Whole genome sequencing identifies putative associations between genomic polymorphisms and clinical response to the antiepileptic drug *levetiracetam*

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ABSTRACT

In the context of pharmacogenomics, whole genome sequencing provides a powerful approach for identifying correlations between response variability to specific drugs and genomic polymorphisms in a population, in an unbiased manner. In this study, we employed whole genome sequencing of DNA samples from patients showing extreme response (n=72) and non-response (n=27) to the antiepileptic drug levetiracetam, in order to identify genomic variants that underlie response to the drug. Although no common SNP (MAF>5%) crossed the conventional genome-wide significance threshold of 5×10^{-8}, we found common polymorphisms in genes *SPNS3*, *HDC*, *MDGA2*, *NSG1* and *RASGEF1C*, which collectively predict clinical response to levetiracetam in our cohort with ~91% predictive accuracy (~94% positive predictive value, ~85% negative predictive value). Among these genes, *HDC*, *NSG1*, *MDGA2 and RASGEF1C* are potentially implicated in synaptic neurotransmission, while *SPNS3* is an atypical solute carrier transporter homologous to *SV2A*, the known molecular target of levetiracetam. Furthermore, we performed gene- and pathway-based statistical analysis on sets of rare and low-frequency variants (MAF<5%) and we identified associations between genes or pathways and response to levetiracetam. Our findings include a) the genes *PRKCB* and *DLG2*, which are involved in glutamatergic neurotransmission, a known target of anticonvulsants, including levetiracetam; b) the genes *FILIP1* and *SEMA6D*, which are involved in axon guidance and modelling of neural connections; and c) pathways with a role in synaptic neurotransmission, such as *WNT5A-dependent internalization of FZD4* and *disinhibition of SNARE formation*. Targeted analysis of genes involved in neurotransmitter release and transport further supports the possibility of association between drug response and genes *NSG1* and *DLG2*. In summary, our approach to utilise whole genome sequencing on subjects with extreme response phenotypes is a feasible route to generate plausible hypotheses for investigating the genetic factors underlying drug response variability in cases of pharmaco-resistant epilepsy.

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INTRODUCTION

The advent of next-generation sequencing (NGS) has made possible the routine reconstruction of an individual's genetic variation profile across their whole genome[1,2], while the introduction of NGS to clinical practice brings closer the promise of personalised medicine for diagnostic sensitivity and therapeutic precision[3,4]. In the context of pharmacogenomics, whole exome and genome sequencing combined with appropriate bioinformatics and statistical analysis has the potential to identify variants that correlate with clinical response to specific drugs, in a comprehensive, high-resolution and unbiased manner[5–12], i.e. without the need for a prior hypothesis regarding the type (e.g. common or rare), location or distribution of genomic polymorphisms across the whole extent of the genome. We employed whole genome sequencing to better understand response variability to the antiepileptic drug levetiracetam (LEV), a third-generation first-line drug for the treatment of both focal and generalised epilepsies, for which high variability of clinical response is observed.

Experiments in mice show that *SV2A*, but not its paralogs *SV2B* and *SV2C*, is the molecular target of LEV[13]. *SV2A* is a synaptic glycoprotein with widespread distribution in the brain[14] and a crucial role in synaptic vesicle exocytosis[15]. Mice deficient in SV2 functionality exhibit severe seizures with a concomitant reduction in (inhibitory) GABAergic neurotransmission[16] and an abnormal presynaptic accumulation of calcium leading to increased neurotransmitter release[17]. LEV inhibits presynaptic calcium channels[18] and calcium-dependent vesicle exocytosis[19], and it reverses synaptic deficits due to overexpression of *SV2A*[20]. However, its exact mechanism of action as an antiepileptic drug is not understood.

It is natural to hypothesize that LEV may act by modifying deregulated *SV2A*-dependent neurotransmission and that variability in SV2A functionality may explain differential responsiveness to treatment with LEV. This view is supported by reports showing that partial loss of SV2A functionality is linked to decreased LEV efficacy in several mice seizure models[21], or that levels of SV2A expression in tumour and peri-tumoral tissue predicts clinical response to LEV in patients with glioma[22]. However, neither common nor rare polymorphisms in *SV2A* (including polymorphisms overlapping its binding site with LEV) are associated with clinical response to the drug, based on targeted sequencing approaches[23,24]. Any role of genetic variation (either rare or common) in other genomic loci as potential predictors of LEV efficacy remains to be elucidated.

We analysed whole genome sequencing (WGS) data from 99 people with epilepsy, classified as extreme responders (n=72) or non-responders to LEV (n=27), aiming to explore the genetic differences between the two groups and to identify rare or common polymorphisms that may be predictive of the response/non response phenotype. Using whole genome sequencing (instead of targeted sequencing or genome-wide SNP arrays) facilitates the search for genetic predictors to LEV in a complete, high-resolution and unbiased manner. At the same time, a targeted search for genomic features associated with response to LEV is still possible. Here, we identified common polymorphisms which collectively predict a substantial fraction of clinical response to the drug in our cohort of patients with epilepsy. Furthermore, analysis of groups of low-frequency variants highlights significant associations between response to LEV and genes involved in synaptic neurotransmission, axon guidance and modelling of neural connections.

METHODS

Sample acquisition and whole genome sequencing

The study was approved by the relevant local ethics committee. Patients provided written informed consent, or in the case of people unable to provide consent, assent was obtained from parents or guardians as permitted within the approved protocol.

Ninety-nine unrelated adults with a range of types of epilepsy were recruited from the National Hospital for Neurology and Neurosurgery. Non-responders (n=27; ~27%) were defined as patients who had failed to respond to at least two of the currently established epilepsy treatments and had not responded to maximum tolerated doses of levetiracetam used for at least 12 months. Extreme responders were defined as patients who became seizure-free for at least 12 months after initiation of levetiracetam and who had not previously responded to at least three appropriately chosen and used antiepileptic drugs (AEDs; n=72; ~73%).

Samples from the above subjects were sequenced at the Oxford Genomics Centre using the HiSeq2500 platform, v3 chemistry and the 100bp paired-end read format (Illumina, San Diego, CA). Sequencing was performed across 2.3 lanes per sample at depth 30X (Figure 1).

Bioinformatics analysis

Reads were mapped to hs37d5 using BWA[25] and duplicate reads were removed using the MarkDuplicates option from the Picard toolkit[26] all with default options. Variants were called simultaneously across all 99 samples with Platypus[27] v0.7.9.3 resulting in a multi-sample VCF file. Read alignments were checked visually using the Integrative Genomics Viewer v2.3.5[28].

In total, ~20M variants were called across all samples (Figure 1). We excluded variants in multi-allelic loci or in sex chromosomes, variants with FILTER flag other than PASS, and variants in homopolymers with running length larger than 8 base pairs (HP>8). We excluded genotypes of low quality (PHRED score GQ<20), and with less than 10 reads covering the variant location (DP<10). We also excluded variants not in Hardy-Weinberg Equilibrium[29] (p-value less than 10^{-6}) and with missing genotypes in more than 2 individuals (~2%). Furthermore, we excluded variants in low complexity regions[30], in poor mappability regions[31], in segmental duplications[32] and in the top 1% most variable genes according to Ingenuity IVA[33]. On the remaining ~8.4M variants, we conducted principal component analysis using the *prcomp* function in R[34] and we identified 7 outlier samples, which were excluded from further analysis (Figure 2A,B). We did not find evidence of association between clinical response and sex in the remaining 92 patients (Figure 2C). The filtered data were annotated using the Ensembl Variant Effect Predictor[35] software v90.5 with allele frequency annotations provided by gnomAD r2.0.1[36] and variant IDs provided by dbSNP[37] build 150. Overall, we reviewed ~3.9M common variants (MAF>5%), and ~4M low-frequency (1%<MAF<5%) and rare variants (MAF<1%) (Figure 2D,E).

Statistical analysis

We conducted single-variant tests on common variants, and gene- and pathway-based tests on low-frequency and rare variants (Figure 1). In the case of common variants, we calculated SNP-specific p-values by applying a two-tailed Fisher's exact test on each common variant (Figure 3A). In a pre-specified second stage, we selected a small subset of variants by using all variants with p-value less than the conventional suggestive genome-wide significance threshold of 10^{-5} (n=23 variants; Table S1 and Figure 3A, white dots) as predictors (along with sex) in a penalised logistic regression model[38] (known as the *LASSO*; Figure 3B). An optimal penalisation parameter was estimated using leave-one-out cross-validation. This resulted in the selection of 10 out of 23 variants with maximal predictive power (Figure 3B, red dots). An additional selection step was applied by filtering out all variants (among those selected by the LASSO in the previous step) that had non-protein-coding gene annotation or were annotated as *intergenic*. This resulted in the final selection of 5 variants with protein-coding gene annotations (Table S1). The reason for this final selection step was to avoid overfitting during the downstream analyses described below and because the selection of variants in protein-coding genes (instead of non-protein coding or intergenic variants) facilitates the subsequent investigation of their possible biological relevance. After variant selection, we conducted an analysis of deviance by examining a series of logistic regression models using response to LEV as the dependent variable (Table S2). The BASIC model includes, besides the intercept, a single predictor, sex. The FULL model includes in addition the genotypes of the previously selected variants. A number of intermediate models are simple extensions of the BASIC model through the inclusion of just one of these variants. Finally, we calculated the predictive power of the FULL model using leave-one-out cross-validation and the accuracy (ACC), sensitivity (TPR), specificity (TNR), positive (PPV) and negative (NPV) predictive values, and Matthews correlation coefficient (MCC) as metrics of predictive power. For completeness, we also conducted auxiliary statistical analyses, which included a genome-wide Bayesian analysis and calculation of bespoke genome-wide significance thresholds (see Supplementary Material for more details).

In the case of rare and low-frequency variants, we first calculated a variant-specific p-value by applying a two-tailed Fisher's exact test, as in the case of the common variants. Subsequently, we aggregated all variant-specific p-values in a gene- or pathway-specific statistic using an appropriately corrected Fisher's product method[39] (see Supplementary Material), which takes into account the effective number of independent variants in a group of variants, thus correcting for correlations between variants in the same gene or pathway. The resulting statistic was used to calculate a gene- (Table S3) or pathway-specific (Table S4) p-value for testing the null hypothesis that none of the variants in the gene/pathway are associated with response to LEV, against the alternative hypothesis that at least one variant in the set is associated with response to LEV. P-values were corrected for multiple hypothesis testing across all genes or pathways using Sidak's method.

Finally, we conducted a targeted analysis of common and rare variants in a set of genes implicated in neurotransmitter transport and release and in a set of genes associated with epilepsy (Table S5). For the common variants, we tested each variant individually using a two-tailed Fisher's exact test of independence, as above. We used Sidak's method for multiplicity correction across all genes in each of the two sets. The effective number of independent variants was estimated by first calculating a gene-specific estimate of the number of independent variants using four alternative methods[39–43], followed by summing these estimates over all genes. All four methods returned consistent results. For the rare variants, we calculated gene-specific p-values followed by multiplicity correction using the Sidak method, as before.

More details on the statistical analysis are given in the Supplementary Material.

RESULTS

Common polymorphisms in genes *SPNS3*, *HDC*, *NSG1*, *MDGA2* and *RASGEF1C* predict clinical response to LEV in our cohort with overall accuracy ~91%

We constructed a statistical model that utilises common genomic variation to predict response to LEV in our cohort. Towards this aim, we first assessed the significance of association between each SNP and response to LEV (Figure 3A). The smallest SNP-specific p-value calculated at this stage was 1.6×10^{-7}, i.e. no p-value crossed the conventional genome-wide significance threshold of 5×10^{-8} (Table S1). This was followed by a principled SNP selection process (see Methods) to identify a minimal set of highly predictive variants (n=5 variants). These are located in the protein-coding genes *SPNS3*, *HDC*, *NSG1*, *MDGA2* and *RASGEF1C*, as indicated by the non-zero coefficients in Figure 1B. Variants with non-zero coefficients in the non-coding genes *RP11-284F21.8*, *RP11-446J8.1* and *RP11-650J17.1*, as well as two intergenic variants in chromosome 15, were not included, in order to keep the model small and avoid overfitting (see Methods for rationale). All these variants are listed in Supplementary Table S1.

At the next stage, we conducted an analysis of deviance on the polymorphisms identified in the previous step (see Methods and Table S2). We found that the inclusion of these SNPs in a logistic regression model reduces the residual deviance from ~107 (BASIC model) to ~28 (FULL model), thus significantly improving the goodness of fit (p-value=1.15×10^{-15} based on a χ^2 test) of the model to the data. The fraction of explained deviance in the data was assessed using a pseudo-R^2 metric, the adjusted D^2, as described in Guisan & Zimmermann[44]. The BASIC and FULL models have an adjusted D^2 equal to 1% and 73%, respectively, which implies that the identified variants in genes *SPNS3*, *HDC*, *NSG1*, *MDGA2* and *RASGEF1C* collectively explain ~72% of the total deviance (Table S2). When considering just a single gene as predictor (as in any of the intermediate models between BASIC and FULL), the improvement in model fit is significant (as indicated by the low p-values). Furthermore, the proportion of explained deviance by SNPs in each gene ranges between 10% (*HDC*) and 21% (*SPNS3*), as inferred by comparing the adjusted D^2 value for each of the intermediate models to the adjusted D^2 value of the BASIC model.

Subsequently, we assessed the predictive power of the FULL model using leave-one-out cross-validation. In brief, this involves fitting the FULL model in all but one subjects and predicting the response phenotype of the held-out subject using the fitted model. This process of model fitting and prediction is repeated until all 92 subjects have been used for prediction. We found that the FULL model correctly predicts clinical response to LEV in 62 responders and 22 non-responders, which corresponds to ~94% sensitivity (TPR) and positive predictive value (PPV), ~85% specificity (TNR) and negative predictive value (NPV), and ~91% overall predictive accuracy

(ACC). The Matthews correlation coefficient (MCC), a balanced performance metric for binary classifiers even when the two classes are of very different size, was equal to ~79%.

Local genomic structure near the identified variants and possible biological relevance

For gene *NSG1* on chromosome 4, three highly correlated SNPs (rs7695197, rs3981 and rs12641832) are located ~5kb upstream of the gene, less than 3kb upstream or downstream of transcription factor binding sites (TFBS) and DNaseI hypersensitivity sites (DHS), and less than 5kb upstream of a small cluster of conserved elements (CE; Figure 4A). The odds ratio for a recessive model (with respect to the ALT allele) is ~23 times in favour of the non-responders, while the corresponding odds ratio for a dominant model is ~2.7 (see Table S1 for the number of homozygous/heterozygous cases in each group). In other words, non-responders to LEV are ~23 times more likely to be homozygous for the alternative allele than responders. *NSG1* (Neuronal Vesicle Trafficking Associated 1) is abundantly expressed in the brain[45,46] and it plays a role in synaptic neurotransmission and plasticity due to its involvement in recycling and trafficking of receptors, such as the glutamate receptor AMPA, the amyloid precursor protein (APP), and the L1 cell adhesion molecule (L1CAM)[47].

The intronic variant rs34570575 in gene *RASGEF1C* on chromosome 5 overlaps a DHS and it is located ~5kb upstream of a TFBS and a cluster of CE (Figure 4B). The odds ratio for a dominant model of inheritance (with respect to the ALT allele) is slightly higher than that of a recessive model (~9.5 and ~8, respectively; Table S1). *RASGEF1C* (RAS guanyl-nucleotide exchange factor domain family member 1C) is abundantly expressed in the brain[45,46]. It belongs to a family of proteins containing the RASGEF domain, which regulates the GTPase activity of RAS-like proteins. These comprise a superfamily of membrane-associated signalling molecules involved in a variety of essential cellular processes, including vesicle trafficking and synaptic function[48–50].

In gene *MDGA2* on chromosome 14, rs1952220 is an intronic variant, less than ~4kb from CE, TFBS and DHS (Figure 4C). The odds ratios for recessive and dominant models (with respect to the ALT allele) are 0.11 and 0.61 in favour of the non-responders, respectively, suggesting a recessive model where non-responders to LEV are ~9 times less likely to be homozygous for the alternative allele than responders (Table S1). The *MDGA2* (MAM Domain Containing Glycosylphosphatidylinositol Anchor 2) mRNA is expressed in the cerebral cortex[45,46]. MDGAs are Ig superfamily cell adhesion molecules that contribute to the radial migration of cortical neurons during early neural development. They play an important, neuroglin-2-dependent role in controlling the function of inhibitory synapses, and they have been associated with autism spectrum disorders and schizophrenia[51,52].

In gene *HDC* on chromosome 15, rs7182203 is an intronic variant that overlaps a TFBS and a DHS, and it is within 5kb of upstream or downstream CE (Figure 4D). From Table S1, the odds ratios for recessive and dominant models (with respect to the ALT allele) are 1.1 and 0.12 in favour of the non-responders, respectively. This implies that patients that respond to LEV are ~8 times more likely to be homozygous or heterozygous for the alternative allele in comparison to non-responders. *HDC* (histidine decarboxylase) is expressed in the brain[45,46], and it catalyses the synthesis of histamine, which is implicated, among others, in neurotransmission and smooth muscle tone. Elevated levels of histamine in the brain appear to suppress seizures and confer neuroprotection, thus antiepileptic agents that boost the levels of histamine in the brain may act by increasing *HDC* activity[53]. Furthermore, *HDC* has been linked to the pathogenesis of Tourette's syndrome[54]. Interestingly, LEV has been used for the treatment of Tourette's syndrome, although its efficacy has not been established[55–57].

Finally, in gene *SPNS3* on chromosome 17, the intronic variants rs2047231, rs2047232 and rs2047233 overlap a DHS and a cluster of CE, and they are located within 5kb of upstream or downstream TFBS (Figure 4E). From Table S1, the odds ratio for a recessive model (with respect to the ALT allele) ranges among these three SNPs between 0.07 and 0.09 in favour of non-responders. This implies that patients responding to LEV are between ~11 and ~14 times more likely to be homozygous for the alternative allele than non-responders. *SPNS3* (a putative sphingolipid transporter 3) is expressed in the cerebral cortex[45,46]. Both *SPNS3* and *SV2A,* the known target of LEV, are atypical solute carrier (SLC) transporters. They belong to the Major Facilitator Superfamily (MFS) of membrane transporters, and they share a common structure consisting of 12 transmembrane segments, which is necessary for optimal transporter activity[58,59].

Tests on sets of low frequency variants (MAF<5%)

Next, we studied variants with MAF<5%, i.e. low-frequency and rare variants. Among the approximately 4M variants with MAF<5%, we focused on the top 5% genotypically most variable variants across all 92 samples in our cohort. These included ~182K variants with MAF between 0.003% and 5%. A common strategy for increasing statistical power when studying low-frequency and rare variants is to analyse sets of variants, instead of individual variants. Therefore, we examined gene- and pathway-based sets of variants (see Methods).

Gene-based tests indicate that low-frequency variants in genes PRKCB, DLG2, FILIP1, SEMA6D and LINC01090 are associated with response to LEV

We conducted 19,824 gene-based tests, which is the number of genes harbouring at least one of the ~182K low-frequency and rare variants in our data. We found that four protein-coding genes (*PRKCB*, *DLG2*, *FILIP1* and *SEMA6D*) and a long intergenic non-protein-coding RNA (*LINC1090*) had a Family-Wise Error Rate (FWER) less than 10%, and they were kept for further study (Table S3 and Figure 5).

The top hit, *PRKCB*, encodes a protein kinase C, a family of serine- and threonine-specific protein kinases, which can be activated by calcium and second messenger diacylglycerol[47]. There are 78 variants in *PRKCB* with MAF between 2.2% and 4.9%. Forty-five of them have p-values less than 0.05 and they aggregate towards the 5' end of the gene (Figure 5A). Associated Reactome pathways are *glutamate binding*, *activation of AMPA receptors* and *synaptic plasticity*[60]. *PRKCB* is implicated in the trafficking of GluR2-containing AMPA receptors[60]. It is known that fast synaptic excitation relevant to epilepsy is mediated mainly by AMPA receptors, thus rendering the latter potential targets of antiepileptic treatment[61]. There is evidence suggesting that LEV interacts with AMPA receptors[62] and that its antiepileptic action is mediated by inhibiting glutamatergic neurotransmission through presynaptic calcium channels[63], but the precise molecular mechanism that mediates its action remains unclear.

A second hit of interest, *DLG2*, encodes a membrane-associated guanylate kinase, which is implicated in the clustering of receptors (including NMDARs), ion channels, and associated signalling proteins at postsynaptic sites of excitatory synapses[47]. We found 208 variants in this gene with MAF between 0.96% and 4.97%, 53 of which have p-values less than 0.05 (Figure 5B). A related Reactome pathway is *protein-protein interactions at synapses*[60]. There is evidence supporting the role of NMDARs in epilepsy, and as a potential therapeutic target of antiepileptic drugs, including LEV[64]. It is possible that LEV blocks epileptiform bursting induced by NMDA *in vitro* without affecting normal synaptic transmission[65] and that it inhibits NMDA-dependent excitatory postsynaptic currents[63], although its precise molecular mechanism of action remains unclear.

Among the remaining three hits (Figure 5C-E), *FILIP1* includes 12 variants (11 with p-values less than 0.01) with MAF between 1.8% and 5%, *SEMA6D* has 41 variants (17 with p-values less than 0.05) with MAF between 1.9% and 5% and *LINC01090* harbours 35 variants (18 with p-values less than 0.01) with MAF between 1.7% and 5%. *FILIP1* encodes a protein that stimulates filamin A degradation, which may regulate cortical neuron migration, dendritic spine morphology, and normal excitatory signalling[47]. *SEMA6D* encodes a transmembrane semaphorin, a class of proteins involved in axon guidance, and maintenance and remodelling of neural connections[47]. Finally, *LINC01090* is transcribed into a long intergenic non-protein-coding RNA[47], which is associated with post-traumatic stress disorder[66].

Pathway-based tests indicate that associations between response to LEV and Reactome pathways are driven mainly by low-frequency variants in gene PRKCB

We conducted tests using gene sets, instead of single genes, as the organisational unit for grouping individual variants together. We have used all pathways from *Reactome*, a curated, peer-reviewed database of interacting signalling and metabolic molecules, which are organised into groups of higher order structures (pathways) with well-defined biological relevance[60]. In total, we considered 2,028 pathways, of which 1,979 harboured at least one of the ~182K low-frequency highly-variable variants in our data. Among these, we identified six pathways with FWER<5% and one pathway with FWER<10% (Table S4).

The top hit is *activation of NF-kappaB (nuclear factor kappaB) in B cells*. NF-kappaB is a ubiquitous transcription factor, which is instrumental in gene regulation relevant to cell death and survival and to the immune system's response to inflammation. The next hit is *WNT5A-dependent internalization of FZD4*. WNT5A regulates multiple intracellular signalling cascades via internalisation of its receptors. These include FZD4, a member of the frizzled gene family, which encode seven-transmembrane domain proteins[47]. Importantly, the WNT5A-dependent uptake of FZD4 occurs in a clathrin-dependent manner[67]. Clathrins are adaptor proteins, which are essential in the formations of synaptic vesicles, and which are known to interact with SV2A, the molecular target of LEV[68].

Another interesting pathway is *disinhibition of SNARE formation*. SNARE is a family of proteins, which are important components of the mechanism responsible for membrane fusion, thus playing an important role in docking of synaptic vesicles with the presynaptic membrane, and neurotransmitter release. It is known that SV2A, the target of LEV, regulates the formation of SNARE complexes: kindling epileptogenesis triggers the long-term accumulation of both SNARE and SV2A in the ipsilateral hippocampus, a molecular process which is reversed by LEV[69].

Next, we asked which genes underlie these findings. In total, in these pathways, there are 108 genes harbouring low-frequency mutations (Table S4). In Figure 6, we illustrate these genes, as well as their pathway membership. *PRKCB* is mutated in all but the least significant pathway with FWER<10%, followed by its paralog, *PRCKA*, which is mutated in three pathways (central panel). The remaining genes are mutated in only 1 or 2 pathways. Furthermore, *PRKCB* and *PRKCA* harbour the largest number of low-frequency mutations, along with *RUNX1* (top panel). However, in *PRKCB*, more than half of these mutations have p-values less than 0.05 (see also Table S3) leading to a low gene- and pathway-based p-value (Tables S3 and S4), while only a very small proportion of mutations in *PRKCA* and *RUNX1* have p-values less than 0.05. Among the other highly mutated genes, *LPR6* and *IKBKB* also harbour a large proportion of mutations with low p-values, but they participate in only 1 and 2 pathways, respectively. We conclude that the significant associations in Table S4 are driven mainly by *PRKCB* in all but the least significant pathway with FWER<10%. Associations in this last pathway (*disassembly of the destruction complex and recruitment of AXIN to the membrane*) are driven mainly by *LRP6*, a transmembrane low density lipoprotein (LDL) receptor[47]. Neuronal *LRP6*-mediated Wnt signalling is critical for synaptic function and cognition[70,71].

Targeted analysis of genes implicated in neurotransmitter transport and release highlights the previously identified genes *NSG1* and *DLG2*, but not *SV2A*, *SV2B* or *SV2C*

Whole genome sequencing permits focused analysis of identified sets of variants, in addition to unbiased analysis over the whole genome. Furthermore, by testing only a small subset of variants, we can ameliorate the effect of multiple hypothesis testing, thus increasing the power of statistical analysis. We conducted targeted analysis of common and rare variants on a set of 294 genes implicated in neurotransmitter transport and release (Table S5). These genes (SYNAPTIC) were identified based on their Gene Ontology[72] terms and they included *SV2A* and its paralogs, *SV2B* and *SV2C*. In addition, we tested all 402 high-confidence (i.e. “green”) genes (EPILEPSY) in the genetic epilepsy syndromes panel v1.35 provided by Genomics England[73] (Table S5).

In the case of SYNAPTIC genes, which harboured ~51K common variants, we found evidence of association with response to LEV in the previously identified gene *NSG1* at a FWER<5% or <10%, depending on the methodology used for calculating the effective number of independent tests (Table S5). Furthermore, when examining the ~2.6K rare variants found in SYNAPTIC genes, *DLG2* was found associated with response to LEV at a FWER<0.1% (Table S5). This is not surprising, since *DLG2* was also found associated with LEV response in the previously conducted gene-based tests. We did not find any evidence of association between LEV response and *SV2A* or its paralogs, *SV2B* and *SV2C*, using either SNP- or gene-based tests. Furthermore, we did not find any evidence of association between ~66K common variants in EPILEPSY genes and response to LEV or between ~3.7K rare variants in the same genes and response to LEV at a FWER<10% (Table S5).

DISCUSSION

Although the anticonvulsant properties of the prominent antiepileptic drug LEV have been linked to the activity levels of its molecular target, the synaptic glycoprotein SV2A[21,22], targeted sequencing did not reveal any associations between common[24] or rare[23] variation in this gene and LEV efficacy. This leaves open the question as to whether genetic variation is a component of response variability and, if so, the identity of the genomic variants underlying clinical response to LEV. In the present study, we followed a whole genome sequencing approach in an unbiased search of genomic polymorphisms that underlie clinical response to this drug.

According to one possible hypothesis for explaining variability in drug response, one or more common polymorphisms occur with different frequencies between responders and non-responders. Our analysis indicates that common polymorphisms in genes *NSG1*, *HDC, MDGA2*, *RASGEF1C* and *SPNS3* collectively predict clinical response to LEV in our cohort with overall accuracy ~91%. These genes are attractive candidates, since the first four are potentially implicated in synaptic neurotransmission, while the fourth is a transmembrane transporter protein homologous to *SV2A*.

A second hypothesis asserts that multiple rare variants act synergistically to influence a patient's response to the drug. Our analysis showed that groups of low-frequency variants in genes *PRKCB*, *DLG2*, *FILIP1* and *SEMA6D*, and in pathways involving *PRKCB* (and *LRP6*) demonstrate significant associations with the response/non-response phenotype.

From a neurophysiological perspective, there are three major, not mutually exclusive hypotheses for explaining pharmaco-resistant epilepsy[74]. First, the drug target hypothesis postulates that alterations in the activity of the molecular target of the drug (e.g. due to genomic polymorphisms coding for the drug-target binding site) result in reduced drug efficacy. Our analysis did not provide any evidence that *SV2A* or its paralogs (*SV2B* and *SV2C*) are associated with response to LEV, in agreement with previous studies[23,24]

Second, the drug transporter hypothesis states that reduced efficacy of antiepileptic drugs are due to low concentration of the drug at its target site due to over-active efflux drug transporters. A common intronic polymorphism in *SPNS3*, a gene homologous to *SV2A*, may be of interest in relation to this hypothesis. Both *SPNS3* and *SV2A* (and its paralogs) are structurally similar to the solute carrier family 22 (SLC22), a large family of transmembrane drug transporters. It should, however, be emphasised that homology (as established through structural similarity) is not definitive proof of biological relevance.

Finally, the intrinsic severity hypothesis postulates that severe epilepsy (manifested, for example, as high-frequency seizures) is linked to reduced response to antiepileptic drugs. Neurophysiological processes that are proposed to underlie the severity of epilepsy include neuroinflammation, aberrations in synaptic neurotransmission, and restructuring of neural networks[75]. Our analysis has identified common and low-frequency polymorphisms in genes and pathways, which are putatively related to these processes; for example, genes *HDC*, *NSG1*, *MDGA2*, *RASGEF1C*, *PRKCB* and *DLG2* (synaptic neurotransmission) and genes *FILIP1* and *SEMA6D* (restructuring of neural networks).

Whilst highlighting the approaches now available through the advent of NGS technologies, the findings in the present study need independent replication and potentially functional validation to confirm their role in determining response to LEV. Furthermore, we expect that the rapidly decreasing cost of WGS will allow conducting similar studies with a larger sample size in the near future. Nevertheless, our approach of using extremes of response is a pragmatic way to derive hypotheses for experimental testing. It is interesting to postulate what the remaining factors are that determine response to LEV. Drug response is likely to be a complex interaction of many factors, including interacting genetic factors, which should be explored through polygenic risk score analysis and integrative analysis of multiple data modalities utilizing machine learning approaches.

In summary, we have identified common and low-frequency variants in genes and pathways, which may influence clinical response to LEV in a cohort of 99 patients with epilepsy. We conclude that whole genome sequencing can be a useful approach for investigating the genomic correlates of pharmaco-resistant epilepsy.

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FIGURES

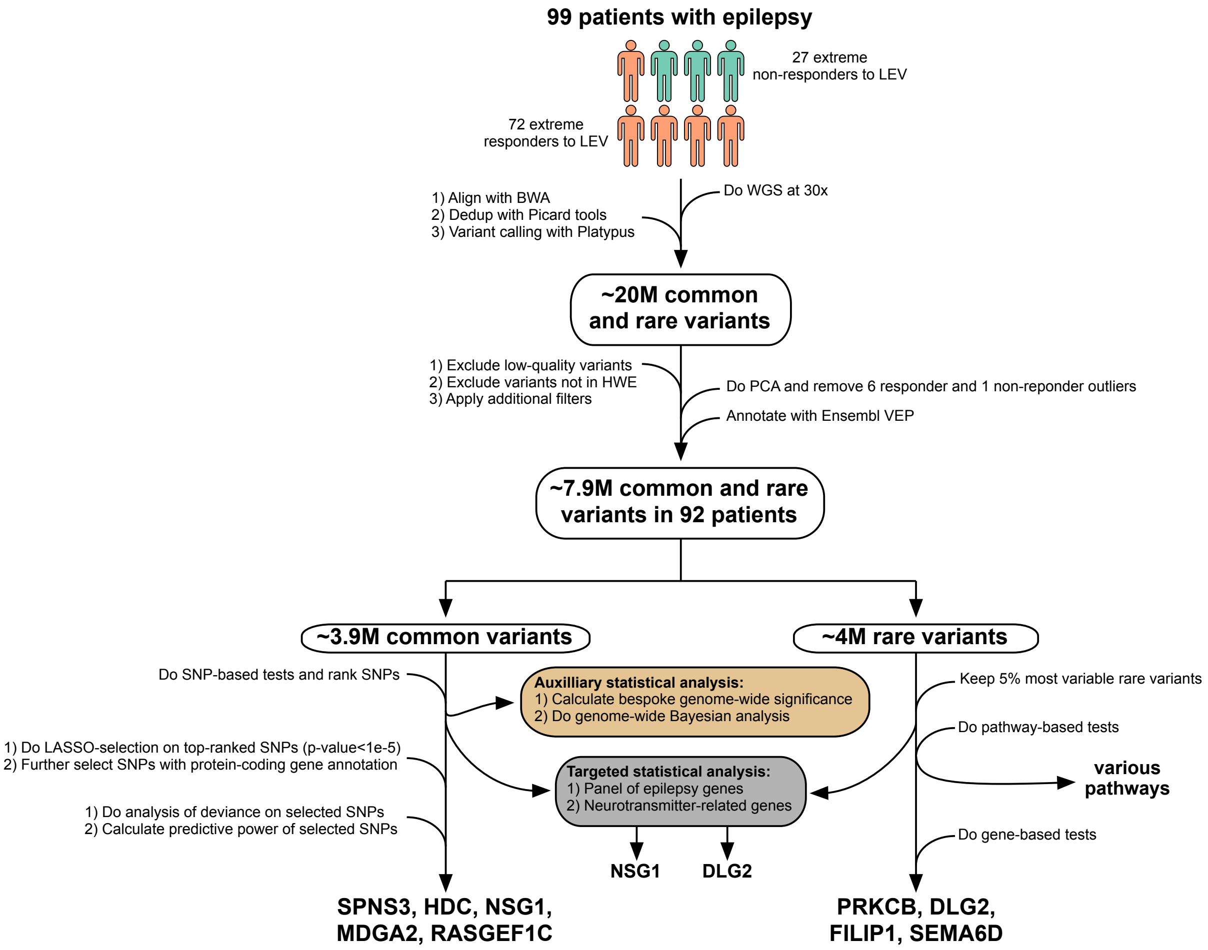

Figure 1: Overview of the study. We recruited 99 patients with epilepsy (72 extreme responders and 27 extreme non-responders to LEV). After performing WGS, alignment and variant calling, we identified ~20M unfiltered variants. After filtering across variants and samples, we ended up with ~3.9M common (MAF>5%) variants and ~4M low-frequency and rare (MAF<5%) variants across 92 patients. Subsequently, we calculated p-values for each common variant using a two-tailed Fisher's exact test. In the next step, we performed penalised logistic regression (LASSO) on all common variants with p-value less than the suggestive genome-wide significance threshold of 10^{-5} (n=23 variants; Supplementary Table S1). This was followed by further selecting variants with protein-coding gene annotation. In the last step, we performed analysis of deviance on the finally selected variants (n=5 variants) and we calculated their collective predictive accuracy using a cross-validation approach. For completeness, we also conducted additional auxiliary statistical analyses on the common variants (see Supplementary Material). In the case of low-frequency and rare variants, we focused on the top 5% most variable variants in our cohort and, by performing gene- and pathway-based tests on these, we identified associations between several genes or pathways and clinical response to LEV. Finally, for both common and low-frequency/rare variants, we conducted targeted analysis on a panel of epilepsy genes and on genes related to neurotransmitter transport and release.

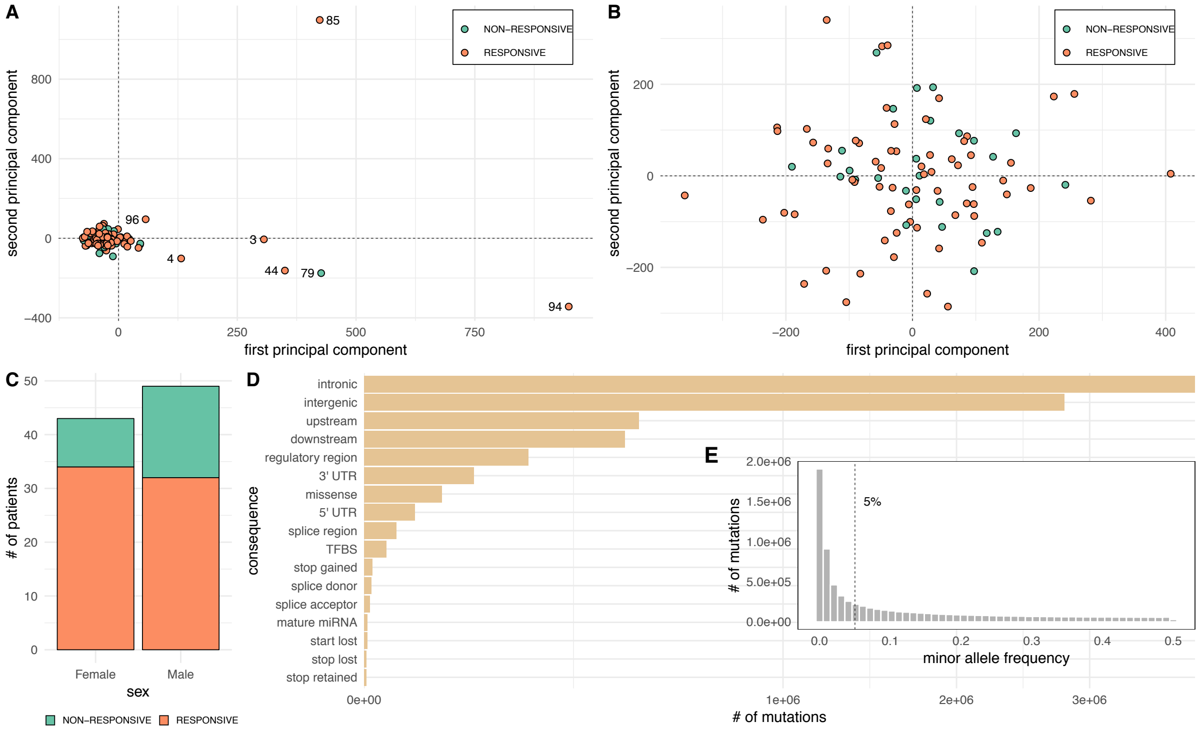

Figure 2: Overview of the WGS data from 99 extreme responders and non-responders to LEV. A) Principal component analysis (PCA) of the matrix of genotypes across all samples and variants. The first two principal components are illustrated. Seven samples appear as outliers. B) Repeating the PCA after removing the seven outliers identified in (A) indicates lack of any stratification (e.g. due to population structure) in the data. C) Number of male and female subjects among responders and non-responders to LEV. There are almost twice as many non-responders among 49 males (n=17), as among 43 females (n=9) in the data. A two-tailed Fisher's exact test of independence indicates that this difference is not statistically significant (odds ratio: 1.99; 95% CI: 0.72-5.86; p-value: 0.17). D) Consequences of all variants identified by WGS. Most variants are intronic, intergenic, or located immediately upstream or downstream of protein-coding genes. E) Minor allele frequencies (MAF) of all variants identified by WGS. A cut-off of 5% was chosen to discriminate between common and low-frequency or rare variants.

