs903506	24 PGAP3	0 intronic	5,804	4	2	7
0.868268	rs903506	24 PGAP3	0 intronic	5,616 NA		2	7
0.856957	rs903506	24 PGAP3	0 intronic	2,734 NA		2	7
0.868578	rs903506	24 PGAP3	0 intronic	0.863	4	2	7
0.882005	rs903506	24 PGAP3	0 intronic	7,183	4	2	7
0.868578	rs903506	24 PGAP3	0 intronic	Oct-23	4	2	5
0.868578	rs903506	24 PGAP3	0 intronic	6,495	4	2	5
0.868578	rs903506	24 PGAP3	0 intronic	2,904	4	4	5
0.868578	rs903506	24 PGAP3	0 intronic	8,827	4	2	5
0.882005	rs903506	24 PGAP3	0 intronic	2,231 NA		2	5
0.882005	rs903506	24 PGAP3	0 intronic	6,072	4	2	5
0.882005	rs903506	24 PGAP3	0 intronic	7,048	4	2	5
0.839156	rs903506	24 PGAP3	0 intronic	3,011	7	4	5

0.882005	rs903506	24 PGAP3	0 intronic	1,035	5	4	5
0.882005	rs903506	24 PGAP3	0 intronic	1,748	5	4	5
0.81282	rs903506	24 PGAP3	0 intronic	1,907 NA		4	5
0.913436	rs903506	24 PGAP3	0 intronic	0.647	5	4	5
0.841584	rs903506	24 PGAP3	0 intronic	5,933	4	1	5
0.913436	rs903506	24 PGAP3	0 intronic	May-16 2b		1	2
0.841584	rs903506	24 PGAP3	0 intronic	8,424	4	1	1
0.841584	rs903506	24 PGAP3:ERE	0:00 intronic	1,877	6	4	5
0.913436	rs903506	24 PGAP3:ERE	0:00 intronic	2,643	6	4	5
0.854662	rs903506	24 PGAP3:ERE	0:00 intronic	1,214 NA		5	5
0.837292	rs903506	24 PGAP3:ERE	0:00 intronic	0.264	6	5	5
0.846386	rs903506	24 PGAP3:ERE	0:00 intronic	0.264	6	5	5
0.921831	rs903506	24 PGAP3:ERE	0:00 intronic	7,231	6	5	5
0.921831	rs903506	24 PGAP3:ERE	0:00 intronic	7,231	6	5	5
0.904873	rs903506	24 PGAP3:ERE	0:00 UTR5	4,818	5	1	5
0.981127	rs903506	24 ERBB2	0 intronic	2,767	5	1	5
0.909361	rs903506	24 ERBB2	0 intronic	7,394	5	1	5
0.909361	rs903506	24 ERBB2	0 intronic	0.539	4	5	5
0.909361	rs903506	24 ERBB2	0 intronic	3,267	5	1	5
0.668816	rs903506	24 ERBB2	0 intronic	1,556 2b		1	7
0.904742	rs903506	24 ERBB2	0 intronic	Apr-74	5	1	4
0.954129	rs903506	24 ERBB2	0 intronic	2,193	6	4	4
0.909361	rs903506	24 ERBB2	0 intronic	3,071	5	4	5
0.918556	rs903506	24 ERBB2	0 intronic	5,026	5	4	5
0.913874	rs903506	24 ERBB2	0 intronic	1,259	5	4	5
0.96823	rs903506	24 ERBB2	0 intronic	2,579	5	4	5
0.918556	rs903506	24 ERBB2	0 intronic	2,296	6	4	5
	1 rs903506	24 ERBB2	0 intronic	4,731	4	2	5
0.964741	rs903506	24 ERBB2	0 intronic	2,449 NA		2	4
0.995291	rs903506	24 ERBB2	0 exonic	23-May	5	3	4
0.794745	rs903506	24 MIEN1	2200 intergenic	0.808 NA		5	14
0.80674	rs903506	24 GRB7	695 upstream	1,901	5	1	14
0.807564	rs903506	24 GRB7	185 downstream	0.157 NA		4	14
0.61497	rs228772	25 PYY	0 intronic	0.471 NA		5	14
0.666016	rs228772	25 PYY	0 intronic	0.718	6	5	14
0.648171	rs228772	25 PYY	0 intronic	3,649	4	1	11
0.747313	rs228772	25 PYY	0 intronic	2,402 NA		5	14
	1 rs1642594	25 PYY	0 intronic	4,158 NA		5	14
	1 rs1642594	25 PYY	0 intronic	3,555 NA		5	14
0.98571	rs1642594	25 PYY	0 intronic	0.652	6	5	14
0.747313	rs228772	25 PYY	0 intronic	4,661 NA		5	14
0.77054	rs228772	25 PYY	0 intronic	1,955 NA		5	14
0.887238	rs1642594	25 PYY	0 intronic	8,211	7	5	14
0.760698	rs228772	25 PYY	0 intronic	Dec-56	4	5	14
	1 rs228772	25 PYY	0 intronic	14.15	4	2	14
	1 rs228772	25 PYY	0 intronic	2,063	5	2	14
	1 rs228772	25 PYY	0 intronic	0.035	7	5	14
	1 rs228772	25 PYY	0 intronic	3,453 NA		1	14

