# Unravelling the Molecular Mechanisms Underlying Variations in Lung Function: an Integrative Genomic Analysis

## Supplementary Materials

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## Contents

# Detailed Methods

## Study Cohorts

### SpiroMeta-CHARGE lung function GWAS

The study subjects' characteristics and the methods for the SpiroMeta CHARGE study have been described in detail (1). Briefly, meta-analyses for cross-sectional lung function measures were undertaken for approximately 2.5 million HapMap II imputed SNPs across 23 individual GWAS studies with a combined sample size of 48,201 adult individuals of European ancestry. The analyses of $FEV_1$ and $FEV_1/FVC$ were adjusted for age, $age^2$, sex and height, and where appropriate study center and ancestry principal components as covariates. The association testing of the inverse-normal–transformed residuals for $FEV_1$ and $FEV_1/FVC$ assumed an additive genetic model and was stratified by ever-smoking versus never-smoking status. Meta-analyses were performed employing inverse-variance weighting (using the inverse of the standard error squared as the weight). The study applied genomic control twice at the study level and also at the meta-analysis level to avoid inflation of the test statistics caused by cryptic population structure or relatedness. Before applying genomic control at the meta-analysis level, the inflation factor ($\lambda_{GC}$) was 1·12 for $FEV_1$ and 1·09 for $FEV_1/FVC$.

### Lung tissue eQTL study

The study subjects' demographics and the methods have been described previously in detail (2). Briefly, lung eQTLs were derived from meta-analysis of non-tumor lung tissue eQTLs from 1,111 patients who underwent lung resection surgery at three participating sites: The University of British Columbia Centre for Heart and Lung Innovation (n=339, Vancouver, Canada), Laval University (n=409, Quebec City, Canada) and the University of Groningen (n=363, Groningen, The Netherlands). Whole-genome gene expression was undertaken on these specimens using an Affymetrix custom array testing 51,627 non-control probesets and normalized using RMA (3). The expression data are available at NCBI Gene Expression Omnibus repository (GEO, http://www.ncbi.nlm.nih.gov/geo) through accession number GSE23546. Genotyping was performed on DNA extracted from blood or lung tissue using the Illumina Human1M-Duo BeadChip array, and imputation was performed using the HapMap II reference panel providing eQTL data on 2,598,263 million SNPs. Using a Benjamini-Hochberg 10% FDR threshold, the study identified 468,300 eQTLs (18% of all SNPs tested) affecting expression of nearby genes within 1Mb from the transcript start site (*cis*) and 16,677 *trans* eQTLs (further than 1Mb away or on a different chromosome) representing 0·64% of all SNPs tested.

Appropriate ethics approval for the lung function GWAS studies and the lung eQTL studies were received from all participating institutions.

### Integration of GWAS and eQTL

To integrate the SNPs which were associated with $FEV_1$ and/or $FEV_1/FVC$ with gene expression in the lung we first merged the 468,300 *cis*, and the 17,182 *trans* eQTLs with SNPs in the SpiroMeta and CHARGE GWAS (2,419,122 SNPs at N effective >50%). Merged SNPs were then filtered to select those with a $P_{GWAS} < 0{\cdot}001$ for association with $FEV_1$ or $FEV_1/FVC$. This threshold was chosen to allow the identification of potentially biologically relevant yet statistically modest associations. Throughout this manuscript we refer to SNPs associated with $FEV_1$ or FEV1/FVC which act as eQTL as lung function eSNPs, and the genes regulated by these SNPs as lung function eSNP-regulated genes. The study design is presented in **Figure 1**. Fold enrichment was calculated as the ratio of the two proportions: The % of GWAS SNPs with $P < 0.001$ that act as eQTLs divided by the proportion of all eQTLs at 10% FDR to all SNPs tested. Enrichment of eSNPs among SpiroMeta-CHARGE GWAS results was calculated using Fisher's exact test.

To validate the enrichment of lung eSNPs among the SpiroMeta-CHARGE GWAS, results from Type II diabetes (T2D) GWAS were overlapped with lung tissue eQTLs. The meta-analysis of T2D diabetes GWAS results for 2,473,442 SNPs from Morris et al. 2012 (4) are publically available at http://www.broadinstitute.org/diabetes. The meta-analysis consists of 12,171 T2D cases and 56,862 controls across 12 GWAS from European descent populations. Each GWAS was imputed at up to 2.5M SNPs using Caucasian (CEU) samples from Phase II of the International HapMap Project. Each SNP with MAF>1% passing QC was tested for association with T2D under an additive model after adjustment for study-specific covariates including indicators of population structure. Full details of genotyping, QC and imputation for each study were presented in Morris et al. (4). The authors made available the complete GWAS results for 2,473,442 SNPs at http://www.broadinstitute.org/diabetes .

Analyses similar to the SpiroMeta-CHARGE lung function GWAS overlap were repeated for T2D GWAS to obtain the QQ plots for lung and blood T2D eSNPs.

Since enrichment in SNPs proximal to genes is expected among GWAS findings, enrichment was performed for all SNPs within 1Mb region from known genes in the SpiroMeta-CHARGE GWAS results, as compared to the complete GWAS results. This included; 1) Downloading all known genes' coordinates from the UCSC Genome Table, build 36/gh18, 2) Identifying regions that are 1Mb from genes coordinates, 3) Extracting all SNPs in the SpiroMeta-CHARGE GWAS results that fall within these genomic coordinates, which mapped to 2,083,834 SNPs, and 4) Generating a QQ plot comparing the distribution of SNPs within 1Mb of genes to all GWAS SNPs.

### Network and pathway enrichment analyses

The lung function eSNP-regulated genes were tested for enrichment in biological processes and pathways using the WEB-based GEne SeT AnaLysis Toolkit (WebGestalt) (5). Gene symbols were used as input for WebGestalt and enrichment for Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (6) and Gene Ontology (GO) processes (7) was undertaken using a hypergeometric model (8) and adjusting for multiple testing using the Benjamini-Hochberg (BH) method (9).

### Association between mRNA levels, $FEV_1$ and $FEV_1$/FVC in eQTL study subjects

For lung function eSNP-regulated genes, the relationship between mRNA levels and lung function measures was examined in 727 of the 1,111 subjects in the lung eQTL study. The selected subjects had the appropriate measures of lung function and did not have a diagnosis (other than COPD or lung cancer) likely to influence lung function. The demographics of this subgroup of subjects are shown in Table 1. A linear regression analysis of the level of expression of each probeset versus $FEV_1$ and $FEV_1$/FVC, adjusted for age, sex, height and smoking status (never-smoker, ex-smoker, current smoker), was undertaken in each of three cohorts separately, and the results were meta-analyzed using a fixed effects model with inverse variance weighting. Benjamini-Hochberg (BH) method (9) was used to adjust for multiple comparisons.

### The direction of effect between mRNA and lung function

The eSNP's allelic effect on $FEV_1$ and $FEV_1$/FVC from the GWAS, and on mRNA from the lung eQTL study was used to infer the predicted direction of effect between the mRNA and lung function measures; we refer to this as the "expected" direction. For example if the T allele of a SNP was associated with lower $FEV_1$ in the GWAS and with higher mRNA levels for a particular gene in the eQTL study then we infer that higher expression for that gene would be associated with lower $FEV_1$ (i.e. negative direction). Independently, we regressed the mRNA levels of lung function eSNP-regulated genes on $FEV_1$ and $FEV_1$/FVC in the 727 eQTL study subjects (see above section), and we refer to the direction of effect for this association as the "observed" direction. For lung function eSNP-regulated probesets that show significant mRNA association with lung function measures, we investigated whether the "observed" direction of effect was concordant with the "expected" direction. Lung function eSNP-regulated probesets that show concordant directions of effect are referred to as "concordant", while those for which the observed direction is opposite to the expected direction (yet significant at a nominal P-value $<0{\cdot}05$) are referred to as "discordant". For probesets that show nominal P-value associations ($P<0.05$) with either FEV1 or FEV1/FVC, the % concordance is the ratio between probesets that show concordant direction of effect to the total number of probesets with $P<0.05$.

### SNP x SNP interaction for HHIP eSNP (rs11100860) and the PTCH1 eSNP (rs10512248)

Given the results from GWAS, eQTL and mRNA associations for the receptor PTCH1, and its ligand HHIP, we proposed that a SNP-SNP interaction on lung function may exist for the two lung eSNPs that regulate their expression: *HHIP* eSNP (rs11100860) and the *PTCH1* eSNP (rs10512248). The interaction testing was undertaken in the 727 individuals from the eQTL study using linear regression on $FEV_1$ and separately $FEV_1$/FVC ratio, adjusting for age, gender, smoking status and height, and including the interaction term between the two SNPs.

### Immunohistochemical staining

To determine the cellular source of nephronectin (NPNT) in human lung, immunohistochemistry was performed on formalin-fixed normal lung tissue from the Centre for Heart Lung Innovation tissue biobank in Vancouver, Canada.

Donor airway sections were deparaffinized and rehydrated and antigens were retrieved by autoclaving the sections in citrate target retrieval solution (Dako) for 15 minutes at 120°C and 30 psi. Endogenous peroxidase was quenched with 3% hydrogen peroxide for 20 minutes and non-specific binding was blocked with 10% goat serum. Slides were incubated overnight with antibodies against human NPNT (Novus Biologicals, Cat# NBP1-83990) or IgG isotype control (Santa Cruz) at 4°C in 5% goat serum. Subsequent to three washes in Tris-buffered saline, sections were incubated with goat anti-rabbit secondary antibody (1:100, Vector Labs) for 2hrs, followed by incubation with streptavidin-horse radish peroxidase (Dako) for 20 minutes. Staining was developed with brown chromogen 3,3-diaminobenzidine (Dako) and counterstained with hematoxylin (Sigma). Slides were then dehydrated and mounted with Cytoseal 60 (Richard-Allan Scientific).

### *In silico* therapeutics using Connectivity Map

To identify potential compounds that could reverse (or induce) COPD-associated genes, the Connectivity Map (CMap) online tool from the Broad Institute (http://www.broadinstitute.org/cmap/) was used (10). CMap hosts a publically available database of transcriptional profiles of existing drugs containing over 7,000 genome-wide transcriptomes from cultured human cells treated with 1,309 bioactive compounds. The CMap online tool uses pattern matching algorithms based on non-parametric rank-ordered Kolmogorov–Smirnov statistics (11). The similarity metric between a test gene signature (a list of genes up- and down- regulated in relation to a phenotype or outcome) and the reference transcriptional profiles is transformed to a 'connectivity score' ranging from -1 to +1 to reflect the similarity or dissimilarity of the expression profiles. A positive connectivity score denotes the degree of similarity and a negative score denotes the dissimilarity between the gene signature of the phenotype and the drug or compounds effect on gene expression in specific cell types. A positive score suggests that the compound may act as an "inducer" of the phenotype while a negative score suggests a "therapeutic" for the disease of interest (12). Since CMap expects a gene signature of up- and down-regulated genes as input, we tested the expression levels of lung function eSNP-regulated genes for association with COPD in a case-control design in individuals from the eQTL study who did not have any other disease apart from smoking related lung diseases. The analysis involved using logistic regression adjusting for age, gender, and smoking status (ex, current and never smoker) in each of the three studies separately, and the results were combined using meta-analysis with a fixed effect model and inverse variance weighting. COPD was defined on Global Initiative for Chronic Obstructive Lung Disease (GOLD) criteria (13). COPD cases were defined as: $FEV_1/FVC < 70\%$ and $FEV_1 < 80\%$ predicted (n=428), and non- COPD cases were defined as $FEV_1/FVC > 70\%$ and $FEV_1 > 80\%$ predicted (n=330). 51 lung function eSNP-regulated genes associated with COPD at nominal P-values of < 0·05 were mapped into Affymetrix platform HG-U133A probe set IDs (33 were remapped) to be used as input for the CMap to query compounds that could reverse or augment the airway obstruction gene signature.

### Pleiotropy of lung function eSNPs

Lung function eSNPs were tested for association with other diseases or traits by integrating them with the National Human Genome Research Institute (NHGRI) GWAS Catalog, which contains the updated top association results from published GWAS data (http://www.genome.gov/gwastudies/, accessed April 2014) (14). All reported associations in the NHGRI GWAS Catalog were used in this analysis without filtering on any P-value thresholds.

### ENCODE data analyses

Analyses were undertaken on lung function eSNPs and lung function eSNP-regulated genes using tools designed to query the Encyclopedia of DNA Elements (ENCODE) data. To gain insight into what transcription factors were enriched in the promoters and 5` regions of lung function eSNP-regulated genes the ENCODE ChIP-Seq Significance Tool (15) was used. Gene symbols were used as input, and "all IDs" was selected as the background region for the hypergeometric test. The 500 bp region upstream from the transcription start sites was selected as the analysis window, and all cell lines were used as input. At the SNP level, lung function eSNPs were tested for enrichment in ENCODE functional annotations using HaploReg v2 publically available software (16). All SNPs in the 1000 Genomes Project CEU population were selected as the background set for analysis of enhancer and DNase hypersensitivity site (DHS) enrichment. For the queried lung function eSNPs, HaploReg calculates the coverage of strong enhancers and DHS in each assayed cell type. If this coverage exceeds that of the background set selected (1000 Genomes Project in this case), a binomial test is performed, and enrichment is reported if it passes an uncorrected significance threshold of 0·05. HaploReg calculates enrichment for DHS and enhancer function sites in multiple cell types assayed as part of both ENCODE (17) and Roadmap Epigenome (18) projects.

### Fetal human lung development transcriptome study

To identify if lung function eSNP-regulated genes are differentially expressed during human lung development, we downloaded and processed the publically available human lung development transcriptome dataset (19). The study included 38 lung RNA samples from 38 subjects (estimated gestational age 7-22 weeks or 53-154 days post-conception) and is available at NCBI Gene Expression Omnibus (GEO, http://www.ncbi.nlm.nih.gov/geo webcite), GSE14334 (Affymetrix Human Genome GeneChip U133 Plus 2.0 microarray platform). Expression values were extracted and normalized from .CEL files using the *Affy* package and the Robust Multi-array Average (RMA) method in R/BioConductor (http://www.bioconductor.org) which transforms expression signals of each probe into a logarithmic base-2 scale. Differential gene expression analysis relative to gestational age was performed using a linear regression model (lmFit) as implemented in the *Limma* package in R/BioConductor. Over/under representation of LFERGs among genes differentially expressed during human lung development was calculated using Fisher's exact test.

### Peripheral blood mononuclear cell (PBMC) eQTL study

We assessed if SpiroMeta-CHARGE SNPs with $P_{\mathrm{GWAS}} < 0{\cdot}001$ act as *cis*-eQTLs meeting 10% FDR in non-transformed PBMCs obtained from 5,311 European subjects (20). The study mapped eQTLs by testing HapMap II imputed genotypes, and quantile normalized log2-transformed gene expression values. The study defines a *cis*-acting eQTL if the SNP position is less than 250 kilobases (Kb) away from the midpoint of the probe. *Trans*-eQTL analysis in the PBMC study was restricted to 4,542 SNPs that were associated with diseases/traits and present in the NHGRI GWAS Catalog (accessed 16 July 2011), and included any combination of SNPs and probes, as long as the distance between the SNP position and midpoint of the probe was > 5 megabases (Mb) (20). Given the study's definition of *trans*-eQTL, we focused our integration analysis on *cis*-eQTLs.

### Statistical analysis

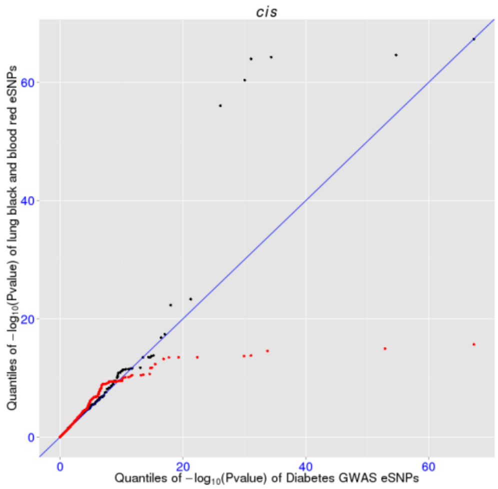
All statistical analyses were performed using R version 3·0·1 (http://www.r-project.org/)

## Supplementary Figures

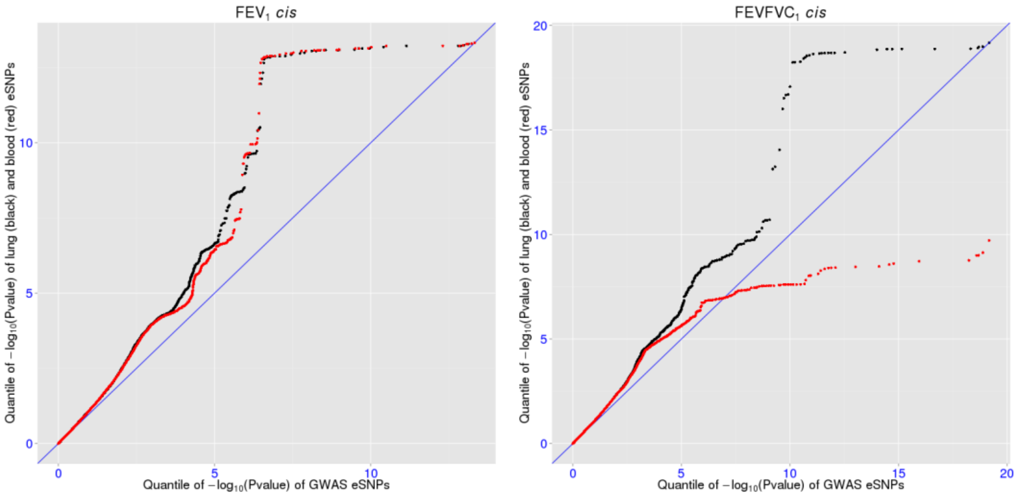
### Supplementary Figure 1: Enrichment in lung and blood *cis* eSNPs in the diabetes GWAS from Morris *et al.*

QQ plot for lung and blood *cis* eSNPs in the diabetes GWAS from Morris *et al.* (upper panel) and for comparison, the lung and blood eSNPs in the $FEV_1$ and $FEV_1$/FVC GWAS from the present study are shown in the lower panel.

**Diabetes eSNPs**

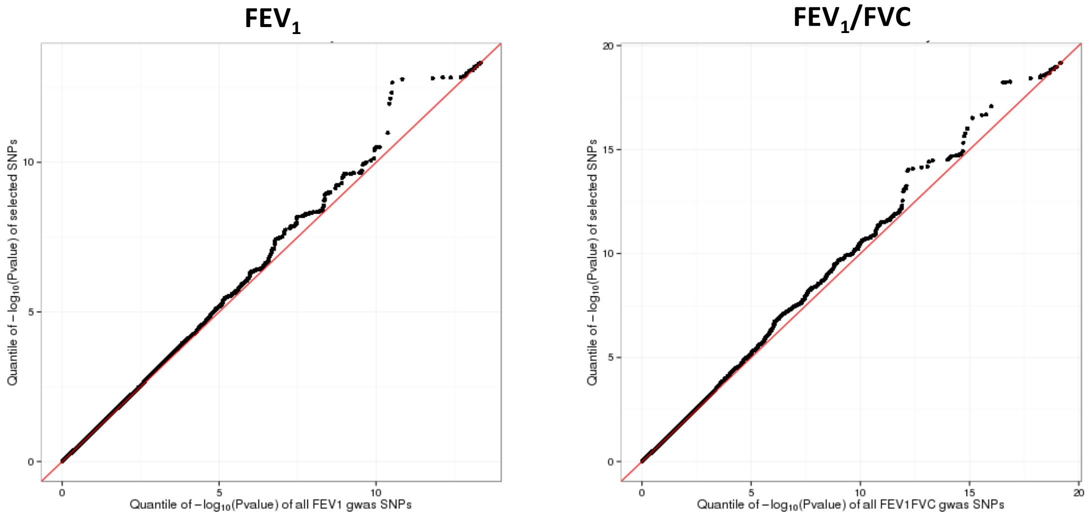


**Lung function eSNPs**



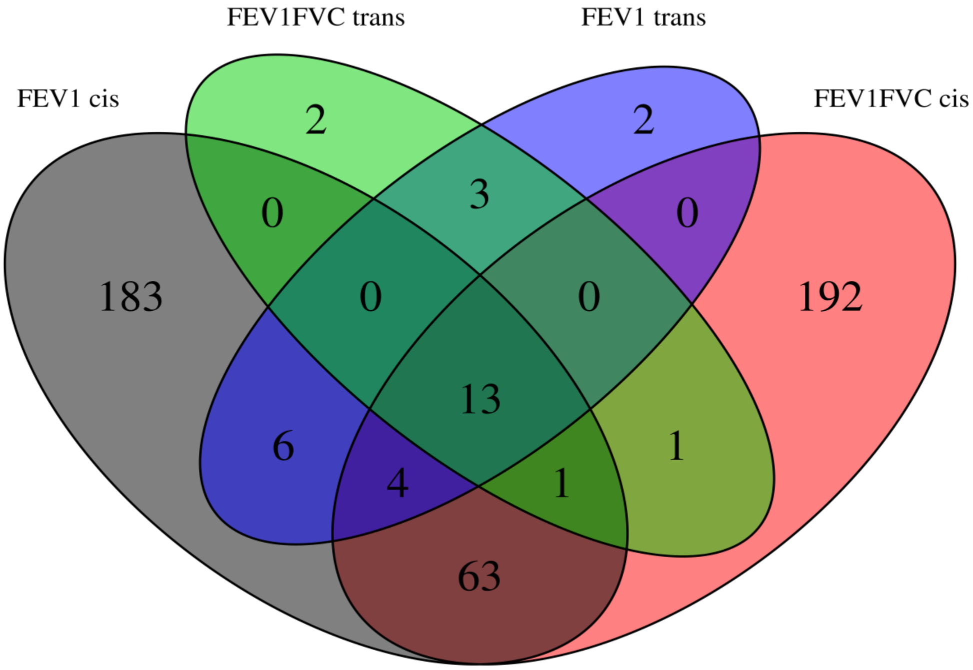
### Supplementary Figure 2: Enrichment of SNPs within 1Mb of genes compared to all SNPs tested in the SpiroMeta-CHARGE GWAS meta-analysis of lung function.

The QQ plot shows slight deviation but only for low P-value GWAS SNPs, suggesting an enrichment of SNPs with low GWAS P-values in the region of 1Mb of a gene. However, the deviation is less than that observed in the QQ plots of lung eQTLs. This suggests that the genomic distance alone of eSNPs do not explain the deviation observed for lung eQTLs, and that the large deviation observed for lung eSNPs is due to the tissue type used for eQTL discovery and its relevance to the phenotype under investigation.



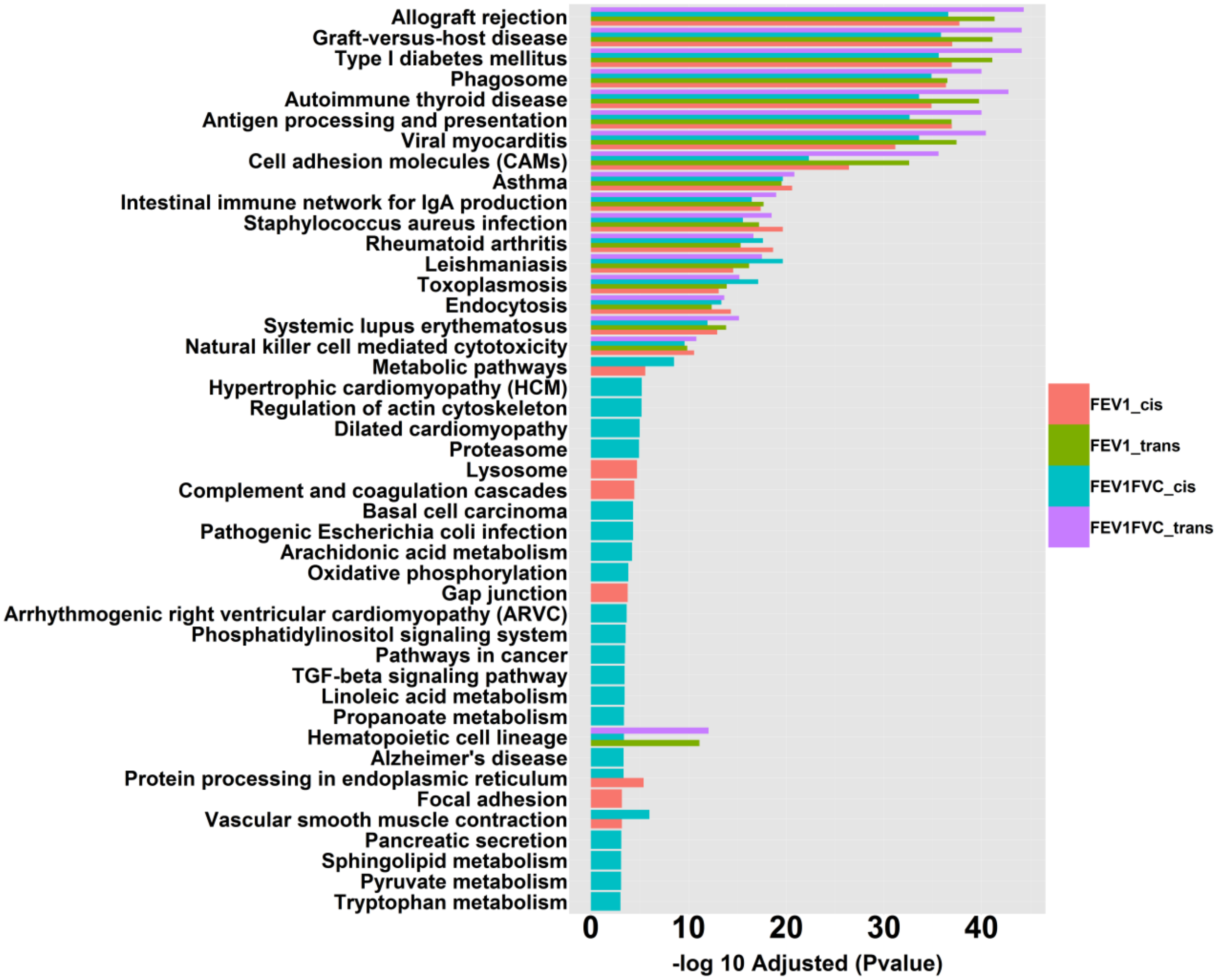
### Supplementary Figure 3: Venn diagram for the overlap between lung function eSNPs

The diagram shows the degree of overlap between the $FEV_1$ and $FEV_1$/FVC *cis* and *trans* regulated genes. Dark grey represent $FEV_1$ *cis*, blue $FEV_1$ *trans*, red $FEV_1$/FVC *cis* and green $FEV_1$/FVC *trans*. The numbers indicate the number of genes shared between the overlapping groups.



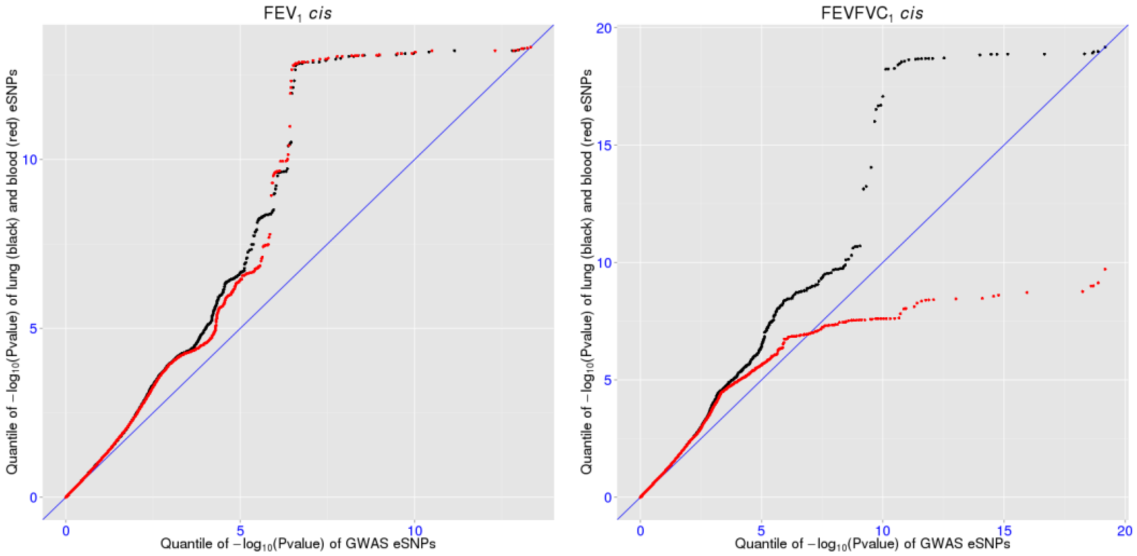
## Supplementary Figure 4: KEGG pathways for lung function eSNP-regulated genes

KEGG pathways and their corresponding false discovery rates (adjusted P-values) for enrichment among lung function eSNP-regulated genes. $FEV_1$ and $FEV_1$/FVC *cis*- and *trans*-regulated genes are assigned a different color indicated by the color legend to the right.



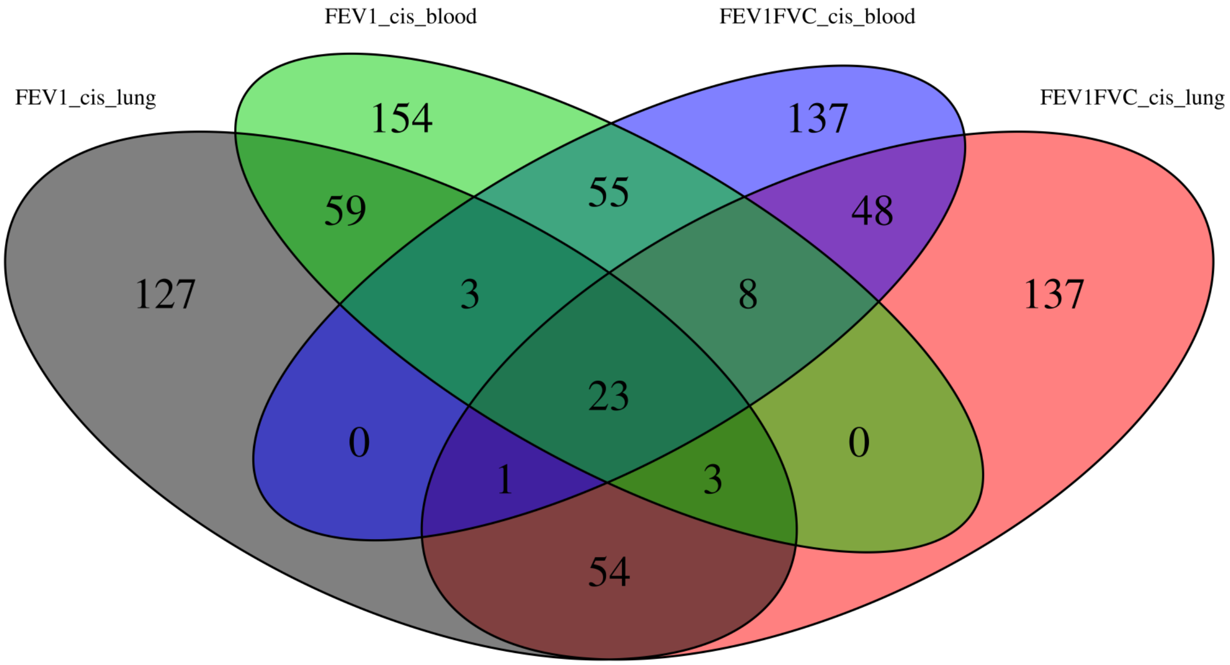
## Supplementary Figure 5: Q-Q plots of blood eSNPs GWAS P values vs. all GWAS SNPs

On the Y axis are quantiles of the distribution of lung function GWAS P values for *cis*-eSNPs identified in blood (in red) and lung (in black). On the X axis are the quantiles of the distribution of lung function GWAS P-values for all the variants (~2.4 million).
For FEV$_1$ (left panel) the systematic deviation of the red line from the expected distribution illustrates that blood *cis*-eSNPs are enriched for association with FEV$_{1,}$ in a similar pattern to lung eSNPs. The deviation is larger for FEV$_1$/FVC lung *cis*-eSNPs (black line) suggesting that eSNPs discovered in the lung are more likely to show association with FEV$_1$/FVC.



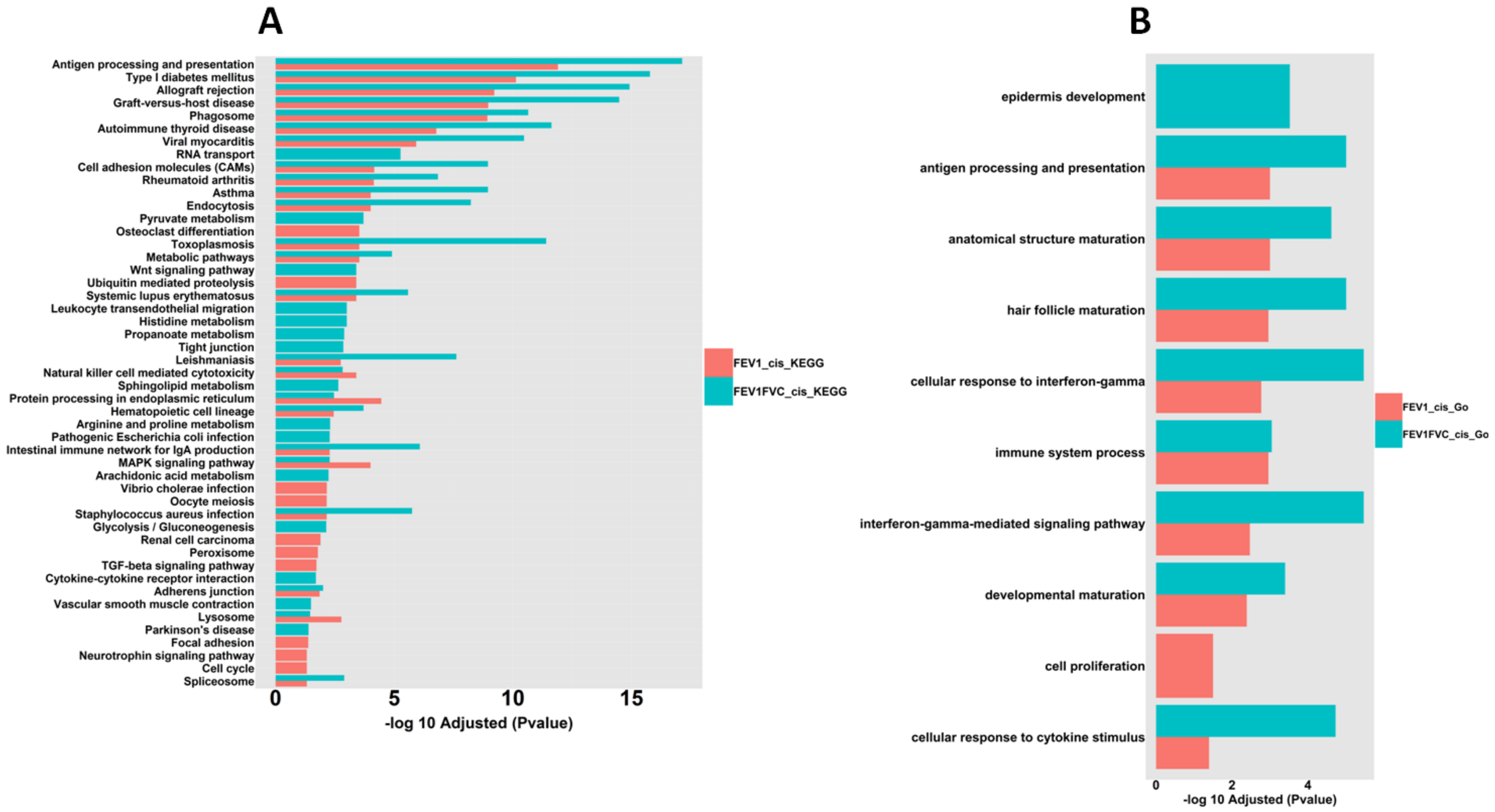
### Supplementary Figure 6: Overlap between blood and lung $FEV_1$ and $FEV_1$/FVC *cis*-regulated genes

Venn diagram showing the degree of overlap between the $FEV_1$ and $FEV_1$/FVC lung and blood *cis* eSNPs-regulated genes. Dark grey represents $FEV_1$ lung, green $FEV_1$ blood, blue $FEV_1$/FVC blood, red $FEV_1$/FVC lung. The numbers indicate the number of genes shared between the overlapping groups.



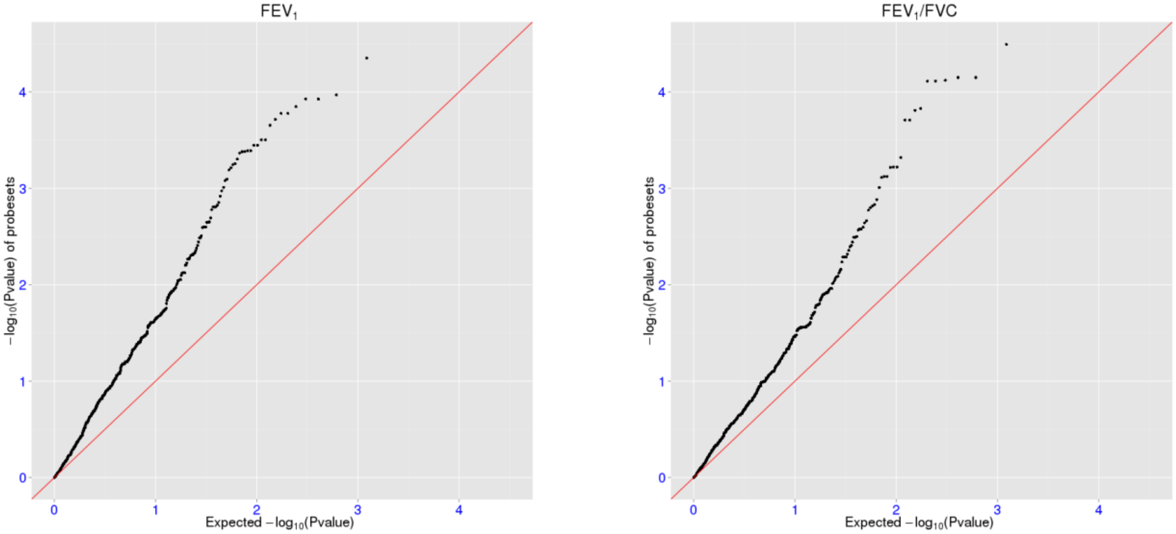
**Supplementary Figure 7 (A and B): Blood eSNPs regulated genes KEGG and GO enrichment analyses**

KEGG pathways (A) and GO processes (B) and their corresponding false discovery rates(adjusted P-values) for enrichment when $FEV_1$ and $FEV_1$/FVC *cis* blood-derived eSNP-regulated genes were used as input. $FEV_1$ and $FEV_1$/FVC blood-derived *cis*-regulated genes are assigned a different color indicated by the color legend to the right.



## Supplementary Figure 8: Q-Q plots for lung function eSNP-regulated genes' associations with lung function measures in individuals from the eQTL study

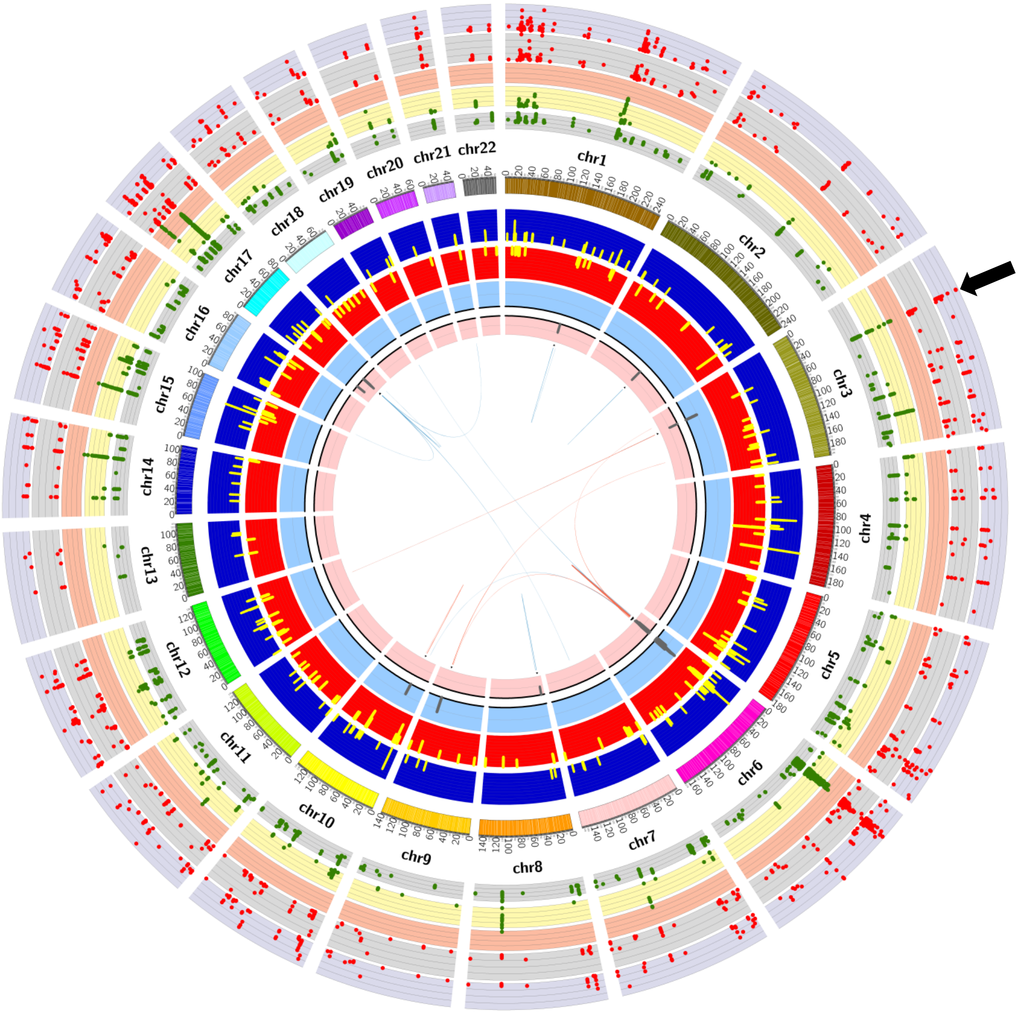
Probesets regulated by lung function eSNPs were tested for association with $FEV_1$ (left) and $FEV_1$/FVC (right) in 727 individuals from the eQTL study. On the Y-axis is the distribution of P-values for the probesets' association with lung function plotted against the expected distribution of P-values under the null hypothesis of no association on the X-axis. The systematic departure of the observed P-values from the expected distribution illustrates that the expression of lung function eSNP-regulated genes are enriched for association with lung function in individuals from the eQTL study.



## Supplementary Figure 9: Summary of eSNPs association

The graph summarizes all eSNP association data described in this study. The colors of circles are described from the innermost to the outermost circle. The lines in the innermost circle depict the *trans* eSNP regulated genes i.e. they connect the eSNP with the gene it regulates in *trans*; red represents FEV$_1$/FVC *trans* and the blue FEV$_1$ trans. First circle: $P_{\mathrm{GWAS}}$ values for FEV$_1$ *trans* eSNPs. Second circle : $P_{\mathrm{GWAS}}$ values for FEV$_1$/FVC *trans* eSNPs. Third circle $P_{\mathrm{GWAS}}$ values for FEV$_1$ *cis* eSNPs. Fourth circle: $P_{\mathrm{GWAS}}$ values for FEV$_1$/FVC *cis* eSNPs. The length of the bars inside these four circles is proportional to the –log10 p value from that particular analysis, so the longer the stronger the association. The height of the points in the circles outside the 22 chromosome labels represent the –log10 P-values from the following analyses: The first three circles represent the $P_{\mathrm{eQTL}}$ value for each lung function eSNP, divided into these P-value ranges:: grey circle represents –log10 ($P_{\mathrm{eQTL}}$ value) range 0-10, yellow –log10 ($P_{\mathrm{eQTL}}$ value) range 10-100, and red –log10 ($P_{\mathrm{eQTL}}$ value) range 100-600. The last two outer circles represents the –log10 P-values of each lung function eSNP-regulated probeset regressed on FEV$_1$ in the grey circle and on FEV$_1$/FVC in the purple circle.

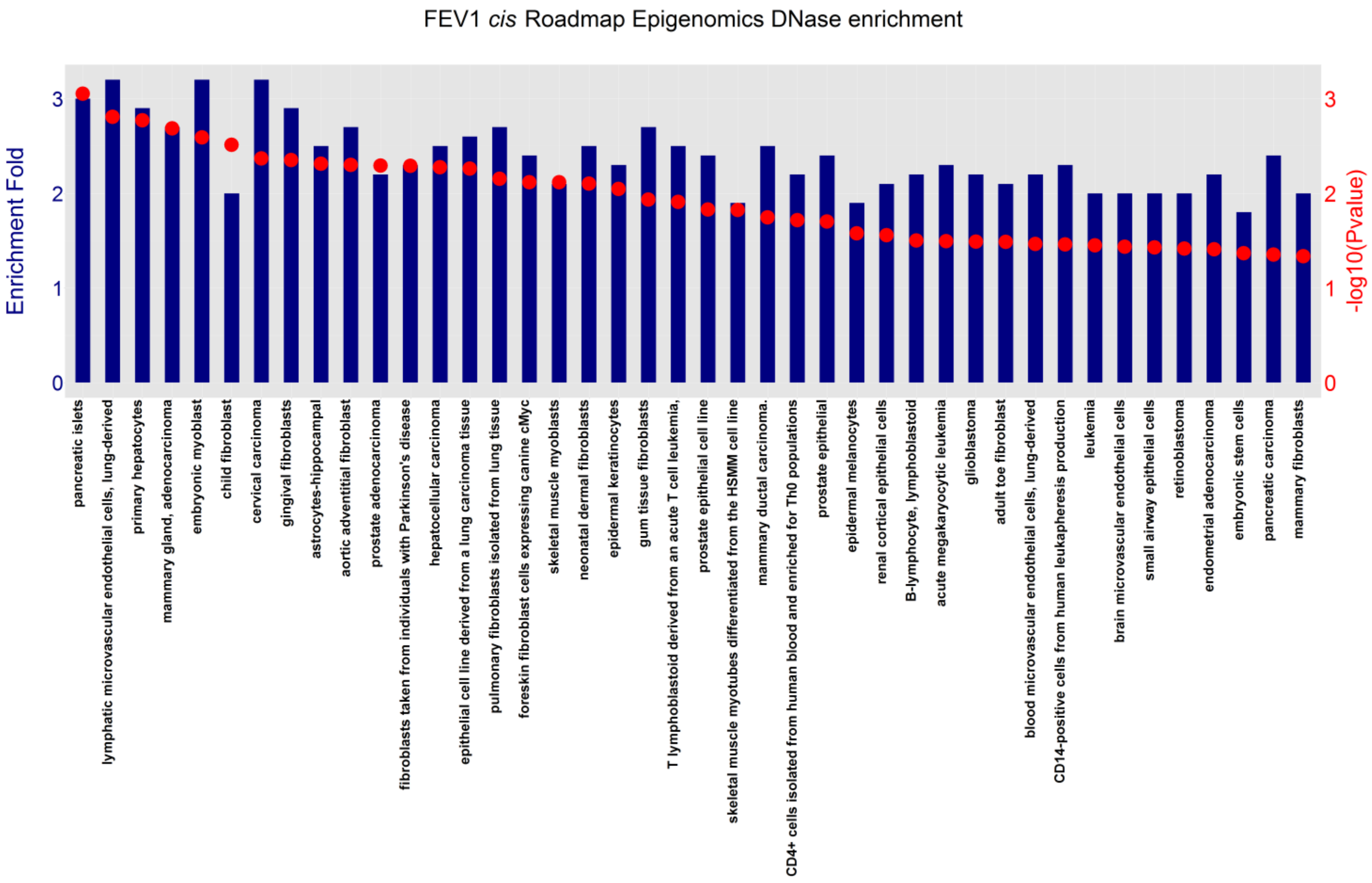
The figure is a way to visualize associations for the three dimensions tested: GWAS, eQTL, and mRNA associations with lung function measures. The graph enables location of regions in the genome with support from all three of these dimensions. For example, the arrow points to a region on chromosome 3 that show good support as indicated by the longer lines for the layers of eQTL and mRNA associations (outer layer).



**Supplementary Figure 10 (A-D): Lung eSNPs enrichment in functional annotations from ENCODE and Roadmap Epigenome projects**

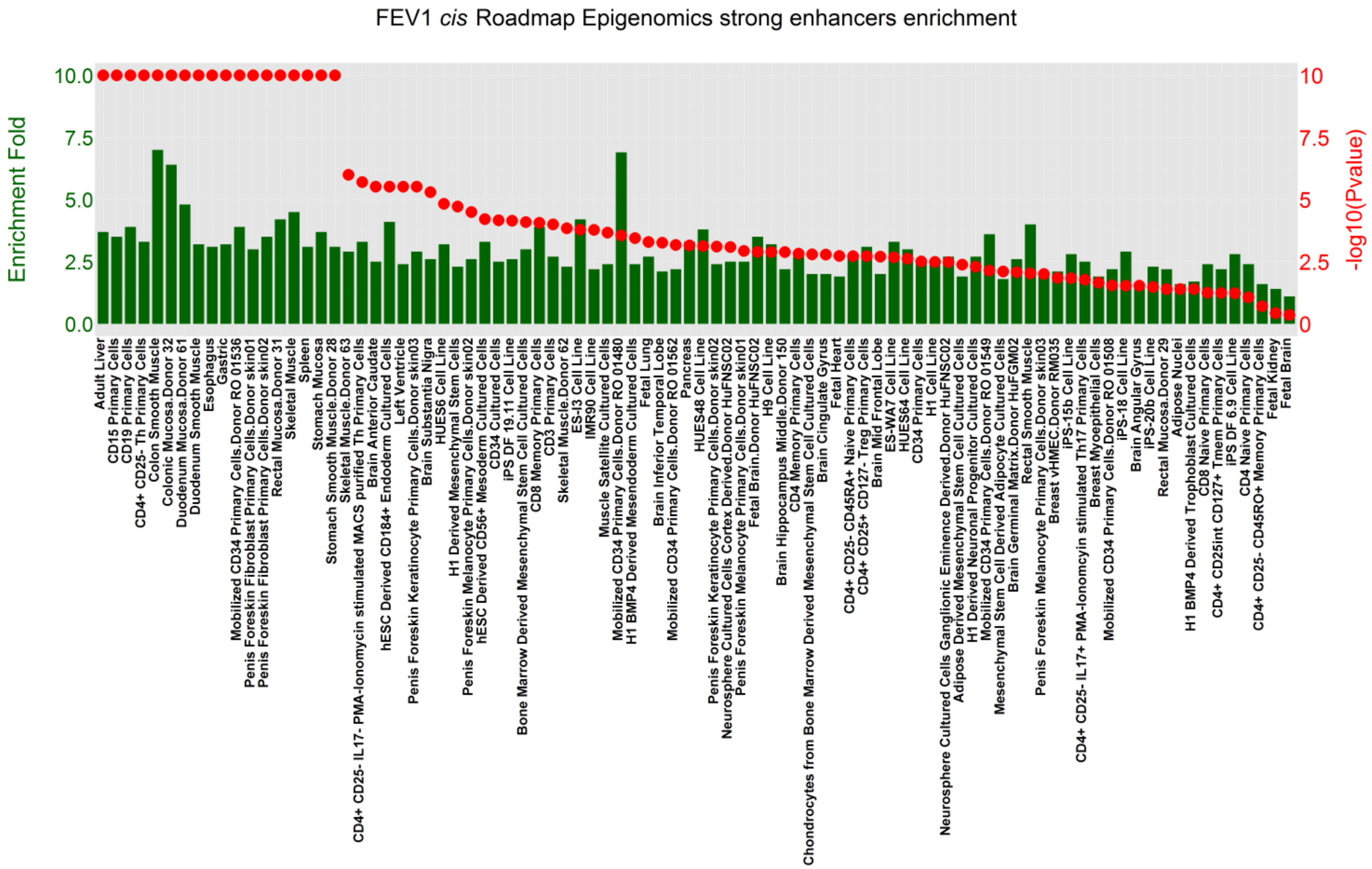
The left Y-axis represents the fold enrichment, in blue for DNase hypersensitivity sites and in green for Enhancers. The right Y-axis represents the-log10(P value) for this enrichment. P values < $2.2\times10^{-16}$ were set to 10 on the Y-axis to aid visualization. A: $FEV_1$ lung *cis*-eSNPs' DNase enrichment in Roadmap Epigenomics. B: $FEV_1$ lung *cis*-eSNPs' enhancer enrichment in Roadmap Epigenomics. C: $FEV_1$/FVC lung *cis*-eSNPs' DNase enrichment in Roadmap Epigenomics. D: $FEV_1$/FVC lung *cis*-eSNPs' enhancer enrichment in Roadmap Epigenomics project.

# Supplementary Figure 10 A

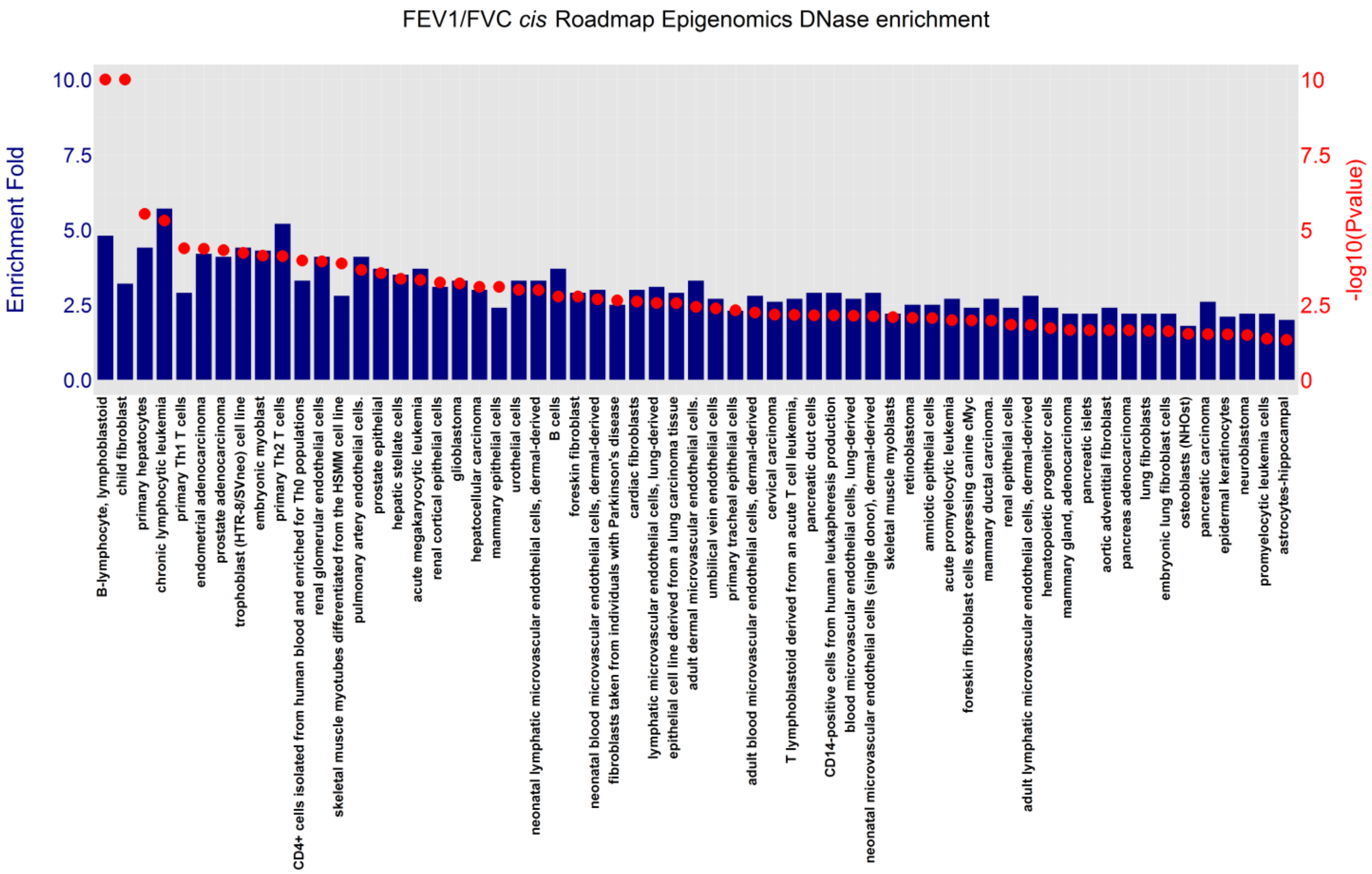


FEV1 *cis* Roadmap Epigenomics DNase enrichment

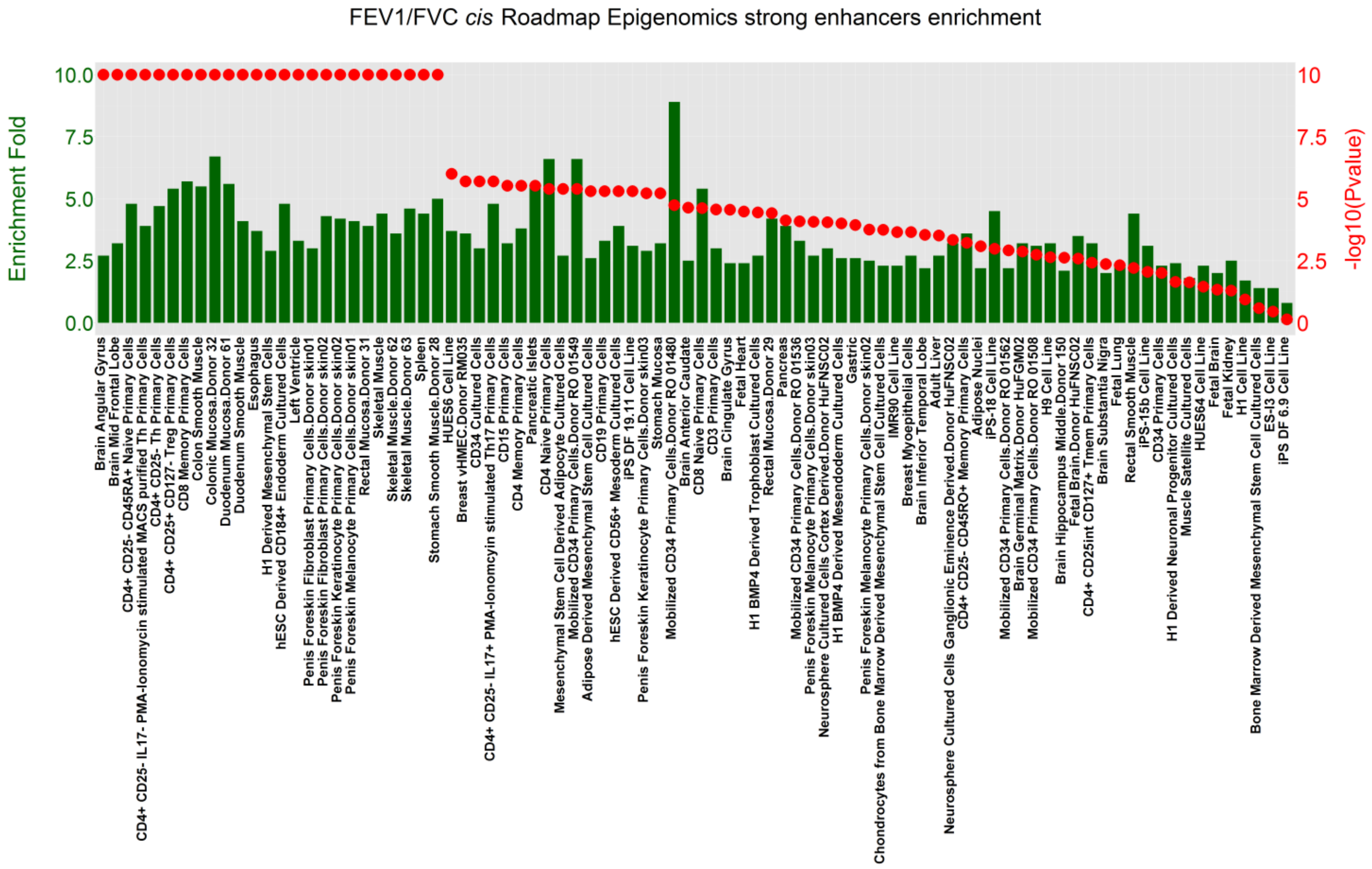
# Supplementary Figure 10 B



# Supplementary Figure 10 C

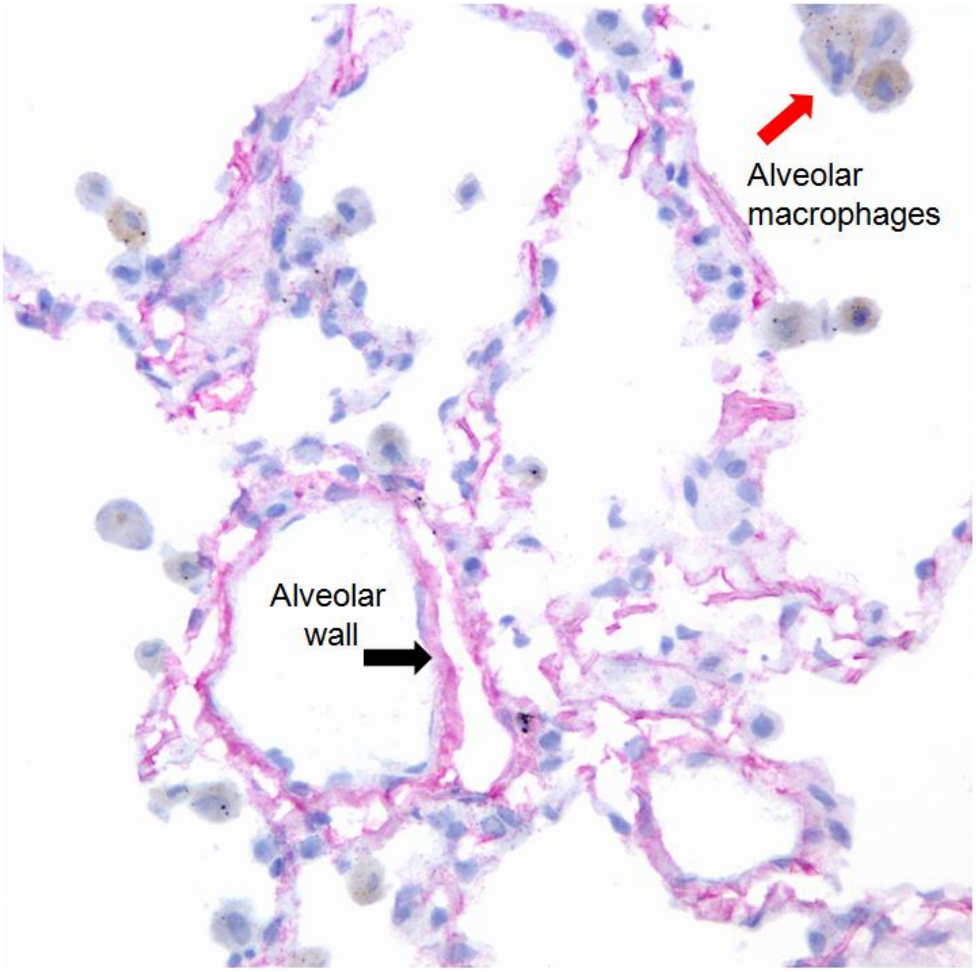


# Supplementary Figure 10 D



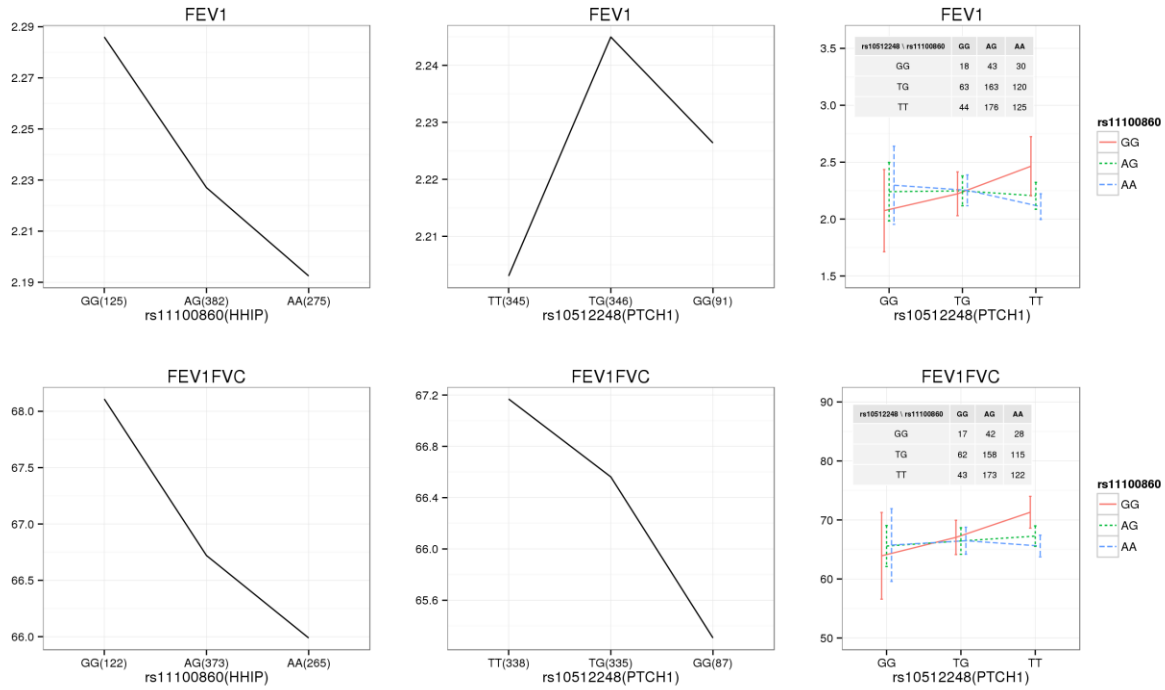
## Supplementary Figure 11: Immunohistochemistry staining of NPNT in human lung tissue

Representative image of NPNT expression in human lung parenchyma by immunohistochemistry. Staining was positive in alveolar walls, likely due to endothelial staining although staining of type I alveolar cells may also be present.  Not shown is positive staining of vascular endothelium in bronchial microvessels and larger pulmonary arteries. Airway epithelial cells and alveolar macrophages were negative for NPNT staining. This shows that NPNT protein is expressed in relevant cell types.



**Supplementary Figure 12: Effect of HHIP and PTCH1 eSNPs on FEV1 (top panel) and FEV1/FVC (bottom panel) in individuals from the eQTL study.**

Genotypes are shown on the X-axis and in parentheses the number of individuals carrying this genotype in the eQTL study. On the Y-axis is $FEV_1$ in litres, or $FEV_1$/FVC. The third figure to the right in the top and bottom panels shows the effect of the PTCH1 genotype on either $FEV_1$ or $FEV_1$/FVC in combination with the HHIP eSNP genotypes. Mean values and their standard errors bars are shown for each genotype.



| rs10512248 \ rs11100860 | GG | AG | AA |
|---|---|---|---|
| GG | 18 | 43 | 30 |
| TG | 63 | 163 | 120 |
| TT | 44 | 176 | 125 |

| rs10512248 \ rs11100860 | GG | AG | AA |
|---|---|---|---|
| GG | 17 | 42 | 28 |
| TG | 62 | 158 | 115 |
| TT | 43 | 173 | 122 |

## Enrichment of lung function eSNP-regulated genes in KEGG pathways

A number of KEGG pathways were significantly enriched among lung function eSNP- regulated genes. The strongest enrichment was for antigen processing and presentation, autoimmune diseases, cell adhesion, and asthma. While the most enriched KEGG pathways were shared across the $FEV_1$ and $FEV_1$/FVC *cis* and *trans*-regulated genes, a number of pathways were unique to either $FEV_1$ or $FEV_1$/FVC. $FEV_1$/FVC *cis*-regulated genes were specifically enriched in Wnt signalling, linoleic acid metabolism, the TGF-beta signalling pathway, arachidonic acid metabolism, regulation of actin cytoskeleton, and dilated cardiomyopathy. $FEV_1$ *cis*-regulated genes were, on the other hand, specifically enriched for genes expressed in focal adhesion and gap junctions.

## Evaluation of lung function eSNP-regulated genes in fetal lung study

Lung function eSNP-regulated genes were significantly enriched among genes differentially expressed during human fetal lung development (1·61 fold, $P= 7{\cdot}1\text{x}10^{-07}$). The relative enrichment fold increased (2·3 fold, $P= 4{\cdot}6\text{x}10^{-06}$) when the analysis was restricted to the lung function eSNP-regulated genes whose mRNA level was associated with either $FEV_1$ or $FEV_1$/FVC in the eQTL study at a nominal $P<0{\cdot}05$ (Supplementary Table 9).

## ENCODE enrichment results

Results from the Roadmap Epigenome revealed enrichment of lung function eSNPs- in DNase Hypersensitivity sites (DHS) and enhancer functions in a number of cell types and tissues including fetal lung, and multiple tissues from the brain. For example, $FEV_1$ *cis*-eSNPs were enriched for strong enhancers in fetal lung tissue, (2.7 fold, $P$= 5.17E-04), $FEV_1$/FVC *cis*-eSNPs (2.4 fold, $P$= 4.86E-03), and $FEV_1$/FVC *trans*-eSNPs (5.8 fold, $P$= 0.046). FEV1 *cis*-eSNPs were enriched in DHS in pulmonary fibroblasts (2.7 fold, $P$= 0.007), small airway epithelial cells (2 fold, $P$=0.037), and lung carcinoma epithelial cell lines (2.6 fold, $P$= 0.006). $FEV_1$/FVC *cis*-eSNPs were enriched for DHS in pulmonary artery endothelial cells (4.1 fold, $P$= 0.0002), lung fibroblasts (2.2 fold, P= 0.023), primary tracheal epithelial cells (2.3 fold, $P$=0.0048), embryonic lung fibroblast cells (2.2 fold, P=0.023), and in a trophoblast cell line (4.4 fold, $P$=5.90E-05), among others.

## Integrative genomics identifies *RBP2*

SNP rs1491106 on chromosome 9 is a lung tissue trans eQTL ($P_{\text{eQTL}} = 9.92\text{x}10^{-19)}$ for retinal binding protein 2 (*RBP2*) which is on chromosome 3. The same SNP was associated with $FEV_1$/FVC with $P_{\text{GWAS}}= 6.02\text{x}10^{-05}$. The T allele was associated with higher $FEV_1$/FVC and higher *RBP2* mRNA expression. In concordance with this allelic effect, the mRNA levels of *RBP*2 in lung tissue were positively associated with $FEV_1$/FVC ($P$=0.02) (i.e. higher levels of *RBP2* associated with better $FEV_1$/FVC).
These relationships provide a potential explanation for the molecular link between the vitamin A pathway and variation in lung function which has been previously proposed (21-25). Checkley *et al*. (24) found that children whose mothers' received supplementary vitamin A during pregnancy had a higher $FEV_1$ and FVC than those who received placebo. Massaro and Massaro (26) showed that vitamin A treatment could partially reverse elastase-induced emphysema in rats and Paiva *et al*. (27) showed that vitamin A treatment could improve lung function in moderately severe COPD patients whose blood levels of vitamin A were low. On the other hand, two clinical trials have shown no benefit of vitamin A supplementation. Mao *et al*. (28) found no benefit of 3 months of treatment with all trans retinoic acid in 20 patients who had severe COPD and Stolk et al (6) failed to show a significant benefit of an agonist of the γ-type retinoic acid receptor on lung density in patients with moderate-to-severe emphysema secondary to severe alpha 1 antitrypsin deficiency (29).

## *HHIP* and *PTCH1* eSNPs interaction effect on $FEV_1$ and $FEV_1$/FVC in the eQTL study

The effect of the *HHIP* eSNP (rs11100860) and the *PTCH1* eSNP (rs10512248) on $FEV_1$ and $FEV_1$/FVC in 727 individuals from the eQTL study was separately performed using linear regression adjusting for age, gender, height and smoking status, under an additive genetic model. The results in the table below show association of rs11100860 (*HHIP*) with $FEV_1$ (*P*=0.02)

| **SNP** | **$FEV_1$/FVC beta** | **$FEV_1$/FVC SE** | **$FEV_1$/FVC P value** | **$FEV_1$ beta** | **$FEV_1$ SE*** | **$FEV_1$ P value** |
|---|---|---|---|---|---|---|
| **rs10512248 (*PTCH1*)** | 0.23 | 0.59 | 0.69 | 0.01 | 0.03 | 0.79 |
| **rs11100860 (*HHIP*)** | -0.95 | 0.57 | 0.09 | -0.08 | 0.03 | **0.02** |

The same test was performed with both SNPs in the model and including an interaction term. When the interaction term was included in the model, SNP rs10512248 (*PTCH1*) showed association with both $FEV_1$ (*P*=0.004) and $FEV_1$/FVC (*P*=0.007) with a significant interaction effect on both $FEV_1$ (*P*=0.003) and $FEV_1$/FVC (*P*=0.006), see table below.

| **SNP** | **$FEV_1$/FVC beta** | **$FEV_1$/FVC SE** | **$FEV_1$/FVC P value** | **$FEV_1$ beta** | **$FEV_1$ SE*** | **$FEV_1$ P value** |
|---|---|---|---|---|---|---|
| **Interaction** | -2.352 | 0.857 | **0.006** | -0.142 | 0.047 | **0.003** |
| **rs10512248 (*PTCH1*)** | 3.195 | 1.180 | **0.007** | 0.187 | 0.065 | **0.004** |
| **rs11100860 (*HHIP*)** | 2.098 | 1.253 | 0.094 | 0.106 | 0.069 | 0.122 |

*SE: standard error

Supplementary Figure 10 above shows the effect of the two SNPs genotypes separately on $FEV_1$, and $FEV_1$/FVC in individuals from the eQTL study, and also shows the interaction effect.

## Supplementary Tables

### Supplementary Table 1: Lung function SNPs enrichment in lung eQTLs at different GWAS P value thresholds

GWAS P value cutoff: The thereshold of GWAS P values from SpiroMeta CHARGE lung function association with $FEV_1$ and $FEV_1$/FVC. No of GWAS SNPs: Nubmer of SNPs in SpiroMeta-CHARGE GWAS meeting this P value threshold. no of lung eQTLs: Number of lung function SNPs that act as lung eQTLs at the 10% FDR genome-wide eQTL significance. Enrichment Fold: the ratio of the two proportions: The % of GWAS SNPs at the assigned GWAS P value threshold that act as eQTLs divided by the proportion of all eQTLs at 10% FDR to all SNPs tested. P value: Fisher's exact test P value.

| GWAS P value cutoff | No of GWAS SNPs | No of lung eQTLs | Enrichment Fold | P value |
|---|---|---|---|---|
| **FEV1 *cis*** | | | | |
| 1.00E-03 | 6615 | 3413 | 2.71 | <1E-323 |
| 1.00E-04 | 1906 | 1186 | 3.26 | <1E-323 |
| 1.00E-05 | 586 | 348 | 3.1 | 4.14E-102 |
| 1.00E-06 | 288 | 181 | 3.28 | 2.64E-59 |
| 1.00E-07 | 143 | 95 | 3.47 | 7.67E-35 |
| 1.00E-08 | 109 | 81 | 3.88 | 1.58E-35 |
| **FEV1 *trans*** | | | | |
| 1.00E-03 | 6615 | 1568 | 37.87 | <1E-323 |
| 1.00E-04 | 1906 | 648 | 51.3 | <1E-323 |
| 1.00E-05 | 586 | 41 | 10.18 | 1.23E-27 |
| 1.00E-06 | 288 | 15 | 7.57 | 2.62E-09 |
| 1.00E-07 | 143 | 1 | 1.01 | 6.28E-01 |
| 1.00E-08 | 109 | 0 | NA | NA |
| **FEV1/FVC *cis*** | | | | |
| 1.00E-03 | 5239 | 2205 | 2.2 | 4.1E-318 |
| 1.00E-04 | 1759 | 973 | 2.89 | 1.35E-248 |
| 1.00E-05 | 835 | 378 | 2.37 | 5.03E-66 |
| 1.00E-06 | 455 | 189 | 2.17 | 4.13E-28 |

| | | | | |
|---|---|---|---|---|
| 1.00E-07 | 346 | 141 | 2.13 | 1.68E-20 |
| 1.00E-08 | 252 | 102 | 2.12 | 4.66E-15 |
| **FEV1/FVC *trans*** | | | | |
| 1.00E-03 | 5239 | 442 | 12.55 | 3.11E-316 |
| 1.00E-04 | 1759 | 183 | 15.26 | 6.97E-148 |
| 1.00E-05 | 835 | 84 | 14.67 | 1.34E-67 |
| 1.00E-06 | 455 | 15 | 4.79 | 9.84E-07 |
| 1.00E-07 | 346 | 9 | 3.78 | 7.76E-04 |
| 1.00E-08 | 252 | 7 | 4.03 | 2.01E-03 |

## Supplementary Table 2: $FEV_1$ *cis*-eSNPs

Table shows the list of $FEV_1$ *cis*-acting lung eSNPs. eSNP: a SNP that is associated with either $FEV_1$ or $FEV_1$/FVC from the SpiroMeta GWAS with $P_{GWAS}$ <0.001 and acts as a *cis* or *trans* eQTL at 10% FDR in lung tissue. eSNP-regulated probeset: Probeset whose expression is regulated by that particular eSNP. GWAS SNP alleles: Two alleles from the GWAS study. GWAS reference allele: Allele used to derive the association test statistics. Reference allele freq in HapMap: The frequency of the GWAS reference allele from the HapMap II project in the Caucasian population (CEU). Chr: chromosome. SNP position: position using NCBI36/hg18 coordinates. GWAS_Pval_ $FEV_1$: eSNP P-value for association with $FEV_1$ from the GWAS study. eQTL Z meta: The Z score of meta analysis results of eQTL study across the three datasets (UBC, Groningen, Laval). eQTL P-value: the eQTL P-value from the lung eQTL study. Log10.pvalue.meta: Log10 of the eQTL P-value. Sequence source ID: the mRNA transcript ID, or the cDNA clone ID that the probeset sequence maps to. Gene Symbol: eSNP regulated gene symbol. eQTL alleles: Two alleles from the eQTL study. GWAS_noncoded_alleles: Alternate allele that was not used to derive the association test statistics in the GWAS study. GWAS_coded_alleles: Allele used to derive the association test statistics in the GWAS study. eQTL_noncoded_alleles: Alternate allele that was not used to derive the association test statistics in the eQTL study. eQTL_coded_alleles: Allele used to derive the association test statistics in the eQTL study. Expected direction of effect of mRNA with lung function: The direction of effect of mRNA on lung function as inferred from the SNP effect on mRNA (from the eQTL study) and on lung function (from the GWAS study).

### FEV1 *cis* lung eSNPs

| eSNP | eSNP regulated probeset | GWAS SNP alleles | GWAS Reference allele | Reference allele freq in HapMap | Chr | SNP Position | GWAS_ Pval_ FEV1 | eQTL Z meta | eQTL P value | log10. pvalue. meta | sequence source ID | Gene Symbol | eQTL-alleles | GWAS_ noncoded_alleles | GWAS_ coded_ alleles | eQTL_ noncoded_alleles | eQTL_ coded_ alleles | Expected Direction Of Effect of mRNA with lung function |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs17331332 | 100129915_ TGI_at | A/G | G | 0.923 | 4 | 107027556 | 1.11E-12 | 4.502 | 6.73E-06 | -5.1719 | NM_001033 047 | NPNT | A_G | A | G | A | G | negative |
| rs1063281 | 100145096_ TGI_at | C/T | T | 0.608 | 2 | 218376977 | 2.43E-10 | -4.309 | 1.64E-05 | -4.7852 | NM_022648 | TNS1 | T_C | C | T | T | C | positive |
| rs10906097 | 100149333_ TGI_at | G/T | T | 0.567 | 10 | 12283827 | 3.32E-09 | 6.077 | 1.22E-09 | -8.912 | NM_006023 | CDC123 | G_T | G | T | G | T | negative |
| rs12509311 | 100139086_ TGI_at | C/T | T | 0.405 | 4 | 145698112 | 4.27E-09 | -5.216 | 1.83E-07 | -6.738 | AK024689 | HHIP | C_T | C | T | C | T | negative |
| rs13141641 | 100133899_ TGI_at | C/T | T | 0.564 | 4 | 145725906 | 1.40E-08 | -4.211 | 2.54E-05 | -4.5948 | AK124396 | Maps to cDNA clone close to HHIP | T_C | C | T | T | C | negative |
| rs13141641 | 100311674_ TGI_at | C/T | T | 0.564 | 4 | 145725906 | 1.40E-08 | -4.095 | 4.22E-05 | -4.3745 | AK098525 | HHIP | T_C | C | T | T | C | negative |
| rs13141641 | 100148028_ TGI_at | C/T | T | 0.564 | 4 | 145725906 | 1.40E-08 | -4.071 | 4.68E-05 | -4.3296 | NM_022475 | HHIP | T_C | C | T | T | C | negative |
| rs11001819 | 100144009_ TGI_at | A/G | G | 0.5 | 10 | 77985230 | 1.42E-08 | 5.722 | 1.05E-08 | -7.9777 | AK125328 | C10orf11 | A_G | A | G | A | G | negative |
| rs2855812 | 100125842_ TGI_at | G/T | T | 0.258 | 6 | 31580699 | 8.57E-08 | 4.986 | 6.16E-07 | -6.2101 | NM_147130 | NCR3 | G_T | G | T | G | T | negative |
| rs1150691 | 100139132_ TGI_at | A/G | G | 0.38 | 6 | 28276012 | 4.34E-07 | -4.019 | 5.85E-05 | -4.2332 | BC035154 |  | G_A | A | G | G | A | negative |
| rs7727320 | 100134215_ TGI_at | C/G | G | 0.733 | 5 | 147812764 | 6.84E-07 | -6.58 | 4.7E-11 | -10.3275 | NM_030793 | FBXO38 | G_C | C | G | G | C | negative |
| rs2579762 | 100124184_ TGI_at | A/C | C | 0.414 | 10 | 77988885 | 7.15E-07 | -6.978 | 2.99E-12 | -11.5237 | DA084722 |  | C_A | A | C | C | A | negative |
| rs10055430 | 100313079_ TGI_at | A/G | G | 0.276 | 5 | 147777732 | 1.02E-06 | 12.615 | 1.75E-36 | -35.7581 | AF251055 | FBXO38 | A_G | A | G | A | G | positive |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2036527 | 100148404_TGI_at | A/G | G | 0.575 | 15 | 76638670 | 2.40E-06 | 6.946 | 3.76E-12 | -11.4251 | NM_002789 | PSMA4 | G_A | A | G | G | A | negative |
| rs599707 | 100139818_TGI_at | C/T | T | 0.093 | 6 | 31916415 | 8.76E-06 | 5.467 | 4.58E-08 | -7.3394 | NM_080686 | BAT2 | T_C | C | T | T | C | positive |
| rs10125253 | 100161091_TGI_at | C/T | T | 0.625 | 9 | 117052662 | 9.99E-06 | 4.414 | 1.01E-05 | -4.9936 | BQ447217 | TNC | C_T | C | T | C | T | negative |
| rs6478156 | 100161091_TGI_at | G/T | T | 0.625 | 9 | 117064513 | 1.04E-05 | 4.414 | 1.01E-05 | -4.9936 | BQ447217 | TNC | G_T | G | T | G | T | negative |
| rs4634439 | 100127556_TGI_at | A/G | G | 0.142 | 6 | 26705983 | 1.22E-05 | 4.343 | 1.41E-05 | -4.8522 | BX640949 | TRIM38 | G_A | A | G | G | A | positive |
| rs1150721 | 100161813_TGI_at | C/G | G | 0.655 | 6 | 28363019 | 1.45E-05 | 7.267 | 3.68E-13 | -12.4347 | NM_032507 | PGBD1 | G_C | C | G | G | C | negative |
| rs11150044 | 100138939_TGI_at | A/C | C | 0.664 | 16 | 76758793 | 1.49E-05 | 5.22 | 1.79E-07 | -6.7473 | NM_016373 | WWOX | A_C | A | C | A | C | positive |
| rs1401705 | 100136657_TGI_at | A/G | G | 0.508 | 2 | 17421443 | 1.76E-05 | 7.202 | 5.93E-13 | -12.2267 | NM_182625 | GEN1 | G_A | A | G | G | A | positive |
| rs1401705 | 100158297_TGI_at | A/G | G | 0.508 | 2 | 17421443 | 1.76E-05 | 5.438 | 5.39E-08 | -7.2686 | ENST00000381254 | GEN1 | G_A | A | G | G | A | positive |
| rs3094086 | 100125489_TGI_at | A/G | G | 0.822 | 6 | 31027370 | 1.86E-05 | 7.907 | 2.64E-15 | -14.5789 | NM_205854 | SFTA2 | G_A | A | G | G | A | negative |
| rs3132581 | 100125489_TGI_at | A/G | G | 0.839 | 6 | 31021437 | 1.96E-05 | -7.907 | 2.64E-15 | -14.5789 | NM_205854 | SFTA2 | A_G | A | G | A | G | negative |
| rs9264740 | 100311757_TGI_at | C/T | T | 0.673 | 6 | 31352310 | 2.15E-05 | 8.067 | 7.2E-16 | -15.1424 | AK095029 | | T_C | C | T | T | C | positive |
| rs3117574 | 100126143_TGI_at | A/G | G | 0.9 | 6 | 31833209 | 2.15E-05 | 8.012 | 1.13E-15 | -14.9475 | NM_019101 | APOM | A_G | A | G | A | G | positive |
| rs12214383 | 100312805_TGI_at | C/T | T | 0.398 | 6 | 28331710 | 2.27E-05 | 5.796 | 6.79E-09 | -8.168 | AI251212 | ZNF165 | C_T | C | T | C | T | negative |
| rs931794 | 100156434_TGI_at | A/G | G | 0.433 | 15 | 76613235 | 2.38E-05 | -10.6 | 3.11E-26 | -25.5072 | NM_000745 | CHRNA5 | A_G | A | G | A | G | positive |
| rs2844559 | 100144394_TGI_at | C/T | T | 0.167 | 6 | 31448054 | 3.09E-05 | 4.674 | 2.95E-06 | -5.5296 | NM_006674 | HCP5 | T_C | C | T | T | C | positive |
| rs9788721 | 100154936_TGI_at | C/T | T | 0.567 | 15 | 76589924 | 3.14E-05 | -16.42 | 1.35E-60 | -59.8686 | AF147302 | | T_C | C | T | T | C | positive |
| rs11650615 | 100139309_TGI_at | C/G | G | 0.271 | 17 | 43478697 | 3.27E-05 | 4.418 | 9.96E-06 | -5.0017 | NM_176096 | CDK5RAP3 | C_G | C | G | C | G | positive |
| rs1864325 | 100161408_TGI_at | C/T | T | 0.195 | 17 | 41333623 | 3.59E-05 | -22.26 | 9E-110 | -109.045 | AY526356 | MAPT | T_C | C | T | T | C | negative |
| rs1864325 | 100148039_TGI_at | C/T | T | 0.195 | 17 | 41333623 | 3.59E-05 | 8.262 | 1.43E-16 | -15.8439 | NM_015443 | KIAA1267 | T_C | C | T | T | C | positive |
| rs7636047 | 100157337_TGI_at | A/G | G | 0.858 | 3 | 197550966 | 3.59E-05 | 5.547 | 2.91E-08 | -7.5367 | AK097068 | | A_G | A | G | A | G | positive |
| rs2524067 | 100309484_TGI_at | A/G | G | 0.175 | 6 | 31353800 | 3.76E-05 | 16.162 | 9.35E-59 | -58.0293 | BC041078 | HLA-C | G_A | A | G | G | A | positive |
| rs17650872 | 100123425_TGI_at | G/T | T | 0.2 | 17 | 41395352 | 3.81E-05 | 22.463 | 9.6E-112 | -111.02 | NM_016834 | MAPT | G_T | G | T | G | T | negative |
| rs1225710 | 100139670_TGI_at | C/T | T | 0.608 | 6 | 28208619 | 3.84E-05 | -6.382 | 1.75E-10 | -9.7575 | Z11773 | ZNF187 | T_C | C | T | T | C | positive |
| rs3812637 | 100160231_TGI_at | C/T | T | 0.725 | 10 | 75238852 | 3.85E-05 | 4.065 | 4.8E-05 | -4.3185 | NM_001001791 | C10orf55 | C_T | C | T | C | T | negative |
| rs2622320 | 100149232_TGI_at | A/T | T | 0.608 | 6 | 28223315 | 3.93E-05 | 4.495 | 6.96E-06 | -5.1576 | ENST00000303290 | | T_A | A | T | T | A | negative |
| rs12577642 | 100308139_TGI_at | A/T | T | 0.271 | 11 | 43685110 | 4.20E-05 | 22.33 | 1.9E-110 | -109.724 | BG741638 | HSD17B12 | T_A | A | T | T | A | positive |
| rs12577642 | 100148450_TGI_at | A/T | T | 0.271 | 11 | 43685110 | 4.20E-05 | -7.391 | 1.46E-13 | -12.8365 | NM_016142 | HSD17B12 | T_A | A | T | T | A | negative |
| rs2524084 | 100304000_TGI_at | A/G | G | 0.308 | 6 | 31349618 | 4.21E-05 | -12.6 | 2.08E-36 | -35.6809 | ENST00000376242 | PSORS1C3 | G_A | A | G | G | A | negative |
| rs2524084 | 100313121_TGI_at | A/G | G | 0.308 | 6 | 31349618 | 4.21E-05 | 7.423 | 1.14E-13 | -12.9412 | AF196489 | HLA-C | G_A | A | G | G | A | positive |
| rs389884 | 100148822_TGI_at | A/G | G | 0.092 | 6 | 32048876 | 4.25E-05 | 5.307 | 1.11E-07 | -6.9529 | NM_004557 | NOTCH4 | G_A | A | G | G | A | positive |

| | | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8023669 | 100157269_ TGI_at | C/T | T | 0.617 | 15 | 81511661 | 4.56E-05 | 4.251 | 2.13E-05 | -4.672 | CA427225 | | C_T | C | T | C | T | negative |
| rs11257655 | 100142010_ TGI_at | C/T | T | 0.259 | 10 | 12347900 | 5.19E-05 | 14.628 | 1.86E-48 | -47.7301 | NM_153498 | CAMK1D | C_T | C | T | C | T | negative |
| rs11257655 | 100139207_ TGI_at | C/T | T | 0.259 | 10 | 12347900 | 5.19E-05 | 13.121 | 2.5E-39 | -38.6027 | BU616230 | CAMK1D | C_T | C | T | C | T | negative |
| rs11257655 | 100301887_ TGI_at | C/T | T | 0.259 | 10 | 12347900 | 5.19E-05 | 11.328 | 9.54E-30 | -29.0206 | NM_020397 | CAMK1D | C_T | C | T | C | T | negative |
| rs11257655 | 100161388_ TGI_at | C/T | T | 0.259 | 10 | 12347900 | 5.19E-05 | 5.37 | 7.87E-08 | -7.1038 | AW900148 | | C_T | C | T | C | T | negative |
| rs12947718 | 100159134_ TGI_at | A/G | G | 0.866 | 17 | 40848884 | 5.98E-05 | -13.19 | 1.03E-39 | -38.9877 | NM_014798 | PLEKHM1 | A_G | A | G | A | G | negative |
| rs1150753 | 100145052_ TGI_at | A/G | G | 0.1 | 6 | 32167845 | 6.02E-05 | -6.072 | 1.26E-09 | -8.8985 | NM_002121 | HLA-DPB1 | G_A | A | G | G | A | negative |
| rs12448215 | 100160204_ TGI_at | G/T | T | 0.075 | 16 | 46890605 | 6.28E-05 | 6.251 | 4.08E-10 | -9.3895 | AK056051 | | T_G | G | T | T | G | positive |
| rs12448215 | 100305657_ TGI_at | G/T | T | 0.075 | 16 | 46890605 | 6.28E-05 | 5.672 | 1.41E-08 | -7.8503 | CB161851 | SIAH1 | T_G | G | T | T | G | positive |
| rs12448215 | 100311980_ TGI_at | G/T | T | 0.075 | 16 | 46890605 | 6.28E-05 | 5.581 | 2.39E-08 | -7.6213 | AK056051 | | T_G | G | T | T | G | positive |
| rs12448215 | 100139154_ TGI_at | G/T | T | 0.075 | 16 | 46890605 | 6.28E-05 | 5.299 | 1.16E-07 | -6.9339 | AK225895 | SIAH1 | T_G | G | T | T | G | positive |
| rs12448215 | 100300599_ TGI_at | G/T | T | 0.075 | 16 | 46890605 | 6.28E-05 | -4.322 | 1.55E-05 | -4.8107 | T95917 | LONP2 | T_G | G | T | T | G | negative |
| rs12445647 | 100134381_ TGI_at | G/T | T | 0.065 | 16 | 46894281 | 6.38E-05 | 4.274 | 1.92E-05 | -4.7167 | AK074775 | LONP2 | G_T | G | T | G | T | negative |
| rs1858173 | 100162004_ TGI_at | A/C | C | 0.233 | 12 | 101151741 | 6.65E-05 | 4.136 | 3.53E-05 | -4.4517 | NM_017915 | C12orf48 | A_C | A | C | A | C | positive |
| rs11635618 | 100306620_ TGI_at | G/T | T | 0.517 | 15 | 81305985 | 6.67E-05 | 12.671 | 8.56E-37 | -36.0674 | BX091006 | | G_T | G | T | G | T | negative |
| rs2076030 | 100311443_ TGI_at | A/G | G | 0.867 | 6 | 26534835 | 6.95E-05 | -5.908 | 3.46E-09 | -8.4606 | AK225208 | LRRC16A | G_A | A | G | G | A | positive |
| rs9878996 | 100145663_ TGI_at | G/T | T | 0.808 | 3 | 120392228 | 7.25E-05 | -4.41 | 1.03E-05 | -4.9856 | NM_212543 | B4GALT4 | G_T | G | T | G | T | positive |
| rs11853359 | 100310339_ TGI_at | A/G | G | 0.702 | 15 | 69408578 | 7.28E-05 | -7.124 | 1.05E-12 | -11.9795 | AY358143 | THSD4 | A_G | A | G | A | G | negative |
| rs11853359 | 100142979_ TGI_at | A/G | G | 0.702 | 15 | 69408578 | 7.28E-05 | -6.894 | 5.43E-12 | -11.2656 | NM_024817 | THSD4 | A_G | A | G | A | G | negative |
| rs11853359 | 100308491_ TGI_at | A/G | G | 0.702 | 15 | 69408578 | 7.28E-05 | -4.305 | 1.67E-05 | -4.7773 | BF969690 | THSD4 | A_G | A | G | A | G | negative |
| rs750214 | 100143321_ TGI_at | A/C | C | 0.617 | 15 | 81531940 | 7.39E-05 | 5.133 | 2.85E-07 | -6.5449 | AK055438 | | C_A | A | C | C | A | positive |
| rs17689182 | 100135158_ TGI_at | C/T | T | 0.195 | 17 | 41139356 | 7.71E-05 | 36.037 | 2.2E-284 | -283.657 | ENST000003 29477 | LRRC37A4 | T_C | C | T | T | C | positive |
| rs826033 | 100150651_ TGI_at | A/G | G | 0.432 | 11 | 73456591 | 7.85E-05 | -5.748 | 9.03E-09 | -8.0443 | NM_025155 | PAAF1 | A_G | A | G | A | G | negative |
| rs826033 | 100133960_ TGI_at | A/G | G | 0.432 | 11 | 73456591 | 7.85E-05 | -4.676 | 2.93E-06 | -5.5338 | NM_182904 | P4HA3 | A_G | A | G | A | G | negative |
| rs418891 | 100130540_ TGI_at | G/T | T | 0.2 | 17 | 41049321 | 8.22E-05 | 35.462 | 1.9E-275 | -274.722 | CA391893 | | G_T | G | T | G | T | negative |
| rs418891 | 100149004_ TGI_at | G/T | T | 0.2 | 17 | 41049321 | 8.22E-05 | 22.603 | 4E-113 | -112.393 | BC017896 | | G_T | G | T | G | T | negative |
| rs418891 | 100151558_ TGI_at | G/T | T | 0.2 | 17 | 41049321 | 8.22E-05 | 18.205 | 4.71E-74 | -73.3269 | AK094165 | | G_T | G | T | G | T | negative |
| rs17763086 | 100306395_ TGI_at | G/T | T | 0.793 | 17 | 41261262 | 8.29E-05 | -10.91 | 1.07E-27 | -26.9718 | BX418439 | MAPT | G_T | G | T | G | T | negative |
| rs3095151 | 100151371_ TGI_at | G/T | T | 0.25 | 6 | 31008129 | 8.59E-05 | 8.279 | 1.24E-16 | -15.9058 | NM_020442 | VARS2 | T_G | G | T | T | G | positive |
| rs3131787 | 100151371_ TGI_at | C/T | T | 0.742 | 6 | 31007503 | 8.79E-05 | -8.279 | 1.24E-16 | -15.9058 | NM_020442 | VARS2 | T_C | C | T | T | C | positive |
| rs2393667 | 100141839_ TGI_at | C/T | T | 0.864 | 6 | 26529324 | 8.93E-05 | 4.65 | 3.32E-06 | -5.4789 | BC014021 | BTN2A2 | C_T | C | T | C | T | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs10223421 | 100313880_TGI_at | G/T | T | 0.176 | 6 | 31498034 | 9.23E-05 | -7.5 | 6.38E-14 | -13.1951 | AA381265 | | T_G | G | T | T | G | positive |
| rs3814354 | 100306705_TGI_at | A/G | G | 0.593 | 2 | 135428127 | 9.42E-05 | 5.35 | 8.8E-08 | -7.0557 | BU733840 | CCNT2 | G_A | A | G | G | A | positive |
| rs2844518 | 100305045_TGI_at | C/T | T | 0.377 | 6 | 31480548 | 9.71E-05 | -12.68 | 7.54E-37 | -36.1228 | D83543 | | T_C | C | T | T | C | negative |
| rs2844518 | 100162706_TGI_at | C/T | T | 0.377 | 6 | 31480548 | 9.71E-05 | -12.03 | 2.47E-33 | -32.607 | D83543 | | T_C | C | T | T | C | negative |
| rs8057015 | 100145017_TGI_at | A/C | C | 0.375 | 16 | 76717963 | 9.79E-05 | 4.035 | 5.46E-05 | -4.2628 | DN993123 | | A_C | A | C | A | C | positive |
| rs6901158 | 100305836_TGI_at | C/T | T | 0.11 | 6 | 32313920 | 9.92E-05 | -5.524 | 3.31E-08 | -7.4797 | CA308455 | HLA-DPA1 | C_T | C | T | C | T | positive |
| rs7132592 | 100125980_TGI_at | C/T | T | 0.383 | 12 | 68178815 | 0.00010242 | 4.523 | 6.1E-06 | -5.2149 | NM_006530 | YEATS4 | T_C | C | T | T | C | positive |
| rs11079720 | 100308628_TGI_at | A/G | G | 0.816 | 17 | 41195788 | 0.00010277 | 43.691 | 0 | -416.252 | BF475443 | LRRC37A4 | A_G | A | G | A | G | positive |
| rs442439 | 100129584_TGI_at | A/G | G | 0.675 | 6 | 28680985 | 0.00010616 | -11.34 | 8.6E-30 | -29.0653 | ENST00000377186 | | A_G | A | G | A | G | negative |
| rs11257555 | 100305260_TGI_at | A/C | C | 0.483 | 10 | 12217424 | 0.00010851 | 6.143 | 8.1E-10 | -9.0916 | CR607709 | SEC61A2 | A_C | A | C | A | C | positive |
| rs826039 | 100145368_TGI_at | A/G | G | 0.525 | 11 | 73460613 | 0.00010916 | -4.974 | 6.56E-07 | -6.1832 | BC035599 | C2CD3 | G_A | A | G | G | A | negative |
| rs7251154 | 100141551_TGI_at | A/G | G | 0.612 | 19 | 46997781 | 0.00011202 | -4.192 | 2.77E-05 | -4.5583 | NM_001817 | CEACAM4 | A_G | A | G | A | G | negative |
| rs710789 | 100303765_TGI_at | C/T | T | 0.617 | 12 | 68190618 | 0.00011273 | 5.199 | 2E-07 | -6.6982 | M21119 | LYZ | C_T | C | T | C | T | positive |
| rs3131038 | 100139688_TGI_at | A/G | G | 0.742 | 6 | 30842059 | 0.00011297 | 9.808 | 1.04E-22 | -21.9829 | AK055657 | HCG18 | A_G | A | G | A | G | positive |
| rs3131038 | 100308127_TGI_at | A/G | G | 0.742 | 6 | 30842059 | 0.00011297 | 9.661 | 4.42E-22 | -21.355 | BG746649 | HCG18 | A_G | A | G | A | G | positive |
| rs1942055 | 100133530_TGI_at | C/G | G | 0.508 | 2 | 135215394 | 0.00011828 | 4.869 | 1.12E-06 | -5.9501 | NM_032143 | ZRANB3 | C_G | C | G | C | G | negative |
| rs12569964 | 100303975_TGI_at | C/T | T | 0.483 | 10 | 12213610 | 0.00012057 | -10.02 | 1.21E-23 | -22.918 | ENST00000378952 | NUDT5 | C_T | C | T | C | T | negative |
| rs12569964 | 100154198_TGI_at | C/T | T | 0.483 | 10 | 12213610 | 0.00012057 | -9.972 | 2.02E-23 | -22.6944 | NM_014142 | NUDT5 | C_T | C | T | C | T | negative |
| rs12569964 | 100129724_TGI_at | C/T | T | 0.483 | 10 | 12213610 | 0.00012057 | 9.101 | 8.95E-20 | -19.0482 | NM_018144 | SEC61A2 | C_T | C | T | C | T | positive |
| rs17034954 | 100152575_TGI_at | C/T | T | 0.042 | 2 | 68180003 | 0.00012059 | -9.478 | 2.59E-21 | -20.5864 | BI462997 | | T_C | C | T | T | C | positive |
| rs17034954 | 100162510_TGI_at | C/T | T | 0.042 | 2 | 68180003 | 0.00012059 | -7.123 | 1.06E-12 | -11.9763 | NM_006333 | | T_C | C | T | T | C | positive |
| rs7308243 | 100303765_TGI_at | A/G | G | 0.381 | 12 | 68176103 | 0.00012836 | 5.199 | 2E-07 | -6.6982 | M21119 | LYZ | G_A | A | G | G | A | positive |
| rs1708678 | 100151676_TGI_at | A/G | G | 0.642 | 4 | 90195490 | 0.00013375 | 6.966 | 3.26E-12 | -11.4867 | AA993242 | | A_G | A | G | A | G | positive |
| rs2046071 | 100301598_TGI_at | A/G | G | 0.533 | 15 | 81304105 | 0.00013535 | 4.498 | 6.86E-06 | -5.1637 | NM_031452 | FAM103A1 | G_A | A | G | G | A | positive |
| rs12150048 | 100304816_TGI_at | C/G | G | 0.789 | 17 | 41183242 | 0.00013738 | -4.802 | 1.57E-06 | -5.8039 | DB041795 | LRRC37A | C_G | C | G | C | G | negative |
| rs12150048 | 100312557_TGI_at | C/G | G | 0.789 | 17 | 41183242 | 0.00013738 | -4.605 | 4.12E-06 | -5.3846 | AI690186 | ARL17P1 | C_G | C | G | C | G | negative |
| rs12230584 | 100303765_TGI_at | A/G | G | 0.646 | 12 | 68174084 | 0.0001378 | 5.199 | 2E-07 | -6.6982 | M21119 | LYZ | A_G | A | G | A | G | positive |
| rs10784784 | 100303765_TGI_at | C/T | T | 0.617 | 12 | 68166150 | 0.00013883 | 5.199 | 2E-07 | -6.6982 | M21119 | LYZ | C_T | C | T | C | T | positive |
| rs3130934 | 100131217_TGI_at | A/C | C | 0.596 | 6 | 31236531 | 0.00014213 | -4.114 | 3.89E-05 | -4.4102 | AK056160 | HCG18 | C_A | A | C | C | A | negative |
| rs9283891 | 100305324_TGI_at | A/G | G | 0.845 | 6 | 31496209 | 0.00014467 | 15.066 | 2.71E-51 | -50.567 | CN480851 | | A_G | A | G | A | G | negative |
| rs9283891 | 100304001_TGI_at | A/G | G | 0.845 | 6 | 31496209 | 0.00014467 | 14.799 | 1.49E-49 | -48.8278 | ENST00000376222 | | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs9896052 | 100140717_TGI_at | A/C | C | 0.683 | 17 | 70930457 | 0.00015845 | 9.378 | 6.72E-21 | -20.1724 | AK091010 | GRB2 | A_C | A | C | A | C | negative |
| rs9896052 | 100304907_TGI_at | A/C | C | 0.683 | 17 | 70930457 | 0.00015845 | 8.982 | 2.66E-19 | -18.5753 | DA646246 | GRB2 | A_C | A | C | A | C | negative |
| rs9896052 | 100158391_TGI_at | A/C | C | 0.683 | 17 | 70930457 | 0.00015845 | -5.261 | 1.43E-07 | -6.8438 | NM_014595 | NT5C | A_C | A | C | A | C | positive |
| rs9896052 | 100143655_TGI_at | A/C | C | 0.683 | 17 | 70930457 | 0.00015845 | -4.325 | 1.53E-05 | -4.8166 | NM_024844 | NUP85 | A_C | A | C | A | C | positive |
| rs11590781 | 100151793_TGI_at | C/T | T | 0.904 | 1 | 219995825 | 0.0001634 | -4.82 | 1.44E-06 | -5.843 | BX114699 | | C_T | C | T | C | T | positive |
| rs8042238 | 100129239_TGI_at | C/T | T | 0.638 | 15 | 76561326 | 0.00016609 | 4.365 | 1.27E-05 | -4.8958 | AW118658 | IREB2 | C_T | C | T | C | T | negative |
| rs2844645 | 100159175_TGI_at | A/G | G | 0.467 | 6 | 31123161 | 0.0001689 | -10.56 | 4.66E-26 | -25.3312 | NM_001010909 | MUC21 | A_G | A | G | A | G | negative |
| rs2844645 | 100309111_TGI_at | A/G | G | 0.467 | 6 | 31123161 | 0.0001689 | -9.211 | 3.23E-20 | -19.4907 | BC105735 | MUC21 | A_G | A | G | A | G | negative |
| rs6819993 | 100149386_TGI_at | A/G | G | 0.8 | 4 | 119558277 | 0.00017183 | 4.534 | 5.79E-06 | -5.2375 | ACA24 | SNORA24 | A_G | A | G | A | G | positive |
| rs799237 | 100155445_TGI_at | C/T | T | 0.6 | 7 | 27092792 | 0.00017217 | -5.981 | 2.22E-09 | -8.6541 | BC031342 | | C_T | C | T | C | T | positive |
| rs799237 | 100308581_TGI_at | C/T | T | 0.6 | 7 | 27092792 | 0.00017217 | -5.717 | 1.08E-08 | -7.9649 | BF593636 | | C_T | C | T | C | T | positive |
| rs799237 | 100160131_TGI_at | C/T | T | 0.6 | 7 | 27092792 | 0.00017217 | -4.122 | 3.76E-05 | -4.4253 | AK022839 | | C_T | C | T | C | T | positive |
| rs3129975 | 100139688_TGI_at | C/T | T | 0.742 | 6 | 30840033 | 0.00017238 | 9.808 | 1.04E-22 | -21.9829 | AK055657 | HCG18 | C_T | C | T | C | T | positive |
| rs3129975 | 100308127_TGI_at | C/T | T | 0.742 | 6 | 30840033 | 0.00017238 | 9.661 | 4.42E-22 | -21.355 | BG746649 | HCG18 | C_T | C | T | C | T | positive |
| rs2734983 | 100309580_TGI_at | A/T | T | 0.824 | 6 | 29928930 | 0.00017723 | -20.08 | 1.06E-89 | -88.9745 | BC035659 | | A_T | A | T | A | T | negative |
| rs2517866 | 100309580_TGI_at | C/T | T | 0.208 | 6 | 29929011 | 0.00017851 | -20.08 | 1.06E-89 | -88.9745 | BC035659 | | T_C | C | T | T | C | negative |
| rs2517866 | 100303756_TGI_at | C/T | T | 0.208 | 6 | 29929011 | 0.00017851 | -10.57 | 4.19E-26 | -25.3774 | M27539 | HLA-A | T_C | C | T | T | C | negative |
| rs3094127 | 100300978_TGI_at | A/G | G | 0.192 | 6 | 30805426 | 0.00017891 | -10.88 | 1.37E-27 | -26.862 | NM_178014 | TUBB | G_A | A | G | G | A | negative |
| rs929615 | 100304233_TGI_at | G/T | T | 0.783 | 12 | 9793766 | 0.00018214 | -5.988 | 2.12E-09 | -8.6728 | ENST00000290855 | CLEC2D | G_T | G | T | G | T | negative |
| rs1050025 | 100309376_TGI_at | C/T | T | 0.217 | 17 | 43503154 | 0.00019238 | -4.622 | 3.8E-06 | -5.4202 | BC052601 | MRPL10 | T_C | C | T | T | C | positive |
| rs701320 | 100158468_TGI_at | A/G | G | 0.161 | 7 | 83444454 | 0.00019863 | -6.542 | 6.07E-11 | -10.2168 | NM_006080 | SEMA3A | G_A | A | G | G | A | positive |
| rs3756208 | 100148345_TGI_at | A/G | G | 0.342 | 4 | 24742767 | 0.00020002 | -5.196 | 2.04E-07 | -6.6912 | AK095450 | | A_G | A | G | A | G | positive |
| rs9483768 | 100133258_TGI_at | A/C | C | 0.19 | 6 | 135240980 | 0.00020582 | -5.087 | 3.64E-07 | -6.4392 | ENST00000367826 | HBS1L | A_C | A | C | A | C | positive |
| rs10500284 | 100127522_TGI_at | A/T | T | 0.408 | 19 | 47046784 | 0.00020907 | -5.125 | 2.98E-07 | -6.5265 | NM_001022 | RPS19 | T_A | A | T | T | A | negative |
| rs10500284 | 100314018_TGI_at | A/T | T | 0.408 | 19 | 47046784 | 0.00020907 | -4.839 | 1.3E-06 | -5.8844 | AA040468 | RPS19 | T_A | A | T | T | A | negative |
| rs9258636 | 100309580_TGI_at | C/T | T | 0.193 | 6 | 29929816 | 0.00021101 | -20.08 | 1.06E-89 | -88.9745 | BC035659 | | T_C | C | T | T | C | negative |
| rs9258636 | 100303756_TGI_at | C/T | T | 0.193 | 6 | 29929816 | 0.00021101 | -10.57 | 4.19E-26 | -25.3774 | M27539 | HLA-A | T_C | C | T | T | C | negative |
| rs2292217 | 100130519_TGI_at | C/T | T | 0.458 | 12 | 50151246 | 0.00021109 | -6.796 | 1.08E-11 | -10.9683 | NM_004858 | SLC4A8 | C_T | C | T | C | T | positive |
| rs3094121 | 100139688_TGI_at | C/T | T | 0.258 | 6 | 30838939 | 0.00021627 | 9.808 | 1.04E-22 | -21.9829 | AK055657 | HCG18 | T_C | C | T | T | C | positive |
| rs3094121 | 100308127_TGI_at | C/T | T | 0.258 | 6 | 30838939 | 0.00021627 | 9.661 | 4.42E-22 | -21.355 | BG746649 | HCG18 | T_C | C | T | T | C | positive |
| rs9475714 | 100138535_TGI_at | A/G | G | 0.325 | 6 | 56497033 | 0.0002178 | 4.113 | 3.91E-05 | -4.4083 | BG251250 | DST | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs1264702 | 100304197_TGI_at | C/T | T | 0.758 | 6 | 30173554 | 0.00022391 | -10.01 | 1.32E-23 | -22.8785 | ENST00000318669 | | T_C | C | T | T | C | positive |
| rs11882587 | 100310092_TGI_at | A/G | G | 0.422 | 19 | 4303959 | 0.00022622 | -5.45 | 5.04E-08 | -7.2978 | BC008288 | UBXN6 | A_G | A | G | A | G | negative |
| rs11133403 | 100147633_TGI_at | C/T | T | 0.647 | 4 | 56170870 | 0.00022865 | -15.17 | 6.03E-52 | -51.2197 | NM_004898 | CLOCK | C_T | C | T | C | T | negative |
| rs11133403 | 100130701_TGI_at | C/T | T | 0.647 | 4 | 56170870 | 0.00022865 | -4.611 | 4.01E-06 | -5.3971 | BC002480 | SRD5A3 | C_T | C | T | C | T | negative |
| rs12593522 | 100138194_TGI_at | A/G | G | 0.847 | 15 | 98008093 | 0.00023065 | -9.275 | 1.78E-20 | -19.7505 | NM_152449 | LYSMD4 | A_G | A | G | A | G | positive |
| rs6938343 | 100149189_TGI_at | C/T | T | 0.276 | 6 | 56337596 | 0.0002348 | 5.151 | 2.59E-07 | -6.5865 | NM_030820 | COL21A1 | C_T | C | T | C | T | positive |
| rs6813853 | 100149386_TGI_at | C/T | T | 0.2 | 4 | 119551778 | 0.00023519 | 4.534 | 5.79E-06 | -5.2375 | ACA24 | SNORA24 | T_C | C | T | T | C | positive |
| rs6811485 | 100149386_TGI_at | A/G | G | 0.2 | 4 | 119556711 | 0.0002375 | -4.534 | 5.79E-06 | -5.2375 | ACA24 | SNORA24 | A_G | A | G | A | G | positive |
| rs7687884 | 100149386_TGI_at | C/T | T | 0.2 | 4 | 119554403 | 0.00023831 | 4.534 | 5.79E-06 | -5.2375 | ACA24 | SNORA24 | T_C | C | T | T | C | positive |
| rs11134779 | 100132327_TGI_at | A/G | G | 0.308 | 5 | 156869344 | 0.00023964 | -4.591 | 4.41E-06 | -5.3554 | NM_033274 | ADAM19 | G_A | A | G | G | A | negative |
| rs1422795 | 100132327_TGI_at | C/T | T | 0.692 | 5 | 156868942 | 0.00024052 | 4.591 | 4.41E-06 | -5.3554 | NM_033274 | ADAM19 | T_C | C | T | T | C | negative |
| rs7613814 | 100301782_TGI_at | C/T | T | 0.583 | 3 | 159768797 | 0.00024351 | 10.639 | 1.96E-26 | -25.7072 | NM_022443 | MLF1 | C_T | C | T | C | T | negative |
| rs7613814 | 100304858_TGI_at | C/T | T | 0.583 | 3 | 159768797 | 0.00024351 | 8.833 | 1.02E-18 | -17.9918 | DA823417 | MLF1 | C_T | C | T | C | T | negative |
| rs7613814 | 100123606_TGI_at | C/T | T | 0.583 | 3 | 159768797 | 0.00024351 | 7.228 | 4.9E-13 | -12.3097 | DB449779 | MLF1 | C_T | C | T | C | T | negative |
| rs7613814 | 100312821_TGI_at | C/T | T | 0.583 | 3 | 159768797 | 0.00024351 | 5.876 | 4.2E-09 | -8.3764 | AI220091 | MLF1 | C_T | C | T | C | T | negative |
| rs1035091 | 100307638_TGI_at | A/T | T | 0.658 | 4 | 24760972 | 0.00024382 | -9.321 | 1.15E-20 | -19.9384 | BM719344 | | T_A | A | T | T | A | positive |
| rs2668628 | 100310659_TGI_at | A/G | G | 0.814 | 17 | 41709662 | 0.00024418 | -44.08 | 0 | -423.593 | AW138870 | | A_G | A | G | A | G | negative |
| rs2668628 | 100133629_TGI_at | A/G | G | 0.814 | 17 | 41709662 | 0.00024418 | -38.82 | 0 | -328.994 | HSS00009365 | | A_G | A | G | A | G | negative |
| rs2668628 | 100134593_TGI_at | A/G | G | 0.814 | 17 | 41709662 | 0.00024418 | -44.52 | 0 | -432.043 | BC066350 | | A_G | A | G | A | G | negative |
| rs2668628 | 100160728_TGI_at | A/G | G | 0.814 | 17 | 41709662 | 0.00024418 | -33.44 | 4E-245 | -244.4 | H23006 | KIAA1267 | A_G | A | G | A | G | negative |
| rs7315029 | 100311305_TGI_at | A/G | G | 0.617 | 12 | 26871782 | 0.00024805 | -5.487 | 4.09E-08 | -7.3885 | AL117608 | FGFR1OP2 | A_G | A | G | A | G | negative |
| rs418914 | 100303991_TGI_at | A/G | G | 0.292 | 6 | 28676507 | 0.00024974 | 14.142 | 2.09E-45 | -44.6793 | ENST00000377186 | | A_G | A | G | A | G | negative |
| rs12716849 | 100161847_TGI_at | A/G | G | 0.433 | 16 | 76725191 | 0.00025349 | 7.793 | 6.54E-15 | -14.1842 | BQ573975 | | A_G | A | G | A | G | positive |
| rs12716849 | 100151362_TGI_at | A/G | G | 0.433 | 16 | 76725191 | 0.00025349 | 4.818 | 1.45E-06 | -5.8386 | H52699 | | A_G | A | G | A | G | positive |
| rs10866659 | 100132327_TGI_at | A/G | G | 0.304 | 5 | 156869621 | 0.00025551 | -4.591 | 4.41E-06 | -5.3554 | NM_033274 | ADAM19 | G_A | A | G | G | A | negative |
| rs10902553 | 100155121_TGI_at | A/G | G | 0.038 | 15 | 98237023 | 0.00025773 | 9.441 | 3.69E-21 | -20.4327 | AK127420 | | G_A | A | G | G | A | negative |
| rs2216386 | 100147399_TGI_at | A/G | G | 0.192 | 3 | 186448393 | 0.00025918 | 5.055 | 4.3E-07 | -6.3661 | NM_001966 | EHHADH | G_A | A | G | G | A | positive |
| rs1913575 | 100149386_TGI_at | C/T | T | 0.793 | 4 | 119554577 | 0.00026675 | 4.534 | 5.79E-06 | -5.2375 | ACA24 | SNORA24 | C_T | C | T | C | T | positive |
| rs7521898 | 100135055_TGI_at | A/G | G | 0.65 | 1 | 148974220 | 0.00026759 | -8.84 | 9.57E-19 | -18.019 | NM_032132 | HORMAD1 | A_G | A | G | A | G | positive |
| rs7511673 | 100135055_TGI_at | A/T | T | 0.35 | 1 | 148974260 | 0.00026812 | -8.84 | 9.57E-19 | -18.019 | NM_032132 | HORMAD1 | T_A | A | T | T | A | positive |
| rs2324142 | 100158126_TGI_at | A/C | C | 0.483 | 17 | 15982031 | 0.00027206 | 6.48 | 9.17E-11 | -10.0375 | NM_004278 | PIGL | A_C | A | C | A | C | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs1317850 | 100305428_TGI_at | C/T | T | 0.267 | 17 | 43476838 | 0.00027558 | -6.258 | 3.9E-10 | -9.409 | CK004660 | | T_C | C | T | T | C | negative |
| rs10898954 | 100156557_TGI_at | C/T | T | 0.467 | 11 | 73467891 | 0.00027597 | 5.038 | 4.7E-07 | -6.3275 | NM_173582 | PGM2L1 | C_T | C | T | C | T | positive |
| rs7197 | 100302940_TGI_at | C/T | T | 0.283 | 6 | 32520558 | 0.00028309 | -18.55 | 8.31E-77 | -76.0805 | NM_002125 | HLA-DRB5 | T_C | C | T | T | C | positive |
| rs7197 | 100311684_TGI_at | C/T | T | 0.283 | 6 | 32520558 | 0.00028309 | -10.33 | 5.05E-25 | -24.2967 | AK098007 | HLA-DQB2 | T_C | C | T | T | C | positive |
| rs7197 | 100304704_TGI_at | C/T | T | 0.283 | 6 | 32520558 | 0.00028309 | 4.963 | 6.94E-07 | -6.1586 | DB344086 | | T_C | C | T | T | C | negative |
| rs7197 | 100161625_TGI_at | C/T | T | 0.283 | 6 | 32520558 | 0.00028309 | 4.73 | 2.25E-06 | -5.6487 | NM_000063 | C2 | T_C | C | T | T | C | negative |
| rs2303644 | 100306708_TGI_at | A/G | G | 0.608 | 5 | 178487651 | 0.00028511 | 4.15 | 3.33E-05 | -4.4782 | BU733456 | | A_G | A | G | A | G | positive |
| rs7312624 | 100309845_TGI_at | A/G | G | 0.225 | 12 | 9787906 | 0.00028519 | 6.946 | 3.76E-12 | -11.4251 | BC019883 | CLEC2D | A_G | A | G | A | G | negative |
| rs7312624 | 100303868_TGI_at | A/G | G | 0.225 | 12 | 9787906 | 0.00028519 | -6.501 | 7.98E-11 | -10.0981 | H17596 | CLEC2D | A_G | A | G | A | G | positive |
| rs10078178 | 100132327_TGI_at | A/T | T | 0.295 | 5 | 156865562 | 0.0002871 | -4.591 | 4.41E-06 | -5.3554 | NM_033274 | ADAM19 | T_A | A | T | T | A | negative |
| rs1611701 | 100309580_TGI_at | C/T | T | 0.203 | 6 | 29935935 | 0.00028972 | -20.08 | 1.06E-89 | -88.9745 | BC035659 | | T_C | C | T | T | C | negative |
| rs1611701 | 100303756_TGI_at | C/T | T | 0.203 | 6 | 29935935 | 0.00028972 | -10.57 | 4.19E-26 | -25.3774 | M27539 | HLA-A | T_C | C | T | T | C | negative |
| rs9392029 | 100139548_TGI_at | C/T | T | 0.083 | 6 | 419252 | 0.00029052 | -7.506 | 6.1E-14 | -13.2149 | AK056564 | EXOC2 | T_C | C | T | T | C | positive |
| rs12456881 | 100129585_TGI_at | C/T | T | 0.242 | 18 | 55328175 | 0.00029089 | -6.043 | 1.51E-09 | -8.8202 | BC046645 | CCBE1 | T_C | C | T | T | C | positive |
| rs12456881 | 100136733_TGI_at | C/T | T | 0.242 | 18 | 55328175 | 0.00029089 | -5.228 | 1.71E-07 | -6.7661 | NM_133459 | CCBE1 | T_C | C | T | T | C | positive |
| rs12456881 | 100129234_TGI_at | C/T | T | 0.242 | 18 | 55328175 | 0.00029089 | -4.829 | 1.37E-06 | -5.8626 | AI822141 | CCBE1 | T_C | C | T | T | C | positive |
| rs8365 | 100158927_TGI_at | C/G | G | 0.831 | 6 | 32256381 | 0.00029327 | -8.348 | 6.94E-17 | -16.1585 | NM_006913 | RNF5 | C_G | C | G | C | G | negative |
| rs12051 | 100129691_TGI_at | A/G | G | 0.375 | 17 | 43458759 | 0.000298 | 5.106 | 3.29E-07 | -6.4827 | NM_018129 | PNPO | G_A | A | G | G | A | negative |
| rs7299039 | 100124630_TGI_at | A/G | G | 0.389 | 12 | 28498283 | 0.00029963 | 4.258 | 2.06E-05 | -4.6856 | NM_018318 | CCDC91 | G_A | A | G | G | A | positive |
| rs2275235 | 100302368_TGI_at | A/G | G | 0.325 | 1 | 148996903 | 0.00030713 | -9.618 | 6.71E-22 | -21.1731 | NM_013384 | LASS2 | G_A | A | G | G | A | positive |
| rs2275235 | 100151271_TGI_at | A/G | G | 0.325 | 1 | 148996903 | 0.00030713 | -8.523 | 1.55E-17 | -16.8083 | NM_181746 | LASS2 | G_A | A | G | G | A | positive |
| rs3095320 | 100303039_TGI_at | A/G | G | 0.305 | 6 | 31195913 | 0.00030753 | -32.82 | 3.1E-236 | -235.515 | NM_001264 | CDSN | G_A | A | G | G | A | positive |
| rs3095320 | 100121628_TGI_at | A/G | G | 0.305 | 6 | 31195913 | 0.00030753 | 18.412 | 1.05E-75 | -74.9777 | NM_014068 | PSORS1C1 | G_A | A | G | G | A | negative |
| rs2239523 | 100303039_TGI_at | C/G | G | 0.688 | 6 | 31197486 | 0.00030981 | 32.82 | 3.1E-236 | -235.515 | NM_001264 | CDSN | G_C | C | G | G | C | positive |
| rs2239523 | 100121628_TGI_at | C/G | G | 0.688 | 6 | 31197486 | 0.00030981 | -18.41 | 1.05E-75 | -74.9777 | NM_014068 | PSORS1C1 | G_C | C | G | G | C | negative |
| rs2277027 | 100132327_TGI_at | A/C | C | 0.308 | 5 | 156864954 | 0.00030983 | 4.591 | 4.41E-06 | -5.3554 | NM_033274 | ADAM19 | A_C | A | C | A | C | negative |
| rs12649925 | 100307345_TGI_at | C/T | T | 0.643 | 4 | 56173264 | 0.00031203 | -7.183 | 6.82E-13 | -12.1662 | BQ013439 | CLOCK | T_C | C | T | T | C | positive |
| rs2160812 | 100147399_TGI_at | A/G | G | 0.808 | 3 | 186443803 | 0.00031285 | 5.055 | 4.3E-07 | -6.3661 | NM_001966 | EHHADH | A_G | A | G | A | G | positive |
| rs7305599 | 100150083_TGI_at | A/G | G | 0.56 | 12 | 50187657 | 0.00031429 | 4.275 | 1.91E-05 | -4.7187 | NM_007210 | GALNT6 | A_G | A | G | A | G | positive |
| rs11683643 | 100143280_TGI_at | A/G | G | 0.692 | 2 | 48718796 | 0.00031527 | -7.651 | 1.99E-14 | -13.7002 | AL049443 | | A_G | A | G | A | G | positive |
| rs8064802 | 100124262_TGI_at | C/T | T | 0.679 | 17 | 41618273 | 0.00031548 | -6.552 | 5.68E-11 | -10.2459 | AK057167 | | C_T | C | T | C | T | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8064802 | 100161122_TGI_at | C/T | T | 0.679 | 17 | 41618273 | 0.00031548 | -4.939 | 7.85E-07 | -6.105 | AF035297 | | C_T | C | T | C | T | positive |
| rs1052708 | 100305949_TGI_at | A/G | G | 0.05 | 10 | 16593361 | 0.00031654 | -13.02 | 9.54E-39 | -38.0204 | BX648556 | PTER | A_G | A | G | A | G | positive |
| rs1052708 | 100124216_TGI_at | A/G | G | 0.05 | 10 | 16593361 | 0.00031654 | -12.57 | 3.13E-36 | -35.5049 | NM_030664 | PTER | A_G | A | G | A | G | positive |
| rs1052708 | 100123512_TGI_at | A/G | G | 0.05 | 10 | 16593361 | 0.00031654 | 8.135 | 4.12E-16 | -15.3852 | NM_001010908 | C1QL3 | A_G | A | G | A | G | negative |
| rs1052708 | 100132235_TGI_at | A/G | G | 0.05 | 10 | 16593361 | 0.00031654 | 4.883 | 1.04E-06 | -5.981 | AK095486 | PTER | A_G | A | G | A | G | negative |
| rs199513 | 100138516_TGI_at | A/G | G | 0.898 | 17 | 42212095 | 0.00031826 | -10.89 | 1.34E-27 | -26.8716 | BC114219 | WNT3 | A_G | A | G | A | G | negative |
| rs6683015 | 100138305_TGI_at | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | 26.875 | 4.3E-159 | -158.366 | NM_178426 | ARNT | T_G | G | T | T | G | positive |
| rs6683015 | 100309723_TGI_at | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | -9.731 | 2.22E-22 | -21.6529 | BC028362 | ARNT | T_G | G | T | T | G | negative |
| rs6683015 | 100310890_TGI_at | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | 8.15 | 3.64E-16 | -15.439 | AL834279 | ARNT | T_G | G | T | T | G | positive |
| rs6683015 | 100313509_TGI_at | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | -6.602 | 4.06E-11 | -10.3919 | AB037811 | FAM63A | T_G | G | T | T | G | negative |
| rs1655921 | 100129349_TGI_at | C/T | T | 0.157 | 6 | 30016168 | 0.00032577 | 19.67 | 3.9E-86 | -85.4092 | NM_002116 | HLA-A | T_C | C | T | T | C | positive |
| rs1655921 | 100160221_TGI_at | C/T | T | 0.157 | 6 | 30016168 | 0.00032577 | 12.286 | 1.08E-34 | -33.9678 | NM_002127 | HLA-G | T_C | C | T | T | C | positive |
| rs1736922 | 100311825_TGI_at | C/T | T | 0.33 | 6 | 29801948 | 0.00032792 | -7.821 | 5.24E-15 | -14.2806 | AK092748 | RP3-377H14.5 | T_C | C | T | T | C | negative |
| rs1736922 | 100303129_TGI_at | C/T | T | 0.33 | 6 | 29801948 | 0.00032792 | -4.186 | 2.84E-05 | -4.5468 | NM_001098479 | HLA-F | T_C | C | T | T | C | negative |
| rs3764919 | 100147399_TGI_at | G/T | T | 0.192 | 3 | 186449252 | 0.00032998 | 5.055 | 4.3E-07 | -6.3661 | NM_001966 | EHHADH | T_G | G | T | T | G | positive |
| rs3094014 | 100302942_TGI_at | A/G | G | 0.817 | 6 | 31541537 | 0.00033158 | -4.996 | 5.85E-07 | -6.2326 | NM_002117 | HLA-C | G_A | A | G | G | A | positive |
| rs11191822 | 100135728_TGI_at | G/T | T | 0.679 | 10 | 105589760 | 0.00033166 | -4.413 | 1.02E-05 | -4.9916 | AK024150 | | G_T | G | T | G | T | negative |
| rs11205383 | 100309243_TGI_at | C/T | T | 0.759 | 1 | 148722437 | 0.00033226 | 4.272 | 1.94E-05 | -4.7128 | BC069280 | | C_T | C | T | C | T | positive |
| rs1724422 | 100133349_TGI_at | A/G | G | 0.392 | 17 | 41133096 | 0.00033584 | 4.167 | 3.09E-05 | -4.5106 | NM_199282 | ARHGAP27 | A_G | A | G | A | G | negative |
| rs6655975 | 100144443_TGI_at | A/G | G | 0.7 | 1 | 148808752 | 0.00033626 | 6.493 | 8.41E-11 | -10.075 | BC038543 | | A_G | A | G | A | G | negative |
| rs2696501 | 100146746_TGI_at | G/T | T | 0.181 | 17 | 41719662 | 0.00033865 | -30.79 | 3.7E-208 | -207.434 | U51706 | | T_G | G | T | T | G | negative |
| rs11231181 | 100135147_TGI_at | A/G | G | 0.742 | 11 | 62190749 | 0.00033886 | -7.795 | 6.44E-15 | -14.1911 | NM_030628 | INTS5 | A_G | A | G | A | G | positive |
| rs11231181 | 100153773_TGI_at | A/G | G | 0.742 | 11 | 62190749 | 0.00033886 | 5.45 | 5.04E-08 | -7.2978 | NM_001085372 | C11orf83 | A_G | A | G | A | G | negative |
| rs9379856 | 100161253_TGI_at | A/C | C | 0.136 | 6 | 26474815 | 0.00033947 | -27.02 | 9.6E-161 | -160.018 | NM_007047 | BTN3A2 | A_C | A | C | A | C | positive |
| rs4489748 | 100122809_TGI_at | C/T | T | 0.742 | 11 | 62189391 | 0.00034313 | 9.984 | 1.79E-23 | -22.7469 | NM_000327 | ROM1 | C_T | C | T | C | T | negative |
| rs10517061 | 100130614_TGI_at | A/T | T | 0.5 | 4 | 24787395 | 0.00034472 | 6.41 | 1.46E-10 | -9.8371 | NM_013367 | ANAPC4 | T_A | A | T | T | A | negative |
| rs7120836 | 100124148_TGI_at | A/G | G | 0.217 | 11 | 3798039 | 0.00034599 | -4.673 | 2.97E-06 | -5.5275 | NM_014489 | | A_G | A | G | A | G | negative |
| rs1264698 | 100141210_TGI_at | A/C | C | 0.242 | 6 | 30175156 | 0.0003472 | 9.305 | 1.34E-20 | -19.8729 | ENST00000318669 | | C_A | A | C | C | A | positive |
| rs2279408 | 100159519_TGI_at | A/G | G | 0.259 | 16 | 4598585 | 0.00034988 | -4.479 | 7.5E-06 | -5.125 | DQ167023 | C16orf5 | A_G | A | G | A | G | negative |
| rs1264697 | 100141210_TGI_at | C/G | G | 0.246 | 6 | 30175547 | 0.00035057 | 9.305 | 1.34E-20 | -19.8729 | ENST00000318669 | | G_C | C | G | G | C | positive |
| rs518442 | 100304943_TGI_at | C/T | T | 0.125 | 18 | 30972885 | 0.00035464 | 5.187 | 2.14E-07 | -6.6702 | DA493437 | ZNF271 | T_C | C | T | T | C | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3130349 | 100158927_ TGI_at | A/G | G | 0.833 | 6 | 32255674 | 0.00035568 | -8.348 | 6.94E-17 | -16.1585 | NM_006913 | RNF5 | A_G | A | G | A | G | negative |
| rs10792356 | 100155082_ TGI_at | C/G | G | 0.267 | 11 | 62197399 | 0.00036166 | -15.54 | 1.89E-54 | -53.7237 | NM_032667 | BSCL2 | C_G | C | G | C | G | negative |
| rs537145 | 100161482_ TGI_at | G/T | T | 0.167 | 18 | 30918852 | 0.00036318 | 4.841 | 1.29E-06 | -5.8888 | NM_014268 | MAPRE2 | G_T | G | T | G | T | positive |
| rs3862206 | 100129463_ TGI_at | G/T | T | 0.76 | 1 | 148682255 | 0.00036417 | 7.706 | 1.3E-14 | -13.8866 | ENST000003 69069 | RPRD2 | T_G | G | T | T | G | negative |
| rs2289469 | 100158135_ TGI_at | A/G | G | 0.831 | 2 | 134930512 | 0.00036745 | -5.554 | 2.79E-08 | -7.5541 | NM_030923 | TMEM163 | A_G | A | G | A | G | positive |
| rs12113381 | 100304931_ TGI_at | C/T | T | 0.102 | 7 | 1109653 | 0.00037104 | -5.685 | 1.31E-08 | -7.8834 | DA547158 | | C_T | C | T | C | T | positive |
| rs12113381 | 100151722_ TGI_at | C/T | T | 0.102 | 7 | 1109653 | 0.00037104 | -4.524 | 6.07E-06 | -5.2169 | NM_182491 | ZFAND2A | C_T | C | T | C | T | positive |
| rs3099840 | 100142285_ TGI_at | A/G | G | 0.183 | 6 | 31538700 | 0.00037313 | 4.022 | 5.77E-05 | -4.2388 | ENST000003 76255 | TCF19 | A_G | A | G | A | G | negative |
| rs2333452 | 100151178_ TGI_at | A/G | G | 0.75 | 4 | 177525930 | 0.00037383 | 6.288 | 3.22E-10 | -9.4927 | AK096223 | | A_G | A | G | A | G | positive |
| rs882520 | 100124297_ TGI_at | A/T | T | 0.533 | 19 | 47081120 | 0.00038556 | -7.155 | 8.37E-13 | -12.0774 | NM_006423 | RABAC1 | A_T | A | T | A | T | negative |
| rs882520 | 100306969_ TGI_at | A/T | T | 0.533 | 19 | 47081120 | 0.00038556 | -6.923 | 4.42E-12 | -11.3544 | BT019964 | RABAC1 | A_T | A | T | A | T | negative |
| rs4958097 | 100143365_ TGI_at | A/T | T | 0.169 | 5 | 133062094 | 0.00039339 | -6.416 | 1.4E-10 | -9.8542 | BX640845 | FSTL4 | T_A | A | T | T | A | positive |
| rs4958097 | 100145132_ TGI_at | A/T | T | 0.169 | 5 | 133062094 | 0.00039339 | -5.386 | 7.2E-08 | -7.1424 | NM_015082 | FSTL4 | T_A | A | T | T | A | positive |
| rs3774051 | 100147399_ TGI_at | C/T | T | 0.192 | 3 | 186424419 | 0.00040173 | 5.055 | 4.3E-07 | -6.3661 | NM_001966 | EHHADH | T_C | C | T | T | C | positive |
| rs2523720 | 100132397_ TGI_at | C/T | T | 0.179 | 6 | 30274865 | 0.000408 | -4.176 | 2.97E-05 | -4.5277 | L19688 | | T_C | C | T | T | C | negative |
| rs911552 | 100311425_ TGI_at | A/G | G | 0.297 | 14 | 103069261 | 0.00041008 | -7.831 | 4.84E-15 | -14.3152 | AK225730 | BAG5 | G_A | A | G | G | A | positive |
| rs1558205 | 100140600_ TGI_at | A/C | C | 0.692 | 6 | 28490241 | 0.0004112 | 7.667 | 1.76E-14 | -13.7543 | BC019888 | | A_C | A | C | A | C | positive |
| rs2240071 | 100136412_ TGI_at | C/G | G | 0.233 | 6 | 30178911 | 0.00041872 | 6.124 | 9.13E-10 | -9.0397 | ENST000003 76791 | HLA-G | G_C | C | G | G | C | positive |
| rs12690556 | 100123120_ TGI_at | A/G | G | 0.817 | 3 | 120455706 | 0.00042018 | -7.464 | 8.39E-14 | -13.0761 | BU742963 | | A_G | A | G | A | G | positive |
| rs10852637 | 100312853_ TGI_at | C/T | T | 0.466 | 16 | 3658493 | 0.00042348 | 6.444 | 1.16E-10 | -9.9342 | AI167680 | CLUAP1 | C_T | C | T | C | T | positive |
| rs10852637 | 100152540_ TGI_at | C/T | T | 0.466 | 16 | 3658493 | 0.00042348 | 6.081 | 1.19E-09 | -8.9229 | NM_015041 | CLUAP1 | C_T | C | T | C | T | positive |
| rs10852637 | 100313559_ TGI_at | C/T | T | 0.466 | 16 | 3658493 | 0.00042348 | 5.771 | 7.88E-09 | -8.1035 | AB014543 | CLUAP1 | C_T | C | T | C | T | positive |
| rs10852637 | 100125900_ TGI_at | C/T | T | 0.466 | 16 | 3658493 | 0.00042348 | 4.569 | 4.9E-06 | -5.3098 | NM_178844 | NLRC3 | C_T | C | T | C | T | positive |
| rs3130380 | 100304636_ TGI_at | A/G | G | 0.858 | 6 | 30387109 | 0.00044216 | -4.555 | 5.24E-06 | -5.2808 | DB503443 | FLOT1 | A_G | A | G | A | G | negative |
| rs1050818 | 100144721_ TGI_at | A/C | C | 0.258 | 1 | 148533183 | 0.00044678 | 10.144 | 3.52E-24 | -23.453 | NM_015203 | RPRD2 | A_C | A | C | A | C | negative |
| rs738416 | 100307496_ TGI_at | A/G | G | 0.108 | 22 | 48482509 | 0.00045115 | -6.38 | 1.77E-10 | -9.7518 | BM977889 | C22orf34 | A_G | A | G | A | G | positive |
| rs7542068 | 100307575_ TGI_at | C/G | G | 0.258 | 1 | 148730396 | 0.00046008 | -7.991 | 1.34E-15 | -14.8734 | BM853911 | MRPS21 | G_C | C | G | G | C | negative |
| rs6446257 | 100156808_ TGI_at | C/T | T | 0.692 | 3 | 49228496 | 0.00047061 | 7.371 | 1.69E-13 | -12.7712 | ENST000003 60934 | | C_T | C | T | C | T | positive |
| rs2844796 | 100123483_ TGI_at | A/G | G | 0.754 | 6 | 30180490 | 0.00047664 | 12.764 | 2.6E-37 | -36.5842 | AK056727 | HCG4P6 | G_A | A | G | G | A | negative |
| rs773139 | 100125670_ TGI_at | A/G | G | 0.108 | 9 | 76852819 | 0.00047685 | 6.815 | 9.43E-12 | -11.0257 | NM_017881 | C9orf95 | A_G | A | G | A | G | positive |
| rs9949 | 100136365_ TGI_at | A/G | G | 0.275 | 8 | 9031922 | 0.00047688 | 5.662 | 1.5E-08 | -7.825 | ENST000003 10455 | PPP1R3B | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs7739357 | 100313766_TGI_at | A/G | G | 0.549 | 6 | 32549619 | 0.00047739 | 19.862 | 8.68E-88 | -87.0616 | AA622265 | HLA-DQA2 | A_G | A | G | A | G | negative |
| rs7739357 | 100160430_TGI_at | A/G | G | 0.549 | 6 | 32549619 | 0.00047739 | 15.143 | 8.43E-52 | -51.0743 | L76566 | HLA-DRB6 | A_G | A | G | A | G | negative |
| rs7739357 | 100129037_TGI_at | A/G | G | 0.549 | 6 | 32549619 | 0.00047739 | 4.742 | 2.12E-06 | -5.6744 | NM_018833 | TAP2 | A_G | A | G | A | G | negative |
| rs1264695 | 100304754_TGI_at | A/G | G | 0.242 | 6 | 30175871 | 0.00047782 | 6.4 | 1.55E-10 | -9.8086 | DB311150 | | G_A | A | G | G | A | positive |
| rs1264695 | 100135776_TGI_at | A/G | G | 0.242 | 6 | 30175871 | 0.00047782 | 4.231 | 2.33E-05 | -4.6333 | NM_170769 | RNF39 | G_A | A | G | G | A | positive |
| rs1611738 | 100309580_TGI_at | A/C | C | 0.797 | 6 | 29939685 | 0.00047855 | -20.08 | 1.06E-89 | -88.9745 | BC035659 | | A_C | A | C | A | C | negative |
| rs1611738 | 100303756_TGI_at | A/C | C | 0.797 | 6 | 29939685 | 0.00047855 | -10.57 | 4.19E-26 | -25.3774 | M27539 | HLA-A | A_C | A | C | A | C | negative |
| rs12757613 | 100311695_TGI_at | G/T | T | 0.082 | 1 | 20244374 | 0.00048038 | -9.303 | 1.37E-20 | -19.8647 | AK097693 | PLA2G5 | G_T | G | T | G | T | positive |
| rs12757613 | 100130289_TGI_at | G/T | T | 0.082 | 1 | 20244374 | 0.00048038 | -8.462 | 2.63E-17 | -16.5803 | ENST00000375108 | PLA2G5 | G_T | G | T | G | T | positive |
| rs911554 | 100126588_TGI_at | G/T | T | 0.302 | 14 | 103069124 | 0.00048406 | 5.7 | 1.2E-08 | -7.9215 | AK023145 | BAG5 | T_G | G | T | T | G | negative |
| rs911554 | 100310380_TGI_at | G/T | T | 0.302 | 14 | 103069124 | 0.00048406 | -4.068 | 4.74E-05 | -4.3241 | AY180163 | KLC1 | T_G | G | T | T | G | positive |
| rs4964023 | 100155895_TGI_at | C/T | T | 0.175 | 12 | 26915043 | 0.00048526 | -4.06 | 4.91E-05 | -4.3092 | AI732946 | | C_T | C | T | C | T | negative |
| rs652348 | 100304943_TGI_at | C/T | T | 0.875 | 18 | 30972241 | 0.00049121 | 5.187 | 2.14E-07 | -6.6702 | DA493437 | ZNF271 | C_T | C | T | C | T | negative |
| rs9800013 | 100123914_TGI_at | A/G | G | 0.216 | 5 | 595023 | 0.00049481 | 11.574 | 5.58E-31 | -30.2532 | BC013821 | | A_G | A | G | A | G | negative |
| rs9800013 | 100146413_TGI_at | A/G | G | 0.216 | 5 | 595023 | 0.00049481 | 5.683 | 1.32E-08 | -7.8783 | ENST00000329849 | | A_G | A | G | A | G | negative |
| rs11111134 | 100151519_TGI_at | C/T | T | 0.783 | 12 | 100939387 | 0.00049609 | -9.381 | 6.53E-21 | -20.1848 | NM_016053 | CCDC53 | T_C | C | T | T | C | negative |
| rs650401 | 100142307_TGI_at | C/T | T | 0.442 | 8 | 109266030 | 0.00050532 | -6.553 | 5.64E-11 | -10.2488 | BX094067 | | T_C | C | T | T | C | negative |
| rs686251 | 100142307_TGI_at | A/C | C | 0.558 | 8 | 109268083 | 0.00050593 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | C_A | A | C | C | A | negative |
| rs2212704 | 100142307_TGI_at | C/T | T | 0.441 | 8 | 109267591 | 0.00050745 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | C_T | C | T | C | T | negative |
| rs2251830 | 100129279_TGI_at | A/C | C | 0.543 | 6 | 31124957 | 0.00050848 | 5.719 | 1.07E-08 | -7.97 | AK094433 | HCG22 | A_C | A | C | A | C | positive |
| rs635624 | 100142307_TGI_at | C/G | G | 0.558 | 8 | 109266975 | 0.00050916 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | G_C | C | G | G | C | negative |
| rs597992 | 100142307_TGI_at | A/T | T | 0.442 | 8 | 109262984 | 0.00050921 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_T | A | T | A | T | negative |
| rs595266 | 100142307_TGI_at | A/G | G | 0.442 | 8 | 109262960 | 0.00051269 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_G | A | G | A | G | negative |
| rs651814 | 100142307_TGI_at | A/G | G | 0.442 | 8 | 109265747 | 0.00051333 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_G | A | G | A | G | negative |
| rs1264709 | 100125007_TGI_at | A/T | T | 0.22 | 6 | 30164455 | 0.00051785 | -12.76 | 2.64E-37 | -36.5787 | AF036974 | C6orf12 | T_A | A | T | T | A | negative |
| rs1264709 | 100158228_TGI_at | A/T | T | 0.22 | 6 | 30164455 | 0.00051785 | 5.676 | 1.38E-08 | -7.8605 | NM_170783 | ZNRD1 | T_A | A | T | T | A | positive |
| rs11591349 | 100152029_TGI_at | A/T | T | 0.466 | 10 | 102734321 | 0.00052066 | -8.977 | 2.78E-19 | -18.5556 | NM_176793 | MRPL43 | A_T | A | T | A | T | negative |
| rs11591349 | 100148949_TGI_at | A/T | T | 0.466 | 10 | 102734321 | 0.00052066 | -8.009 | 1.16E-15 | -14.9369 | NM_176792 | MRPL43 | A_T | A | T | A | T | negative |
| rs11591349 | 100134957_TGI_at | A/T | T | 0.466 | 10 | 102734321 | 0.00052066 | 4.844 | 1.27E-06 | -5.8953 | NM_032112 | MRPL43 | A_T | A | T | A | T | positive |
| rs3134940 | 100158927_TGI_at | C/T | T | 0.84 | 6 | 32257794 | 0.00052123 | 8.348 | 6.94E-17 | -16.1585 | NM_006913 | RNF5 | T_C | C | T | T | C | negative |
| rs594405 | 100142307_TGI_at | A/G | G | 0.442 | 8 | 109262783 | 0.00052174 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs9869645 | 100146385_TGI_at | A/G | G | 0.817 | 3 | 120445316 | 0.00052269 | -4.637 | 3.54E-06 | -5.4516 | NM_152538 | IGSF11 | A_G | A | G | A | G | positive |
| rs9869645 | 100157247_TGI_at | A/G | G | 0.817 | 3 | 120445316 | 0.00052269 | 4.021 | 5.8E-05 | -4.2369 | NM_020231 | KTELC1 | A_G | A | G | A | G | negative |
| rs10477360 | 100147290_TGI_at | A/G | G | 0.525 | 5 | 147384474 | 0.0005246 | -5.27 | 1.36E-07 | -6.8651 | NM_001001325 | | A_G | A | G | A | G | positive |
| rs10477360 | 100160780_TGI_at | A/G | G | 0.525 | 5 | 147384474 | 0.0005246 | 4.882 | 1.05E-06 | -5.9787 | NM_006846 | SPINK5 | A_G | A | G | A | G | negative |
| rs688746 | 100142307_TGI_at | A/G | G | 0.558 | 8 | 109294901 | 0.00052461 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | G_A | A | G | G | A | negative |
| rs1668178 | 100142307_TGI_at | A/G | G | 0.442 | 8 | 109260876 | 0.00052604 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_G | A | G | A | G | negative |
| rs6070706 | 100126253_TGI_at | C/T | T | 0.109 | 20 | 57061634 | 0.00053202 | -10.01 | 1.36E-23 | -22.8653 | NM_198976 | TH1L | C_T | C | T | C | T | negative |
| rs6070706 | 100306923_TGI_at | C/T | T | 0.109 | 20 | 57061634 | 0.00053202 | -7.549 | 4.39E-14 | -13.3579 | BU166368 | TH1L | C_T | C | T | C | T | negative |
| rs6070706 | 100130622_TGI_at | C/T | T | 0.109 | 20 | 57061634 | 0.00053202 | -6.108 | 1.01E-09 | -8.9962 | NM_016045 | SLMO2 | C_T | C | T | C | T | negative |
| rs6070706 | 100152090_TGI_at | C/T | T | 0.109 | 20 | 57061634 | 0.00053202 | 4.574 | 4.79E-06 | -5.3201 | BX464861 | SLMO2 | C_T | C | T | C | T | positive |
| rs3768015 | 100151271_TGI_at | A/G | G | 0.675 | 1 | 149079578 | 0.00053261 | -8.523 | 1.55E-17 | -16.8083 | NM_181746 | LASS2 | A_G | A | G | A | G | positive |
| rs613644 | 100142307_TGI_at | A/G | G | 0.558 | 8 | 109258170 | 0.00053355 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | G_A | A | G | G | A | negative |
| rs612265 | 100142307_TGI_at | A/G | G | 0.442 | 8 | 109257826 | 0.00053563 | -6.553 | 5.64E-11 | -10.2488 | BX094067 | | G_A | A | G | G | A | negative |
| rs610452 | 100142307_TGI_at | C/T | T | 0.567 | 8 | 109257439 | 0.00053675 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | T_C | C | T | T | C | negative |
| rs7015513 | 100152431_TGI_at | A/C | C | 0.508 | 8 | 109331746 | 0.00053841 | 23.37 | 8.6E-121 | -120.064 | AW293012 | EIF3E | A_C | A | C | A | C | negative |
| rs598477 | 100142307_TGI_at | G/T | T | 0.442 | 8 | 109257050 | 0.00054163 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | G_T | G | T | G | T | negative |
| rs602384 | 100142307_TGI_at | C/G | G | 0.558 | 8 | 109257361 | 0.00054203 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | G_C | C | G | G | C | negative |
| rs2071407 | 100305763_TGI_at | C/T | T | 0.283 | 14 | 103056893 | 0.00054294 | 5.925 | 3.12E-09 | -8.5054 | CA426758 | XRCC3 | T_C | C | T | T | C | negative |
| rs3130047 | 100151160_TGI_at | C/T | T | 0.108 | 6 | 31718458 | 0.0005452 | -4.156 | 3.24E-05 | -4.4896 | NM_001623 | AIF1 | T_C | C | T | T | C | negative |
| rs2652804 | 100145725_TGI_at | C/T | T | 0.353 | 15 | 61161309 | 0.00054747 | 11.249 | 2.34E-29 | -28.6304 | NM_001018007 | TPM1 | T_C | C | T | T | C | negative |
| rs2652804 | 100156621_TGI_at | C/T | T | 0.353 | 15 | 61161309 | 0.00054747 | 7.24 | 4.49E-13 | -12.3481 | NM_001018005 | TPM1 | T_C | C | T | T | C | negative |
| rs11856316 | 100141670_TGI_at | A/C | C | 0.314 | 15 | 81312346 | 0.00055632 | -7.134 | 9.75E-13 | -12.011 | NM_004644 | AP3B2 | C_A | A | C | C | A | positive |
| rs598022 | 100142307_TGI_at | C/T | T | 0.442 | 8 | 109256935 | 0.00055888 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | C_T | C | T | C | T | negative |
| rs597649 | 100142307_TGI_at | G/T | T | 0.558 | 8 | 109256894 | 0.00055954 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | T_G | G | T | T | G | negative |
| rs660816 | 100142307_TGI_at | C/T | T | 0.442 | 8 | 109247224 | 0.00056018 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | C_T | C | T | C | T | negative |
| rs7024579 | 100124395_TGI_at | C/T | T | 0.246 | 9 | 138240234 | 0.00056121 | -5.159 | 2.48E-07 | -6.6051 | NM_181701 | QSOX2 | C_T | C | T | C | T | positive |
| rs673356 | 100142307_TGI_at | A/T | T | 0.442 | 8 | 109254335 | 0.00056124 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_T | A | T | A | T | negative |
| rs2523721 | 100137319_TGI_at | C/T | T | 0.225 | 6 | 30274245 | 0.00056161 | 7.986 | 1.39E-15 | -14.8558 | NM_001004349 | | T_C | C | T | T | C | positive |
| rs2523721 | 100310523_TGI_at | C/T | T | 0.225 | 6 | 30274245 | 0.00056161 | -7.299 | 2.9E-13 | -12.5377 | AW473609 | | T_C | C | T | T | C | negative |
| rs677330 | 100142307_TGI_at | A/G | G | 0.442 | 8 | 109246748 | 0.00056517 | 6.553 | 5.64E-11 | -10.2488 | BX094067 | | A_G | A | G | A | G | negative |
| rs3130626 | 100151160_TGI_at | A/G | G | 0.108 | 6 | 31706468 | 0.00056583 | 4.156 | 3.24E-05 | -4.4896 | NM_001623 | AIF1 | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3094211 | 100303039_ TGI_at | A/G | G | 0.305 | 6 | 31194381 | 0.00056799 | -32.82 | 3.1E-236 | -235.515 | NM_001264 | CDSN | G_A | A | G | G | A | positive |
| rs3094211 | 100121628_ TGI_at | A/G | G | 0.305 | 6 | 31194381 | 0.00056799 | 18.412 | 1.05E-75 | -74.9777 | NM_014068 | PSORS1C1 | G_A | A | G | G | A | negative |
| rs16924301 | 100145578_ TGI_at | A/G | G | 0.158 | 9 | 6296093 | 0.00057259 | -7.28 | 3.34E-13 | -12.4765 | AF147316 | | G_A | A | G | G | A | positive |
| rs6904608 | 100142471_ TGI_at | C/T | T | 0.508 | 6 | 32435705 | 0.00057619 | 4.428 | 9.51E-06 | -5.0218 | AK057104 | | T_C | C | T | T | C | positive |
| rs7807028 | 100305640_ TGI_at | A/G | G | 0.108 | 7 | 23563699 | 0.0005807 | -5.238 | 1.62E-07 | -6.7896 | CB243396 | C7orf46 | G_A | A | G | G | A | positive |
| rs7807028 | 100158666_ TGI_at | A/G | G | 0.108 | 7 | 23563699 | 0.0005807 | -5.219 | 1.8E-07 | -6.745 | BX106492 | | G_A | A | G | G | A | positive |
| rs9267522 | 100151160_ TGI_at | A/G | G | 0.108 | 6 | 31711749 | 0.00058706 | 4.156 | 3.24E-05 | -4.4896 | NM_001623 | AIF1 | A_G | A | G | A | G | negative |
| rs1045599 | 100125319_ TGI_at | C/T | T | 0.533 | 17 | 15820635 | 0.00059088 | -33.92 | 3.1E-252 | -251.515 | NM_001042 698 | ZSWIM7 | T_C | C | T | T | C | negative |
| rs2911709 | 100132932_ TGI_at | A/G | G | 0.181 | 1 | 215684325 | 0.00059158 | -5.448 | 5.09E-08 | -7.2929 | NM_018040 | GPATCH2 | A_G | A | G | A | G | positive |
| rs4680444 | 100305399_ TGI_at | A/G | G | 0.275 | 3 | 159743208 | 0.00059382 | -20.62 | 1.71E-94 | -93.7679 | CN266276 | | G_A | A | G | G | A | negative |
| rs4680444 | 100153916_ TGI_at | A/G | G | 0.275 | 3 | 159743208 | 0.00059382 | -20.04 | 2.42E-89 | -88.6164 | AK097794 | | G_A | A | G | G | A | negative |
| rs9651832 | 100137632_ TGI_at | C/T | T | 0.367 | 12 | 28286689 | 0.00059648 | 7.903 | 2.72E-15 | -14.565 | BC035168 | | C_T | C | T | C | T | negative |
| rs11064872 | 100309959_ TGI_at | A/G | G | 0.983 | 12 | 108977042 | 0.00059773 | -4.58 | 4.65E-06 | -5.3326 | BC014223 | GIT2 | A_G | A | G | A | G | positive |
| rs2516400 | 100161520_ TGI_at | A/G | G | 0.688 | 6 | 31589084 | 0.00059953 | 7.593 | 3.13E-14 | -13.505 | NM_005931 | MICB | G_A | A | G | G | A | negative |
| rs16829104 | 100305399_ TGI_at | A/G | G | 0.725 | 3 | 159741114 | 0.00060381 | -20.62 | 1.71E-94 | -93.7679 | CN266276 | | A_G | A | G | A | G | negative |
| rs1592971 | 100129603_ TGI_at | A/G | G | 0.8 | 5 | 156951767 | 0.00061657 | 4.976 | 6.49E-07 | -6.1877 | AK055284 | | G_A | A | G | G | A | positive |
| rs1592971 | 100141348_ TGI_at | A/G | G | 0.8 | 5 | 156951767 | 0.00061657 | 4.599 | 4.25E-06 | -5.3721 | NM_001099 287 | | G_A | A | G | G | A | positive |
| rs885912 | 100137319_ TGI_at | A/C | C | 0.786 | 6 | 30282612 | 0.00062276 | -7.986 | 1.39E-15 | -14.8558 | NM_001004 349 | | C_A | A | C | C | A | positive |
| rs885912 | 100310523_ TGI_at | A/C | C | 0.786 | 6 | 30282612 | 0.00062276 | 7.299 | 2.9E-13 | -12.5377 | AW473609 | | C_A | A | C | C | A | negative |
| rs17628958 | 100305399_ TGI_at | C/G | G | 0.725 | 3 | 159739261 | 0.00062429 | -20.62 | 1.71E-94 | -93.7679 | CN266276 | | C_G | C | G | C | G | negative |
| rs3117583 | 100151160_ TGI_at | A/G | G | 0.108 | 6 | 31727555 | 0.00062536 | -4.156 | 3.24E-05 | -4.4896 | NM_001623 | AIF1 | G_A | A | G | G | A | negative |
| rs3134996 | 100312946_ TGI_at | A/T | T | 0.593 | 6 | 32744844 | 0.00062562 | -14.64 | 1.52E-48 | -47.8195 | AF522251 | HLA- DRB1 | A_T | A | T | A | T | positive |
| rs3134996 | 100304009_ TGI_at | A/T | T | 0.593 | 6 | 32744844 | 0.00062562 | -13.95 | 3.06E-44 | -43.5144 | ENST000003 74943 | HLA- DQB1 | A_T | A | T | A | T | positive |
| rs3134996 | 100302941_ TGI_at | A/T | T | 0.593 | 6 | 32744844 | 0.00062562 | -13.93 | 4.4E-44 | -43.3562 | NM_002123 | HLA- DQB1 | A_T | A | T | A | T | positive |
| rs3134996 | 100300398_ TGI_at | A/T | T | 0.593 | 6 | 32744844 | 0.00062562 | -13.82 | 1.99E-43 | -42.7022 | X03068 | HLA- DQB1 | A_T | A | T | A | T | positive |
| rs3134996 | 100161395_ TGI_at | A/T | T | 0.593 | 6 | 32744844 | 0.00062562 | -5.96 | 2.52E-09 | -8.5982 | AK225657 | TAP2 | A_T | A | T | A | T | positive |
| rs4499917 | 100145604_ TGI_at | A/C | C | 0.746 | 6 | 56494557 | 0.00062746 | -4.041 | 5.32E-05 | -4.2739 | BC038763 | | C_A | A | C | C | A | positive |
| rs7663650 | 100301711_ TGI_at | C/T | T | 0.35 | 4 | 55925876 | 0.00062766 | 7.781 | 7.2E-15 | -14.1429 | NM_024592 | SRD5A3 | C_T | C | T | C | T | negative |
| rs7663650 | 100129781_ TGI_at | C/T | T | 0.35 | 4 | 55925876 | 0.00062766 | 5.808 | 6.32E-09 | -8.1991 | ENST000003 81322 | CLOCK | C_T | C | T | C | T | negative |
| rs2894189 | 100300925_ TGI_at | A/C | C | 0.55 | 6 | 31325794 | 0.00062767 | -6.888 | 5.66E-12 | -11.2473 | NM_181717 | HCG27 | C_A | A | C | C | A | negative |
| rs6901497 | 100302369_ TGI_at | A/G | G | 0.992 | 6 | 26808488 | 0.00063701 | 11.742 | 7.76E-32 | -31.11 | NM_013375 | ABT1 | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs1117490 | 100137319_TGI_at | C/T | T | 0.781 | 6 | 30278489 | 0.00065163 | -7.986 | 1.39E-15 | -14.8558 | NM_001004349 | | T_C | C | T | T | C | positive |
| rs1117490 | 100310523_TGI_at | C/T | T | 0.781 | 6 | 30278489 | 0.00065163 | 7.299 | 2.9E-13 | -12.5377 | AW473609 | | T_C | C | T | T | C | negative |
| rs515271 | 100310631_TGI_at | A/G | G | 0.842 | 11 | 125532146 | 0.00065407 | -10.89 | 1.36E-27 | -26.8668 | AW196521 | RPUSD4 | A_G | A | G | A | G | negative |
| rs515271 | 100143437_TGI_at | A/G | G | 0.842 | 11 | 125532146 | 0.00065407 | 5.958 | 2.55E-09 | -8.5929 | NM_032795 | RPUSD4 | A_G | A | G | A | G | positive |
| rs2458216 | 100136496_TGI_at | C/T | T | 0.178 | 17 | 41702739 | 0.00065483 | -21.89 | 3.4E-106 | -105.471 | AK095802 | MAPT | T_C | C | T | T | C | negative |
| rs2532335 | 100136496_TGI_at | A/G | G | 0.183 | 17 | 41702874 | 0.00065688 | -21.89 | 3.4E-106 | -105.471 | AK095802 | MAPT | G_A | A | G | G | A | negative |
| rs8046429 | 100122211_TGI_at | A/G | G | 0.553 | 16 | 75769346 | 0.00065802 | -7.616 | 2.62E-14 | -13.5823 | NM_014940 | MON1B | G_A | A | G | G | A | positive |
| rs2726490 | 100160580_TGI_at | C/T | T | 0.575 | 4 | 106490971 | 0.00066111 | -8.525 | 1.53E-17 | -16.8158 | BM977451 | PPA2 | C_T | C | T | C | T | negative |
| rs2726490 | 100307499_TGI_at | C/T | T | 0.575 | 4 | 106490971 | 0.00066111 | -8.523 | 1.55E-17 | -16.8083 | BM977451 | PPA2 | C_T | C | T | C | T | negative |
| rs2248373 | 100128894_TGI_at | C/T | T | 0.417 | 6 | 31554525 | 0.00066132 | -6.416 | 1.4E-10 | -9.8542 | NM_181717 | HCG27 | C_T | C | T | C | T | negative |
| rs2248373 | 100142732_TGI_at | C/T | T | 0.417 | 6 | 31554525 | 0.00066132 | -6.174 | 6.66E-10 | -9.1766 | NM_138282 | ATP6V1G2 | C_T | C | T | C | T | negative |
| rs1264705 | 100138030_TGI_at | C/G | G | 0.858 | 6 | 30171653 | 0.00066249 | 4.604 | 4.14E-06 | -5.3825 | U58024 | HLA-G | C_G | C | G | C | G | positive |
| rs11205386 | 100156777_TGI_at | C/T | T | 0.192 | 1 | 148748362 | 0.00066304 | 6.07 | 1.28E-09 | -8.8931 | NM_018997 | MRPS21 | T_C | C | T | T | C | positive |
| rs11611575 | 100158197_TGI_at | A/G | G | 0.217 | 12 | 31731994 | 0.00066732 | 10.585 | 3.5E-26 | -25.4562 | XM_084845 | | A_G | A | G | A | G | positive |
| rs1549237 | 100305138_TGI_at | A/T | T | 0.525 | 5 | 147387587 | 0.00067064 | -8.537 | 1.38E-17 | -16.8609 | CU445838 | SPINK5 | T_A | A | T | T | A | negative |
| rs2499855 | 100155887_TGI_at | C/T | T | 0.892 | 1 | 160196385 | 0.00067166 | 9.202 | 3.51E-20 | -19.4543 | NM_007348 | ATF6 | C_T | C | T | C | T | negative |
| rs2499855 | 100304092_TGI_at | C/T | T | 0.892 | 1 | 160196385 | 0.00067166 | 4.508 | 6.54E-06 | -5.1841 | ENST00000367942 | ATF6 | C_T | C | T | C | T | negative |
| rs6501822 | 100159529_TGI_at | A/G | G | 0.85 | 17 | 71051226 | 0.00067239 | -4.128 | 3.66E-05 | -4.4366 | NM_207346 | TSEN54 | A_G | A | G | A | G | positive |
| rs1726744 | 100309263_TGI_at | A/C | C | 0.525 | 11 | 73543430 | 0.00067291 | 4.836 | 1.32E-06 | -5.8779 | BC068486 | RAB6A | A_C | A | C | A | C | negative |
| rs3824658 | 100132638_TGI_at | C/T | T | 0.802 | 10 | 7645073 | 0.00067442 | 7.948 | 1.9E-15 | -14.7223 | NM_030569 | ITIH5 | C_T | C | T | C | T | negative |
| rs3824658 | 100159682_TGI_at | C/T | T | 0.802 | 10 | 7645073 | 0.00067442 | -4.065 | 4.8E-05 | -4.3185 | ENST00000298441 | ITIH5 | C_T | C | T | C | T | positive |
| rs12473839 | 100144954_TGI_at | C/T | T | 0.367 | 2 | 135354514 | 0.00067482 | 6.406 | 1.49E-10 | -9.8257 | AK075041 | CCNT2 | T_C | C | T | T | C | negative |
| rs3932521 | 100311360_TGI_at | A/G | G | 0.492 | 6 | 87875317 | 0.00068051 | -11.34 | 8.51E-30 | -29.0702 | AL050201 | C6orf162 | G_A | A | G | G | A | positive |
| rs3932521 | 100306590_TGI_at | A/G | G | 0.492 | 6 | 87875317 | 0.00068051 | -4.4 | 1.08E-05 | -4.9656 | BX099470 | SLC35A1 | G_A | A | G | G | A | positive |
| rs2523716 | 100137319_TGI_at | C/T | T | 0.225 | 6 | 30278504 | 0.00068464 | 7.986 | 1.39E-15 | -14.8558 | NM_001004349 | | T_C | C | T | T | C | positive |
| rs2523716 | 100310523_TGI_at | C/T | T | 0.225 | 6 | 30278504 | 0.00068464 | -7.299 | 2.9E-13 | -12.5377 | AW473609 | | T_C | C | T | T | C | negative |
| rs2779212 | 100162676_TGI_at | C/T | T | 0.467 | 17 | 15817380 | 0.00068944 | 52.52 | 0 | -600.787 | BC066344 | ZSWIM7 | C_T | C | T | C | T | positive |
| rs1807304 | 100152779_TGI_at | A/G | G | 0.212 | 11 | 63616327 | 0.00069363 | -6.234 | 4.55E-10 | -9.3423 | BF509821 | | G_A | A | G | G | A | positive |
| rs17264866 | 100148761_TGI_at | C/G | G | 0.233 | 1 | 39795364 | 0.00069411 | 6.703 | 2.04E-11 | -10.69 | NM_022120 | OXCT2 | C_G | C | G | C | G | negative |
| rs4954192 | 100144954_TGI_at | C/T | T | 0.353 | 2 | 135349451 | 0.00070055 | 6.406 | 1.49E-10 | -9.8257 | AK075041 | CCNT2 | T_C | C | T | T | C | negative |
| rs7547017 | 100156028_TGI_at | C/T | T | 0.592 | 1 | 169868825 | 0.0007034 | -5.47 | 4.5E-08 | -7.3468 | AL035296 | VAMP4 | C_T | C | T | C | T | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2248289 | 100123483_TGI_at | C/T | T | 0.758 | 6 | 30180700 | 0.00070517 | 12.764 | 2.6E-37 | -36.5842 | AK056727 | HCG4P6 | T_C | C | T | T | C | negative |
| rs6430553 | 100144954_TGI_at | C/T | T | 0.367 | 2 | 135347870 | 0.00070935 | 6.406 | 1.49E-10 | -9.8257 | AK075041 | CCNT2 | T_C | C | T | T | C | negative |
| rs9341077 | 100303655_TGI_at | C/T | T | 0.992 | 6 | 152464821 | 0.00071157 | 4.683 | 2.83E-06 | -5.5487 | NM_000125 | ESR1 | C_T | C | T | C | T | negative |
| rs11042032 | 100130569_TGI_at | A/T | T | 0.509 | 11 | 8653448 | 0.00071393 | 11.769 | 5.64E-32 | -31.2488 | AK000908 | | A_T | A | T | A | T | negative |
| rs11042032 | 100145297_TGI_at | A/T | T | 0.509 | 11 | 8653448 | 0.00071393 | 9.838 | 7.72E-23 | -22.1122 | ENST00000299550 | TRIM66 | A_T | A | T | A | T | negative |
| rs3117579 | 100151160_TGI_at | G/T | T | 0.108 | 6 | 31741475 | 0.00071756 | -4.156 | 3.24E-05 | -4.4896 | NM_001623 | AIF1 | T_G | G | T | T | G | negative |
| rs1862362 | 100300070_TGI_at | A/G | G | 0.442 | 5 | 150510872 | 0.00072239 | 5.418 | 6.03E-08 | -7.2199 | Y00097 | ANXA6 | A_G | A | G | A | G | positive |
| rs1862362 | 100129059_TGI_at | A/G | G | 0.442 | 5 | 150510872 | 0.00072239 | 4.94 | 7.81E-07 | -6.1072 | NM_001155 | ANXA6 | A_G | A | G | A | G | positive |
| rs1800209 | 100146692_TGI_at | A/G | G | 0.125 | 13 | 76472984 | 0.00072322 | -5.527 | 3.26E-08 | -7.4871 | NM_006493 | CLN5 | A_G | A | G | A | G | negative |
| rs2526625 | 100146735_TGI_at | A/C | C | 0.737 | 7 | 19009885 | 0.0007244 | -12.84 | 9.29E-38 | -37.0318 | NM_178423 | HDAC9 | A_C | A | C | A | C | positive |
| rs10499135 | 100121877_TGI_at | A/G | G | 0.433 | 6 | 126668026 | 0.00072484 | -4.05 | 5.12E-05 | -4.2906 | NM_001012507 | C6orf173 | A_G | A | G | A | G | negative |
| rs6502482 | 100146347_TGI_at | C/G | G | 0.517 | 17 | 15839966 | 0.00072553 | 11.671 | 1.79E-31 | -30.7464 | NM_000676 | ADORA2B | G_C | C | G | G | C | positive |
| rs6502482 | 100300365_TGI_at | C/G | G | 0.517 | 17 | 15839966 | 0.00072553 | 10.838 | 2.27E-27 | -26.6432 | X68487 | ADORA2B | G_C | C | G | G | C | positive |
| rs2471338 | 100303520_TGI_at | G/T | T | 0.64 | 4 | 2963905 | 0.00072647 | -15.95 | 2.85E-57 | -56.5453 | NM_001004057 | GRK4 | T_G | G | T | T | G | negative |
| rs2471338 | 100134728_TGI_at | G/T | T | 0.64 | 4 | 2963905 | 0.00072647 | -12.19 | 3.74E-34 | -33.4275 | NM_001004056 | GRK4 | T_G | G | T | T | G | negative |
| rs629996 | 100139300_TGI_at | C/T | T | 0.466 | 8 | 109324382 | 0.00073622 | 4.873 | 1.1E-06 | -5.9589 | NM_014673 | TTC35 | C_T | C | T | C | T | negative |
| rs629996 | 100129666_TGI_at | C/T | T | 0.466 | 8 | 109324382 | 0.00073622 | 4.398 | 1.09E-05 | -4.9616 | NM_001146 | ANGPT1 | C_T | C | T | C | T | negative |
| rs512375 | 100311300_TGI_at | G/T | T | 0.55 | 2 | 135001749 | 0.00073732 | 5.206 | 1.93E-07 | -6.7145 | AL122044 | TMEM163 | T_G | G | T | T | G | negative |
| rs1265758 | 100302735_TGI_at | A/G | G | 0.509 | 6 | 32431507 | 0.00074626 | -4.162 | 3.16E-05 | -4.501 | NM_004381 | ATF6B | G_A | A | G | G | A | negative |
| rs735765 | 100145476_TGI_at | A/G | G | 0.842 | 6 | 28278276 | 0.00075298 | -8.255 | 1.52E-16 | -15.8184 | XM_940433 | ZNF389 | G_A | A | G | G | A | positive |
| rs4970926 | 100161206_TGI_at | C/T | T | 0.517 | 1 | 148940308 | 0.00075885 | -5.376 | 7.62E-08 | -7.1183 | NM_004436 | ENSA | C_T | C | T | C | T | negative |
| rs4970926 | 100125530_TGI_at | C/T | T | 0.517 | 1 | 148940308 | 0.00075885 | 4.144 | 3.41E-05 | -4.4669 | NM_004079 | CTSS | C_T | C | T | C | T | positive |
| rs3130618 | 100151160_TGI_at | A/C | C | 0.892 | 6 | 31740113 | 0.00075906 | -4.156 | 3.24E-05 | -4.4896 | NM_001623 | AIF1 | A_C | A | C | A | C | negative |
| rs6430552 | 100144954_TGI_at | C/T | T | 0.362 | 2 | 135339278 | 0.00076295 | -6.406 | 1.49E-10 | -9.8257 | AK075041 | CCNT2 | C_T | C | T | C | T | negative |
| rs1483267 | 100306816_TGI_at | C/T | T | 0.208 | 11 | 103219640 | 0.00076369 | -5.899 | 3.66E-09 | -8.4369 | BU616629 | PDGFD | T_C | C | T | T | C | negative |
| rs1483267 | 100132001_TGI_at | C/T | T | 0.208 | 11 | 103219640 | 0.00076369 | -4.466 | 7.97E-06 | -5.0986 | BU616629 | PDGFD | T_C | C | T | T | C | negative |
| rs2960785 | 100300632_TGI_at | C/T | T | 0.578 | 7 | 26918664 | 0.00076661 | -4.158 | 3.21E-05 | -4.4934 | S79869 | HOXA1 | C_T | C | T | C | T | positive |
| rs2050188 | 100126591_TGI_at | C/T | T | 0.633 | 6 | 32447875 | 0.0007672 | 4.062 | 4.87E-05 | -4.3129 | NM_002119 | HLA-DOA | T_C | C | T | T | C | positive |
| rs1344 | 100128577_TGI_at | A/G | G | 0.442 | 1 | 145585897 | 0.00076866 | -14.41 | 4.68E-47 | -46.3301 | NM_016361 | ACP6 | A_G | A | G | A | G | positive |
| rs7163730 | 100313804_TGI_at | A/G | G | 0.208 | 15 | 76601736 | 0.0007702 | -6.15 | 7.75E-10 | -9.1108 | AA532820 | | G_A | A | G | G | A | positive |
| rs134025 | 100307164_TGI_at | G/T | T | 0.533 | 22 | 26374057 | 0.00077521 | -4.128 | 3.66E-05 | -4.4366 | BQ446922 | MN1 | G_T | G | T | G | T | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs4660808 | 100133670_ TGI_at | C/T | T | 0.233 | 1 | 39791096 | 0.00077739 | 7.092 | 1.32E-12 | -11.8788 | ENST000003 31856 | | C_T | C | T | C | T | negative |
| rs4660808 | 100148761_ TGI_at | C/T | T | 0.233 | 1 | 39791096 | 0.00077739 | 6.703 | 2.04E-11 | -10.69 | NM_022120 | OXCT2 | C_T | C | T | C | T | negative |
| rs4660808 | 100313726_ TGI_at | C/T | T | 0.233 | 1 | 39791096 | 0.00077739 | 4.893 | 9.93E-07 | -6.003 | AA732526 | | C_T | C | T | C | T | negative |
| rs2236783 | 100138467_ TGI_at | A/G | G | 0.149 | 2 | 136310628 | 0.00077878 | -12.57 | 3.05E-36 | -35.5159 | BT006710 | DARS | G_A | A | G | G | A | positive |
| rs2236783 | 100148961_ TGI_at | A/G | G | 0.149 | 2 | 136310628 | 0.00077878 | -7.771 | 7.79E-15 | -14.1086 | BC008774 | MCM6 | G_A | A | G | G | A | positive |
| rs2236783 | 100305043_ TGI_at | A/G | G | 0.149 | 2 | 136310628 | 0.00077878 | -5.354 | 8.6E-08 | -7.0653 | D84557 | MCM6 | G_A | A | G | G | A | positive |
| rs2236783 | 100310941_ TGI_at | A/G | G | 0.149 | 2 | 136310628 | 0.00077878 | 4.73 | 2.25E-06 | -5.6487 | AL833322 | ZRANB3 | G_A | A | G | G | A | negative |
| rs2523713 | 100137319_ TGI_at | A/G | G | 0.775 | 6 | 30281309 | 0.00077912 | 7.986 | 1.39E-15 | -14.8558 | NM_001004 349 | | A_G | A | G | A | G | positive |
| rs2523713 | 100310523_ TGI_at | A/G | G | 0.775 | 6 | 30281309 | 0.00077912 | -7.299 | 2.9E-13 | -12.5377 | AW473609 | | A_G | A | G | A | G | negative |
| rs10103957 | 100154661_ TGI_at | C/T | T | 0.117 | 8 | 144670152 | 0.0007797 | -4.84 | 1.3E-06 | -5.8866 | NM_145201 | NAPRT1 | T_C | C | T | T | C | positive |
| rs9951973 | 100313618_ TGI_at | C/G | G | 0.567 | 18 | 18808314 | 0.00078172 | -7.576 | 3.56E-14 | -13.4481 | AA928204 | | G_C | C | G | G | C | negative |
| rs2844776 | 100137319_ TGI_at | C/T | T | 0.789 | 6 | 30279806 | 0.00078445 | -7.986 | 1.39E-15 | -14.8558 | NM_001004 349 | | T_C | C | T | T | C | positive |
| rs2844776 | 100310523_ TGI_at | C/T | T | 0.789 | 6 | 30279806 | 0.00078445 | 7.299 | 2.9E-13 | -12.5377 | AW473609 | | T_C | C | T | T | C | negative |
| rs4656342 | 100305118_ TGI_at | C/G | G | 0.212 | 1 | 160209115 | 0.00078568 | -4.297 | 1.73E-05 | -4.7616 | CV805370 | ATF6 | G_C | C | G | G | C | negative |
| rs3094064 | 100313972_ TGI_at | A/G | G | 0.858 | 6 | 30404232 | 0.0007861 | 4.858 | 1.19E-06 | -5.926 | AA159392 | FLOT1 | G_A | A | G | G | A | negative |
| rs7532311 | 100310881_ TGI_at | C/T | T | 0.933 | 1 | 23581073 | 0.00078944 | -7.466 | 8.27E-14 | -13.0827 | AL834485 | ZNF436 | C_T | C | T | C | T | positive |
| rs7532311 | 100127649_ TGI_at | C/T | T | 0.933 | 1 | 23581073 | 0.00078944 | -6.493 | 8.41E-11 | -10.075 | ENST000003 74608 | ZNF436 | C_T | C | T | C | T | positive |
| rs566890 | 100300284_ TGI_at | G/T | T | 0.758 | 18 | 8787189 | 0.00079715 | -6.818 | 9.23E-12 | -11.0347 | XM_031357 | KIAA0802 | G_T | G | T | G | T | negative |
| rs9268877 | 100125275_ TGI_at | A/G | G | 0.55 | 6 | 32539125 | 0.0007974 | -9.149 | 5.75E-20 | -19.2406 | BG755321 | HLA- DRB1 | A_G | A | G | A | G | positive |
| rs4969481 | 100124485_ TGI_at | C/T | T | 0.017 | 17 | 77586501 | 0.00079912 | 8.802 | 1.34E-18 | -17.8716 | NM_016286 | DCXR | C_T | C | T | C | T | positive |
| rs4969481 | 100151685_ TGI_at | C/T | T | 0.017 | 17 | 77586501 | 0.00079912 | -4.426 | 9.6E-06 | -5.0177 | NM_144998 | STRA13 | C_T | C | T | C | T | negative |
| rs7037371 | 100155123_ TGI_at | C/T | T | 0.453 | 9 | 38006247 | 0.00080136 | -4.657 | 3.21E-06 | -5.4937 | AK098185 | MCART1 | T_C | C | T | T | C | positive |
| rs7037371 | 100146140_ TGI_at | C/T | T | 0.453 | 9 | 38006247 | 0.00080136 | -4.354 | 1.34E-05 | -4.8739 | ENST000003 77724 | WDR32 | T_C | C | T | T | C | positive |
| rs11874249 | 100312458_ TGI_at | C/T | T | 0.768 | 18 | 55329317 | 0.00080491 | -5.798 | 6.71E-09 | -8.1732 | AI822141 | CCBE1 | C_T | C | T | C | T | positive |
| rs971570 | 100137319_ TGI_at | A/C | C | 0.225 | 6 | 30280492 | 0.00080571 | 7.986 | 1.39E-15 | -14.8558 | NM_001004 349 | | C_A | A | C | C | A | positive |
| rs971570 | 100310523_ TGI_at | A/C | C | 0.225 | 6 | 30280492 | 0.00080571 | -7.299 | 2.9E-13 | -12.5377 | AW473609 | | C_A | A | C | C | A | negative |
| rs7758054 | 100306458_ TGI_at | A/T | T | 0.708 | 6 | 56507690 | 0.00080853 | 5.086 | 3.66E-07 | -6.4369 | BX364902 | DST | T_A | A | T | T | A | negative |
| rs6776974 | 100309898_ TGI_at | A/G | G | 0.115 | 3 | 114737213 | 0.0008098 | 4.686 | 2.79E-06 | -5.555 | BC016799 | WDR52 | G_A | A | G | G | A | negative |
| rs6776974 | 100126013_ TGI_at | A/G | G | 0.115 | 3 | 114737213 | 0.0008098 | 4.404 | 1.06E-05 | -4.9736 | ENST000003 08346 | WDR52 | G_A | A | G | G | A | negative |
| rs6776974 | 100157274_ TGI_at | A/G | G | 0.115 | 3 | 114737213 | 0.0008098 | 4.035 | 5.46E-05 | -4.2628 | NM_018338 | WDR52 | G_A | A | G | G | A | negative |
| rs17162316 | 100306509_ TGI_at | C/G | G | 0.133 | 1 | 27050494 | 0.00081397 | 8.093 | 5.82E-16 | -15.235 | BX282734 | PIGV | G_C | C | G | G | C | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs17162316 | 100137081_TGI_at | C/G | G | 0.133 | 1 | 27050494 | 0.00081397 | 7.622 | 2.5E-14 | -13.6025 | NM_017837 | PIGV | G_C | C | G | G | C | positive |
| rs17162316 | 100136478_TGI_at | C/G | G | 0.133 | 1 | 27050494 | 0.00081397 | 5.595 | 2.21E-08 | -7.6564 | NM_139135 | ARID1A | G_C | C | G | G | C | positive |
| rs17162316 | 100149978_TGI_at | C/G | G | 0.133 | 1 | 27050494 | 0.00081397 | 4.834 | 1.34E-06 | -5.8735 | NM_021969 | NR0B2 | G_C | C | G | G | C | positive |
| rs2804529 | 100309207_TGI_at | A/T | T | 0.775 | 10 | 76608269 | 0.00081766 | 4.518 | 6.24E-06 | -5.2046 | BC072407 | VDAC2 | A_T | A | T | A | T | negative |
| rs2804529 | 100153741_TGI_at | A/T | T | 0.775 | 10 | 76608269 | 0.00081766 | 4.072 | 4.66E-05 | -4.3315 | NM_003375 | VDAC2 | A_T | A | T | A | T | negative |
| rs6566060 | 100306063_TGI_at | C/T | T | 0.136 | 18 | 71009457 | 0.00081809 | 5.15 | 2.6E-07 | -6.5842 | BX647730 | ZADH2 | C_T | C | T | C | T | positive |
| rs6566060 | 100134955_TGI_at | C/T | T | 0.136 | 18 | 71009457 | 0.00081809 | 4.767 | 1.87E-06 | -5.7282 | BC010734 | ZADH2 | C_T | C | T | C | T | positive |
| rs7017868 | 100122765_TGI_at | A/G | G | 0.492 | 8 | 8910703 | 0.00081963 | -6.362 | 1.99E-10 | -9.7008 | AL137679 | THEX1 | A_G | A | G | A | G | positive |
| rs7017868 | 100152809_TGI_at | A/G | G | 0.492 | 8 | 8910703 | 0.00081963 | -4.077 | 4.56E-05 | -4.3408 | NM_153332 | THEX1 | A_G | A | G | A | G | positive |
| rs7617480 | 100160114_TGI_at | A/C | C | 0.75 | 3 | 49185736 | 0.00082127 | -9.965 | 2.17E-23 | -22.6638 | AK001120 | | A_C | A | C | A | C | negative |
| rs7617480 | 100162155_TGI_at | A/C | C | 0.75 | 3 | 49185736 | 0.00082127 | -4.469 | 7.86E-06 | -5.1047 | AF017306 | USP4 | A_C | A | C | A | C | negative |
| rs7617480 | 100155972_TGI_at | A/C | C | 0.75 | 3 | 49185736 | 0.00082127 | -4.056 | 4.99E-05 | -4.3017 | AK223292 | USP4 | A_C | A | C | A | C | negative |
| rs11720657 | 100313943_TGI_at | A/G | G | 0.729 | 3 | 49367624 | 0.00082261 | -5.823 | 5.78E-09 | -8.2381 | AA229292 | CCDC51 | A_G | A | G | A | G | negative |
| rs2036291 | 100305792_TGI_at | A/G | G | 0.433 | 3 | 153549483 | 0.00082893 | -4.1 | 4.13E-05 | -4.3839 | CA414870 | MBNL1 | G_A | A | G | G | A | positive |
| rs2021722 | 100137319_TGI_at | C/T | T | 0.225 | 6 | 30282110 | 0.00082989 | 7.986 | 1.39E-15 | -14.8558 | NM_001004349 | | T_C | C | T | T | C | positive |
| rs2021722 | 100310523_TGI_at | C/T | T | 0.225 | 6 | 30282110 | 0.00082989 | -7.299 | 2.9E-13 | -12.5377 | AW473609 | | T_C | C | T | T | C | negative |
| rs4792827 | 100150806_TGI_at | C/T | T | 0.417 | 17 | 41487141 | 0.00083184 | -4.871 | 1.11E-06 | -5.9545 | AK025172 | | C_T | C | T | C | T | negative |
| rs4930826 | 100150849_TGI_at | A/T | T | 0.367 | 12 | 28618585 | 0.00083233 | 4.672 | 2.98E-06 | -5.5254 | AK092571 | | T_A | A | T | T | A | positive |
| rs6430547 | 100304349_TGI_at | C/T | T | 0.358 | 2 | 135328892 | 0.00083459 | 8.036 | 9.28E-16 | -15.0324 | EB387822 | CCNT2 | T_C | C | T | T | C | negative |
| rs2395150 | 100302735_TGI_at | A/G | G | 0.483 | 6 | 32434023 | 0.00083535 | -4.162 | 3.16E-05 | -4.501 | NM_004381 | ATF6B | A_G | A | G | A | G | negative |
| rs702688 | 100131401_TGI_at | A/G | G | 0.617 | 5 | 56226743 | 0.00083818 | 17.931 | 6.75E-72 | -71.1704 | NM_153706 | C5orf35 | A_G | A | G | A | G | positive |
| rs2836362 | 100136326_TGI_at | C/T | T | 0.661 | 21 | 38686654 | 0.00085623 | -7.751 | 9.12E-15 | -14.0401 | U17624 | | C_T | C | T | C | T | positive |
| rs6772483 | 100150755_TGI_at | A/G | G | 0.608 | 3 | 159898693 | 0.00085624 | -15.28 | 9.77E-53 | -52.0099 | NM_024996 | GFM1 | A_G | A | G | A | G | positive |
| rs6772483 | 100141104_TGI_at | A/G | G | 0.608 | 3 | 159898693 | 0.00085624 | -7.225 | 5.01E-13 | -12.3001 | BC049210 | GFM1 | A_G | A | G | A | G | positive |
| rs6772483 | 100301664_TGI_at | A/G | G | 0.608 | 3 | 159898693 | 0.00085624 | -5.2 | 1.99E-07 | -6.7005 | NM_024996 | GFM1 | A_G | A | G | A | G | positive |
| rs3129061 | 100303994_TGI_at | C/T | T | 0.245 | 6 | 29777979 | 0.00085648 | -27.25 | 1.9E-163 | -162.732 | ENST00000376881 | ZFP57 | T_C | C | T | T | C | negative |
| rs3129061 | 100311606_TGI_at | C/T | T | 0.245 | 6 | 29777979 | 0.00085648 | -13.54 | 9.33E-42 | -41.0301 | AK125274 | HLA-F | T_C | C | T | T | C | negative |
| rs3129061 | 100300348_TGI_at | C/T | T | 0.245 | 6 | 29777979 | 0.00085648 | 11.558 | 6.73E-31 | -30.1723 | X81001 | HCG2P7 | T_C | C | T | T | C | positive |
| rs3129061 | 100143227_TGI_at | C/T | T | 0.245 | 6 | 29777979 | 0.00085648 | 9.975 | 1.96E-23 | -22.7075 | X81001 | HCG2P7 | T_C | C | T | T | C | positive |
| rs3129061 | 100141578_TGI_at | C/T | T | 0.245 | 6 | 29777979 | 0.00085648 | 4.022 | 5.77E-05 | -4.2388 | NM_001003807 | RP3-377H14.5 | T_C | C | T | T | C | positive |
| rs11944404 | 100302095_TGI_at | C/T | T | 0.508 | 4 | 145890321 | 0.00085734 | 4.118 | 3.82E-05 | -4.4177 | NM_017493 | OTUD4 | C_T | C | T | C | T | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs16877282 | 100303540_TGI_at | A/G | G | 0.921 | 5 | 6468844 | 0.0008595 | 5.394 | 6.89E-08 | -7.1617 | NM_001001702 | | A_G | A | G | A | G | positive |
| rs16877282 | 100138705_TGI_at | A/G | G | 0.921 | 5 | 6468844 | 0.0008595 | 4.106 | 4.03E-05 | -4.3952 | NM_001001702 | | A_G | A | G | A | G | positive |
| rs6699701 | 100122866_TGI_at | C/T | T | 0.3 | 1 | 28171538 | 0.00086249 | -12.96 | 2.04E-38 | -37.6913 | ENST00000373871 | EYA3 | C_T | C | T | C | T | negative |
| rs4500045 | 100121683_TGI_at | A/G | G | 0.567 | 8 | 82180487 | 0.00086266 | 4.528 | 5.95E-06 | -5.2252 | AW404907 | | A_G | A | G | A | G | negative |
| rs9272346 | 100311704_TGI_at | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | -20.08 | 1.06E-89 | -88.9745 | AK097297 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs9272346 | 100126665_TGI_at | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | -11.49 | 1.45E-30 | -29.8395 | NM_032741 | AGPAT1 | G_A | A | G | G | A | positive |
| rs9272346 | 100135327_TGI_at | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | -8.603 | 7.77E-18 | -17.1098 | NM_006411 | AGPAT1 | G_A | A | G | G | A | positive |
| rs9272346 | 100157567_TGI_at | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | -7.449 | 9.41E-14 | -13.0266 | NM_182549 | HLA-DQB2 | G_A | A | G | G | A | positive |
| rs1474589 | 100135231_TGI_at | G/T | T | 0.075 | 6 | 28429523 | 0.00087547 | 4.235 | 2.29E-05 | -4.641 | BC032507 | PGBD1 | T_G | G | T | T | G | positive |
| rs2524005 | 100138253_TGI_at | A/G | G | 0.767 | 6 | 30007656 | 0.00087652 | -4.574 | 4.79E-06 | -5.3201 | CR933629 | HCG8 | G_A | A | G | G | A | positive |
| rs4968255 | 100306281_TGI_at | C/T | T | 0.225 | 17 | 42667812 | 0.00088646 | -11.75 | 6.98E-32 | -31.1562 | BX537519 | C17orf57 | T_C | C | T | T | C | negative |
| rs4968255 | 100308684_TGI_at | C/T | T | 0.225 | 17 | 42667812 | 0.00088646 | -4.07 | 4.7E-05 | -4.3278 | BF224332 | | T_C | C | T | T | C | negative |
| rs4968255 | 100149604_TGI_at | C/T | T | 0.225 | 17 | 42667812 | 0.00088646 | -4.04 | 5.35E-05 | -4.272 | AA430297 | | T_C | C | T | T | C | negative |
| rs3816125 | 100311198_TGI_at | A/G | G | 0.467 | 18 | 42855609 | 0.00089082 | -7.139 | 9.4E-13 | -12.0268 | AL512748 | KATNAL2 | G_A | A | G | G | A | positive |
| rs2937121 | 100300793_TGI_at | G/T | T | 0.558 | 16 | 68427910 | 0.00089223 | 4.093 | 4.26E-05 | -4.3708 | NM_199423 | WWP2 | T_G | G | T | T | G | positive |
| rs255751 | 100139549_TGI_at | C/T | T | 0.741 | 5 | 53355274 | 0.00089348 | 4.232 | 2.32E-05 | -4.6352 | BQ024800 | | C_T | C | T | C | T | positive |
| rs164867 | 100311884_TGI_at | A/G | G | 0.842 | 1 | 13741114 | 0.00089483 | -4.322 | 1.55E-05 | -4.8107 | AK075345 | PDPN | A_G | A | G | A | G | negative |
| rs2534674 | 100138417_TGI_at | C/T | T | 0.433 | 6 | 31573082 | 0.00089905 | -11.36 | 6.39E-30 | -29.1944 | AK055022 | | T_C | C | T | T | C | positive |
| rs1415148 | 100308717_TGI_at | A/G | G | 0.625 | 1 | 148972379 | 0.00090016 | -8.318 | 8.95E-17 | -16.0484 | BF115327 | GOLPH3L | A_G | A | G | A | G | positive |
| rs1415148 | 100159164_TGI_at | A/G | G | 0.625 | 1 | 148972379 | 0.00090016 | -5.716 | 1.09E-08 | -7.9623 | BM928226 | GOLPH3L | A_G | A | G | A | G | positive |
| rs1415148 | 100143466_TGI_at | A/G | G | 0.625 | 1 | 148972379 | 0.00090016 | -5.675 | 1.39E-08 | -7.858 | BX405157 | GOLPH3L | A_G | A | G | A | G | positive |
| rs565203 | 100135523_TGI_at | C/T | T | 0.615 | 8 | 8670367 | 0.00090256 | -4.296 | 1.74E-05 | -4.7597 | NM_194284 | CLDN23 | C_T | C | T | C | T | positive |
| rs689623 | 100136633_TGI_at | C/T | T | 0.025 | 11 | 94287761 | 0.00090447 | -5.228 | 1.71E-07 | -6.7661 | AK093699 | AMOTL1 | T_C | C | T | T | C | negative |
| rs2836371 | 100136326_TGI_at | C/T | T | 0.661 | 21 | 38695398 | 0.00090532 | -7.751 | 9.12E-15 | -14.0401 | U17624 | | C_T | C | T | C | T | positive |
| rs12067677 | 100137694_TGI_at | C/T | T | 0.202 | 1 | 26284558 | 0.0009087 | -10.09 | 5.99E-24 | -23.2223 | NM_032588 | TRIM63 | T_C | C | T | T | C | positive |
| rs7644148 | 100129450_TGI_at | A/G | G | 0.7 | 3 | 49520245 | 0.00091339 | -6.063 | 1.34E-09 | -8.8742 | ENST00000273598 | NICN1 | A_G | A | G | A | G | negative |
| rs2015353 | 100132808_TGI_at | C/T | T | 0.542 | 17 | 15814000 | 0.00091586 | -6.449 | 1.13E-10 | -9.9485 | NM_017775 | TTC19 | C_T | C | T | C | T | negative |
| rs7739034 | 100139965_TGI_at | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | 12.744 | 3.37E-37 | -36.4728 | BX537746 | ZNF292 | C_T | C | T | C | T | positive |
| rs7739034 | 100144708_TGI_at | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | 9.494 | 2.22E-21 | -20.653 | AL050201 | C6orf162 | C_T | C | T | C | T | positive |
| rs7739034 | 100147499_TGI_at | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | -9.265 | 1.95E-20 | -19.7098 | ENST00000369572 | C6orf164 | C_T | C | T | C | T | negative |
| rs7739034 | 100128463_TGI_at | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | -7.513 | 5.78E-14 | -13.2382 | AK022079 | | C_T | C | T | C | T | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs7739034 | 100134209_TGI_at | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | -7.043 | 1.88E-12 | -11.7255 | R62370 | | C_T | C | T | C | T | negative |
| rs7739034 | 100143632_TGI_at | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | -6.651 | 2.91E-11 | -10.5359 | BC070260 | C6orf162 | C_T | C | T | C | T | negative |
| rs2938852 | 100305257_TGI_at | G/T | T | 0.225 | 10 | 76583884 | 0.00091873 | 5.232 | 1.68E-07 | -6.7755 | CR609899 | VDAC2 | T_G | G | T | T | G | negative |
| rs6602776 | 100149806_TGI_at | C/T | T | 0.219 | 10 | 15049510 | 0.00092222 | -9.739 | 2.06E-22 | -21.687 | NM_001080836 | MEIG1 | C_T | C | T | C | T | negative |
| rs738415 | 100307496_TGI_at | A/G | G | 0.892 | 22 | 48481817 | 0.00092642 | 6.38 | 1.77E-10 | -9.7518 | BM977889 | C22orf34 | A_G | A | G | A | G | positive |
| rs4836224 | 100145444_TGI_at | A/C | C | 0.427 | 5 | 122120774 | 0.00092655 | -4.102 | 4.1E-05 | -4.3876 | AK026718 | | A_C | A | C | A | C | positive |
| rs213238 | 100143968_TGI_at | C/T | T | 0.619 | 6 | 28429972 | 0.00093426 | 18.763 | 1.52E-78 | -77.8193 | NM_145909 | ZNF323 | T_C | C | T | T | C | negative |
| rs213238 | 100301615_TGI_at | C/T | T | 0.619 | 6 | 28429972 | 0.00093426 | 18.279 | 1.22E-74 | -73.9149 | NM_030899 | ZNF323 | T_C | C | T | T | C | negative |
| rs4929941 | 100136729_TGI_at | C/T | T | 0.642 | 11 | 8581527 | 0.00093587 | 6.157 | 7.41E-10 | -9.13 | AW138771 | TRIM66 | C_T | C | T | C | T | negative |
| rs4929941 | 100162298_TGI_at | C/T | T | 0.642 | 11 | 8581527 | 0.00093587 | -5.674 | 1.4E-08 | -7.8554 | ENST00000356931 | RPL27A | C_T | C | T | C | T | positive |
| rs9843440 | 100135841_TGI_at | A/C | C | 0.567 | 3 | 186472127 | 0.00093639 | 4.485 | 7.29E-06 | -5.1372 | BC011030 | EHHADH | A_C | A | C | A | C | positive |
| rs9843440 | 100155000_TGI_at | A/C | C | 0.567 | 3 | 186472127 | 0.00093639 | 4.076 | 4.58E-05 | -4.339 | NM_001025266 | C3orf70 | A_C | A | C | A | C | positive |
| rs685912 | 100304878_TGI_at | A/T | T | 0.192 | 18 | 30915253 | 0.00093695 | 4.362 | 1.29E-05 | -4.8898 | DA748162 | ZNF271 | T_A | A | T | T | A | negative |
| rs7732013 | 100309539_TGI_at | C/T | T | 0.025 | 5 | 35192289 | 0.00093718 | -4.045 | 5.23E-05 | -4.2813 | BC037857 | RAD1 | T_C | C | T | T | C | positive |
| rs2527197 | 100129573_TGI_at | A/G | G | 0.192 | 7 | 158428021 | 0.00093792 | 5.56 | 2.7E-08 | -7.569 | NM_018051 | WDR60 | G_A | A | G | G | A | positive |
| rs2527197 | 100301867_TGI_at | A/G | G | 0.192 | 7 | 158428021 | 0.00093792 | 4.282 | 1.85E-05 | -4.7323 | NM_020728 | FAM62B | G_A | A | G | G | A | positive |
| rs2527197 | 100136204_TGI_at | A/G | G | 0.192 | 7 | 158428021 | 0.00093792 | 4.046 | 5.21E-05 | -4.2832 | NM_017760 | NCAPG2 | G_A | A | G | G | A | positive |
| rs4983579 | 100151496_TGI_at | A/G | G | 0.792 | 14 | 104626441 | 0.00094072 | -4.286 | 1.82E-05 | -4.7401 | NM_177533 | NUDT14 | A_G | A | G | A | G | positive |
| rs17339831 | 100122984_TGI_at | C/G | G | 0.839 | 5 | 142724285 | 0.00094465 | -10.81 | 3.22E-27 | -26.4916 | NM_001018074 | NR3C1 | C_G | C | G | C | G | negative |
| rs17339831 | 100129487_TGI_at | C/G | G | 0.839 | 5 | 142724285 | 0.00094465 | -7.219 | 5.24E-13 | -12.2809 | U01351 | NR3C1 | C_G | C | G | C | G | negative |
| rs2521222 | 100128819_TGI_at | C/T | T | 0.517 | 7 | 24508049 | 0.00095026 | -6.465 | 1.01E-10 | -9.9944 | NM_016447 | MPP6 | C_T | C | T | C | T | positive |
| rs2521222 | 100136557_TGI_at | C/T | T | 0.517 | 7 | 24508049 | 0.00095026 | -4.439 | 9.04E-06 | -5.0439 | BC012034 | MPP6 | C_T | C | T | C | T | positive |
| rs17356867 | 100136066_TGI_at | C/T | T | 0.783 | 1 | 26321436 | 0.00095448 | -10.29 | 7.98E-25 | -24.0979 | AI884856 | | C_T | C | T | C | T | positive |
| rs17356867 | 100154120_TGI_at | C/T | T | 0.783 | 1 | 26321436 | 0.00095448 | 4.535 | 5.76E-06 | -5.2396 | NM_006314 | CNKSR1 | C_T | C | T | C | T | negative |
| rs4790 | 100311439_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | -15.31 | 6.17E-53 | -52.21 | AK225357 | PCBP2 | C_T | C | T | C | T | negative |
| rs4790 | 100302531_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | -12.1 | 1.08E-33 | -32.9657 | NM_006301 | MAP3K12 | C_T | C | T | C | T | negative |
| rs4790 | 100131043_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | 9.702 | 2.96E-22 | -21.5292 | NM_005016 | PCBP2 | C_T | C | T | C | T | positive |
| rs4790 | 100302664_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | 8.836 | 9.92E-19 | -18.0035 | NM_005016.2 | PCBP2 | C_T | C | T | C | T | positive |
| rs4790 | 100137523_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | 7.349 | 2E-13 | -12.6996 | BC071942 | PCBP2 | C_T | C | T | C | T | positive |
| rs4790 | 100306859_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | -5.852 | 4.86E-09 | -8.3136 | BU538613 | MAP3K12 | C_T | C | T | C | T | negative |
| rs4790 | 100137986_TGI_at | C/T | T | 0.068 | 12 | 52159633 | 0.0009565 | -4.05 | 5.12E-05 | -4.2906 | NM_173860 | HOXC12 | C_T | C | T | C | T | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs12446197 | 100122963_TGI_at | A/G | G | 0.449 | 16 | 68412370 | 0.00095679 | 11.446 | 2.46E-30 | -29.6086 | AL833251 | PDXDC2 | A_G | A | G | A | G | positive |
| rs12446197 | 100310948_TGI_at | A/G | G | 0.449 | 16 | 68412370 | 0.00095679 | 5.438 | 5.39E-08 | -7.2686 | AL833251 | PDXDC2 | A_G | A | G | A | G | positive |
| rs2293476 | 100302787_TGI_at | C/G | G | 0.767 | 1 | 39809434 | 0.0009581 | -5.611 | 2.01E-08 | -7.6965 | NM_003819 | PABPC4 | G_C | C | G | G | C | positive |
| rs1147761 | 100122767_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | 12.189 | 3.56E-34 | -33.4488 | CA417101 | C18orf10 | T_C | C | T | T | C | negative |
| rs1147761 | 100305245_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | 10.374 | 3.26E-25 | -24.4873 | CR614442 | C18orf10 | T_C | C | T | T | C | negative |
| rs1147761 | 100135353_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | 9.567 | 1.1E-21 | -20.9584 | BG420782 | C18orf10 | T_C | C | T | T | C | negative |
| rs1147761 | 100308899_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | 8.935 | 4.07E-19 | -18.3902 | BE548302 | C18orf10 | T_C | C | T | T | C | negative |
| rs1147761 | 100126219_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | -8.403 | 4.35E-17 | -16.3613 | BC037214 | | T_C | C | T | T | C | positive |
| rs1147761 | 100160039_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | 5.041 | 4.63E-07 | -6.3343 | AA702940 | | T_C | C | T | T | C | negative |
| rs1147761 | 100146695_TGI_at | C/T | T | 0.733 | 18 | 32655158 | 0.00095955 | -4.534 | 5.79E-06 | -5.2375 | XM_001128998 | BRUNOL4 | T_C | C | T | T | C | positive |
| rs8897 | 100124708_TGI_at | C/T | T | 0.3 | 3 | 49435411 | 0.00096089 | 10.719 | 8.29E-27 | -26.0815 | NM_000481 | AMT | T_C | C | T | T | C | positive |
| rs8897 | 100138300_TGI_at | C/T | T | 0.3 | 3 | 49435411 | 0.00096089 | -7.763 | 8.29E-15 | -14.0812 | NM_001664 | RHOA | T_C | C | T | T | C | negative |
| rs8897 | 100314021_TGI_at | C/T | T | 0.3 | 3 | 49435411 | 0.00096089 | 7.369 | 1.72E-13 | -12.7647 | AA034951 | ARIH2 | T_C | C | T | T | C | positive |
| rs8897 | 100130226_TGI_at | C/T | T | 0.3 | 3 | 49435411 | 0.00096089 | 4.789 | 1.68E-06 | -5.7757 | NM_016453 | NCKIPSD | T_C | C | T | T | C | positive |
| rs12071062 | 100137694_TGI_at | G/T | T | 0.8 | 1 | 26284786 | 0.00096158 | -10.09 | 5.99E-24 | -23.2223 | NM_032588 | TRIM63 | G_T | G | T | G | T | positive |
| rs6009826 | 100149241_TGI_at | A/T | T | 0.892 | 22 | 48476247 | 0.00097183 | -6.14 | 8.25E-10 | -9.0834 | AK128192 | | A_T | A | T | A | T | negative |
| rs6009826 | 100129499_TGI_at | A/T | T | 0.892 | 22 | 48476247 | 0.00097183 | -5.418 | 6.03E-08 | -7.2199 | ENST00000380976 | C22orf34 | A_T | A | T | A | T | negative |
| rs13175787 | 100153252_TGI_at | A/G | G | 0.092 | 5 | 175759469 | 0.00097351 | -15.77 | 4.85E-56 | -55.3144 | NM_138820 | HIGD2A | G_A | A | G | G | A | negative |
| rs13175787 | 100134693_TGI_at | A/G | G | 0.092 | 5 | 175759469 | 0.00097351 | -10.91 | 1.08E-27 | -26.967 | NM_007097 | CLTB | G_A | A | G | G | A | negative |
| rs13175787 | 100141815_TGI_at | A/G | G | 0.092 | 5 | 175759469 | 0.00097351 | -5.313 | 1.08E-07 | -6.9672 | NM_016391 | NOP16 | G_A | A | G | G | A | negative |
| rs7631174 | 100304176_TGI_at | C/T | T | 0.608 | 3 | 101396592 | 0.00097419 | -6.366 | 1.94E-10 | -9.7122 | ENST00000333147 | C3orf26 | C_T | C | T | C | T | negative |
| rs7631174 | 100159492_TGI_at | C/T | T | 0.608 | 3 | 101396592 | 0.00097419 | -5.925 | 3.12E-09 | -8.5054 | NM_032359 | C3orf26 | C_T | C | T | C | T | negative |
| rs3129909 | 100302735_TGI_at | A/G | G | 0.483 | 6 | 32433688 | 0.00097429 | -4.162 | 3.16E-05 | -4.501 | NM_004381 | ATF6B | A_G | A | G | A | G | negative |
| rs1046089 | 100126781_TGI_at | A/G | G | 0.675 | 6 | 31710946 | 0.00098195 | 7.007 | 2.44E-12 | -11.6135 | NM_025262 | LY6G5C | A_G | A | G | A | G | positive |
| rs1046089 | 100162932_TGI_at | A/G | G | 0.675 | 6 | 31710946 | 0.00098195 | 5.4 | 6.66E-08 | -7.1763 | BF064119 | | A_G | A | G | A | G | positive |
| rs1046089 | 100138357_TGI_at | A/G | G | 0.675 | 6 | 31710946 | 0.00098195 | 4.464 | 8.04E-06 | -5.0945 | NM_033177 | BAT4 | A_G | A | G | A | G | positive |
| rs9878610 | 100157152_TGI_at | A/G | G | 0.75 | 3 | 134002566 | 0.00098489 | 6.52 | 7.03E-11 | -10.153 | AK095050 | TMEM108 | A_G | A | G | A | G | negative |
| rs9878610 | 100139628_TGI_at | A/G | G | 0.75 | 3 | 134002566 | 0.00098489 | 6.388 | 1.68E-10 | -9.7745 | NM_023943 | TMEM108 | A_G | A | G | A | G | negative |
| rs2369832 | 100159303_TGI_at | C/T | T | 0.2 | 3 | 133920080 | 0.00098505 | -11.33 | 9.43E-30 | -29.0256 | NM_153240 | NPHP3 | C_T | C | T | C | T | negative |
| rs2369832 | 100143326_TGI_at | C/T | T | 0.2 | 3 | 133920080 | 0.00098505 | -9.986 | 1.76E-23 | -22.7557 | AK094015 | NPHP3 | C_T | C | T | C | T | negative |
| rs2369832 | 100311821_TGI_at | C/T | T | 0.2 | 3 | 133920080 | 0.00098505 | -9.345 | 9.19E-21 | -20.0367 | AK092910 | NPHP3 | C_T | C | T | C | T | negative |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2369832 | 100313479_ TGI_at | C/T | T | 0.2 | 3 | 133920080 | 0.00098505 | -8.28 | 1.23E-16 | -15.9095 | AB056657 | NPHP3 | C_T | C | T | C | T | negative |
| rs7983607 | 100162913_ TGI_at | G/T | T | 0.6 | 13 | 49339455 | 0.00098909 | -4.855 | 1.2E-06 | -5.9194 | AF034756 | KPNA3 | G_T | G | T | G | T | positive |
| rs7983607 | 100141096_ TGI_at | G/T | T | 0.6 | 13 | 49339455 | 0.00098909 | -4.506 | 6.61E-06 | -5.1801 | DQ892644 | KPNA3 | G_T | G | T | G | T | positive |
| rs1233699 | 100148250_ TGI_at | A/T | T | 0.75 | 6 | 28277137 | 0.00099046 | -5.134 | 2.84E-07 | -6.5472 | BC040524 | ZSCAN12 L1 | A_T | A | T | A | T | negative |
| rs1233699 | 100144299_ TGI_at | A/T | T | 0.75 | 6 | 28277137 | 0.00099046 | 4.387 | 1.15E-05 | -4.9396 | AK130456 |  | A_T | A | T | A | T | positive |
| rs12089989 | 100306322_ TGI_at | A/G | G | 0.627 | 1 | 148982406 | 0.00099395 | 7.499 | 6.43E-14 | -13.1917 | BX470720 | ARNT | A_G | A | G | A | G | negative |
| rs6933779 | 100155331_ TGI_at | C/T | T | 0.129 | 6 | 31488711 | 0.00099556 | 24.623 | 7.2E-134 | -133.145 | BC035656 |  | T_C | C | T | T | C | negative |
| rs6933779 | 100300038_ TGI_at | C/T | T | 0.129 | 6 | 31488711 | 0.00099556 | -5.477 | 4.33E-08 | -7.3639 | Z33453 | HLA-B | T_C | C | T | T | C | positive |
| rs1135403 | 100304832_ TGI_at | G/T | T | 0.625 | 15 | 61132011 | 0.00099797 | 7.9 | 2.79E-15 | -14.5545 | DA897550 | TPM1 | G_T | G | T | G | T | negative |
| rs7756729 | 100311276_ TGI_at | C/T | T | 0.975 | 6 | 142617815 | 0.00099882 | -5.069 | 4E-07 | -6.398 | AL136684 | VTA1 | C_T | C | T | C | T | positive |
| rs7756729 | 100153205_ TGI_at | C/T | T | 0.975 | 6 | 142617815 | 0.00099882 | -4.965 | 6.87E-07 | -6.163 | NM_016485 | VTA1 | C_T | C | T | C | T | positive |
| rs12179134 | 100150625_ TGI_at | A/G | G | 0.19 | 6 | 27783448 | 0.00099903 | -4.765 | 1.89E-06 | -5.7239 | NM_001076 781 | ZNF391 | G_A | A | G | G | A | negative |

## Supplementary Table 3: FEV$_1$ *trans*-eSNPs

Table shows the list of FEV$_1$ *trans* acting eSNPs. Header definitions are the same as Supplementary Table 2.

| **FEV1 *trans lung* eSNPs** | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| eSNP | eSNP regulated probeset | GWAS SNP alleles | GWAS Reference allele | Reference allele freq in HapMap | Chr | SNP Position | GWAS_ Pval_ FEV1 | eQTL Z meta | eQTL P value | log10. pvalue. meta | sequence source ID | Gene Symbol | eQTL-alleles | GWAS_ noncoded_alleles | GWAS_ coded_ alleles | eQTL_ noncoded_alleles | eQTL_coded_alleles | Expected Direction Of Effect of mRNA with lung function |
| rs9468413 | 100311443_TGI_at | A/C | C | 0.15 | 6 | 28797651 | 7.06E-06 | -6.347 | 2.2E-10 | -9.6585 | AK225208 | LRRC16A | A_C | A | C | A | C | positive |
| rs13193532 | 100303994_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 1.16E-05 | 15.855 | 1.3E-56 | -55.8866 | ENST00000376881 | ZFP57 | A_G | A | G | A | G | negative |
| rs13193532 | 100311606_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 1.16E-05 | 8.712 | 3E-18 | -17.525 | AK125274 | HLA-F | A_G | A | G | A | G | negative |
| rs13193532 | 100309580_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 1.16E-05 | 14.14 | 2.2E-45 | -44.667 | BC035659 | | A_G | A | G | A | G | negative |
| rs3132450 | 100300398_TGI_at | A/G | G | 0.092 | 6 | 31704117 | 4.30E-05 | 8.067 | 7.2E-16 | -15.1424 | X03068 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs3132450 | 100304009_TGI_at | A/G | G | 0.092 | 6 | 31704117 | 4.30E-05 | 8.117 | 4.8E-16 | -15.3207 | ENST00000374943 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs3132450 | 100302941_TGI_at | A/G | G | 0.092 | 6 | 31704117 | 4.30E-05 | 8.05 | 8.3E-16 | -15.082 | NM_002123 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs1264377 | 100141210_TGI_at | A/G | G | 0.808 | 6 | 30872886 | 4.98E-05 | -6.813 | 9.6E-12 | -11.0196 | ENST00000318669 | | G_A | A | G | G | A | positive |
| rs1264377 | 100304197_TGI_at | A/G | G | 0.808 | 6 | 30872886 | 4.98E-05 | -7.127 | 1E-12 | -11.9889 | ENST00000318669 | | G_A | A | G | G | A | positive |
| rs2523454 | 100138030_TGI_at | A/G | G | 0.633 | 6 | 31475844 | 5.16E-05 | -7.135 | 9.7E-13 | -12.0142 | U58024 | HLA-G | G_A | A | G | G | A | positive |
| rs2959945 | 100149004_TGI_at | C/T | T | 0.807 | 17 | 40931011 | 5.22E-05 | -22.348 | 1E-110 | -109.899 | BC017896 | | C_T | C | T | C | T | negative |
| rs156737 | 100129584_TGI_at | A/G | G | 0.367 | 6 | 28003192 | 6.18E-05 | -8.424 | 3.6E-17 | -16.4391 | ENST00000377186 | | G_A | A | G | G | A | negative |
| rs156737 | 100303991_TGI_at | A/G | G | 0.367 | 6 | 28003192 | 6.18E-05 | -11.734 | 8.5E-32 | -31.0689 | ENST00000377186 | | G_A | A | G | G | A | negative |
| rs6430549 | 100138467_TGI_at | A/G | G | 0.405 | 2 | 1.35E+08 | 6.58E-05 | -8.143 | 3.9E-16 | -15.4139 | BT006710 | DARS | G_A | A | G | G | A | positive |
| rs418891 | 100124649_TGI_at | G/T | T | 0.2 | 17 | 41049321 | 8.22E-05 | 9.184 | 4.2E-20 | -19.3816 | AA446387 | | G_T | G | T | G | T | negative |
| rs418891 | 100144981_TGI_at | G/T | T | 0.2 | 17 | 41049321 | 8.22E-05 | 21.403 | 1E-101 | -100.902 | BQ777623 | | G_T | G | T | G | T | negative |
| rs418891 | 100138516_TGI_at | G/T | T | 0.2 | 17 | 41049321 | 8.22E-05 | 9.953 | 2.4E-23 | -22.6114 | BC114219 | WNT3 | G_T | G | T | G | T | negative |
| rs3130934 | 100126665_TGI_at | A/C | C | 0.596 | 6 | 31236531 | 0.000142 | 7.481 | 7.4E-14 | -13.1322 | NM_032741 | AGPAT1 | C_A | A | C | C | A | positive |
| rs13191227 | 100161253_TGI_at | C/G | G | 0.929 | 6 | 27498094 | 0.000154 | 18.173 | 8.4E-74 | -73.0734 | NM_007047 | BTN3A2 | C_G | C | G | C | G | positive |
| rs878918 | 100124262_TGI_at | A/G | G | 0.339 | 17 | 41387462 | 0.000184 | 6.568 | 5.1E-11 | -10.2925 | AK057167 | | A_G | A | G | A | G | positive |
| rs2668628 | 100162323_TGI_at | A/G | G | 0.814 | 17 | 41709662 | 0.000244 | -40.342 | 0 | -355.106 | AF338199 | | A_G | A | G | A | G | negative |
| rs3093975 | 100139688_TGI_at | A/G | G | 0.797 | 6 | 31614117 | 0.000254 | 6.474 | 9.5E-11 | -10.0203 | AK055657 | HCG18 | A_G | A | G | A | G | positive |
| rs7197 | 100152956_TGI_at | C/T | T | 0.283 | 6 | 32520558 | 0.000283 | -6.936 | 4E-12 | -11.3943 | BC053580 | | T_C | C | T | T | C | positive |
| rs3132649 | 100162706_TGI_at | A/G | G | 0.858 | 6 | 30429036 | 0.000313 | 8.594 | 8.4E-18 | -17.0758 | D83543 | | G_A | A | G | G | A | negative |
| rs3132649 | 100305045_T | A/G | G | 0.858 | 6 | 30429036 | 0.000313 | 8.679 | 4E-18 | -17.3987 | D83543 | | G_A | A | G | G | A | negative |

| | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | |
| rs9268144 | 100309484_TGI_at | C/T | T | 0.908 | 6 | 32365177 | 0.000325 | 9.648 | 5E-22 | -21.3 | BC041078 | HLA-C | C_T | C | T | C | T | positive |
| rs3129950 | 100300978_TGI_at | C/G | G | 0.908 | 6 | 32466179 | 0.000329 | -6.748 | 1.5E-11 | -10.8242 | NM_178014 | TUBB | C_G | C | G | C | G | negative |
| rs3094627 | 100162706_TGI_at | C/T | T | 0.858 | 6 | 30429461 | 0.000437 | -8.594 | 8.4E-18 | -17.0758 | D83543 | | C_T | C | T | C | T | negative |
| rs3094627 | 100305045_TGI_at | C/T | T | 0.858 | 6 | 30429461 | 0.000437 | -8.679 | 4E-18 | -17.3987 | D83543 | | C_T | C | T | C | T | negative |
| rs199439 | 100300682_TGI_at | A/G | G | 0.192 | 17 | 42148686 | 0.000472 | 6.883 | 5.9E-12 | -11.2321 | R48770 | BRWD1 | A_G | A | G | A | G | negative |
| rs7739357 | 100127159_TGI_at | A/G | G | 0.549 | 6 | 32549619 | 0.000477 | 19.796 | 3.2E-87 | -86.4918 | NM_021983 | HLA-DRB4 | A_G | A | G | A | G | negative |
| rs1264695 | merck.AK128290_at | A/G | G | 0.242 | 6 | 30175871 | 0.000478 | 10.796 | 3.6E-27 | -26.4443 | NA | NA | G_A | A | G | G | A | positive |
| rs3130374 | 100305045_TGI_at | C/T | T | 0.142 | 6 | 30429315 | 0.000485 | 8.679 | 4E-18 | -17.3987 | D83543 | | C_T | C | T | C | T | negative |
| rs3130374 | 100162706_TGI_at | C/T | T | 0.142 | 6 | 30429315 | 0.000485 | 8.594 | 8.4E-18 | -17.0758 | D83543 | | C_T | C | T | C | T | negative |
| rs538628 | 100308628_TGI_at | C/G | G | 0.814 | 17 | 42142496 | 0.00049 | 36.033 | 3E-284 | -283.594 | BF475443 | LRRC37A4 | C_G | C | G | C | G | positive |
| rs538628 | 100159134_TGI_at | C/G | G | 0.814 | 17 | 42142496 | 0.00049 | -11.594 | 4.4E-31 | -30.3546 | NM_014798 | PLEKHM1 | C_G | C | G | C | G | negative |
| rs538628 | 100135158_TGI_at | C/G | G | 0.814 | 17 | 42142496 | 0.00049 | 31.05 | 1E-211 | -210.943 | ENST00000329477 | LRRC37A4 | C_G | C | G | C | G | positive |
| rs3130375 | 100162706_TGI_at | A/C | C | 0.866 | 6 | 30429711 | 0.000543 | -8.594 | 8.4E-18 | -17.0758 | D83543 | | A_C | A | C | A | C | negative |
| rs3130375 | 100305045_TGI_at | A/C | C | 0.866 | 6 | 30429711 | 0.000543 | -8.679 | 4E-18 | -17.3987 | D83543 | | A_C | A | C | A | C | negative |
| rs3134930 | 100139572_TGI_at | C/T | T | 0.06 | 6 | 32299598 | 0.000571 | -17.86 | 2.4E-71 | -70.6168 | NM_022555 | HLA-DRB3 | T_C | C | T | T | C | negative |
| rs3094061 | 100162706_TGI_at | A/C | C | 0.142 | 6 | 30429168 | 0.000592 | -8.594 | 8.4E-18 | -17.0758 | D83543 | | C_A | A | C | C | A | negative |
| rs3094061 | 100305045_TGI_at | A/C | C | 0.142 | 6 | 30429168 | 0.000592 | -8.679 | 4E-18 | -17.3987 | D83543 | | C_A | A | C | C | A | negative |
| rs2248373 | 100302940_TGI_at | C/T | T | 0.417 | 6 | 31554525 | 0.000661 | 6.31 | 2.8E-10 | -9.5543 | NM_002125 | HLA-DRB5 | C_T | C | T | C | T | positive |
| rs3130825 | 100308127_TGI_at | C/G | G | 0.89 | 6 | 29331472 | 0.00076 | 6.85 | 7.4E-12 | -11.1316 | BG746649 | HCG18 | C_G | C | G | C | G | positive |
| rs9257744 | 100301615_TGI_at | A/C | C | 0.242 | 6 | 29414329 | 0.000761 | 8.037 | 9.2E-16 | -15.0359 | NM_030899 | ZNF323 | A_C | A | C | A | C | negative |
| rs9257744 | 100143968_TGI_at | A/C | C | 0.242 | 6 | 29414329 | 0.000761 | 8.116 | 4.8E-16 | -15.3171 | NM_145909 | ZNF323 | A_C | A | C | A | C | negative |
| rs7832968 | 100311514_TGI_at | A/G | G | 0.534 | 8 | 8690299 | 0.000772 | -6.428 | 1.3E-10 | -9.8884 | AK129982 | | A_G | A | G | A | G | negative |
| rs7832968 | 100312826_TGI_at | A/G | G | 0.534 | 8 | 8690299 | 0.000772 | -6.233 | 4.6E-10 | -9.3395 | AI217876 | | A_G | A | G | A | G | negative |
| rs172328 | 100123483_TGI_at | C/T | T | 0.14 | 6 | 28898507 | 0.000784 | -8.985 | 2.6E-19 | -18.5871 | AK056727 | HCG4P6 | T_C | C | T | T | C | negative |
| rs172328 | 100160221_TGI_at | C/T | T | 0.14 | 6 | 28898507 | 0.000784 | 8.494 | 2E-17 | -16.6997 | NM_002127 | HLA-G | T_C | C | T | T | C | positive |
| rs172328 | 100125007_TGI_at | C/T | T | 0.14 | 6 | 28898507 | 0.000784 | -8.095 | 5.7E-16 | -15.2421 | AF036974 | C6orf12 | T_C | C | T | T | C | negative |
| rs172328 | 100303756_TGI_at | C/T | T | 0.14 | 6 | 28898507 | 0.000784 | -7.69 | 1.5E-14 | -13.8323 | M27539 | HLA-A | T_C | C | T | T | C | negative |
| rs172328 | 100129349_TGI_at | C/T | T | 0.14 | 6 | 28898507 | 0.000784 | 14.655 | 1.3E-48 | -47.9025 | NM_002116 | HLA-A | T_C | C | T | T | C | positive |
| rs16836230 | 100136516_TGI_at | C/G | G | 0.759 | 1 | 1.49E+08 | 0.000799 | -7.184 | 6.8E-13 | -12.1694 | hCT1834979.1 | | C_G | C | G | C | G | negative |
| rs3130453 | 100311825_TGI_at | C/T | T | 0.467 | 6 | 31232828 | 0.000858 | 6.623 | 3.5E-11 | -10.4535 | AK092748 | RP3-377H14.5 | C_T | C | T | C | T | negative |
| rs9272346 | 100158347_T | A/G | G | 0.45 | 6 | 32712350 | 0.000863 | - | 5.1E-24 | -23.2887 | BF966155 | C19orf6 | G_A | A | G | G | A | positive |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | 10.107 | | | | | | | | | | |
| rs9272346 | 100303039_TGI_at | A/G | G | 0.45 | 6 | 32712350 | 0.000863 | -7.529 | 5.1E-14 | -13.2913 | NM_001264 | CDSN | G_A | A | G | G | A | positive |
| rs9272346 | 100300305_TGI_at | A/G | G | 0.45 | 6 | 32712350 | 0.000863 | -6.341 | 2.3E-10 | -9.6415 | XM_001130818 | | G_A | A | G | G | A | positive |
| rs2015353 | 100159981_TGI_at | C/T | T | 0.542 | 17 | 15814000 | 0.000916 | 6.92 | 4.5E-12 | -11.3452 | XM_936321 | | C_T | C | T | C | T | positive |
| rs3870339 | 100148878_TGI_at | A/T | T | 0.294 | 3 | 49511867 | 0.000959 | -30.127 | 2E-199 | -198.668 | AA011598 | | T_A | A | T | T | A | negative |
| rs200994 | 100141839_TGI_at | G/T | T | 0.25 | 6 | 27921792 | 0.000964 | 6.604 | 4E-11 | -10.3977 | BC014021 | BTN2A2 | T_G | G | T | T | G | positive |
| rs1794282 | 100126143_TGI_at | C/T | T | 0.083 | 6 | 32774504 | 0.00097 | 6.437 | 1.2E-10 | -9.9141 | NM_019101 | APOM | T_C | C | T | T | C | positive |

## Supplementary Table 4: FEV$_1$/FVC *cis*-eSNPs

Table shows the list of FEV$_1$/FVC *cis* acting eSNPs. Header definitions are the same as Supplementary Table 2.

**FEV1/FVC *cis lung* eSNPs**

| eSNP | eSNP regulated probeset | GWAS SNP alleles | GWAS Reference allele | Reference allele freq in HapMap | Chr | SNP Position | GWAS_ Pval_ FEV1/FVC | eQTL Z meta | eQTL P value | log10. pvalue. meta | sequence source ID | Gene Symbol | eQTL-alleles | GWAS_ noncoded_ alleles | GWAS_ coded_ alleles | eQTL_ noncoded_alleles | eQTL_ coded_ alleles | Expected Direction Of Effect of mRNA with lung function |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs12509311 | 100139086_TGI_at | C/T | T | 0.405 | 4 | 145698112 | 5.91E-19 | -5.216 | 1.8E-07 | -6.738 | AK024689 | cDNA clone map to HHIP | C_T | C | T | C | T | negative |
| rs13141641 | 100148028_TGI_at | C/T | T | 0.564 | 4 | 145725906 | 8.45E-18 | -4.071 | 4.7E-05 | -4.3296 | NM_022475 | HHIP | T_C | C | T | T | C | negative |
| rs13141641 | 100133899_TGI_at | C/T | T | 0.564 | 4 | 145725906 | 8.45E-18 | -4.211 | 2.5E-05 | -4.5948 | AK124396 | cDNA clone map to region upstream of HHIP | T_C | C | T | T | C | negative |
| rs2070600 | 100143779_TGI_at | C/T | T | 0.05 | 6 | 32259421 | 9.07E-15 | 4.36 | 1.3E-05 | -4.8858 | NM_172197 | AGER | T_C | C | T | T | C | negative |
| rs2070600 | 100313510_TGI_at | C/T | T | 0.05 | 6 | 32259421 | 9.07E-15 | 4.607 | 4.1E-06 | -5.3888 | AB036432 | AGER | T_C | C | T | T | C | negative |
| rs11853359 | 100308491_TGI_at | A/G | G | 0.702 | 15 | 69408578 | 7.40E-14 | -4.305 | 1.7E-05 | -4.7773 | BF969690 | THSD4 | A_G | A | G | A | G | negative |
| rs11853359 | 100142979_TGI_at | A/G | G | 0.702 | 15 | 69408578 | 7.40E-14 | -6.894 | 5.4E-12 | -11.266 | NM_024817 | THSD4 | A_G | A | G | A | G | negative |
| rs11853359 | 100310339_TGI_at | A/G | G | 0.702 | 15 | 69408578 | 7.40E-14 | -7.124 | 1E-12 | -11.98 | AY358143 | THSD4 | A_G | A | G | A | G | negative |
| rs2856437 | 100125191_TGI_at | A/G | G | 0.95 | 6 | 32265342 | 4.99E-10 | -4.428 | 9.5E-06 | -5.0218 | NM_020056 | HLA-DQA2 | G_A | A | G | G | A | negative |
| rs10906097 | 100149333_TGI_at | G/T | T | 0.567 | 10 | 12283827 | 3.43E-09 | 6.077 | 1.2E-09 | -8.912 | NM_006023 | CDC123 | G_T | G | T | G | T | negative |
| rs6657613 | 100307969_TGI_at | A/T | T | 0.534 | 1 | 17200787 | 3.55E-09 | -7.108 | 1.2E-12 | -11.929 | BI715270 | | A_T | A | T | A | T | positive |
| rs2028467 | 100130228_TGI_at | A/G | G | 0.65 | 15 | 69424902 | 4.16E-09 | -4.596 | 4.3E-06 | -5.3658 | U79293 | | G_A | A | G | G | A | negative |
| rs805284 | 100309111_TGI_at | A/G | G | 0.95 | 6 | 31790008 | 3.39E-08 | 4.234 | 2.3E-05 | -4.6391 | BC105735 | MUC21 | G_A | A | G | G | A | positive |
| rs805284 | 100159175_TGI_at | A/G | G | 0.95 | 6 | 31790008 | 3.39E-08 | 4.946 | 7.6E-07 | -6.1206 | NM_001010909 | MUC21 | G_A | A | G | G | A | positive |
| rs1865736 | 100150862_TGI_at | A/G | G | 0.75 | 12 | 94771960 | 3.76E-08 | -8.603 | 7.8E-18 | -17.11 | BX108644 | | A_G | A | G | A | G | positive |
| rs4784887 | 100142706_TGI_at | A/G | G | 0.358 | 16 | 56623125 | 8.02E-08 | 4.973 | 6.6E-07 | -6.181 | NM_002428 | MMP15 | A_G | A | G | A | G | negative |
| rs7730971 | 100147290_TGI_at | C/G | G | 0.583 | 5 | 147771053 | 1.69E-07 | 5.094 | 3.5E-07 | -6.4552 | NM_001001325 | | C_G | C | G | C | G | positive |
| rs756345 | 100148014_TGI_at | A/G | G | 0.667 | 4 | 90292237 | 2.26E-07 | 4.053 | 5.1E-05 | -4.2961 | NM_145715 | TIGD2 | G_A | A | G | G | A | negative |
| rs1481345 | 100303767_TGI_at | C/T | T | 0.373 | 1 | 216894478 | 1.52E-06 | -4.686 | 2.8E-06 | -5.555 | M19154 | TGFB2 | T_C | C | T | T | C | negative |
| rs7550829 | 100309227_TGI_at | C/T | T | 0.075 | 1 | 17230164 | 1.74E-06 | -4.518 | 6.2E-06 | -5.2046 | BC070363 | | C_T | C | T | C | T | negative |
| rs7550829 | 100155522_TGI_at | C/T | T | 0.075 | 1 | 17230164 | 1.74E-06 | -5.055 | 4.3E-07 | -6.3661 | BC070363 | | C_T | C | T | C | T | negative |
| rs599707 | 100139818_T | C/T | T | 0.093 | 6 | 31916415 | 1.90E-06 | 5.467 | 4.6E-08 | -7.3394 | NM_080686 | BAT2 | T_C | C | T | T | C | positive |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | GI_at |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| rs153918 | 100306800_TGI_at | A/T | T | 0.509 | 5 | 95063783 | 2.14E-06 | 6.762 | 1.4E-11 | -10.866 | BU619786 | RHOBTB3 | T_A | A | T | T | A | positive |
| rs153918 | 100126558_TGI_at | A/T | T | 0.509 | 5 | 95063783 | 2.14E-06 | 7.31 | 2.7E-13 | -12.573 | NM_014899 | RHOBTB3 | T_A | A | T | T | A | positive |
| rs213002 | 100143194_TGI_at | A/C | C | 0.475 | 5 | 95058745 | 2.17E-06 | 6.794 | 1.1E-11 | -10.962 | BC020231 | RHOBTB3 | A_C | A | C | A | C | positive |
| rs173879 | 100143194_TGI_at | C/G | G | 0.517 | 5 | 95058021 | 2.27E-06 | 6.794 | 1.1E-11 | -10.962 | BC020231 | RHOBTB3 | G_C | C | G | G | C | positive |
| rs2548131 | 100143194_TGI_at | C/T | T | 0.517 | 5 | 95054602 | 2.27E-06 | 6.794 | 1.1E-11 | -10.962 | BC020231 | RHOBTB3 | T_C | C | T | T | C | positive |
| rs169883 | 100154919_TGI_at | C/T | T | 0.483 | 5 | 95059597 | 2.32E-06 | -6.939 | 3.9E-12 | -11.404 | AK057894 | RHOBTB3 | T_C | C | T | T | C | positive |
| rs2609260 | 100160946_TGI_at | C/T | T | 0.822 | 4 | 90055842 | 2.71E-06 | 7.071 | 1.5E-12 | -11.813 | NM_014883 | FAM13A1 | C_T | C | T | C | T | negative |
| rs2609260 | 100312038_TGI_at | C/T | T | 0.822 | 4 | 90055842 | 2.71E-06 | 6.311 | 2.8E-10 | -9.5571 | AK027138 | FAM13A1 | C_T | C | T | C | T | negative |
| rs2609260 | 100151492_TGI_at | C/T | T | 0.822 | 4 | 90055842 | 2.71E-06 | 7.285 | 3.2E-13 | -12.493 | AK023526 |  | C_T | C | T | C | T | negative |
| rs3117574 | 100126143_TGI_at | A/G | G | 0.9 | 6 | 31833209 | 2.75E-06 | 8.012 | 1.1E-15 | -14.948 | NM_019101 | APOM | A_G | A | G | A | G | positive |
| rs316398 | 100309522_TGI_at | A/G | G | 0.2 | 5 | 43073783 | 2.80E-06 | 5.274 | 1.3E-07 | -6.8746 | BC039088 |  | G_A | A | G | G | A | positive |
| rs316398 | 100155226_TGI_at | A/G | G | 0.2 | 5 | 43073783 | 2.80E-06 | 4.88 | 1.1E-06 | -5.9743 | AK075204 | hCG_2039148 | G_A | A | G | G | A | positive |
| rs316398 | 100129380_TGI_at | A/G | G | 0.2 | 5 | 43073783 | 2.80E-06 | 6.767 | 1.3E-11 | -10.881 | ENST00000314957 |  | G_A | A | G | G | A | positive |
| rs316398 | 100123880_TGI_at | A/G | G | 0.2 | 5 | 43073783 | 2.80E-06 | 6.08 | 1.2E-09 | -8.9202 | BC039088 |  | G_A | A | G | G | A | positive |
| rs3891175 | 100305836_TGI_at | C/T | T | 0.167 | 6 | 32742445 | 3.24E-06 | 6.962 | 3.4E-12 | -11.474 | CA308455 | HLA-DPA1 | T_C | C | T | T | C | positive |
| rs11257655 | 100139207_TGI_at | C/T | T | 0.259 | 10 | 12347900 | 3.47E-06 | 13.121 | 2.5E-39 | -38.603 | BU616230 | CAMK1D | C_T | C | T | C | T | negative |
| rs11257655 | 100142010_TGI_at | C/T | T | 0.259 | 10 | 12347900 | 3.47E-06 | 14.628 | 1.9E-48 | -47.73 | NM_153498 | CAMK1D | C_T | C | T | C | T | negative |
| rs11257655 | 100161388_TGI_at | C/T | T | 0.259 | 10 | 12347900 | 3.47E-06 | 5.37 | 7.9E-08 | -7.1038 | AW900148 |  | C_T | C | T | C | T | negative |
| rs11257655 | 100301887_TGI_at | C/T | T | 0.259 | 10 | 12347900 | 3.47E-06 | 11.328 | 9.5E-30 | -29.021 | NM_020397 | CAMK1D | C_T | C | T | C | T | negative |
| rs10076733 | 100158314_TGI_at | G/T | T | 0.233 | 5 | 131788630 | 3.91E-06 | 4.217 | 2.5E-05 | -4.6063 | BC043424 |  | G_T | G | T | G | T | negative |
| rs6450094 | 100135535_TGI_at | A/G | G | 0.75 | 5 | 52258508 | 4.50E-06 | -4.342 | 1.4E-05 | -4.8502 | X17033 | ITGA2 | A_G | A | G | A | G | negative |
| rs2548993 | 100123073_TGI_at | A/G | G | 0.283 | 5 | 131836768 | 7.97E-06 | 6.364 | 2E-10 | -9.7065 | NM_003060 | SLC22A5 | A_G | A | G | A | G | negative |
| rs7209622 | 100308887_TGI_at | C/G | G | 0.509 | 17 | 25280933 | 9.67E-06 | -4.337 | 1.4E-05 | -4.8403 | BE614389 | ANKRD13B | C_G | C | G | C | G | positive |
| rs7209622 | 100159312_TGI_at | C/G | G | 0.509 | 17 | 25280933 | 9.67E-06 | -4.194 | 2.7E-05 | -4.5621 | NM_152345 | ANKRD13B | C_G | C | G | C | G | positive |
| rs8042238 | 100129239_TGI_at | C/T | T | 0.638 | 15 | 76561326 | 9.85E-06 | 4.365 | 1.3E-05 | -4.8958 | AW118658 | IREB2 | C_T | C | T | C | T | negative |
| rs3219190 | 100149313_TGI_at | C/T | T | 0.875 | 6 | 31605954 | 1.00E-05 | 4.408 | 1E-05 | -4.9816 | NM_007161 | LST1 | T_C | C | T | T | C | positive |
| rs2036527 | 100148404_TGI_at | A/G | G | 0.575 | 15 | 76638670 | 1.19E-05 | 6.946 | 3.8E-12 | -11.425 | NM_002789 | PSMA4 | G_A | A | G | G | A | negative |
| rs17310361 | 100305819_TGI_at | C/T | T | 0.908 | 11 | 72911372 | 1.28E-05 | 5.503 | 3.7E-08 | -7.4278 | CA311483 | FAM168A | C_T | C | T | C | T | negative |
| rs1063281 | 100145096_TGI_at | C/T | T | 0.608 | 2 | 218376977 | 1.37E-05 | -4.309 | 1.6E-05 | -4.7852 | NM_022648 | TNS1 | T_C | C | T | T | C | positive |
| rs7727320 | 100134215_TGI_at | C/G | G | 0.733 | 5 | 147812764 | 1.55E-05 | -6.58 | 4.7E-11 | -10.328 | NM_030793 | FBXO38 | G_C | C | G | G | C | negative |
| rs3743024 | 100306577_T | A/G | G | 0.4 | 15 | 39906263 | 1.56E-05 | -9.895 | 4.4E-23 | -22.359 | BX102344 | MGA | G_A | A | G | G | A | positive |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs10777747 | 100310201_TGI_at | A/G | G | 0.331 | 12 | 94788101 | 1.58E-05 | -4.409 | 1E-05 | -4.9836 | BC002505 | SNRPF | A_G | A | G | A | G | negative |
| rs10777749 | 100145491_TGI_at | A/G | G | 0.678 | 12 | 94801091 | 1.60E-05 | -8.625 | 6.4E-18 | -17.193 | NM_003095 | SNRPF | A_G | A | G | A | G | positive |
| rs7308921 | 100310201_TGI_at | A/G | G | 0.333 | 12 | 94788666 | 1.77E-05 | -4.409 | 1E-05 | -4.9836 | BC002505 | SNRPF | A_G | A | G | A | G | negative |
| rs7925226 | 100301195_TGI_at | A/G | G | 0.093 | 11 | 72815010 | 1.94E-05 | 10.498 | 8.8E-26 | -25.054 | NM_152222 | RELT | A_G | A | G | A | G | positive |
| rs2844518 | 100305045_TGI_at | C/T | T | 0.377 | 6 | 31480548 | 2.09E-05 | -12.681 | 7.5E-37 | -36.123 | D83543 | | T_C | C | T | T | C | negative |
| rs2844518 | 100162706_TGI_at | C/T | T | 0.377 | 6 | 31480548 | 2.09E-05 | -12.03 | 2.5E-33 | -32.607 | D83543 | | T_C | C | T | T | C | negative |
| rs2076600 | 100310898_TGI_at | A/G | G | 0.817 | 1 | 17209978 | 2.14E-05 | -5.015 | 5.3E-07 | -6.2754 | AL834169 | CROCC | G_A | A | G | G | A | negative |
| rs2076600 | 100124110_TGI_at | A/G | G | 0.817 | 1 | 17209978 | 2.14E-05 | -4.618 | 3.9E-06 | -5.4118 | AK128484 | CROCCL1 | G_A | A | G | G | A | negative |
| rs1200348 | 100154811_TGI_at | C/T | T | 0.492 | 15 | 39608460 | 2.19E-05 | -8.226 | 1.9E-16 | -15.713 | NM_015540 | RPAP1 | T_C | C | T | T | C | negative |
| rs10519717 | 100311674_TGI_at | C/T | T | 0.867 | 4 | 145699790 | 2.48E-05 | -4.155 | 3.3E-05 | -4.4877 | AK098525 | HHIP | C_T | C | T | C | T | negative |
| rs931794 | 100156434_TGI_at | A/G | G | 0.433 | 15 | 76613235 | 2.67E-05 | -10.596 | 3.1E-26 | -25.507 | NM_000745 | CHRNA5 | A_G | A | G | A | G | positive |
| rs931794 | 100313804_TGI_at | A/G | G | 0.433 | 15 | 76613235 | 2.67E-05 | 6.086 | 1.2E-09 | -8.9364 | AA532820 | | A_G | A | G | A | G | negative |
| rs9273363 | 100302941_TGI_at | A/C | C | 0.683 | 6 | 32734250 | 2.72E-05 | -12.547 | 4.1E-36 | -35.384 | NM_002123 | HLA-DQB1 | C_A | A | C | C | A | positive |
| rs9273363 | 100304009_TGI_at | A/C | C | 0.683 | 6 | 32734250 | 2.72E-05 | -12.742 | 3.5E-37 | -36.462 | ENST00000374943 | HLA-DQB1 | C_A | A | C | C | A | positive |
| rs9273363 | 100300398_TGI_at | A/C | C | 0.683 | 6 | 32734250 | 2.72E-05 | -12.614 | 1.8E-36 | -35.753 | X03068 | HLA-DQB1 | C_A | A | C | C | A | positive |
| rs2726490 | 100160580_TGI_at | C/T | T | 0.575 | 4 | 106490971 | 2.80E-05 | -8.525 | 1.5E-17 | -16.816 | BM977451 | PPA2 | C_T | C | T | C | T | negative |
| rs2726490 | 100307499_TGI_at | C/T | T | 0.575 | 4 | 106490971 | 2.80E-05 | -8.523 | 1.6E-17 | -16.808 | BM977451 | PPA2 | C_T | C | T | C | T | negative |
| rs10055430 | 100313079_TGI_at | A/G | G | 0.276 | 5 | 147777732 | 2.89E-05 | 12.615 | 1.7E-36 | -35.758 | AF251055 | FBXO38 | A_G | A | G | A | G | positive |
| rs7957346 | 100137266_TGI_at | A/C | C | 0.508 | 12 | 94784605 | 2.94E-05 | 9.818 | 9.4E-23 | -22.026 | NM_021229 | NTN4 | C_A | A | C | C | A | negative |
| rs9944249 | 100129019_TGI_at | G/T | T | 0.442 | 15 | 39634468 | 3.34E-05 | 15.354 | 3.3E-53 | -52.478 | NM_006293 | TYRO3 | G_T | G | T | G | T | positive |
| rs9944249 | 100124857_TGI_at | G/T | T | 0.442 | 15 | 39634468 | 3.34E-05 | 6.724 | 1.8E-11 | -10.753 | NM_002220 | ITPKA | G_T | G | T | G | T | positive |
| rs9944249 | 100154412_TGI_at | G/T | T | 0.442 | 15 | 39634468 | 3.34E-05 | 23.806 | 3E-125 | -124.54 | NM_206961 | LTK | G_T | G | T | G | T | positive |
| rs9944249 | 100305514_TGI_at | G/T | T | 0.442 | 15 | 39634468 | 3.34E-05 | 4.785 | 1.7E-06 | -5.767 | CD558726 | TMEM87A | G_T | G | T | G | T | positive |
| rs8053376 | 100149583_TGI_at | A/G | G | 0.575 | 16 | 18867252 | 3.48E-05 | 4.946 | 7.6E-07 | -6.1206 | AA773342 | ARL6IP1 | A_G | A | G | A | G | positive |
| rs890498 | 100302252_TGI_at | C/G | G | 0.417 | 15 | 39898590 | 3.68E-05 | 5.795 | 6.8E-09 | -8.1654 | NM_014994 | MAPKBP1 | C_G | C | G | C | G | positive |
| rs890498 | 100157433_TGI_at | C/G | G | 0.417 | 15 | 39898590 | 3.68E-05 | -4.127 | 3.7E-05 | -4.4347 | ENST00000309874 | | C_G | C | G | C | G | negative |
| rs1862874 | 100125704_TGI_at | A/T | T | 0.78 | 5 | 156626536 | 3.79E-05 | 4.583 | 4.6E-06 | -5.3388 | NM_001037333 | CYFIP2 | A_T | A | T | A | T | positive |
| rs11191751 | 100150425_TGI_at | A/G | G | 0.133 | 10 | 105381715 | 3.80E-05 | 4.83 | 1.4E-06 | -5.8648 | W57592 | SH3PXD2A | G_A | A | G | G | A | negative |
| rs2844559 | 100144394_TGI_at | C/T | T | 0.167 | 6 | 31448054 | 3.83E-05 | 4.674 | 3E-06 | -5.5296 | NM_006674 | HCP5 | T_C | C | T | T | C | positive |
| rs4567782 | 100305934_TGI_at | A/C | C | 0.482 | 17 | 25292926 | 4.02E-05 | 5.974 | 2.3E-09 | -8.6354 | BX648689 | EFCAB5 | A_C | A | C | A | C | negative |
| rs2009746 | 100154936_T | A/G | G | 0.405 | 15 | 76541157 | 4.12E-05 | 17.254 | 1E-66 | -65.981 | AF147302 | | G_A | A | G | G | A | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs3781352 | 100150425_TGI_at | C/T | T | 0.133 | 10 | 105379476 | 4.17E-05 | 4.83 | 1.4E-06 | -5.8648 | W57592 | SH3PXD2A | T_C | C | T | T | C | negative |
| rs11653487 | 100300166_TGI_at | C/T | T | 0.55 | 17 | 34196157 | 4.19E-05 | 4.098 | 4.2E-05 | -4.3801 | XM_372668 | ARL5C | C_T | C | T | C | T | negative |
| rs9921330 | 100147953_TGI_at | A/G | G | 0.822 | 16 | 73884902 | 4.55E-05 | 4.623 | 3.8E-06 | -5.4222 | NM_006324 | CFDP1 | A_G | A | G | A | G | negative |
| rs2303644 | 100306708_TGI_at | A/G | G | 0.608 | 5 | 178487651 | 4.60E-05 | 4.15 | 3.3E-05 | -4.4782 | BU733456 | | A_G | A | G | A | G | positive |
| rs11080616 | 100142718_TGI_at | A/G | G | 0.817 | 18 | 12951999 | 4.90E-05 | 7.793 | 6.5E-15 | -14.184 | NM_032142 | CEP192 | A_G | A | G | A | G | positive |
| rs11080616 | 100154727_TGI_at | A/G | G | 0.817 | 18 | 12951999 | 4.90E-05 | 6.652 | 2.9E-11 | -10.539 | AK096548 | CEP192 | A_G | A | G | A | G | positive |
| rs2855812 | 100161520_TGI_at | G/T | T | 0.258 | 6 | 31580699 | 5.11E-05 | 7.236 | 4.6E-13 | -12.335 | NM_005931 | MICB | G_T | G | T | G | T | negative |
| rs2568494 | 100132425_TGI_at | A/G | G | 0.582 | 15 | 76528019 | 5.25E-05 | 4.118 | 3.8E-05 | -4.4177 | NM_001083612 | | A_G | A | G | A | G | positive |
| rs17331332 | 100129915_TGI_at | A/G | G | 0.923 | 4 | 107027556 | 5.30E-05 | 4.502 | 6.7E-06 | -5.1719 | NM_001033047 | NPNT | A_G | A | G | A | G | negative |
| rs8022046 | 100127661_TGI_at | A/G | G | 0.224 | 14 | 74348055 | 5.80E-05 | -4.33 | 1.5E-05 | -4.8265 | NM_014239 | EIF2B2 | A_G | A | G | A | G | negative |
| rs131284 | 100141331_TGI_at | C/T | T | 0.425 | 22 | 28487589 | 6.04E-05 | -12.616 | 1.7E-36 | -35.764 | NM_013387 | | T_C | C | T | T | C | negative |
| rs6593973 | 100300216_TGI_at | A/G | G | 0.912 | 1 | 204152539 | 6.35E-05 | -4.186 | 2.8E-05 | -4.5468 | XM_209271 | | A_G | A | G | A | G | negative |
| rs6593973 | 100155586_TGI_at | A/G | G | 0.912 | 1 | 204152539 | 6.35E-05 | 4.123 | 3.7E-05 | -4.4272 | NM_152491 | PM20D1 | A_G | A | G | A | G | positive |
| rs6593973 | 100151213_TGI_at | A/G | G | 0.912 | 1 | 204152539 | 6.35E-05 | 4.846 | 1.3E-06 | -5.8997 | AK097788 | | A_G | A | G | A | G | positive |
| rs4924575 | 100147021_TGI_at | C/T | T | 0.405 | 15 | 39884218 | 6.36E-05 | 10.094 | 5.9E-24 | -23.231 | ENST00000335032 | JMJD7-PLA2G4B | C_T | C | T | C | T | positive |
| rs6444749 | 100155944_TGI_at | C/T | T | 0.575 | 3 | 195028932 | 7.39E-05 | 5.361 | 8.3E-08 | -7.0822 | BX099811 | | C_T | C | T | C | T | positive |
| rs2834449 | 100155146_TGI_at | C/T | T | 0.366 | 21 | 34623226 | 7.40E-05 | -5.709 | 1.1E-08 | -7.9445 | NM_172201 | KCNE2 | T_C | C | T | T | C | negative |
| rs2834449 | 100145031_TGI_at | C/T | T | 0.366 | 21 | 34623226 | 7.40E-05 | -6.193 | 5.9E-10 | -9.2289 | NM_032476 | MRPS6 | T_C | C | T | T | C | negative |
| rs713718 | 100160585_TGI_at | G/T | T | 0.592 | 22 | 28644092 | 7.82E-05 | -11.645 | 2.4E-31 | -30.614 | ENST00000323630 | MTMR3 | G_T | G | T | G | T | negative |
| rs713718 | 100131090_TGI_at | G/T | T | 0.592 | 22 | 28644092 | 7.82E-05 | 4.46 | 8.2E-06 | -5.0864 | NM_003634 | NIPSNAP1 | G_T | G | T | G | T | positive |
| rs713718 | 100308994_TGI_at | G/T | T | 0.592 | 22 | 28644092 | 7.82E-05 | -11.13 | 9E-29 | -28.048 | BC151217 | MTMR3 | G_T | G | T | G | T | negative |
| rs9469220 | 100157567_TGI_at | A/G | G | 0.6 | 6 | 32766288 | 8.12E-05 | 13.302 | 2.3E-40 | -39.647 | NM_182549 | HLA-DQB2 | A_G | A | G | A | G | negative |
| rs9469220 | 100311684_TGI_at | A/G | G | 0.6 | 6 | 32766288 | 8.12E-05 | 11.979 | 4.6E-33 | -32.339 | AK098007 | HLA-DQB2 | A_G | A | G | A | G | negative |
| rs9469220 | 100311704_TGI_at | A/G | G | 0.6 | 6 | 32766288 | 8.12E-05 | 11.67 | 1.8E-31 | -30.741 | AK097297 | HLA-DQB1 | A_G | A | G | A | G | negative |
| rs9469220 | 100142471_TGI_at | A/G | G | 0.6 | 6 | 32766288 | 8.12E-05 | -5.639 | 1.7E-08 | -7.7669 | AK057104 | | A_G | A | G | A | G | positive |
| rs12649925 | 100129781_TGI_at | C/T | T | 0.643 | 4 | 56173264 | 8.48E-05 | 4.311 | 1.6E-05 | -4.7891 | ENST00000381322 | CLOCK | T_C | C | T | T | C | negative |
| rs12649925 | 100307345_TGI_at | C/T | T | 0.643 | 4 | 56173264 | 8.48E-05 | -7.183 | 6.8E-13 | -12.166 | BQ013439 | CLOCK | T_C | C | T | T | C | positive |
| rs10512248 | 100141529_TGI_at | G/T | T | 0.683 | 9 | 97299524 | 9.27E-05 | 4.394 | 1.1E-05 | -4.9536 | NM_001083602 | PTCH1 | G_T | G | T | G | T | positive |
| rs1042173 | 100136117_TGI_at | A/C | C | 0.433 | 17 | 25549137 | 9.40E-05 | 4.88 | 1.1E-06 | -5.9743 | AK000606 | GOSR1 | C_A | A | C | C | A | positive |
| rs8025614 | 100306182_TGI_at | A/G | G | 0.454 | 15 | 39930204 | 0.0001031 | 7.056 | 1.7E-12 | -11.766 | BX640787 | MAPKBP1 | A_G | A | G | A | G | negative |
| rs3134940 | 100158927_T | C/T | T | 0.84 | 6 | 32257794 | 0.000106 | 8.348 | 6.9E-17 | -16.159 | NM_006913 | RNF5 | T_C | C | T | T | C | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs5752972 | 100302806_TGI_at | A/T | T | 0.592 | 22 | 28580312 | 0.0001087 | 4.822 | 1.4E-06 | -5.8473 | NM_003634 | NIPSNAP1 | A_T | A | T | A | T | positive |
| rs6088580 | 100300977_TGI_at | C/G | G | 0.5 | 20 | 32748714 | 0.0001137 | -20.554 | 7.1E-94 | -93.15 | NM_178025 | GGT7 | G_C | C | G | G | C | negative |
| rs6088580 | 100307620_TGI_at | C/G | G | 0.5 | 20 | 32748714 | 0.0001137 | 12.72 | 4.6E-37 | -36.339 | BM742377 | ITCH | G_C | C | G | G | C | positive |
| rs6088580 | 100143040_TGI_at | C/G | G | 0.5 | 20 | 32748714 | 0.0001137 | 6.154 | 7.6E-10 | -9.1218 | NM_181509 | MAP1LC3A | G_C | C | G | G | C | positive |
| rs2077543 | 100156388_TGI_at | C/G | G | 0.628 | 15 | 39919492 | 0.0001148 | -20.843 | 1.8E-96 | -95.753 | BC113983 | MAPKBP1 | C_G | C | G | C | G | negative |
| rs9272775 | 100302940_TGI_at | C/T | T | 0.592 | 6 | 32718235 | 0.000115 | 9.782 | 1.3E-22 | -21.871 | NM_002125 | HLA-DRB5 | C_T | C | T | C | T | negative |
| rs1146045 | 100155944_TGI_at | C/T | T | 0.575 | 3 | 195032102 | 0.0001155 | -5.361 | 8.3E-08 | -7.0822 | BX099811 | | T_C | C | T | T | C | positive |
| rs1043515 | 100123137_TGI_at | A/G | G | 0.575 | 17 | 34175722 | 0.0001222 | 5.312 | 1.1E-07 | -6.9649 | NM_003559 | PIP4K2B | G_A | A | G | G | A | positive |
| rs1043515 | 100304243_TGI_at | A/G | G | 0.575 | 17 | 34175722 | 0.0001222 | 5.19 | 2.1E-07 | -6.6772 | ENST00000269554 | PIP4K2B | G_A | A | G | G | A | positive |
| rs1043515 | 100134576_TGI_at | A/G | G | 0.575 | 17 | 34175722 | 0.0001222 | 5.948 | 2.7E-09 | -8.5663 | NM_002795 | PSMB3 | G_A | A | G | G | A | positive |
| rs9672671 | 100150740_TGI_at | C/T | T | 0.417 | 15 | 39704367 | 0.0001242 | 4.537 | 5.7E-06 | -5.2437 | NM_005090 | JMJD7-PLA2G4B | C_T | C | T | C | T | positive |
| rs9672671 | 100134750_TGI_at | C/T | T | 0.417 | 15 | 39704367 | 0.0001242 | 8.223 | 2E-16 | -15.702 | NM_016642 | SPTBN5 | C_T | C | T | C | T | positive |
| rs316408 | 100157324_TGI_at | C/T | T | 0.167 | 5 | 43102531 | 0.0001269 | -6.872 | 6.3E-12 | -11.199 | AK056817 | | T_C | C | T | T | C | negative |
| rs178415 | 100126167_TGI_at | G/T | T | 0.167 | 5 | 43113975 | 0.0001275 | 6.069 | 1.3E-09 | -8.8904 | BM992182 | | T_G | G | T | T | G | positive |
| rs178415 | 100157820_TGI_at | G/T | T | 0.167 | 5 | 43113975 | 0.0001275 | -4.602 | 4.2E-06 | -5.3784 | AK097396 | | T_G | G | T | T | G | negative |
| rs17602686 | 100136812_TGI_at | A/C | C | 0.149 | 15 | 49456917 | 0.0001276 | -4.041 | 5.3E-05 | -4.2739 | AL602112 | | C_A | A | C | C | A | positive |
| rs1574407 | 100147117_TGI_at | C/T | T | 0.167 | 5 | 43088648 | 0.0001277 | 9.063 | 1.3E-19 | -18.897 | NM_003432 | ZNF131 | C_T | C | T | C | T | negative |
| rs1574407 | 100155899_TGI_at | C/T | T | 0.167 | 5 | 43088648 | 0.0001277 | 4.342 | 1.4E-05 | -4.8502 | AK057759 | | C_T | C | T | C | T | negative |
| rs140701 | 100305644_TGI_at | C/T | T | 0.417 | 17 | 25562658 | 0.0001278 | -4.019 | 5.8E-05 | -4.2332 | CB241458 | CPD | T_C | C | T | T | C | negative |
| rs10859966 | 100140090_TGI_at | C/T | T | 0.658 | 12 | 94777506 | 0.0001292 | -4.137 | 3.5E-05 | -4.4536 | NM_182496 | CCDC38 | C_T | C | T | C | T | positive |
| rs2235910 | 100135390_TGI_at | G/T | T | 0.675 | 1 | 17298416 | 0.0001331 | -6.916 | 4.6E-12 | -11.333 | AB030176 | PADI2 | T_G | G | T | T | G | negative |
| rs2235910 | 100143443_TGI_at | G/T | T | 0.675 | 1 | 17298416 | 0.0001331 | -13.808 | 2.3E-43 | -42.642 | NM_007365 | PADI2 | T_G | G | T | T | G | negative |
| rs3826397 | 100305428_TGI_at | C/T | T | 0.667 | 17 | 43864446 | 0.0001419 | -7.046 | 1.8E-12 | -11.735 | CK004660 | | C_T | C | T | C | T | negative |
| rs11133403 | 100130701_TGI_at | C/T | T | 0.647 | 4 | 56170870 | 0.0001431 | -4.611 | 4E-06 | -5.3971 | BC002480 | SRD5A3 | C_T | C | T | C | T | negative |
| rs11133403 | 100147633_TGI_at | C/T | T | 0.647 | 4 | 56170870 | 0.0001431 | -15.165 | 6E-52 | -51.22 | NM_004898 | CLOCK | C_T | C | T | C | T | negative |
| rs11133403 | 100301711_TGI_at | C/T | T | 0.647 | 4 | 56170870 | 0.0001431 | -6.8 | 1E-11 | -10.98 | NM_024592 | SRD5A3 | C_T | C | T | C | T | negative |
| rs9435732 | 100133163_TGI_at | C/T | T | 0.175 | 1 | 17180745 | 0.0001431 | -5.788 | 7.1E-09 | -8.1473 | NM_017459 | MFAP2 | C_T | C | T | C | T | negative |
| rs2716943 | 100155542_TGI_at | G/T | T | 0.221 | 17 | 5483296 | 0.0001438 | 5.29 | 1.2E-07 | -6.9125 | BC065242 | RABEP1 | G_T | G | T | G | T | negative |
| rs2596501 | 100300038_TGI_at | C/T | T | 0.424 | 6 | 31429190 | 0.0001522 | -7.111 | 1.2E-12 | -11.939 | Z33453 | HLA-B | T_C | C | T | T | C | positive |
| rs3851706 | 100148972_TGI_at | A/G | G | 0.675 | 16 | 15858148 | 0.0001534 | -4.07 | 4.7E-05 | -4.3278 | NM_144600 | C16orf63 | G_A | A | G | G | A | positive |
| rs12037222 | 100302787_T | A/G | G | 0.763 | 1 | 39837548 | 0.0001543 | 5.951 | 2.7E-09 | -8.5743 | NM_003819 | PABPC4 | A_G | A | G | A | G | positive |