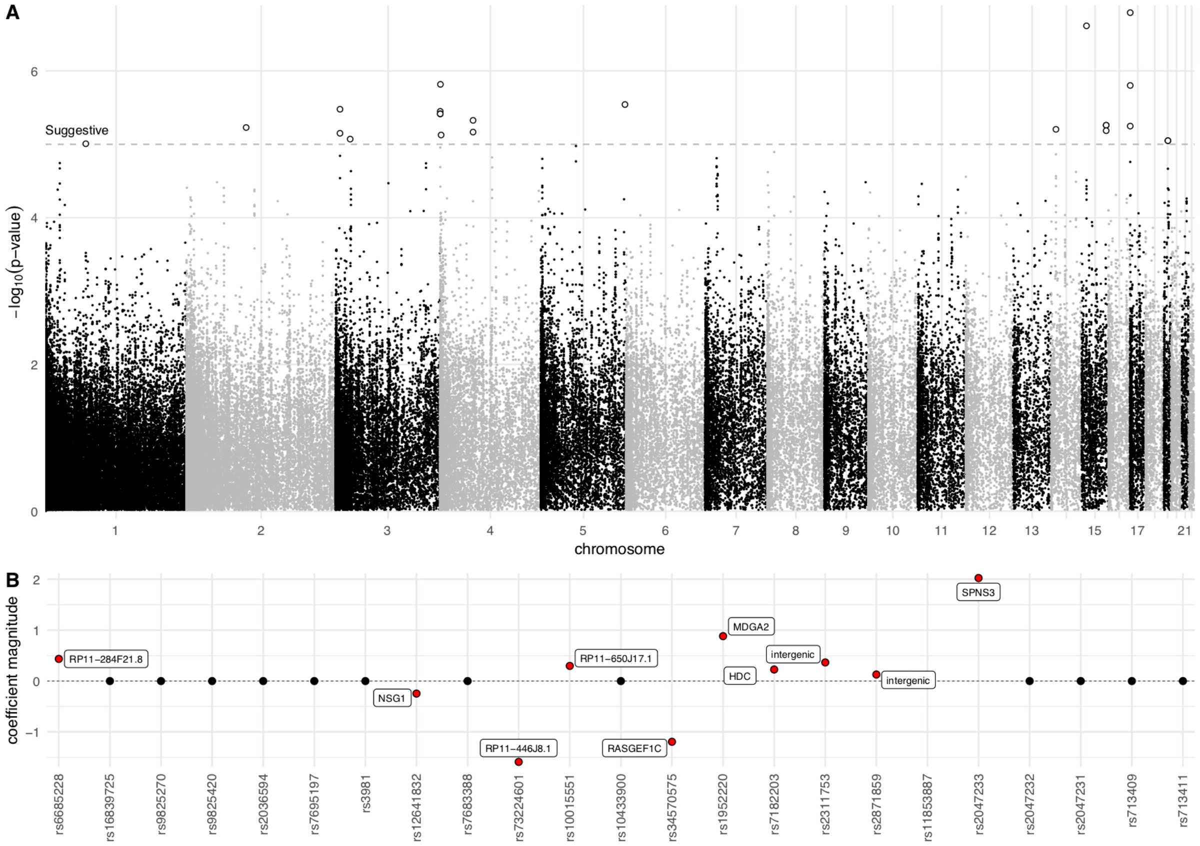

Figure 3: Genome-wide selection of a minimal set of common (MAF>5%) variants with maximal predictive power. A) Manhattan plot summarising SNP-based tests using a two-tailed Fisher's exact test of independence. All variants with p-values below a suggestive significance threshold of 10^{-5} are indicated with white circles (n=23). B) Summary of variable selection using penalised logistic regression (LASSO). All SNPs crossing the suggestive genome-wide significance threshold in (A) were used as predictors. Variants selected through this process have non-zero regression coefficients (red dots). Among these, the variants with protein-coding gene annotation (i.e. *SPNS3*, *HDC*, *MDGA2*, *NSG1* and *RASGEF1C*) were selected for further analysis.

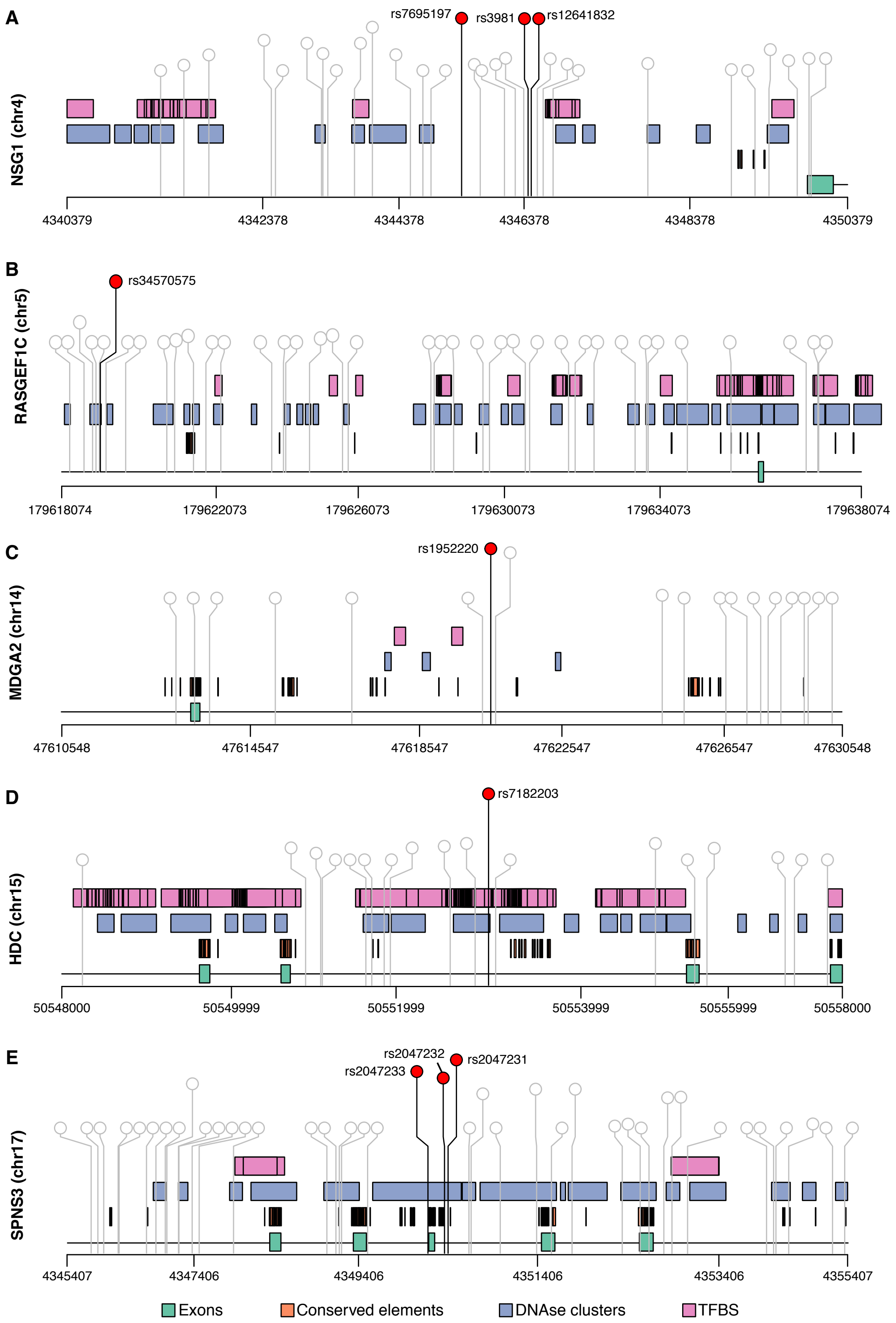

Figure 4: Local genomic structure near the most significant SNPs in genes *NSG1*, *RASGEF1C*, *MDGA2*, *HDC* and *SPNS3*. Common variants in these genes are strong predictors of clinical response to LEV in our cohort. SNPs crossing the suggestive genome-wide significance threshold of 10^{-5} are indicated in red.

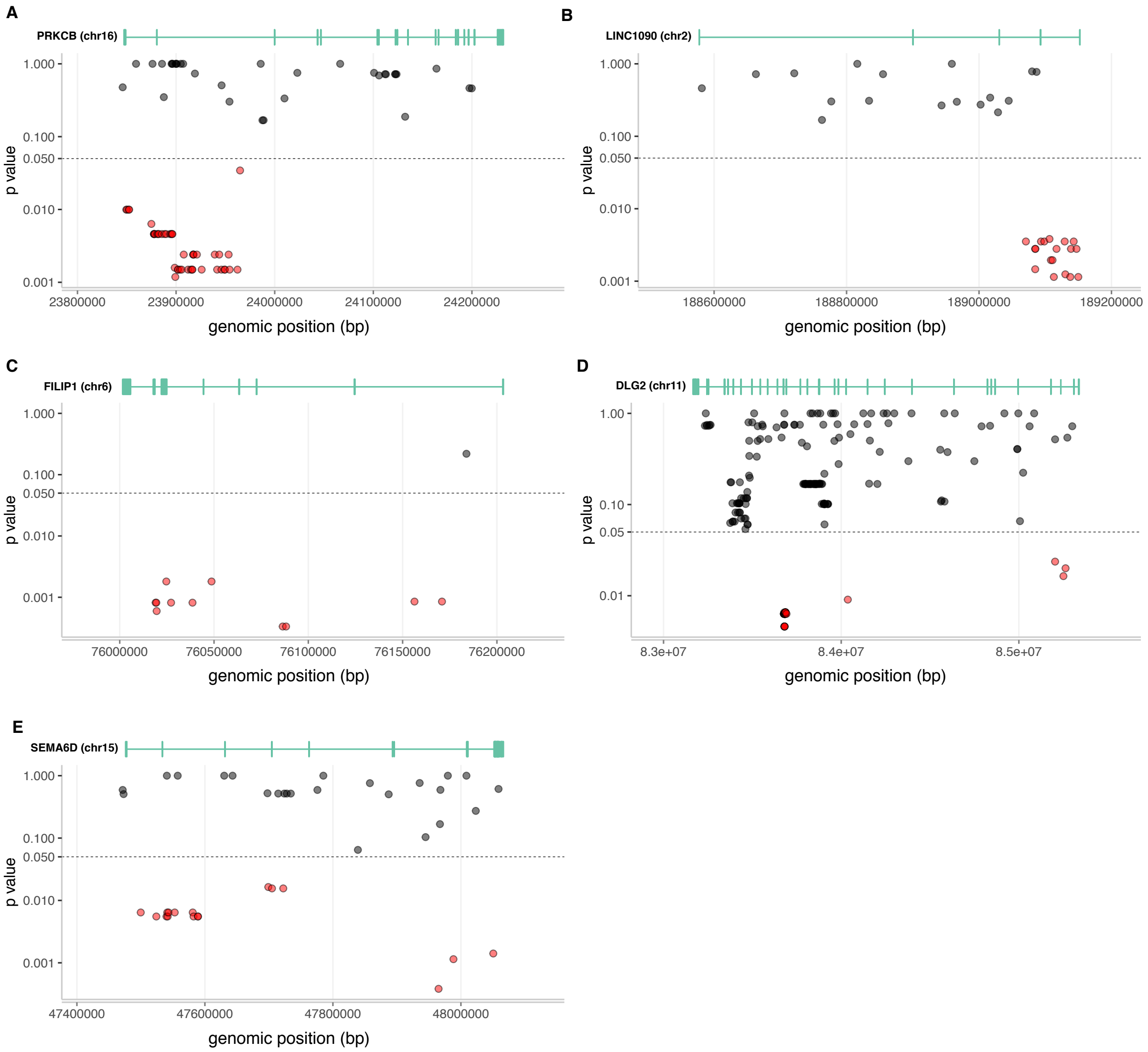

Figure 5: Distribution of rare variants along genes *PRKCB*, *LINC01090*, *FILIP1*, *DLG2* and *SEMA6D*. Based on gene-based tests, these genes are significantly associated with response to LEV at a FWER<10%. Rare variants with p-values below 5% (calculated using a two-tailed Fisher's exact test of independence) are indicated in red.

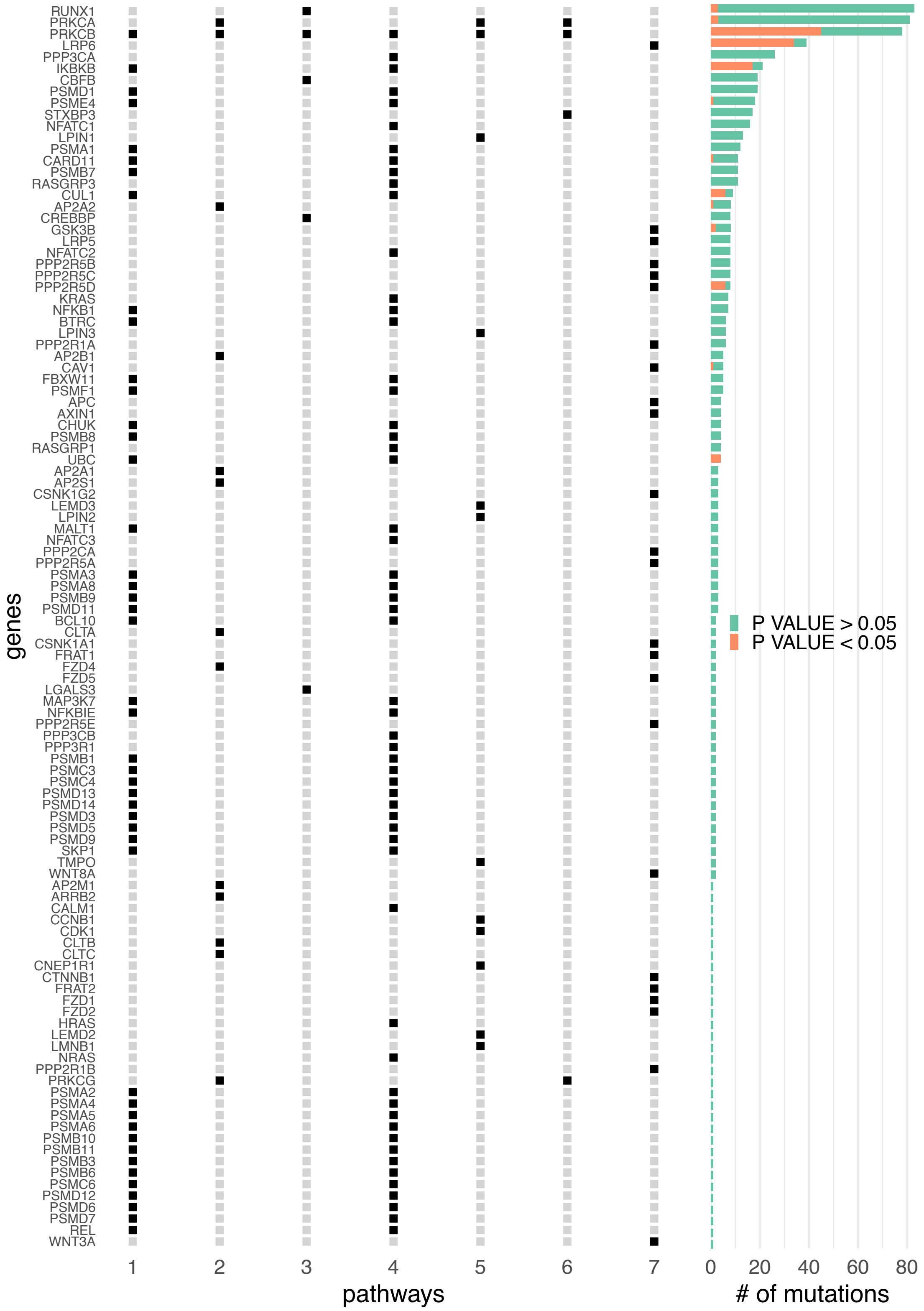

Figure 6: Summary of the results from Reactome pathway-based tests. In the left panel, pathways are as follows: *1-Activation of NF-kappaB in B cells; 2-WNT5A-dependent internalization of FZD4; 3-RUNX1 regulates transcription of genes involved in differentiation of myeloid cells; 4-Downstream signalling events of B Cell Receptor (BCR); 5-Depolymerisation of the Nuclear Lamina; 6-Disinhibition of SNARE formation; 7-Disassembly of the*

destruction complex and recruitment of AXIN to the membrane. Among all genes harbouring the highest number of rare variants (*RUNX1*, *PRKCA*, *PRKCB*, *LRP6*), *PRKCB* and *LRP6* have the highest proportion of rare variants with p-values less than 5% (right panel). *PRKCB* is participating in all but one pathway, with the remaining genes participating in only 1, 2 or 3 pathways (left panel).

SUPPLEMENTARY MATERIAL
Whole genome sequencing identifies putative associations between genomic polymorphisms and clinical response to the antiepileptic drug *levetiracetam*

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STATISTICAL METHODS

Statistical tests on single variants

For each common variant (and without assuming a particular genetic model), we constructed a 2x3 contingency table of counts, where the rows correspond to responders and non-responders (i.e. controls and cases, respectively), and the columns correspond to Ref/Ref, Ref/Alt and Alt/Alt genotypes. We analysed each such SNP-specific table using a two-sided Fisher's exact test of independence, which unlike the χ^2 test or the Cohran-Armitage test for trend under an additive genetic model, is applicable even when the counts in any cell of the contingency matrix become very small (e.g. <5).

Auxiliary statistical analysis of single variants

The genome-wide significance threshold for Type 1 error control due to multiple hypothesis testing is usually set at 5×10^{-8}, although it has been suggested[1] that this can be relaxed to the less stringent value of 10^{-7}. In this study, we have calculated a bespoke significance threshold using the Sidak correction[2], in order to keep the family-wise error rate (FWER) below α=10%. Specifically, we calculated the significance threshold as $p_{thr} = 1-(1-\alpha)^{1/Neff}$, where *Neff* is the effective number of independent tests. For the calculation of *Neff*, we split each chromosome in a large number of blocks each containing 1000 variants, we calculate *Neff* in each block, and we sum the block-specific *Neff* values across all chromosomes to obtain a genome-wide estimate of *Neff*. For the actual calculation of *Neff* in each block, we applied four different methods[3–7], all of which operate on the eigenvalues of the correlation matrix of the SNP allele counts. Depending on which method is used, the estimated effective number of independent tests/SNPs was approximately equal to 3.6M[3,4], 358K[5], 259K[6] or 161K[7], leading to genome-wide significance thresholds equal to 3.0×10^{-8}, 3.0×10^{-7}, 4.1×10^{-7} and 6.6×10^{-7}, respectively (Figure S1A; Table S1). Two SNPs (rs7182203 in gene *HDC* and rs2047231 in gene *SPNS3*, with p-values 2.43×10^{-7} and 1.60×10^{-7}, respectively) are above the three least conservative thresholds[5–7], while 21 additional SNPs are above a suggestive significance threshold of 10^{-5} (Figure S1A; Table S6).

We have also applied a Bayesian approach to single-variant association testing, as previously described[8] (Figure S1B; Table S6). Specifically, we calculated the retrospective posterior probability of association (*rPPA*) for each SNP, which can be directly interpreted as the probability (given the data) that a particular SNP genotype is associated with the phenotype[8]. For each variant, we write: $rPPA = PO \times (1 - PO)^{-1}$, where $PO = BF \times \pi \times (1 - \pi)^{-1}$. In the previous expression, PO are the posterior odds, BF is the Bayes factor, and π is the prior probability of association for the variant. This prior probability typically falls between 10^{-4} and 10^{-6}, according to Stephens & Balding[8]. The Bayes factor is equal to:

$$BF = \frac{DirMult(n_{N0}, n_{N1}, n_{N2}|a, b, c) \times DirMult(n_{R0}, n_{R1}, n_{R2}|a, b, c)}{DirMult(n_0, n_1, n_2|a, b, c)}$$

where *DirMult(...)* is the Dirichlet-Multinomial distribution; n_{X0}, n_{X1}, n_{X2} are the number of responders (X=R) and non-responders (X=N) with Ref/Ref, Ref/Alt and Alt/Alt genotypes, respectively; n_0, n_1, n_2 are the total number of patients in each of the above genotype categories; and *a, b, c* are the prior values of the concentration parameters of the Dirichlet-Multinomial distribution.

Although Bayesian approaches are, in principle, applicable regardless of the sample size or the number of variants entering the analysis, the calculation of *rPPA* requires an explicit choice of priors π, a, b and c. Here, we have assumed that π=10^{-4}, i.e. we expect a priori that 1 out of every 10K SNPs is truly associated with the phenotype (values of *rPPA* for π equal to 10^{-5} or 10^{-6} are also given in Table S6). The priors *a, b* and *c* were set either equal to 1 (flat prior), or equal to the empirical values $(\mathrm{a, b, c}) = \left(\frac{n_0}{n}, \frac{n_1}{n}, \frac{n_2}{n}\right)$, where n=n_0+n_1+n_2 is the total number of patients. Both options return similar results, although the empirical prior is less conservative (see Table S6).

Under these explicit prior assumptions, we see that the previously identified variants rs7182203 (*HDC*) and rs2047231 (*SPNS3*) have *rPPA* values above 50%, i.e. they are more likely than not to be associated with drug response (Figure S1B; Table S6). In addition, the following variants also have an *rPPA* of more than 50%: rs7683388 (*HTRA3*), rs7695197 (*NSG1*), rs3981 (*NSG1*) and rs12641832 (*NSG1*).

Statistical tests on groups of low-frequency and rare variants

There are various approaches for testing groups of low-frequency and rare variants[9–11]. In this study, we followed a two-stage approach to group-based tests: a) first, we calculated for each variant in a group a p-value using a two-sided Fisher's exact test, as we did for the common variants, and b) we combined all variant-specific p-values in the same group into a group-specific statistic using an appropriately scaled Fisher's product method, which accounts for correlations between variants in the group[7]:

$$T = -2\frac{Meff}{M}\sum_{i=1}^{M}\log p_i$$

where M is the total number of variants in the group, *Meff* is the effective number of uncorrelated variants in the group, and p_i is the variant-specific p-value from Fisher's test. This statistic can be used to measure the strength of evidence that a particular group is associated with the response phenotype, and its distribution is approximated by a χ^2 distribution with $2 \times Meff$ degrees of freedom[7], which is used to derive a group-specific p-value, p_j. Assuming N total groups, we use the Sidak correction to calculate an adjusted-for-multiplicity p-value, $p_{adj,j} = 1 - (1 - p_j)^N$. Groups are defined as either genes or pathways.

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SUPPLEMENTARY FIGURES

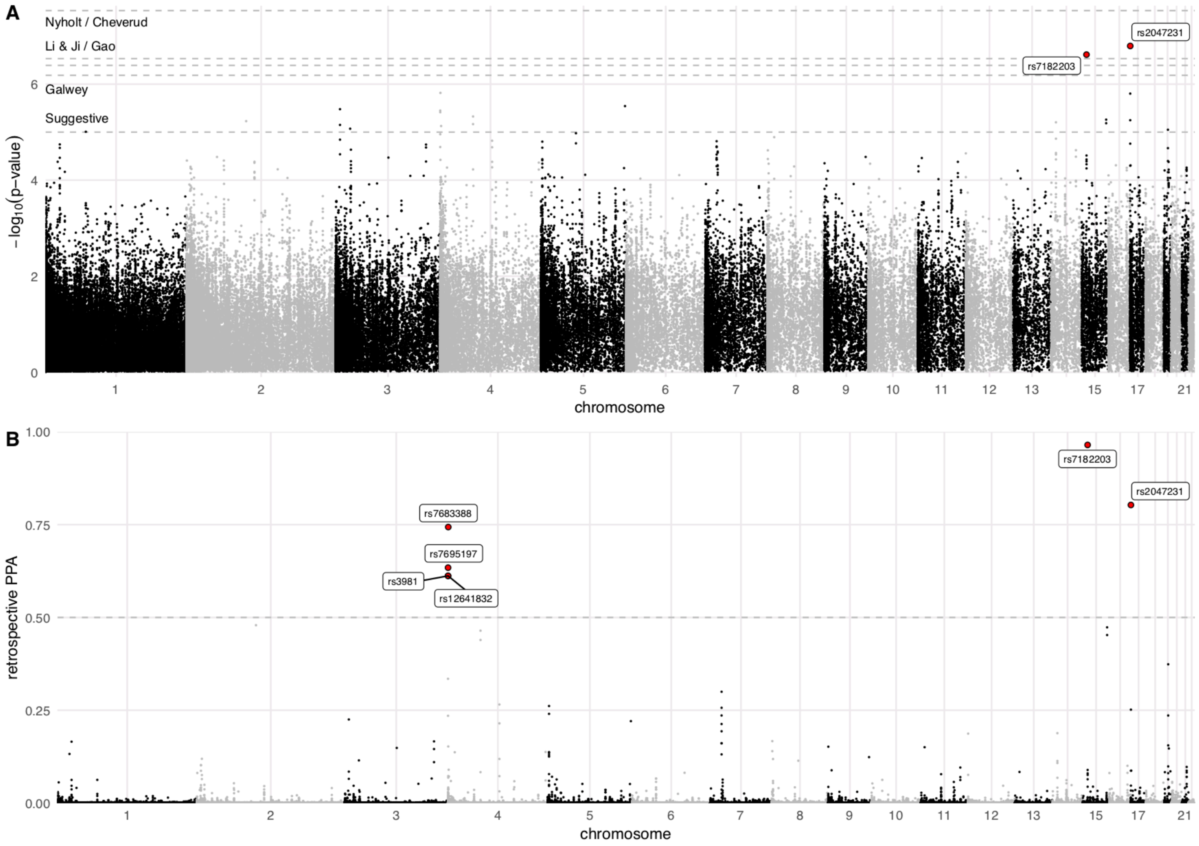

Figure S1: Auxiliary statistical analysis of common (MAF>5%) variants across the whole genome. A) Manhattan plot summarising SNP-based tests using a two-tailed Fisher's exact test of independence. Genome-wide significance thresholds (calculated using four different methodologies) are indicated, including a suggestive significance threshold of 10^{-5}. Two variants (in red) cross the three least conservative thresholds and they could be considered statistically significant with respect to these thresholds. B) Manhattan plot summarising the Bayesian analysis of single SNPs. We assumed a prior retrospective probability of association (rPPA) equal to $\pi=10^{-4}$. Variants with rPPA values above 50% are more likely than not to be associated with response to the drug.

SUPPLEMENTARY TABLES

Table S1: Summary of all common variants with p-values less than a suggestive genome-wide significance threshold of 10^{-5} (n=23). Among these, those selected by the LASSO are indicated in green and orange (n=10; also see Figure 3B). The variants indicated in green (n=5) have protein-coding genes annotations and they were selected for further analysis. Those indicated in orange (n=5) have non-protein-coding gene annotations or are annotated as *intergenic* and they were not selected for further analysis. In order to avoid division by zero in the calculation of odds ratios, the matrix of counts for each variant was pre-processed using Lidstone smoothing with pseudo-count parameter equal to 1 (i.e. add-one smoothing).

Table S2: Analysis of deviance using seven different logistic regression models of increasing complexity. The BASIC model includes only sex and the intercept as predictors. The FULL model includes in addition five SNPs from genes *SPNS3*, *HDC*, *NSG1, RASGEF1C* and *MDGA2*, which were previously selected using penalised logistic regression. Intermediate models include only sex, the intercept and the SNP harboured by the indicated gene. DF: degrees of freedom

Table S3: Summary of gene-based tests. Only genes with FWER<10% are shown. The low-frequency variants harboured by these genes are listed in the second spreadsheet.

Table S4: Summary of Reactome pathway-based tests. Only pathways with FWER<10% are shown. The rare variants harboured by genes in these pathways are listed in the second spreadsheet.

Table S5: Summary of results from the targeted analysis. We list the results from SNP- and gene-based tests on SYNAPTIC and EPILEPSY genes. A complete list of genes in each of these two groups is also provided in the last spreadsheet.

Table S6: Summary of results from the auxiliary statistical analysis on common variants. Only variants with a p-value below a suggestive genome-wide significance threshold of 10^{-5} are presented. P-values were corrected for multiplicity using Sidak's method and four different estimates of the effective number of independent tests, as indicated. The results of Bayesian analysis for different choices of the priors π (10^{-4}, 10^{-5} and 10^{-6}) and (a, b, c) (flat or empirical) are also given. rPPA: retrospective probability of association. FWER: family-wise error rate.

Table S1

CHROM	POS	REF	ALT	MINOR ALLELE	ID	CONSEQUENCE	AF	MAF	SYMBOL	P VALUE	# RESPONDERS			# NON-RESPONDERS			% RESPONDERS			% NON-RESPONDERS			ODDS RATIO	
											Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Dominant model	Recessive model
17	4350407	G	C	G	rs2047231	intronic	0.82	0.18	SPNS3	1.60E-07	1	4	60	0	15	10	2.94	7.35	89.71	3.57	57.14	39.29	0.82	0.07
15	50553000	G	A	A	rs7182203	intronic	0.26	0.26	HDC	2.43E-07	21	35	10	22	0	4	31.88	52.17	15.94	79.31	3.45	17.24	0.12	1.10
4	8291102	C	T	T	rs7683388	intronic	0.39	0.39	HTRA3	1.52E-06	26	40	0	13	5	8	39.13	59.42	1.45	48.28	20.69	31.03	0.69	30.60
17	4350182	T	C	T	rs2047233	intronic	0.88	0.12	SPNS3	1.58E-06	0	3	63	0	13	13	1.45	5.80	92.75	3.45	48.28	48.28	0.41	0.07
5	179619074	T	C	C	rs34570575	intronic	0.10	0.10	RASGEF1C	2.87E-06	57	9	0	9	14	2	84.06	14.49	1.45	35.71	53.57	10.71	9.49	8.16
3	37604012	T	G	G	rs9825420	intronic	0.18	0.18	ITGA9	3.32E-06	58	6	2	11	15	0	85.51	10.14	4.35	41.38	55.17	3.45	8.36	0.79
4	4345379	T	C	C	rs7695197	upstream	0.31	0.31	NSG1	3.55E-06	34	31	1	7	8	11	50.72	46.38	2.90	27.59	31.03	41.38	2.70	23.65
4	4346427	G	A	A	rs3981	upstream	0.32	0.32	NSG1	3.84E-06	34	30	1	7	8	11	51.47	45.59	2.94	27.59	31.03	41.38	2.78	23.29
4	4346465	T	C	C	rs12641832	upstream	0.33	0.33	NSG1	3.84E-06	34	30	1	7	8	11	51.47	45.59	2.94	27.59	31.03	41.38	2.78	23.29
4	113961039	G	T	G	rs10015551	intronic, non-coding transcript	0.57	0.43	RP11-650J17.1	4.72E-06	6	29	31	2	23	0	10.14	43.48	46.38	10.71	85.71	3.57	0.94	0.04
15	99100580	A	G	A	rs2311753	intergenic	0.79	0.21		5.49E-06	0	24	42	9	8	9	1.45	36.23	62.32	34.48	31.03	34.48	0.03	0.32
15	99101462	A	G	A	rs2871859	intergenic	0.79	0.21		5.49E-06	0	24	42	9	8	9	1.45	36.23	62.32	34.48	31.03	34.48	0.03	0.32
17	4350367	A	G	A	rs2047232	intronic	0.88	0.12	SPNS3	5.64E-06	0	4	62	0	13	13	1.45	7.25	91.30	3.45	48.28	48.28	0.41	0.09
2	156765630	T	C	C	rs16839725	intergenic	0.29	0.29		5.90E-06	40	15	11	3	19	4	59.42	23.19	17.39	13.79	68.97	17.24	9.15	0.99
14	47620548	C	T	C	rs1952220	intronic	0.87	0.13	MDGA2	6.25E-06	2	17	47	1	20	5	4.35	26.09	69.57	6.90	72.41	20.69	0.61	0.11
15	99102128	A	G	A	rs11853887	intergenic	0.76	0.24		6.52E-06	0	25	41	9	8	9	1.45	37.68	60.87	34.48	31.03	34.48	0.03	0.34
4	113961811	C	T	C	rs10433900	intronic, non-coding transcript	0.52	0.48	RP11-650J17.1	6.81E-06	9	27	30	3	22	0	14.49	40.58	44.93	14.29	82.14	3.57	1.02	0.05
3	37603952	T	A	A	rs9825270	intronic	0.19	0.19	ITGA9	7.07E-06	58	7	1	11	15	0	85.51	11.59	2.90	41.38	55.17	3.45	8.36	1.20
4	16428073	G	A	A	rs73224601	intronic, non-coding transcript	0.10	0.10	RP11-446J8.1	7.46E-06	64	1	0	16	9	1	95.59	2.94	1.47	58.62	34.48	6.90	15.29	4.96
3	72015276	C	A	A	rs2036594	intergenic	0.17	0.17		8.48E-06	61	2	3	15	11	0	89.86	4.35	5.80	55.17	41.38	3.45	7.20	0.58
19	46569619	A	G	A	rs713409	intronic	0.53	0.47	IGFL4	8.91E-06	18	24	23	3	22	0	27.94	36.76	35.29	14.29	82.14	3.57	2.33	0.07
19	46569630	A	G	A	rs713411	intronic	0.53	0.47	IGFL4	8.91E-06	18	24	23	3	22	0	27.94	36.76	35.29	14.29	82.14	3.57	2.33	0.07
1	156486009	G	A	G	rs6685228	downstream	0.76	0.24	RP11-284F21.8	9.82E-06	1	9	56	0	16	10	2.90	14.49	82.61	3.45	58.62	37.93	0.84	0.13

Table S2

MODEL	DF		DEVIANCE		P VALUE	D2	D2 (adj.)
	Residual	Null	Residual	Null			
BASIC	90	91	107.38	109.55	-	0.02	0.01
BASIC + HDC	89	91	95.43	109.55	5.44E-04	0.13	0.11
BASIC + NSG1	89	91	91.83	109.55	8.03E-05	0.16	0.14
BASIC + MDGA2	89	91	89.68	109.55	2.58E-05	0.18	0.16
BASIC + RASGEF1C	89	91	84.62	109.55	1.84E-06	0.23	0.21
BASIC + SPNS3	89	91	83.49	109.55	1.02E-06	0.24	0.22
FULL	86	91	28.04	109.55	1.15E-15	0.74	0.73

Table S3 (A): Significant results from gene-based tests

SYMBOL	# MUTATIONS All	# MUTATIONS p value < 0.05	P VALUE (GENE-BASED)	FWER	GENE ONTOLOGY	REACTOME
PRKCB	78	45	8.24E-08	0.0016	transferase activity, transferring phosphorus-containing groups, protein tyrosine kinase activity	glutamate binding, activation of AMPA receptors, synaptic plasticity
LINC01090	35	18	1.45E-07	0.0029	-	-
DLG2	208	53	6.25E-07	0.0123	kinase binding, guanylate kinase activity	protein-protein interactions at synapses
FILIP1	12	11	7.79E-07	0.0153	cytoplasm, nucleolus, plasma membrane, actin cytoskeleton	-
SEMA6D	41	17	4.87E-06	0.0921	semaphorin receptor binding	axon guidance, semaphorin interactions

Table S3 (B): Variants with MAF<5% in significant genes

CHROM	POS	REF	ALT	MINOR ALLELE	ID	CONSEQUENCE	AF	MAF	SYMBOL	P VALUE	# RESPONDERS			# NON-RESPONDERS		
											Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt
2	188581504	C	T	T	rs10497687	intronic,non_coding_transcript	0.0495	0.0495	LINC01090	0.46031	60	6	0	22	4	0
2	188663115	C	G	G	rs116771909	intronic,non_coding_transcript	0.0371	0.0371	LINC01090	0.72009	57	8	0	23	2	0
2	188721064	T	C	C	rs7557550	intronic,non_coding_transcript	0.0361	0.0361	LINC01090	0.74016	57	9	0	20	4	0
2	188762907	A	T	T	rs116655447	intronic,non_coding_transcript	0.0293	0.0293	LINC01090	0.16792	55	11	0	25	1	0
2	188776942	T	C	C	rs75411057	intronic,non_coding_transcript	0.0254	0.0254	LINC01090	0.30238	58	7	0	20	5	0
2	188816239	C	G	G	rs112295437	intronic,non_coding_transcript	0.0367	0.0367	LINC01090	1.00000	58	8	0	23	3	0
2	188833988	C	A	A	rs115319205	intronic,non_coding_transcript	0.0176	0.0176	LINC01090	0.30912	59	7	0	21	5	0
2	188855089	C	T	T	rs17262471	intronic,non_coding_transcript	0.0277	0.0277	LINC01090	0.72009	57	8	0	23	2	0
2	188943459	A	C	C	rs77663937	intronic,non_coding_transcript	0.0499	0.0499	LINC01090	0.26662	53	13	0	17	8	0
2	188959003	T	C	C	rs7349373	intronic,non_coding_transcript	0.0434	0.0434	LINC01090	1.00000	58	8	0	22	2	0
2	188966511	C	T	T	rs76695614	intronic,non_coding_transcript	0.0174	0.0174	LINC01090	0.29927	59	7	0	20	5	0
2	189002372	G	A	A	rs77231981	intronic,non_coding_transcript	0.0404	0.0404	LINC01090	0.27341	58	7	1	20	6	0
2	189016852	A	G	G	rs1439880	intronic,non_coding_transcript	0.0387	0.0387	LINC01090	0.34130	57	9	0	19	6	0
2	189028697	A	G	G	rs62181870	intronic,non_coding_transcript	0.0386	0.0386	LINC01090	0.21415	57	9	0	18	6	0
2	189044856	A	C	C	rs75344621	intronic,non_coding_transcript	0.0231	0.0231	LINC01090	0.30912	59	7	0	21	5	0
2	189070772	C	T	T	rs73041656	intronic,non_coding_transcript	0.0370	0.0370	LINC01090	0.00353	62	4	0	18	8	0
2	189080123	A	G	G	rs72897997	intronic,non_coding_transcript	0.0295	0.0295	LINC01090	0.78552	59	6	1	22	3	0
2	189084759	T	G	G	rs73043732	intronic,non_coding_transcript	0.0377	0.0377	LINC01090	0.00279	62	4	0	17	8	0
2	189084858	G	A	A	rs16829913	intronic,non_coding_transcript	0.0311	0.0311	LINC01090	0.00146	63	3	0	18	8	0
2	189085132	T	C	C	rs16829916	intronic,non_coding_transcript	0.0421	0.0421	LINC01090	0.00279	62	4	0	17	8	0
2	189086909	A	G	G	rs17235639	intronic,non_coding_transcript	0.0486	0.0486	LINC01090	0.77339	53	13	0	19	6	0
2	189093576	A	G	G	rs139110719	intronic,non_coding_transcript	0.0345	0.0345	LINC01090	0.00353	62	4	0	18	8	0
2	189098538	T	C	C	rs77518981	intronic,non_coding_transcript	0.0346	0.0346	LINC01090	0.00353	62	4	0	18	8	0
2	189106416	C	T	T	rs4536617	intronic,non_coding_transcript	0.0346	0.0346	LINC01090	0.00382	61	4	0	18	8	0
2	189108567	A	G	G	rs34477786	intronic,non_coding_transcript	0.0489	0.0489	LINC01090	0.00195	61	5	0	16	9	0
2	189110995	A	C	C	rs72903517	intronic,non_coding_transcript	0.0493	0.0493	LINC01090	0.00195	61	5	0	16	9	0
2	189112992	A	G	G	rs76427030	intronic,non_coding_transcript	0.0304	0.0304	LINC01090	0.00114	63	3	0	17	8	0
2	189117009	A	G	G	rs74596536	intronic,non_coding_transcript	0.0380	0.0380	LINC01090	0.00279	62	4	0	17	8	0
2	189129357	G	A	A	rs79376882	intronic,non_coding_transcript	0.0339	0.0339	LINC01090	0.00353	62	4	0	18	8	0
2	189130332	T	A	A	rs78784062	intronic,non_coding_transcript	0.0306	0.0306	LINC01090	0.00124	62	3	0	17	8	0
2	189137825	G	T	T	rs78533331	intronic,non_coding_transcript	0.0305	0.0305	LINC01090	0.00114	63	3	0	17	8	0
2	189138858	A	T	T	rs76319142	intronic,non_coding_transcript	0.0339	0.0339	LINC01090	0.00279	62	4	0	17	8	0
2	189142943	A	T	T	rs60688387	intronic,non_coding_transcript	0.0378	0.0378	LINC01090	0.00353	62	4	0	18	8	0
2	189147226	C	T	T	rs75927445	intronic,non_coding_transcript	0.0377	0.0377	LINC01090	0.00279	62	4	0	17	8	0
2	189149922	C	T	T	rs4490147	intronic,non_coding_transcript	0.0311	0.0311	LINC01090	0.00114	63	3	0	17	8	0
6	76019039	G	A	A	rs13217015	intronic	0.0499	0.0499	FILIP1	0.00082	61	5	0	16	9	1
6	76019395	C	G	G	rs13217241	intronic	0.0495	0.0495	FILIP1	0.00082	61	5	0	16	9	1
6	76019584	A	T	T	rs13217398	intronic	0.0495	0.0495	FILIP1	0.00060	61	5	0	15	9	1