1	rs228772	25 NAGS	0 intronic	Oct-62 NA		1	2
1	rs228772	25 NAGS	0 intronic	1,833 NA		1	1
1	rs228772	25 NAGS	0 intronic	8,083 NA		1	2
1	rs228772	25 NAGS	0 intronic	4,718	4	1	2
1	rs228772	25 NAGS	0 UTR3	0.619	4	2	5
1	rs228772	25 TMEM101	1054 intergenic	2,493 NA		4	5
1	rs228772	25 TMEM101	302 downstrea	Mar-92 NA		3	5
1	rs228772	25 TMEM101	165 downstrea	2,517 NA		3	5
1	rs228772	25 TMEM101	0 UTR3	2,241 3a		2	4
0.969609	rs228772	25 U3	4521 intergenic	4,419	5	4	4
0.866762	rs228772	25 LSM12	0 intronic	5,828 NA		4	5
0.969609	rs228772	25 LSM12	0 intronic	Oct-92	5	4	4
1	rs228772	25 LSM12	0 intronic	6,652 NA		4	5
1	rs228772	25 LSM12	0 intronic	2,186 NA		4	5
1	rs228772	25 LSM12	0 intronic	0.036	7	4	5
1	rs228772	25 LSM12	0 intronic	0.753	7	4	5
1	rs9913925	25 HDAC5	0 intronic	8,383 2b		4	4
0.624638	20:512728	26 RP4-723E3	0 ncRNA_int	Nov-41 NA		5	15
0.968309	20:512728	26 RP4-723E3	4845 intergenic	3,568 NA		7	15
1	20:512728	26 RP4-723E3	5831 intergenic	Jan-36	7	9	15
1	20:512728	26 RP4-723E3	5831 NA	1,282 NA		9	15