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| | GI_at | | | | | | | | | | | | | | | | | |
| rs886424 | 100303756_TGI_at | C/T | T | 0.193 | 6 | 30889981 | 0.0001549 | -7.814 | 5.5E-15 | -14.257 | M27539 | HLA-A | T_C | C | T | T | C | negative |
| rs2834440 | 100128165_TGI_at | A/G | G | 0.381 | 21 | 34612369 | 0.000155 | 4.097 | 4.2E-05 | -4.3783 | ENST00000361850 | C21orf82 | A_G | A | G | A | G | negative |
| rs17358468 | 100123896_TGI_at | C/T | T | 0.192 | 3 | 180509886 | 0.0001694 | -6.184 | 6.3E-10 | -9.2041 | AF085833 | | T_C | C | T | T | C | negative |
| rs7514452 | 100136037_TGI_at | C/T | T | 0.733 | 1 | 152704708 | 0.0001703 | -5.454 | 4.9E-08 | -7.3076 | NM_207308 | NUP210L | C_T | C | T | C | T | positive |
| rs2076607 | 100158208_TGI_at | C/T | T | 0.678 | 1 | 17295247 | 0.0001731 | -5.002 | 5.7E-07 | -6.2461 | AK055895 | NBPF1 | C_T | C | T | C | T | positive |
| rs2076607 | 100307733_TGI_at | C/T | T | 0.678 | 1 | 17295247 | 0.0001731 | -4.098 | 4.2E-05 | -4.3801 | BM665403 | | C_T | C | T | C | T | positive |
| rs4903262 | 100152363_TGI_at | A/G | G | 0.617 | 14 | 74410571 | 0.0001768 | -5.249 | 1.5E-07 | -6.8155 | AI566819 | TMED10 | A_G | A | G | A | G | positive |
| rs316413 | 100157820_TGI_at | C/T | T | 0.167 | 5 | 43129786 | 0.0001772 | 4.602 | 4.2E-06 | -5.3784 | AK097396 | | C_T | C | T | C | T | negative |
| rs2842895 | 100307951_TGI_at | C/G | G | 0.408 | 6 | 7051315 | 0.0001858 | 7.683 | 1.6E-14 | -13.809 | BI770221 | RREB1 | C_G | C | G | C | G | negative |
| rs3742783 | 100129848_TGI_at | C/T | T | 0.258 | 14 | 74446761 | 0.0001946 | 8.721 | 2.8E-18 | -17.56 | ENST00000238662 | MLH3 | T_C | C | T | T | C | negative |
| rs3742783 | 100146446_TGI_at | C/T | T | 0.258 | 14 | 74446761 | 0.0001946 | -9.033 | 1.7E-19 | -18.777 | NM_001040108 | MLH3 | T_C | C | T | T | C | positive |
| rs3742783 | 100302585_TGI_at | C/T | T | 0.258 | 14 | 74446761 | 0.0001946 | 9.549 | 1.3E-21 | -20.883 | NM_005784 | MLH3 | T_C | C | T | T | C | negative |
| rs3742783 | 100151060_TGI_at | C/T | T | 0.258 | 14 | 74446761 | 0.0001946 | -8.489 | 2.1E-17 | -16.681 | CA311614 | MLH3 | T_C | C | T | T | C | positive |
| rs11066028 | 100161262_TGI_at | A/C | C | 0.325 | 12 | 110729553 | 0.0001955 | 5.464 | 4.7E-08 | -7.3321 | NM_001034025 | ERP29 | A_C | A | C | A | C | positive |
| rs11066028 | 100300653_TGI_at | A/C | C | 0.325 | 12 | 110729553 | 0.0001955 | 5.888 | 3.9E-09 | -8.4079 | R93151 | ERP29 | A_C | A | C | A | C | positive |
| rs10866685 | 100154320_TGI_at | A/G | G | 0.909 | 5 | 157037289 | 0.0001978 | -4.16 | 3.2E-05 | -4.4972 | DB357058 | SGCD | A_G | A | G | A | G | negative |
| rs4660808 | 100133670_TGI_at | C/T | T | 0.233 | 1 | 39791096 | 0.000198 | 7.092 | 1.3E-12 | -11.879 | ENST00000331856 | | C_T | C | T | C | T | negative |
| rs4660808 | 100148761_TGI_at | C/T | T | 0.233 | 1 | 39791096 | 0.000198 | 6.703 | 2E-11 | -10.69 | NM_022120 | OXCT2 | C_T | C | T | C | T | negative |
| rs4660808 | 100313726_TGI_at | C/T | T | 0.233 | 1 | 39791096 | 0.000198 | 4.893 | 9.9E-07 | -6.003 | AA732526 | | C_T | C | T | C | T | negative |
| rs8365 | 100158927_TGI_at | C/G | G | 0.831 | 6 | 32256381 | 0.000201 | -8.348 | 6.9E-17 | -16.159 | NM_006913 | RNF5 | C_G | C | G | C | G | negative |
| rs2716931 | 100135777_TGI_at | C/T | T | 0.275 | 17 | 5511168 | 0.0002078 | -4.33 | 1.5E-05 | -4.8265 | NM_001083585 | RABEP1 | C_T | C | T | C | T | positive |
| rs17264866 | 100148761_TGI_at | C/G | G | 0.233 | 1 | 39795364 | 0.0002099 | 6.703 | 2E-11 | -10.69 | NM_022120 | OXCT2 | C_G | C | G | C | G | negative |
| rs7790478 | 100153459_TGI_at | A/G | G | 0.875 | 7 | 128135641 | 0.0002138 | 5.248 | 1.5E-07 | -6.8132 | NM_001012454 | FAM71F2 | A_G | A | G | A | G | negative |
| rs17565905 | 100154198_TGI_at | A/G | G | 0.692 | 10 | 12279950 | 0.0002174 | -7.381 | 1.6E-13 | -12.804 | NM_014142 | NUDT5 | A_G | A | G | A | G | negative |
| rs17565905 | 100303975_TGI_at | A/G | G | 0.692 | 10 | 12279950 | 0.0002174 | -7.032 | 2E-12 | -11.691 | ENST00000378952 | NUDT5 | A_G | A | G | A | G | negative |
| rs17565905 | 100129724_TGI_at | A/G | G | 0.692 | 10 | 12279950 | 0.0002174 | 4.941 | 7.8E-07 | -6.1095 | NM_018144 | SEC61A2 | A_G | A | G | A | G | positive |
| rs4934284 | 100304251_TGI_at | C/G | G | 0.108 | 10 | 82267277 | 0.0002211 | -12.212 | 2.7E-34 | -33.572 | ENST00000265450 | TSPAN14 | G_C | C | G | G | C | negative |
| rs4934284 | 100161068_TGI_at | C/G | G | 0.108 | 10 | 82267277 | 0.0002211 | -4.38 | 1.2E-05 | -4.9256 | NM_032333 | C10orf58 | G_C | C | G | G | C | negative |
| rs4934284 | 100150788_TGI_at | C/G | G | 0.108 | 10 | 82267277 | 0.0002211 | -12.272 | 1.3E-34 | -33.893 | NM_030927 | TSPAN14 | G_C | C | G | G | C | negative |
| rs12548626 | 100307977_TGI_at | A/C | C | 0.843 | 8 | 17754380 | 0.0002346 | -6.714 | 1.9E-11 | -10.723 | BI666677 | ASAH1 | A_C | A | C | A | C | negative |
| rs12548626 | 100308495_T | A/C | C | 0.843 | 8 | 17754380 | 0.0002346 | -6.956 | 3.5E-12 | -11.456 | BF965720 | ASAH1 | A_C | A | C | A | C | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs12548626 | 100303798_TGI_at | A/C | C | 0.843 | 8 | 17754380 | 0.0002346 | -5.181 | 2.2E-07 | -6.6562 | L27841 | PCM1 | A_C | A | C | A | C | negative |
| rs12548626 | 100312395_TGI_at | A/C | C | 0.843 | 8 | 17754380 | 0.0002346 | -4.238 | 2.3E-05 | -4.6468 | AI924817 | PCM1 | A_C | A | C | A | C | negative |
| rs12548626 | 100134179_TGI_at | A/C | C | 0.843 | 8 | 17754380 | 0.0002346 | -4.962 | 7E-07 | -6.1563 | ENST00000325083 | PCM1 | A_C | A | C | A | C | negative |
| rs3130349 | 100158927_TGI_at | A/G | G | 0.833 | 6 | 32255674 | 0.0002376 | -8.348 | 6.9E-17 | -16.159 | NM_006913 | RNF5 | A_G | A | G | A | G | negative |
| rs1294416 | 100136210_TGI_at | A/G | G | 0.5 | 6 | 6686326 | 0.0002478 | 5.66 | 1.5E-08 | -7.82 | BC039678 | | A_G | A | G | A | G | positive |
| rs2394685 | 100141210_TGI_at | A/G | G | 0.533 | 6 | 29853418 | 0.000249 | 11.175 | 5.4E-29 | -28.267 | ENST00000318669 | | A_G | A | G | A | G | positive |
| rs2394685 | 100304197_TGI_at | A/G | G | 0.533 | 6 | 29853418 | 0.000249 | 11.309 | 1.2E-29 | -28.927 | ENST00000318669 | | A_G | A | G | A | G | positive |
| rs7274854 | 100138660_TGI_at | A/C | C | 0.661 | 20 | 32692333 | 0.0002505 | 4.438 | 9.1E-06 | -5.0419 | NM_080476 | PIGU | A_C | A | C | A | C | positive |
| rs3742786 | 100151794_TGI_at | A/G | G | 0.442 | 14 | 74442764 | 0.0002513 | 10.878 | 1.5E-27 | -26.833 | NM_031464 | RPS6KL1 | G_A | A | G | G | A | negative |
| rs12937167 | 100150055_TGI_at | A/G | G | 0.123 | 17 | 34249707 | 0.0002673 | 4.784 | 1.7E-06 | -5.7649 | BX647429 | PCGF2 | A_G | A | G | A | G | negative |
| rs12937167 | 100140755_TGI_at | A/G | G | 0.123 | 17 | 34249707 | 0.0002673 | 6.863 | 6.7E-12 | -11.171 | AL566957 | PCGF2 | A_G | A | G | A | G | negative |
| rs712313 | 100145206_TGI_at | G/T | T | 0.681 | 14 | 34476664 | 0.0002765 | -5.934 | 3E-09 | -8.5292 | DA538705 | | G_T | G | T | G | T | positive |
| rs16896742 | 100160221_TGI_at | A/G | G | 0.398 | 6 | 30030719 | 0.0002769 | 11.356 | 6.9E-30 | -29.16 | NM_002127 | HLA-G | A_G | A | G | A | G | positive |
| rs12579299 | 100148776_TGI_at | A/G | G | 0.195 | 12 | 93966373 | 0.000286 | -4.137 | 3.5E-05 | -4.4536 | NM_018838 | NDUFA12 | A_G | A | G | A | G | positive |
| rs12579299 | 100151388_TGI_at | A/G | G | 0.195 | 12 | 93966373 | 0.000286 | 4.512 | 6.4E-06 | -5.1923 | CA503082 | FGD6 | A_G | A | G | A | G | negative |
| rs4978425 | 100160095_TGI_at | A/T | T | 0.483 | 9 | 112177221 | 0.000291 | -5.17 | 2.3E-07 | -6.6306 | BG571099 | SVEP1 | A_T | A | T | A | T | negative |
| rs10774192 | 100313404_TGI_at | C/T | T | 0.683 | 12 | 424352 | 0.0002957 | 8.239 | 1.7E-16 | -15.76 | AB209999 | JARID1A | C_T | C | T | C | T | negative |
| rs10774192 | 100134025_TGI_at | C/T | T | 0.683 | 12 | 424352 | 0.0002957 | 5.933 | 3E-09 | -8.5266 | NM_032358 | CCDC77 | C_T | C | T | C | T | negative |
| rs324013 | 100310285_TGI_at | C/T | T | 0.483 | 12 | 55796928 | 0.0002971 | 11.826 | 2.9E-32 | -31.543 | AY615283 | STAT6 | C_T | C | T | C | T | positive |
| rs10902208 | 100313840_TGI_at | A/G | G | 0.767 | 11 | 719570 | 0.0002979 | 4.029 | 5.6E-05 | -4.2517 | AA452033 | | A_G | A | G | A | G | positive |
| rs10902208 | 100132055_TGI_at | A/G | G | 0.767 | 11 | 719570 | 0.0002979 | -4.338 | 1.4E-05 | -4.8423 | NM_182612 | PDDC1 | A_G | A | G | A | G | negative |
| rs7575189 | 100129209_TGI_at | A/G | G | 0.425 | 2 | 173723414 | 0.0003009 | -5.478 | 4.3E-08 | -7.3664 | NM_016653 | | G_A | A | G | G | A | negative |
| rs2327351 | 100140380_TGI_at | A/G | G | 0.208 | 6 | 133889569 | 0.0003085 | 5.861 | 4.6E-09 | -8.3372 | AK093513 | | A_G | A | G | A | G | positive |
| rs4801272 | 100150898_TGI_at | C/G | G | 0.45 | 19 | 63669275 | 0.0003128 | -5.787 | 7.2E-09 | -8.1448 | NM_012254 | SLC27A5 | G_C | C | G | G | C | positive |
| rs1003879 | 100302735_TGI_at | A/G | G | 0.742 | 6 | 32407570 | 0.0003188 | -4.954 | 7.3E-07 | -6.1384 | NM_004381 | ATF6B | A_G | A | G | A | G | negative |
| rs290198 | 100301468_TGI_at | C/T | T | 0.542 | 11 | 85097315 | 0.0003255 | -5.321 | 1E-07 | -6.9863 | NM_032943 | SYTL2 | C_T | C | T | C | T | positive |
| rs290198 | 100123986_TGI_at | C/T | T | 0.542 | 11 | 85097315 | 0.0003255 | -8.76 | 2E-18 | -17.709 | AK222710 | SYTL2 | C_T | C | T | C | T | positive |
| rs3132947 | 100148822_TGI_at | G/T | T | 0.167 | 6 | 32284760 | 0.0003261 | -5.408 | 6.4E-08 | -7.1956 | NM_004557 | NOTCH4 | G_T | G | T | G | T | positive |
| rs11745587 | 100309997_TGI_at | A/G | G | 0.595 | 5 | 131824821 | 0.0003288 | 5.409 | 6.3E-08 | -7.1981 | BC012325 | SLC22A5 | A_G | A | G | A | G | positive |
| rs4493117 | 100136626_TGI_at | A/G | G | 0.525 | 17 | 25513896 | 0.0003328 | 5.358 | 8.4E-08 | -7.075 | BU754208 | SLC6A4 | G_A | A | G | G | A | negative |
| rs3115627 | 100311606_T | A/G | G | 0.4 | 6 | 29928257 | 0.0003401 | 10.97 | 5.3E-28 | -27.274 | AK125274 | HLA-F | G_A | A | G | G | A | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | GI_at |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| rs3129840 | 100137319_TGI_at | C/G | G | 0.808 | 6 | 30415321 | 0.0003443 | 6.648 | 3E-11 | -10.527 | NM_001004349 |  | C_G | C | G | C | G | positive |
| rs2147215 | 100152113_TGI_at | C/T | T | 0.75 | 6 | 18515569 | 0.0003452 | -7.82 | 5.3E-15 | -14.277 | BE274992 | RNF144B | C_T | C | T | C | T | negative |
| rs3805389 | 100137237_TGI_at | A/G | G | 0.758 | 4 | 56177507 | 0.0003489 | -4.791 | 1.7E-06 | -5.78 | NM_006681 | NMU | A_G | A | G | A | G | positive |
| rs1592971 | 100141348_TGI_at | A/G | G | 0.8 | 5 | 156951767 | 0.0003499 | 4.599 | 4.2E-06 | -5.3721 | NM_001099287 |  | G_A | A | G | G | A | positive |
| rs4801273 | 100127780_TGI_at | A/G | G | 0.458 | 19 | 63692085 | 0.0003546 | 12.319 | 7.2E-35 | -34.145 | BC067232 |  | A_G | A | G | A | G | positive |
| rs2523720 | 100132397_TGI_at | C/T | T | 0.179 | 6 | 30274865 | 0.0003651 | -4.176 | 3E-05 | -4.5277 | L19688 |  | T_C | C | T | T | C | negative |
| rs9883000 | 100124708_TGI_at | C/T | T | 0.208 | 3 | 49642695 | 0.0003692 | -6.458 | 1.1E-10 | -9.9743 | NM_000481 | AMT | C_T | C | T | C | T | positive |
| rs3132935 | 100148822_TGI_at | A/G | G | 0.167 | 6 | 32279053 | 0.0003747 | -5.408 | 6.4E-08 | -7.1956 | NM_004557 | NOTCH4 | A_G | A | G | A | G | positive |
| rs3094067 | 100303994_TGI_at | G/T | T | 0.858 | 6 | 30407224 | 0.0003867 | 14.548 | 6E-48 | -47.221 | ENST00000376881 | ZFP57 | T_G | G | T | T | G | negative |
| rs2571997 | 100133464_TGI_at | A/C | C | 0.525 | 7 | 99352353 | 0.0004125 | 6.052 | 1.4E-09 | -8.8445 | NM_013440 | PILRB | C_A | A | C | C | A | positive |
| rs2571997 | 100300966_TGI_at | A/C | C | 0.525 | 7 | 99352353 | 0.0004125 | 6.178 | 6.5E-10 | -9.1876 | NM_178238 | PILRB | C_A | A | C | C | A | positive |
| rs2571997 | 100301456_TGI_at | A/C | C | 0.525 | 7 | 99352353 | 0.0004125 | 20.202 | 9.4E-91 | -90.027 | NM_033017 | TRIM4 | C_A | A | C | C | A | positive |
| rs2517618 | 100309580_TGI_at | A/G | G | 0.808 | 6 | 30266106 | 0.0004152 | -13.503 | 1.5E-41 | -40.824 | BC035659 |  | A_G | A | G | A | G | negative |
| rs2571998 | 100133464_TGI_at | A/G | G | 0.534 | 7 | 99349308 | 0.0004161 | 6.052 | 1.4E-09 | -8.8445 | NM_013440 | PILRB | G_A | A | G | G | A | positive |
| rs2571998 | 100300966_TGI_at | A/G | G | 0.534 | 7 | 99349308 | 0.0004161 | 6.178 | 6.5E-10 | -9.1876 | NM_178238 | PILRB | G_A | A | G | G | A | positive |
| rs2571998 | 100301456_TGI_at | A/G | G | 0.534 | 7 | 99349308 | 0.0004161 | 20.202 | 9.4E-91 | -90.027 | NM_033017 | TRIM4 | G_A | A | G | G | A | positive |
| rs7260359 | 100148378_TGI_at | C/T | T | 0.405 | 19 | 50506748 | 0.0004161 | -4.24 | 2.2E-05 | -4.6507 | NM_001824 | CKM | C_T | C | T | C | T | negative |
| rs6938656 | 100135979_TGI_at | C/T | T | 0.108 | 6 | 41364098 | 0.000418 | 4.167 | 3.1E-05 | -4.5106 | NM_018643 | TREM1 | T_C | C | T | T | C | negative |
| rs1019497 | 100302468_TGI_at | A/C | C | 0.943 | 19 | 58002621 | 0.0004248 | -7.039 | 1.9E-12 | -11.713 | NM_006969 | ZNF28 | A_C | A | C | A | C | negative |
| rs2355237 | 100130314_TGI_at | A/G | G | 0.417 | 1 | 237924147 | 0.0004252 | 5.165 | 2.4E-07 | -6.619 | AL832284 |  | G_A | A | G | G | A | positive |
| rs2287312 | 100302139_TGI_at | A/G | G | 0.175 | 3 | 180552862 | 0.000434 | 4.723 | 2.3E-06 | -5.6338 | NM_016331 | ZNF639 | G_A | A | G | G | A | positive |
| rs1866400 | 100132051_TGI_at | C/T | T | 0.167 | 15 | 39311528 | 0.0004344 | 4.92 | 8.7E-07 | -6.0628 | NM_016013 | NDUFAF1 | T_C | C | T | T | C | positive |
| rs1866400 | 100307916_TGI_at | C/T | T | 0.167 | 15 | 39311528 | 0.0004344 | -4.837 | 1.3E-06 | -5.88 | BI907154 | C15orf57 | T_C | C | T | T | C | negative |
| rs2034647 | 100305328_TGI_at | A/C | C | 0.617 | 2 | 173655759 | 0.0004346 | -5.883 | 4E-09 | -8.3948 | CN479035 |  | A_C | A | C | A | C | negative |
| rs1368528 | 100130355_TGI_at | A/C | C | 0.831 | 4 | 101514882 | 0.0004396 | 4.911 | 9.1E-07 | -6.0428 | AI417595 |  | A_C | A | C | A | C | positive |
| rs11153162 | 100133695_TGI_at | A/C | C | 0.742 | 6 | 97311015 | 0.0004419 | 4.03 | 5.6E-05 | -4.2535 | NM_014165 | C6orf66 | A_C | A | C | A | C | negative |
| rs3094622 | 100158228_TGI_at | A/G | G | 0.134 | 6 | 30435931 | 0.0004473 | 5.277 | 1.3E-07 | -6.8817 | NM_170783 | ZNRD1 | G_A | A | G | G | A | positive |
| rs6894249 | 100149872_TGI_at | A/G | G | 0.424 | 5 | 131825446 | 0.0004578 | 4.774 | 1.8E-06 | -5.7433 | DB546169 |  | A_G | A | G | A | G | negative |
| rs6894249 | 100150988_TGI_at | A/G | G | 0.424 | 5 | 131825446 | 0.0004578 | 6.001 | 2E-09 | -8.7075 | U46120 |  | A_G | A | G | A | G | negative |
| rs6894249 | 100307273_TGI_at | A/G | G | 0.424 | 5 | 131825446 | 0.0004578 | 5.346 | 9E-08 | -7.0461 | BQ188640 |  | A_G | A | G | A | G | negative |
| rs11868086 | 100139113_T | A/G | G | 0.342 | 17 | 25351708 | 0.0004654 | -4.929 | 8.3E-07 | -6.0827 | U65090 | CPD | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs7135334 | 100160044_TGI_at | C/T | T | 0.7 | 12 | 68719461 | 0.0004691 | 5.847 | 5E-09 | -8.3006 | ENST00000325555 | RAB3IP | C_T | C | T | C | T | negative |
| rs6881684 | 100141348_TGI_at | A/T | T | 0.793 | 5 | 156957935 | 0.0004694 | 4.599 | 4.2E-06 | -5.3721 | NM_001099287 | | T_A | A | T | T | A | positive |
| rs12257568 | 100157818_TGI_at | C/T | T | 0.408 | 10 | 105512865 | 0.0004731 | -6.128 | 8.9E-10 | -9.0507 | AK056784 | | C_T | C | T | C | T | negative |
| rs2572009 | 100162662_TGI_at | A/G | G | 0.525 | 7 | 99326941 | 0.0004745 | 6.664 | 2.7E-11 | -10.574 | ENST00000310771 | PILRB | G_A | A | G | G | A | positive |
| rs6681207 | 100162507_TGI_at | C/T | T | 0.758 | 1 | 152783841 | 0.0004757 | 8.463 | 2.6E-17 | -16.584 | NM_017582 | UBE2Q1 | C_T | C | T | C | T | negative |
| rs6681207 | 100158499_TGI_at | C/T | T | 0.758 | 1 | 152783841 | 0.0004757 | 11.081 | 1.6E-28 | -27.809 | NM_182499 | TDRD10 | C_T | C | T | C | T | negative |
| rs7138545 | 100302085_TGI_at | C/G | G | 0.576 | 12 | 94024858 | 0.0004764 | 4.808 | 1.5E-06 | -5.8169 | NM_017599.2 | VEZT | C_G | C | G | C | G | negative |
| rs7138545 | 100146416_TGI_at | C/G | G | 0.576 | 12 | 94024858 | 0.0004764 | 4.907 | 9.2E-07 | -6.034 | NM_018351 | FGD6 | C_G | C | G | C | G | negative |
| rs2394250 | 100136412_TGI_at | G/T | T | 0.438 | 6 | 30051635 | 0.0004795 | 10.06 | 8.3E-24 | -23.081 | ENST00000376791 | HLA-G | G_T | G | T | G | T | positive |
| rs3119331 | 100302581_TGI_at | A/T | T | 0.203 | 1 | 184701141 | 0.000484 | 5.469 | 4.5E-08 | -7.3443 | NM_005807 | PRG4 | T_A | A | T | T | A | positive |
| rs12116935 | 100312774_TGI_at | A/G | G | 0.417 | 1 | 36562133 | 0.0004844 | 8.648 | 5.2E-18 | -17.281 | AI287629 | C1orf113 | A_G | A | G | A | G | positive |
| rs12116935 | 100129400_TGI_at | A/G | G | 0.417 | 1 | 36562133 | 0.0004844 | 17.427 | 5.1E-68 | -67.288 | ENST00000373137 | C1orf113 | A_G | A | G | A | G | positive |
| rs12116935 | 100149702_TGI_at | A/G | G | 0.417 | 1 | 36562133 | 0.0004844 | 16.193 | 5.7E-59 | -58.248 | NM_024676 | C1orf113 | A_G | A | G | A | G | positive |
| rs4855833 | 100124708_TGI_at | A/G | G | 0.792 | 3 | 49632445 | 0.000485 | -6.458 | 1.1E-10 | -9.9743 | NM_000481 | AMT | G_A | A | G | G | A | positive |
| rs2814954 | 100149686_TGI_at | A/T | T | 0.192 | 6 | 34806124 | 0.0004856 | -6.429 | 1.3E-10 | -9.8913 | BC026164 | UHRF1BP1 | T_A | A | T | T | A | positive |
| rs2131108 | 100124708_TGI_at | A/G | G | 0.208 | 3 | 49640394 | 0.0004864 | -6.458 | 1.1E-10 | -9.9743 | NM_000481 | AMT | A_G | A | G | A | G | positive |
| rs241549 | 100146392_TGI_at | C/T | T | 0.408 | 14 | 55614413 | 0.0004942 | 5.657 | 1.5E-08 | -7.8124 | BF110341 | PELI2 | C_T | C | T | C | T | negative |
| rs912576 | 100140992_TGI_at | A/G | G | 0.018 | 1 | 51777843 | 0.0004948 | -4.465 | 8E-06 | -5.0965 | NM_001981 | EPS15 | G_A | A | G | G | A | positive |
| rs10085400 | 100132261_TGI_at | A/C | C | 0.808 | 7 | 3867717 | 0.0004965 | -4.88 | 1.1E-06 | -5.9743 | AK074083 | SDK1 | A_C | A | C | A | C | positive |
| rs2763979 | 100126781_TGI_at | C/T | T | 0.325 | 6 | 31902571 | 0.0004984 | -5.016 | 5.3E-07 | -6.2777 | NM_025262 | LY6G5C | C_T | C | T | C | T | positive |
| rs9824435 | 100138300_TGI_at | C/T | T | 0.792 | 3 | 49649347 | 0.0005 | -5.728 | 1E-08 | -7.993 | NM_001664 | RHOA | C_T | C | T | C | T | negative |
| rs6915220 | 100155331_TGI_at | A/T | T | 0.241 | 6 | 31515800 | 0.000502 | 27.212 | 5E-163 | -162.33 | BC035656 | | T_A | A | T | T | A | negative |
| rs2527919 | 100151170_TGI_at | C/T | T | 0.508 | 7 | 99332449 | 0.0005046 | 4.864 | 1.2E-06 | -5.9392 | NM_001185 | AZGP1 | T_C | C | T | T | C | positive |
| rs9380150 | 100303129_TGI_at | C/T | T | 0.642 | 6 | 30118471 | 0.0005068 | 4.675 | 2.9E-06 | -5.5317 | NM_001098479 | HLA-F | C_T | C | T | C | T | negative |
| rs9996936 | 100135910_TGI_at | C/G | G | 0.237 | 4 | 56162396 | 0.0005104 | 5.68 | 1.3E-08 | -7.8706 | BC034006 | | G_C | C | G | G | C | negative |
| rs1080197 | 100132596_TGI_at | C/T | T | 0.839 | 1 | 169342621 | 0.0005109 | -4.385 | 1.2E-05 | -4.9356 | AL833218 | FMO2 | C_T | C | T | C | T | positive |
| rs437179 | 100142732_TGI_at | A/C | C | 0.65 | 6 | 32036993 | 0.0005169 | -6.323 | 2.6E-10 | -9.5909 | NM_138282 | ATP6V1G2 | C_A | A | C | C | A | positive |
| rs437179 | 100304704_TGI_at | A/C | C | 0.65 | 6 | 32036993 | 0.0005169 | -8.559 | 1.1E-17 | -16.944 | DB344086 | | C_A | A | C | C | A | positive |
| rs648997 | 100308316_TGI_at | C/T | T | 0.328 | 12 | 110461159 | 0.0005189 | -4.166 | 3.1E-05 | -4.5087 | BG428456 | ALDH2 | C_T | C | T | C | T | negative |
| rs1586827 | 100124708_TGI_at | C/T | T | 0.208 | 3 | 49646228 | 0.0005274 | 6.458 | 1.1E-10 | -9.9743 | NM_000481 | AMT | T_C | C | T | T | C | positive |
| rs2329021 | 100124708_T | A/G | G | 0.208 | 3 | 49654076 | 0.0005317 | 6.458 | 1.1E-10 | -9.9743 | NM_000481 | AMT | G_A | A | G | G | A | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | GI_at |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| rs722599 | 100160610_TGI_at | C/T | T | 0.7 | 14 | 74397196 | 0.0005329 | 4.282 | 1.9E-05 | -4.7323 | ENST00000238571 | YLPM1 | C_T | C | T | C | T | negative |
| rs2277948 | 100129603_TGI_at | C/T | T | 0.883 | 5 | 157030811 | 0.000535 | 5.375 | 7.7E-08 | -7.1159 | AK055284 |  | T_C | C | T | T | C | negative |
| rs13210025 | 100129291_TGI_at | A/C | C | 0.185 | 6 | 26762796 | 0.0005425 | -4.147 | 3.4E-05 | -4.4726 | BC031943 |  | C_A | A | C | C | A | negative |
| rs8019631 | 100307819_TGI_at | G/T | T | 0.492 | 14 | 87590455 | 0.000548 | 5.211 | 1.9E-07 | -6.7262 | BM470754 | GALC | G_T | G | T | G | T | negative |
| rs484932 | 100310831_TGI_at | A/C | C | 0.95 | 9 | 134231409 | 0.0005486 | -5.366 | 8.1E-08 | -7.0942 | AU121573 | SETX | A_C | A | C | A | C | negative |
| rs3812637 | 100160231_TGI_at | C/T | T | 0.725 | 10 | 75238852 | 0.0005505 | 4.065 | 4.8E-05 | -4.3185 | NM_001001791 | C10orf55 | C_T | C | T | C | T | negative |
| rs2284163 | 100133405_TGI_at | G/T | T | 0.342 | 6 | 30186994 | 0.000552 | -5.142 | 2.7E-07 | -6.5657 | ENST00000376704 | TRIM10 | G_T | G | T | G | T | negative |
| rs2284163 | 100126192_TGI_at | G/T | T | 0.342 | 6 | 30186994 | 0.000552 | -5.477 | 4.3E-08 | -7.3639 | NM_003449 | TRIM26 | G_T | G | T | G | T | negative |
| rs4713237 | 100304754_TGI_at | G/T | T | 0.691 | 6 | 29805660 | 0.0005528 | 13.794 | 2.8E-43 | -42.558 | DB311150 |  | T_G | G | T | T | G | positive |
| rs4713237 | 100311825_TGI_at | G/T | T | 0.691 | 6 | 29805660 | 0.0005528 | -14.898 | 3.4E-50 | -49.469 | AK092748 | RP3-377H14.5 | T_G | G | T | T | G | negative |
| rs440454 | 100303617_TGI_at | A/G | G | 0.65 | 6 | 32035321 | 0.0005541 | -4.349 | 1.4E-05 | -4.864 | NM_000500 | CYP21A2 | G_A | A | G | G | A | positive |
| rs440454 | 100303672_TGI_at | A/G | G | 0.65 | 6 | 32035321 | 0.0005541 | -5.386 | 7.2E-08 | -7.1424 | NG_001111 |  | G_A | A | G | G | A | positive |
| rs2359239 | 100160610_TGI_at | C/T | T | 0.3 | 14 | 74396524 | 0.0005559 | -4.282 | 1.9E-05 | -4.7323 | ENST00000238571 | YLPM1 | C_T | C | T | C | T | negative |
| rs6459154 | 100149189_TGI_at | C/T | T | 0.229 | 6 | 56315296 | 0.0005561 | 5.168 | 2.4E-07 | -6.626 | NM_030820 | COL21A1 | C_T | C | T | C | T | positive |
| rs9861291 | 100313107_TGI_at | C/G | G | 0.533 | 3 | 180274372 | 0.0005565 | -6.273 | 3.5E-10 | -9.4508 | AF214561 | KCNMB3 | C_G | C | G | C | G | negative |
| rs9861291 | 100142264_TGI_at | C/G | G | 0.533 | 3 | 180274372 | 0.0005565 | 5.079 | 3.8E-07 | -6.4209 | NM_022470 | ZMAT3 | C_G | C | G | C | G | positive |
| rs9861291 | 100133838_TGI_at | C/G | G | 0.533 | 3 | 180274372 | 0.0005565 | -6.031 | 1.6E-09 | -8.788 | NM_171828 | KCNMB3 | C_G | C | G | C | G | negative |
| rs4964087 | 100150316_TGI_at | G/T | T | 0.625 | 12 | 63353456 | 0.0005587 | -4.665 | 3.1E-06 | -5.5106 | AF242771 |  | G_T | G | T | G | T | positive |
| rs1078341 | 100124865_TGI_at | A/G | G | 0.792 | 3 | 49660596 | 0.0005589 | 5.303 | 1.1E-07 | -6.9434 | NM_005777 | RBM6 | A_G | A | G | A | G | positive |
| rs1078341 | 100156808_TGI_at | A/G | G | 0.792 | 3 | 49660596 | 0.0005589 | 5.044 | 4.6E-07 | -6.3411 | ENST00000360934 |  | A_G | A | G | A | G | positive |
| rs3745601 | 100132449_TGI_at | A/G | G | 0.917 | 19 | 10085548 | 0.0005595 | -4.023 | 5.7E-05 | -4.2406 | NM_031917 | ANGPTL6 | A_G | A | G | A | G | negative |
| rs9261431 | 100131217_TGI_at | C/G | G | 0.658 | 6 | 30194401 | 0.0005661 | 6.595 | 4.3E-11 | -10.371 | AK056160 | HCG18 | G_C | C | G | G | C | positive |
| rs1352889 | 100124708_TGI_at | C/T | T | 0.208 | 3 | 49627152 | 0.0005753 | -6.458 | 1.1E-10 | -9.9743 | NM_000481 | AMT | C_T | C | T | C | T | positive |
| rs2734934 | 100135776_TGI_at | C/T | T | 0.482 | 6 | 29975776 | 0.00058 | 5.461 | 4.7E-08 | -7.3247 | NM_170769 | RNF39 | C_T | C | T | C | T | positive |
| rs2734934 | 100138253_TGI_at | C/T | T | 0.482 | 6 | 29975776 | 0.00058 | 4.074 | 4.6E-05 | -4.3352 | CR933629 | HCG8 | C_T | C | T | C | T | positive |
| rs12368672 | 100156721_TGI_at | C/G | G | 0.4 | 12 | 55798737 | 0.0005806 | 12.872 | 6.5E-38 | -37.189 | NM_003153 | STAT6 | G_C | C | G | G | C | negative |
| rs12368672 | 100305452_TGI_at | C/G | G | 0.4 | 12 | 55798737 | 0.0005806 | -4.386 | 1.2E-05 | -4.9376 | CF455116 | STAT6 | G_C | C | G | G | C | positive |
| rs2749592 | 100300887_TGI_at | A/C | C | 0.7 | 10 | 38298848 | 0.000598 | -7.066 | 1.6E-12 | -11.797 | NM_182829 | HSD17B7P2 | C_A | A | C | C | A | positive |
| rs2749592 | 100154037_TGI_at | A/C | C | 0.7 | 10 | 38298848 | 0.000598 | 6.142 | 8.1E-10 | -9.0889 | ENST00000374633 | ZNF25 | C_A | A | C | C | A | negative |
| rs2749592 | 100304014_TGI_at | A/C | C | 0.7 | 10 | 38298848 | 0.000598 | 5.452 | 5E-08 | -7.3027 | ENST00000374633 | ZNF25 | C_A | A | C | C | A | negative |
| rs1548029 | 100148527_T | A/C | C | 0.333 | 19 | 51001043 | 0.0006041 | - | 1.4E-24 | -23.869 | NM_001081 | DMPK | A_C | A | C | A | C | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | 10.237 | | | 562 | | | | | | | |
| rs7554937 | 100159938_TGI_at | A/G | G | 0.754 | 1 | 217991288 | 0.0006052 | 4.538 | 5.7E-06 | -5.2457 | AK097467 | SLC30A10 | A_G | A | G | A | G | positive |
| rs11829776 | 100302084_TGI_at | C/T | T | 0.808 | 12 | 94055573 | 0.0006105 | 5.963 | 2.5E-09 | -8.6062 | NM_017599 | VEZT | C_T | C | T | C | T | positive |
| rs11829776 | 100306202_TGI_at | C/T | T | 0.808 | 12 | 94055573 | 0.0006105 | -4.152 | 3.3E-05 | -4.482 | BX538322 | FGD6 | C_T | C | T | C | T | negative |
| rs11829776 | 100305406_TGI_at | C/T | T | 0.808 | 12 | 94055573 | 0.0006105 | 4.668 | 3E-06 | -5.5169 | CK904578 | VEZT | C_T | C | T | C | T | positive |
| rs6843986 | 100151676_TGI_at | A/G | G | 0.612 | 4 | 90238388 | 0.0006159 | 4.258 | 2.1E-05 | -4.6856 | AA993242 | | G_A | A | G | G | A | positive |
| rs4705862 | 100132153_TGI_at | A/T | T | 0.458 | 5 | 131841118 | 0.0006173 | 6.901 | 5.2E-12 | -11.287 | NM_133482 | RAD50 | A_T | A | T | A | T | negative |
| rs12359870 | 100158065_TGI_at | A/G | G | 0.61 | 10 | 133935549 | 0.0006208 | 5.039 | 4.7E-07 | -6.3298 | NM_173575 | STK32C | A_G | A | G | A | G | positive |
| rs9834356 | 100139628_TGI_at | C/T | T | 0.258 | 3 | 134044307 | 0.0006212 | 6.292 | 3.1E-10 | -9.5039 | NM_023943 | TMEM108 | T_C | C | T | T | C | negative |
| rs7562974 | 100306345_TGI_at | C/T | T | 0.667 | 2 | 213615402 | 0.0006266 | 8.035 | 9.4E-16 | -15.029 | BX456521 | IKZF2 | C_T | C | T | C | T | positive |
| rs4144361 | 100132831_TGI_at | A/G | G | 0.492 | 14 | 87602987 | 0.0006279 | -4.052 | 5.1E-05 | -4.2943 | BC029479 | | A_G | A | G | A | G | positive |
| rs4144361 | 100161240_TGI_at | A/G | G | 0.492 | 14 | 87602987 | 0.0006279 | -4.691 | 2.7E-06 | -5.5656 | AL832767 | | A_G | A | G | A | G | positive |
| rs9870430 | 100157152_TGI_at | C/T | T | 0.733 | 3 | 134077510 | 0.0006284 | 6.492 | 8.5E-11 | -10.072 | AK095050 | TMEM108 | C_T | C | T | C | T | negative |
| rs1611715 | 100143227_TGI_at | A/C | C | 0.433 | 6 | 29937461 | 0.0006301 | 12.95 | 2.3E-38 | -37.629 | X81001 | HCG2P7 | A_C | A | C | A | C | positive |
| rs1611715 | 100300348_TGI_at | A/C | C | 0.433 | 6 | 29937461 | 0.0006301 | 14.535 | 7.3E-48 | -47.138 | X81001 | HCG2P7 | A_C | A | C | A | C | positive |
| rs3748976 | 100311790_TGI_at | G/T | T | 0.114 | 16 | 12805079 | 0.0006317 | -4.422 | 9.8E-06 | -5.0097 | AK093854 | | T_G | G | T | T | G | negative |
| rs10252169 | 100142556_TGI_at | A/G | G | 0.8 | 7 | 3866392 | 0.0006335 | -5.164 | 2.4E-07 | -6.6167 | BX505598 | | A_G | A | G | A | G | positive |
| rs11669741 | 100125493_TGI_at | C/T | T | 0.558 | 19 | 63652293 | 0.0006361 | 17.459 | 2.9E-68 | -67.532 | NM_003433 | ZNF132 | C_T | C | T | C | T | negative |
| rs11669741 | 100127553_TGI_at | C/T | T | 0.558 | 19 | 63652293 | 0.0006361 | 5.356 | 8.5E-08 | -7.0701 | NM_173548 | ZNF584 | C_T | C | T | C | T | negative |
| rs4801589 | 100307917_TGI_at | C/G | G | 0.433 | 19 | 63645210 | 0.000643 | -5.332 | 9.7E-08 | -7.0126 | BI871359 | RPS5 | G_C | C | G | G | C | positive |
| rs4801589 | 100139275_TGI_at | C/G | G | 0.433 | 19 | 63645210 | 0.000643 | -4.336 | 1.5E-05 | -4.8383 | NM_001009 | RPS5 | G_C | C | G | G | C | positive |
| rs10495573 | 100307726_TGI_at | G/T | T | 0.758 | 2 | 9629611 | 0.0006465 | -4.309 | 1.6E-05 | -4.7852 | BM669527 | ADAM17 | T_G | G | T | T | G | negative |
| rs3796051 | 100127813_TGI_at | G/T | T | 0.508 | 2 | 64771574 | 0.0006488 | 5.275 | 1.3E-07 | -6.8769 | BU569200 | | G_T | G | T | G | T | negative |
| rs1934983 | 100303586_TGI_at | A/G | G | 0.269 | 10 | 96791919 | 0.0006511 | -4.343 | 1.4E-05 | -4.8522 | NM_000771 | CYP2C9 | G_A | A | G | G | A | negative |
| rs2571992 | 100126573_TGI_at | A/G | G | 0.525 | 7 | 99357852 | 0.0006557 | -27.089 | 1E-161 | -160.88 | AK092892 | TRIM4 | G_A | A | G | G | A | negative |
| rs8076343 | 100301317_TGI_at | C/T | T | 0.683 | 17 | 34235398 | 0.0006573 | 5.675 | 1.4E-08 | -7.858 | NM_138687 | PIP4K2B | C_T | C | T | C | T | negative |
| rs11625046 | 100121711_TGI_at | G/T | T | 0.642 | 14 | 34566762 | 0.0006591 | 7.882 | 3.2E-15 | -14.492 | AI962446 | FAM177A1 | G_T | G | T | G | T | negative |
| rs3094127 | 100300978_TGI_at | A/G | G | 0.192 | 6 | 30805426 | 0.0006599 | -10.884 | 1.4E-27 | -26.862 | NM_178014 | TUBB | G_A | A | G | G | A | negative |
| rs2834463 | 100301107_TGI_at | A/G | G | 0.373 | 21 | 34639337 | 0.000664 | 6.119 | 9.4E-10 | -9.0261 | NM_153751 | C21orf82 | A_G | A | G | A | G | negative |
| rs12664426 | 100302815_TGI_at | C/T | T | 0.076 | 6 | 27187899 | 0.0006648 | 4.126 | 3.7E-05 | -4.4328 | NM_003519 | HIST1H2BL | T_C | C | T | T | C | negative |
| rs12585929 | 100162913_TGI_at | A/G | G | 0.966 | 13 | 49277184 | 0.000665 | -5.832 | 5.5E-09 | -8.2615 | AF034756 | KPNA3 | A_G | A | G | A | G | negative |
| rs7084673 | 100128225_T | A/G | G | 0.62 | 10 | 94157067 | 0.000667 | -4.623 | 3.8E-06 | -5.4222 | NM_152429 | FGFBP3 | A_G | A | G | A | G | negative |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs7084673 | 100305748_TGI_at | A/G | G | 0.62 | 10 | 94157067 | 0.000667 | -4.977 | 6.5E-07 | -6.1899 | CA431227 | 5-Mar | A_G | A | G | A | G | negative |
| rs7084673 | 100148133_TGI_at | A/G | G | 0.62 | 10 | 94157067 | 0.000667 | -5.525 | 3.3E-08 | -7.4822 | NM_017824 | 5-Mar | A_G | A | G | A | G | negative |
| rs12889403 | 100311425_TGI_at | C/T | T | 0.308 | 14 | 103104499 | 0.0006675 | -8.402 | 4.4E-17 | -16.358 | AK225730 | BAG5 | C_T | C | T | C | T | positive |
| rs9393754 | 100302369_TGI_at | G/T | T | 0.158 | 6 | 26861110 | 0.0006743 | 9.438 | 3.8E-21 | -20.42 | NM_013375 | ABT1 | T_G | G | T | T | G | positive |
| rs10253113 | 100127501_TGI_at | A/G | G | 0.381 | 7 | 129796547 | 0.0006782 | 4.569 | 4.9E-06 | -5.3098 | NM_177524 | MEST | G_A | A | G | G | A | positive |
| rs10253113 | 100308753_TGI_at | A/G | G | 0.381 | 7 | 129796547 | 0.0006782 | 4.232 | 2.3E-05 | -4.6352 | BF037602 | MEST | G_A | A | G | G | A | positive |
| rs12149831 | 100140312_TGI_at | A/G | G | 0.383 | 16 | 11713513 | 0.0006789 | -4.268 | 2E-05 | -4.705 | NM_015914 | TXNDC11 | A_G | A | G | A | G | negative |
| rs7637711 | 100314021_TGI_at | A/G | G | 0.208 | 3 | 49804657 | 0.0006791 | -4.944 | 7.7E-07 | -6.1161 | AA034951 | ARIH2 | A_G | A | G | A | G | positive |
| rs9877231 | 100139628_TGI_at | A/G | G | 0.258 | 3 | 134045296 | 0.0006816 | 6.292 | 3.1E-10 | -9.5039 | NM_023943 | TMEM108 | G_A | A | G | G | A | negative |
| rs1513261 | 100139628_TGI_at | C/T | T | 0.258 | 3 | 134043066 | 0.0006843 | -6.292 | 3.1E-10 | -9.5039 | NM_023943 | TMEM108 | C_T | C | T | C | T | negative |
| rs173141 | 100129443_TGI_at | C/T | T | 0.765 | 13 | 91232737 | 0.0006901 | -8.943 | 3.8E-19 | -18.422 | NM_004466 | GPC5 | T_C | C | T | T | C | negative |
| rs2070721 | 100304804_TGI_at | G/T | T | 0.534 | 5 | 131853741 | 0.0006928 | 4.11 | 4E-05 | -4.4027 | DB096867 | RAD50 | T_G | G | T | T | G | negative |
| rs10239342 | 100308753_TGI_at | G/T | T | 0.605 | 7 | 129796548 | 0.0006978 | 4.232 | 2.3E-05 | -4.6352 | BF037602 | MEST | G_T | G | T | G | T | positive |
| rs10239342 | 100127501_TGI_at | G/T | T | 0.605 | 7 | 129796548 | 0.0006978 | 4.569 | 4.9E-06 | -5.3098 | NM_177524 | MEST | G_T | G | T | G | T | positive |
| rs9803853 | 100147593_TGI_at | C/T | T | 0.6 | 1 | 50866596 | 0.0007034 | 5.071 | 4E-07 | -6.4026 | AF242772 | | C_T | C | T | C | T | negative |
| rs494620 | 100162932_TGI_at | A/G | G | 0.617 | 6 | 31946692 | 0.0007081 | -4.741 | 2.1E-06 | -5.6723 | BF064119 | | A_G | A | G | A | G | positive |
| rs3871468 | 100141578_TGI_at | C/T | T | 0.69 | 6 | 29785620 | 0.0007094 | 10.222 | 1.6E-24 | -23.801 | NM_001003807 | RP3-377H14.5 | T_C | C | T | T | C | positive |
| rs529834 | 100121858_TGI_at | A/C | C | 0.254 | 6 | 47908536 | 0.0007157 | -4.4 | 1.1E-05 | -4.9656 | AK123835 | C6orf138 | C_A | A | C | C | A | positive |
| rs1264334 | 100125489_TGI_at | A/G | G | 0.658 | 6 | 30952239 | 0.0007221 | -10.108 | 5.1E-24 | -23.293 | NM_205854 | SFTA2 | G_A | A | G | G | A | negative |
| rs9263970 | 100142285_TGI_at | A/C | C | 0.198 | 6 | 31294580 | 0.0007237 | -4.96 | 7E-07 | -6.1519 | ENST00000376255 | TCF19 | C_A | A | C | C | A | positive |
| rs9263970 | 100311757_TGI_at | A/C | C | 0.198 | 6 | 31294580 | 0.0007237 | -5.827 | 5.6E-09 | -8.2485 | AK095029 | | C_A | A | C | C | A | positive |
| rs9263970 | 100129279_TGI_at | A/C | C | 0.198 | 6 | 31294580 | 0.0007237 | 4.176 | 3E-05 | -4.5277 | AK094433 | HCG22 | C_A | A | C | C | A | negative |
| rs16867083 | 100126288_TGI_at | C/T | T | 0.758 | 2 | 9684892 | 0.0007306 | -4.508 | 6.5E-06 | -5.1841 | NM_003183 | ADAM17 | C_T | C | T | C | T | positive |
| rs11205746 | 100147593_TGI_at | A/G | G | 0.4 | 1 | 50866278 | 0.0007331 | 5.071 | 4E-07 | -6.4026 | AF242772 | | G_A | A | G | G | A | negative |
| rs1341164 | 100123290_TGI_at | C/T | T | 0.7 | 10 | 96790863 | 0.0007339 | -4.38 | 1.2E-05 | -4.9256 | NM_000771 | CYP2C9 | C_T | C | T | C | T | negative |
| rs11709734 | 100129450_TGI_at | A/G | G | 0.208 | 3 | 49720239 | 0.0007359 | 4.487 | 7.2E-06 | -5.1413 | ENST00000273598 | NICN1 | A_G | A | G | A | G | negative |
| rs8032589 | 100309540_TGI_at | C/T | T | 0.817 | 15 | 39288775 | 0.0007503 | -4.143 | 3.4E-05 | -4.465 | BC037835 | | C_T | C | T | C | T | negative |
| rs7257999 | 100127527_TGI_at | C/G | G | 0.441 | 19 | 63656672 | 0.0007511 | 8.542 | 1.3E-17 | -16.88 | AK124458 | | G_C | C | G | G | C | negative |
| rs9402187 | 100150758_TGI_at | A/G | G | 0.275 | 6 | 130214002 | 0.0007515 | -5.087 | 3.6E-07 | -6.4392 | NM_001010876 | C6orf191 | A_G | A | G | A | G | positive |
| rs729438 | 100142037_TGI_at | A/G | G | 0.683 | 14 | 103162542 | 0.0007528 | 7.049 | 1.8E-12 | -11.744 | NM_005552 | KLC1 | A_G | A | G | A | G | positive |
| rs729438 | 100126588_T | A/G | G | 0.683 | 14 | 103162542 | 0.0007528 | 7.787 | 6.9E-15 | -14.164 | AK023145 | BAG5 | A_G | A | G | A | G | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs3094064 | 100313972_TGI_at | A/G | G | 0.858 | 6 | 30404232 | 0.000758 | 4.858 | 1.2E-06 | -5.926 | AA159392 | FLOT1 | G_A | A | G | G | A | negative |
| rs744459 | 100156369_TGI_at | A/G | G | 0.974 | 1 | 149608041 | 0.0007615 | -4.142 | 3.4E-05 | -4.4631 | AK096600 | CGN | G_A | A | G | G | A | positive |
| rs744459 | 100140105_TGI_at | A/G | G | 0.974 | 1 | 149608041 | 0.0007615 | 4.24 | 2.2E-05 | -4.6507 | NM_020239 | CDC42SE1 | G_A | A | G | G | A | negative |
| rs4793870 | 100147773_TGI_at | C/T | T | 0.314 | 17 | 43936183 | 0.0007708 | -8.252 | 1.6E-16 | -15.808 | NM_002145 | HOXB2 | C_T | C | T | C | T | negative |
| rs13193532 | 100145476_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | -4.368 | 1.3E-05 | -4.9017 | XM_940433 | ZNF389 | A_G | A | G | A | G | positive |
| rs13193532 | 100301615_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 5.413 | 6.2E-08 | -7.2078 | NM_030899 | ZNF323 | A_G | A | G | A | G | negative |
| rs13193532 | 100129584_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 7.185 | 6.7E-13 | -12.173 | ENST00000377186 | | A_G | A | G | A | G | negative |
| rs13193532 | 100303991_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 9.034 | 1.7E-19 | -18.781 | ENST00000377186 | | A_G | A | G | A | G | negative |
| rs13193532 | 100143968_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 5.504 | 3.7E-08 | -7.4303 | NM_145909 | ZNF323 | A_G | A | G | A | G | negative |
| rs13193532 | 100140600_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | -5.315 | 1.1E-07 | -6.972 | BC019888 | | A_G | A | G | A | G | positive |
| rs11658065 | 100139631_TGI_at | G/T | T | 0.221 | 17 | 78559945 | 0.0007781 | 4.072 | 4.7E-05 | -4.3315 | NM_022158 | FN3K | G_T | G | T | G | T | negative |
| rs11658065 | 100159829_TGI_at | G/T | T | 0.221 | 17 | 78559945 | 0.0007781 | 5.476 | 4.4E-08 | -7.3615 | NM_024619 | | G_T | G | T | G | T | negative |
| rs11658065 | 100312006_TGI_at | G/T | T | 0.221 | 17 | 78559945 | 0.0007781 | -7.354 | 1.9E-13 | -12.716 | AK054757 | B3GNTL1 | G_T | G | T | G | T | positive |
| rs4889484 | 100311952_TGI_at | A/G | G | 0.259 | 16 | 72807754 | 0.0007795 | -4.345 | 1.4E-05 | -4.8561 | AK057096 | | G_A | A | G | G | A | negative |
| rs4889484 | 100303831_TGI_at | A/G | G | 0.259 | 16 | 72807754 | 0.0007795 | -4.741 | 2.1E-06 | -5.6723 | H99664 | PSMD7 | G_A | A | G | G | A | negative |
| rs11572093 | 100303586_TGI_at | C/T | T | 0.297 | 10 | 96814396 | 0.00078 | -4.343 | 1.4E-05 | -4.8522 | NM_000771 | CYP2C9 | T_C | C | T | T | C | negative |
| rs3094121 | 100308127_TGI_at | C/T | T | 0.258 | 6 | 30838939 | 0.0007803 | 9.661 | 4.4E-22 | -21.355 | BG746649 | HCG18 | T_C | C | T | T | C | positive |
| rs3094121 | 100139688_TGI_at | C/T | T | 0.258 | 6 | 30838939 | 0.0007803 | 9.808 | 1E-22 | -21.983 | AK055657 | HCG18 | T_C | C | T | T | C | positive |
| rs2535326 | 100125489_TGI_at | C/T | T | 0.347 | 6 | 30940042 | 0.0007806 | 10.108 | 5.1E-24 | -23.293 | NM_205854 | SFTA2 | T_C | C | T | T | C | negative |
| rs2517754 | 100123483_TGI_at | A/G | G | 0.554 | 6 | 30004659 | 0.0007822 | -23.198 | 5E-119 | -118.32 | AK056727 | HCG4P6 | A_G | A | G | A | G | negative |
| rs9292669 | 100310722_TGI_at | C/G | G | 0.664 | 5 | 37791792 | 0.0007848 | 6.444 | 1.2E-10 | -9.9342 | AV753237 | | C_G | C | G | C | G | negative |
| rs1559239 | 100157946_TGI_at | A/G | G | 0.867 | 19 | 57981787 | 0.0007881 | 15.652 | 3.2E-55 | -54.492 | AK131231 | ZNF600 | A_G | A | G | A | G | positive |
| rs291484 | 100123597_TGI_at | A/G | G | 0.672 | 3 | 73960039 | 0.0007896 | -4.055 | 5E-05 | -4.2999 | ENST00000383700 | | A_G | A | G | A | G | negative |
| rs6457622 | 100160430_TGI_at | A/C | C | 0.384 | 6 | 32772141 | 0.0007945 | 12.591 | 2.4E-36 | -35.626 | L76566 | HLA-DRB6 | A_C | A | C | A | C | positive |
| rs6457622 | 100312946_TGI_at | A/C | C | 0.384 | 6 | 32772141 | 0.0007945 | -12.879 | 5.9E-38 | -37.228 | AF522251 | HLA-DRB1 | A_C | A | C | A | C | negative |
| rs9428015 | 100126116_TGI_at | A/G | G | 0.33 | 1 | 89041928 | 0.0008049 | -4.618 | 3.9E-06 | -5.4118 | NM_018284 | GBP3 | A_G | A | G | A | G | negative |
| rs9428015 | 100135988_TGI_at | A/G | G | 0.33 | 1 | 89041928 | 0.0008049 | -5.47 | 4.5E-08 | -7.3468 | NM_001008661 | CCBL2 | A_G | A | G | A | G | negative |
| rs9428015 | 100303452_TGI_at | A/G | G | 0.33 | 1 | 89041928 | 0.0008049 | -6.44 | 1.2E-10 | -9.9227 | NM_001008661 | CCBL2 | A_G | A | G | A | G | negative |
| rs6866959 | 100149905_TGI_at | A/G | G | 0.883 | 5 | 157072081 | 0.0008056 | -4.331 | 1.5E-05 | -4.8285 | NM_173491 | LSM11 | G_A | A | G | G | A | negative |
| rs6456762 | 100148923_TGI_at | G/T | T | 0.112 | 6 | 27038278 | 0.0008091 | -7.436 | 1E-13 | -12.984 | NM_024639 | ZNF322A | T_G | G | T | T | G | positive |
| rs6456762 | 100307519_T | G/T | T | 0.112 | 6 | 27038278 | 0.0008091 | 20.661 | 7.8E-95 | -94.109 | BM971125 | | T_G | G | T | T | G | negative |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  | GI_at |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| rs6456762 | 100129276_TGI_at | G/T | T | 0.112 | 6 | 27038278 | 0.0008091 | 8.9 | 5.6E-19 | -18.253 | BU732657 |  | T_G | G | T | T | G | negative |
| rs12375394 | 100136594_TGI_at | C/T | T | 0.18 | 8 | 10726622 | 0.0008101 | -4.198 | 2.7E-05 | -4.5698 | AK056119 |  | C_T | C | T | C | T | positive |
| rs9266813 | 100304001_TGI_at | C/G | G | 0.206 | 6 | 31489300 | 0.0008102 | 15.088 | 1.9E-51 | -50.712 | ENST00000376222 |  | G_C | C | G | G | C | negative |
| rs9266813 | 100305324_TGI_at | C/G | G | 0.206 | 6 | 31489300 | 0.0008102 | 15.195 | 3.8E-52 | -51.418 | CN480851 |  | G_C | C | G | G | C | negative |
| rs7812140 | 100157804_TGI_at | A/G | G | 0.083 | 7 | 149536980 | 0.0008145 | 5.313 | 1.1E-07 | -6.9672 | AY102072 |  | G_A | A | G | G | A | positive |
| rs2517681 | 100153401_TGI_at | C/T | T | 0.453 | 6 | 30040309 | 0.0008198 | 4.731 | 2.2E-06 | -5.6509 | BQ005238 | TRIM26 | T_C | C | T | T | C | positive |
| rs4906335 | 100306300_TGI_at | A/C | C | 0.716 | 14 | 103090894 | 0.0008201 | -6.915 | 4.7E-12 | -11.33 | BX505087 | C14orf153 | A_C | A | C | A | C | negative |
| rs9467772 | 100161253_TGI_at | A/T | T | 0.158 | 6 | 26604557 | 0.0008219 | -16.63 | 4.2E-62 | -61.374 | NM_007047 | BTN3A2 | A_T | A | T | A | T | positive |
| rs9467772 | 100127556_TGI_at | A/T | T | 0.158 | 6 | 26604557 | 0.0008219 | -4.322 | 1.5E-05 | -4.8107 | BX640949 | TRIM38 | A_T | A | T | A | T | positive |
| rs11969000 | 100304633_TGI_at | C/T | T | 0.155 | 6 | 35210386 | 0.000822 | -5.138 | 2.8E-07 | -6.5565 | DB511695 | TCP11 | T_C | C | T | T | C | negative |
| rs4695356 | 100124251_TGI_at | A/G | G | 0.358 | 4 | 47884898 | 0.0008248 | 6.904 | 5.1E-12 | -11.296 | NM_000087 | CNGA1 | A_G | A | G | A | G | negative |
| rs4695356 | 100163169_TGI_at | A/G | G | 0.358 | 4 | 47884898 | 0.0008248 | 6.778 | 1.2E-11 | -10.914 | CN366905 | CNGA1 | A_G | A | G | A | G | negative |
| rs746423 | 100144365_TGI_at | C/T | T | 0.208 | 12 | 52703526 | 0.0008322 | 4.288 | 1.8E-05 | -4.744 | NM_153693 | HOXC6 | C_T | C | T | C | T | positive |
| rs746423 | 100148000_TGI_at | C/T | T | 0.208 | 12 | 52703526 | 0.0008322 | 4.221 | 2.4E-05 | -4.614 | BC020349 | HOXC6 | C_T | C | T | C | T | positive |
| rs746423 | 100309835_TGI_at | C/T | T | 0.208 | 12 | 52703526 | 0.0008322 | 5.155 | 2.5E-07 | -6.5958 | BC020349 | HOXC6 | C_T | C | T | C | T | positive |
| rs536889 | 100304757_TGI_at | C/T | T | 0.25 | 6 | 47926832 | 0.0008331 | 5.66 | 1.5E-08 | -7.82 | DB309312 | OPN5 | T_C | C | T | T | C | negative |
| rs7772549 | 100125842_TGI_at | C/T | T | 0.767 | 6 | 31515622 | 0.0008438 | 5.033 | 4.8E-07 | -6.3162 | NM_147130 | NCR3 | C_T | C | T | C | T | negative |
| rs4081763 | 100307330_TGI_at | A/T | T | 0.195 | 16 | 73938298 | 0.0008476 | -4.334 | 1.5E-05 | -4.8344 | BQ016861 | BCAR1 | T_A | A | T | T | A | positive |
| rs11024750 | 100142627_TGI_at | A/G | G | 0.655 | 11 | 18626055 | 0.0008476 | -4.075 | 4.6E-05 | -4.3371 | NM_002301 | LDHC | G_A | A | G | G | A | negative |
| rs1383264 | 100129037_TGI_at | A/T | T | 0.483 | 6 | 32847945 | 0.000849 | 8.549 | 1.2E-17 | -16.906 | NM_018833 | TAP2 | T_A | A | T | T | A | negative |
| rs1383264 | 100133511_TGI_at | A/T | T | 0.483 | 6 | 32847945 | 0.000849 | 6.965 | 3.3E-12 | -11.484 | NM_002120 | HLA-DOB | T_A | A | T | T | A | negative |
| rs1383264 | 100161395_TGI_at | A/T | T | 0.483 | 6 | 32847945 | 0.000849 | -11.369 | 6E-30 | -29.224 | AK225657 | TAP2 | T_A | A | T | T | A | positive |
| rs4368711 | 100132327_TGI_at | C/T | T | 0.233 | 5 | 156877249 | 0.0008522 | -5.818 | 6E-09 | -8.2251 | NM_033274 | ADAM19 | T_C | C | T | T | C | negative |
| rs1472568 | 100162335_TGI_at | C/G | G | 0.387 | 1 | 19639019 | 0.0008538 | -6.869 | 6.5E-12 | -11.189 | ENST00000375158 |  | C_G | C | G | C | G | positive |
| rs8045779 | 100151120_TGI_at | C/T | T | 0.883 | 16 | 12814562 | 0.0008573 | -5.25 | 1.5E-07 | -6.8179 | ENST00000261660 |  | C_T | C | T | C | T | negative |
| rs3131038 | 100139688_TGI_at | A/G | G | 0.742 | 6 | 30842059 | 0.0008582 | 9.808 | 1E-22 | -21.983 | AK055657 | HCG18 | A_G | A | G | A | G | positive |
| rs3131038 | 100308127_TGI_at | A/G | G | 0.742 | 6 | 30842059 | 0.0008582 | 9.661 | 4.4E-22 | -21.355 | BG746649 | HCG18 | A_G | A | G | A | G | positive |
| rs11191822 | 100135728_TGI_at | G/T | T | 0.679 | 10 | 105589760 | 0.0008595 | -4.413 | 1E-05 | -4.9916 | AK024150 |  | G_T | G | T | G | T | negative |
| rs13051329 | 100136800_TGI_at | C/T | T | 0.11 | 21 | 34244759 | 0.0008622 | -5.582 | 2.4E-08 | -7.6238 | NM_001697 | ATP5O | T_C | C | T | T | C | positive |
| rs4947349 | 100145052_TGI_at | G/T | T | 0.1 | 6 | 32855768 | 0.0008668 | -6.572 | 5E-11 | -10.304 | NM_002121 | HLA-DPB1 | T_G | G | T | T | G | negative |
| rs3016009 | 100138417_T | C/T | T | 0.304 | 6 | 31559940 | 0.0008686 | 8.215 | 2.1E-16 | -15.673 | AK055022 |  | T_C | C | T | T | C | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs2524142 | 100313121_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -5.119 | 3.1E-07 | -6.5126 | AF196489 | HLA-C | G_C | C | G | G | C | positive |
| rs2524142 | 100302942_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -5.026 | 5E-07 | -6.3003 | NM_002117 | HLA-C | G_C | C | G | G | C | positive |
| rs2524142 | 100313880_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -11.677 | 1.7E-31 | -30.777 | AA381265 | | G_C | C | G | G | C | positive |
| rs2524142 | 100128894_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -8.938 | 4E-19 | -18.402 | NM_181717 | HCG27 | G_C | C | G | G | C | positive |
| rs2524142 | 100309484_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -23.877 | 5E-126 | -125.27 | BC041078 | HLA-C | G_C | C | G | G | C | positive |
| rs2524142 | 100300925_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -9.316 | 1.2E-20 | -19.918 | NM_181717 | HCG27 | G_C | C | G | G | C | positive |
| rs32086 | 100156891_TGI_at | C/G | G | 0.15 | 5 | 156059547 | 0.0008737 | -7.213 | 5.5E-13 | -12.262 | NM_000337 | SGCD | G_C | C | G | G | C | positive |
| rs32086 | 100313731_TGI_at | C/G | G | 0.15 | 5 | 156059547 | 0.0008737 | -6.174 | 6.7E-10 | -9.1766 | AA723953 | SGCD | G_C | C | G | G | C | positive |
| rs32086 | 100144469_TGI_at | C/G | G | 0.15 | 5 | 156059547 | 0.0008737 | -5.868 | 4.4E-09 | -8.3555 | AI022514 | SGCD | G_C | C | G | G | C | positive |
| rs11771259 | 100154998_TGI_at | C/G | G | 0.123 | 7 | 7243740 | 0.0008739 | 14.61 | 2.4E-48 | -47.615 | NM_020156 | C1GALT1 | C_G | C | G | C | G | negative |
| rs11771259 | 100124335_TGI_at | C/G | G | 0.123 | 7 | 7243740 | 0.0008739 | 6.123 | 9.2E-10 | -9.037 | AK023557 | | C_G | C | G | C | G | negative |
| rs11771259 | 100147343_TGI_at | C/G | G | 0.123 | 7 | 7243740 | 0.0008739 | 6.05 | 1.4E-09 | -8.8391 | AI672489 | | C_G | C | G | C | G | negative |
| rs9472507 | 100122981_TGI_at | A/G | G | 0.692 | 6 | 45652166 | 0.000875 | 4.182 | 2.9E-05 | -4.5392 | BX108677 | RUNX2 | G_A | A | G | G | A | positive |
| rs2744966 | 100131760_TGI_at | A/G | G | 0.2 | 6 | 34693909 | 0.0008757 | 4.046 | 5.2E-05 | -4.2832 | BC146646 | ITPR3 | G_A | A | G | G | A | negative |
| rs6435126 | 100122090_TGI_at | A/G | G | 0.534 | 2 | 202671347 | 0.0008901 | -7.088 | 1.4E-12 | -11.866 | BC015915 | FZD7 | A_G | A | G | A | G | positive |
| rs7196681 | 100138939_TGI_at | A/C | C | 0.458 | 16 | 76853299 | 0.0008943 | 7.347 | 2E-13 | -12.693 | NM_016373 | WWOX | A_C | A | C | A | C | positive |
| rs7196681 | 100143315_TGI_at | A/C | C | 0.458 | 16 | 76853299 | 0.0008943 | -6.808 | 9.9E-12 | -11.005 | NM_130791 | WWOX | A_C | A | C | A | C | negative |
| rs2289739 | 100141553_TGI_at | G/T | T | 0.383 | 15 | 39588804 | 0.0008958 | 4.553 | 5.3E-06 | -5.2767 | BX648343 | | G_T | G | T | G | T | positive |
| rs626339 | 100306966_TGI_at | C/T | T | 0.675 | 1 | 111530848 | 0.0008973 | 4.165 | 3.1E-05 | -4.5067 | BU069696 | TMEM77 | C_T | C | T | C | T | positive |
| rs12320166 | 100158197_TGI_at | A/G | G | 0.225 | 12 | 31794812 | 0.0009004 | 10.626 | 2.3E-26 | -25.647 | XM_084845 | | A_G | A | G | A | G | positive |
| rs3131290 | 100135327_TGI_at | A/G | G | 0.684 | 6 | 32291153 | 0.0009047 | 10.147 | 3.4E-24 | -23.466 | NM_006411 | AGPAT1 | A_G | A | G | A | G | positive |
| rs3131290 | 100126665_TGI_at | A/G | G | 0.684 | 6 | 32291153 | 0.0009047 | 14.336 | 1.3E-46 | -45.885 | NM_032741 | AGPAT1 | A_G | A | G | A | G | positive |
| rs3130380 | 100304636_TGI_at | A/G | G | 0.858 | 6 | 30387109 | 0.0009066 | -4.555 | 5.2E-06 | -5.2808 | DB503443 | FLOT1 | A_G | A | G | A | G | negative |
| rs9929566 | 100307707_TGI_at | C/T | T | 0.392 | 16 | 75682603 | 0.0009133 | 5.755 | 8.7E-09 | -8.0623 | BM677564 | MON1B | C_T | C | T | C | T | negative |
| rs17394376 | 100132347_TGI_at | A/G | G | 0.681 | 1 | 19596687 | 0.0009139 | -4.753 | 2E-06 | -5.6981 | AK021935 | | A_G | A | G | A | G | negative |
| rs3130474 | 100303039_TGI_at | C/T | T | 0.336 | 6 | 31307235 | 0.0009146 | 11.129 | 9.1E-29 | -28.043 | NM_001264 | CDSN | T_C | C | T | T | C | positive |
| rs1264705 | 100129349_TGI_at | C/G | G | 0.858 | 6 | 30171653 | 0.000915 | 12.935 | 2.9E-38 | -37.544 | NM_002116 | HLA-A | C_G | C | G | C | G | positive |
| rs1264705 | 100138030_TGI_at | C/G | G | 0.858 | 6 | 30171653 | 0.000915 | 4.604 | 4.1E-06 | -5.3825 | U58024 | HLA-G | C_G | C | G | C | G | positive |
| rs9975829 | 100130835_TGI_at | A/G | G | 0.345 | 21 | 33781365 | 0.0009194 | 5.661 | 1.5E-08 | -7.8225 | BQ070130 | SON | A_G | A | G | A | G | negative |
| rs9975829 | 100127382_TGI_at | A/G | G | 0.345 | 21 | 33781365 | 0.0009194 | 9.354 | 8.4E-21 | -20.074 | NM_006134 | TMEM50B | A_G | A | G | A | G | negative |
| rs9975829 | 100310797_T | A/G | G | 0.345 | 21 | 33781365 | 0.0009194 | -8.942 | 3.8E-19 | -18.418 | AV648346 | IFNGR2 | A_G | A | G | A | G | positive |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | | | | | | | | | | | |
| rs9975829 | 100308980_TGI_at | A/G | G | 0.345 | 21 | 33781365 | 0.0009194 | -6.537 | 6.3E-11 | -10.202 | BE144260 | IFNGR2 | A_G | A | G | A | G | positive |
| rs8109951 | 100306689_TGI_at | C/T | T | 0.345 | 19 | 50981343 | 0.0009195 | -9.353 | 8.5E-21 | -20.07 | BU741440 | | C_T | C | T | C | T | negative |
| rs11649804 | 100153419_TGI_at | A/C | C | 0.758 | 17 | 17637480 | 0.0009197 | 5.491 | 4E-08 | -7.3983 | ENST00000318094 | TOM1L2 | A_C | A | C | A | C | negative |
| rs11649804 | 100129852_TGI_at | A/C | C | 0.758 | 17 | 17637480 | 0.0009197 | 5.858 | 4.7E-09 | -8.3293 | AK096528 | | A_C | A | C | A | C | negative |
| rs2247056 | 100121628_TGI_at | C/T | T | 0.388 | 6 | 31373469 | 0.0009199 | -12.695 | 6.3E-37 | -36.201 | NM_014068 | PSORS1C1 | C_T | C | T | C | T | positive |
| rs17481834 | 100145697_TGI_at | A/G | G | 0.144 | 2 | 37381853 | 0.0009287 | 7.362 | 1.8E-13 | -12.742 | AK122883 | PRKD3 | G_A | A | G | G | A | negative |
| rs2579762 | 100124184_TGI_at | A/C | C | 0.414 | 10 | 77988885 | 0.0009312 | -6.978 | 3E-12 | -11.524 | DA084722 | | C_A | A | C | C | A | negative |
| rs9870755 | 100160114_TGI_at | C/T | T | 0.176 | 3 | 49784845 | 0.000936 | -13.279 | 3.1E-40 | -39.514 | AK001120 | | T_C | C | T | T | C | negative |
| rs9870755 | 100137568_TGI_at | C/T | T | 0.176 | 3 | 49784845 | 0.000936 | -4.216 | 2.5E-05 | -4.6044 | AB058754 | AMIGO3 | T_C | C | T | T | C | negative |
| rs7880493 | 100310951_TGI_at | C/T | T | 0.191 | 1 | 169327657 | 0.000937 | 4.28 | 1.9E-05 | -4.7284 | AL833218 | FMO2 | C_T | C | T | C | T | positive |
| rs12145992 | 100141567_TGI_at | A/G | G | 0.771 | 1 | 3750169 | 0.0009409 | 4.739 | 2.1E-06 | -5.668 | NM_014704 | KIAA0562 | A_G | A | G | A | G | positive |
| rs8004430 | 100308140_TGI_at | C/T | T | 0.89 | 14 | 74241436 | 0.0009453 | 21.807 | 2E-105 | -104.7 | BG741360 | KIAA0317 | C_T | C | T | C | T | negative |
| rs8004430 | 100126667_TGI_at | C/T | T | 0.89 | 14 | 74241436 | 0.0009453 | 18.239 | 2.5E-74 | -73.597 | NM_001039479 | KIAA0317 | C_T | C | T | C | T | negative |
| rs997154 | 100301474_TGI_at | A/G | G | 0.833 | 14 | 22534322 | 0.0009455 | 4.854 | 1.2E-06 | -5.9172 | NM_032876 | JUB | A_G | A | G | A | G | positive |
| rs10463321 | 100300564_TGI_at | G/T | T | 0.791 | 5 | 151304098 | 0.0009468 | -14.265 | 3.6E-46 | -45.442 | U32519 | G3BP1 | G_T | G | T | G | T | positive |
| rs10463321 | 100158823_TGI_at | G/T | T | 0.791 | 5 | 151304098 | 0.0009468 | -4.171 | 3E-05 | -4.5182 | AK001582 | | G_T | G | T | G | T | positive |
| rs9263967 | 100304000_TGI_at | A/G | G | 0.45 | 6 | 31294224 | 0.0009473 | -9.099 | 9.1E-20 | -19.04 | ENST00000376242 | PSORS1C3 | G_A | A | G | G | A | positive |
| rs9472463 | 100300937_TGI_at | A/G | G | 0.975 | 6 | 45398612 | 0.0009482 | 6.334 | 2.4E-10 | -9.6218 | NM_181356 | SUPT3H | A_G | A | G | A | G | positive |
| rs2070729 | 100136084_TGI_at | A/C | C | 0.533 | 5 | 131847820 | 0.0009491 | 4.824 | 1.4E-06 | -5.8517 | BX648423 | | C_A | A | C | C | A | negative |
| rs2735048 | 100310523_TGI_at | A/G | G | 0.57 | 6 | 29841680 | 0.0009537 | 6.796 | 1.1E-11 | -10.968 | AW473609 | | G_A | A | G | G | A | positive |
| rs7603424 | 100307074_TGI_at | A/G | G | 0.892 | 2 | 229317612 | 0.0009541 | 4.465 | 8E-06 | -5.0965 | BQ771727 | PID1 | A_G | A | G | A | G | negative |
| rs7603424 | 100157087_TGI_at | A/G | G | 0.892 | 2 | 229317612 | 0.0009541 | 4.153 | 3.3E-05 | -4.4839 | NM_017933 | PID1 | A_G | A | G | A | G | negative |
| rs9558323 | 100149341_TGI_at | A/G | G | 0.613 | 13 | 87534298 | 0.0009571 | 4.342 | 1.4E-05 | -4.8502 | NM_015567 | SLITRK5 | G_A | A | G | G | A | negative |
| rs32070 | 100307171_TGI_at | A/G | G | 0.15 | 5 | 156047396 | 0.0009584 | -6.619 | 3.6E-11 | -10.442 | BQ446019 | | G_A | A | G | G | A | positive |
| rs32070 | 100130704_TGI_at | A/G | G | 0.15 | 5 | 156047396 | 0.0009584 | -6.348 | 2.2E-10 | -9.6613 | AF010236 | | G_A | A | G | G | A | positive |
| rs32070 | 100142964_TGI_at | A/G | G | 0.15 | 5 | 156047396 | 0.0009584 | -5.082 | 3.7E-07 | -6.4277 | NM_172244 | SGCD | G_A | A | G | G | A | positive |
| rs11868035 | 100136519_TGI_at | A/G | G | 0.767 | 17 | 17655826 | 0.0009606 | -9.945 | 2.7E-23 | -22.577 | S66168 | SREBF1 | A_G | A | G | A | G | positive |
| rs11868035 | 100301274_TGI_at | A/G | G | 0.767 | 17 | 17655826 | 0.0009606 | 4.574 | 4.8E-06 | -5.3201 | NM_144678 | TOM1L2 | A_G | A | G | A | G | negative |
| rs11868035 | 100153419_TGI_at | A/G | G | 0.767 | 17 | 17655826 | 0.0009606 | 5.491 | 4E-08 | -7.3983 | ENST00000318094 | TOM1L2 | A_G | A | G | A | G | negative |
| rs11632927 | 100130789_TGI_at | A/C | C | 0.742 | 15 | 98158249 | 0.0009633 | -11.125 | 9.5E-29 | -28.023 | BX110580 | | A_C | A | C | A | C | positive |
| rs602875 | 100313766_T | A/G | G | 0.19 | 6 | 32681607 | 0.0009653 | - | 3.2E-31 | -30.492 | AA622265 | HLA-DQA2 | A_G | A | G | A | G | positive |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | GI_at | | | | | | | 11.621 | | | | | | | | | | |
| rs602875 | 100125275_TGI_at | A/G | G | 0.19 | 6 | 32681607 | 0.0009653 | 9.958 | 2.3E-23 | -22.633 | BG755321 | HLA-DRB1 | A_G | A | G | A | G | negative |
| rs2009879 | 100309078_TGI_at | C/T | T | 0.466 | 21 | 34575174 | 0.0009655 | -4.946 | 7.6E-07 | -6.1206 | BC112087 | KCNE2 | T_C | C | T | T | C | negative |
| rs11809504 | 100129207_TGI_at | A/T | T | 0.169 | 1 | 169356844 | 0.0009671 | 4.695 | 2.7E-06 | -5.5741 | BT006979 | FMO2 | A_T | A | T | A | T | positive |
| rs11809504 | 100162242_TGI_at | A/T | T | 0.169 | 1 | 169356844 | 0.0009671 | 5.27 | 1.4E-07 | -6.8651 | NM_001460 | FMO2 | A_T | A | T | A | T | positive |
| rs1264331 | 100161807_TGI_at | G/T | T | 0.317 | 6 | 30954809 | 0.0009741 | 5.046 | 4.5E-07 | -6.3457 | NM_001954 | DDR1 | T_G | G | T | T | G | negative |
| rs2295687 | 100306484_TGI_at | A/G | G | 0.617 | 14 | 22490936 | 0.0009743 | 7.041 | 1.9E-12 | -11.719 | BX346609 | RBM23 | A_G | A | G | A | G | positive |
| rs2295687 | 100135911_TGI_at | A/G | G | 0.617 | 14 | 22490936 | 0.0009743 | 7.536 | 4.8E-14 | -13.315 | NM_001077352 | RBM23 | A_G | A | G | A | G | positive |
| rs2295687 | 100310197_TGI_at | A/G | G | 0.617 | 14 | 22490936 | 0.0009743 | 7.629 | 2.4E-14 | -13.626 | BC002566 | RBM23 | A_G | A | G | A | G | positive |
| rs2295687 | 100146509_TGI_at | A/G | G | 0.617 | 14 | 22490936 | 0.0009743 | -16.584 | 9.1E-62 | -61.041 | NM_017815 | C14orf94 | A_G | A | G | A | G | negative |
| rs3129975 | 100139688_TGI_at | C/T | T | 0.742 | 6 | 30840033 | 0.0009788 | 9.808 | 1E-22 | -21.983 | AK055657 | HCG18 | C_T | C | T | C | T | positive |
| rs3129975 | 100308127_TGI_at | C/T | T | 0.742 | 6 | 30840033 | 0.0009788 | 9.661 | 4.4E-22 | -21.355 | BG746649 | HCG18 | C_T | C | T | C | T | positive |
| rs925284 | 100154282_TGI_at | C/T | T | 0.458 | 17 | 43940889 | 0.0009789 | -4.444 | 8.8E-06 | -5.054 | NM_004502 | HOXB7 | C_T | C | T | C | T | negative |
| rs221032 | 100122367_TGI_at | C/T | T | 0.267 | 1 | 16398136 | 0.0009815 | 4.526 | 6E-06 | -5.221 | NM_153213 | ARHGEF19 | T_C | C | T | T | C | negative |
| rs221032 | 100143670_TGI_at | C/T | T | 0.267 | 1 | 16398136 | 0.0009815 | -6.405 | 1.5E-10 | -9.8228 | NM_030907 | C1orf89 | T_C | C | T | T | C | positive |
| rs221032 | 100313238_TGI_at | C/T | T | 0.267 | 1 | 16398136 | 0.0009815 | 4.69 | 2.7E-06 | -5.5635 | AF088037 | ARHGEF19 | T_C | C | T | T | C | negative |
| rs2535331 | 100151371_TGI_at | A/G | G | 0.683 | 6 | 30924249 | 0.0009841 | 14.274 | 3.2E-46 | -45.498 | NM_020442 | VARS2 | G_A | A | G | G | A | positive |
| rs486023 | 100304225_TGI_at | A/G | G | 0.675 | 11 | 100148347 | 0.0009849 | 4.105 | 4E-05 | -4.3933 | ENST00000298824 | | G_A | A | G | G | A | positive |
| rs3094066 | 100125007_TGI_at | C/T | T | 0.043 | 6 | 30386724 | 0.0009894 | -8.176 | 2.9E-16 | -15.533 | AF036974 | C6orf12 | T_C | C | T | T | C | negative |
| rs6736194 | 100160466_TGI_at | C/G | G | 0.492 | 2 | 11417509 | 0.0009919 | -4.548 | 5.4E-06 | -5.2663 | AI379509 | ROCK2 | G_C | C | G | G | C | positive |
| rs6736194 | 100124316_TGI_at | C/G | G | 0.492 | 2 | 11417509 | 0.0009919 | -7.332 | 2.3E-13 | -12.645 | NM_152391 | PQLC3 | G_C | C | G | G | C | positive |
| rs6736194 | 100311377_TGI_at | C/G | G | 0.492 | 2 | 11417509 | 0.0009919 | -5.867 | 4.4E-09 | -8.3529 | AL049383 | ROCK2 | G_C | C | G | G | C | positive |
| rs6736194 | 100159613_TGI_at | C/G | G | 0.492 | 2 | 11417509 | 0.0009919 | 5.397 | 6.8E-08 | -7.169 | BU753251 | ROCK2 | G_C | C | G | G | C | negative |
| rs6736194 | 100306938_TGI_at | C/G | G | 0.492 | 2 | 11417509 | 0.0009919 | 4.091 | 4.3E-05 | -4.367 | BU159594 | ROCK2 | G_C | C | G | G | C | negative |
| rs17565336 | 100162242_TGI_at | A/G | G | 0.167 | 1 | 169371713 | 0.0009924 | 5.27 | 1.4E-07 | -6.8651 | NM_001460 | FMO2 | A_G | A | G | A | G | positive |
| rs17565336 | 100129207_TGI_at | A/G | G | 0.167 | 1 | 169371713 | 0.0009924 | 4.695 | 2.7E-06 | -5.5741 | BT006979 | FMO2 | A_G | A | G | A | G | positive |
| rs2744973 | 100128579_TGI_at | C/T | T | 0.23 | 6 | 34688199 | 0.0009954 | -14.227 | 6.2E-46 | -45.206 | NM_017754 | UHRF1BP1 | T_C | C | T | T | C | positive |
| rs2744973 | 100159916_TGI_at | C/T | T | 0.23 | 6 | 34688199 | 0.0009954 | 5.582 | 2.4E-08 | -7.6238 | NM_003093 | SNRPC | T_C | C | T | T | C | negative |
| rs678946 | 100157332_TGI_at | C/T | T | 0.15 | 9 | 134857508 | 0.0009958 | 4.136 | 3.5E-05 | -4.4517 | NM_012087 | GTF3C5 | C_T | C | T | C | T | positive |
| rs13029949 | 100122720_TGI_at | A/G | G | 0.664 | 2 | 173696496 | 0.0009995 | -4.317 | 1.6E-05 | -4.8009 | AB208974 | | A_G | A | G | A | G | positive |

## Supplementary Table 5: FEV$_1$/FVC *trans*-eSNPs

Table shows the list of FEV$_1$/FVC *trans* acting eSNPs. Header definitions are the same as Supplementary Table 2.

| FEV1/FVC *trans* lung eSNPs | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| eSNP | eSNP regulated probeset | GWAS SNP alleles | GWAS Reference allele | Reference allele freq in HapMap | Chr | SNP Position | GWAS_Pval_ FEV1/FVC | eQTL Z meta | eQTL P value | log10.pvalue.meta | sequence source ID | Gene Symbol | eQTL-alleles | GWAS_noncoded_alleles | GWAS_coded_alleles | eQTL_noncoded_alleles | eQTL_coded_alleles | Expected Direction Of Effect of mRNA with lung function |
| rs1264376 | 100141210_TGI_at | A/C | C | 0.817 | 6 | 30873558 | 0.0005327 | -6.222 | 4.9E-10 | -9.309 | ENST00000318669 | | C_A | A | C | C | A | positive |
| rs1264376 | 100304197_TGI_at | A/C | C | 0.817 | 6 | 30873558 | 0.0005327 | -6.643 | 3.1E-11 | -10.512 | ENST00000318669 | | C_A | A | C | C | A | positive |
| rs1264705 | 100161253_TGI_at | C/G | G | 0.858 | 6 | 30171653 | 0.000915 | 12.654 | 1.1E-36 | -35.973 | NM_007047 | BTN3A2 | C_G | C | G | C | G | positive |
| rs13193532 | 100123483_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 8.722 | 2.7E-18 | -17.563 | AK056727 | HCG4P6 | A_G | A | G | A | G | negative |
| rs13193532 | 100311606_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 8.712 | 3E-18 | -17.525 | AK125274 | HLA-F | A_G | A | G | A | G | negative |
| rs13193532 | 100125007_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 7.841 | 4.5E-15 | -14.35 | AF036974 | C6orf12 | A_G | A | G | A | G | negative |
| rs13193532 | 100309580_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 14.14 | 2.2E-45 | -44.667 | BC035659 | | A_G | A | G | A | G | negative |
| rs13193532 | 100129349_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | -14.425 | 3.6E-47 | -46.443 | NM_002116 | HLA-A | A_G | A | G | A | G | positive |
| rs13193532 | 100160221_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | -8.123 | 4.5E-16 | -15.342 | NM_002127 | HLA-G | A_G | A | G | A | G | positive |
| rs13193532 | 100303994_TGI_at | A/G | G | 0.145 | 6 | 28730893 | 0.0007709 | 15.855 | 1.3E-56 | -55.887 | ENST00000376881 | ZFP57 | A_G | A | G | A | G | negative |
| rs1491106 | 100309242_TGI_at | G/T | T | 0.383 | 9 | 108523338 | 6.02E-05 | -8.836 | 9.9E-19 | -18.004 | BC069296 | RBP2 | T_G | G | T | T | G | positive |
| rs1491106 | 100161662_TGI_at | G/T | T | 0.383 | 9 | 108523338 | 6.02E-05 | -9.188 | 4E-20 | -19.398 | NM_004164 | RBP2 | T_G | G | T | T | G | positive |
| rs149356 | 100153237_TGI_at | C/T | T | 0.5 | 5 | 95059521 | 2.32E-06 | 8.097 | 5.6E-16 | -15.249 | ENST00000296731 | RHOBTB3 | T_C | C | T | T | C | positive |
| rs153911 | 100153237_TGI_at | C/T | T | 0.517 | 5 | 95059055 | 2.08E-06 | 8.097 | 5.6E-16 | -15.249 | ENST00000296731 | RHOBTB3 | T_C | C | T | T | C | positive |
| rs2206030 | 100307218_TGI_at | C/T | T | 0.275 | 6 | 35512332 | 0.0001716 | -6.929 | 4.2E-12 | -11.373 | BQ379815 | | T_C | C | T | T | C | negative |
| rs2247056 | 100308127_TGI_at | C/T | T | 0.388 | 6 | 31373469 | 0.0009199 | -7.972 | 1.6E-15 | -14.807 | BG746649 | HCG18 | C_T | C | T | C | T | positive |
| rs2247056 | 100139688_TGI_at | C/T | T | 0.388 | 6 | 31373469 | 0.0009199 | -7.629 | 2.4E-14 | -13.626 | AK055657 | HCG18 | C_T | C | T | C | T | positive |
| rs2524142 | 100122819_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -6.36 | 2E-10 | -9.6952 | NM_001001961 | OR13C3 | G_C | C | G | G | C | positive |
| rs2524142 | 100138030_TGI_at | C/G | G | 0.602 | 6 | 31371501 | 0.0008719 | -7.254 | 4E-13 | -12.393 | U58024 | HLA-G | G_C | C | G | G | C | positive |
| rs2734934 | 100159186_TGI_at | C/T | T | 0.482 | 6 | 29975776 | 0.00058 | 6.335 | 2.4E-10 | -9.6246 | AK057519 | | C_T | C | T | C | T | positive |
| rs2749592 | 100123769_TGI_at | A/C | C | 0.7 | 10 | 38298848 | 0.000598 | 7.344 | 2.1E-13 | -12.683 | AK092104 | | C_A | A | C | C | A | negative |
| rs3095330 | merck.AK128290_at | A/G | G | 0.191 | 6 | 30801612 | 9.22E-05 | 6.73 | 1.7E-11 | -10.77 | NA | NA | G_A | A | G | G | A | positive |
| rs3129950 | 100300978_TGI_at | C/G | G | 0.908 | 6 | 32466179 | 5.68E-06 | -6.748 | 1.5E-11 | -10.824 | NM_178014 | TUBB | C_G | C | G | C | G | negative |

| | | | | | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3130374 | 100162706_TGI_at | C/T | T | 0.142 | 6 | 30429315 | 0.0009504 | 8.594 | 8.4E-18 | -17.076 | D83543 | | C_T | C | T | C | T | negative |
| rs3130374 | 100305045_TGI_at | C/T | T | 0.142 | 6 | 30429315 | 0.0009504 | 8.679 | 4E-18 | -17.399 | D83543 | | C_T | C | T | C | T | negative |
| rs3131784 | 100311825_TGI_at | C/T | T | 0.542 | 6 | 31011927 | 0.0008625 | -8.498 | 1.9E-17 | -16.715 | AK092748 | RP3-377H14.5 | T_C | C | T | T | C | negative |
| rs3131934 | 100303756_TGI_at | C/T | T | 0.808 | 6 | 31039823 | 6.08E-06 | 7.422 | 1.2E-13 | -12.938 | M27539 | HLA-A | T_C | C | T | T | C | negative |
| rs3132450 | 100300398_TGI_at | A/G | G | 0.092 | 6 | 31704117 | 6.75E-05 | 8.067 | 7.2E-16 | -15.142 | X03068 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs3132450 | 100304009_TGI_at | A/G | G | 0.092 | 6 | 31704117 | 6.75E-05 | 8.117 | 4.8E-16 | -15.321 | ENST00000374943 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs3132450 | 100302941_TGI_at | A/G | G | 0.092 | 6 | 31704117 | 6.75E-05 | 8.05 | 8.3E-16 | -15.082 | NM_002123 | HLA-DQB1 | G_A | A | G | G | A | positive |
| rs3132473 | 100303991_TGI_at | A/T | T | 0.88 | 6 | 31516308 | 1.56E-05 | -6.216 | 5.1E-10 | -9.2924 | ENST00000377186 | | A_T | A | T | A | T | negative |
| rs3794968 | 100304214_TGI_at | C/G | G | 0.569 | 19 | 63678611 | 0.0002434 | -8.58 | 9.5E-18 | -17.023 | ENST00000307164 | | C_G | C | G | C | G | positive |
| rs4713279 | 100155331_TGI_at | A/T | T | 0.635 | 6 | 30052875 | 0.000706 | 6.223 | 4.9E-10 | -9.3118 | BC035656 | | T_A | A | T | T | A | positive |
| rs602875 | 100139572_TGI_at | A/G | G | 0.19 | 6 | 32681607 | 0.0009653 | 20.758 | 1E-95 | -94.984 | NM_022555 | HLA-DRB3 | A_G | A | G | A | G | negative |
| rs6457622 | 100127159_TGI_at | A/C | C | 0.384 | 6 | 32772141 | 0.0007945 | 11.412 | 3.6E-30 | -29.439 | NM_021983 | HLA-DRB4 | A_C | A | C | A | C | positive |
| rs9267444 | 100125275_TGI_at | A/G | G | 0.678 | 6 | 31591437 | 0.0006843 | -6.34 | 2.3E-10 | -9.6387 | BG755321 | HLA-DRB1 | A_G | A | G | A | G | negative |
| rs9268144 | 100309484_TGI_at | C/T | T | 0.908 | 6 | 32365177 | 2.78E-05 | 9.648 | 5E-22 | -21.3 | BC041078 | HLA-C | C_T | C | T | C | T | positive |
| rs9275576 | 100126143_TGI_at | C/T | T | 0.092 | 6 | 32787304 | 6.85E-06 | 6.713 | 1.9E-11 | -10.72 | NM_019101 | APOM | T_C | C | T | T | C | positive |
| rs9824435 | 100148878_TGI_at | C/T | T | 0.792 | 3 | 49649347 | 0.0005 | -18.418 | 9.4E-76 | -75.026 | AA011598 | | C_T | C | T | C | T | negative |

**Supplementary Table 6: Summary of integration of SpiroMeta-CHARGE GWAS results with PBMCs eQTLs**

eSNPs refer to the number of SpiroMeta-CHARGE GWAS SNPs with $P_{\mathrm{GWAS}} < 0.001$ acting as PBMCs *cis*-eQTL at the 10% FDR.

| **Integration of lung function GWAS with blood eQTLs** | | |
|---|---|---|
| **GWAS trait** | **FEV$_1$** | **FEV$_1$/FVC** |
| **Number of SNPs with $P_{\mathrm{GWAS}}$<0.001** | 6615 | 5239 |
| **Number of blood eSNPs** | 3001 | 1958 |
| **Number of probesets** | 367 | 334 |
| **Number of genes** | 306 | 276 |

## Supplementary Table 7: Blood eQTL GWAS integration results

The two tables show the list of $FEV_1$ (Table 7A) and $FEV_1$/FVC (Table 7B) *cis*-acting blood eSNPs. eSNP: SNP that is associated with either $FEV_1$ or $FEV_1$/FVC from the SpiroMeta GWAS with $P_{GWAS}$ <0.001, and acting as *cis* blood eQTL at 10% FDR in blood tissue. eQTL regulated Probe Name: Probeset whose expression is under genetic control by that particular eSNP. GWAS SNP alleles: Two alleles from the GWAS study. GWAS reference allele: Allele used to derive the association test statistics. Reference allele freq in HapMap: The frequency of the GWAS reference allele from the HapMap II project in the Caucasian population (CEU). Chr: chromosome. SNP position: position using NCBI36/hg18 coordinates. GWAS_Pval_ $FEV_1$/ GWAS_Pval_ $FEV_1$/FVC: eSNP P value for association with $FEV_1$ or $FEV_1$/FVC from the GWAS study. Blood eQTL regulated gene: Gene regulated by the eSNP in blood. eQTL regulated Probe Name: Probe regulated by the eSNP in blood. eQTL SNP alleles: SNP alleles from the blood eQTL study. Allele Assessed: Allele used to drive the eQTL test statistics. eQTL overall Z Score: Meta-analysis Z score from the blood eQTL individual studies. FDR: False discovery rate adjusted P value. Gene Name: eSNP regulated gene name.