6	76024704	G	A	A	rs62415695	missense	0.0184	0.0184	FILIP1	0.00181	65	1	0	20	5	1
6	76027221	A	G	G	rs13198000	intronic	0.0485	0.0485	FILIP1	0.00082	61	5	0	16	9	1
6	76038587	G	C	C	rs13193201	intronic	0.0490	0.0490	FILIP1	0.00082	61	5	0	16	9	1
6	76048681	G	T	T	rs78980779	intronic	0.0192	0.0192	FILIP1	0.00181	65	1	0	20	5	1
6	76086411	G	A	A	rs13203246	intronic	0.0499	0.0499	FILIP1	0.00033	62	4	0	16	9	1
6	76088207	A	C	C	rs13211248	intronic	0.0499	0.0499	FILIP1	0.00033	62	4	0	16	9	1
6	76156294	G	A	A	rs34747139	intronic	0.0454	0.0454	FILIP1	0.00085	62	4	0	16	8	1
6	76170874	C	A	A	rs9443176	intronic	0.0416	0.0416	FILIP1	0.00085	62	4	0	16	8	1
6	76183844	G	A	A	rs72877517	intronic	0.0447	0.0447	FILIP1	0.21916	52	13	0	23	2	0
11	83232915	G	A	A	rs114513645	intronic	0.0474	0.0474	DLG2	0.73157	57	8	0	21	4	0
11	83237817	C	G	G	rs1155272	intronic	0.0455	0.0455	DLG2	1.00000	57	9	0	22	4	0
11	83242900	G	A	A	rs117159938	intronic	0.0424	0.0424	DLG2	0.73017	58	8	0	21	4	0
11	83244370	T	C	C	rs996925	intronic	0.0456	0.0456	DLG2	0.74690	57	9	0	21	4	0
11	83255284	T	C	C	rs116983205	intronic	0.0428	0.0428	DLG2	0.73017	58	8	0	21	4	0
11	83259388	A	C	C	rs118015302	intronic	0.0464	0.0464	DLG2	0.74690	57	9	0	21	4	0
11	83264917	A	G	G	rs17463588	intronic	0.0256	0.0256	DLG2	0.74690	57	9	0	21	4	0
11	83375180	A	T	T	rs12791719	intronic	0.0398	0.0398	DLG2	0.06279	58	8	0	18	8	0
11	83377015	C	A	A	rs977822	intronic	0.0335	0.0335	DLG2	0.17547	59	7	0	19	6	0
11	83380474	G	A	A	rs34718216	intronic	0.0336	0.0336	DLG2	0.17547	59	7	0	19	6	0
11	83387738	C	T	T	rs76751610	intronic	0.0333	0.0333	DLG2	0.10333	59	7	0	19	5	1
11	83389547	A	T	T	rs12803579	intronic	0.0343	0.0343	DLG2	0.06500	58	8	0	18	6	1
11	83389577	C	A	A	rs34839973	intronic	0.0398	0.0398	DLG2	0.06500	58	8	0	18	6	1
11	83400031	C	T	T	rs34843650	intronic	0.0345	0.0345	DLG2	0.06500	58	8	0	18	6	1
11	83405196	A	G	G	rs12806068	intronic	0.0319	0.0319	DLG2	0.08178	59	7	0	19	6	1
11	83413022	A	G	G	rs1892949	intronic	0.0320	0.0320	DLG2	0.10333	59	7	0	19	5	1
11	83417779	C	T	T	rs71465553	intronic	0.0317	0.0317	DLG2	0.10333	59	7	0	19	5	1
11	83418812	C	T	T	rs12787861	intronic	0.0329	0.0329	DLG2	0.08178	59	7	0	19	6	1
11	83424657	A	G	G	rs34514322	intronic	0.0320	0.0320	DLG2	0.10333	59	7	0	19	5	1
11	83424825	T	C	C	rs34994208	intronic	0.0330	0.0330	DLG2	0.10333	59	7	0	19	5	1
11	83427143	A	C	C	rs35954003	intronic	0.0327	0.0327	DLG2	0.08178	59	7	0	19	6	1
11	83427549	C	T	T	rs118106162	intronic	0.0327	0.0327	DLG2	0.10333	59	7	0	19	5	1
11	83427586	G	A	A	rs117792962	intronic	0.0326	0.0326	DLG2	0.10333	59	7	0	19	5	1
11	83429731	G	A	A	rs71465554	intronic	0.0317	0.0317	DLG2	0.17547	59	7	0	19	6	0
11	83430048	G	A	A	rs116872257	intronic	0.0316	0.0316	DLG2	0.08178	59	7	0	19	6	1
11	83436606	G	T	T	rs35301519	intronic	0.0327	0.0327	DLG2	0.07030	58	8	0	19	6	1
11	83436879	C	T	T	rs17481934	intronic	0.0328	0.0328	DLG2	0.11742	58	8	0	19	5	1
11	83451753	T	C	C	rs36110284	intronic	0.0344	0.0344	DLG2	0.11742	58	8	0	19	5	1
11	83454878	G	A	A	rs12792825	intronic	0.0331	0.0331	DLG2	0.07030	58	8	0	19	6	1
11	83460859	T	C	C	rs12786565	intronic	0.0405	0.0405	DLG2	0.05388	57	8	0	18	7	1
11	83461366	T	C	C	rs71465556	intronic	0.0345	0.0345	DLG2	0.07030	58	8	0	19	6	1

11	83462110	A	C	C	rs71465557	intronic	0.0344	0.0344	DLG2	0.11742	58	8	0	19	5	1
11	83462245	T	C	C	rs34873133	intronic	0.0403	0.0403	DLG2	0.10134	57	9	0	18	6	1
11	83469530	C	T	T	rs4456272	intronic	0.0342	0.0342	DLG2	0.11742	58	8	0	19	5	1
11	83469764	A	T	T	rs71465559	intronic	0.0365	0.0365	DLG2	0.11742	58	8	0	19	5	1
11	83471488	C	G	G	rs148662532	intronic	0.0124	0.0124	DLG2	0.13742	62	3	0	22	3	1
11	83473103	C	A	A	rs34520201	intronic	0.0445	0.0445	DLG2	0.06038	57	9	0	18	7	1
11	83473291	C	T	T	rs35047639	intronic	0.0441	0.0441	DLG2	0.06038	57	9	0	18	7	1
11	83478153	C	T	T	rs76663974	intronic	0.0409	0.0409	DLG2	0.79699	57	8	1	23	2	0
11	83481286	G	A	A	rs79417402	intronic	0.0346	0.0346	DLG2	0.20777	58	8	0	20	6	0
11	83482085	C	T	T	rs61900028	intronic	0.0374	0.0374	DLG2	0.49988	56	10	0	23	2	0
11	83482647	A	C	C	rs12802155	intronic	0.0322	0.0322	DLG2	0.34130	57	9	0	19	6	0
11	83485395	T	C	C	rs71468352	intronic	0.0307	0.0307	DLG2	0.19653	58	8	0	19	6	0
11	83499391	C	T	T	rs77713322	intronic	0.0304	0.0304	DLG2	0.79699	57	8	1	23	2	0
11	83510016	G	A	A	rs80098460	intronic	0.0215	0.0215	DLG2	1.00000	57	9	0	22	3	0
11	83524658	C	T	T	rs12362201	intronic	0.0449	0.0449	DLG2	0.33478	54	12	0	23	2	0
11	83529668	A	T	T	rs78005836	intronic	0.0224	0.0224	DLG2	0.49839	59	7	0	22	4	0
11	83530139	T	C	C	rs117322638	intronic	0.0227	0.0227	DLG2	0.72340	57	7	0	22	4	0
11	83543747	C	T	T	rs80100935	intronic	0.0355	0.0355	DLG2	0.52285	62	3	1	22	3	0
11	83555201	C	A	A	rs76144509	intronic	0.0461	0.0461	DLG2	0.75217	56	10	0	23	3	0
11	83558415	C	T	T	rs72958255	intronic	0.0260	0.0260	DLG2	0.72086	57	9	0	23	2	0
11	83589911	C	T	T	rs17146314	intronic	0.0462	0.0462	DLG2	0.52280	54	11	1	24	2	0
11	83636021	C	T	T	rs11233813	intronic	0.0453	0.0453	DLG2	0.70191	60	6	0	22	3	0
11	83664354	G	A	A	rs79392602	intronic	0.0490	0.0490	DLG2	0.54308	54	12	0	23	3	0
11	83677047	T	C	C	rs34747709	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83677711	A	G	G	rs34310426	intronic	0.0462	0.0462	DLG2	0.00633	52	14	0	24	0	1
11	83677783	T	G	G	rs34826061	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83678621	C	G	G	rs35494684	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83678640	C	A	A	rs34197413	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83678730	T	C	C	rs12282675	intronic	0.0484	0.0484	DLG2	0.75015	55	11	0	22	3	0
11	83678734	T	A	A	rs71465567	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83678887	T	C	C	rs4133461	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83678920	A	C	C	rs963090	intronic	0.0464	0.0464	DLG2	0.00657	51	14	0	24	0	1
11	83679015	A	C	C	rs12290311	intronic	0.0497	0.0497	DLG2	0.75015	55	11	0	22	3	0
11	83679413	T	C	C	rs7482523	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83679979	T	C	C	rs71465568	intronic	0.0464	0.0464	DLG2	0.00460	52	14	0	25	0	1
11	83680070	G	A	A	rs71465569	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83680280	A	G	G	rs35693607	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83680391	G	C	C	rs12796172	intronic	0.0464	0.0464	DLG2	0.00460	52	14	0	25	0	1
11	83680397	T	C	C	rs11233866	intronic	0.0373	0.0373	DLG2	1.00000	56	9	1	23	3	0
11	83680596	T	C	C	rs34716185	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1

11	83680906	A	G	G	rs35240755	intronic	0.0461	0.0461	DLG2	0.00460	52	14	0	25	0	1
11	83681204	C	T	T	rs12790276	intronic	0.0463	0.0463	DLG2	0.00460	52	14	0	25	0	1
11	83681379	C	T	T	rs35307147	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83681457	G	C	C	rs35268360	intronic	0.0462	0.0462	DLG2	0.00460	52	14	0	25	0	1
11	83681470	G	A	A	rs34655432	intronic	0.0462	0.0462	DLG2	0.00633	52	14	0	24	0	1
11	83681548	G	A	A	rs34949067	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83682356	A	G	G	rs35540097	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83683244	G	T	T	rs71465571	intronic	0.0473	0.0473	DLG2	0.00633	52	14	0	24	0	1
11	83683312	A	G	G	rs71465572	intronic	0.0474	0.0474	DLG2	0.00633	52	14	0	24	0	1
11	83683445	G	A	A	rs12804617	intronic	0.0474	0.0474	DLG2	0.00633	52	14	0	24	0	1
11	83683640	A	G	G	rs12804532	intronic	0.0473	0.0473	DLG2	0.00633	52	14	0	24	0	1
11	83683790	G	C	C	rs12805402	intronic	0.0473	0.0473	DLG2	0.00633	52	14	0	24	0	1
11	83683815	T	A	A	rs34912232	intronic	0.0474	0.0474	DLG2	0.00633	52	14	0	24	0	1
11	83683854	C	T	T	rs35024645	intronic	0.0474	0.0474	DLG2	0.00633	52	14	0	24	0	1
11	83683932	G	A	A	rs36114419	intronic	0.0473	0.0473	DLG2	0.00633	52	14	0	24	0	1
11	83684393	G	C	C	rs34272592	intronic	0.0474	0.0474	DLG2	0.00633	52	14	0	24	0	1
11	83684792	A	T	T	rs35812794	intronic	0.0470	0.0470	DLG2	0.00633	52	14	0	24	0	1
11	83684934	A	G	G	rs71468355	intronic	0.0471	0.0471	DLG2	0.00633	52	14	0	24	0	1
11	83684949	C	T	T	rs71468356	intronic	0.0472	0.0472	DLG2	0.00633	52	14	0	24	0	1
11	83685111	T	C	C	rs77093335	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83685208	A	T	T	rs77985485	intronic	0.0463	0.0463	DLG2	0.00657	51	14	0	24	0	1
11	83685270	A	G	G	rs80349643	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83685317	G	A	A	rs79892044	intronic	0.0464	0.0464	DLG2	0.00657	51	14	0	24	0	1
11	83685451	T	G	G	rs71465573	intronic	0.0462	0.0462	DLG2	0.00657	51	14	0	24	0	1
11	83685540	T	G	G	rs71465574	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83685725	A	C	C	rs12794213	intronic	0.0462	0.0462	DLG2	0.00633	52	14	0	24	0	1
11	83685924	C	T	T	rs34436974	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83686159	T	C	C	rs71465575	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83686254	A	G	G	rs71465576	intronic	0.0463	0.0463	DLG2	0.00633	52	14	0	24	0	1
11	83686428	A	G	G	rs71465577	intronic	0.0462	0.0462	DLG2	0.00657	51	14	0	24	0	1
11	83686440	A	T	T	rs71465578	intronic	0.0464	0.0464	DLG2	0.00657	51	14	0	24	0	1
11	83686572	A	G	G	rs71465579	intronic	0.0463	0.0463	DLG2	0.00657	51	14	0	24	0	1
11	83686609	A	G	G	rs71465580	intronic	0.0463	0.0463	DLG2	0.00657	51	14	0	24	0	1
11	83686635	A	G	G	rs71465581	intronic	0.0463	0.0463	DLG2	0.00657	51	14	0	24	0	1
11	83692232	T	G	G	rs34756786	intronic	0.0464	0.0464	DLG2	0.00633	52	14	0	24	0	1
11	83735515	G	A	A	rs80196056	intronic	0.0475	0.0475	DLG2	0.75015	55	11	0	22	3	0
11	83737618	G	A	A	rs17146592	intronic	0.0491	0.0491	DLG2	0.74966	55	11	0	23	3	0
11	83767440	G	A	A	rs11233892	intronic	0.0480	0.0480	DLG2	0.74966	55	11	0	23	3	0
11	83778678	A	G	G	rs35239124	intronic	0.0441	0.0441	DLG2	0.47692	55	10	1	24	1	0
11	83786559	T	C	C	rs34012933	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0

11	83791441	T	C	C	rs17561231	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83796163	T	C	C	rs2187553	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83798382	G	A	A	rs34309181	intronic	0.0389	0.0389	DLG2	0.16792	55	11	0	25	1	0
11	83798496	T	C	C	rs34846175	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83798802	T	C	C	rs34045362	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83802683	G	T	T	rs34899787	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83803464	A	G	G	rs71469619	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83807535	T	C	C	rs17495791	intronic	0.0142	0.0142	DLG2	0.43524	58	7	0	24	1	0
11	83813177	T	C	C	rs75925390	intronic	0.0387	0.0387	DLG2	0.16792	55	11	0	25	1	0
11	83814433	G	C	C	rs71469623	intronic	0.0387	0.0387	DLG2	0.16784	54	11	0	25	1	0
11	83821405	C	T	T	rs12808867	intronic	0.0387	0.0387	DLG2	0.16792	55	11	0	25	1	0
11	83821870	C	A	A	rs12785867	intronic	0.0386	0.0386	DLG2	0.16812	55	11	0	24	1	0
11	83827128	G	T	T	rs75687645	intronic	0.0439	0.0439	DLG2	1.00000	55	9	2	21	4	0
11	83828197	G	C	C	rs12808314	intronic	0.0378	0.0378	DLG2	0.16792	55	11	0	25	1	0
11	83828665	T	C	C	rs71469624	intronic	0.0379	0.0379	DLG2	0.16792	55	11	0	25	1	0
11	83830087	C	T	T	rs35992468	intronic	0.0378	0.0378	DLG2	0.16812	55	11	0	24	1	0
11	83839007	G	A	A	rs116913890	intronic	0.0445	0.0445	DLG2	1.00000	55	9	2	21	4	0
11	83839703	C	A	A	rs71469625	intronic	0.0387	0.0387	DLG2	0.16812	55	11	0	24	1	0
11	83844499	T	C	C	rs34770791	intronic	0.0388	0.0388	DLG2	0.16812	55	11	0	24	1	0
11	83846946	G	A	A	rs35615041	intronic	0.0388	0.0388	DLG2	0.16792	55	11	0	25	1	0
11	83850610	T	C	C	rs71469626	intronic	0.0387	0.0387	DLG2	0.16812	55	11	0	24	1	0
11	83851228	G	A	A	rs71469627	intronic	0.0387	0.0387	DLG2	0.16812	55	11	0	24	1	0
11	83855558	A	C	C	rs12788130	intronic	0.0385	0.0385	DLG2	0.16792	55	11	0	25	1	0
11	83856459	T	C	C	rs34337231	intronic	0.0385	0.0385	DLG2	0.16812	55	11	0	24	1	0
11	83857766	T	C	C	rs35969270	intronic	0.0385	0.0385	DLG2	0.16733	54	11	0	24	1	0
11	83860894	G	A	A	rs71469629	intronic	0.0386	0.0386	DLG2	0.16812	55	11	0	24	1	0
11	83862352	T	G	G	rs71469630	intronic	0.0384	0.0384	DLG2	0.16812	55	11	0	24	1	0
11	83866720	A	T	T	rs11233929	intronic	0.0467	0.0467	DLG2	1.00000	55	9	2	21	4	0
11	83867612	T	C	C	rs71469631	intronic	0.0385	0.0385	DLG2	0.16812	55	11	0	24	1	0
11	83875056	A	C	C	rs35910823	intronic	0.0385	0.0385	DLG2	0.16812	55	11	0	24	1	0
11	83878183	T	C	C	rs12801364	intronic	0.0381	0.0381	DLG2	0.16812	55	11	0	24	1	0
11	83880139	A	T	T	rs373152600	intronic	0.0378	0.0378	DLG2	0.17020	55	11	0	23	1	0
11	83882227	C	T	T	rs78328809	intronic	0.0450	0.0450	DLG2	1.00000	55	9	2	22	4	0
11	83888454	C	G	G	rs12808048	intronic	0.0381	0.0381	DLG2	0.16812	55	11	0	24	1	0
11	83890296	T	C	C	rs12799079	intronic	0.0409	0.0409	DLG2	0.10154	53	13	0	23	1	0
11	83892801	C	T	T	rs34386657	intronic	0.0360	0.0360	DLG2	0.16812	55	11	0	24	1	0
11	83899234	A	G	G	rs11233934	intronic	0.0486	0.0486	DLG2	0.75113	55	9	2	20	5	0
11	83900060	A	G	G	rs34042104	intronic	0.0407	0.0407	DLG2	0.10130	53	13	0	24	1	0
11	83903212	A	T	T	rs73517787	intronic	0.0439	0.0439	DLG2	0.10130	53	13	0	24	1	0
11	83903240	A	G	G	rs74448633	intronic	0.0406	0.0406	DLG2	0.10130	53	13	0	24	1	0

11	83903511	C	T	T	rs35502448	intronic	0.0403	0.0403	DLG2	0.10282	53	13	0	25	1	0
11	83905317	G	A	A	rs73517792	intronic	0.0491	0.0491	DLG2	0.21764	53	13	0	24	2	0
11	83906010	C	G	G	rs12800271	intronic	0.0402	0.0402	DLG2	0.06055	52	13	0	25	1	0
11	83907441	G	A	A	rs77892201	intronic	0.0482	0.0482	DLG2	0.10130	53	13	0	24	1	0
11	83907455	C	T	T	rs79602990	intronic	0.0408	0.0408	DLG2	0.10130	53	13	0	24	1	0
11	83908287	T	C	C	rs59681368	intronic	0.0474	0.0474	DLG2	0.10130	53	13	0	24	1	0
11	83908345	G	A	A	rs75344440	intronic	0.0407	0.0407	DLG2	0.10121	52	13	0	24	1	0
11	83922479	G	C	C	rs71469640	intronic	0.0409	0.0409	DLG2	0.10130	53	13	0	24	1	0
11	83924357	T	C	C	rs75384284	intronic	0.0425	0.0425	DLG2	0.10130	53	13	0	24	1	0
11	83926691	A	G	G	rs34664733	intronic	0.0427	0.0427	DLG2	0.10130	53	13	0	24	1	0
11	83942171	T	C	C	rs11233957	intronic	0.0324	0.0324	DLG2	1.00000	56	9	1	22	3	0
11	83954261	T	C	C	rs74818442	intronic	0.0199	0.0199	DLG2	1.00000	60	5	1	22	2	0
11	83961660	C	G	G	rs17159833	intronic	0.0290	0.0290	DLG2	0.49839	59	7	0	22	4	0
11	83965933	A	T	T	rs11233966	intronic	0.0402	0.0402	DLG2	1.00000	55	10	1	22	4	0
11	83979308	C	A	A	rs11233971	intronic	0.0214	0.0214	DLG2	0.75945	61	4	1	23	2	0
11	83985299	C	G	G	rs17500125	intronic	0.0475	0.0475	DLG2	0.27806	56	10	0	24	1	0
11	83987664	C	T	T	rs80140888	intronic	0.0442	0.0442	DLG2	0.54181	53	13	0	22	3	0
11	84037134	C	T	T	rs72959544	intronic	0.0356	0.0356	DLG2	0.00907	60	4	1	18	7	0
11	84051729	G	A	A	rs61899215	intronic	0.0246	0.0246	DLG2	0.59212	58	7	1	25	1	0
11	84073212	A	G	G	rs116901444	intronic	0.0215	0.0215	DLG2	0.75945	61	4	1	23	2	0
11	84124557	A	T	T	rs11234016	intronic	0.0224	0.0224	DLG2	1.00000	60	5	1	23	2	0
11	84148078	C	T	T	rs12793229	intronic	0.0264	0.0264	DLG2	0.76318	60	5	1	25	1	0
11	84157083	A	G	G	rs71468372	intronic	0.0382	0.0382	DLG2	0.16938	62	3	1	21	4	0
11	84161506	A	C	C	rs79104196	intronic	0.0439	0.0439	DLG2	0.50269	55	11	0	23	2	0
11	84168666	C	T	T	rs11234035	intronic	0.0493	0.0493	DLG2	1.00000	53	11	2	21	4	0
11	84203688	C	T	T	rs11234045	intronic	0.0406	0.0406	DLG2	0.16812	55	11	0	24	1	0
11	84216892	T	C	C	rs17808372	intronic	0.0481	0.0481	DLG2	0.37817	51	15	0	22	3	0
11	84238326	T	C	C	rs1367538	intronic	0.0237	0.0237	DLG2	1.00000	59	6	1	24	2	0
11	84257549	C	T	T	rs11234071	intronic	0.0237	0.0237	DLG2	1.00000	59	6	1	23	2	0
11	84265771	G	A	A	rs111685275	intronic	0.0452	0.0452	DLG2	0.77969	54	9	3	21	4	0
11	84298759	G	A	A	rs77693614	intronic	0.0238	0.0238	DLG2	1.00000	59	6	1	23	2	0
11	84378128	T	C	C	rs71469652	intronic	0.0463	0.0463	DLG2	0.29927	59	7	0	20	5	0
11	84395708	C	A	A	rs118128180	intronic	0.0434	0.0434	DLG2	1.00000	56	10	0	22	4	0
11	84557455	T	G	G	rs113083358	intronic	0.0281	0.0281	DLG2	0.39891	58	8	0	21	3	1
11	84561099	T	G	G	rs117287296	intronic	0.0452	0.0452	DLG2	0.10783	62	4	0	20	5	0
11	84565540	C	A	A	rs1943717	intronic	0.0408	0.0408	DLG2	0.11105	62	4	0	21	5	0
11	84580040	A	C	C	rs76074207	intronic	0.0387	0.0387	DLG2	1.00000	57	9	0	23	3	0
11	84581522	T	C	C	rs7125471	intronic	0.0493	0.0493	DLG2	0.10783	62	4	0	20	5	0
11	84598257	T	G	G	rs76429934	intronic	0.0278	0.0278	DLG2	0.37598	58	7	0	21	3	1
11	84639183	G	C	C	rs72955531	intronic	0.0437	0.0437	DLG2	1.00000	62	3	1	24	1	0

11	84749449	C	T	T	rs74775461	intronic	0.0437	0.0437	DLG2	0.29927	59	7	0	20	5	0
11	84789864	A	G	G	rs111410955	intronic	0.0255	0.0255	DLG2	0.72086	57	9	0	23	2	0
11	84837883	G	A	A	rs35003694	intronic	0.0397	0.0397	DLG2	0.73017	58	8	0	21	4	0
11	84918461	T	C	C	rs112844595	intronic	0.0206	0.0206	DLG2	1.00000	57	9	0	22	3	0
11	84991145	C	T	T	rs189136848	intronic	0.0096	0.0096	DLG2	0.40582	59	6	1	25	0	0
11	84991169	C	A	A	rs192808445	intronic	0.0096	0.0096	DLG2	0.40582	59	6	1	25	0	0
11	84996976	A	G	G	rs35695258	intronic	0.0145	0.0145	DLG2	1.00000	58	7	0	23	2	0
11	85006195	A	T	T	rs1016636	intronic	0.0388	0.0388	DLG2	0.06574	60	5	0	19	6	0
11	85024079	T	C	C	rs185755081	intronic	0.0097	0.0097	DLG2	0.22343	59	6	1	26	0	0
11	85060360	C	G	G	rs12794044	intronic	0.0157	0.0157	DLG2	0.72129	58	8	0	23	2	0
11	85086043	A	T	T	rs35395221	intronic	0.0142	0.0142	DLG2	1.00000	59	7	0	23	2	0
11	85203814	C	T	T	rs77687788	intronic	0.0399	0.0399	DLG2	0.02367	62	4	0	19	6	0
11	85203882	G	A	A	rs75993784	intronic	0.0431	0.0431	DLG2	0.51888	57	9	0	20	5	0
11	85250747	G	A	A	rs7939547	intronic	0.0393	0.0393	DLG2	0.01641	61	5	0	18	7	0
11	85262722	T	C	C	rs7931722	intronic	0.0394	0.0394	DLG2	0.02002	62	4	0	18	6	0
11	85272815	T	G	G	rs505238	intronic	0.0310	0.0310	DLG2	0.54181	53	13	0	22	3	0
11	85300458	G	A	A	rs576722	intronic	0.0191	0.0191	DLG2	0.72218	57	9	0	24	2	0
15	47471564	A	G	G	rs146546695	upstream	0.0428	0.0428	SEMA6D	0.59042	57	8	1	24	1	0
15	47472960	G	A	A	rs79135353	upstream	0.0407	0.0407	SEMA6D	0.50649	58	8	0	21	5	0
15	47499732	G	A	A	rs77819625	intronic	0.0189	0.0189	SEMA6D	0.00641	64	1	1	21	5	0
15	47524094	T	C	C	rs80085470	intronic	0.0192	0.0192	SEMA6D	0.00553	64	1	1	20	5	0
15	47540002	A	G	G	rs78106502	intronic	0.0408	0.0408	SEMA6D	0.00553	64	1	1	20	5	0
15	47540559	A	G	G	rs11856688	intronic	0.0462	0.0462	SEMA6D	1.00000	58	8	0	22	3	0
15	47541152	C	T	T	rs117884763	intronic	0.0211	0.0211	SEMA6D	0.00641	64	1	1	21	5	0
15	47541811	C	T	T	rs76035674	intronic	0.0210	0.0210	SEMA6D	0.00553	64	1	1	20	5	0
15	47543232	T	C	C	rs76999103	intronic	0.0192	0.0192	SEMA6D	0.00641	64	1	1	21	5	0
15	47552814	A	G	G	rs78673643	intronic	0.0216	0.0216	SEMA6D	0.00641	64	1	1	21	5	0
15	47557518	C	T	T	rs72731766	intronic	0.0276	0.0276	SEMA6D	1.00000	57	8	1	23	3	0
15	47580975	A	G	G	rs7174561	intronic	0.0320	0.0320	SEMA6D	0.00641	64	1	1	21	5	0
15	47582288	C	G	G	rs78142733	intronic	0.0217	0.0217	SEMA6D	0.00553	64	1	1	20	5	0
15	47589031	T	G	G	rs17358151	intronic	0.0211	0.0211	SEMA6D	0.00553	64	1	1	20	5	0
15	47589185	G	T	T	rs75474152	intronic	0.0259	0.0259	SEMA6D	0.00553	64	1	1	20	5	0
15	47630156	C	T	T	rs77144407	intronic	0.0389	0.0389	SEMA6D	1.00000	58	8	0	23	3	0
15	47643236	C	T	T	rs117401545	intronic	0.0375	0.0375	SEMA6D	1.00000	58	8	0	22	3	0
15	47697796	G	C	C	rs61998609	intronic	0.0429	0.0429	SEMA6D	0.52276	53	12	1	24	2	0
15	47699041	T	C	C	rs76187847	intronic	0.0220	0.0220	SEMA6D	0.01640	63	2	0	20	4	1
15	47704791	G	A	A	rs79372522	intronic	0.0268	0.0268	SEMA6D	0.01558	64	2	0	20	4	1
15	47714563	C	A	A	rs16959446	intronic	0.0437	0.0437	SEMA6D	0.51682	53	12	1	23	2	0
15	47722435	A	G	G	rs111589399	intronic	0.0238	0.0238	SEMA6D	0.01558	64	2	0	20	4	1
15	47724040	G	A	A	rs4775685	intronic	0.0437	0.0437	SEMA6D	0.51682	53	12	1	23	2	0

15	47727933	T	C	C	rs74787996	intronic	0.0492	0.0492	SEMA6D	0.51682	53	12	1	23	2	0
15	47734225	T	A	A	rs76552436	intronic	0.0498	0.0498	SEMA6D	0.51682	53	12	1	23	2	0
15	47775809	G	A	A	rs61998616	intronic	0.0283	0.0283	SEMA6D	0.59042	57	8	1	24	1	0
15	47785052	T	G	G	rs75701467	intronic	0.0200	0.0200	SEMA6D	1.00000	55	11	0	22	4	0
15	47839035	A	G	G	rs72733864	intronic	0.0498	0.0498	SEMA6D	0.06460	61	5	0	19	6	0
15	47857783	G	C	C	rs61998619	intronic	0.0297	0.0297	SEMA6D	0.75945	59	6	1	24	1	0
15	47887164	G	A	A	rs117833852	intronic	0.0268	0.0268	SEMA6D	0.50269	55	11	0	23	2	0
15	47935535	T	C	C	rs76732631	intronic	0.0290	0.0290	SEMA6D	0.76310	59	5	1	25	1	0
15	47944782	T	C	C	rs1369639	intronic	0.0472	0.0472	SEMA6D	0.10353	54	12	0	24	1	0
15	47965075	A	G	G	rs72735833	intronic	0.0394	0.0394	SEMA6D	0.00038	64	2	0	17	8	0
15	47967262	C	T	T	rs17386817	intronic	0.0191	0.0191	SEMA6D	0.16733	54	11	0	24	1	0
15	47967971	C	T	T	rs79207249	intronic	0.0329	0.0329	SEMA6D	0.59212	58	7	1	25	1	0
15	47979578	G	A	A	rs17327778	intronic	0.0463	0.0463	SEMA6D	1.00000	58	7	0	22	3	0
15	47988326	G	A	A	rs72735842	intronic	0.0386	0.0386	SEMA6D	0.00114	63	3	0	17	8	0
15	48008619	A	G	G	rs72735850	upstream	0.0478	0.0478	SEMA6D	1.00000	60	5	1	23	2	0
15	48023229	A	G	G	rs150484536	intronic	0.0274	0.0274	SEMA6D	0.27275	56	9	0	24	1	0
15	48050564	C	T	T	rs56376571	intronic	0.0209	0.0209	SEMA6D	0.00141	64	2	0	18	7	0
15	48058769	T	A	A	rs16960071	intronic	0.0263	0.0263	SEMA6D	0.61255	63	3	0	23	2	0
16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.47621	60	5	1	22	4	0
16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.00994	0	11	55	1	0	25
16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.00994	0	11	55	1	0	25
16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.00994	0	11	55	1	0	25
16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.00994	0	11	55	1	0	25
16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.00000	59	7	0	23	3	0
16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.00633	0	14	52	1	0	24
16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.00000	59	7	0	23	3	0
16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.00460	0	14	52	1	0	25
16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.00460	0	14	52	1	0	25
16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.00460	0	14	52	1	0	25
16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.00460	0	14	52	1	0	25
16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.00460	0	14	52	1	0	25
16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.00460	0	14	52	1	0	25
16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.00460	0	14	52	1	0	25
16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.00460	0	14	52	1	0	25
16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.00000	59	7	0	23	3	0
16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.34868	61	4	1	22	4	0
16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.00460	0	14	52	1	0	25
16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.00460	0	14	52	1	0	25
16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.00460	0	14	52	1	0	25
16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.00460	0	14	52	1	0	25

16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.00000	59	7	0	23	3	0
16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.00460	0	14	52	1	0	25
16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.00000	59	7	0	23	3	0
16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.00460	0	14	52	1	0	25
16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.00000	59	7	0	22	3	0
16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.00159	0	17	49	1	0	24
16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.00118	0	17	49	1	0	25
16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.00000	59	7	0	23	3	0
16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.00000	59	7	0	23	3	0
16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.00000	59	7	0	23	3	0
16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.00149	0	16	50	1	0	25
16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.00149	0	16	49	1	0	25
16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.00149	0	16	50	1	0	25
16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.00000	59	7	0	23	3	0
16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.00149	0	16	50	1	0	25
16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.00000	59	7	0	23	3	0
16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.00240	0	16	50	1	0	24
16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.00149	0	16	50	1	0	25
16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.00149	0	16	50	1	0	25
16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.00149	0	16	50	1	0	25
16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.00149	0	16	50	1	0	25
16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.00240	0	16	50	1	0	24
16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.00240	0	16	50	1	0	24
16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.00240	0	16	50	1	0	24
16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.73476	58	8	0	22	4	0
16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.00240	0	16	50	1	0	24
16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.00149	0	16	50	1	0	25
16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.00240	0	16	50	1	0	24
16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.00149	0	16	49	1	0	25
16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.00240	0	16	50	1	0	24
16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.00149	0	16	50	1	0	25
16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.50649	58	8	0	21	5	0
16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.00149	0	16	50	1	0	25
16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.00149	0	16	50	1	0	25
16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.00240	0	16	50	1	0	24
16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.30238	58	7	0	20	5	0
16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.00149	0	16	50	1	0	25
16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.00149	0	16	50	1	0	25
16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.03433	0	15	51	0	1	25
16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.00000	53	12	0	21	4	0

16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.16792	0	11	55	0	1	25
16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.16812	0	11	55	0	1	24
16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.33476	54	12	0	24	2	0
16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.75217	56	10	0	23	3	0
16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.00000	57	9	0	23	3	0
16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.75217	56	10	0	23	3	0
16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.69190	60	4	1	25	0	0
16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.72129	58	8	0	23	2	0
16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.71919	58	8	0	24	2	0
16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.72129	58	8	0	23	2	0
16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.72009	57	8	0	23	2	0
16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.72009	57	8	0	23	2	0
16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.18770	59	7	0	21	4	1
16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.85826	57	7	2	22	4	0
16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.46312	59	6	0	22	4	0
16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.46031	60	6	0	22	4	0

Table S4 (A): Significant results from pathway-based tests

REACTOME PATHWAY	# MUTATIONS All	 p value < 0.05	P VALUE (P/WAY-BASED)	FWER
Activation of NF-kappaB in B cells	264	74	4.89E-09	9.68E-06
WNT5A-dependent internalization of FZD4	187	49	1.31E-06	2.59E-03
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	190	48	1.33E-06	2.64E-03
Downstream signaling events of B Cell Receptor (BCR)	345	74	4.60E-06	9.05E-03
Depolymerisation of the Nuclear Lamina	191	48	5.88E-06	1.16E-02
Disinhibition of SNARE formation	177	48	6.89E-06	1.35E-02
Disassembly of the destruction complex and recruitment of AXIN to the membrane	123	43	3.67E-05	7.00E-02