uniqID	rsID	chr	pos	non_effect_allele	effect_allele
1:954777:A:C	rs61766299	1	954777	A	C
1:956852:C:T	rs9777931	1	956852	T	C
1:959169:C:G	rs3845292	1	959169	C	G
1:960409:C:G	rs4970392	1	960409	C	G
1:984302:C:T	rs9442391	1	984302	C	T
1:1018144:C:T	rs9442395	1	1018144	C	T
7:28173522:C:T	rs702815	7	28173522	T	C
7:28174957:A:G	rs849136	7	28174957	G	A
9:37192988:A:C	rs10973246	9	37192988	C	A
9:37198176:C:T	rs10973250	9	37198176	C	T
9:37295658:A:G	rs10973291	9	37295658	A	G
17:26216090:C:T	rs7224724	17	26216090	C	T
17:26216356:A:G	rs9903233	17	26216356	A	G
17:26216397:A:G	rs7220420	17	26216397	G	A
17:26220355:G:T	rs4063521	17	26220355	T	G
17:37810218:C:G	rs881844	17	37810218	G	C
17:37815899:A:G	rs11658786	17	37815899	A	G
17:37821435:G:T	rs931992	17	37821435	T	G
17:37822311:A:C	rs1053651	17	37822311	C	A
17:37828496:C:T	rs2952151	17	37828496	C	T
17:37828745:A:G	rs2941503	17	37828745	G	A
17:37828787:A:G	rs907087	17	37828787	A	G
17:37830900:A:G	rs2941504	17	37830900	G	A
17:37831304:C:G	rs10558975	17	37831304	G	C
17:37832704:A:G	rs2941505	17	37832704	G	A
17:37832735:C:T	rs2952152	17	37832735	C	T
17:37833035:A:G	rs2941506	17	37833035	G	A
17:37833805:C:T	rs9675194	17	37833805	C	T
17:37833842:C:T	rs2313171	17	37833842	C	T
17:37834541:C:T	rs12150298	17	37834541	C	T
17:37834715:A:G	rs12150603	17	37834715	A	G
17:37834977:G:T	rs8077172	17	37834977	T	G
17:37834998:C:T	rs8078228	17	37834998	T	C
17:37835240:C:T	rs1018246	17	37835240	T	C
17:37835755:C:T	rs11078919	17	37835755	C	T
17:37836353:C:T	rs9303274	17	37836353	C	T
17:37836581:A:G	rs12940986	17	37836581	A	G
17:37843550:C:T	rs2517954	17	37843550	C	T
17:37843681:C:T	rs2517955	17	37843681	T	C
17:37843859:A:G	rs2517956	17	37843859	A	G
17:37854507:G:T	rs2934971	17	37854507	T	G
17:37861718:C:T	rs2952155	17	37861718	C	T
17:37879762:A:G	rs903506	17	37879762	A	G
17:42085352:C:G	rs170639	17	42085352	C	G
17:42086180:C:T	rs640631	17	42086180	T	C
17:42088853:A:G	rs12889	17	42088853	A	G
17:42155838:A:G	rs9913925	17	42155838	A	G