### Supplementary Table 7A : $FEV_1$ blood eSNPs

| eSNP | GWAS SNP alleles | GWAS reference allele | Reference allele freq in HapMap | Chr | eSNP Position | GWAS_ Pval_ FEV1 | Blood eQTL regulated gene | eQTL P Value | eQTL regulated Probe Name | eQTL SNP alleles | Allele Assessed | Overall Z Score | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2499856 | A/G | G | 0.89 | 1 | 160193261 | 0.000990367 | ATF6 | 2.25E-44 | 5420343 | G/A | A | -13.97402 | 0 |
| rs7983607 | G/T | T | 0.6 | 13 | 49339455 | 0.000989086 | DLEU1 | 5.02E-15 | 5490053 | T/G | T | 7.8264223 | 0 |
| rs4786427 | A/G | G | 0.367 | 16 | 3658445 | 0.000986722 | CLUAP1 | 4.05E-07 | 6980477 | A/G | G | 5.0667841 | 0.0001085 |
| rs1046089 | A/G | G | 0.675 | 6 | 31710946 | 0.000981945 | AIF1 | 9.80E-06 | 1940047 | G/A | A | -4.421746 | 0.0044955 |
| rs1046089 | A/G | G | 0.675 | 6 | 31710946 | 0.000981945 | LY6G5C | 1.32E-34 | 3520647 | G/A | A | -12.26977 | 0 |
| rs1046089 | A/G | G | 0.675 | 6 | 31710946 | 0.000981945 | HSPA1B | 2.74E-34 | 3850433 | G/A | A | -12.21038 | 0 |
| rs3806925 | A/G | G | 0.783 | 5 | 147144605 | 0.000979792 | JAKMIP2 | 1.97E-09 | 2100253 | G/A | A | 6.0004349 | 0 |
| rs3008230 | A/G | G | 0.2 | 1 | 26273918 | 0.000979362 | PAFAH2 | 4.14E-07 | 610600 | A/G | G | -5.062543 | 0.0001085 |
| rs7631174 | C/T | T | 0.608 | 3 | 101396592 | 0.000974191 | C3orf26 | 3.30E-33 | 3610372 | C/T | C | 12.006072 | 0 |
| rs13175787 | A/G | G | 0.092 | 5 | 175759469 | 0.000973505 | NOP16 | 1.27E-12 | 380370 | A/G | G | 7.0980765 | 0 |
| rs13175787 | A/G | G | 0.092 | 5 | 175759469 | 0.000973505 | CLTB | 2.08E-13 | 1110095 | A/G | G | -7.343695 | 0 |
| rs13175787 | A/G | G | 0.092 | 5 | 175759469 | 0.000973505 | HIGD2A | 9.81E-198 | 7510315 | A/G | G | -33.07862 | 0 |
| rs6009826 | A/T | T | 0.892 | 22 | 48476247 | 0.000971829 | - | 3.31E-36 | 2760019 | T/A | A | 12.564696 | 0 |
| rs7199132 | C/T | T | 0.491 | 16 | 74007540 | 0.00097149 | CFDP1 | 1.84E-11 | 6200494 | T/C | C | 6.718156 | 0 |
| rs1794282 | C/T | T | 0.083 | 6 | 32774504 | 0.000969799 | PSMB9 | 1.43E-11 | 6450692 | C/T | T | 6.75462 | 0 |
| rs710755 | C/T | T | 0.383 | 12 | 68257980 | 0.000969324 | CCT2 | 1.79E-14 | 7100288 | T/C | T | 7.6649591 | 0 |
| rs7224888 | C/T | T | 0.908 | 17 | 44601162 | 0.00096505 | GNGT2 | 5.64E-11 | 2760138 | T/C | C | -6.553121 | 0 |
| rs11855722 | A/C | C | 0.292 | 15 | 81542424 | 0.000964787 | AC105339.9,HOMER2 | 0.000146931 | 1570767 | C/A | C | -3.796234 | 0.0553337 |
| rs11855722 | A/C | C | 0.292 | 15 | 81542424 | 0.000964787 | AC105339.9,HOMER2 | 3.42E-17 | 3850630 | C/A | C | -8.431366 | 0 |
| rs8897 | C/T | T | 0.3 | 3 | 49435411 | 0.000960886 | AMT | 3.47E-53 | 940450 | C/T | T | -15.35151 | 0 |
| rs202540 | C/T | T | 0.462 | 20 | 1613172 | 0.000960629 | SIRPG | 1.32E-90 | 2680050 | C/T | T | -20.18539 | 0 |
| rs1147761 | C/T | T | 0.733 | 18 | 32655158 | 0.000959554 | C18orf10 | 2.44E-09 | 2690541 | C/T | C | 5.9655912 | 0 |
| rs1147761 | C/T | T | 0.733 | 18 | 32655158 | 0.000959554 | C18orf10 | 4.21E-182 | 3140110 | C/T | C | -28.77673 | 0 |
| rs3870339 | A/T | T | 0.294 | 3 | 49511867 | 0.000959233 | C3orf62 | 0.000134865 | 130280 | A/T | T | -3.817429 | 0.0511033 |
| rs4790 | C/T | T | 0.068 | 12 | 52159633 | 0.000956495 | MFSD5 | 1.32E-06 | 6900600 | C/T | T | 4.8361331 | 0.0004486 |
| rs16839527 | C/T | T | 0.821 | 3 | 133915547 | 0.000951554 | ACAD11 | 9.81E-198 | 1820746 | T/C | C | -32.51813 | 0 |
| rs2521222 | C/T | T | 0.517 | 7 | 24508049 | 0.000950256 | DFNA5 | 1.27E-48 | 580403 | C/T | T | -14.65426 | 0 |
| rs3866330 | C/T | T | 0.3 | 3 | 49557998 | 0.000948415 | TCTA | 2.38E-05 | 540100 | C/T | T | -4.225891 | 0.0108242 |
| rs4983579 | A/G | G | 0.792 | 14 | 104626441 | 0.000940723 | NUDT14 | 4.31E-08 | 110092 | G/A | A | 5.4777819 | 1.64E-05 |
| rs4983579 | A/G | G | 0.792 | 14 | 104626441 | 0.000940723 | C14orf79 | 0.000124648 | 3180445 | G/A | A | 3.836815 | 0.0474467 |
| rs4983579 | A/G | G | 0.792 | 14 | 104626441 | 0.000940723 | GPR132 | 4.70E-11 | 5870692 | G/A | A | -6.580068 | 0 |
| rs916090 | C/T | T | 0.407 | 12 | 68161285 | 0.000938217 | LYZ | 3.01E-11 | 3710504 | T/C | T | -6.646273 | 0 |
| rs2463463 | C/T | T | 0.358 | 2 | 10493875 | 0.00093594 | HPCAL1 | 1.55E-12 | 520184 | C/T | T | -7.069969 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs252906 | A/C | C | 0.386 | 5 | 56154947 | 0.000930293 | C5orf35 | 5.56E-186 | 6100239 | C/A | C | -29.0852 | 0 |
| rs4649033 | A/G | G | 0.55 | 1 | 25080216 | 0.000930224 | RUNX3 | 2.47E-15 | 1440564 | A/G | G | 7.9152479 | 0 |
| rs11646677 | C/T | T | 0.475 | 16 | 73966482 | 0.00092934 | ADAT1 | 1.45E-07 | 1710204 | T/C | T | 5.2592123 | 3.18E-05 |
| rs2295786 | A/T | T | 0.317 | 10 | 105606472 | 0.000924724 | SLK | 5.27E-09 | 670470 | T/A | T | -5.838465 | 0 |
| rs10413359 | C/T | T | 0.408 | 19 | 46962846 | 0.000923429 | CEACAM6 | 1.17E-08 | 7400377 | T/C | T | 5.7038303 | 0 |
| rs7739034 | C/T | T | 0.5 | 6 | 87942905 | 0.0009162 | - | 6.30E-08 | 3390541 | T/C | C | 5.4100226 | 1.62E-05 |
| rs11610714 | A/G | G | 0.618 | 12 | 102735570 | 0.000915928 | NT5DC3 | 1.02E-37 | 6330348 | G/A | A | -12.83691 | 0 |
| rs2015353 | C/T | T | 0.542 | 17 | 15814000 | 0.000915855 | TTC19 | 1.27E-24 | 7040168 | T/C | C | 10.243262 | 0 |
| rs2684833 | C/G | G | 0.633 | 18 | 42973426 | 0.000913945 | HDHD2 | 1.20E-06 | 6370477 | G/C | C | -4.855038 | 0.0003905 |
| rs11735949 | C/G | G | 0.72 | 4 | 151294657 | 0.00091387 | LRBA | 0.000100658 | 6020291 | G/C | C | 3.8890758 | 0.0393347 |
| rs6501820 | C/G | G | 0.147 | 17 | 71029879 | 0.000912922 | TSEN54 | 5.90E-35 | 4890092 | C/G | G | 12.334738 | 0 |
| rs11928090 | A/G | G | 0.3 | 3 | 49579908 | 0.000906487 | UBA7 | 2.27E-11 | 2850202 | A/G | G | -6.687504 | 0 |
| rs11928090 | A/G | G | 0.3 | 3 | 49579908 | 0.000906487 | GMPPB,AMIGO3 | 6.86E-10 | 4830458 | A/G | G | 6.1693136 | 0 |
| rs2836371 | C/T | T | 0.661 | 21 | 38695398 | 0.000905322 | KCNJ15 | 6.08E-06 | 1050215 | T/C | C | -4.523721 | 0.0027438 |
| rs565203 | C/T | T | 0.615 | 8 | 8670367 | 0.000902561 | MFHAS1 | 3.77E-62 | 4260243 | C/T | C | -16.63684 | 0 |
| rs10904094 | C/T | T | 0.633 | 10 | 3820122 | 0.000901619 | - | 9.92E-07 | 2340215 | C/T | C | -4.893383 | 0.000272 |
| rs6507719 | A/T | T | 0.483 | 18 | 42835308 | 0.000899276 | PIAS2 | 6.88E-08 | 2320735 | T/A | T | -5.394227 | 1.62E-05 |
| rs2534674 | C/T | T | 0.433 | 6 | 31573082 | 0.00089905 | LST1 | 4.51E-06 | 770471 | T/C | T | -4.586307 | 0.0020394 |
| rs2534674 | C/T | T | 0.433 | 6 | 31573082 | 0.00089905 | TNF | 5.82E-21 | 2640301 | T/C | T | 9.393241 | 0 |
| rs2534674 | C/T | T | 0.433 | 6 | 31573082 | 0.00089905 | MICB | 3.46E-23 | 3170064 | T/C | T | -9.918751 | 0 |
| rs2534674 | C/T | T | 0.433 | 6 | 31573082 | 0.00089905 | CSNK2B | 1.85E-11 | 3450156 | T/C | T | 6.7172211 | 0 |
| rs6456804 | G/T | T | 0.083 | 6 | 28093367 | 0.000897992 | - | 2.18E-06 | 3370463 | G/T | T | 4.7359397 | 0.0008391 |
| rs12415919 | A/G | G | 0.018 | 10 | 29139022 | 0.000888733 | BAMBI | 2.25E-08 | 430050 | A/G | G | 5.5918088 | 0 |
| rs4968255 | C/T | T | 0.225 | 17 | 42667812 | 0.000886463 | ITGB3 | 0.000255184 | 1470685 | C/T | T | 3.6571084 | 0.088308 |
| rs12483553 | A/G | G | 0.904 | 21 | 45750521 | 0.000879488 | SLC19A1 | 7.76E-11 | 4230184 | G/A | A | 6.5053887 | 0 |
| rs2524005 | A/G | G | 0.767 | 6 | 30007656 | 0.000876518 | TRIM10 | 1.76E-17 | 1990110 | G/A | A | -8.508472 | 0 |
| rs2524005 | A/G | G | 0.767 | 6 | 30007656 | 0.000876518 | ZNRD1 | 5.46E-05 | 4890112 | G/A | A | 4.0348025 | 0.0230087 |
| rs2524005 | A/G | G | 0.767 | 6 | 30007656 | 0.000876518 | HCG9 | 9.77E-07 | 5960541 | G/A | A | 4.8963271 | 0.000272 |
| rs2524005 | A/G | G | 0.767 | 6 | 30007656 | 0.000876518 | - | 8.93E-05 | 6040187 | G/A | A | -3.918119 | 0.0350704 |
| rs10483080 | C/G | G | 0.117 | 21 | 45750430 | 0.000873532 | COL18A1,SLC19A1 | 2.15E-33 | 5290132 | G/C | G | 12.041733 | 0 |
| rs3129046 | A/G | G | 0.796 | 6 | 29778631 | 0.000870104 | HLA-F | 9.65E-09 | 5220070 | G/A | A | 5.7368243 | 0 |
| rs11694508 | G/T | T | 0.088 | 2 | 228168488 | 0.000869934 | MFF | 7.71E-12 | 2100068 | G/T | T | -6.843997 | 0 |
| rs1343921 | C/T | T | 0.492 | 4 | 90166485 | 0.000867715 | TIGD2 | 7.89E-07 | 1820497 | T/C | C | 4.9380569 | 0.0002434 |
| rs9272346 | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | - | 3.59E-23 | 620544 | G/A | G | 9.9148527 | 0 |
| rs9272346 | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | AL662789.11 | 0.000282763 | 2100066 | G/A | G | 3.6306833 | 0.0958659 |
| rs9272346 | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | HLA-DRA | 7.46E-12 | 2570564 | G/A | G | 6.8487684 | 0 |
| rs9272346 | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | HLA-DRB5 | 2.07E-121 | 6370315 | G/A | G | 23.430904 | 0 |
| rs9272346 | A/G | G | 0.45 | 6 | 32712350 | 0.00086271 | PSMB9,TAP1 | 0.000158601 | 7330392 | G/A | G | 3.7773073 | 0.0588038 |
| rs4500045 | A/G | G | 0.567 | 8 | 82180487 | 0.000862657 | AC012533.11,PAG1 | 6.94E-09 | 1240228 | A/G | A | 5.7925336 | 0 |
| rs4500045 | A/G | G | 0.567 | 8 | 82180487 | 0.000862657 | PAG1 | 1.47E-17 | 3610709 | A/G | A | 8.5299328 | 0 |
| rs16877282 | A/G | G | 0.921 | 5 | 6468844 | 0.000859498 | - | 7.00E-05 | 3170576 | G/A | A | -3.976241 | 0.0284393 |
| rs16877282 | A/G | G | 0.921 | 5 | 6468844 | 0.000859498 | MED10 | 2.02E-15 | 5720056 | G/A | A | 7.9400912 | 0 |
| rs6878780 | C/T | T | 0.562 | 5 | 122121639 | 0.000856875 | SNX2 | 1.67E-18 | 5550736 | T/C | C | -8.777876 | 0 |
| rs3129061 | C/T | T | 0.245 | 6 | 29777979 | 0.000856482 | GABBR1 | 3.45E-09 | 7550328 | C/T | T | 5.9087939 | 0 |
| rs2997446 | C/G | G | 0.2 | 1 | 26260828 | 0.00085566 | STMN1 | 5.33E-06 | 3460707 | C/G | G | -4.551562 | 0.0022984 |
| rs4792709 | A/T | T | 0.525 | 17 | 15833166 | 0.000849779 | ADORA2B | 4.26E-22 | 2060040 | T/A | A | 9.6646021 | 0 |
| rs9568348 | C/T | T | 0.931 | 13 | 49366723 | 0.000849255 | - | 0.000185785 | 7150735 | T/C | C | 3.7377053 | 0.0670319 |
| rs178820 | A/G | G | 0.458 | 17 | 16031510 | 0.000843867 | TTC19,NCOR1 | 1.31E-25 | 270646 | G/A | A | 10.460714 | 0 |
| rs12583 | G/T | T | 0.302 | 3 | 49546466 | 0.000836193 | NICN1 | 9.81E-198 | 3390722 | G/T | T | 30.135893 | 0 |
| rs2976958 | C/T | T | 0.65 | 8 | 8274087 | 0.000835045 | AC068353.34 | 6.48E-06 | 3370242 | T/C | C | -4.510254 | 0.0029516 |
| rs2561563 | A/C | C | 0.075 | 19 | 45841484 | 0.000825229 | EGLN2 | 1.71E-11 | 1400408 | A/C | C | -6.729166 | 0 |
| rs2561563 | A/C | C | 0.075 | 19 | 45841484 | 0.000825229 | LTBP4 | 5.13E-11 | 4290315 | A/C | C | -6.56721 | 0 |
| rs6566060 | C/T | T | 0.136 | 18 | 71009457 | 0.000818093 | ZADH2 | 5.38E-17 | 6040743 | T/C | T | 8.3780006 | 0 |
| rs17162316 | C/G | G | 0.133 | 1 | 27050494 | 0.000813972 | ZDHHC18 | 3.92E-69 | 540274 | C/G | G | 17.573742 | 0 |
| rs17162316 | C/G | G | 0.133 | 1 | 27050494 | 0.000813972 | PIGV | 9.23E-28 | 2070279 | C/G | G | -10.92028 | 0 |
| rs17162316 | C/G | G | 0.133 | 1 | 27050494 | 0.000813972 | ARID1A | 1.41E-122 | 6280411 | C/G | G | -23.5454 | 0 |
| rs6776974 | A/G | G | 0.115 | 3 | 114737213 | 0.000809796 | SIDT1 | 0.00029256 | 7000026 | A/G | G | 3.6219937 | 0.0985437 |
| rs778524 | A/G | G | 0.233 | 3 | 23469516 | 0.00080239 | UBE2E2 | 1.54E-09 | 5270021 | A/G | G | -6.040095 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs16836230 | C/G | G | 0.759 | 1 | 148588957 | 0.000799478 | AL138795.21-3,MRPS21 | 3.56E-26 | 3890500 | G/C | C | 10.583437 | 0 |
| rs4969481 | C/T | T | 0.017 | 17 | 77586501 | 0.000799122 | SLC16A3 | 1.05E-15 | 110719 | T/C | T | 8.021159 | 0 |
| rs4969481 | C/T | T | 0.017 | 17 | 77586501 | 0.000799122 | STRA13 | 6.50E-12 | 270605 | T/C | T | -6.868327 | 0 |
| rs4969481 | C/T | T | 0.017 | 17 | 77586501 | 0.000799122 | LRRC45 | 1.08E-07 | 1500048 | T/C | T | 5.3129324 | 3.20E-05 |
| rs4969481 | C/T | T | 0.017 | 17 | 77586501 | 0.000799122 | DCXR | 9.81E-198 | 6660132 | T/C | T | 33.545665 | 0 |
| rs17162190 | A/G | G | 0.825 | 1 | 26745419 | 0.000797522 | RPS6KA1 | 5.60E-20 | 4730739 | G/A | A | 9.1518496 | 0 |
| rs2298605 | C/T | T | 0.525 | 8 | 109341182 | 0.000794138 | - | 4.68E-35 | 4730162 | T/C | T | 12.353247 | 0 |
| rs12459996 | G/T | T | 0.075 | 19 | 46448746 | 0.000792004 | HNRNPUL1 | 3.86E-16 | 5890156 | T/G | T | -8.142858 | 0 |
| rs8015723 | A/G | G | 0.208 | 14 | 102965662 | 0.000787555 | EIF5 | 1.97E-05 | 5050110 | G/A | G | 4.2689732 | 0.0091892 |
| rs8015723 | A/G | G | 0.208 | 14 | 102965662 | 0.000787555 | EIF5 | 9.68E-33 | 5670468 | G/A | G | 11.916822 | 0 |
| rs10883916 | A/G | G | 0.691 | 10 | 105570526 | 0.000787475 | SLK | 3.35E-08 | 4060021 | G/A | A | 5.5223012 | 0 |
| rs10103957 | C/T | T | 0.117 | 8 | 144670152 | 0.000779696 | - | 3.58E-17 | 520639 | T/C | T | 8.4261057 | 0 |
| rs2236783 | A/G | G | 0.149 | 2 | 136310628 | 0.000778778 | MCM6 | 1.31E-116 | 5690274 | G/A | G | 22.955313 | 0 |
| rs2236783 | A/G | G | 0.149 | 2 | 136310628 | 0.000778778 | DARS | 5.44E-72 | 6840711 | G/A | G | 17.94307 | 0 |
| rs4660808 | C/T | T | 0.233 | 1 | 39791096 | 0.000777388 | MACF1 | 2.56E-25 | 6370739 | C/T | T | 10.39696 | 0 |
| rs7163730 | A/G | G | 0.208 | 15 | 76601736 | 0.000770202 | PSMA4 | 2.37E-23 | 4040711 | G/A | G | -9.956339 | 0 |
| rs10418984 | C/T | T | 0.15 | 19 | 36530218 | 0.000769869 | TSHZ3 | 4.54E-19 | 1260066 | C/T | T | 8.9230189 | 0 |
| rs4970988 | A/G | G | 0.675 | 1 | 149216686 | 0.000769765 | LASS2 | 2.94E-25 | 3370121 | G/A | A | 10.383824 | 0 |
| rs4970988 | A/G | G | 0.675 | 1 | 149216686 | 0.000769765 | BNIPL | 1.74E-07 | 4390372 | G/A | A | -5.225129 | 4.75E-05 |
| rs4970988 | A/G | G | 0.675 | 1 | 149216686 | 0.000769765 | CDC42SE1,C1orf56 | 3.66E-07 | 4540288 | G/A | A | -5.085972 | 0.0001088 |
| rs4970988 | A/G | G | 0.675 | 1 | 149216686 | 0.000769765 | SETDB1 | 8.37E-05 | 6450722 | G/A | A | -3.933755 | 0.0331704 |
| rs11693759 | A/G | G | 0.814 | 2 | 128318236 | 0.00076706 | MYO7B | 4.87E-06 | 2230600 | G/A | A | -4.570503 | 0.0021328 |
| rs2960785 | C/T | T | 0.578 | 7 | 26918664 | 0.000766605 | - | 2.16E-192 | 5340519 | T/C | T | -29.58767 | 0 |
| rs2960785 | C/T | T | 0.578 | 7 | 26918664 | 0.000766605 | HOXA5,HOXA3 | 9.59E-57 | 6620437 | T/C | T | -15.87407 | 0 |
| rs4970926 | C/T | T | 0.517 | 1 | 148940308 | 0.000758853 | MCL1 | 1.13E-05 | 7380100 | T/C | C | -4.390282 | 0.0051633 |
| rs8455 | C/T | T | 0.408 | 3 | 159871474 | 0.000757142 | GFM1,LXN | 6.49E-41 | 60670 | T/C | T | -13.39489 | 0 |
| rs13270096 | A/G | G | 0.74 | 8 | 91529516 | 0.000753619 | - | 2.16E-10 | 1820768 | G/A | A | -6.349933 | 0 |
| rs13270096 | A/G | G | 0.74 | 8 | 91529516 | 0.000753619 | TMEM64 | 0.000274124 | 6270600 | G/A | A | -3.638696 | 0.0936847 |
| rs735765 | A/G | G | 0.842 | 6 | 28278276 | 0.000752978 | ZKSCAN4 | 2.29E-20 | 3390053 | G/A | A | 9.2481341 | 0 |
| rs5742761 | C/G | G | 0.147 | 14 | 22122938 | 0.000748703 | DAD1 | 5.10E-31 | 4220181 | C/G | G | 11.581979 | 0 |
| rs268769 | C/T | T | 0.508 | 3 | 57914614 | 0.000737563 | FLNB | 3.77E-09 | 5220767 | C/T | C | -5.894097 | 0 |
| rs7725846 | C/T | T | 0.471 | 5 | 156870548 | 0.000737526 | CYFIP2 | 4.04E-10 | 3520020 | C/T | T | 6.2526819 | 0 |
| rs916888 | C/T | T | 0.783 | 17 | 42218292 | 0.000734659 | NSF | 1.40E-13 | 5260138 | T/C | C | 7.3968893 | 0 |
| rs1800209 | A/G | G | 0.125 | 13 | 76472984 | 0.000723221 | CLN5 | 2.74E-08 | 1740040 | G/A | G | -5.557052 | 0 |
| rs1862362 | A/G | G | 0.442 | 5 | 150510872 | 0.000722388 | ANXA6 | 7.43E-57 | 450671 | G/A | G | 15.890138 | 0 |
| rs1862362 | A/G | G | 0.442 | 5 | 150510872 | 0.000722388 | ANXA6 | 6.07E-91 | 2490598 | G/A | G | 20.223657 | 0 |
| rs11042032 | A/T | T | 0.509 | 11 | 8653448 | 0.000713934 | C11orf17 | 5.86E-09 | 2190753 | T/A | T | 5.8206132 | 0 |
| rs11042032 | A/T | T | 0.509 | 11 | 8653448 | 0.000713934 | C11orf17 | 5.53E-07 | 3180288 | T/A | T | 5.0069351 | 0.0001691 |
| rs11042032 | A/T | T | 0.509 | 11 | 8653448 | 0.000713934 | C11orf17 | 1.96E-25 | 6270112 | T/A | T | 10.422236 | 0 |
| rs12112550 | C/G | G | 0.139 | 7 | 129907172 | 0.000711903 | CPA5 | 2.36E-49 | 1450056 | C/G | G | 14.767994 | 0 |
| rs16938170 | A/G | G | 0.661 | 11 | 45079758 | 0.000708789 | TP53I11 | 2.17E-09 | 70440 | G/A | A | 5.984948 | 0 |
| rs16938170 | A/G | G | 0.661 | 11 | 45079758 | 0.000708789 | TP53I11 | 0.000111911 | 6350376 | G/A | A | 3.8632847 | 0.0432691 |
| rs479763 | C/T | T | 0.158 | 11 | 67531704 | 0.00070684 | UNC93B1 | 1.83E-12 | 4780612 | C/T | T | -7.047368 | 0 |
| rs479763 | C/T | T | 0.158 | 11 | 67531704 | 0.00070684 | TCIRG1 | 4.43E-24 | 6480333 | C/T | T | -10.12167 | 0 |
| rs1051065 | C/T | T | 0.281 | 12 | 9797334 | 0.000706161 | - | 0.000153338 | 3610333 | T/C | T | 3.7856559 | 0.0573552 |
| rs7547017 | C/T | T | 0.592 | 1 | 169868825 | 0.000703402 | VAMP4 | 2.83E-11 | 2100722 | T/C | C | 6.6550401 | 0 |
| rs7547017 | C/T | T | 0.592 | 1 | 169868825 | 0.000703402 | VAMP4 | 4.59E-08 | 3870520 | T/C | C | 5.4665429 | 1.64E-05 |
| rs1807304 | A/G | G | 0.212 | 11 | 63616327 | 0.000693633 | PRDX5 | 4.70E-09 | 520750 | A/G | G | -5.8575 | 0 |
| rs1807304 | A/G | G | 0.212 | 11 | 63616327 | 0.000693633 | - | 1.22E-12 | 940750 | A/G | G | 7.1032127 | 0 |
| rs1807304 | A/G | G | 0.212 | 11 | 63616327 | 0.000693633 | PRDX5 | 1.57E-14 | 2630056 | A/G | G | -7.6817 | 0 |
| rs7954012 | A/T | T | 0.763 | 12 | 31795525 | 0.000691059 | C12orf35 | 5.57E-10 | 7510424 | T/A | A | -6.202296 | 0 |
| rs7954012 | A/T | T | 0.763 | 12 | 31795525 | 0.000691059 | C12orf35 | 5.25E-12 | 7570477 | T/A | A | -6.898649 | 0 |
| rs7526415 | A/G | G | 0.233 | 1 | 25052908 | 0.000688715 | CLIC4 | 0.000197651 | 3170762 | A/G | G | 3.7220538 | 0.0711306 |
| rs4837587 | A/G | G | 0.575 | 9 | 118324965 | 0.000688436 | TRIM32,ASTN2 | 7.87E-05 | 5670088 | G/A | A | 3.9483375 | 0.0312626 |
| rs7204927 | C/G | G | 0.55 | 16 | 56683661 | 0.000677989 | C16orf57 | 6.01E-05 | 2750360 | G/C | C | -4.012603 | 0.0250991 |
| rs7204927 | C/G | G | 0.55 | 16 | 56683661 | 0.000677989 | ZNF319 | 1.27E-21 | 3180315 | G/C | C | -9.552367 | 0 |
| rs7204927 | C/G | G | 0.55 | 16 | 56683661 | 0.000677989 | CSNK2A2 | 5.62E-06 | 4150176 | G/C | C | 4.5402132 | 0.0024237 |
| rs7204927 | C/G | G | 0.55 | 16 | 56683661 | 0.000677989 | C16orf80 | 6.57E-05 | 5360630 | G/C | C | -3.9914 | 0.0269431 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs11763462 | A/G | G | 0.129 | 7 | 129993518 | 0.000676544 | AC007938.1 | 6.58E-09 | 2030386 | A/G | G | 5.8014169 | 0 |
| rs2499855 | C/T | T | 0.892 | 1 | 160196385 | 0.000671659 | FCRLB | 1.62E-15 | 4730204 | T/C | C | 7.9675853 | 0 |
| rs3130564 | C/T | T | 0.283 | 6 | 31209653 | 0.000662753 | HCG27 | 1.23E-19 | 3800358 | C/T | T | -9.066274 | 0 |
| rs12285938 | C/T | T | 0.971 | 11 | 10555328 | 0.000661598 | MRVI1,AC009532.9 | 1.29E-07 | 2320750 | T/C | C | 5.280216 | 3.19E-05 |
| rs12285938 | C/T | T | 0.971 | 11 | 10555328 | 0.000661598 | RNF141 | 4.15E-06 | 4220372 | T/C | C | -4.603899 | 0.0018124 |
| rs2248373 | C/T | T | 0.417 | 6 | 31554525 | 0.000661319 | ATP6V1G2,BAT1 | 1.56E-13 | 1260538 | T/C | T | -7.382212 | 0 |
| rs8046429 | A/G | G | 0.553 | 16 | 75769346 | 0.000658015 | MON1B | 4.11E-153 | 5310674 | G/A | A | -26.3586 | 0 |
| rs515271 | A/G | G | 0.842 | 11 | 125532146 | 0.00065407 | RPUSD4 | 1.62E-49 | 2100608 | G/A | A | -14.7935 | 0 |
| rs4875 | C/T | T | 0.392 | 3 | 159803291 | 0.000652582 | GFM1 | 1.55E-25 | 3440195 | T/C | T | -10.44471 | 0 |
| rs9366653 | A/G | G | 0.867 | 6 | 26462226 | 0.00065204 | HIST1H2AC,HIST1H2BD,HIST1H4A | 6.97E-18 | 290730 | G/A | A | -8.615501 | 0 |
| rs9366653 | A/G | G | 0.867 | 6 | 26462226 | 0.00065204 | HIST1H4C,HIST1H4A | 1.81E-06 | 3890349 | G/A | A | 4.7732456 | 0.0006669 |
| rs6901497 | A/G | G | 0.992 | 6 | 26808488 | 0.000637008 | - | 4.93E-40 | 290273 | G/A | A | 13.243586 | 0 |
| rs6901497 | A/G | G | 0.992 | 6 | 26808488 | 0.000637008 | HMGN4 | 6.54E-10 | 5270689 | G/A | A | -6.176924 | 0 |
| rs6901497 | A/G | G | 0.992 | 6 | 26808488 | 0.000637008 | ABT1 | 1.13E-05 | 6480392 | G/A | A | -4.391373 | 0.0051633 |
| rs2183269 | C/T | T | 0.681 | 1 | 68441018 | 0.000634057 | GPR177 | 6.55E-08 | 1570441 | T/C | C | 5.4031417 | 1.62E-05 |
| rs2183269 | C/T | T | 0.681 | 1 | 68441018 | 0.000634057 | GPR177 | 8.58E-16 | 4250711 | T/C | C | 8.0457108 | 0 |
| rs2183269 | C/T | T | 0.681 | 1 | 68441018 | 0.000634057 | GPR177 | 5.44E-14 | 6940280 | T/C | C | 7.5211212 | 0 |
| rs3786320 | A/C | C | 0.975 | 18 | 30951841 | 0.000621055 | ZNF397OS,ZNF397 | 3.08E-05 | 2320673 | C/A | A | -4.167957 | 0.0137229 |
| rs13072540 | A/C | C | 0.422 | 3 | 153476864 | 0.000619991 | MBNL1 | 2.43E-79 | 160253 | C/A | C | -18.86009 | 0 |
| rs1592971 | A/G | G | 0.8 | 5 | 156951767 | 0.00061657 | THG1L | 3.33E-29 | 4730348 | G/A | A | -11.21803 | 0 |
| rs1592971 | A/G | G | 0.8 | 5 | 156951767 | 0.00061657 | CYFIP2 | 0.000104801 | 6100768 | G/A | A | 3.879302 | 0.041001 |
| rs1592971 | A/G | G | 0.8 | 5 | 156951767 | 0.00061657 | ADAM19 | 9.71E-45 | 6900209 | G/A | A | -14.0337 | 0 |
| rs7216411 | C/T | T | 0.712 | 17 | 43443943 | 0.000612489 | SNX11 | 7.20E-38 | 130446 | T/C | C | 12.863832 | 0 |
| rs6602563 | C/T | T | 0.568 | 10 | 12210180 | 0.000587888 | DHTKD1 | 5.75E-07 | 6250075 | T/C | C | -4.999493 | 0.0001689 |
| rs4889366 | A/G | G | 0.703 | 16 | 80278919 | 0.000583779 | AC099524.5 | 2.40E-08 | 360626 | A/G | A | 5.5807995 | 0 |
| rs4946151 | C/G | G | 0.583 | 6 | 116701982 | 0.000580482 | FAM26F | 2.52E-13 | 6590646 | G/C | C | -7.31792 | 0 |
| rs6499263 | C/T | T | 0.45 | 16 | 68447650 | 0.000563855 | WWP2 | 1.95E-10 | 3800603 | T/C | T | 6.365191 | 0 |
| rs7024579 | C/T | T | 0.246 | 9 | 138240234 | 0.000561212 | C9orf151 | 3.54E-08 | 3830605 | T/C | T | 5.5122662 | 0 |
| rs613214 | A/C | C | 0.367 | 11 | 125542572 | 0.00055931 | FOXRED1 | 8.19E-19 | 1240309 | C/A | C | 8.8575313 | 0 |
| rs613214 | A/C | C | 0.367 | 11 | 125542572 | 0.00055931 | DCPS | 5.43E-07 | 1500129 | C/A | C | -5.010771 | 0.0001538 |
| rs3773663 | A/G | G | 0.558 | 3 | 30705876 | 0.000556378 | TGFBR2 | 3.91E-34 | 6560091 | A/G | A | -12.18145 | 0 |
| rs2652804 | C/T | T | 0.353 | 15 | 61161309 | 0.000547472 | LACTB | 4.69E-13 | 460373 | C/T | T | -7.234145 | 0 |
| rs2652804 | C/T | T | 0.353 | 15 | 61161309 | 0.000547472 | LACTB | 3.31E-72 | 1570669 | C/T | T | -17.97072 | 0 |
| rs2652804 | C/T | T | 0.353 | 15 | 61161309 | 0.000547472 | - | 3.27E-14 | 3940762 | C/T | T | -7.587176 | 0 |
| rs2071407 | C/T | T | 0.283 | 14 | 103056893 | 0.00054294 | XRCC3,KLC1 | 0.000112279 | 670014 | T/C | T | -3.862497 | 0.0433828 |
| rs1783537 | A/G | G | 0.48 | 11 | 73647399 | 0.000536557 | PGM2L1 | 2.29E-06 | 7210093 | G/A | A | -4.726503 | 0.0009108 |
| rs2766533 | A/G | G | 0.483 | 6 | 35793468 | 0.000534651 | RPL10A | 0.000224078 | 4040100 | G/A | G | 3.690399 | 0.0791117 |
| rs3786343 | C/T | T | 0.342 | 18 | 59798875 | 0.000533086 | SERPINB8 | 6.58E-07 | 1770376 | T/C | T | -4.973431 | 0.0002141 |
| rs3786343 | C/T | T | 0.342 | 18 | 59798875 | 0.000533086 | SERPINB8 | 4.13E-09 | 3400672 | T/C | T | -5.878863 | 0 |
| rs6755 | A/G | G | 0.552 | 6 | 116677948 | 0.000532652 | TSPYL4 | 4.28E-05 | 610521 | G/A | A | 4.0918895 | 0.0183132 |
| rs6755 | A/G | G | 0.552 | 6 | 116677948 | 0.000532652 | NT5DC1 | 8.20E-25 | 6960129 | G/A | A | 10.285416 | 0 |
| rs3768015 | A/G | G | 0.675 | 1 | 149079578 | 0.000532611 | CDC42SE1,C1orf56 | 2.51E-11 | 4480192 | G/A | A | -6.672622 | 0 |
| rs3768015 | A/G | G | 0.675 | 1 | 149079578 | 0.000532611 | LASS2 | 7.75E-23 | 6380154 | G/A | A | 9.8377691 | 0 |
| rs6070706 | C/T | T | 0.109 | 20 | 57061634 | 0.00053202 | TH1L,CTSZ | 2.33E-114 | 4390288 | C/T | T | -22.72893 | 0 |
| rs6070706 | C/T | T | 0.109 | 20 | 57061634 | 0.00053202 | TH1L,CTSZ | 2.28E-83 | 6250017 | C/T | T | -19.34427 | 0 |
| rs12208776 | G/T | T | 0.508 | 6 | 7640417 | 0.000531178 | BMP6 | 8.02E-07 | 6980064 | G/T | G | -4.934812 | 0.0002433 |
| rs3134940 | C/T | T | 0.84 | 6 | 32257794 | 0.000521231 | SKIV2L | 3.34E-14 | 5560541 | T/C | C | -7.584488 | 0 |
| rs11591349 | A/T | T | 0.466 | 10 | 102734321 | 0.000520655 | SEMA4G,MRPL43 | 5.78E-47 | 6620181 | T/A | T | -14.39255 | 0 |
| rs3136555 | C/G | G | 0.958 | 5 | 54434096 | 0.000518149 | GZMA | 3.39E-05 | 3420612 | G/C | C | 4.1459272 | 0.015027 |
| rs1264709 | A/T | T | 0.22 | 6 | 30164455 | 0.000517854 | ZNRD1 | 1.06E-18 | 4060255 | A/T | T | -8.828489 | 0 |
| rs2867301 | C/T | T | 0.375 | 1 | 148920419 | 0.000504189 | CTSS | 3.64E-157 | 6330484 | T/C | T | 26.709614 | 0 |
| rs11836637 | C/T | T | 0.904 | 12 | 50208747 | 0.000503566 | SLC4A8 | 1.85E-14 | 6200196 | T/C | C | -7.66092 | 0 |
| rs911554 | G/T | T | 0.302 | 14 | 103069124 | 0.000484057 | BAG5 | 1.35E-13 | 130669 | T/G | T | 7.4015563 | 0 |
| rs1264695 | A/G | G | 0.242 | 6 | 30175871 | 0.000477822 | ZNRD1 | 2.81E-06 | 4050673 | A/G | G | 4.6846262 | 0.0010651 |
| rs1877723 | C/T | T | 0.302 | 4 | 2816597 | 0.00047691 | ADD1 | 3.28E-11 | 5900685 | C/T | T | 6.63326 | 0 |
| rs773139 | A/G | G | 0.108 | 9 | 76852819 | 0.000476851 | C9orf95 | 3.58E-39 | 1980180 | A/G | G | 13.093659 | 0 |
| rs2844796 | A/G | G | 0.754 | 6 | 30180490 | 0.000476638 | PPP1R11 | 5.87E-09 | 620376 | G/A | A | 5.820494 | 0 |
| rs6446257 | C/T | T | 0.692 | 3 | 49228496 | 0.000470609 | DALRD3,WDR6 | 1.93E-82 | 70707 | T/C | C | 19.233909 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs6446257 | C/T | T | 0.692 | 3 | 49228496 | 0.000470609 | ARIH2 | 0.000107504 | 1010682 | T/C | C | -3.87312 | 0.0418287 |
| rs6446257 | C/T | T | 0.692 | 3 | 49228496 | 0.000470609 | USP4 | 0.000119964 | 6290435 | T/C | C | -3.846344 | 0.0459255 |
| rs6446257 | C/T | T | 0.692 | 3 | 49228496 | 0.000470609 | QRICH1 | 1.24E-12 | 7320743 | T/C | C | 7.1012219 | 0 |
| rs7556628 | C/T | T | 0.683 | 1 | 26557777 | 0.000467268 | CD52 | 3.19E-06 | 20129 | T/C | C | 4.6582614 | 0.0012783 |
| rs3926468 | A/C | C | 0.422 | 3 | 57485447 | 0.000453639 | PDE12 | 0.000112371 | 3060154 | A/C | C | -3.862286 | 0.0434633 |
| rs1050818 | A/C | C | 0.258 | 1 | 148533183 | 0.000446782 | PRPF3 | 7.44E-05 | 2260615 | A/C | C | 3.9617955 | 0.0300606 |
| rs2517645 | C/T | T | 0.792 | 6 | 30230602 | 0.000444181 | TRIM10 | 4.44E-28 | 110255 | T/C | C | -10.98645 | 0 |
| rs3823158 | A/T | T | 0.875 | 6 | 26571250 | 0.000442395 | HIST1H4H | 8.40E-06 | 2970019 | T/A | A | 4.4549237 | 0.0039579 |
| rs2815708 | C/T | T | 0.336 | 1 | 28220078 | 0.000441869 | ATPIF1 | 8.10E-12 | 3780068 | C/T | T | -6.836933 | 0 |
| rs555502 | A/G | G | 0.717 | 20 | 2794397 | 0.00043175 | MRPS26 | 2.61E-06 | 3310445 | G/A | A | -4.699684 | 0.0010238 |
| rs6504280 | G/T | T | 0.717 | 17 | 43915068 | 0.000426775 | HOXB4 | 2.62E-05 | 2120008 | T/G | G | -4.203993 | 0.011984 |
| rs6504280 | G/T | T | 0.717 | 17 | 43915068 | 0.000426775 | HOXB2 | 1.84E-72 | 3460097 | T/G | G | -18.00338 | 0 |
| rs8073371 | C/T | T | 0.217 | 17 | 43451275 | 0.000424334 | MRPL10 | 7.78E-12 | 6180154 | C/T | T | -6.842781 | 0 |
| rs1075728 | A/G | G | 0.558 | 19 | 47154628 | 0.000424135 | RABAC1 | 4.11E-120 | 70634 | A/G | A | 23.303378 | 0 |
| rs10852637 | C/T | T | 0.466 | 16 | 3658493 | 0.000423479 | - | 2.91E-48 | 2230129 | C/T | C | 14.597775 | 0 |
| rs11780215 | A/G | G | 0.15 | 8 | 118126719 | 0.000413779 | RAD21 | 5.26E-08 | 2260551 | A/G | G | -5.44243 | 1.63E-05 |
| rs911552 | A/G | G | 0.297 | 14 | 103069261 | 0.000410077 | CKB | 7.50E-17 | 4150066 | G/A | G | -8.33896 | 0 |
| rs12678078 | A/G | G | 0.875 | 8 | 144649443 | 0.000406893 | ZC3H3 | 7.80E-17 | 4760538 | G/A | A | -8.334273 | 0 |
| rs11869081 | A/G | G | 0.783 | 17 | 27891141 | 0.000405419 | CDK5R1 | 9.52E-05 | 2750280 | G/A | A | 3.9024613 | 0.037441 |
| rs330905 | A/T | T | 0.271 | 8 | 9030961 | 0.000403482 | PPP1R3B | 2.54E-05 | 3940682 | T/A | T | 4.2115011 | 0.0113676 |
| rs330905 | A/T | T | 0.271 | 8 | 9030961 | 0.000403482 | PPP1R3B | 3.67E-19 | 5870608 | T/A | T | 8.9467559 | 0 |
| rs1076976 | A/G | G | 0.683 | 19 | 46985789 | 0.00039784 | CEACAM3 | 7.05E-05 | 1850139 | G/A | A | 3.9747497 | 0.0285443 |
| rs11580810 | C/T | T | 0.729 | 1 | 148674347 | 0.000396177 | AL138795.21-3,MRPS21 | 7.53E-18 | 3830671 | T/C | C | 8.606708 | 0 |
| rs7212620 | A/T | T | 0.325 | 17 | 70973525 | 0.000389295 | KIAA0195 | 1.92E-32 | 380743 | A/T | T | 11.859676 | 0 |
| rs7212620 | A/T | T | 0.325 | 17 | 70973525 | 0.000389295 | MRPS7 | 4.13E-15 | 1580129 | A/T | T | -7.851009 | 0 |
| rs3104405 | A/C | C | 0.344 | 6 | 32790286 | 0.00038584 | HLA-DMA | 2.63E-10 | 540563 | C/A | C | 6.3194094 | 0 |
| rs4745763 | A/C | C | 0.295 | 10 | 76504927 | 0.000384097 | COMTD1 | 6.81E-06 | 6960377 | C/A | C | 4.4997112 | 0.0030883 |
| rs9612418 | C/T | T | 0.062 | 22 | 22427015 | 0.000383285 | VPREB3 | 1.80E-37 | 4640768 | T/C | T | 12.792817 | 0 |
| rs8076163 | C/T | T | 0.267 | 17 | 43475324 | 0.000382862 | SP2 | 1.17E-07 | 1260201 | C/T | T | 5.2988934 | 3.20E-05 |
| rs2004100 | C/T | T | 0.271 | 8 | 144625874 | 0.00037728 | ZNF696 | 3.81E-12 | 3310523 | T/C | T | -6.944139 | 0 |
| rs2333452 | A/G | G | 0.75 | 4 | 177525930 | 0.000373833 | - | 5.22E-15 | 7050026 | G/A | A | -7.821777 | 0 |
| rs12113381 | C/T | T | 0.102 | 7 | 1109653 | 0.000371044 | C7orf50,GPR30 | 1.78E-12 | 270593 | C/T | T | -7.0506 | 0 |
| rs12113381 | C/T | T | 0.102 | 7 | 1109653 | 0.000371044 | ZFAND2A | 1.96E-37 | 870379 | C/T | T | -12.78625 | 0 |
| rs12113381 | C/T | T | 0.102 | 7 | 1109653 | 0.000371044 | C7orf50,GPR146 | 3.81E-06 | 7100092 | C/T | T | -4.621646 | 0.0015875 |
| rs2289469 | A/G | G | 0.831 | 2 | 134930512 | 0.000367448 | MGAT5 | 1.06E-98 | 2230382 | G/A | A | -21.08633 | 0 |
| rs6800914 | A/G | G | 0.397 | 3 | 159804868 | 0.000366769 | MFSD1 | 1.60E-06 | 510288 | G/A | G | 4.7981464 | 0.0005948 |
| rs178810 | C/T | T | 0.517 | 17 | 16038155 | 0.000364935 | TRPV2 | 7.48E-05 | 4390301 | T/C | C | 3.9606062 | 0.0301287 |
| rs10792356 | C/G | G | 0.267 | 11 | 62197399 | 0.000361661 | ZBTB3,TTC9C | 0.000182126 | 3830682 | C/G | G | 3.7426564 | 0.0660135 |
| rs7531698 | A/G | G | 0.297 | 1 | 26563332 | 0.000357977 | ZNF683 | 7.66E-06 | 7650451 | A/G | G | 4.4744717 | 0.0035518 |
| rs2294119 | C/T | T | 0.125 | 8 | 144638112 | 0.000353022 | NAPRT1 | 6.32E-54 | 3360131 | T/C | T | 15.461402 | 0 |
| rs2279408 | A/G | G | 0.259 | 16 | 4598585 | 0.000349882 | MGRN1 | 1.07E-12 | 1510414 | A/G | G | -7.121372 | 0 |
| rs11903357 | C/T | T | 0.322 | 2 | 150959444 | 0.000348271 | - | 9.15E-05 | 4730113 | C/T | T | -3.912266 | 0.0358904 |
| rs7120836 | A/G | G | 0.217 | 11 | 3798039 | 0.000345988 | RHOG | 5.50E-10 | 4010753 | G/A | G | 6.2042763 | 0 |
| rs10517061 | A/T | T | 0.5 | 4 | 24787395 | 0.000344721 | ANAPC4 | 5.01E-69 | 6450021 | T/A | A | 17.559871 | 0 |
| rs11231181 | A/G | G | 0.742 | 11 | 62190749 | 0.000338858 | INTS5 | 3.93E-86 | 4810288 | G/A | A | 19.669603 | 0 |
| rs11191822 | G/T | T | 0.679 | 10 | 105589760 | 0.000331663 | SH3PXD2A | 6.93E-40 | 3460451 | T/G | G | -13.21791 | 0 |
| rs3129950 | C/G | G | 0.908 | 6 | 32466179 | 0.000328693 | HLA-DRA | 1.87E-19 | 270168 | G/C | C | 9.0208556 | 0 |
| rs6683015 | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | MCL1 | 6.86E-05 | 610750 | T/G | G | 3.9813232 | 0.0280315 |
| rs6683015 | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | CTSK | 7.76E-101 | 1430278 | T/G | G | 21.31794 | 0 |
| rs6683015 | G/T | T | 0.528 | 1 | 149014035 | 0.00032145 | ARNT | 8.10E-10 | 2640338 | T/G | G | 6.1430608 | 0 |
| rs2285579 | A/T | T | 0.517 | 17 | 15987570 | 0.00031701 | PIGL | 1.76E-11 | 6110367 | T/A | A | 6.7245165 | 0 |
| rs1052708 | A/G | G | 0.05 | 10 | 16593361 | 0.000316538 | PTER | 2.28E-23 | 6130382 | A/G | G | 9.9600932 | 0 |
| rs11683643 | A/G | G | 0.692 | 2 | 48718796 | 0.000315274 | STON1-GTF2A1L | 0.000197338 | 4230730 | A/G | A | 3.7224592 | 0.0710804 |
| rs1110304 | A/G | G | 0.358 | 1 | 203542648 | 0.000309431 | DSTYK | 7.52E-06 | 5560360 | A/G | G | -4.4784 | 0.0034556 |
| rs6127688 | A/G | G | 0.737 | 20 | 54244231 | 0.000303665 | C20orf108 | 2.39E-07 | 770561 | G/A | A | 5.1659478 | 9.42E-05 |
| rs7634335 | G/T | T | 0.742 | 3 | 57665513 | 0.000303489 | ARF4 | 2.85E-08 | 6770176 | T/G | G | 5.5503943 | 0 |
| rs11204675 | G/T | T | 0.458 | 1 | 148837609 | 0.000299637 | C1orf138 | 6.15E-05 | 4050497 | T/G | T | 4.0071961 | 0.0254341 |
| rs12051 | A/G | G | 0.375 | 17 | 43458759 | 0.000297999 | SNX11 | 3.20E-09 | 430445 | A/G | G | -5.921316 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs1434232 | A/G | G | 0.271 | 15 | 97921346 | 0.000296271 | MEF2A | 7.79E-06 | 6400132 | A/G | G | 4.4710638 | 0.0035915 |
| rs9392029 | C/T | T | 0.083 | 6 | 419252 | 0.000290524 | EXOC2 | 7.93E-09 | 2970390 | C/T | T | 5.7700113 | 0 |
| rs17637597 | C/T | T | 0.733 | 11 | 62195326 | 0.000286846 | BSCL2 | 1.64E-25 | 6900224 | T/C | C | -10.43941 | 0 |
| rs2960784 | C/G | G | 0.6 | 7 | 26917430 | 0.000285549 | HOXA4,HOXA3 | 8.40E-06 | 7160553 | G/C | G | -4.454653 | 0.0039579 |
| rs7312624 | A/G | G | 0.225 | 12 | 9787906 | 0.000285192 | AC007068.17,CLEC2D | 6.34E-09 | 2570132 | G/A | G | 5.8077003 | 0 |
| rs7312624 | A/G | G | 0.225 | 12 | 9787906 | 0.000285192 | AC007068.17,CLEC2D | 9.20E-05 | 3520129 | G/A | G | 3.9108504 | 0.036255 |
| rs7312624 | A/G | G | 0.225 | 12 | 9787906 | 0.000285192 | CLEC12A | 0.000298959 | 3780358 | G/A | G | 3.6162534 | 0.0997749 |
| rs7312624 | A/G | G | 0.225 | 12 | 9787906 | 0.000285192 | - | 4.00E-13 | 4010681 | G/A | G | -7.255586 | 0 |
| rs7312624 | A/G | G | 0.225 | 12 | 9787906 | 0.000285192 | AC007068.17,CLEC2D | 1.58E-57 | 5490341 | G/A | G | -15.98685 | 0 |
| rs7312624 | A/G | G | 0.225 | 12 | 9787906 | 0.000285192 | CLECL1 | 7.24E-05 | 6370414 | G/A | G | -3.968493 | 0.0294058 |
| rs7645318 | A/T | T | 0.525 | 3 | 11661475 | 0.000284804 | VGLL4 | 6.77E-11 | 2340075 | A/T | T | 6.5257757 | 0 |
| rs7547496 | C/T | T | 0.317 | 1 | 26563068 | 0.000284407 | SH3BGRL3 | 7.01E-09 | 6280240 | C/T | T | 5.7908405 | 0 |
| rs934925 | C/G | G | 0.775 | 16 | 4584049 | 0.000267967 | C16orf5 | 3.53E-05 | 130709 | G/C | C | 4.1362495 | 0.0155737 |
| rs934925 | C/G | G | 0.775 | 16 | 4584049 | 0.000267967 | NMRAL1 | 3.54E-16 | 540524 | G/C | C | 8.1532237 | 0 |
| rs307222 | A/C | C | 0.11 | 11 | 13490469 | 0.000265925 | FAR1 | 0.000283202 | 5090309 | C/A | C | 3.630336 | 0.0960815 |
| rs17718831 | A/G | G | 0.395 | 3 | 71640555 | 0.00026399 | FOXP1 | 5.05E-14 | 1500309 | G/A | G | 7.5306621 | 0 |
| rs17694496 | C/T | T | 0.808 | 14 | 52401429 | 0.000261447 | ERO1L | 7.06E-12 | 4780671 | T/C | C | 6.8565917 | 0 |
| rs12173854 | A/G | G | 0.136 | 6 | 26479658 | 0.000248948 | BTN3A2 | 9.81E-198 | 4610674 | A/G | G | -39.79358 | 0 |
| rs16952265 | A/G | G | 0.775 | 17 | 43539882 | 0.000248103 | PNPO | 3.19E-20 | 3180600 | G/A | A | -9.212565 | 0 |
| rs17510173 | A/C | C | 0.083 | 11 | 43465745 | 0.00024111 | TTC17 | 1.58E-07 | 1090204 | A/C | C | -5.242674 | 4.76E-05 |
| rs7720419 | A/T | T | 0.407 | 5 | 642343 | 0.000230701 | AC010442.7-3 | 2.12E-07 | 2760068 | T/A | T | -5.188756 | 9.45E-05 |
| rs10883560 | C/G | G | 0.448 | 10 | 102663697 | 0.000228698 | FAM178A | 2.27E-18 | 6510368 | G/C | G | -8.742941 | 0 |
| rs3130557 | C/T | T | 0.167 | 6 | 31202682 | 0.000228097 | HLA-C | 1.75E-24 | 7150630 | C/T | T | 10.212331 | 0 |
| rs2596560 | C/T | T | 0.746 | 6 | 31463297 | 0.000227683 | HCP5 | 5.51E-10 | 780600 | T/C | C | -6.2038 | 0 |
| rs11882587 | A/G | G | 0.422 | 19 | 4303959 | 0.000226224 | UBXN6 | 5.89E-22 | 2120689 | G/A | G | -9.631525 | 0 |
| rs4944036 | A/G | G | 0.558 | 11 | 73459362 | 0.000220776 | PAAF1 | 3.28E-12 | 3290170 | G/A | G | 6.9651236 | 0 |
| rs6438503 | C/T | T | 0.817 | 3 | 120413076 | 0.000211976 | B4GALT4 | 3.16E-60 | 2000646 | T/C | C | 16.369464 | 0 |
| rs3129840 | C/G | G | 0.808 | 6 | 30415321 | 0.000211295 | HLA-E | 5.99E-21 | 1030747 | G/C | C | 9.3903663 | 0 |
| rs13311400 | A/G | G | 0.6 | 7 | 26921271 | 0.000200675 | SKAP2 | 9.81E-198 | 6040008 | G/A | G | -32.97631 | 0 |
| rs13311400 | A/G | G | 0.6 | 7 | 26921271 | 0.000200675 | SKAP2 | 9.81E-198 | 7160360 | G/A | G | -56.89102 | 0 |
| rs1978 | A/T | T | 0.867 | 6 | 26485552 | 0.000188541 | BTN2A2 | 6.52E-07 | 5420709 | T/A | A | 4.9751709 | 0.0002141 |
| rs10895506 | C/T | T | 0.258 | 11 | 103047628 | 0.000185484 | PDGFD | 4.53E-06 | 5690139 | T/C | T | -4.58573 | 0.0020394 |
| rs929615 | G/T | T | 0.783 | 12 | 9793766 | 0.000182138 | CLEC2B | 1.47E-17 | 2490161 | T/G | G | 8.529243 | 0 |
| rs929615 | G/T | T | 0.783 | 12 | 9793766 | 0.000182138 | CLEC12A | 0.000193465 | 3170601 | T/G | G | 3.7275464 | 0.0698485 |
| rs2517866 | C/T | T | 0.208 | 6 | 29929011 | 0.000178514 | HLA-G | 1.16E-43 | 2070088 | C/T | T | -13.85652 | 0 |
| rs11590781 | C/T | T | 0.904 | 1 | 219995825 | 0.000163397 | DUSP10 | 7.40E-05 | 3780707 | T/C | C | -3.963328 | 0.0299747 |
| rs4453265 | C/T | T | 0.533 | 11 | 73462974 | 0.000158933 | UCP2 | 1.78E-48 | 6580059 | T/C | T | 14.631319 | 0 |
| rs9896052 | A/C | C | 0.683 | 17 | 70930457 | 0.000158448 | GRB2 | 6.31E-07 | 940039 | C/A | A | -4.981659 | 0.0002145 |
| rs9896052 | A/C | C | 0.683 | 17 | 70930457 | 0.000158448 | MIF4GD | 2.82E-08 | 1110243 | C/A | A | -5.552369 | 0 |
| rs9896052 | A/C | C | 0.683 | 17 | 70930457 | 0.000158448 | GRB2 | 1.64E-29 | 7380725 | C/A | A | -11.28044 | 0 |
| rs9273363 | A/C | C | 0.683 | 6 | 32734250 | 0.000149431 | TAP2 | 8.78E-12 | 2650156 | C/A | A | -6.825254 | 0 |
| rs9273363 | A/C | C | 0.683 | 6 | 32734250 | 0.000149431 | TAP2 | 4.22E-14 | 3940477 | C/A | A | -7.554109 | 0 |
| rs6696174 | A/T | T | 0.442 | 1 | 219271136 | 0.000144606 | HLX | 9.62E-05 | 1050309 | T/A | T | -3.90001 | 0.0377684 |
| rs6696174 | A/T | T | 0.442 | 1 | 219271136 | 0.000144606 | HLX | 2.97E-08 | 4230753 | T/A | T | -5.543163 | 0 |
| rs9358938 | C/T | T | 0.121 | 6 | 26495525 | 0.000143036 | BTN3A1 | 1.62E-10 | 3130600 | C/T | T | -6.393727 | 0 |
| rs3130934 | A/C | C | 0.596 | 6 | 31236531 | 0.000142131 | TCF19 | 1.46E-06 | 3890097 | C/A | A | 4.8161403 | 0.0005368 |
| rs4797754 | C/G | G | 0.406 | 18 | 13242862 | 0.000138465 | CEP192 | 6.96E-10 | 4490154 | G/C | G | 6.1671014 | 0 |
| rs10876192 | A/G | G | 0.458 | 12 | 50197076 | 0.000137708 | GALNT6 | 3.30E-35 | 4490164 | G/A | G | -12.38152 | 0 |
| rs2227564 | C/T | T | 0.223 | 10 | 75343107 | 0.000132257 | PLAU,C10orf55 | 3.38E-16 | 5360670 | C/T | T | 8.1589221 | 0 |
| rs10444582 | A/C | C | 0.375 | 12 | 68154677 | 0.000131031 | YEATS4 | 3.72E-05 | 3370747 | C/A | C | -4.124508 | 0.0161096 |
| rs12402939 | A/C | C | 0.375 | 1 | 148881718 | 0.000123853 | ARNT | 1.36E-05 | 2190040 | C/A | C | -4.35037 | 0.0061334 |
| rs1150758 | C/G | G | 0.842 | 6 | 32136127 | 0.000122106 | DOM3Z | 7.67E-11 | 4150482 | G/C | C | -6.507138 | 0 |
| rs1150758 | C/G | G | 0.842 | 6 | 32136127 | 0.000122106 | HSPA1A | 0.000172789 | 6380717 | G/C | C | 3.755904 | 0.063141 |
| rs684402 | C/T | T | 0.883 | 18 | 30894282 | 0.000121709 | MAPRE2 | 2.79E-43 | 3400360 | T/C | C | 13.793565 | 0 |
| rs12569964 | C/T | T | 0.483 | 10 | 12213610 | 0.000120567 | SEC61A2 | 4.45E-37 | 5700364 | T/C | T | 12.722254 | 0 |
| rs10221243 | A/G | G | 0.792 | 17 | 41568087 | 0.000117596 | LRRC37A,ARL17 | 2.16E-08 | 1030706 | G/A | A | 5.5984854 | 0 |
| rs2072803 | C/G | G | 0.867 | 6 | 26500494 | 0.000111928 | HIST1H2AC,HIST1H2BD,HIST1H4A | 5.05E-11 | 6200669 | G/C | C | -6.569438 | 0 |
| rs6985207 | A/C | C | 0.455 | 8 | 8641833 | 0.000111876 | - | 6.53E-52 | 1850156 | C/A | A | 15.159929 | 0 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs910527 | C/T | T | 0.667 | 20 | 24975078 | 0.000106306 | CST7 | 3.75E-12 | 4810341 | T/C | C | 6.9462045 | 0 |
| rs910527 | C/T | T | 0.667 | 20 | 24975078 | 0.000106306 | ACSS1 | 4.94E-10 | 5220377 | T/C | C | -6.22114 | 0 |
| rs9858538 | C/T | T | 0.8 | 3 | 186538170 | 0.000104551 | EHHADH | 0.000179105 | 4880382 | T/C | C | -3.746856 | 0.0652328 |
| rs2242256 | C/G | G | 0.258 | 10 | 75267552 | 0.000101126 | CAMK2G | 5.88E-07 | 1010475 | C/G | G | -4.995103 | 0.0001842 |
| rs213230 | A/G | G | 0.242 | 6 | 28438243 | 9.72E-05 | ZKSCAN3 | 3.22E-08 | 3400605 | A/G | G | 5.5293363 | 0 |
| rs1150709 | C/T | T | 0.61 | 6 | 28315342 | 9.45E-05 | ZNF193 | 2.07E-70 | 4830220 | T/C | C | -17.73991 | 0 |
| rs1592 | A/C | C | 0.392 | 2 | 135438613 | 9.42E-05 | CCNT2 | 4.13E-14 | 3520382 | C/A | A | -7.556984 | 0 |
| rs3131787 | C/T | T | 0.742 | 6 | 31007503 | 8.79E-05 | VARSL | 8.53E-144 | 1500753 | T/C | C | -25.53282 | 0 |
| rs2070450 | A/G | G | 0.975 | 22 | 22408513 | 8.49E-05 | SMARCB1 | 4.01E-07 | 150021 | G/A | A | -5.068769 | 0.0001085 |
| rs8010247 | A/G | G | 0.214 | 14 | 103003309 | 7.76E-05 | MARK3 | 2.35E-27 | 7570706 | G/A | G | 10.835121 | 0 |
| rs2768551 | A/G | G | 0.858 | 6 | 109377349 | 6.92E-05 | SESN1 | 3.70E-05 | 1240553 | G/A | A | 4.1252196 | 0.0160986 |
| rs2544029 | C/T | T | 0.3 | 12 | 46481224 | 6.66E-05 | RPAP3 | 5.43E-08 | 2000392 | T/C | T | -5.436764 | 1.63E-05 |
| rs2544029 | C/T | T | 0.3 | 12 | 46481224 | 6.66E-05 | SLC48A1 | 5.29E-32 | 2900139 | T/C | T | 11.774503 | 0 |
| rs17426064 | C/T | T | 0.2 | 17 | 41184469 | 6.36E-05 | - | 5.75E-105 | 1070368 | C/T | T | 21.758431 | 0 |
| rs9858592 | C/T | T | 0.542 | 3 | 99919443 | 6.36E-05 | ST3GAL6 | 0.000114132 | 5260440 | T/C | C | -3.858538 | 0.0439132 |
| rs1056237 | A/C | C | 0.375 | 6 | 52503716 | 6.32E-05 | PAQR8 | 1.07E-13 | 2070451 | A/C | C | 7.431428 | 0 |
| rs7232963 | C/T | T | 0.3 | 18 | 18845192 | 6.24E-05 | RBBP8 | 4.35E-19 | 6580672 | C/T | T | -8.927693 | 0 |
| rs10445335 | A/T | T | 0.795 | 17 | 41290685 | 6.08E-05 | - | 9.81E-198 | 240152 | T/A | A | 41.386696 | 0 |
| rs4630591 | C/T | T | 0.192 | 17 | 41548345 | 6.04E-05 | KIAA1267 | 3.03E-34 | 1850079 | C/T | T | -12.20232 | 0 |
| rs1531681 | A/G | G | 0.425 | 6 | 28334857 | 5.91E-05 | ZNF187 | 4.13E-11 | 5390259 | G/A | G | -6.599235 | 0 |
| rs17498135 | C/T | T | 0.1 | 1 | 90121935 | 5.90E-05 | LRRC8D | 0.000111454 | 2650100 | C/T | T | 3.8643374 | 0.0432691 |
| rs11038358 | A/G | G | 0.625 | 11 | 45199134 | 5.51E-05 | PRDM11,AC103681.4 | 5.49E-06 | 5090221 | A/G | A | -4.545237 | 0.002382 |
| rs2959945 | C/T | T | 0.807 | 17 | 40931011 | 5.22E-05 | SH3D20 | 6.32E-45 | 7330070 | T/C | C | -14.06419 | 0 |
| rs8023669 | C/T | T | 0.617 | 15 | 81511661 | 4.56E-05 | AC024270.6 | 7.85E-14 | 3460296 | C/T | C | 7.4728403 | 0 |
| rs12577642 | A/T | T | 0.271 | 11 | 43685110 | 4.20E-05 | HSD17B12 | 4.71E-58 | 6280050 | A/T | T | -16.06211 | 0 |
| rs9393777 | C/T | T | 0.858 | 6 | 27050006 | 4.08E-05 | HIST1H2BK | 1.90E-05 | 6110630 | T/C | C | 4.2767252 | 0.0088757 |
| rs1635298 | A/T | T | 0.208 | 17 | 41100127 | 3.99E-05 | LRRC37A4,AC091132.16-2,AC091132.16-1 | 6.10E-10 | 3890041 | A/T | T | -6.187848 | 0 |
| rs2855804 | C/T | T | 0.255 | 6 | 31575344 | 3.76E-05 | BAT3 | 3.24E-05 | 5340382 | C/T | T | 4.155911 | 0.0143743 |
| rs10178728 | A/T | T | 0.845 | 2 | 239024860 | 3.56E-05 | ASB1 | 8.64E-20 | 1820347 | T/A | A | -9.104914 | 0 |
| rs2248617 | C/T | T | 0.373 | 6 | 31556512 | 3.17E-05 | - | 3.90E-91 | 580452 | C/T | T | 20.245572 | 0 |
| rs9788721 | C/T | T | 0.567 | 15 | 76589924 | 3.14E-05 | IREB2 | 2.63E-70 | 6020328 | T/C | C | -17.72632 | 0 |
| rs2516417 | C/G | G | 0.308 | 6 | 31567615 | 2.87E-05 | - | 1.21E-167 | 1440603 | C/G | G | -27.59713 | 0 |
| rs11000787 | C/T | T | 0.276 | 10 | 75254389 | 2.47E-05 | NDST2 | 2.63E-47 | 110561 | C/T | T | -14.44698 | 0 |
| rs931794 | A/G | G | 0.433 | 15 | 76613235 | 2.38E-05 | PSMA4 | 1.13E-11 | 3420543 | G/A | G | 6.7892636 | 0 |
| rs886424 | C/T | T | 0.193 | 6 | 30889981 | 2.17E-05 | IER3 | 7.28E-60 | 1190367 | C/T | T | 16.318799 | 0 |
| rs6788718 | A/G | G | 0.058 | 3 | 191765028 | 2.01E-05 | IL1RAP,AC108747.5-1 | 2.23E-15 | 4880632 | A/G | G | 7.9278718 | 0 |
| rs6729330 | C/T | T | 0.408 | 2 | 218402541 | 1.96E-05 | TNS1 | 3.72E-53 | 6250110 | T/C | C | -15.34683 | 0 |
| rs11150044 | A/C | C | 0.664 | 16 | 76758793 | 1.49E-05 | WWOX | 0.000250254 | 6450189 | C/A | A | -3.662025 | 0.0868126 |
| rs1264353 | A/C | C | 0.831 | 6 | 30895741 | 1.17E-05 | FLOT1 | 9.05E-42 | 3780181 | C/A | A | 13.540314 | 0 |
| rs10041283 | C/G | G | 0.25 | 5 | 147756991 | 4.81E-06 | FBXO38 | 3.05E-22 | 7570139 | C/G | G | 9.6988421 | 0 |
| rs2553449 | C/T | T | 0.358 | 4 | 106918341 | 2.96E-06 | GSTCD | 3.17E-05 | 5360487 | T/C | T | 4.1613972 | 0.0139802 |
| rs2855812 | G/T | T | 0.258 | 6 | 31580699 | 8.57E-08 | BAT1 | 5.41E-06 | 160132 | G/T | T | 4.5482482 | 0.0023256 |
| rs2855812 | G/T | T | 0.258 | 6 | 31580699 | 8.57E-08 | LTA | 1.02E-10 | 1030743 | G/T | T | -6.463757 | 0 |
| rs17331332 | A/G | G | 0.923 | 4 | 107027556 | 1.11E-12 | INTS12 | 2.28E-11 | 4860553 | G/A | A | -6.686626 | 0 |

## Supplementary Table 7B: FEV$_1$/FVC blood eSNPs

| eSNP | GWAS SNP alleles | GWAS reference allele | Reference allele freq in HapMap | Chr | eSNP Position | GWAS_Pval_FEV1/FVC | Blood eQTL reguated gene | eQTL P Value | eQTL regulated Probe Name | eQTL SNP alleles | Allele Assessed | eQTL overall Z Score | FDR |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2282041 | A/G | G | 0.11 | 9 | 97288208 | 3.37E-09 | PTCH1 | 8.82E-20 | 1410289 | G/A | G | 9.103 | 0 |
| rs11203280 | G/T | T | 0.258 | 1 | 17215370 | 5.78E-08 | CROCC | 3.49E-06 | 610424 | T/G | T | 4.640 | 0.0014476 |
| rs4784887 | A/G | G | 0.358 | 16 | 56623125 | 8.02E-08 | C16orf80 | 1.20E-05 | 5360630 | A/G | G | 4.378 | 0.00539981 |
| rs7199132 | C/T | T | 0.491 | 16 | 74007540 | 8.48E-08 | CFDP1 | 1.84E-11 | 6200494 | T/C | C | 6.718 | 0 |
| rs1364078 | C/T | T | 0.473 | 16 | 73954382 | 1.17E-07 | ADAT1 | 1.29E-07 | 1710204 | T/C | T | 5.280 | 3.19E-05 |
| rs2596560 | C/T | T | 0.746 | 6 | 31463297 | 1.30E-06 | HCP5 | 5.51E-10 | 780600 | T/C | C | -6.204 | 0 |
| rs9319483 | C/T | T | 0.696 | 16 | 73903292 | 2.28E-06 | TMEM170A | 9.97E-09 | 6370019 | T/C | C | 5.731 | 0 |
| rs316398 | A/G | G | 0.2 | 5 | 43073783 | 2.80E-06 | - | 6.16E-62 | 5340278 | A/G | G | 16.607 | 0 |
| rs316398 | A/G | G | 0.2 | 5 | 43073783 | 2.80E-06 | C5orf39 | 1.22E-10 | 7330523 | A/G | G | -6.437 | 0 |
| rs3891175 | C/T | T | 0.167 | 6 | 32742445 | 3.24E-06 | - | 1.18E-35 | 620544 | C/T | T | -12.464 | 0 |
| rs2548993 | A/G | G | 0.283 | 5 | 131836768 | 7.97E-06 | SLC22A4 | 2.04E-24 | 4850168 | G/A | G | 10.198 | 0 |
| rs2548993 | A/G | G | 0.283 | 5 | 131836768 | 7.97E-06 | SLC22A5 | 1.94E-68 | 7050180 | G/A | G | 17.483 | 0 |
| rs2040406 | A/G | G | 0.112 | 6 | 32710985 | 1.30E-05 | HLA-DRA | 6.60E-29 | 270168 | A/G | G | 11.157 | 0 |
| rs10853135 | A/G | G | 0.534 | 17 | 25212801 | 2.25E-05 | SSH2 | 1.50E-92 | 2810468 | A/G | G | -20.405 | 0 |
| rs12920639 | A/C | C | 0.212 | 16 | 56671641 | 2.48E-05 | CSNK2A2 | 1.02E-08 | 4150176 | A/C | C | 5.728 | 0 |
| rs7251067 | A/G | G | 0.88 | 19 | 18461056 | 2.54E-05 | LRRC25,PGPEP1 | 4.63E-06 | 3850678 | G/A | A | -4.581 | 0.0020657 |
| rs7251067 | A/G | G | 0.88 | 19 | 18461056 | 2.54E-05 | LRRC25,PGPEP1 | 2.51E-10 | 5310397 | G/A | A | -6.327 | 0 |
| rs7251067 | A/G | G | 0.88 | 19 | 18461056 | 2.54E-05 | - | 4.15E-18 | 6550358 | G/A | A | -8.675 | 0 |
| rs11134736 | A/G | G | 0.778 | 5 | 156769091 | 2.62E-05 | CYFIP2 | 1.35E-09 | 6100768 | G/A | A | 6.062 | 0 |
| rs931794 | A/G | G | 0.433 | 15 | 76613235 | 2.67E-05 | PSMA4 | 1.13E-11 | 3420543 | G/A | G | 6.789 | 0 |
| rs7125978 | A/G | G | 0.9 | 11 | 72716877 | 2.90E-05 | ARHGEF17 | 1.75E-43 | 1660020 | G/A | A | 13.827 | 0 |
| rs7957346 | A/C | C | 0.508 | 12 | 94784605 | 2.94E-05 | SNRPF | 5.50E-14 | 650301 | C/A | C | 7.520 | 0 |
| rs2238104 | G/T | T | 0.442 | 12 | 6057926 | 3.08E-05 | CD9 | 7.88E-06 | 6250487 | T/G | T | 4.469 | 0.00365836 |
| rs2303693 | C/T | T | 0.142 | 19 | 18418673 | 3.44E-05 | ELL,PGPEP1 | 3.30E-52 | 6650086 | C/T | T | 15.205 | 0 |
| rs8053376 | A/G | G | 0.575 | 16 | 18867252 | 3.48E-05 | RPS15A | 2.16E-13 | 7100717 | G/A | A | -7.338 | 0 |
| rs10752641 | C/G | G | 0.322 | 1 | 152698666 | 3.64E-05 | IL6R | 3.09E-13 | 1780603 | G/C | G | 7.291 | 0 |
| rs10752641 | C/G | G | 0.322 | 1 | 152698666 | 3.64E-05 | IL6R | 1.06E-05 | 5870685 | G/C | G | 4.406 | 0.00477446 |
| rs140126 | C/T | T | 0.425 | 22 | 28477038 | 3.67E-05 | THOC5 | 2.76E-07 | 3060561 | T/C | T | 5.139 | 9.39E-05 |
| rs890498 | C/G | G | 0.417 | 15 | 39898590 | 3.68E-05 | - | 3.01E-06 | 1300747 | G/C | G | 4.670 | 0.00114959 |
| rs890498 | C/G | G | 0.417 | 15 | 39898590 | 3.68E-05 | EHD4 | 5.40E-21 | 6400647 | G/C | G | 9.401 | 0 |
| rs9305545 | A/G | G | 0.224 | 21 | 34517691 | 3.83E-05 | MRPS6 | 2.94E-16 | 6400195 | A/G | G | -8.176 | 0 |
| rs2656065 | A/G | G | 0.603 | 15 | 76537604 | 4.29E-05 | IREB2 | 1.03E-87 | 6020328 | G/A | A | -19.854 | 0 |
| rs3741149 | C/T | T | 0.1 | 11 | 72698732 | 4.34E-05 | - | 4.42E-09 | 2630601 | C/T | T | -5.868 | 0 |
| rs12604345 | C/T | T | 0.183 | 18 | 12958223 | 4.49E-05 | CEP192 | 6.69E-35 | 4490154 | C/T | T | -12.325 | 0 |
| rs11080616 | A/G | G | 0.817 | 18 | 12951999 | 4.90E-05 | SEH1L | 0.000126693 | 1580286 | G/A | A | -3.833 | 0.04810034 |
| rs9348970 | C/G | G | 0.825 | 6 | 35261543 | 5.03E-05 | ZNF76 | 2.08E-10 | 4640333 | G/C | C | -6.356 | 0 |
| rs9568348 | C/T | T | 0.931 | 13 | 49366723 | 5.08E-05 | - | 0.000185785 | 7150735 | T/C | C | 3.738 | 0.06703193 |
| rs2855812 | G/T | T | 0.258 | 6 | 31580699 | 5.11E-05 | LTA | 1.02E-10 | 1030743 | G/T | T | -6.464 | 0 |
| rs2855812 | G/T | T | 0.258 | 6 | 31580699 | 5.11E-05 | TNF | 4.77E-14 | 2640301 | G/T | T | -7.538 | 0 |
| rs17331332 | A/G | G | 0.923 | 4 | 107027556 | 5.30E-05 | INTS12 | 2.28E-11 | 4860553 | G/A | A | -6.687 | 0 |
| rs1042719 | C/G | G | 0.698 | 5 | 148187640 | 5.71E-05 | ADRB2 | 4.32E-23 | 7570326 | G/C | C | -9.896 | 0 |
| rs140119 | A/T | T | 0.575 | 22 | 28468149 | 5.95E-05 | ZMAT5 | 1.95E-10 | 5420068 | T/A | A | 6.365 | 0 |
| rs4240872 | C/T | T | 0.683 | 1 | 152702819 | 6.15E-05 | UBAP2L | 1.18E-11 | 7610152 | T/C | C | 6.783 | 0 |
| rs17678767 | C/G | G | 0.398 | 15 | 39883714 | 6.42E-05 | JMJD7-PLA2G4B | 1.61E-42 | 2350722 | G/C | G | 13.667 | 0 |
| rs1473781 | A/G | G | 0.583 | 15 | 39606209 | 6.48E-05 | RPAP1 | 3.10E-21 | 1450678 | G/A | A | -9.459 | 0 |
| rs7596847 | A/T | T | 0.825 | 2 | 238985857 | 7.57E-05 | ASB1 | 2.52E-19 | 1820347 | T/A | A | -8.988 | 0 |
| rs12505696 | C/T | T | 0.322 | 4 | 90150093 | 7.64E-05 | TIGD2 | 1.58E-05 | 1820497 | T/C | T | 4.317 | 0.00737962 |
| rs2097572 | A/G | G | 0.125 | 1 | 165997407 | 7.65E-05 | MPZL1 | 6.18E-07 | 7000431 | A/G | G | 4.985 | 0.00021456 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs713718 | G/T | T | 0.592 | 22 | 28644092 | 7.82E-05 | MTMR3 | 3.68E-78 | 460039 | T/G | G | 18.716 | 0 |
| rs713718 | G/T | T | 0.592 | 22 | 28644092 | 7.82E-05 | MTMR3 | 3.21E-16 | 5720577 | T/G | G | 8.165 | 0 |
| rs9469220 | A/G | G | 0.6 | 6 | 32766288 | 8.12E-05 | PSMB9,TAP1 | 1.98E-05 | 7330392 | G/A | G | 4.268 | 0.00925551 |
| rs7764819 | G/T | T | 0.897 | 6 | 32788554 | 8.79E-05 | TAP2 | 4.78E-18 | 3940477 | T/G | G | 8.658 | 0 |
| rs10418984 | C/T | T | 0.15 | 19 | 36530218 | 9.44E-05 | TSHZ3 | 4.54E-19 | 1260066 | C/T | T | 8.923 | 0 |
| rs10041283 | C/G | G | 0.25 | 5 | 147756991 | 9.75E-05 | FBXO38 | 3.05E-22 | 7570139 | C/G | G | 9.699 | 0 |
| rs11191741 | A/G | G | 0.688 | 10 | 105352094 | 9.75E-05 | USMG5,hsa-mir-1307 | 2.02E-08 | 2320253 | A/G | A | 5.610 | 0 |
| rs893185 | A/C | C | 0.45 | 19 | 63681307 | 0.000101514 | CHMP2A | 2.32E-05 | 3130022 | C/A | A | -4.232 | 0.01067167 |
| rs893185 | A/C | C | 0.45 | 19 | 63681307 | 0.000101514 | ZNF446 | 0.000200489 | 5810767 | C/A | A | 3.719 | 0.07215723 |
| rs3130557 | C/T | T | 0.167 | 6 | 31202682 | 0.000108095 | HLA-C | 1.75E-24 | 7150630 | C/T | T | 10.212 | 0 |
| rs6088580 | C/G | G | 0.5 | 20 | 32748714 | 0.000113679 | GGT7 | 3.49E-24 | 2680161 | G/C | G | 10.145 | 0 |
| rs9272775 | C/T | T | 0.592 | 6 | 32718235 | 0.000115046 | PSMB9 | 3.02E-11 | 1940180 | T/C | T | 6.646 | 0 |
| rs9272775 | C/T | T | 0.592 | 6 | 32718235 | 0.000115046 | AL662789.11 | 0.00014169 | 2100066 | T/C | T | 3.805 | 0.05359816 |
| rs9272775 | C/T | T | 0.592 | 6 | 32718235 | 0.000115046 | HLA-DRA | 3.62E-28 | 2570564 | T/C | T | 11.005 | 0 |
| rs9272775 | C/T | T | 0.592 | 6 | 32718235 | 0.000115046 | HLA-DOB | 2.35E-20 | 3450338 | T/C | T | 9.245 | 0 |
| rs9272775 | C/T | T | 0.592 | 6 | 32718235 | 0.000115046 | HLA-DRB5 | 5.37E-101 | 6370315 | T/C | T | 21.335 | 0 |
| rs131298 | A/G | G | 0.558 | 22 | 28510001 | 0.000125066 | ZMAT5,UCRC | 5.35E-89 | 6380563 | G/A | A | 20.001 | 0 |
| rs7137731 | C/T | T | 0.585 | 12 | 94015130 | 0.000125913 | NR2C1 | 3.21E-07 | 1470521 | T/C | C | 5.111 | 0.0001092 |
| rs4946151 | C/G | G | 0.583 | 6 | 116701982 | 0.000134504 | FAM26F | 2.52E-13 | 6590646 | G/C | C | -7.318 | 0 |
| rs2014725 | C/T | T | 0.325 | 1 | 17289840 | 0.000134928 | PADI2 | 1.36E-56 | 4730746 | C/T | T | -15.852 | 0 |
| rs165685 | C/T | T | 0.208 | 22 | 19249755 | 0.000137154 | MED15 | 3.29E-26 | 6770672 | T/C | T | -10.591 | 0 |
| rs2245090 | C/G | G | 0.767 | 17 | 5469488 | 0.000139732 | NUP88 | 0.000171825 | 3800678 | G/C | C | 3.757 | 0.06278352 |
| rs1264353 | A/C | C | 0.831 | 6 | 30895741 | 0.000144601 | FLOT1 | 9.05E-42 | 3780181 | C/A | A | 13.540 | 0 |
| rs17093914 | C/T | T | 0.258 | 14 | 74433394 | 0.000148685 | ACYP1 | 0.000161685 | 5910148 | C/T | T | -3.772 | 0.05990211 |
| rs2596501 | C/T | T | 0.424 | 6 | 31429190 | 0.000152153 | HCG27 | 6.43E-13 | 3800358 | T/C | T | 7.191 | 0 |
| rs886424 | C/T | T | 0.193 | 6 | 30889981 | 0.000154946 | IER3 | 7.28E-60 | 1190367 | C/T | T | 16.319 | 0 |
| rs1007636 | C/T | T | 0.85 | 6 | 33012019 | 0.000157542 | HLA-DMB | 1.03E-12 | 4900731 | T/C | C | -7.126 | 0 |
| rs1150758 | C/G | G | 0.842 | 6 | 32136127 | 0.000159595 | DOM3Z | 7.67E-11 | 4150482 | G/C | C | -6.507 | 0 |
| rs1150758 | C/G | G | 0.842 | 6 | 32136127 | 0.000159595 | HSPA1A | 0.000172789 | 6380717 | G/C | C | 3.756 | 0.06314103 |
| rs2227564 | C/T | T | 0.223 | 10 | 75343107 | 0.000162638 | PLAU,C10orf55 | 3.38E-16 | 5360670 | C/T | T | 8.159 | 0 |
| rs2070063 | A/G | G | 0.392 | 2 | 64715559 | 0.000167913 | SERTAD2 | 1.43E-09 | 2070367 | G/A | G | 6.053 | 0 |
| rs973879 | C/T | T | 0.375 | 14 | 74367480 | 0.00016799 | - | 0.000298498 | 6900167 | T/C | T | 3.617 | 0.09968472 |
| rs7514452 | C/T | T | 0.733 | 1 | 152704708 | 0.000170284 | AQP10 | 7.49E-05 | 2340577 | T/C | C | -3.960 | 0.03012869 |
| rs2206030 | C/T | T | 0.275 | 6 | 35512332 | 0.000171601 | RPL10A | 1.67E-07 | 4040100 | C/T | T | 5.233 | 4.76E-05 |
| rs2076607 | C/T | T | 0.678 | 1 | 17295247 | 0.000173089 | SDHB | 6.40E-06 | 3370195 | T/C | C | 4.513 | 0.00289567 |
| rs6088568 | A/C | C | 0.342 | 20 | 32729632 | 0.000182231 | MAP1LC3A | 7.35E-36 | 5490240 | C/A | C | 12.501 | 0 |
| rs3738814 | A/G | G | 0.373 | 1 | 17204263 | 0.000182318 | ATP13A2 | 5.45E-12 | 7100326 | G/A | G | -6.893 | 0 |
| rs16868886 | A/G | G | 0.917 | 5 | 39475736 | 0.000187282 | DAB2 | 1.82E-08 | 610152 | G/A | A | -5.628 | 0 |
| rs16868886 | A/G | G | 0.917 | 5 | 39475736 | 0.000187282 | DAB2 | 3.20E-12 | 3930367 | G/A | A | -6.969 | 0 |
| rs6692872 | A/G | G | 0.105 | 1 | 3695845 | 0.000190512 | LRRC47 | 0.000108301 | 2000132 | A/G | G | -3.871 | 0.04191167 |
| rs3742783 | C/T | T | 0.258 | 14 | 74446761 | 0.000194627 | MLH3 | 6.50E-12 | 7560274 | C/T | T | -6.868 | 0 |
| rs11066028 | A/C | C | 0.325 | 12 | 110729553 | 0.000195496 | ERP29 | 1.42E-05 | 830730 | A/C | C | -4.340 | 0.00660274 |
| rs11066028 | A/C | C | 0.325 | 12 | 110729553 | 0.000195496 | ERP29 | 1.86E-14 | 4120333 | A/C | C | -7.660 | 0 |
| rs4660808 | C/T | T | 0.233 | 1 | 39791096 | 0.00019805 | MACF1 | 2.56E-25 | 6370739 | C/T | T | 10.397 | 0 |
| rs9919666 | A/G | G | 0.776 | 11 | 73968529 | 0.000210482 | PGM2L1 | 2.97E-06 | 7210093 | G/A | A | 4.673 | 0.00109186 |
| rs731952 | C/T | T | 0.273 | 14 | 74436200 | 0.00021095 | EIF2B2 | 1.85E-43 | 3130079 | C/T | T | -13.823 | 0 |
| rs6088575 | A/G | G | 0.342 | 20 | 32737064 | 0.000212044 | ACSS2 | 1.30E-25 | 4490524 | G/A | G | 10.461 | 0 |
| rs17565905 | A/G | G | 0.692 | 10 | 12279950 | 0.000217397 | SEC61A2 | 3.16E-11 | 5700364 | G/A | A | -6.639 | 0 |
| rs5752962 | G/T | T | 0.45 | 22 | 28518245 | 0.000220674 | ZMAT5,ASCC2 | 3.23E-99 | 1570523 | T/G | T | -21.143 | 0 |
| rs4934284 | C/G | G | 0.108 | 10 | 82267277 | 0.000221125 | - | 9.68E-23 | 2340414 | G/C | G | -9.815 | 0 |
| rs4934284 | C/G | G | 0.108 | 10 | 82267277 | 0.000221125 | C10orf57 | 1.30E-08 | 5960168 | G/C | G | -5.686 | 0 |
| rs12236402 | C/T | T | 0.092 | 9 | 119302174 | 0.000227311 | TLR4 | 1.12E-06 | 1500180 | T/C | T | 4.870 | 0.00036139 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs11660634 | A/G | G | 0.867 | 18 | 13153125 | 0.000229552 | SEH1L | 0.000132266 | 6760504 | G/A | A | -3.822 | 0.05014577 |
| rs12548626 | A/C | C | 0.843 | 8 | 17754380 | 0.000234642 | ASAH1 | 5.71E-07 | 2030482 | C/A | A | 5.001 | 0.00016892 |
| rs12548626 | A/C | C | 0.843 | 8 | 17754380 | 0.000234642 | PCM1 | 8.10E-15 | 6180022 | C/A | A | 7.766 | 0 |
| rs1888825 | G/T | T | 0.808 | 6 | 35338518 | 0.000239495 | DEF6 | 1.85E-132 | 1570255 | T/G | G | -24.491 | 0 |
| rs652888 | A/G | G | 0.2 | 6 | 31959213 | 0.000244675 | C6orf48 | 5.09E-05 | 6280601 | A/G | G | -4.052 | 0.0214875 |
| rs592229 | G/T | T | 0.508 | 6 | 32038420 | 0.000247407 | RDBP | 4.86E-15 | 1820538 | G/T | G | -7.831 | 0 |
| rs575013 | A/C | C | 0.525 | 11 | 85128084 | 0.000249485 | SYTL2 | 2.80E-87 | 2100274 | C/A | A | 19.803 | 0 |
| rs575013 | A/C | C | 0.525 | 11 | 85128084 | 0.000249485 | SYTL2 | 1.27E-129 | 6760037 | C/A | A | 24.223 | 0 |
| rs154977 | C/G | G | 0.675 | 6 | 33007996 | 0.000260632 | HLA-DPB1 | 2.89E-13 | 1050360 | C/G | C | 7.300 | 0 |
| rs13211886 | G/T | T | 0.108 | 6 | 41387766 | 0.000261841 | TREML2 | 2.54E-07 | 7380180 | G/T | T | 5.155 | 9.41E-05 |
| rs2242256 | C/G | G | 0.258 | 10 | 75267552 | 0.000262059 | CAMK2G | 5.88E-07 | 1010475 | C/G | G | -4.995 | 0.00018416 |
| rs12937167 | A/G | G | 0.123 | 17 | 34249707 | 0.000267313 | PCGF2 | 6.46E-07 | 3830296 | G/A | G | 4.977 | 0.0002142 |
| rs181095 | C/T | T | 0.792 | 7 | 87925775 | 0.000283774 | STEAP4 | 8.19E-11 | 540091 | T/C | C | -6.497 | 0 |
| rs2716934 | A/T | T | 0.336 | 17 | 5511762 | 0.000294372 | MIS12 | 0.000245989 | 1050017 | T/A | T | 3.666 | 0.08536697 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | TSPAN4,AP006623.1 | 8.67E-20 | 110661 | G/A | A | 9.104 | 0 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | LRDD | 7.93E-07 | 580242 | G/A | A | -4.937 | 0.00024331 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | PNPLA2 | 1.26E-26 | 1190463 | G/A | A | 10.680 | 0 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | TMEM80 | 5.96E-06 | 1580707 | G/A | A | -4.528 | 0.00263158 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | CD151 | 1.07E-35 | 1940132 | G/A | A | -12.472 | 0 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | POLR2L | 1.42E-12 | 6200017 | G/A | A | -7.082 | 0 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | CD151 | 3.51E-75 | 6330474 | G/A | A | -18.347 | 0 |
| rs10902208 | A/G | G | 0.767 | 11 | 719570 | 0.000297858 | CD151 | 6.13E-23 | 6550259 | G/A | A | -9.861 | 0 |
| rs9380261 | C/G | G | 0.827 | 6 | 31613763 | 0.000305143 | AIF1 | 2.71E-06 | 1940047 | G/C | C | -4.691 | 0.00103741 |
| rs6088578 | C/T | T | 0.325 | 20 | 32745265 | 0.000305874 | ACSS2 | 5.69E-21 | 4670544 | T/C | T | 9.396 | 0 |
| rs657605 | C/T | T | 0.783 | 1 | 111538160 | 0.000307042 | DENND2D | 1.57E-13 | 6020327 | T/C | C | 7.381 | 0 |
| rs2571391 | A/C | C | 0.388 | 6 | 30031817 | 0.000317863 | - | 6.07E-05 | 1660452 | C/A | C | 4.010 | 0.02523006 |
| rs2020939 | A/G | G | 0.6 | 17 | 25574858 | 0.000319488 | BLMH | 5.04E-06 | 2850577 | A/G | A | 4.563 | 0.00217298 |
| rs4904411 | C/T | T | 0.492 | 14 | 87580008 | 0.000319569 | GALC | 7.14E-60 | 3440491 | T/C | T | 16.320 | 0 |
| rs6538597 | A/C | C | 0.417 | 12 | 94037328 | 0.000333485 | VEZT | 2.08E-13 | 2000195 | C/A | C | 7.343 | 0 |
| rs1965193 | C/T | T | 0.275 | 12 | 32019486 | 0.00033598 | C12orf35 | 2.43E-11 | 7510424 | C/T | T | -6.678 | 0 |
| rs6669395 | A/G | G | 0.591 | 1 | 36426304 | 0.000336186 | FAM176B,C1orf113 | 7.68E-10 | 7100561 | G/A | A | -6.151 | 0 |
| rs3734263 | A/G | G | 0.083 | 6 | 34946407 | 0.000336909 | ANKS1A | 3.65E-09 | 5390064 | A/G | G | 5.899 | 0 |
| rs2071596 | A/G | G | 0.85 | 6 | 31614670 | 0.000338557 | BAT1 | 8.25E-23 | 160132 | G/A | A | -9.831 | 0 |
| rs2071596 | A/G | G | 0.85 | 6 | 31614670 | 0.000338557 | LST1 | 1.80E-07 | 770471 | G/A | A | 5.219 | 4.74E-05 |
| rs2235980 | A/G | G | 0.533 | 6 | 116672197 | 0.00035713 | TSPYL4 | 2.22E-05 | 610521 | G/A | A | 4.242 | 0.01033741 |
| rs7744809 | A/G | G | 0.561 | 6 | 116659759 | 0.00036016 | NT5DC1 | 6.02E-26 | 6960129 | G/A | A | 10.534 | 0 |
| rs593226 | A/G | G | 0.317 | 12 | 110478269 | 0.000370228 | ATXN2 | 7.16E-07 | 1090400 | G/A | G | 4.957 | 0.00022883 |
| rs1886461 | A/G | G | 0.733 | 14 | 61014635 | 0.000376963 | PRKCH | 3.04E-05 | 3290731 | G/A | A | -4.171 | 0.0135396 |
| rs3851294 | A/G | G | 0.875 | 1 | 203397036 | 0.000390864 | DSTYK | 1.60E-88 | 5560360 | G/A | A | 19.947 | 0 |
| rs644045 | A/G | G | 0.625 | 6 | 31991936 | 0.000415835 | NEU1 | 0.000132912 | 4200692 | A/G | A | -3.821 | 0.05032172 |
| rs7260359 | C/T | T | 0.405 | 19 | 50506748 | 0.000416121 | CKM | 1.33E-15 | 1580592 | T/C | C | 7.992 | 0 |
| rs7260359 | C/T | T | 0.405 | 19 | 50506748 | 0.000416121 | VASP | 2.15E-05 | 2320356 | T/C | C | 4.249 | 0.01002422 |
| rs7260359 | C/T | T | 0.405 | 19 | 50506748 | 0.000416121 | KLC3 | 7.13E-15 | 2340500 | T/C | C | -7.782 | 0 |
| rs6938656 | C/T | T | 0.108 | 6 | 41364098 | 0.000417992 | TREM1 | 2.06E-11 | 3310091 | C/T | T | -6.702 | 0 |
| rs10839 | A/T | T | 0.325 | 1 | 39917405 | 0.00043771 | HPCAL4 | 1.10E-142 | 5220524 | T/A | T | 25.433 | 0 |
| rs1368528 | A/C | C | 0.831 | 4 | 101514882 | 0.000439617 | DDIT4L | 0.000273486 | 380019 | C/A | A | 3.639 | 0.09330758 |
| rs11153162 | A/C | C | 0.742 | 6 | 97311015 | 0.000441876 | C6orf66 | 6.31E-05 | 430309 | C/A | A | -4.001 | 0.02600102 |
| rs11153162 | A/C | C | 0.742 | 6 | 97311015 | 0.000441876 | C6orf66 | 0.000151865 | 1940435 | C/A | A | -3.788 | 0.05693728 |
| rs17098453 | C/T | T | 0.267 | 14 | 61014320 | 0.000449234 | TMEM30B | 0.000141347 | 670754 | C/T | T | 3.806 | 0.05355891 |
| rs17579009 | C/T | T | 0.127 | 6 | 110897677 | 0.000450261 | SLC22A16 | 2.48E-68 | 2480072 | T/C | T | -17.469 | 0 |
| rs10037531 | C/T | T | 0.475 | 5 | 156738482 | 0.000458965 | CYFIP2 | 3.36E-16 | 3520020 | C/T | T | 8.160 | 0 |
| rs140110 | A/G | G | 0.433 | 22 | 28461148 | 0.000459871 | NIPSNAP1 | 5.58E-07 | 5490131 | G/A | A | 5.005 | 0.00016913 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs4759277 | A/C | C | 0.692 | 12 | 55819957 | 0.000466036 | TMEM194A | 2.28E-12 | 1110494 | C/A | A | 7.016 | 0 |
| rs6881684 | A/T | T | 0.793 | 5 | 156957935 | 0.000469438 | ADAM19 | 4.57E-45 | 6900209 | T/A | A | -14.087 | 0 |
| rs2572009 | A/G | G | 0.525 | 7 | 99326941 | 0.000474478 | ZNF3,ZSCAN21 | 2.78E-07 | 940576 | G/A | A | -5.138 | 9.39E-05 |
| rs2572009 | A/G | G | 0.525 | 7 | 99326941 | 0.000474478 | COPS6 | 1.63E-07 | 6350114 | G/A | A | -5.237 | 4.76E-05 |
| rs1048705 | A/T | T | 0.525 | 7 | 99326876 | 0.000475477 | TRIM4 | 9.81E-198 | 2810674 | T/A | A | -58.956 | 0 |
| rs737280 | C/T | T | 0.667 | 12 | 110679359 | 0.000482652 | TMEM116 | 4.91E-46 | 2070736 | T/C | C | 14.244 | 0 |
| rs3119331 | A/T | T | 0.203 | 1 | 184701141 | 0.000484004 | TPR | 6.23E-40 | 6770014 | A/T | T | -13.226 | 0 |
| rs12116935 | A/G | G | 0.417 | 1 | 36562133 | 0.000484364 | LSM10 | 0.000230505 | 160255 | G/A | G | 3.683 | 0.08114622 |
| rs241549 | C/T | T | 0.408 | 14 | 55614413 | 0.000494171 | PELI2 | 6.82E-08 | 3840491 | C/T | T | 5.396 | 1.62E-05 |
| rs912576 | A/G | G | 0.018 | 1 | 51777843 | 0.000494776 | EPS15 | 1.00E-06 | 1510035 | A/G | G | 4.891 | 0.0002719 |
| rs2763979 | C/T | T | 0.325 | 6 | 31902571 | 0.000498388 | LY6G5C | 9.89E-22 | 3520647 | C/T | T | -9.578 | 0 |
| rs2763979 | C/T | T | 0.325 | 6 | 31902571 | 0.000498388 | LSM2 | 7.11E-05 | 4540349 | C/T | T | -3.973 | 0.02882085 |
| rs9824435 | C/T | T | 0.792 | 3 | 49649347 | 0.000500011 | NICN1 | 2.07E-78 | 3390722 | T/C | C | 18.747 | 0 |
| rs4419885 | C/G | G | 0.65 | 9 | 138106255 | 0.000500271 | NACC2 | 5.78E-62 | 3400709 | G/C | C | 16.611 | 0 |
| rs17102847 | A/G | G | 0.25 | 14 | 74394533 | 0.000501392 | DLSTP | 5.15E-05 | 6450681 | A/G | G | -4.049 | 0.02175705 |
| rs2527919 | C/T | T | 0.508 | 7 | 99332449 | 0.000504637 | CNPY4 | 1.14E-05 | 6200743 | T/C | C | -4.388 | 0.00520343 |
| rs662333 | A/G | G | 0.259 | 11 | 121084155 | 0.000505389 | SORL1 | 0.000226735 | 2480274 | A/G | G | 3.687 | 0.0798429 |
| rs7569851 | C/G | G | 0.5 | 2 | 15869728 | 0.00051637 | - | 0.000286068 | 7560768 | G/C | G | -3.628 | 0.09663989 |
| rs437179 | A/C | C | 0.65 | 6 | 32036993 | 0.000516908 | SKIV2L | 1.12E-30 | 5560541 | A/C | A | -11.514 | 0 |
| rs2431501 | A/T | T | 0.358 | 5 | 176538658 | 0.000517272 | RAB24 | 1.23E-34 | 2360022 | A/T | T | -12.275 | 0 |
| rs648997 | C/T | T | 0.328 | 12 | 110461159 | 0.00051891 | SH2B3 | 7.49E-31 | 6560301 | T/C | T | -11.549 | 0 |
| rs4870313 | A/G | G | 0.825 | 6 | 155167835 | 0.00051971 | RBM16 | 1.74E-05 | 7200070 | G/A | A | -4.296 | 0.00818157 |
| rs11000787 | C/T | T | 0.276 | 10 | 75254389 | 0.000526192 | NDST2 | 2.63E-47 | 110561 | C/T | T | -14.447 | 0 |
| rs6538592 | A/G | G | 0.414 | 12 | 94026878 | 0.000527518 | NDUFA12 | 1.51E-81 | 5090050 | G/A | G | -19.127 | 0 |
| rs3743553 | C/T | T | 0.31 | 16 | 56587554 | 0.000536314 | C16orf57 | 2.17E-22 | 2750360 | C/T | T | -9.733 | 0 |
| rs2517645 | C/T | T | 0.792 | 6 | 30230602 | 0.000540143 | TRIM10 | 4.44E-28 | 110255 | T/C | C | -10.986 | 0 |
| rs4855882 | G/T | T | 0.792 | 3 | 49690358 | 0.000545351 | UBA7 | 1.08E-70 | 2850202 | T/G | G | -17.776 | 0 |
| rs484932 | A/C | C | 0.95 | 9 | 134231409 | 0.000548595 | TTF1 | 1.84E-05 | 1340114 | C/A | A | 4.283 | 0.00852766 |
| rs9861291 | C/G | G | 0.533 | 3 | 180274372 | 0.000556515 | - | 4.00E-13 | 1510608 | G/C | C | -7.256 | 0 |
| rs9861291 | C/G | G | 0.533 | 3 | 180274372 | 0.000556515 | ZMAT3 | 1.34E-06 | 3140543 | G/C | C | -4.834 | 0.00044863 |
| rs1078341 | A/G | G | 0.792 | 3 | 49660596 | 0.000558894 | AMT | 1.69E-20 | 940450 | G/A | A | -9.281 | 0 |
| rs1078341 | A/G | G | 0.792 | 3 | 49660596 | 0.000558894 | GMPPB,AMIGO3 | 6.51E-08 | 6020228 | G/A | A | 5.404 | 1.62E-05 |
| rs9261431 | C/G | G | 0.658 | 6 | 30194401 | 0.000566114 | RPP21 | 1.14E-05 | 830739 | C/G | C | -4.390 | 0.00516334 |
| rs9261431 | C/G | G | 0.658 | 6 | 30194401 | 0.000566114 | HLA-L | 2.44E-06 | 5130768 | C/G | C | 4.713 | 0.00096746 |
| rs380149 | A/G | G | 0.377 | 1 | 25268346 | 0.000569638 | RHD | 5.60E-07 | 5220615 | G/A | G | -5.004 | 0.00016913 |
| rs4713858 | A/G | G | 0.839 | 6 | 35510763 | 0.000571224 | PPARD | 8.93E-06 | 2630168 | G/A | A | -4.442 | 0.00419522 |
| rs7306887 | C/T | T | 0.6 | 12 | 94761226 | 0.000574119 | AMDHD1 | 4.21E-08 | 6520112 | T/C | C | -5.482 | 1.64E-05 |
| rs2734934 | C/T | T | 0.482 | 6 | 29975776 | 0.000579978 | HLA-F | 9.65E-159 | 5220070 | T/C | T | -26.845 | 0 |
| rs6680302 | A/G | G | 0.425 | 1 | 36426127 | 0.000580541 | TRAPPC3 | 1.24E-16 | 1740674 | G/A | G | 8.280 | 0 |
| rs12368672 | C/G | G | 0.4 | 12 | 55798737 | 0.000580575 | STAT6 | 9.81E-198 | 1660397 | G/C | G | -37.203 | 0 |
| rs2806372 | C/T | T | 0.142 | 6 | 109328696 | 0.000585302 | SESN1 | 1.55E-09 | 1240553 | C/T | T | 6.039 | 0 |
| rs2749592 | A/C | C | 0.7 | 10 | 38298848 | 0.00059796 | ZNF248 | 1.84E-06 | 6620608 | A/C | A | -4.770 | 0.00068158 |
| rs11632040 | C/T | T | 0.972 | 15 | 48162576 | 0.000598719 | ATP8B4 | 7.08E-06 | 1820270 | T/C | C | 4.491 | 0.00325364 |
| rs7140568 | C/T | T | 0.317 | 14 | 103111127 | 0.000599246 | BAG5 | 2.89E-169 | 130669 | T/C | T | 27.732 | 0 |
| rs2252551 | A/G | G | 0.192 | 6 | 34730654 | 0.000601178 | C6orf106 | 1.69E-07 | 5900504 | G/A | G | 5.230 | 4.75E-05 |
| rs2968787 | C/T | T | 0.466 | 2 | 55119289 | 0.00060551 | RTN4 | 7.11E-20 | 2230161 | C/T | T | -9.126 | 0 |
| rs6729330 | C/T | T | 0.408 | 2 | 218402541 | 0.000606793 | TNS1 | 3.72E-53 | 6250110 | T/C | C | -15.347 | 0 |
| rs3743554 | A/C | C | 0.681 | 16 | 56587693 | 0.000609804 | ZNF319 | 1.39E-85 | 3180315 | C/A | A | -19.606 | 0 |
| rs10918760 | C/T | T | 0.358 | 1 | 165998722 | 0.000622298 | MPZL1 | 6.32E-06 | 2490470 | T/C | T | 4.516 | 0.00289608 |
| rs2744963 | A/G | G | 0.8 | 6 | 34700709 | 0.000622419 | C6orf106 | 3.31E-07 | 7320110 | G/A | A | 5.105 | 0.00010917 |
| rs4490505 | A/G | G | 0.698 | 4 | 157356553 | 0.000623346 | - | 1.31E-09 | 4070138 | G/A | A | 6.066 | 0 |
| rs17318297 | C/G | G | 0.103 | 7 | 7256463 | 0.000629817 | C1GALT1 | 8.73E-10 | 580066 | C/G | G | 6.131 | 0 |
| rs1611715 | A/C | C | 0.433 | 6 | 29937461 | 0.00063012 | HLA-G | 9.81E-198 | 2070088 | C/A | C | 32.493 | 0 |
| rs799466 | C/T | T | 0.642 | 14 | 34573077 | 0.000635252 | KIAA0391 | 2.42E-39 | 6560427 | T/C | C | -13.123 | 0 |
| rs799466 | C/T | T | 0.642 | 14 | 34573077 | 0.000635252 | SRP54 | 1.18E-11 | 6860553 | T/C | C | 6.783 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs11146315 | C/T | T | 0.392 | 10 | 133955839 | 0.000635809 | STK32C | 2.84E-130 | 2450435 | T/C | T | 24.285 | 0 |
| rs11669741 | C/T | T | 0.558 | 19 | 63652293 | 0.000636058 | ZNF132,ZNF584 | 2.57E-24 | 4730187 | T/C | T | 10.175 | 0 |
| rs3772503 | C/T | T | 0.825 | 3 | 59955464 | 0.000641831 | FHIT | 1.70E-12 | 7150142 | T/C | C | -7.057 | 0 |
| rs4801589 | C/G | G | 0.433 | 19 | 63645210 | 0.000642963 | MZF1 | 1.28E-08 | 1030053 | G/C | C | -5.689 | 0 |
| rs8076343 | C/T | T | 0.683 | 17 | 34235398 | 0.000657272 | CCDC49 | 2.53E-31 | 730253 | T/C | C | 11.642 | 0 |
| rs2834058 | A/G | G | 0.85 | 21 | 33295942 | 0.000664766 | OLIG1 | 1.95E-07 | 2030403 | G/A | A | -5.204 | 6.31E-05 |
| rs12664426 | C/T | T | 0.076 | 6 | 27187899 | 0.000664844 | HIST1H2BK | 5.64E-09 | 6110630 | C/T | T | -5.827 | 0 |
| rs10212471 | A/G | G | 0.258 | 3 | 134042081 | 0.000665856 | ACAD11 | 1.29E-30 | 1820746 | A/G | G | -11.502 | 0 |
| rs12889403 | C/T | T | 0.308 | 14 | 103104499 | 0.000667546 | XRCC3,KLC1 | 5.88E-05 | 670014 | T/C | T | 4.018 | 0.02476325 |
| rs12889403 | C/T | T | 0.308 | 14 | 103104499 | 0.000667546 | BAG5 | 6.74E-09 | 6550349 | T/C | T | 5.797 | 0 |
| rs10983314 | A/T | T | 0.333 | 9 | 118514893 | 0.000669585 | TRIM32,ASTN2 | 9.52E-07 | 5670088 | A/T | T | 4.902 | 0.00027231 |
| rs4767293 | A/G | G | 0.4 | 12 | 110947679 | 0.000675833 | ALDH2 | 1.93E-33 | 840253 | G/A | G | 12.051 | 0 |
| rs7637711 | A/G | G | 0.208 | 3 | 49804657 | 0.00067913 | GMPPB,AMIGO3 | 4.53E-20 | 4830458 | A/G | G | 9.175 | 0 |
| rs2070721 | G/T | T | 0.534 | 5 | 131853741 | 0.000692848 | SLC22A4 | 2.91E-46 | 6040398 | T/G | G | 14.280 | 0 |
| rs7232135 | C/T | T | 0.807 | 18 | 13037983 | 0.000693533 | SEH1L | 5.01E-09 | 580196 | T/C | C | -5.847 | 0 |
| rs518425 | A/G | G | 0.25 | 15 | 76670868 | 0.000696244 | PSMA4 | 1.27E-21 | 4040711 | G/A | G | -9.552 | 0 |
| rs10239342 | G/T | T | 0.605 | 7 | 129796548 | 0.000697846 | CPA5 | 1.36E-15 | 1450056 | G/T | G | -7.989 | 0 |
| rs1048466 | A/G | G | 0.692 | 12 | 421811 | 0.000698286 | JARID1A | 1.24E-25 | 730068 | G/A | A | -10.466 | 0 |
| rs1048466 | A/G | G | 0.692 | 12 | 421811 | 0.000698286 | CCDC77 | 1.98E-48 | 3850291 | G/A | A | -14.624 | 0 |
| rs2516510 | C/T | T | 0.693 | 6 | 31557893 | 0.000699745 | BAT3 | 0.000151865 | 5340382 | T/C | C | 3.788 | 0.05693728 |
| rs494620 | A/G | G | 0.617 | 6 | 31946692 | 0.000708115 | HSPA1B | 8.71E-108 | 3850433 | G/A | A | 22.054 | 0 |
| rs883058 | A/T | T | 0.633 | 1 | 52089819 | 0.000715714 | TXNDC12 | 6.16E-05 | 7160274 | T/A | A | 4.007 | 0.0254564 |
| rs7597198 | C/T | T | 0.758 | 2 | 55109374 | 0.000722858 | RTN4 | 8.10E-10 | 6770189 | T/C | C | 6.143 | 0 |
| rs2405308 | A/G | G | 0.775 | 1 | 222819988 | 0.000723803 | CNIH4 | 1.32E-11 | 6400332 | A/G | A | 6.767 | 0 |
| rs4731689 | C/T | T | 0.383 | 7 | 129797075 | 0.000731721 | AC007938.1 | 1.39E-05 | 2030386 | T/C | T | -4.345 | 0.00624057 |
| rs9807819 | C/T | T | 0.342 | 19 | 50931438 | 0.000740901 | FBXO46 | 1.42E-06 | 3610452 | T/C | T | 4.822 | 0.00049224 |
| rs9807819 | C/T | T | 0.342 | 19 | 50931438 | 0.000740901 | DMWD | 3.84E-07 | 3850731 | T/C | T | -5.077 | 0.00010868 |
| rs3094694 | C/T | T | 0.775 | 6 | 30559883 | 0.000749723 | HLA-E | 1.03E-30 | 1030747 | T/C | C | 11.521 | 0 |
| rs8032589 | C/T | T | 0.817 | 15 | 39288775 | 0.00075029 | AC012652.1 | 4.83E-11 | 6760192 | T/C | C | -6.576 | 0 |
| rs1022088 | A/T | T | 0.328 | 17 | 43934789 | 0.00076151 | HOXB2 | 9.81E-198 | 3460097 | T/A | T | -59.274 | 0 |
| rs4806117 | A/G | G | 0.667 | 19 | 40418875 | 0.000763129 | USF2 | 3.00E-09 | 7210382 | G/A | A | 5.932 | 0 |
| rs9393737 | A/G | G | 0.805 | 6 | 26725285 | 0.000763165 | ABT1 | 5.59E-05 | 6480392 | G/A | A | -4.030 | 0.02347279 |
| rs10859997 | C/T | T | 0.108 | 12 | 94909490 | 0.000771319 | LTA4H | 9.22E-12 | 1430524 | C/T | T | -6.818 | 0 |
| rs10859997 | C/T | T | 0.108 | 12 | 94909490 | 0.000771319 | HAL | 8.45E-24 | 6840468 | C/T | T | -10.058 | 0 |
| rs10859997 | C/T | T | 0.108 | 12 | 94909490 | 0.000771319 | HAL | 1.53E-07 | 6960274 | C/T | T | -5.249 | 4.76E-05 |
| rs1087298 | A/G | G | 0.4 | 4 | 185509610 | 0.000771701 | IRF2 | 2.87E-10 | 580722 | G/A | G | -6.306 | 0 |
| rs11645506 | A/C | C | 0.593 | 16 | 11703080 | 0.00077232 | TXNDC11 | 1.51E-11 | 10746 | C/A | A | -6.747 | 0 |
| rs1561073 | A/T | T | 0.336 | 3 | 11617114 | 0.000780236 | VGLL4 | 0.000104887 | 5220491 | A/T | T | 3.879 | 0.04100099 |
| rs1561073 | A/T | T | 0.336 | 3 | 11617114 | 0.000780236 | ATG7 | 7.81E-07 | 5220754 | A/T | T | -4.940 | 0.00024342 |
| rs13146503 | C/T | T | 0.633 | 4 | 47886593 | 0.000780642 | TXK | 1.52E-10 | 1190138 | T/C | C | -6.403 | 0 |
| rs2517754 | A/G | G | 0.554 | 6 | 30004659 | 0.00078218 | PPP1R11 | 7.08E-27 | 620376 | G/A | A | -10.734 | 0 |
| rs10054755 | A/G | G | 0.092 | 5 | 156743623 | 0.000786997 | ITK | 4.02E-05 | 7560632 | A/G | G | 4.106 | 0.01710595 |
| rs3004047 | A/G | G | 0.85 | 6 | 26818370 | 0.000787241 | HMGN4 | 7.87E-93 | 5270689 | G/A | A | -20.437 | 0 |
| rs9428015 | A/G | G | 0.33 | 1 | 89041928 | 0.000804915 | CCBL2 | 2.02E-35 | 770630 | A/G | G | -12.421 | 0 |
| rs9428015 | A/G | G | 0.33 | 1 | 89041928 | 0.000804915 | CCBL2,RBMXL1 | 0.000123135 | 2760538 | A/G | G | -3.840 | 0.04693106 |
| rs9428015 | A/G | G | 0.33 | 1 | 89041928 | 0.000804915 | GTF2B | 4.94E-07 | 4880215 | A/G | G | 5.029 | 0.00013878 |
| rs17345997 | C/T | T | 0.192 | 1 | 203546235 | 0.000805248 | NUAK2 | 0.000241037 | 380202 | C/T | T | 3.672 | 0.08405331 |
| rs17345997 | C/T | T | 0.192 | 1 | 203546235 | 0.000805248 | NUAK2 | 2.46E-14 | 840356 | C/T | T | 7.624 | 0 |
| rs6866959 | A/G | G | 0.883 | 5 | 157072081 | 0.000805552 | THG1L | 4.56E-36 | 4730348 | G/A | A | -12.539 | 0 |
| rs893186 | A/C | C | 0.558 | 19 | 63660991 | 0.000808957 | CHMP2A | 6.43E-05 | 4260762 | C/A | C | -3.997 | 0.02656986 |
| rs6456762 | G/T | T | 0.112 | 6 | 27038278 | 0.000809091 | - | 3.56E-57 | 3390050 | G/T | T | -15.936 | 0 |
| rs6599143 | A/G | G | 0.583 | 3 | 41140620 | 0.000809906 | CTNNB1 | 4.68E-16 | 3800671 | G/A | A | 8.119 | 0 |
| rs6933716 | C/T | T | 0.242 | 6 | 7070708 | 0.000815403 | RREB1 | 1.51E-05 | 4060187 | T/C | T | 4.328 | 0.0071048 |
| rs2517681 | C/T | T | 0.453 | 6 | 30040309 | 0.000819787 | ZNRD1 | 0.00016761 | 4050673 | C/T | T | -3.763 | 0.06149453 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
|  |  |  |  |  |  |  |  | 9 |  |  |  |  |  |
| rs2517681 | C/T | T | 0.453 | 6 | 30040309 | 0.000819787 | ZNRD1 | 7.79E-46 | 4060255 | C/T | T | -14.212 | 0 |
| rs4906335 | A/C | C | 0.716 | 14 | 103090894 | 0.000820092 | CKB | 8.32E-17 | 4150066 | C/A | A | 8.327 | 0 |
| rs4906335 | A/C | C | 0.716 | 14 | 103090894 | 0.000820092 | EIF5 | 1.19E-06 | 5670468 | C/A | A | -4.857 | 0.00039051 |
| rs2243393 | A/G | G | 0.675 | 1 | 111527549 | 0.000829852 | CEPT1 | 4.23E-11 | 2190730 | G/A | A | 6.596 | 0 |
| rs746423 | C/T | T | 0.208 | 12 | 52703526 | 0.000832249 | SMUG1 | 3.57E-09 | 1050386 | C/T | T | 5.903 | 0 |
| rs746423 | C/T | T | 0.208 | 12 | 52703526 | 0.000832249 | - | 4.59E-06 | 5550458 | C/T | T | 4.583 | 0.00205253 |
| rs11024750 | A/G | G | 0.655 | 11 | 18626055 | 0.0008476 | LDHC | 1.41E-05 | 110291 | G/A | A | -4.343 | 0.00645648 |
| rs1383264 | A/T | T | 0.483 | 6 | 32847945 | 0.00084902 | HLA-DMA | 3.44E-06 | 540563 | T/A | A | 4.642 | 0.00143437 |
| rs1383264 | A/T | T | 0.483 | 6 | 32847945 | 0.00084902 | TAP2 | 1.43E-101 | 2650156 | T/A | A | -21.397 | 0 |
| rs10747851 | C/G | G | 0.767 | 12 | 58261381 | 0.000852498 | - | 9.22E-06 | 1430682 | G/C | C | -4.435 | 0.00424522 |
| rs11656386 | C/T | T | 0.067 | 17 | 72125682 | 0.000854262 | ST6GALNAC2 | 1.33E-20 | 6420164 | C/T | T | -9.306 | 0 |
| rs12783892 | A/G | G | 0.602 | 10 | 133930159 | 0.000856348 | JAKMIP3 | 0.000161426 | 5960364 | A/G | A | -3.773 | 0.05961079 |
| rs11191822 | G/T | T | 0.679 | 10 | 105589760 | 0.000859514 | SLK | 7.39E-09 | 670470 | T/G | G | -5.782 | 0 |
| rs11191822 | G/T | T | 0.679 | 10 | 105589760 | 0.000859514 | SH3PXD2A | 6.93E-40 | 3460451 | T/G | G | -13.218 | 0 |
| rs11191822 | G/T | T | 0.679 | 10 | 105589760 | 0.000859514 | SLK | 9.05E-07 | 4060021 | T/G | G | -4.911 | 0.00025746 |
| rs9492413 | C/T | T | 0.225 | 6 | 130259478 | 0.000861974 | L3MBTL3 | 0.00029256 | 770128 | T/C | T | 3.622 | 0.09854369 |
| rs13051329 | C/T | T | 0.11 | 21 | 34244759 | 0.000862235 | - | 2.92E-28 | 6580703 | C/T | T | -11.024 | 0 |
| rs4947349 | G/T | T | 0.1 | 6 | 32855768 | 0.000866826 | PSMB9 | 1.86E-18 | 6450692 | G/T | T | 8.766 | 0 |
| rs3016009 | C/T | T | 0.304 | 6 | 31559940 | 0.000868605 | - | 3.26E-141 | 1440603 | C/T | T | -25.299 | 0 |
| rs2524142 | C/G | G | 0.602 | 6 | 31371501 | 0.000871928 | ATP6V1G2,BAT1 | 3.70E-10 | 1260538 | G/C | C | -6.266 | 0 |
| rs4910431 | A/G | G | 0.255 | 11 | 9045221 | 0.000877427 | C11orf17 | 7.75E-05 | 6270112 | A/G | G | -3.952 | 0.03105098 |
| rs3869130 | C/T | T | 0.173 | 6 | 31518730 | 0.000878382 | MICB | 3.05E-23 | 3170064 | T/C | T | -9.931 | 0 |
| rs626339 | C/T | T | 0.675 | 1 | 111530848 | 0.00089735 | CEPT1 | 2.66E-08 | 5870403 | T/C | C | 5.562 | 0 |
| rs3131290 | A/G | G | 0.684 | 6 | 32291153 | 0.000904741 | GPSM3,NOTCH4 | 5.08E-09 | 7160390 | G/A | A | -5.845 | 0 |
| rs11846869 | A/G | G | 0.667 | 14 | 87609522 | 0.000906224 | GALC | 1.48E-11 | 3360524 | G/A | A | -6.750 | 0 |
| rs11846869 | A/G | G | 0.667 | 14 | 87609522 | 0.000906224 | GPR65 | 5.92E-12 | 6550273 | G/A | A | -6.882 | 0 |
| rs11846869 | A/G | G | 0.667 | 14 | 87609522 | 0.000906224 | GPR65 | 8.89E-12 | 7570367 | G/A | A | -6.824 | 0 |
| rs9929566 | C/T | T | 0.392 | 16 | 75682603 | 0.000913312 | MON1B | 5.71E-29 | 5310674 | C/T | C | 11.170 | 0 |
| rs12203019 | A/G | G | 0.75 | 6 | 18512991 | 0.000918548 | IBRDC2 | 1.28E-15 | 70630 | G/A | A | -7.997 | 0 |
| rs9975829 | A/G | G | 0.345 | 21 | 33781365 | 0.000919387 | TMEM50B | 4.51E-52 | 3460307 | A/G | G | 15.184 | 0 |
| rs9975829 | A/G | G | 0.345 | 21 | 33781365 | 0.000919387 | - | 1.38E-127 | 4480647 | A/G | G | -24.029 | 0 |
| rs9975829 | A/G | G | 0.345 | 21 | 33781365 | 0.000919387 | IL10RB | 0.000228164 | 5670719 | A/G | G | 3.686 | 0.08030933 |
| rs11649804 | A/C | C | 0.758 | 17 | 17637480 | 0.000919721 | ATPAF2 | 0.000268642 | 3780239 | C/A | A | 3.644 | 0.09174061 |
| rs11649804 | A/C | C | 0.758 | 17 | 17637480 | 0.000919721 | SREBF1 | 1.76E-20 | 6840044 | C/A | A | -9.276 | 0 |
| rs2093169 | C/T | T | 0.158 | 6 | 26603078 | 0.000924589 | BTN3A2 | 7.38E-154 | 4610674 | C/T | T | -26.424 | 0 |
| rs2093169 | C/T | T | 0.158 | 6 | 26603078 | 0.000924589 | BTN2A2 | 0.000257784 | 5420709 | C/T | T | 3.655 | 0.08892445 |
| rs17481834 | A/G | G | 0.144 | 2 | 37381853 | 0.000928695 | CEBPZ,EIF2AK2,AC007390.5 | 3.60E-07 | 4760373 | A/G | G | 5.089 | 0.00010895 |
| rs17481834 | A/G | G | 0.144 | 2 | 37381853 | 0.000928695 | QPCT | 4.31E-16 | 5570139 | A/G | G | -8.129 | 0 |
| rs10910097 | C/T | T | 0.2 | 1 | 2511290 | 0.000939314 | TNFRSF14 | 2.54E-16 | 6520725 | T/C | T | 8.194 | 0 |
| rs4600917 | C/T | T | 0.592 | 4 | 107049094 | 0.000939467 | GSTCD | 0.000158729 | 5360487 | T/C | C | 3.777 | 0.05882564 |
| rs2736428 | C/T | T | 0.295 | 6 | 31951903 | 0.000939984 | CSNK2B | 6.95E-85 | 3450156 | C/T | T | -19.523 | 0 |
| rs2736428 | C/T | T | 0.295 | 6 | 31951903 | 0.000939984 | BAT3 | 0.000140776 | 4260736 | C/T | T | 3.807 | 0.05342764 |
| rs2736428 | C/T | T | 0.295 | 6 | 31951903 | 0.000939984 | HSPA1L | 3.17E-12 | 6280471 | C/T | T | 6.970 | 0 |
| rs12145992 | A/G | G | 0.771 | 1 | 3750169 | 0.00094085 | KIAA0562 | 1.02E-47 | 6650288 | G/A | A | -14.512 | 0 |
| rs1075654 | A/G | G | 0.867 | 9 | 135918097 | 0.000943683 | BRD3 | 4.56E-17 | 6660626 | G/A | A | 8.398 | 0 |
| rs997154 | A/G | G | 0.833 | 14 | 22534322 | 0.000945533 | PRMT5 | 1.23E-49 | 3850520 | G/A | A | -14.812 | 0 |
| rs997154 | A/G | G | 0.833 | 14 | 22534322 | 0.000945533 | PRMT5 | 3.22E-63 | 5700520 | G/A | A | -16.784 | 0 |
| rs7964078 | A/G | G | 0.225 | 12 | 31795203 | 0.000946278 | C12orf35 | 8.09E-11 | 7570477 | A/G | G | -6.499 | 0 |
| rs10463321 | G/T | T | 0.791 | 5 | 151304098 | 0.000946839 | ATOX1 | 3.26E-22 | 5560131 | T/G | G | -9.692 | 0 |
| rs10463321 | G/T | T | 0.791 | 5 | 151304098 | 0.000946839 | G3BP1 | 5.93E-07 | 6520730 | T/G | G | 4.994 | 0.00018405 |
| rs2070729 | A/C | C | 0.533 | 5 | 131847820 | 0.000949106 | IRF1 | 4.51E-10 | 6250064 | C/A | A | -6.236 | 0 |

| | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs11868035 | A/G | G | 0.767 | 17 | 17655826 | 0.000960595 | SREBF1 | 5.31E-59 | 3390343 | G/A | A | -16.197 | 0 |
| rs966087 | A/C | C | 0.3 | 5 | 126198809 | 0.000961572 | - | 1.75E-05 | 870561 | C/A | C | 4.295 | 0.00818157 |
| rs2268248 | A/G | G | 0.941 | 21 | 34108970 | 0.000962871 | ITSN1 | 5.77E-05 | 6420575 | G/A | A | -4.022 | 0.02409376 |
| rs6673832 | A/G | G | 0.125 | 1 | 183225534 | 0.0009638 | C1orf25 | 3.31E-08 | 4890647 | A/G | G | -5.524 | 0 |
| rs11672342 | A/G | G | 0.871 | 19 | 34958442 | 0.000966871 | C19orf12 | 3.33E-08 | 6370377 | G/A | A | -5.523 | 0 |
| rs16841336 | C/T | T | 0.833 | 1 | 157167751 | 0.000968436 | PYHIN1 | 4.12E-10 | 2000451 | T/C | C | 6.250 | 0 |
| rs16841336 | C/T | T | 0.833 | 1 | 157167751 | 0.000968436 | PYHIN1 | 9.24E-09 | 7000270 | T/C | C | 5.744 | 0 |
| rs16841336 | C/T | T | 0.833 | 1 | 157167751 | 0.000968436 | PYHIN1 | 1.67E-23 | 7330538 | T/C | C | 9.991 | 0 |
| rs1264331 | G/T | T | 0.317 | 6 | 30954809 | 0.000974071 | VARSL | 9.81E-198 | 1500753 | T/G | T | 41.179 | 0 |
| rs2295687 | A/G | G | 0.617 | 14 | 22490936 | 0.000974329 | RBM23 | 3.64E-22 | 2190743 | G/A | A | -9.681 | 0 |
| rs2295687 | A/G | G | 0.617 | 14 | 22490936 | 0.000974329 | RBM23 | 6.75E-16 | 3610092 | G/A | A | -8.075 | 0 |
| rs2295687 | A/G | G | 0.617 | 14 | 22490936 | 0.000974329 | MRPL52 | 3.32E-08 | 7000692 | G/A | A | 5.524 | 0 |
| rs925284 | C/T | T | 0.458 | 17 | 43940889 | 0.00097893 | HOXB4 | 5.23E-15 | 2120008 | T/C | T | -7.821 | 0 |
| rs221032 | C/T | T | 0.267 | 1 | 16398136 | 0.00098155 | SPATA21,C1orf144 | 7.02E-10 | 2030044 | T/C | T | 6.166 | 0 |
| rs221032 | C/T | T | 0.267 | 1 | 16398136 | 0.00098155 | ARHGEF19 | 2.39E-40 | 6250546 | T/C | T | -13.298 | 0 |
| rs10992662 | C/G | G | 0.467 | 9 | 94969016 | 0.000986164 | NINJ1 | 1.31E-22 | 7380706 | G/C | G | -9.785 | 0 |
| rs2243429 | G/T | T | 0.367 | 6 | 31554799 | 0.00098963 | - | 7.31E-91 | 580452 | G/T | T | 20.215 | 0 |
| rs6736194 | C/G | G | 0.492 | 2 | 11417509 | 0.00099193 | ROCK2 | 3.97E-08 | 5670333 | C/G | C | -5.492 | 0 |
| rs6736194 | C/G | G | 0.492 | 2 | 11417509 | 0.00099193 | PQLC3 | 1.17E-05 | 7000382 | C/G | C | -4.383 | 0.00532356 |
| rs13051785 | C/T | T | 0.125 | 21 | 34245156 | 0.000995159 | AP000569.1 | 6.06E-10 | 1990156 | C/T | T | -6.189 | 0 |
| rs13029949 | A/G | G | 0.664 | 2 | 173696496 | 0.000999497 | ZAK | 3.91E-05 | 3360431 | G/A | A | 4.113 | 0.01670154 |
| rs13029949 | A/G | G | 0.664 | 2 | 173696496 | 0.000999497 | ZAK | 5.61E-20 | 4670059 | G/A | A | 9.152 | 0 |

## Supplementary Table 8: Blood and lung regulated genes GO pathways

Gene Ontology processes: Biological processes enriched among tested genes. FDR: False Discovery Rate.

| **Pathway enrichment analyses of lung function eSNP-regulated genes in lung and blood** | |
|---|---|
| **Blood eSNP- regulated genes enrichment in Gene Ontology Processes** | **FDR** |
| NK T cell differentiation | 0.0422 |
| immune system process | 0.0422 |
| positive regulation of immune system process | 0.0422 |
| negative regulation of cellular process | 0.0422 |
| cell proliferation | 0.0422 |
| negative regulation of biological process | 0.0422 |
| cytokine-mediated signaling pathway | 0.0422 |
| positive regulation of cell differentiation | 0.0422 |
| | |
| **Lung eSNP- regulated genes enrichment in Gene Ontology Processes** | **FDR** |
| hair follicle maturation | 9.00E-04 |
| anatomical structure maturation | 9.00E-04 |
| developmental maturation | 0.0029 |
| interferon-gamma-mediated signaling pathway | 0.0045 |
| exogen | 0.0045 |
| hair cycle | 0.0056 |
| antigen processing and presentation of exogenous peptide antigen | 0.0056 |
| hair cycle process | 0.0056 |
| molting cycle | 0.0056 |
| hair follicle development | 0.0056 |
| molting cycle process | 0.0056 |
| antigen processing and presentation of exogenous antigen | 0.0057 |
| cellular response to interferon-gamma | 0.0059 |
| antigen processing and presentation | 0.0073 |
| antigen processing and presentation of peptide antigen | 0.0136 |
| response to interferon-gamma | 0.0191 |
| antigen processing and presentation of exogenous peptide antigen via MHC class II | 0.036 |
| antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | 0.0376 |

| | |
|---|---|
| antigen processing and presentation of peptide antigen via MHC class II | 0.0376 |
| | |
| **Shared blood and lung eSNP- regulated genes enrichment in Gene Ontology Processes** | **FDR** |
| antigen processing and presentation | 2.00E-04 |
| exogen | 2.00E-04 |
| antigen processing and presentation of exogenous peptide antigen | 2.00E-04 |
| antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent | 2.00E-04 |
| antigen processing and presentation of exogenous antigen | 2.00E-04 |
| antigen processing and presentation of peptide antigen | 3.00E-04 |
| hair follicle maturation | 3.00E-04 |
| antigen processing and presentation of exogenous peptide antigen via MHC class I | 3.00E-04 |
| anatomical structure maturation | 8.00E-04 |
| antigen processing and presentation of peptide antigen via MHC class I | 0.0011 |
| antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 0.0019 |
| hair cycle process | 0.0021 |
| molting cycle process | 0.0021 |
| hair follicle development | 0.0021 |
| hair cycle | 0.0022 |
| molting cycle | 0.0022 |
| cellular response to interferon-gamma | 0.0034 |
| developmental maturation | 0.0035 |
| epidermis development | 0.0095 |
| response to interferon-gamma | 0.0095 |
| interferon-gamma-mediated signaling pathway | 0.0121 |
| negative regulation of mononuclear cell proliferation | 0.0248 |
| negative regulation of lymphocyte proliferation | 0.0248 |
| negative regulation of leukocyte proliferation | 0.029 |
| regulation of leukocyte activation | 0.038 |
| centrosome organization | 0.0463 |

## Supplementary Table 9: Fetal lung development results

Table shows the results of human fetal lung differential gene expression for lung function eSNP-regulated genes. Probeset: The probeset from the Affymetrix U133 Plus 2.0 mapping to the lung function eSNP-regulated gene. Gene symbol: the gene tested for differential expression. Log Fold change: log fold change of probeset in relation to gestational age in days. P value: differential expression unadjusted P value. FDR adjusted P value: False discovery rate adjusted P value. Gene Name: Full name of tested gene.