Table S4 (B): Variants with MAF<5% in signifiant pathways

REACTOME PATHWAY	CHROM	POS	REF	ALT	MINOR ALLELE	ID	CONSEQUENCE	AF	MAF	SYMBOL	P VALUE	# RESPONDERS			# NON-RESPONDERS		
												Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt
Activation of NF-kappaB in B cells	1	85738304	T	G	G	rs141532778	intronic	0.0265	0.0265	BCL10	0.1949	59	7	0	24	1	1
Activation of NF-kappaB in B cells	1	85742155	G	A	A	rs78416998	5_prime_UTR	0.0349	0.0349	BCL10	0.7734	60	5	1	23	3	0
Activation of NF-kappaB in B cells	1	109959684	G	A	A	rs12119154	intronic	0.0463	0.0463	PSMA5	0.3842	59	7	0	22	3	1
Activation of NF-kappaB in B cells	2	54106726	G	A	A	rs78542544	intronic	0.0466	0.0466	PSME4	0.0565	56	10	0	25	0	0
Activation of NF-kappaB in B cells	2	54109699	G	A	A	rs75679248	intronic	0.0345	0.0345	PSME4	1.0000	57	9	0	22	3	0
Activation of NF-kappaB in B cells	2	54112612	T	G	G	rs115678984	intronic	0.0340	0.0340	PSME4	0.7302	58	8	0	21	4	0
Activation of NF-kappaB in B cells	2	54116463	C	T	T	rs805403	intronic	0.0376	0.0376	PSME4	0.2083	62	4	0	21	4	0
Activation of NF-kappaB in B cells	2	54119870	T	C	C	rs77215245	intronic	0.0487	0.0487	PSME4	0.6362	55	10	1	23	2	0
Activation of NF-kappaB in B cells	2	54121956	T	C	C	rs79436269	intronic	0.0498	0.0498	PSME4	0.6362	55	10	1	23	2	0
Activation of NF-kappaB in B cells	2	54131546	T	C	C	rs78887562	intronic	0.0467	0.0467	PSME4	0.0565	56	10	0	25	0	0
Activation of NF-kappaB in B cells	2	54132737	G	A	A	rs75125553	intronic	0.0493	0.0493	PSME4	0.6407	54	10	1	24	2	0
Activation of NF-kappaB in B cells	2	54148310	G	C	C	rs74545963	intronic	0.0348	0.0348	PSME4	1.0000	57	9	0	23	3	0
Activation of NF-kappaB in B cells	2	54153284	A	G	G	rs62139281	intronic	0.0226	0.0226	PSME4	0.0237	62	4	0	19	6	0
Activation of NF-kappaB in B cells	2	54161109	A	C	C	rs74627832	intronic	0.0468	0.0468	PSME4	0.0565	56	10	0	25	0	0
Activation of NF-kappaB in B cells	2	54166671	C	T	T	rs79435818	intronic	0.0317	0.0317	PSME4	1.0000	58	8	0	23	3	0
Activation of NF-kappaB in B cells	2	54166800	A	G	G	rs76811723	intronic	0.0317	0.0317	PSME4	1.0000	58	8	0	22	3	0
Activation of NF-kappaB in B cells	2	54176733	C	A	A	rs115660490	intronic	0.0366	0.0366	PSME4	0.7213	58	8	0	23	2	0
Activation of NF-kappaB in B cells	2	54182973	T	A	A	rs114515761	intronic	0.0346	0.0346	PSME4	0.7192	58	8	0	24	2	0
Activation of NF-kappaB in B cells	2	54188394	T	A	A	rs11692784	intronic	0.0346	0.0346	PSME4	0.7192	58	8	0	24	2	0
Activation of NF-kappaB in B cells	2	54198172	G	A	A	rs141622297	upstream	0.0360	0.0360	PSME4	0.7192	58	8	0	24	2	0
Activation of NF-kappaB in B cells	2	54201823	G	A	A	rs74336645	upstream	0.0362	0.0362	PSME4	0.7213	58	8	0	23	2	0
Activation of NF-kappaB in B cells	2	61155012	C	G	G	rs79263888	3_prime_UTR	0.0229	0.0229	REL	0.7522	56	10	0	23	3	0
Activation of NF-kappaB in B cells	2	162169482	G	A	A	rs7605885	intronic	0.0425	0.0425	PSMD14	0.8183	56	9	1	21	4	0
Activation of NF-kappaB in B cells	2	162215335	C	T	T	rs6722186	intronic	0.0427	0.0427	PSMD14	1.0000	56	9	1	22	4	0
Activation of NF-kappaB in B cells	2	231921109	G	A	A	rs3754982	upstream	0.0430	0.0430	PSMD1	0.0899	60	6	0	25	0	1
Activation of NF-kappaB in B cells	2	231926692	G	A	A	rs80031661	intronic	0.0429	0.0429	PSMD1	0.0899	60	6	0	25	0	1
Activation of NF-kappaB in B cells	2	231932134	T	C	C	rs78964764	intronic	0.0433	0.0433	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231933408	C	T	T	rs13424110	intronic	0.0476	0.0476	PSMD1	0.1782	59	7	0	20	4	1
Activation of NF-kappaB in B cells	2	231937539	T	C	C	rs2288148	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231939526	A	G	G	rs12620983	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231947467	A	G	G	rs11694724	intronic	0.0411	0.0411	PSMD1	0.2744	57	9	0	24	1	0
Activation of NF-kappaB in B cells	2	231949569	T	C	C	rs2303354	intronic	0.0433	0.0433	PSMD1	0.0876	59	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231950847	T	G	G	rs78363488	intronic	0.0407	0.0407	PSMD1	0.4353	57	8	0	24	1	0
Activation of NF-kappaB in B cells	2	231967886	T	C	C	rs12616914	intronic	0.0436	0.0436	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231979258	A	G	G	rs17586405	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231982950	T	C	C	rs60707561	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	231983382	T	G	G	rs17619636	intronic	0.0478	0.0478	PSMD1	0.0899	60	6	0	25	0	1
Activation of NF-kappaB in B cells	2	231998010	G	A	A	rs77199363	intronic	0.0431	0.0431	PSMD1	0.0899	60	6	0	25	0	1
Activation of NF-kappaB in B cells	2	232003189	C	T	T	rs80121410	intronic	0.0408	0.0408	PSMD1	0.2744	57	9	0	24	1	0
Activation of NF-kappaB in B cells	2	232021354	T	C	C	rs115196328	intronic	0.0402	0.0402	PSMD1	0.5418	53	13	0	22	3	0
Activation of NF-kappaB in B cells	2	232025880	C	T	T	rs76901853	intronic	0.0472	0.0472	PSMD1	0.0863	60	6	0	24	0	1
Activation of NF-kappaB in B cells	2	232036567	G	A	A	rs11674175	intronic	0.0409	0.0409	PSMD1	0.2744	57	9	0	24	1	0
Activation of NF-kappaB in B cells	2	232041640	G	A	A	rs111612792	downstream	0.0413	0.0413	PSMD1	0.2719	57	9	0	25	1	0
Activation of NF-kappaB in B cells	3	63994801	G	A	A	rs62252370	downstream	0.0360	0.0360	PSMD6	1.0000	58	8	0	23	3	0
Activation of NF-kappaB in B cells	4	103436737	T	C	C	rs79590323	intronic	0.0393	0.0393	NFKB1	0.4981	56	10	0	24	2	0
Activation of NF-kappaB in B cells	4	103441152	G	A	A	rs74833382	intronic	0.0318	0.0318	NFKB1	0.7621	59	6	1	25	1	0
Activation of NF-kappaB in B cells	4	103441742	G	A	A	rs78900265	intronic	0.0393	0.0393	NFKB1	0.4999	56	10	0	23	2	0
Activation of NF-kappaB in B cells	4	103465229	C	T	T	rs76016852	intronic	0.0414	0.0414	NFKB1	0.4999	56	10	0	23	2	0
Activation of NF-kappaB in B cells	4	103534557	C	T	T	rs4648117	intronic	0.0416	0.0416	NFKB1	0.7621	59	6	1	25	1	0
Activation of NF-kappaB in B cells	4	103535905	C	T	T	rs4648127	intronic	0.0389	0.0389	NFKB1	0.4974	55	10	0	24	2	0
Activation of NF-kappaB in B cells	4	103542005	G	T	T	rs997476	downstream	0.0397	0.0397	NFKB1	0.4981	56	10	0	24	2	0
Activation of NF-kappaB in B cells	5	133505097	T	C	C	rs34751193	intronic	0.0303	0.0303	SKP1	0.7497	55	11	0	23	3	0
Activation of NF-kappaB in B cells	5	133512605	G	T	T	rs11538030	5_prime_UTR	0.0356	0.0356	SKP1	0.6295	55	9	2	24	2	0
Activation of NF-kappaB in B cells	5	171287624	C	G	C	rs702109	downstream	0.9605	0.0395	FBXW11	0.1356	0	13	52	1	2	22
Activation of NF-kappaB in B cells	5	171319929	T	C	C	rs17569783	intronic	0.0456	0.0456	FBXW11	1.0000	59	6	1	23	2	0
Activation of NF-kappaB in B cells	5	171387634	G	A	A	rs72835279	intronic	0.0450	0.0450	FBXW11	1.0000	59	6	1	24	2	0
Activation of NF-kappaB in B cells	5	171420105	G	C	C	rs72835287	intronic	0.0441	0.0441	FBXW11	0.2719	57	9	0	25	1	0
Activation of NF-kappaB in B cells	5	171424137	T	G	G	rs72835288	intronic	0.0465	0.0465	FBXW11	1.0000	59	6	1	24	2	0
Activation of NF-kappaB in B cells	6	32810147	G	T	T	rs41270496	intronic	0.0323	0.0323	PSMB8	0.4984	59	7	0	22	4	0

Activation of NF-kappaB in B cells	6	32811224	A	T	T	rs72854938	intronic	0.0322	0.0322	PSMB8	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	6	32811366	G	T	T	rs72854939	intronic	0.0322	0.0322	PSMB8	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	6	32826688	G	T	T	rs115353581	intronic	0.0219	0.0219	PSMB9	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	6	32832218	A	T	T	rs116481206	downstream	0.0219	0.0219	PSMB9	0.4862	59	7	0	21	4	0
Activation of NF-kappaB in B cells	6	44227224	C	T	T	rs28362860	intronic	0.0269	0.0269	NFKBIE	0.4603	60	6	0	22	4	0
Activation of NF-kappaB in B cells	6	44233216	G	C	C	rs28362857	missense	0.0296	0.0296	NFKBIE	0.0685	61	5	0	20	6	0
Activation of NF-kappaB in B cells	6	91239702	T	A	A	rs62409064	intronic	0.0407	0.0407	MAP3K7	0.4940	58	7	1	20	5	0
Activation of NF-kappaB in B cells	6	91296810	C	T	T	rs34016005	upstream	0.0303	0.0303	MAP3K7	0.4762	60	5	1	22	4	0
Activation of NF-kappaB in B cells	6	170851525	G	A	A	rs12200064	intronic	0.0431	0.0431	PSMB1	0.3694	59	5	2	26	0	0
Activation of NF-kappaB in B cells	6	170858332	G	A	A	rs17860779	intronic	0.0420	0.0420	PSMB1	1.0000	59	6	1	23	2	0
Activation of NF-kappaB in B cells	7	2955476	G	C	C	rs41336352	intronic	0.0400	0.0400	CARD11	1.0000	58	8	0	22	3	0
Activation of NF-kappaB in B cells	7	2966334	G	A	A	rs41448444	intronic	0.0454	0.0454	CARD11	0.7213	58	8	0	23	2	0
Activation of NF-kappaB in B cells	7	2968105	C	A	A	rs71527417	intronic	0.0472	0.0472	CARD11	0.0436	49	16	1	25	1	0
Activation of NF-kappaB in B cells	7	2970297	C	T	T	rs41386651	intronic	0.0410	0.0410	CARD11	0.7386	56	8	0	22	4	0
Activation of NF-kappaB in B cells	7	2970866	C	T	T	rs9648301	intronic	0.0444	0.0444	CARD11	1.0000	57	9	0	22	4	0
Activation of NF-kappaB in B cells	7	3029796	G	C	C	rs12700500	intronic	0.0454	0.0454	CARD11	1.0000	59	7	0	22	3	0
Activation of NF-kappaB in B cells	7	3042802	G	A	A	rs35579453	intronic	0.0363	0.0363	CARD11	1.0000	57	9	0	22	4	0
Activation of NF-kappaB in B cells	7	3052087	G	A	A	rs75468256	intronic	0.0407	0.0407	CARD11	0.2020	62	4	0	20	4	0
Activation of NF-kappaB in B cells	7	3072512	T	C	C	rs6975176	intronic	0.0452	0.0452	CARD11	1.0000	61	4	1	25	1	0
Activation of NF-kappaB in B cells	7	3073243	G	A	A	rs78353391	intronic	0.0427	0.0427	CARD11	0.0650	56	8	0	18	8	0
Activation of NF-kappaB in B cells	7	3079195	G	T	T	rs62439353	intronic	0.0400	0.0400	CARD11	0.7348	58	8	0	22	4	0
Activation of NF-kappaB in B cells	7	42971385	G	A	A	rs76256519	intronic	0.0432	0.0432	PSMA2	0.1923	61	5	0	21	3	1
Activation of NF-kappaB in B cells	7	148411091	C	T	T	rs11764941	intronic	0.0416	0.0416	CUL1	0.0082	58	8	0	16	9	1
Activation of NF-kappaB in B cells	7	148422581	A	G	G	rs11760399	intronic	0.0409	0.0409	CUL1	0.0158	57	9	0	16	9	1
Activation of NF-kappaB in B cells	7	148427470	A	T	T	rs17625893	intronic	0.0188	0.0188	CUL1	0.3091	59	7	0	21	5	0
Activation of NF-kappaB in B cells	7	148453031	C	G	G	rs4726991	intronic	0.0427	0.0427	CUL1	0.0164	61	5	0	18	7	0
Activation of NF-kappaB in B cells	7	148455710	A	G	G	rs73158225	intronic	0.0426	0.0426	CUL1	0.0333	61	5	0	19	7	0
Activation of NF-kappaB in B cells	7	148456174	T	G	G	rs17537343	intronic	0.0430	0.0430	CUL1	0.0164	61	5	0	18	7	0
Activation of NF-kappaB in B cells	7	148458141	C	T	T	rs73158226	intronic	0.0426	0.0426	CUL1	0.0616	61	5	0	18	6	0
Activation of NF-kappaB in B cells	7	148470413	T	C	C	rs73158234	intronic	0.0423	0.0423	CUL1	0.0333	61	5	0	19	7	0
Activation of NF-kappaB in B cells	7	148502252	T	C	C	rs77948593	downstream	0.0395	0.0395	CUL1	1.0000	59	6	1	23	2	0
Activation of NF-kappaB in B cells	8	42125339	T	C	C	rs76361874	upstream	0.0303	0.0303	IKBKB	0.0653	59	7	0	25	0	1
Activation of NF-kappaB in B cells	8	42127643	A	C	C	rs17875739	upstream	0.0241	0.0241	IKBKB	0.0653	59	7	0	25	0	1
Activation of NF-kappaB in B cells	8	42128072	T	A	A	rs62507976	upstream	0.0296	0.0296	IKBKB	0.4157	61	5	0	23	2	1
Activation of NF-kappaB in B cells	8	42135678	T	G	G	rs17875740	intronic	0.0335	0.0335	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42138781	G	C	C	rs80313154	intronic	0.0274	0.0274	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42142316	G	A	A	rs79881854	intronic	0.0326	0.0326	IKBKB	0.0321	58	8	0	24	0	1
Activation of NF-kappaB in B cells	8	42145446	A	G	G	rs17875744	intronic	0.0327	0.0327	IKBKB	0.0272	57	9	0	25	0	1
Activation of NF-kappaB in B cells	8	42150794	C	T	T	rs79123247	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42154866	A	G	G	rs78342373	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42155029	G	A	A	rs112141582	intronic	0.0267	0.0267	IKBKB	0.0321	58	8	0	24	0	1
Activation of NF-kappaB in B cells	8	42158881	A	G	G	rs75230171	intronic	0.0327	0.0327	IKBKB	0.0321	58	8	0	24	0	1
Activation of NF-kappaB in B cells	8	42159022	C	T	T	rs79460550	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42161317	G	A	A	rs113993388	intronic	0.0280	0.0280	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42162675	C	T	T	rs17875700	intronic	0.0338	0.0338	IKBKB	0.0321	58	8	0	24	0	1
Activation of NF-kappaB in B cells	8	42170928	C	T	T	rs76891399	intronic	0.0325	0.0325	IKBKB	0.0321	58	8	0	24	0	1
Activation of NF-kappaB in B cells	8	42173677	G	T	T	rs17875746	intronic	0.0322	0.0322	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42180084	G	A	A	rs17875721	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42180328	G	T	T	rs17875751	intronic	0.0327	0.0327	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42180679	G	A	A	rs78599265	intronic	0.0333	0.0333	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42186989	C	T	T	rs17875731	intronic	0.0324	0.0324	IKBKB	0.0330	58	8	0	25	0	1
Activation of NF-kappaB in B cells	8	42188334	G	T	T	rs79200457	intronic	0.0325	0.0325	IKBKB	0.0666	58	7	0	25	0	1
Activation of NF-kappaB in B cells	9	123578733	G	A	A	rs10384	3_prime_UTR	0.0186	0.0186	PSMD5	0.3096	61	5	0	23	1	1
Activation of NF-kappaB in B cells	9	123598623	A	G	G	rs62581704	intronic	0.0476	0.0476	PSMD5	0.3820	62	4	0	24	1	1
Activation of NF-kappaB in B cells	9	127118932	G	A	A	rs117300833	intronic	0.0270	0.0270	PSMB7	0.3024	58	7	0	20	5	0
Activation of NF-kappaB in B cells	9	127119442	G	A	A	rs16927388	intronic	0.0435	0.0435	PSMB7	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	9	127119799	G	A	A	rs56058032	intronic	0.0172	0.0172	PSMB7	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	9	127141846	G	C	C	rs79069085	intronic	0.0178	0.0178	PSMB7	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	9	127143001	T	A	A	rs76699962	intronic	0.0448	0.0448	PSMB7	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	9	127144906	A	C	C	rs79321634	intronic	0.0239	0.0239	PSMB7	0.2833	59	6	0	21	5	0
Activation of NF-kappaB in B cells	9	127145687	T	C	C	rs77214542	intronic	0.0335	0.0335	PSMB7	1.0000	58	8	0	23	3	0

Activation of NF-kappaB in B cells	9	127145878	G	C	C	rs41274376	intronic	0.0237	0.0237	PSMB7	0.3091	59	7	0	21	5	0
Activation of NF-kappaB in B cells	9	127151807	T	G	G	rs114451602	intronic	0.0301	0.0301	PSMB7	0.5095	60	5	1	26	0	0
Activation of NF-kappaB in B cells	9	127172515	T	C	C	rs140504275	intronic	0.0204	0.0204	PSMB7	0.1666	60	6	0	20	5	0
Activation of NF-kappaB in B cells	9	127177053	C	T	T	rs73588260	intronic	0.0344	0.0344	PSMB7	0.7366	57	8	0	22	4	0
Activation of NF-kappaB in B cells	10	101958770	C	T	T	rs12764732	intronic	0.0464	0.0464	CHUK	0.7209	57	9	0	23	2	0
Activation of NF-kappaB in B cells	10	101958858	T	G	G	rs17883365	intronic	0.0229	0.0229	CHUK	1.0000	61	5	0	24	2	0
Activation of NF-kappaB in B cells	10	101961171	G	A	A	rs17885986	intronic	0.0496	0.0496	CHUK	0.6322	57	8	1	21	4	1
Activation of NF-kappaB in B cells	10	101979482	T	C	C	rs12764370	intronic	0.0302	0.0302	CHUK	0.7209	57	9	0	23	2	0
Activation of NF-kappaB in B cells	10	103121589	C	T	T	rs11190960	intronic	0.0325	0.0325	BTRC	0.2234	59	6	1	26	0	0
Activation of NF-kappaB in B cells	10	103165858	G	A	A	rs145847638	intronic	0.0278	0.0278	BTRC	0.4058	59	6	1	25	0	0
Activation of NF-kappaB in B cells	10	103180336	G	A	A	rs11191003	intronic	0.0274	0.0274	BTRC	0.2234	59	6	1	26	0	0
Activation of NF-kappaB in B cells	10	103231195	T	C	C	rs34711120	intronic	0.0435	0.0435	BTRC	0.7302	58	8	0	21	4	0
Activation of NF-kappaB in B cells	10	103272221	C	T	T	rs12774622	intronic	0.0257	0.0257	BTRC	0.7970	57	8	1	23	2	0
Activation of NF-kappaB in B cells	10	103298099	G	T	T	rs4151060	missense	0.0289	0.0289	BTRC	0.6362	55	10	1	23	2	0
Activation of NF-kappaB in B cells	11	242014	T	A	A	rs17727753	intronic	0.0189	0.0189	PSMD13	1.0000	60	5	1	24	2	0
Activation of NF-kappaB in B cells	11	249105	G	A	A	rs11601352	intronic	0.0465	0.0465	PSMD13	0.7522	56	10	0	23	3	0
Activation of NF-kappaB in B cells	11	14528592	T	A	A	rs11023241	intronic	0.0417	0.0417	PSMA1	0.6117	57	8	1	23	2	1
Activation of NF-kappaB in B cells	11	14531031	C	T	T	rs78398913	intronic	0.0273	0.0273	PSMA1	1.0000	56	9	0	22	4	0
Activation of NF-kappaB in B cells	11	14537004	A	G	G	rs74589503	intronic	0.0418	0.0418	PSMA1	0.4981	56	10	0	24	2	0
Activation of NF-kappaB in B cells	11	14540827	C	T	T	rs79966935	intronic	0.0233	0.0233	PSMA1	0.7222	57	9	0	24	2	0
Activation of NF-kappaB in B cells	11	14541179	A	T	T	rs61883612	intronic	0.0441	0.0441	PSMA1	0.7666	55	11	0	21	5	0
Activation of NF-kappaB in B cells	11	14556220	C	T	T	rs34162548	intronic	0.0376	0.0376	PSMA1	1.0000	55	11	0	21	4	0
Activation of NF-kappaB in B cells	11	14588324	G	A	A	rs78854818	intronic	0.0413	0.0413	PSMA1	1.0000	59	6	1	24	2	0
Activation of NF-kappaB in B cells	11	14602698	T	G	G	rs17567703	intronic	0.0418	0.0418	PSMA1	1.0000	58	8	0	23	3	0
Activation of NF-kappaB in B cells	11	14622982	G	A	A	rs16930367	intronic	0.0250	0.0250	PSMA1	0.7192	58	8	0	24	2	0
Activation of NF-kappaB in B cells	11	14627135	G	A	A	rs55760529	intronic	0.0485	0.0485	PSMA1	1.0000	56	9	1	23	3	0
Activation of NF-kappaB in B cells	11	14633490	G	A	A	rs11023274	intronic	0.0317	0.0317	PSMA1	1.0000	56	9	1	23	3	0
Activation of NF-kappaB in B cells	11	14648387	G	A	A	rs79123458	intronic	0.0412	0.0412	PSMA1	1.0000	59	6	1	24	2	0
Activation of NF-kappaB in B cells	11	47441683	C	T	T	rs72903900	intronic	0.0375	0.0375	PSMC3	0.8389	59	5	2	23	3	0
Activation of NF-kappaB in B cells	11	47449591	G	A	A	rs116930066	upstream	0.0311	0.0311	PSMC3	0.5028	56	9	0	24	2	0
Activation of NF-kappaB in B cells	12	122349404	T	G	G	rs113810917	intronic	0.0229	0.0229	PSMD9	0.1282	57	8	1	25	0	0
Activation of NF-kappaB in B cells	12	122351293	A	C	C	rs73229956	intronic	0.0288	0.0288	PSMD9	0.2597	54	11	1	24	1	0
Activation of NF-kappaB in B cells	12	125395161	G	C	C	rs113660988	downstream	0.0428	0.0428	UBC	0.0064	64	1	1	21	5	0
Activation of NF-kappaB in B cells	12	125395728	C	T	T	rs112205208	downstream	0.0429	0.0429	UBC	0.0064	64	1	1	21	5	0
Activation of NF-kappaB in B cells	12	125398911	C	T	T	rs112043091	5_prime_UTR	0.0430	0.0430	UBC	0.0064	64	1	1	21	5	0
Activation of NF-kappaB in B cells	12	125399133	C	T	T	rs41276688	5_prime_UTR	0.0434	0.0434	UBC	0.0064	64	1	1	21	5	0
Activation of NF-kappaB in B cells	14	23512430	C	T	T	rs78162644	3_prime_UTR	0.0459	0.0459	PSMB11	1.0000	57	9	0	22	4	0
Activation of NF-kappaB in B cells	14	35787993	A	T	T	rs12890150	downstream	0.0324	0.0324	PSMA6	0.5321	62	3	1	23	3	0
Activation of NF-kappaB in B cells	14	53178728	T	C	C	rs117516552	intronic	0.0276	0.0276	PSMC6	0.7209	57	9	0	23	2	0
Activation of NF-kappaB in B cells	14	58710711	C	G	G	rs117328560	upstream	0.0280	0.0280	PSMA3	0.4999	56	10	0	23	2	0
Activation of NF-kappaB in B cells	14	58729996	C	G	G	rs111364917	intronic	0.0397	0.0397	PSMA3	0.4984	59	7	0	22	4	0
Activation of NF-kappaB in B cells	14	58731398	T	G	G	rs117955444	intronic	0.0210	0.0210	PSMA3	1.0000	59	7	0	22	3	0
Activation of NF-kappaB in B cells	15	78834476	A	G	G	rs41280046	intronic	0.0393	0.0393	PSMA4	0.7087	60	6	0	23	3	0
Activation of NF-kappaB in B cells	16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.4762	60	5	1	22	4	0
Activation of NF-kappaB in B cells	16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.0099	0	11	55	1	0	25
Activation of NF-kappaB in B cells	16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Activation of NF-kappaB in B cells	16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Activation of NF-kappaB in B cells	16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.0099	0	11	55	1	0	25
Activation of NF-kappaB in B cells	16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.0063	0	14	52	1	0	24
Activation of NF-kappaB in B cells	16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.3487	61	4	1	22	4	0

Activation of NF-kappaB in B cells	16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Activation of NF-kappaB in B cells	16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	22	3	0
Activation of NF-kappaB in B cells	16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.0016	0	17	49	1	0	24
Activation of NF-kappaB in B cells	16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.0012	0	17	49	1	0	25
Activation of NF-kappaB in B cells	16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.0015	0	16	49	1	0	25
Activation of NF-kappaB in B cells	16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.0000	59	7	0	23	3	0
Activation of NF-kappaB in B cells	16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.7348	58	8	0	22	4	0
Activation of NF-kappaB in B cells	16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.0015	0	16	49	1	0	25
Activation of NF-kappaB in B cells	16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.5065	58	8	0	21	5	0
Activation of NF-kappaB in B cells	16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.0024	0	16	50	1	0	24
Activation of NF-kappaB in B cells	16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.3024	58	7	0	20	5	0
Activation of NF-kappaB in B cells	16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.0015	0	16	50	1	0	25
Activation of NF-kappaB in B cells	16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.0343	0	15	51	0	1	25
Activation of NF-kappaB in B cells	16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.0000	53	12	0	21	4	0
Activation of NF-kappaB in B cells	16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.1679	0	11	55	0	1	25
Activation of NF-kappaB in B cells	16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.1681	0	11	55	0	1	24
Activation of NF-kappaB in B cells	16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.3348	54	12	0	24	2	0
Activation of NF-kappaB in B cells	16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.7522	56	10	0	23	3	0
Activation of NF-kappaB in B cells	16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.0000	57	9	0	23	3	0
Activation of NF-kappaB in B cells	16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.7522	56	10	0	23	3	0
Activation of NF-kappaB in B cells	16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.6919	60	4	1	25	0	0
Activation of NF-kappaB in B cells	16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.7213	58	8	0	23	2	0
Activation of NF-kappaB in B cells	16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.7192	58	8	0	24	2	0
Activation of NF-kappaB in B cells	16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.7213	58	8	0	23	2	0
Activation of NF-kappaB in B cells	16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Activation of NF-kappaB in B cells	16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Activation of NF-kappaB in B cells	16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.1877	59	7	0	21	4	1
Activation of NF-kappaB in B cells	16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.8583	57	7	2	22	4	0
Activation of NF-kappaB in B cells	16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.4631	59	6	0	22	4	0
Activation of NF-kappaB in B cells	16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.4603	60	6	0	22	4	0
Activation of NF-kappaB in B cells	16	67973569	C	T	T	rs17240392	upstream	0.0497	0.0497	PSMB10	0.4984	59	7	0	22	4	0

Activation of NF-kappaB in B cells	16	74334545	G	T	T	rs149977784	intronic	0.0196	0.0196	PSMD7	1.0000	62	2	2	26	0	0
Activation of NF-kappaB in B cells	17	4702206	C	A	A	rs71368518	downstream	0.0416	0.0416	PSMB6	1.0000	56	9	1	23	3	0
Activation of NF-kappaB in B cells	17	30778483	C	T	T	rs117117721	intronic	0.0190	0.0190	PSMD11	1.0000	59	7	0	22	3	0
Activation of NF-kappaB in B cells	17	30791889	C	T	T	rs35225085	intronic	0.0427	0.0427	PSMD11	0.4999	56	10	0	23	2	0
Activation of NF-kappaB in B cells	17	30794889	C	G	G	rs35177842	intronic	0.0430	0.0430	PSMD11	0.4999	56	10	0	23	2	0
Activation of NF-kappaB in B cells	17	36920050	C	T	T	rs118080693	intronic	0.0415	0.0415	PSMB3	0.1732	63	3	0	25	0	1
Activation of NF-kappaB in B cells	17	38144079	G	T	T	rs118009374	intronic	0.0189	0.0189	PSMD3	0.8767	53	11	2	20	5	0
Activation of NF-kappaB in B cells	17	38154396	C	T	T	rs118034841	downstream	0.0176	0.0176	PSMD3	0.0569	56	10	0	26	0	0
Activation of NF-kappaB in B cells	17	65334270	T	A	A	rs146515782	3_prime_UTR	0.0418	0.0418	PSMD12	1.0000	58	8	0	23	3	0
Activation of NF-kappaB in B cells	18	23711373	G	T	T	rs79820119	upstream	0.0407	0.0407	PSMA8	0.2218	53	13	0	23	2	0
Activation of NF-kappaB in B cells	18	23715815	T	G	G	rs4800242	intronic	0.0460	0.0460	PSMA8	0.7043	59	6	0	22	3	0
Activation of NF-kappaB in B cells	18	23774138	C	A	A	rs79452515	downstream	0.0424	0.0424	PSMA8	0.2993	59	7	0	20	5	0
Activation of NF-kappaB in B cells	18	56333866	G	A	A	rs72958690	upstream	0.0368	0.0368	MALT1	0.8183	56	9	1	21	4	0
Activation of NF-kappaB in B cells	18	56338792	G	A	A	rs56142402	5_prime_UTR	0.0327	0.0327	MALT1	0.8110	57	8	1	22	4	0
Activation of NF-kappaB in B cells	18	56363534	A	C	C	rs55825071	intronic	0.0377	0.0377	MALT1	0.6531	56	9	1	20	5	0
Activation of NF-kappaB in B cells	19	40472450	A	C	C	rs147915270	upstream	0.0382	0.0382	PSMC4	1.0000	58	7	1	22	3	0
Activation of NF-kappaB in B cells	19	40475070	T	G	G	rs139876278	upstream	0.0147	0.0147	PSMC4	0.2725	63	2	1	23	3	0
Activation of NF-kappaB in B cells	20	1128622	T	C	C	rs74871431	intronic	0.0320	0.0320	PSMF1	0.7087	60	6	0	23	3	0
Activation of NF-kappaB in B cells	20	1146048	C	T	T	rs17716261	3_prime_UTR	0.0279	0.0279	PSMF1	0.4532	60	6	0	21	4	0
Activation of NF-kappaB in B cells	20	1149980	C	T	T	rs77625408	downstream	0.0254	0.0254	PSMF1	0.7495	54	11	0	23	3	0
Activation of NF-kappaB in B cells	20	1152323	C	T	T	rs34552580	downstream	0.0323	0.0323	PSMF1	1.0000	59	5	1	24	2	0
Activation of NF-kappaB in B cells	20	1155154	G	A	A	rs78313102	intronic,non_coding_transcript	0.0258	0.0258	PSMF1	1.0000	58	7	0	23	3	0
WNT5A-dependent internalization of FZD4	3	183896966	G	A	A	rs2231217	intronic	0.0406	0.0406	AP2M1	0.7980	57	8	1	24	2	0
WNT5A-dependent internalization of FZD4	5	175838749	T	A	A	rs72807224	intronic	0.0466	0.0466	CLTB	0.0974	60	5	1	20	6	0
WNT5A-dependent internalization of FZD4	9	36189647	T	C	C	rs3739608	upstream	0.0486	0.0486	CLTA	0.4858	59	6	1	21	5	0
WNT5A-dependent internalization of FZD4	9	36201064	G	A	A	rs10972788	intronic	0.0274	0.0274	CLTA	0.2818	60	6	0	21	5	0
WNT5A-dependent internalization of FZD4	11	941844	C	T	T	rs10902236	intronic	0.0339	0.0339	AP2A2	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	11	965671	C	T	T	rs74045443	intronic	0.0489	0.0489	AP2A2	0.4662	58	6	0	22	4	0
WNT5A-dependent internalization of FZD4	11	966609	C	T	T	rs7394613	intronic	0.0457	0.0457	AP2A2	0.0005	64	2	0	18	7	1
WNT5A-dependent internalization of FZD4	11	967822	C	T	T	rs117367662	intronic	0.0338	0.0338	AP2A2	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	11	970818	C	T	T	rs74045446	intronic	0.0491	0.0491	AP2A2	0.4474	60	6	0	20	4	0
WNT5A-dependent internalization of FZD4	11	971884	A	G	G	rs7945582	intronic	0.0470	0.0470	AP2A2	0.6640	56	9	1	21	5	0
WNT5A-dependent internalization of FZD4	11	978921	C	T	T	rs7122686	intronic	0.0468	0.0468	AP2A2	0.8183	56	9	1	21	4	0
WNT5A-dependent internalization of FZD4	11	986568	G	C	C	rs112772664	intronic	0.0457	0.0457	AP2A2	0.4532	60	6	0	21	4	0
WNT5A-dependent internalization of FZD4	11	86653253	G	A	A	rs79378895	downstream	0.0478	0.0478	FZD4	0.7222	57	9	0	24	2	0
WNT5A-dependent internalization of FZD4	11	86657419	A	G	G	rs72963441	3_prime_UTR	0.0393	0.0393	FZD4	0.5065	58	8	0	21	5	0
WNT5A-dependent internalization of FZD4	16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.4762	60	5	1	22	4	0
WNT5A-dependent internalization of FZD4	16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.0099	0	11	55	1	0	25
WNT5A-dependent internalization of FZD4	16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
WNT5A-dependent internalization of FZD4	16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
WNT5A-dependent internalization of FZD4	16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.0099	0	11	55	1	0	25
WNT5A-dependent internalization of FZD4	16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.0063	0	14	52	1	0	24
WNT5A-dependent internalization of FZD4	16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.3487	61	4	1	22	4	0
WNT5A-dependent internalization of FZD4	16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.0000	59	7	0	23	3	0

WNT5A-dependent internalization of FZD4	16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
WNT5A-dependent internalization of FZD4	16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	22	3	0
WNT5A-dependent internalization of FZD4	16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.0016	0	17	49	1	0	24
WNT5A-dependent internalization of FZD4	16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.0012	0	17	49	1	0	25
WNT5A-dependent internalization of FZD4	16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.0015	0	16	49	1	0	25
WNT5A-dependent internalization of FZD4	16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.7348	58	8	0	22	4	0
WNT5A-dependent internalization of FZD4	16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.0015	0	16	49	1	0	25
WNT5A-dependent internalization of FZD4	16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.5065	58	8	0	21	5	0
WNT5A-dependent internalization of FZD4	16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.0024	0	16	50	1	0	24
WNT5A-dependent internalization of FZD4	16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.3024	58	7	0	20	5	0
WNT5A-dependent internalization of FZD4	16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.0015	0	16	50	1	0	25
WNT5A-dependent internalization of FZD4	16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.0343	0	15	51	0	1	25
WNT5A-dependent internalization of FZD4	16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.0000	53	12	0	21	4	0
WNT5A-dependent internalization of FZD4	16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.1679	0	11	55	0	1	25
WNT5A-dependent internalization of FZD4	16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.1681	0	11	55	0	1	24
WNT5A-dependent internalization of FZD4	16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.3348	54	12	0	24	2	0
WNT5A-dependent internalization of FZD4	16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.7522	56	10	0	23	3	0
WNT5A-dependent internalization of FZD4	16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.0000	57	9	0	23	3	0
WNT5A-dependent internalization of FZD4	16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.7522	56	10	0	23	3	0
WNT5A-dependent internalization of FZD4	16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.6919	60	4	1	25	0	0
WNT5A-dependent internalization of FZD4	16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.7213	58	8	0	23	2	0
WNT5A-dependent internalization of FZD4	16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.7192	58	8	0	24	2	0
WNT5A-dependent internalization of FZD4	16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.7213	58	8	0	23	2	0
WNT5A-dependent internalization of FZD4	16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
WNT5A-dependent internalization of FZD4	16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
WNT5A-dependent internalization of FZD4	16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.1877	59	7	0	21	4	1
WNT5A-dependent internalization of FZD4	16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.8583	57	7	2	22	4	0
WNT5A-dependent internalization of FZD4	16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.4631	59	6	0	22	4	0
WNT5A-dependent internalization of FZD4	16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.4603	60	6	0	22	4	0
WNT5A-dependent internalization of FZD4	17	4626173	A	G	G	rs78082978	downstream	0.0315	0.0315	ARRB2	0.8212	55	10	1	23	3	0
WNT5A-dependent internalization of FZD4	17	33953109	G	A	A	rs225253	intronic	0.0178	0.0178	AP2B1	0.2428	58	7	1	26	0	0
WNT5A-dependent internalization of FZD4	17	33990042	T	C	C	rs75950451	intronic	0.0469	0.0469	AP2B1	0.8528	56	8	2	23	2	0
WNT5A-dependent internalization of FZD4	17	34003398	C	T	T	rs79010821	intronic	0.0386	0.0386	AP2B1	0.1965	58	8	0	19	6	0
WNT5A-dependent internalization of FZD4	17	34006300	T	A	A	rs79688427	intronic	0.0389	0.0389	AP2B1	0.2078	58	8	0	20	6	0
WNT5A-dependent internalization of FZD4	17	34051124	T	G	G	rs11653803	3_prime_UTR	0.0341	0.0341	AP2B1	0.7192	58	8	0	24	2	0
WNT5A-dependent internalization of FZD4	17	57746013	C	T	T	rs117419555	intronic	0.0437	0.0437	CLTC	1.0000	57	9	0	23	3	0
WNT5A-dependent internalization of FZD4	17	64305051	A	G	G	rs78357146	intronic	0.0186	0.0186	PRKCA	0.7209	57	9	0	23	2	0

WNT5A-dependent internalization of FZD4	17	64315409	T	C	C	rs80130647	intronic	0.0184	0.0184	PRKCA	0.7043	59	6	0	22	3	0
WNT5A-dependent internalization of FZD4	17	64318385	G	A	A	rs12150623	intronic	0.0343	0.0343	PRKCA	0.7595	61	4	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64320040	C	T	T	rs139317720	intronic	0.0229	0.0229	PRKCA	1.0000	62	3	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64326068	T	G	G	rs12951126	intronic	0.0260	0.0260	PRKCA	1.0000	58	8	0	23	3	0
WNT5A-dependent internalization of FZD4	17	64343295	A	C	C	rs72843901	intronic	0.0457	0.0457	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64344650	C	T	T	rs72846606	intronic	0.0454	0.0454	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64344788	C	T	T	rs72846607	intronic	0.0457	0.0457	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64346204	A	G	G	rs12150367	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64349104	C	T	T	rs72846609	intronic	0.0497	0.0497	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64351542	G	C	C	rs28592028	intronic	0.0453	0.0453	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64352431	T	G	G	rs544435459	intronic	0.0451	0.0451	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64354597	T	C	C	rs72846612	intronic	0.0451	0.0451	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64358121	C	G	G	rs72846614	intronic	0.0451	0.0451	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64359354	T	C	C	rs72846615	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64365593	C	T	T	rs72846677	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64367534	C	T	T	rs72846678	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64369822	A	G	G	rs72846681	intronic	0.0451	0.0451	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64375194	T	C	C	rs72846695	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64377301	C	A	A	rs113134992	intronic	0.0448	0.0448	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64382507	C	G	G	rs79461368	intronic	0.0453	0.0453	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64389524	C	T	T	rs77682324	intronic	0.0403	0.0403	PRKCA	0.7621	59	6	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64395773	T	C	C	rs78584531	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64396570	T	G	G	rs72838208	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64396695	A	G	G	rs74329211	intronic	0.0432	0.0432	PRKCA	0.7302	58	8	0	21	4	0
WNT5A-dependent internalization of FZD4	17	64396883	G	A	A	rs72838209	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64398013	G	A	A	rs75125285	intronic	0.0295	0.0295	PRKCA	0.7632	60	5	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64400648	C	T	T	rs72838214	intronic	0.0452	0.0452	PRKCA	0.4788	55	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64402141	G	T	T	rs10221238	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64405430	T	A	A	rs72838216	intronic	0.0453	0.0453	PRKCA	0.4725	56	9	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64410564	C	T	T	rs9972974	intronic	0.0390	0.0390	PRKCA	0.7632	60	5	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64412921	G	A	A	rs62070391	intronic	0.0426	0.0426	PRKCA	0.7621	59	6	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64424382	C	T	T	rs62070395	intronic	0.0425	0.0425	PRKCA	0.7595	59	6	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64429928	G	A	A	rs117729211	intronic	0.0272	0.0272	PRKCA	0.0477	60	6	0	19	6	1
WNT5A-dependent internalization of FZD4	17	64431874	G	A	A	rs72838278	intronic	0.0426	0.0426	PRKCA	0.7642	57	6	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64432202	A	G	G	rs62070397	intronic	0.0427	0.0427	PRKCA	0.7621	59	6	1	25	1	0
WNT5A-dependent internalization of FZD4	17	64432881	A	G	G	rs62070398	intronic	0.0426	0.0426	PRKCA	0.7595	59	6	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64438732	A	T	T	rs113684166	intronic	0.0445	0.0445	PRKCA	0.2744	57	9	0	24	1	0
WNT5A-dependent internalization of FZD4	17	64441204	T	C	C	rs75005068	intronic	0.0469	0.0469	PRKCA	0.2719	57	9	0	25	1	0
WNT5A-dependent internalization of FZD4	17	64441759	C	A	A	rs78330327	intronic	0.0465	0.0465	PRKCA	0.2710	56	9	0	25	1	0
WNT5A-dependent internalization of FZD4	17	64445337	A	C	C	rs118090701	intronic	0.0387	0.0387	PRKCA	1.0000	58	6	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64445856	A	G	G	rs12451388	intronic	0.0449	0.0449	PRKCA	0.2744	57	9	0	24	1	0
WNT5A-dependent internalization of FZD4	17	64447721	G	A	A	rs12452749	intronic	0.0462	0.0462	PRKCA	0.2786	57	9	0	23	1	0
WNT5A-dependent internalization of FZD4	17	64450113	G	C	C	rs80162292	intronic	0.0461	0.0461	PRKCA	0.2710	56	9	0	25	1	0
WNT5A-dependent internalization of FZD4	17	64453194	A	G	G	rs111776777	intronic	0.0442	0.0442	PRKCA	0.8716	54	10	2	23	3	0
WNT5A-dependent internalization of FZD4	17	64458036	C	T	T	rs113153197	intronic	0.0339	0.0339	PRKCA	0.1678	54	11	0	25	1	0
WNT5A-dependent internalization of FZD4	17	64462111	T	G	G	rs79239451	intronic	0.0464	0.0464	PRKCA	0.2744	57	9	0	24	1	0
WNT5A-dependent internalization of FZD4	17	64462288	G	A	A	rs80080003	intronic	0.0305	0.0305	PRKCA	0.1706	56	10	0	25	1	0
WNT5A-dependent internalization of FZD4	17	64483589	G	T	T	rs79070174	intronic	0.0391	0.0391	PRKCA	1.0000	59	6	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64487077	T	G	G	rs78149509	intronic	0.0200	0.0200	PRKCA	0.0381	63	3	0	21	4	1
WNT5A-dependent internalization of FZD4	17	64494906	A	G	G	rs117168126	intronic	0.0300	0.0300	PRKCA	1.0000	59	6	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64501943	C	T	T	rs7217954	intronic	0.0422	0.0422	PRKCA	1.0000	59	7	0	23	3	0
WNT5A-dependent internalization of FZD4	17	64519790	G	A	A	rs11659067	intronic	0.0498	0.0498	PRKCA	0.0125	62	3	0	19	6	0
WNT5A-dependent internalization of FZD4	17	64525002	A	T	T	rs77462363	intronic	0.0380	0.0380	PRKCA	1.0000	59	6	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64544723	C	T	T	rs116879811	intronic	0.0274	0.0274	PRKCA	1.0000	60	6	0	24	2	0
WNT5A-dependent internalization of FZD4	17	64559535	A	G	G	rs227907	intronic	0.0478	0.0478	PRKCA	0.2800	55	11	0	21	3	1
WNT5A-dependent internalization of FZD4	17	64561055	G	A	A	rs62071706	intronic	0.0238	0.0238	PRKCA	0.1546	60	5	0	21	4	1
WNT5A-dependent internalization of FZD4	17	64590951	A	T	T	rs11867591	intronic	0.0449	0.0449	PRKCA	0.2122	57	8	0	20	6	0
WNT5A-dependent internalization of FZD4	17	64604776	C	T	T	rs117539643	intronic	0.0479	0.0479	PRKCA	0.6653	51	11	2	23	3	0
WNT5A-dependent internalization of FZD4	17	64608923	T	C	C	rs72845947	intronic	0.0440	0.0440	PRKCA	0.7355	57	7	2	21	4	0
WNT5A-dependent internalization of FZD4	17	64610285	T	C	C	rs72845948	intronic	0.0445	0.0445	PRKCA	0.8583	57	7	2	22	4	0
WNT5A-dependent internalization of FZD4	17	64610480	A	C	C	rs17759657	intronic	0.0444	0.0444	PRKCA	0.8583	57	7	2	22	4	0