MAF	gwasP	beta	se	r2	IndSigSNP	GenomicLocus
0.4404	0.0001371	0.0822986227211	0.0216	0.666382	rs9442391	1
0.4473	7.32E-02	0.0859024290007	0.0217	0.65504	rs9442391	1
0.4503	0.0001528	0.0829983354992	0.0219	0.713069	rs9442391	1
0.4404	8.78E-03	0.0970994871297	0.0219	0.824816	rs9442391	1
0.4364	3.88E-03	0.0999991692905	0.0216		1 rs9442391	1
0.4414	0.002115	0.0648978315778	0.0211	0.683074	rs9442391	1
0.2584	0.009935	0.0553022477847	0.0215	0.683395	rs10226758	7
0.2584	0.01041	0.0548952993716	0.0214	0.683395	rs10226758	7
0.1461	4.27E-02	-0.103695236339	0.0253	0.922382	rs4483247	10
0.1461	3.95E-02	-0.104094650537	0.0253	0.922382	rs4483247	10
0.1471	3.84E-02	-0.104505325881	0.0254	0.930295	rs4483247	10
0.3022	6.53E-03	0.0944006754215	0.0209	0.973199	rs7218395	23
0.3022	6.95E-03	0.0930986452544	0.0207	0.973199	rs7218395	23
0.2435	0.001408	0.0701042536729	0.022	0.752624	rs7218395	23
0.3032	1.08E-02	0.0911013350303	0.0207	0.977732	rs7218395	23
0.332	0.00333	0.0600032523358	0.0204	0.695709	rs903506	24
0.326	0.002181	0.0625991417565	0.0204	0.717135	rs903506	24
0.326	0.002004	0.0632001258861	0.0205	0.717135	rs903506	24
0.2783	0.001838	0.0674997573466	0.0217	0.635016	rs903506	24
0.3141	0.0002256	0.0777015076639	0.0211	0.828601	rs903506	24
0.3141	0.0002186	0.0778957893081	0.0211	0.828601	rs903506	24
0.3111	0.0002733	0.0767017482634	0.0211	0.815947	rs903506	24
0.3101	0.000362	0.0750981960059	0.021	0.819962	rs903506	24
0.325	NA	NA	NA	0.894031	rs903506	24
0.3191	0.0005183	0.0750981960059	0.0216	0.894611	rs903506	24
0.3181	0.0002297	0.0763960667533	0.0207	0.890365	rs903506	24
0.3191	0.0002287	0.0764979709727	0.0207	0.894611	rs903506	24
0.325	0.0005149	0.0713993070303	0.0205	0.868578	rs903506	24
0.3241	0.0004974	0.0715017216887	0.0205	0.864368	rs903506	24
0.325	0.0004454	0.0721997240344	0.0205	0.868578	rs903506	24
0.328	0.0003674	0.0731017517981	0.0205	0.882005	rs903506	24
0.325	0.0004473	0.0720973808404	0.0205	0.868578	rs903506	24
0.325	0.000447	0.0720973808404	0.0205	0.868578	rs903506	24
0.325	0.0004492	0.0720973808404	0.0206	0.868578	rs903506	24
0.325	0.0004651	0.0719019692891	0.0206	0.868578	rs903506	24
0.328	0.0003754	0.0729995008835	0.0205	0.882005	rs903506	24
0.328	0.0003933	0.0728042655546	0.0205	0.882005	rs903506	24
0.3191	3.53E-02	0.0853975755122	0.0206	0.841584	rs903506	24
0.335	1.92E-02	0.0870030436216	0.0204	0.913436	rs903506	24
0.3191	3.60E-02	0.0852965742221	0.0206	0.841584	rs903506	24
0.3101	6.76E-02	0.0871955266997	0.0219	0.909361	rs903506	24
0.2505	0.0001084	0.0874979252725	0.0226	0.668816	rs903506	24
0.328	2.05e-06	0.0983963218562	0.0207		1 rs903506	24
0.0328	2.27E-02	0.179901965275	0.0425		1 rs228772	25
0.0328	1.21E-02	0.185200741295	0.0423		1 rs228772	25
0.0328	2.36E-02	0.179500915857	0.0425		1 rs228772	25
0.1262	2.82E-03	-0.131499173268	0.0281		1 rs9913925	25

nearestGene	dist	func	CADD	RDB	minChrState	commonChrState
AGRN		725 upstream	4,289	4	1	2
AGRN		0 intronic	Nov-81	4	1	2
AGRN		0 intronic	0.069	3a	2	7
AGRN		0 intronic	3,401	4	1	7
AGRN		0 exonic	Mar-13	4	4	5
C1orf159		0 UTR3	1,347	4	3	5
JAZF1		0 intronic	1,109	4	5	5
JAZF1		0 intronic	8,683	4	5	5
ZCCHC7		0 intronic	20-Jan	4	2	5
ZCCHC7		0 intronic	5,898	3a	2	5
ZCCHC7		0 intronic	1,882	4	2	5
RP1-66C13.4:LYRM9	0:00	intronic	6,021	4	2	5
RP1-66C13.4:LYRM9	0:00	intronic	0.565	4	5	5
RP1-66C13.4:LYRM9	0:00	intronic	0.077	2b	5	5
RP1-66C13.4:LYRM9	0:00	UTR5	14-Aug	2b	1	1
STARD3		0 intronic	4,856	2b	2	5
STARD3		0 intronic	May-21	4	2	4
TCAP		0 UTR5	3,558	2b	1	5
TCAP		0 exonic	15-Jul	4	1	7
PGAP3		0 UTR3	3,808	2b	2	7
PGAP3		0 UTR3	1,933	4	2	5
PGAP3		0 UTR3	5,518	2b	2	5
PGAP3		0 exonic	16.51	4	2	5
PGAP3		0 intronic	15-Feb	4	2	7
PGAP3		0 intronic	0.924	3a	2	7
PGAP3		0 intronic	8,336	4	2	7
PGAP3		0 intronic	8,419	3a	2	7
PGAP3		0 intronic	5,338	4	2	7
PGAP3		0 intronic	5,804	4	2	7
PGAP3		0 intronic	0.863	4	2	7
PGAP3		0 intronic	7,183	4	2	7
PGAP3		0 intronic	Oct-23	4	2	5
PGAP3		0 intronic	6,495	4	2	5
PGAP3		0 intronic	2,904	4	4	5
PGAP3		0 intronic	8,827	4	2	5
PGAP3		0 intronic	6,072	4	2	5
PGAP3		0 intronic	7,048	4	2	5
PGAP3		0 intronic	5,933	4	1	5
PGAP3		0 intronic	May-16	2b	1	2
PGAP3		0 intronic	8,424	4	1	1
ERBB2		0 intronic	0.539	4	5	5
ERBB2		0 intronic	1,556	2b	1	7
ERBB2		0 intronic	4,731	4	2	5
NAGS		0 intronic	4,718	4	1	2
NAGS		0 UTR3	0.619	4	2	5
TMEM101		0 UTR3	2,241	3a	2	4
HDAC5		0 intronic	8,383	2b	4	4