**Evaluation of lung function eSNP-regulated genes in fetal lung study**

| Probeset | Gene Symbol | log Fold Change | P Value | FDR adjusted P value | Gene Name |
|---|---|---|---|---|---|
| 203832_at | SNRPF | -0.01259 | 7.50E-14 | 1.37E-10 | small nuclear ribonucleoprotein polypeptide F |
| 228268_at | FMO2 | 0.036657 | 2.18E-12 | 1.55E-09 | flavin containing monooxygenase 2 (non-functional) |
| 223503_at | TMEM163 | 0.032838 | 8.23E-12 | 4.23E-09 | transmembrane protein 163 |
| 201865_x_at | NR3C1 | 0.012522 | 8.69E-12 | 4.36E-09 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) |
| 211726_s_at | FMO2 | 0.042972 | 1.29E-11 | 5.71E-09 | flavin containing monooxygenase 2 (non-functional) |
| 211671_s_at | NR3C1 | 0.012931 | 1.65E-11 | 6.85E-09 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) |
| 219588_s_at | NCAPG2 | -0.020856 | 1.76E-11 | 7.13E-09 | non-SMC condensin II complex, subunit G2 |
| 223315_at | NTN4 | 0.035134 | 2.05E-11 | 8.11E-09 | netrin 4 |
| 211714_x_at | TUBB | -0.019597 | 2.32E-11 | 8.88E-09 | tubulin, beta class I |
| 209026_x_at | TUBB | -0.020294 | 4.95E-11 | 1.53E-08 | tubulin, beta class I |
| 1552626_a_at | TMEM163 | 0.021971 | 5.64E-11 | 1.71E-08 | transmembrane protein 163 |
| 208812_x_at | HLA-C | 0.019142 | 8.72E-11 | 2.40E-08 | major histocompatibility complex, class I, C |
| 221978_at | HLA-F | 0.012529 | 1.60E-09 | 1.89E-07 | major histocompatibility complex, class I, F |
| 214459_x_at | HLA-C | 0.016972 | 2.68E-09 | 2.83E-07 | major histocompatibility complex, class I, C |
| 205659_at | HDAC9 | 0.017554 | 3.84E-09 | 3.74E-07 | histone deacetylase 9 |
| 201930_at | MCM6 | -0.01892 | 4.73E-09 | 4.47E-07 | minichromosome maintenance complex component 6 |
| 219556_at | C16orf5 | -0.011259 | 7.42E-09 | 6.35E-07 | chromosome 16 open reading frame 59 |
| 219901_at | FGD6 | -0.015788 | 1.07E-08 | 8.49E-07 | FYVE, RhoGEF and PH domain containing 6 |
| 223232_s_at | CGN | 0.01569 | 1.16E-08 | 9.10E-07 | cingulin |
| 216526_x_at | HLA-C | 0.01905 | 1.63E-08 | 1.20E-06 | major histocompatibility complex, class I, C |
| 228286_at | GEN1 | -0.01513 | 3.63E-08 | 2.24E-06 | GEN1 Holliday junction 5' flap endonuclease |
| 201400_at | PSMB3 | -0.011404 | 4.75E-08 | 2.75E-06 | proteasome (prosome, macropain) subunit, beta type, 3 |
| 230135_at | HHIP | 0.013116 | 4.97E-08 | 2.84E-06 | hedgehog interacting protein |
| 209815_at | PTCH1 | -0.012304 | 5.23E-08 | 2.96E-06 | patched 1 |
| 221748_s_at | TNS1 | 0.011381 | 6.24E-08 | 3.36E-06 | tensin 1 |
| 204670_x_at | HLA-DRB1 | 0.016926 | 7.94E-08 | 4.08E-06 |  |
| 201342_at | SNRPC | -0.007621 | 8.76E-08 | 4.41E-06 | small nuclear ribonucleoprotein polypeptide C |

| | | | | | |
|---|---|---|---|---|---|
| 206082_at | HCP5 | 0.012002 | 9.44E-08 | 4.70E-06 | HLA complex P5 (non-protein coding) |
| 211432_s_at | TYRO3 | -0.009619 | 9.98E-08 | 4.90E-06 | TYRO3 protein tyrosine kinase |
| 227978_s_at | ZADH2 | -0.011211 | 1.04E-07 | 5.08E-06 | zinc binding alcohol dehydrogenase domain containing 2 |
| 225911_at | NPNT | 0.011368 | 1.44E-07 | 6.65E-06 | nephronectin |
| 228153_at | RNF144B | 0.010728 | 1.71E-07 | 7.65E-06 | ring finger protein 144B |
| 201503_at | G3BP1 | -0.010579 | 2.58E-07 | 1.05E-05 | GTPase activating protein (SH3 domain) binding protein 1 |
| 209140_x_at | HLA-B | 0.018404 | 2.69E-07 | 1.08E-05 | major histocompatibility complex, class I, B |
| 228707_at | CLDN23 | 0.018583 | 3.36E-07 | 1.29E-05 | claudin 23 |
| 223434_at | GBP3 | 0.032958 | 3.96E-07 | 1.47E-05 | guanylate binding protein 3 |
| 212254_s_at | DST | 0.009279 | 5.07E-07 | 1.81E-05 | dystonin |
| 201229_s_at | ARIH2 | -0.008679 | 5.55E-07 | 1.96E-05 | ariadne homolog 2 (Drosophila) |
| 1555137_a_at | FGD6 | -0.018119 | 6.14E-07 | 2.13E-05 | FYVE, RhoGEF and PH domain containing 6 |
| 216321_s_at | NR3C1 | 0.011428 | 7.23E-07 | 2.42E-05 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) |
| 215016_x_at | DST | 0.007317 | 8.37E-07 | 2.73E-05 | dystonin |
| 206116_s_at | TPM1 | -0.016995 | 9.39E-07 | 2.98E-05 | tropomyosin 1 (alpha) |
| 203396_at | PSMA4 | -0.006499 | 9.43E-07 | 2.99E-05 | proteasome (prosome, macropain) subunit, alpha type, 4 |
| 1556037_s_at | HHIP | 0.013832 | 1.04E-06 | 3.23E-05 | hedgehog interacting protein |
| 205429_s_at | MPP6 | -0.009311 | 1.18E-06 | 3.57E-05 | membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6) |
| 223639_s_at | ZNRD1 | -0.005906 | 1.48E-06 | 4.27E-05 | zinc ribbon domain containing 1 |
| 230152_at | WDR52 | 0.006115 | 2.00E-06 | 5.43E-05 | WD repeat domain 52 |
| 223100_s_at | NUDT5 | -0.009016 | 2.13E-06 | 5.72E-05 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 |
| 228009_x_at | ZNRD1 | -0.006566 | 2.22E-06 | 5.88E-05 | zinc ribbon domain containing 1 |
| 201725_at | CDC123 | -0.009694 | 2.26E-06 | 5.97E-05 | cell division cycle 123 |
| 212320_at | TUBB | -0.011371 | 2.30E-06 | 6.06E-05 | tubulin, beta class I |
| 215620_at | RREB1 | 0.017055 | 2.50E-06 | 6.48E-05 | ras responsive element binding protein 1 |
| 212204_at | TMEM87A | 0.010342 | 2.72E-06 | 6.93E-05 | transmembrane protein 87A |
| 201709_s_at | NIPSNAP1 | -0.006725 | 2.75E-06 | 6.99E-05 | nipsnap homolog 1 (C. elegans) |
| 229099_at | C11orf83 | -0.00958 | 2.91E-06 | 7.35E-05 | chromosome 11 open reading frame 83 |
| 235411_at | PGBD1 | -0.012246 | 5.87E-06 | 0.000129 | piggyBac transposable element derived 1 |
| 212877_at | KLC1 | -0.010218 | 5.91E-06 | 0.000129 | kinesin light chain 1 |
| 238977_at | MCM6 | -0.011494 | 6.14E-06 | 0.000133 | minichromosome maintenance complex component 6 |
| 200818_at | ATP5O | -0.006382 | 6.15E-06 | 0.000133 | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit |
| 201425_at | ALDH2 | 0.006104 | 6.22E-06 | 0.000135 | aldehyde dehydrogenase 2 family (mitochondrial) |
| 213932_x_at | HLA-A | 0.010991 | 7.87E-06 | 0.000163 | major histocompatibility complex, class I, A |
| 210081_at | AGER | 0.015055 | 9.51E-06 | 0.000191 | advanced glycosylation end product-specific receptor |
| 209316_s_at | HBS1L | -0.008165 | 9.64E-06 | 0.000193 | HBS1-like (S. cerevisiae) |
| 201708_s_at | NIPSNAP1 | -0.011737 | 1.09E-05 | 0.000213 | nipsnap homolog 1 (C. elegans) |

| | | | | | |
|---|---|---|---|---|---|
| 203306_s_at | SLC35A1 | 0.007064 | 1.15E-05 | 0.000223 | solute carrier family 35 (CMP-sialic acid transporter), member A1 |
| 224919_at | MRPS6 | -0.00767 | 1.17E-05 | 0.000225 | mitochondrial ribosomal protein S6 |
| 222750_s_at | SRD5A3 | -0.011133 | 1.22E-05 | 0.000233 | steroid 5 alpha-reductase 3 |
| 223066_at | SNAPIN | -0.008931 | 1.23E-05 | 0.000234 | SNAP-associated protein |
| 223233_s_at | CGN | 0.009922 | 1.25E-05 | 0.000238 | cingulin |
| 203023_at | NOP16 | -0.011542 | 1.29E-05 | 0.000244 | NOP16 nucleolar protein |
| 1555814_a_at | RHOA | -0.016511 | 1.42E-05 | 0.000261 | ras homolog family member A |
| 211935_at | ARL6IP1 | -0.008659 | 1.45E-05 | 0.000266 | ADP-ribosylation factor-like 6 interacting protein 1 |
| 216005_at | TNC | 0.010384 | 1.60E-05 | 0.000288 | tenascin C |
| 213414_s_at | RPS19 | -0.004828 | 1.64E-05 | 0.000294 | ribosomal protein S19 |
| 232617_at | CTSS | 0.014528 | 1.69E-05 | 0.000302 | cathepsin S |
| 209312_x_at | HLA-DRB1 | 0.022929 | 1.93E-05 | 0.000335 | |
| 209312_x_at | HLA-DRB5 | 0.022929 | 1.93E-05 | 0.000335 | |
| 223244_s_at | NDUFA12 | -0.005283 | 2.05E-05 | 0.000352 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12 |
| 225007_at | G3BP1 | -0.006534 | 2.08E-05 | 0.000355 | GTPase activating protein (SH3 domain) binding protein 1 |
| 206805_at | SEMA3A | -0.01091 | 2.11E-05 | 0.00036 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A |
| 220219_s_at | LRRC37A4 | -0.009125 | 2.34E-05 | 0.000391 | |
| 220219_s_at | LRRC37A | -0.009125 | 2.34E-05 | 0.000391 | |
| 208306_x_at | HLA-DRB1 | 0.012052 | 2.37E-05 | 0.000394 | |
| 202649_x_at | RPS19 | -0.00408 | 2.50E-05 | 0.000412 | ribosomal protein S19 |
| 221246_x_at | TNS1 | 0.006511 | 2.54E-05 | 0.000416 | tensin 1 |
| 223116_at | BCAR1 | 0.00642 | 2.63E-05 | 0.000428 | breast cancer anti-estrogen resistance 1 |
| 204460_s_at | RAD1 | -0.009673 | 2.70E-05 | 0.000436 | RAD1 homolog (S. pombe) |
| 205453_at | HOXB2 | -0.009306 | 2.81E-05 | 0.00045 | homeobox B2 |
| 223325_at | TXNDC11 | 0.007009 | 2.96E-05 | 0.000469 | thioredoxin domain containing 11 |
| 201514_s_at | G3BP1 | -0.009372 | 2.98E-05 | 0.000472 | GTPase activating protein (SH3 domain) binding protein 1 |
| 211911_x_at | HLA-B | 0.014517 | 3.01E-05 | 0.000475 | major histocompatibility complex, class I, B |
| 234977_at | ZADH2 | -0.009075 | 3.22E-05 | 0.000502 | zinc binding alcohol dehydrogenase domain containing 2 |
| 204982_at | GIT2 | 0.012336 | 3.52E-05 | 0.000537 | G protein-coupled receptor kinase interacting ArfGAP 2 |
| 214011_s_at | NOP16 | -0.009273 | 3.52E-05 | 0.000537 | NOP16 nucleolar protein |
| 227977_at | ZADH2 | -0.0071 | 3.66E-05 | 0.000555 | zinc binding alcohol dehydrogenase domain containing 2 |
| 219434_at | TREM1 | 0.006023 | 3.68E-05 | 0.000557 | triggering receptor expressed on myeloid cells 1 |
| 221875_x_at | HLA-F | 0.012392 | 3.76E-05 | 0.000566 | major histocompatibility complex, class I, F |
| 219304_s_at | PDGFD | 0.01116 | 3.86E-05 | 0.000579 | platelet derived growth factor D |
| 218911_at | YEATS4 | -0.013147 | 3.96E-05 | 0.000591 | YEATS domain containing 4 |
| 211799_x_at | HLA-C | 0.012352 | 3.96E-05 | 0.000591 | major histocompatibility complex, class I, C |
| 220017_x_at | CYP2C9 | 0.007304 | 4.19E-05 | 0.000619 | cytochrome P450, family 2, subfamily C, polypeptide 9 |

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|---|---|---|---|---|---|
| 200024_at | RPS5 | -0.007298 | 4.21E-05 | 0.000621 | ribosomal protein S5 |
| 201064_s_at | PABPC4 | -0.005815 | 4.58E-05 | 0.000663 | poly(A) binding protein, cytoplasmic 4 (inducible form) |
| 235562_at | C3orf70 | -0.01161 | 4.68E-05 | 0.000675 | chromosome 3 open reading frame 70 |
| 228030_at | RBM6 | 0.013317 | 5.10E-05 | 0.000723 | RNA binding motif protein 6 |
| 203705_s_at | FZD7 | -0.008033 | 5.14E-05 | 0.000728 | frizzled family receptor 7 |
| 242447_at | C3orf70 | -0.015337 | 5.22E-05 | 0.000736 | chromosome 3 open reading frame 70 |
| 201152_s_at | MBNL1 | 0.005758 | 5.68E-05 | 0.000787 | muscleblind-like splicing regulator 1 |
| 204806_x_at | HLA-F | 0.011406 | 6.67E-05 | 0.000889 | major histocompatibility complex, class I, F |
| 216025_x_at | CYP2C9 | 0.007504 | 6.76E-05 | 0.000899 | cytochrome P450, family 2, subfamily C, polypeptide 9 |
| 200059_s_at | RHOA | -0.008264 | 7.02E-05 | 0.000925 | ras homolog family member A |
| 219860_at | LY6G5C | 0.006324 | 7.13E-05 | 0.000937 | lymphocyte antigen 6 complex, locus G5C |
| 215785_s_at | CYFIP2 | 0.008934 | 7.18E-05 | 0.000942 | cytoplasmic FMR1 interacting protein 2 |
| 222824_at | NUDT5 | -0.01371 | 7.34E-05 | 0.000958 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 |
| 204740_at | CNKSR1 | 0.007296 | 8.28E-05 | 0.00105 | connector enhancer of kinase suppressor of Ras 1 |
| 244849_at | SEMA3A | -0.007624 | 8.55E-05 | 0.001073 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A |
| 205671_s_at | HLA-DOB | 0.005683 | 9.03E-05 | 0.001121 | major histocompatibility complex, class II, DO beta |
| 210216_x_at | RAD1 | -0.007564 | 9.18E-05 | 0.001136 | RAD1 homolog (S. pombe) |
| 218864_at | TNS1 | 0.013539 | 9.70E-05 | 0.001185 | tensin 1 |
| 209329_x_at | HIGD2A | -0.006677 | 0.000103 | 0.00124 | HIG1 hypoxia inducible domain family, member 2A |
| 207823_s_at | AIF1 | 0.007108 | 0.000103 | 0.001242 | allograft inflammatory factor 1 |
| 206117_at | TPM1 | -0.008402 | 0.000105 | 0.001257 | tropomyosin 1 (alpha) |
| 216299_s_at | XRCC3 | -0.005846 | 0.00011 | 0.001307 | X-ray repair complementing defective repair in Chinese hamster cells 3 |
| 228851_s_at | ENSA | -0.015066 | 0.00011 | 0.001312 | endosulfine alpha |
| 213252_at | SH3PXD2A | 0.010466 | 0.00011 | 0.001312 | SH3 and PX domains 2A |
| 214552_s_at | RABEP1 | -0.011557 | 0.00012 | 0.001396 | rabaptin, RAB GTPase binding effector protein 1 |
| 201081_s_at | PIP4K2B | -0.008697 | 0.00012 | 0.001402 | phosphatidylinositol-5-phosphate 4-kinase, type II, beta |
| 216954_x_at | ATP5O | -0.004178 | 0.000124 | 0.001435 | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit |
| 209478_at | STRA13 | -0.00599 | 0.000137 | 0.001555 | stimulated by retinoic acid 13 |
| 205247_at | NOTCH4 | 0.007708 | 0.000139 | 0.001577 | notch 4 |
| 205447_s_at | MAP3K12 | 0.006617 | 0.00014 | 0.001578 | mitogen-activated protein kinase kinase kinase 12 |
| 208729_x_at | HLA-B | 0.01303 | 0.000148 | 0.001649 | major histocompatibility complex, class I, B |
| 201331_s_at | STAT6 | 0.007193 | 0.000164 | 0.001795 | signal transducer and activator of transcription 6, interleukin-4 induced |
| 223274_at | TCF19 | -0.011072 | 0.000181 | 0.001941 | transcription factor 19 |
| 218827_s_at | CEP192 | -0.010408 | 0.00019 | 0.002013 | centrosomal protein 192kDa |
| 212787_at | YLPM1 | -0.007914 | 0.000193 | 0.002039 | YLP motif containing 1 |
| 218361_at | GOLPH3L | 0.006956 | 0.000209 | 0.002172 | golgi phosphoprotein 3-like |
| 239012_at | RNF144B | 0.009385 | 0.000217 | 0.002241 | ring finger protein 144B |

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|---|---|---|---|---|---|
| 226270_at | EXOC2 | -0.005588 | 0.00022 | 0.002264 | exocyst complex component 2 |
| 211990_at | HLA-DPA1 | 0.024811 | 0.000226 | 0.002307 | major histocompatibility complex, class II, DP alpha 1 |
| 223868_s_at | WWOX | -0.008257 | 0.000237 | 0.002402 | WW domain containing oxidoreductase |
| 211431_s_at | TYRO3 | -0.006252 | 0.000238 | 0.002406 | TYRO3 protein tyrosine kinase |
| 228706_s_at | CLDN23 | 0.007283 | 0.00024 | 0.002427 | claudin 23 |
| 209791_at | PADI2 | 0.010887 | 0.000254 | 0.002536 | peptidyl arginine deiminase, type II |
| 225064_at | RABEP1 | -0.009833 | 0.000261 | 0.002589 | rabaptin, RAB GTPase binding effector protein 1 |
| 211529_x_at | HLA-G | 0.009531 | 0.000264 | 0.002613 | major histocompatibility complex, class I, G |
| 227049_at | ZADH2 | -0.007044 | 0.000268 | 0.002645 | zinc binding alcohol dehydrogenase domain containing 2 |
| 215313_x_at | HLA-A | 0.011332 | 0.000274 | 0.002692 | major histocompatibility complex, class I, A |
| 203136_at | RABAC1 | -0.009644 | 0.000281 | 0.002748 | Rab acceptor 1 (prenylated) |
| 205874_at | ITPKA | -0.004534 | 0.000292 | 0.002826 | inositol-trisphosphate 3-kinase A |
| 222997_s_at | MRPS21 | -0.007528 | 0.000305 | 0.002925 | mitochondrial ribosomal protein S21 |
| 211084_x_at | PRKD3 | -0.006073 | 0.000305 | 0.002925 | protein kinase D3 |
| 222798_at | PTER | 0.008522 | 0.000327 | 0.003099 | phosphotriesterase related |
| 202596_at | ENSA | -0.007189 | 0.000335 | 0.003157 | endosulfine alpha |
| 224437_s_at | VTA1 | -0.008584 | 0.000344 | 0.003224 | Vps20-associated 1 homolog (S. cerevisiae) |
| 225398_at | RPUSD4 | -0.005924 | 0.000357 | 0.003315 | RNA pseudouridylate synthase domain containing 4 |
| 205299_s_at | BTN2A2 | 0.005489 | 0.000358 | 0.003319 | butyrophilin, subfamily 2, member A2 |
| 228148_at | ZNF584 | -0.00641 | 0.000375 | 0.003433 | zinc finger protein 584 |
| 225916_at | ZNF131 | -0.008073 | 0.000383 | 0.003482 | uncharacterized LOC100506639 /// zinc finger protein 131 |
| 237466_s_at | HHIP | 0.011955 | 0.000387 | 0.003508 | hedgehog interacting protein |
| 218677_at | S100A14 | 0.014248 | 0.000407 | 0.003653 | S100 calcium binding protein A14 |
| 205891_at | ADORA2B | 0.011987 | 0.000413 | 0.003693 | adenosine A2b receptor |
| 1554239_s_at | ZADH2 | -0.004573 | 0.000426 | 0.003779 | zinc binding alcohol dehydrogenase domain containing 2 |
| 225903_at | PIGU | -0.006147 | 0.000443 | 0.003906 | phosphatidylinositol glycan anchor biosynthesis, class U |
| 219095_at | JMJD7-PLA2G4B | 0.006064 | 0.000469 | 0.004073 | |
| 201645_at | TNC | 0.008993 | 0.000492 | 0.004229 | tenascin C |
| 223021_x_at | VTA1 | -0.01085 | 0.000497 | 0.004263 | Vps20-associated 1 homolog (S. cerevisiae) |
| 206007_at | PRG4 | 0.005306 | 0.000513 | 0.004373 | proteoglycan 4 |
| 211654_x_at | HLA-DQB1 | 0.009481 | 0.000516 | 0.004397 | major histocompatibility complex, class II, DQ beta 1 |
| 201705_at | PSMD7 | -0.006466 | 0.000528 | 0.004476 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 7 |
| 223022_s_at | VTA1 | -0.005003 | 0.000528 | 0.004476 | Vps20-associated 1 homolog (S. cerevisiae) |
| 233724_at | ARNT | 0.009216 | 0.000544 | 0.004578 | aryl hydrocarbon receptor nuclear translocator |
| 1007_s_at | DDR1 | 0.006749 | 0.000551 | 0.004625 | discoidin domain receptor tyrosine kinase 1 /// microRNA 4640 |
| 210986_s_at | TPM1 | -0.006644 | 0.000555 | 0.004649 | tropomyosin 1 (alpha) |
| 230296_at | C16orf5 | 0.004906 | 0.000568 | 0.004735 | chromosome 16 open reading frame 52 /// uncharacterized LOC101060634 |

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|---|---|---|---|---|---|
| 225618_at | ARHGAP27 | 0.005121 | 0.000574 | 0.004774 | Rho GTPase activating protein 27 |
| 1559050_at | HCG27 | 0.004367 | 0.000599 | 0.004926 | HLA complex group 27 (non-protein coding) /// uncharacterized LOC100996357 |
| 1566722_a_at | SVEP1 | -0.003794 | 0.000609 | 0.004992 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |
| 221898_at | PDPN | 0.01019 | 0.000618 | 0.005045 | podoplanin |
| 211528_x_at | HLA-G | 0.008192 | 0.000623 | 0.005075 | major histocompatibility complex, class I, G |
| 205682_x_at | APOM | -0.00522 | 0.000646 | 0.005216 | apolipoprotein M |
| 232262_at | PIGL | 0.006448 | 0.000694 | 0.005527 | phosphatidylinositol glycan anchor biosynthesis, class L |
| 206417_at | CNGA1 | 0.004999 | 0.000733 | 0.005769 | cyclic nucleotide gated channel alpha 1 |
| 215193_x_at | HLA-DRB3 | 0.016142 | 0.000745 | 0.005843 | |
| 215193_x_at | HLA-DRB1 | 0.016142 | 0.000745 | 0.005843 | |
| 202901_x_at | CTSS | 0.009749 | 0.000753 | 0.005898 | cathepsin S |
| 205222_at | EHHADH | -0.007597 | 0.000763 | 0.005956 | enoyl-CoA, hydratase/3-hydroxyacyl CoA dehydrogenase |
| 229103_at | WNT3 | -0.006992 | 0.000807 | 0.006218 | wingless-type MMTV integration site family, member 3 |
| 230619_at | ARNT | 0.012049 | 0.000825 | 0.006318 | aryl hydrocarbon receptor nuclear translocator |
| 201045_s_at | RAB6A | -0.007067 | 0.000855 | 0.006493 | RAB6A, member RAS oncogene family |
| 1555136_at | FGD6 | -0.004583 | 0.000887 | 0.00668 | FYVE, RhoGEF and PH domain containing 6 |
| 221856_s_at | FAM63A | 0.00672 | 0.000907 | 0.006785 | family with sequence similarity 63, member A |
| 218236_s_at | PRKD3 | -0.007154 | 0.000924 | 0.006886 | protein kinase D3 |
| 36612_at | FAM168A | -0.006499 | 0.000934 | 0.006943 | family with sequence similarity 168, member A |
| 236231_at | ZNF271 | -0.006467 | 0.000946 | 0.007005 | zinc finger protein 271 |
| 226878_at | HLA-DOA | 0.0058 | 0.000961 | 0.007083 | major histocompatibility complex, class II, DO alpha |
| 214910_s_at | APOM | -0.00505 | 0.00102 | 0.007422 | apolipoprotein M |
| 210200_at | WWP2 | 0.004834 | 0.001068 | 0.00768 | WW domain containing E3 ubiquitin protein ligase 2 |
| 212553_at | RPRD2 | 0.006574 | 0.00112 | 0.007936 | regulation of nuclear pre-mRNA domain containing 2 |
| 242297_at | RREB1 | 0.009184 | 0.001135 | 0.008021 | ras responsive element binding protein 1 |
| 223675_s_at | VEZT | -0.00528 | 0.001147 | 0.008084 | vezatin, adherens junctions transmembrane protein |
| 209765_at | ADAM19 | 0.005527 | 0.001152 | 0.008109 | ADAM metallopeptidase domain 19 |
| 203568_s_at | TRIM38 | 0.00482 | 0.001155 | 0.008121 | tripartite motif containing 38 |
| 227968_at | PDDC1 | -0.005655 | 0.00124 | 0.008579 | Parkinson disease 7 domain containing 1 |
| 221503_s_at | KPNA3 | -0.008792 | 0.001241 | 0.008583 | karyopherin alpha 3 (importin alpha 4) |
| 203706_s_at | FZD7 | -0.004963 | 0.001328 | 0.009049 | frizzled family receptor 7 |
| 239538_at | ZRANB3 | -0.007721 | 0.001356 | 0.009195 | zinc finger, RAN-binding domain containing 3 |
| 212613_at | BTN3A2 | 0.010795 | 0.001404 | 0.009466 | butyrophilin, subfamily 3, member A2 |
| 201965_s_at | SETX | -0.005674 | 0.001499 | 0.009949 | senataxin |
| 203223_at | RABEP1 | -0.00918 | 0.001536 | 0.010121 | rabaptin, RAB GTPase binding effector protein 1 |
| 209315_at | HBS1L | -0.004573 | 0.001565 | 0.010283 | HBS1-like (S. cerevisiae) |

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|---|---|---|---|---|---|
| 201153_s_at | MBNL1 | 0.003776 | 0.001616 | 0.010528 | muscleblind-like splicing regulator 1 |
| 1569061_at | IQGAP3 | -0.002617 | 0.001626 | 0.010576 | IQ motif containing GTPase activating protein 3 |
| 211991_s_at | HLA-DPA1 | 0.014811 | 0.001635 | 0.01062 | major histocompatibility complex, class II, DP alpha 1 |
| 1562939_at | LRRC16A | 0.007314 | 0.001636 | 0.010628 | leucine rich repeat containing 16A |
| 232296_s_at | GFM1 | -0.007516 | 0.001706 | 0.010973 | G elongation factor, mitochondrial 1 |
| 222441_x_at | SLMO2 | -0.007966 | 0.001742 | 0.011155 | slowmo homolog 2 (Drosophila) |
| 219349_s_at | EXOC2 | -0.008476 | 0.001754 | 0.011219 | exocyst complex component 2 |
| 225379_at | MAPT | 0.004651 | 0.001785 | 0.011374 | microtubule-associated protein tau |
| 208522_s_at | PTCH1 | -0.005371 | 0.001796 | 0.01142 | patched 1 |
| 235549_at | RNF144B | 0.003573 | 0.001817 | 0.011528 | ring finger protein 144B |
| 222835_at | THSD4 | -0.007446 | 0.001862 | 0.01175 | thrombospondin, type I, domain containing 4 |
| 236808_at | FGFR1OP2 | 0.014074 | 0.00191 | 0.011976 | FGFR1 oncogene partner 2 |
| 1555594_a_at | MBNL1 | -0.009777 | 0.001984 | 0.012315 | muscleblind-like splicing regulator 1 |
| 205298_s_at | BTN2A2 | 0.005476 | 0.002032 | 0.012555 | butyrophilin, subfamily 2, member A2 |
| 211009_s_at | ZNF271 | -0.008834 | 0.002043 | 0.012599 | zinc finger protein 271 |
| 1553243_at | ITIH5 | 0.008437 | 0.002055 | 0.01265 | inter-alpha-trypsin inhibitor heavy chain family, member 5 |
| 217851_s_at | SLMO2 | -0.007368 | 0.002081 | 0.012761 | slowmo homolog 2 (Drosophila) |
| 219064_at | ITIH5 | 0.00953 | 0.002094 | 0.012822 | inter-alpha-trypsin inhibitor heavy chain family, member 5 |
| 231371_at | TDRD10 | 0.00473 | 0.002115 | 0.012913 | tudor domain containing 10 |
| 212202_s_at | TMEM87A | 0.006788 | 0.002125 | 0.012961 | transmembrane protein 87A |
| 231929_at | IKZF2 | 0.007728 | 0.002139 | 0.013029 | IKAROS family zinc finger 2 (Helios) |
| 235839_at | C22orf34 | -0.006772 | 0.002152 | 0.013088 | chromosome 22 open reading frame 34 |
| 210987_x_at | TPM1 | -0.00657 | 0.002265 | 0.013604 | tropomyosin 1 (alpha) |
| 233117_at | MAPT | 0.002943 | 0.002266 | 0.013609 | microtubule-associated protein tau |
| 223703_at | C10orf11 | 0.008054 | 0.00227 | 0.013626 | chromosome 10 open reading frame 11 |
| 222860_s_at | PDGFD | 0.005597 | 0.00229 | 0.013712 | platelet derived growth factor D |
| 221125_s_at | KCNMB3 | 0.004863 | 0.002299 | 0.013757 | potassium large conductance calcium-activated channel, subfamily M beta member 3 |
| 204783_at | MLF1 | 0.009984 | 0.002396 | 0.014209 | myeloid leukemia factor 1 |
| 215032_at | RREB1 | 0.009146 | 0.002447 | 0.014442 | ras responsive element binding protein 1 |
| 213656_s_at | KLC1 | 0.004931 | 0.002505 | 0.014708 | kinesin light chain 1 |
| 214421_x_at | CYP2C9 | 0.005921 | 0.00254 | 0.014876 | cytochrome P450, family 2, subfamily C, polypeptide 9 |
| 207169_x_at | DDR1 | 0.007798 | 0.002634 | 0.015281 | discoidin domain receptor tyrosine kinase 1 /// microRNA 4640 |
| 213537_at | HLA-DPA1 | 0.004386 | 0.002648 | 0.01535 | major histocompatibility complex, class II, DP alpha 1 |
| 211530_x_at | HLA-G | 0.006732 | 0.00277 | 0.015866 | major histocompatibility complex, class I, G |
| 213851_at | TMEM110 | -0.006996 | 0.002801 | 0.016005 | transmembrane protein 110 |
| 209472_at | CCBL2 | -0.006813 | 0.00289 | 0.0164 | cysteine conjugate-beta lyase 2 |
| 209816_at | PTCH1 | -0.010953 | 0.003077 | 0.017182 | patched 1 |

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|---|---|---|---|---|---|
| 228747_at | SEC61A2 | -0.003538 | 0.003186 | 0.017654 | Sec61 alpha 2 subunit (S. cerevisiae) |
| 229983_at | TIGD2 | -0.008178 | 0.003249 | 0.017926 | tigger transposable element derived 2 |
| 238076_at | GATAD2B | -0.009359 | 0.003277 | 0.018039 | GATA zinc finger domain containing 2B |
| 223524_s_at | TMEM108 | 0.00581 | 0.003559 | 0.019191 | transmembrane protein 108 |
| 225892_at | IREB2 | -0.006456 | 0.003567 | 0.019223 | iron-responsive element binding protein 2 |
| 1562516_at | WDR60 | 0.012704 | 0.003684 | 0.019688 | WD repeat domain 60 |
| 244163_at | SEMA3A | -0.007105 | 0.003753 | 0.019961 | sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A |
| 209480_at | HLA-DQB1 | 0.008919 | 0.003827 | 0.020276 | major histocompatibility complex, class II, DQ beta 1 |
| 215814_at | DST | 0.00355 | 0.00383 | 0.020278 | dystonin |
| 223012_at | UBXN6 | 0.004907 | 0.003923 | 0.020657 | microRNA 4746 /// UBX domain protein 6 |
| 225459_at | AMOTL1 | -0.007033 | 0.00404 | 0.021137 | angiomotin like 1 |
| 229538_s_at | IQGAP3 | -0.011687 | 0.00405 | 0.021168 | IQ motif containing GTPase activating protein 3 |
| 242618_at | HCG18 | -0.008072 | 0.004093 | 0.021338 | HLA complex group 18 (non-protein coding) |
| 217563_at | CLOCK | 0.003841 | 0.004099 | 0.021361 | clock circadian regulator |
| 222623_s_at | ZNF639 | -0.004248 | 0.004115 | 0.021431 | zinc finger protein 639 |
| 238453_at | FGFBP3 | -0.006837 | 0.004168 | 0.021645 | fibroblast growth factor binding protein 3 |
| 217190_x_at | ESR1 | -0.004576 | 0.004241 | 0.021942 | estrogen receptor 1 |
| 244056_at | SFTA2 | 0.013793 | 0.004288 | 0.022122 | surfactant associated 2 |
| 213551_x_at | PCGF2 | 0.003384 | 0.004493 | 0.022894 | polycomb group ring finger 2 |
| 1557267_s_at | GEN1 | -0.00861 | 0.00452 | 0.023004 | GEN1 Holliday junction 5' flap endonuclease |
| 200929_at | TMED10 | -0.006826 | 0.004554 | 0.023127 | transmembrane emp24-like trafficking protein 10 (yeast) |
| 60528_at | JMJD7-PLA2G4B | 0.00573 | 0.004655 | 0.023533 | |
| 225158_at | GFM1 | -0.007784 | 0.004758 | 0.023941 | G elongation factor, mitochondrial 1 |
| 228905_at | PCM1 | -0.007757 | 0.004826 | 0.024195 | pericentriolar material 1 |
| 215669_at | HLA-DRB4 | 0.003911 | 0.004868 | 0.024361 | major histocompatibility complex, class II, DR beta 4 |
| 206247_at | MICB | 0.0115 | 0.004881 | 0.024407 | MHC class I polypeptide-related sequence B |
| 238007_at | ZNF271 | -0.00839 | 0.004909 | 0.024501 | zinc finger protein 271 |
| 217046_s_at | AGER | 0.006586 | 0.005074 | 0.025147 | advanced glycosylation end product-specific receptor |
| 227116_at | MON1B | -0.007683 | 0.005093 | 0.025214 | MON1 homolog B (yeast) |
| 237844_at | ZNF131 | 0.003858 | 0.00522 | 0.025674 | uncharacterized LOC100506639 /// zinc finger protein 131 |
| 1553389_at | NPHP3 | 0.007109 | 0.005269 | 0.02587 | nephronophthisis 3 (adolescent) |
| 201964_at | SETX | -0.004718 | 0.005381 | 0.026267 | senataxin |
| 212366_at | ZNF292 | 0.007912 | 0.005583 | 0.02699 | zinc finger protein 292 |
| 241939_at | IQGAP3 | 0.004543 | 0.005705 | 0.027401 | IQ motif containing GTPase activating protein 3 |
| 219280_at | BRWD1 | 0.00509 | 0.005844 | 0.02789 | bromodomain and WD repeat domain containing 1 |
| 203793_x_at | PCGF2 | 0.003896 | 0.005896 | 0.028082 | polycomb group ring finger 2 |

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|---|---|---|---|---|---|
| 213819_s_at | FLOT1 | 0.003805 | 0.006082 | 0.028734 | flotillin 1 |
| 226799_at | FGD6 | -0.007879 | 0.006237 | 0.029308 | FYVE, RhoGEF and PH domain containing 6 |
| 210142_x_at | FLOT1 | 0.005311 | 0.006279 | 0.029473 | flotillin 1 |
| 225725_at | ZMAT3 | -0.006752 | 0.006316 | 0.029594 | zinc finger, matrin-type 3 |
| 214525_x_at | MLH3 | 0.004996 | 0.006329 | 0.029652 | mutL homolog 3 (E. coli) |
| 227634_at | STK32C | -0.004851 | 0.006496 | 0.030209 | serine/threonine kinase 32C |
| 208697_s_at | EIF3E | -0.003238 | 0.006629 | 0.030679 | eukaryotic translation initiation factor 3, subunit E |
| 209846_s_at | BTN3A2 | 0.011753 | 0.006837 | 0.031383 | butyrophilin, subfamily 3, member A2 |
| 228704_s_at | CLDN23 | 0.002451 | 0.007064 | 0.03219 | claudin 23 |
| 221747_at | TNS1 | 0.006149 | 0.007145 | 0.032437 | tensin 1 |
| 243444_at | SRD5A3 | -0.004907 | 0.007187 | 0.03257 | steroid 5 alpha-reductase 3 |
| 219214_s_at | NT5C | -0.00452 | 0.007245 | 0.032776 | 5', 3'-nucleotidase, cytosolic |
| 223771_at | TMEM87A | 0.00514 | 0.007309 | 0.032946 | transmembrane protein 87A |
| 201866_s_at | NR3C1 | 0.004575 | 0.007364 | 0.033135 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) |
| 202197_at | MTMR3 | 0.004521 | 0.007494 | 0.033554 | myotubularin related protein 3 |
| 218413_s_at | ZNF639 | -0.003082 | 0.007542 | 0.03371 | zinc finger protein 639 |
| 215434_x_at | NBPF1 | -0.00703 | 0.007759 | 0.034385 | neuroblastoma breakpoint family, member 1 |
| 203792_x_at | PCGF2 | 0.006122 | 0.007779 | 0.034464 | polycomb group ring finger 2 |
| 224521_s_at | CCDC77 | -0.00737 | 0.007966 | 0.035092 | coiled-coil domain containing 77 |
| 216008_s_at | ARIH2 | -0.004162 | 0.008263 | 0.036082 | ariadne homolog 2 (Drosophila) |
| 214666_x_at | IREB2 | -0.007905 | 0.008474 | 0.036772 | iron-responsive element binding protein 2 |
| 230027_s_at | MRPL43 | -0.006271 | 0.008848 | 0.037989 | mitochondrial ribosomal protein L43 |
| 210330_at | SGCD | 0.002775 | 0.008849 | 0.037989 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 218722_s_at | CCDC51 | -0.005141 | 0.008933 | 0.038273 | coiled-coil domain containing 51 |
| 210749_x_at | DDR1 | 0.007368 | 0.009092 | 0.038768 | discoidin domain receptor tyrosine kinase 1 /// microRNA 4640 |
| 242422_at | G3BP1 | -0.00816 | 0.009164 | 0.039028 | GTPase activating protein (SH3 domain) binding protein 1 |
| 217550_at | ATF6 | 0.00567 | 0.00926 | 0.039325 | activating transcription factor 6 |
| 231860_at | BRWD1 | 0.01159 | 0.009271 | 0.039362 | bromodomain and WD repeat domain containing 1 |
| 224058_s_at | HSD17B7P2 | 0.004951 | 0.009294 | 0.039437 | hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2 |
| 204022_at | WWP2 | -0.003887 | 0.009413 | 0.039806 | WW domain containing E3 ubiquitin protein ligase 2 |
| 232598_at | NUP210L | 0.002473 | 0.009797 | 0.040981 | nucleoporin 210kDa-like |
| 235626_at | CAMK1D | -0.005598 | 0.009839 | 0.041121 | calcium/calmodulin-dependent protein kinase ID |
| 208209_s_at | C4BPB | -0.00328 | 0.009922 | 0.041409 | complement component 4 binding protein, beta |
| 235415_at | RPRD2 | 0.003579 | 0.010131 | 0.04203 | regulation of nuclear pre-mRNA domain containing 2 |
| 218014_at | NUP85 | -0.005692 | 0.01021 | 0.042264 | nucleoporin 85kDa |
| 203567_s_at | TRIM38 | 0.004963 | 0.010269 | 0.042454 | tripartite motif containing 38 |
| 1559584_a_at | C16orf5 | 0.005676 | 0.01028 | 0.04249 | chromosome 16 open reading frame 54 |

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|---|---|---|---|---|---|
| 212878_s_at | KLC1 | -0.004669 | 0.010391 | 0.042856 | kinesin light chain 1 |
| 225161_at | GFM1 | -0.006246 | 0.010568 | 0.043434 | G elongation factor, mitochondrial 1 |
| 217973_at | DCXR | -0.005194 | 0.010881 | 0.044389 | dicarbonyl/L-xylulose reductase |
| 204294_at | AMT | 0.004768 | 0.010984 | 0.044692 | aminomethyltransferase |
| 219816_s_at | RBM23 | -0.005157 | 0.011034 | 0.044849 | RNA binding motif protein 23 |
| 216200_at | PLEKHM1 | 0.003888 | 0.011909 | 0.047498 | pleckstrin homology domain containing, family M (with RUN domain) member 1 |
| 213394_at | MAPKBP1 | 0.003486 | 0.01194 | 0.047592 | mitogen-activated protein kinase binding protein 1 |
| 1560715_at | P4HA3 | 0.002786 | 0.012075 | 0.047967 | prolyl 4-hydroxylase, alpha polypeptide III |
| 240111_at | RHOBTB3 | 0.005419 | 0.012094 | 0.048024 | Rho-related BTB domain containing 3 |
| 203480_s_at | OTUD4 | 0.003731 | 0.012558 | 0.04932 | OTU domain containing 4 |
| 217887_s_at | EPS15 | -0.00537 | 0.012692 | 0.049734 | epidermal growth factor receptor pathway substrate 15 |
| 221491_x_at | HLA-DRB1 | 0.005079 | 0.012815 | 0.050088 | |
| 221491_x_at | HLA-DRB5 | 0.005079 | 0.012815 | 0.050088 | |
| 221491_x_at | HLA-DRB3 | 0.005079 | 0.012815 | 0.050088 | |
| 218405_at | ABT1 | -0.005104 | 0.0131 | 0.050956 | activator of basal transcription 1 |
| 1554113_a_at | SLC4A8 | 0.004469 | 0.0134 | 0.051875 | solute carrier family 4, sodium bicarbonate cotransporter, member 8 |
| 219956_at | GALNT6 | -0.003137 | 0.013555 | 0.052312 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) |
| 212368_at | ZNF292 | 0.007377 | 0.0136 | 0.052447 | zinc finger protein 292 |
| 1558111_at | MBNL1 | 0.009869 | 0.013869 | 0.053296 | muscleblind-like splicing regulator 1 |
| 226198_at | TOM1L2 | 0.00541 | 0.014463 | 0.05499 | target of myb1-like 2 (chicken) |
| 218917_s_at | ARID1A | -0.003522 | 0.014565 | 0.055252 | AT rich interactive domain 1A (SWI-like) |
| 224543_at | SVEP1 | -0.004738 | 0.014601 | 0.055368 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |
| 214930_at | SLITRK5 | -0.009264 | 0.014661 | 0.055546 | SLIT and NTRK-like family, member 5 |
| 225321_s_at | PILRB | 0.007357 | 0.014856 | 0.056081 | paired immunoglobin-like type 2 receptor beta |
| 219499_at | SEC61A2 | -0.003403 | 0.015175 | 0.056977 | Sec61 alpha 2 subunit (S. cerevisiae) |
| 214638_s_at | CCNT2 | -0.005342 | 0.015375 | 0.057529 | cyclin T2 |
| 207661_s_at | SH3PXD2A | 0.006971 | 0.015618 | 0.058191 | SH3 and PX domains 2A |
| 229467_at | PCBP2 | 0.007739 | 0.015733 | 0.058476 | poly(rC) binding protein 2 |
| 1554050_at | SMPDL3B | 0.004465 | 0.015828 | 0.05874 | sphingomyelin phosphodiesterase, acid-like 3B |
| 224817_at | SH3PXD2A | 0.003452 | 0.015863 | 0.058819 | SH3 and PX domains 2A |
| 232914_s_at | SYTL2 | 0.005023 | 0.016048 | 0.059321 | synaptotagmin-like 2 |
| 213532_at | ADAM17 | 0.00412 | 0.016325 | 0.06004 | ADAM metallopeptidase domain 17 |
| 235239_at | QSOX2 | -0.003451 | 0.016355 | 0.06011 | quiescin Q6 sulfhydryl oxidase 2 |
| 208749_x_at | FLOT1 | 0.004587 | 0.017339 | 0.062878 | flotillin 1 |
| 228954_at | LYSMD4 | -0.004842 | 0.017531 | 0.063399 | LysM, putative peptidoglycan-binding, domain containing 4 |
| 225208_s_at | FAM103A1 | -0.003243 | 0.01772 | 0.063892 | family with sequence similarity 103, member A1 |

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|---|---|---|---|---|---|
| 232098_at | DST | 0.008602 | 0.018184 | 0.06511 | dystonin |
| 239768_x_at | GPATCH2 | -0.004892 | 0.018253 | 0.065318 | G patch domain containing 2 |
| 1570032_at | AP3B2 | 0.003531 | 0.018281 | 0.065404 | adaptor-related protein complex 3, beta 2 subunit |
| 220220_at | LRRC37A4 | -0.007345 | 0.018412 | 0.065751 | leucine rich repeat containing 37, member A4, pseudogene |
| 220220_at | LRRC37A | -0.007345 | 0.018412 | 0.065751 | leucine rich repeat containing 37, member A4, pseudogene |
| 232975_at | HCG18 | -0.004568 | 0.018582 | 0.066222 | HLA complex group 18 (non-protein coding) |
| 202308_at | SREBF1 | 0.005109 | 0.018883 | 0.067044 | sterol regulatory element binding transcription factor 1 |
| 221502_at | KPNA3 | -0.003779 | 0.019013 | 0.067381 | karyopherin alpha 3 (importin alpha 4) |
| 229641_at | CCBE1 | -0.00462 | 0.019394 | 0.0684 | collagen and calcium binding EGF domains 1 |
| 226819_at | LSM11 | -0.003178 | 0.019486 | 0.068616 | LSM11, U7 small nuclear RNA associated |
| 226650_at | ZFAND2A | 0.005519 | 0.019484 | 0.068616 | zinc finger, AN1-type domain 2A |
| 223090_x_at | VEZT | -0.003701 | 0.019682 | 0.069127 | vezatin, adherens junctions transmembrane protein |
| 226394_at | 5-Mar | -0.005946 | 0.020062 | 0.070135 | membrane-associated ring finger (C3HC4) 5 |
| 204778_x_at | HOXB7 | -0.004351 | 0.020766 | 0.071996 | homeobox B7 |
| 204778_x_at | HOXB7 | -0.004351 | 0.020766 | 0.071996 | NULL |
| 221486_at | ENSA | -0.003945 | 0.021185 | 0.073106 | endosulfine alpha |
| 1556285_s_at | PPA2 | -0.006873 | 0.02124 | 0.073278 | pyrophosphatase (inorganic) 2 |
| 227531_at | CLOCK | -0.003217 | 0.022008 | 0.075254 | clock circadian regulator |
| 202016_at | MEST | -0.003181 | 0.022096 | 0.075479 | mesoderm specific transcript |
| 222662_at | PPP1R3B | 0.005286 | 0.022574 | 0.07669 | protein phosphatase 1, regulatory subunit 3B |
| 236150_at | HYKK | 0.00299 | 0.023109 | 0.078089 | hydroxylysine kinase |
| 209349_at | RAD50 | -0.005146 | 0.023427 | 0.078861 | RAD50 homolog (S. cerevisiae) |
| 213865_at | DCBLD2 | 0.004718 | 0.023577 | 0.079201 | discoidin, CUB and LCCL domain containing 2 |
| 229120_s_at | CDC42SE1 | -0.006921 | 0.023678 | 0.079456 | CDC42 small effector 1 |
| 1556283_s_at | FGFR1OP2 | -0.004547 | 0.023958 | 0.080126 | FGFR1 oncogene partner 2 |
| 228303_at | GALNT6 | -0.003912 | 0.025049 | 0.082746 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) |
| 210578_at | TRIM10 | 0.002311 | 0.025266 | 0.083263 | tripartite motif containing 10 |
| 201189_s_at | ITPR3 | 0.004745 | 0.025523 | 0.083888 | inositol 1,4,5-trisphosphate receptor, type 3 |
| 1558300_at | EFCAB5 | 0.00292 | 0.025982 | 0.084951 | EF-hand calcium binding domain 5 |
| 1558658_at | ZNF391 | 0.002284 | 0.026001 | 0.084992 | zinc finger protein 391 |
| 210514_x_at | HLA-G | 0.005627 | 0.026245 | 0.085631 | major histocompatibility complex, class I, G |
| 215319_at | ATP8B3 | 0.003196 | 0.026624 | 0.08652 | ATPase, aminophospholipid transporter, class I, type 8B, member 3 |
| 1554499_s_at | PPA2 | -0.002964 | 0.026888 | 0.087085 | pyrophosphatase (inorganic) 2 |
| 204031_s_at | PCBP2 | -0.003045 | 0.027418 | 0.088388 | poly(rC) binding protein 2 |
| 1554580_a_at | WWP2 | 0.005026 | 0.028002 | 0.089831 | WW domain containing E3 ubiquitin protein ligase 2 |
| 229663_at | LONP2 | 0.003909 | 0.028045 | 0.089933 | lon peptidase 2, peroxisomal |
| 220741_s_at | PPA2 | -0.003849 | 0.028442 | 0.090882 | pyrophosphatase (inorganic) 2 |

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|---|---|---|---|---|---|
| 229660_at | C16orf5 | -0.004754 | 0.028457 | 0.090913 | chromosome 16 open reading frame 55 |
| 230811_at | C16orf5 | -0.006126 | 0.029934 | 0.094384 | chromosome 16 open reading frame 55 |
| 228703_at | P4HA3 | 0.002886 | 0.030121 | 0.094814 | prolyl 4-hydroxylase, alpha polypeptide III |
| 1565799_at | RAB3IP | 0.001569 | 0.030523 | 0.095823 | RAB3A interacting protein |
| 244396_at | G3BP1 | -0.006815 | 0.031056 | 0.097088 | GTPase activating protein (SH3 domain) binding protein 1 |
| 237169_at | TNC | 0.005642 | 0.03118 | 0.097375 | tenascin C |
| 203928_x_at | MAPT | 0.00302 | 0.031335 | 0.097749 | microtubule-associated protein tau |
| 218697_at | NCKIPSD | 0.005036 | 0.031406 | 0.097921 | NCK interacting protein with SH3 domain |
| 1553048_a_at | PIP4K2B | -0.005603 | 0.03151 | 0.098127 | phosphatidylinositol-5-phosphate 4-kinase, type II, beta |
| 215871_at | PLA2G5 | -0.002312 | 0.03166 | 0.098474 | phospholipase A2, group V |
| 232229_at | SETX | -0.004706 | 0.031672 | 0.098491 | senataxin |
| 232431_at | NR3C1 | 0.007839 | 0.03208 | 0.099472 | nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) |
| 217184_s_at | LTK | 0.003627 | 0.032753 | 0.101032 | leukocyte receptor tyrosine kinase |
| 208779_x_at | DDR1 | 0.005011 | 0.032779 | 0.101094 | discoidin domain receptor tyrosine kinase 1 /// microRNA 4640 |
| 214659_x_at | YLPM1 | -0.004968 | 0.033212 | 0.102036 | YLP motif containing 1 |
| 211106_at | SUPT3H | 0.005334 | 0.033235 | 0.102074 | suppressor of Ty 3 homolog (S. cerevisiae) |
| 230730_at | SGCD | -0.009009 | 0.033399 | 0.102437 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 219608_s_at | FBXO38 | -0.006691 | 0.033802 | 0.103349 | F-box protein 38 |
| 223967_at | ANGPTL6 | -0.005639 | 0.034309 | 0.10448 | angiopoietin-like 6 |
| 237897_at | ADAM17 | -0.003408 | 0.034315 | 0.104494 | ADAM metallopeptidase domain 17 |
| 242720_at | ITIH4 | 0.004003 | 0.034529 | 0.10493 | inter-alpha-trypsin inhibitor heavy chain family, member 4 |
| 201137_s_at | HLA-DPB1 | 0.005744 | 0.035342 | 0.106813 | major histocompatibility complex, class II, DP beta 1 |
| 212044_s_at | RPL27A | -0.008988 | 0.035446 | 0.107004 | ribosomal protein L27a |
| 203417_at | MFAP2 | -0.005658 | 0.036143 | 0.108589 | microfibrillar-associated protein 2 |
| 202980_s_at | SIAH1 | -0.003724 | 0.036823 | 0.110053 | siah E3 ubiquitin protein ligase 1 |
| 1562446_at | ZNF391 | 0.00302 | 0.037056 | 0.110501 | zinc finger protein 391 |
| 238158_at | MEIG1 | 0.002743 | 0.037065 | 0.110521 | meiosis expressed gene 1 homolog (mouse) |
| 219132_at | PELI2 | 0.004562 | 0.037196 | 0.11081 | pellino E3 ubiquitin protein ligase family member 2 |
| 228366_at | PPA2 | 0.003788 | 0.038373 | 0.113449 | pyrophosphatase (inorganic) 2 |
| 243536_x_at | ARHGAP27 | -0.002279 | 0.038417 | 0.113556 | Rho GTPase activating protein 27 |
| 237813_at | PCBP2 | -0.004376 | 0.039504 | 0.115819 | poly(rC) binding protein 2 |
| 207519_at | SLC6A4 | 0.003385 | 0.039701 | 0.116182 | solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 |
| 203610_s_at | TRIM38 | 0.00505 | 0.040039 | 0.116927 | tripartite motif containing 38 |
| 226506_at | THSD4 | -0.003705 | 0.04063 | 0.118207 | thrombospondin, type I, domain containing 4 |
| 242224_at | GPATCH2 | -0.005899 | 0.041018 | 0.119025 | G patch domain containing 2 |
| 235149_at | PGM2L1 | 0.002576 | 0.041226 | 0.119467 | phosphoglucomutase 2-like 1 |
| 239446_x_at | DCBLD2 | -0.003854 | 0.041274 | 0.119583 | discoidin, CUB and LCCL domain containing 2 |

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|---|---|---|---|---|---|
| 202902_s_at | CTSS | 0.006648 | 0.041491 | 0.120059 | cathepsin S |
| 219733_s_at | SLC27A5 | -0.002491 | 0.041584 | 0.120258 | solute carrier family 27 (fatty acid transporter), member 5 |
| 210600_s_at | GRK4 | -0.002966 | 0.041864 | 0.120793 | G protein-coupled receptor kinase 4 |
| 242432_at | LRRC37A | 0.002905 | 0.041874 | 0.120808 | leucine rich repeat containing 37, member A2 |
| 236026_at | GPATCH2 | -0.006467 | 0.042048 | 0.121169 | G patch domain containing 2 |
| 212945_s_at | MGA | 0.002561 | 0.042536 | 0.12219 | MGA, MAX dimerization protein |
| 225393_at | GATAD2B | 0.004569 | 0.044276 | 0.125711 | GATA zinc finger domain containing 2B |
| 201048_x_at | RAB6A | -0.005408 | 0.044635 | 0.126447 | RAB6A, member RAS oncogene family |
| 216994_s_at | RUNX2 | 0.00207 | 0.044776 | 0.126755 | runt-related transcription factor 2 |
| 229119_s_at | ZSWIM7 | -0.005898 | 0.044825 | 0.126855 | zinc finger, SWIM-type containing 7 |
| 216018_at | RNF5 | -0.002472 | 0.044846 | 0.126886 | ring finger protein 5, E3 ubiquitin protein ligase |
| 201623_s_at | DARS | -0.007445 | 0.046263 | 0.12986 | aspartyl-tRNA synthetase |
| 228719_at | ZSWIM7 | -0.007025 | 0.046392 | 0.130111 | zinc finger, SWIM-type containing 7 |
| 211810_s_at | GALC | -0.006485 | 0.046972 | 0.131339 | galactosylceramidase |
| 243619_at | FGFR1OP2 | 0.005596 | 0.047013 | 0.13142 | FGFR1 oncogene partner 2 |
| 206401_s_at | MAPT | 0.003718 | 0.04704 | 0.131474 | microtubule-associated protein tau |
| 200982_s_at | ANXA6 | -0.005499 | 0.047101 | 0.131585 | annexin A6 |
| 220669_at | OTUD4 | 0.002472 | 0.047151 | 0.13169 | OTU domain containing 4 |
| 1555816_at | THSD4 | -0.001405 | 0.04721 | 0.131766 | thrombospondin, type I, domain containing 4 |
| 225496_s_at | SYTL2 | 0.005059 | 0.04775 | 0.132775 | synaptotagmin-like 2 |
| 223861_at | HORMAD1 | 0.001422 | 0.047864 | 0.133043 | HORMA domain containing 1 |
| 1564640_at | MGA | 0.003266 | 0.048092 | 0.133474 | MGA, MAX dimerization protein |
| 237109_at | TOM1L2 | -0.00221 | 0.048236 | 0.133758 | target of myb1-like 2 (chicken) |
| 227146_at | QSOX2 | -0.003052 | 0.048266 | 0.133801 | quiescin Q6 sulfhydryl oxidase 2 |
| 1552669_at | PPP1R3B | 0.002614 | 0.049456 | 0.136189 | protein phosphatase 1, regulatory subunit 3B |
| 242451_x_at | RPS19 | 0.00249 | 0.050043 | 0.137335 | ribosomal protein S19 |
| 214713_at | YLPM1 | 0.003403 | 0.050357 | 0.137911 | YLP motif containing 1 |
| 224671_at | MRPL10 | -0.003038 | 0.050653 | 0.138528 | mitochondrial ribosomal protein L10 |
| 1554594_at | ARHGAP27 | 0.00186 | 0.050785 | 0.138763 | Rho GTPase activating protein 27 |
| 204455_at | DST | 0.004443 | 0.051156 | 0.139448 | dystonin |
| 225202_at | RHOBTB3 | -0.003639 | 0.052096 | 0.141232 | Rho-related BTB domain containing 3 |
| 1555476_at | IREB2 | 0.003901 | 0.052286 | 0.141592 | iron-responsive element binding protein 2 |
| 201943_s_at | CPD | -0.006528 | 0.052642 | 0.142294 | carboxypeptidase D |
| 206533_at | CHRNA5 | -0.002563 | 0.053383 | 0.14375 | cholinergic receptor, nicotinic, alpha 5 (neuronal) |
| 233015_at | MBNL1 | -0.00264 | 0.053479 | 0.143953 | muscleblind-like splicing regulator 1 |
| 205185_at | SPINK5 | 0.009671 | 0.053753 | 0.144397 | serine peptidase inhibitor, Kazal type 5 |
| 203365_s_at | MMP15 | 0.004185 | 0.054547 | 0.145893 | matrix metallopeptidase 15 (membrane-inserted) |

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|---|---|---|---|---|---|
| 213889_at | PIGL | 0.004049 | 0.055108 | 0.146934 | phosphatidylinositol glycan anchor biosynthesis, class L |
| 238886_at | TMED10 | -0.004666 | 0.056546 | 0.149593 | transmembrane emp24-like trafficking protein 10 (yeast) |
| 229553_at | PGM2L1 | 0.00552 | 0.057203 | 0.15085 | phosphoglucomutase 2-like 1 |
| 201332_s_at | STAT6 | 0.005816 | 0.058265 | 0.152836 | signal transducer and activator of transcription 6, interleukin-4 induced |
| 229912_at | SDK1 | -0.003579 | 0.058438 | 0.153162 | sidekick cell adhesion molecule 1 |
| 213247_at | SVEP1 | -0.00304 | 0.058569 | 0.153374 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |
| 214937_x_at | PCM1 | -0.003011 | 0.059039 | 0.154352 | pericentriolar material 1 |
| 228083_at | CACNA2D4 | 0.003131 | 0.059102 | 0.154443 | calcium channel, voltage-dependent, alpha 2/delta subunit 4 |
| 205654_at | C4BPA | 0.007699 | 0.060029 | 0.156217 | complement component 4 binding protein, alpha |
| 215551_at | ESR1 | -0.001932 | 0.060617 | 0.157361 | estrogen receptor 1 |
| 221283_at | RUNX2 | 0.002151 | 0.060898 | 0.157815 | runt-related transcription factor 2 |
| 205330_at | MN1 | -0.005258 | 0.061924 | 0.159657 | meningioma (disrupted in balanced translocation) 1 |
| 206858_s_at | HOXC6 | 0.008337 | 0.062602 | 0.160883 | homeobox C6 |
| 219916_s_at | RNF39 | 0.002611 | 0.062724 | 0.16109 | ring finger protein 39 |
| 209728_at | HLA-DRB4 | 0.00629 | 0.062861 | 0.161352 | major histocompatibility complex, class II, DR beta 4 |
| 201047_x_at | RAB6A | 0.002416 | 0.064219 | 0.163762 | RAB6A, member RAS oncogene family |
| 225879_at | TSEN54 | -0.002286 | 0.065538 | 0.166216 | tRNA splicing endonuclease 54 homolog (S. cerevisiae) |
| 218157_x_at | CDC42SE1 | -0.005702 | 0.065666 | 0.166433 | CDC42 small effector 1 |
| 243805_at | CCBE1 | -0.004823 | 0.065797 | 0.166646 | collagen and calcium binding EGF domains 1 |
| 221487_s_at | ENSA | -0.004604 | 0.066506 | 0.167752 | endosulfine alpha |
| 66053_at | BSCL2 | -0.004689 | 0.067059 | 0.168774 | heterogeneous nuclear ribonucleoprotein U-like 2 /// HNRNPUL2-BSCL2 readthrough |
| 206284_x_at | CLTB | -0.003805 | 0.067109 | 0.168831 | clathrin, light chain B |
| 213702_x_at | ASAH1 | 0.003689 | 0.068265 | 0.170943 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 |
| 205074_at | SLC22A5 | 0.003327 | 0.068974 | 0.172182 | solute carrier family 22 (organic cation/carnitine transporter), member 5 |
| 1568702_a_at | PAAF1 | 0.003679 | 0.071363 | 0.176478 | proteasomal ATPase-associated factor 1 |
| 210980_s_at | ASAH1 | 0.003469 | 0.071769 | 0.177171 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 |
| 244250_at | ANXA6 | 0.002261 | 0.071836 | 0.177285 | annexin A6 |
| 236295_s_at | NLRC3 | 0.00466 | 0.072519 | 0.178457 | NLR family, CARD domain containing 3 |
| 223098_s_at | LONP2 | -0.003565 | 0.07331 | 0.179877 | lon peptidase 2, peroxisomal |
| 204645_at | CCNT2 | -0.003708 | 0.073497 | 0.180224 | cyclin T2 |
| 233898_s_at | FGFR1OP2 | -0.004486 | 0.073675 | 0.180556 | FGFR1 oncogene partner 2 |
| 227314_at | ITGA2 | 0.00532 | 0.074298 | 0.181642 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) |
| 207350_s_at | VAMP4 | -0.003897 | 0.074796 | 0.182476 | vesicle-associated membrane protein 4 |
| 223775_at | HHIP | 0.00692 | 0.075395 | 0.183512 | hedgehog interacting protein |
| 225220_at | SNORA24 | 0.004497 | 0.075612 | 0.183868 | small nucleolar RNA host gene 8 (non-protein coding) /// small nucleolar RNA, H/ACA box 24 |
| 202198_s_at | MTMR3 | -0.003133 | 0.078247 | 0.188316 | myotubularin related protein 3 |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| 219153_s_at | THSD4 | 0.002457 | 0.078557 | 0.188837 | thrombospondin, type I, domain containing 4 |
| 231708_at | C2CD3 | -0.002163 | 0.07967 | 0.190644 | C2 calcium-dependent domain containing 3 |
| 214420_s_at | CYP2C9 | 0.001858 | 0.079946 | 0.19112 | cytochrome P450, family 2, subfamily C, polypeptide 9 |
| 227221_at | ZMAT3 | -0.003085 | 0.08019 | 0.191525 | zinc finger, matrin-type 3 |
| 223384_s_at | TRIM4 | 0.003484 | 0.080541 | 0.19211 | tripartite motif containing 4 |
| 203644_s_at | MON1B | -0.004234 | 0.081221 | 0.193287 | MON1 homolog B (yeast) |
| 230074_s_at | C16orf5 | 0.002769 | 0.08137 | 0.193534 | chromosome 16 open reading frame 58 |
| 232295_at | GFM1 | -0.00237 | 0.081391 | 0.193564 | G elongation factor, mitochondrial 1 |
| 206023_at | NMU | -0.007425 | 0.082894 | 0.196031 | neuromedin U |
| 203479_s_at | OTUD4 | 0.003649 | 0.083361 | 0.196729 | OTU domain containing 4 |
| 1555520_at | PTCH1 | -0.008242 | 0.083505 | 0.196973 | patched 1 |
| 209909_s_at | TGFB2 | -0.006443 | 0.085401 | 0.19991 | transforming growth factor, beta 2 |
| 223534_s_at | RPS6KL1 | 0.002083 | 0.085682 | 0.200369 | ribosomal protein S6 kinase-like 1 |
| 214859_at | FSTL4 | 0.001908 | 0.085752 | 0.200474 | follistatin-like 4 |
| 225092_at | RABEP1 | -0.003852 | 0.087003 | 0.202635 | rabaptin, RAB GTPase binding effector protein 1 |
| 1560391_at | PIGL | 0.003448 | 0.088184 | 0.204699 | phosphatidylinositol glycan anchor biosynthesis, class L |
| 226941_at | ATF6 | 0.002738 | 0.089035 | 0.206123 | activating transcription factor 6 |
| 226471_at | GGT7 | 0.002485 | 0.090712 | 0.208952 | gamma-glutamyltransferase 7 |
| 1554287_at | TRIM4 | -0.007183 | 0.091689 | 0.210599 | tripartite motif containing 4 |
| 228175_at | SLC4A8 | 0.002764 | 0.092425 | 0.211801 | solute carrier family 4, sodium bicarbonate cotransporter, member 8 |
| 204630_s_at | GOSR1 | 0.003047 | 0.093097 | 0.212884 | golgi SNAP receptor complex member 1 |
| 220613_s_at | SYTL2 | 0.002603 | 0.093353 | 0.213381 | synaptotagmin-like 2 |
| 219600_s_at | TMEM50B | -0.005733 | 0.094167 | 0.214676 | transmembrane protein 50B |
| 231696_x_at | TMEM50B | 0.002109 | 0.095978 | 0.217489 | transmembrane protein 50B |
| 205745_x_at | ADAM17 | 0.003804 | 0.096478 | 0.218332 | ADAM metallopeptidase domain 17 |
| 225973_at | TAP2 | 0.006135 | 0.097537 | 0.21997 | transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) |
| 205225_at | ESR1 | 0.002255 | 0.097837 | 0.220406 | estrogen receptor 1 |
| 209876_at | GIT2 | -0.002157 | 0.098419 | 0.221271 | G protein-coupled receptor kinase interacting ArfGAP 2 |
| 228852_at | ENSA | 0.004094 | 0.09869 | 0.221688 | endosulfine alpha |
| 217978_s_at | UBE2Q1 | 0.002432 | 0.09921 | 0.222545 | ubiquitin-conjugating enzyme E2Q family member 1 |
| 239943_x_at | PIGL | -0.002058 | 0.099835 | 0.223451 | phosphatidylinositol glycan anchor biosynthesis, class L |
| 210329_s_at | SGCD | -0.001898 | 0.10149 | 0.226026 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 223263_s_at | FGFR1OP2 | -0.005275 | 0.101632 | 0.226259 | FGFR1 oncogene partner 2 |
| 1554121_at | HSD17B12 | 0.001467 | 0.103478 | 0.229341 | hydroxysteroid (17-beta) dehydrogenase 12 |
| 234114_at | ZNRD1 | -0.001848 | 0.105491 | 0.232456 | zinc ribbon domain containing 1 |
| 1552737_s_at | WWP2 | -0.002917 | 0.106045 | 0.233292 | WW domain containing E3 ubiquitin protein ligase 2 |
| 201086_x_at | SON | 0.001735 | 0.107062 | 0.234869 | SON DNA binding protein |

|  |  |  |  |  |  |
|---|---|---|---|---|---|
| 220757_s_at | UBXN6 | 0.002875 | 0.107149 | 0.23502 | microRNA 4746 /// UBX domain protein 6 |
| 223772_s_at | TMEM87A | 0.002286 | 0.108861 | 0.237652 | transmembrane protein 87A |
| 230506_at | C6orf164 | -0.002584 | 0.109991 | 0.239402 | chromosome 6 open reading frame 164 |
| 1558756_at | C2CD3 | 0.001469 | 0.111095 | 0.241074 | C2 calcium-dependent domain containing 3 |
| 205873_at | PIGL | 0.002512 | 0.111853 | 0.242086 | phosphatidylinositol glycan anchor biosynthesis, class L |
| 239929_at | PM20D1 | 0.00208 | 0.111947 | 0.242241 | peptidase M20 domain containing 1 |
| 206178_at | PLA2G5 | 0.003033 | 0.112017 | 0.242364 | phospholipase A2, group V |
| 1557384_at | ZNF131 | -0.004898 | 0.113207 | 0.244185 | uncharacterized LOC100506639 /// zinc finger protein 131 |
| 207205_at | CEACAM4 | 0.001998 | 0.113378 | 0.244389 | carcinoembryonic antigen-related cell adhesion molecule 4 |
| 220407_s_at | TGFB2 | -0.005211 | 0.11414 | 0.245568 | transforming growth factor, beta 2 |
| 1552939_at | ANGPT1 | 0.001283 | 0.114268 | 0.2458 | angiopoietin 1 |
| 216419_at | CROCC | 0.005211 | 0.11473 | 0.24639 | ciliary rootlet coiled-coil, rootletin |
| 216049_at | RHOBTB3 | 0.002212 | 0.115297 | 0.247286 | Rho-related BTB domain containing 3 |
| 204085_s_at | CLN5 | -0.004498 | 0.116383 | 0.248835 | ceroid-lipofuscinosis, neuronal 5 |
| 1558648_at | C15orf57 | 0.002322 | 0.117444 | 0.25043 | chromosome 15 open reading frame 57 |
| 1554234_at | KATNAL2 | 0.002046 | 0.118804 | 0.252395 | katanin p60 subunit A-like 2 |
| 232231_at | RUNX2 | 0.005302 | 0.120785 | 0.25551 | runt-related transcription factor 2 |
| 229184_at | CCNT2 | 0.002545 | 0.12092 | 0.255721 | cyclin T2 |
| 220435_at | SLC30A10 | 0.002243 | 0.120922 | 0.255721 | solute carrier family 30, member 10 |
| 210579_s_at | TRIM10 | 0.001306 | 0.122383 | 0.257793 | tripartite motif containing 10 |
| 1554384_at | PADI2 | 0.00164 | 0.123984 | 0.260253 | peptidyl arginine deiminase, type II |
| 238890_at | BRWD1 | 0.00301 | 0.124933 | 0.261673 | bromodomain and WD repeat domain containing 1 |
| 216114_at | NCKIPSD | 0.002537 | 0.125784 | 0.262917 | NCK interacting protein with SH3 domain |
| 229962_at | LRRC37A | -0.002851 | 0.125944 | 0.263105 | leucine rich repeat containing 37, member A3 |
| 1558875_at | SREBF1 | -0.001795 | 0.127488 | 0.265478 | sterol regulatory element binding transcription factor 1 |
| 225210_s_at | FAM103A1 | -0.002751 | 0.127538 | 0.265562 | family with sequence similarity 103, member A1 |
| 220406_at | TGFB2 | 0.001968 | 0.128114 | 0.266364 | transforming growth factor, beta 2 |
| 213748_at | TRIM66 | 0.004232 | 0.128718 | 0.267256 | tripartite motif containing 66 |
| 206192_at | CDSN | 0.002955 | 0.130172 | 0.269161 | corneodesmosin |
| 216661_x_at | CYP2C9 | 0.003203 | 0.130451 | 0.269551 | cytochrome P450, family 2, subfamily C, polypeptide 9 |
| 227060_at | RELT | 0.002038 | 0.131967 | 0.271608 | RELT tumor necrosis factor receptor |
| 235080_at | CLUAP1 | 0.001865 | 0.1329 | 0.273024 | clusterin associated protein 1 |
| 213480_at | VAMP4 | 0.003252 | 0.133737 | 0.27421 | vesicle-associated membrane protein 4 |
| 222624_s_at | ZNF639 | -0.002535 | 0.135279 | 0.276461 | zinc finger protein 639 |
| 210747_at | HLA-DQB1 | 0.001426 | 0.135786 | 0.277091 | major histocompatibility complex, class II, DQ beta 1 |
| 226170_at | EYA3 | -0.001989 | 0.136621 | 0.278075 | eyes absent homolog 3 (Drosophila) |
| 214639_s_at | HOXA1 | -0.003678 | 0.137035 | 0.278678 | homeobox A1 |

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|---|---|---|---|---|---|
| 1568914_at | OPN5 | 0.001531 | 0.138611 | 0.280906 | opsin 5 |
| 1557350_at | G3BP1 | 0.003419 | 0.139307 | 0.281992 | GTPase activating protein (SH3 domain) binding protein 1 |
| 209328_x_at | HIGD2A | -0.001753 | 0.140407 | 0.283606 | HIG1 hypoxia inducible domain family, member 2A |
| 221740_x_at | LRRC37A | 0.003578 | 0.142784 | 0.287155 | leucine rich repeat containing 37, member A2 |
| 213743_at | CCNT2 | 0.002928 | 0.145785 | 0.291362 | cyclin T2 |
| 213199_at | C2CD3 | 0.00169 | 0.145804 | 0.291371 | C2 calcium-dependent domain containing 3 |
| 1553129_at | SVEP1 | -0.003101 | 0.146174 | 0.291852 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |
| 226956_at | MTMR3 | -0.002254 | 0.147991 | 0.294425 | myotubularin related protein 3 |
| 207056_s_at | SLC4A8 | -0.001416 | 0.148567 | 0.295283 | solute carrier family 4, sodium bicarbonate cotransporter, member 8 |
| 209314_s_at | HBS1L | -0.004584 | 0.152108 | 0.300353 | HBS1-like (S. cerevisiae) |
| 221996_s_at | CLTB | 0.00187 | 0.152458 | 0.300858 | clathrin, light chain B |
| 221627_at | TRIM10 | 0.002084 | 0.153877 | 0.302655 | tripartite motif containing 10 |
| 204810_s_at | CKM | 0.002191 | 0.154615 | 0.303736 | creatine kinase, muscle |
| 206088_at | LRRC37A | 0.006229 | 0.155204 | 0.304565 | leucine rich repeat containing 37, member A3 |
| 204838_s_at | MLH3 | 0.003479 | 0.156221 | 0.305917 | mutL homolog 3 (E. coli) |
| 1562803_at | LRRC37A | 0.001317 | 0.157479 | 0.307571 | leucine rich repeat containing 37, member A5, pseudogene |
| 220954_s_at | PILRB | 0.004776 | 0.157613 | 0.307789 | paired immunoglobin-like type 2 receptor beta |
| 1553973_a_at | SPINK6 | 0.002 | 0.158875 | 0.30938 | serine peptidase inhibitor, Kazal type 6 |
| 220067_at | SPTBN5 | 0.002052 | 0.15908 | 0.309689 | spectrin, beta, non-erythrocytic 5 |
| 212357_at | FAM168A | -0.002203 | 0.159176 | 0.309785 | family with sequence similarity 168, member A |
| 238526_at | RAB3IP | -0.002621 | 0.159298 | 0.309974 | RAB3A interacting protein |
| 217094_s_at | ITCH | -0.002205 | 0.159923 | 0.310885 | itchy E3 ubiquitin protein ligase |
| 215920_s_at | PDXDC2 | 0.003284 | 0.160711 | 0.311868 |  |
| 232524_x_at | ANAPC4 | -0.002597 | 0.160869 | 0.312107 | anaphase promoting complex subunit 4 |
| 1552760_at | HDAC9 | 0.001141 | 0.161268 | 0.31275 | histone deacetylase 9 |
| 210828_s_at | ARNT | 0.003355 | 0.161295 | 0.31278 | aryl hydrocarbon receptor nuclear translocator |
| 208365_s_at | GRK4 | -0.002364 | 0.163123 | 0.315295 | G protein-coupled receptor kinase 4 |
| 226200_at | VARS2 | -0.002755 | 0.16498 | 0.317682 | valyl-tRNA synthetase 2, mitochondrial |
| 1558304_s_at | TSEN54 | -0.001782 | 0.165472 | 0.318255 | tRNA splicing endonuclease 54 homolog (S. cerevisiae) |
| 202762_at | ROCK2 | 0.002828 | 0.168339 | 0.32238 | Rho-associated, coiled-coil containing protein kinase 2 |
| 244478_at | LRRC37A | 0.002329 | 0.168877 | 0.32298 | leucine rich repeat containing 37, member A3 |
| 212253_x_at | DST | 0.003306 | 0.168987 | 0.3231 | dystonin |
| 204461_x_at | RAD1 | -0.002428 | 0.169446 | 0.323728 | RAD1 homolog (S. pombe) |
| 1560543_at | GRK4 | -0.001185 | 0.170247 | 0.324782 | G protein-coupled receptor kinase 4 |
| 212671_s_at | HLA-DQA2 | 0.006685 | 0.170743 | 0.325398 |  |
| 220362_at | PSORS1C1 | 0.001145 | 0.171408 | 0.32629 | psoriasis susceptibility 1 candidate 1 |
| 201228_s_at | ARIH2 | -0.002478 | 0.172995 | 0.328512 | ariadne homolog 2 (Drosophila) |

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|---|---|---|---|---|---|
| 217323_at | HLA-DRB6 | 0.001261 | 0.174393 | 0.330339 | major histocompatibility complex, class II, DR beta 6 (pseudogene) |
| 215523_at | ZNF391 | 0.00298 | 0.177137 | 0.333837 | zinc finger protein 391 |
| 222537_s_at | CDC42SE1 | -0.002359 | 0.177478 | 0.334238 | CDC42 small effector 1 |
| 220154_at | DST | -0.003985 | 0.177718 | 0.334541 | dystonin |
| 207106_s_at | LTK | 0.002775 | 0.179119 | 0.336437 | leukocyte receptor tyrosine kinase |
| 203166_at | CFDP1 | -0.001796 | 0.181229 | 0.339044 | craniofacial development protein 1 |
| 218957_s_at | PAAF1 | -0.002719 | 0.181558 | 0.339466 | proteasomal ATPase-associated factor 1 |
| 235084_x_at | TRIM38 | 0.002977 | 0.181652 | 0.339586 | tripartite motif containing 38 |
| 242812_at | HCG18 | -0.003313 | 0.182279 | 0.340546 | HLA complex group 18 (non-protein coding) |
| 226465_s_at | SON | -0.003209 | 0.183458 | 0.342029 | SON DNA binding protein |
| 217558_at | CYP2C9 | 0.001529 | 0.183529 | 0.342087 | cytochrome P450, family 2, subfamily C, polypeptide 9 |
| 227720_at | ANKRD13B | -0.002418 | 0.184295 | 0.343107 | ankyrin repeat domain 13B |
| 217163_at | ESR1 | 0.001047 | 0.185239 | 0.344266 | estrogen receptor 1 |
| 216973_s_at | HOXB7 | 0.002265 | 0.185505 | 0.34456 | homeobox B7 |
| 216973_s_at | HOXB7 | 0.002265 | 0.185505 | 0.34456 | NULL |
| 1556284_at | PPA2 | 0.001102 | 0.186327 | 0.345556 | pyrophosphatase (inorganic) 2 |
| 205806_at | ROM1 | -0.001953 | 0.186974 | 0.346327 | retinal outer segment membrane protein 1 |
| 243417_at | ZADH2 | 0.003245 | 0.18808 | 0.347819 | zinc binding alcohol dehydrogenase domain containing 2 |
| 218222_x_at | ARNT | 0.002391 | 0.191199 | 0.351886 | aryl hydrocarbon receptor nuclear translocator |
| 201080_at | PIP4K2B | -0.001832 | 0.195609 | 0.357451 | phosphatidylinositol-5-phosphate 4-kinase, type II, beta |
| 216679_at | DDR1 | 0.001862 | 0.197349 | 0.359633 | DDR1 antisense RNA 1 (head to head) |
| 216458_at | PQLC3 | -0.001429 | 0.197347 | 0.359633 | PQ loop repeat containing 3 |
| 212876_at | B4GALT4 | 0.001791 | 0.202532 | 0.36575 | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4 |
| 231910_at | NUDT14 | 0.001483 | 0.203964 | 0.367606 | nudix (nucleoside diphosphate linked moiety X)-type motif 14 |
| 225577_at | HCG18 | -0.002564 | 0.205302 | 0.369215 | HLA complex group 18 (non-protein coding) |
| 241846_at | HCG18 | 0.001399 | 0.210323 | 0.375098 | HLA complex group 18 (non-protein coding) |
| 1560767_at | HCG22 | 0.001723 | 0.210931 | 0.375925 | HLA complex group 22 (non-protein coding) |
| 236273_at | NBPF1 | 0.003463 | 0.211339 | 0.376396 | neuroblastoma breakpoint family, member 1 |
| 218863_s_at | TNS1 | 0.002382 | 0.21237 | 0.377666 | tensin 1 |
| 1568789_at | UHRF1BP1 | 0.00161 | 0.212868 | 0.378305 | UHRF1 binding protein 1 |
| 222907_x_at | TMEM50B | -0.003487 | 0.215227 | 0.381214 | transmembrane protein 50B |
| 213095_x_at | AIF1 | 0.002256 | 0.21595 | 0.382009 | allograft inflammatory factor 1 |
| 1558839_at | MAPKBP1 | -0.002473 | 0.218202 | 0.384604 | mitogen-activated protein kinase binding protein 1 |
| 217216_x_at | MLH3 | 0.002477 | 0.219647 | 0.386277 | mutL homolog 3 (E. coli) |
| 1554487_a_at | ATF6B | -0.002619 | 0.221392 | 0.388504 | activating transcription factor 6 beta |
| 220132_s_at | CLEC2D | -0.001833 | 0.222441 | 0.38972 | C-type lectin domain family 2, member D |
| 204125_at | NDUFAF1 | -0.00261 | 0.226359 | 0.394016 | NADH dehydrogenase (ubiquinone) complex I, assembly factor 1 |

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|---|---|---|---|---|---|
| 207263_x_at | VEZT | 0.003279 | 0.227206 | 0.39502 | vezatin, adherens junctions transmembrane protein |
| 204769_s_at | TAP2 | -0.002341 | 0.227322 | 0.395155 | transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) |
| 211235_s_at | ESR1 | 0.002278 | 0.230834 | 0.399407 | estrogen receptor 1 |
| 203929_s_at | MAPT | -0.00281 | 0.23287 | 0.40195 | microtubule-associated protein tau |
| 1567853_at | ZNF28 | -0.001055 | 0.232934 | 0.401987 | zinc finger protein 28 |
| 214741_at | ZNF131 | -0.003769 | 0.23474 | 0.404252 | uncharacterized LOC100506639 /// zinc finger protein 131 |
| 224378_x_at | MAP1LC3A | 0.002519 | 0.234835 | 0.404333 | microtubule-associated protein 1 light chain 3 alpha |
| 216527_at | HCG18 | -0.003121 | 0.236995 | 0.407014 | HLA complex group 18 (non-protein coding) |
| 228426_at | CLEC2D | 0.001924 | 0.238349 | 0.40866 | C-type lectin domain family 2, member D |
| 234530_s_at | ZNRD1 | 0.001154 | 0.238433 | 0.408765 | zinc ribbon domain containing 1 |
| 1559174_at | RAB6A | -0.001805 | 0.240638 | 0.41119 | RAB6A, member RAS oncogene family |
| 226658_at | PDPN | -0.003384 | 0.24249 | 0.413168 | podoplanin |
| 201187_s_at | ITPR3 | -0.001877 | 0.242522 | 0.413183 | inositol 1,4,5-trisphosphate receptor, type 3 |
| 216649_at | RREB1 | -0.001448 | 0.243563 | 0.414324 | ras responsive element binding protein 1 |
| 209908_s_at | TGFB2 | -0.003711 | 0.243809 | 0.414588 | transforming growth factor, beta 2 |
| 215535_s_at | AGPAT1 | 0.002977 | 0.243985 | 0.41481 | 1-acylglycerol-3-phosphate O-acyltransferase 1 |
| 207402_at | ZNF132 | -0.002205 | 0.244132 | 0.41492 | zinc finger protein 132 |
| 242972_at | HCG18 | 0.004192 | 0.248654 | 0.420357 | HLA complex group 18 (non-protein coding) |
| 1569062_s_at | IQGAP3 | -0.001264 | 0.25186 | 0.423913 | IQ motif containing GTPase activating protein 3 |
| 238417_at | PGM2L1 | 0.001964 | 0.251913 | 0.423951 | phosphoglucomutase 2-like 1 |
| 219552_at | SVEP1 | -0.003591 | 0.251921 | 0.423951 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |
| 1554984_a_at | HLA-DOB | 0.001563 | 0.252812 | 0.425024 | major histocompatibility complex, class II, DO beta |
| 230215_at | SEC61A2 | 0.001454 | 0.256166 | 0.428576 | Sec61 alpha 2 subunit (S. cerevisiae) |
| 243704_at | GPATCH2 | 0.001937 | 0.257273 | 0.429657 | G patch domain containing 2 |
| 220378_at | TCP11 | 0.001255 | 0.258873 | 0.431587 | t-complex 11, testis-specific |
| 230794_at | PELI2 | 0.001243 | 0.259595 | 0.432291 | pellino E3 ubiquitin protein ligase family member 2 |
| 226527_at | RPRD2 | 0.001825 | 0.262108 | 0.435 | regulation of nuclear pre-mRNA domain containing 2 |
| 205609_at | ANGPT1 | 0.002397 | 0.263765 | 0.437034 | angiopoietin 1 |
| 237866_at | PID1 | 0.000985 | 0.266201 | 0.439622 | phosphotyrosine interaction domain containing 1 |
| 243441_at | HOXB7 | 0.001649 | 0.266369 | 0.43983 | homeobox B7 |
| 243441_at | HOXB7 | 0.001649 | 0.266369 | 0.43983 | NULL |
| 207174_at | GPC5 | -0.005084 | 0.267146 | 0.440624 | glypican 5 |
| 216116_at | NCKIPSD | 0.001179 | 0.268991 | 0.442717 | NCK interacting protein with SH3 domain |
| 214252_s_at | CLN5 | -0.002866 | 0.270087 | 0.44404 | ceroid-lipofuscinosis, neuronal 5 |
| 236588_at | CFDP1 | -0.001578 | 0.270353 | 0.444303 | craniofacial development protein 1 |
| 1558931_at | LRRC16A | -0.001032 | 0.270547 | 0.444476 | leucine rich repeat containing 16A |
| 1555419_a_at | ASAH1 | -0.004544 | 0.271255 | 0.445371 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 |

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|---|---|---|---|---|---|
| 222256_s_at | JMJD7-PLA2G4B | -0.001836 | 0.271494 | 0.44559 | |
| 212854_x_at | NBPF1 | -0.001486 | 0.273708 | 0.447968 | neuroblastoma breakpoint family, member 1 |
| 203704_s_at | RREB1 | 0.001621 | 0.275693 | 0.450311 | ras responsive element binding protein 1 |
| 227029_at | FAM177A1 | -0.003077 | 0.279761 | 0.45464 | family with sequence similarity 177, member A1 |
| 217886_at | EPS15 | 0.001783 | 0.280517 | 0.455545 | epidermal growth factor receptor pathway substrate 15 |
| 241402_at | TSEN54 | -0.001331 | 0.2814 | 0.456462 | tRNA splicing endonuclease 54 homolog (S. cerevisiae) |
| 201940_at | CPD | -0.002657 | 0.281989 | 0.456998 | carboxypeptidase D |
| 209996_x_at | PCM1 | -0.003058 | 0.282587 | 0.457492 | pericentriolar material 1 |
| 1560814_a_at | C15orf57 | -0.003691 | 0.283822 | 0.458763 | chromosome 15 open reading frame 57 |
| 1553191_at | DST | -0.002004 | 0.284291 | 0.459273 | dystonin |
| 229424_s_at | ARHGAP27 | 0.002169 | 0.286223 | 0.461194 | Rho GTPase activating protein 27 |
| 214574_x_at | LST1 | 0.001462 | 0.286429 | 0.461396 | leukocyte specific transcript 1 |
| 1554385_a_at | PADI2 | 0.001968 | 0.28691 | 0.461864 | peptidyl arginine deiminase, type II |
| 201085_s_at | SON | -0.002772 | 0.287998 | 0.46314 | SON DNA binding protein |
| 227673_at | ZNRD1 | 0.001583 | 0.288236 | 0.463394 | zinc ribbon domain containing 1 |
| 208428_at | TAP2 | 0.001361 | 0.288436 | 0.463594 | transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) |
| 221147_x_at | WWOX | -0.001757 | 0.28904 | 0.464182 | WW domain containing oxidoreductase |
| 208748_s_at | FLOT1 | -0.002496 | 0.289228 | 0.464394 | flotillin 1 |
| 206683_at | ZNF165 | -0.002348 | 0.289504 | 0.464705 | zinc finger protein 165 |
| 233173_x_at | GTF3C5 | -0.001323 | 0.292391 | 0.467824 | general transcription factor IIIC, polypeptide 5, 63kDa |
| 236927_at | SVEP1 | 0.001293 | 0.292927 | 0.468371 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |
| 220999_s_at | CYFIP2 | 0.001878 | 0.294703 | 0.470244 | cytoplasmic FMR1 interacting protein 2 |
| 1566984_at | LRRC37A | 0.001771 | 0.295349 | 0.470958 | NULL /// leucine rich repeat containing 37, member A16, pseudogene |
| 205172_x_at | CLTB | -0.001327 | 0.296796 | 0.472491 | clathrin, light chain B |
| 237867_s_at | PID1 | -0.001802 | 0.298964 | 0.474562 | phosphotyrosine interaction domain containing 1 |
| 1553512_at | HOXC12 | 0.002004 | 0.299175 | 0.474751 | homeobox C12 |
| 233301_at | OXCT2 | 0.001048 | 0.301175 | 0.476619 | 3-oxoacid CoA transferase 2 |
| 226917_s_at | ANAPC4 | -0.002086 | 0.303144 | 0.478739 | anaphase promoting complex subunit 4 |
| 235788_at | HCG18 | -0.002479 | 0.30716 | 0.482822 | HLA complex group 18 (non-protein coding) |
| 220256_s_at | OXCT2 | -0.001496 | 0.307698 | 0.483461 | 3-oxoacid CoA transferase 2 |
| 216946_at | HLA-DOA | -0.001185 | 0.307969 | 0.483704 | major histocompatibility complex, class II, DO alpha |
| 37996_s_at | DMPK | 0.003238 | 0.308667 | 0.484366 | dystrophia myotonica-protein kinase |
| 206410_at | NR0B2 | 0.001375 | 0.309463 | 0.485172 | nuclear receptor subfamily 0, group B, member 2 |
| 228001_at | TMEM50B | 0.00237 | 0.312512 | 0.488341 | transmembrane protein 50B |
| 1569839_s_at | LRRC37A | 0.001604 | 0.312919 | 0.48868 | leucine rich repeat containing 37, member A5, pseudogene |
| 235253_at | RAD1 | -0.002337 | 0.314578 | 0.490394 | RAD1 homolog (S. pombe) |

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|---|---|---|---|---|---|
| 211142_x_at | HLA-DOA | -0.001406 | 0.320533 | 0.496492 | major histocompatibility complex, class II, DO alpha |
| 219920_s_at | AMIGO3 | -0.001798 | 0.323599 | 0.499528 | adhesion molecule with Ig-like domain 3 /// GDP-mannose pyrophosphorylase B |
| 241599_at | LSM11 | -0.001391 | 0.326146 | 0.501943 | LSM11, U7 small nuclear RNA associated |
| 238848_at | OTUD4 | 0.001636 | 0.331527 | 0.507397 | OTU domain containing 4 |
| 231734_at | RBP2 | -0.001476 | 0.331561 | 0.507421 | retinol binding protein 2, cellular |
| 221057_at | SPATA1 | 0.001147 | 0.333556 | 0.509533 | spermatogenesis associated 1 |
| 229835_s_at | SLMO2 | -0.004202 | 0.335287 | 0.511376 | slowmo homolog 2 (Drosophila) |
| 1557065_at | YLPM1 | 0.003044 | 0.335901 | 0.51207 | YLP motif containing 1 |
| 222480_at | UBE2Q1 | -0.002037 | 0.336131 | 0.512335 | ubiquitin-conjugating enzyme E2Q family member 1 |
| 228535_at | RAD1 | -0.001858 | 0.336306 | 0.512502 | RAD1 homolog (S. pombe) |
| 230721_at | C16orf5 | -0.001945 | 0.339793 | 0.516105 | chromosome 16 open reading frame 52 /// uncharacterized LOC101060634 |
| 213489_at | MAPRE2 | 0.001955 | 0.34008 | 0.516454 | microtubule-associated protein, RP/EB family, member 2 |
| 218221_at | ARNT | 0.001683 | 0.340438 | 0.516739 | aryl hydrocarbon receptor nuclear translocator |
| 215051_x_at | AIF1 | 0.001713 | 0.341786 | 0.518081 | allograft inflammatory factor 1 |
| 1552690_a_at | CACNA2D4 | 0.001227 | 0.344144 | 0.520529 | calcium channel, voltage-dependent, alpha 2/delta subunit 4 |
| 221257_x_at | FBXO38 | 0.001945 | 0.345131 | 0.521388 | F-box protein 38 |
| 1552314_a_at | EYA3 | -0.001259 | 0.346852 | 0.523336 | eyes absent homolog 3 (Drosophila) |
| 1555060_a_at | IKZF2 | 0.002138 | 0.347627 | 0.524133 | IKAROS family zinc finger 2 (Helios) |
| 227351_at | C16orf5 | -0.001755 | 0.35026 | 0.526777 | chromosome 16 open reading frame 52 /// uncharacterized LOC101060634 |
| 204770_at | TAP2 | 0.001812 | 0.3526 | 0.529407 | transporter 2, ATP-binding cassette, sub-family B (MDR/TAP) |
| 231960_at | BRWD1 | 0.001922 | 0.352991 | 0.529706 | bromodomain and WD repeat domain containing 1 |
| 210649_s_at | ARID1A | -0.002682 | 0.353901 | 0.530534 | AT rich interactive domain 1A (SWI-like) |
| 210629_x_at | LST1 | -0.0014 | 0.355857 | 0.532748 | leukocyte specific transcript 1 |
| 201216_at | ERP29 | -0.001582 | 0.356836 | 0.533676 | endoplasmic reticulum protein 29 |
| 211043_s_at | CLTB | -0.001763 | 0.357739 | 0.53448 | clathrin, light chain B |
| 222190_s_at | C16orf5 | 0.00195 | 0.360401 | 0.537171 | chromosome 16 open reading frame 58 |
| 228375_at | IGSF11 | 0.001004 | 0.36125 | 0.538008 | immunoglobulin superfamily, member 11 |
| 209327_s_at | NOP16 | -0.001646 | 0.361297 | 0.538063 | NOP16 nucleolar protein |
| 216918_s_at | DST | 0.001381 | 0.361336 | 0.538077 | dystonin |
| 1556672_a_at | RBM6 | 0.002861 | 0.364103 | 0.540818 | RNA binding motif protein 6 |
| 219078_at | GPATCH2 | 0.001902 | 0.370014 | 0.546247 | G patch domain containing 2 |
| 218628_at | CCDC53 | -0.002407 | 0.372437 | 0.548573 | coiled-coil domain containing 53 |
| 213589_s_at | B3GNTL1 | -0.001332 | 0.375757 | 0.551605 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 |
| 225397_at | C15orf57 | 0.002215 | 0.376188 | 0.551964 | chromosome 15 open reading frame 57 |
| 232365_at | SIAH1 | -0.003027 | 0.37683 | 0.552572 | siah E3 ubiquitin protein ligase 1 |
| 242112_at | LSM11 | 0.002002 | 0.377194 | 0.552885 | LSM11, U7 small nuclear RNA associated |
| 213021_at | GOSR1 | -0.001341 | 0.379173 | 0.554684 | golgi SNAP receptor complex member 1 |

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|---|---|---|---|---|---|
| 244622_at | BRWD1 | 0.001683 | 0.379322 | 0.554857 | bromodomain and WD repeat domain containing 1 |
| 202976_s_at | RHOBTB3 | -0.002199 | 0.382824 | 0.558113 | Rho-related BTB domain containing 3 |
| 218582_at | 5-Mar | -0.001772 | 0.383377 | 0.558636 | membrane-associated ring finger (C3HC4) 5 |
| 219573_at | LRRC16A | -0.001995 | 0.383985 | 0.55921 | leucine rich repeat containing 16A |
| 214762_at | ATP6V1G2 | -0.001318 | 0.386277 | 0.561584 | ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2 |
| 216648_s_at | RREB1 | -0.001306 | 0.388197 | 0.563407 | ras responsive element binding protein 1 |
| 244192_x_at | USP4 | -0.001027 | 0.390682 | 0.565766 | ubiquitin specific peptidase 4 (proto-oncogene) |
| 232442_at | BCAR1 | -0.001598 | 0.392312 | 0.567106 | breast cancer anti-estrogen resistance 1 |
| 207611_at | HIST1H2BL | 0.000747 | 0.392998 | 0.567738 | histone cluster 1, H2bl |
| 1559518_at | HSD17B12 | -0.00068 | 0.39461 | 0.569135 | hydroxysteroid (17-beta) dehydrogenase 12 |
| 1565800_x_at | RAB3IP | -0.000634 | 0.396103 | 0.570493 | RAB3A interacting protein |
| 228840_at | AMOTL1 | -0.001432 | 0.396602 | 0.570998 | angiomotin like 1 |
| 218800_at | SRD5A3 | -0.001484 | 0.402555 | 0.576245 | steroid 5 alpha-reductase 3 |
| 1553047_at | PIP4K2B | 0.001426 | 0.406043 | 0.579292 | phosphatidylinositol-5-phosphate 4-kinase, type II, beta |
| 216459_x_at | DDR1 | 0.001225 | 0.406411 | 0.579609 | DDR1 antisense RNA 1 (head to head) |
| 235409_at | MGA | -0.002753 | 0.408728 | 0.581649 | MGA, MAX dimerization protein |
| 202975_s_at | RHOBTB3 | 0.002283 | 0.410353 | 0.583013 | Rho-related BTB domain containing 3 |
| 213543_at | SGCD | 0.002345 | 0.411742 | 0.584363 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 1553227_s_at | BRWD1 | 0.001222 | 0.41177 | 0.584373 | bromodomain and WD repeat domain containing 1 |
| 1555609_a_at | ZMAT3 | -0.001071 | 0.415681 | 0.587817 | zinc finger, matrin-type 3 |
| 242463_x_at | ZNF600 | -0.002228 | 0.420127 | 0.591854 | zinc finger protein 600 |
| 211581_x_at | LST1 | 0.001543 | 0.421208 | 0.592736 | leukocyte specific transcript 1 |
| 238688_at | TPM1 | 0.002519 | 0.421885 | 0.593368 | tropomyosin 1 (alpha) |
| 235057_at | ITCH | 0.002024 | 0.423133 | 0.594671 | itchy E3 ubiquitin protein ligase |
| 230427_s_at | BAG5 | -0.001909 | 0.426472 | 0.59756 | BCL2-associated athanogene 5 |
| 235277_at | AMOTL1 | -0.001556 | 0.428713 | 0.599424 | angiomotin like 1 |
| 223442_at | NICN1 | 0.001213 | 0.42874 | 0.599429 | nicolin 1 |
| 229256_at | PGM2L1 | 0.002117 | 0.429918 | 0.600495 | phosphoglucomutase 2-like 1 |
| 221818_at | INTS5 | -0.000989 | 0.431757 | 0.602018 | integrator complex subunit 5 |
| 206274_s_at | CROCC | 0.001648 | 0.433478 | 0.603559 | ciliary rootlet coiled-coil, rootletin |
| 231927_at | ATF6 | -0.00146 | 0.434533 | 0.60455 | activating transcription factor 6 |
| 235410_at | NPHP3 | 0.002018 | 0.436664 | 0.606632 | nephronophthisis 3 (adolescent) |
| 208096_s_at | COL21A1 | -0.001399 | 0.437116 | 0.607044 | collagen, type XXI, alpha 1 |
| 211556_at | MAPRE2 | 0.000606 | 0.439096 | 0.608727 | microtubule-associated protein, RP/EB family, member 2 |
| 224124_at | ZRANB3 | -0.000883 | 0.439111 | 0.608732 | zinc finger, RAN-binding domain containing 3 |
| 1555199_at | GOSR1 | 0.001053 | 0.441068 | 0.610687 | golgi SNAP receptor complex member 1 |
| 221282_x_at | RUNX2 | 0.000901 | 0.442879 | 0.612294 | runt-related transcription factor 2 |

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|---|---|---|---|---|---|
| 214419_s_at | CYP2C9 | 0.000914 | 0.446398 | 0.615463 | cytochrome P450, family 2, subfamily C, polypeptide 9 |
| 214988_s_at | SON | 0.000724 | 0.447071 | 0.616143 | SON DNA binding protein |
| 243883_at | MMP15 | 0.001101 | 0.448062 | 0.617074 | matrix metallopeptidase 15 (membrane-inserted) |
| 1554533_at | C2 | 0.000679 | 0.449749 | 0.618586 | complement component 2 |
| 202981_x_at | SIAH1 | 0.000745 | 0.450932 | 0.619621 | siah E3 ubiquitin protein ligase 1 |
| 215810_x_at | DST | 0.000933 | 0.451582 | 0.620186 | dystonin |
| 217001_x_at | HLA-DOA | 0.001391 | 0.451739 | 0.62034 | major histocompatibility complex, class II, DO alpha |
| 225558_at | GIT2 | -0.001535 | 0.452452 | 0.620904 | G protein-coupled receptor kinase interacting ArfGAP 2 |
| 219744_at | FN3K | 0.000922 | 0.45477 | 0.623031 | fructosamine 3 kinase |
| 201942_s_at | CPD | -0.002727 | 0.454933 | 0.62313 | carboxypeptidase D |
| 206506_s_at | SUPT3H | 0.001455 | 0.456055 | 0.624284 | suppressor of Ty 3 homolog (S. cerevisiae) |
| 211504_x_at | ROCK2 | 0.001006 | 0.457171 | 0.625192 | Rho-associated, coiled-coil containing protein kinase 2 |
| 221842_s_at | ZNF131 | -0.001921 | 0.461774 | 0.629049 | uncharacterized LOC100506639 /// zinc finger protein 131 |
| 51146_at | PIGV | 0.001716 | 0.462371 | 0.629532 | phosphatidylinositol glycan anchor biosynthesis, class V |
| 225856_at | CLOCK | -0.001066 | 0.463013 | 0.630093 | clock circadian regulator |
| 213264_at | PCBP2 | -0.001184 | 0.463132 | 0.630163 | poly(rC) binding protein 2 |
| 217964_at | TTC19 | -0.000971 | 0.463534 | 0.630408 | tetratricopeptide repeat domain 19 |
| 223523_at | TMEM108 | -0.001714 | 0.464059 | 0.630763 | transmembrane protein 108 |
| 202682_s_at | USP4 | 0.001268 | 0.467151 | 0.633297 | ubiquitin specific peptidase 4 (proto-oncogene) |
| 232011_s_at | MAP1LC3A | -0.001838 | 0.469097 | 0.635021 | microtubule-associated protein 1 light chain 3 alpha |
| 229466_at | TRIM66 | -0.001088 | 0.469615 | 0.635467 | tripartite motif containing 66 |
| 233644_at | KATNAL2 | -0.000907 | 0.478751 | 0.643217 | katanin p60 subunit A-like 2 |
| 223674_s_at | CDC42SE1 | -0.000953 | 0.478961 | 0.643393 | CDC42 small effector 1 |
| 220246_at | CAMK1D | -0.001296 | 0.479165 | 0.643478 | calcium/calmodulin-dependent protein kinase ID |
| 217876_at | GTF3C5 | -0.001268 | 0.479283 | 0.643552 | general transcription factor IIIC, polypeptide 5, 63kDa |
| 226135_at | UHRF1BP1 | -0.001153 | 0.47926 | 0.643552 | UHRF1 binding protein 1 |
| 216208_s_at | ATF6B | -0.00154 | 0.482636 | 0.6468 | activating transcription factor 6 beta |
| 214492_at | SGCD | 0.000795 | 0.486721 | 0.650278 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 1554910_at | PRKD3 | -0.001162 | 0.488222 | 0.651491 | protein kinase D3 |
| 235522_at | CLEC2D | -0.001956 | 0.489231 | 0.652344 | C-type lectin domain family 2, member D |
| 1564482_at | ATP5O | 0.001008 | 0.494817 | 0.656941 | ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit |
| 203168_at | ATF6B | -0.001342 | 0.49535 | 0.65744 | activating transcription factor 6 beta |
| 224159_x_at | TRIM4 | 0.001691 | 0.496742 | 0.65868 | tripartite motif containing 4 |
| 206193_s_at | CDSN | 0.000972 | 0.497516 | 0.659179 | corneodesmosin |
| 1558967_s_at | HCG18 | -0.000946 | 0.500394 | 0.661694 | HLA complex group 18 (non-protein coding) |
| 1557303_at | NT5C | 0.000973 | 0.500975 | 0.66222 | 5', 3'-nucleotidase, cytosolic |
| 204417_at | GALC | -0.001295 | 0.502081 | 0.663187 | galactosylceramidase |

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|---|---|---|---|---|---|
| 229600_s_at | CPD | 0.000649 | 0.503201 | 0.664229 | carboxypeptidase D |
| 225153_at | GFM1 | 0.000984 | 0.503455 | 0.664408 | G elongation factor, mitochondrial 1 |
| 221103_s_at | WDR52 | 0.001549 | 0.506238 | 0.666889 | WD repeat domain 52 |
| 204084_s_at | CLN5 | -0.001799 | 0.507454 | 0.667686 | ceroid-lipofuscinosis, neuronal 5 |
| 227057_at | ARHGAP27 | 0.001381 | 0.508102 | 0.668163 | Rho GTPase activating protein 27 |
| 231250_at | HOXB7 | 0.000594 | 0.509515 | 0.669184 | homeobox B7 |
| 231250_at | HOXB7 | 0.000594 | 0.509515 | 0.669184 | NULL |
| 219238_at | PIGV | 0.001353 | 0.509664 | 0.669331 | phosphatidylinositol glycan anchor biosynthesis, class V |
| 234818_at | TMEM108 | -0.000827 | 0.510492 | 0.670023 | transmembrane protein 108 |
| 218545_at | CCDC91 | 0.001577 | 0.517174 | 0.675582 | coiled-coil domain containing 91 |
| 223747_x_at | WWOX | -0.001092 | 0.518356 | 0.676625 | WW domain containing oxidoreductase |
| 231816_s_at | UBE2Q1 | 0.001014 | 0.519954 | 0.677818 | ubiquitin-conjugating enzyme E2Q family member 1 |
| 228315_at | ZMAT3 | -0.001526 | 0.524381 | 0.681431 | zinc finger, matrin-type 3 |
| 237679_at | TRIM66 | -0.000613 | 0.526474 | 0.682965 | tripartite motif containing 66 |
| 219628_at | ZMAT3 | -0.000787 | 0.526642 | 0.683087 | zinc finger, matrin-type 3 |
| 236235_at | ITCH | -0.002027 | 0.536052 | 0.690916 | itchy E3 ubiquitin protein ligase |
| 229717_at | AMIGO3 | -0.000656 | 0.542085 | 0.695731 | adhesion molecule with Ig-like domain 3 /// GDP-mannose pyrophosphorylase B |
| 1557531_a_at | C10orf55 | 0.000482 | 0.547168 | 0.699864 | chromosome 10 open reading frame 55 |
| 226470_at | GGT7 | 0.001253 | 0.547751 | 0.700346 | gamma-glutamyltransferase 7 |
| 230173_at | TRIM4 | -0.000785 | 0.550524 | 0.702536 | tripartite motif containing 4 |
| 218967_s_at | PTER | -0.001958 | 0.551287 | 0.703077 | phosphotriesterase related |
| 201624_at | DARS | 0.001519 | 0.557929 | 0.708554 | aspartyl-tRNA synthetase |
| 1556282_at | FGFR1OP2 | 0.000836 | 0.558453 | 0.708909 | FGFR1 oncogene partner 2 |
| 221095_s_at | KCNE2 | 0.000811 | 0.560821 | 0.710825 | potassium voltage-gated channel, Isk-related family, member 2 |
| 215666_at | HLA-DRB4 | 0.000547 | 0.564111 | 0.71349 | major histocompatibility complex, class II, DR beta 4 |
| 209997_x_at | PCM1 | -0.001226 | 0.564649 | 0.713832 | pericentriolar material 1 |
| 216048_s_at | RHOBTB3 | -0.001167 | 0.569931 | 0.71826 | Rho-related BTB domain containing 3 |
| 226114_at | ZNF436 | -0.001135 | 0.570342 | 0.718612 | zinc finger protein 436 |
| 211010_s_at | NCR3 | 0.000772 | 0.57136 | 0.719256 | natural cytotoxicity triggering receptor 3 |
| 242009_at | SLC6A4 | -0.001104 | 0.571366 | 0.719256 | solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 |
| 1558532_at | TPM1 | -0.000507 | 0.573973 | 0.721358 | tropomyosin 1 (alpha) |
| 1552670_a_at | PPP1R3B | -0.001675 | 0.575485 | 0.722478 | protein phosphatase 1, regulatory subunit 3B |
| 1564684_at | BTN2A2 | 0.000583 | 0.57824 | 0.724655 | butyrophilin, subfamily 2, member A2 |
| 213833_x_at | NOP16 | -0.000694 | 0.584604 | 0.729541 | NOP16 nucleolar protein |
| 236859_at | RUNX2 | -0.000464 | 0.58819 | 0.732638 | runt-related transcription factor 2 |
| 241989_at | GRK4 | -0.001419 | 0.588798 | 0.733015 | G protein-coupled receptor kinase 4 |
| 223089_at | VEZT | 0.001564 | 0.59262 | 0.736079 | vezatin, adherens junctions transmembrane protein |

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|---|---|---|---|---|---|
| 208906_at | BSCL2 | -0.000891 | 0.594209 | 0.737468 | Berardinelli-Seip congenital lipodystrophy 2 (seipin) /// HNRNPUL2-BSCL2 readthrough |
| 231236_at | ZFP57 | 0.000977 | 0.596489 | 0.738972 | ZFP57 zinc finger protein |
| 218795_at | ACP6 | 0.001148 | 0.597189 | 0.739487 | acid phosphatase 6, lysophosphatidic |
| 231914_at | NUDT14 | -0.00122 | 0.600924 | 0.742222 | nudix (nucleoside diphosphate linked moiety X)-type motif 14 |
| 1552758_at | HDAC9 | 0.000557 | 0.601297 | 0.742499 | histone deacetylase 9 |
| 211234_x_at | ESR1 | -0.000791 | 0.604248 | 0.744435 | estrogen receptor 1 |
| 231399_at | RAB3IP | -0.000978 | 0.609062 | 0.747931 | RAB3A interacting protein |
| 217869_at | HSD17B12 | 0.000785 | 0.611159 | 0.749621 | hydroxysteroid (17-beta) dehydrogenase 12 |
| 239615_at | SLC22A5 | -0.000581 | 0.611513 | 0.749903 | solute carrier family 22 (organic cation/carnitine transporter), member 5 |
| 205448_s_at | MAP3K12 | 0.000646 | 0.611906 | 0.750151 | mitogen-activated protein kinase kinase kinase 12 |
| 234948_at | SLC27A5 | -0.000811 | 0.618664 | 0.755353 | solute carrier family 27 (fatty acid transporter), member 5 |
| 1555817_s_at | THSD4 | 0.000511 | 0.62013 | 0.756535 | thrombospondin, type I, domain containing 4 |
| 1555745_a_at | LYZ | -0.002028 | 0.625264 | 0.760585 | lysozyme |
| 1554844_at | EYA3 | 0.000455 | 0.626972 | 0.761804 | eyes absent homolog 3 (Drosophila) |
| 219439_at | C1GALT1 | -0.001074 | 0.627003 | 0.761826 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 |
| 210979_at | ASAH1 | 0.000517 | 0.630871 | 0.764961 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 |
| 230793_at | LRRC16A | -0.001915 | 0.631106 | 0.765144 | leucine rich repeat containing 16A |
| 240602_at | HBS1L | 0.000543 | 0.63146 | 0.765421 | HBS1-like (S. cerevisiae) |
| 1569448_at | PGM2L1 | 0.000712 | 0.631991 | 0.765711 | phosphoglucomutase 2-like 1 |
| 234393_at | HDAC9 | -0.000746 | 0.632482 | 0.766048 | histone deacetylase 9 |
| 226857_at | ARHGEF19 | -0.001052 | 0.634875 | 0.767603 | Rho guanine nucleotide exchange factor (GEF) 19 |
| 211760_s_at | VAMP4 | -0.001344 | 0.635661 | 0.768204 | vesicle-associated membrane protein 4 |
| 214239_x_at | PCGF2 | -0.000565 | 0.635768 | 0.768242 | polycomb group ring finger 2 |
| 32836_at | AGPAT1 | 0.001287 | 0.636303 | 0.768632 | 1-acylglycerol-3-phosphate O-acyltransferase 1 |
| 205678_at | AP3B2 | -0.00065 | 0.641355 | 0.772481 | adaptor-related protein complex 3, beta 2 subunit |
| 236858_s_at | RUNX2 | 0.000436 | 0.649211 | 0.778463 | runt-related transcription factor 2 |
| 1564511_a_at | FSTL4 | 0.000715 | 0.64984 | 0.778958 | follistatin-like 4 |
| 222565_s_at | PRKD3 | -0.000833 | 0.650561 | 0.779399 | protein kinase D3 |
| 240786_at | NOTCH4 | -0.000577 | 0.650653 | 0.779458 | notch 4 |
| 201151_s_at | MBNL1 | -0.000965 | 0.652448 | 0.780531 | muscleblind-like splicing regulator 1 |
| 213902_at | ASAH1 | 0.000862 | 0.65527 | 0.78252 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 |
| 1560136_at | ARL5C | -0.000524 | 0.657231 | 0.783936 | ADP-ribosylation factor-like 5C |
| 213517_at | PCBP2 | 0.001543 | 0.657632 | 0.784266 | poly(rC) binding protein 2 |
| 235429_at | EIF3E | 0.001231 | 0.657835 | 0.784418 | eukaryotic translation initiation factor 3, subunit E |
| 209111_at | RNF5 | -0.000768 | 0.66252 | 0.787977 | ring finger protein 5, E3 ubiquitin protein ligase |
| 225579_at | PQLC3 | 0.00132 | 0.664318 | 0.789137 | PQ loop repeat containing 3 |

| | | | | | |
|---|---|---|---|---|---|
| 234115_s_at | ZNRD1 | 0.000516 | 0.665686 | 0.790177 | zinc ribbon domain containing 1 |
| 224369_s_at | FBXO38 | 0.000732 | 0.665876 | 0.790318 | F-box protein 38 |
| 219077_s_at | WWOX | 0.0012 | 0.666466 | 0.790572 | WW domain containing oxidoreductase |
| 1559496_at | PPA2 | -0.001492 | 0.667282 | 0.791145 | pyrophosphatase (inorganic) 2 |
| 231743_at | WNT3 | -0.000778 | 0.668888 | 0.792159 | wingless-type MMTV integration site family, member 3 |
| 214820_at | BRWD1 | 0.001055 | 0.670275 | 0.793162 | bromodomain and WD repeat domain containing 1 |
| 227219_x_at | MAP1LC3A | 0.00083 | 0.670494 | 0.793336 | microtubule-associated protein 1 light chain 3 alpha |
| 210695_s_at | WWOX | -0.00065 | 0.671736 | 0.794148 | WW domain containing oxidoreductase |
| 202985_s_at | BAG5 | -0.000635 | 0.671945 | 0.794308 | BCL2-associated athanogene 5 |
| 211233_x_at | ESR1 | 0.000675 | 0.671969 | 0.794308 | estrogen receptor 1 |
| 225182_at | TMEM50B | -0.000927 | 0.671963 | 0.794308 | transmembrane protein 50B |
| 244835_at | C16orf5 | -0.000671 | 0.673282 | 0.795361 | chromosome 16 open reading frame 52 |
| 1554122_a_at | HSD17B12 | -0.000689 | 0.674009 | 0.795894 | hydroxysteroid (17-beta) dehydrogenase 12 |
| 223049_at | GRB2 | -0.00049 | 0.677276 | 0.798423 | growth factor receptor-bound protein 2 |
| 239101_at | ITCH | 0.000737 | 0.679998 | 0.800458 | itchy E3 ubiquitin protein ligase |
| 230026_at | MRPL43 | 0.001917 | 0.687128 | 0.805741 | mitochondrial ribosomal protein L43 |
| 209901_x_at | AIF1 | -0.000673 | 0.69132 | 0.808944 | allograft inflammatory factor 1 |
| 215870_s_at | PLA2G5 | -0.000517 | 0.694057 | 0.810517 | phospholipase A2, group V |
| 37201_at | ITIH4 | 0.000579 | 0.694973 | 0.811187 | inter-alpha-trypsin inhibitor heavy chain family, member 4 |
| 1558301_a_at | EFCAB5 | 0.000315 | 0.695245 | 0.811382 | EF-hand calcium binding domain 5 |
| 211582_x_at | LST1 | 0.00076 | 0.701394 | 0.8156 | leukocyte specific transcript 1 |
| 228121_at | TGFB2 | 0.000778 | 0.702343 | 0.816322 | transforming growth factor, beta 2 |
| 203930_s_at | MAPT | -0.000371 | 0.704514 | 0.817715 | microtubule-associated protein tau |
| 202461_at | EIF2B2 | 0.000721 | 0.705611 | 0.818202 | eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa |
| 226107_at | C1GALT1 | 0.00097 | 0.706422 | 0.818835 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 |
| 229407_at | SDK1 | -0.000744 | 0.708038 | 0.820083 | sidekick cell adhesion molecule 1 |
| 221128_at | ADAM19 | -0.000622 | 0.710416 | 0.821897 | ADAM metallopeptidase domain 19 |
| 211800_s_at | USP4 | 0.000467 | 0.711178 | 0.822551 | ubiquitin specific peptidase 4 (proto-oncogene) |
| 225450_at | AMOTL1 | -0.000477 | 0.712108 | 0.823237 | angiomotin like 1 |
| 211662_s_at | VDAC2 | -0.000419 | 0.715003 | 0.825369 | voltage-dependent anion channel 2 |
| 244485_at | HLA-DPB1 | 0.000323 | 0.716655 | 0.826683 | major histocompatibility complex, class II, DP beta 1 |
| 218441_s_at | RPAP1 | 0.000654 | 0.717753 | 0.827412 | RNA polymerase II associated protein 1 |
| 237320_at | FAM71F2 | -0.000483 | 0.718359 | 0.827803 | family with sequence similarity 71, member F2 |
| 219251_s_at | WDR60 | 0.000617 | 0.722753 | 0.830682 | WD repeat domain 60 |
| 210701_at | CFDP1 | 0.001279 | 0.724966 | 0.832214 | craniofacial development protein 1 |
| 235164_at | ZNF25 | 0.000745 | 0.729288 | 0.835264 | zinc finger protein 25 |
| 240337_at | RHOA | 0.000328 | 0.729739 | 0.835606 | ras homolog family member A |

| | | | | | |
|---|---|---|---|---|---|
| 228935_at | SLC4A8 | 0.000481 | 0.730051 | 0.835892 | solute carrier family 4, sodium bicarbonate cotransporter, member 8 |
| 233500_x_at | CLEC2D | -0.000504 | 0.732483 | 0.837485 | C-type lectin domain family 2, member D |
| 217066_s_at | DMPK | -0.000714 | 0.733951 | 0.838531 | dystrophia myotonica-protein kinase |
| 220903_at | GFM1 | 0.000298 | 0.742295 | 0.844202 | G elongation factor, mitochondrial 1 |
| 213263_s_at | PCBP2 | 0.00061 | 0.744108 | 0.845518 | poly(rC) binding protein 2 |
| 215075_s_at | GRB2 | 0.000462 | 0.749767 | 0.849131 | growth factor receptor-bound protein 2 |
| 224332_s_at | MRPL43 | -0.00072 | 0.755607 | 0.852989 | mitochondrial ribosomal protein L43 |
| 207591_s_at | ARID1A | -0.000547 | 0.757079 | 0.853911 | AT rich interactive domain 1A (SWI-like) |
| 36552_at | C2CD3 | 0.000467 | 0.75941 | 0.855286 | C2 calcium-dependent domain containing 3 |
| 234323_at | THSD4 | -0.000354 | 0.759757 | 0.855466 | thrombospondin, type I, domain containing 4 |
| 221455_s_at | WNT3 | -0.000427 | 0.76171 | 0.856941 | wingless-type MMTV integration site family, member 3 |
| 1557620_a_at | CCDC38 | 0.000414 | 0.765554 | 0.859678 | coiled-coil domain containing 38 |
| 222653_at | PNPO | 0.00042 | 0.768643 | 0.861683 | pyridoxamine 5'-phosphate oxidase |
| 218740_s_at | CDK5RAP3 | -0.000561 | 0.768679 | 0.861696 | CDK5 regulatory subunit associated protein 3 |
| 214840_at | TOM1L2 | 0.000503 | 0.768734 | 0.861723 | target of myb1-like 2 (chicken) |
| 204879_at | PDPN | 0.00063 | 0.771453 | 0.863302 | podoplanin |
| 224911_s_at | DCBLD2 | -0.000493 | 0.776878 | 0.867066 | discoidin, CUB and LCCL domain containing 2 |
| 226062_x_at | FAM63A | -0.000989 | 0.77735 | 0.867433 | family with sequence similarity 63, member A |
| 242549_at | PRKD3 | 0.00081 | 0.77783 | 0.867738 | protein kinase D3 |
| 233165_at | NCKIPSD | -0.000471 | 0.781467 | 0.870174 | NCK interacting protein with SH3 domain |
| 237776_at | ZADH2 | -0.000366 | 0.782543 | 0.870815 | zinc binding alcohol dehydrogenase domain containing 2 |
| 206313_at | HLA-DOA | 0.000402 | 0.783772 | 0.87159 | major histocompatibility complex, class II, DO alpha |
| 224686_x_at | LRRC37A | 0.000531 | 0.788972 | 0.875115 | leucine rich repeat containing 37, member A2 |
| 202501_at | MAPRE2 | 0.000414 | 0.80193 | 0.883872 | microtubule-associated protein, RP/EB family, member 2 |
| 235432_at | NPHP3 | -0.000583 | 0.803165 | 0.884564 | nephronophthisis 3 (adolescent) |
| 230175_s_at | DCBLD2 | 0.001408 | 0.804789 | 0.885611 | discoidin, CUB and LCCL domain containing 2 |
| 53968_at | INTS5 | -0.000394 | 0.805378 | 0.885888 | integrator complex subunit 5 |
| 228185_at | ZNF25 | -0.000618 | 0.806929 | 0.886954 | zinc finger protein 25 |
| 223471_at | RAB3IP | 0.000546 | 0.807397 | 0.88725 | RAB3A interacting protein |
| 233557_s_at | MON1B | 0.000488 | 0.808888 | 0.888093 | MON1 homolog B (yeast) |
| 209744_x_at | ITCH | 0.000404 | 0.812002 | 0.890042 | itchy E3 ubiquitin protein ligase |
| 214118_x_at | PCM1 | -0.000325 | 0.812335 | 0.890247 | pericentriolar material 1 |
| 238853_at | RAB3IP | 0.000457 | 0.813669 | 0.89113 | RAB3A interacting protein |
| 1570571_at | CCDC91 | 0.000749 | 0.817332 | 0.893503 | coiled-coil domain containing 91 |
| 209743_s_at | ITCH | 0.000494 | 0.817799 | 0.893808 | itchy E3 ubiquitin protein ligase |
| 238997_at | PSORS1C3 | 0.000222 | 0.819799 | 0.894982 | psoriasis susceptibility 1 candidate 3 (non-protein coding) |
| 1566721_at | SVEP1 | 0.000278 | 0.821496 | 0.896101 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 |

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|---|---|---|---|---|---|
| 219093_at | PID1 | 0.000608 | 0.822207 | 0.896555 | phosphotyrosine interaction domain containing 1 |
| 214622_at | CYP21A2 | -0.000251 | 0.822836 | 0.896891 | cytochrome P450, family 21, subfamily A, polypeptide 2 |
| 203052_at | C2 | 0.000349 | 0.823993 | 0.897421 | complement component 2 |
| 236972_at | TRIM63 | -0.000292 | 0.827079 | 0.899499 | tripartite motif containing 63, E3 ubiquitin protein ligase |
| 56748_at | TRIM10 | 0.000246 | 0.827297 | 0.899665 | tripartite motif containing 10 |
| 206379_at | EYA3 | -0.000268 | 0.82976 | 0.901036 | eyes absent homolog 3 (Drosophila) |
| 239704_at | RNF144B | 0.000348 | 0.831779 | 0.902344 | ring finger protein 144B |
| 222187_x_at | G3BP1 | 0.000442 | 0.833379 | 0.903279 | GTPase activating protein (SH3 domain) binding protein 1 |
| 229008_at | WDR60 | 0.000286 | 0.835139 | 0.904312 | WD repeat domain 60 |
| 204784_s_at | MLF1 | 0.000633 | 0.83965 | 0.907275 | myeloid leukemia factor 1 |
| 201967_at | RBM6 | 0.00034 | 0.84238 | 0.908999 | RNA binding motif protein 6 |
| 226707_at | NAPRT1 | -0.00058 | 0.850124 | 0.91373 | nicotinate phosphoribosyltransferase domain containing 1 |
| 1565910_at | FSTL4 | -0.000184 | 0.850994 | 0.91427 | follistatin-like 4 |
| 243142_at | FGD6 | 0.000164 | 0.854621 | 0.916474 | FYVE, RhoGEF and PH domain containing 6 |
| 202174_s_at | PCM1 | 0.000216 | 0.856013 | 0.917462 | pericentriolar material 1 |
| 215663_at | MBNL1 | -0.000131 | 0.860459 | 0.919972 | muscleblind-like splicing regulator 1 |
| 208233_at | PDPN | 0.000123 | 0.860519 | 0.919984 | podoplanin |
| 226826_at | LSM11 | -0.000431 | 0.86231 | 0.921059 | LSM11, U7 small nuclear RNA associated |
| 232288_at | PDXDC2 | -0.000228 | 0.86655 | 0.923704 |  |
| 202702_at | TRIM26 | 0.000256 | 0.869753 | 0.925278 | tripartite motif containing 26 |
| 230934_at | STK32C | 0.000219 | 0.870868 | 0.925838 | serine/threonine kinase 32C |
| 205608_s_at | ANGPT1 | 0.000383 | 0.870977 | 0.925908 | angiopoietin 1 |
| 225446_at | BRWD1 | 0.00027 | 0.877217 | 0.929853 | bromodomain and WD repeat domain containing 1 |
| 244092_at | ZRANB3 | 0.000221 | 0.88712 | 0.935713 | zinc finger, RAN-binding domain containing 3 |
| 223099_s_at | LONP2 | -0.00022 | 0.899086 | 0.942975 | lon peptidase 2, peroxisomal |
| 234813_at | TMEM108 | 0.000155 | 0.902126 | 0.94472 | transmembrane protein 108 |
| 205746_s_at | ADAM17 | 0.000267 | 0.903507 | 0.945403 | ADAM metallopeptidase domain 17 |
| 239457_at | ATP8B3 | -0.000203 | 0.903619 | 0.945449 | ATPase, aminophospholipid transporter, class I, type 8B, member 3 |
| 214181_x_at | LST1 | 0.000206 | 0.905283 | 0.946483 | leukocyte specific transcript 1 |
| 205334_at | S100A1 | -0.000223 | 0.905601 | 0.946682 | S100 calcium binding protein A1 |
| 222710_at | AMIGO3 | -0.000117 | 0.905758 | 0.946751 | adhesion molecule with Ig-like domain 3 /// GDP-mannose pyrophosphorylase B |
| 233245_at | UHRF1BP1 | -0.000193 | 0.906559 | 0.947315 | UHRF1 binding protein 1 |
| 228602_at | SGCD | -0.000415 | 0.906807 | 0.947388 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) |
| 225584_at | HCG18 | -0.000292 | 0.90708 | 0.947493 | HLA complex group 18 (non-protein coding) |
| 201188_s_at | ITPR3 | 0.000299 | 0.907963 | 0.948047 | inositol 1,4,5-trisphosphate receptor, type 3 |
| 217411_s_at | RREB1 | -0.000215 | 0.912164 | 0.950283 | ras responsive element binding protein 1 |
| 210763_x_at | NCR3 | 0.000121 | 0.912392 | 0.950463 | natural cytotoxicity triggering receptor 3 |

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|---|---|---|---|---|---|
| 231016_s_at | ARNT | 0.00036 | 0.913121 | 0.95077 | aryl hydrocarbon receptor nuclear translocator |
| 201230_s_at | ARIH2 | 0.000154 | 0.921511 | 0.956122 | ariadne homolog 2 (Drosophila) |
| 223262_s_at | FGFR1OP2 | 0.000153 | 0.927196 | 0.959505 | FGFR1 oncogene partner 2 |
| 213975_s_at | LYZ | -0.000609 | 0.929875 | 0.961094 | lysozyme |
| 226469_s_at | GGT7 | -0.000162 | 0.932268 | 0.962571 | gamma-glutamyltransferase 7 |
| 211583_x_at | NCR3 | 0.000101 | 0.933412 | 0.963129 | natural cytotoxicity triggering receptor 3 |
| 211507_s_at | MTMR3 | -0.000152 | 0.934398 | 0.963564 | myotubularin related protein 3 |
| 238900_at | HLA-DRB5 | 7.95E-05 | 0.936774 | 0.964759 |  |
| 238900_at | HLA-DRB3 | 7.95E-05 | 0.936774 | 0.964759 |  |
| 238900_at | HLA-DRB1 | 7.95E-05 | 0.936774 | 0.964759 |  |
| 218511_s_at | PNPO | 0.000124 | 0.937525 | 0.965188 | pyridoxamine 5'-phosphate oxidase |
| 202984_s_at | BAG5 | -0.000269 | 0.938969 | 0.966056 | BCL2-associated athanogene 5 |
| 217891_at | C16orf5 | -0.000192 | 0.941556 | 0.967613 | chromosome 16 open reading frame 58 |
| 201941_at | CPD | 0.000148 | 0.943203 | 0.968436 | carboxypeptidase D |
| 221002_s_at | TSPAN14 | -0.000146 | 0.943487 | 0.968499 | tetraspanin 14 |
| 226113_at | ZNF436 | 0.00014 | 0.944134 | 0.968987 | zinc finger protein 436 |
| 211627_x_at | ESR1 | 6.44E-05 | 0.945229 | 0.969515 | estrogen receptor 1 |
| 215633_x_at | LST1 | -0.000122 | 0.946156 | 0.970091 | leukocyte specific transcript 1 |
| 1554704_at | ATP8B3 | 7.73E-05 | 0.946998 | 0.970531 | ATPase, aminophospholipid transporter, class I, type 8B, member 3 |
| 215055_at | B3GNTL1 | 9.04E-05 | 0.947562 | 0.970805 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 |
| 203952_at | ATF6 | -8.36E-05 | 0.948439 | 0.971165 | activating transcription factor 6 |
| 242324_x_at | CCBE1 | -0.000138 | 0.952696 | 0.973697 | collagen and calcium binding EGF domains 1 |
| 232036_at | KLC1 | -6.59E-05 | 0.952896 | 0.973752 | kinesin light chain 1 |
| 244747_at | NPNT | -8.36E-05 | 0.955454 | 0.975276 | nephronectin |
| 215536_at | HLA-DQB2 | -7.15E-05 | 0.961751 | 0.978812 | major histocompatibility complex, class II, DQ beta 2 |
| 204577_s_at | CLUAP1 | 8.60E-05 | 0.961792 | 0.978822 | clusterin associated protein 1 |
| 204980_at | CLOCK | -7.50E-05 | 0.962934 | 0.979578 | clock circadian regulator |
| 1562991_at | ZNF292 | 3.61E-05 | 0.964192 | 0.980347 | zinc finger protein 292 |
| 242261_at | IREB2 | -0.000138 | 0.967366 | 0.982205 | iron-responsive element binding protein 2 |
| 212152_x_at | ARID1A | -8.11E-05 | 0.968023 | 0.982439 | AT rich interactive domain 1A (SWI-like) |
| 208393_s_at | RAD50 | 9.06E-05 | 0.969328 | 0.983156 | RAD50 homolog (S. cerevisiae) |
| 212717_at | PLEKHM1 | -4.76E-05 | 0.971096 | 0.983909 | pleckstrin homology domain containing, family M (with RUN domain) member 1 |
| 220567_at | IKZF2 | -4.05E-05 | 0.971546 | 0.984182 | IKAROS family zinc finger 2 (Helios) |
| 233657_at | OPN5 | -3.90E-05 | 0.973307 | 0.985091 | opsin 5 |
| 205309_at | SMPDL3B | -6.30E-05 | 0.977664 | 0.987344 | sphingomyelin phosphodiesterase, acid-like 3B |
| 201642_at | IFNGR2 | -3.28E-05 | 0.977885 | 0.987422 | interferon gamma receptor 2 (interferon gamma transducer 1) |
| 213538_at | SON | 4.51E-05 | 0.978601 | 0.987907 | SON DNA binding protein |

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|---|---|---|---|---|---|
| 226105_at | C1GALT1 | -4.72E-05 | 0.979465 | 0.988361 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 |
| 205032_at | ITGA2 | -6.14E-05 | 0.979704 | 0.988472 | integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) |
| 213020_at | GOSR1 | -4.13E-05 | 0.980421 | 0.988909 | golgi SNAP receptor complex member 1 |
| 241811_x_at | SLC6A4 | -2.06E-05 | 0.983308 | 0.990464 | solute carrier family 6 (neurotransmitter transporter, serotonin), member 4 |
| 223314_at | TSPAN14 | 3.92E-05 | 0.985344 | 0.991742 | tetraspanin 14 |
| 209309_at | AZGP1 | 1.50E-05 | 0.98956 | 0.994233 | alpha-2-glycoprotein 1, zinc-binding |
| 207022_s_at | LDHC | -1.94E-05 | 0.9903 | 0.994684 | lactate dehydrogenase C |
| 215552_s_at | ESR1 | -1.11E-05 | 0.994078 | 0.996661 | estrogen receptor 1 |
| 228432_at | RAB3IP | 7.69E-06 | 0.994759 | 0.996913 | RAB3A interacting protein |
| 204576_s_at | CLUAP1 | 1.04E-05 | 0.995378 | 0.997262 | clusterin associated protein 1 |
| 212352_s_at | TMED10 | 4.81E-06 | 0.995957 | 0.997532 | transmembrane emp24-like trafficking protein 10 (yeast) |
| 227932_at | ARIH2 | -7.16E-06 | 0.997204 | 0.998372 | ariadne homolog 2 (Drosophila) |
| 204779_s_at | HOXB7 | 1.93E-06 | 0.999228 | 0.999557 | homeobox B7 |
| 204779_s_at | HOXB7 | 1.93E-06 | 0.999228 | 0.999557 | NULL |
| 210540_s_at | B4GALT4 | -1.24E-06 | 0.999437 | 0.999675 | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4 |

## Supplementary Table 10: Probesets regression on lung function in individuals from the eQTL study

Table shows results of regression of eSNP-regulated probesets versus FEV$_1$ and FEV$_1$/FVC in 727 individuals from the eQTL study. Probeset ID: probeset tested for association. Gene Symbol: The gene the probeset maps to. Expected direction: the direction of mRNA and lung function inferred from the eSNP's direction of effect on lung function from the GWAS, and its effect on mRNA expression from the eQTL study. Expected vs. observed direction of effect: Whether the observed direction of effect (identified by testing probeset association with lung function measures in the eQTL study) is concordant with the expected one. Concordant means the effect is in the same direction and Discordant means the effect is in the opposite direction. FEV$_1$ Beta: the effect estimate of probeset regression on FEV$_1$ in individuals from the eQTL study. FEV$_1$ SE: the standard error of probeset regression on FEV$_1$ in individuals from the eQTL study. FEV$_1$ P value: the P value for probeset regression on FEV$_1$ in individuals from the eQTL study. FEV$_1$ FDR: the False Discovery Rate (FDR) of associations with FEV$_1$. FEV$_1$/FVC Beta: the effect estimate of probeset regression on FEV$_1$/FVC in individuals from the eQTL study. FEV$_1$/FVC SE: the standard error of probeset regression on FEV$_1$/FVC in individuals from the eQTL study. FEV$_1$/FVC P value: the P value for probeset regression on FEV$_1$/FVC in individuals from the eQTL study. FEV$_1$/FVC FDR: the False Discovery Rate (FDR) of associations with FEV$_1$/FVC