WNT5A-dependent internalization of FZD4	17	64612838	C	T	T	rs16959714	intronic	0.0338	0.0338	PRKCA	0.4353	57	8	0	24	1	0
WNT5A-dependent internalization of FZD4	17	64614717	T	C	C	rs17686540	intronic	0.0442	0.0442	PRKCA	0.7355	57	7	2	21	4	0
WNT5A-dependent internalization of FZD4	17	64626385	G	A	A	rs74352723	intronic	0.0460	0.0460	PRKCA	0.2744	57	9	0	24	1	0
WNT5A-dependent internalization of FZD4	17	64628634	A	G	G	rs117353888	intronic	0.0437	0.0437	PRKCA	0.2521	54	11	0	18	7	0
WNT5A-dependent internalization of FZD4	17	64660047	G	C	C	rs146141011	intronic	0.0484	0.0484	PRKCA	1.0000	53	9	2	22	4	0
WNT5A-dependent internalization of FZD4	17	64671047	C	T	T	rs16959942	intronic	0.0496	0.0496	PRKCA	0.1706	56	10	0	25	1	0
WNT5A-dependent internalization of FZD4	17	64712634	T	C	C	rs78121420	intronic	0.0465	0.0465	PRKCA	1.0000	57	7	2	23	3	0
WNT5A-dependent internalization of FZD4	17	64713847	G	T	T	rs112934229	intronic	0.0464	0.0464	PRKCA	1.0000	57	7	2	23	3	0
WNT5A-dependent internalization of FZD4	17	64723880	G	A	A	rs79547774	intronic	0.0264	0.0264	PRKCA	1.0000	57	9	0	23	3	0
WNT5A-dependent internalization of FZD4	17	64738427	A	C	C	rs117138620	intronic	0.0400	0.0400	PRKCA	0.3055	58	8	0	23	2	1
WNT5A-dependent internalization of FZD4	17	64748431	G	T	T	rs141177250	intronic	0.0153	0.0153	PRKCA	0.7595	59	6	1	24	1	0
WNT5A-dependent internalization of FZD4	17	64755018	T	C	C	rs74831470	intronic	0.0226	0.0226	PRKCA	0.7976	56	9	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64760870	A	G	G	rs77904275	intronic	0.0307	0.0307	PRKCA	0.5233	53	11	1	24	2	0
WNT5A-dependent internalization of FZD4	17	64762410	C	G	G	rs113025478	intronic	0.0307	0.0307	PRKCA	0.6398	54	11	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64763235	T	C	C	rs77635068	intronic	0.0306	0.0306	PRKCA	0.6398	54	11	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64771614	C	T	T	rs80238933	intronic	0.0297	0.0297	PRKCA	0.6398	54	11	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64776847	G	A	A	rs113542727	intronic	0.0297	0.0297	PRKCA	0.5228	54	11	1	24	2	0
WNT5A-dependent internalization of FZD4	17	64791836	G	C	C	rs56884788	intronic	0.0390	0.0390	PRKCA	0.6362	55	10	1	23	2	0
WNT5A-dependent internalization of FZD4	17	64792863	G	C	C	rs72838636	intronic	0.0484	0.0484	PRKCA	0.6470	57	8	1	21	5	0
WNT5A-dependent internalization of FZD4	19	47342929	G	A	A	rs17716171	intronic	0.0468	0.0468	AP2S1	0.3121	57	8	1	20	5	1
WNT5A-dependent internalization of FZD4	19	47352639	A	G	G	rs78730097	intronic	0.0144	0.0144	AP2S1	1.0000	60	5	1	24	2	0
WNT5A-dependent internalization of FZD4	19	47353083	T	A	A	rs117750880	intronic	0.0252	0.0252	AP2S1	0.7632	60	5	1	25	1	0
WNT5A-dependent internalization of FZD4	19	50279933	G	T	T	rs79075745	intronic	0.0372	0.0372	AP2A1	0.7560	55	10	0	21	5	0
WNT5A-dependent internalization of FZD4	19	50282053	G	A	A	rs62129179	intronic	0.0227	0.0227	AP2A1	0.2039	62	4	0	21	2	1
WNT5A-dependent internalization of FZD4	19	50297520	T	C	C	rs62129182	intronic	0.0212	0.0212	AP2A1	0.3151	62	4	0	23	2	1
WNT5A-dependent internalization of FZD4	19	54401602	G	C	C	rs41311973	intronic	0.0163	0.0163	PRKCG	0.7213	58	8	0	23	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	14	55593382	G	A	A	rs149885215	upstream	0.0492	0.0492	LGALS3	1.0000	56	9	1	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	14	55598617	G	T	T	rs78793419	intronic	0.0375	0.0375	LGALS3	0.4984	59	7	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3782471	G	C	C	rs75401475	intronic	0.0208	0.0208	CREBBP	1.0000	58	8	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3796252	T	C	C	rs116481265	intronic	0.0390	0.0390	CREBBP	0.7549	56	10	0	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3857035	T	G	G	rs130038	intronic	0.0341	0.0341	CREBBP	0.5065	58	8	0	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3876864	T	C	C	rs77292571	intronic	0.0215	0.0215	CREBBP	0.7348	58	8	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3880659	A	G	G	rs12447449	intronic	0.0347	0.0347	CREBBP	1.0000	57	8	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3881494	T	C	C	rs113198082	intronic	0.0497	0.0497	CREBBP	0.2977	54	12	0	22	3	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3888283	A	T	T	rs35581149	intronic	0.0268	0.0268	CREBBP	1.0000	57	9	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	3901493	T	C	C	rs113653086	intronic	0.0332	0.0332	CREBBP	0.3346	58	8	0	20	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.4762	60	5	1	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.0099	0	11	55	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.0099	0	11	55	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.0063	0	14	52	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.3487	61	4	1	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.0000	59	7	0	23	3	0

RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.0016	0	17	49	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.0012	0	17	49	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.0015	0	16	49	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.7348	58	8	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.0015	0	16	49	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.5065	58	8	0	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.0024	0	16	50	1	0	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.3024	58	7	0	20	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.0015	0	16	50	1	0	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.0343	0	15	51	0	1	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.0000	53	12	0	21	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.1679	0	11	55	0	1	25
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.1681	0	11	55	0	1	24
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.3348	54	12	0	24	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.7522	56	10	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.0000	57	9	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.7522	56	10	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.6919	60	4	1	25	0	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.7213	58	8	0	23	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.7192	58	8	0	24	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.7213	58	8	0	23	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.1877	59	7	0	21	4	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.8583	57	7	2	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.4631	59	6	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.4603	60	6	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67058614	T	G	G	rs116975210	upstream	0.0256	0.0256	CBFB	0.2078	58	8	0	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67059547	T	C	C	rs118064296	upstream	0.0255	0.0255	CBFB	0.2078	58	8	0	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67060518	C	A	A	rs78843766	upstream	0.0407	0.0407	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67064218	C	T	T	rs115088567	intronic	0.0408	0.0408	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67065005	T	G	G	rs60915579	intronic	0.0410	0.0410	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67077985	A	T	T	rs16957128	intronic	0.0410	0.0410	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67081133	C	A	A	rs116271212	intronic	0.0409	0.0409	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67087645	T	C	C	rs34968486	intronic	0.0413	0.0413	CBFB	1.0000	59	7	0	23	3	0

RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67089554	C	T	T	rs115947495	intronic	0.0409	0.0409	CBFB	1.0000	59	7	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67092389	T	C	C	rs58448340	intronic	0.0410	0.0410	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67097563	C	G	G	rs146692508	intronic	0.0409	0.0409	CBFB	1.0000	59	7	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67110174	G	A	A	rs115775129	intronic	0.0409	0.0409	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67113178	A	G	G	rs78817904	intronic	0.0407	0.0407	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67121057	G	C	C	rs114556591	intronic	0.0408	0.0408	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67121931	C	G	G	rs80188152	intronic	0.0408	0.0408	CBFB	1.0000	59	7	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67122543	A	G	G	rs2204708	intronic	0.0407	0.0407	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67127104	C	T	T	rs116154207	intronic	0.0408	0.0408	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67128349	G	C	C	rs115375898	intronic	0.0408	0.0408	CBFB	1.0000	59	7	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	16	67138195	C	G	G	rs76658185	downstream	0.0409	0.0409	CBFB	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36161662	G	C	C	rs75192893	3_prime_UTR	0.0252	0.0252	RUNX1	1.0000	61	4	1	24	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36258223	T	C	C	rs2734472	intronic	0.0207	0.0207	RUNX1	0.0718	55	11	0	24	1	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36279730	T	C	C	rs79087516	intronic	0.0328	0.0328	RUNX1	0.7285	62	3	1	24	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36298914	T	C	C	rs2051392	intronic	0.0378	0.0378	RUNX1	0.0576	28	30	8	6	19	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36360816	C	T	T	rs118131631	intronic	0.0328	0.0328	RUNX1	1.0000	58	8	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36385772	G	A	A	rs78097430	intronic	0.0312	0.0312	RUNX1	1.0000	60	5	1	24	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36389539	C	T	T	rs77728098	intronic	0.0493	0.0493	RUNX1	1.0000	58	7	1	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36392564	A	G	G	rs71329093	intronic	0.0314	0.0314	RUNX1	1.0000	58	8	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36400441	C	G	G	rs75967349	intronic	0.0294	0.0294	RUNX1	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36405472	C	G	G	rs75102343	intronic	0.0365	0.0365	RUNX1	0.0087	52	14	0	26	0	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36420012	T	C	C	rs55800826	intronic	0.0435	0.0435	RUNX1	0.7065	51	14	1	19	7	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36420200	T	G	G	rs77398576	intronic	0.0289	0.0289	RUNX1	0.2818	60	6	0	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36445895	T	C	C	rs78203858	intronic	0.0402	0.0402	RUNX1	1.0000	57	9	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36481863	C	A	A	rs9305560	intronic	0.0454	0.0454	RUNX1	0.8770	56	8	2	22	2	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36525063	G	T	T	rs79134632	intronic	0.0303	0.0303	RUNX1	0.0320	54	12	0	25	0	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36525900	T	C	C	rs62216988	intronic	0.0414	0.0414	RUNX1	0.1174	57	9	0	23	1	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36531645	A	C	C	rs2834807	intronic	0.0357	0.0357	RUNX1	1.0000	58	8	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36540870	T	C	C	rs9984209	intronic	0.0153	0.0153	RUNX1	0.7929	59	6	1	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36549995	T	C	C	rs76673048	intronic	0.0153	0.0153	RUNX1	0.7855	59	6	1	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36554527	C	T	T	rs80172635	intronic	0.0341	0.0341	RUNX1	0.1028	53	13	0	25	1	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36578831	T	A	T	rs8132151	intronic	0.9516	0.0484	RUNX1	0.2734	1	7	58	0	6	20
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36600490	G	A	A	rs113393734	intronic	0.0338	0.0338	RUNX1	0.5316	56	9	0	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36615789	T	G	G	rs76608041	intronic	0.0356	0.0356	RUNX1	0.4862	59	7	0	21	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36644806	C	T	T	rs73192907	intronic	0.0329	0.0329	RUNX1	0.7549	56	10	0	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36651166	C	T	T	rs78150243	intronic	0.0348	0.0348	RUNX1	0.4984	59	7	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36678254	G	A	A	rs77468602	intronic	0.0288	0.0288	RUNX1	1.0000	56	10	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36679979	A	G	G	rs75531812	intronic	0.0486	0.0486	RUNX1	0.4353	58	8	0	24	1	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36682912	T	A	A	rs66699816	intronic	0.0476	0.0476	RUNX1	0.3666	4	34	28	0	11	14
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36714201	C	A	A	rs2242721	intronic	0.0422	0.0422	RUNX1	1.0000	57	9	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36741936	A	G	G	rs2242724	intronic	0.0446	0.0446	RUNX1	0.5457	56	10	0	20	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36777301	C	T	T	rs113799213	intronic	0.0482	0.0482	RUNX1	0.7348	58	8	0	22	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36790637	C	T	T	rs73197362	intronic	0.0471	0.0471	RUNX1	0.1026	56	9	0	18	6	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36817202	G	T	T	rs76384559	intronic	0.0472	0.0472	RUNX1	0.7302	58	8	0	21	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36827331	G	C	C	rs62217064	intronic	0.0304	0.0304	RUNX1	0.4532	60	6	0	21	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36887862	G	A	A	rs73201472	intronic	0.0285	0.0285	RUNX1	0.0370	61	4	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36904158	A	G	G	rs78159534	intronic	0.0382	0.0382	RUNX1	1.0000	58	7	1	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36978701	C	T	T	rs141048458	intronic	0.0137	0.0137	RUNX1	0.7043	59	6	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	36988765	A	G	G	rs117334794	intronic	0.0137	0.0137	RUNX1	1.0000	59	7	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37001252	G	A	A	rs147475775	intronic	0.0133	0.0133	RUNX1	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37041204	A	T	T	rs9978750	intronic	0.0430	0.0430	RUNX1	1.0000	58	8	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37111438	C	T	T	rs2835112	intronic	0.0109	0.0109	RUNX1	1.0000	58	8	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37145469	A	G	G	rs78766167	intronic	0.0338	0.0338	RUNX1	0.8583	57	8	1	22	3	1
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37146205	T	C	C	rs2835139	intronic	0.0440	0.0440	RUNX1	1.0000	56	10	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37165262	T	G	G	rs79838028	intronic	0.0208	0.0208	RUNX1	0.7681	60	5	1	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37168627	C	A	A	rs9976429	intronic	0.0381	0.0381	RUNX1	1.0000	59	7	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37201847	G	A	A	rs2835146	intronic	0.0109	0.0109	RUNX1	1.0000	58	8	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37220269	T	A	A	rs141274106	intronic	0.0109	0.0109	RUNX1	1.0000	58	8	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37276929	C	T	T	rs75561514	intronic	0.0138	0.0138	RUNX1	1.0000	61	4	1	24	2	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37283402	C	T	T	rs79437318	intronic	0.0284	0.0284	RUNX1	0.7681	60	5	1	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37314583	C	T	T	rs35256126	intronic	0.0349	0.0349	RUNX1	0.1421	59	6	1	19	6	0

RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37316253	T	C	C	rs35676489	intronic	0.0484	0.0484	RUNX1	1.0000	57	9	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37318065	G	A	A	rs112248952	intronic	0.0352	0.0352	RUNX1	1.0000	58	8	0	22	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37323869	A	G	G	rs17813817	intronic	0.0353	0.0353	RUNX1	0.1603	57	6	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37325386	A	G	G	rs74524623	intronic	0.0186	0.0186	RUNX1	0.3387	61	4	1	21	4	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37327434	G	C	C	rs35296624	intronic	0.0356	0.0356	RUNX1	0.2734	58	7	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37327713	G	C	C	rs35137377	intronic	0.0355	0.0355	RUNX1	0.2734	58	7	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37331245	G	C	C	rs13049450	intronic	0.0354	0.0354	RUNX1	0.1521	59	6	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37332139	G	T	T	rs75887851	intronic	0.0458	0.0458	RUNX1	0.4799	58	6	1	20	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37332988	C	T	T	rs79662622	intronic	0.0372	0.0372	RUNX1	0.2734	58	7	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37333615	C	T	T	rs34303222	intronic	0.0353	0.0353	RUNX1	0.2734	58	7	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37335408	T	A	A	rs35338421	intronic	0.0354	0.0354	RUNX1	0.2734	58	7	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37342778	C	T	T	rs13047609	intronic	0.0320	0.0320	RUNX1	0.6499	56	8	1	21	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37343254	G	T	T	rs13048435	intronic	0.0319	0.0319	RUNX1	0.4348	57	8	1	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37345637	G	A	A	rs13052673	intronic	0.0474	0.0474	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37346157	A	G	G	rs915742	intronic	0.0473	0.0473	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37347057	C	T	T	rs2835194	intronic	0.0475	0.0475	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37348386	A	G	G	rs34544538	intronic	0.0472	0.0472	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37350173	C	T	T	rs71330629	intronic	0.0472	0.0472	RUNX1	0.1227	55	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37351306	C	T	T	rs2835205	intronic	0.0476	0.0476	RUNX1	0.1139	55	9	1	17	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37351459	T	C	C	rs56317271	intronic	0.0472	0.0472	RUNX1	0.1117	56	9	1	17	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37351802	C	T	T	rs13048310	intronic	0.0473	0.0473	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37352953	T	C	C	rs13046307	intronic	0.0473	0.0473	RUNX1	0.1117	56	9	1	17	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37353681	T	C	C	rs71330630	intronic	0.0473	0.0473	RUNX1	0.1227	55	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37357051	C	T	T	rs28665789	5_prime_UTR	0.0498	0.0498	RUNX1	1.0000	56	9	0	23	3	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37361832	A	C	C	rs36028697	intronic	0.0476	0.0476	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37362718	C	A	A	rs2835215	intronic	0.0476	0.0476	RUNX1	0.1117	56	9	1	17	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37363385	A	G	G	rs2835216	intronic	0.0477	0.0477	RUNX1	0.1196	56	9	1	18	8	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37364473	A	G	G	rs13047560	intronic	0.0432	0.0432	RUNX1	0.3739	56	10	0	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37366389	A	T	T	rs34327189	intronic	0.0459	0.0459	RUNX1	0.7528	55	10	0	20	5	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37368100	C	G	G	rs55824509	intronic	0.0431	0.0431	RUNX1	0.3739	56	10	0	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37369628	C	T	T	rs13049536	intronic	0.0431	0.0431	RUNX1	0.3612	56	10	0	19	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37370442	G	A	A	rs13050761	intronic	0.0430	0.0430	RUNX1	0.3739	56	10	0	20	6	0
RUNX1 regulates transcription of genes involved in differentiation of myeloid cells	21	37371181	C	T	T	rs71330631	intronic	0.0433	0.0433	RUNX1	0.3788	55	10	0	20	6	0
Downstream signaling events of B Cell Receptor (BCR)	1	85738304	T	G	G	rs141532778	intronic	0.0265	0.0265	BCL10	0.1949	59	7	0	24	1	1
Downstream signaling events of B Cell Receptor (BCR)	1	85742155	G	A	A	rs78416998	5_prime_UTR	0.0349	0.0349	BCL10	0.7734	60	5	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	1	109959684	G	A	A	rs12119154	intronic	0.0463	0.0463	PSMA5	0.3842	59	7	0	22	3	1
Downstream signaling events of B Cell Receptor (BCR)	1	115255717	T	C	C	rs9724630	intronic	0.0490	0.0490	NRAS	0.0910	60	6	0	20	6	0
Downstream signaling events of B Cell Receptor (BCR)	2	33674504	A	G	G	rs17013001	intronic	0.0406	0.0406	RASGRP3	0.2744	57	9	0	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	33707486	A	G	G	rs17648515	intronic	0.0454	0.0454	RASGRP3	0.7549	56	10	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	2	33715019	A	C	C	rs17595032	intronic	0.0422	0.0422	RASGRP3	0.7549	56	10	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	2	33717791	T	A	A	rs12470632	intronic	0.0329	0.0329	RASGRP3	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	33718749	G	A	A	rs72804240	intronic	0.0274	0.0274	RASGRP3	0.3739	56	10	0	20	6	0
Downstream signaling events of B Cell Receptor (BCR)	2	33723194	T	C	C	rs34719322	intronic	0.0204	0.0204	RASGRP3	0.5590	61	4	1	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	2	33725279	T	C	C	rs34958143	intronic	0.0231	0.0231	RASGRP3	0.7348	58	8	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	2	33725706	A	T	T	rs72785908	intronic	0.0406	0.0406	RASGRP3	0.1706	56	10	0	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	33732446	A	G	G	rs80205916	intronic	0.0361	0.0361	RASGRP3	0.7632	60	5	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	33758737	C	T	T	rs56197103	intronic	0.0426	0.0426	RASGRP3	0.7384	55	9	1	21	3	1
Downstream signaling events of B Cell Receptor (BCR)	2	33760191	A	G	G	rs148641284	intronic	0.0360	0.0360	RASGRP3	0.7469	57	9	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	2	54106726	G	A	A	rs78542544	intronic	0.0466	0.0466	PSME4	0.0565	56	10	0	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	2	54109699	G	A	A	rs75679248	intronic	0.0345	0.0345	PSME4	1.0000	57	9	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	2	54112612	T	G	G	rs115678984	intronic	0.0340	0.0340	PSME4	0.7302	58	8	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	2	54116463	C	T	T	rs805403	intronic	0.0376	0.0376	PSME4	0.2083	62	4	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	2	54119870	T	C	C	rs77215245	intronic	0.0487	0.0487	PSME4	0.6362	55	10	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54121956	T	C	C	rs79436269	intronic	0.0498	0.0498	PSME4	0.6362	55	10	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54131546	T	C	C	rs78887562	intronic	0.0467	0.0467	PSME4	0.0565	56	10	0	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	2	54132737	G	A	A	rs75125553	intronic	0.0493	0.0493	PSME4	0.6407	54	10	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54148310	G	C	C	rs74545963	intronic	0.0348	0.0348	PSME4	1.0000	57	9	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	2	54153284	A	G	G	rs62139281	intronic	0.0226	0.0226	PSME4	0.0237	62	4	0	19	6	0
Downstream signaling events of B Cell Receptor (BCR)	2	54161109	A	C	C	rs74627832	intronic	0.0468	0.0468	PSME4	0.0565	56	10	0	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	2	54166671	C	T	T	rs79435818	intronic	0.0317	0.0317	PSME4	1.0000	58	8	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	2	54166800	A	G	G	rs76811723	intronic	0.0317	0.0317	PSME4	1.0000	58	8	0	22	3	0

Downstream signaling events of B Cell Receptor (BCR)	2	54176733	C	A	A	rs115660490	intronic	0.0366	0.0366	PSME4	0.7213	58	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54182973	T	A	A	rs114515761	intronic	0.0346	0.0346	PSME4	0.7192	58	8	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54188394	T	A	A	rs11692784	intronic	0.0346	0.0346	PSME4	0.7192	58	8	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54198172	G	A	A	rs141622297	upstream	0.0360	0.0360	PSME4	0.7192	58	8	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	54201823	G	A	A	rs74336645	upstream	0.0362	0.0362	PSME4	0.7213	58	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	2	61155012	C	G	G	rs79263888	3_prime_UTR	0.0229	0.0229	REL	0.7522	56	10	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	2	68411185	T	C	C	rs72832011	intronic	0.0451	0.0451	PPP3R1	0.0653	59	7	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	68413244	T	A	A	rs72832013	intronic	0.0455	0.0455	PPP3R1	0.0621	59	7	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	162169482	G	A	A	rs7605885	intronic	0.0425	0.0425	PSMD14	0.8183	56	9	1	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	2	162215335	C	T	T	rs6722186	intronic	0.0427	0.0427	PSMD14	1.0000	56	9	1	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	2	231921109	G	A	A	rs3754982	upstream	0.0430	0.0430	PSMD1	0.0899	60	6	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231926692	G	A	A	rs80031661	intronic	0.0429	0.0429	PSMD1	0.0899	60	6	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231932134	T	C	C	rs78964764	intronic	0.0433	0.0433	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231933408	C	T	T	rs13424110	intronic	0.0476	0.0476	PSMD1	0.1782	59	7	0	20	4	1
Downstream signaling events of B Cell Receptor (BCR)	2	231937539	T	C	C	rs2288148	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231939526	A	G	G	rs12620983	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231947467	A	G	G	rs11694724	intronic	0.0411	0.0411	PSMD1	0.2744	57	9	0	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	231949569	T	C	C	rs2303354	intronic	0.0433	0.0433	PSMD1	0.0876	59	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231950847	T	G	G	rs78363488	intronic	0.0407	0.0407	PSMD1	0.4353	57	8	0	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	231967886	T	C	C	rs12616914	intronic	0.0436	0.0436	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231979258	A	G	G	rs17586405	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231982950	T	C	C	rs60707561	intronic	0.0434	0.0434	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231983382	T	G	G	rs17619636	intronic	0.0478	0.0478	PSMD1	0.0899	60	6	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	231998010	G	A	A	rs77199363	intronic	0.0431	0.0431	PSMD1	0.0899	60	6	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	232003189	C	T	T	rs80121410	intronic	0.0408	0.0408	PSMD1	0.2744	57	9	0	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	232021354	T	C	C	rs115196328	intronic	0.0402	0.0402	PSMD1	0.5418	53	13	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	2	232025880	C	T	T	rs76901853	intronic	0.0472	0.0472	PSMD1	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	2	232036567	G	A	A	rs11674175	intronic	0.0409	0.0409	PSMD1	0.2744	57	9	0	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	2	232041640	G	A	A	rs111612792	downstream	0.0413	0.0413	PSMD1	0.2719	57	9	0	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	3	63994801	G	A	A	rs62252370	downstream	0.0360	0.0360	PSMD6	1.0000	58	8	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	4	102027455	C	T	T	rs78657301	intronic	0.0019	0.0019	PPP3CA	0.7980	57	8	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102030909	T	C	C	rs143246322	intronic	0.0331	0.0331	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102046408	C	T	T	rs79507245	intronic	0.0394	0.0394	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102046629	C	T	T	rs74675949	intronic	0.0393	0.0393	PPP3CA	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102047770	T	C	C	rs78209620	intronic	0.0395	0.0395	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102047812	A	G	G	rs78888749	intronic	0.0394	0.0394	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102049484	A	G	G	rs113609659	intronic	0.0394	0.0394	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102059408	A	G	G	rs111885453	intronic	0.0393	0.0393	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102060085	C	A	A	rs150119589	intronic	0.0392	0.0392	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102061144	C	T	T	rs113496555	intronic	0.0392	0.0392	PPP3CA	0.4985	55	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102061766	T	C	C	rs116229517	intronic	0.0392	0.0392	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102061822	C	T	T	rs112122964	intronic	0.0393	0.0393	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102062069	G	A	A	rs74631130	intronic	0.0392	0.0392	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102063270	T	C	C	rs111752790	intronic	0.0421	0.0421	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102064126	A	T	T	rs113744576	intronic	0.0439	0.0439	PPP3CA	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102064899	T	C	C	rs112973280	intronic	0.0500	0.0500	PPP3CA	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102065144	G	A	A	rs112695279	intronic	0.0497	0.0497	PPP3CA	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102065533	G	A	A	rs75372805	intronic	0.0392	0.0392	PPP3CA	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102065719	T	C	C	rs17240082	intronic	0.0496	0.0496	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102071777	C	T	T	rs112522326	intronic	0.0439	0.0439	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102073273	G	A	A	rs111792710	intronic	0.0391	0.0391	PPP3CA	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102105924	C	T	T	rs80191143	intronic	0.0153	0.0153	PPP3CA	1.0000	60	5	1	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	4	102128007	A	C	C	rs75423137	intronic	0.0447	0.0447	PPP3CA	0.6398	54	11	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	102158097	G	A	A	rs116097940	intronic	0.0226	0.0226	PPP3CA	0.3171	60	6	0	23	1	1
Downstream signaling events of B Cell Receptor (BCR)	4	102159289	C	T	T	rs13133951	intronic	0.0215	0.0215	PPP3CA	0.3221	60	6	0	24	1	1
Downstream signaling events of B Cell Receptor (BCR)	4	102174349	T	C	C	rs114543570	intronic	0.0466	0.0466	PPP3CA	0.7621	59	6	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	4	103436737	T	C	C	rs79590323	intronic	0.0393	0.0393	NFKB1	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	103441152	G	A	A	rs74833382	intronic	0.0318	0.0318	NFKB1	0.7621	59	6	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	4	103441742	G	A	A	rs78900265	intronic	0.0393	0.0393	NFKB1	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	103465229	C	T	T	rs76016852	intronic	0.0414	0.0414	NFKB1	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	103534557	C	T	T	rs4648117	intronic	0.0416	0.0416	NFKB1	0.7621	59	6	1	25	1	0

Downstream signaling events of B Cell Receptor (BCR)	4	103535905	C	T	T	rs4648127	intronic	0.0389	0.0389	NFKB1	0.4974	55	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	4	103542005	G	T	T	rs997476	downstream	0.0397	0.0397	NFKB1	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	5	133505097	T	C	C	rs34751193	intronic	0.0303	0.0303	SKP1	0.7497	55	11	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	5	133512605	G	T	T	rs11538030	5_prime_UTR	0.0356	0.0356	SKP1	0.6295	55	9	2	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	5	171287624	C	G	C	rs702109	downstream	0.9605	0.0395	FBXW11	0.1356	0	13	52	1	2	22
Downstream signaling events of B Cell Receptor (BCR)	5	171319929	T	C	C	rs17569783	intronic	0.0456	0.0456	FBXW11	1.0000	59	6	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	5	171387634	G	A	A	rs72835279	intronic	0.0450	0.0450	FBXW11	1.0000	59	6	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	5	171420105	G	C	C	rs72835287	intronic	0.0441	0.0441	FBXW11	0.2719	57	9	0	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	5	171424137	T	G	G	rs72835288	intronic	0.0465	0.0465	FBXW11	1.0000	59	6	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	6	32810147	G	T	T	rs41270496	intronic	0.0323	0.0323	PSMB8	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	32811224	A	T	T	rs72854938	intronic	0.0322	0.0322	PSMB8	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	32811366	G	T	T	rs72854939	intronic	0.0322	0.0322	PSMB8	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	32826688	G	T	T	rs115353581	intronic	0.0219	0.0219	PSMB9	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	32832218	A	T	T	rs116481206	downstream	0.0219	0.0219	PSMB9	0.4862	59	7	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	44227224	C	T	T	rs28362860	intronic	0.0269	0.0269	NFKBIE	0.4603	60	6	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	44233216	G	C	C	rs28362857	missense	0.0296	0.0296	NFKBIE	0.0685	61	5	0	20	6	0
Downstream signaling events of B Cell Receptor (BCR)	6	91239702	T	A	A	rs62409064	intronic	0.0407	0.0407	MAP3K7	0.4940	58	7	1	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	6	91296810	C	T	T	rs34016005	upstream	0.0303	0.0303	MAP3K7	0.4762	60	5	1	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	6	170851525	G	A	A	rs12200064	intronic	0.0431	0.0431	PSMB1	0.3694	59	5	2	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	6	170858332	G	A	A	rs17860779	intronic	0.0420	0.0420	PSMB1	1.0000	59	6	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	7	2955476	G	C	C	rs41336352	intronic	0.0400	0.0400	CARD11	1.0000	58	8	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	7	2966334	G	A	A	rs41448444	intronic	0.0454	0.0454	CARD11	0.7213	58	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	7	2968105	C	A	A	rs71527417	intronic	0.0472	0.0472	CARD11	0.0436	49	16	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	7	2970297	C	T	T	rs41386651	intronic	0.0410	0.0410	CARD11	0.7386	56	8	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	7	2970866	C	T	T	rs9648301	intronic	0.0444	0.0444	CARD11	1.0000	57	9	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	7	3029796	G	C	C	rs12700500	intronic	0.0454	0.0454	CARD11	1.0000	59	7	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	7	3042802	G	A	A	rs35579453	intronic	0.0363	0.0363	CARD11	1.0000	57	9	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	7	3052087	G	A	A	rs75468256	intronic	0.0407	0.0407	CARD11	0.2020	62	4	0	20	4	0
Downstream signaling events of B Cell Receptor (BCR)	7	3072512	T	C	C	rs6975176	intronic	0.0452	0.0452	CARD11	1.0000	61	4	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	7	3073243	G	A	A	rs78353391	intronic	0.0427	0.0427	CARD11	0.0650	56	8	0	18	8	0
Downstream signaling events of B Cell Receptor (BCR)	7	3079195	G	T	T	rs62439353	intronic	0.0400	0.0400	CARD11	0.7348	58	8	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	7	42971385	G	A	A	rs76256519	intronic	0.0432	0.0432	PSMA2	0.1923	61	5	0	21	3	1
Downstream signaling events of B Cell Receptor (BCR)	7	148411091	C	T	T	rs11764941	intronic	0.0416	0.0416	CUL1	0.0082	58	8	0	16	9	1
Downstream signaling events of B Cell Receptor (BCR)	7	148422581	A	G	G	rs11760399	intronic	0.0409	0.0409	CUL1	0.0158	57	9	0	16	9	1
Downstream signaling events of B Cell Receptor (BCR)	7	148427470	A	T	T	rs17625893	intronic	0.0188	0.0188	CUL1	0.3091	59	7	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	7	148453031	C	G	G	rs4726991	intronic	0.0427	0.0427	CUL1	0.0164	61	5	0	18	7	0
Downstream signaling events of B Cell Receptor (BCR)	7	148455710	A	G	G	rs73158225	intronic	0.0426	0.0426	CUL1	0.0333	61	5	0	19	7	0
Downstream signaling events of B Cell Receptor (BCR)	7	148456174	T	G	G	rs17537343	intronic	0.0430	0.0430	CUL1	0.0164	61	5	0	18	7	0
Downstream signaling events of B Cell Receptor (BCR)	7	148458141	C	T	T	rs73158226	intronic	0.0426	0.0426	CUL1	0.0616	61	5	0	18	6	0
Downstream signaling events of B Cell Receptor (BCR)	7	148470413	T	C	C	rs73158234	intronic	0.0423	0.0423	CUL1	0.0333	61	5	0	19	7	0
Downstream signaling events of B Cell Receptor (BCR)	7	148502252	T	C	C	rs77948593	downstream	0.0395	0.0395	CUL1	1.0000	59	6	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	8	42125339	T	C	C	rs76361874	upstream	0.0303	0.0303	IKBKB	0.0653	59	7	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42127643	A	C	C	rs17875739	upstream	0.0241	0.0241	IKBKB	0.0653	59	7	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42128072	T	A	A	rs62507976	upstream	0.0296	0.0296	IKBKB	0.4157	61	5	0	23	2	1
Downstream signaling events of B Cell Receptor (BCR)	8	42135678	T	G	G	rs17875740	intronic	0.0335	0.0335	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42138781	G	C	C	rs80313154	intronic	0.0274	0.0274	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42142316	G	A	A	rs79881854	intronic	0.0326	0.0326	IKBKB	0.0321	58	8	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42145446	A	G	G	rs17875744	intronic	0.0327	0.0327	IKBKB	0.0272	57	9	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42150794	C	T	T	rs79123247	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42154866	A	G	G	rs78342373	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42155029	G	A	A	rs112141582	intronic	0.0267	0.0267	IKBKB	0.0321	58	8	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42158881	A	G	G	rs75230171	intronic	0.0327	0.0327	IKBKB	0.0321	58	8	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42159022	C	T	T	rs79460550	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42161317	G	A	A	rs113993388	intronic	0.0280	0.0280	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42162675	C	T	T	rs17875700	intronic	0.0338	0.0338	IKBKB	0.0321	58	8	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42170928	C	T	T	rs76891399	intronic	0.0325	0.0325	IKBKB	0.0321	58	8	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42173677	G	T	T	rs17875746	intronic	0.0322	0.0322	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42180084	G	A	A	rs17875721	intronic	0.0326	0.0326	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42180328	G	T	T	rs17875751	intronic	0.0327	0.0327	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42180679	G	A	A	rs78599265	intronic	0.0333	0.0333	IKBKB	0.0330	58	8	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	8	42186989	C	T	T	rs17875731	intronic	0.0324	0.0324	IKBKB	0.0330	58	8	0	25	0	1