uniqID	rsID	chr	pos	non_effect	effect_allele	MAF	gwasP	beta
1:954777:A:C	rs61766299	1	954777	A	C	0.4404	0.00013710	0.0822986
1:956852:C:T	rs9777931	1	956852	T	C	0.4473	7.32E-02	0.0859024
1:959169:C:G	rs3845292	1	959169	C	G	0.4503	0.00015280	0.0829983
1:960409:C:G	rs4970392	1	960409	C	G	0.4404	8.78E-03	0.0970994
1:1018144:C:T	rs9442395	1	1018144	C	T	0.4414	0.002115	0.0648978
17:26216090:C:T	rs7224724	17	26216090	C	T	0.3022	6.53E-03	0.0944006
17:26216356:A:G	rs9903233	17	26216356	A	G	0.3022	6.95E-03	0.0930986
17:26216397:A:G	rs7220420	17	26216397	G	A	0.2435	0.001408	0.0701042
17:26220355:G:T	rs4063521	17	26220355	T	G	0.3032	1.08E-02	0.0911013
17:37843550:C:T	rs2517954	17	37843550	C	T	0.3191	3.53E-02	0.0853975
17:37843681:C:T	rs2517955	17	37843681	T	C	0.335	1.92E-02	0.0870030
17:37843859:A:G	rs2517956	17	37843859	A	G	0.3191	3.60E-02	0.0852965
17:42155838:A:G	rs9913925	17	42155838	A	G	0.1262	2.82E-03	-0.131499

se	r2	IndSigSNP	GenomicL	nearestGene	dist	func	CADD	RDB
0.0216	0.666382	rs9442391	1	AGRN	725	upstream	4,289	4
0.0217	0.65504	rs9442391	1	AGRN	0	intronic	Nov-81	4
0.0219	0.713069	rs9442391	1	AGRN	0	intronic	0.069	3a
0.0219	0.824816	rs9442391	1	AGRN	0	intronic	3,401	4
0.0211	0.683074	rs9442391	1	C1orf159	0	UTR3	1,347	4
0.0209	0.973199	rs7218395	23	RP1-66C13.4:LYRM9	0:00	intronic	6,021	4
0.0207	0.973199	rs7218395	23	RP1-66C13.4:LYRM9	0:00	intronic	0.565	4
0.022	0.752624	rs7218395	23	RP1-66C13.4:LYRM9	0:00	intronic	0.077	2b
0.0207	0.977732	rs7218395	23	RP1-66C13.4:LYRM9	0:00	UTR5	14-Aug	2b
0.0206	0.841584	rs903506	24	PGAP3	0	intronic	5,933	4
0.0204	0.913436	rs903506	24	PGAP3	0	intronic	May-16	2b
0.0206	0.841584	rs903506	24	PGAP3	0	intronic	8,424	4
0.0281		1 rs9913925	25	HDAC5	0	intronic	8,383	2b