**Probesets regression on lung function in individuals from the eQTL study**

| **Probeset ID** | **Gene Symbol** | **expected Direction** | **Expected vs. Observed Direction** | **FEV$_1$ Beta** | **FEV$_1$ SE** | **FEV$_1$ P.value** | **FEV$_1$ FDR** | **FEV$_1$/FVC Beta** | **FEV$_1$/FVC SE** | **FEV$_1$/FVC P.value** | **FEV$_1$/FVC FDR** |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 100121628_TGI_at | PSORS1C1 | negative | Concordant | -1.03144 | 0.535445 | 0.054064 | 0.292957 | -11.9985 | 9.7679 | 0.219312 | 0.623069 |
| 100121628_TGI_at | PSORS1C1 | positive | Discordant | -1.03144 | 0.535445 | 0.054064 | 0.292957 | -11.9985 | 9.7679 | 0.219312 | 0.623069 |
| 100121683_TGI_at |  | negative | Concordant | -1.07881 | 1.211022 | 0.373021 | 0.695504 | -34.8638 | 21.92013 | 0.111724 | 0.507597 |
| 100121711_TGI_at | FAM177A1 | negative | Concordant | -0.16286 | 0.726381 | 0.822594 | 0.942561 | -11.3558 | 13.12554 | 0.386946 | 0.739358 |
| 100121858_TGI_at | C6orf138 | positive | Concordant | -0.10952 | 0.753989 | 0.884509 | 0.965743 | 7.067203 | 13.87676 | 0.610553 | 0.860732 |
| 100121877_TGI_at | C6orf173 | negative | Concordant | -0.14568 | 0.102001 | 0.153219 | 0.4583 | -3.90328 | 1.874375 | 0.037302 | 0.342664 |
| 100122090_TGI_at | FZD7 | positive | Discordant | 0.0347 | 0.196162 | 0.859591 | 0.95732 | -4.8359 | 3.551078 | 0.173257 | 0.56775 |
| 100122178_TGI_at | C4BPA | negative | Discordant | -0.00246 | 0.004387 | 0.574888 | 0.821133 | -0.06578 | 0.080327 | 0.412858 | 0.761037 |
| 100122211_TGI_at | MON1B | positive | Discordant | -0.15835 | 0.154787 | 0.306311 | 0.622924 | -2.15976 | 2.828895 | 0.445186 | 0.773355 |
| 100122367_TGI_at | ARHGEF19 | negative | Discordant | 0.449859 | 0.343183 | 0.189911 | 0.501991 | 6.284997 | 6.309703 | 0.319209 | 0.671733 |
| 100122720_TGI_at |  | positive | Discordant | -0.56348 | 0.352175 | 0.109598 | 0.417621 | -8.17187 | 6.465436 | 0.206255 | 0.608241 |
| 100122765_TGI_at | THEX1 | positive | Discordant | -0.04712 | 0.162786 | 0.772249 | 0.923606 | -1.5403 | 2.936312 | 0.599882 | 0.860732 |
| 100122767_TGI_at | C18orf10 | negative | Discordant | 0.248803 | 0.136316 | 0.067972 | 0.322578 | 0.782616 | 2.504975 | 0.754718 | 0.930374 |
| 100122809_TGI_at | ROM1 | negative | Concordant | -1.5379 | 0.416394 | 0.000221 | 0.02741 | -15.5544 | 7.808124 | 0.046363 | 0.38285 |
| 100122819_TGI_at | OR13C3 | positive | Discordant | 0.482221 | 2.571653 | 0.851258 | 0.953541 | -6.57446 | 47.00315 | 0.888761 | 0.97411 |
| 100122866_TGI_at | EYA3 | negative | Concordant | -0.04819 | 0.116804 | 0.679953 | 0.883837 | -0.91241 | 2.145789 | 0.670685 | 0.89459 |
| 100122963_TGI_at | PDXDC2 | positive | Discordant | -0.00847 | 0.01247 | 0.497107 | 0.774427 | 0.377056 | 0.229798 | 0.100836 | 0.486596 |
| 100122981_TGI_at | RUNX2 | positive | Concordant | 0.271839 | 0.305728 | 0.373921 | 0.695685 | 11.84435 | 5.620383 | 0.035084 | 0.334258 |
| 100122984_TGI_at | NR3C1 | negative | Discordant | 0.129479 | 0.034719 | 0.000192 | 0.02741 | 1.69345 | 0.633934 | 0.007555 | 0.192653 |
| 100123073_TGI_at | SLC22A5 | negative | Discordant | 0.079958 | 0.118357 | 0.499313 | 0.774427 | 1.208121 | 2.152708 | 0.574654 | 0.847029 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100123120_TGI_at | | positive | Discordant | -0.52737 | 0.622251 | 0.396706 | 0.704177 | 10.33162 | 11.37578 | 0.363766 | 0.726694 |
| 100123137_TGI_at | PIP4K2B | positive | Concordant | 0.13816 | 0.052084 | 0.007987 | 0.125898 | 0.947781 | 0.961355 | 0.324192 | 0.673202 |
| 100123290_TGI_at | CYP2C9 | negative | Discordant | -2.98077 | 3.601892 | 0.407922 | 0.711479 | 14.22858 | 65.14896 | 0.827117 | 0.957068 |
| 100123425_TGI_at | MAPT | negative | Concordant | -0.71372 | 0.546728 | 0.191744 | 0.503948 | -8.9073 | 9.839724 | 0.365339 | 0.728158 |
| 100123483_TGI_at | HCG4P6 | negative | Concordant | -1.2919 | 1.440374 | 0.369762 | 0.692406 | -51.549 | 25.89688 | 0.04653 | 0.38285 |
| 100123483_TGI_at | HCG4P6 | negative | Concordant | -1.2919 | 1.440374 | 0.369762 | 0.692406 | -51.549 | 25.89688 | 0.04653 | 0.38285 |
| 100123483_TGI_at | HCG4P6 | negative | Concordant | -1.2919 | 1.440374 | 0.369762 | 0.692406 | -51.549 | 25.89688 | 0.04653 | 0.38285 |
| 100123483_TGI_at | HCG4P6 | negative | Concordant | -1.2919 | 1.440374 | 0.369762 | 0.692406 | -51.549 | 25.89688 | 0.04653 | 0.38285 |
| 100123512_TGI_at | C1QL3 | negative | Discordant | 0.420478 | 0.647334 | 0.515981 | 0.780157 | 18.8838 | 11.58717 | 0.103162 | 0.486596 |
| 100123597_TGI_at | | negative | Discordant | 5.010515 | 2.224378 | 0.024288 | 0.203166 | 47.56727 | 41.38723 | 0.250423 | 0.638503 |
| 100123606_TGI_at | MLF1 | negative | Concordant | -0.03832 | 0.086423 | 0.657437 | 0.875236 | 0.097852 | 1.560399 | 0.949998 | 0.994854 |
| 100123769_TGI_at | | negative | Discordant | -0.42794 | 0.392688 | 0.275819 | 0.587555 | 2.173034 | 7.148941 | 0.761154 | 0.934186 |
| 100123880_TGI_at | | positive | Discordant | -0.15924 | 0.527479 | 0.762738 | 0.923606 | -2.93051 | 9.555288 | 0.759079 | 0.933506 |
| 100123896_TGI_at | | negative | Discordant | 0.148003 | 0.064386 | 0.021522 | 0.201777 | 0.936677 | 1.162957 | 0.420574 | 0.764753 |
| 100123914_TGI_at | | negative | Discordant | 0.083569 | 0.077868 | 0.28318 | 0.595914 | -0.15564 | 1.416399 | 0.912503 | 0.980193 |
| 100123986_TGI_at | SYTL2 | positive | Concordant | 0.017916 | 0.115384 | 0.876604 | 0.965712 | 1.313888 | 2.083808 | 0.528353 | 0.825639 |
| 100124110_TGI_at | CROCCL1 | negative | Concordant | -0.02834 | 0.033294 | 0.394652 | 0.704177 | -0.1475 | 0.603026 | 0.80677 | 0.950782 |
| 100124148_TGI_at | | negative | Discordant | 0.102172 | 0.09774 | 0.295865 | 0.616622 | 2.291673 | 1.776707 | 0.197105 | 0.598854 |
| 100124184_TGI_at | | negative | Concordant | 0.251383 | 0.386746 | 0.515697 | 0.780157 | -5.39879 | 7.043287 | 0.443369 | 0.772392 |
| 100124184_TGI_at | | negative | Discordant | 0.251383 | 0.386746 | 0.515697 | 0.780157 | -5.39879 | 7.043287 | 0.443369 | 0.772392 |
| 100124216_TGI_at | PTER | positive | Concordant | -0.00013 | 0.15285 | 0.999312 | 0.99936 | -4.08516 | 2.736186 | 0.135434 | 0.536498 |
| 100124251_TGI_at | CNGA1 | negative | Concordant | -1.49789 | 1.164968 | 0.198521 | 0.50837 | -18.853 | 21.0186 | 0.369736 | 0.730277 |
| 100124262_TGI_at | | positive | Concordant | 0.185246 | 0.160435 | 0.248237 | 0.553268 | 0.389141 | 2.935902 | 0.894553 | 0.975569 |
| 100124262_TGI_at | | positive | Concordant | 0.185246 | 0.160435 | 0.248237 | 0.553268 | 0.389141 | 2.935902 | 0.894553 | 0.975569 |
| 100124297_TGI_at | RABAC1 | negative | Concordant | -0.10476 | 0.055003 | 0.056832 | 0.304155 | -1.13093 | 0.999528 | 0.257859 | 0.640563 |
| 100124316_TGI_at | PQLC3 | positive | Concordant | 0.067251 | 0.041046 | 0.101336 | 0.403443 | 0.597433 | 0.74809 | 0.424516 | 0.764753 |
| 100124335_TGI_at | | negative | Concordant | -0.01774 | 0.22635 | 0.937527 | 0.981686 | -2.8292 | 4.076862 | 0.487704 | 0.802352 |
| 100124395_TGI_at | QSOX2 | positive | Discordant | -0.10989 | 0.180267 | 0.542133 | 0.794833 | 4.658527 | 3.244846 | 0.151096 | 0.553455 |
| 100124485_TGI_at | DCXR | positive | Discordant | -0.06385 | 0.046618 | 0.170815 | 0.470154 | -1.87421 | 0.855329 | 0.028436 | 0.301895 |
| 100124630_TGI_at | CCDC91 | positive | Concordant | -0.03416 | 0.114847 | 0.766164 | 0.923606 | 1.344282 | 2.070936 | 0.516262 | 0.820274 |
| 100124649_TGI_at | | negative | Concordant | -3.71212 | 3.660262 | 0.310502 | 0.62316 | -62.4944 | 66.1245 | 0.344607 | 0.698071 |
| 100124708_TGI_at | AMT | positive | Concordant | 0.167924 | 0.090239 | 0.062761 | 0.31384 | 2.800188 | 1.66758 | 0.093115 | 0.469363 |
| 100124708_TGI_at | AMT | positive | Concordant | 0.167924 | 0.090239 | 0.062761 | 0.31384 | 2.800188 | 1.66758 | 0.093115 | 0.469363 |
| 100124857_TGI_at | ITPKA | positive | Concordant | -0.88786 | 1.163244 | 0.445307 | 0.733564 | -0.87072 | 21.00837 | 0.96694 | 0.999082 |
| 100124865_TGI_at | RBM6 | positive | Concordant | 0.083308 | 0.06751 | 0.217201 | 0.523093 | 2.332627 | 1.231266 | 0.058159 | 0.413224 |
| 100125007_TGI_at | C6orf12 | negative | Concordant | -0.17012 | 0.464519 | 0.714187 | 0.899455 | 11.81391 | 8.448786 | 0.162024 | 0.560509 |
| 100125007_TGI_at | C6orf12 | negative | Concordant | -0.17012 | 0.464519 | 0.714187 | 0.899455 | 11.81391 | 8.448786 | 0.162024 | 0.560509 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100125007_TGI_at | C6orf12 | negative | Discordant | -0.17012 | 0.464519 | 0.714187 | 0.899455 | 11.81391 | 8.448786 | 0.162024 | 0.560509 |
| 100125007_TGI_at | C6orf12 | negative | Discordant | -0.17012 | 0.464519 | 0.714187 | 0.899455 | 11.81391 | 8.448786 | 0.162024 | 0.560509 |
| 100125191_TGI_at | HLA-DQA2 | negative | Discordant | 1.116749 | 0.520928 | 0.032051 | 0.234777 | 16.09414 | 9.486978 | 0.089802 | 0.460698 |
| 100125275_TGI_at | HLA-DRB1 | negative | Concordant | -0.00185 | 0.013128 | 0.888113 | 0.965743 | -0.15769 | 0.236136 | 0.504273 | 0.814654 |
| 100125275_TGI_at | HLA-DRB1 | negative | Concordant | -0.00185 | 0.013128 | 0.888113 | 0.965743 | -0.15769 | 0.236136 | 0.504273 | 0.814654 |
| 100125275_TGI_at | HLA-DRB1 | positive | Discordant | -0.00185 | 0.013128 | 0.888113 | 0.965743 | -0.15769 | 0.236136 | 0.504273 | 0.814654 |
| 100125319_TGI_at | ZSWIM7 | negative | Discordant | 0.203902 | 0.104932 | 0.051994 | 0.285485 | 2.023544 | 1.899727 | 0.286796 | 0.64733 |
| 100125489_TGI_at | SFTA2 | negative | Discordant | 0.005885 | 0.012117 | 0.627216 | 0.852345 | 0.04712 | 0.22032 | 0.830649 | 0.957068 |
| 100125489_TGI_at | SFTA2 | negative | Discordant | 0.005885 | 0.012117 | 0.627216 | 0.852345 | 0.04712 | 0.22032 | 0.830649 | 0.957068 |
| 100125493_TGI_at | ZNF132 | negative | Concordant | 0.036263 | 0.317806 | 0.909156 | 0.971934 | -6.09989 | 5.722658 | 0.28646 | 0.64733 |
| 100125530_TGI_at | CTSS | positive | Concordant | -0.00383 | 0.012983 | 0.767931 | 0.923606 | -0.41316 | 0.234777 | 0.078438 | 0.447721 |
| 100125670_TGI_at | C9orf95 | positive | Concordant | 0.009874 | 0.068232 | 0.884938 | 0.965743 | 0.021014 | 1.239417 | 0.986472 | 0.999082 |
| 100125704_TGI_at | CYFIP2 | positive | Discordant | -0.03238 | 0.106255 | 0.760542 | 0.923606 | -2.30508 | 1.907175 | 0.226802 | 0.623069 |
| 100125842_TGI_at | NCR3 | negative | Concordant | -0.22024 | 0.287299 | 0.443318 | 0.733269 | -5.97655 | 5.165976 | 0.24731 | 0.638503 |
| 100125842_TGI_at | NCR3 | negative | Concordant | -0.22024 | 0.287299 | 0.443318 | 0.733269 | -5.97655 | 5.165976 | 0.24731 | 0.638503 |
| 100125900_TGI_at | NLRC3 | positive | Concordant | 0.025086 | 0.069174 | 0.716867 | 0.899455 | -0.11409 | 1.252571 | 0.927425 | 0.989025 |
| 100125980_TGI_at | YEATS4 | positive | Concordant | 0.193792 | 0.236038 | 0.411633 | 0.711479 | 1.079233 | 4.275737 | 0.800725 | 0.9484 |
| 100126013_TGI_at | WDR52 | negative | Concordant | -0.02515 | 0.123008 | 0.837972 | 0.949702 | -0.82958 | 2.206869 | 0.706985 | 0.915742 |
| 100126116_TGI_at | GBP3 | negative | Discordant | -0.03155 | 0.030858 | 0.306649 | 0.622924 | 0.109219 | 0.556983 | 0.84454 | 0.958398 |
| 100126124_TGI_at | S100A1 | positive | Discordant | -0.22779 | 0.290916 | 0.433612 | 0.724358 | -3.13325 | 5.192869 | 0.546259 | 0.83676 |
| 100126143_TGI_at | APOM | positive | Discordant | 0.667582 | 0.39942 | 0.094647 | 0.39476 | -5.90336 | 7.2218 | 0.413679 | 0.761037 |
| 100126143_TGI_at | APOM | positive | Discordant | 0.667582 | 0.39942 | 0.094647 | 0.39476 | -5.90336 | 7.2218 | 0.413679 | 0.761037 |
| 100126143_TGI_at | APOM | positive | Concordant | 0.667582 | 0.39942 | 0.094647 | 0.39476 | -5.90336 | 7.2218 | 0.413679 | 0.761037 |
| 100126143_TGI_at | APOM | positive | Concordant | 0.667582 | 0.39942 | 0.094647 | 0.39476 | -5.90336 | 7.2218 | 0.413679 | 0.761037 |
| 100126167_TGI_at | | positive | Discordant | 0.104423 | 0.736698 | 0.887281 | 0.965743 | -3.42737 | 13.28974 | 0.796487 | 0.9484 |
| 100126192_TGI_at | TRIM26 | negative | Concordant | -0.05286 | 0.140732 | 0.707182 | 0.896688 | -3.76134 | 2.579485 | 0.144792 | 0.549177 |
| 100126219_TGI_at | | positive | Concordant | 0.74625 | 0.268332 | 0.005418 | 0.099945 | 8.505875 | 4.867585 | 0.080559 | 0.447721 |
| 100126253_TGI_at | TH1L | negative | Concordant | -0.05495 | 0.085237 | 0.519136 | 0.781408 | -0.21101 | 1.548772 | 0.891628 | 0.974832 |
| 100126288_TGI_at | ADAM17 | positive | Concordant | 0.004616 | 0.071101 | 0.948239 | 0.984579 | 0.623071 | 1.285298 | 0.627841 | 0.870942 |
| 100126558_TGI_at | RHOBTB3 | positive | Concordant | -0.03421 | 0.061793 | 0.579886 | 0.82238 | 1.733299 | 1.122007 | 0.12239 | 0.516945 |
| 100126573_TGI_at | TRIM4 | negative | Concordant | -0.16585 | 0.112963 | 0.14206 | 0.445546 | -2.98396 | 2.062116 | 0.147887 | 0.550292 |
| 100126588_TGI_at | BAG5 | negative | Concordant | -0.08514 | 0.066738 | 0.202064 | 0.509426 | -0.06626 | 1.213594 | 0.956459 | 0.995701 |
| 100126588_TGI_at | BAG5 | positive | Discordant | -0.08514 | 0.066738 | 0.202064 | 0.509426 | -0.06626 | 1.213594 | 0.956459 | 0.995701 |
| 100126591_TGI_at | HLA-DOA | positive | Concordant | 0.008631 | 0.011276 | 0.444021 | 0.733269 | -0.13078 | 0.204567 | 0.522634 | 0.821114 |
| 100126665_TGI_at | AGPAT1 | positive | Discordant | -0.06454 | 0.072179 | 0.371214 | 0.693627 | -1.0562 | 1.298329 | 0.415926 | 0.761788 |
| 100126665_TGI_at | AGPAT1 | positive | Discordant | -0.06454 | 0.072179 | 0.371214 | 0.693627 | -1.0562 | 1.298329 | 0.415926 | 0.761788 |
| 100126665_TGI_at | AGPAT1 | positive | Discordant | -0.06454 | 0.072179 | 0.371214 | 0.693627 | -1.0562 | 1.298329 | 0.415926 | 0.761788 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100126667_TGI_at | KIAA0317 | negative | Discordant | 0.176307 | 0.141013 | 0.211191 | 0.516353 | 3.244058 | 2.565758 | 0.206099 | 0.608241 |
| 100126781_TGI_at | LY6G5C | positive | Discordant | -0.27725 | 0.243955 | 0.255752 | 0.564215 | -2.04016 | 4.520176 | 0.651741 | 0.887779 |
| 100126781_TGI_at | LY6G5C | positive | Discordant | -0.27725 | 0.243955 | 0.255752 | 0.564215 | -2.04016 | 4.520176 | 0.651741 | 0.887779 |
| 100127159_TGI_at | HLA-DRB4 | positive | Concordant | 0.001887 | 0.002714 | 0.487008 | 0.765308 | 0.052041 | 0.048923 | 0.287453 | 0.64733 |
| 100127159_TGI_at | HLA-DRB4 | negative | Discordant | 0.001887 | 0.002714 | 0.487008 | 0.765308 | 0.052041 | 0.048923 | 0.287453 | 0.64733 |
| 100127382_TGI_at | TMEM50B | negative | Discordant | 0.057924 | 0.042586 | 0.173781 | 0.475293 | 1.56554 | 0.772497 | 0.042704 | 0.366575 |
| 100127501_TGI_at | MEST | positive | Discordant | -0.05271 | 0.026523 | 0.046904 | 0.269292 | -0.53347 | 0.488648 | 0.274949 | 0.64407 |
| 100127522_TGI_at | RPS19 | negative | Concordant | -0.02683 | 0.014222 | 0.059218 | 0.307435 | -0.74948 | 0.257563 | 0.003615 | 0.125383 |
| 100127527_TGI_at | | negative | Discordant | -0.14087 | 0.625791 | 0.821891 | 0.942561 | -2.36257 | 11.34186 | 0.834991 | 0.957588 |
| 100127553_TGI_at | ZNF584 | negative | Concordant | -0.37426 | 0.187119 | 0.045487 | 0.269292 | -1.76922 | 3.407684 | 0.603631 | 0.860732 |
| 100127556_TGI_at | TRIM38 | positive | Discordant | -0.1607 | 0.057079 | 0.004873 | 0.09827 | -3.85458 | 1.034888 | 0.000196 | 0.024226 |
| 100127556_TGI_at | TRIM38 | positive | Discordant | -0.1607 | 0.057079 | 0.004873 | 0.09827 | -3.85458 | 1.034888 | 0.000196 | 0.024226 |
| 100127649_TGI_at | ZNF436 | positive | Concordant | 0.398921 | 0.231404 | 0.084724 | 0.373119 | 5.365446 | 4.218303 | 0.203393 | 0.606239 |
| 100127661_TGI_at | EIF2B2 | negative | Concordant | -0.22619 | 0.161503 | 0.161347 | 0.461656 | -4.51738 | 2.965764 | 0.127715 | 0.529803 |
| 100127780_TGI_at | | positive | Discordant | -0.09283 | 0.081496 | 0.254677 | 0.563278 | -0.49246 | 1.460957 | 0.736058 | 0.92225 |
| 100127813_TGI_at | | negative | Concordant | -2.17753 | 2.134918 | 0.307748 | 0.622924 | -38.0767 | 38.429 | 0.321767 | 0.67176 |
| 100128165_TGI_at | C21orf82 | negative | Concordant | -3.0377 | 0.862929 | 0.000431 | 0.033986 | -51.7732 | 15.71048 | 0.000983 | 0.065533 |
| 100128225_TGI_at | FGFBP3 | negative | Discordant | 0.625554 | 0.315895 | 0.047674 | 0.269292 | 7.336234 | 5.693291 | 0.197546 | 0.598854 |
| 100128463_TGI_at | | negative | Discordant | 0.561017 | 0.194516 | 0.003925 | 0.091961 | 8.201414 | 3.545683 | 0.020719 | 0.273703 |
| 100128577_TGI_at | ACP6 | positive | Discordant | -0.01465 | 0.145561 | 0.919839 | 0.972561 | -1.59375 | 2.638111 | 0.545761 | 0.83676 |
| 100128579_TGI_at | UHRF1BP1 | positive | Discordant | 0.076209 | 0.074462 | 0.306086 | 0.622924 | 0.214732 | 1.348828 | 0.873512 | 0.966864 |
| 100128819_TGI_at | MPP6 | positive | Discordant | -1.81321 | 0.955647 | 0.05778 | 0.306533 | -4.61047 | 17.29752 | 0.789824 | 0.947133 |
| 100128894_TGI_at | HCG27 | negative | Concordant | -0.30271 | 0.371719 | 0.415441 | 0.713242 | 2.282034 | 6.666022 | 0.732096 | 0.92225 |
| 100128894_TGI_at | HCG27 | positive | Concordant | -0.30271 | 0.371719 | 0.415441 | 0.713242 | 2.282034 | 6.666022 | 0.732096 | 0.92225 |
| 100129019_TGI_at | TYRO3 | positive | Discordant | -0.3323 | 0.220922 | 0.13254 | 0.440276 | -0.74935 | 4.094867 | 0.8548 | 0.963575 |
| 100129037_TGI_at | TAP2 | negative | Concordant | 0.68505 | 0.494496 | 0.165946 | 0.464112 | -4.58976 | 8.934076 | 0.607436 | 0.860732 |
| 100129037_TGI_at | TAP2 | negative | Discordant | 0.68505 | 0.494496 | 0.165946 | 0.464112 | -4.58976 | 8.934076 | 0.607436 | 0.860732 |
| 100129059_TGI_at | ANXA6 | positive | Discordant | -0.62689 | 0.280742 | 0.02555 | 0.20322 | -14.072 | 5.212794 | 0.006944 | 0.188142 |
| 100129207_TGI_at | FMO2 | positive | Discordant | 0.009171 | 0.014142 | 0.516683 | 0.780157 | -0.09015 | 0.255749 | 0.72447 | 0.921701 |
| 100129209_TGI_at | | negative | Discordant | -0.16951 | 0.13155 | 0.197554 | 0.508246 | 0.709245 | 2.392495 | 0.76689 | 0.93779 |
| 100129234_TGI_at | CCBE1 | positive | Concordant | 0.418042 | 0.178174 | 0.018963 | 0.201777 | 5.901351 | 3.253251 | 0.06968 | 0.427671 |
| 100129239_TGI_at | IREB2 | negative | Concordant | 0.525664 | 0.438226 | 0.230323 | 0.532507 | -3.92444 | 7.915373 | 0.620035 | 0.865125 |
| 100129239_TGI_at | IREB2 | negative | Discordant | 0.525664 | 0.438226 | 0.230323 | 0.532507 | -3.92444 | 7.915373 | 0.620035 | 0.865125 |
| 100129276_TGI_at | | negative | Discordant | 2.232726 | 0.654389 | 0.000645 | 0.034954 | 18.38725 | 11.9354 | 0.123423 | 0.516945 |
| 100129279_TGI_at | HCG22 | positive | Concordant | 0.348495 | 1.808092 | 0.847161 | 0.952951 | -27.9018 | 33.03407 | 0.398313 | 0.74587 |
| 100129279_TGI_at | HCG22 | negative | Concordant | 0.348495 | 1.808092 | 0.847161 | 0.952951 | -27.9018 | 33.03407 | 0.398313 | 0.74587 |
| 100129291_TGI_at | | negative | Concordant | -0.51169 | 0.840622 | 0.542723 | 0.794833 | -11.0012 | 15.25121 | 0.470704 | 0.794832 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100129349_TGI_at | HLA-A | positive | Concordant | 0.006637 | 0.004318 | 0.124239 | 0.431533 | 0.067097 | 0.079832 | 0.400647 | 0.748623 |
| 100129349_TGI_at | HLA-A | positive | Concordant | 0.006637 | 0.004318 | 0.124239 | 0.431533 | 0.067097 | 0.079832 | 0.400647 | 0.748623 |
| 100129349_TGI_at | HLA-A | positive | Concordant | 0.006637 | 0.004318 | 0.124239 | 0.431533 | 0.067097 | 0.079832 | 0.400647 | 0.748623 |
| 100129349_TGI_at | HLA-A | positive | Concordant | 0.006637 | 0.004318 | 0.124239 | 0.431533 | 0.067097 | 0.079832 | 0.400647 | 0.748623 |
| 100129380_TGI_at | | positive | Discordant | 0.070745 | 0.52215 | 0.892226 | 0.965743 | -2.65177 | 9.507971 | 0.780322 | 0.941122 |
| 100129400_TGI_at | C1orf113 | positive | Discordant | 0.122963 | 0.205289 | 0.549189 | 0.797566 | 1.260316 | 3.784775 | 0.739137 | 0.92225 |
| 100129443_TGI_at | GPC5 | negative | Concordant | 0.360007 | 0.687668 | 0.600614 | 0.832554 | -0.01437 | 12.48933 | 0.999082 | 0.999082 |
| 100129450_TGI_at | NICN1 | negative | Discordant | -0.05493 | 0.13115 | 0.67535 | 0.883837 | 0.832631 | 2.364205 | 0.724701 | 0.921701 |
| 100129450_TGI_at | NICN1 | negative | Concordant | -0.05493 | 0.13115 | 0.67535 | 0.883837 | 0.832631 | 2.364205 | 0.724701 | 0.921701 |
| 100129463_TGI_at | RPRD2 | negative | Discordant | 0.298014 | 0.118314 | 0.011775 | 0.150127 | 2.774774 | 2.177824 | 0.202627 | 0.606239 |
| 100129487_TGI_at | NR3C1 | negative | Discordant | 0.153224 | 0.040276 | 0.000142 | 0.02741 | 1.88327 | 0.742803 | 0.011233 | 0.215815 |
| 100129499_TGI_at | C22orf34 | negative | Concordant | -0.1895 | 0.1268 | 0.135047 | 0.443506 | -2.04383 | 2.314443 | 0.377196 | 0.730287 |
| 100129573_TGI_at | WDR60 | positive | Discordant | 0.034302 | 0.068428 | 0.616174 | 0.841142 | 0.877696 | 1.241615 | 0.479629 | 0.80052 |
| 100129584_TGI_at | | negative | Discordant | 3.168682 | 4.358657 | 0.467235 | 0.751563 | 1.16045 | 78.60241 | 0.988221 | 0.999082 |
| 100129584_TGI_at | | negative | Discordant | 3.168682 | 4.358657 | 0.467235 | 0.751563 | 1.16045 | 78.60241 | 0.988221 | 0.999082 |
| 100129584_TGI_at | | negative | Discordant | 3.168682 | 4.358657 | 0.467235 | 0.751563 | 1.16045 | 78.60241 | 0.988221 | 0.999082 |
| 100129585_TGI_at | CCBE1 | positive | Concordant | 0.191858 | 0.195645 | 0.326768 | 0.641332 | 5.183769 | 3.574089 | 0.146954 | 0.549177 |
| 100129603_TGI_at | | positive | Concordant | 1.20403 | 3.002799 | 0.688443 | 0.889538 | 20.77091 | 55.16836 | 0.706545 | 0.915742 |
| 100129603_TGI_at | | negative | Discordant | 1.20403 | 3.002799 | 0.688443 | 0.889538 | 20.77091 | 55.16836 | 0.706545 | 0.915742 |
| 100129666_TGI_at | ANGPT1 | negative | Discordant | 0.001816 | 0.025734 | 0.943737 | 0.983056 | 0.19417 | 0.470411 | 0.679777 | 0.901173 |
| 100129691_TGI_at | PNPO | negative | Concordant | -0.03181 | 0.111573 | 0.775531 | 0.923606 | -3.732 | 2.008659 | 0.063175 | 0.421332 |
| 100129724_TGI_at | SEC61A2 | positive | Concordant | 0.305444 | 0.321903 | 0.342686 | 0.66319 | 4.850961 | 5.786391 | 0.40184 | 0.749237 |
| 100129724_TGI_at | SEC61A2 | positive | Concordant | 0.305444 | 0.321903 | 0.342686 | 0.66319 | 4.850961 | 5.786391 | 0.40184 | 0.749237 |
| 100129781_TGI_at | CLOCK | negative | Concordant | -1.09433 | 0.438264 | 0.012526 | 0.155142 | -19.0549 | 7.915976 | 0.016078 | 0.240338 |
| 100129781_TGI_at | CLOCK | negative | Concordant | -1.09433 | 0.438264 | 0.012526 | 0.155142 | -19.0549 | 7.915976 | 0.016078 | 0.240338 |
| 100129848_TGI_at | MLH3 | negative | Concordant | 0.468038 | 0.282946 | 0.098095 | 0.398532 | 0.142803 | 5.163964 | 0.977938 | 0.999082 |
| 100129852_TGI_at | | negative | Concordant | 0.207559 | 0.610124 | 0.733712 | 0.910662 | 3.797809 | 11.34232 | 0.737749 | 0.92225 |
| 100129915_TGI_at | NPNT | negative | Discordant | 0.013216 | 0.009918 | 0.182668 | 0.49021 | 0.458524 | 0.180245 | 0.010962 | 0.215815 |
| 100129915_TGI_at | NPNT | negative | Discordant | 0.013216 | 0.009918 | 0.182668 | 0.49021 | 0.458524 | 0.180245 | 0.010962 | 0.215815 |
| 100130226_TGI_at | NCKIPSD | positive | Discordant | -0.21057 | 0.104141 | 0.043183 | 0.265194 | -1.93538 | 1.897177 | 0.307663 | 0.670538 |
| 100130228_TGI_at | | negative | Discordant | -0.06857 | 0.113495 | 0.545745 | 0.796047 | 3.115943 | 2.078964 | 0.133927 | 0.536498 |
| 100130289_TGI_at | PLA2G5 | positive | Concordant | 0.196658 | 0.259104 | 0.447857 | 0.733676 | 4.98771 | 4.679199 | 0.286454 | 0.64733 |
| 100130314_TGI_at | | positive | Discordant | -0.65916 | 0.286447 | 0.021384 | 0.201777 | -16.2672 | 5.059825 | 0.001305 | 0.080793 |
| 100130355_TGI_at | | positive | Concordant | 0.13685 | 0.060661 | 0.024073 | 0.203166 | 3.011282 | 1.0913 | 0.005792 | 0.161978 |
| 100130519_TGI_at | SLC4A8 | positive | Concordant | 3.236132 | 1.02304 | 0.00156 | 0.054107 | 55.66682 | 18.56278 | 0.00271 | 0.106802 |
| 100130540_TGI_at | | negative | Concordant | -0.07531 | 0.094884 | 0.427351 | 0.719444 | -2.6987 | 1.738634 | 0.120615 | 0.516945 |
| 100130569_TGI_at | | negative | Discordant | 0.350542 | 0.153726 | 0.02259 | 0.203023 | 6.267922 | 2.818593 | 0.026163 | 0.301895 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100130614_TGI_at | ANAPC4 | negative | Discordant | 0.115718 | 0.051764 | 0.025384 | 0.20322 | 1.339181 | 0.943321 | 0.155711 | 0.560509 |
| 100130622_TGI_at | SLMO2 | negative | Concordant | -0.10457 | 0.110918 | 0.345795 | 0.666231 | 1.059934 | 1.998017 | 0.59577 | 0.860732 |
| 100130701_TGI_at | SRD5A3 | negative | Concordant | -0.15498 | 0.057985 | 0.007524 | 0.121882 | -2.37872 | 1.040558 | 0.022254 | 0.287971 |
| 100130701_TGI_at | SRD5A3 | negative | Concordant | -0.15498 | 0.057985 | 0.007524 | 0.121882 | -2.37872 | 1.040558 | 0.022254 | 0.287971 |
| 100130704_TGI_at | | positive | Concordant | 0.24199 | 0.14552 | 0.096326 | 0.398532 | 3.809352 | 2.640941 | 0.149183 | 0.550391 |
| 100130789_TGI_at | | positive | Concordant | 0.640799 | 0.338482 | 0.058337 | 0.306533 | 11.45281 | 6.133147 | 0.061851 | 0.421332 |
| 100130835_TGI_at | SON | negative | Concordant | -0.07155 | 0.179123 | 0.689576 | 0.889676 | -2.176 | 3.261795 | 0.504697 | 0.814654 |
| 100131043_TGI_at | PCBP2 | positive | Discordant | -0.0409 | 0.027771 | 0.140849 | 0.445546 | -0.91478 | 0.505198 | 0.070183 | 0.427671 |
| 100131090_TGI_at | NIPSNAP1 | positive | Discordant | -0.03602 | 0.131936 | 0.784841 | 0.928221 | -2.06016 | 2.379202 | 0.386542 | 0.739358 |
| 100131217_TGI_at | HCG18 | positive | Concordant | 0.086066 | 0.205011 | 0.674622 | 0.883837 | 0.207023 | 3.746184 | 0.955929 | 0.995701 |
| 100131217_TGI_at | HCG18 | negative | Discordant | 0.086066 | 0.205011 | 0.674622 | 0.883837 | 0.207023 | 3.746184 | 0.955929 | 0.995701 |
| 100131401_TGI_at | C5orf35 | positive | Discordant | -0.31897 | 0.277229 | 0.249915 | 0.55558 | -8.16106 | 5.041984 | 0.105529 | 0.491902 |
| 100131579_TGI_at | CACNA2D4 | negative | Concordant | 0.218601 | 0.838257 | 0.794262 | 0.930575 | -9.15938 | 15.36276 | 0.551037 | 0.837177 |
| 100131760_TGI_at | ITPR3 | negative | Discordant | 0.031858 | 2.483572 | 0.989765 | 0.996398 | 19.62455 | 44.93823 | 0.662329 | 0.888268 |
| 100131939_TGI_at | IQGAP3 | negative | Concordant | -0.35498 | 1.587213 | 0.823028 | 0.942561 | -9.19648 | 28.70217 | 0.748657 | 0.928592 |
| 100132001_TGI_at | PDGFD | negative | Concordant | -0.43773 | 0.187376 | 0.019485 | 0.201777 | -6.62947 | 3.374673 | 0.049475 | 0.39368 |
| 100132051_TGI_at | NDUFAF1 | positive | Discordant | -0.03274 | 0.169904 | 0.847219 | 0.952951 | -4.74037 | 3.066744 | 0.122169 | 0.516945 |
| 100132055_TGI_at | PDDC1 | negative | Discordant | 0.056941 | 0.036515 | 0.118909 | 0.427778 | 0.900073 | 0.661363 | 0.173534 | 0.56775 |
| 100132153_TGI_at | RAD50 | negative | Discordant | 0.046131 | 0.150272 | 0.758854 | 0.923606 | 1.759798 | 2.709422 | 0.516009 | 0.820274 |
| 100132235_TGI_at | PTER | negative | Discordant | 0.001491 | 0.390338 | 0.996951 | 0.999257 | 1.407376 | 7.065751 | 0.84212 | 0.958398 |
| 100132261_TGI_at | SDK1 | positive | Discordant | -0.11824 | 0.081559 | 0.147129 | 0.452342 | -2.73976 | 1.471965 | 0.062703 | 0.421332 |
| 100132327_TGI_at | ADAM19 | negative | Concordant | -0.09904 | 0.069309 | 0.153032 | 0.4583 | -1.30955 | 1.252523 | 0.295777 | 0.656435 |
| 100132327_TGI_at | ADAM19 | negative | Concordant | -0.09904 | 0.069309 | 0.153032 | 0.4583 | -1.30955 | 1.252523 | 0.295777 | 0.656435 |
| 100132347_TGI_at | | negative | Discordant | -0.23737 | 0.272498 | 0.3837 | 0.702316 | 2.304164 | 5.005822 | 0.645303 | 0.88421 |
| 100132374_TGI_at | ITIH4 | positive | Discordant | -0.03192 | 0.184103 | 0.862361 | 0.95732 | -0.88877 | 3.414988 | 0.794666 | 0.9484 |
| 100132397_TGI_at | | negative | Concordant | 0.03342 | 0.132193 | 0.800411 | 0.931838 | -0.80621 | 2.443445 | 0.741438 | 0.922277 |
| 100132397_TGI_at | | negative | Concordant | 0.03342 | 0.132193 | 0.800411 | 0.931838 | -0.80621 | 2.443445 | 0.741438 | 0.922277 |
| 100132425_TGI_at | | positive | Discordant | -0.23534 | 0.718351 | 0.743208 | 0.911402 | -10.2459 | 13.05519 | 0.43256 | 0.767727 |
| 100132449_TGI_at | ANGPTL6 | negative | Concordant | 0.426588 | 1.272325 | 0.737412 | 0.910662 | -16.8621 | 22.99029 | 0.463287 | 0.787588 |
| 100132596_TGI_at | FMO2 | positive | Concordant | 0.014553 | 0.01026 | 0.156071 | 0.459406 | 0.113195 | 0.185278 | 0.541233 | 0.83348 |
| 100132638_TGI_at | ITIH5 | negative | Discordant | 0.290947 | 0.084284 | 0.000556 | 0.034954 | 5.924929 | 1.562228 | 0.000149 | 0.022389 |
| 100132808_TGI_at | TTC19 | negative | Discordant | 0.06934 | 0.049816 | 0.163942 | 0.461656 | 2.835117 | 0.89765 | 0.001587 | 0.080912 |
| 100132831_TGI_at | | positive | Concordant | 0.39167 | 0.473087 | 0.407726 | 0.711479 | 9.637805 | 8.607681 | 0.262852 | 0.64407 |
| 100132932_TGI_at | GPATCH2 | positive | Concordant | 0.255638 | 0.196964 | 0.194324 | 0.506885 | 6.275664 | 3.541481 | 0.076387 | 0.447721 |
| 100133163_TGI_at | MFAP2 | negative | Concordant | -0.14498 | 0.113317 | 0.200747 | 0.509426 | -0.77088 | 2.076584 | 0.710468 | 0.915742 |
| 100133258_TGI_at | HBS1L | positive | Discordant | -0.08013 | 0.235037 | 0.733175 | 0.910662 | 1.623536 | 4.249383 | 0.702414 | 0.915742 |
| 100133349_TGI_at | ARHGAP27 | negative | Concordant | 0.018979 | 0.138083 | 0.890676 | 0.965743 | 2.689982 | 2.504981 | 0.282889 | 0.64733 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100133405_TGI_at | TRIM10 | negative | Discordant | 1.905958 | 1.024485 | 0.062828 | 0.31384 | 12.20625 | 18.37284 | 0.506458 | 0.814654 |
| 100133464_TGI_at | PILRB | positive | Concordant | 0.006125 | 0.013649 | 0.653645 | 0.873359 | 0.272585 | 0.248797 | 0.273248 | 0.64407 |
| 100133511_TGI_at | HLA-DOB | negative | Concordant | -0.01186 | 0.091007 | 0.896272 | 0.966995 | -2.29004 | 1.628965 | 0.159777 | 0.560509 |
| 100133530_TGI_at | ZRANB3 | negative | Concordant | -2.1438 | 1.021766 | 0.035893 | 0.238611 | -45.7264 | 18.70497 | 0.014501 | 0.228584 |
| 100133629_TGI_at | | negative | Concordant | -0.10995 | 0.097627 | 0.26007 | 0.572286 | -2.75074 | 1.745249 | 0.114995 | 0.509594 |
| 100133670_TGI_at | | negative | Discordant | 0.15613 | 0.153651 | 0.309565 | 0.622924 | 2.42323 | 2.793505 | 0.385695 | 0.739358 |
| 100133670_TGI_at | | negative | Discordant | 0.15613 | 0.153651 | 0.309565 | 0.622924 | 2.42323 | 2.793505 | 0.385695 | 0.739358 |
| 100133695_TGI_at | C6orf66 | negative | Concordant | -0.20664 | 0.092089 | 0.024839 | 0.203166 | -2.51517 | 1.676249 | 0.133491 | 0.536498 |
| 100133810_TGI_at | TMEM110 | negative | Concordant | -0.13634 | 0.081588 | 0.094706 | 0.39476 | -1.77643 | 1.501635 | 0.236811 | 0.631062 |
| 100133838_TGI_at | KCNMB3 | negative | Concordant | -0.11186 | 0.400782 | 0.780162 | 0.926576 | -0.94916 | 7.309672 | 0.896686 | 0.976666 |
| 100133899_TGI_at | | negative | Concordant | -0.00961 | 0.012039 | 0.424876 | 0.718939 | -0.30028 | 0.218075 | 0.16853 | 0.564154 |
| 100133899_TGI_at | | negative | Concordant | -0.00961 | 0.012039 | 0.424876 | 0.718939 | -0.30028 | 0.218075 | 0.16853 | 0.564154 |
| 100133960_TGI_at | P4HA3 | negative | Concordant | -0.57495 | 0.468593 | 0.219835 | 0.523661 | 0.101083 | 8.524368 | 0.990539 | 0.999082 |
| 100134025_TGI_at | CCDC77 | negative | Discordant | 0.218307 | 0.136056 | 0.108595 | 0.417621 | 0.509992 | 2.479429 | 0.837033 | 0.957828 |
| 100134179_TGI_at | PCM1 | negative | Discordant | 0.066149 | 0.043195 | 0.125667 | 0.431533 | 0.721053 | 0.802878 | 0.36914 | 0.730277 |
| 100134209_TGI_at | | negative | Discordant | 2.472337 | 0.638234 | 0.000107 | 0.02741 | 35.08858 | 11.62315 | 0.002537 | 0.104756 |
| 100134215_TGI_at | FBXO38 | negative | Concordant | -0.00903 | 0.064947 | 0.889384 | 0.965743 | 1.048977 | 1.179456 | 0.373802 | 0.730277 |
| 100134215_TGI_at | FBXO38 | negative | Discordant | -0.00903 | 0.064947 | 0.889384 | 0.965743 | 1.048977 | 1.179456 | 0.373802 | 0.730277 |
| 100134381_TGI_at | LONP2 | negative | Concordant | -0.32248 | 0.187999 | 0.086283 | 0.373243 | -7.07718 | 3.402868 | 0.037547 | 0.342664 |
| 100134576_TGI_at | PSMB3 | positive | Discordant | -0.04234 | 0.03321 | 0.20232 | 0.509426 | -1.11311 | 0.608113 | 0.067186 | 0.426441 |
| 100134593_TGI_at | | negative | Concordant | -0.03344 | 0.023617 | 0.156844 | 0.459406 | -0.5952 | 0.424497 | 0.160878 | 0.560509 |
| 100134693_TGI_at | CLTB | negative | Concordant | -0.00946 | 0.026828 | 0.724384 | 0.905521 | -0.1708 | 0.487433 | 0.726034 | 0.921701 |
| 100134728_TGI_at | GRK4 | negative | Concordant | -0.88634 | 0.696885 | 0.203422 | 0.509426 | -0.4964 | 12.98726 | 0.969511 | 0.999082 |
| 100134750_TGI_at | SPTBN5 | positive | Discordant | -0.59659 | 0.470159 | 0.204475 | 0.509426 | -14.2227 | 8.615011 | 0.098755 | 0.486596 |
| 100134955_TGI_at | ZADH2 | positive | Concordant | 0.67267 | 0.315924 | 0.033236 | 0.236522 | 6.62415 | 5.755104 | 0.24973 | 0.638503 |
| 100134957_TGI_at | MRPL43 | positive | Discordant | -0.00417 | 0.063914 | 0.948018 | 0.984579 | -1.41727 | 1.156531 | 0.220405 | 0.623069 |
| 100135055_TGI_at | HORMAD1 | positive | Discordant | -0.15181 | 1.308033 | 0.907604 | 0.971472 | -16.6633 | 23.12736 | 0.471215 | 0.794832 |
| 100135147_TGI_at | INTS5 | positive | Discordant | -0.31203 | 0.171695 | 0.069165 | 0.324142 | -4.10899 | 3.146028 | 0.191523 | 0.588831 |
| 100135158_TGI_at | LRRC37A4 | positive | Concordant | 0.406425 | 0.264305 | 0.124119 | 0.431533 | 8.279898 | 4.822686 | 0.086004 | 0.455195 |
| 100135158_TGI_at | LRRC37A4 | positive | Concordant | 0.406425 | 0.264305 | 0.124119 | 0.431533 | 8.279898 | 4.822686 | 0.086004 | 0.455195 |
| 100135231_TGI_at | PGBD1 | positive | Discordant | -0.18819 | 0.206979 | 0.363243 | 0.692406 | 0.244565 | 3.806621 | 0.948773 | 0.994854 |
| 100135327_TGI_at | AGPAT1 | positive | Discordant | -1.05755 | 0.49987 | 0.034375 | 0.23826 | -11.0197 | 9.0838 | 0.225086 | 0.623069 |
| 100135327_TGI_at | AGPAT1 | positive | Discordant | -1.05755 | 0.49987 | 0.034375 | 0.23826 | -11.0197 | 9.0838 | 0.225086 | 0.623069 |
| 100135353_TGI_at | C18orf10 | negative | Discordant | 0.236565 | 0.27149 | 0.383559 | 0.702316 | -1.94169 | 4.95263 | 0.69502 | 0.91172 |
| 100135390_TGI_at | PADI2 | negative | Concordant | -3.11078 | 1.165205 | 0.007591 | 0.121882 | -45.7281 | 21.05357 | 0.029857 | 0.302098 |
| 100135523_TGI_at | CLDN23 | positive | Concordant | 0.116873 | 0.042715 | 0.006216 | 0.108753 | 1.439887 | 0.777307 | 0.063968 | 0.423359 |
| 100135535_TGI_at | ITGA2 | negative | Discordant | -0.06965 | 0.06262 | 0.266034 | 0.578075 | 0.792145 | 1.129259 | 0.483007 | 0.80052 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100135728_TGI_at | | negative | Discordant | 0.089501 | 0.23236 | 0.700104 | 0.894706 | 1.074292 | 4.326709 | 0.803908 | 0.950782 |
| 100135728_TGI_at | | negative | Discordant | 0.089501 | 0.23236 | 0.700104 | 0.894706 | 1.074292 | 4.326709 | 0.803908 | 0.950782 |
| 100135776_TGI_at | RNF39 | positive | Discordant | -0.30152 | 0.334888 | 0.367922 | 0.692406 | 0.671348 | 6.031482 | 0.911373 | 0.980193 |
| 100135776_TGI_at | RNF39 | positive | Concordant | -0.30152 | 0.334888 | 0.367922 | 0.692406 | 0.671348 | 6.031482 | 0.911373 | 0.980193 |
| 100135777_TGI_at | RABEP1 | positive | Concordant | 0.004558 | 0.089358 | 0.959315 | 0.988973 | 1.521793 | 1.630479 | 0.350644 | 0.705761 |
| 100135841_TGI_at | EHHADH | positive | Concordant | 1.059621 | 0.742725 | 0.153676 | 0.4583 | -5.79221 | 13.33149 | 0.663943 | 0.888331 |
| 100135910_TGI_at | | negative | Discordant | -0.17048 | 1.120235 | 0.879043 | 0.965743 | 9.563207 | 20.35248 | 0.638441 | 0.878617 |
| 100135911_TGI_at | RBM23 | positive | Concordant | 0.030088 | 0.045023 | 0.503954 | 0.776148 | 0.577193 | 0.81981 | 0.481397 | 0.80052 |
| 100135979_TGI_at | TREM1 | negative | Concordant | -0.00063 | 0.011374 | 0.95598 | 0.988973 | -0.2145 | 0.205014 | 0.295425 | 0.656435 |
| 100135988_TGI_at | CCBL2 | negative | Discordant | 0.176949 | 0.08691 | 0.04175 | 0.260411 | 0.627761 | 1.589206 | 0.692831 | 0.91172 |
| 100136037_TGI_at | NUP210L | positive | Concordant | -1.06927 | 1.373881 | 0.436402 | 0.724829 | 0.698195 | 25.13769 | 0.977842 | 0.999082 |
| 100136066_TGI_at | | positive | Concordant | 0.811626 | 0.965208 | 0.400414 | 0.704177 | -12.9101 | 17.28147 | 0.455034 | 0.779673 |
| 100136084_TGI_at | | negative | Concordant | -0.3981 | 0.277729 | 0.151744 | 0.4583 | -7.03745 | 5.248148 | 0.17994 | 0.575675 |
| 100136117_TGI_at | GOSR1 | positive | Discordant | -0.17656 | 0.117317 | 0.132325 | 0.440276 | -3.54385 | 2.138241 | 0.097445 | 0.486596 |
| 100136204_TGI_at | NCAPG2 | positive | Discordant | -0.16601 | 0.109045 | 0.127917 | 0.431533 | -0.43075 | 2.009912 | 0.830303 | 0.957068 |
| 100136210_TGI_at | | positive | Discordant | -2.49802 | 2.850911 | 0.380911 | 0.702316 | -77.4756 | 51.53067 | 0.132714 | 0.536498 |
| 100136326_TGI_at | | positive | Discordant | -0.51042 | 0.385872 | 0.18591 | 0.49443 | 3.805056 | 6.993672 | 0.586392 | 0.851595 |
| 100136365_TGI_at | PPP1R3B | negative | Concordant | -0.12888 | 0.171124 | 0.451367 | 0.736977 | -2.29881 | 3.08882 | 0.456733 | 0.781041 |
| 100136412_TGI_at | HLA-G | positive | Concordant | 0.03779 | 0.14456 | 0.793774 | 0.930575 | 3.265398 | 2.627832 | 0.214008 | 0.62081 |
| 100136412_TGI_at | HLA-G | positive | Concordant | 0.03779 | 0.14456 | 0.793774 | 0.930575 | 3.265398 | 2.627832 | 0.214008 | 0.62081 |
| 100136478_TGI_at | ARID1A | positive | Concordant | 0.098125 | 0.099886 | 0.325918 | 0.641332 | 2.619035 | 1.803907 | 0.146538 | 0.549177 |
| 100136496_TGI_at | MAPT | negative | Concordant | -0.2285 | 0.222195 | 0.30378 | 0.622924 | -6.31193 | 3.989076 | 0.11358 | 0.507597 |
| 100136516_TGI_at | | negative | Concordant | -1.11497 | 0.733795 | 0.128646 | 0.432311 | -17.2585 | 13.3737 | 0.196885 | 0.598854 |
| 100136519_TGI_at | SREBF1 | positive | Discordant | -0.2513 | 0.456335 | 0.581845 | 0.82238 | -4.21727 | 8.521074 | 0.620655 | 0.865125 |
| 100136557_TGI_at | MPP6 | positive | Discordant | -0.40499 | 0.148174 | 0.006272 | 0.108753 | -5.88735 | 2.659763 | 0.026864 | 0.301895 |
| 100136594_TGI_at | | positive | Concordant | -0.0381 | 0.225289 | 0.865713 | 0.958586 | 5.133074 | 4.108305 | 0.211505 | 0.619509 |
| 100136626_TGI_at | SLC6A4 | negative | Discordant | 0.022976 | 0.026835 | 0.391887 | 0.704177 | 1.251246 | 0.48378 | 0.009699 | 0.205089 |
| 100136633_TGI_at | AMOTL1 | negative | Concordant | -0.14284 | 0.087328 | 0.101908 | 0.403443 | -0.92664 | 1.585475 | 0.558914 | 0.839094 |
| 100136657_TGI_at | GEN1 | positive | Discordant | -1.61092 | 0.526842 | 0.00223 | 0.065414 | -17.9373 | 9.552259 | 0.060407 | 0.415658 |
| 100136729_TGI_at | TRIM66 | negative | Concordant | -1.90158 | 2.092611 | 0.363503 | 0.692406 | 0.068533 | 38.06303 | 0.998563 | 0.999082 |
| 100136733_TGI_at | CCBE1 | positive | Concordant | 0.199442 | 0.102942 | 0.052694 | 0.287332 | 0.399405 | 1.875815 | 0.831387 | 0.957068 |
| 100136800_TGI_at | ATP5O | positive | Discordant | 0.027707 | 0.022789 | 0.224056 | 0.529887 | -0.31296 | 0.412261 | 0.447779 | 0.773355 |
| 100136812_TGI_at | | positive | Discordant | -0.20423 | 0.250751 | 0.415364 | 0.713242 | -2.73008 | 4.55267 | 0.548729 | 0.837177 |
| 100137081_TGI_at | PIGV | positive | Concordant | 0.015011 | 0.10485 | 0.88616 | 0.965743 | -0.74472 | 1.913445 | 0.697124 | 0.913 |
| 100137237_TGI_at | NMU | positive | Discordant | -0.03609 | 0.050313 | 0.473149 | 0.75471 | -0.98536 | 0.890261 | 0.268373 | 0.64407 |
| 100137266_TGI_at | NTN4 | negative | Discordant | 0.086093 | 0.040263 | 0.032495 | 0.234777 | 1.365129 | 0.726389 | 0.060199 | 0.415658 |
| 100137319_TGI_at | | positive | Discordant | -0.97543 | 0.627129 | 0.119852 | 0.429388 | -24.877 | 11.28112 | 0.027441 | 0.301895 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100137319_TGI_at | | positive | Discordant | -0.97543 | 0.627129 | 0.119852 | 0.429388 | -24.877 | 11.28112 | 0.027441 | 0.301895 |
| 100137523_TGI_at | PCBP2 | positive | Discordant | -0.01149 | 0.018255 | 0.529179 | 0.785614 | -0.33603 | 0.330011 | 0.308566 | 0.670538 |
| 100137568_TGI_at | AMIGO3 | negative | Discordant | -0.6285 | 0.525334 | 0.231548 | 0.533011 | 3.514233 | 9.872121 | 0.721859 | 0.921701 |
| 100137632_TGI_at | | negative | Discordant | 0.092506 | 0.172512 | 0.591799 | 0.827564 | 0.611284 | 3.141546 | 0.845721 | 0.958484 |
| 100137671_TGI_at | SPINK6 | negative | Concordant | -6.84247 | 1.899115 | 0.000315 | 0.033986 | -117.501 | 34.24572 | 0.000601 | 0.052609 |
| 100137671_TGI_at | SPINK6 | negative | Concordant | -6.84247 | 1.899115 | 0.000315 | 0.033986 | -117.501 | 34.24572 | 0.000601 | 0.052609 |
| 100137694_TGI_at | TRIM63 | positive | Discordant | -1.08506 | 0.415622 | 0.009036 | 0.135075 | -25.0097 | 7.422092 | 0.000753 | 0.055876 |
| 100137986_TGI_at | HOXC12 | negative | Concordant | -4.61211 | 5.117572 | 0.367466 | 0.692406 | -186.752 | 95.38771 | 0.050251 | 0.39368 |
| 100138030_TGI_at | HLA-G | positive | Concordant | 0.036154 | 0.78981 | 0.963489 | 0.989745 | 5.583503 | 14.15887 | 0.693325 | 0.91172 |
| 100138030_TGI_at | HLA-G | positive | Discordant | 0.036154 | 0.78981 | 0.963489 | 0.989745 | 5.583503 | 14.15887 | 0.693325 | 0.91172 |
| 100138030_TGI_at | HLA-G | positive | Discordant | 0.036154 | 0.78981 | 0.963489 | 0.989745 | 5.583503 | 14.15887 | 0.693325 | 0.91172 |
| 100138030_TGI_at | HLA-G | positive | Concordant | 0.036154 | 0.78981 | 0.963489 | 0.989745 | 5.583503 | 14.15887 | 0.693325 | 0.91172 |
| 100138194_TGI_at | LYSMD4 | positive | Discordant | -0.23397 | 0.222179 | 0.292316 | 0.610694 | 4.352397 | 4.047052 | 0.282174 | 0.64733 |
| 100138253_TGI_at | HCG8 | positive | Concordant | 0.876048 | 0.378758 | 0.020725 | 0.201777 | 7.498354 | 6.908647 | 0.277763 | 0.64407 |
| 100138253_TGI_at | HCG8 | positive | Concordant | 0.876048 | 0.378758 | 0.020725 | 0.201777 | 7.498354 | 6.908647 | 0.277763 | 0.64407 |
| 100138300_TGI_at | RHOA | negative | Discordant | 0.010188 | 0.016048 | 0.52553 | 0.784224 | 0.406762 | 0.291068 | 0.162269 | 0.560509 |
| 100138300_TGI_at | RHOA | negative | Discordant | 0.010188 | 0.016048 | 0.52553 | 0.784224 | 0.406762 | 0.291068 | 0.162269 | 0.560509 |
| 100138305_TGI_at | ARNT | positive | Concordant | 0.133015 | 0.041652 | 0.001406 | 0.054107 | 0.890806 | 0.776753 | 0.25145 | 0.638503 |
| 100138357_TGI_at | BAT4 | positive | Discordant | 0.075486 | 0.152621 | 0.620886 | 0.845068 | -2.744 | 2.767704 | 0.321473 | 0.67176 |
| 100138417_TGI_at | | positive | Concordant | 0.393646 | 1.66577 | 0.813189 | 0.939541 | 23.97344 | 30.11784 | 0.426039 | 0.764753 |
| 100138417_TGI_at | | positive | Concordant | 0.393646 | 1.66577 | 0.813189 | 0.939541 | 23.97344 | 30.11784 | 0.426039 | 0.764753 |
| 100138467_TGI_at | DARS | positive | Concordant | 0.053596 | 0.04482 | 0.231771 | 0.533011 | -0.92508 | 0.811163 | 0.254103 | 0.638503 |
| 100138467_TGI_at | DARS | positive | Concordant | 0.053596 | 0.04482 | 0.231771 | 0.533011 | -0.92508 | 0.811163 | 0.254103 | 0.638503 |
| 100138516_TGI_at | WNT3 | negative | Concordant | -0.09878 | 0.137821 | 0.473544 | 0.75471 | 0.839401 | 2.470571 | 0.734037 | 0.92225 |
| 100138516_TGI_at | WNT3 | negative | Concordant | -0.09878 | 0.137821 | 0.473544 | 0.75471 | 0.839401 | 2.470571 | 0.734037 | 0.92225 |
| 100138535_TGI_at | DST | negative | Discordant | 0.095114 | 0.064509 | 0.14037 | 0.445546 | 1.743224 | 1.167782 | 0.135499 | 0.536498 |
| 100138660_TGI_at | PIGU | positive | Discordant | -0.2504 | 0.203679 | 0.218922 | 0.523661 | -3.77796 | 3.710794 | 0.308631 | 0.670538 |
| 100138705_TGI_at | | positive | Concordant | 1.21734 | 0.708031 | 0.085554 | 0.373119 | 10.14066 | 12.67436 | 0.423657 | 0.764753 |
| 100138939_TGI_at | WWOX | positive | Discordant | -0.18299 | 0.168341 | 0.277037 | 0.588704 | -1.81845 | 3.093692 | 0.556671 | 0.839094 |
| 100138939_TGI_at | WWOX | positive | Discordant | -0.18299 | 0.168341 | 0.277037 | 0.588704 | -1.81845 | 3.093692 | 0.556671 | 0.839094 |
| 100139086_TGI_at | | negative | Concordant | -0.18559 | 0.114581 | 0.105294 | 0.409927 | -4.23367 | 2.071872 | 0.041012 | 0.360043 |
| 100139086_TGI_at | | negative | Concordant | -0.18559 | 0.114581 | 0.105294 | 0.409927 | -4.23367 | 2.071872 | 0.041012 | 0.360043 |
| 100139113_TGI_at | CPD | negative | Concordant | -0.16097 | 0.115602 | 0.163774 | 0.461656 | -1.20956 | 2.082697 | 0.561397 | 0.840641 |
| 100139132_TGI_at | | negative | Discordant | 1.827743 | 0.803892 | 0.022989 | 0.203023 | 11.21652 | 14.74753 | 0.446914 | 0.773355 |
| 100139154_TGI_at | SIAH1 | positive | Concordant | 0.205311 | 0.087973 | 0.019607 | 0.201777 | 1.858242 | 1.613251 | 0.249378 | 0.638503 |
| 100139207_TGI_at | CAMK1D | negative | Discordant | 0.155146 | 0.067663 | 0.021853 | 0.201777 | 1.593415 | 1.215403 | 0.189852 | 0.587863 |
| 100139207_TGI_at | CAMK1D | negative | Discordant | 0.155146 | 0.067663 | 0.021853 | 0.201777 | 1.593415 | 1.215403 | 0.189852 | 0.587863 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100139275_TGI_at | RPS5 | positive | Discordant | -0.01432 | 0.011246 | 0.202884 | 0.509426 | -0.58231 | 0.204483 | 0.004403 | 0.136346 |
| 100139300_TGI_at | TTC35 | negative | Discordant | 0.048196 | 0.059517 | 0.418056 | 0.716053 | 1.290349 | 1.076292 | 0.230573 | 0.623069 |
| 100139309_TGI_at | CDK5RAP3 | positive | Concordant | 0.031879 | 0.036843 | 0.386894 | 0.702944 | -0.01169 | 0.674775 | 0.986178 | 0.999082 |
| 100139548_TGI_at | EXOC2 | positive | Concordant | 0.215184 | 0.171557 | 0.209733 | 0.516353 | -0.49183 | 3.112474 | 0.874443 | 0.966864 |
| 100139549_TGI_at | | positive | Concordant | 0.268623 | 0.333129 | 0.420034 | 0.716053 | -0.9569 | 5.988911 | 0.873056 | 0.966864 |
| 100139572_TGI_at | HLA-DRB3 | negative | Concordant | -0.00161 | 0.003641 | 0.659004 | 0.875236 | -0.02006 | 0.066169 | 0.761787 | 0.934186 |
| 100139572_TGI_at | HLA-DRB3 | negative | Discordant | -0.00161 | 0.003641 | 0.659004 | 0.875236 | -0.02006 | 0.066169 | 0.761787 | 0.934186 |
| 100139628_TGI_at | TMEM108 | negative | Concordant | -0.09829 | 0.082771 | 0.235023 | 0.537639 | -1.78155 | 1.511326 | 0.238478 | 0.632294 |
| 100139628_TGI_at | TMEM108 | negative | Concordant | -0.09829 | 0.082771 | 0.235023 | 0.537639 | -1.78155 | 1.511326 | 0.238478 | 0.632294 |
| 100139631_TGI_at | FN3K | negative | Discordant | 1.416161 | 1.769621 | 0.423559 | 0.718641 | 16.73237 | 32.80477 | 0.61001 | 0.860732 |
| 100139670_TGI_at | ZNF187 | positive | Concordant | 0.238367 | 0.176846 | 0.177698 | 0.481451 | -1.12774 | 3.219081 | 0.726092 | 0.921701 |
| 100139688_TGI_at | HCG18 | positive | Concordant | 0.159831 | 0.092288 | 0.083296 | 0.371725 | 1.858809 | 1.690618 | 0.271556 | 0.64407 |
| 100139688_TGI_at | HCG18 | positive | Concordant | 0.159831 | 0.092288 | 0.083296 | 0.371725 | 1.858809 | 1.690618 | 0.271556 | 0.64407 |
| 100139688_TGI_at | HCG18 | positive | Concordant | 0.159831 | 0.092288 | 0.083296 | 0.371725 | 1.858809 | 1.690618 | 0.271556 | 0.64407 |
| 100139688_TGI_at | HCG18 | positive | Concordant | 0.159831 | 0.092288 | 0.083296 | 0.371725 | 1.858809 | 1.690618 | 0.271556 | 0.64407 |
| 100139818_TGI_at | BAT2 | positive | Discordant | -0.13035 | 0.14771 | 0.377505 | 0.700281 | -1.28999 | 2.711299 | 0.634229 | 0.874208 |
| 100139818_TGI_at | BAT2 | positive | Discordant | -0.13035 | 0.14771 | 0.377505 | 0.700281 | -1.28999 | 2.711299 | 0.634229 | 0.874208 |
| 100139929_TGI_at | ATP8B3 | positive | Concordant | 0.671291 | 1.01026 | 0.506387 | 0.776148 | 8.378 | 18.21575 | 0.645565 | 0.88421 |
| 100139965_TGI_at | ZNF292 | positive | Concordant | 0.087632 | 0.059858 | 0.143191 | 0.44657 | -0.37521 | 1.080773 | 0.728466 | 0.922014 |
| 100140090_TGI_at | CCDC38 | positive | Discordant | 1.013146 | 3.809248 | 0.790262 | 0.929308 | -3.79056 | 69.37597 | 0.956427 | 0.995701 |
| 100140105_TGI_at | CDC42SE1 | negative | Discordant | 0.015982 | 0.10885 | 0.883273 | 0.965743 | 0.652466 | 1.965962 | 0.739979 | 0.92225 |
| 100140312_TGI_at | TXNDC11 | negative | Discordant | 0.038321 | 0.029573 | 0.195046 | 0.506885 | 0.824985 | 0.535086 | 0.123127 | 0.516945 |
| 100140380_TGI_at | | positive | Concordant | 1.049817 | 1.158629 | 0.364891 | 0.692406 | 29.32398 | 21.44353 | 0.171469 | 0.567301 |
| 100140600_TGI_at | | positive | Concordant | 0.440837 | 0.257551 | 0.086961 | 0.373243 | 4.076303 | 4.76401 | 0.392194 | 0.744053 |
| 100140600_TGI_at | | positive | Concordant | 0.440837 | 0.257551 | 0.086961 | 0.373243 | 4.076303 | 4.76401 | 0.392194 | 0.744053 |
| 100140717_TGI_at | GRB2 | negative | Concordant | -0.06957 | 0.064554 | 0.281187 | 0.593566 | -2.21347 | 1.171212 | 0.058772 | 0.413224 |
| 100140755_TGI_at | PCGF2 | negative | Discordant | 0.205376 | 0.149119 | 0.168432 | 0.467042 | 2.41984 | 2.702878 | 0.370636 | 0.730277 |
| 100140992_TGI_at | EPS15 | positive | Concordant | 0.096567 | 0.046083 | 0.036125 | 0.238611 | 2.21291 | 0.838994 | 0.00835 | 0.195664 |
| 100141096_TGI_at | KPNA3 | positive | Concordant | 0.110691 | 0.251789 | 0.660212 | 0.875236 | 5.155846 | 4.557195 | 0.257902 | 0.640563 |
| 100141104_TGI_at | GFM1 | positive | Discordant | -0.4624 | 0.310685 | 0.136667 | 0.445546 | -2.26586 | 5.675668 | 0.689728 | 0.910189 |
| 100141210_TGI_at | | positive | Concordant | 0.467985 | 0.295067 | 0.112732 | 0.419479 | 11.87695 | 5.39679 | 0.027754 | 0.301895 |
| 100141210_TGI_at | | positive | Concordant | 0.467985 | 0.295067 | 0.112732 | 0.419479 | 11.87695 | 5.39679 | 0.027754 | 0.301895 |
| 100141210_TGI_at | | positive | Concordant | 0.467985 | 0.295067 | 0.112732 | 0.419479 | 11.87695 | 5.39679 | 0.027754 | 0.301895 |
| 100141210_TGI_at | | positive | Concordant | 0.467985 | 0.295067 | 0.112732 | 0.419479 | 11.87695 | 5.39679 | 0.027754 | 0.301895 |
| 100141331_TGI_at | | negative | Discordant | -0.04614 | 0.182319 | 0.800226 | 0.931838 | 1.645187 | 3.30035 | 0.61814 | 0.865125 |
| 100141348_TGI_at | | positive | Discordant | -2.07627 | 0.687413 | 0.002524 | 0.069066 | -20.9941 | 12.79471 | 0.100831 | 0.486596 |
| 100141348_TGI_at | | positive | Discordant | -2.07627 | 0.687413 | 0.002524 | 0.069066 | -20.9941 | 12.79471 | 0.100831 | 0.486596 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100141529_TGI_at | PTCH1 | positive | Concordant | 0.88309 | 0.310311 | 0.00443 | 0.09827 | 19.17145 | 5.591695 | 0.000607 | 0.052609 |
| 100141551_TGI_at | CEACAM4 | negative | Concordant | -1.10913 | 0.331746 | 0.000828 | 0.039874 | -10.4838 | 6.039709 | 0.082597 | 0.447876 |
| 100141553_TGI_at | | positive | Concordant | 0.027214 | 0.026532 | 0.30504 | 0.622924 | -0.01575 | 0.486798 | 0.974194 | 0.999082 |
| 100141567_TGI_at | KIAA0562 | positive | Concordant | -0.30347 | 0.259563 | 0.242336 | 0.546504 | 0.771706 | 4.760215 | 0.871215 | 0.966864 |
| 100141578_TGI_at | RP3-377H14.5 | positive | Discordant | 1.024245 | 1.468364 | 0.485464 | 0.765268 | -1.8791 | 26.6354 | 0.943757 | 0.994854 |
| 100141578_TGI_at | RP3-377H14.5 | positive | Concordant | 1.024245 | 1.468364 | 0.485464 | 0.765268 | -1.8791 | 26.6354 | 0.943757 | 0.994854 |
| 100141670_TGI_at | AP3B2 | positive | Discordant | -1.3057 | 1.165735 | 0.262684 | 0.574815 | -5.64337 | 21.06814 | 0.788805 | 0.947133 |
| 100141815_TGI_at | NOP16 | negative | Concordant | -0.15629 | 0.046628 | 0.000803 | 0.039874 | -1.55405 | 0.854186 | 0.06886 | 0.426441 |
| 100141839_TGI_at | BTN2A2 | positive | Concordant | 0.09689 | 0.086923 | 0.26499 | 0.577252 | -0.08265 | 1.574574 | 0.95814 | 0.996052 |
| 100141839_TGI_at | BTN2A2 | positive | Concordant | 0.09689 | 0.086923 | 0.26499 | 0.577252 | -0.08265 | 1.574574 | 0.95814 | 0.996052 |
| 100142010_TGI_at | CAMK1D | negative | Discordant | 0.111735 | 0.060783 | 0.066023 | 0.319057 | 0.751102 | 1.099225 | 0.494416 | 0.804238 |
| 100142010_TGI_at | CAMK1D | negative | Discordant | 0.111735 | 0.060783 | 0.066023 | 0.319057 | 0.751102 | 1.099225 | 0.494416 | 0.804238 |
| 100142037_TGI_at | KLC1 | positive | Discordant | -0.57338 | 0.226269 | 0.011274 | 0.150127 | -5.67063 | 4.106074 | 0.167269 | 0.564154 |
| 100142264_TGI_at | ZMAT3 | positive | Discordant | -0.0142 | 0.052056 | 0.785015 | 0.928221 | -1.32101 | 0.94792 | 0.163444 | 0.562324 |
| 100142285_TGI_at | TCF19 | positive | Concordant | -0.14923 | 0.272749 | 0.584298 | 0.82238 | -0.01257 | 4.96706 | 0.997981 | 0.999082 |
| 100142285_TGI_at | TCF19 | negative | Concordant | -0.14923 | 0.272749 | 0.584298 | 0.82238 | -0.01257 | 4.96706 | 0.997981 | 0.999082 |
| 100142307_TGI_at | | negative | Discordant | 1.201167 | 2.207441 | 0.586342 | 0.82392 | 29.20765 | 39.90534 | 0.464215 | 0.787622 |
| 100142471_TGI_at | | positive | Concordant | 0.194054 | 0.126568 | 0.125225 | 0.431533 | 4.002349 | 2.285359 | 0.079894 | 0.447721 |
| 100142471_TGI_at | | positive | Concordant | 0.194054 | 0.126568 | 0.125225 | 0.431533 | 4.002349 | 2.285359 | 0.079894 | 0.447721 |
| 100142556_TGI_at | | positive | Discordant | -0.54668 | 0.262786 | 0.037496 | 0.24443 | -6.57714 | 4.761118 | 0.167148 | 0.564154 |
| 100142627_TGI_at | LDHC | negative | Concordant | -0.75288 | 1.128172 | 0.50455 | 0.776148 | -59.7831 | 20.24414 | 0.003146 | 0.116559 |
| 100142706_TGI_at | MMP15 | negative | Discordant | 0.06972 | 0.045619 | 0.126435 | 0.431533 | 0.891102 | 0.819554 | 0.276904 | 0.64407 |
| 100142718_TGI_at | CEP192 | positive | Discordant | 0.141317 | 0.104638 | 0.176845 | 0.480641 | 0.849904 | 1.904087 | 0.655339 | 0.887779 |
| 100142732_TGI_at | ATP6V1G2 | positive | Discordant | -0.18124 | 0.153745 | 0.238459 | 0.539802 | -3.44559 | 2.820438 | 0.22184 | 0.623069 |
| 100142732_TGI_at | ATP6V1G2 | negative | Concordant | -0.18124 | 0.153745 | 0.238459 | 0.539802 | -3.44559 | 2.820438 | 0.22184 | 0.623069 |
| 100142964_TGI_at | SGCD | positive | Concordant | -0.14137 | 0.463734 | 0.760483 | 0.923606 | 0.660291 | 8.482427 | 0.937954 | 0.994139 |
| 100142979_TGI_at | THSD4 | negative | Concordant | -0.04999 | 0.113623 | 0.659945 | 0.875236 | 2.480079 | 2.049756 | 0.226302 | 0.623069 |
| 100142979_TGI_at | THSD4 | negative | Discordant | -0.04999 | 0.113623 | 0.659945 | 0.875236 | 2.480079 | 2.049756 | 0.226302 | 0.623069 |
| 100143040_TGI_at | MAP1LC3A | positive | Concordant | -0.10686 | 0.092425 | 0.247601 | 0.553268 | 1.304625 | 1.680857 | 0.437651 | 0.771226 |
| 100143194_TGI_at | RHOBTB3 | positive | Discordant | -0.12908 | 0.06325 | 0.04127 | 0.259282 | -0.427 | 1.150592 | 0.710555 | 0.915742 |
| 100143227_TGI_at | HCG2P7 | positive | Concordant | 0.954469 | 0.50573 | 0.059119 | 0.307435 | 2.136766 | 9.266532 | 0.817634 | 0.952807 |
| 100143227_TGI_at | HCG2P7 | positive | Concordant | 0.954469 | 0.50573 | 0.059119 | 0.307435 | 2.136766 | 9.266532 | 0.817634 | 0.952807 |
| 100143280_TGI_at | | positive | Discordant | -0.09518 | 0.093304 | 0.3077 | 0.622924 | -1.84968 | 1.704466 | 0.277834 | 0.64407 |
| 100143315_TGI_at | WWOX | negative | Concordant | -0.43272 | 0.499959 | 0.38676 | 0.702944 | -13.1182 | 9.089473 | 0.148956 | 0.550391 |
| 100143321_TGI_at | | positive | Concordant | 0.733755 | 0.371397 | 0.048193 | 0.269569 | 10.77791 | 6.80856 | 0.113423 | 0.507597 |
| 100143326_TGI_at | NPHP3 | negative | Discordant | 0.057246 | 0.226123 | 0.800143 | 0.931838 | -0.09964 | 4.108483 | 0.980652 | 0.999082 |
| 100143365_TGI_at | FSTL4 | positive | Concordant | 0.157793 | 0.168769 | 0.349807 | 0.672468 | 6.034025 | 3.04125 | 0.047249 | 0.38285 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100143437_TGI_at | RPUSD4 | positive | Discordant | -0.33647 | 0.110165 | 0.002256 | 0.065414 | -6.34859 | 2.001506 | 0.001514 | 0.080912 |
| 100143443_TGI_at | PADI2 | negative | Concordant | -0.06016 | 0.017456 | 0.000568 | 0.034954 | -1.23797 | 0.312793 | 7.56E-05 | 0.01669 |
| 100143466_TGI_at | GOLPH3L | positive | Concordant | 0.262987 | 0.420253 | 0.531458 | 0.787648 | -13.9496 | 7.642949 | 0.067977 | 0.426441 |
| 100143632_TGI_at | C6orf162 | negative | Discordant | -0.01526 | 0.550899 | 0.977908 | 0.996398 | -4.80396 | 10.01385 | 0.631418 | 0.873211 |
| 100143655_TGI_at | NUP85 | positive | Discordant | -0.00927 | 0.087053 | 0.91518 | 0.972561 | -0.68765 | 1.575476 | 0.662494 | 0.888268 |
| 100143670_TGI_at | C1orf89 | positive | Discordant | -1.07806 | 0.674213 | 0.109824 | 0.417621 | -27.2082 | 12.10524 | 0.024599 | 0.301895 |
| 100143779_TGI_at | AGER | negative | Discordant | 0.021044 | 0.008122 | 0.009572 | 0.140655 | 0.372513 | 0.149187 | 0.012527 | 0.215815 |
| 100143968_TGI_at | ZNF323 | negative | Discordant | 0.127744 | 0.064172 | 0.046518 | 0.269292 | 1.430725 | 1.161772 | 0.218135 | 0.623069 |
| 100143968_TGI_at | ZNF323 | negative | Discordant | 0.127744 | 0.064172 | 0.046518 | 0.269292 | 1.430725 | 1.161772 | 0.218135 | 0.623069 |
| 100143968_TGI_at | ZNF323 | negative | Discordant | 0.127744 | 0.064172 | 0.046518 | 0.269292 | 1.430725 | 1.161772 | 0.218135 | 0.623069 |
| 100144009_TGI_at | C10orf11 | negative | Discordant | -0.89213 | 1.238197 | 0.471214 | 0.75471 | -6.09183 | 22.55523 | 0.787095 | 0.946479 |
| 100144299_TGI_at | | positive | Concordant | 0.418339 | 0.321222 | 0.192802 | 0.505013 | 4.372663 | 5.747651 | 0.446792 | 0.773355 |
| 100144365_TGI_at | HOXC6 | positive | Discordant | -0.16132 | 0.091369 | 0.077465 | 0.355356 | -2.01195 | 1.695831 | 0.235461 | 0.630076 |
| 100144394_TGI_at | HCP5 | positive | Concordant | 0.000809 | 0.037768 | 0.982908 | 0.996398 | 0.080034 | 0.681564 | 0.906522 | 0.980193 |
| 100144394_TGI_at | HCP5 | positive | Concordant | 0.000809 | 0.037768 | 0.982908 | 0.996398 | 0.080034 | 0.681564 | 0.906522 | 0.980193 |
| 100144443_TGI_at | | negative | Concordant | -2.86378 | 0.836025 | 0.000614 | 0.034954 | -34.4259 | 15.45824 | 0.025946 | 0.301895 |
| 100144469_TGI_at | SGCD | positive | Discordant | 0.088853 | 0.370043 | 0.810241 | 0.939143 | 0.563456 | 6.720199 | 0.93318 | 0.99272 |
| 100144708_TGI_at | C6orf162 | positive | Concordant | 0.16083 | 0.252485 | 0.524134 | 0.783489 | -3.14292 | 4.569727 | 0.491597 | 0.804238 |
| 100144721_TGI_at | RPRD2 | negative | Concordant | -0.01997 | 0.112717 | 0.859352 | 0.95732 | -2.97687 | 2.040319 | 0.144558 | 0.549177 |
| 100144954_TGI_at | CCNT2 | negative | Discordant | 0.24909 | 0.175745 | 0.156385 | 0.459406 | 3.253948 | 3.192047 | 0.308017 | 0.670538 |
| 100144981_TGI_at | | negative | Concordant | -1.1111 | 1.093687 | 0.309666 | 0.622924 | -16.5551 | 20.27996 | 0.414313 | 0.761037 |
| 100145017_TGI_at | | positive | Concordant | 0.558302 | 2.04525 | 0.784872 | 0.928221 | -11.0942 | 36.90479 | 0.763706 | 0.935216 |
| 100145031_TGI_at | MRPS6 | negative | Concordant | -0.01742 | 0.031425 | 0.579355 | 0.82238 | -1.43944 | 0.571264 | 0.011744 | 0.215815 |
| 100145052_TGI_at | HLA-DPB1 | negative | Discordant | 0.027637 | 0.053756 | 0.607163 | 0.833901 | -0.13442 | 0.97055 | 0.889845 | 0.97411 |
| 100145052_TGI_at | HLA-DPB1 | negative | Discordant | 0.027637 | 0.053756 | 0.607163 | 0.833901 | -0.13442 | 0.97055 | 0.889845 | 0.97411 |
| 100145066_TGI_at | SMPDL3B | positive | Discordant | -0.22382 | 0.159235 | 0.159849 | 0.461656 | -0.61027 | 2.903131 | 0.833503 | 0.957149 |
| 100145096_TGI_at | TNS1 | positive | Discordant | -0.09184 | 0.24471 | 0.707422 | 0.896688 | 6.365906 | 4.499239 | 0.157102 | 0.560509 |
| 100145096_TGI_at | TNS1 | positive | Concordant | -0.09184 | 0.24471 | 0.707422 | 0.896688 | 6.365906 | 4.499239 | 0.157102 | 0.560509 |
| 100145132_TGI_at | FSTL4 | positive | Concordant | 0.982409 | 1.814114 | 0.588138 | 0.825106 | 51.69083 | 32.90707 | 0.116226 | 0.509594 |
| 100145206_TGI_at | | positive | Discordant | -0.72147 | 0.948223 | 0.446738 | 0.733564 | -11.3935 | 17.20189 | 0.507752 | 0.815224 |
| 100145297_TGI_at | TRIM66 | negative | Concordant | -0.11459 | 0.30057 | 0.703034 | 0.895052 | 2.847049 | 5.537534 | 0.607156 | 0.860732 |
| 100145368_TGI_at | C2CD3 | negative | Concordant | -0.12192 | 0.139398 | 0.381779 | 0.702316 | -2.82603 | 2.547082 | 0.267208 | 0.64407 |
| 100145444_TGI_at | | positive | Concordant | 2.060943 | 0.867811 | 0.017555 | 0.200263 | 35.03336 | 15.80433 | 0.026644 | 0.301895 |
| 100145476_TGI_at | ZNF389 | positive | Concordant | 2.43492 | 1.555867 | 0.117585 | 0.424774 | 4.739578 | 28.42623 | 0.86758 | 0.966864 |
| 100145476_TGI_at | ZNF389 | positive | Concordant | 2.43492 | 1.555867 | 0.117585 | 0.424774 | 4.739578 | 28.42623 | 0.86758 | 0.966864 |
| 100145491_TGI_at | SNRPF | positive | Discordant | -0.30437 | 0.235679 | 0.196542 | 0.507149 | -2.11269 | 4.268185 | 0.62061 | 0.865125 |
| 100145578_TGI_at | | positive | Discordant | -0.03205 | 0.265685 | 0.903984 | 0.970639 | 1.528862 | 4.86178 | 0.753168 | 0.930374 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100145604_TGI_at | | positive | Concordant | 1.114221 | 0.908146 | 0.219853 | 0.523661 | 11.15601 | 16.29648 | 0.493618 | 0.804238 |
| 100145663_TGI_at | B4GALT4 | positive | Discordant | -0.20377 | 0.073017 | 0.00526 | 0.099945 | -1.16487 | 1.319556 | 0.377357 | 0.730287 |
| 100145697_TGI_at | PRKD3 | negative | Concordant | -0.02052 | 0.154044 | 0.894042 | 0.966502 | 0.487195 | 2.808406 | 0.862276 | 0.966864 |
| 100145725_TGI_at | TPM1 | negative | Concordant | -0.01101 | 0.014855 | 0.458595 | 0.740412 | 0.147703 | 0.269963 | 0.584294 | 0.851595 |
| 100146140_TGI_at | WDR32 | positive | Concordant | 0.057136 | 0.249801 | 0.819082 | 0.941835 | -2.10706 | 4.5579 | 0.643874 | 0.88421 |
| 100146347_TGI_at | ADORA2B | positive | Discordant | -0.40624 | 0.143845 | 0.004741 | 0.09827 | -3.01859 | 2.621329 | 0.249506 | 0.638503 |
| 100146385_TGI_at | IGSF11 | positive | Discordant | 0.012626 | 0.929224 | 0.989159 | 0.996398 | 9.308254 | 16.6101 | 0.575209 | 0.847029 |
| 100146392_TGI_at | PELI2 | negative | Discordant | 2.054106 | 1.637901 | 0.209802 | 0.516353 | 17.54444 | 30.0553 | 0.559396 | 0.839094 |
| 100146413_TGI_at | | negative | Discordant | 0.58475 | 0.69938 | 0.4031 | 0.707466 | -18.5258 | 12.72876 | 0.145551 | 0.549177 |
| 100146416_TGI_at | FGD6 | negative | Discordant | 0.541704 | 0.172283 | 0.001665 | 0.055523 | 8.189259 | 3.14201 | 0.009151 | 0.203425 |
| 100146446_TGI_at | MLH3 | positive | Discordant | -0.00598 | 0.195597 | 0.975592 | 0.996398 | -1.9118 | 3.547974 | 0.589996 | 0.855396 |
| 100146509_TGI_at | C14orf94 | negative | Concordant | -0.03927 | 0.048731 | 0.420382 | 0.716053 | -1.63056 | 0.876528 | 0.062851 | 0.421332 |
| 100146692_TGI_at | CLN5 | negative | Discordant | 0.037493 | 0.090559 | 0.67886 | 0.883837 | -0.60573 | 1.628029 | 0.709846 | 0.915742 |
| 100146695_TGI_at | BRUNOL4 | positive | Concordant | 0.848751 | 0.582293 | 0.144951 | 0.450369 | 18.66306 | 10.64106 | 0.079452 | 0.447721 |
| 100146735_TGI_at | HDAC9 | positive | Concordant | 1.689386 | 0.744088 | 0.023183 | 0.203023 | 20.13628 | 13.48987 | 0.135517 | 0.536498 |
| 100146746_TGI_at | | negative | Concordant | -0.03173 | 0.052707 | 0.547225 | 0.796047 | -0.92731 | 0.949731 | 0.32887 | 0.675664 |
| 100147021_TGI_at | JMJD7-PLA2G4B | positive | Discordant | -0.16102 | 0.121322 | 0.184449 | 0.492054 | -4.05258 | 2.216017 | 0.067435 | 0.426441 |
| 100147117_TGI_at | ZNF131 | negative | Concordant | -0.44931 | 0.455633 | 0.324075 | 0.641332 | -5.80932 | 8.332161 | 0.485667 | 0.80052 |
| 100147290_TGI_at | | positive | Discordant | -4.67728 | 3.162762 | 0.139178 | 0.445546 | -33.896 | 57.92831 | 0.558456 | 0.839094 |
| 100147290_TGI_at | | positive | Discordant | -4.67728 | 3.162762 | 0.139178 | 0.445546 | -33.896 | 57.92831 | 0.558456 | 0.839094 |
| 100147343_TGI_at | | negative | Discordant | -0.09211 | 0.150445 | 0.54037 | 0.794069 | -0.62194 | 2.715406 | 0.818837 | 0.952928 |
| 100147399_TGI_at | EHHADH | positive | Concordant | 0.253106 | 0.171378 | 0.139706 | 0.445546 | 2.239724 | 3.103648 | 0.470514 | 0.794832 |
| 100147499_TGI_at | C6orf164 | negative | Discordant | 0.548522 | 2.498595 | 0.826236 | 0.942561 | 10.81225 | 45.25801 | 0.811181 | 0.951684 |
| 100147593_TGI_at | | negative | Concordant | 0.67991 | 0.819524 | 0.406742 | 0.711479 | 3.593513 | 14.92925 | 0.809786 | 0.951333 |
| 100147633_TGI_at | CLOCK | negative | Discordant | -0.21976 | 0.256747 | 0.39202 | 0.704177 | -2.78741 | 4.65568 | 0.549365 | 0.837177 |
| 100147633_TGI_at | CLOCK | negative | Concordant | -0.21976 | 0.256747 | 0.39202 | 0.704177 | -2.78741 | 4.65568 | 0.549365 | 0.837177 |
| 100147773_TGI_at | HOXB2 | negative | Concordant | -0.55948 | 0.228878 | 0.014508 | 0.169974 | -8.67467 | 4.20614 | 0.039171 | 0.353766 |
| 100147953_TGI_at | CFDP1 | negative | Concordant | -0.06195 | 0.040258 | 0.12385 | 0.431533 | -0.76601 | 0.724621 | 0.290457 | 0.650713 |
| 100148000_TGI_at | HOXC6 | positive | Discordant | -0.61054 | 1.861337 | 0.742904 | 0.911402 | -43.1607 | 33.93923 | 0.203478 | 0.606239 |
| 100148014_TGI_at | TIGD2 | negative | Discordant | 0.382443 | 0.213074 | 0.072673 | 0.336937 | 1.930072 | 3.851375 | 0.616274 | 0.865125 |
| 100148028_TGI_at | HHIP | negative | Concordant | -0.22769 | 0.107742 | 0.034578 | 0.23826 | -2.7467 | 1.963776 | 0.161908 | 0.560509 |
| 100148028_TGI_at | HHIP | negative | Concordant | -0.22769 | 0.107742 | 0.034578 | 0.23826 | -2.7467 | 1.963776 | 0.161908 | 0.560509 |
| 100148039_TGI_at | KIAA1267 | positive | Concordant | 0.030684 | 0.027425 | 0.263208 | 0.574815 | 0.547031 | 0.499974 | 0.273903 | 0.64407 |
| 100148133_TGI_at | 5-Mar | negative | Discordant | -0.00631 | 0.077944 | 0.9355 | 0.981518 | 1.624913 | 1.404254 | 0.247217 | 0.638503 |
| 100148250_TGI_at | ZSCAN12L1 | negative | Concordant | -0.9567 | 1.771267 | 0.589113 | 0.825139 | 7.442036 | 31.69126 | 0.814341 | 0.952807 |
| 100148345_TGI_at | | positive | Discordant | 0.115881 | 0.461618 | 0.801789 | 0.931838 | 1.784558 | 8.429034 | 0.832329 | 0.957068 |
| 100148378_TGI_at | CKM | negative | Concordant | 0.044106 | 1.750278 | 0.979896 | 0.996398 | -4.629 | 31.63959 | 0.883681 | 0.971042 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100148404_TGI_at | PSMA4 | negative | Discordant | 0.014379 | 0.028267 | 0.610959 | 0.836812 | 0.093579 | 0.50914 | 0.854172 | 0.963575 |
| 100148404_TGI_at | PSMA4 | negative | Discordant | 0.014379 | 0.028267 | 0.610959 | 0.836812 | 0.093579 | 0.50914 | 0.854172 | 0.963575 |
| 100148450_TGI_at | HSD17B12 | negative | Discordant | 0.049942 | 0.024444 | 0.041043 | 0.259282 | 0.847961 | 0.44198 | 0.055041 | 0.403041 |
| 100148527_TGI_at | DMPK | negative | Discordant | 0.003274 | 0.068072 | 0.961638 | 0.989745 | 1.54131 | 1.2681 | 0.224195 | 0.623069 |
| 100148761_TGI_at | OXCT2 | negative | Concordant | -1.09327 | 0.602524 | 0.069604 | 0.324444 | -19.1741 | 11.09848 | 0.084054 | 0.452639 |
| 100148761_TGI_at | OXCT2 | negative | Concordant | -1.09327 | 0.602524 | 0.069604 | 0.324444 | -19.1741 | 11.09848 | 0.084054 | 0.452639 |
| 100148776_TGI_at | NDUFA12 | positive | Discordant | 0.00888 | 0.030781 | 0.772962 | 0.923606 | -0.34342 | 0.556157 | 0.536918 | 0.828306 |
| 100148822_TGI_at | NOTCH4 | positive | Concordant | 0.020254 | 0.031155 | 0.515627 | 0.780157 | 1.356207 | 0.565369 | 0.016449 | 0.241715 |
| 100148822_TGI_at | NOTCH4 | positive | Discordant | 0.020254 | 0.031155 | 0.515627 | 0.780157 | 1.356207 | 0.565369 | 0.016449 | 0.241715 |
| 100148878_TGI_at | | negative | Concordant | -0.47266 | 0.910685 | 0.603753 | 0.832729 | -1.32464 | 16.49395 | 0.93599 | 0.993272 |
| 100148878_TGI_at | | negative | Concordant | -0.47266 | 0.910685 | 0.603753 | 0.832729 | -1.32464 | 16.49395 | 0.93599 | 0.993272 |
| 100148923_TGI_at | ZNF322A | positive | Concordant | 0.214509 | 0.088794 | 0.0157 | 0.181497 | 2.945791 | 1.61581 | 0.068287 | 0.426441 |
| 100148949_TGI_at | MRPL43 | negative | Discordant | 0.283806 | 0.408541 | 0.487255 | 0.765308 | 7.281009 | 7.443412 | 0.327985 | 0.675446 |
| 100148961_TGI_at | MCM6 | positive | Discordant | -0.06593 | 0.159263 | 0.678911 | 0.883837 | -4.18093 | 2.86336 | 0.14425 | 0.549177 |
| 100148972_TGI_at | C16orf63 | positive | Discordant | 0.111636 | 0.070603 | 0.113839 | 0.421787 | 0.006072 | 1.276121 | 0.996203 | 0.999082 |
| 100149004_TGI_at | | negative | Concordant | -0.01547 | 0.044316 | 0.727009 | 0.906931 | -0.62011 | 0.807388 | 0.442458 | 0.772392 |
| 100149004_TGI_at | | negative | Concordant | -0.01547 | 0.044316 | 0.727009 | 0.906931 | -0.62011 | 0.807388 | 0.442458 | 0.772392 |
| 100149189_TGI_at | COL21A1 | positive | Concordant | 0.117706 | 0.061231 | 0.054563 | 0.293829 | 0.982692 | 1.120163 | 0.380337 | 0.734414 |
| 100149189_TGI_at | COL21A1 | positive | Concordant | 0.117706 | 0.061231 | 0.054563 | 0.293829 | 0.982692 | 1.120163 | 0.380337 | 0.734414 |
| 100149232_TGI_at | | negative | Concordant | 0.243663 | 5.16427 | 0.962368 | 0.989745 | -33.2792 | 93.08831 | 0.720716 | 0.921701 |
| 100149241_TGI_at | | negative | Concordant | -0.0037 | 0.129609 | 0.977204 | 0.996398 | -0.96094 | 2.34263 | 0.68166 | 0.902289 |
| 100149313_TGI_at | LST1 | positive | Discordant | -0.0002 | 0.0102 | 0.984547 | 0.996398 | -0.24353 | 0.184762 | 0.187481 | 0.584699 |
| 100149333_TGI_at | CDC123 | negative | Discordant | 0.045829 | 0.057497 | 0.425412 | 0.718939 | 0.77029 | 1.050191 | 0.463268 | 0.787588 |
| 100149333_TGI_at | CDC123 | negative | Discordant | 0.045829 | 0.057497 | 0.425412 | 0.718939 | 0.77029 | 1.050191 | 0.463268 | 0.787588 |
| 100149341_TGI_at | SLITRK5 | negative | Discordant | 0.97696 | 0.599259 | 0.103042 | 0.404243 | 11.03933 | 10.79218 | 0.306355 | 0.670538 |
| 100149386_TGI_at | SNORA24 | positive | Discordant | -0.23202 | 0.1355 | 0.086833 | 0.373243 | -2.4487 | 2.493683 | 0.326119 | 0.673202 |
| 100149583_TGI_at | ARL6IP1 | positive | Discordant | -3.67508 | 1.83986 | 0.045773 | 0.269292 | -82.2529 | 33.1722 | 0.013154 | 0.219318 |
| 100149604_TGI_at | | negative | Concordant | -6.42014 | 2.28389 | 0.004938 | 0.09827 | -58.0746 | 41.51006 | 0.161799 | 0.560509 |
| 100149686_TGI_at | UHRF1BP1 | positive | Discordant | -0.5249 | 0.528966 | 0.321048 | 0.639882 | -6.64741 | 9.505919 | 0.48437 | 0.80052 |
| 100149702_TGI_at | C1orf113 | positive | Discordant | 0.615403 | 0.910261 | 0.498994 | 0.774427 | 2.977737 | 16.65591 | 0.858111 | 0.964752 |
| 100149806_TGI_at | MEIG1 | negative | Discordant | 0.884925 | 1.046542 | 0.397793 | 0.704177 | 3.129251 | 18.80906 | 0.867866 | 0.966864 |
| 100149872_TGI_at | | negative | Discordant | 0.04037 | 0.093609 | 0.666276 | 0.879862 | 1.860902 | 1.71473 | 0.277813 | 0.64407 |
| 100149905_TGI_at | LSM11 | negative | Discordant | 0.562094 | 1.055617 | 0.594394 | 0.829561 | 7.938418 | 19.06465 | 0.677121 | 0.901173 |
| 100149978_TGI_at | NR0B2 | positive | Concordant | 0.364252 | 0.172673 | 0.034902 | 0.23826 | 8.076013 | 3.175346 | 0.01098 | 0.215815 |
| 100150055_TGI_at | PCGF2 | negative | Discordant | 0.214509 | 0.188225 | 0.254435 | 0.563278 | 3.081283 | 3.459108 | 0.37305 | 0.730277 |
| 100150083_TGI_at | GALNT6 | positive | Discordant | -0.14323 | 0.244258 | 0.557626 | 0.805583 | -4.13531 | 4.383158 | 0.345449 | 0.698145 |
| 100150316_TGI_at | | positive | Concordant | -0.01162 | 0.793546 | 0.988318 | 0.996398 | -0.09461 | 14.29798 | 0.99472 | 0.999082 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100150425_TGI_at | SH3PXD2A | negative | Concordant | -0.31794 | 0.173508 | 0.066887 | 0.320394 | -0.29548 | 3.143554 | 0.925114 | 0.987775 |
| 100150625_TGI_at | ZNF391 | negative | Discordant | 2.465018 | 1.551072 | 0.112007 | 0.419479 | 16.48258 | 28.54678 | 0.563677 | 0.84115 |
| 100150651_TGI_at | PAAF1 | negative | Discordant | 0.107438 | 0.10048 | 0.284956 | 0.598201 | -1.24657 | 1.819952 | 0.493376 | 0.804238 |
| 100150740_TGI_at | JMJD7-PLA2G4B | positive | Concordant | 0.071429 | 0.130449 | 0.583995 | 0.82238 | 0.813086 | 2.426353 | 0.737545 | 0.92225 |
| 100150755_TGI_at | GFM1 | positive | Discordant | -0.10269 | 0.079317 | 0.195411 | 0.506885 | -1.94363 | 1.440495 | 0.177248 | 0.571841 |
| 100150758_TGI_at | C6orf191 | positive | Discordant | -2.87561 | 3.651574 | 0.43099 | 0.722949 | -130.159 | 65.49769 | 0.046897 | 0.38285 |
| 100150788_TGI_at | TSPAN14 | negative | Concordant | -0.11693 | 0.064161 | 0.068383 | 0.322578 | -0.52765 | 1.172623 | 0.652732 | 0.887779 |
| 100150806_TGI_at | | negative | Concordant | 0.141352 | 0.307528 | 0.645776 | 0.870774 | -1.49617 | 5.687193 | 0.792491 | 0.947801 |
| 100150849_TGI_at | | positive | Discordant | -2.01444 | 3.389327 | 0.55228 | 0.800714 | -82.3139 | 61.76885 | 0.182659 | 0.575874 |
| 100150862_TGI_at | | positive | Concordant | 5.868991 | 6.97445 | 0.400069 | 0.704177 | 7.977419 | 127.481 | 0.950103 | 0.994854 |
| 100150898_TGI_at | SLC27A5 | positive | Discordant | -0.7071 | 0.3378 | 0.036328 | 0.238611 | -14.9312 | 6.1824 | 0.01573 | 0.240338 |
| 100150988_TGI_at | | negative | Discordant | 1.575514 | 1.916331 | 0.410991 | 0.711479 | 22.11159 | 35.24583 | 0.530428 | 0.825639 |
| 100151060_TGI_at | MLH3 | positive | Discordant | -1.06501 | 0.630294 | 0.091086 | 0.387115 | -10.6192 | 11.4187 | 0.35238 | 0.707207 |
| 100151120_TGI_at | | negative | Concordant | -0.0382 | 0.111446 | 0.731776 | 0.910662 | -2.02207 | 2.029065 | 0.318981 | 0.671733 |
| 100151160_TGI_at | AIF1 | negative | Discordant | -0.00175 | 0.011214 | 0.876039 | 0.965712 | -0.14307 | 0.204327 | 0.4838 | 0.80052 |
| 100151170_TGI_at | AZGP1 | positive | Discordant | -0.01622 | 0.011263 | 0.14971 | 0.4583 | -0.3295 | 0.201505 | 0.102011 | 0.486596 |
| 100151178_TGI_at | | positive | Concordant | 0.385641 | 0.343299 | 0.261294 | 0.573524 | -1.27396 | 6.208138 | 0.837409 | 0.957828 |
| 100151213_TGI_at | | positive | Concordant | -0.25395 | 1.424118 | 0.858472 | 0.95732 | 30.9523 | 26.19082 | 0.237285 | 0.631062 |
| 100151271_TGI_at | LASS2 | positive | Concordant | 0.132089 | 0.053474 | 0.013505 | 0.162627 | 1.209807 | 0.97796 | 0.21606 | 0.622339 |
| 100151362_TGI_at | | positive | Concordant | 0.680167 | 0.415594 | 0.101711 | 0.403443 | 4.24599 | 7.612265 | 0.576993 | 0.847029 |
| 100151371_TGI_at | VARS2 | positive | Discordant | -0.28608 | 0.120874 | 0.017946 | 0.201777 | -2.44473 | 2.195725 | 0.265535 | 0.64407 |
| 100151371_TGI_at | VARS2 | positive | Discordant | -0.28608 | 0.120874 | 0.017946 | 0.201777 | -2.44473 | 2.195725 | 0.265535 | 0.64407 |
| 100151388_TGI_at | FGD6 | negative | Discordant | 0.305943 | 0.096358 | 0.001498 | 0.054107 | 4.104722 | 1.752416 | 0.019164 | 0.2703 |
| 100151492_TGI_at | | negative | Discordant | 0.089935 | 0.052863 | 0.088886 | 0.379625 | 1.373734 | 0.958503 | 0.151798 | 0.553455 |
| 100151496_TGI_at | NUDT14 | positive | Concordant | 0.135458 | 0.064466 | 0.035621 | 0.238611 | 1.853568 | 1.169963 | 0.113126 | 0.507597 |
| 100151519_TGI_at | CCDC53 | negative | Discordant | 0.09346 | 0.059557 | 0.116593 | 0.424731 | 1.163021 | 1.088896 | 0.285488 | 0.64733 |
| 100151558_TGI_at | | negative | Concordant | 0.031528 | 0.161158 | 0.844897 | 0.952951 | -2.60309 | 3.015544 | 0.388014 | 0.739358 |
| 100151666_TGI_at | SPATA1 | negative | Concordant | -0.16845 | 0.36196 | 0.641651 | 0.867881 | -7.54926 | 6.479662 | 0.24399 | 0.638503 |
| 100151676_TGI_at | | positive | Concordant | 1.335389 | 1.003306 | 0.183193 | 0.49021 | -3.52578 | 17.93412 | 0.844144 | 0.958398 |
| 100151676_TGI_at | | positive | Discordant | 1.335389 | 1.003306 | 0.183193 | 0.49021 | -3.52578 | 17.93412 | 0.844144 | 0.958398 |
| 100151685_TGI_at | STRA13 | negative | Concordant | -0.00282 | 0.067323 | 0.966618 | 0.991785 | -0.10211 | 1.246273 | 0.934702 | 0.993121 |
| 100151722_TGI_at | ZFAND2A | positive | Discordant | -0.06429 | 0.046196 | 0.164003 | 0.461656 | -0.24496 | 0.853386 | 0.774081 | 0.941122 |
| 100151793_TGI_at | | positive | Discordant | -1.76447 | 1.253109 | 0.159108 | 0.461656 | -31.3958 | 22.65368 | 0.165776 | 0.564154 |
| 100151794_TGI_at | RPS6KL1 | negative | Concordant | -0.82993 | 0.414008 | 0.045002 | 0.269084 | -13.5379 | 7.485994 | 0.070539 | 0.427671 |
| 100152029_TGI_at | MRPL43 | negative | Discordant | 0.041733 | 0.063795 | 0.512998 | 0.780157 | -0.17486 | 1.165556 | 0.880749 | 0.969048 |
| 100152090_TGI_at | SLMO2 | positive | Discordant | -0.1979 | 0.134047 | 0.139845 | 0.445546 | -2.06753 | 2.412304 | 0.391403 | 0.744053 |
| 100152113_TGI_at | RNF144B | negative | Concordant | 0.016122 | 0.271908 | 0.952718 | 0.986866 | 1.775197 | 4.953135 | 0.720045 | 0.921701 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100152363_TGI_at | TMED10 | positive | Concordant | 0.928583 | 0.465745 | 0.046179 | 0.269292 | 15.056 | 8.515647 | 0.077054 | 0.447721 |
| 100152431_TGI_at | EIF3E | negative | Discordant | 0.21124 | 0.296913 | 0.476804 | 0.758512 | 4.62804 | 5.42218 | 0.393361 | 0.744637 |
| 100152540_TGI_at | CLUAP1 | positive | Concordant | 0.071054 | 0.078814 | 0.3673 | 0.692406 | 1.401236 | 1.426303 | 0.32589 | 0.673202 |
| 100152575_TGI_at | | positive | Concordant | 0.160886 | 0.114821 | 0.161159 | 0.461656 | -0.48401 | 2.063042 | 0.814513 | 0.952807 |
| 100152779_TGI_at | | positive | Discordant | -0.60249 | 0.500242 | 0.228435 | 0.531663 | -18.4592 | 9.003694 | 0.040347 | 0.360043 |
| 100152809_TGI_at | THEX1 | positive | Discordant | -0.64806 | 0.299673 | 0.030575 | 0.228521 | -9.44423 | 5.419544 | 0.081399 | 0.447876 |
| 100152956_TGI_at | | positive | Concordant | 0.126053 | 1.303816 | 0.922981 | 0.974694 | 8.494102 | 23.91487 | 0.722454 | 0.921701 |
| 100153205_TGI_at | VTA1 | positive | Concordant | 0.219813 | 0.124874 | 0.078359 | 0.357565 | 2.501718 | 2.281936 | 0.272941 | 0.64407 |
| 100153237_TGI_at | RHOBTB3 | positive | Concordant | -0.03328 | 0.081867 | 0.684395 | 0.885627 | 0.717701 | 1.496368 | 0.631492 | 0.873211 |
| 100153252_TGI_at | HIGD2A | negative | Discordant | 0.024138 | 0.071757 | 0.736578 | 0.910662 | -2.23097 | 1.297223 | 0.085467 | 0.455195 |
| 100153401_TGI_at | TRIM26 | positive | Concordant | 0.598819 | 0.925031 | 0.517405 | 0.780157 | 15.05946 | 16.97547 | 0.375008 | 0.730277 |
| 100153419_TGI_at | TOM1L2 | negative | Concordant | -0.50347 | 0.304254 | 0.097969 | 0.398532 | -8.86395 | 5.591803 | 0.112928 | 0.507597 |
| 100153459_TGI_at | FAM71F2 | negative | Discordant | 0.260488 | 2.173083 | 0.904586 | 0.970639 | 25.80619 | 39.78534 | 0.516574 | 0.820274 |
| 100153741_TGI_at | VDAC2 | negative | Concordant | -0.12353 | 0.043994 | 0.004987 | 0.09827 | -1.77089 | 0.804821 | 0.027782 | 0.301895 |
| 100153773_TGI_at | C11orf83 | negative | Concordant | -0.52115 | 0.348296 | 0.134578 | 0.443506 | -7.46216 | 6.365744 | 0.241102 | 0.637303 |
| 100153916_TGI_at | | negative | Concordant | 0.037585 | 0.27288 | 0.890451 | 0.965743 | -9.98403 | 4.911143 | 0.042059 | 0.364653 |
| 100154037_TGI_at | ZNF25 | negative | Discordant | 0.457142 | 0.196775 | 0.02017 | 0.201777 | 7.797254 | 3.554279 | 0.028252 | 0.301895 |
| 100154120_TGI_at | CNKSR1 | negative | Discordant | 0.082524 | 0.096921 | 0.394513 | 0.704177 | 2.794681 | 1.77987 | 0.116378 | 0.509594 |
| 100154198_TGI_at | NUDT5 | negative | Concordant | -0.11579 | 0.066713 | 0.082614 | 0.371725 | -2.11353 | 1.203706 | 0.079113 | 0.447721 |
| 100154198_TGI_at | NUDT5 | negative | Concordant | -0.11579 | 0.066713 | 0.082614 | 0.371725 | -2.11353 | 1.203706 | 0.079113 | 0.447721 |
| 100154282_TGI_at | HOXB7 | negative | Concordant | -0.55996 | 0.195498 | 0.00418 | 0.09536 | -10.7414 | 3.519403 | 0.002273 | 0.098532 |
| 100154320_TGI_at | SGCD | negative | Discordant | 0.451207 | 0.197164 | 0.022109 | 0.201777 | 6.129356 | 3.590952 | 0.087843 | 0.457481 |
| 100154412_TGI_at | LTK | positive | Concordant | 0.145185 | 0.115996 | 0.210703 | 0.516353 | 5.954987 | 2.112227 | 0.004813 | 0.143891 |
| 100154603_TGI_at | SNAPIN | positive | Concordant | -0.00638 | 0.118591 | 0.957087 | 0.988973 | -0.2684 | 2.138264 | 0.900108 | 0.978198 |
| 100154661_TGI_at | NAPRT1 | positive | Discordant | -0.11235 | 0.144002 | 0.435263 | 0.724829 | -4.15667 | 2.612167 | 0.111549 | 0.507597 |
| 100154727_TGI_at | CEP192 | positive | Concordant | 1.095571 | 0.996083 | 0.271385 | 0.580964 | 27.66046 | 17.81956 | 0.120602 | 0.516945 |
| 100154811_TGI_at | RPAP1 | negative | Concordant | -0.28971 | 0.16855 | 0.085641 | 0.373119 | -4.26814 | 3.04709 | 0.161296 | 0.560509 |
| 100154919_TGI_at | RHOBTB3 | positive | Concordant | -0.06717 | 0.062309 | 0.281025 | 0.593566 | 0.753271 | 1.132949 | 0.50613 | 0.814654 |
| 100154936_TGI_at | | positive | Concordant | 0.266797 | 0.084329 | 0.001557 | 0.054107 | 2.512052 | 1.535748 | 0.101898 | 0.486596 |
| 100154936_TGI_at | | positive | Concordant | 0.266797 | 0.084329 | 0.001557 | 0.054107 | 2.512052 | 1.535748 | 0.101898 | 0.486596 |
| 100154998_TGI_at | C1GALT1 | negative | Concordant | -0.29758 | 0.128043 | 0.020123 | 0.201777 | -4.75696 | 2.329108 | 0.041112 | 0.360043 |
| 100155000_TGI_at | C3orf70 | positive | Concordant | 8.20E-05 | 0.102254 | 0.99936 | 0.99936 | 1.099202 | 1.852341 | 0.552905 | 0.837177 |
| 100155082_TGI_at | BSCL2 | negative | Concordant | -0.00351 | 0.032671 | 0.914486 | 0.972561 | 0.311064 | 0.595829 | 0.601621 | 0.860732 |
| 100155121_TGI_at | | negative | Concordant | -0.0393 | 0.163231 | 0.809715 | 0.939143 | -0.345 | 2.962342 | 0.907288 | 0.980193 |
| 100155123_TGI_at | MCART1 | positive | Discordant | -0.03094 | 0.256461 | 0.903984 | 0.970639 | -0.07369 | 4.773789 | 0.987685 | 0.999082 |
| 100155146_TGI_at | KCNE2 | negative | Concordant | -1.46303 | 1.172276 | 0.21202 | 0.516353 | -43.0903 | 21.35722 | 0.043633 | 0.370881 |
| 100155226_TGI_at | hCG_2039148 | positive | Concordant | 0.378948 | 0.245004 | 0.121935 | 0.431533 | 4.387885 | 4.454345 | 0.324585 | 0.673202 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100155331_TGI_at | | negative | Discordant | 0.322665 | 0.153188 | 0.035176 | 0.23826 | 5.448107 | 2.797105 | 0.051443 | 0.39368 |
| 100155331_TGI_at | | positive | Concordant | 0.322665 | 0.153188 | 0.035176 | 0.23826 | 5.448107 | 2.797105 | 0.051443 | 0.39368 |
| 100155331_TGI_at | | negative | Discordant | 0.322665 | 0.153188 | 0.035176 | 0.23826 | 5.448107 | 2.797105 | 0.051443 | 0.39368 |
| 100155432_TGI_at | GATAD2B | negative | Concordant | 0.008164 | 0.046876 | 0.861745 | 0.95732 | 0.210517 | 0.862281 | 0.807123 | 0.950782 |
| 100155445_TGI_at | | positive | Discordant | -0.06009 | 0.086791 | 0.488741 | 0.766255 | -1.79265 | 1.57193 | 0.254113 | 0.638503 |
| 100155522_TGI_at | | negative | Concordant | -0.02292 | 0.015052 | 0.127801 | 0.431533 | -0.50595 | 0.273659 | 0.06448 | 0.423515 |
| 100155542_TGI_at | RABEP1 | negative | Concordant | -0.05686 | 0.160548 | 0.723207 | 0.905521 | -1.62121 | 2.900558 | 0.57621 | 0.847029 |
| 100155586_TGI_at | PM20D1 | positive | Discordant | -1.93954 | 1.45501 | 0.182529 | 0.49021 | -32.2345 | 26.93025 | 0.231321 | 0.623069 |
| 100155887_TGI_at | ATF6 | negative | Concordant | -0.14302 | 0.056617 | 0.011535 | 0.150127 | -2.54707 | 1.03273 | 0.01365 | 0.223291 |
| 100155895_TGI_at | | negative | Concordant | -0.82 | 2.47448 | 0.740356 | 0.911402 | 30.61613 | 44.96566 | 0.495949 | 0.80522 |
| 100155899_TGI_at | | negative | Concordant | 0.123922 | 0.466084 | 0.790331 | 0.929308 | -6.51718 | 8.38751 | 0.437153 | 0.771226 |
| 100155944_TGI_at | | positive | Concordant | 4.030662 | 2.407593 | 0.094102 | 0.39476 | 78.57488 | 43.17354 | 0.068762 | 0.426441 |
| 100155972_TGI_at | USP4 | negative | Concordant | -0.04464 | 0.030666 | 0.145504 | 0.450369 | -0.51252 | 0.558354 | 0.358666 | 0.718159 |
| 100156028_TGI_at | VAMP4 | negative | Concordant | -0.50212 | 0.247181 | 0.042216 | 0.26144 | -6.53595 | 4.496184 | 0.146039 | 0.549177 |
| 100156369_TGI_at | CGN | positive | Concordant | -0.06124 | 0.163898 | 0.708672 | 0.896962 | 2.364804 | 2.970239 | 0.425935 | 0.764753 |
| 100156388_TGI_at | MAPKBP1 | negative | Concordant | -0.67011 | 0.478794 | 0.16164 | 0.461656 | -7.53385 | 8.86636 | 0.395486 | 0.745404 |
| 100156434_TGI_at | CHRNA5 | positive | Discordant | 0.140732 | 1.11144 | 0.89924 | 0.968499 | 3.640105 | 19.90915 | 0.854927 | 0.963575 |
| 100156434_TGI_at | CHRNA5 | positive | Concordant | 0.140732 | 1.11144 | 0.89924 | 0.968499 | 3.640105 | 19.90915 | 0.854927 | 0.963575 |
| 100156557_TGI_at | PGM2L1 | positive | Discordant | -0.03347 | 0.151329 | 0.824958 | 0.942561 | -0.17384 | 2.72976 | 0.949224 | 0.994854 |
| 100156621_TGI_at | TPM1 | negative | Concordant | -0.23824 | 0.187162 | 0.203059 | 0.509426 | 1.261701 | 3.429472 | 0.712948 | 0.915742 |
| 100156721_TGI_at | STAT6 | negative | Discordant | 0.019569 | 0.013259 | 0.139979 | 0.445546 | 0.247577 | 0.240959 | 0.304203 | 0.669401 |
| 100156777_TGI_at | MRPS21 | positive | Discordant | -0.0698 | 0.234692 | 0.76616 | 0.923606 | -3.32245 | 4.236176 | 0.432862 | 0.767727 |
| 100156808_TGI_at | | positive | Discordant | -0.26103 | 0.674739 | 0.69886 | 0.894706 | -10.5947 | 12.1773 | 0.384279 | 0.739358 |
| 100156808_TGI_at | | positive | Discordant | -0.26103 | 0.674739 | 0.69886 | 0.894706 | -10.5947 | 12.1773 | 0.384279 | 0.739358 |
| 100156891_TGI_at | SGCD | positive | Concordant | 0.263052 | 0.18291 | 0.150391 | 0.4583 | 3.651225 | 3.322807 | 0.271839 | 0.64407 |
| 100157087_TGI_at | PID1 | negative | Concordant | 0.002221 | 0.021682 | 0.918403 | 0.972561 | -0.45518 | 0.391486 | 0.244955 | 0.638503 |
| 100157152_TGI_at | TMEM108 | negative | Discordant | 0.365015 | 0.194833 | 0.061003 | 0.311116 | 3.020002 | 3.57102 | 0.397722 | 0.74587 |
| 100157152_TGI_at | TMEM108 | negative | Discordant | 0.365015 | 0.194833 | 0.061003 | 0.311116 | 3.020002 | 3.57102 | 0.397722 | 0.74587 |
| 100157247_TGI_at | KTELC1 | negative | Concordant | -0.33216 | 0.129097 | 0.010085 | 0.143335 | -5.44208 | 2.337817 | 0.01992 | 0.2703 |
| 100157269_TGI_at | | negative | Discordant | 1.883371 | 1.259758 | 0.134908 | 0.443506 | 38.73575 | 22.6068 | 0.086629 | 0.455195 |
| 100157274_TGI_at | WDR52 | negative | Concordant | -0.04814 | 0.224434 | 0.83015 | 0.945698 | -3.00679 | 4.0164 | 0.454082 | 0.779582 |
| 100157324_TGI_at | | negative | Concordant | -0.17651 | 0.279987 | 0.528416 | 0.785614 | -5.35986 | 5.117199 | 0.294906 | 0.656435 |
| 100157332_TGI_at | GTF3C5 | positive | Discordant | 0.044536 | 0.105071 | 0.671667 | 0.882327 | 0.091077 | 1.906736 | 0.961903 | 0.998766 |
| 100157337_TGI_at | | positive | Discordant | -0.26083 | 0.111604 | 0.019435 | 0.201777 | -1.26209 | 2.031939 | 0.534517 | 0.826976 |
| 100157433_TGI_at | | negative | Concordant | -0.95008 | 0.446327 | 0.033282 | 0.236522 | -19.1544 | 8.047083 | 0.017299 | 0.249971 |
| 100157567_TGI_at | HLA-DQB2 | positive | Concordant | 0.017681 | 0.042817 | 0.679655 | 0.883837 | -0.45568 | 0.767455 | 0.552673 | 0.837177 |
| 100157567_TGI_at | HLA-DQB2 | negative | Concordant | 0.017681 | 0.042817 | 0.679655 | 0.883837 | -0.45568 | 0.767455 | 0.552673 | 0.837177 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100157804_TGI_at | | positive | Concordant | 0.704556 | 0.215158 | 0.001058 | 0.04587 | 8.133873 | 3.90841 | 0.037423 | 0.342664 |
| 100157818_TGI_at | | negative | Discordant | 2.371581 | 1.078199 | 0.027837 | 0.209866 | 72.46862 | 19.15629 | 0.000155 | 0.022389 |
| 100157820_TGI_at | | negative | Concordant | -0.20321 | 0.286998 | 0.478907 | 0.760462 | -8.7964 | 5.208326 | 0.091237 | 0.462585 |
| 100157946_TGI_at | ZNF600 | positive | Concordant | 0.026401 | 0.123833 | 0.831175 | 0.945698 | 0.092336 | 2.254192 | 0.967326 | 0.999082 |
| 100158065_TGI_at | STK32C | positive | Discordant | 0.032593 | 0.319068 | 0.918638 | 0.972561 | -0.92347 | 5.814448 | 0.873808 | 0.966864 |
| 100158126_TGI_at | PIGL | positive | Discordant | -0.23742 | 0.527522 | 0.652669 | 0.873359 | -0.07704 | 9.657085 | 0.993635 | 0.999082 |
| 100158135_TGI_at | TMEM163 | positive | Concordant | 0.066417 | 0.046571 | 0.153824 | 0.4583 | 0.856743 | 0.852565 | 0.314945 | 0.671386 |
| 100158197_TGI_at | | positive | Discordant | -2.02826 | 1.079839 | 0.060341 | 0.309558 | -38.3712 | 19.5722 | 0.049938 | 0.39368 |
| 100158197_TGI_at | | positive | Discordant | -2.02826 | 1.079839 | 0.060341 | 0.309558 | -38.3712 | 19.5722 | 0.049938 | 0.39368 |
| 100158208_TGI_at | NBPF1 | positive | Concordant | 0.00499 | 0.425935 | 0.990652 | 0.996398 | 0.839512 | 7.719216 | 0.913396 | 0.980193 |
| 100158228_TGI_at | ZNRD1 | positive | Discordant | -0.69139 | 0.179604 | 0.000118 | 0.02741 | -12.9695 | 3.264002 | 7.08E-05 | 0.01669 |
| 100158228_TGI_at | ZNRD1 | positive | Discordant | -0.69139 | 0.179604 | 0.000118 | 0.02741 | -12.9695 | 3.264002 | 7.08E-05 | 0.01669 |
| 100158297_TGI_at | GEN1 | positive | Discordant | -0.23093 | 0.150607 | 0.125189 | 0.431533 | -0.70036 | 2.762901 | 0.799893 | 0.9484 |
| 100158314_TGI_at | | negative | Discordant | 0.651572 | 1.190554 | 0.584183 | 0.82238 | 27.04989 | 21.80888 | 0.214859 | 0.620942 |
| 100158347_TGI_at | C19orf6 | positive | Discordant | 0.529064 | 0.920631 | 0.565511 | 0.813007 | -3.64971 | 17.14399 | 0.831416 | 0.957068 |
| 100158391_TGI_at | NT5C | positive | Concordant | 0.080785 | 0.105382 | 0.443325 | 0.733269 | -0.3478 | 1.913484 | 0.85577 | 0.963575 |
| 100158468_TGI_at | SEMA3A | positive | Discordant | -1.21865 | 0.948326 | 0.198774 | 0.50837 | -20.3436 | 17.02526 | 0.232124 | 0.623069 |
| 100158499_TGI_at | TDRD10 | negative | Discordant | -0.01955 | 0.0581 | 0.73645 | 0.910662 | 1.068075 | 1.063148 | 0.315073 | 0.671386 |
| 100158666_TGI_at | | positive | Discordant | -0.12089 | 0.180909 | 0.503998 | 0.776148 | -7.98311 | 3.2 | 0.012606 | 0.215815 |
| 100158823_TGI_at | | positive | Concordant | 4.751005 | 3.639973 | 0.191814 | 0.503948 | 56.85272 | 65.8478 | 0.38792 | 0.739358 |
| 100158927_TGI_at | RNF5 | negative | Discordant | 0.017846 | 0.048732 | 0.714211 | 0.899455 | 0.889654 | 0.880826 | 0.312485 | 0.671386 |
| 100158927_TGI_at | RNF5 | negative | Discordant | 0.017846 | 0.048732 | 0.714211 | 0.899455 | 0.889654 | 0.880826 | 0.312485 | 0.671386 |
| 100159134_TGI_at | PLEKHM1 | negative | Concordant | -0.04329 | 0.105662 | 0.682042 | 0.883903 | -1.51022 | 1.913909 | 0.430067 | 0.767727 |
| 100159134_TGI_at | PLEKHM1 | negative | Concordant | -0.04329 | 0.105662 | 0.682042 | 0.883903 | -1.51022 | 1.913909 | 0.430067 | 0.767727 |
| 100159164_TGI_at | GOLPH3L | positive | Concordant | 0.192166 | 0.37258 | 0.606015 | 0.833901 | -9.47055 | 6.747501 | 0.160449 | 0.560509 |
| 100159175_TGI_at | MUC21 | negative | Concordant | -0.04331 | 0.036296 | 0.232723 | 0.533786 | -0.08746 | 0.653864 | 0.893599 | 0.975569 |
| 100159175_TGI_at | MUC21 | positive | Discordant | -0.04331 | 0.036296 | 0.232723 | 0.533786 | -0.08746 | 0.653864 | 0.893599 | 0.975569 |
| 100159186_TGI_at | | positive | Concordant | 0.710658 | 2.480065 | 0.774458 | 0.923606 | 54.07002 | 44.52591 | 0.224614 | 0.623069 |
| 100159303_TGI_at | NPHP3 | negative | Discordant | 0.19283 | 0.120338 | 0.109067 | 0.417621 | 3.006515 | 2.182603 | 0.168361 | 0.564154 |
| 100159312_TGI_at | ANKRD13B | positive | Concordant | -0.0543 | 0.087545 | 0.535069 | 0.791076 | 0.103393 | 1.615016 | 0.948954 | 0.994854 |
| 100159322_TGI_at | C4BPB | positive | Discordant | -0.07305 | 0.169631 | 0.666747 | 0.879862 | 1.522009 | 3.048734 | 0.61762 | 0.865125 |
| 100159492_TGI_at | C3orf26 | negative | Concordant | -0.13837 | 0.093729 | 0.139862 | 0.445546 | -4.55074 | 1.721095 | 0.008191 | 0.195664 |
| 100159519_TGI_at | C16orf5 | negative | Concordant | -0.10842 | 0.110497 | 0.326486 | 0.641332 | -2.24868 | 2.010806 | 0.263439 | 0.64407 |
| 100159529_TGI_at | TSEN54 | positive | Discordant | -0.47161 | 0.208126 | 0.023453 | 0.203166 | -5.80255 | 3.844226 | 0.131192 | 0.536498 |
| 100159613_TGI_at | ROCK2 | negative | Discordant | -0.14292 | 0.086469 | 0.098369 | 0.398532 | 2.672743 | 1.574226 | 0.089543 | 0.460698 |
| 100159682_TGI_at | ITIH5 | positive | Concordant | 0.112063 | 0.036702 | 0.002263 | 0.065414 | 2.281692 | 0.67864 | 0.000773 | 0.055876 |
| 100159829_TGI_at | | negative | Concordant | -0.14469 | 0.164125 | 0.378007 | 0.700281 | -3.92701 | 3.002085 | 0.190841 | 0.588823 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 100159916_TGI_at | SNRPC | negative | Concordant | 0.018658 | 0.05933 | 0.753156 | 0.919699 | -0.43261 | 1.08234 | 0.689381 | 0.910189 |
| 100159938_TGI_at | SLC30A10 | positive | Concordant | 1.7367 | 1.135802 | 0.126252 | 0.431533 | 32.32693 | 20.37768 | 0.112651 | 0.507597 |
| 100159981_TGI_at | | positive | Discordant | -0.38691 | 0.58035 | 0.504974 | 0.776148 | 2.670703 | 10.54079 | 0.799984 | 0.9484 |
| 100160039_TGI_at | | negative | Discordant | 1.021335 | 1.043488 | 0.327693 | 0.641332 | 2.692547 | 18.71317 | 0.885591 | 0.971908 |
| 100160044_TGI_at | RAB3IP | negative | Discordant | 0.003269 | 0.044871 | 0.941928 | 0.983056 | -0.05078 | 0.81095 | 0.950076 | 0.994854 |
| 100160095_TGI_at | SVEP1 | negative | Concordant | -0.6195 | 0.530255 | 0.24268 | 0.546504 | -9.95452 | 9.392642 | 0.289226 | 0.649634 |
| 100160114_TGI_at | | negative | Concordant | -0.39561 | 0.719273 | 0.582307 | 0.82238 | -10.7404 | 13.21827 | 0.416479 | 0.761788 |
| 100160114_TGI_at | | negative | Concordant | -0.39561 | 0.719273 | 0.582307 | 0.82238 | -10.7404 | 13.21827 | 0.416479 | 0.761788 |
| 100160131_TGI_at | | positive | Discordant | -0.15433 | 0.581166 | 0.79058 | 0.929308 | -8.90272 | 10.4748 | 0.395371 | 0.745404 |
| 100160204_TGI_at | | positive | Concordant | 0.22307 | 0.096677 | 0.021035 | 0.201777 | 2.26618 | 1.77689 | 0.202181 | 0.606239 |
| 100160221_TGI_at | HLA-G | positive | Discordant | -0.47057 | 0.591408 | 0.426222 | 0.718939 | -2.99079 | 10.61352 | 0.778104 | 0.941122 |
| 100160221_TGI_at | HLA-G | positive | Discordant | -0.47057 | 0.591408 | 0.426222 | 0.718939 | -2.99079 | 10.61352 | 0.778104 | 0.941122 |
| 100160221_TGI_at | HLA-G | positive | Discordant | -0.47057 | 0.591408 | 0.426222 | 0.718939 | -2.99079 | 10.61352 | 0.778104 | 0.941122 |
| 100160221_TGI_at | HLA-G | positive | Discordant | -0.47057 | 0.591408 | 0.426222 | 0.718939 | -2.99079 | 10.61352 | 0.778104 | 0.941122 |
| 100160231_TGI_at | C10orf55 | negative | Concordant | -1.10166 | 1.565543 | 0.481625 | 0.762065 | -13.7078 | 28.02473 | 0.624749 | 0.868396 |
| 100160231_TGI_at | C10orf55 | negative | Concordant | -1.10166 | 1.565543 | 0.481625 | 0.762065 | -13.7078 | 28.02473 | 0.624749 | 0.868396 |
| 100160430_TGI_at | HLA-DRB6 | negative | Discordant | -0.19979 | 0.528119 | 0.705209 | 0.896505 | 3.667363 | 9.494486 | 0.699302 | 0.913095 |
| 100160430_TGI_at | HLA-DRB6 | positive | Concordant | -0.19979 | 0.528119 | 0.705209 | 0.896505 | 3.667363 | 9.494486 | 0.699302 | 0.913095 |
| 100160466_TGI_at | ROCK2 | positive | Concordant | 0.076739 | 0.131448 | 0.559355 | 0.805583 | 5.500907 | 2.380364 | 0.020835 | 0.273703 |
| 100160580_TGI_at | PPA2 | negative | Concordant | -0.18174 | 0.215512 | 0.399052 | 0.704177 | 0.596344 | 3.912585 | 0.878858 | 0.968426 |
| 100160580_TGI_at | PPA2 | negative | Discordant | -0.18174 | 0.215512 | 0.399052 | 0.704177 | 0.596344 | 3.912585 | 0.878858 | 0.968426 |
| 100160585_TGI_at | MTMR3 | negative | Discordant | 0.177949 | 0.150261 | 0.23631 | 0.53916 | 3.91929 | 2.700501 | 0.146691 | 0.549177 |
| 100160610_TGI_at | YLPM1 | negative | Discordant | -0.23235 | 1.052477 | 0.825272 | 0.942561 | 22.86796 | 19.1335 | 0.232017 | 0.623069 |
| 100160728_TGI_at | KIAA1267 | negative | Concordant | -2.31542 | 1.099001 | 0.035131 | 0.23826 | -34.7479 | 19.8276 | 0.079688 | 0.447721 |
| 100160780_TGI_at | SPINK5 | negative | Concordant | -0.07384 | 0.02447 | 0.002549 | 0.069066 | -0.78294 | 0.449692 | 0.081674 | 0.447876 |
| 100160946_TGI_at | FAM13A1 | negative | Discordant | -0.00948 | 0.044737 | 0.832258 | 0.945698 | 0.154061 | 0.814041 | 0.849893 | 0.961955 |
| 100161068_TGI_at | C10orf58 | negative | Concordant | -0.08343 | 0.047481 | 0.078912 | 0.358205 | -2.249 | 0.851389 | 0.008252 | 0.195664 |
| 100161091_TGI_at | TNC | negative | Concordant | -0.23807 | 0.149996 | 0.11247 | 0.419479 | 1.427875 | 2.723024 | 0.60002 | 0.860732 |
| 100161091_TGI_at | TNC | negative | Concordant | -0.23807 | 0.149996 | 0.11247 | 0.419479 | 1.427875 | 2.723024 | 0.60002 | 0.860732 |
| 100161122_TGI_at | | positive | Discordant | 0.019279 | 0.182859 | 0.916035 | 0.972561 | -0.41645 | 3.494831 | 0.905147 | 0.980193 |
| 100161206_TGI_at | ENSA | negative | Discordant | 0.021179 | 0.027208 | 0.436336 | 0.724829 | 0.224886 | 0.498077 | 0.651623 | 0.887779 |
| 100161240_TGI_at | | positive | Concordant | 0.713745 | 0.437002 | 0.10241 | 0.40359 | 6.345266 | 7.908873 | 0.422381 | 0.764753 |
| 100161253_TGI_at | BTN3A2 | positive | Discordant | 0.046426 | 0.034089 | 0.173232 | 0.47529 | -0.17534 | 0.618617 | 0.776838 | 0.941122 |
| 100161253_TGI_at | BTN3A2 | positive | Discordant | 0.046426 | 0.034089 | 0.173232 | 0.47529 | -0.17534 | 0.618617 | 0.776838 | 0.941122 |
| 100161253_TGI_at | BTN3A2 | positive | Concordant | 0.046426 | 0.034089 | 0.173232 | 0.47529 | -0.17534 | 0.618617 | 0.776838 | 0.941122 |
| 100161253_TGI_at | BTN3A2 | positive | Concordant | 0.046426 | 0.034089 | 0.173232 | 0.47529 | -0.17534 | 0.618617 | 0.776838 | 0.941122 |
| 100161262_TGI_at | ERP29 | positive | Concordant | -0.4584 | 0.485505 | 0.345086 | 0.666231 | -2.13975 | 8.868769 | 0.809348 | 0.951333 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100161388_TGI_at | | negative | Discordant | 2.475021 | 1.339559 | 0.064655 | 0.314919 | 1.7443 | 24.8614 | 0.944066 | 0.994854 |
| 100161388_TGI_at | | negative | Discordant | 2.475021 | 1.339559 | 0.064655 | 0.314919 | 1.7443 | 24.8614 | 0.944066 | 0.994854 |
| 100161395_TGI_at | TAP2 | positive | Discordant | -0.01401 | 0.016284 | 0.38964 | 0.703787 | -0.05948 | 0.295169 | 0.840297 | 0.958398 |
| 100161395_TGI_at | TAP2 | positive | Concordant | -0.01401 | 0.016284 | 0.38964 | 0.703787 | -0.05948 | 0.295169 | 0.840297 | 0.958398 |
| 100161408_TGI_at | MAPT | negative | Concordant | -0.48641 | 0.262683 | 0.06407 | 0.314919 | -9.99068 | 4.727026 | 0.034556 | 0.334258 |
| 100161482_TGI_at | MAPRE2 | positive | Discordant | 0.040398 | 0.102011 | 0.692094 | 0.891598 | 1.270476 | 1.846313 | 0.49138 | 0.804238 |
| 100161520_TGI_at | MICB | negative | Concordant | -0.09742 | 0.068201 | 0.153182 | 0.4583 | -1.58134 | 1.229229 | 0.198286 | 0.599003 |
| 100161520_TGI_at | MICB | negative | Concordant | -0.09742 | 0.068201 | 0.153182 | 0.4583 | -1.58134 | 1.229229 | 0.198286 | 0.599003 |
| 100161625_TGI_at | C2 | negative | Discordant | 0.025246 | 0.015608 | 0.105774 | 0.409927 | 0.125471 | 0.281009 | 0.655236 | 0.887779 |
| 100161662_TGI_at | RBP2 | positive | Concordant | 0.063281 | 0.084652 | 0.454739 | 0.737526 | 2.930082 | 1.528984 | 0.055319 | 0.403041 |
| 100161807_TGI_at | DDR1 | negative | Discordant | 0.023531 | 0.02619 | 0.368941 | 0.692406 | 0.919385 | 0.477769 | 0.054313 | 0.403041 |
| 100161813_TGI_at | PGBD1 | negative | Discordant | 0.319423 | 0.616097 | 0.604137 | 0.832729 | 17.0943 | 11.20283 | 0.127037 | 0.529525 |
| 100161847_TGI_at | | positive | Concordant | 0.484726 | 0.381696 | 0.204111 | 0.509426 | 2.34416 | 6.87073 | 0.732968 | 0.92225 |
| 100162004_TGI_at | C12orf48 | positive | Discordant | -1.01421 | 0.819048 | 0.215611 | 0.522164 | -9.69477 | 14.77341 | 0.511676 | 0.818492 |
| 100162155_TGI_at | USP4 | negative | Concordant | -0.03238 | 0.031452 | 0.303195 | 0.622924 | -0.16651 | 0.575459 | 0.772311 | 0.941122 |
| 100162242_TGI_at | FMO2 | positive | Concordant | -0.01369 | 0.047954 | 0.775255 | 0.923606 | 0.448383 | 0.875455 | 0.608531 | 0.860732 |
| 100162298_TGI_at | RPL27A | positive | Discordant | -0.80228 | 0.43404 | 0.064544 | 0.314919 | -9.23591 | 8.098146 | 0.25408 | 0.638503 |
| 100162323_TGI_at | | negative | Concordant | -0.02201 | 0.033144 | 0.506689 | 0.776148 | -0.64904 | 0.601352 | 0.280452 | 0.647173 |
| 100162335_TGI_at | | positive | Concordant | 0.808703 | 0.694826 | 0.244467 | 0.549102 | 16.84405 | 12.50779 | 0.178082 | 0.571841 |
| 100162507_TGI_at | UBE2Q1 | negative | Discordant | 0.641297 | 0.326422 | 0.049457 | 0.274869 | 16.99439 | 5.909394 | 0.00403 | 0.129398 |
| 100162510_TGI_at | | positive | Concordant | 0.010448 | 0.05499 | 0.849317 | 0.952951 | 0.107586 | 0.990325 | 0.91349 | 0.980193 |
| 100162662_TGI_at | PILRB | positive | Concordant | -0.11281 | 0.182918 | 0.537421 | 0.791076 | 2.020598 | 3.346557 | 0.545987 | 0.83676 |
| 100162676_TGI_at | ZSWIM7 | positive | Discordant | -0.02263 | 0.038683 | 0.558594 | 0.805583 | -0.11328 | 0.703369 | 0.872055 | 0.966864 |
| 100162706_TGI_at | | negative | Discordant | 0.290338 | 0.230447 | 0.207708 | 0.514523 | 4.039861 | 4.234941 | 0.340116 | 0.692604 |
| 100162706_TGI_at | | negative | Discordant | 0.290338 | 0.230447 | 0.207708 | 0.514523 | 4.039861 | 4.234941 | 0.340116 | 0.692604 |
| 100162706_TGI_at | | negative | Discordant | 0.290338 | 0.230447 | 0.207708 | 0.514523 | 4.039861 | 4.234941 | 0.340116 | 0.692604 |
| 100162706_TGI_at | | negative | Discordant | 0.290338 | 0.230447 | 0.207708 | 0.514523 | 4.039861 | 4.234941 | 0.340116 | 0.692604 |
| 100162913_TGI_at | KPNA3 | positive | Concordant | 0.050549 | 0.186026 | 0.78583 | 0.928221 | 1.123446 | 3.390146 | 0.740353 | 0.92225 |
| 100162913_TGI_at | KPNA3 | negative | Discordant | 0.050549 | 0.186026 | 0.78583 | 0.928221 | 1.123446 | 3.390146 | 0.740353 | 0.92225 |
| 100162932_TGI_at | | positive | Discordant | -0.2024 | 0.857577 | 0.81342 | 0.939541 | -0.2724 | 15.47799 | 0.985959 | 0.999082 |
| 100162932_TGI_at | | positive | Concordant | -0.2024 | 0.857577 | 0.81342 | 0.939541 | -0.2724 | 15.47799 | 0.985959 | 0.999082 |
| 100163169_TGI_at | CNGA1 | negative | Concordant | -3.03056 | 1.231214 | 0.013838 | 0.164352 | -49.3135 | 22.71946 | 0.029966 | 0.302098 |
| 100300038_TGI_at | HLA-B | positive | Concordant | 0.009601 | 0.007949 | 0.227133 | 0.530862 | 0.108396 | 0.144012 | 0.451635 | 0.77692 |
| 100300038_TGI_at | HLA-B | positive | Concordant | 0.009601 | 0.007949 | 0.227133 | 0.530862 | 0.108396 | 0.144012 | 0.451635 | 0.77692 |
| 100300070_TGI_at | ANXA6 | positive | Discordant | -0.00128 | 0.018379 | 0.944505 | 0.983056 | -0.44452 | 0.334948 | 0.184461 | 0.579448 |
| 100300166_TGI_at | ARL5C | negative | Discordant | -7.72589 | 9.416507 | 0.411952 | 0.711479 | -2.87566 | 171.9134 | 0.986654 | 0.999082 |
| 100300216_TGI_at | | negative | Concordant | -0.05119 | 0.138269 | 0.711193 | 0.898841 | 0.088097 | 2.510611 | 0.972008 | 0.999082 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100300284_TGI_at | KIAA0802 | negative | Discordant | 0.02804 | 0.170376 | 0.869275 | 0.961303 | 4.670012 | 3.137289 | 0.136606 | 0.538352 |
| 100300305_TGI_at | | positive | Discordant | -0.57393 | 0.696562 | 0.409974 | 0.711479 | -8.81289 | 12.62021 | 0.48498 | 0.80052 |
| 100300348_TGI_at | HCG2P7 | positive | Concordant | 1.545728 | 0.697666 | 0.026721 | 0.20322 | 2.266632 | 12.76293 | 0.859041 | 0.964752 |
| 100300348_TGI_at | HCG2P7 | positive | Concordant | 1.545728 | 0.697666 | 0.026721 | 0.20322 | 2.266632 | 12.76293 | 0.859041 | 0.964752 |
| 100300365_TGI_at | ADORA2B | positive | Discordant | -0.41999 | 0.169128 | 0.013018 | 0.158968 | -2.74163 | 3.083827 | 0.373983 | 0.730277 |
| 100300398_TGI_at | HLA-DQB1 | positive | Concordant | -0.00056 | 0.005976 | 0.925102 | 0.975746 | -0.17773 | 0.107811 | 0.099242 | 0.486596 |
| 100300398_TGI_at | HLA-DQB1 | positive | Concordant | -0.00056 | 0.005976 | 0.925102 | 0.975746 | -0.17773 | 0.107811 | 0.099242 | 0.486596 |
| 100300398_TGI_at | HLA-DQB1 | positive | Discordant | -0.00056 | 0.005976 | 0.925102 | 0.975746 | -0.17773 | 0.107811 | 0.099242 | 0.486596 |
| 100300398_TGI_at | HLA-DQB1 | positive | Discordant | -0.00056 | 0.005976 | 0.925102 | 0.975746 | -0.17773 | 0.107811 | 0.099242 | 0.486596 |
| 100300564_TGI_at | G3BP1 | positive | Discordant | -0.03729 | 0.105938 | 0.724834 | 0.905521 | -0.94109 | 1.925433 | 0.625005 | 0.868396 |
| 100300599_TGI_at | LONP2 | negative | Discordant | -0.11221 | 0.396135 | 0.776971 | 0.924052 | -9.45284 | 7.204584 | 0.1895 | 0.587863 |
| 100300632_TGI_at | HOXA1 | positive | Discordant | -0.28048 | 0.974834 | 0.773563 | 0.923606 | -14.7217 | 17.68158 | 0.405069 | 0.752024 |
| 100300653_TGI_at | ERP29 | positive | Concordant | -1.66861 | 1.789854 | 0.351202 | 0.673656 | 20.75709 | 32.33008 | 0.520849 | 0.821114 |
| 100300682_TGI_at | BRWD1 | negative | Discordant | 0.593834 | 0.378103 | 0.116284 | 0.424731 | 11.09354 | 6.80915 | 0.103268 | 0.486596 |
| 100300793_TGI_at | WWP2 | positive | Concordant | 0.066986 | 0.147909 | 0.650628 | 0.873359 | 2.151447 | 2.684196 | 0.422829 | 0.764753 |
| 100300887_TGI_at | HSD17B7P2 | positive | Discordant | -3.57658 | 2.792504 | 0.200272 | 0.509426 | -76.1417 | 51.00217 | 0.135461 | 0.536498 |
| 100300925_TGI_at | HCG27 | negative | Concordant | -0.35 | 0.360893 | 0.332131 | 0.647095 | -0.01759 | 6.472809 | 0.997832 | 0.999082 |
| 100300925_TGI_at | HCG27 | positive | Concordant | -0.35 | 0.360893 | 0.332131 | 0.647095 | -0.01759 | 6.472809 | 0.997832 | 0.999082 |
| 100300937_TGI_at | SUPT3H | positive | Discordant | -0.01095 | 0.507624 | 0.982793 | 0.996398 | -4.1228 | 9.39359 | 0.660738 | 0.888268 |
| 100300966_TGI_at | PILRB | positive | Concordant | 0.005635 | 0.014557 | 0.698692 | 0.894706 | 0.26832 | 0.265306 | 0.311844 | 0.671386 |
| 100300977_TGI_at | GGT7 | negative | Concordant | -0.25442 | 0.178858 | 0.154898 | 0.459406 | -3.61924 | 3.332786 | 0.277501 | 0.64407 |
| 100300978_TGI_at | TUBB | negative | Discordant | 0.003287 | 0.018675 | 0.860283 | 0.95732 | -0.18891 | 0.34072 | 0.579281 | 0.848373 |
| 100300978_TGI_at | TUBB | negative | Concordant | 0.003287 | 0.018675 | 0.860283 | 0.95732 | -0.18891 | 0.34072 | 0.579281 | 0.848373 |
| 100300978_TGI_at | TUBB | negative | Concordant | 0.003287 | 0.018675 | 0.860283 | 0.95732 | -0.18891 | 0.34072 | 0.579281 | 0.848373 |
| 100300978_TGI_at | TUBB | negative | Discordant | 0.003287 | 0.018675 | 0.860283 | 0.95732 | -0.18891 | 0.34072 | 0.579281 | 0.848373 |
| 100301072_TGI_at | CACNA2D4 | negative | Discordant | 0.605817 | 0.432317 | 0.161116 | 0.461656 | 1.585091 | 8.066636 | 0.844219 | 0.958398 |
| 100301107_TGI_at | C21orf82 | negative | Concordant | -1.16318 | 0.516158 | 0.024225 | 0.203166 | -32.4794 | 9.300726 | 0.000479 | 0.051931 |
| 100301195_TGI_at | RELT | positive | Concordant | -0.0447 | 0.115836 | 0.699602 | 0.894706 | -0.1377 | 2.13321 | 0.94853 | 0.994854 |
| 100301274_TGI_at | TOM1L2 | negative | Concordant | -2.7848 | 2.022828 | 0.168609 | 0.467042 | -33.4894 | 37.0796 | 0.366433 | 0.728664 |
| 100301317_TGI_at | PIP4K2B | negative | Concordant | 0.169839 | 0.51567 | 0.741886 | 0.911402 | -5.29445 | 9.255248 | 0.567289 | 0.842191 |
| 100301456_TGI_at | TRIM4 | positive | Concordant | 0.342414 | 0.203631 | 0.092657 | 0.391872 | 8.104867 | 3.701762 | 0.028563 | 0.301895 |
| 100301468_TGI_at | SYTL2 | positive | Discordant | -0.05332 | 0.106159 | 0.615449 | 0.841142 | -0.30256 | 1.929869 | 0.875419 | 0.966864 |
| 100301474_TGI_at | JUB | positive | Concordant | 0.154531 | 0.104633 | 0.139705 | 0.445546 | 1.784557 | 1.91281 | 0.350845 | 0.705761 |
| 100301598_TGI_at | FAM103A1 | positive | Discordant | -0.16478 | 0.103209 | 0.110354 | 0.417803 | -2.10915 | 1.874131 | 0.260418 | 0.643256 |
| 100301615_TGI_at | ZNF323 | negative | Discordant | 0.127687 | 0.056753 | 0.024457 | 0.203166 | 1.385609 | 1.027979 | 0.177692 | 0.571841 |
| 100301615_TGI_at | ZNF323 | negative | Discordant | 0.127687 | 0.056753 | 0.024457 | 0.203166 | 1.385609 | 1.027979 | 0.177692 | 0.571841 |
| 100301615_TGI_at | ZNF323 | negative | Discordant | 0.127687 | 0.056753 | 0.024457 | 0.203166 | 1.385609 | 1.027979 | 0.177692 | 0.571841 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100301664_TGI_at | GFM1 | positive | Discordant | -0.06659 | 0.082587 | 0.420079 | 0.716053 | -0.1844 | 1.501779 | 0.902277 | 0.979066 |
| 100301711_TGI_at | SRD5A3 | negative | Concordant | -1.91655 | 0.754966 | 0.01113 | 0.150127 | -16.4779 | 13.68099 | 0.228421 | 0.623069 |
| 100301711_TGI_at | SRD5A3 | negative | Concordant | -1.91655 | 0.754966 | 0.01113 | 0.150127 | -16.4779 | 13.68099 | 0.228421 | 0.623069 |
| 100301782_TGI_at | MLF1 | negative | Concordant | -0.05174 | 0.037778 | 0.170817 | 0.470154 | -0.227 | 0.684918 | 0.740321 | 0.92225 |
| 100301867_TGI_at | FAM62B | positive | Concordant | 0.024744 | 0.044668 | 0.579617 | 0.82238 | 1.583924 | 0.814319 | 0.051764 | 0.39368 |
| 100301887_TGI_at | CAMK1D | negative | Discordant | 2.384967 | 0.911435 | 0.008878 | 0.135075 | 16.13255 | 16.78626 | 0.336524 | 0.688127 |
| 100301887_TGI_at | CAMK1D | negative | Discordant | 2.384967 | 0.911435 | 0.008878 | 0.135075 | 16.13255 | 16.78626 | 0.336524 | 0.688127 |
| 100302084_TGI_at | VEZT | positive | Concordant | 0.286762 | 0.330868 | 0.386109 | 0.702944 | 11.3808 | 5.962429 | 0.056294 | 0.406724 |
| 100302085_TGI_at | VEZT | negative | Discordant | 0.132919 | 0.084833 | 0.117155 | 0.424774 | 2.840007 | 1.541732 | 0.065462 | 0.426441 |
| 100302095_TGI_at | OTUD4 | negative | Concordant | -1.82258 | 1.240342 | 0.14172 | 0.445546 | -11.6131 | 22.33877 | 0.603158 | 0.860732 |
| 100302139_TGI_at | ZNF639 | positive | Concordant | 1.581028 | 0.685692 | 0.021125 | 0.201777 | 30.15333 | 12.51211 | 0.015956 | 0.240338 |
| 100302252_TGI_at | MAPKBP1 | positive | Concordant | 0.45792 | 0.966801 | 0.635753 | 0.861247 | 21.68467 | 17.56692 | 0.217053 | 0.623069 |
| 100302368_TGI_at | LASS2 | positive | Concordant | 0.108713 | 0.048558 | 0.025168 | 0.20322 | 0.875545 | 0.884657 | 0.322321 | 0.67176 |
| 100302369_TGI_at | ABT1 | negative | Discordant | 0.031202 | 0.390013 | 0.936234 | 0.981518 | -4.37971 | 7.043195 | 0.534049 | 0.826976 |
| 100302369_TGI_at | ABT1 | positive | Concordant | 0.031202 | 0.390013 | 0.936234 | 0.981518 | -4.37971 | 7.043195 | 0.534049 | 0.826976 |
| 100302468_TGI_at | ZNF28 | negative | Discordant | 0.110047 | 0.177731 | 0.535801 | 0.791076 | 1.444765 | 3.200462 | 0.651684 | 0.887779 |
| 100302531_TGI_at | MAP3K12 | negative | Concordant | -0.02875 | 0.046545 | 0.536769 | 0.791076 | -0.66647 | 0.862517 | 0.439695 | 0.772392 |
| 100302581_TGI_at | PRG4 | positive | Concordant | -0.06413 | 0.096957 | 0.508352 | 0.777321 | 1.635725 | 1.841216 | 0.374329 | 0.730277 |
| 100302585_TGI_at | MLH3 | negative | Concordant | 0.332267 | 0.244693 | 0.174498 | 0.475754 | -0.38674 | 4.449974 | 0.930745 | 0.991346 |
| 100302664_TGI_at | PCBP2 | positive | Discordant | -0.03299 | 0.024569 | 0.179345 | 0.4844 | -0.76585 | 0.446509 | 0.08631 | 0.455195 |
| 100302735_TGI_at | ATF6B | negative | Discordant | -0.00153 | 0.055534 | 0.977983 | 0.996398 | 0.777386 | 1.014242 | 0.443397 | 0.772392 |
| 100302735_TGI_at | ATF6B | negative | Concordant | -0.00153 | 0.055534 | 0.977983 | 0.996398 | 0.777386 | 1.014242 | 0.443397 | 0.772392 |
| 100302787_TGI_at | PABPC4 | positive | Discordant | -0.1217 | 0.0341 | 0.000359 | 0.033986 | -2.42543 | 0.6135 | 7.70E-05 | 0.01669 |
| 100302787_TGI_at | PABPC4 | positive | Discordant | -0.1217 | 0.0341 | 0.000359 | 0.033986 | -2.42543 | 0.6135 | 7.70E-05 | 0.01669 |
| 100302806_TGI_at | NIPSNAP1 | positive | Discordant | -0.05456 | 0.098335 | 0.578989 | 0.82238 | -2.76986 | 1.773655 | 0.118366 | 0.515693 |
| 100302815_TGI_at | HIST1H2BL | negative | Discordant | -2.57929 | 12.57549 | 0.83749 | 0.949702 | -7.29649 | 227.8509 | 0.974454 | 0.999082 |
| 100302940_TGI_at | HLA-DRB5 | positive | Discordant | 0.001381 | 0.002691 | 0.607872 | 0.833901 | -0.00266 | 0.048906 | 0.956654 | 0.995701 |
| 100302940_TGI_at | HLA-DRB5 | positive | Discordant | 0.001381 | 0.002691 | 0.607872 | 0.833901 | -0.00266 | 0.048906 | 0.956654 | 0.995701 |
| 100302940_TGI_at | HLA-DRB5 | negative | Concordant | 0.001381 | 0.002691 | 0.607872 | 0.833901 | -0.00266 | 0.048906 | 0.956654 | 0.995701 |
| 100302941_TGI_at | HLA-DQB1 | positive | Discordant | -0.00067 | 0.00598 | 0.91089 | 0.972183 | -0.17579 | 0.107823 | 0.10302 | 0.486596 |
| 100302941_TGI_at | HLA-DQB1 | positive | Concordant | -0.00067 | 0.00598 | 0.91089 | 0.972183 | -0.17579 | 0.107823 | 0.10302 | 0.486596 |
| 100302941_TGI_at | HLA-DQB1 | positive | Discordant | -0.00067 | 0.00598 | 0.91089 | 0.972183 | -0.17579 | 0.107823 | 0.10302 | 0.486596 |
| 100302941_TGI_at | HLA-DQB1 | positive | Concordant | -0.00067 | 0.00598 | 0.91089 | 0.972183 | -0.17579 | 0.107823 | 0.10302 | 0.486596 |
| 100302942_TGI_at | HLA-C | positive | Discordant | 0.002743 | 0.009391 | 0.770221 | 0.923606 | 0.01649 | 0.171527 | 0.923413 | 0.987175 |
| 100302942_TGI_at | HLA-C | positive | Discordant | 0.002743 | 0.009391 | 0.770221 | 0.923606 | 0.01649 | 0.171527 | 0.923413 | 0.987175 |
| 100303039_TGI_at | CDSN | positive | Discordant | 0.401506 | 0.570635 | 0.481674 | 0.762065 | 6.570551 | 10.46708 | 0.530178 | 0.825639 |
| 100303039_TGI_at | CDSN | positive | Discordant | 0.401506 | 0.570635 | 0.481674 | 0.762065 | 6.570551 | 10.46708 | 0.530178 | 0.825639 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100303039_TGI_at | CDSN | positive | Discordant | 0.401506 | 0.570635 | 0.481674 | 0.762065 | 6.570551 | 10.46708 | 0.530178 | 0.825639 |
| 100303129_TGI_at | HLA-F | negative | Concordant | 0.008651 | 0.030039 | 0.773355 | 0.923606 | -0.31159 | 0.544153 | 0.566905 | 0.842191 |
| 100303129_TGI_at | HLA-F | negative | Discordant | 0.008651 | 0.030039 | 0.773355 | 0.923606 | -0.31159 | 0.544153 | 0.566905 | 0.842191 |
| 100303445_TGI_at | SMPDL3B | positive | Discordant | -0.09417 | 0.204889 | 0.645799 | 0.870774 | 1.547695 | 3.749135 | 0.679743 | 0.901173 |
| 100303452_TGI_at | CCBL2 | negative | Concordant | 0.005483 | 0.067958 | 0.935691 | 0.981518 | -1.65601 | 1.25107 | 0.185611 | 0.580956 |
| 100303520_TGI_at | GRK4 | negative | Concordant | 0.306409 | 0.71829 | 0.669684 | 0.881057 | 3.155442 | 13.60715 | 0.816619 | 0.952807 |
| 100303540_TGI_at | | positive | Concordant | 0.850424 | 0.766318 | 0.267105 | 0.578522 | 7.027278 | 13.73969 | 0.60903 | 0.860732 |
| 100303586_TGI_at | CYP2C9 | negative | Discordant | -0.36479 | 1.092285 | 0.738403 | 0.910662 | 12.63878 | 19.62442 | 0.519554 | 0.821114 |
| 100303617_TGI_at | CYP21A2 | positive | Discordant | -1.65391 | 1.022921 | 0.10591 | 0.409927 | -36.2658 | 18.5626 | 0.050736 | 0.39368 |
| 100303655_TGI_at | ESR1 | negative | Discordant | 0.046241 | 0.080646 | 0.566385 | 0.813007 | -2.52025 | 1.44172 | 0.080449 | 0.447721 |
| 100303672_TGI_at | | positive | Discordant | -0.55892 | 0.748291 | 0.455106 | 0.737526 | -8.57537 | 13.82598 | 0.535102 | 0.826976 |
| 100303756_TGI_at | HLA-A | negative | Concordant | -0.00037 | 0.014772 | 0.98001 | 0.996398 | -0.25493 | 0.268316 | 0.342064 | 0.694542 |
| 100303756_TGI_at | HLA-A | negative | Concordant | -0.00037 | 0.014772 | 0.98001 | 0.996398 | -0.25493 | 0.268316 | 0.342064 | 0.694542 |
| 100303756_TGI_at | HLA-A | negative | Concordant | -0.00037 | 0.014772 | 0.98001 | 0.996398 | -0.25493 | 0.268316 | 0.342064 | 0.694542 |
| 100303756_TGI_at | HLA-A | negative | Concordant | -0.00037 | 0.014772 | 0.98001 | 0.996398 | -0.25493 | 0.268316 | 0.342064 | 0.694542 |
| 100303765_TGI_at | LYZ | positive | Discordant | -0.00844 | 0.015972 | 0.597054 | 0.829561 | -0.24403 | 0.288877 | 0.398254 | 0.74587 |
| 100303767_TGI_at | TGFB2 | negative | Discordant | 0.267226 | 0.102204 | 0.008932 | 0.135075 | 5.812331 | 1.828011 | 0.001475 | 0.080912 |
| 100303798_TGI_at | PCM1 | negative | Discordant | 0.11057 | 0.049657 | 0.025968 | 0.20322 | 1.469007 | 0.907091 | 0.105346 | 0.491902 |
| 100303831_TGI_at | PSMD7 | negative | Concordant | -0.1237 | 0.10291 | 0.229364 | 0.531707 | -1.0252 | 1.883948 | 0.58632 | 0.851595 |
| 100303868_TGI_at | CLEC2D | positive | Discordant | -0.79267 | 0.625661 | 0.205181 | 0.509719 | -28.0219 | 11.20945 | 0.012425 | 0.215815 |
| 100303975_TGI_at | NUDT5 | negative | Concordant | -0.0965 | 0.063716 | 0.129882 | 0.434779 | -1.6816 | 1.149804 | 0.143601 | 0.549177 |
| 100303975_TGI_at | NUDT5 | negative | Concordant | -0.0965 | 0.063716 | 0.129882 | 0.434779 | -1.6816 | 1.149804 | 0.143601 | 0.549177 |
| 100303991_TGI_at | | negative | Concordant | -1.4705 | 3.433189 | 0.668418 | 0.880727 | -16.314 | 62.03557 | 0.792567 | 0.947801 |
| 100303991_TGI_at | | negative | Concordant | -1.4705 | 3.433189 | 0.668418 | 0.880727 | -16.314 | 62.03557 | 0.792567 | 0.947801 |
| 100303991_TGI_at | | negative | Concordant | -1.4705 | 3.433189 | 0.668418 | 0.880727 | -16.314 | 62.03557 | 0.792567 | 0.947801 |
| 100303991_TGI_at | | negative | Concordant | -1.4705 | 3.433189 | 0.668418 | 0.880727 | -16.314 | 62.03557 | 0.792567 | 0.947801 |
| 100303994_TGI_at | ZFP57 | negative | Concordant | -0.57344 | 0.270059 | 0.033721 | 0.237694 | -8.12073 | 4.95285 | 0.101087 | 0.486596 |
| 100303994_TGI_at | ZFP57 | negative | Concordant | -0.57344 | 0.270059 | 0.033721 | 0.237694 | -8.12073 | 4.95285 | 0.101087 | 0.486596 |
| 100303994_TGI_at | ZFP57 | negative | Concordant | -0.57344 | 0.270059 | 0.033721 | 0.237694 | -8.12073 | 4.95285 | 0.101087 | 0.486596 |
| 100303994_TGI_at | ZFP57 | negative | Concordant | -0.57344 | 0.270059 | 0.033721 | 0.237694 | -8.12073 | 4.95285 | 0.101087 | 0.486596 |
| 100304000_TGI_at | PSORS1C3 | positive | Discordant | -1.08419 | 0.918801 | 0.237998 | 0.539802 | -17.4864 | 16.95958 | 0.302511 | 0.667372 |
| 100304000_TGI_at | PSORS1C3 | negative | Concordant | -1.08419 | 0.918801 | 0.237998 | 0.539802 | -17.4864 | 16.95958 | 0.302511 | 0.667372 |
| 100304001_TGI_at | | negative | Discordant | 0.078264 | 0.042053 | 0.062734 | 0.31384 | 1.903057 | 0.757606 | 0.012007 | 0.215815 |
| 100304001_TGI_at | | negative | Discordant | 0.078264 | 0.042053 | 0.062734 | 0.31384 | 1.903057 | 0.757606 | 0.012007 | 0.215815 |
| 100304009_TGI_at | HLA-DQB1 | positive | Concordant | -0.00052 | 0.005866 | 0.928805 | 0.978462 | -0.17287 | 0.105858 | 0.102454 | 0.486596 |
| 100304009_TGI_at | HLA-DQB1 | positive | Discordant | -0.00052 | 0.005866 | 0.928805 | 0.978462 | -0.17287 | 0.105858 | 0.102454 | 0.486596 |
| 100304009_TGI_at | HLA-DQB1 | positive | Concordant | -0.00052 | 0.005866 | 0.928805 | 0.978462 | -0.17287 | 0.105858 | 0.102454 | 0.486596 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100304009_TGI_at | HLA-DQB1 | positive | Discordant | -0.00052 | 0.005866 | 0.928805 | 0.978462 | -0.17287 | 0.105858 | 0.102454 | 0.486596 |
| 100304014_TGI_at | ZNF25 | negative | Discordant | 0.557478 | 0.221009 | 0.011655 | 0.150127 | 9.824254 | 4.004834 | 0.014163 | 0.227397 |
| 100304092_TGI_at | ATF6 | negative | Concordant | -0.21146 | 0.071863 | 0.003255 | 0.080734 | -2.75004 | 1.315652 | 0.036596 | 0.342664 |
| 100304176_TGI_at | C3orf26 | negative | Concordant | -0.28305 | 0.149445 | 0.058225 | 0.306533 | -8.66161 | 2.757934 | 0.001686 | 0.081206 |
| 100304197_TGI_at | | positive | Concordant | 0.289243 | 0.203534 | 0.155286 | 0.459406 | 7.838387 | 3.713589 | 0.034795 | 0.334258 |
| 100304197_TGI_at | | positive | Concordant | 0.289243 | 0.203534 | 0.155286 | 0.459406 | 7.838387 | 3.713589 | 0.034795 | 0.334258 |
| 100304197_TGI_at | | positive | Concordant | 0.289243 | 0.203534 | 0.155286 | 0.459406 | 7.838387 | 3.713589 | 0.034795 | 0.334258 |
| 100304197_TGI_at | | positive | Concordant | 0.289243 | 0.203534 | 0.155286 | 0.459406 | 7.838387 | 3.713589 | 0.034795 | 0.334258 |
| 100304214_TGI_at | | positive | Concordant | -0.03046 | 0.363666 | 0.933243 | 0.981518 | 10.34441 | 6.636086 | 0.119041 | 0.516042 |
| 100304225_TGI_at | | positive | Concordant | 0.076829 | 0.268723 | 0.774952 | 0.923606 | 5.050527 | 4.861995 | 0.298909 | 0.661107 |
| 100304233_TGI_at | CLEC2D | negative | Discordant | 0.004749 | 0.042789 | 0.911632 | 0.972183 | -0.77545 | 0.772034 | 0.315172 | 0.671386 |
| 100304243_TGI_at | PIP4K2B | positive | Concordant | 0.254905 | 0.098607 | 0.009736 | 0.140692 | 1.82503 | 1.810177 | 0.313356 | 0.671386 |
| 100304251_TGI_at | TSPAN14 | negative | Concordant | -0.11237 | 0.06843 | 0.100551 | 0.403443 | -0.55258 | 1.253032 | 0.659217 | 0.888268 |
| 100304349_TGI_at | CCNT2 | negative | Discordant | 0.185461 | 0.157259 | 0.238265 | 0.539802 | 2.031494 | 2.851635 | 0.47622 | 0.799852 |
| 100304633_TGI_at | TCP11 | negative | Concordant | -0.02395 | 1.758384 | 0.989132 | 0.996398 | 7.510979 | 32.33811 | 0.816333 | 0.952807 |
| 100304636_TGI_at | FLOT1 | negative | Concordant | -0.30344 | 0.310666 | 0.328705 | 0.641863 | -6.53695 | 5.70002 | 0.251452 | 0.638503 |
| 100304636_TGI_at | FLOT1 | negative | Concordant | -0.30344 | 0.310666 | 0.328705 | 0.641863 | -6.53695 | 5.70002 | 0.251452 | 0.638503 |
| 100304704_TGI_at | | negative | Concordant | -0.33445 | 0.142084 | 0.018577 | 0.201777 | -4.63773 | 2.672283 | 0.082653 | 0.447876 |
| 100304704_TGI_at | | positive | Discordant | -0.33445 | 0.142084 | 0.018577 | 0.201777 | -4.63773 | 2.672283 | 0.082653 | 0.447876 |
| 100304754_TGI_at | | positive | Discordant | -2.0596 | 1.021339 | 0.04374 | 0.265194 | -5.20626 | 18.68003 | 0.780469 | 0.941122 |
| 100304754_TGI_at | | positive | Discordant | -2.0596 | 1.021339 | 0.04374 | 0.265194 | -5.20626 | 18.68003 | 0.780469 | 0.941122 |
| 100304757_TGI_at | OPN5 | negative | Discordant | -0.79103 | 1.128463 | 0.483315 | 0.763268 | -2.52288 | 20.14726 | 0.900348 | 0.978198 |
| 100304804_TGI_at | RAD50 | negative | Discordant | -0.2105 | 0.48703 | 0.665585 | 0.879862 | 5.280843 | 8.850162 | 0.550711 | 0.837177 |
| 100304816_TGI_at | LRRC37A | negative | Concordant | -10.7771 | 8.765919 | 0.218908 | 0.523661 | -275.974 | 161.823 | 0.088119 | 0.457481 |
| 100304832_TGI_at | TPM1 | negative | Concordant | -0.09738 | 0.038623 | 0.011692 | 0.150127 | -0.70356 | 0.707424 | 0.319961 | 0.671733 |
| 100304858_TGI_at | MLF1 | negative | Concordant | -0.36864 | 0.366127 | 0.313999 | 0.627275 | -0.37541 | 6.589616 | 0.954569 | 0.995701 |
| 100304878_TGI_at | ZNF271 | negative | Concordant | -0.82661 | 0.283925 | 0.003598 | 0.086663 | -11.7151 | 5.248259 | 0.025602 | 0.301895 |
| 100304907_TGI_at | GRB2 | negative | Concordant | -0.1462 | 0.182497 | 0.423062 | 0.718641 | -3.57247 | 3.341417 | 0.285002 | 0.64733 |
| 100304931_TGI_at | | positive | Discordant | -0.12238 | 0.472218 | 0.79551 | 0.930779 | 2.669442 | 8.552861 | 0.754956 | 0.930374 |
| 100304943_TGI_at | ZNF271 | negative | Concordant | -0.31079 | 0.111718 | 0.005404 | 0.099945 | -4.40629 | 2.07004 | 0.033287 | 0.328895 |
| 100305043_TGI_at | MCM6 | positive | Discordant | -0.19296 | 0.096059 | 0.04456 | 0.268286 | -3.78141 | 1.731042 | 0.028928 | 0.301895 |
| 100305045_TGI_at | | negative | Discordant | 0.295687 | 0.267348 | 0.268726 | 0.578522 | 5.943985 | 4.911427 | 0.226188 | 0.623069 |
| 100305045_TGI_at | | negative | Discordant | 0.295687 | 0.267348 | 0.268726 | 0.578522 | 5.943985 | 4.911427 | 0.226188 | 0.623069 |
| 100305045_TGI_at | | negative | Discordant | 0.295687 | 0.267348 | 0.268726 | 0.578522 | 5.943985 | 4.911427 | 0.226188 | 0.623069 |
| 100305045_TGI_at | | negative | Discordant | 0.295687 | 0.267348 | 0.268726 | 0.578522 | 5.943985 | 4.911427 | 0.226188 | 0.623069 |
| 100305118_TGI_at | ATF6 | negative | Concordant | -3.35742 | 1.842742 | 0.068459 | 0.322578 | -25.8624 | 33.56609 | 0.441009 | 0.772392 |
| 100305138_TGI_at | SPINK5 | negative | Concordant | -0.26541 | 0.115541 | 0.021611 | 0.201777 | -8.47861 | 2.038604 | 3.20E-05 | 0.01669 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| 100305245_TGI_at | C18orf10 | negative | Discordant | -0.00931 | 0.068453 | 0.891776 | 0.965743 | -0.35086 | 1.254734 | 0.77976 | 0.941122 |
| 100305257_TGI_at | VDAC2 | negative | Concordant | -0.18499 | 0.057126 | 0.001203 | 0.049662 | -2.02653 | 1.049954 | 0.053593 | 0.403041 |
| 100305260_TGI_at | SEC61A2 | positive | Concordant | 0.330299 | 0.23635 | 0.162263 | 0.461656 | 7.938051 | 4.332643 | 0.066929 | 0.426441 |
| 100305324_TGI_at | | negative | Discordant | 0.085338 | 0.041264 | 0.038633 | 0.249963 | 1.863943 | 0.744354 | 0.012276 | 0.215815 |
| 100305324_TGI_at | | negative | Discordant | 0.085338 | 0.041264 | 0.038633 | 0.249963 | 1.863943 | 0.744354 | 0.012276 | 0.215815 |
| 100305328_TGI_at | | negative | Concordant | -0.17769 | 0.171565 | 0.300343 | 0.622924 | -0.65968 | 3.092558 | 0.831085 | 0.957068 |
| 100305399_TGI_at | | negative | Concordant | -0.03294 | 0.044219 | 0.45635 | 0.738164 | -1.3955 | 0.79562 | 0.079434 | 0.447721 |
| 100305406_TGI_at | VEZT | positive | Concordant | 0.06867 | 0.293896 | 0.815253 | 0.939926 | 7.224928 | 5.346247 | 0.176567 | 0.571841 |
| 100305428_TGI_at | | negative | Concordant | -0.15077 | 0.229057 | 0.510385 | 0.779055 | -4.67889 | 4.108833 | 0.254812 | 0.638503 |
| 100305428_TGI_at | | negative | Concordant | -0.15077 | 0.229057 | 0.510385 | 0.779055 | -4.67889 | 4.108833 | 0.254812 | 0.638503 |
| 100305452_TGI_at | STAT6 | positive | Concordant | -0.04376 | 0.049751 | 0.379072 | 0.700757 | 0.264434 | 0.933024 | 0.776858 | 0.941122 |
| 100305514_TGI_at | TMEM87A | positive | Concordant | 1.425445 | 1.904338 | 0.454143 | 0.737526 | 1.437756 | 34.40639 | 0.966668 | 0.999082 |
| 100305640_TGI_at | C7orf46 | positive | Discordant | -0.36383 | 0.371567 | 0.327493 | 0.641332 | -8.31408 | 6.794059 | 0.221055 | 0.623069 |
| 100305644_TGI_at | CPD | negative | Discordant | -0.05995 | 0.114991 | 0.602147 | 0.832633 | 0.037432 | 2.063378 | 0.985526 | 0.999082 |
| 100305657_TGI_at | SIAH1 | positive | Concordant | 0.064976 | 0.122374 | 0.595447 | 0.829561 | 1.434883 | 2.257116 | 0.524962 | 0.823042 |
| 100305748_TGI_at | 5-Mar | negative | Discordant | -0.01801 | 0.077649 | 0.8166 | 0.940229 | 0.980383 | 1.402378 | 0.484498 | 0.80052 |
| 100305763_TGI_at | XRCC3 | negative | Concordant | 0.029702 | 0.056816 | 0.601129 | 0.832554 | 1.439214 | 1.023005 | 0.159472 | 0.560509 |
| 100305792_TGI_at | MBNL1 | positive | Discordant | -0.07813 | 0.081744 | 0.339209 | 0.659405 | 0.667271 | 1.490173 | 0.654311 | 0.887779 |
| 100305819_TGI_at | FAM168A | negative | Concordant | -0.09298 | 0.157328 | 0.554542 | 0.80265 | -3.14333 | 2.852914 | 0.27055 | 0.64407 |
| 100305836_TGI_at | HLA-DPA1 | positive | Discordant | -0.01836 | 0.028669 | 0.521946 | 0.782375 | -0.98654 | 0.521171 | 0.058369 | 0.413224 |
| 100305836_TGI_at | HLA-DPA1 | positive | Discordant | -0.01836 | 0.028669 | 0.521946 | 0.782375 | -0.98654 | 0.521171 | 0.058369 | 0.413224 |
| 100305934_TGI_at | EFCAB5 | negative | Discordant | 1.449708 | 4.54927 | 0.749978 | 0.918405 | 8.649579 | 83.41942 | 0.917417 | 0.98319 |
| 100305949_TGI_at | PTER | positive | Concordant | 0.028639 | 0.144993 | 0.84342 | 0.952951 | -3.91018 | 2.600437 | 0.132668 | 0.536498 |
| 100306063_TGI_at | ZADH2 | positive | Concordant | 0.314969 | 0.147125 | 0.032288 | 0.234777 | 3.371507 | 2.679509 | 0.208299 | 0.612188 |
| 100306182_TGI_at | MAPKBP1 | negative | Concordant | -1.06114 | 1.241235 | 0.392601 | 0.704177 | -18.9022 | 22.66921 | 0.404378 | 0.752024 |
| 100306202_TGI_at | FGD6 | negative | Concordant | 0.968121 | 0.960834 | 0.313654 | 0.627275 | 1.733991 | 17.42186 | 0.920718 | 0.985509 |
| 100306281_TGI_at | C17orf57 | negative | Discordant | -0.01681 | 0.283393 | 0.952702 | 0.986866 | -5.85103 | 5.108841 | 0.252095 | 0.638503 |
| 100306300_TGI_at | C14orf153 | negative | Concordant | -0.15223 | 0.203383 | 0.45416 | 0.737526 | -5.22416 | 3.679858 | 0.155705 | 0.560509 |
| 100306322_TGI_at | ARNT | negative | Discordant | 0.196726 | 0.177939 | 0.268909 | 0.578522 | 1.030125 | 3.208577 | 0.74817 | 0.928592 |
| 100306345_TGI_at | IKZF2 | positive | Concordant | 0.158867 | 0.069742 | 0.02273 | 0.203023 | 1.383126 | 1.266629 | 0.274844 | 0.64407 |
| 100306395_TGI_at | MAPT | negative | Concordant | -1.7718 | 2.035115 | 0.383965 | 0.702316 | -13.9302 | 36.92028 | 0.705948 | 0.915742 |
| 100306458_TGI_at | DST | negative | Discordant | 0.073341 | 0.052632 | 0.163474 | 0.461656 | 1.30994 | 0.95575 | 0.170503 | 0.566383 |
| 100306484_TGI_at | RBM23 | positive | Concordant | 0.097542 | 0.094871 | 0.303881 | 0.622924 | 1.080929 | 1.735612 | 0.53342 | 0.826976 |
| 100306509_TGI_at | PIGV | positive | Discordant | 0.056086 | 0.29476 | 0.849093 | 0.952951 | -3.6583 | 5.352415 | 0.4943 | 0.804238 |
| 100306577_TGI_at | MGA | positive | Concordant | 0.927929 | 0.347315 | 0.007546 | 0.121882 | 4.993106 | 6.31562 | 0.42918 | 0.767727 |
| 100306590_TGI_at | SLC35A1 | positive | Concordant | 0.224581 | 0.055011 | 4.46E-05 | 0.02741 | 3.063569 | 0.999264 | 0.002171 | 0.098532 |
| 100306620_TGI_at | | negative | Discordant | 0.280554 | 0.231236 | 0.225023 | 0.53015 | 4.904176 | 4.216942 | 0.244842 | 0.638503 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100306689_TGI_at | | negative | Concordant | -0.36759 | 0.373327 | 0.324805 | 0.641332 | -4.83309 | 6.892204 | 0.483153 | 0.80052 |
| 100306705_TGI_at | CCNT2 | positive | Concordant | 0.098085 | 0.062211 | 0.114875 | 0.422151 | 0.936811 | 1.137456 | 0.410166 | 0.759859 |
| 100306708_TGI_at | | positive | Discordant | -1.5188 | 0.430354 | 0.000417 | 0.033986 | -9.43288 | 8.206094 | 0.250351 | 0.638503 |
| 100306708_TGI_at | | positive | Discordant | -1.5188 | 0.430354 | 0.000417 | 0.033986 | -9.43288 | 8.206094 | 0.250351 | 0.638503 |
| 100306800_TGI_at | RHOBTB3 | positive | Concordant | -0.14416 | 0.155131 | 0.352758 | 0.675146 | 1.534641 | 2.816438 | 0.585831 | 0.851595 |
| 100306816_TGI_at | PDGFD | negative | Concordant | -2.24829 | 0.817266 | 0.005942 | 0.10732 | -27.7566 | 14.70586 | 0.0591 | 0.413224 |
| 100306859_TGI_at | MAP3K12 | negative | Concordant | -0.05007 | 0.130271 | 0.700698 | 0.894706 | -1.14814 | 2.405598 | 0.633164 | 0.874129 |
| 100306923_TGI_at | TH1L | negative | Discordant | 0.280693 | 0.184173 | 0.127492 | 0.431533 | 1.741988 | 3.318578 | 0.599639 | 0.860732 |
| 100306938_TGI_at | ROCK2 | negative | Discordant | -0.38711 | 0.217113 | 0.074588 | 0.343979 | 4.142867 | 3.964601 | 0.296039 | 0.656435 |
| 100306966_TGI_at | TMEM77 | positive | Discordant | 0.028581 | 0.062559 | 0.647774 | 0.87208 | -1.79817 | 1.133359 | 0.112606 | 0.507597 |
| 100306969_TGI_at | RABAC1 | negative | Concordant | -0.0613 | 0.043967 | 0.163249 | 0.461656 | -0.85961 | 0.796805 | 0.280666 | 0.647173 |
| 100307074_TGI_at | PID1 | negative | Concordant | -0.27858 | 0.22312 | 0.211821 | 0.516353 | -9.4297 | 4.051898 | 0.019953 | 0.2703 |
| 100307164_TGI_at | MN1 | positive | Discordant | -0.02558 | 0.042461 | 0.546918 | 0.796047 | -0.40181 | 0.767688 | 0.600696 | 0.860732 |
| 100307171_TGI_at | | positive | Concordant | 0.144769 | 0.087567 | 0.09828 | 0.398532 | 2.195199 | 1.589751 | 0.167327 | 0.564154 |
| 100307218_TGI_at | | negative | Concordant | -1.40927 | 0.427449 | 0.000977 | 0.044603 | -11.499 | 7.80163 | 0.140503 | 0.548723 |
| 100307273_TGI_at | | negative | Discordant | 0.06064 | 0.096153 | 0.528263 | 0.785614 | 2.112548 | 1.749361 | 0.227197 | 0.623069 |
| 100307330_TGI_at | BCAR1 | positive | Concordant | -1.8017 | 0.910437 | 0.047823 | 0.269292 | 0.552132 | 16.61592 | 0.973492 | 0.999082 |
| 100307345_TGI_at | CLOCK | positive | Concordant | 0.028469 | 0.28169 | 0.919498 | 0.972561 | 1.874254 | 5.089517 | 0.712681 | 0.915742 |
| 100307345_TGI_at | CLOCK | positive | Concordant | 0.028469 | 0.28169 | 0.919498 | 0.972561 | 1.874254 | 5.089517 | 0.712681 | 0.915742 |
| 100307496_TGI_at | C22orf34 | positive | Concordant | 0.081075 | 0.16213 | 0.617031 | 0.841142 | 1.146644 | 2.959178 | 0.698396 | 0.913095 |
| 100307499_TGI_at | PPA2 | negative | Discordant | 0.03369 | 0.177699 | 0.849632 | 0.952951 | 0.528238 | 3.221665 | 0.869759 | 0.966864 |
| 100307499_TGI_at | PPA2 | negative | Discordant | 0.03369 | 0.177699 | 0.849632 | 0.952951 | 0.528238 | 3.221665 | 0.869759 | 0.966864 |
| 100307519_TGI_at | | negative | Discordant | 0.066092 | 0.092172 | 0.47334 | 0.75471 | 2.296434 | 1.681721 | 0.172088 | 0.567301 |
| 100307575_TGI_at | MRPS21 | negative | Concordant | -0.10181 | 0.064012 | 0.111716 | 0.419479 | -3.05724 | 1.166852 | 0.008791 | 0.200574 |
| 100307611_TGI_at | IQGAP3 | negative | Concordant | -0.35767 | 0.986025 | 0.716803 | 0.899455 | -9.61801 | 18.23364 | 0.597855 | 0.860732 |
| 100307620_TGI_at | ITCH | positive | Discordant | -0.00048 | 0.061246 | 0.993768 | 0.998374 | 0.126096 | 1.103369 | 0.909014 | 0.980193 |
| 100307638_TGI_at | | positive | Concordant | -0.06126 | 0.351836 | 0.861766 | 0.95732 | -8.68156 | 6.397721 | 0.174788 | 0.569705 |
| 100307707_TGI_at | MON1B | negative | Discordant | 0.241686 | 0.104576 | 0.020826 | 0.201777 | 0.968843 | 1.901482 | 0.610388 | 0.860732 |
| 100307726_TGI_at | ADAM17 | negative | Concordant | -1.52433 | 1.027229 | 0.137829 | 0.445546 | -7.3862 | 18.8447 | 0.695094 | 0.91172 |
| 100307733_TGI_at | | positive | Concordant | 0.166143 | 0.083959 | 0.047833 | 0.269292 | 2.74875 | 1.52948 | 0.072307 | 0.432347 |
| 100307819_TGI_at | GALC | negative | Discordant | 0.137073 | 0.079227 | 0.083606 | 0.371725 | 1.276398 | 1.428905 | 0.371713 | 0.730277 |
| 100307865_TGI_at | CACNA2D4 | negative | Concordant | 0.845736 | 0.936237 | 0.366348 | 0.692406 | -4.3939 | 17.32674 | 0.799812 | 0.9484 |
| 100307916_TGI_at | C15orf57 | negative | Concordant | -0.32915 | 0.346203 | 0.341739 | 0.662836 | -7.89973 | 6.358554 | 0.214097 | 0.62081 |
| 100307917_TGI_at | RPS5 | positive | Discordant | -0.02277 | 0.010628 | 0.032174 | 0.234777 | -0.55673 | 0.193019 | 0.003923 | 0.129398 |
| 100307951_TGI_at | RREB1 | negative | Discordant | 0.214649 | 0.091121 | 0.01849 | 0.201777 | 2.087889 | 1.649118 | 0.20549 | 0.608241 |
| 100307969_TGI_at | | positive | Discordant | -0.26172 | 0.45958 | 0.569026 | 0.815447 | -0.37077 | 8.437238 | 0.964949 | 0.999082 |
| 100307977_TGI_at | ASAH1 | negative | Discordant | 0.062117 | 0.051434 | 0.227162 | 0.530862 | 1.029729 | 0.926857 | 0.266573 | 0.64407 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100308127_TGI_at | HCG18 | positive | Concordant | 0.338034 | 0.164378 | 0.03974 | 0.25522 | 3.873615 | 3.003514 | 0.197157 | 0.598854 |
| 100308127_TGI_at | HCG18 | positive | Concordant | 0.338034 | 0.164378 | 0.03974 | 0.25522 | 3.873615 | 3.003514 | 0.197157 | 0.598854 |
| 100308127_TGI_at | HCG18 | positive | Concordant | 0.338034 | 0.164378 | 0.03974 | 0.25522 | 3.873615 | 3.003514 | 0.197157 | 0.598854 |
| 100308127_TGI_at | HCG18 | positive | Concordant | 0.338034 | 0.164378 | 0.03974 | 0.25522 | 3.873615 | 3.003514 | 0.197157 | 0.598854 |
| 100308139_TGI_at | HSD17B12 | positive | Concordant | 0.114052 | 0.056537 | 0.043665 | 0.265194 | 1.847343 | 1.026148 | 0.071818 | 0.432347 |
| 100308140_TGI_at | KIAA0317 | negative | Discordant | 0.483263 | 0.256984 | 0.060038 | 0.309558 | 3.674323 | 4.681477 | 0.432533 | 0.767727 |
| 100308316_TGI_at | ALDH2 | negative | Discordant | 0.338015 | 0.109512 | 0.002025 | 0.06502 | 2.477063 | 1.993196 | 0.213956 | 0.62081 |
| 100308400_TGI_at | C1orf77 | negative | Concordant | -0.16345 | 4.530606 | 0.971221 | 0.99533 | -25.9163 | 83.21209 | 0.75546 | 0.930374 |
| 100308435_TGI_at | DCBLD2 | negative | Discordant | 5.320472 | 4.404618 | 0.227074 | 0.530862 | 115.6525 | 80.72053 | 0.151929 | 0.553455 |
| 100308491_TGI_at | THSD4 | negative | Concordant | -0.14324 | 0.18899 | 0.448498 | 0.733676 | 2.681299 | 3.419788 | 0.433008 | 0.767727 |
| 100308491_TGI_at | THSD4 | negative | Discordant | -0.14324 | 0.18899 | 0.448498 | 0.733676 | 2.681299 | 3.419788 | 0.433008 | 0.767727 |
| 100308495_TGI_at | ASAH1 | negative | Discordant | 1.067431 | 1.189853 | 0.36966 | 0.692406 | 25.55143 | 21.83552 | 0.24193 | 0.637547 |
| 100308581_TGI_at | | positive | Discordant | 0.00789 | 0.067161 | 0.90648 | 0.971468 | -0.80399 | 1.217268 | 0.508943 | 0.815626 |
| 100308628_TGI_at | LRRC37A4 | positive | Concordant | 0.102841 | 0.055312 | 0.062985 | 0.31384 | 1.778532 | 0.995369 | 0.073969 | 0.439253 |
| 100308628_TGI_at | LRRC37A4 | positive | Concordant | 0.102841 | 0.055312 | 0.062985 | 0.31384 | 1.778532 | 0.995369 | 0.073969 | 0.439253 |
| 100308684_TGI_at | | negative | Concordant | -2.02484 | 4.903359 | 0.679644 | 0.883837 | 15.30473 | 89.58474 | 0.864349 | 0.966864 |
| 100308717_TGI_at | GOLPH3L | positive | Concordant | 0.426222 | 0.591866 | 0.471444 | 0.75471 | -10.3821 | 10.80133 | 0.33646 | 0.688127 |
| 100308753_TGI_at | MEST | positive | Discordant | -0.33132 | 0.270772 | 0.2211 | 0.525188 | -2.46276 | 4.875357 | 0.613458 | 0.863422 |
| 100308887_TGI_at | ANKRD13B | positive | Concordant | -0.13084 | 0.195402 | 0.503128 | 0.776148 | 1.241776 | 3.612309 | 0.731025 | 0.92225 |
| 100308899_TGI_at | C18orf10 | negative | Discordant | 0.412442 | 0.734306 | 0.574336 | 0.821133 | 3.855222 | 13.59996 | 0.776814 | 0.941122 |
| 100308980_TGI_at | IFNGR2 | positive | Discordant | -1.72495 | 1.745871 | 0.323144 | 0.641332 | -5.17702 | 31.84765 | 0.870868 | 0.966864 |
| 100308994_TGI_at | MTMR3 | negative | Discordant | 0.035862 | 0.120838 | 0.766636 | 0.923606 | 2.907028 | 2.178629 | 0.182093 | 0.575874 |
| 100309078_TGI_at | KCNE2 | negative | Concordant | -1.10053 | 0.793282 | 0.165346 | 0.463931 | -31.9282 | 14.42121 | 0.02683 | 0.301895 |
| 100309111_TGI_at | MUC21 | positive | Discordant | -0.12498 | 0.096628 | 0.195855 | 0.506885 | -0.76848 | 1.729694 | 0.656836 | 0.888268 |
| 100309111_TGI_at | MUC21 | negative | Concordant | -0.12498 | 0.096628 | 0.195855 | 0.506885 | -0.76848 | 1.729694 | 0.656836 | 0.888268 |
| 100309207_TGI_at | VDAC2 | negative | Concordant | -0.1752 | 0.050307 | 0.000497 | 0.034954 | -1.76826 | 0.92179 | 0.055074 | 0.403041 |
| 100309227_TGI_at | | negative | Concordant | -0.01833 | 0.015087 | 0.2243 | 0.529887 | -0.39799 | 0.274087 | 0.14649 | 0.549177 |
| 100309242_TGI_at | RBP2 | positive | Concordant | 0.092854 | 0.090071 | 0.302587 | 0.622924 | 3.621108 | 1.620001 | 0.025401 | 0.301895 |
| 100309243_TGI_at | | positive | Concordant | 0.377619 | 0.194357 | 0.052026 | 0.285485 | 1.488375 | 3.587644 | 0.678243 | 0.901173 |
| 100309263_TGI_at | RAB6A | negative | Concordant | -0.0994 | 0.117173 | 0.396248 | 0.704177 | -3.28877 | 2.12589 | 0.121861 | 0.516945 |
| 100309376_TGI_at | MRPL10 | positive | Discordant | -0.04356 | 0.063296 | 0.491303 | 0.767563 | -1.38523 | 1.157197 | 0.231284 | 0.623069 |
| 100309484_TGI_at | HLA-C | positive | Discordant | -0.00398 | 0.008877 | 0.65376 | 0.873359 | -0.11637 | 0.162492 | 0.473881 | 0.797777 |
| 100309484_TGI_at | HLA-C | positive | Discordant | -0.00398 | 0.008877 | 0.65376 | 0.873359 | -0.11637 | 0.162492 | 0.473881 | 0.797777 |
| 100309484_TGI_at | HLA-C | positive | Discordant | -0.00398 | 0.008877 | 0.65376 | 0.873359 | -0.11637 | 0.162492 | 0.473881 | 0.797777 |
| 100309484_TGI_at | HLA-C | positive | Discordant | -0.00398 | 0.008877 | 0.65376 | 0.873359 | -0.11637 | 0.162492 | 0.473881 | 0.797777 |
| 100309522_TGI_at | | positive | Discordant | -0.50127 | 0.728408 | 0.491346 | 0.767563 | -10.5378 | 13.19177 | 0.424395 | 0.764753 |
| 100309539_TGI_at | RAD1 | positive | Discordant | -0.61638 | 0.230704 | 0.007546 | 0.121882 | -3.97787 | 4.171639 | 0.340311 | 0.692604 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100309540_TGI_at | | negative | Concordant | 0.139824 | 0.170785 | 0.412951 | 0.711787 | -2.39755 | 3.07643 | 0.435787 | 0.771076 |
| 100309580_TGI_at | | negative | Concordant | -0.58258 | 0.525928 | 0.267987 | 0.578522 | -3.0438 | 9.702947 | 0.75375 | 0.930374 |
| 100309580_TGI_at | | negative | Concordant | -0.58258 | 0.525928 | 0.267987 | 0.578522 | -3.0438 | 9.702947 | 0.75375 | 0.930374 |
| 100309580_TGI_at | | negative | Concordant | -0.58258 | 0.525928 | 0.267987 | 0.578522 | -3.0438 | 9.702947 | 0.75375 | 0.930374 |
| 100309580_TGI_at | | negative | Concordant | -0.58258 | 0.525928 | 0.267987 | 0.578522 | -3.0438 | 9.702947 | 0.75375 | 0.930374 |
| 100309723_TGI_at | ARNT | negative | Discordant | 0.078689 | 0.077301 | 0.308694 | 0.622924 | 0.309575 | 1.411268 | 0.82637 | 0.957068 |
| 100309835_TGI_at | HOXC6 | positive | Discordant | -0.79771 | 2.354381 | 0.734747 | 0.910662 | -43.0164 | 42.3154 | 0.30936 | 0.670538 |
| 100309845_TGI_at | CLEC2D | negative | Discordant | 0.003155 | 0.044217 | 0.943116 | 0.983056 | -0.65868 | 0.801266 | 0.411049 | 0.75987 |
| 100309898_TGI_at | WDR52 | negative | Discordant | 0.047599 | 0.124706 | 0.702691 | 0.895052 | -0.44507 | 2.246678 | 0.842966 | 0.958398 |
| 100309959_TGI_at | GIT2 | positive | Discordant | -0.24798 | 0.226134 | 0.272803 | 0.582563 | -9.14893 | 4.123853 | 0.026518 | 0.301895 |
| 100309997_TGI_at | SLC22A5 | positive | Concordant | 0.013652 | 0.765508 | 0.985772 | 0.996398 | 8.007604 | 13.82536 | 0.562456 | 0.840775 |
| 100310092_TGI_at | UBXN6 | negative | Concordant | -0.07855 | 0.049828 | 0.114911 | 0.422151 | -1.97059 | 0.903897 | 0.029249 | 0.301895 |
| 100310151_TGI_at | S100A14 | negative | Discordant | 0.059888 | 0.040821 | 0.142349 | 0.445546 | 0.889023 | 0.739528 | 0.229306 | 0.623069 |
| 100310197_TGI_at | RBM23 | positive | Concordant | 0.03072 | 0.051027 | 0.547155 | 0.796047 | 0.505859 | 0.92484 | 0.5844 | 0.851595 |
| 100310201_TGI_at | SNRPF | negative | Concordant | 0.020415 | 0.056166 | 0.716253 | 0.899455 | -1.03708 | 1.042822 | 0.319984 | 0.671733 |
| 100310285_TGI_at | STAT6 | positive | Discordant | -0.04299 | 0.049843 | 0.388362 | 0.702944 | -0.52212 | 0.916609 | 0.568935 | 0.843191 |
| 100310339_TGI_at | THSD4 | negative | Discordant | 0.042846 | 0.104342 | 0.681342 | 0.883903 | 3.995135 | 1.877898 | 0.033383 | 0.328895 |
| 100310339_TGI_at | THSD4 | negative | Concordant | 0.042846 | 0.104342 | 0.681342 | 0.883903 | 3.995135 | 1.877898 | 0.033383 | 0.328895 |
| 100310380_TGI_at | KLC1 | positive | Discordant | -0.00307 | 0.203214 | 0.987942 | 0.996398 | -0.04437 | 3.725871 | 0.990498 | 0.999082 |
| 100310523_TGI_at | | negative | Discordant | 0.330144 | 0.179739 | 0.06624 | 0.319057 | 0.829463 | 3.278177 | 0.800248 | 0.9484 |
| 100310523_TGI_at | | positive | Concordant | 0.330144 | 0.179739 | 0.06624 | 0.319057 | 0.829463 | 3.278177 | 0.800248 | 0.9484 |
| 100310631_TGI_at | RPUSD4 | negative | Concordant | -5.22032 | 3.02993 | 0.084903 | 0.373119 | -63.4489 | 55.86787 | 0.256084 | 0.639841 |
| 100310659_TGI_at | | negative | Concordant | -0.03988 | 0.028835 | 0.166665 | 0.464625 | -0.71071 | 0.518091 | 0.170128 | 0.566383 |
| 100310722_TGI_at | | negative | Discordant | -0.05836 | 0.091249 | 0.522486 | 0.782375 | 0.109491 | 1.652888 | 0.947185 | 0.994854 |
| 100310797_TGI_at | IFNGR2 | positive | Concordant | -0.12985 | 0.759769 | 0.864298 | 0.958243 | 3.373096 | 13.75742 | 0.806314 | 0.950782 |
| 100310831_TGI_at | SETX | negative | Discordant | 0.696155 | 0.455226 | 0.126202 | 0.431533 | 3.583021 | 8.350568 | 0.667869 | 0.892207 |
| 100310881_TGI_at | ZNF436 | positive | Concordant | 0.532183 | 0.240131 | 0.026676 | 0.20322 | 6.952119 | 4.424885 | 0.11615 | 0.509594 |
| 100310890_TGI_at | ARNT | positive | Discordant | -0.2071 | 0.390811 | 0.596171 | 0.829561 | -4.24549 | 7.16131 | 0.55329 | 0.837177 |
| 100310898_TGI_at | CROCC | negative | Concordant | -0.13569 | 0.081894 | 0.097537 | 0.398532 | -0.82847 | 1.486827 | 0.577386 | 0.847029 |
| 100310941_TGI_at | ZRANB3 | negative | Concordant | -1.59682 | 0.71852 | 0.026258 | 0.20322 | -25.7623 | 13.24396 | 0.05175 | 0.39368 |
| 100310948_TGI_at | PDXDC2 | positive | Discordant | -0.03004 | 0.119454 | 0.801447 | 0.931838 | 2.915708 | 2.17815 | 0.180696 | 0.575874 |
| 100310951_TGI_at | FMO2 | positive | Concordant | 0.015957 | 0.009689 | 0.099568 | 0.401512 | 0.155219 | 0.175209 | 0.375668 | 0.730277 |
| 100311198_TGI_at | KATNAL2 | positive | Discordant | -0.28436 | 1.43 | 0.842377 | 0.952951 | -27.7879 | 25.9686 | 0.284593 | 0.64733 |
| 100311276_TGI_at | VTA1 | positive | Concordant | 0.246076 | 0.107518 | 0.022096 | 0.201777 | 2.936077 | 1.955736 | 0.133287 | 0.536498 |
| 100311300_TGI_at | TMEM163 | negative | Discordant | 0.021492 | 0.027329 | 0.431616 | 0.722949 | 0.401785 | 0.497084 | 0.418926 | 0.764651 |
| 100311305_TGI_at | FGFR1OP2 | negative | Discordant | 0.006214 | 0.086757 | 0.942896 | 0.983056 | -0.6897 | 1.562959 | 0.65901 | 0.888268 |
| 100311360_TGI_at | C6orf162 | positive | Concordant | 0.3802 | 0.261499 | 0.145967 | 0.450369 | -0.54485 | 4.753283 | 0.908742 | 0.980193 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100311377_TGI_at | ROCK2 | positive | Concordant | -0.00903 | 0.06056 | 0.881455 | 0.965743 | 2.551229 | 1.094408 | 0.019745 | 0.2703 |
| 100311425_TGI_at | BAG5 | positive | Discordant | -0.97355 | 0.381503 | 0.010714 | 0.149822 | -9.90941 | 7.036811 | 0.159065 | 0.560509 |
| 100311425_TGI_at | BAG5 | positive | Discordant | -0.97355 | 0.381503 | 0.010714 | 0.149822 | -9.90941 | 7.036811 | 0.159065 | 0.560509 |
| 100311439_TGI_at | PCBP2 | negative | Discordant | 0.070284 | 0.040574 | 0.083228 | 0.371725 | 0.548795 | 0.741777 | 0.459398 | 0.784051 |
| 100311443_TGI_at | LRRC16A | positive | Concordant | 0.59502 | 0.384947 | 0.122173 | 0.431533 | 1.900576 | 6.990788 | 0.785723 | 0.946142 |
| 100311443_TGI_at | LRRC16A | positive | Concordant | 0.59502 | 0.384947 | 0.122173 | 0.431533 | 1.900576 | 6.990788 | 0.785723 | 0.946142 |
| 100311514_TGI_at | | negative | Discordant | 0.043569 | 0.030495 | 0.153086 | 0.4583 | 0.325173 | 0.556255 | 0.558834 | 0.839094 |
| 100311606_TGI_at | HLA-F | negative | Concordant | -0.35939 | 0.290963 | 0.216771 | 0.523093 | -7.02704 | 5.262837 | 0.181805 | 0.575874 |
| 100311606_TGI_at | HLA-F | negative | Concordant | -0.35939 | 0.290963 | 0.216771 | 0.523093 | -7.02704 | 5.262837 | 0.181805 | 0.575874 |
| 100311606_TGI_at | HLA-F | negative | Concordant | -0.35939 | 0.290963 | 0.216771 | 0.523093 | -7.02704 | 5.262837 | 0.181805 | 0.575874 |
| 100311606_TGI_at | HLA-F | negative | Concordant | -0.35939 | 0.290963 | 0.216771 | 0.523093 | -7.02704 | 5.262837 | 0.181805 | 0.575874 |
| 100311674_TGI_at | HHIP | negative | Concordant | -0.12982 | 0.0518 | 0.012204 | 0.153347 | -2.76918 | 0.940206 | 0.003227 | 0.116559 |
| 100311674_TGI_at | HHIP | negative | Concordant | -0.12982 | 0.0518 | 0.012204 | 0.153347 | -2.76918 | 0.940206 | 0.003227 | 0.116559 |
| 100311684_TGI_at | HLA-DQB2 | positive | Discordant | -1.67896 | 2.203654 | 0.44612 | 0.733564 | -29.7934 | 39.5181 | 0.450899 | 0.77692 |
| 100311684_TGI_at | HLA-DQB2 | negative | Concordant | -1.67896 | 2.203654 | 0.44612 | 0.733564 | -29.7934 | 39.5181 | 0.450899 | 0.77692 |
| 100311695_TGI_at | PLA2G5 | positive | Discordant | 0.090085 | 0.203988 | 0.658766 | 0.875236 | 5.066138 | 3.675839 | 0.168133 | 0.564154 |
| 100311704_TGI_at | HLA-DQB1 | negative | Concordant | -1.00735 | 0.493489 | 0.041224 | 0.259282 | -13.2256 | 8.949491 | 0.139459 | 0.547108 |
| 100311704_TGI_at | HLA-DQB1 | positive | Discordant | -1.00735 | 0.493489 | 0.041224 | 0.259282 | -13.2256 | 8.949491 | 0.139459 | 0.547108 |
| 100311757_TGI_at | | positive | Discordant | 0.410783 | 0.522701 | 0.431935 | 0.722949 | 0.138787 | 9.529064 | 0.98838 | 0.999082 |
| 100311757_TGI_at | | positive | Discordant | 0.410783 | 0.522701 | 0.431935 | 0.722949 | 0.138787 | 9.529064 | 0.98838 | 0.999082 |
| 100311790_TGI_at | | negative | Concordant | -0.12422 | 0.143894 | 0.387988 | 0.702944 | -3.14816 | 2.599065 | 0.225794 | 0.623069 |
| 100311821_TGI_at | NPHP3 | negative | Discordant | 0.307539 | 0.419881 | 0.463898 | 0.747582 | 2.936807 | 7.7375 | 0.704276 | 0.915742 |
| 100311825_TGI_at | RP3-377H14.5 | negative | Concordant | -0.69787 | 0.31057 | 0.024635 | 0.203166 | -15.6869 | 5.609522 | 0.005166 | 0.149307 |
| 100311825_TGI_at | RP3-377H14.5 | negative | Concordant | -0.69787 | 0.31057 | 0.024635 | 0.203166 | -15.6869 | 5.609522 | 0.005166 | 0.149307 |
| 100311825_TGI_at | RP3-377H14.5 | negative | Concordant | -0.69787 | 0.31057 | 0.024635 | 0.203166 | -15.6869 | 5.609522 | 0.005166 | 0.149307 |
| 100311825_TGI_at | RP3-377H14.5 | negative | Concordant | -0.69787 | 0.31057 | 0.024635 | 0.203166 | -15.6869 | 5.609522 | 0.005166 | 0.149307 |
| 100311884_TGI_at | PDPN | negative | Concordant | -0.11502 | 0.176595 | 0.514857 | 0.780157 | -0.07829 | 3.202098 | 0.980494 | 0.999082 |
| 100311952_TGI_at | | negative | Discordant | 0.012891 | 0.054742 | 0.813835 | 0.939541 | 0.661086 | 1.010725 | 0.513066 | 0.819204 |
| 100311980_TGI_at | | positive | Concordant | 0.085486 | 0.046195 | 0.064233 | 0.314919 | 0.856148 | 0.856479 | 0.317498 | 0.671733 |
| 100312006_TGI_at | B3GNTL1 | positive | Discordant | -0.3121 | 0.289729 | 0.281379 | 0.593566 | -1.13262 | 5.317065 | 0.831315 | 0.957068 |
| 100312038_TGI_at | FAM13A1 | negative | Discordant | 0.045729 | 0.053775 | 0.395109 | 0.704177 | 0.550697 | 0.972151 | 0.571072 | 0.844914 |
| 100312395_TGI_at | PCM1 | negative | Discordant | 0.046677 | 0.042319 | 0.27004 | 0.579517 | 0.860332 | 0.779331 | 0.26962 | 0.64407 |
| 100312458_TGI_at | CCBE1 | positive | Concordant | 0.122289 | 0.041564 | 0.003259 | 0.080734 | 1.878093 | 0.753585 | 0.012695 | 0.215815 |
| 100312557_TGI_at | ARL17P1 | negative | Discordant | 6.173858 | 4.98463 | 0.215501 | 0.522164 | 31.55564 | 90.88606 | 0.728441 | 0.922014 |
| 100312774_TGI_at | C1orf113 | positive | Concordant | 9.480586 | 7.224678 | 0.189436 | 0.501991 | 146.0066 | 134.3133 | 0.27701 | 0.64407 |
| 100312805_TGI_at | ZNF165 | negative | Concordant | -0.28608 | 0.277198 | 0.302058 | 0.622924 | -5.02492 | 4.972064 | 0.312193 | 0.671386 |
| 100312821_TGI_at | MLF1 | negative | Concordant | -0.71294 | 1.586072 | 0.653071 | 0.873359 | 12.45864 | 28.57795 | 0.662871 | 0.888268 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| 100312826_TGI_at | | negative | Discordant | 0.081649 | 0.21144 | 0.699381 | 0.894706 | 1.110673 | 3.910411 | 0.776388 | 0.941122 |
| 100312853_TGI_at | CLUAP1 | positive | Concordant | 0.056995 | 0.084149 | 0.498211 | 0.774427 | 1.526935 | 1.525777 | 0.316943 | 0.671733 |
| 100312946_TGI_at | HLA-DRB1 | negative | Concordant | 0.003646 | 0.004328 | 0.399556 | 0.704177 | -0.05008 | 0.078251 | 0.522156 | 0.821114 |
| 100312946_TGI_at | HLA-DRB1 | positive | Concordant | 0.003646 | 0.004328 | 0.399556 | 0.704177 | -0.05008 | 0.078251 | 0.522156 | 0.821114 |
| 100313079_TGI_at | FBXO38 | positive | Concordant | 0.130743 | 0.084392 | 0.121325 | 0.431533 | 1.678469 | 1.532978 | 0.273557 | 0.64407 |
| 100313079_TGI_at | FBXO38 | positive | Concordant | 0.130743 | 0.084392 | 0.121325 | 0.431533 | 1.678469 | 1.532978 | 0.273557 | 0.64407 |
| 100313107_TGI_at | KCNMB3 | negative | Concordant | 0.001465 | 0.300802 | 0.996115 | 0.999257 | 0.20371 | 5.467429 | 0.970279 | 0.999082 |
| 100313121_TGI_at | HLA-C | positive | Concordant | 0.010729 | 0.009263 | 0.246754 | 0.552806 | 0.183093 | 0.168118 | 0.276122 | 0.64407 |
| 100313121_TGI_at | HLA-C | positive | Concordant | 0.010729 | 0.009263 | 0.246754 | 0.552806 | 0.183093 | 0.168118 | 0.276122 | 0.64407 |
| 100313238_TGI_at | ARHGEF19 | negative | Discordant | 0.071318 | 0.22599 | 0.75232 | 0.919699 | 2.683109 | 4.161531 | 0.519095 | 0.821114 |
| 100313404_TGI_at | JARID1A | negative | Concordant | 0.147906 | 0.179074 | 0.408832 | 0.711479 | -1.85366 | 3.220017 | 0.564839 | 0.841435 |
| 100313479_TGI_at | NPHP3 | negative | Concordant | 0.036373 | 0.137277 | 0.791037 | 0.929308 | -1.9085 | 2.491408 | 0.443658 | 0.772392 |
| 100313509_TGI_at | FAM63A | negative | Discordant | 0.126794 | 0.063732 | 0.046648 | 0.269292 | 1.490058 | 1.213063 | 0.219318 | 0.623069 |
| 100313510_TGI_at | AGER | negative | Discordant | 0.018265 | 0.00618 | 0.003122 | 0.080734 | 0.293586 | 0.113281 | 0.009551 | 0.205089 |
| 100313559_TGI_at | CLUAP1 | positive | Discordant | 0.040452 | 0.083726 | 0.628988 | 0.853415 | 1.017272 | 1.514862 | 0.501884 | 0.813334 |
| 100313618_TGI_at | | negative | Discordant | -0.30392 | 0.999132 | 0.760987 | 0.923606 | -12.8552 | 18.07526 | 0.476959 | 0.799852 |
| 100313726_TGI_at | | negative | Concordant | -0.01212 | 0.093342 | 0.896729 | 0.966995 | -0.63131 | 1.707425 | 0.711571 | 0.915742 |
| 100313726_TGI_at | | negative | Concordant | -0.01212 | 0.093342 | 0.896729 | 0.966995 | -0.63131 | 1.707425 | 0.711571 | 0.915742 |
| 100313731_TGI_at | SGCD | positive | Discordant | 0.021706 | 0.414816 | 0.958269 | 0.988973 | 0.059012 | 7.556665 | 0.993769 | 0.999082 |
| 100313766_TGI_at | HLA-DQA2 | negative | Discordant | 0.000864 | 0.006185 | 0.888876 | 0.965743 | 0.071559 | 0.111975 | 0.522785 | 0.821114 |
| 100313766_TGI_at | HLA-DQA2 | positive | Concordant | 0.000864 | 0.006185 | 0.888876 | 0.965743 | 0.071559 | 0.111975 | 0.522785 | 0.821114 |
| 100313804_TGI_at | | positive | Discordant | -0.67386 | 0.559855 | 0.228732 | 0.531663 | -11.535 | 10.21043 | 0.25859 | 0.640563 |
| 100313804_TGI_at | | negative | Concordant | -0.67386 | 0.559855 | 0.228732 | 0.531663 | -11.535 | 10.21043 | 0.25859 | 0.640563 |
| 100313840_TGI_at | | positive | Discordant | 0.399325 | 0.376757 | 0.28919 | 0.605622 | 1.051329 | 6.909751 | 0.879067 | 0.968426 |
| 100313880_TGI_at | | positive | Discordant | 0.021939 | 0.138965 | 0.874555 | 0.965712 | 1.342558 | 2.516327 | 0.593661 | 0.859272 |
| 100313880_TGI_at | | positive | Concordant | 0.021939 | 0.138965 | 0.874555 | 0.965712 | 1.342558 | 2.516327 | 0.593661 | 0.859272 |
| 100313943_TGI_at | CCDC51 | negative | Concordant | -0.16809 | 0.059399 | 0.004657 | 0.09827 | -2.14976 | 1.069842 | 0.044493 | 0.37452 |
| 100313972_TGI_at | FLOT1 | negative | Concordant | -0.53465 | 0.831871 | 0.520412 | 0.781971 | -9.65369 | 15.33014 | 0.528878 | 0.825639 |
| 100313972_TGI_at | FLOT1 | negative | Concordant | -0.53465 | 0.831871 | 0.520412 | 0.781971 | -9.65369 | 15.33014 | 0.528878 | 0.825639 |
| 100314018_TGI_at | RPS19 | negative | Concordant | -0.01449 | 0.006539 | 0.026691 | 0.20322 | -0.31815 | 0.118406 | 0.00721 | 0.189429 |
| 100314021_TGI_at | ARIH2 | positive | Discordant | -0.43667 | 0.116011 | 0.000167 | 0.02741 | -3.5702 | 2.109056 | 0.090494 | 0.46152 |
| 100314021_TGI_at | ARIH2 | positive | Discordant | -0.43667 | 0.116011 | 0.000167 | 0.02741 | -3.5702 | 2.109056 | 0.090494 | 0.46152 |