Downstream signaling events of B Cell Receptor (BCR)	8	42188334	G	T	T	rs79200457	intronic	0.0325	0.0325	IKBKB	0.0666	58	7	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	9	123578733	G	A	A	rs10384	3_prime_UTR	0.0186	0.0186	PSMD5	0.3096	61	5	0	23	1	1
Downstream signaling events of B Cell Receptor (BCR)	9	123598623	A	G	G	rs62581704	intronic	0.0476	0.0476	PSMD5	0.3820	62	4	0	24	1	1
Downstream signaling events of B Cell Receptor (BCR)	9	127118932	G	A	A	rs117300833	intronic	0.0270	0.0270	PSMB7	0.3024	58	7	0	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	9	127119442	G	A	A	rs16927388	intronic	0.0435	0.0435	PSMB7	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	9	127119799	G	A	A	rs56058032	intronic	0.0172	0.0172	PSMB7	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	9	127141846	G	C	C	rs79069085	intronic	0.0178	0.0178	PSMB7	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	9	127143001	T	A	A	rs76699962	intronic	0.0448	0.0448	PSMB7	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	9	127144906	A	C	C	rs79321634	intronic	0.0239	0.0239	PSMB7	0.2833	59	6	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	9	127145687	T	C	C	rs77214542	intronic	0.0335	0.0335	PSMB7	1.0000	58	8	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	9	127145878	G	C	C	rs41274376	intronic	0.0237	0.0237	PSMB7	0.3091	59	7	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	9	127151807	T	G	G	rs114451602	intronic	0.0301	0.0301	PSMB7	0.5095	60	5	1	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	9	127172515	T	C	C	rs140504275	intronic	0.0204	0.0204	PSMB7	0.1666	60	6	0	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	9	127177053	C	T	T	rs73588260	intronic	0.0344	0.0344	PSMB7	0.7366	57	8	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	10	75203331	A	T	T	rs12775630	intronic	0.0464	0.0464	PPP3CB	0.8528	56	8	2	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	10	75243476	G	A	A	rs72814306	intronic	0.0163	0.0163	PPP3CB	0.2725	63	2	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	10	101958770	C	T	T	rs12764732	intronic	0.0464	0.0464	CHUK	0.7209	57	9	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	10	101958858	T	G	G	rs17883365	intronic	0.0229	0.0229	CHUK	1.0000	61	5	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	10	101961171	G	A	A	rs17885986	intronic	0.0496	0.0496	CHUK	0.6322	57	8	1	21	4	1
Downstream signaling events of B Cell Receptor (BCR)	10	101979482	T	C	C	rs12764370	intronic	0.0302	0.0302	CHUK	0.7209	57	9	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	10	103121589	C	T	T	rs11190960	intronic	0.0325	0.0325	BTRC	0.2234	59	6	1	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	10	103165858	G	A	A	rs145847638	intronic	0.0278	0.0278	BTRC	0.4058	59	6	1	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	10	103180336	G	A	A	rs11191003	intronic	0.0274	0.0274	BTRC	0.2234	59	6	1	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	10	103231195	T	C	C	rs34711120	intronic	0.0435	0.0435	BTRC	0.7302	58	8	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	10	103272221	C	T	T	rs12774622	intronic	0.0257	0.0257	BTRC	0.7970	57	8	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	10	103298099	G	T	T	rs4151060	missense	0.0289	0.0289	BTRC	0.6362	55	10	1	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	242014	T	A	A	rs17727753	intronic	0.0189	0.0189	PSMD13	1.0000	60	5	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	249105	G	A	A	rs11601352	intronic	0.0465	0.0465	PSMD13	0.7522	56	10	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	11	527311	T	G	G	rs117011293	downstream	0.0497	0.0497	HRAS	0.4157	61	5	0	23	2	1
Downstream signaling events of B Cell Receptor (BCR)	11	14528592	T	A	A	rs11023241	intronic	0.0417	0.0417	PSMA1	0.6117	57	8	1	23	2	1
Downstream signaling events of B Cell Receptor (BCR)	11	14531031	C	T	T	rs78398913	intronic	0.0273	0.0273	PSMA1	1.0000	56	9	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	11	14537004	A	G	G	rs74589503	intronic	0.0418	0.0418	PSMA1	0.4981	56	10	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	14540827	C	T	T	rs79966935	intronic	0.0233	0.0233	PSMA1	0.7222	57	9	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	14541179	A	T	T	rs61883612	intronic	0.0441	0.0441	PSMA1	0.7666	55	11	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	11	14556220	C	T	T	rs34162548	intronic	0.0376	0.0376	PSMA1	1.0000	55	11	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	11	14588324	G	A	A	rs78854818	intronic	0.0413	0.0413	PSMA1	1.0000	59	6	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	14602698	T	G	G	rs17567703	intronic	0.0418	0.0418	PSMA1	1.0000	58	8	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	11	14622982	G	A	A	rs16930367	intronic	0.0250	0.0250	PSMA1	0.7192	58	8	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	14627135	G	A	A	rs55760529	intronic	0.0485	0.0485	PSMA1	1.0000	56	9	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	11	14633490	G	A	A	rs11023274	intronic	0.0317	0.0317	PSMA1	1.0000	56	9	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	11	14648387	G	A	A	rs79123458	intronic	0.0412	0.0412	PSMA1	1.0000	59	6	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	11	47441683	C	T	T	rs72903900	intronic	0.0375	0.0375	PSMC3	0.8389	59	5	2	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	11	47449591	G	A	A	rs116930066	upstream	0.0311	0.0311	PSMC3	0.5028	56	9	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	12	25374046	T	C	C	rs117991169	intronic	0.0070	0.0070	KRAS	1.0000	63	2	1	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	12	25384938	C	T	T	rs187995827	intronic	0.0218	0.0218	KRAS	0.6900	61	4	1	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	12	25389886	T	C	C	rs61761102	intronic	0.0354	0.0354	KRAS	1.0000	57	7	2	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	12	25393865	A	C	C	rs17388893	intronic	0.0338	0.0338	KRAS	1.0000	57	7	2	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	12	25395953	T	C	C	rs61761078	intronic	0.0309	0.0309	KRAS	0.5904	57	8	1	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	12	25397593	A	C	C	rs61761074	intronic	0.0336	0.0336	KRAS	0.3096	61	5	0	23	1	1
Downstream signaling events of B Cell Receptor (BCR)	12	25398972	C	T	T	rs17329975	intronic	0.0340	0.0340	KRAS	1.0000	57	7	2	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	12	122349404	T	G	G	rs113810917	intronic	0.0229	0.0229	PSMD9	0.1282	57	8	1	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	12	122351293	A	C	C	rs73229956	intronic	0.0288	0.0288	PSMD9	0.2597	54	11	1	24	1	0
Downstream signaling events of B Cell Receptor (BCR)	12	125395161	G	C	C	rs113660988	downstream	0.0428	0.0428	UBC	0.0064	64	1	1	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	12	125395728	C	T	T	rs112205208	downstream	0.0429	0.0429	UBC	0.0064	64	1	1	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	12	125398911	C	T	T	rs112043091	5_prime_UTR	0.0430	0.0430	UBC	0.0064	64	1	1	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	12	125399133	C	T	T	rs41276688	5_prime_UTR	0.0434	0.0434	UBC	0.0064	64	1	1	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	14	23512430	C	T	T	rs78162644	3_prime_UTR	0.0459	0.0459	PSMB11	1.0000	57	9	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	14	35787993	A	T	T	rs12890150	downstream	0.0324	0.0324	PSMA6	0.5321	62	3	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	14	53178728	T	C	C	rs117516552	intronic	0.0276	0.0276	PSMC6	0.7209	57	9	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	14	58710711	C	G	G	rs117328560	upstream	0.0280	0.0280	PSMA3	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	14	58729996	C	G	G	rs111364917	intronic	0.0397	0.0397	PSMA3	0.4984	59	7	0	22	4	0

Downstream signaling events of B Cell Receptor (BCR)	14	58731398	T	G	G	rs117955444	intronic	0.0210	0.0210	PSMA3	1.0000	59	7	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	14	90868665	A	G	G	rs34825576	intronic	0.0382	0.0382	CALM1	0.5425	53	13	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	15	38801129	C	T	T	rs12901652	intronic	0.0478	0.0478	RASGRP1	0.0703	56	9	1	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	15	38803689	G	A	A	rs28710819	intronic	0.0461	0.0461	RASGRP1	0.7703	53	13	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	15	38805185	A	C	C	rs55888286	intronic	0.0498	0.0498	RASGRP1	0.7632	60	5	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	15	38816519	G	A	A	rs35925499	intronic	0.0463	0.0463	RASGRP1	0.7302	58	8	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	15	78834476	A	G	G	rs41280046	intronic	0.0393	0.0393	PSMA4	0.7087	60	6	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.4762	60	5	1	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.0099	0	11	55	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.0099	0	11	55	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.0063	0	14	52	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.3487	61	4	1	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.0016	0	17	49	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.0012	0	17	49	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.0015	0	16	49	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.7348	58	8	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.0015	0	16	49	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.5065	58	8	0	21	5	0

Downstream signaling events of B Cell Receptor (BCR)	16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.0024	0	16	50	1	0	24
Downstream signaling events of B Cell Receptor (BCR)	16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.3024	58	7	0	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.0015	0	16	50	1	0	25
Downstream signaling events of B Cell Receptor (BCR)	16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.0343	0	15	51	0	1	25
Downstream signaling events of B Cell Receptor (BCR)	16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.0000	53	12	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.1679	0	11	55	0	1	25
Downstream signaling events of B Cell Receptor (BCR)	16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.1681	0	11	55	0	1	24
Downstream signaling events of B Cell Receptor (BCR)	16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.3348	54	12	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.7522	56	10	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.0000	57	9	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.7522	56	10	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.6919	60	4	1	25	0	0
Downstream signaling events of B Cell Receptor (BCR)	16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.7213	58	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.7192	58	8	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.7213	58	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.1877	59	7	0	21	4	1
Downstream signaling events of B Cell Receptor (BCR)	16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.8583	57	7	2	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.4631	59	6	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.4603	60	6	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	67973569	C	T	T	rs17240392	upstream	0.0497	0.0497	PSMB10	0.4984	59	7	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	16	68137486	G	T	T	rs78479045	intronic	0.0183	0.0183	NFATC3	0.7734	60	5	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	68165961	G	C	C	rs75914405	intronic	0.0183	0.0183	NFATC3	0.7734	60	5	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	16	68170298	C	T	T	rs117300105	intronic	0.0352	0.0352	NFATC3	0.1078	62	4	0	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	16	74334545	G	T	T	rs149977784	intronic	0.0196	0.0196	PSMD7	1.0000	62	2	2	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	17	4702206	C	A	A	rs71368518	downstream	0.0416	0.0416	PSMB6	1.0000	56	9	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	17	30778483	C	T	T	rs117117721	intronic	0.0190	0.0190	PSMD11	1.0000	59	7	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	17	30791889	C	T	T	rs35225085	intronic	0.0427	0.0427	PSMD11	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	17	30794889	C	G	G	rs35177842	intronic	0.0430	0.0430	PSMD11	0.4999	56	10	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	17	36920050	C	T	T	rs118080693	intronic	0.0415	0.0415	PSMB3	0.1732	63	3	0	25	0	1
Downstream signaling events of B Cell Receptor (BCR)	17	38144079	G	T	T	rs118009374	intronic	0.0189	0.0189	PSMD3	0.8767	53	11	2	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	17	38154396	C	T	T	rs118034841	downstream	0.0176	0.0176	PSMD3	0.0569	56	10	0	26	0	0
Downstream signaling events of B Cell Receptor (BCR)	17	65334270	T	A	A	rs146515782	3_prime_UTR	0.0418	0.0418	PSMD12	1.0000	58	8	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	18	23711373	G	T	T	rs79820119	upstream	0.0407	0.0407	PSMA8	0.2218	53	13	0	23	2	0
Downstream signaling events of B Cell Receptor (BCR)	18	23715815	T	G	G	rs4800242	intronic	0.0460	0.0460	PSMA8	0.7043	59	6	0	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	18	23774138	C	A	A	rs79452515	downstream	0.0424	0.0424	PSMA8	0.2993	59	7	0	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	18	56333866	G	A	A	rs72958690	upstream	0.0368	0.0368	MALT1	0.8183	56	9	1	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	18	56338792	G	A	A	rs56142402	5_prime_UTR	0.0327	0.0327	MALT1	0.8110	57	8	1	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	18	56363534	A	C	C	rs55825071	intronic	0.0377	0.0377	MALT1	0.6531	56	9	1	20	5	0
Downstream signaling events of B Cell Receptor (BCR)	18	77161434	C	T	T	rs73007652	intronic	0.0439	0.0439	NFATC1	1.0000	54	12	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	18	77181200	C	T	T	rs4799054	intronic	0.0312	0.0312	NFATC1	0.3820	62	4	0	24	1	1
Downstream signaling events of B Cell Receptor (BCR)	18	77193040	G	A	A	rs142796661	intronic	0.0417	0.0417	NFATC1	0.4442	53	12	0	21	4	1
Downstream signaling events of B Cell Receptor (BCR)	18	77197508	G	A	A	rs117121680	intronic	0.0416	0.0416	NFATC1	0.3172	52	13	0	21	4	1
Downstream signaling events of B Cell Receptor (BCR)	18	77199322	C	T	T	rs75588847	intronic	0.0455	0.0455	NFATC1	0.3091	59	7	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	18	77199460	G	A	A	rs62096887	intronic	0.0211	0.0211	NFATC1	1.0000	60	6	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	18	77211908	G	A	A	rs55953864	intronic	0.0480	0.0480	NFATC1	0.3091	59	7	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	18	77212989	G	T	T	rs73007700	intronic	0.0438	0.0438	NFATC1	0.5065	58	8	0	21	5	0
Downstream signaling events of B Cell Receptor (BCR)	18	77239775	G	A	A	rs117383241	intronic	0.0246	0.0246	NFATC1	0.7113	59	6	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	18	77241715	G	A	A	rs117246954	intronic	0.0175	0.0175	NFATC1	0.7222	57	9	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	18	77256499	A	G	G	rs62096906	intronic	0.0466	0.0466	NFATC1	1.0000	53	12	0	22	4	0
Downstream signaling events of B Cell Receptor (BCR)	18	77275049	A	G	G	rs113507668	intronic	0.0393	0.0393	NFATC1	1.0000	58	7	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	18	77278071	G	A	A	rs116844899	intronic	0.0231	0.0231	NFATC1	1.0000	59	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	18	77279921	G	A	A	rs79426764	intronic	0.0497	0.0497	NFATC1	0.2606	51	15	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	18	77279961	A	G	G	rs76389821	intronic	0.0306	0.0306	NFATC1	0.2710	56	9	0	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	19	40472450	A	C	C	rs147915270	upstream	0.0382	0.0382	PSMC4	1.0000	58	7	1	22	3	0
Downstream signaling events of B Cell Receptor (BCR)	19	40475070	T	G	G	rs139876278	upstream	0.0147	0.0147	PSMC4	0.2725	63	2	1	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	20	1128622	T	C	C	rs74871431	intronic	0.0320	0.0320	PSMF1	0.7087	60	6	0	23	3	0

Downstream signaling events of B Cell Receptor (BCR)	20	1146048	C	T	T	rs17716261	3_prime_UTR	0.0279	0.0279	PSMF1	0.4532	60	6	0	21	4	0
Downstream signaling events of B Cell Receptor (BCR)	20	1149980	C	T	T	rs77625408	downstream	0.0254	0.0254	PSMF1	0.7495	54	11	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	20	1152323	C	T	T	rs34552580	downstream	0.0323	0.0323	PSMF1	1.0000	59	5	1	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	20	1155154	G	A	A	rs78313102	intronic,non_coding_transcript	0.0258	0.0258	PSMF1	1.0000	58	7	0	23	3	0
Downstream signaling events of B Cell Receptor (BCR)	20	50001132	C	T	T	rs75343958	downstream	0.0191	0.0191	NFATC2	0.0863	60	6	0	24	0	1
Downstream signaling events of B Cell Receptor (BCR)	20	50014957	G	A	A	rs77379100	intronic	0.0207	0.0207	NFATC2	0.7222	57	9	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	20	50113131	A	C	C	rs73128899	intronic	0.0467	0.0467	NFATC2	0.7632	60	5	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	20	50113240	A	G	G	rs73128900	intronic	0.0466	0.0466	NFATC2	0.7632	60	5	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	20	50124126	C	T	T	rs6013204	intronic	0.0473	0.0473	NFATC2	1.0000	60	6	0	24	2	0
Downstream signaling events of B Cell Receptor (BCR)	20	50129716	T	C	C	rs17728960	intronic	0.0477	0.0477	NFATC2	0.7621	59	6	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	20	50143470	C	T	T	rs77042341	intronic	0.0367	0.0367	NFATC2	0.7631	59	5	1	25	1	0
Downstream signaling events of B Cell Receptor (BCR)	20	50170376	T	G	G	rs80208372	intronic	0.0480	0.0480	NFATC2	1.0000	55	10	0	22	4	0
Depolymerisation of the Nuclear Lamina	2	11819328	G	A	A	rs140904588	intronic	0.0333	0.0333	LPIN1	0.1086	59	5	0	25	0	1
Depolymerisation of the Nuclear Lamina	2	11848161	C	G	G	rs77534915	intronic	0.0360	0.0360	LPIN1	0.6828	61	5	0	23	3	0
Depolymerisation of the Nuclear Lamina	2	11882703	A	C	C	rs80102993	intronic	0.0434	0.0434	LPIN1	0.4984	59	7	0	22	4	0
Depolymerisation of the Nuclear Lamina	2	11885139	C	T	T	rs74899248	intronic	0.0444	0.0444	LPIN1	0.4984	59	7	0	22	4	0
Depolymerisation of the Nuclear Lamina	2	11885972	C	G	G	rs78733123	intronic	0.0354	0.0354	LPIN1	0.4393	60	6	0	23	2	1
Depolymerisation of the Nuclear Lamina	2	11894527	C	G	G	rs75421235	intronic	0.0416	0.0416	LPIN1	0.7222	57	9	0	24	2	0
Depolymerisation of the Nuclear Lamina	2	11895388	C	T	T	rs11694928	intronic	0.0498	0.0498	LPIN1	0.5065	58	8	0	21	5	0
Depolymerisation of the Nuclear Lamina	2	11911946	G	A	A	rs111726318	intronic	0.0471	0.0471	LPIN1	0.2818	60	6	0	21	5	0
Depolymerisation of the Nuclear Lamina	2	11943082	C	T	T	rs4669781	missense	0.0342	0.0342	LPIN1	0.1706	56	10	0	25	1	0
Depolymerisation of the Nuclear Lamina	2	11945495	A	C	C	rs79025286	intronic	0.0282	0.0282	LPIN1	0.2744	57	9	0	24	1	0
Depolymerisation of the Nuclear Lamina	2	11955603	C	T	T	rs75560733	intronic	0.0410	0.0410	LPIN1	0.5425	53	13	0	23	3	0
Depolymerisation of the Nuclear Lamina	2	11963271	A	C	C	rs56163146	intronic	0.0449	0.0449	LPIN1	0.4984	59	7	0	22	4	0
Depolymerisation of the Nuclear Lamina	2	11968029	A	G	G	rs34857485	downstream	0.0304	0.0304	LPIN1	0.4098	61	5	0	24	1	1
Depolymerisation of the Nuclear Lamina	5	68462801	C	G	G	rs8192259	upstream	0.0444	0.0444	CCNB1	0.7688	54	11	0	21	5	0
Depolymerisation of the Nuclear Lamina	5	126143504	C	T	C	rs2973605	intronic	0.9641	0.0359	LMNB1	1.0000	1	8	57	0	3	22
Depolymerisation of the Nuclear Lamina	6	33746837	C	T	T	rs151266730	intronic	0.0122	0.0122	LEMD2	0.5321	62	3	1	23	3	0
Depolymerisation of the Nuclear Lamina	10	62548390	G	A	A	rs3213056	intronic	0.0326	0.0326	CDK1	0.7469	57	9	0	21	4	0
Depolymerisation of the Nuclear Lamina	12	65578819	T	G	G	rs75563741	intronic	0.0221	0.0221	LEMD3	0.4862	59	7	0	21	4	0
Depolymerisation of the Nuclear Lamina	12	65586630	A	G	G	rs78691095	intronic	0.0389	0.0389	LEMD3	0.8053	57	8	1	21	4	0
Depolymerisation of the Nuclear Lamina	12	65594504	A	G	G	rs74809372	intronic	0.0234	0.0234	LEMD3	0.2781	56	10	0	24	1	0
Depolymerisation of the Nuclear Lamina	12	98930771	G	A	A	rs57467331	downstream	0.0354	0.0354	TMPO	0.4862	59	7	0	21	4	0
Depolymerisation of the Nuclear Lamina	12	98932013	G	C	C	rs76069997	downstream	0.0352	0.0352	TMPO	0.4984	59	7	0	22	4	0
Depolymerisation of the Nuclear Lamina	16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.4762	60	5	1	22	4	0
Depolymerisation of the Nuclear Lamina	16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.0099	0	11	55	1	0	25
Depolymerisation of the Nuclear Lamina	16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Depolymerisation of the Nuclear Lamina	16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Depolymerisation of the Nuclear Lamina	16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.0099	0	11	55	1	0	25
Depolymerisation of the Nuclear Lamina	16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.0063	0	14	52	1	0	24
Depolymerisation of the Nuclear Lamina	16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.3487	61	4	1	22	4	0
Depolymerisation of the Nuclear Lamina	16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Depolymerisation of the Nuclear Lamina	16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	22	3	0

Depolymerisation of the Nuclear Lamina	16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.0016	0	17	49	1	0	24
Depolymerisation of the Nuclear Lamina	16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.0012	0	17	49	1	0	25
Depolymerisation of the Nuclear Lamina	16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.0015	0	16	49	1	0	25
Depolymerisation of the Nuclear Lamina	16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.7348	58	8	0	22	4	0
Depolymerisation of the Nuclear Lamina	16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.0015	0	16	49	1	0	25
Depolymerisation of the Nuclear Lamina	16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.5065	58	8	0	21	5	0
Depolymerisation of the Nuclear Lamina	16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.0024	0	16	50	1	0	24
Depolymerisation of the Nuclear Lamina	16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.3024	58	7	0	20	5	0
Depolymerisation of the Nuclear Lamina	16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.0015	0	16	50	1	0	25
Depolymerisation of the Nuclear Lamina	16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.0343	0	15	51	0	1	25
Depolymerisation of the Nuclear Lamina	16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.0000	53	12	0	21	4	0
Depolymerisation of the Nuclear Lamina	16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.1679	0	11	55	0	1	25
Depolymerisation of the Nuclear Lamina	16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.1681	0	11	55	0	1	24
Depolymerisation of the Nuclear Lamina	16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.3348	54	12	0	24	2	0
Depolymerisation of the Nuclear Lamina	16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.7522	56	10	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.0000	57	9	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.7522	56	10	0	23	3	0
Depolymerisation of the Nuclear Lamina	16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.6919	60	4	1	25	0	0
Depolymerisation of the Nuclear Lamina	16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.7213	58	8	0	23	2	0
Depolymerisation of the Nuclear Lamina	16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.7192	58	8	0	24	2	0
Depolymerisation of the Nuclear Lamina	16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.7213	58	8	0	23	2	0
Depolymerisation of the Nuclear Lamina	16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Depolymerisation of the Nuclear Lamina	16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Depolymerisation of the Nuclear Lamina	16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.1877	59	7	0	21	4	1
Depolymerisation of the Nuclear Lamina	16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.8583	57	7	2	22	4	0
Depolymerisation of the Nuclear Lamina	16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.4631	59	6	0	22	4	0
Depolymerisation of the Nuclear Lamina	16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.4603	60	6	0	22	4	0
Depolymerisation of the Nuclear Lamina	16	50058523	C	T	T	rs111253683	5_prime_UTR	0.0302	0.0302	CNEP1R1	0.5717	61	4	1	23	3	0
Depolymerisation of the Nuclear Lamina	17	64305051	A	G	G	rs78357146	intronic	0.0186	0.0186	PRKCA	0.7209	57	9	0	23	2	0
Depolymerisation of the Nuclear Lamina	17	64315409	T	C	C	rs80130647	intronic	0.0184	0.0184	PRKCA	0.7043	59	6	0	22	3	0
Depolymerisation of the Nuclear Lamina	17	64318385	G	A	A	rs12150623	intronic	0.0343	0.0343	PRKCA	0.7595	61	4	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64320040	C	T	T	rs139317720	intronic	0.0229	0.0229	PRKCA	1.0000	62	3	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64326068	T	G	G	rs12951126	intronic	0.0260	0.0260	PRKCA	1.0000	58	8	0	23	3	0
Depolymerisation of the Nuclear Lamina	17	64343295	A	C	C	rs72843901	intronic	0.0457	0.0457	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64344650	C	T	T	rs72846606	intronic	0.0454	0.0454	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64344788	C	T	T	rs72846607	intronic	0.0457	0.0457	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64346204	A	G	G	rs12150367	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0

Depolymerisation of the Nuclear Lamina	17	64349104	C	T	T	rs72846609	intronic	0.0497	0.0497	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64351542	G	C	C	rs28592028	intronic	0.0453	0.0453	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64352431	T	G	G	rs544435459	intronic	0.0451	0.0451	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64354597	T	C	C	rs72846612	intronic	0.0451	0.0451	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64358121	C	G	G	rs72846614	intronic	0.0451	0.0451	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64359354	T	C	C	rs72846615	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64365593	C	T	T	rs72846677	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64367534	C	T	T	rs72846678	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64369822	A	G	G	rs72846681	intronic	0.0451	0.0451	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64375194	T	C	C	rs72846695	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64377301	C	A	A	rs113134992	intronic	0.0448	0.0448	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64382507	C	G	G	rs79461368	intronic	0.0453	0.0453	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64389524	C	T	T	rs77682324	intronic	0.0403	0.0403	PRKCA	0.7621	59	6	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64395773	T	C	C	rs78584531	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64396570	T	G	G	rs72838208	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64396695	A	G	G	rs74329211	intronic	0.0432	0.0432	PRKCA	0.7302	58	8	0	21	4	0
Depolymerisation of the Nuclear Lamina	17	64396883	G	A	A	rs72838209	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64398013	G	A	A	rs75125285	intronic	0.0295	0.0295	PRKCA	0.7632	60	5	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64400648	C	T	T	rs72838214	intronic	0.0452	0.0452	PRKCA	0.4788	55	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64402141	G	T	T	rs10221238	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64405430	T	A	A	rs72838216	intronic	0.0453	0.0453	PRKCA	0.4725	56	9	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64410564	C	T	T	rs9972974	intronic	0.0390	0.0390	PRKCA	0.7632	60	5	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64412921	G	A	A	rs62070391	intronic	0.0426	0.0426	PRKCA	0.7621	59	6	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64424382	C	T	T	rs62070395	intronic	0.0425	0.0425	PRKCA	0.7595	59	6	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64429928	G	A	A	rs117729211	intronic	0.0272	0.0272	PRKCA	0.0477	60	6	0	19	6	1
Depolymerisation of the Nuclear Lamina	17	64431874	G	A	A	rs72838278	intronic	0.0426	0.0426	PRKCA	0.7642	57	6	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64432202	A	G	G	rs62070397	intronic	0.0427	0.0427	PRKCA	0.7621	59	6	1	25	1	0
Depolymerisation of the Nuclear Lamina	17	64432881	A	G	G	rs62070398	intronic	0.0426	0.0426	PRKCA	0.7595	59	6	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64438732	A	T	T	rs113684166	intronic	0.0445	0.0445	PRKCA	0.2744	57	9	0	24	1	0
Depolymerisation of the Nuclear Lamina	17	64441204	T	C	C	rs75005068	intronic	0.0469	0.0469	PRKCA	0.2719	57	9	0	25	1	0
Depolymerisation of the Nuclear Lamina	17	64441759	C	A	A	rs78330327	intronic	0.0465	0.0465	PRKCA	0.2710	56	9	0	25	1	0
Depolymerisation of the Nuclear Lamina	17	64445337	A	C	C	rs118090701	intronic	0.0387	0.0387	PRKCA	1.0000	58	6	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64445856	A	G	G	rs12451388	intronic	0.0449	0.0449	PRKCA	0.2744	57	9	0	24	1	0
Depolymerisation of the Nuclear Lamina	17	64447721	G	A	A	rs12452749	intronic	0.0462	0.0462	PRKCA	0.2786	57	9	0	23	1	0
Depolymerisation of the Nuclear Lamina	17	64450113	G	C	C	rs80162292	intronic	0.0461	0.0461	PRKCA	0.2710	56	9	0	25	1	0
Depolymerisation of the Nuclear Lamina	17	64453194	A	G	G	rs111776777	intronic	0.0442	0.0442	PRKCA	0.8716	54	10	2	23	3	0
Depolymerisation of the Nuclear Lamina	17	64458036	C	T	T	rs113153197	intronic	0.0339	0.0339	PRKCA	0.1678	54	11	0	25	1	0
Depolymerisation of the Nuclear Lamina	17	64462111	T	G	G	rs79239451	intronic	0.0464	0.0464	PRKCA	0.2744	57	9	0	24	1	0
Depolymerisation of the Nuclear Lamina	17	64462288	G	A	A	rs80080003	intronic	0.0305	0.0305	PRKCA	0.1706	56	10	0	25	1	0
Depolymerisation of the Nuclear Lamina	17	64483589	G	T	T	rs79070174	intronic	0.0391	0.0391	PRKCA	1.0000	59	6	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64487077	T	G	G	rs78149509	intronic	0.0200	0.0200	PRKCA	0.0381	63	3	0	21	4	1
Depolymerisation of the Nuclear Lamina	17	64494906	A	G	G	rs117168126	intronic	0.0300	0.0300	PRKCA	1.0000	59	6	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64501943	C	T	T	rs7217954	intronic	0.0422	0.0422	PRKCA	1.0000	59	7	0	23	3	0
Depolymerisation of the Nuclear Lamina	17	64519790	G	A	A	rs11659067	intronic	0.0498	0.0498	PRKCA	0.0125	62	3	0	19	6	0
Depolymerisation of the Nuclear Lamina	17	64525002	A	T	T	rs77462363	intronic	0.0380	0.0380	PRKCA	1.0000	59	6	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64544723	C	T	T	rs116879811	intronic	0.0274	0.0274	PRKCA	1.0000	60	6	0	24	2	0
Depolymerisation of the Nuclear Lamina	17	64559535	A	G	G	rs227907	intronic	0.0478	0.0478	PRKCA	0.2800	55	11	0	21	3	1
Depolymerisation of the Nuclear Lamina	17	64561055	G	A	A	rs62071706	intronic	0.0238	0.0238	PRKCA	0.1546	60	5	0	21	4	1
Depolymerisation of the Nuclear Lamina	17	64590951	A	T	T	rs11867591	intronic	0.0449	0.0449	PRKCA	0.2122	57	8	0	20	6	0
Depolymerisation of the Nuclear Lamina	17	64604776	C	T	T	rs117539643	intronic	0.0479	0.0479	PRKCA	0.6653	51	11	2	23	3	0
Depolymerisation of the Nuclear Lamina	17	64608923	T	C	C	rs72845947	intronic	0.0440	0.0440	PRKCA	0.7355	57	7	2	21	4	0
Depolymerisation of the Nuclear Lamina	17	64610285	T	C	C	rs72845948	intronic	0.0445	0.0445	PRKCA	0.8583	57	7	2	22	4	0
Depolymerisation of the Nuclear Lamina	17	64610480	A	C	C	rs17759657	intronic	0.0444	0.0444	PRKCA	0.8583	57	7	2	22	4	0
Depolymerisation of the Nuclear Lamina	17	64612838	C	T	T	rs16959714	intronic	0.0338	0.0338	PRKCA	0.4353	57	8	0	24	1	0
Depolymerisation of the Nuclear Lamina	17	64614717	T	C	C	rs17686540	intronic	0.0442	0.0442	PRKCA	0.7355	57	7	2	21	4	0
Depolymerisation of the Nuclear Lamina	17	64626385	G	A	A	rs74352723	intronic	0.0460	0.0460	PRKCA	0.2744	57	9	0	24	1	0
Depolymerisation of the Nuclear Lamina	17	64628634	A	G	G	rs117353888	intronic	0.0437	0.0437	PRKCA	0.2521	54	11	0	18	7	0
Depolymerisation of the Nuclear Lamina	17	64660047	G	C	C	rs146141011	intronic	0.0484	0.0484	PRKCA	1.0000	53	9	2	22	4	0
Depolymerisation of the Nuclear Lamina	17	64671047	C	T	T	rs16959942	intronic	0.0496	0.0496	PRKCA	0.1706	56	10	0	25	1	0
Depolymerisation of the Nuclear Lamina	17	64712634	T	C	C	rs78121420	intronic	0.0465	0.0465	PRKCA	1.0000	57	7	2	23	3	0
Depolymerisation of the Nuclear Lamina	17	64713847	G	T	T	rs112934229	intronic	0.0464	0.0464	PRKCA	1.0000	57	7	2	23	3	0

Depolymerisation of the Nuclear Lamina	17	64723880	G	A	A	rs79547774	intronic	0.0264	0.0264	PRKCA	1.0000	57	9	0	23	3	0
Depolymerisation of the Nuclear Lamina	17	64738427	A	C	C	rs117138620	intronic	0.0400	0.0400	PRKCA	0.3055	58	8	0	23	2	1
Depolymerisation of the Nuclear Lamina	17	64748431	G	T	T	rs141177250	intronic	0.0153	0.0153	PRKCA	0.7595	59	6	1	24	1	0
Depolymerisation of the Nuclear Lamina	17	64755018	T	C	C	rs74831470	intronic	0.0226	0.0226	PRKCA	0.7976	56	9	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64760870	A	G	G	rs77904275	intronic	0.0307	0.0307	PRKCA	0.5233	53	11	1	24	2	0
Depolymerisation of the Nuclear Lamina	17	64762410	C	G	G	rs113025478	intronic	0.0307	0.0307	PRKCA	0.6398	54	11	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64763235	T	C	C	rs77635068	intronic	0.0306	0.0306	PRKCA	0.6398	54	11	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64771614	C	T	T	rs80238933	intronic	0.0297	0.0297	PRKCA	0.6398	54	11	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64776847	G	A	A	rs113542727	intronic	0.0297	0.0297	PRKCA	0.5228	54	11	1	24	2	0
Depolymerisation of the Nuclear Lamina	17	64791836	G	C	C	rs56884788	intronic	0.0390	0.0390	PRKCA	0.6362	55	10	1	23	2	0
Depolymerisation of the Nuclear Lamina	17	64792863	G	C	C	rs72838636	intronic	0.0484	0.0484	PRKCA	0.6470	57	8	1	21	5	0
Depolymerisation of the Nuclear Lamina	18	2967168	A	T	T	rs145394193	intronic	0.0160	0.0160	LPIN2	0.7192	58	8	0	24	2	0
Depolymerisation of the Nuclear Lamina	18	3015946	A	G	G	rs77361064	upstream	0.0479	0.0479	LPIN2	1.0000	57	9	0	22	4	0
Depolymerisation of the Nuclear Lamina	18	3016562	T	C	C	rs76840312	upstream	0.0473	0.0473	LPIN2	1.0000	57	9	0	22	4	0
Depolymerisation of the Nuclear Lamina	20	39968020	A	T	T	rs117029881	upstream	0.0108	0.0108	LPIN3	0.7632	60	5	1	25	1	0
Depolymerisation of the Nuclear Lamina	20	39971848	T	C	C	rs79070826	intronic	0.0382	0.0382	LPIN3	1.0000	61	4	1	25	1	0
Depolymerisation of the Nuclear Lamina	20	39977650	C	T	T	rs78339899	intronic	0.0345	0.0345	LPIN3	1.0000	61	4	1	25	1	0
Depolymerisation of the Nuclear Lamina	20	39982743	C	T	T	rs7269761	intronic	0.0405	0.0405	LPIN3	1.0000	60	4	1	25	1	0
Depolymerisation of the Nuclear Lamina	20	39984988	G	A	A	rs79649817	intronic	0.0295	0.0295	LPIN3	1.0000	61	4	1	25	1	0
Depolymerisation of the Nuclear Lamina	20	39989181	C	T	T	rs2235594	3_prime_UTR	0.0462	0.0462	LPIN3	1.0000	60	4	1	25	1	0
Disinhibition of SNARE formation	1	109285777	G	A	A	rs61797290	upstream	0.0453	0.0453	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109290893	C	T	T	rs1004424	intronic	0.0414	0.0414	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109291952	G	T	T	rs61797292	intronic	0.0458	0.0458	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109292062	G	A	A	rs61797293	intronic	0.0417	0.0417	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109293596	T	C	C	rs61797294	intronic	0.0465	0.0465	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109295260	C	G	G	rs41299559	intronic	0.0458	0.0458	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109300874	A	G	G	rs61797297	intronic	0.0444	0.0444	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109308400	C	G	G	rs61797304	intronic	0.0450	0.0450	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109310759	A	G	G	rs76989906	intronic	0.0458	0.0458	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109311501	T	G	G	rs74406644	intronic	0.0458	0.0458	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	1	109316394	A	C	C	rs61797328	intronic	0.0458	0.0458	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109317182	C	T	T	rs74727654	intronic	0.0459	0.0459	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109324694	A	G	G	rs61797330	intronic	0.0413	0.0413	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109334327	A	C	C	rs61797332	intronic	0.0415	0.0415	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109341648	T	G	G	rs61797348	intronic	0.0458	0.0458	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109347906	G	C	C	rs61797351	intronic	0.0415	0.0415	STXBP3	0.2699	60	6	0	21	3	1
Disinhibition of SNARE formation	1	109351109	A	G	G	rs61797354	intronic	0.0419	0.0419	STXBP3	0.2789	60	6	0	22	3	1
Disinhibition of SNARE formation	16	23845860	G	T	T	rs72777910	upstream	0.0300	0.0300	PRKCB	0.4762	60	5	1	22	4	0
Disinhibition of SNARE formation	16	23849482	T	C	T	rs2023670	intronic	0.9513	0.0487	PRKCB	0.0099	0	11	55	1	0	25
Disinhibition of SNARE formation	16	23850240	A	G	A	rs11074581	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Disinhibition of SNARE formation	16	23851956	T	C	T	rs7189210	intronic	0.9663	0.0337	PRKCB	0.0099	0	11	55	1	0	25
Disinhibition of SNARE formation	16	23852415	A	T	A	rs2188359	intronic	0.9528	0.0472	PRKCB	0.0099	0	11	55	1	0	25
Disinhibition of SNARE formation	16	23859391	A	G	G	rs62030647	intronic	0.0226	0.0226	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23874933	A	C	A	rs6497691	intronic	0.9663	0.0337	PRKCB	0.0063	0	14	52	1	0	24
Disinhibition of SNARE formation	16	23876099	C	T	T	rs79131874	intronic	0.0303	0.0303	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23877500	A	G	A	rs8059885	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23877606	A	G	A	rs8060048	intronic	0.9644	0.0356	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23877781	G	A	G	rs8060718	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23878470	C	T	C	rs12935004	intronic	0.9657	0.0343	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23880851	C	T	C	rs8061523	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23881930	G	A	G	rs8047121	intronic	0.9662	0.0338	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23882469	T	C	T	rs1468129	intronic	0.9663	0.0337	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23885608	A	T	A	rs8044732	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23885751	A	G	G	rs62031692	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23887574	G	T	T	rs79034087	intronic	0.0290	0.0290	PRKCB	0.3487	61	4	1	22	4	0
Disinhibition of SNARE formation	16	23888354	C	T	C	rs7404417	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23889896	T	C	T	rs8063823	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23893893	G	A	G	rs11647359	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23895034	A	G	A	rs6497695	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23895443	A	G	G	rs62028075	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23895884	T	C	T	rs9944348	intronic	0.9665	0.0335	PRKCB	0.0046	0	14	52	1	0	25