minChr	Stacommon	CleQTL gene	eQTL tissue
1	2	RP11-5407.17	eQTLcatalogue/BrainSeq
1	2	AGRN, RP11-5407.17	eQTLcatalogue/BrainSeq
2	7	RP11-5407.17	eQTLcatalogue/BrainSeq
1	7	C1orf159, RP11-465B22.3,	eQTLcatalogue/BrainSeq
3	5	C1orf159, RP11-465B22.3,	eQTLcatalogue/BrainSeq
2	5	NOS2	PsychENCODE_eQTLs:CM
5	5	NOS2	PsychENCODE_eQTLs:CM
5	5	NOS2	PsychENCODE_eQTLs:CM
1	1	NOS2	PsychENCODE_eQTLs:CM
1	5	ORMDL3	PsychENCODE_eQTLs, CM
1	2	ORMDL3	CMC_SVA_cis
1	1	ORMDL3	CMC_SVA_cis
4	4	SLC25A39, RUNDC3A	xQTLServer_eQTLs, CMC

Hci cell type

Promoter_anchored_loops, Adult_Cortex

Promoter_anchored_loops, Adult_Cortex

Promoter_anchored_loops, Adult_Cortex, EP_links_oneway

Promoter_anchored_loops, EP_links_oneway

Promoter_anchored_loops

Promoter_anchored_loops, Hippocampus, Fetal_Cortex, Adult_Cortex, Neural_Progenitor_Cell

Promoter_anchored_loops, Hippocampus, Fetal_Cortex, Adult_Cortex, Neural_Progenitor_Cell

Promoter_anchored_loops, Hippocampus, Fetal_Cortex, Adult_Cortex, Neural_Progenitor_Cell

Promoter_anchored_loops, Hippocampus, Fetal_Cortex, Adult_Cortex, Neural_Progenitor_Cell

Adult_Cortex

Adult_Cortex

Adult_Cortex

Adult_Cortex, Fetal_Cortex

Rebuttal Letter

Dear Editor,

We are pleased to have an opportunity to revise our manuscript entitled “Functional Annotation of Bipolar Disorder 2 Risk Location Implicates Novel Susceptibility Genes” (NPS-2024-6-5 INVITED). In the revised manuscript, we have carefully considered the reviewers’ comments and suggestions, which were very helpful overall. Herein, we have attempted to reply to each comment point-by-point. After addressing the issues raised, we feel the quality of the paper is much increased. We hope that the reviewers and the editor will be satisfied with the further amendments.

Sincerely and respectfully yours.

Dr. Güneş Şayan Can

Reviewer 1:

Comments to authors

In their manuscript authors conducted a re-analysis of previously published GWAS data to specifically identify genes associated with BD2. The manuscript requires more detailed description in some sections.

Authors should provide the reference for the PGC-BD study used to run FUMA.

Authors’ response: We thank the reviewer. The PGC-BD data (Mullins et al. 2021) used in this study has been cited can be found as reference #8 under the “References” section. Also, this study is now cited under the Methods section, Line 78.

Reviewer 1:

Moreover, they should also provide details on the number of BD 2 samples included in the reference dataset. Authors reported the sample size, but it is not clear how the data were managed. Was the FUMA analysis run on a sub-sample from PGC only including BD2 samples? how was this performed exactly?