Disinhibition of SNARE formation	16	23896089	T	C	C	rs74572166	intronic	0.0245	0.0245	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23896209	C	A	C	rs9302418	intronic	0.9664	0.0336	PRKCB	0.0046	0	14	52	1	0	25
Disinhibition of SNARE formation	16	23896438	G	T	T	rs62028076	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	22	3	0
Disinhibition of SNARE formation	16	23898605	A	T	A	rs933290	intronic	0.9632	0.0368	PRKCB	0.0016	0	17	49	1	0	24
Disinhibition of SNARE formation	16	23899211	A	T	A	rs12926245	intronic	0.9632	0.0368	PRKCB	0.0012	0	17	49	1	0	25
Disinhibition of SNARE formation	16	23899610	G	A	A	rs17753246	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23899951	G	A	A	rs62028077	intronic	0.0254	0.0254	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23900716	T	C	C	rs62028078	intronic	0.0252	0.0252	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23901896	C	T	C	rs6497696	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23901948	A	C	A	rs6497697	intronic	0.9630	0.0370	PRKCB	0.0015	0	16	49	1	0	25
Disinhibition of SNARE formation	16	23904058	A	G	A	rs886115	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23904781	G	A	A	rs17753509	intronic	0.0253	0.0253	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23905676	C	T	C	rs7200610	intronic	0.9631	0.0369	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23907177	A	C	C	rs17810011	intronic	0.0251	0.0251	PRKCB	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	16	23907765	C	T	C	rs9925890	intronic	0.9632	0.0368	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23912174	A	G	A	rs12448249	intronic	0.9519	0.0481	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23914915	C	A	C	rs1004186	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23916258	G	A	G	rs1004187	intronic	0.9632	0.0368	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23916521	G	C	G	rs1008654	intronic	0.9633	0.0367	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23917335	G	A	G	rs6497699	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23917465	C	G	C	rs7186538	intronic	0.9645	0.0355	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23917700	C	A	C	rs7187091	intronic	0.9646	0.0354	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23919088	C	T	T	rs78322646	intronic	0.0278	0.0278	PRKCB	0.7348	58	8	0	22	4	0
Disinhibition of SNARE formation	16	23921083	C	T	C	rs6497702	intronic	0.9647	0.0353	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23925936	C	G	C	rs11074588	intronic	0.9649	0.0351	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23939212	G	A	G	rs11074590	intronic	0.9650	0.0350	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23941628	C	A	C	rs2005671	intronic	0.9647	0.0353	PRKCB	0.0015	0	16	49	1	0	25
Disinhibition of SNARE formation	16	23943749	T	C	T	rs9302420	intronic	0.9649	0.0351	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23945985	T	G	T	rs195989	intronic	0.9651	0.0349	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23946157	G	A	A	rs76973283	intronic	0.0302	0.0302	PRKCB	0.5065	58	8	0	21	5	0
Disinhibition of SNARE formation	16	23949175	G	C	G	rs2560403	intronic	0.9657	0.0343	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23949438	A	G	A	rs195985	intronic	0.9658	0.0342	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23953265	T	C	T	rs2560404	intronic	0.9656	0.0344	PRKCB	0.0024	0	16	50	1	0	24
Disinhibition of SNARE formation	16	23954128	T	C	C	rs17810486	intronic	0.0308	0.0308	PRKCB	0.3024	58	7	0	20	5	0
Disinhibition of SNARE formation	16	23954253	G	A	G	rs195994	intronic	0.9653	0.0347	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23962258	G	C	G	rs196000	intronic	0.9659	0.0341	PRKCB	0.0015	0	16	50	1	0	25
Disinhibition of SNARE formation	16	23964858	T	A	T	rs196003	intronic	0.9647	0.0353	PRKCB	0.0343	0	15	51	0	1	25
Disinhibition of SNARE formation	16	23985814	C	T	T	rs72779914	intronic	0.0487	0.0487	PRKCB	1.0000	53	12	0	21	4	0
Disinhibition of SNARE formation	16	23987552	A	G	A	rs169030	intronic	0.9709	0.0291	PRKCB	0.1679	0	11	55	0	1	25
Disinhibition of SNARE formation	16	23988755	T	C	T	rs196013	intronic	0.9681	0.0319	PRKCB	0.1681	0	11	55	0	1	24
Disinhibition of SNARE formation	16	24009919	A	G	G	rs75622923	intronic	0.0319	0.0319	PRKCB	0.3348	54	12	0	24	2	0
Disinhibition of SNARE formation	16	24022944	C	T	T	rs111746132	intronic	0.0229	0.0229	PRKCB	0.7522	56	10	0	23	3	0
Disinhibition of SNARE formation	16	24066378	G	A	A	rs113426570	intronic	0.0216	0.0216	PRKCB	1.0000	57	9	0	23	3	0
Disinhibition of SNARE formation	16	24100759	T	A	A	rs11643939	intronic	0.0294	0.0294	PRKCB	0.7522	56	10	0	23	3	0
Disinhibition of SNARE formation	16	24105816	G	A	A	rs56316329	intronic	0.0251	0.0251	PRKCB	0.6919	60	4	1	25	0	0
Disinhibition of SNARE formation	16	24111853	T	C	C	rs55959083	intronic	0.0431	0.0431	PRKCB	0.7213	58	8	0	23	2	0
Disinhibition of SNARE formation	16	24112768	G	A	A	rs117056307	intronic	0.0430	0.0430	PRKCB	0.7192	58	8	0	24	2	0
Disinhibition of SNARE formation	16	24122052	G	A	A	rs117467859	intronic	0.0433	0.0433	PRKCB	0.7213	58	8	0	23	2	0
Disinhibition of SNARE formation	16	24122492	C	T	T	rs72779977	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Disinhibition of SNARE formation	16	24123560	G	A	A	rs60261043	intronic	0.0457	0.0457	PRKCB	0.7201	57	8	0	23	2	0
Disinhibition of SNARE formation	16	24132273	G	A	A	rs62027458	intronic	0.0232	0.0232	PRKCB	0.1877	59	7	0	21	4	1
Disinhibition of SNARE formation	16	24164042	G	T	T	rs72779989	intronic	0.0487	0.0487	PRKCB	0.8583	57	7	2	22	4	0
Disinhibition of SNARE formation	16	24197496	A	T	T	rs79699525	intronic	0.0261	0.0261	PRKCB	0.4631	59	6	0	22	4	0
Disinhibition of SNARE formation	16	24199852	C	T	T	rs78424166	intronic	0.0359	0.0359	PRKCB	0.4603	60	6	0	22	4	0
Disinhibition of SNARE formation	17	64305051	A	G	G	rs78357146	intronic	0.0186	0.0186	PRKCA	0.7209	57	9	0	23	2	0
Disinhibition of SNARE formation	17	64315409	T	C	C	rs80130647	intronic	0.0184	0.0184	PRKCA	0.7043	59	6	0	22	3	0
Disinhibition of SNARE formation	17	64318385	G	A	A	rs12150623	intronic	0.0343	0.0343	PRKCA	0.7595	61	4	1	23	2	0
Disinhibition of SNARE formation	17	64320040	C	T	T	rs139317720	intronic	0.0229	0.0229	PRKCA	1.0000	62	3	1	24	1	0
Disinhibition of SNARE formation	17	64326068	T	G	G	rs12951126	intronic	0.0260	0.0260	PRKCA	1.0000	58	8	0	23	3	0
Disinhibition of SNARE formation	17	64343295	A	C	C	rs72843901	intronic	0.0457	0.0457	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64344650	C	T	T	rs72846606	intronic	0.0454	0.0454	PRKCA	0.4725	56	9	1	24	1	0

Disinhibition of SNARE formation	17	64344788	C	T	T	rs72846607	intronic	0.0457	0.0457	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64346204	A	G	G	rs12150367	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64349104	C	T	T	rs72846609	intronic	0.0497	0.0497	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64351542	G	C	C	rs28592028	intronic	0.0453	0.0453	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64352431	T	G	G	rs544435459	intronic	0.0451	0.0451	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64354597	T	C	C	rs72846612	intronic	0.0451	0.0451	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64358121	C	G	G	rs72846614	intronic	0.0451	0.0451	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64359354	T	C	C	rs72846615	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64365593	C	T	T	rs72846677	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64367534	C	T	T	rs72846678	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64369822	A	G	G	rs72846681	intronic	0.0451	0.0451	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64375194	T	C	C	rs72846695	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64377301	C	A	A	rs113134992	intronic	0.0448	0.0448	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64382507	C	G	G	rs79461368	intronic	0.0453	0.0453	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64389524	C	T	T	rs77682324	intronic	0.0403	0.0403	PRKCA	0.7621	59	6	1	25	1	0
Disinhibition of SNARE formation	17	64395773	T	C	C	rs78584531	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64396570	T	G	G	rs72838208	intronic	0.0452	0.0452	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64396695	A	G	G	rs74329211	intronic	0.0432	0.0432	PRKCA	0.7302	58	8	0	21	4	0
Disinhibition of SNARE formation	17	64396883	G	A	A	rs72838209	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64398013	G	A	A	rs75125285	intronic	0.0295	0.0295	PRKCA	0.7632	60	5	1	25	1	0
Disinhibition of SNARE formation	17	64400648	C	T	T	rs72838214	intronic	0.0452	0.0452	PRKCA	0.4788	55	9	1	25	1	0
Disinhibition of SNARE formation	17	64402141	G	T	T	rs10221238	intronic	0.0452	0.0452	PRKCA	0.4770	56	9	1	25	1	0
Disinhibition of SNARE formation	17	64405430	T	A	A	rs72838216	intronic	0.0453	0.0453	PRKCA	0.4725	56	9	1	24	1	0
Disinhibition of SNARE formation	17	64410564	C	T	T	rs9972974	intronic	0.0390	0.0390	PRKCA	0.7632	60	5	1	25	1	0
Disinhibition of SNARE formation	17	64412921	G	A	A	rs62070391	intronic	0.0426	0.0426	PRKCA	0.7621	59	6	1	25	1	0
Disinhibition of SNARE formation	17	64424382	C	T	T	rs62070395	intronic	0.0425	0.0425	PRKCA	0.7595	59	6	1	24	1	0
Disinhibition of SNARE formation	17	64429928	G	A	A	rs117729211	intronic	0.0272	0.0272	PRKCA	0.0477	60	6	0	19	6	1
Disinhibition of SNARE formation	17	64431874	G	A	A	rs72838278	intronic	0.0426	0.0426	PRKCA	0.7642	57	6	1	25	1	0
Disinhibition of SNARE formation	17	64432202	A	G	G	rs62070397	intronic	0.0427	0.0427	PRKCA	0.7621	59	6	1	25	1	0
Disinhibition of SNARE formation	17	64432881	A	G	G	rs62070398	intronic	0.0426	0.0426	PRKCA	0.7595	59	6	1	24	1	0
Disinhibition of SNARE formation	17	64438732	A	T	T	rs113684166	intronic	0.0445	0.0445	PRKCA	0.2744	57	9	0	24	1	0
Disinhibition of SNARE formation	17	64441204	T	C	C	rs75005068	intronic	0.0469	0.0469	PRKCA	0.2719	57	9	0	25	1	0
Disinhibition of SNARE formation	17	64441759	C	A	A	rs78330327	intronic	0.0465	0.0465	PRKCA	0.2710	56	9	0	25	1	0
Disinhibition of SNARE formation	17	64445337	A	C	C	rs118090701	intronic	0.0387	0.0387	PRKCA	1.0000	58	6	1	23	2	0
Disinhibition of SNARE formation	17	64445856	A	G	G	rs12451388	intronic	0.0449	0.0449	PRKCA	0.2744	57	9	0	24	1	0
Disinhibition of SNARE formation	17	64447721	G	A	A	rs12452749	intronic	0.0462	0.0462	PRKCA	0.2786	57	9	0	23	1	0
Disinhibition of SNARE formation	17	64450113	G	C	C	rs80162292	intronic	0.0461	0.0461	PRKCA	0.2710	56	9	0	25	1	0
Disinhibition of SNARE formation	17	64453194	A	G	G	rs111776777	intronic	0.0442	0.0442	PRKCA	0.8716	54	10	2	23	3	0
Disinhibition of SNARE formation	17	64458036	C	T	T	rs113153197	intronic	0.0339	0.0339	PRKCA	0.1678	54	11	0	25	1	0
Disinhibition of SNARE formation	17	64462111	T	G	G	rs79239451	intronic	0.0464	0.0464	PRKCA	0.2744	57	9	0	24	1	0
Disinhibition of SNARE formation	17	64462288	G	A	A	rs80080003	intronic	0.0305	0.0305	PRKCA	0.1706	56	10	0	25	1	0
Disinhibition of SNARE formation	17	64483589	G	T	T	rs79070174	intronic	0.0391	0.0391	PRKCA	1.0000	59	6	1	23	2	0
Disinhibition of SNARE formation	17	64487077	T	G	G	rs78149509	intronic	0.0200	0.0200	PRKCA	0.0381	63	3	0	21	4	1
Disinhibition of SNARE formation	17	64494906	A	G	G	rs117168126	intronic	0.0300	0.0300	PRKCA	1.0000	59	6	1	23	2	0
Disinhibition of SNARE formation	17	64501943	C	T	T	rs7217954	intronic	0.0422	0.0422	PRKCA	1.0000	59	7	0	23	3	0
Disinhibition of SNARE formation	17	64519790	G	A	A	rs11659067	intronic	0.0498	0.0498	PRKCA	0.0125	62	3	0	19	6	0
Disinhibition of SNARE formation	17	64525002	A	T	T	rs77462363	intronic	0.0380	0.0380	PRKCA	1.0000	59	6	1	23	2	0
Disinhibition of SNARE formation	17	64544723	C	T	T	rs116879811	intronic	0.0274	0.0274	PRKCA	1.0000	60	6	0	24	2	0
Disinhibition of SNARE formation	17	64559535	A	G	G	rs227907	intronic	0.0478	0.0478	PRKCA	0.2800	55	11	0	21	3	1
Disinhibition of SNARE formation	17	64561055	G	A	A	rs62071706	intronic	0.0238	0.0238	PRKCA	0.1546	60	5	0	21	4	1
Disinhibition of SNARE formation	17	64590951	A	T	T	rs11867591	intronic	0.0449	0.0449	PRKCA	0.2122	57	8	0	20	6	0
Disinhibition of SNARE formation	17	64604776	C	T	T	rs117539643	intronic	0.0479	0.0479	PRKCA	0.6653	51	11	2	23	3	0
Disinhibition of SNARE formation	17	64608923	T	C	C	rs72845947	intronic	0.0440	0.0440	PRKCA	0.7355	57	7	2	21	4	0
Disinhibition of SNARE formation	17	64610285	T	C	C	rs72845948	intronic	0.0445	0.0445	PRKCA	0.8583	57	7	2	22	4	0
Disinhibition of SNARE formation	17	64610480	A	C	C	rs17759657	intronic	0.0444	0.0444	PRKCA	0.8583	57	7	2	22	4	0
Disinhibition of SNARE formation	17	64612838	C	T	T	rs16959714	intronic	0.0338	0.0338	PRKCA	0.4353	57	8	0	24	1	0
Disinhibition of SNARE formation	17	64614717	T	C	C	rs17686540	intronic	0.0442	0.0442	PRKCA	0.7355	57	7	2	21	4	0
Disinhibition of SNARE formation	17	64626385	G	A	A	rs74352723	intronic	0.0460	0.0460	PRKCA	0.2744	57	9	0	24	1	0
Disinhibition of SNARE formation	17	64628634	A	G	G	rs117353888	intronic	0.0437	0.0437	PRKCA	0.2521	54	11	0	18	7	0
Disinhibition of SNARE formation	17	64660047	G	C	C	rs146141011	intronic	0.0484	0.0484	PRKCA	1.0000	53	9	2	22	4	0
Disinhibition of SNARE formation	17	64671047	C	T	T	rs16959942	intronic	0.0496	0.0496	PRKCA	0.1706	56	10	0	25	1	0

Disinhibition of SNARE formation	17	64712634	T	C	C	rs78121420	intronic	0.0465	0.0465	PRKCA	1.0000	57	7	2	23	3	0
Disinhibition of SNARE formation	17	64713847	G	T	T	rs112934229	intronic	0.0464	0.0464	PRKCA	1.0000	57	7	2	23	3	0
Disinhibition of SNARE formation	17	64723880	G	A	A	rs79547774	intronic	0.0264	0.0264	PRKCA	1.0000	57	9	0	23	3	0
Disinhibition of SNARE formation	17	64738427	A	C	C	rs117138620	intronic	0.0400	0.0400	PRKCA	0.3055	58	8	0	23	2	1
Disinhibition of SNARE formation	17	64748431	G	T	T	rs141177250	intronic	0.0153	0.0153	PRKCA	0.7595	59	6	1	24	1	0
Disinhibition of SNARE formation	17	64755018	T	C	C	rs74831470	intronic	0.0226	0.0226	PRKCA	0.7976	56	9	1	23	2	0
Disinhibition of SNARE formation	17	64760870	A	G	G	rs77904275	intronic	0.0307	0.0307	PRKCA	0.5233	53	11	1	24	2	0
Disinhibition of SNARE formation	17	64762410	C	G	G	rs113025478	intronic	0.0307	0.0307	PRKCA	0.6398	54	11	1	23	2	0
Disinhibition of SNARE formation	17	64763235	T	C	C	rs77635068	intronic	0.0306	0.0306	PRKCA	0.6398	54	11	1	23	2	0
Disinhibition of SNARE formation	17	64771614	C	T	T	rs80238933	intronic	0.0297	0.0297	PRKCA	0.6398	54	11	1	23	2	0
Disinhibition of SNARE formation	17	64776847	G	A	A	rs113542727	intronic	0.0297	0.0297	PRKCA	0.5228	54	11	1	24	2	0
Disinhibition of SNARE formation	17	64791836	G	C	C	rs56884788	intronic	0.0390	0.0390	PRKCA	0.6362	55	10	1	23	2	0
Disinhibition of SNARE formation	17	64792863	G	C	C	rs72838636	intronic	0.0484	0.0484	PRKCA	0.6470	57	8	1	21	5	0
Disinhibition of SNARE formation	19	54401602	G	C	C	rs41311973	intronic	0.0163	0.0163	PRKCG	0.7213	58	8	0	23	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	1	212485607	A	T	A	rs351381	intronic	0.9528	0.0472	PPP2R5A	0.2993	0	7	59	0	5	20
Disassembly of the destruction complex and recruitment of AXIN to the membrane	1	212505662	A	G	G	rs17665257	intronic	0.0348	0.0348	PPP2R5A	0.6148	59	6	1	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	1	212507249	C	T	T	rs61828730	intronic	0.0408	0.0408	PPP2R5A	0.8011	58	7	1	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	1	228204651	G	A	A	rs12747212	intronic	0.0465	0.0465	WNT3A	0.1984	58	8	0	23	1	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	2	208631211	A	T	T	rs74471859	3_prime_UTR	0.0420	0.0420	FZD5	0.2352	56	10	0	19	7	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	2	208632817	G	A	A	rs35994626	missense	0.0418	0.0418	FZD5	0.2352	56	10	0	19	7	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	41241993	A	G	G	rs11564437	intronic	0.0255	0.0255	CTNNB1	0.2725	63	2	1	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119663780	G	A	A	rs114872182	intronic	0.0222	0.0222	GSK3B	0.8074	61	4	1	24	1	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119674978	G	C	C	rs115950158	intronic	0.0384	0.0384	GSK3B	0.2761	56	10	0	23	1	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119734170	T	C	C	rs116755725	intronic	0.0237	0.0237	GSK3B	0.0397	54	11	1	26	0	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119736734	T	C	C	rs78796384	intronic	0.0177	0.0177	GSK3B	0.1282	57	8	1	25	0	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119752368	T	A	A	rs78883820	intronic	0.0403	0.0403	GSK3B	1.0000	52	13	1	20	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119785723	C	T	T	rs75142045	intronic	0.0236	0.0236	GSK3B	0.0391	54	11	1	25	0	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119795926	C	T	T	rs75192446	intronic	0.0409	0.0409	GSK3B	1.0000	52	13	1	20	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	3	119816610	G	A	A	rs114798987	upstream	0.0229	0.0229	GSK3B	0.0646	61	5	0	19	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	112077680	T	C	C	rs62363988	intronic	0.0273	0.0273	APC	0.7207	62	3	1	23	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	112124405	C	T	T	rs62364020	intronic	0.0266	0.0266	APC	0.7207	62	3	1	23	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	112141114	C	G	G	rs62364022	intronic	0.0270	0.0270	APC	0.7207	62	3	1	23	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	112164747	A	G	G	rs62364023	intronic	0.0271	0.0271	APC	0.7285	62	3	1	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	133551516	A	G	G	rs75368011	intronic	0.0484	0.0484	PPP2CA	0.0685	61	5	0	20	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	133553213	T	A	A	rs79758263	intronic	0.0483	0.0483	PPP2CA	0.0646	61	5	0	19	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	133554676	A	G	G	rs71587522	intronic	0.0288	0.0288	PPP2CA	0.7497	55	11	0	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	137417081	A	G	G	rs60251892	upstream	0.0479	0.0479	WNT8A	0.4762	60	5	1	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	137429148	C	T	T	rs146145625	downstream	0.0305	0.0305	WNT8A	1.0000	57	8	0	22	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	148887275	C	A	A	rs114967510	intronic	0.0299	0.0299	CSNK1A1	1.0000	56	10	0	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	5	148921266	C	T	T	rs114031822	intronic	0.0172	0.0172	CSNK1A1	1.0000	58	7	0	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42955700	G	A	A	rs150318932	intronic	0.0184	0.0184	PPP2R5D	0.0188	62	2	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42956855	C	G	G	rs139678883	intronic	0.0185	0.0185	PPP2R5D	0.0179	63	2	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42956915	G	A	A	rs116911410	intronic	0.0185	0.0185	PPP2R5D	0.0179	63	2	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42958019	T	C	C	rs9462861	intronic	0.0181	0.0181	PPP2R5D	0.1111	62	4	0	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42958084	A	G	G	rs114754270	intronic	0.0185	0.0185	PPP2R5D	0.0179	63	2	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42967569	G	A	A	rs143336223	intronic	0.0182	0.0182	PPP2R5D	0.0179	63	2	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42970465	A	G	G	rs78833196	intronic	0.0403	0.0403	PPP2R5D	0.2977	54	12	0	22	3	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	6	42978824	C	T	T	rs41274902	intronic	0.0182	0.0182	PPP2R5D	0.0179	63	2	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	7	90892588	C	T	T	rs78521924	upstream	0.0215	0.0215	FZD1	0.7469	57	9	0	21	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	7	116165233	C	T	T	rs45498702	intronic	0.0462	0.0462	CAV1	0.2078	58	8	0	20	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	7	116187330	G	A	A	rs1474511	intronic	0.0342	0.0342	CAV1	0.0534	59	7	0	18	7	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	7	116192330	C	T	T	rs75022895	intronic	0.0478	0.0478	CAV1	0.0150	58	8	0	16	9	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	7	116193508	A	T	T	rs117052851	intronic	0.0304	0.0304	CAV1	1.0000	56	10	0	21	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	7	116197908	C	T	T	rs35902398	intronic	0.0348	0.0348	CAV1	0.2428	58	7	1	26	0	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	10	99076980	G	C	C	rs11189125	upstream	0.0428	0.0428	FRAT1	1.0000	60	5	1	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	10	99081117	G	A	A	rs11189129	3_prime_UTR	0.0422	0.0422	FRAT1	1.0000	60	5	1	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	10	99097398	T	C	C	rs35502594	upstream	0.0344	0.0344	FRAT2	0.4762	60	5	1	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64690070	G	A	A	rs147029783	upstream	0.0444	0.0444	PPP2R5B	0.3373	55	11	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64691910	T	G	G	rs76436719	upstream	0.0440	0.0440	PPP2R5B	0.3373	55	11	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64692312	A	G	G	rs60798873	5_prime_UTR	0.0441	0.0441	PPP2R5B	0.3373	55	11	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64692356	C	T	T	rs61024397	5_prime_UTR	0.0441	0.0441	PPP2R5B	0.3373	55	11	0	24	2	0

Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64694023	A	T	T	rs57393537	intronic	0.0442	0.0442	PPP2R5B	0.3373	55	11	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64695020	T	G	G	rs885999	intronic	0.0443	0.0443	PPP2R5B	0.3348	54	11	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64697950	C	T	T	rs111934356	splice_region,intronic	0.0384	0.0384	PPP2R5B	0.5002	55	9	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	64700976	T	C	C	rs10488702	intronic	0.0458	0.0458	PPP2R5B	0.7222	57	9	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68105602	G	A	A	rs74968229	intronic	0.0413	0.0413	LRP5	1.0000	57	9	0	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68109822	T	C	C	rs4988311	intronic	0.0434	0.0434	LRP5	0.8249	55	10	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68111672	A	G	G	rs314756	intronic	0.0470	0.0470	LRP5	0.5316	56	9	0	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68176016	C	T	T	rs76884287	intronic	0.0481	0.0481	LRP5	0.7302	58	8	0	21	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68192362	C	G	G	rs75776943	intronic	0.0486	0.0486	LRP5	0.3091	59	7	0	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68205117	T	C	C	rs137864217	intronic	0.0205	0.0205	LRP5	0.4984	59	7	0	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68214505	C	G	G	rs78471927	intronic	0.0482	0.0482	LRP5	0.7227	58	7	0	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	68214890	G	A	A	rs79320300	intronic	0.0441	0.0441	LRP5	0.4984	59	7	0	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	11	111624412	A	G	A	rs4322429	intronic	0.9540	0.0460	PPP2R1B	0.2775	2	13	51	0	2	24
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12267520	G	A	A	rs12826332	downstream	0.0468	0.0468	LRP6	0.0422	61	4	0	20	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12267823	T	C	C	rs34372334	downstream	0.0471	0.0471	LRP6	0.0410	62	4	0	20	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12269960	G	A	A	rs3741792	3_prime_UTR	0.0471	0.0471	LRP6	0.0237	62	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12270560	A	G	G	rs71457129	3_prime_UTR	0.0470	0.0470	LRP6	0.0250	61	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12271574	C	T	T	rs71457130	3_prime_UTR	0.0469	0.0469	LRP6	0.0237	62	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12275297	A	G	G	rs71457131	intronic	0.0317	0.0317	LRP6	0.2078	58	8	0	20	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12287013	T	A	A	rs12819810	intronic	0.0495	0.0495	LRP6	0.0237	62	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12287589	C	T	T	rs12819916	intronic	0.0496	0.0496	LRP6	0.0237	62	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12295552	T	G	G	rs34694539	intronic	0.0496	0.0496	LRP6	0.0250	61	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12297091	A	G	G	rs71457134	intronic	0.0496	0.0496	LRP6	0.0410	62	4	0	20	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12315857	T	C	C	rs2300230	intronic	0.0496	0.0496	LRP6	0.0237	62	4	0	19	5	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12321526	G	A	A	rs11054719	intronic	0.0210	0.0210	LRP6	1.0000	58	8	0	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12324058	G	A	A	rs113794654	intronic	0.0315	0.0315	LRP6	1.0000	60	5	1	24	1	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12324841	A	G	G	rs12833575	intronic	0.0327	0.0327	LRP6	0.3477	57	9	0	20	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12325932	C	G	G	rs76038196	intronic	0.0382	0.0382	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12326027	C	G	G	rs75049047	intronic	0.0381	0.0381	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12326128	C	T	T	rs76299027	intronic	0.0380	0.0380	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12328826	T	C	C	rs78024436	intronic	0.0382	0.0382	LRP6	0.0351	62	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12337956	C	T	T	rs77595426	intronic	0.0383	0.0383	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12346016	G	A	A	rs79359989	intronic	0.0383	0.0383	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12350029	A	G	G	rs187847468	intronic	0.0383	0.0383	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12357470	T	A	A	rs75431901	intronic	0.0382	0.0382	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12364411	T	C	C	rs17374170	intronic	0.0382	0.0382	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12369072	C	A	A	rs75798211	intronic	0.0468	0.0468	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12370932	C	T	T	rs77970482	intronic	0.0381	0.0381	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12372047	T	G	G	rs117001679	intronic	0.0383	0.0383	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12374101	A	G	G	rs75253855	intronic	0.0383	0.0383	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12378128	C	T	T	rs11054733	intronic	0.0209	0.0209	LRP6	1.0000	57	8	0	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12378158	C	T	T	rs78815657	intronic	0.0383	0.0383	LRP6	0.0400	62	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12378767	T	C	C	rs117299638	intronic	0.0379	0.0379	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12378920	C	T	T	rs80214149	intronic	0.0383	0.0383	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12384668	G	A	A	rs77157509	intronic	0.0376	0.0376	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12388356	A	C	C	rs77588531	intronic	0.0383	0.0383	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12391576	T	C	C	rs75155789	intronic	0.0380	0.0380	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12398849	T	G	G	rs116946061	intronic	0.0380	0.0380	LRP6	0.0335	63	3	0	20	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12404270	C	T	T	rs78533154	intronic	0.0384	0.0384	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12414109	G	T	T	rs149872900	intronic	0.0383	0.0383	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12414920	T	C	C	rs147798710	intronic	0.0383	0.0383	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	12	12416595	A	C	C	rs117775212	intronic	0.0383	0.0383	LRP6	0.0381	63	3	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	63877780	T	G	G	rs76445028	intronic	0.0431	0.0431	PPP2R5E	0.3158	53	13	0	21	4	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	63977051	C	A	A	rs17766076	intronic	0.0436	0.0436	PPP2R5E	0.6433	56	9	1	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102253838	T	C	C	rs151299721	intronic	0.0229	0.0229	PPP2R5C	0.4981	56	10	0	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102274571	A	T	T	rs76294435	intronic	0.0481	0.0481	PPP2R5C	0.2818	60	6	0	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102287985	G	A	A	rs80152381	intronic	0.0425	0.0425	PPP2R5C	1.0000	54	11	0	21	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102326654	C	T	T	rs80319248	intronic	0.0269	0.0269	PPP2R5C	0.7348	58	8	0	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102338112	A	G	G	rs2476521	intronic	0.0458	0.0458	PPP2R5C	0.0565	56	10	0	25	0	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102339600	T	C	C	rs116995481	intronic	0.0294	0.0294	PPP2R5C	0.0569	56	10	0	26	0	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102344254	C	T	T	rs8012434	intronic	0.0449	0.0449	PPP2R5C	0.7192	58	8	0	24	2	0

Disassembly of the destruction complex and recruitment of AXIN to the membrane	14	102395021	T	C	T	rs1741145	downstream	0.9636	0.0364	PPP2R5C	0.7522	0	10	56	0	3	23
Disassembly of the destruction complex and recruitment of AXIN to the membrane	16	337655	A	G	G	rs45530432	3_prime_UTR	0.0218	0.0218	AXIN1	0.5928	57	7	1	25	1	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	16	350846	A	G	A	rs214245	intronic	0.9604	0.0396	AXIN1	0.2078	0	8	58	0	6	20
Disassembly of the destruction complex and recruitment of AXIN to the membrane	16	351517	A	G	A	rs214242	intronic	0.9533	0.0467	AXIN1	0.2078	0	8	58	0	6	20
Disassembly of the destruction complex and recruitment of AXIN to the membrane	16	392392	C	G	G	rs118100148	intronic	0.0492	0.0492	AXIN1	1.0000	51	14	0	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	17	42641345	G	C	C	rs75575961	downstream	0.0180	0.0180	FZD2	0.6957	60	6	0	21	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	1948218	C	T	T	rs117285549	intronic	0.0293	0.0293	CSNK1G2	0.6148	59	6	1	22	4	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	1952808	G	A	A	rs74415283	intronic	0.0236	0.0236	CSNK1G2	0.3091	59	7	0	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	1957031	G	T	T	rs34956563	intronic	0.0245	0.0245	CSNK1G2	0.7980	57	8	1	24	2	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	52710886	A	G	G	rs62109206	intronic	0.0217	0.0217	PPP2R1A	0.8074	61	4	1	24	1	1
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	52716143	G	A	A	rs74536039	intronic	0.0445	0.0445	PPP2R1A	0.8249	55	10	1	21	5	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	52720738	C	T	T	rs77810569	intronic	0.0478	0.0478	PPP2R1A	0.5544	55	10	1	20	6	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	52726288	G	A	A	rs77891912	intronic	0.0456	0.0456	PPP2R1A	0.5418	53	13	0	22	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	52729981	C	T	T	rs111484780	3_prime_UTR	0.0455	0.0455	PPP2R1A	0.5425	53	13	0	23	3	0
Disassembly of the destruction complex and recruitment of AXIN to the membrane	19	52734671	T	C	C	rs76856298	downstream	0.0447	0.0447	PPP2R1A	0.5425	53	13	0	23	3	0

Table S5 (A): SNP-based tests in SYNAPTIC genes (only the top 20 SNPs are shown)

CHROM	POS	REF	ALT	MINOR ALLELE	ID	CONSEQUENCE	AF	MAF	SYMBOL	P VALUE	FWER				# RESPONDERS			# NON-RESPONDERS			% RESPONDERS			% NON-RESPONDERS			ODDS RATIO	
											Neff=3,704 (Galwey)	Neff=6,074 (Gao)	Neff=6,169 (Li & Ji)	Neff=43,119 (Nyholt/Cheverud)	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Dominant model	Recessive model
4	4345379	T	C	C	rs7695197	upstream	0.31	0.31	NSG1	3.55E-06	0.013	0.021	0.022	0.14	34	31	1	7	8	11	50.72	46.38	2.90	27.59	31.03	41.38	2.70	23.65
4	4346427	G	A	A	rs3981	upstream	0.32	0.32	NSG1	3.84E-06	0.014	0.023	0.023	0.15	34	30	1	7	8	11	51.47	45.59	2.94	27.59	31.03	41.38	2.78	23.29
4	4346465	T	C	C	rs12641832	upstream	0.33	0.33	NSG1	3.84E-06	0.014	0.023	0.023	0.15	34	30	1	7	8	11	51.47	45.59	2.94	27.59	31.03	41.38	2.78	23.29
4	4351540	G	A	A	rs34402391	intronic	0.34	0.34	NSG1	1.10E-05	0.040	0.065	0.066	0.38	33	30	2	6	8	11	50.00	45.59	4.41	25.00	32.14	42.86	3.00	16.25
17	11348500	A	G	G	rs9900468	intronic	0.21	0.21	SHISA6	4.92E-05	0.167	0.258	0.262	0.88	43	14	9	8	18	0	63.77	21.74	14.49	31.03	65.52	3.45	3.91	0.21
5	75425227	T	G	G	rs10514059	intronic	0.22	0.22	SV2C	1.34E-04	0.391	0.556	0.562	1.00	41	24	1	5	17	4	60.87	36.23	2.90	20.69	62.07	17.24	5.96	6.98
19	15900659	A	G	G	rs7249737	upstream	0.08	0.08	OR10H5	2.14E-04	0.548	0.728	0.734	1.00	53	12	1	10	15	0	78.26	18.84	2.90	39.29	57.14	3.57	5.56	1.24
4	4357296	A	G	A	rs10937867	intronic	0.62	0.38	NSG1	3.37E-04	0.713	0.871	0.875	1.00	9	33	24	2	3	21	14.49	49.28	36.23	10.34	13.79	75.86	1.47	5.53
10	50815871	T	C	C	rs75287762	upstream	0.08	0.08	SLC18A3	3.74E-04	0.750	0.897	0.901	1.00	59	7	0	14	12	0	86.96	11.59	1.45	51.72	44.83	3.45	6.22	2.43
19	15906476	G	C	C	rs62106069	downstream	0.08	0.08	OR10H5	3.90E-04	0.764	0.906	0.910	1.00	52	11	1	11	15	0	79.10	17.91	2.99	41.38	55.17	3.45	5.36	1.16
13	47440800	T	C	C	rs9567743	intronic	0.18	0.18	HTR2A	3.92E-04	0.766	0.908	0.911	1.00	28	31	7	21	2	1	42.03	46.38	11.59	81.48	11.11	7.41	0.16	0.61
11	84340842	T	G	G	rs17807944	intronic	0.22	0.22	DLG2	4.15E-04	0.785	0.920	0.923	1.00	30	32	4	21	2	3	44.93	47.83	7.25	75.86	10.34	13.79	0.26	2.05
7	157825498	C	T	C	rs6953551	intronic	0.70	0.30	PTPRN2	4.37E-04	0.802	0.930	0.932	1.00	1	26	38	2	1	22	2.94	39.71	57.35	10.71	7.14	82.14	0.25	3.42
19	15855434	C	A	A	rs56108924	downstream	0.10	0.10	OR10H3	5.33E-04	0.861	0.961	0.963	1.00	52	13	1	10	15	1	76.81	20.29	2.90	37.93	55.17	6.90	5.42	2.48
6	34036642	G	T	T	rs1906954	intronic	0.06	0.06	GRM4	5.86E-04	0.886	0.972	0.973	1.00	62	2	0	18	8	0	94.03	4.48	1.49	65.52	31.03	3.45	8.29	2.36
19	15910817	T	C	C	rs55908984	downstream	0.07	0.07	OR10H5	6.49E-04	0.910	0.981	0.982	1.00	53	12	1	11	15	0	78.26	18.84	2.90	41.38	55.17	3.45	5.10	1.20
19	15907908	C	T	T	rs62106071	downstream	0.08	0.08	OR10H5	6.54E-04	0.911	0.981	0.982	1.00	52	12	1	11	15	0	77.94	19.12	2.94	41.38	55.17	3.45	5.01	1.18
19	15908978	C	T	T	rs72995365	downstream	0.07	0.07	OR10H5	6.54E-04	0.911	0.981	0.982	1.00	52	12	1	11	15	0	77.94	19.12	2.94	41.38	55.17	3.45	5.01	1.18
6	44192158	T	C	C	rs1886884	intronic	0.47	0.47	SLC29A1	6.72E-04	0.917	0.983	0.984	1.00	9	33	23	14	8	4	14.71	50.00	35.29	51.72	31.03	17.24	0.16	0.38
2	50882657	C	T	C	rs9752732	intronic	0.82	0.18	NRXN1	7.31E-04	0.933	0.988	0.989	1.00	2	11	53	2	13	10	4.35	17.39	78.26	10.71	50.00	39.29	0.38	0.18

Table S5 (B): Gene-based tests in SYNAPTIC genes

SYMBOL	# MUTATIONS	P VALUE	FWER
DLG2	208	6.25E-07	0.000137
SLC6A4	2	1.86E-03	0.336693
DAGLA	5	8.14E-03	0.834428
SHISA9	15	3.74E-02	0.999771
SCRIB	2	4.25E-02	0.999928
SV2B	17	6.11E-02	0.999999
PPFIA4	3	6.33E-02	0.999999
PRKCZ	5	6.61E-02	1.000000
NAAA	1	7.03E-02	1.000000
SYT17	4	7.47E-02	1.000000
USP46	3	7.60E-02	1.000000
GRIA1	38	8.74E-02	1.000000
FNTA	2	9.10E-02	1.000000
HRH2	7	9.10E-02	1.000000
GRM1	17	9.16E-02	1.000000
AP3D1	3	9.35E-02	1.000000
LYPD6B	7	9.43E-02	1.000000
DTNBP1	16	9.86E-02	1.000000
RAP1A	16	9.99E-02	1.000000
SLC6A7	1	1.04E-01	1.000000
SRC	1	1.20E-01	1.000000
APBA1	3	1.22E-01	1.000000
DNM3	36	1.29E-01	1.000000
STX3	5	1.29E-01	1.000000
KIF17	4	1.49E-01	1.000000
OR56A4	2	1.62E-01	1.000000
ATP1A2	2	1.62E-01	1.000000
DOC2B	8	1.63E-01	1.000000
SV2C	12	1.71E-01	1.000000
DAG1	4	1.72E-01	1.000000
SNCG	1	1.75E-01	1.000000
FRRS1L	4	1.76E-01	1.000000
BRSK1	2	1.78E-01	1.000000
GLUL	2	1.80E-01	1.000000
RAB11A	2	1.92E-01	1.000000
WNT7A	3	1.93E-01	1.000000
HTR1D	2	2.01E-01	1.000000
GABBR1	30	2.02E-01	1.000000
STXBP1	10	2.02E-01	1.000000
SLC6A15	4	2.10E-01	1.000000
SHISA6	15	2.18E-01	1.000000
DNM2	12	2.25E-01	1.000000
DDC	6	2.28E-01	1.000000
HTR1E	29	2.32E-01	1.000000
FLOT1	2	2.37E-01	1.000000
RPH3A	13	2.58E-01	1.000000
KCNC4	3	2.62E-01	1.000000

EFNB2	2	2.67E-01	1.000000
COLQ	7	2.83E-01	1.000000
SLC1A7	8	2.87E-01	1.000000
CTNND1	4	2.88E-01	1.000000
SYN3	46	2.88E-01	1.000000
NUMB	10	2.90E-01	1.000000
GRM4	2	2.92E-01	1.000000
SLC6A9	3	3.00E-01	1.000000
KIF5C	5	3.01E-01	1.000000
UNC13A	7	3.15E-01	1.000000
SNAPIN	1	3.22E-01	1.000000
SLC18A1	3	3.27E-01	1.000000
SYT1	41	3.29E-01	1.000000
ALDH5A1	6	3.29E-01	1.000000
HTR4	12	3.93E-01	1.000000
PDE1B	2	3.97E-01	1.000000
HTR5A	3	4.00E-01	1.000000
HSPA8	3	4.05E-01	1.000000
AP2B1	5	4.14E-01	1.000000
HRAS	1	4.16E-01	1.000000
CNIH2	2	4.16E-01	1.000000
ICA1	32	4.20E-01	1.000000
CPLX2	8	4.25E-01	1.000000
CACNA1B	5	4.45E-01	1.000000
CLSTN1	5	4.64E-01	1.000000
NPTXR	2	4.68E-01	1.000000
CHRM5	5	4.74E-01	1.000000
AKAP9	1	4.86E-01	1.000000
BAIAP3	1	4.86E-01	1.000000
CACNG2	14	4.89E-01	1.000000
SLC6A13	3	4.93E-01	1.000000
CHRM3	37	4.97E-01	1.000000
ADRB1	1	4.98E-01	1.000000
CHRM1	1	4.98E-01	1.000000
CHAT	1	5.03E-01	1.000000
LRTOMT	1	5.06E-01	1.000000
HRH1	6	5.09E-01	1.000000
SYT2	3	5.09E-01	1.000000
SLC6A18	2	5.11E-01	1.000000
NF1	6	5.13E-01	1.000000
GAD1	6	5.25E-01	1.000000
SLC30A1	2	5.50E-01	1.000000
SLC17A6	3	5.69E-01	1.000000
SLC6A20	10	5.75E-01	1.000000
SNCA	3	5.80E-01	1.000000
STX1A	3	5.83E-01	1.000000
SLC6A12	3	5.83E-01	1.000000
CACNG7	2	5.83E-01	1.000000

NRG1	103	5.83E-01	1.000000
UNC13B	5	5.85E-01	1.000000
NPTX1	2	5.90E-01	1.000000
SLC1A2	12	6.06E-01	1.000000
LYNX1	4	6.33E-01	1.000000
DOC2A	1	6.47E-01	1.000000
EPS8	7	6.54E-01	1.000000
ATP2A2	2	6.58E-01	1.000000
ARHGAP44	47	6.59E-01	1.000000
SLC22A1	2	6.72E-01	1.000000
SLC38A1	7	6.81E-01	1.000000
RHOT1	8	6.95E-01	1.000000
NRXN1	77	6.98E-01	1.000000
SLC32A1	1	7.19E-01	1.000000
SLC5A7	2	7.23E-01	1.000000
OR5T3	1	7.30E-01	1.000000
SYT12	3	7.31E-01	1.000000
SYT7	4	7.36E-01	1.000000
PRKCI	2	7.44E-01	1.000000
SLC6A17	7	7.51E-01	1.000000
CALY	1	7.52E-01	1.000000
HTR6	2	7.52E-01	1.000000
PPFIA1	2	7.55E-01	1.000000
GABRA2	18	7.59E-01	1.000000
PPP1R9A	15	7.60E-01	1.000000
ALDH9A1	3	7.65E-01	1.000000
DRD3	1	7.68E-01	1.000000
SLC18A2	2	7.74E-01	1.000000
NRXN2	5	7.79E-01	1.000000
SLC1A3	14	7.88E-01	1.000000
HOMER1	5	7.88E-01	1.000000
CHRM2	12	7.88E-01	1.000000
SLC6A2	6	7.92E-01	1.000000
SLC1A6	3	7.94E-01	1.000000
DRD4	1	7.96E-01	1.000000
AP2M1	1	7.98E-01	1.000000
HIP1	17	7.99E-01	1.000000
PATE1	4	8.06E-01	1.000000
CPLX1	5	8.09E-01	1.000000
CACNG4	3	8.09E-01	1.000000
LYPD6	4	8.11E-01	1.000000
CHRNB4	2	8.17E-01	1.000000
PPFIA3	3	8.17E-01	1.000000
GPER1	4	8.18E-01	1.000000
GSG1L	19	8.23E-01	1.000000
NPTX2	2	8.24E-01	1.000000
DAGLB	1	8.25E-01	1.000000
ADAM10	12	8.30E-01	1.000000

KIF5A	3	8.38E-01	1.000000
SLC6A16	2	8.45E-01	1.000000
MCTP1	45	8.46E-01	1.000000
PRIMA1	7	8.48E-01	1.000000
DRD2	7	8.50E-01	1.000000
NIPSNAP1	2	8.58E-01	1.000000
SLC6A6	7	8.61E-01	1.000000
RAB8A	2	8.65E-01	1.000000
GAD2	2	8.78E-01	1.000000
LIN7A	12	8.80E-01	1.000000
GPHN	62	8.92E-01	1.000000
GRIP1	24	8.98E-01	1.000000
YWHAE	23	9.12E-01	1.000000
SYT11	3	9.16E-01	1.000000
PATE4	7	9.24E-01	1.000000
RIMS1	17	9.24E-01	1.000000
CACNA1A	19	9.26E-01	1.000000
SYNJ1	3	9.27E-01	1.000000
GRIN1	5	9.29E-01	1.000000
SLC6A3	4	9.32E-01	1.000000
SNAP25	8	9.33E-01	1.000000
CAMK2A	5	9.38E-01	1.000000
SLC6A5	6	9.38E-01	1.000000
RIMS2	39	9.39E-01	1.000000
SLC17A8	6	9.41E-01	1.000000
SNCAIP	5	9.43E-01	1.000000
CACNG3	7	9.48E-01	1.000000
SLC22A2	3	9.50E-01	1.000000
HTR7	5	9.51E-01	1.000000
SLC6A19	2	9.53E-01	1.000000
ITGB3	9	9.55E-01	1.000000
NSG1	6	9.61E-01	1.000000
RIMS4	6	9.62E-01	1.000000
MAPK10	19	9.70E-01	1.000000
SYN2	56	9.79E-01	1.000000
SYT5	3	9.82E-01	1.000000
EPS15	8	9.84E-01	1.000000
PAH	4	9.85E-01	1.000000
NRXN3	187	9.90E-01	1.000000
DGKI	40	9.90E-01	1.000000
AGTPBP1	6	9.93E-01	1.000000
HTR2A	26	9.94E-01	1.000000
LRRC7	34	9.95E-01	1.000000
GPC6	98	9.97E-01	1.000000
ADORA1	12	9.98E-01	1.000000
COMT	5	9.98E-01	1.000000
NAALAD2	23	9.98E-01	1.000000
PPFIA2	47	9.98E-01	1.000000

MEF2C	39	9.99E-01	1.000000
SLC6A11	21	9.99E-01	1.000000
PTPRN2	90	1.00E+00	1.000000
SNPH	4	1.00E+00	1.000000
NOS1	11	1.00E+00	1.000000
GRM5	13	1.00E+00	1.000000
DLG1	72	1.00E+00	1.000000
CACNG5	12	1.00E+00	1.000000
ABAT	14	1.00E+00	1.000000
CPT1C	1	1.00E+00	1.000000
DLG4	1	1.00E+00	1.000000
DNM1	1	1.00E+00	1.000000
GRASP	1	1.00E+00	1.000000
GRIP2	4	1.00E+00	1.000000
HRH3	1	1.00E+00	1.000000
HRH4	1	1.00E+00	1.000000
HTR1F	1	1.00E+00	1.000000
KCNMB4	3	1.00E+00	1.000000
LGI1	1	1.00E+00	1.000000
OR11H4	1	1.00E+00	1.000000
PPT1	1	1.00E+00	1.000000
PSCA	1	1.00E+00	1.000000
RAB3A	1	1.00E+00	1.000000
RIMS3	2	1.00E+00	1.000000
SHISA7	1	1.00E+00	1.000000
SLC29A1	1	1.00E+00	1.000000
SLC6A1	4	1.00E+00	1.000000
SNAP47	2	1.00E+00	1.000000
SYT4	1	1.00E+00	1.000000

Table S5 (C): SNP-based tests in EPILEPSY genes (only the top 20 SNPs are shown)

											FWER				# RESPONDERS			# NON-RESPONDERS			% RESPONDERS			% NON-RESPONDERS			ODDS RATIO	
CHROM	POS	REF	ALT	MINOR ALLELE	ID	CONSEQUENCE	AF	MAF	SYMBOL	P VALUE	Neff=4,205 (Galwey)	Neff=6,797 (Gao)	Neff=7,141 (Li & Ji)	Neff=55,488 (Nyholt/Cheverud)	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Ref/Ref	Ref/Alt	Alt/Alt	Dominant model	Recessive model
7	75690988	A	C	C	rs10216079	intronic	0.20	0.20	MDH2	2.65E-05	0.105	0.165	0.172	0.770	37	26	2	26	0	0	55.88	39.71	4.41	93.10	3.45	3.45	0.09	0.77
7	75677578	G	T	T	rs2286828	intronic	0.21	0.21	MDH2	2.66E-05	0.106	0.165	0.173	0.771	38	26	2	26	0	0	56.52	39.13	4.35	93.10	3.45	3.45	0.10	0.79
7	75677739	G	A	A	rs2286829	intronic	0.21	0.21	MDH2	2.66E-05	0.106	0.165	0.173	0.771	38	26	2	26	0	0	56.52	39.13	4.35	93.10	3.45	3.45	0.10	0.79
7	75686007	G	A	A	rs867973	intronic	0.18	0.18	MDH2	2.66E-05	0.106	0.165	0.173	0.771	38	26	2	26	0	0	56.52	39.13	4.35	93.10	3.45	3.45	0.10	0.79
7	75688672	G	A	A	rs78587454	intronic	0.18	0.18	MDH2	2.66E-05	0.106	0.165	0.173	0.771	38	26	2	26	0	0	56.52	39.13	4.35	93.10	3.45	3.45	0.10	0.79
7	75695081	G	A	A	rs3779419	intronic	0.23	0.23	MDH2	2.66E-05	0.106	0.165	0.173	0.771	38	26	2	26	0	0	56.52	39.13	4.35	93.10	3.45	3.45	0.10	0.79
16	90008296	T	C	C	rs11644157	downstream	0.06	0.06	TUBB3	1.30E-04	0.420	0.586	0.604	0.999	62	3	0	16	10	0	92.65	5.88	1.47	58.62	37.93	3.45	8.89	2.39
9	87388848	G	A	G	rs4877288	intronic	0.63	0.37	NTRK2	2.36E-04	0.629	0.799	0.814	1.000	16	36	14	1	7	16	24.64	53.62	21.74	7.41	29.63	62.96	4.09	6.12
16	90003359	G	A	A	rs4534840	downstream	0.11	0.11	TUBB3	2.41E-04	0.637	0.805	0.821	1.000	62	4	0	15	10	0	91.30	7.25	1.45	57.14	39.29	3.57	7.88	2.52
16	78331490	A	G	G	rs73574528	intronic	0.14	0.14	WWOX	2.80E-04	0.692	0.851	0.865	1.000	31	29	6	23	2	0	46.38	43.48	10.14	85.71	10.71	3.57	0.14	0.33
16	89991963	C	T	T	rs62052213	intronic	0.08	0.08	TUBB3	3.05E-04	0.723	0.874	0.887	1.000	59	5	0	15	11	0	89.55	8.96	1.49	55.17	41.38	3.45	6.96	2.36
16	89998157	G	A	A	rs62052214	intronic	0.06	0.06	TUBB3	3.34E-04	0.754	0.896	0.908	1.000	62	4	0	16	10	0	91.30	7.25	1.45	58.62	37.93	3.45	7.41	2.43
16	90007025	A	G	G	rs11640500	downstream	0.06	0.06	TUBB3	3.34E-04	0.754	0.896	0.908	1.000	62	4	0	16	10	0	91.30	7.25	1.45	58.62	37.93	3.45	7.41	2.43
16	90008896	G	A	A	rs74251586	downstream	0.06	0.06	TUBB3	3.34E-04	0.754	0.896	0.908	1.000	62	4	0	16	10	0	91.30	7.25	1.45	58.62	37.93	3.45	7.41	2.43
16	90008928	C	A	A	rs79886664	downstream	0.06	0.06	TUBB3	3.34E-04	0.754	0.896	0.908	1.000	62	4	0	16	10	0	91.30	7.25	1.45	58.62	37.93	3.45	7.41	2.43
9	87382724	T	C	T	rs2378671	intronic	0.53	0.47	NTRK2	4.61E-04	0.856	0.956	0.963	1.000	16	36	14	1	8	16	24.64	53.62	21.74	7.14	32.14	60.71	4.25	5.56
9	87384534	G	A	G	rs10746750	intronic	0.59	0.41	NTRK2	4.61E-04	0.856	0.956	0.963	1.000	16	36	14	1	8	16	24.64	53.62	21.74	7.14	32.14	60.71	4.25	5.56
9	87392582	C	T	C	rs10465180	intronic	0.63	0.37	NTRK2	4.61E-04	0.856	0.956	0.963	1.000	16	36	14	1	8	16	24.64	53.62	21.74	7.14	32.14	60.71	4.25	5.56
9	87394720	G	C	G	rs1778971	intronic	0.59	0.41	NTRK2	4.61E-04	0.856	0.956	0.963	1.000	16	36	14	1	8	16	24.64	53.62	21.74	7.14	32.14	60.71	4.25	5.56
9	87395810	A	G	A	rs1778970	intronic	0.59	0.41	NTRK2	4.61E-04	0.856	0.956	0.963	1.000	16	36	14	1	8	16	24.64	53.62	21.74	7.14	32.14	60.71	4.25	5.56

Table S5 (D): Gene-based tests in EPILEPSY genes

SYMBOL	# MUTATIONS	P VALUE	FWER
RTN4IP1	19	0.0056	0.7923
DYRK1A	30	0.0069	0.8579
PEX6	4	0.0150	0.9856
KCNB1	35	0.0210	0.9974
TBC1D24	2	0.0212	0.9976
PRRT2	1	0.0303	0.9998
SLC13A5	3	0.0343	0.9999
PRICKLE1	8	0.0420	1.0000
GALC	8	0.0475	1.0000
ALG6	4	0.0541	1.0000
SETD5	5	0.0563	1.0000
MDH2	2	0.0597	1.0000
SURF1	2	0.0683	1.0000
CHRNB2	1	0.0685	1.0000
PIGO	1	0.0697	1.0000
PSAP	1	0.0701	1.0000
SYNGAP1	3	0.0712	1.0000
NHLRC1	6	0.0723	1.0000
PAFAH1B1	4	0.0857	1.0000
GRIN2B	55	0.0901	1.0000
PCDH12	1	0.0941	1.0000
IDH2	2	0.0960	1.0000
RNASEH2C	1	0.1006	1.0000
EPM2A	11	0.1089	1.0000
KCNJ10	2	0.1098	1.0000
ALG8	2	0.1136	1.0000
CLN8	1	0.1162	1.0000
COQ9	2	0.1162	1.0000
GABRB2	95	0.1235	1.0000
ARFGEF2	2	0.1289	1.0000
NDUFV1	3	0.1289	1.0000
NTRK2	111	0.1497	1.0000
PEX7	2	0.1528	1.0000
DYNC1H1	7	0.1535	1.0000
DHX30	1	0.1630	1.0000
SCN2A	8	0.1671	1.0000
FRRS1L	4	0.1757	1.0000
GLUL	2	0.1796	1.0000
TBCK	10	0.1802	1.0000
FAR1	1	0.1809	1.0000
LYST	3	0.1836	1.0000
SLC12A5	2	0.1890	1.0000
COL4A2	21	0.1898	1.0000
STXBP1	10	0.2022	1.0000
AKT1	2	0.2033	1.0000
CIC	2	0.2096	1.0000
OCLN	4	0.2120	1.0000

MFF	2	0.2171	1.0000
KCNK4	1	0.2176	1.0000
HLCS	26	0.2329	1.0000
TRPM6	6	0.2398	1.0000
PCCB	5	0.2403	1.0000
TRAK1	4	0.2448	1.0000
GOSR2	2	0.2558	1.0000
AP3B2	5	0.2578	1.0000
HACE1	6	0.2670	1.0000
GTPBP2	1	0.2672	1.0000
RMND1	2	0.2780	1.0000
MOCS2	1	0.2781	1.0000
SMARCC2	1	0.2818	1.0000
LIAS	1	0.2834	1.0000
SETBP1	35	0.2839	1.0000
AIMP1	2	0.2845	1.0000
NAGA	4	0.2919	1.0000
DENND5A	2	0.2945	1.0000
ASPA	2	0.2947	1.0000
EIF3F	4	0.2955	1.0000
KIF5C	5	0.3007	1.0000
SCN3A	2	0.3009	1.0000
AKT3	36	0.3086	1.0000
EEF1A2	3	0.3161	1.0000
TUBB3	1	0.3163	1.0000
ALDH5A1	6	0.3294	1.0000
EPG5	9	0.3296	1.0000
ARID1B	52	0.3372	1.0000
CNNM2	6	0.3418	1.0000
GNB1	4	0.3438	1.0000
DNM1L	6	0.3441	1.0000
SLC25A12	2	0.3477	1.0000
NSD1	6	0.3554	1.0000
STAG1	22	0.3685	1.0000
COQ4	1	0.3739	1.0000
TANGO2	1	0.3842	1.0000
EIF2B5	15	0.3876	1.0000
HSD17B4	7	0.3885	1.0000
SLC25A22	2	0.4034	1.0000
COL4A1	36	0.4116	1.0000
SCN8A	10	0.4148	1.0000
AMT	1	0.4157	1.0000
HRAS	1	0.4157	1.0000
NDE1	2	0.4209	1.0000
NPRL3	3	0.4213	1.0000
PIK3R2	10	0.4223	1.0000
RORB	6	0.4236	1.0000
HCN2	6	0.4346	1.0000

TSEN2	3	0.4435	1.0000
IFIH1	6	0.4476	1.0000
POMT1	1	0.4554	1.0000
CACNA1E	41	0.4576	1.0000
ADAR	2	0.4603	1.0000
DEAF1	3	0.4644	1.0000
KARS	2	0.4671	1.0000
FBXO11	3	0.4680	1.0000
RHOBTB2	1	0.4762	1.0000
PDHX	1	0.4770	1.0000
PHACTR1	13	0.4879	1.0000
ATP1A1	4	0.4892	1.0000
D2HGDH	2	0.4905	1.0000
PEX19	4	0.4909	1.0000
ALG11	1	0.4981	1.0000
WDR62	1	0.4984	1.0000
ZBTB18	1	0.4999	1.0000
CAD	1	0.5027	1.0000
GABRA1	6	0.5037	1.0000
PTS	1	0.5065	1.0000
ROGDI	2	0.5065	1.0000
TSC2	2	0.5134	1.0000
BOLA3	2	0.5275	1.0000
MTHFR	1	0.5316	1.0000
PRMT7	1	0.5321	1.0000
TREX1	1	0.5357	1.0000
RTTN	6	0.5359	1.0000
RNASET2	4	0.5373	1.0000
KCTD3	2	0.5374	1.0000
TSC1	1	0.5425	1.0000
SCARB2	5	0.5434	1.0000
MFSD8	2	0.5449	1.0000
TSEN54	2	0.5494	1.0000
PACS1	10	0.5497	1.0000
CPA6	14	0.5516	1.0000
NDUFAF2	17	0.5585	1.0000
STRADA	3	0.5586	1.0000
MTOR	4	0.5639	1.0000
FARS2	41	0.5675	1.0000
SZT2	6	0.5676	1.0000
CHRNA2	3	0.5718	1.0000
SEPSECS	2	0.5833	1.0000
ALDH7A1	6	0.5897	1.0000
KCNJ11	2	0.5934	1.0000
NACC1	4	0.5977	1.0000
GABRG2	4	0.6056	1.0000
SLC1A2	12	0.6065	1.0000
PACS2	7	0.6074	1.0000

RORA	44	0.6079	1.0000
STAMBP	5	0.6188	1.0000
BTD	8	0.6306	1.0000
SUCLA2	5	0.6335	1.0000
GM2A	3	0.6363	1.0000
SCN9A	10	0.6665	1.0000
NARS2	8	0.6707	1.0000
TBCD	13	0.6804	1.0000
PLAA	18	0.6829	1.0000
NRXN1	77	0.6977	1.0000
EHMT1	13	0.7075	1.0000
CHRNA4	14	0.7080	1.0000
PHGDH	4	0.7089	1.0000
CTNNA2	104	0.7096	1.0000
KCNQ2	9	0.7130	1.0000
PPP3CA	26	0.7133	1.0000
PEX10	1	0.7184	1.0000
MMADHC	1	0.7209	1.0000
FGF12	40	0.7212	1.0000
PEX2	7	0.7237	1.0000
ARG1	1	0.7302	1.0000
ARV1	1	0.7302	1.0000
GRIN2D	1	0.7302	1.0000
MOGS	1	0.7348	1.0000
GABBR2	52	0.7352	1.0000
ALG9	3	0.7375	1.0000
MOCS1	3	0.7376	1.0000
WDR45B	2	0.7491	1.0000
COG7	1	0.7495	1.0000
BCKDHB	6	0.7555	1.0000
NGLY1	7	0.7558	1.0000
PNPO	1	0.7632	1.0000
KCNQ5	73	0.7653	1.0000
UBA5	3	0.7681	1.0000
PEX13	1	0.7700	1.0000
ST3GAL5	21	0.7868	1.0000
RELN	35	0.7913	1.0000
MAP2K2	1	0.7929	1.0000
UBE3A	13	0.7931	1.0000
BRAT1	8	0.7952	1.0000
CC2D2A	1	0.8053	1.0000
PEX1	3	0.8154	1.0000
FUT8	10	0.8211	1.0000
ALPL	6	0.8235	1.0000
ATP6V1A	1	0.8279	1.0000
BRAF	8	0.8333	1.0000
PCCA	10	0.8353	1.0000
EML1	17	0.8395	1.0000

PMM2	2	0.8427	1.0000
CACNA1D	18	0.8588	1.0000
MACF1	10	0.8590	1.0000
KCNQ3	42	0.8659	1.0000
GNAO1	2	0.8733	1.0000
PIGN	6	0.8744	1.0000
EMX2	2	0.8790	1.0000
TBL1XR1	11	0.8817	1.0000
RARS2	3	0.8826	1.0000
MAP2K1	4	0.8827	1.0000
KCNC1	2	0.8856	1.0000
NDUFS4	3	0.8906	1.0000
GPHN	62	0.8916	1.0000
MLC1	4	0.8939	1.0000
RALA	9	0.8992	1.0000
ZEB2	2	0.9072	1.0000
ACOX1	27	0.9095	1.0000
PIGG	5	0.9100	1.0000
MTR	9	0.9148	1.0000
NBEA	114	0.9155	1.0000
DOCK7	10	0.9209	1.0000
GRIN2A	15	0.9219	1.0000
CACNA1A	19	0.9256	1.0000
SYNJ1	3	0.9266	1.0000
GRIN1	5	0.9294	1.0000
SPTAN1	3	0.9369	1.0000
KCNT1	2	0.9374	1.0000
UNC80	6	0.9424	1.0000
CREBBP	8	0.9467	1.0000
PIK3CA	21	0.9479	1.0000
GLDC	6	0.9496	1.0000
SLC6A19	2	0.9526	1.0000
KCNA2	15	0.9546	1.0000
SLC2A1	3	0.9552	1.0000
CACNA1G	2	0.9572	1.0000
NDUFAF5	18	0.9579	1.0000
KRAS	7	0.9583	1.0000
FBXL4	13	0.9583	1.0000
RNASEH2B	4	0.9592	1.0000
SMARCA2	15	0.9601	1.0000
QDPR	8	0.9604	1.0000
WASF1	6	0.9627	1.0000
FKTN	3	0.9627	1.0000
WWOX	224	0.9631	1.0000
CHD2	7	0.9687	1.0000
GCH1	4	0.9728	1.0000
TCF4	27	0.9782	1.0000
DIAPH1	10	0.9782	1.0000

DEPDC5	103	0.9810	1.0000
DPYD	46	0.9836	1.0000
CYFIP2	8	0.9836	1.0000
PAH	4	0.9849	1.0000
NDUFA10	4	0.9886	1.0000
KIF1A	13	0.9888	1.0000
MBD5	56	0.9889	1.0000
GLB1	8	0.9929	1.0000
PTEN	6	0.9957	1.0000
HECW2	55	0.9965	1.0000
PLCB1	55	0.9971	1.0000
GRIA4	14	0.9984	1.0000
HCN1	14	0.9985	1.0000
MEF2C	39	0.9991	1.0000
KIF2A	7	0.9994	1.0000
GNAQ	16	0.9996	1.0000
MAGI2	175	0.9998	1.0000
GABRB3	20	0.9999	1.0000
GNB5	33	0.9999	1.0000
CNTNAP2	372	1.0000	1.0000
ABAT	14	1.0000	1.0000
AMPD2	1	1.0000	1.0000
CLTC	1	1.0000	1.0000
DNM1	1	1.0000	1.0000
EFTUD2	1	1.0000	1.0000
FGFR3	1	1.0000	1.0000
GSS	1	1.0000	1.0000
HEPACAM	3	1.0000	1.0000
HEXA	2	1.0000	1.0000
ITPA	1	1.0000	1.0000
LGI1	1	1.0000	1.0000
MBOAT7	1	1.0000	1.0000
OTUD6B	1	1.0000	1.0000
POMGNT1	1	1.0000	1.0000
PPT1	1	1.0000	1.0000
RAB18	1	1.0000	1.0000
RFT1	3	1.0000	1.0000
SLC35A1	2	1.0000	1.0000
SLC6A1	4	1.0000	1.0000
TUBB2A	1	1.0000	1.0000
VARS	1	1.0000	1.0000
WDR73	1	1.0000	1.0000

Table S5 (E): Lists of SYNAPTIC and EPILEPSY genes

GENES	
SYNAPTIC	EPILEPSY
AC136616.1	AARS
RAP1A	ADSL
SYT12	ALDH7A1
HTR7	ALG11
PPFIA2	ALG13
DNM3	ARHGEF9
SLC6A15	ARX
SLC17A8	ATP1A3
KCNMB4	ATP6V0A2
DOC2A	ATRX
SLC30A1	BRAT1
CHRM3	BSCL2
SYN1	CACNA1D
PRIMA1	CDKL5
SLC10A4	CHD2
ATP1A2	CHRNA2
CPT1C	CHRNA4
IQSEC2	CHRNB2
PNKD	CIC
SLC6A13	CLN8
CACNG3	CLTC
NF1	CNKSR2
HTR6	CNTNAP2
SLC6A11	CPA6
EFNB2	CYFIP2
SV2B	DEPDC5
SYNJ1	DIAPH1
HRH4	DNM1
ARHGAP44	DOCK7
FLOT1	DPYD
DTNBP1	DYRK1A
SYT8	EHMT1
CASK	EML1
P2RY11	EPG5
CPLX3	EPM2A
CHAT	FOXG1
SLC6A6	GABBR2
GRIP2	GABRA1
PPT1	GABRB3
SLC18A3	GABRG2
SLC6A20	GLYCTK
FRRS1L	GNAO1
CTNND1	GPAA1
PRKCI	GRIN1
SLC6A1	GRIN2A
RIMS1	GRIN2B

NRXN3
GPC6
SLC18A1
LRTOMT
DDC
SV2C
HTR1E
BRSK1
RIMS2
HRH1
DAGLB
EPS15
COMT
KIF17
NUMB
SLC6A4
GFAP
CAMK2A
SLC6A7
SHISA9
FNTA
LGI1
SNCG
STX1A
DLG4
MAOA
ALDH5A1
MAOB
SRC
SLC1A2
SLC6A19
AP2B1
HCRT
GPER1
CHRM5
SLC6A18
DRD3
BAIAP3
SHISA6
NAALAD2
CPLX4
OR11H4
NRXN2
SLC1A3
CACNG5
CACNG4
SHISA7
LYNX1

GSS
HCN1
HECW2
HMGCL
HNRNPH2
HNRNPU
HTRA2
IDH2
IER3IP1
IQSEC2
ITPA
KCNA2
KCNB1
KCNC1
KCNJ10
KCNQ2
KCNQ3
KCNT1
KCTD7
KIF1BP
LGI1
MBD5
MBOAT7
MDH2
MECP2
MEF2C
MFF
MOGS
MTOR
NACC1
NEXMIF
PCDH19
PIGA
PIGN
PIGT
PLCB1
PLPBP
PNKP
PNPO
POLG
PRODH
PRRT2
PURA
QARS
RANBP2
SCARB2
SCN1A
SCN1B

SLURP2
STX3
SYN3
PRKCZ
UNC13B
NSG1
SYT17
UNC13A
GCHFR
NPTXR
DRD1
PPFIA1
CHRNB4
GRM1
SLC6A3
APBA1
HRH2
CPLX2
YWHAE
PDZD11
OR56A5
CPLX1
OR56A4
OR56A1
SLC6A9
RAB3A
ADAM10
DRD2
SLC1A6
VAMP2
SLC6A8
RHOT1
DNM1
ATP2A2
DLG3
SV2A
CACNG2
SLC6A16
STX1B
NPTX2
GRIA1
HTR1D
NPTX1
STX4
OR6T1
ITGB3
SLC38A1
SNAP25

SCN2A
SCN8A
SCN9A
SETD5
SIK1
SLC12A5
SLC13A5
SLC16A2
SLC1A2
SLC25A1
SLC25A22
SLC2A1
SLC35A2
SLC6A1
SLC6A19
SLC9A6
SPTAN1
STRADA
STX1B
STXBP1
SUOX
SYNGAP1
SYNJ1
SZT2
TBC1D24
TCF4
TPP1
TRAK1
TRPM6
UBE2A
UBE3A
WDR45
WDR45B
WWOX
ZEB2
ABAT
ACOX1
ADAR
ADGRG1
ADPRHL2
AIMP1
AKT1
AKT3
ALDH5A1
ALG1
ALG3
ALG6
ALG8

SYT7
ARC
PSCA
SCRIB
RAB3GAP1
GABBR1
PPP1R9A
DNAJC5
GRIPAP1
HTR2C
CACNG7
RIMS3
HRAS
CACNG8
CHRM2
PATE1
PATE4
DAGLA
OR10H2
OR10H3
GRM4
OR10H5
SLC6A14
GABRQ
AC114267.1
EPS8
SYN2
CACNA1B
OR13F1
DGKI
HRH3
WNT7A
LIN7B
NRG1
GRASP
GAD2
HPCA
HOMER1
PORCN
HTR4
OR10H4
KIF5C
SNAPIN
SLC17A7
LYPD6B
ACHE
PPFIA3
KIF5A

ALG9
ALPL
AMPD2
AMT
AP3B2
ARFGEF2
ARG1
ARID1B
ARV1
ASPA
ATP1A1
ATP6V1A
ATP7A
BCKDHA
BCKDHB
BCS1L
BOLA3
BRAF
BTD
C12orf57
CACNA1A
CACNA1E
CACNA1G
CAD
CASK
CC2D2A
CLCN4
CLN3
CNNM2
COG7
COL18A1
COL4A1
COL4A2
COQ2
COQ4
COQ9
CREBBP
CSTB
CTNNA2
CTSD
D2HGDH
DCX
DDX3X
DEAF1
DENND5A
DHCR7
DHDDS
DHX30

AP3D1
GPHN
HTR1F
LYPD6
FLOT2
SNCA
RIMS4
LRRC7
ICA1
TH
CNIH2
DRD4
RPH3A
SLC29A1
DVL1
GHSR
NAAA
COLQ
CLSTN1
SLC22A2
SYT5
HIP1
DNM2
SLC1A7
CHRM1
SLC18A2
ASIC1
DLG2
ABAT
AKAP9
SYT4
SLC29A2
RAB8A
HTR1B
DOC2B
NRXN1
OPHN1
DMD
OR5T2
OR5T3
OR5T1
SLC17A6
GABRA2
DRD5
SLC6A2
SNCAIP
MEF2C
AGTPBP1

DNM1L
DPAGT1
DPM1
DYNC1H1
EARS2
EEF1A2
EFTUD2
EIF2B2
EIF2B4
EIF2B5
EIF2S3
EIF3F
EMX2
ETHE1
EXOSC3
FAR1
FARS2
FBXL4
FBXO11
FGF12
FGFR3
FH
FKTN
FLNA
FOLR1
FRRS1L
FUCA1
FUT8
GABRB2
GALC
GAMT
GBA
GCH1
GFAP
GFM1
GLB1
GLDC
GLUD1
GLUL
GM2A
GNAQ
GNB1
GNB5
GOSR2
GPHN
GRIA4
GRIN2D
GTPBP2

STXBP1
SLC22A1
CALY
VPS35
PAH
SYT2
SLC6A5
ZNF219
GRIP1
HSPA8
GRIN1
SLC32A1
ALDH9A1
SLC6A17
SNAP47
KCNC4
PPFIA4
RAB11A
HTR5A
NOS1
ADORA1
HTR2B
CHRM4
ADRB1
ERBIN
HTR2A
CLN3
MCTP1
HTR1A
CACNA1A
SLC6A12
DAG1
GRM5
GRIN3B
MAPK10
NIPSNAP1
SNPH
SLC5A7
USP46
PDE1B
LIN7A
SYT11
GLUL
FMR1
PTPRN2
PRKN
SYT1
GAD1

HACE1
HAX1
HCFC1
HCN2
HEPACAM
HEXA
HLCS
HRAS
HSD17B4
IFIH1
IKBKG
IRF2BPL
KARS
KCNA1
KCNJ11
KCNK4
KCNQ5
KCTD3
KIF1A
KIF2A
KIF5C
KRAS
LIAS
LYST
MACF1
MAF
MAGI2
MAP2K1
MAP2K2
MED12
MFSD8
MLC1
MMACHC
MMADHC
MOCS1
MOCS2
MPDU1
MTHFR
MTR
NAGA
NARS2
NBEA
NDE1
NDUFA1
NDUFA10
NDUFAF2
NDUFAF5
NDUFS4

PEBP1
LIN7C
DLG1
OR10J5
GSG1L
GPC4
TSPOAP1
AP2M1

NDUFS8
NDUFV1
NGLY1
NHLRC1
NPRL3
NRXN1
NSD1
NSDHL
NTRK2
OCLN
OPHN1
OTUD6B
PACS1
PACS2
PAFAH1B1
PAH
PCCA
PCCB
PCDH12
PDHA1
PDHX
PET100
PEX1
PEX10
PEX12
PEX13
PEX19
PEX2
PEX3
PEX6
PEX7
PHACTR1
PHGDH
PIGG
PIGO
PIGW
PIK3CA
PIK3R2
PLAA
PMM2
POMGNT1
POMT1
PPP3CA
PPT1
PRICKLE1
PRMT7
PSAP
PTEN

PTPN23
PTS
QDPR
RAB11B
RAB18
RALA
RARS2
RELN
RFT1
RHOBTB2
RMND1
RNASEH2A
RNASEH2B
RNASEH2C
RNASET2
ROGDI
RORA
RORB
RTN4IP1
RTTN
SAMHD1
SCN3A
SCO1
SCO2
SEPSECS
SETBP1
SLC1A4
SLC25A12
SLC35A1
SLC6A8
SMARCA2
SMARCC2
SMS
SNORD118
ST3GAL5
STAG1
STAMBP
SUCLA2
SURF1
SYN1
TANGO2
TBCD
TBCK
TBL1XR1
TMEM70
TREX1
TRIM8
TSC1

TSC2
TSEN2
TSEN54
TUBA1A
TUBB2A
TUBB2B
TUBB3
TUBB4A
TUBG1
UBA5
UFM1
UNC80
VARS
WASF1
WDR62
WDR73
YWHAG
ZBTB18
ATN1
CSTB

Table S6

											FWER				rPPA (flat prior)			rPPA (empirical prior)		
CHROM	POS	REF	ALT	MINOR ALLELE	ID	CONSEQUENCE	AF	MAF	SYMBOL	P VALUE	Neff=160,965 (Galwey)	Neff=258,715 (Gao)	Neff=357,717 (Li & Ji)	Neff=3,577,371 (Nyholt/Cheverud)	π=1e-4	π=1e-5	π=1e-6	π=1e-4	π=1e-5	π=1e-6
17	4350407	G	C	G	rs2047231	intronic	0.82	0.18	SPNS3	1.60E-07	0.026	0.041	0.056	0.437	0.80	0.29	0.04	0.97	0.78	0.26
15	50553000	G	A	A	rs7182203	intronic	0.26	0.26	HDC	2.43E-07	0.038	0.061	0.083	0.581	0.96	0.73	0.21	0.98	0.84	0.35
4	8291102	C	T	T	rs7683388	intronic	0.39	0.39	HTRA3	1.52E-06	0.217	0.326	0.420	0.996	0.74	0.22	0.03	0.95	0.65	0.16
17	4350182	T	C	T	rs2047233	intronic	0.88	0.12	SPNS3	1.58E-06	0.224	0.335	0.431	0.996	0.25	0.03	0.00	0.77	0.25	0.03
5	179619074	T	C	C	rs34570575	intronic	0.10	0.10	RASGEF1C	2.87E-06	0.370	0.524	0.642	1.000	0.22	0.03	0.00	0.64	0.15	0.02
3	37604012	T	G	G	rs9825420	intronic	0.18	0.18	ITGA9	3.32E-06	0.414	0.577	0.695	1.000	0.23	0.03	0.00	0.68	0.17	0.02
4	4345379	T	C	C	rs7695197	upstream	0.31	0.31	NSG1	3.55E-06	0.436	0.601	0.720	1.000	0.63	0.15	0.02	0.60	0.13	0.01
4	4346427	G	A	A	rs3981	upstream	0.32	0.32	NSG1	3.84E-06	0.461	0.630	0.747	1.000	0.61	0.14	0.02	0.57	0.12	0.01
4	4346465	T	C	C	rs12641832	upstream	0.33	0.33	NSG1	3.84E-06	0.461	0.630	0.747	1.000	0.61	0.14	0.02	0.57	0.12	0.01
4	113961039	G	T	G	rs10015551	intronic, non-coding transcript	0.57	0.43	RP11-650J17.1	4.72E-06	0.532	0.705	0.815	1.000	0.46	0.08	0.01	0.69	0.19	0.02
15	99100580	A	G	A	rs2311753	intergenic	0.79	0.21		5.49E-06	0.587	0.758	0.860	1.000	0.47	0.08	0.01	0.84	0.34	0.05
15	99101462	A	G	A	rs2871859	intergenic	0.79	0.21		5.49E-06	0.587	0.758	0.860	1.000	0.47	0.08	0.01	0.84	0.34	0.05
17	4350367	A	G	A	rs2047232	intronic	0.88	0.12	SPNS3	5.64E-06	0.597	0.768	0.867	1.000	0.09	0.01	0.00	0.45	0.08	0.01
2	156765630	T	C	C	rs16839725	intergenic	0.29	0.29		5.90E-06	0.613	0.783	0.879	1.000	0.48	0.08	0.01	0.29	0.04	0.00
14	47620548	C	T	C	rs1952220	intronic	0.87	0.13	MDGA2	6.25E-06	0.634	0.801	0.893	1.000	0.19	0.02	0.00	0.09	0.01	0.00
15	99102128	A	G	A	rs11853887	intergenic	0.76	0.24		6.52E-06	0.650	0.815	0.903	1.000	0.45	0.08	0.01	0.83	0.32	0.05
4	113961811	C	T	C	rs10433900	intronic, non-coding transcript	0.52	0.48	RP11-650J17.1	6.81E-06	0.666	0.828	0.912	1.000	0.44	0.07	0.01	0.66	0.16	0.02
3	37603952	T	A	A	rs9825270	intronic	0.19	0.19	ITGA9	7.07E-06	0.679	0.839	0.920	1.000	0.08	0.01	0.00	0.39	0.06	0.01
4	16428073	G	A	A	rs73224601	intronic, non-coding transcript	0.10	0.10	RP11-446J8.1	7.46E-06	0.699	0.855	0.931	1.000	0.07	0.01	0.00	0.55	0.11	0.01
3	72015276	C	A	A	rs2036594	intergenic	0.17	0.17		8.48E-06	0.745	0.889	0.952	1.000	0.11	0.01	0.00	0.57	0.12	0.01
19	46569619	A	G	A	rs713409	intronic	0.53	0.47	IGFL4	8.91E-06	0.762	0.900	0.959	1.000	0.37	0.06	0.01	0.70	0.19	0.02
19	46569630	A	G	A	rs713411	intronic	0.53	0.47	IGFL4	8.91E-06	0.762	0.900	0.959	1.000	0.37	0.06	0.01	0.70	0.19	0.02
1	156486009	G	A	G	rs6685228	downstream	0.76	0.24	RP11-284F21.8	9.82E-06	0.794	0.921	0.970	1.000	0.06	0.01	0.00	0.31	0.04	0.00