Authors’ response: We have added more detailed information about the data that was used in this study, how it was obtained and managed, with explicit details on the sample sizes. Yes, the FUMA analysis was run on a sub-sample from PGC only including BD2 samples, with the help of individual level data being labeled with the type of BD (i.e., BD1 or BD2). The following text was added to the Methods section, between Lines 76-86:

“.....The largest BD2 GWAS data we used in our study is a subset of a GWAS meta-analysis of 57 BD cohorts collected in Europe, North America and Australia, totaling 41,917 individuals with BD (cases) and 371,549 controls [8]. The BD sample in this meta-analysis consisted of BD1 (25,060 cases), BD2 (6,781 cases) and BD NOS (not otherwise specified) (10,076 cases). The included cases met international consensus criteria for lifetime BD (DSM-IV, ICD-9 or ICD-10), as determined using structured diagnostic interviews, clinician-administered checklists or medical record review. The authors shared individual-level genotype and phenotype data for 52 cohorts (5 cohorts were excluded) with Psychiatric Genomics Consortium (PGC). In PGC, these data are available as 3 different GWAS

summary statistics files for all BD cases, BD1 cases only and BD2 cases only
([https://figshare.com/articles/dataset/PGC3 bipolar disorder GWAS summary statistics/14102594](https://figshare.com/articles/dataset/PGC3_bipolar_disorder_GWAS_summary_statistics/14102594))."

Reviewer 1:

The p-value reported for the "Independently Significant SNPs" is not in line with the standard for GWAS studies. Authors should explain the criteria to set this threshold.

Authors' response: We have added the rationale behind using a 'sub-threshold' significance level and provided references (reference#15-17) to some of the supporting literature in the Methods section, Lines 92-98, as follows:

".....Independently Significant SNPs: These are SNPs with a p-value below 5×10^{-5} and are independent from each other with $r^2 < 0.6$. While Some SNPs below the conventional genome-wide significance threshold ($p < 5 \times 10^{-8}$) is commonly used in genomic studies, this approach is applied at the expense of the false-negative rate [15]. Indeed, several studies have shown that a substantial portion of variants with 'sub-threshold' significance ($p < 5 \times 10^{-5}$) may still indicate actual disease risk loci [16, 17]. In a study by Wang et al., they examined SNPs associated with cardiac QT interval, finding that 'sub-threshold' SNPs ($p < 5 \times 10^{-5}$) were significantly present in predicted cardiac enhancers [18]."

In short, the main idea behind using a sub-threshold significance level is that use of the conventional genome-wide significance level of $p < 5 \times 10^{-8}$ could cause missing some critical variants that do not reach significance level due to limitations of the GWAS and therefore lead to increased false-negative rate.

Reviewer 1:

Overall, the manuscript would benefit from professional proof-reading.

Authors' response: We have thoroughly reviewed the manuscript to correct the grammatical mistakes and make improvements to the text for clarity and better reading.

Reviewer 2:

Comments to authors

Abstract: The abstract puts the research into a general and specific background and explains broadly why the study matters. Key findings are provided. It should be noted that the research question should be formulated more precisely in the abstract and/or at least in the introduction.

Authors' response: We would like to thank the reviewer for this constructive criticism. We agree and have modified the abstract accordingly to state the research question more precisely. We believe the following statements in the abstract should address this concern, between Lines 15-17:

".....However, in contrast to bipolar 1 disorder, studies investigating causal and functional genes are lacking. This study aims to identify and prioritize causal genetic variants and genes for BD2 by analyzing brain-specific gene expression markers, to improve the understanding of its genetic underpinnings and support advancements in diagnosis, treatment and prognosis."

Reviewer 2:

General remarks: Care should be taken to ensure that abbreviations are used correctly and written out in full when first mentioned.

Authors' response: We have gone through the manuscript to make the necessary corrections with regard to this point; gene names were italicized while protein names were not, and all abbreviations were written out in full when first mentioned.

Reviewer 2:

In addition, the study has not been approved by an ethics committee. This should be obtained in any case!

Authors' response: We would like to thank the reviewer for raising this point. Accordingly, we applied to the Ethics Review Committee of Izmir Biomedicine and Genome Center (IBG) with application title "Functional Annotation of Bipolar 2 Disorder Risk Loci and Investigation of New Susceptibility Genes" and have obtained their approval with the **protocol number 2024-033**. This point has been added under the Statement of Ethics section between Lines 261-263.