## Supplementary Table 11: Percentage concordance of mRNA associations at different GWAS P value cutoffs for eSNPs

The table shows the % concordance of mRNA associations for different GWAS P value cutoffs. The concordance was calculated for $FEV_1$ and for $FEV_1$/FVC GWAS, separately. eSNP GWAS P value cutoff: The GWAS P value cutoff for eSNPs that regulate the expression of probesets in lung tissue. No. of Concordant: Number of concordant probesets ( compared to the expected given the SNP effect on lung function and probeset expression). No. of Discordant: Number of discordant probesets at this GWAS P value for eSNPs. Concordance percentage: % of concordant probesets to all eSNP-regulated probeset at this GWAS cutoff.

| **Percentage concordance of mRNA associations at different GWAS P value cutoffs for eSNPs** | | | |
|---|---|---|---|
| **$FEV_1$** | | | |
| eSNP GWAS P value cutoff | No. of Concordant | No. of Discordant | Concordance percentage |
| 0.001 | 103 | 77 | 57 |
| 1.00E-04 | 28 | 17 | 62 |
| 1.00E-05 | 6 | 3 | 67 |
| 1.00E-06 | 6 | 3 | 67 |
| 1.00E-07 | 6 | 2 | 75 |
| 1.00E-08 | 2 | 2 | 50 |
| | | | |
| **$FEV_1$/FVC** | | | |
| eSNP GWAS P value cutoff | No. of Concordant | No. of Discordant | Concordance percentage |
| 0.001 | 85 | 80 | 52 |
| 1.00E-04 | 19 | 17 | 53 |
| 1.00E-05 | 5 | 10 | 33 |
| 1.00E-06 | 5 | 4 | 56 |
| 1.00E-07 | 5 | 4 | 56 |
| 1.00E-08 | 5 | 4 | 56 |

## Supplementary Table 12: Lung eSNPs at 4q31 in LD with the functional SNPs reported in Zhou *et al*. 2012

The table shows lung tissue eSNPs identified in this study in the HHIP region at 4q31 and their LD ( R Squared and D prime) with two functional SNPs identified *in vitro* in Zhou *et al.* (30). Coordinate_HG18 referes to the SNPs position using human genome build 18.

| **Lung eSNPs at 4q31 in LD with the functional SNPs reported in Zhou et al. 2012** | | | | | |
|---|---|---|---|---|---|
| Functional SNP in Zhou *et al.* | Proxy eSNP in the current manuscript | Distance (bp) | RSquared | DPrime | Coordinate_HG18 |
| rs6537296 | rs1542725 | 400 | 0.935 | 1 | 145707784 |
| | rs7655625 | 2019 | 0.935 | 1 | 145705365 |
| | rs11100860 | 8795 | 0.935 | 1 | 145698589 |
| | ***rs12509311*** | 9272 | 0.935 | 1 | 145698112 |
| | rs995758 | 9733 | 0.935 | 1 | 145697651 |
| | rs6842889 | 8054 | 0.9 | 0.965 | 145699330 |
| | ***rs13141641*** | 18522 | 0.869 | 0.964 | 145725906 |
| | rs10013495 | 17704 | 0.118 | 1 | 145725088 |
| | rs10519717 | 7594 | 0.109 | 1 | 145699790 |
| | rs6852830 | 18624 | 0.109 | 1 | 145726008 |
| | rs1996020 | 23260 | 0.109 | 1 | 145730644 |
| | rs2130338 | 21733 | 0.054 | 0.73 | 145685651 |
| | rs11938704 | 44564 | 0.028 | 0.51 | 145662820 |
| | rs6854832 | 46175 | 0.028 | 0.51 | 145661209 |
| | rs4835638 | 48641 | 0.028 | 0.51 | 145658743 |
| rs1542725 | rs7655625 | 2419 | 1 | 1 | 145705365 |
| | rs11100860 | 9195 | 1 | 1 | 145698589 |
| | rs12509311 | 9672 | 1 | 1 | 145698112 |
| | rs995758 | 10133 | 1 | 1 | 145697651 |
| | rs6842889 | 8454 | 0.967 | 1 | 145699330 |
| | rs6537296 | 400 | 0.935 | 1 | 145707384 |
| | rs13141641 | 18122 | 0.933 | 0.966 | 145725906 |
| | rs10013495 | 17304 | 0.126 | 1 | 145725088 |
| | ***rs10519717*** | 7994 | 0.117 | 1 | 145699790 |
| | rs6852830 | 18224 | 0.117 | 1 | 145726008 |
| | rs1996020 | 22860 | 0.117 | 1 | 145730644 |

| | | | | | |
|---|---|---|---|---|---|
| | rs2130338 | 22133 | 0.061 | 0.75 | 145685651 |
| | rs11938704 | 44964 | 0.035 | 0.544 | 145662820 |
| | rs6854832 | 46575 | 0.035 | 0.544 | 145661209 |
| | rs4835638 | 49041 | 0.035 | 0.544 | 145658743 |

## Supplementary Table 13: Lung eSNPs shared with blood/sputum eQTLs reported in Castaldi *et al.* 2015

The paper by Castaldi *et al*. 21 integrated SNPs from 5812 COPD cases and 3955 controls with blood and sputum eQTLs from 121 COPD subjects. SNPs associated with both gene expression and COPD susceptibility at an FDR of 10% were observed for 36 unique probesets at 19 distinct genomic loci.

The Table shows the lung eSNPs identified in this study along with their eQTL P values and the probestes they regulate. The Table also shows the COPD and gene expression q-values, and the tissue where the SNP function as an eQTL(blood, sputum or both) and the gene(s) they regulate in these tissues.

| **Lung eSNPs shared with blood/sputum eQTLs reported in Castaldi et al. 2015** | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| **Lung function eSNP results** | | | **eQTL results in Castaldi et al.** | | | | | | |
| **eSNP** | **Lung eQTL P value** | **Lung eQTL regulated probeset** | **COPD GWAS q-value** | **Sample** | **Best blood eQTL q-value** | **Best sputum eQTL q-value** | **eQTL gene** | **eQTL gene 2** | **eQTL gene 3** |
| rs12914385 | 3.45E-47 | IREB2 | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs12914385 | 7.39E-06 | Maps to en Expressed Sequence Taq located between IREB2 and PSMA4 genes | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs12914385 | 3.75E-18 | CHRNA5 | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs12914385 | 7.80E-10 | PSMA4 | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs1394371 | 4.10E-17 | CHRNA5 | 0.003 | Blood | 0.06 | >0.1 | WDR61 | | |
| rs1394371 | 9.00E-06 | Maps to en Expressed Sequence Taq located between IREB2 and PSMA4 genes | 0.003 | Blood | 0.06 | >0.1 | WDR61 | | |
| rs1394371 | 7.71E-42 | IREB2 | 0.003 | Blood | 0.06 | >0.1 | WDR61 | | |
| rs1394371 | 2.10E-10 | PSMA4 | 0.003 | Blood | 0.06 | >0.1 | WDR61 | | |
| rs2869967 | 1.74E-06 | FAM13A1 | <0.001 | Blood | 0.029 | >0.1 | FAM13A | | |
| rs720485 | 5.98E-07 | HHIP | <0.001 | Blood | 0.089 | >0.1 | HHIP | | |
| | | | | | | | | | |
| rs12914385 | 3.75E-18 | CHRNA5 | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs12914385 | 7.39E-06 | Maps to en Expressed Sequence Taq located between IREB2 and PSMA4 genes | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs12914385 | 7.80E-10 | PSMA4 | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs12914385 | 3.45E-47 | IREB2 | <0.001 | Both | <0.001 | 0.02 | IREB2 | CHRNA3 | PSMA4 |
| rs720485 | 5.98E-07 | HHIP | <0.001 | Blood | 0.089 | >0.1 | HHIP | | |

## Supplementary Table 14: Pleiotropy of lung function eSNPs from GWAS catalog

Table shows the result of integrating eSNPs with published associations from the GWAS catalog. Supplementary Table 14A shows the results for all lung function eSNPs, and supplementary Table 14B shows the results for the best lung function eSNP per probeset.
eSNP: SNP that is associated with either FEV$_1$ or FEV$_1$/FVC from the SpiroMeta GWAS with $P_{\text{GWAS}}$ <0.001, which also acts as a *cis* or *trans* lung eQTL at 10% FDR in lung tissue. Chr: chromosome. eSNP Position: position using NCBI36/hg18 coordinates. GWAS_P value: eSNP P value for association with lung function from the GWAS study. eQTL Z meta: The Z score of meta-analysis results of eQTL study across the three datasets ( UBC, Groningen, Laval). eQTL -log10.pvalue: the –log10 of eQTL p value from the lung eQTL study.. eSNP regulated gene: gene whose expression is regulated by the eSNP. eQTL_study: Whether the SNP is associated with FEV$_1$ or FEV$_1$/FVC and acts as a *cis*- or *trans*-eQTL. eQTL_alleles: two eQTL SNP alleles from the eQTL study. Note: The SNP data in the GWAS catalog has been mapped to dbSNP Build 137 and Genome Assembly, GRCh37/hg19. PUBMEDID: PubMed identification number. DISEASE/TRAIT: Disease or trait examined in study. P-VALUE: Reported p-value for strongest SNP risk allele (linked to dbGaP Association Browser). OR or BETA: Reported odds ratio or beta-coefficient associated with strongest SNP risk allele.

**Pleiotropy of all lung function eSNPs in the NHGRI GWAS Catalog**

| eSNP | Chr | GWAS_P value | eQTL Z meta | eQTL - log10. pvalue | eSNP regulated Gene | eQTL_study | eQTL_alleles | PUBMEDID | Disease.Trait | p.Value | OR.or.beta |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs1466535 | 12 | 5.76E-04 | -10.15 | -23.4797 | STAT6 | FEV1FVC_cis | G_A | 22055160 | Abdominal aortic aneurysm | 5.00E-10 | 1.15 |
| rs1466535 | 12 | 5.76E-04 | 9.823 | -22.0475 | STAT6 | FEV1FVC_cis | G_A | 22055160 | Abdominal aortic aneurysm | 5.00E-10 | 1.15 |
| rs12310399 | 12 | 1.20E-04 | 4.642 | -5.4621 | VEZT | FEV1FVC_cis | C_T | 23648065 | Adverse response to chemotherapy (neutropenia/leucopenia) (paclitaxel + carboplatin) | 2.00E-07 | 1.85 |
| rs12310399 | 12 | 1.20E-04 | 4.824 | -5.8517 | FGD6 | FEV1FVC_cis | C_T | 23648065 | Adverse response to chemotherapy (neutropenia/leucopenia) (paclitaxel + carboplatin) | 2.00E-07 | 1.85 |
| rs11755724 | 6 | 1.44E-04 | -5.526 | -7.4846 | RREB1 | FEV1FVC_cis | A_G | 20385826 | Age-related macular degeneration | 1.00E-06 | 1.15 |
| rs8321 | 6 | 3.72E-04 | -12.508 | -35.1707 |  | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 4.467 | -5.1006 |  | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -4.771 | -5.7368 | FLOT1 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 7.796 | -14.1945 | HCG18 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 12.972 | -37.7536 | HLA-A | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -6.051 | -8.8418 | TUBB | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -4.829 | -5.8626 | RP3-377H14.5 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -4.518 | -5.2046 | FLOT1 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 6.502 | -10.101 |  | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 4.526 | -5.221 | HLA-G | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 12.486 | -35.0505 | BTN3A2 | FEV1_trans | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 7.79 | -14.1739 | HLA-G | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 5.06 | -6.3775 | HCG2P7 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -6.197 | -9.24 | HLA-F | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 5.616 | -7.709 |  | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -7.181 | -12.1599 |  | FEV1_trans | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -7.155 | -12.0774 |  | FEV1_trans | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -7.948 | -14.7223 | C6orf12 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8321 | 6 | 3.72E-04 | 5.051 | -6.357 | ZNRD1 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 7.45 | -13.0299 | HCG18 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 8.125 | -15.3493 | HLA-C | FEV1_trans | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -7.822 | -14.2841 | HLA-A | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -4.972 | -6.1787 | SFTA2 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 4.949 | -6.1273 | VARS2 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | 4.344 | -4.8541 | HCG2P7 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -14.213 | -45.1186 | ZFP57 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -9.092 | -19.0122 | HLA-DRB3 | FEV1_trans | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -8.022 | -14.9828 | HCG4P6 | FEV1_cis | C_A | 19115949 | AIDS progression | 5.00E-07 | NR |
| rs17486278 | 15 | 1.29E-05 | -5.602 | -7.6739 | | FEV1_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.29E-05 | 15.148 | -51.1073 | | FEV1_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.27E-05 | 15.148 | -51.1073 | | FEV1FVC_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.27E-05 | -5.602 | -7.6739 | | FEV1FVC_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.27E-05 | -6.945 | -11.422 | PSMA4 | FEV1FVC_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.29E-05 | -6.945 | -11.422 | PSMA4 | FEV1_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.29E-05 | 10.207 | -23.734 | CHRNA5 | FEV1_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs17486278 | 15 | 1.27E-05 | 10.207 | -23.734 | CHRNA5 | FEV1FVC_cis | C_A | 22837378 | Airflow obstruction | 2.00E-07 | 1.18 |
| rs2044029 | 15 | 4.68E-05 | 4.115 | -4.4121 | THSD4 | FEV1_cis | G_A | 22837378 | Airflow obstruction | 1.00E-07 | 1.17 |
| rs2044029 | 15 | 4.68E-05 | 4.506 | -5.1801 | THSD4 | FEV1_cis | G_A | 22837378 | Airflow obstruction | 1.00E-07 | 1.17 |
| rs2044029 | 15 | 6.21E-10 | 4.115 | -4.4121 | THSD4 | FEV1FVC_cis | G_A | 22837378 | Airflow obstruction | 1.00E-07 | 1.17 |
| rs2044029 | 15 | 6.21E-10 | 4.506 | -5.1801 | THSD4 | FEV1FVC_cis | G_A | 22837378 | Airflow obstruction | 1.00E-07 | 1.17 |
| rs8031948 | 15 | 6.68E-05 | 6.904 | -11.2962 | PSMA4 | FEV1FVC_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 1.72E-05 | -16.147 | -57.9236 | | FEV1_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 6.68E-05 | -10.474 | -24.9441 | CHRNA5 | FEV1FVC_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 6.68E-05 | 5.755 | -8.0623 | | FEV1FVC_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 1.72E-05 | 6.904 | -11.2962 | PSMA4 | FEV1_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 1.72E-05 | 5.755 | -8.0623 | | FEV1_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 1.72E-05 | -10.474 | -24.9441 | CHRNA5 | FEV1_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs8031948 | 15 | 6.68E-05 | -16.147 | -57.9236 | | FEV1FVC_cis | G_T | 22837378 | Airflow obstruction | 3.00E-09 | 1.22 |
| rs11745587 | 5 | 3.29E-04 | -5.747 | -8.0417 | RAD50 | FEV1FVC_cis | A_G | 22561531 | Asthma | 2.00E-06 | 1.26 |
| rs11745587 | 5 | 3.29E-04 | -5.296 | -6.9268 | | FEV1FVC_cis | A_G | 22561531 | Asthma | 2.00E-06 | 1.26 |
| rs11745587 | 5 | 3.29E-04 | -5.217 | -6.7403 | | FEV1FVC_cis | A_G | 22561531 | Asthma | 2.00E-06 | 1.26 |
| rs11745587 | 5 | 3.29E-04 | -4.761 | -5.7153 | | FEV1FVC_cis | A_G | 22561531 | Asthma | 2.00E-06 | 1.26 |
| rs11745587 | 5 | 3.29E-04 | 5.409 | -7.1981 | SLC22A5 | FEV1FVC_cis | A_G | 22561531 | Asthma | 2.00E-06 | 1.26 |
| rs9272346 | 6 | 8.63E-04 | -10.049 | -23.0324 | HLA-DQB2 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | 16.482 | -60.3061 | HLA-DRB4 | FEV1_trans | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -11.492 | -29.8395 | AGPAT1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -10.107 | -23.2887 | C19orf6 | FEV1_trans | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -13.665 | -41.7844 | HLA-DQB1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -12.808 | -36.83 | HLA-DRB5 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -10.924 | -27.053 | HLA-DRB1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -8.603 | -17.1098 | AGPAT1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -5.675 | -7.858 | TAP2 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -13.463 | -40.588 | HLA-DQB1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -20.082 | -88.9745 | HLA-DQB1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |

|  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs9272346 | 6 | 8.63E-04 | -7.449 | -13.0266 | HLA-DQB2 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -6.341 | -9.6415 |  | FEV1_trans | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | 14.33 | -45.8473 | HLA-DRB6 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -13.484 | -40.7116 | HLA-DQB1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | 16.468 | -60.2055 | HLA-DQA2 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -7.529 | -13.2913 | CDSN | FEV1_trans | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs9272346 | 6 | 8.63E-04 | -7.577 | -13.4514 | HLA-DRB1 | FEV1_cis | G_A | 23181788 | Asthma | 2.00E-08 | NR |
| rs404860 | 6 | 9.95E-10 | -5.575 | -7.6064 | HLA-DQA2 | FEV1FVC_cis | C_T | 21804548 | Asthma | 4.00E-23 | 1.21 |
| rs3132581 | 6 | 1.96E-05 | -7.907 | -14.5789 | SFTA2 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 6.528 | -10.1762 | VARS2 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 5.843 | -8.2901 |  | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 6.65 | -10.533 | CDSN | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 7.87 | -14.4502 | HCG18 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -6.798 | -10.9744 | HLA-A | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -4.153 | -4.4839 | C6orf12 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -4.521 | -5.2108 | MICB | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -8.814 | -17.9181 | ZFP57 | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -9.935 | -22.5329 | HLA-DRB3 | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -9.099 | -19.0402 |  | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 7.87 | -14.4502 | HCG18 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 6.319 | -9.5796 | HLA-G | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar | 2.00E-07 | NR |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | disorder, major depressive disorder, and schizophrenia (combined) | | |
| rs3132581 | 6 | 2.00E-05 | -9.215 | -19.5069 | | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 6.319 | -9.5796 | HLA-G | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -8.935 | -18.3902 | | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -7.201 | -12.2235 | HCG4P6 | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 9.364 | -20.1148 | BTN3A2 | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 7.759 | -14.0675 | HLA-C | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -9.099 | -19.0402 | | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 5.001 | -6.2439 | PSORS1C3 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 7.564 | -13.408 | HCG18 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -6.774 | -10.9022 | TUBB | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -7.201 | -12.2235 | HCG4P6 | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -8.814 | -17.9181 | ZFP57 | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 5.379 | -7.1255 | PSORS1C1 | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 5.001 | -6.2439 | PSORS1C3 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 4.987 | -6.2124 | APOM | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 7.259 | -12.409 | HLA-A | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention | 2.00E-07 | NR |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | | |
| rs3132581 | 6 | 2.00E-05 | 5.843 | -8.2901 | | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -6.774 | -10.9022 | TUBB | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 6.528 | -10.1762 | VARS2 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | 7.259 | -12.409 | HLA-A | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -9.935 | -22.5329 | HLA-DRB3 | FEV1_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 9.364 | -20.1148 | BTN3A2 | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -4.153 | -4.4839 | C6orf12 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -7.907 | -14.5789 | SFTA2 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -4.521 | -5.2108 | MICB | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | -6.798 | -10.9744 | HLA-A | FEV1FVC_trans | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -8.935 | -18.3902 | | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 7.759 | -14.0675 | HLA-C | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 1.96E-05 | -9.215 | -19.5069 | | FEV1_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 4.987 | -6.2124 | APOM | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 5.379 | -7.1255 | PSORS1C1 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3132581 | 6 | 2.00E-05 | 6.65 | -10.533 | CDSN | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs3132581 | 6 | 2.00E-05 | 7.564 | -13.408 | HCG18 | FEV1FVC_cis | A_G | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-07 | NR |
| rs8321 | 6 | 3.72E-04 | -12.508 | -35.1707 | | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 4.467 | -5.1006 | | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -4.771 | -5.7368 | FLOT1 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 7.796 | -14.1945 | HCG18 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 12.972 | -37.7536 | HLA-A | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -6.051 | -8.8418 | TUBB | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -4.829 | -5.8626 | RP3-377H14.5 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -4.518 | -5.2046 | FLOT1 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 6.502 | -10.101 | | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 4.526 | -5.221 | HLA-G | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 12.486 | -35.0505 | BTN3A2 | FEV1_trans | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 7.79 | -14.1739 | HLA-G | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 5.06 | -6.3775 | HCG2P7 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -6.197 | -9.24 | HLA-F | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and | 8.00E-09 | 1.08 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | schizophrenia (combined) | | |
| rs8321 | 6 | 3.72E-04 | 5.616 | -7.709 | | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -7.181 | -12.1599 | | FEV1_trans | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -7.155 | -12.0774 | | FEV1_trans | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -7.948 | -14.7223 | C6orf12 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 5.051 | -6.357 | ZNRD1 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 7.45 | -13.0299 | HCG18 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 8.125 | -15.3493 | HLA-C | FEV1_trans | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -7.822 | -14.2841 | HLA-A | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -4.972 | -6.1787 | SFTA2 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 4.949 | -6.1273 | VARS2 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | 4.344 | -4.8541 | HCG2P7 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -14.213 | -45.1186 | ZFP57 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -9.092 | -19.0122 | HLA-DRB3 | FEV1_trans | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs8321 | 6 | 3.72E-04 | -8.022 | -14.9828 | HCG4P6 | FEV1_cis | C_A | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 8.00E-09 | 1.08 |
| rs2021722 | 6 | 8.30E-04 | 8.098 | -15.2528 | BTN3A2 | FEV1_trans | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -6.243 | -9.3673 | | FEV1_trans | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar | 2.00E-12 | NR |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | | disorder, major depressive disorder, and schizophrenia (combined) | | |
| rs2021722 | 6 | 8.30E-04 | -5.741 | -8.0263 | RP3-377H14.5 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | 7.986 | -14.8558 | | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | 5.632 | -7.7493 | VARS2 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -8.291 | -15.9496 | | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -4.559 | -5.2891 | SFTA2 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -6.859 | -11.159 | HLA-DRB3 | FEV1_trans | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -5.559 | -7.5665 | HCG18 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -7.299 | -12.5377 | | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -6.046 | -8.8283 | TUBB | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -5.535 | -7.5069 | HCG18 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -6.821 | -11.0438 | ZFP57 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | 8.616 | -17.1591 | HLA-A | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | -7.685 | -13.8153 | HCG4P6 | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | 5.038 | -6.3275 | HLA-G | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs2021722 | 6 | 8.30E-04 | 5.922 | -8.4975 | CDSN | FEV1_cis | T_C | 23453885 | Autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia (combined) | 2.00E-12 | NR |
| rs886424 | 6 | 1.55E-04 | -9.77 | -21.8197 | | FEV1FVC_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs886424 | 6 | 1.55E-04 | 5.16 | -6.6074 | APOM | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -10.72 | -26.0862 | HLA-DRB3 | FEV1_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 5.268 | -6.8604 | PSORS1C1 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 6.223 | -9.3118 | CDSN | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -7.777 | -14.1292 | | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 4.228 | -4.6275 | PSORS1C3 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 4.362 | -4.8898 | HCG2P7 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -6.23 | -9.3312 | HCG4P6 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 9.644 | -21.283 | BTN3A2 | FEV1FVC_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -7.777 | -14.1292 | | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -9.77 | -21.8197 | | FEV1_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 7.591 | -13.4983 | HCG18 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -6.23 | -9.3312 | HCG4P6 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 5.268 | -6.8604 | PSORS1C1 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 5.417 | -7.2175 | VARS2 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 8.902 | -18.2608 | HLA-A | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 4.655 | -5.4895 | HCG2P7 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 5.417 | -7.2175 | VARS2 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 4.655 | -5.4895 | HCG2P7 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -7.814 | -14.2565 | HLA-A | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 7.704 | -13.8798 | HCG18 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 5.16 | -6.6074 | APOM | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -11.161 | -28.1988 | ZFP57 | FEV1FVC_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -4.302 | -4.7714 | MICB | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -6.216 | -9.2924 | SFTA2 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -4.302 | -4.7714 | MICB | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -7.87 | -14.4502 | | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -6.216 | -9.2924 | SFTA2 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 4.775 | -5.7454 | | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -7.851 | -14.3843 | TUBB | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 4.228 | -4.6275 | PSORS1C3 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -7.87 | -14.4502 | | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -6.141 | -9.0862 | C6orf12 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 8.902 | -18.2608 | HLA-A | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -7.851 | -14.3843 | TUBB | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 7.591 | -13.4983 | HCG18 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -6.141 | -9.0862 | C6orf12 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 7.704 | -13.8798 | HCG18 | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 4.362 | -4.8898 | HCG2P7 | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 9.644 | -21.283 | BTN3A2 | FEV1_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -10.72 | -26.0862 | HLA-DRB3 | FEV1FVC_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 4.775 | -5.7454 | | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 8.885 | -18.1944 | HLA-C | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 6.223 | -9.3118 | CDSN | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | 5.918 | -8.4869 | HLA-G | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | -11.161 | -28.1988 | ZFP57 | FEV1_trans | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 8.885 | -18.1944 | HLA-C | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 2.17E-05 | 5.918 | -8.4869 | HLA-G | FEV1_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs886424 | 6 | 1.55E-04 | -7.814 | -14.2565 | HLA-A | FEV1FVC_cis | T_C | 22688191 | Bipolar disorder and schizophrenia | 9.00E-07 | 1.37 |
| rs2524005 | 6 | 8.77E-04 | 5.336 | -7.0222 | C6orf12 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -6.843 | -11.1104 | HCG18 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 10.263 | -23.9853 | HLA-F | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 5.034 | -6.3184 | | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -5.342 | -7.0366 | HLA-G | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 4.095 | -4.3745 | TUBB | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 12.616 | -35.7636 | HCG4P6 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | 5.00E-07 | 1.32 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2524005 | 6 | 8.77E-04 | 4.774 | -5.7433 | | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -4.574 | -5.3201 | HCG8 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 6.306 | -9.5431 | RP3-377H14.5 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -6.875 | -11.2077 | HCG18 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 17.127 | -65.0299 | ZFP57 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -9.622 | -21.19 | HLA-G | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -5.309 | -6.9577 | | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -6.672 | -10.598 | CDSN | FEV1_trans | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 7.73 | -13.9684 | HLA-A | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -6.795 | -10.9653 | HCG2P7 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 4.203 | -4.5794 | SFTA2 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -8.723 | -17.5671 | | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -6.686 | -10.6395 | BTN3A2 | FEV1_trans | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -7.903 | -14.565 | HCG2P7 | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -10.438 | -24.7792 | NA | FEV1_trans | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | 14.942 | -49.7554 | | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -8.366 | -16.2247 | | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs2524005 | 6 | 8.77E-04 | -16.667 | -61.6426 | HLA-A | FEV1_cis | G_A | 22688191 | Bipolar disorder and schizophrenia | | 5.00E-07 | 1.32 |
| rs1864325 | 17 | 3.59E-05 | -34.904 | -266.1894 | | FEV1_trans | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | 8.262 | -15.8439 | KIAA1267 | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -26.735 | -156.734 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -22.26 | -109.0446 | MAPT | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -29.648 | -192.4438 | KIAA1267 | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | 34.399 | -258.5834 | LRRC37A4 | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -30.698 | -206.2181 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -7.895 | -14.5371 | | FEV1_trans | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -16.459 | -60.141 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -39.86 | -346.7067 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -19.131 | -80.8558 | | FEV1_trans | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -12.517 | -35.2199 | PLEKHM1 | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -4.795 | -5.7887 | LRRC37A | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -21.737 | -104.0376 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -22.247 | -108.9187 | MAPT | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -10.293 | -24.1205 | MAPT | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -39.701 | -343.958 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | 41.554 | -376.6726 | LRRC37A4 | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -34.026 | -253.0365 | | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -6.183 | -9.2014 | BRWD1 | FEV1_trans | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -21.784 | -104.4827 | MAPT | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |
| rs1864325 | 17 | 3.59E-05 | -9.803 | -21.9614 | WNT3 | FEV1_cis | T_C | 22504420 | Bone mineral density | | 5.00E-11 | 0.04 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8014204 | 14 | 3.33E-04 | -7.397 | -12.8561 | MLH3 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | -6.67 | -10.5921 | MLH3 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | 12.21 | -33.5608 | KIAA0317 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | 6.063 | -8.8742 | MLH3 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | 7.062 | -11.7848 | MLH3 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | -4.42 | -5.0057 | TMED10 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | 10.679 | -25.894 | RPS6KL1 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs8014204 | 14 | 3.33E-04 | 16.85 | -62.9792 | KIAA0317 | FEV1FVC_cis | A_G | 21490707 | Caffeine consumption | 5.00E-06 | 0.07 |
| rs2187668 | 6 | 2.05E-06 | -6.623 | -10.4535 | RNF5 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 9.985 | -22.7513 | HLA-DQB1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 5.044 | -6.3411 | HLA-DQB2 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 8.741 | -17.6363 | HLA-C | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 4.389 | -4.9436 | NOTCH4 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -8.762 | -17.7171 | ZFP57 | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 5.791 | -8.1551 | HLA-DQB1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -5.404 | -7.1859 | HLA-DPB1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 9.954 | -22.6157 | HLA-DQB1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -5.688 | -7.891 | HLA-DRB1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 4.661 | -5.5021 | HLA-DPA1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -7.936 | -14.6803 | | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 5.539 | -7.5168 | HLA-DQA2 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 6.721 | -10.7436 | APOM | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -15.376 | -52.625 | HLA-DRB3 | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 7.801 | -14.2117 | HLA-A | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 5.14 | -6.5611 | AGPAT1 | FEV1FVC_cis | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -6.471 | -10.0116 | HCG4P6 | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | 6.599 | -10.3831 | BTN3A2 | FEV1FVC_trans | T_C | 17558408 | Celiac disease | 1.00E-19 | 7.04 |
| rs2187668 | 6 | 2.05E-06 | -6.623 | -10.4535 | RNF5 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 9.985 | -22.7513 | HLA-DQB1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 5.044 | -6.3411 | HLA-DQB2 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 8.741 | -17.6363 | HLA-C | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 4.389 | -4.9436 | NOTCH4 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | -8.762 | -17.7171 | ZFP57 | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 5.791 | -8.1551 | HLA-DQB1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | -5.404 | -7.1859 | HLA-DPB1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 9.954 | -22.6157 | HLA-DQB1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | -5.688 | -7.891 | HLA-DRB1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 4.661 | -5.5021 | HLA-DPA1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | -7.936 | -14.6803 | | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 5.539 | -7.5168 | HLA-DQA2 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 6.721 | -10.7436 | APOM | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | -15.376 | -52.625 | HLA-DRB3 | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 7.801 | -14.2117 | HLA-A | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2187668 | 6 | 2.05E-06 | 5.14 | -6.5611 | AGPAT1 | FEV1FVC_cis | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | -6.471 | -10.0116 | HCG4P6 | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs2187668 | 6 | 2.05E-06 | 6.599 | -10.3831 | BTN3A2 | FEV1FVC_trans | T_C | 20190752 | Celiac disease | 1.00E-50 | 6.23 |
| rs652888 | 6 | 2.45E-04 | 4.297 | -4.7616 | HLA-DRB5 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 6.19 | -9.2207 | HCG18 | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 4.036 | -4.2646 | PSORS1C1 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -5.31 | -6.9601 | | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -9.984 | -22.7469 | HLA-DRB3 | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 5.289 | -6.9101 | APOM | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -6.266 | -9.4313 | HCG4P6 | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 9.501 | -20.6822 | HLA-DQB1 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -5.035 | -6.3207 | | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -6.26 | -9.4146 | C6orf12 | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -9.613 | -21.152 | ZFP57 | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 6.165 | -9.1519 | HLA-C | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 9.602 | -21.1056 | HLA-DQB1 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 5.976 | -8.6408 | HLA-DQB1 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 9.605 | -21.1183 | HLA-DQB1 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -5.818 | -8.2251 | RNF5 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -4.142 | -4.4631 | SFTA2 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 7.552 | -13.3679 | HLA-A | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | -7.683 | -13.8085 | | FEV1FVC_trans | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 4.51 | -5.1882 | ATP6V1G2 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 4.342 | -4.8502 | CDSN | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs652888 | 6 | 2.45E-04 | 5.347 | -7.0485 | AGPAT1 | FEV1FVC_cis | G_A | 23760081 | Chronic hepatitis B infection | 7.00E-13 | 1.38 |
| rs1419881 | 6 | 2.53E-04 | 4.778 | -5.7519 | PSORS1C1 | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | 4.888 | -5.992 | | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | 7.054 | -11.7598 | | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | 5.335 | -7.0198 | | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | 6.347 | -9.6585 | HCG4P6 | FEV1_trans | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | -4.192 | -4.5583 | VARS2 | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | 4.674 | -5.5296 | SFTA2 | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | -14.643 | -47.8258 | CDSN | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs1419881 | 6 | 2.53E-04 | 7.022 | -11.6601 | | FEV1_cis | G_A | 23760081 | Chronic hepatitis B infection | 1.00E-18 | 1.37 |
| rs13118928 | 4 | 5.04E-09 | -5.042 | -6.3366 | | FEV1_cis | A_G | 20173748 | Chronic obstructive pulmonary disease | 5.00E-07 | 1.25 |
| rs13118928 | 4 | 1.31E-19 | -5.042 | -6.3366 | | FEV1FVC_cis | A_G | 20173748 | Chronic obstructive pulmonary disease | 5.00E-07 | 1.25 |
| rs13141641 | 4 | 1.40E-08 | -4.211 | -4.5948 | | FEV1_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 8.45E-18 | -5.104 | -6.4781 | | FEV1FVC_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 1.40E-08 | -4.071 | -4.3296 | HHIP | FEV1_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 8.45E-18 | -4.211 | -4.5948 | | FEV1FVC_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 1.40E-08 | -4.095 | -4.3745 | HHIP | FEV1_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 8.45E-18 | -4.095 | -4.3745 | HHIP | FEV1FVC_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 8.45E-18 | -4.071 | -4.3296 | HHIP | FEV1FVC_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs13141641 | 4 | 1.40E-08 | -5.104 | -6.4781 | | FEV1_cis | T_C | 22080838 | Chronic obstructive pulmonary disease | 3.00E-07 | 1.32 |
| rs1828591 | 4 | 1.44E-19 | -5.092 | -6.4506 | | FEV1FVC_cis | A_G | 19300482 | Chronic obstructive pulmonary disease | 1.00E-07 | 1.38 |
| rs1828591 | 4 | 4.86E-09 | -5.092 | -6.4506 | | FEV1_cis | A_G | 19300482 | Chronic obstructive pulmonary disease | 1.00E-07 | 1.38 |
| rs13180 | 15 | 1.97E-04 | 4.298 | -4.7636 | IREB2 | FEV1_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 2.00E-08 | 1.3 |
| rs13180 | 15 | 1.55E-05 | -11.807 | -31.4447 | | FEV1FVC_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 2.00E-08 | 1.3 |
| rs13180 | 15 | 1.55E-05 | 4.298 | -4.7636 | IREB2 | FEV1FVC_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 2.00E-08 | 1.3 |
| rs13180 | 15 | 1.97E-04 | -11.807 | -31.4447 | | FEV1_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 2.00E-08 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | 16.228 | -58.4952 | | FEV1FVC_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs8034191 | 15 | 2.07E-05 | -6.679 | -10.6187 | PSMA4 | FEV1_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8034191 | 15 | 9.65E-06 | -5.697 | -7.9139 | | FEV1FVC_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs8034191 | 15 | 9.65E-06 | -6.679 | -10.6187 | PSMA4 | FEV1FVC_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs8034191 | 15 | 2.07E-05 | 10.413 | -24.665 | CHRNA5 | FEV1_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs8034191 | 15 | 9.65E-06 | 10.413 | -24.665 | CHRNA5 | FEV1FVC_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs8034191 | 15 | 2.07E-05 | -5.697 | -7.9139 | | FEV1_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs8034191 | 15 | 2.07E-05 | 16.228 | -58.4952 | | FEV1_cis | C_T | 19300482 | Chronic obstructive pulmonary disease | 1.00E-10 | 1.4 |
| rs7671167 | 4 | 1.27E-09 | 4.139 | -4.4574 | FAM13A1 | FEV1FVC_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 1.00E-11 | 1.32 |
| rs7671167 | 4 | 1.27E-09 | 4.739 | -5.668 | FAM13A1 | FEV1FVC_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 1.00E-11 | 1.32 |
| rs7671167 | 4 | 1.27E-09 | 4.662 | -5.5042 | | FEV1FVC_cis | C_T | 20173748 | Chronic obstructive pulmonary disease | 1.00E-11 | 1.32 |
| rs2071278 | 6 | 1.66E-04 | 4.135 | -4.4498 | BAT2 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 5.075 | -6.4117 | HLA-DQB2 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 6.528 | -10.1762 | APOM | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 5.075 | -6.4117 | HLA-DQB2 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 4.582 | -5.3367 | HLA-DPA1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -7.9 | -14.5545 | ZFP57 | FEV1_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -7.535 | -13.3113 | | FEV1FVC_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 4.651 | -5.4811 | | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 4.135 | -4.4498 | BAT2 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 8.313 | -16.0301 | HLA-DQB1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 6.061 | -8.8688 | AGPAT1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 4.316 | -4.7989 | AGPAT1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 5.556 | -7.559 | HLA-DQB1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -7.388 | -12.8267 | | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 6.061 | -8.8688 | AGPAT1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -4.757 | -5.7067 | HLA-DPB1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -7.819 | -14.2737 | | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 6.91 | -11.3146 | HLA-A | FEV1FVC_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -4.757 | -5.7067 | HLA-DPB1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -6.834 | -11.0831 | RNF5 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 5.031 | -6.3116 | NOTCH4 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 4.582 | -5.3367 | HLA-DPA1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 8.313 | -16.0301 | HLA-DQB1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -4.785 | -5.767 | MICB | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 5.556 | -7.559 | HLA-DQB1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 8.35 | -16.1658 | HLA-DQB1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 7.958 | -14.7574 | BTN3A2 | FEV1FVC_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -6.879 | -11.2199 | HCG4P6 | FEV1FVC_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -7.388 | -12.8267 | | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -7.9 | -14.5545 | ZFP57 | FEV1FVC_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 6.528 | -10.1762 | APOM | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -11.26 | -28.6845 | HLA-DRB3 | FEV1_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 8.291 | -15.9496 | HLA-DQB1 | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -7.535 | -13.3113 | | FEV1_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 7.958 | -14.7574 | BTN3A2 | FEV1_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -11.26 | -28.6845 | HLA-DRB3 | FEV1FVC_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 4.651 | -5.4811 | | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -7.819 | -14.2737 | | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -4.785 | -5.767 | MICB | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 5.031 | -6.3116 | NOTCH4 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 8.35 | -16.1658 | HLA-DQB1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2071278 | 6 | 1.66E-04 | 6.91 | -11.3146 | HLA-A | FEV1_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | -6.834 | -11.0831 | RNF5 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 4.316 | -4.7989 | AGPAT1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | 6.749 | -10.8272 | HLA-C | FEV1_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 6.749 | -10.8272 | HLA-C | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 1.66E-04 | -6.879 | -11.2199 | HCG4P6 | FEV1_trans | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2071278 | 6 | 8.30E-06 | 8.291 | -15.9496 | HLA-DQB1 | FEV1FVC_cis | G_A | 23028341 | Complement C3 and C4 levels | 4.00E-72 | 0.13 |
| rs2229238 | 1 | 1.93E-04 | 5.448 | -7.2929 | NUP210L | FEV1FVC_cis | C_T | 22319020 | Coronary heart disease | 7.00E-07 | 1.45 |
| rs2229238 | 1 | 1.93E-04 | -7.655 | -13.7137 | UBE2Q1 | FEV1FVC_cis | C_T | 22319020 | Coronary heart disease | 7.00E-07 | 1.45 |
| rs2229238 | 1 | 1.93E-04 | -9.748 | -21.7255 | TDRD10 | FEV1FVC_cis | C_T | 22319020 | Coronary heart disease | 7.00E-07 | 1.45 |
| rs12037222 | 1 | 1.54E-04 | -6.411 | -9.8399 | OXCT2 | FEV1FVC_cis | A_G | 21300955 | C-reactive protein | 6.00E-11 | 0.05 |
| rs12037222 | 1 | 1.54E-04 | -6.985 | -11.5454 | | FEV1FVC_cis | A_G | 21300955 | C-reactive protein | 6.00E-11 | 0.05 |
| rs12037222 | 1 | 1.54E-04 | -4.871 | -5.9545 | | FEV1FVC_cis | A_G | 21300955 | C-reactive protein | 6.00E-11 | 0.05 |
| rs12037222 | 1 | 1.54E-04 | 5.951 | -8.5743 | PABPC4 | FEV1FVC_cis | A_G | 21300955 | C-reactive protein | 6.00E-11 | 0.05 |
| rs9469220 | 6 | 8.12E-05 | 9.494 | -20.653 | HLA-DQB1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | -7.309 | -12.57 | HLA-DRB1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 9.341 | -20.0203 | HLA-DQB1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 9.005 | -18.6662 | HLA-DRB3 | FEV1FVC_trans | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 5.183 | -6.6609 | HLA-DOB | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 6.017 | -8.7504 | TAP2 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 7.011 | -11.6259 | HLA-DRB5 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | -5.175 | -6.6422 | HLA-DQA2 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 4.708 | -5.6018 | HLA-DRB1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | -8.299 | -15.9788 | HLA-C | FEV1FVC_trans | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 9.51 | -20.7197 | HLA-DQB1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 11.67 | -30.7413 | HLA-DQB1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | -5.892 | -8.4184 | TAP2 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 11.979 | -32.3393 | HLA-DQB2 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 4.885 | -5.9854 | AGPAT1 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | -5.639 | -7.7669 | | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 6.179 | -9.1904 | ZFP57 | FEV1FVC_trans | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs9469220 | 6 | 8.12E-05 | 13.302 | -39.6471 | HLA-DQB2 | FEV1FVC_cis | A_G | 17554300 | Crohn's disease | 2.00E-06 | 1.14 |
| rs7765379 | 6 | 8.99E-05 | -5.464 | -7.3321 | HLA-DRB6 | FEV1FVC_cis | G_T | 23266558 | Crohn's disease | 9.00E-59 | 1.93 |
| rs7765379 | 6 | 8.99E-05 | -7.342 | -12.6769 | HLA-DQA2 | FEV1FVC_cis | G_T | 23266558 | Crohn's disease | 9.00E-59 | 1.93 |
| rs7765379 | 6 | 8.99E-05 | -4.069 | -4.3259 | HLA-DPA1 | FEV1FVC_cis | G_T | 23266558 | Crohn's disease | 9.00E-59 | 1.93 |
| rs7765379 | 6 | 8.99E-05 | 5.044 | -6.3411 | HLA-DQB1 | FEV1FVC_cis | G_T | 23266558 | Crohn's disease | 9.00E-59 | 1.93 |
| rs611744 | 8 | 4.96E-04 | 6.461 | -9.9829 | | FEV1_cis | A_G | 21732829 | Dupuytren's disease | 8.00E-15 | 1.33 |
| rs611744 | 8 | 4.96E-04 | 17.641 | -68.9232 | EIF3E | FEV1_cis | A_G | 21732829 | Dupuytren's disease | 8.00E-15 | 1.33 |
| rs6457617 | 6 | 6.99E-04 | -6.78 | -10.9202 | HLA-DQB2 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | 6.367 | -9.715 | HLA-DRB4 | FEV1FVC_trans | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | -6.804 | -10.9925 | HLA-DQB2 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | -9.9 | -22.3806 | HLA-DQB1 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | -10.077 | -23.156 | HLA-DQB1 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | -9.377 | -20.1683 | HLA-DRB5 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | 7.243 | -12.3577 | HLA-DRB6 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs6457617 | 6 | 6.99E-04 | -10.042 | -23.0016 | HLA-DQB1 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | -11.217 | -28.473 | HLA-DQB1 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | -9.658 | -21.3423 | HLA-DRB3 | FEV1FVC_trans | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs6457617 | 6 | 6.99E-04 | 6.159 | -9.1355 | HLA-DQA2 | FEV1FVC_cis | C_T | 21841780 | Graves' disease | 7.00E-33 | 1.4 |
| rs4660293 | 1 | 1.74E-04 | -5.335 | -7.0198 | PABPC4 | FEV1FVC_cis | A_G | 20686565 | HDL cholesterol | 4.00E-10 | 0.48 |
| rs4660293 | 1 | 1.74E-04 | 6.185 | -9.2069 | OXCT2 | FEV1FVC_cis | A_G | 20686565 | HDL cholesterol | 4.00E-10 | 0.48 |
| rs4660293 | 1 | 1.74E-04 | 4.836 | -5.8779 | | FEV1FVC_cis | A_G | 20686565 | HDL cholesterol | 4.00E-10 | 0.48 |
| rs4660293 | 1 | 1.74E-04 | 7.041 | -11.7193 | | FEV1FVC_cis | A_G | 20686565 | HDL cholesterol | 4.00E-10 | 0.48 |
| rs563519 | 11 | 4.47E-04 | -8.26 | -15.8366 | RPUSD4 | FEV1_cis | C_T | 20445134 | Heart failure | 3.00E-06 | 1.45 |
| rs3738814 | 1 | 1.82E-04 | -6.854 | -11.1438 | | FEV1FVC_cis | G_A | 20189936 | Height | 2.00E-07 | 0.06 |
| rs3738814 | 1 | 1.82E-04 | 5.78 | -8.1267 | MFAP2 | FEV1FVC_cis | G_A | 20189936 | Height | 2.00E-07 | 0.06 |
| rs3738814 | 1 | 1.82E-04 | 5.25 | -6.8179 | PADI2 | FEV1FVC_cis | G_A | 20189936 | Height | 2.00E-07 | 0.06 |
| rs6855629 | 4 | 1.77E-05 | -5.801 | -8.181 | PPA2 | FEV1_cis | A_G | 23563607 | Height | 2.00E-08 | 1.14 |
| rs6855629 | 4 | 8.31E-05 | -5.801 | -8.181 | PPA2 | FEV1FVC_cis | A_G | 23563607 | Height | 2.00E-08 | 1.14 |
| rs6855629 | 4 | 8.31E-05 | -6.078 | -8.9147 | PPA2 | FEV1FVC_cis | A_G | 23563607 | Height | 2.00E-08 | 1.14 |
| rs6855629 | 4 | 1.77E-05 | -6.078 | -8.9147 | PPA2 | FEV1_cis | A_G | 23563607 | Height | 2.00E-08 | 1.14 |
| rs1043515 | 17 | 1.22E-04 | 5.948 | -8.5663 | PSMB3 | FEV1FVC_cis | G_A | 20881960 | Height | 3.00E-10 | 0.02 |
| rs1043515 | 17 | 1.22E-04 | 5.19 | -6.6772 | PIP4K2B | FEV1FVC_cis | G_A | 20881960 | Height | 3.00E-10 | 0.02 |
| rs1043515 | 17 | 1.22E-04 | 5.312 | -6.9649 | PIP4K2B | FEV1FVC_cis | G_A | 20881960 | Height | 3.00E-10 | 0.02 |
| rs1043515 | 17 | 1.22E-04 | -4.171 | -4.5182 | PIP4K2B | FEV1FVC_cis | G_A | 20881960 | Height | 3.00E-10 | 0.02 |
| rs10512248 | 9 | 9.27E-05 | 4.394 | -4.9536 | PTCH1 | FEV1FVC_cis | G_T | 18391952 | Height | 4.00E-11 | 0.05 |
| rs2834442 | 21 | 9.36E-04 | -4.068 | -4.3241 | C21orf82 | FEV1FVC_cis | T_A | 20881960 | Height | 5.00E-12 | 0.03 |
| rs2834442 | 21 | 9.36E-04 | -5.723 | -7.9802 | MRPS6 | FEV1FVC_cis | T_A | 20881960 | Height | 5.00E-12 | 0.03 |
| rs2834442 | 21 | 9.36E-04 | -4.715 | -5.6167 | KCNE2 | FEV1FVC_cis | T_A | 20881960 | Height | 5.00E-12 | 0.03 |
| rs2834442 | 21 | 9.36E-04 | -5.837 | -8.2745 | C21orf82 | FEV1FVC_cis | T_A | 20881960 | Height | 5.00E-12 | 0.03 |
| rs2247056 | 6 | 9.20E-04 | -4.726 | -5.6402 | HLA-C | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | 7.947 | -14.7188 | | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -9.237 | -19.596 | HCG27 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -6.324 | -9.5937 | OR13C3 | FEV1FVC_trans | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -12.695 | -36.2005 | PSORS1C1 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -5.254 | -6.8273 | | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -8.859 | -18.0929 | HCG27 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -8.035 | -15.0288 | PSORS1C3 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -11.546 | -30.1116 | | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | 8.136 | -15.3888 | | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -7.972 | -14.8065 | HCG18 | FEV1FVC_trans | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -7.061 | -11.7817 | HLA-G | FEV1FVC_trans | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -5.781 | -8.1293 | ATP6V1G2 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -4.795 | -5.7887 | HLA-C | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -6.202 | -9.2538 | HLA-B | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | 7.993 | -14.8804 | | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -6.646 | -10.5212 | VARS2 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | 6.241 | -9.3617 | CDSN | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -23.259 | -118.938 | HLA-C | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -7.629 | -13.626 | HCG18 | FEV1FVC_trans | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | -4.485 | -5.1372 | | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2247056 | 6 | 9.20E-04 | 4.759 | -5.711 | SFTA2 | FEV1FVC_cis | C_T | 23563607 | Height | 4.00E-12 | 1.18 |
| rs2284746 | 1 | 2.47E-09 | 5.216 | -6.738 | MFAP2 | FEV1FVC_cis | C_G | 23563607 | Height | 5.00E-15 | 1.17 |
| rs2284746 | 1 | 2.47E-09 | 6.339 | -9.6359 | PADI2 | FEV1FVC_cis | C_G | 23563607 | Height | 5.00E-15 | 1.17 |
| rs2284746 | 1 | 2.47E-09 | -6.004 | -8.7155 | | FEV1FVC_cis | C_G | 23563607 | Height | 5.00E-15 | 1.17 |
| rs6457620 | 6 | 2.92E-04 | -10.123 | -23.3597 | HLA-DQB1 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | -6.836 | -11.0892 | HLA- | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB2 | | | | | | |
| rs6457620 | 6 | 2.92E-04 | -11.236 | -28.5664 | HLA-DQB1 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | -9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | 6.208 | -9.2703 | HLA-DQA2 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | -9.376 | -20.1642 | HLA-DRB5 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | -10.152 | -23.4886 | HLA-DQB1 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | -6.796 | -10.9683 | HLA-DQB2 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | -9.645 | -21.2873 | HLA-DRB3 | FEV1FVC_trans | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | 7.348 | -12.6964 | HLA-DRB6 | FEV1FVC_cis | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs6457620 | 6 | 2.92E-04 | 6.447 | -9.9428 | HLA-DRB4 | FEV1FVC_trans | G_C | 20881960 | Height | 2.00E-16 | 0.03 |
| rs2284746 | 1 | 2.47E-09 | 5.216 | -6.738 | MFAP2 | FEV1FVC_cis | C_G | 20881960 | Height | 4.00E-29 | 0.04 |
| rs2284746 | 1 | 2.47E-09 | 6.339 | -9.6359 | PADI2 | FEV1FVC_cis | C_G | 20881960 | Height | 4.00E-29 | 0.04 |
| rs2284746 | 1 | 2.47E-09 | -6.004 | -8.7155 | | FEV1FVC_cis | C_G | 20881960 | Height | 4.00E-29 | 0.04 |
| rs3130544 | 6 | 1.04E-04 | 4.446 | -5.0581 | PSORS1C3 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 6.758 | -10.8542 | HCG18 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -8.778 | -17.7788 | | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -4.411 | -4.9876 | MICB | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -12.63 | -35.8408 | HLA-DRB3 | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 6.319 | -9.5796 | APOM | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 5.3 | -6.9363 | VARS2 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -12.63 | -35.8408 | HLA-DRB3 | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 8.421 | -16.428 | BTN3A2 | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 4.068 | -4.3241 | | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 4.068 | -4.3241 | | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 6.711 | -10.7138 | PSORS1C1 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 4.523 | -5.2149 | BAT2 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 4.446 | -5.0581 | PSORS1C3 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 6.758 | -10.8542 | HCG18 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -9.011 | -18.69 | | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -6.178 | -9.1876 | C6orf12 | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -10.696 | -25.9736 | ZFP57 | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 6.319 | -9.5796 | APOM | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -9.845 | -22.1424 | | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -6.453 | -9.96 | SFTA2 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 6.988 | -11.5547 | CDSN | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 8.313 | -16.0301 | HLA-A | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -6.936 | -11.3943 | TUBB | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 4.523 | -5.2149 | BAT2 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 6.454 | -9.9628 | HCG18 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -9.011 | -18.69 | | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -9.845 | -22.1424 | | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 6.454 | -9.9628 | HCG18 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -6.657 | -10.5537 | HLA-A | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 8.313 | -16.0301 | HLA-A | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 5.738 | -8.0186 | | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -6.936 | -11.3943 | TUBB | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 11.246 | -28.6156 | HLA-C | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -6.657 | -10.5537 | HLA-A | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -10.696 | -25.9736 | ZFP57 | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 5.3 | -6.9363 | VARS2 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -6.831 | -11.074 | HCG4P6 | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -6.453 | -9.96 | SFTA2 | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3130544 | 6 | 1.07E-04 | 5.738 | -8.0186 |  | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 11.246 | -28.6156 | HLA-C | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 8.421 | -16.428 | BTN3A2 | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -6.831 | -11.074 | HCG4P6 | FEV1_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | 6.711 | -10.7138 | PSORS1C1 | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | -8.778 | -17.7788 |  | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -6.178 | -9.1876 | C6orf12 | FEV1FVC_trans | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.04E-04 | -4.411 | -4.9876 | MICB | FEV1FVC_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs3130544 | 6 | 1.07E-04 | 6.988 | -11.5547 | CDSN | FEV1_cis | A_C | 23263863 | Hematology traits | 5.00E-07 | 0.02 |
| rs389884 | 6 | 4.25E-05 | -13.236 | -39.2647 | HLA-DRB3 | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -7.831 | -14.3152 |  | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -13.236 | -39.2647 | HLA-DRB3 | FEV1FVC_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -10.181 | -23.6179 | ZFP57 | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -7.906 | -14.5755 |  | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -6.1 | -8.9744 | RNF5 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -6.377 | -9.7433 | HCG4P6 | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 4.097 | -4.3783 | HCP5 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 5.307 | -6.9529 | NOTCH4 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 4.534 | -5.2375 | HLA-DQA2 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -4.208 | -4.589 | MICB | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 8.591 | -17.0644 | HLA-DQB1 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -8.457 | -16.5617 |  | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 6.287 | -9.4899 | HCG18 | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 8.479 | -16.6437 | HLA-A | FEV1FVC_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 4.097 | -4.3783 | HCP5 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 5.932 | -8.5239 | PSORS1C1 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 5.307 | -6.9529 | NOTCH4 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -10.181 | -23.6179 | ZFP57 | FEV1FVC_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 8.681 | -17.4064 | HLA-DQB1 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 8.643 | -17.2616 | HLA-DQB1 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 8.643 | -17.2616 | HLA-DQB1 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 5.106 | -6.4827 | AGPAT1 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 4.932 | -6.0894 |  | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 7.364 | -12.7484 | APOM | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | -6.176 | -9.1821 | TUBB | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 4.932 | -6.0894 |  | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 8.681 | -17.4064 | HLA-DQB1 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 10.306 | -24.1791 | HLA-C | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 6.287 | -9.4899 | HCG18 | FEV1FVC_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -4.208 | -4.589 | MICB | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 10.306 | -24.1791 | HLA-C | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 8.479 | -16.6437 | HLA-A | FEV1_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 5.932 | -8.5239 | PSORS1C1 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 8.356 | -16.1879 | BTN3A2 | FEV1FVC_trans | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 4.534 | -5.2375 | HLA-DQA2 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 4.84 | -5.8866 | HLA-DQB1 | FEV1_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 4.893 | -6.003 | CDSN | FEV1FVC_cis | G_A | 23263863 | Hematology traits | 2.00E-08 | 0.03 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| rs389884 | 6 | 2.40E-06 | -6.176 | -9.1821 | TUBB | FEV1FVC_trans | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 5.106 | -6.4827 | AGPAT1 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -8.457 | -16.5617 | | FEV1FVC_trans | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 8.356 | -16.1879 | BTN3A2 | FEV1_trans | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -6.377 | -9.7433 | HCG4P6 | FEV1FVC_trans | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 4.91 | -6.0406 | BAT2 | FEV1_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 4.893 | -6.003 | CDSN | FEV1_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -7.831 | -14.3152 | | FEV1FVC_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 7.364 | -12.7484 | APOM | FEV1_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -7.906 | -14.5755 | | FEV1FVC_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 4.91 | -6.0406 | BAT2 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 4.25E-05 | 8.591 | -17.0644 | HLA-DQB1 | FEV1_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | -6.1 | -8.9744 | RNF5 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs389884 | 6 | 2.40E-06 | 4.84 | -5.8866 | HLA-DQB1 | FEV1FVC_cis | G_A | 23263863 | Hematology traits | | 2.00E-08 | 0.03 |
| rs9357152 | 6 | 1.31E-04 | -7.753 | -14.047 | HLA-DQB1 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9357152 | 6 | 1.31E-04 | -4.037 | -4.2665 | AGPAT1 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9357152 | 6 | 1.31E-04 | -7.545 | -13.3446 | HLA-DQB2 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9357152 | 6 | 1.31E-04 | -8.544 | -16.8872 | HLA-DQB2 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9357152 | 6 | 1.31E-04 | -5.925 | -8.5054 | AGPAT1 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9357152 | 6 | 1.31E-04 | 5.015 | -6.2754 | HLA-DRB6 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9357152 | 6 | 1.31E-04 | -6.316 | -9.5712 | HLA-DRB1 | FEV1FVC_cis | A_G | 21896673 | HPV seropositivity | | 1.00E-14 | NR |
| rs9469220 | 6 | 8.12E-05 | 9.494 | -20.653 | HLA-DQB1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | -7.309 | -12.57 | HLA-DRB1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 9.341 | -20.0203 | HLA-DQB1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 9.005 | -18.6662 | HLA-DRB3 | FEV1FVC_trans | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 5.183 | -6.6609 | HLA-DOB | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 6.017 | -8.7504 | TAP2 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 7.011 | -11.6259 | HLA-DRB5 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | -5.175 | -6.6422 | HLA-DQA2 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 4.708 | -5.6018 | HLA-DRB1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | -8.299 | -15.9788 | HLA-C | FEV1FVC_trans | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 9.51 | -20.7197 | HLA-DQB1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 11.67 | -30.7413 | HLA-DQB1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | -5.892 | -8.4184 | TAP2 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 11.979 | -32.3393 | HLA-DQB2 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 4.885 | -5.9854 | AGPAT1 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | -5.639 | -7.7669 | | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 6.179 | -9.1904 | ZFP57 | FEV1FVC_trans | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs9469220 | 6 | 8.12E-05 | 13.302 | -39.6471 | HLA-DQB2 | FEV1FVC_cis | A_G | 23146381 | IgE levels | | 2.00E-07 | 0.09 |
| rs2571391 | 6 | 3.18E-04 | -11.925 | -32.0571 | HCG4P6 | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 4.697 | -5.5784 | | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | -4.6 | -5.3742 | | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | -7.419 | -12.9281 | ZFP57 | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 10.176 | -23.5955 | HLA-G | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | -4.403 | -4.9716 | HCG18 | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 6.03 | -8.7853 | RP3- | FEV1FVC_cis | A_C | 22075330 | IgE levels | | 1.00E-15 | 0.06 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | 377H14.5 | | | | | | |
| rs2571391 | 6 | 3.18E-04 | 5.34 | -7.0318 | HCG18 | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 13.561 | -41.1662 | HCG2P7 | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 6.405 | -9.8228 | | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | -6.552 | -10.2459 | RP3-377H14.5 | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 8.946 | -18.4334 | HLA-G | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 4.35 | -4.866 | RNF39 | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 12.039 | -32.6544 | HCG2P7 | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | -9.615 | -21.1605 | HLA-F | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | -4.152 | -4.482 | | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs2571391 | 6 | 3.18E-04 | 11.202 | -28.3994 | HLA-A | FEV1FVC_cis | A_C | 22075330 | IgE levels | 1.00E-15 | 0.06 |
| rs592229 | 6 | 2.47E-04 | -5.727 | -7.9905 | HLA-DQB2 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.612 | -5.3992 | AGPAT1 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.864 | -5.9392 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 7.217 | -12.2745 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 5.517 | -7.4624 | HLA-DRB6 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 7.858 | -14.4086 | PSORS1C1 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 6.414 | -9.8485 | HLA-DRB4 | FEV1FVC_trans | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.346 | -4.8581 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.143 | -4.465 | HLA-C | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.258 | -4.6856 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 11.623 | -30.5019 | HLA-C | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -8.107 | -15.285 | HLA-DRB5 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -5.154 | -6.5935 | HLA-DQB2 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -5.851 | -8.311 | AGPAT1 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.913 | -6.0472 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.27 | -4.7089 | HLA-B | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.621 | -5.4181 | CDSN | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.885 | -5.9854 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 5.395 | -7.1642 | HLA-DQA2 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 9.00E-06 | 0.15 |
| rs722599 | 14 | 5.33E-04 | 6.973 | -11.5083 | RPS6KL1 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | -7.188 | -12.1821 | MLH3 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | 11.186 | -28.321 | KIAA0317 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | 13.638 | -41.6234 | KIAA0317 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | 6.53 | -10.182 | MLH3 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | -6.585 | -10.3421 | MLH3 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | 4.282 | -4.7323 | YLPM1 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs722599 | 14 | 5.33E-04 | 7.47 | -13.0959 | MLH3 | FEV1FVC_cis | C_T | 23382691 | IgG glycosylation | 8.00E-06 | 0.14 |
| rs592229 | 6 | 2.47E-04 | -5.727 | -7.9905 | HLA-DQB2 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.612 | -5.3992 | AGPAT1 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.864 | -5.9392 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 7.217 | -12.2745 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 5.517 | -7.4624 | HLA-DRB6 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 7.858 | -14.4086 | PSORS1C1 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 6.414 | -9.8485 | HLA-DRB4 | FEV1FVC_trans | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.346 | -4.8581 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.143 | -4.465 | HLA-C | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.258 | -4.6856 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 11.623 | -30.5019 | HLA-C | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -8.107 | -15.285 | HLA-DRB5 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -5.154 | -6.5935 | HLA-DQB2 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -5.851 | -8.311 | AGPAT1 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs592229 | 6 | 2.47E-04 | -4.913 | -6.0472 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 4.27 | -4.7089 | HLA-B | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.621 | -5.4181 | CDSN | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | -4.885 | -5.9854 | | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs592229 | 6 | 2.47E-04 | 5.395 | -7.1642 | HLA-DQA2 | FEV1FVC_cis | G_T | 23382691 | IgG glycosylation | 4.00E-06 | 0.15 |
| rs2187668 | 6 | 2.05E-06 | -6.623 | -10.4535 | RNF5 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 9.985 | -22.7513 | HLA-DQB1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 5.044 | -6.3411 | HLA-DQB2 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 8.741 | -17.6363 | HLA-C | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 4.389 | -4.9436 | NOTCH4 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | -8.762 | -17.7171 | ZFP57 | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 5.791 | -8.1551 | HLA-DQB1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | -5.404 | -7.1859 | HLA-DPB1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 9.954 | -22.6157 | HLA-DQB1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | -5.688 | -7.891 | HLA-DRB1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 4.661 | -5.5021 | HLA-DPA1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | -7.936 | -14.6803 | | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 5.539 | -7.5168 | HLA-DQA2 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 6.721 | -10.7436 | APOM | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | -15.376 | -52.625 | HLA-DRB3 | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 7.801 | -14.2117 | HLA-A | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 5.14 | -6.5611 | AGPAT1 | FEV1FVC_cis | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | -6.471 | -10.0116 | HCG4P6 | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2187668 | 6 | 2.05E-06 | 6.599 | -10.3831 | BTN3A2 | FEV1FVC_trans | T_C | 20694011 | Immunoglobulin A | 2.00E-33 | 2.53 |
| rs2609255 | 4 | 8.99E-07 | 6.866 | -11.1803 | FAM13A1 | FEV1FVC_cis | G_T | 23583980 | Interstitial lung disease | 2.00E-11 | 1.29 |
| rs2609255 | 4 | 8.99E-07 | 6.488 | -10.0606 | | FEV1FVC_cis | G_T | 23583980 | Interstitial lung disease | 2.00E-11 | 1.29 |
| rs2609255 | 4 | 8.99E-07 | 6.12 | -9.0288 | FAM13A1 | FEV1FVC_cis | G_T | 23583980 | Interstitial lung disease | 2.00E-11 | 1.29 |
| rs1981997 | 17 | 6.72E-05 | -4.627 | -5.4306 | LRRC37A | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -30.372 | -201.8903 | KIAA1267 | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -22.175 | -108.2228 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -35.722 | -278.7445 | | FEV1_trans | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -10.545 | -25.2711 | MAPT | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -34.359 | -257.9857 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -22.085 | -107.356 | MAPT | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | 43.159 | -406.2134 | LRRC37A4 | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -19.509 | -84.0359 | | FEV1_trans | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | 7.959 | -14.7609 | KIAA1267 | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -8.305 | -16.0008 | | FEV1_trans | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -12.586 | -35.5984 | PLEKHM1 | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -40.603 | -359.6966 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | - | - | MAPT | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 21.678 | 103.4802 | | | | | | | |
| rs1981997 | 17 | 6.72E-05 | -40.802 | -363.2164 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -17.126 | -65.0224 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -22.303 | -109.4615 | MAPT | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -9.764 | -21.794 | WNT3 | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | 35.653 | -277.6743 | LRRC37A4 | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -31.574 | -218.0757 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs1981997 | 17 | 6.72E-05 | -27.27 | -163.0165 | | FEV1_cis | A_G | 23583980 | Interstitial lung disease | 9.00E-14 | 1.41 |
| rs9303525 | 17 | 4.02E-05 | -21.526 | -102.0512 | MAPT | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -30.311 | -201.0856 | KIAA1267 | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | 34.606 | -261.6877 | LRRC37A4 | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -16.971 | -63.8709 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | 4.663 | -5.5064 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -10.586 | -25.4608 | MAPT | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -22.122 | -107.7119 | MAPT | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -31.102 | -211.6453 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -39.986 | -348.8927 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -8.412 | -16.3946 | | FEV1_trans | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | 41.484 | -375.4097 | LRRC37A4 | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -22.052 | -107.0391 | MAPT | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -34.966 | -267.1309 | | FEV1_trans | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -4.532 | -5.2334 | LRRC37A | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -9.852 | -22.1727 | WNT3 | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -27.016 | -160.0183 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -33.912 | -251.3533 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -19.331 | -82.5307 | | FEV1_trans | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -21.949 | -106.0529 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -40.164 | -351.9926 | | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | 7.815 | -14.2599 | KIAA1267 | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs9303525 | 17 | 4.02E-05 | -12.392 | -34.5395 | PLEKHM1 | FEV1_cis | G_A | 22504418 | Intracranial volume | 8.00E-15 | 14.9 |
| rs602875 | 6 | 9.65E-04 | -9.325 | -19.9547 | HLA-DQB1 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -6.66 | -10.5625 | HLA-DRB6 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -9.327 | -19.9629 | HLA-DQB1 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -6.88 | -11.2229 | AGPAT1 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -5.944 | -8.5557 | HLA-DRB5 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -7.947 | -14.7188 | HLA- | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB1 | | | | | | |
| rs602875 | 6 | 9.65E-04 | 9.958 | -22.6332 | HLA-DRB1 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -4.023 | -4.2406 | AGPAT1 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -11.621 | -30.4917 | HLA-DQA2 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -10.569 | -25.3821 | HLA-DRB4 | FEV1FVC_trans | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | 20.758 | -94.9838 | HLA-DRB3 | FEV1FVC_trans | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -10.161 | -23.5287 | HLA-DQB2 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -4.678 | -5.5381 | APOM | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs602875 | 6 | 9.65E-04 | -9.282 | -19.779 | HLA-DQB1 | FEV1FVC_cis | A_G | 20018961 | Leprosy | 5.00E-27 | 1.61 |
| rs4324798 | 6 | 6.53E-04 | -4.262 | -4.6933 | ZNF323 | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 14.937 | -49.7228 | BTN3A2 | FEV1_trans | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 12.242 | -33.7319 | HLA-A | FEV1_trans | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -4.799 | -5.7973 | | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 4.551 | -5.2725 | ZNF187 | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -6.397 | -9.8001 | C6orf12 | FEV1_trans | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -4.289 | -4.746 | RP3-377H14.5 | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -6.878 | -11.2168 | | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 6.909 | -11.3115 | HLA-C | FEV1_trans | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -7.079 | -11.838 | HLA-DRB3 | FEV1_trans | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 5.472 | -7.3517 | | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -4.283 | -4.7343 | ZNF323 | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -5.304 | -6.9458 | HLA-F | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 6.188 | -9.2152 | ZNF389 | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -12.64 | -35.896 | ZFP57 | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -11.058 | -27.6978 | | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | -6.743 | -10.8093 | HCG4P6 | FEV1_trans | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs4324798 | 6 | 6.53E-04 | 4.833 | -5.8713 | | FEV1_cis | A_G | 19836008 | Lung adenocarcinoma | 2.00E-08 | 1.16 |
| rs3117582 | 6 | 4.03E-06 | 8.327 | -16.0814 | | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -7.885 | -14.5023 | HLA-DQB1 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -4.83 | -5.8648 | NOTCH4 | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -10.358 | -24.4146 | HLA-C | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 10.224 | -23.8102 | ZFP57 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 8.361 | -16.2063 | | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -4.883 | -5.981 | AGPAT1 | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 8.704 | -17.4943 | | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -5.191 | -6.6795 | BAT2 | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 6.944 | -11.4189 | HCG4P6 | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -7.833 | -14.3221 | HLA-DQB1 | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 8.361 | -16.2063 | | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 8.327 | -16.0814 | | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -4.913 | -6.0472 | | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -7.521 | -13.2647 | APOM | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 13.186 | -38.9762 | HLA-DRB3 | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -7.81 | -14.2427 | HLA-DQB1 | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -5.977 | -8.6434 | PSORS1C1 | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 4.599 | -5.3721 | MICB | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 6.314 | -9.5656 | TUBB | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -5.191 | -6.6795 | BAT2 | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -7.885 | -14.5023 | HLA- | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB1 | | | | | | |
| rs3117582 | 6 | 1.09E-05 | -7.833 | -14.3221 | HLA-DQB1 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 6.944 | -11.4189 | HCG4P6 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 13.186 | -38.9762 | HLA-DRB3 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -4.913 | -6.0472 | | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -8.688 | -17.4331 | HLA-A | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -10.358 | -24.4146 | HLA-C | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -5.977 | -8.6434 | PSORS1C1 | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 8.704 | -17.4943 | | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -5.232 | -6.7755 | CDSN | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 5.551 | -7.5466 | RNF5 | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 4.599 | -5.3721 | MICB | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 5.551 | -7.5466 | RNF5 | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -8.039 | -15.043 | BTN3A2 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -8.688 | -17.4331 | HLA-A | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -7.521 | -13.2647 | APOM | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -5.232 | -6.7755 | CDSN | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 6.314 | -9.5656 | TUBB | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | -8.039 | -15.043 | BTN3A2 | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 10.224 | -23.8102 | ZFP57 | FEV1FVC_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -7.81 | -14.2427 | HLA-DQB1 | FEV1_trans | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | 5.211 | -6.7262 | SFTA2 | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -4.883 | -5.981 | AGPAT1 | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 1.09E-05 | -4.83 | -5.8648 | NOTCH4 | FEV1_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs3117582 | 6 | 4.03E-06 | 5.211 | -6.7262 | SFTA2 | FEV1FVC_cis | T_G | 19836008 | Lung adenocarcinoma | 5.00E-12 | 1.22 |
| rs1051730 | 15 | 2.22E-05 | 6.88 | -11.2229 | PSMA4 | FEV1_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 1.46E-05 | 5.825 | -8.2433 | | FEV1FVC_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 2.22E-05 | -15.029 | -50.3241 | | FEV1_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 1.46E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1FVC_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 2.22E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 1.46E-05 | 6.88 | -11.2229 | PSMA4 | FEV1FVC_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 2.22E-05 | 5.825 | -8.2433 | | FEV1_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs1051730 | 15 | 1.46E-05 | -15.029 | -50.3241 | | FEV1FVC_cis | G_A | 19836008 | Lung adenocarcinoma | 2.00E-51 | 1.31 |
| rs8034191 | 15 | 9.65E-06 | 16.228 | -58.4952 | | FEV1FVC_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 2.07E-05 | -6.679 | -10.6187 | PSMA4 | FEV1_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 9.65E-06 | -5.697 | -7.9139 | | FEV1FVC_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 9.65E-06 | -6.679 | -10.6187 | PSMA4 | FEV1FVC_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 2.07E-05 | 10.413 | -24.665 | CHRNA5 | FEV1_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 9.65E-06 | 10.413 | -24.665 | CHRNA5 | FEV1FVC_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 2.07E-05 | -5.697 | -7.9139 | | FEV1_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs8034191 | 15 | 2.07E-05 | 16.228 | -58.4952 | | FEV1_cis | C_T | 18780872 | Lung cancer | 1.00E-08 | 1.38 |
| rs3117582 | 6 | 4.03E-06 | 8.327 | -16.0814 | | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.885 | -14.5023 | HLA-DQB1 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -4.83 | -5.8648 | NOTCH4 | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -10.358 | -24.4146 | HLA-C | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 10.224 | -23.8102 | ZFP57 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 8.361 | -16.2063 | | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -4.883 | -5.981 | AGPAT1 | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 8.704 | -17.4943 | | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -5.191 | -6.6795 | BAT2 | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 6.944 | -11.4189 | HCG4P6 | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.833 | -14.3221 | HLA- | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB1 | | | | | | |
| rs3117582 | 6 | 1.09E-05 | 8.361 | -16.2063 | | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 8.327 | -16.0814 | | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -4.913 | -6.0472 | | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.521 | -13.2647 | APOM | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 13.186 | -38.9762 | HLA-DRB3 | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.81 | -14.2427 | HLA-DQB1 | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -5.977 | -8.6434 | PSORS1C1 | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 4.599 | -5.3721 | MICB | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 6.314 | -9.5656 | TUBB | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -5.191 | -6.6795 | BAT2 | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.885 | -14.5023 | HLA-DQB1 | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.833 | -14.3221 | HLA-DQB1 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 6.944 | -11.4189 | HCG4P6 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 13.186 | -38.9762 | HLA-DRB3 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -4.913 | -6.0472 | | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -8.688 | -17.4331 | HLA-A | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -10.358 | -24.4146 | HLA-C | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -5.977 | -8.6434 | PSORS1C1 | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 8.704 | -17.4943 | | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -5.232 | -6.7755 | CDSN | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 5.551 | -7.5466 | RNF5 | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 4.599 | -5.3721 | MICB | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 5.551 | -7.5466 | RNF5 | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -8.039 | -15.043 | BTN3A2 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -8.688 | -17.4331 | HLA-A | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.521 | -13.2647 | APOM | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -5.232 | -6.7755 | CDSN | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 6.314 | -9.5656 | TUBB | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -8.039 | -15.043 | BTN3A2 | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 10.224 | -23.8102 | ZFP57 | FEV1FVC_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.81 | -14.2427 | HLA-DQB1 | FEV1_trans | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 5.211 | -6.7262 | SFTA2 | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -4.883 | -5.981 | AGPAT1 | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -4.83 | -5.8648 | NOTCH4 | FEV1_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 5.211 | -6.7262 | SFTA2 | FEV1FVC_cis | T_G | 18978787 | Lung cancer | 5.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 8.327 | -16.0814 | | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.885 | -14.5023 | HLA-DQB1 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -4.83 | -5.8648 | NOTCH4 | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -10.358 | -24.4146 | HLA-C | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 10.224 | -23.8102 | ZFP57 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 8.361 | -16.2063 | | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -4.883 | -5.981 | AGPAT1 | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 8.704 | -17.4943 | | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -5.191 | -6.6795 | BAT2 | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 6.944 | -11.4189 | HCG4P6 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.833 | -14.3221 | HLA-DQB1 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 8.361 | -16.2063 | | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 8.327 | -16.0814 | | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -4.913 | -6.0472 | | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.521 | -13.2647 | APOM | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3117582 | 6 | 4.03E-06 | 13.186 | -38.9762 | HLA-DRB3 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.81 | -14.2427 | HLA-DQB1 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -5.977 | -8.6434 | PSORS1C1 | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 4.599 | -5.3721 | MICB | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 6.314 | -9.5656 | TUBB | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -5.191 | -6.6795 | BAT2 | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -7.885 | -14.5023 | HLA-DQB1 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.833 | -14.3221 | HLA-DQB1 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 6.944 | -11.4189 | HCG4P6 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 13.186 | -38.9762 | HLA-DRB3 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -4.913 | -6.0472 | | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -8.688 | -17.4331 | HLA-A | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -10.358 | -24.4146 | HLA-C | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -5.977 | -8.6434 | PSORS1C1 | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 8.704 | -17.4943 | | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -5.232 | -6.7755 | CDSN | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 5.551 | -7.5466 | RNF5 | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 4.599 | -5.3721 | MICB | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 5.551 | -7.5466 | RNF5 | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -8.039 | -15.043 | BTN3A2 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -8.688 | -17.4331 | HLA-A | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.521 | -13.2647 | APOM | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -5.232 | -6.7755 | CDSN | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 6.314 | -9.5656 | TUBB | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | -8.039 | -15.043 | BTN3A2 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 10.224 | -23.8102 | ZFP57 | FEV1FVC_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -7.81 | -14.2427 | HLA-DQB1 | FEV1_trans | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | 5.211 | -6.7262 | SFTA2 | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -4.883 | -5.981 | AGPAT1 | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 1.09E-05 | -4.83 | -5.8648 | NOTCH4 | FEV1_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs3117582 | 6 | 4.03E-06 | 5.211 | -6.7262 | SFTA2 | FEV1FVC_cis | T_G | 19654303 | Lung cancer | 4.00E-10 | 1.24 |
| rs1051730 | 15 | 2.22E-05 | 6.88 | -11.2229 | PSMA4 | FEV1_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 1.46E-05 | 5.825 | -8.2433 | | FEV1FVC_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 2.22E-05 | -15.029 | -50.3241 | | FEV1_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 1.46E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1FVC_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 2.22E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 1.46E-05 | 6.88 | -11.2229 | PSMA4 | FEV1FVC_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 2.22E-05 | 5.825 | -8.2433 | | FEV1_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs1051730 | 15 | 1.46E-05 | -15.029 | -50.3241 | | FEV1FVC_cis | G_A | 18978790 | Lung cancer | 1.00E-15 | 1.35 |
| rs8034191 | 15 | 9.65E-06 | 16.228 | -58.4952 | | FEV1FVC_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | -6.679 | -10.6187 | PSMA4 | FEV1_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | -5.697 | -7.9139 | | FEV1FVC_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | -6.679 | -10.6187 | PSMA4 | FEV1FVC_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | 10.413 | -24.665 | CHRNA5 | FEV1_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | 10.413 | -24.665 | CHRNA5 | FEV1FVC_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | -5.697 | -7.9139 | | FEV1_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | 16.228 | -58.4952 | | FEV1_cis | C_T | 18385676 | Lung cancer | 3.00E-18 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | 16.228 | -58.4952 | | FEV1FVC_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | -6.679 | -10.6187 | PSMA4 | FEV1_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | -5.697 | -7.9139 | | FEV1FVC_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | -6.679 | -10.6187 | PSMA4 | FEV1FVC_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | 10.413 | -24.665 | CHRNA5 | FEV1_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8034191 | 15 | 9.65E-06 | 10.413 | -24.665 | CHRNA5 | FEV1FVC_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | -5.697 | -7.9139 | | FEV1_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 2.07E-05 | 16.228 | -58.4952 | | FEV1_cis | C_T | 18385738 | Lung cancer | 5.00E-20 | 1.3 |
| rs8034191 | 15 | 9.65E-06 | 16.228 | -58.4952 | | FEV1FVC_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 2.07E-05 | -6.679 | -10.6187 | PSMA4 | FEV1_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 9.65E-06 | -5.697 | -7.9139 | | FEV1FVC_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 9.65E-06 | -6.679 | -10.6187 | PSMA4 | FEV1FVC_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 2.07E-05 | 10.413 | -24.665 | CHRNA5 | FEV1_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 9.65E-06 | 10.413 | -24.665 | CHRNA5 | FEV1FVC_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 2.07E-05 | -5.697 | -7.9139 | | FEV1_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs8034191 | 15 | 2.07E-05 | 16.228 | -58.4952 | | FEV1_cis | C_T | 19654303 | Lung cancer | 3.00E-26 | 1.29 |
| rs12373124 | 17 | 5.83E-04 | -16.361 | -59.44 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | 7.134 | -12.011 | KIAA1267 | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -4.397 | -4.9596 | LRRC37A | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -10.278 | -24.0528 | MAPT | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -37.281 | -303.4769 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -20.758 | -94.9838 | MAPT | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -30.235 | -200.0853 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -34.355 | -257.9259 | | FEV1_trans | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -20.908 | -96.3441 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -8.449 | -16.5319 | | FEV1_trans | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -12.111 | -33.0345 | PLEKHM1 | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -21.094 | -98.0443 | MAPT | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -37.482 | -306.7424 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -21.4 | -100.8742 | MAPT | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -32.658 | -233.2098 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | 39.525 | -340.9282 | LRRC37A4 | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -29.109 | -185.5588 | KIAA1267 | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -19.003 | -79.793 | | FEV1_trans | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -9.177 | -19.3533 | WNT3 | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | -25.79 | -145.94 | | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs12373124 | 17 | 5.83E-04 | 33.013 | -238.2768 | LRRC37A4 | FEV1_cis | C_T | 22693459 | Male-pattern baldness | 5.00E-10 | 1.33 |
| rs7617480 | 3 | 8.21E-04 | 8.861 | -18.1007 | AMT | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -7.094 | -11.8851 | RHOA | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -24.479 | -131.6069 | | FEV1_trans | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -4.784 | -5.7649 | CCDC51 | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -4.056 | -4.3017 | USP4 | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | 5.919 | -8.4896 | ARIH2 | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -9.965 | -22.6638 | | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -5.061 | -6.3798 | NICN1 | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | -4.469 | -5.1047 | USP4 | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs7617480 | 3 | 8.21E-04 | 6.695 | -10.6662 | | FEV1_cis | A_C | 21102462 | Menarche (age at onset) | 3.00E-08 | 2.4 |
| rs494620 | 6 | 7.08E-04 | -4.541 | -5.2519 | | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs494620 | 6 | 7.08E-04 | -4.741 | -5.6723 | | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs494620 | 6 | 7.08E-04 | -8.473 | -16.6213 | HLA-C | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs494620 | 6 | 7.08E-04 | -6.645 | -10.5182 | PSORS1C1 | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs494620 | 6 | 7.08E-04 | -4.833 | -5.8713 | HLA-DRB6 | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs494620 | 6 | 7.08E-04 | -4.848 | -5.9041 | VARS2 | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs494620 | 6 | 7.08E-04 | -4.058 | -4.3054 | ATP6V1G2 | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs494620 | 6 | 7.08E-04 | 4.377 | -4.9196 | AGPAT1 | FEV1FVC_cis | A_G | 19448619 | Menopause (age at onset) | 5.00E-07 | 0.3 |
| rs1046089 | 6 | 9.82E-04 | 4.373 | -4.9117 | HLA-C | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | -5.049 | -6.3525 | TUBB | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | -7.153 | -12.0711 | HLA-DRB3 | FEV1_trans | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 5.125 | -6.5265 | ATP6V1G2 | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | -5.407 | -7.1932 | | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 7.007 | -11.6135 | LY6G5C | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 4.19 | -4.5545 | APOM | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 4.464 | -5.0945 | BAT4 | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | -5.481 | -7.3737 | | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | -5.205 | -6.7122 | MICB | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 5.833 | -8.2641 | HLA-DRB5 | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 5.4 | -7.1763 | | FEV1_cis | A_G | 23307926 | Menopause (age at onset) | 4.00E-11 | 0.19 |
| rs1046089 | 6 | 9.82E-04 | 4.373 | -4.9117 | HLA-C | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | -5.049 | -6.3525 | TUBB | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | -7.153 | -12.0711 | HLA-DRB3 | FEV1_trans | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | 5.125 | -6.5265 | ATP6V1G2 | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | -5.407 | -7.1932 | | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | 7.007 | -11.6135 | LY6G5C | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | 4.19 | -4.5545 | APOM | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | 4.464 | -5.0945 | BAT4 | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | -5.481 | -7.3737 | | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | -5.205 | -6.7122 | MICB | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | 5.833 | -8.2641 | HLA-DRB5 | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs1046089 | 6 | 9.82E-04 | 5.4 | -7.1763 | | FEV1_cis | A_G | 22267201 | Menopause (age at onset) | 2.00E-16 | 0.21 |
| rs3099844 | 6 | 5.81E-06 | 4.02 | -4.2351 | NOTCH4 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 6.856 | -11.1499 | HLA-DQB1 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -7.979 | -14.8311 | | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 4.181 | -4.5373 | AGPAT1 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -5.801 | -8.181 | MICB | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 6.917 | -11.336 | HLA-DQB1 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 4.02 | -4.2351 | NOTCH4 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -5.827 | -8.2485 | RNF5 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 5.9 | -8.4395 | CDSN | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 9.177 | -19.3533 | HLA-A | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -10.947 | -27.1631 | ZFP57 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -7.274 | -12.4572 | HCG4P6 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 6.784 | -10.9322 | APOM | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 4.651 | -5.4811 | | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -12.634 | -35.8629 | HLA-DRB3 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 4.651 | -5.4811 | | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -7.979 | -14.8311 | | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -8.39 | -16.3132 | | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -10.947 | -27.1631 | ZFP57 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 6.917 | -11.336 | HLA-DQB1 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 4.165 | -4.5067 | PSORS1C3 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3099844 | 6 | 5.81E-06 | -5.491 | -7.3983 | SFTA2 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 4.181 | -4.5373 | AGPAT1 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 4.165 | -4.5067 | PSORS1C3 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 5.9 | -8.4395 | CDSN | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 7.797 | -14.1979 | BTN3A2 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -7.37 | -12.7679 | TUBB | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 4.753 | -5.6981 | BAT2 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -5.801 | -8.181 | MICB | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -5.491 | -7.3983 | SFTA2 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 10.097 | -23.2444 | HLA-C | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -8.037 | -15.0359 | | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 4.965 | -6.163 | PSORS1C1 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 4.753 | -5.6981 | BAT2 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 6.862 | -11.1681 | HLA-DQB1 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 5.083 | -6.43 | | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 10.097 | -23.2444 | HLA-C | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 4.965 | -6.163 | PSORS1C1 | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 9.177 | -19.3533 | HLA-A | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | 6.862 | -11.1681 | HLA-DQB1 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -5.827 | -8.2485 | RNF5 | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 5.083 | -6.43 | | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -12.634 | -35.8629 | HLA-DRB3 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -7.37 | -12.7679 | TUBB | FEV1FVC_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 7.797 | -14.1979 | BTN3A2 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 6.856 | -11.1499 | HLA-DQB1 | FEV1_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -8.39 | -16.3132 | | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | 6.784 | -10.9322 | APOM | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 1.92E-07 | -8.037 | -15.0359 | | FEV1_cis | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs3099844 | 6 | 5.81E-06 | -7.274 | -12.4572 | HCG4P6 | FEV1FVC_trans | A_C | 22399527 | Metabolic syndrome | 2.00E-08 | 0.15 |
| rs11172113 | 12 | 1.36E-06 | -6.632 | -10.48 | STAT6 | FEV1FVC_cis | C_T | 22683712 | Migraine | 3.00E-08 | 1.16 |
| rs11172113 | 12 | 1.36E-06 | 5.705 | -7.9343 | STAT6 | FEV1FVC_cis | C_T | 22683712 | Migraine | 3.00E-08 | 1.16 |
| rs11172113 | 12 | 1.36E-06 | -6.632 | -10.48 | STAT6 | FEV1FVC_cis | C_T | 21666692 | Migraine | 4.00E-09 | 1.11 |
| rs11172113 | 12 | 1.36E-06 | 5.705 | -7.9343 | STAT6 | FEV1FVC_cis | C_T | 21666692 | Migraine | 4.00E-09 | 1.11 |
| rs11172113 | 12 | 1.36E-06 | -6.632 | -10.48 | STAT6 | FEV1FVC_cis | C_T | 23793025 | Migraine | 4.00E-19 | 1.11 |
| rs11172113 | 12 | 1.36E-06 | 5.705 | -7.9343 | STAT6 | FEV1FVC_cis | C_T | 23793025 | Migraine | 4.00E-19 | 1.11 |
| rs11172113 | 12 | 1.36E-06 | -6.632 | -10.48 | STAT6 | FEV1FVC_cis | C_T | 23793025 | Migraine - clinic-based | 1.00E-06 | 1.12 |
| rs11172113 | 12 | 1.36E-06 | 5.705 | -7.9343 | STAT6 | FEV1FVC_cis | C_T | 23793025 | Migraine - clinic-based | 1.00E-06 | 1.12 |
| rs11172113 | 12 | 1.36E-06 | -6.632 | -10.48 | STAT6 | FEV1FVC_cis | C_T | 23793025 | Migraine without aura | 1.00E-10 | 1.15 |
| rs11172113 | 12 | 1.36E-06 | 5.705 | -7.9343 | STAT6 | FEV1FVC_cis | C_T | 23793025 | Migraine without aura | 1.00E-10 | 1.15 |
| rs11755724 | 6 | 1.44E-04 | -5.526 | -7.4846 | RREB1 | FEV1FVC_cis | A_G | 21833088 | Multiple sclerosis | 3.00E-06 | 1.08 |
| rs2040406 | 6 | 1.30E-05 | 5.721 | -7.9751 | APOM | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 9.561 | -20.9332 | HLA-DQB1 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 7.114 | -11.948 | HLA-DQB1 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 8.143 | -15.4139 | HLA-C | FEV1FVC_trans | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 9.555 | -20.908 | HLA-DQB1 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 7.107 | -11.9259 | HLA-DQA2 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | -7.146 | -12.0489 | HLA-DRB1 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 4.154 | -4.4858 | HLA-DRB5 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 6.488 | -10.0606 | HLA-DRB4 | FEV1FVC_trans | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 6.61 | -10.4153 | HLA-DQB2 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2040406 | 6 | 1.30E-05 | -17.824 | -70.337 | HLA-DRB3 | FEV1FVC_trans | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | -7.138 | -12.0237 | ZFP57 | FEV1FVC_trans | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 4.198 | -4.5698 | NOTCH4 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | -6.362 | -9.7008 | RNF5 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 9.556 | -20.9122 | HLA-DQB1 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 4.474 | -5.1148 | HLA-DRB6 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs2040406 | 6 | 1.30E-05 | 5.819 | -8.2277 | AGPAT1 | FEV1FVC_cis | G_A | 20453840 | Multiple sclerosis | 1.00E-20 | 2.05 |
| rs3130544 | 6 | 1.04E-04 | 4.446 | -5.0581 | PSORS1C3 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 6.758 | -10.8542 | HCG18 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -8.778 | -17.7788 | | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -4.411 | -4.9876 | MICB | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -12.63 | -35.8408 | HLA-DRB3 | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 6.319 | -9.5796 | APOM | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 5.3 | -6.9363 | VARS2 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -12.63 | -35.8408 | HLA-DRB3 | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 8.421 | -16.428 | BTN3A2 | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 4.068 | -4.3241 | | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 4.068 | -4.3241 | | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 6.711 | -10.7138 | PSORS1C1 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 4.523 | -5.2149 | BAT2 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 4.446 | -5.0581 | PSORS1C3 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 6.758 | -10.8542 | HCG18 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -9.011 | -18.69 | | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -6.178 | -9.1876 | C6orf12 | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -10.696 | -25.9736 | ZFP57 | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 6.319 | -9.5796 | APOM | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -9.845 | -22.1424 | | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -6.453 | -9.96 | SFTA2 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 6.988 | -11.5547 | CDSN | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 8.313 | -16.0301 | HLA-A | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -6.936 | -11.3943 | TUBB | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 4.523 | -5.2149 | BAT2 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 6.454 | -9.9628 | HCG18 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -9.011 | -18.69 | | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -9.845 | -22.1424 | | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 6.454 | -9.9628 | HCG18 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -6.657 | -10.5537 | HLA-A | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 8.313 | -16.0301 | HLA-A | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 5.738 | -8.0186 | | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -6.936 | -11.3943 | TUBB | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 11.246 | -28.6156 | HLA-C | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -6.657 | -10.5537 | HLA-A | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -10.696 | -25.9736 | ZFP57 | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 5.3 | -6.9363 | VARS2 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -6.831 | -11.074 | HCG4P6 | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -6.453 | -9.96 | SFTA2 | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 5.738 | -8.0186 | | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 11.246 | -28.6156 | HLA-C | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | 8.421 | -16.428 | BTN3A2 | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -6.831 | -11.074 | HCG4P6 | FEV1_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | 6.711 | -10.7138 | PSORS1C1 | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.07E-04 | -8.778 | -17.7788 | | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -6.178 | -9.1876 | C6orf12 | FEV1FVC_trans | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3130544 | 6 | 1.04E-04 | -4.411 | -4.9876 | MICB | FEV1FVC_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |

|  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3130544 | 6 | 1.07E-04 | 6.988 | -11.5547 | CDSN | FEV1_cis | A_C | 23055271 | Myasthenia gravis | 2.00E-90 | 5.64 |
| rs3099844 | 6 | 5.81E-06 | 4.02 | -4.2351 | NOTCH4 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 6.856 | -11.1499 | HLA-DQB1 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -7.979 | -14.8311 |  | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 4.181 | -4.5373 | AGPAT1 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -5.801 | -8.181 | MICB | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 6.917 | -11.336 | HLA-DQB1 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 4.02 | -4.2351 | NOTCH4 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -5.827 | -8.2485 | RNF5 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 5.9 | -8.4395 | CDSN | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 9.177 | -19.3533 | HLA-A | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -10.947 | -27.1631 | ZFP57 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -7.274 | -12.4572 | HCG4P6 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 6.784 | -10.9322 | APOM | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 4.651 | -5.4811 |  | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -12.634 | -35.8629 | HLA-DRB3 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 4.651 | -5.4811 |  | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -7.979 | -14.8311 |  | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -8.39 | -16.3132 |  | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -10.947 | -27.1631 | ZFP57 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 6.917 | -11.336 | HLA-DQB1 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 4.165 | -4.5067 | PSORS1C3 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -5.491 | -7.3983 | SFTA2 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 4.181 | -4.5373 | AGPAT1 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 4.165 | -4.5067 | PSORS1C3 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 5.9 | -8.4395 | CDSN | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 7.797 | -14.1979 | BTN3A2 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -7.37 | -12.7679 | TUBB | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 4.753 | -5.6981 | BAT2 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -5.801 | -8.181 | MICB | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -5.491 | -7.3983 | SFTA2 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 10.097 | -23.2444 | HLA-C | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -8.037 | -15.0359 |  | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 4.965 | -6.163 | PSORS1C1 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 4.753 | -5.6981 | BAT2 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 6.862 | -11.1681 | HLA-DQB1 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 5.083 | -6.43 |  | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 10.097 | -23.2444 | HLA-C | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 4.965 | -6.163 | PSORS1C1 | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 9.177 | -19.3533 | HLA-A | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | 6.862 | -11.1681 | HLA-DQB1 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | -5.827 | -8.2485 | RNF5 | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 5.083 | -6.43 |  | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -12.634 | -35.8629 | HLA-DRB3 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -7.37 | -12.7679 | TUBB | FEV1FVC_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 7.797 | -14.1979 | BTN3A2 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 6.856 | -11.1499 | HLA-DQB1 | FEV1_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -8.39 | -16.3132 |  | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 1.92E-07 | 6.784 | -10.9322 | APOM | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3099844 | 6 | 1.92E-07 | -8.037 | -15.0359 | | FEV1_cis | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs3099844 | 6 | 5.81E-06 | -7.274 | -12.4572 | HCG4P6 | FEV1FVC_trans | A_C | 20662065 | Neonatal lupus | 5.00E-10 | 3.34 |
| rs2187668 | 6 | 2.05E-06 | -6.623 | -10.4535 | RNF5 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 9.985 | -22.7513 | HLA-DQB1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 5.044 | -6.3411 | HLA-DQB2 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 8.741 | -17.6363 | HLA-C | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 4.389 | -4.9436 | NOTCH4 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | -8.762 | -17.7171 | ZFP57 | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 5.791 | -8.1551 | HLA-DQB1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | -5.404 | -7.1859 | HLA-DPB1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 9.954 | -22.6157 | HLA-DQB1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | -5.688 | -7.891 | HLA-DRB1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 4.661 | -5.5021 | HLA-DPA1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | -7.936 | -14.6803 | | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 5.539 | -7.5168 | HLA-DQA2 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 6.721 | -10.7436 | APOM | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | -15.376 | -52.625 | HLA-DRB3 | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 7.801 | -14.2117 | HLA-A | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 5.14 | -6.5611 | AGPAT1 | FEV1FVC_cis | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | -6.471 | -10.0116 | HCG4P6 | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs2187668 | 6 | 2.05E-06 | 6.599 | -10.3831 | BTN3A2 | FEV1FVC_trans | T_C | 21323541 | Nephropathy (idiopathic membranous) | 8.00E-93 | 4.32 |
| rs1051730 | 15 | 2.22E-05 | 6.88 | -11.2229 | PSMA4 | FEV1_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 1.46E-05 | 5.825 | -8.2433 | | FEV1FVC_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 2.22E-05 | -15.029 | -50.3241 | | FEV1_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 1.46E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1FVC_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 2.22E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 1.46E-05 | 6.88 | -11.2229 | PSMA4 | FEV1FVC_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 2.22E-05 | 5.825 | -8.2433 | | FEV1_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1051730 | 15 | 1.46E-05 | -15.029 | -50.3241 | | FEV1FVC_cis | G_A | 18385739 | Nicotine dependence | 6.00E-20 | 0.1 |
| rs1048466 | 12 | 6.98E-04 | 5.795 | -8.1654 | CCDC77 | FEV1FVC_cis | A_G | 23563609 | Obesity (early onset extreme) | 8.00E-08 | 1.22 |
| rs1048466 | 12 | 6.98E-04 | 8.157 | -15.4641 | JARID1A | FEV1FVC_cis | A_G | 23563609 | Obesity (early onset extreme) | 8.00E-08 | 1.22 |
| rs8040868 | 15 | 2.98E-06 | -5.501 | -7.4229 | PSMA4 | FEV1_cis | C_T | 23251661 | Obesity-related traits | 6.00E-08 | 0.05 |
| rs8040868 | 15 | 1.14E-06 | 8.376 | -16.2616 | CHRNA5 | FEV1FVC_cis | C_T | 23251661 | Obesity-related traits | 6.00E-08 | 0.05 |
| rs8040868 | 15 | 1.14E-06 | -5.501 | -7.4229 | PSMA4 | FEV1FVC_cis | C_T | 23251661 | Obesity-related traits | 6.00E-08 | 0.05 |
| rs8040868 | 15 | 2.98E-06 | 14.535 | -47.1384 | | FEV1_cis | C_T | 23251661 | Obesity-related traits | 6.00E-08 | 0.05 |
| rs8040868 | 15 | 2.98E-06 | 8.376 | -16.2616 | CHRNA5 | FEV1_cis | C_T | 23251661 | Obesity-related traits | 6.00E-08 | 0.05 |
| rs8040868 | 15 | 1.14E-06 | 14.535 | -47.1384 | | FEV1FVC_cis | C_T | 23251661 | Obesity-related traits | 6.00E-08 | 0.05 |
| rs17631303 | 17 | 6.08E-05 | -9.59 | -21.0551 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -9.59 | -21.0551 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -7.178 | -12.1503 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -7.178 | -12.1503 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | 7.389 | -12.8299 | KIAA1267 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | 7.389 | -12.8299 | KIAA1267 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | - | - | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation | 1.00E-08 | NR |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 27.148 | 161.5729 | | | | | carriers | | |
| rs17631303 | 17 | 6.08E-05 | -27.148 | -161.5729 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -32.548 | -231.6508 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -32.548 | -231.6508 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -14.571 | -47.367 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -14.571 | -47.367 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -4.153 | -4.4839 | ARL17P1 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -4.153 | -4.4839 | ARL17P1 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -29.514 | -190.7204 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -29.514 | -190.7204 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -23.35 | -119.8607 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -23.35 | -119.8607 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -19.296 | -82.2363 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -19.296 | -82.2363 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -19.616 | -84.9473 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -19.616 | -84.9473 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -8.745 | -17.6517 | WNT3 | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -8.745 | -17.6517 | WNT3 | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -26.051 | -148.8825 | KIAA1267 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -26.051 | -148.8825 | KIAA1267 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -19.622 | -84.9986 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -19.622 | -84.9986 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -28.944 | -183.4764 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -28.944 | -183.4764 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -17.042 | -64.3971 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -17.042 | -64.3971 | | FEV1_trans | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | 30.255 | -200.3483 | LRRC37A4 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | 30.255 | -200.3483 | LRRC37A4 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -32.499 | -230.958 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -32.499 | -230.958 | | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | -18.418 | -75.0259 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | - | -75.0259 | MAPT | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation | 1.00E-08 | 1.27 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 18.418 | | | | | | carriers | | |
| rs17631303 | 17 | 6.08E-05 | -13.109 | -38.534 | PLEKHM1 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | -13.109 | -38.534 | PLEKHM1 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs17631303 | 17 | 6.08E-05 | 35.221 | -271.0205 | LRRC37A4 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | NR |
| rs17631303 | 17 | 6.08E-05 | 35.221 | -271.0205 | LRRC37A4 | FEV1_cis | G_A | 23544013 | Ovarian cancer in BRCA1 mutation carriers | 1.00E-08 | 1.27 |
| rs199533 | 17 | 2.23E-04 | 32.542 | -231.5659 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 29.536 | -191.0028 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 19.764 | -86.2162 | MAPT | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | -4.367 | -4.8998 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | -7.239 | -12.3449 | KIAA1267 | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 9.693 | -21.4909 | MAPT | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 37.117 | -300.8256 | | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 39.445 | -339.5555 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 19.981 | -88.0937 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 31.515 | -217.2666 | KIAA1267 | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 6.433 | -9.9027 | BRWD1 | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 37.073 | -300.1162 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 16.19 | -58.2267 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 39.625 | -342.648 | | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 11.494 | -29.8495 | PLEKHM1 | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | -30.536 | -204.0617 | LRRC37A4 | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 10.72 | -26.0862 | WNT3 | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 4.428 | -5.0218 | LRRC37A | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 19.474 | -83.7389 | MAPT | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 8.823 | -17.953 | | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 20.195 | -89.9653 | | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | 19.836 | -86.8369 | MAPT | FEV1_cis | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs199533 | 17 | 2.23E-04 | -35.534 | -275.8333 | LRRC37A4 | FEV1_trans | G_A | 20711177 | Parkinson's disease | 1.00E-06 | 1.35 |
| rs415430 | 17 | 3.59E-04 | 18.352 | -74.4973 | MAPT | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 34.659 | -262.4856 | | FEV1_trans | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | -27.917 | -170.7801 | LRRC37A4 | FEV1_trans | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 10.861 | -26.7525 | WNT3 | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 11.347 | -29.1149 | PLEKHM1 | FEV1_trans | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | -4.438 | -5.0419 | | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 17.98 | -71.5536 | MAPT | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 14.439 | -46.5315 | | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 18.764 | -77.8275 | | FEV1_trans | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | -7.02 | -11.6539 | KIAA1267 | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 8.599 | -17.0947 | MAPT | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 18.442 | -75.2185 | MAPT | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 37.019 | -299.2468 | | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 29.78 | -194.1492 | | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 29.213 | -186.8775 | KIAA1267 | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |

|  |  |  |  |  |  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs415430 | 17 | 3.59E-04 | -32.664 | -233.2949 | LRRC37A4 | FEV1_trans | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 18.89 | -78.8606 |  | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 36.635 | -293.1006 |  | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 4.553 | -5.2767 | LRRC37A | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 34.177 | -255.2748 |  | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 28.215 | -174.417 |  | FEV1_cis | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs415430 | 17 | 3.59E-04 | 8.401 | -16.3539 |  | FEV1_trans | T_C | 21812969 | Parkinson's disease | 7.00E-07 | NR |
| rs11012 | 17 | 5.47E-05 | -18.48 | -75.5241 | MAPT | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -19.329 | -82.5139 | MAPT | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -19.6 | -84.8107 | MAPT | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -17.023 | -64.2561 |  | FEV1_trans | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -29.461 | -190.0409 |  | FEV1_trans | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -4.164 | -4.5048 | ARL17P1 | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -14.601 | -47.5579 |  | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -7.191 | -12.1917 |  | FEV1_trans | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -19.617 | -84.9559 |  | FEV1_trans | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -8.657 | -17.3148 | WNT3 | FEV1_trans | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | 35.133 | -269.675 | LRRC37A4 | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -32.471 | -230.5626 |  | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -23.321 | -119.5663 |  | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | 30.215 | -199.8225 | LRRC37A4 | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -32.522 | -231.283 |  | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -26.064 | -149.0298 | KIAA1267 | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -9.626 | -21.2069 | MAPT | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -28.88 | -182.6718 |  | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -27.124 | -161.2897 |  | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | 7.383 | -12.8103 | KIAA1267 | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11012 | 17 | 5.47E-05 | -13.103 | -38.4996 | PLEKHM1 | FEV1_cis | T_C | 20070850 | Parkinson's disease | 6.00E-08 | 1.43 |
| rs11868035 | 17 | 9.61E-04 | 5.71 | -7.947 |  | FEV1FVC_cis | A_G | 21738487 | Parkinson's disease | 6.00E-08 | 1.18 |
| rs11868035 | 17 | 9.61E-04 | -9.945 | -22.5765 | SREBF1 | FEV1FVC_cis | A_G | 21738487 | Parkinson's disease | 6.00E-08 | 1.18 |
| rs11868035 | 17 | 9.61E-04 | 4.574 | -5.3201 | TOM1L2 | FEV1FVC_cis | A_G | 21738487 | Parkinson's disease | 6.00E-08 | 1.18 |
| rs11868035 | 17 | 9.61E-04 | 5.491 | -7.3983 | TOM1L2 | FEV1FVC_cis | A_G | 21738487 | Parkinson's disease | 6.00E-08 | 1.18 |
| rs8070723 | 17 | 5.13E-05 | 16.887 | -63.2512 |  | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 31.365 | -215.2164 |  | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | -8.014 | -14.9545 | KIAA1267 | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 9.878 | -22.2852 | WNT3 | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | -35.125 | -269.5528 | LRRC37A4 | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 8.336 | -16.1144 |  | FEV1_trans | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 19.423 | -83.307 |  | FEV1_trans | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 27.223 | -162.4596 |  | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 21.594 | - | MAPT | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | 102.6893 | | | | | | | |
| rs8070723 | 17 | 5.13E-05 | 10.574 | -25.4052 | MAPT | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 22.1 | -107.5002 | MAPT | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 40.54 | -358.5859 | | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | -42.207 | -388.5565 | LRRC37A4 | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 12.647 | -35.9347 | PLEKHM1 | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 4.588 | -5.3492 | LRRC37A | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 22.085 | -107.356 | MAPT | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 40.708 | -361.5517 | | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 35.43 | -274.2294 | | FEV1_trans | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 21.98 | -106.3492 | | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 30.297 | -200.9012 | KIAA1267 | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs8070723 | 17 | 5.13E-05 | 34.112 | -254.3101 | | FEV1_cis | A_G | 21044948 | Parkinson's disease | 7.00E-12 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 4.541 | -5.2519 | LRRC37A | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 10.583 | -25.4469 | MAPT | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 22.014 | -106.6747 | MAPT | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 8.317 | -16.0447 | | FEV1_trans | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 31.818 | -221.4378 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | -7.841 | -14.3497 | KIAA1267 | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 9.733 | -21.6614 | WNT3 | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 30.336 | -201.4152 | KIAA1267 | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 27.225 | -162.4833 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | -43.403 | -410.8022 | LRRC37A4 | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 21.505 | -101.8545 | MAPT | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 34.511 | -260.2607 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 19.656 | -85.2893 | | FEV1_trans | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 35.913 | -281.7179 | | FEV1_trans | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | -35.744 | -279.0862 | LRRC37A4 | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 17.18 | -65.4261 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 22.105 | -107.5483 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 40.796 | -363.11 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 40.5 | -357.8815 | | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 12.707 | -36.2671 | PLEKHM1 | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs12185268 | 17 | 2.66E-05 | 22.257 | -109.0155 | MAPT | FEV1_cis | A_G | 21738487 | Parkinson's disease | 3.00E-14 | 1.3 |
| rs199533 | 17 | 2.23E-04 | 32.542 | -231.5659 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 29.536 | -191.0028 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 19.764 | -86.2162 | MAPT | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | -4.367 | -4.8998 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | -7.239 | -12.3449 | KIAA1267 | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs199533 | 17 | 2.23E-04 | 9.693 | -21.4909 | MAPT | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 37.117 | -300.8256 | | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 39.445 | -339.5555 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 19.981 | -88.0937 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 31.515 | -217.2666 | KIAA1267 | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 6.433 | -9.9027 | BRWD1 | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 37.073 | -300.1162 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 16.19 | -58.2267 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 39.625 | -342.648 | | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 11.494 | -29.8495 | PLEKHM1 | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | -30.536 | -204.0617 | LRRC37A4 | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 10.72 | -26.0862 | WNT3 | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 4.428 | -5.0218 | LRRC37A | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 19.474 | -83.7389 | MAPT | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 8.823 | -17.953 | | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 20.195 | -89.9653 | | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | 19.836 | -86.8369 | MAPT | FEV1_cis | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs199533 | 17 | 2.23E-04 | -35.534 | -275.8333 | LRRC37A4 | FEV1_trans | G_A | 19915575 | Parkinson's disease | 1.00E-14 | 1.28 |
| rs393152 | 17 | 1.03E-04 | 34.747 | -263.8129 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | -7.806 | -14.2289 | KIAA1267 | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 22.377 | -110.1809 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 9.664 | -21.3678 | WNT3 | FEV1_trans | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 31.875 | -222.2269 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 17.505 | -67.882 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 30.612 | -205.0719 | KIAA1267 | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 19.791 | -86.4487 | | FEV1_trans | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | -35.981 | -282.7803 | LRRC37A4 | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 12.679 | -36.1118 | PLEKHM1 | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 36.12 | -284.9582 | | FEV1_trans | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 8.454 | -16.5505 | | FEV1_trans | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 10.636 | -25.6933 | MAPT | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 27.448 | -165.1343 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 21.621 | -102.9432 | MAPT | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | -43.605 | -414.6207 | LRRC37A4 | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 40.769 | -362.6315 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 22.087 | -107.3752 | MAPT | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 4.595 | -5.3638 | LRRC37A | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 22.262 | -109.0639 | MAPT | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs393152 | 17 | 1.03E-04 | 40.981 | -366.3972 | | FEV1_cis | A_G | 19915575 | Parkinson's disease | 2.00E-16 | 1.3 |
| rs199515 | 17 | 3.22E-04 | -37.269 | -303.2825 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs199515 | 17 | 3.22E-04 | -34.902 | -266.1591 | | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -18.068 | -72.2446 | MAPT | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -18.816 | -78.253 | | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -34.372 | -258.1798 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -8.359 | -16.1989 | | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -4.503 | -5.1739 | LRRC37A | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | 6.94 | -11.4066 | KIAA1267 | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | 4.433 | -5.0318 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -14.344 | -45.9349 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -28.268 | -175.0679 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -18.536 | -75.9755 | MAPT | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | 28.362 | -176.2252 | LRRC37A4 | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -29.928 | -196.0702 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -36.878 | -296.9825 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -11.284 | -28.8029 | PLEKHM1 | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -18.49 | -75.6046 | MAPT | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -8.686 | -17.4255 | MAPT | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -6.215 | -9.2897 | BRWD1 | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -18.895 | -78.9017 | | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | 33.148 | -240.2181 | LRRC37A4 | FEV1_trans | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -10.819 | -26.5531 | WNT3 | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs199515 | 17 | 3.22E-04 | -29.201 | -186.7251 | KIAA1267 | FEV1_cis | G_C | 22451204 | Parkinson's disease | 3.00E-17 | 1.32 |
| rs2942168 | 17 | 1.01E-04 | -22.077 | -107.2791 | MAPT | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -21.624 | -102.9714 | MAPT | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | 35.981 | -282.7803 | LRRC37A4 | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -41.013 | -366.9673 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | 7.812 | -14.2496 | KIAA1267 | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -31.887 | -222.3932 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -36.135 | -285.1938 | | FEV1_trans | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -19.797 | -86.5004 | | FEV1_trans | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -40.804 | -363.2519 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -10.634 | -25.684 | MAPT | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | 43.602 | -414.5639 | LRRC37A4 | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -17.497 | -67.821 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -8.464 | -16.5878 | | FEV1_trans | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2942168 | 17 | 1.01E-04 | -22.262 | -109.0639 | MAPT | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -34.777 | -264.2662 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -9.665 | -21.372 | WNT3 | FEV1_trans | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -27.455 | -165.2179 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -4.582 | -5.3367 | LRRC37A | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -12.683 | -36.1339 | PLEKHM1 | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -30.645 | -205.5113 | KIAA1267 | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs2942168 | 17 | 1.01E-04 | -22.377 | -110.1809 | | FEV1_cis | A_G | 21292315 | Parkinson's disease | 1.00E-28 | 1.27 |
| rs10043775 | 5 | 1.64E-04 | -11.686 | -30.823 | FBXO38 | FEV1_cis | C_T | 22699663 | Periodontal microbiota | 2.00E-06 | 2.06 |
| rs10043775 | 5 | 1.64E-04 | -4.162 | -4.501 | | FEV1_cis | C_T | 22699663 | Periodontal microbiota | 2.00E-06 | 2.06 |
| rs10043775 | 5 | 1.64E-04 | 6.395 | -9.7944 | FBXO38 | FEV1_cis | C_T | 22699663 | Periodontal microbiota | 2.00E-06 | 2.06 |
| rs10043775 | 5 | 4.96E-04 | 6.395 | -9.7944 | FBXO38 | FEV1FVC_cis | C_T | 22699663 | Periodontal microbiota | 2.00E-06 | 2.06 |
| rs10043775 | 5 | 4.96E-04 | -4.162 | -4.501 | | FEV1FVC_cis | C_T | 22699663 | Periodontal microbiota | 2.00E-06 | 2.06 |
| rs10043775 | 5 | 4.96E-04 | -11.686 | -30.823 | FBXO38 | FEV1FVC_cis | C_T | 22699663 | Periodontal microbiota | 2.00E-06 | 2.06 |
| rs2070729 | 5 | 9.49E-04 | 4.937 | -6.1005 | SLC22A5 | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | 6.585 | -10.3421 | RAD50 | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | 4.824 | -5.8517 | | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | -4.56 | -5.2911 | SLC22A5 | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | 4.058 | -4.3054 | RAD50 | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | 4.407 | -4.9796 | | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | 5.227 | -6.7638 | | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs2070729 | 5 | 9.49E-04 | 5.012 | -6.2687 | | FEV1FVC_cis | C_A | 22139419 | Platelet counts | 1.00E-10 | 2.39 |
| rs997154 | 14 | 9.46E-04 | 4.854 | -5.9172 | JUB | FEV1FVC_cis | A_G | 23704328 | Primary tooth development (number of teeth) | 3.00E-08 | 0.15 |
| rs997154 | 14 | 9.46E-04 | -8.957 | -18.4767 | C14orf94 | FEV1FVC_cis | A_G | 23704328 | Primary tooth development (number of teeth) | 3.00E-08 | 0.15 |
| rs997154 | 14 | 9.46E-04 | 4.854 | -5.9172 | JUB | FEV1FVC_cis | A_G | 23704328 | Primary tooth development (time to first tooth eruption) | 7.00E-06 | 0.14 |
| rs997154 | 14 | 9.46E-04 | -8.957 | -18.4767 | C14orf94 | FEV1FVC_cis | A_G | 23704328 | Primary tooth development (time to first tooth eruption) | 7.00E-06 | 0.14 |
| rs8070723 | 17 | 5.13E-05 | 16.887 | -63.2512 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 31.365 | -215.2164 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | -8.014 | -14.9545 | KIAA1267 | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 9.878 | -22.2852 | WNT3 | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | -35.125 | -269.5528 | LRRC37A4 | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 8.336 | -16.1144 | | FEV1_trans | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 19.423 | -83.307 | | FEV1_trans | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 27.223 | -162.4596 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 21.594 | -102.6893 | MAPT | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 10.574 | -25.4052 | MAPT | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 22.1 | -107.5002 | MAPT | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 40.54 | -358.5859 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | -42.207 | -388.5565 | LRRC37A4 | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 12.647 | -35.9347 | PLEKHM1 | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 4.588 | -5.3492 | LRRC37A | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs8070723 | 17 | 5.13E-05 | 22.085 | -107.356 | MAPT | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 40.708 | -361.5517 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 35.43 | -274.2294 | | FEV1_trans | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 21.98 | -106.3492 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 30.297 | -200.9012 | KIAA1267 | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs8070723 | 17 | 5.13E-05 | 34.112 | -254.3101 | | FEV1_cis | A_G | 21685912 | Progressive supranuclear palsy | 2.00E-118 | 5.11 |
| rs3134792 | 6 | 3.42E-04 | 6.308 | -9.5487 | HCG4P6 | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -6.673 | -10.601 | PSORS1C1 | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -4.445 | -5.0561 | NOTCH4 | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -4.836 | -5.8779 | | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 8.592 | -17.0682 | | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -8.056 | -15.1033 | BTN3A2 | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -8.071 | -15.1566 | HLA-A | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 6.347 | -9.6585 | TUBB | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 6.454 | -9.9628 | C6orf12 | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 4.332 | -4.8304 | RNF5 | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 4.332 | -4.8304 | RNF5 | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -5.732 | -8.0033 | APOM | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -5.461 | -7.3247 | CDSN | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 5.122 | -6.5195 | SFTA2 | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -5.732 | -8.0033 | APOM | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -12.3 | -34.043 | HLA-C | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 6.347 | -9.6585 | TUBB | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -4.836 | -5.8779 | | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -4.152 | -4.482 | HLA-C | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 6.454 | -9.9628 | C6orf12 | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -5.461 | -7.3247 | CDSN | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 12.331 | -34.2099 | HLA-DRB3 | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 5.325 | -6.9959 | MICB | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 5.325 | -6.9959 | MICB | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 11.003 | -27.4322 | ZFP57 | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 8.592 | -17.0682 | | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 6.308 | -9.5487 | HCG4P6 | FEV1FVC_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 8.782 | -17.7943 | | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 12.331 | -34.2099 | HLA-DRB3 | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -6.673 | -10.601 | PSORS1C1 | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | -4.445 | -5.0561 | NOTCH4 | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -4.152 | -4.482 | HLA-C | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 11.003 | -27.4322 | ZFP57 | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -12.3 | -34.043 | HLA-C | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 8.782 | -17.7943 | | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -8.071 | -15.1566 | HLA-A | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 5.122 | -6.5195 | SFTA2 | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | 8.67 | -17.3644 | | FEV1_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.42E-04 | -8.056 | -15.1033 | BTN3A2 | FEV1_trans | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs3134792 | 6 | 3.27E-05 | 8.67 | -17.3644 | | FEV1FVC_cis | T_G | 18364390 | Psoriasis | 1.00E-09 | NR |
| rs1150668 | 6 | 2.82E-04 | 15.469 | -53.2505 | ZNF323 | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | 5.27 | -6.8651 | PGBD1 | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | 4.81 | -5.8212 | ZNF165 | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | 4.256 | -4.6817 | | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | 11.046 | -27.6398 | | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | 14.969 | -49.9316 | ZNF323 | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | -5.527 | -7.4871 | ZNF187 | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs1150668 | 6 | 2.82E-04 | 8.706 | -17.502 | | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs1150668 | 6 | 2.82E-04 | -6.071 | -8.8958 | | FEV1_cis | T_G | 23449627 | Pubertal anthropometrics | 2.00E-07 | 0.06 |
| rs2637266 | 10 | 9.57E-06 | -6.109 | -8.9989 | | FEV1_cis | G_A | 23932459 | Pulmonary function | 2.00E-06 | NR |
| rs13147758 | 4 | 2.68E-19 | -4.981 | -6.1989 | | FEV1FVC_cis | A_G | 19300500 | Pulmonary function | 8.00E-11 | 0.1 |
| rs13147758 | 4 | 5.99E-09 | -4.981 | -6.1989 | | FEV1_cis | A_G | 19300500 | Pulmonary function | 8.00E-11 | 0.1 |
| rs11172113 | 12 | 1.36E-06 | -6.632 | -10.48 | STAT6 | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 8.00E-06 | NR |
| rs11172113 | 12 | 1.36E-06 | 5.705 | -7.9343 | STAT6 | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 8.00E-06 | NR |
| rs1036429 | 12 | 1.24E-08 | 8.119 | -15.3279 | SNRPF | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 1.00E-07 | NR |
| rs1036429 | 12 | 1.24E-08 | 7.845 | -14.3636 | | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 1.00E-07 | NR |
| rs2857595 | 6 | 7.86E-08 | 7.759 | -14.0675 | ZFP57 | FEV1FVC_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -4.328 | -4.8226 | | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -4.35 | -4.866 | HLA-DRB6 | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 7.261 | -12.4154 | | FEV1_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -7.587 | -13.4849 | PSORS1C1 | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 7.105 | -11.9197 | | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -4.328 | -4.8226 | | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -7.587 | -13.4849 | PSORS1C1 | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 13.925 | -43.3501 | HLA-DRB3 | FEV1FVC_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -4.837 | -5.88 | ATP6V1G2 | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 7.759 | -14.0675 | ZFP57 | FEV1_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 4.257 | -4.6836 | | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 13.925 | -43.3501 | HLA-DRB3 | FEV1_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -4.471 | -5.1087 | APOM | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -5.227 | -6.7638 | | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 4.691 | -5.5656 | HLA-DRB1 | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -9.134 | -19.1804 | HLA-C | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -4.471 | -5.1087 | APOM | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 7.261 | -12.4154 | | FEV1FVC_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -6.682 | -10.6276 | BTN3A2 | FEV1_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -9.134 | -19.1804 | HLA-C | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 4.257 | -4.6836 | | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 7.097 | -11.8945 | | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 7.097 | -11.8945 | | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 4.691 | -5.5656 | HLA-DRB1 | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | -4.866 | -5.9436 | CDSN | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -4.35 | -4.866 | HLA-DRB6 | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -4.866 | -5.9436 | CDSN | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -6.682 | -10.6276 | BTN3A2 | FEV1FVC_trans | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 7.105 | -11.9197 | | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | 5.545 | -7.5317 | TUBB | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -5.227 | -6.7638 | | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 1.46E-05 | 5.545 | -7.5317 | TUBB | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs2857595 | 6 | 7.86E-08 | -4.837 | -5.88 | ATP6V1G2 | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-08 | NR |
| rs11001819 | 10 | 1.42E-08 | 5.722 | -7.9777 | C10orf11 | FEV1_cis | A_G | 23284291 | Pulmonary function (interaction) | 5.00E-08 | NR |
| rs11001819 | 10 | 1.42E-08 | 5.764 | -8.0854 | | FEV1_cis | A_G | 23284291 | Pulmonary function (interaction) | 5.00E-08 | NR |
| rs2571445 | 2 | 9.83E-11 | -4.271 | -4.7109 | TNS1 | FEV1_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-09 | NR |
| rs2571445 | 2 | 4.46E-06 | -4.271 | -4.7109 | TNS1 | FEV1FVC_cis | G_A | 23284291 | Pulmonary function (interaction) | 8.00E-09 | NR |
| rs7764819 | 6 | 8.79E-05 | 5.046 | -6.3457 | HLA-DQB1 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs7764819 | 6 | 8.79E-05 | 5.046 | -6.3457 | HLA-DQB1 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs7764819 | 6 | 8.79E-05 | -7.347 | -12.6931 | HLA-DQA2 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs7764819 | 6 | 8.79E-05 | -7.347 | -12.6931 | HLA-DQA2 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs7764819 | 6 | 8.79E-05 | -4.069 | -4.3259 | HLA-DPA1 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs7764819 | 6 | 8.79E-05 | -4.069 | -4.3259 | HLA-DPA1 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs7764819 | 6 | 8.79E-05 | -5.468 | -7.3419 | HLA-DRB6 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs7764819 | 6 | 8.79E-05 | -5.468 | -7.3419 | HLA-DRB6 | FEV1FVC_cis | G_T | 23284291 | Pulmonary function (interaction) | 4.00E-09 | 0 |
| rs2869967 | 4 | 2.08E-11 | -4.782 | -5.7606 | FAM13A1 | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 5.00E-11 | NR |
| rs2277027 | 5 | 3.10E-04 | 4.591 | -5.3554 | ADAM19 | FEV1_cis | A_C | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs2277027 | 5 | 6.65E-09 | 4.591 | -5.3554 | ADAM19 | FEV1FVC_cis | A_C | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs2284746 | 1 | 2.47E-09 | 5.216 | -6.738 | MFAP2 | FEV1FVC_cis | C_G | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs2284746 | 1 | 2.47E-09 | 6.339 | -9.6359 | PADI2 | FEV1FVC_cis | C_G | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs2284746 | 1 | 2.47E-09 | -6.004 | -8.7155 | | FEV1FVC_cis | C_G | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.19E-08 | -8.578 | -17.0153 | CAMK1D | FEV1_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.19E-08 | -6.539 | -10.2081 | CAMK1D | FEV1_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.28E-10 | -7.687 | -13.8221 | CAMK1D | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.28E-10 | -8.578 | -17.0153 | CAMK1D | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.19E-08 | -7.687 | -13.8221 | CAMK1D | FEV1_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.28E-10 | -6.539 | -10.2081 | CAMK1D | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.28E-10 | -4.896 | -6.0096 | CDC123 | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs7068966 | 10 | 1.19E-08 | -4.896 | -6.0096 | CDC123 | FEV1_cis | C_T | 23284291 | Pulmonary function (interaction) | 2.00E-11 | NR |
| rs17331332 | 4 | 5.30E-05 | 4.502 | -5.1719 | NPNT | FEV1FVC_cis | A_G | 23284291 | Pulmonary function (interaction) | 1.00E-16 | NR |
| rs17331332 | 4 | 1.11E-12 | 4.502 | -5.1719 | NPNT | FEV1_cis | A_G | 23284291 | Pulmonary function (interaction) | 1.00E-16 | NR |
| rs1980057 | 4 | 4.07E-09 | -5.04 | -6.3321 | | FEV1_cis | C_T | 23284291 | Pulmonary function (interaction) | 5.00E-18 | NR |
| rs1980057 | 4 | 1.06E-19 | -5.04 | -6.3321 | | FEV1FVC_cis | C_T | 23284291 | Pulmonary function (interaction) | 5.00E-18 | NR |
| rs2070600 | 6 | 9.07E-15 | -6.854 | -11.1438 | HLA-DQA2 | FEV1FVC_cis | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs2070600 | 6 | 9.07E-15 | 4.733 | -5.6552 | HLA-DRB1 | FEV1FVC_cis | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs2070600 | 6 | 9.07E-15 | 4.36 | -4.8858 | AGER | FEV1FVC_cis | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs2070600 | 6 | 9.07E-15 | -7.616 | -13.5823 | HLA-DRB6 | FEV1FVC_cis | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs2070600 | 6 | 9.07E-15 | -9.585 | -21.0341 | HLA-DRB4 | FEV1FVC_trans | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs2070600 | 6 | 9.07E-15 | -4.867 | -5.9458 | | FEV1FVC_cis | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs2070600 | 6 | 9.07E-15 | 4.607 | -5.3888 | AGER | FEV1FVC_cis | T_C | 23284291 | Pulmonary function (interaction) | 1.00E-21 | NR |
| rs6457617 | 6 | 6.99E-04 | -6.78 | -10.9202 | HLA-DQB2 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | 6.367 | -9.715 | HLA-DRB4 | FEV1FVC_trans | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -6.804 | -10.9925 | HLA-DQB2 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -9.9 | -22.3806 | HLA-DQB1 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -10.077 | -23.156 | HLA-DQB1 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -9.377 | -20.1683 | HLA-DRB5 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | 7.243 | -12.3577 | HLA-DRB6 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -10.042 | -23.0016 | HLA-DQB1 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -11.217 | -28.473 | HLA-DQB1 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | -9.658 | -21.3423 | HLA-DRB3 | FEV1FVC_trans | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs6457617 | 6 | 6.99E-04 | 6.159 | -9.1355 | HLA-DQA2 | FEV1FVC_cis | C_T | 18668548 | Rheumatoid arthritis | 1.00E-09 | NR |
| rs7765379 | 6 | 8.99E-05 | -5.464 | -7.3321 | HLA-DRB6 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | -5.464 | -7.3321 | HLA-DRB6 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | -7.342 | -12.6769 | HLA-DQA2 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | -7.342 | -12.6769 | HLA-DQA2 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | -4.069 | -4.3259 | HLA-DPA1 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | -4.069 | -4.3259 | HLA-DPA1 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | 5.044 | -6.3411 | HLA-DQB1 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs7765379 | 6 | 8.99E-05 | 5.044 | -6.3411 | HLA-DQB1 | FEV1FVC_cis | G_T | 21452313 | Rheumatoid arthritis | 5.00E-23 | 2.51 |
| rs6457617 | 6 | 6.99E-04 | -6.78 | -10.9202 | HLA-DQB2 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs6457617 | 6 | 6.99E-04 | 6.367 | -9.715 | HLA-DRB4 | FEV1FVC_trans | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -6.804 | -10.9925 | HLA-DQB2 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -9.9 | -22.3806 | HLA-DQB1 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -10.077 | -23.156 | HLA-DQB1 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -9.377 | -20.1683 | HLA-DRB5 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | 7.243 | -12.3577 | HLA-DRB6 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -10.042 | -23.0016 | HLA-DQB1 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -11.217 | -28.473 | HLA-DQB1 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -9.658 | -21.3423 | HLA-DRB3 | FEV1FVC_trans | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | 6.159 | -9.1355 | HLA-DQA2 | FEV1FVC_cis | C_T | 17554300 | Rheumatoid arthritis | 5.00E-75 | 2.36 |
| rs6457620 | 6 | 2.92E-04 | -10.123 | -23.3597 | HLA-DQB1 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -6.836 | -11.0892 | HLA-DQB2 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -11.236 | -28.5664 | HLA-DQB1 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | 6.208 | -9.2703 | HLA-DQA2 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -9.376 | -20.1642 | HLA-DRB5 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -10.152 | -23.4886 | HLA-DQB1 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -6.796 | -10.9683 | HLA-DQB2 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | -9.645 | -21.2873 | HLA-DRB3 | FEV1FVC_trans | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | 7.348 | -12.6964 | HLA-DRB6 | FEV1FVC_cis | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs6457620 | 6 | 2.92E-04 | 6.447 | -9.9428 | HLA-DRB4 | FEV1FVC_trans | G_C | 18794853 | Rheumatoid arthritis | 4.00E-186 | 2.55 |
| rs1046089 | 6 | 9.82E-04 | 4.373 | -4.9117 | HLA-C | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | -5.049 | -6.3525 | TUBB | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | -7.153 | -12.0711 | HLA-DRB3 | FEV1_trans | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | 5.125 | -6.5265 | ATP6V1G2 | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | -5.407 | -7.1932 | | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | 7.007 | -11.6135 | LY6G5C | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | 4.19 | -4.5545 | APOM | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | 4.464 | -5.0945 | BAT4 | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | -5.481 | -7.3737 | | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | -5.205 | -6.7122 | MICB | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | 5.833 | -8.2641 | HLA-DRB5 | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs1046089 | 6 | 9.82E-04 | 5.4 | -7.1763 | | FEV1_cis | A_G | 23894747 | Schizophrenia | 4.00E-06 | 1.3 |
| rs10911902 | 1 | 4.28E-04 | -4.955 | -6.1407 | PRG4 | FEV1FVC_cis | C_T | 18347602 | Schizophrenia | 2.00E-06 | 1.79 |
| rs3132935 | 6 | 3.75E-04 | 7.838 | -14.3393 | RNF5 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -8.684 | -17.4178 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -7.489 | -13.1586 | AGPAT1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -4.891 | -5.9986 | HLA-DRB5 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 6.827 | -11.0619 | | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.362 | -7.0846 | APOM | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -8.74 | -17.6324 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 8.218 | -15.6842 | ZFP57 | FEV1FVC_trans | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.459 | -7.3198 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 10.529 | -25.1972 | HLA-DRB3 | FEV1FVC_trans | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3132935 | 6 | 3.75E-04 | 6.525 | -10.1675 | | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.933 | -8.5266 | AGPAT1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -8.848 | -18.0501 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 7.125 | -11.9826 | | FEV1FVC_trans | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.408 | -7.1956 | NOTCH4 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 5.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 7.838 | -14.3393 | RNF5 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -8.684 | -17.4178 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -7.489 | -13.1586 | AGPAT1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -4.891 | -5.9986 | HLA-DRB5 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 6.827 | -11.0619 | | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.362 | -7.0846 | APOM | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -8.74 | -17.6324 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 8.218 | -15.6842 | ZFP57 | FEV1FVC_trans | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.459 | -7.3198 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 10.529 | -25.1972 | HLA-DRB3 | FEV1FVC_trans | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 6.525 | -10.1675 | | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.933 | -8.5266 | AGPAT1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -8.848 | -18.0501 | HLA-DQB1 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | 7.125 | -11.9826 | | FEV1FVC_trans | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3132935 | 6 | 3.75E-04 | -5.408 | -7.1956 | NOTCH4 | FEV1FVC_cis | A_G | 23894747 | Schizophrenia | 3.00E-07 | 1.25 |
| rs3131296 | 6 | 5.10E-05 | 4.74 | -5.6702 | NOTCH4 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 8.56 | -16.9474 | HLA-DQB1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 5.143 | -6.568 | HLA-DQB2 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -5.574 | -7.6039 | HLA-DPB1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 5.143 | -6.568 | HLA-DQB2 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -10.659 | -25.8005 | HLA-DRB3 | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 5.121 | -6.5172 | HLA-DPA1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 5.257 | -6.8344 | AGPAT1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -7.997 | -14.8945 | | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 7.851 | -14.3843 | HLA-C | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -6.456 | -9.9686 | TUBB | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 6.271 | -9.4452 | HLA-DQB1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -8.285 | -15.9277 | ZFP57 | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 4.925 | -6.0739 | | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 4.925 | -6.0739 | | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -6.778 | -10.9142 | HCG4P6 | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -8.285 | -15.9277 | ZFP57 | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 8.088 | -15.2172 | BTN3A2 | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 5.121 | -6.5172 | HLA-DPA1 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -6.456 | -9.9686 | TUBB | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 6.271 | -9.4452 | HLA-DQB1 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -4.241 | -4.6526 | | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 8.56 | -16.9474 | HLA-DQB1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 8.486 | -16.6698 | HLA-DQB1 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -7.997 | -14.8945 | | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 8.56 | -16.9474 | HLA- | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB1 | | | | | | |
| rs3131296 | 6 | 5.10E-05 | -7.757 | -14.0607 | | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 7.397 | -12.8561 | HLA-A | FEV1_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -10.659 | -25.8005 | HLA-DRB3 | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -6.875 | -11.2077 | RNF5 | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -4.207 | -4.5871 | | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 6.374 | -9.7348 | APOM | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -4.911 | -6.0428 | MICB | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -7.896 | -14.5406 | | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -4.911 | -6.0428 | MICB | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -5.574 | -7.6039 | HLA-DPB1 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 4.74 | -5.6702 | NOTCH4 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -4.207 | -4.5871 | | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 8.56 | -16.9474 | HLA-DQB1 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | -7.896 | -14.5406 | | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 5.257 | -6.8344 | AGPAT1 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -7.757 | -14.0607 | | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 6.374 | -9.7348 | APOM | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 5.10E-05 | 7.851 | -14.3843 | HLA-C | FEV1_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 8.088 | -15.2172 | BTN3A2 | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -4.241 | -4.6526 | | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 7.397 | -12.8561 | HLA-A | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | 8.486 | -16.6698 | HLA-DQB1 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -6.778 | -10.9142 | HCG4P6 | FEV1FVC_trans | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs3131296 | 6 | 2.43E-06 | -6.875 | -11.2077 | RNF5 | FEV1FVC_cis | T_C | 19571808 | Schizophrenia | 2.00E-10 | 1.19 |
| rs17693963 | 6 | 3.38E-04 | 16.884 | -63.2291 | BTN3A2 | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | 11.075 | -27.7802 | HLA-A | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | 5.089 | -6.4437 | | FEV1_cis | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -4.742 | -5.6744 | ZNF323 | FEV1_cis | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -7 | -11.5918 | HCG4P6 | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | 6.167 | -9.1574 | ZNF389 | FEV1_cis | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -10.735 | -26.1566 | ZFP57 | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -9.848 | -22.1554 | | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -6.567 | -10.2896 | C6orf12 | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -6.637 | -10.4947 | HLA-DRB3 | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | 6.727 | -10.7615 | HLA-C | FEV1_trans | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs17693963 | 6 | 3.38E-04 | -4.826 | -5.856 | ZNF323 | FEV1_cis | C_A | 22688191 | Schizophrenia | 3.00E-11 | 1.24 |
| rs2021722 | 6 | 8.30E-04 | 8.098 | -15.2528 | BTN3A2 | FEV1_trans | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -6.243 | -9.3673 | | FEV1_trans | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -5.741 | -8.0263 | RP3-377H14.5 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | 7.986 | -14.8558 | | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | 5.632 | -7.7493 | VARS2 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -8.291 | -15.9496 | | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -4.559 | -5.2891 | SFTA2 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -6.859 | -11.159 | HLA-DRB3 | FEV1_trans | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -5.559 | -7.5665 | HCG18 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -7.299 | -12.5377 | | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -6.046 | -8.8283 | TUBB | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -5.535 | -7.5069 | HCG18 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -6.821 | -11.0438 | ZFP57 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | 8.616 | -17.1591 | HLA-A | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | -7.685 | -13.8153 | HCG4P6 | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2021722 | 6 | 8.30E-04 | 5.038 | -6.3275 | HLA-G | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2021722 | 6 | 8.30E-04 | 5.922 | -8.4975 | CDSN | FEV1_cis | T_C | 21926974 | Schizophrenia | 2.00E-12 | 1.15 |
| rs2523722 | 6 | 4.95E-04 | -6.95 | -11.4374 | ZFP57 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -7.106 | -11.9228 | | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -8.366 | -16.2247 | | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -4.635 | -5.4474 | SFTA2 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -6.07 | -8.8931 | TUBB | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -6.765 | -10.8751 | HLA-DRB3 | FEV1_trans | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | 4.937 | -6.1005 | HLA-G | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | 5.899 | -8.4369 | CDSN | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | 7.746 | -14.023 | | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -4.924 | -6.0716 | HCG18 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | 8.399 | -16.3465 | BTN3A2 | FEV1_trans | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | 5.675 | -7.858 | VARS2 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -4.979 | -6.1944 | HCG18 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | 8.305 | -16.0008 | HLA-A | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -5.214 | -6.7333 | RP3-377H14.5 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs2523722 | 6 | 4.95E-04 | -7.923 | -14.6348 | HCG4P6 | FEV1_cis | T_C | 22883433 | Schizophrenia | 1.00E-16 | 1.25 |
| rs12914385 | 15 | 2.95E-06 | -14.428 | -46.4623 | | FEV1_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.95E-06 | 6.149 | -9.1081 | PSMA4 | FEV1_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.28E-05 | 4.482 | -5.1311 | | FEV1FVC_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.28E-05 | 6.149 | -9.1081 | PSMA4 | FEV1FVC_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.95E-06 | -8.686 | -17.4255 | CHRNA5 | FEV1_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.28E-05 | -8.686 | -17.4255 | CHRNA5 | FEV1FVC_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.95E-06 | 4.482 | -5.1311 | | FEV1_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs12914385 | 15 | 2.28E-05 | -14.428 | -46.4623 | | FEV1FVC_cis | C_T | 23022100 | Serum albumin level | 6.00E-07 | 0.01 |
| rs2036527 | 15 | 2.40E-06 | 5.597 | -7.6614 | | FEV1_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 2.40E-06 | -15.89 | -56.1289 | | FEV1_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 1.19E-05 | -15.89 | -56.1289 | | FEV1FVC_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 1.19E-05 | -10.34 | -24.333 | CHRNA5 | FEV1FVC_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 1.19E-05 | 6.946 | -11.4251 | PSMA4 | FEV1FVC_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 2.40E-06 | -10.34 | -24.333 | CHRNA5 | FEV1_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 2.40E-06 | 6.946 | -11.4251 | PSMA4 | FEV1_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs2036527 | 15 | 1.19E-05 | 5.597 | -7.6614 | | FEV1FVC_cis | G_A | 22832964 | Smoking behavior | 2.00E-08 | 0.04 |
| rs1051730 | 15 | 2.22E-05 | 6.88 | -11.2229 | PSMA4 | FEV1_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 1.46E-05 | 5.825 | -8.2433 | | FEV1FVC_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 2.22E-05 | -15.029 | -50.3241 | | FEV1_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 1.46E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1FVC_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 2.22E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 1.46E-05 | 6.88 | -11.2229 | PSMA4 | FEV1FVC_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 2.22E-05 | 5.825 | -8.2433 | | FEV1_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 1.46E-05 | -15.029 | -50.3241 | | FEV1FVC_cis | G_A | 20418889 | Smoking behavior | 2.00E-66 | 0.08 |
| rs1051730 | 15 | 2.22E-05 | 6.88 | -11.2229 | PSMA4 | FEV1_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 1.46E-05 | 5.825 | -8.2433 | | FEV1FVC_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 2.22E-05 | -15.029 | -50.3241 | | FEV1_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 1.46E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1FVC_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 2.22E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 1.46E-05 | 6.88 | -11.2229 | PSMA4 | FEV1FVC_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 2.22E-05 | 5.825 | -8.2433 | | FEV1_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 1.46E-05 | -15.029 | -50.3241 | | FEV1FVC_cis | G_A | 20418888 | Smoking behavior | 2.00E-69 | 0.8 |
| rs1051730 | 15 | 2.22E-05 | 6.88 | -11.2229 | PSMA4 | FEV1_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs1051730 | 15 | 1.46E-05 | 5.825 | -8.2433 | | FEV1FVC_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs1051730 | 15 | 2.22E-05 | - | -50.3241 | | FEV1_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | 15.029 | | | | | | | | |
| rs1051730 | 15 | 1.46E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1FVC_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs1051730 | 15 | 2.22E-05 | -10.13 | -23.3908 | CHRNA5 | FEV1_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs1051730 | 15 | 1.46E-05 | 6.88 | -11.2229 | PSMA4 | FEV1FVC_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs1051730 | 15 | 2.22E-05 | 5.825 | -8.2433 | | FEV1_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs1051730 | 15 | 1.46E-05 | -15.029 | -50.3241 | | FEV1FVC_cis | G_A | 20418890 | Smoking behavior | 3.00E-73 | 1.02 |
| rs2734583 | 6 | 3.19E-06 | -7.131 | -12.0016 | TUBB | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 5.3 | -6.9363 | PSORS1C1 | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -5.775 | -8.1138 | SFTA2 | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -7.131 | -12.0016 | TUBB | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -8.89 | -18.2139 | | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -11.077 | -27.7899 | ZFP57 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -11.077 | -27.7899 | ZFP57 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -7.181 | -12.1599 | HCG4P6 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -4.087 | -4.3595 | HLA-DRB1 | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -8.513 | -16.7709 | | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -5.412 | -7.2053 | RNF5 | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 8.181 | -15.5505 | BTN3A2 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 6.616 | -10.4329 | APOM | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -5.537 | -7.5119 | MICB | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -5.775 | -8.1138 | SFTA2 | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 8.181 | -15.5505 | BTN3A2 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -4.087 | -4.3595 | HLA-DRB1 | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -8.614 | -17.1515 | | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -6.189 | -9.2179 | C6orf12 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 5.783 | -8.1344 | CDSN | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 6.525 | -10.1675 | HLA-DQB1 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -6.189 | -9.2179 | C6orf12 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 6.492 | -10.0721 | HLA-DQB1 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 6.525 | -10.1675 | HLA-DQB1 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 4.703 | -5.5911 | | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -5.537 | -7.5119 | MICB | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 4.703 | -5.5911 | | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2734583 | 6 | 3.19E-06 | 6.492 | -10.0721 | HLA-DQB1 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -8.614 | -17.1515 | | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 4.457 | -5.0803 | BAT2 | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -12.779 | -36.6679 | HLA-DRB3 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 6.616 | -10.4329 | APOM | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 9.638 | -21.2576 | HLA-A | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 4.425 | -5.0157 | NOTCH4 | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 10.44 | -24.7883 | HLA-C | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 10.44 | -24.7883 | HLA-C | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 4.457 | -5.0803 | BAT2 | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -5.412 | -7.2053 | RNF5 | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -7.181 | -12.1599 | HCG4P6 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 6.493 | -10.075 | HLA-DQB1 | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -8.89 | -18.2139 | | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 5.3 | -6.9363 | PSORS1C1 | FEV1FVC_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | -8.513 | -16.7709 | | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | 6.493 | -10.075 | HLA-DQB1 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 5.38E-06 | -12.779 | -36.6679 | HLA-DRB3 | FEV1FVC_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 9.638 | -21.2576 | HLA-A | FEV1_trans | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 5.783 | -8.1344 | CDSN | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2734583 | 6 | 3.19E-06 | 4.425 | -5.0157 | NOTCH4 | FEV1_cis | G_A | 21912425 | Stevens-Johnson syndrome and toxic epidermal necrolysis (SJS-TEN) | 2.00E-08 | 66.8 |
| rs2187668 | 6 | 2.05E-06 | -6.623 | -10.4535 | RNF5 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 9.985 | -22.7513 | HLA-DQB1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 5.044 | -6.3411 | HLA-DQB2 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 8.741 | -17.6363 | HLA-C | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 4.389 | -4.9436 | NOTCH4 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -8.762 | -17.7171 | ZFP57 | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 5.791 | -8.1551 | HLA-DQB1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -5.404 | -7.1859 | HLA-DPB1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 9.954 | -22.6157 | HLA-DQB1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -5.688 | -7.891 | HLA-DRB1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 4.661 | -5.5021 | HLA-DPA1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -7.936 | -14.6803 | | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 5.539 | -7.5168 | HLA- | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQA2 | | | | | | |
| rs2187668 | 6 | 2.05E-06 | 6.721 | -10.7436 | APOM | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -15.376 | -52.625 | HLA-DRB3 | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 7.801 | -14.2117 | HLA-A | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 5.14 | -6.5611 | AGPAT1 | FEV1FVC_cis | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -6.471 | -10.0116 | HCG4P6 | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | 6.599 | -10.3831 | BTN3A2 | FEV1FVC_trans | T_C | 18204098 | Systemic lupus erythematosus | 3.00E-21 | NR |
| rs2187668 | 6 | 2.05E-06 | -6.623 | -10.4535 | RNF5 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 9.985 | -22.7513 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 5.044 | -6.3411 | HLA-DQB2 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 8.741 | -17.6363 | HLA-C | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 4.389 | -4.9436 | NOTCH4 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | -8.762 | -17.7171 | ZFP57 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 5.791 | -8.1551 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | -5.404 | -7.1859 | HLA-DPB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 9.954 | -22.6157 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | -5.688 | -7.891 | HLA-DRB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 4.661 | -5.5021 | HLA-DPA1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 9.973 | -22.6988 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | -7.936 | -14.6803 | | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 5.539 | -7.5168 | HLA-DQA2 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 6.721 | -10.7436 | APOM | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | -15.376 | -52.625 | HLA-DRB3 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 7.801 | -14.2117 | HLA-A | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 5.14 | -6.5611 | AGPAT1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | -6.471 | -10.0116 | HCG4P6 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs2187668 | 6 | 2.05E-06 | 6.599 | -10.3831 | BTN3A2 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-28 | 2.23 |
| rs1150754 | 6 | 1.81E-04 | -5.498 | -7.4155 | HLA-DPB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 4.105 | -4.3933 | | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 6.187 | -9.2124 | BTN3A2 | FEV1_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 4.258 | -4.6856 | CDSN | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -6.379 | -9.749 | | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 8.875 | -18.1553 | HLA-C | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 6.723 | -10.7495 | HLA-DQB1 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 6.672 | -10.598 | HLA-DQB1 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 7.436 | -12.9839 | HLA-A | FEV1_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -6.581 | -10.3304 | | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -5.444 | -7.2832 | RNF5 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -11.453 | -29.6437 | HLA-DRB3 | FEV1_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -5.444 | -7.2832 | RNF5 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -4.515 | -5.1985 | MICB | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -5.498 | -7.4155 | HLA-DPB1 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -4.515 | -5.1985 | MICB | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 4.105 | -4.3933 | | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -5.396 | -7.1666 | HLA-DQB2 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 6.929 | -11.3728 | APOM | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 6.689 | -10.6484 | HLA- | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB1 | | | | | | |
| rs1150754 | 6 | 1.81E-04 | 6.929 | -11.3728 | APOM | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -8.104 | -15.2742 | ZFP57 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 6.187 | -9.2124 | BTN3A2 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -7.609 | -13.5587 | | FEV1_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 6.689 | -10.6484 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 4.258 | -4.6856 | CDSN | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -6.273 | -9.4508 | HCG4P6 | FEV1_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 5.193 | -6.6842 | NOTCH4 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -8.104 | -15.2742 | ZFP57 | FEV1_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -6.273 | -9.4508 | HCG4P6 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 6.723 | -10.7495 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 6.672 | -10.598 | HLA-DQB1 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | -6.379 | -9.749 | | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 8.875 | -18.1553 | HLA-C | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -11.453 | -29.6437 | HLA-DRB3 | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 5.193 | -6.6842 | NOTCH4 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -6.581 | -10.3304 | | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.15E-04 | 4.141 | -4.4612 | BAT2 | FEV1_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 4.141 | -4.4612 | BAT2 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | 7.436 | -12.9839 | HLA-A | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -5.396 | -7.1666 | HLA-DQB2 | FEV1FVC_cis | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs1150754 | 6 | 1.81E-04 | -7.609 | -13.5587 | | FEV1FVC_trans | T_C | 21408207 | Systemic lupus erythematosus | 6.00E-29 | 2.21 |
| rs3131379 | 6 | 3.07E-05 | 9.979 | -22.725 | ZFP57 | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 8.827 | -17.9685 | | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -5.804 | -8.1888 | PSORS1C1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -4.462 | -5.0905 | HLA-DQA2 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 6.677 | -10.6128 | HCG4P6 | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -4.462 | -5.0905 | HLA-DQA2 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -5.067 | -6.3935 | NOTCH4 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 8.192 | -15.5902 | | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 13.307 | -39.6762 | HLA-DRB3 | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 6.379 | -9.749 | TUBB | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -5.067 | -6.3935 | NOTCH4 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -8.602 | -17.106 | HLA-A | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -5.224 | -6.7567 | CDSN | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -10.329 | -24.2832 | HLA-C | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -8.602 | -17.106 | HLA-A | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 8.107 | -15.285 | | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 6.677 | -10.6128 | HCG4P6 | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -4.488 | -5.1433 | HLA-DQB1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -7.996 | -14.891 | APOM | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -8.201 | -15.6227 | HLA-DQB1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 13.307 | -39.6762 | HLA-DRB3 | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -7.996 | -14.891 | APOM | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 4.791 | -5.78 | MICB | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -4.488 | -5.1433 | HLA-DQB1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -5.324 | -6.9935 | BAT2 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs3131379 | 6 | 3.07E-05 | -7.808 | -14.2358 | BTN3A2 | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -4.757 | -5.7067 | | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 5.991 | -8.6808 | RNF5 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 6.379 | -9.749 | TUBB | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 8.192 | -15.5902 | | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -6.535 | -10.1965 | HCG18 | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 8.107 | -15.285 | | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -7.808 | -14.2358 | BTN3A2 | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -5.224 | -6.7567 | CDSN | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -4.757 | -5.7067 | | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -8.254 | -15.8148 | HLA-DQB1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 6.214 | -9.2869 | C6orf12 | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -5.804 | -8.1888 | PSORS1C1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 4.735 | -5.6594 | SFTA2 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -8.201 | -15.6227 | HLA-DQB1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -6.535 | -10.1965 | HCG18 | FEV1_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 4.023 | -4.2406 | HLA-DRB1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 6.214 | -9.2869 | C6orf12 | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -8.184 | -15.5613 | HLA-DQB1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -5.108 | -6.4873 | AGPAT1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 4.735 | -5.6594 | SFTA2 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -5.108 | -6.4873 | AGPAT1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 9.979 | -22.725 | ZFP57 | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 4.791 | -5.78 | MICB | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | -8.254 | -15.8148 | HLA-DQB1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -10.329 | -24.2832 | HLA-C | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | 8.827 | -17.9685 | | FEV1FVC_trans | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -5.324 | -6.9935 | BAT2 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 5.991 | -8.6808 | RNF5 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 2.35E-06 | -8.184 | -15.5613 | HLA-DQB1 | FEV1FVC_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs3131379 | 6 | 3.07E-05 | 4.023 | -4.2406 | HLA-DRB1 | FEV1_cis | G_A | 18204446 | Systemic lupus erythematosus | 2.00E-52 | 2.36 |
| rs6457617 | 6 | 6.99E-04 | -6.78 | -10.9202 | HLA-DQB2 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | 6.367 | -9.715 | HLA-DRB4 | FEV1FVC_trans | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -6.804 | -10.9925 | HLA-DQB2 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -9.9 | -22.3806 | HLA-DQB1 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -10.077 | -23.156 | HLA-DQB1 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -9.377 | -20.1683 | HLA-DRB5 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | 7.243 | -12.3577 | HLA-DRB6 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -10.042 | -23.0016 | HLA-DQB1 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -11.217 | -28.473 | HLA-DQB1 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -9.658 | -21.3423 | HLA-DRB3 | FEV1FVC_trans | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | 6.159 | -9.1355 | HLA-DQA2 | FEV1FVC_cis | C_T | 20383147 | Systemic sclerosis | 4.00E-17 | 1.37 |
| rs6457617 | 6 | 6.99E-04 | -6.78 | -10.9202 | HLA-DQB2 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | 6.367 | -9.715 | HLA-DRB4 | FEV1FVC_trans | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | -6.804 | -10.9925 | HLA-DQB2 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| rs6457617 | 6 | 6.99E-04 | -9.9 | -22.3806 | HLA-DQB1 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | -10.077 | -23.156 | HLA-DQB1 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | -9.377 | -20.1683 | HLA-DRB5 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | 7.243 | -12.3577 | HLA-DRB6 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | -10.042 | -23.0016 | HLA-DQB1 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | -11.217 | -28.473 | HLA-DQB1 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | -9.658 | -21.3423 | HLA-DRB3 | FEV1FVC_trans | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs6457617 | 6 | 6.99E-04 | 6.159 | -9.1355 | HLA-DQA2 | FEV1FVC_cis | C_T | 21750679 | Systemic sclerosis | 2.00E-37 | 1.61 |
| rs2736428 | 6 | 9.40E-04 | 4.53 | -5.2293 | | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2736428 | 6 | 9.40E-04 | -4.471 | -5.1087 | VARS2 | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2736428 | 6 | 9.40E-04 | -4.229 | -4.6294 | ATF6B | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2736428 | 6 | 9.40E-04 | 4.632 | -5.4411 | | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2736428 | 6 | 9.40E-04 | -5.195 | -6.6888 | HLA-C | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2736428 | 6 | 9.40E-04 | -4.02 | -4.2351 | PSORS1C1 | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2736428 | 6 | 9.40E-04 | -4.11 | -4.4027 | | FEV1FVC_cis | T_C | 20421499 | Telomere length | 3.00E-06 | 0.05 |
| rs2247056 | 6 | 9.20E-04 | -4.726 | -5.6402 | HLA-C | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | 7.947 | -14.7188 | | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -9.237 | -19.596 | HCG27 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -6.324 | -9.5937 | OR13C3 | FEV1FVC_trans | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -12.695 | -36.2005 | PSORS1C1 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -5.254 | -6.8273 | | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -8.859 | -18.0929 | HCG27 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -8.035 | -15.0288 | PSORS1C3 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -11.546 | -30.1116 | | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | 8.136 | -15.3888 | | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -7.972 | -14.8065 | HCG18 | FEV1FVC_trans | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -7.061 | -11.7817 | HLA-G | FEV1FVC_trans | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -5.781 | -8.1293 | ATP6V1G2 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -4.795 | -5.7887 | HLA-C | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -6.202 | -9.2538 | HLA-B | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | 7.993 | -14.8804 | | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -6.646 | -10.5212 | VARS2 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | 6.241 | -9.3617 | CDSN | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -23.259 | -118.938 | HLA-C | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -7.629 | -13.626 | HCG18 | FEV1FVC_trans | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | -4.485 | -5.1372 | | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2247056 | 6 | 9.20E-04 | 4.759 | -5.711 | SFTA2 | FEV1FVC_cis | C_T | 20686565 | Triglycerides | 2.00E-15 | 2.99 |
| rs2647044 | 6 | 2.71E-06 | 10.435 | -24.7654 | HLA-DQB1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 4.656 | -5.4916 | NOTCH4 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -8.557 | -16.9361 | ZFP57 | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -13.927 | -43.3623 | HLA-DRB3 | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 5.088 | -6.4415 | AGPAT1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 4.325 | -4.8166 | HLA-DRB5 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -5.21 | -6.7239 | HLA-DPB1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 7.463 | -13.0728 | HLA-A | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -6.216 | -9.2924 | | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 10.433 | -24.7563 | HLA-DQB1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -4.845 | -5.8975 | HLA-DRB1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs2647044 | 6 | 2.71E-06 | 6.271 | -9.4452 | APOM | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 4.341 | -4.8482 | HLA-DPA1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 6.196 | -9.2372 | HLA-DQB1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 10.416 | -24.6786 | HLA-DQB1 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 8.408 | -16.3798 | HLA-C | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -7.491 | -13.1653 | | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 6.408 | -9.8314 | BTN3A2 | FEV1FVC_trans | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | 4.335 | -4.8364 | HLA-DQB2 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs2647044 | 6 | 2.71E-06 | -6.137 | -9.0752 | RNF5 | FEV1FVC_cis | A_G | 17632545 | Type 1 diabetes | 1.00E-16 | 8.3 |
| rs9272346 | 6 | 8.63E-04 | -10.049 | -23.0324 | HLA-DQB2 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | 16.482 | -60.3061 | HLA-DRB4 | FEV1_trans | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -11.492 | -29.8395 | AGPAT1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -10.107 | -23.2887 | C19orf6 | FEV1_trans | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -13.665 | -41.7844 | HLA-DQB1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -12.808 | -36.83 | HLA-DRB5 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -10.924 | -27.053 | HLA-DRB1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -8.603 | -17.1098 | AGPAT1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -5.675 | -7.858 | TAP2 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -13.463 | -40.588 | HLA-DQB1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -20.082 | -88.9745 | HLA-DQB1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -7.449 | -13.0266 | HLA-DQB2 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -6.341 | -9.6415 | | FEV1_trans | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | 14.33 | -45.8473 | HLA-DRB6 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -13.484 | -40.7116 | HLA-DQB1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | 16.468 | -60.2055 | HLA-DQA2 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -7.529 | -13.2913 | CDSN | FEV1_trans | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -7.577 | -13.4514 | HLA-DRB1 | FEV1_cis | G_A | 18978792 | Type 1 diabetes | 6.00E-129 | NR |
| rs9272346 | 6 | 8.63E-04 | -10.049 | -23.0324 | HLA-DQB2 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | 16.482 | -60.3061 | HLA-DRB4 | FEV1_trans | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -11.492 | -29.8395 | AGPAT1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -10.107 | -23.2887 | C19orf6 | FEV1_trans | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -13.665 | -41.7844 | HLA-DQB1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -12.808 | -36.83 | HLA-DRB5 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -10.924 | -27.053 | HLA-DRB1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -8.603 | -17.1098 | AGPAT1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -5.675 | -7.858 | TAP2 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -13.463 | -40.588 | HLA-DQB1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -20.082 | -88.9745 | HLA-DQB1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -7.449 | -13.0266 | HLA- | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |

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|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | DQB2 | | | | | | |
| rs9272346 | 6 | 8.63E-04 | -6.341 | -9.6415 | | FEV1_trans | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | 14.33 | -45.8473 | HLA-DRB6 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -13.484 | -40.7116 | HLA-DQB1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | 16.468 | -60.2055 | HLA-DQA2 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -7.529 | -13.2913 | CDSN | FEV1_trans | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs9272346 | 6 | 8.63E-04 | -7.577 | -13.4514 | HLA-DRB1 | FEV1_cis | G_A | 17554300 | Type 1 diabetes | 5.00E-134 | 5.49 |
| rs6723108 | 2 | 3.44E-05 | -5.4 | -7.1763 | CCNT2 | FEV1_cis | G_T | 23209189 | Type 2 diabetes | 7.00E-08 | 1.27 |
| rs6723108 | 2 | 3.44E-05 | -4.165 | -4.5067 | CCNT2 | FEV1_cis | G_T | 23209189 | Type 2 diabetes | 7.00E-08 | 1.27 |
| rs6723108 | 2 | 3.44E-05 | -4.835 | -5.8757 | ZRANB3 | FEV1_cis | G_T | 23209189 | Type 2 diabetes | 7.00E-08 | 1.27 |
| rs6723108 | 2 | 3.44E-05 | 6.514 | -10.1356 | DARS | FEV1_trans | G_T | 23209189 | Type 2 diabetes | 7.00E-08 | 1.27 |
| rs6723108 | 2 | 3.44E-05 | -4.124 | -4.429 | TMEM163 | FEV1_cis | G_T | 23209189 | Type 2 diabetes | 7.00E-08 | 1.27 |
| rs6723108 | 2 | 3.44E-05 | -4.441 | -5.048 | ZRANB3 | FEV1_cis | G_T | 23209189 | Type 2 diabetes | 7.00E-08 | 1.27 |
| rs11257655 | 10 | 3.47E-06 | 11.328 | -29.0206 | CAMK1D | FEV1FVC_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 5.19E-05 | 14.628 | -47.7301 | CAMK1D | FEV1_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 5.19E-05 | 4.381 | -4.9276 | NUDT5 | FEV1_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 3.47E-06 | 5.37 | -7.1038 | | FEV1FVC_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 5.19E-05 | 13.121 | -38.6027 | CAMK1D | FEV1_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 3.47E-06 | 14.628 | -47.7301 | CAMK1D | FEV1FVC_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 5.19E-05 | 11.328 | -29.0206 | CAMK1D | FEV1_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 3.47E-06 | 4.601 | -5.3763 | NUDT5 | FEV1FVC_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 3.47E-06 | 13.121 | -38.6027 | CAMK1D | FEV1FVC_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 5.19E-05 | 4.601 | -5.3763 | NUDT5 | FEV1_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 5.19E-05 | 5.37 | -7.1038 | | FEV1_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs11257655 | 10 | 3.47E-06 | 4.381 | -4.9276 | NUDT5 | FEV1FVC_cis | C_T | 22961080 | Type 2 diabetes | 7.00E-09 | 1.15 |
| rs12779790 | 10 | 8.73E-05 | -10.753 | -26.2414 | CAMK1D | FEV1_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 8.73E-05 | -4.812 | -5.8256 | NUDT5 | FEV1_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 8.73E-05 | -4.65 | -5.4789 | NUDT5 | FEV1_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 4.47E-04 | -4.812 | -5.8256 | NUDT5 | FEV1FVC_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 4.47E-04 | -12.746 | -36.4839 | CAMK1D | FEV1FVC_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 4.47E-04 | -4.65 | -5.4789 | NUDT5 | FEV1FVC_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 4.47E-04 | -11.711 | -30.951 | CAMK1D | FEV1FVC_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 4.47E-04 | -4.633 | -5.4432 | | FEV1FVC_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 8.73E-05 | -11.711 | -30.951 | CAMK1D | FEV1_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 8.73E-05 | -12.746 | -36.4839 | CAMK1D | FEV1_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 8.73E-05 | -4.633 | -5.4432 | | FEV1_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs12779790 | 10 | 4.47E-04 | -10.753 | -26.2414 | CAMK1D | FEV1FVC_cis | G_A | 18372903 | Type 2 diabetes | 1.00E-10 | 1.11 |
| rs9268877 | 6 | 7.97E-04 | 4.643 | -5.4642 | TAP2 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -9.309 | -19.8893 | HLA-DRB5 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -4.44 | -5.046 | TAP2 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -5.87 | -8.3607 | HLA-DQB1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -4.696 | -5.5763 | HLA-DQB1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -5.693 | -7.9037 | AGPAT1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -6.472 | -10.0145 | CDSN | FEV1_trans | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | 19.723 | -85.8637 | HLA-DQA2 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -4.704 | -5.5933 | HLA-DQB1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | 19.601 | -84.8193 | HLA-DRB4 | FEV1_trans | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs9268877 | 6 | 7.97E-04 | -4.808 | -5.8169 | HLA-DQB1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -9.149 | -19.2406 | HLA-DRB1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | 14.985 | -50.0361 | HLA-DRB6 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -10.354 | -24.3965 | HLA-DRB1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | -4.96 | -6.1519 | AGPAT1 | FEV1_cis | A_G | 18836448 | Ulcerative colitis | 6.00E-18 | 1.45 |
| rs9268877 | 6 | 7.97E-04 | 4.643 | -5.4642 | TAP2 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -9.309 | -19.8893 | HLA-DRB5 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -4.44 | -5.046 | TAP2 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -5.87 | -8.3607 | HLA-DQB1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -4.696 | -5.5763 | HLA-DQB1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -5.693 | -7.9037 | AGPAT1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -6.472 | -10.0145 | CDSN | FEV1_trans | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | 19.723 | -85.8637 | HLA-DQA2 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -4.704 | -5.5933 | HLA-DQB1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | 19.601 | -84.8193 | HLA-DRB4 | FEV1_trans | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -4.808 | -5.8169 | HLA-DQB1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -9.149 | -19.2406 | HLA-DRB1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | 14.985 | -50.0361 | HLA-DRB6 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -10.354 | -24.3965 | HLA-DRB1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs9268877 | 6 | 7.97E-04 | -4.96 | -6.1519 | AGPAT1 | FEV1_cis | A_G | 19915572 | Ulcerative colitis | 4.00E-23 | NR |
| rs4767364 | 12 | 7.59E-04 | -5.209 | -6.7216 | ERP29 | FEV1FVC_cis | A_G | 21437268 | Upper aerodigestive tract cancers | 2.00E-08 | 1.13 |
| rs4767364 | 12 | 7.59E-04 | -5.776 | -8.1164 | ERP29 | FEV1FVC_cis | A_G | 21437268 | Upper aerodigestive tract cancers | 2.00E-08 | 1.13 |
| rs4970988 | 1 | 7.70E-04 | 9.453 | -20.4825 | ARNT | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -9.503 | -20.6905 | LASS2 | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | 7.188 | -12.1821 | ARNT | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -7.031 | -11.6881 | GOLPH3L | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | 4.168 | -4.5125 | MRPS21 | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -8.486 | -16.6698 | LASS2 | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -7.731 | -13.9718 | HORMAD1 | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -4.762 | -5.7174 | GOLPH3L | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -5.497 | -7.4131 | ARNT | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | -23.972 | -126.2637 | ARNT | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | 4.276 | -4.7206 | | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs4970988 | 1 | 7.70E-04 | 5.832 | -8.2615 | FAM63A | FEV1_cis | A_G | 23263486 | Urate levels | 1.00E-07 | 0.03 |
| rs2842895 | 6 | 1.86E-04 | 7.683 | -13.8085 | RREB1 | FEV1FVC_cis | C_G | 22589738 | Visceral adipose tissue adjusted for BMI | 4.00E-06 | NR |
| rs2842895 | 6 | 1.86E-04 | 7.683 | -13.8085 | RREB1 | FEV1FVC_cis | C_G | 22589738 | Visceral adipose tissue adjusted for BMI | 4.00E-06 | NR |
| rs6904029 | 6 | 3.67E-04 | 6.21 | -9.2759 | ZFP57 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -7.448 | -13.0233 | RP3-377H14.5 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -5.805 | -8.1913 | HCG18 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -5.393 | -7.1593 | | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -7.597 | -13.5185 | | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | 4.447 | -5.0601 | TRIM10 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | 6.458 | -9.9743 | HCG18 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -9.558 | -20.9206 | HLA-A | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -8.785 | -17.8059 | HLA-G | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | 6.687 | -10.6425 | HCG18 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -10.076 | -23.1516 | HCG2P7 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -4.594 | -5.3617 | RNF39 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| rs6904029 | 6 | 3.67E-04 | -11.383 | -29.294 | HCG2P7 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | 7.915 | -14.6069 | HLA-F | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | 10.796 | -26.4443 | HCG4P6 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | -8.761 | -17.7133 | HLA-G | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs6904029 | 6 | 3.67E-04 | 9.005 | -18.6662 | RP3-377H14.5 | FEV1FVC_cis | A_G | 20410501 | Vitiligo | 1.00E-21 | 1.49 |
| rs3095254 | 6 | 9.77E-04 | 6.649 | -10.53 | | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -7.176 | -12.144 | | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | 15.903 | -56.219 | CDSN | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -4.344 | -4.8541 | | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -4.365 | -4.8958 | | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -6.83 | -11.071 | | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -5.781 | -8.1293 | HCG27 | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -6.76 | -10.8601 | PSORS1C3 | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -4.94 | -6.1072 | HCG27 | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | -7.232 | -12.3225 | PSORS1C1 | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |
| rs3095254 | 6 | 9.77E-04 | 4.123 | -4.4272 | AGPAT1 | FEV1_cis | G_C | 21738478 | White blood cell types | 6.00E-11 | 0.07 |

## Supplementary Table 15: ChIP Seq Significance tool results

Table shows a list of transcription factors enriched among *cis* acting lung function eSNP-regulated genes. Transcription binding significance is calculated using a hypergeometric test followed by multiple hypothesis correction using the method of Benjamini and Hochberg FDR method. Factor: transcription factor that is enriched. Q-value: minimum false discovery rate at which a transcription factor can still be considered significant. Only transcription factors with a q-value < .05 are reported. Factor Rank: The rank of enriched transcription factors.

| **Transcription factor enrichment among lung function *cis* eSNP- regulated genes** | | | | | | |
|---|---|---|---|---|---|---|
| **FEV$_1$ cis eSNP-regulated genes** | | | | **FEV$_1$/FVC cis eSNP-regulated genes** | | |
| Factor | Q-value | Factor Rank | | Factor | Q-value | Factor Rank |
| CmycEstro | 1.04E-03 | 1 | | Pol2 | 4.19E-07 | 1 |
| NfkbTnfa | 1.04E-03 | 1 | | Ebf1 | 8.69E-05 | 2 |
| P300 | 1.04E-03 | 1 | | Sin3a | 1.83E-03 | 3 |
| Pol2 | 1.04E-03 | 1 | | Cmyc | 2.41E-03 | 4 |
| CmycSerumstvd | 1.21E-03 | 5 | | NfkbTnfa | 3.06E-03 | 5 |
| Mybl2 | 1.21E-03 | 5 | | P300 | 3.06E-03 | 5 |
| Nrsf | 1.21E-03 | 5 | | Pml | 3.06E-03 | 5 |
| Pml | 1.21E-03 | 5 | | Taf1 | 3.06E-03 | 5 |
| Taf1 | 1.21E-03 | 5 | | Yy1 | 3.06E-03 | 5 |
| Tbp | 1.21E-03 | 5 | | Chd2 | 3.27E-03 | 10 |
| Yy1 | 1.21E-03 | 5 | | Max | 3.27E-03 | 10 |
| Elf1 | 1.66E-03 | 12 | | Elf1 | 4.12E-03 | 12 |
| Hnf4g | 1.90E-03 | 13 | | Pol2Ifng6h | 4.12E-03 | 12 |
| Maff | 1.90E-03 | 13 | | Maz | 4.48E-03 | 14 |
| Mxi1 | 2.25E-03 | 15 | | Arid3a | 5.46E-03 | 15 |
| Mta3 | 2.28E-03 | 16 | | Cfos | 5.46E-03 | 15 |
| Sin3a | 2.30E-03 | 17 | | E2f6 | 5.46E-03 | 15 |
| Cebpz | 2.85E-03 | 18 | | Rfx5 | 5.46E-03 | 15 |
| Creb1 | 2.85E-03 | 18 | | Tbp | 5.46E-03 | 15 |
| Phf8 | 2.85E-03 | 18 | | Prdm1 | 5.66E-03 | 20 |
| Plu1 | 2.85E-03 | 18 | | Mxi1 | 5.82E-03 | 21 |
| Rad21 | 2.85E-03 | 18 | | Pol2Ifng30 | 6.23E-03 | 22 |
| Znf143 | 2.85E-03 | 18 | | Pol2Tam | 6.23E-03 | 22 |
| Chd2 | 3.00E-03 | 24 | | Pol2s2 | 6.23E-03 | 22 |
| Stat1Ifng30 | 3.00E-03 | 24 | | Ctcf | 9.05E-03 | 25 |
| Usf2 | 3.47E-03 | 26 | | Irf1Ifng6h | 9.05E-03 | 25 |
| Usf1 | 3.71E-03 | 27 | | Tcf12 | 9.05E-03 | 25 |

|  |  |  |  |  |  |  |
|---|---|---|---|---|---|---|
| Foxa2 | 4.16E-03 | 28 |  | Ets1 | 9.54E-03 | 28 |
| Gabp | 4.16E-03 | 28 |  | Cebpz | 9.94E-03 | 29 |
| Hnf4a | 4.16E-03 | 28 |  | Pou2f2 | 1.10E-02 | 30 |
| Pol2Serumstim | 4.16E-03 | 28 |  | Creb1 | 1.11E-02 | 31 |
| Pou2f2 | 4.16E-03 | 28 |  | Pol2Ifna30 | 1.11E-02 | 31 |
| CmycIfng30 | 4.17E-03 | 33 |  | Nrsf | 1.25E-02 | 33 |
| CmycSerumstim | 4.42E-03 | 34 |  | Pol2Ifna6h | 1.25E-02 | 33 |
| Foxm1 | 4.81E-03 | 35 |  | Ap2gamma | 1.28E-02 | 35 |
| Pol2s2 | 4.81E-03 | 35 |  | CmycIfng30 | 1.31E-02 | 36 |
| Runx3 | 4.92E-03 | 37 |  | Smc3 | 1.58E-02 | 37 |
| E2f6 | 5.22E-03 | 38 |  | Nfyb | 1.76E-02 | 38 |
| Pol2Tam | 5.32E-03 | 39 |  | Phf8 | 1.76E-02 | 38 |
| Cmyc | 5.54E-03 | 40 |  | Pu1 | 1.76E-02 | 38 |
| Pol2Etoh01 | 5.54E-03 | 40 |  | Hdac2 | 1.93E-02 | 41 |
| Pu1 | 5.54E-03 | 40 |  | Runx3 | 1.99E-02 | 42 |
| Corest | 6.11E-03 | 43 |  | Sp1 | 2.10E-02 | 43 |
| Tf3c | 6.73E-03 | 44 |  | Tead4 | 2.10E-02 | 43 |
| Arid3a | 7.26E-03 | 45 |  | Rad21 | 2.14E-02 | 45 |
| Smc3 | 7.40E-03 | 46 |  | Ap2alpha | 2.16E-02 | 46 |
| Ebf1 | 8.92E-03 | 47 |  | Pax5 | 2.16E-02 | 46 |
| Sp1 | 8.92E-03 | 47 |  | Pol2Serumstim | 2.43E-02 | 48 |
| Max | 9.79E-03 | 49 |  | Tblr1 | 2.43E-02 | 48 |
| Pol2Ifng6h | 9.90E-03 | 50 |  | Stat1Ifng30 | 3.04E-02 | 50 |
| Mafk | 1.00E-02 | 51 |  | E2f4 | 3.12E-02 | 51 |
| Pol2Serumstvd | 1.00E-02 | 51 |  | Hnf4a | 3.12E-02 | 51 |
| Srebp1 | 1.04E-02 | 53 |  | Ikzf1 | 3.16E-02 | 53 |
| Bcl3 | 1.07E-02 | 54 |  | Pol2Serumstvd | 3.50E-02 | 54 |
| Tcf12 | 1.07E-02 | 54 |  | Bcl3 | 3.56E-02 | 55 |
| Cbx3 | 1.20E-02 | 56 |  | Rbbp5 | 3.77E-02 | 56 |
| Rfx5 | 1.25E-02 | 57 |  | Znf143 | 3.77E-02 | 56 |
| Hae2f1 | 1.38E-02 | 58 |  | Plu1 | 4.03E-02 | 58 |
| Tead4 | 1.38E-02 | 58 |  | Rxra | 4.18E-02 | 59 |
| Foxa1 | 1.38E-02 | 60 |  | Atf1 | 4.26E-02 | 60 |
| Atf2 | 1.40E-02 | 61 |  | CtcfEstro | 4.38E-02 | 61 |
| Maz | 1.40E-02 | 62 |  | CtcfSerumstvd | 4.44E-02 | 62 |
| Stat1Ifng6h | 1.40E-02 | 62 |  | Gtf2f1 | 4.82E-02 | 63 |
| Irf4 | 1.47E-02 | 64 |  |  |  |  |

| | | | | | | |
|---|---|---|---|---|---|---|
| Zbtb33 | 1.56E-02 | 65 | | | | |
| Prdm1 | 1.59E-02 | 66 | | | | |
| Gtf2f1 | 1.64E-02 | 67 | | | | |
| Mbd4 | 1.64E-02 | 67 | | | | |
| CmycIfng6h | 1.67E-02 | 69 | | | | |
| Chd1 | 1.71E-02 | 70 | | | | |
| Pol2Ifng30 | 1.74E-02 | 71 | | | | |
| CmycVeh | 1.88E-02 | 72 | | | | |
| Ikzf1 | 1.88E-02 | 72 | | | | |
| Nanog | 1.88E-02 | 72 | | | | |
| Nr2f2 | 1.88E-02 | 72 | | | | |
| Pol2Ifna30 | 1.88E-02 | 72 | | | | |
| Elk4 | 1.90E-02 | 77 | | | | |
| CmycIfna6h | 1.90E-02 | 78 | | | | |
| Elk1 | 1.90E-02 | 79 | | | | |
| Brca1 | 1.99E-02 | 80 | | | | |
| Whip | 2.01E-02 | 81 | | | | |
| CmycTam14h | 2.19E-02 | 82 | | | | |
| Ctcf | 2.49E-02 | 83 | | | | |
| Gata1 | 2.80E-02 | 84 | | | | |
| Irf1Ifng6h | 2.80E-02 | 84 | | | | |
| Mef2c | 2.80E-02 | 84 | | | | |
| E2f4 | 2.83E-02 | 87 | | | | |
| Tcf3 | 2.83E-02 | 88 | | | | |
| Znf263 | 2.96E-02 | 89 | | | | |
| Pax5 | 3.07E-02 | 90 | | | | |
| Pgc1a | 3.10E-02 | 91 | | | | |
| Gata3 | 3.10E-02 | 92 | | | | |
| Srf | 3.10E-02 | 92 | | | | |
| Stat3 | 3.10E-02 | 92 | | | | |
| CmycEtoh01 | 3.18E-02 | 95 | | | | |
| Bhlhe40 | 3.23E-02 | 96 | | | | |
| Trim28 | 3.34E-02 | 97 | | | | |
| Pol2Ifna6h | 3.48E-02 | 98 | | | | |
| Stat2Ifna6h | 3.63E-02 | 99 | | | | |
| Tcf7l2 | 3.73E-02 | 100 | | | | |
| Six5 | 3.74E-02 | 101 | | | | |

| | | | | | | |
|---|---|---|---|---|---|---|
| Rxra | 3.83E-02 | 102 | | | | |
| Nfya | 4.25E-02 | 103 | | | | |
| Atf1 | 4.30E-02 | 104 | | | | |
| Hdac2 | 4.30E-02 | 104 | | | | |
| Nfic | 4.34E-02 | 106 | | | | |
| Stat1 | 4.34E-02 | 106 | | | | |
| Zeb1 | 4.34E-02 | 106 | | | | |
| Eralpha | 4.36E-02 | 109 | | | | |
| Cebpb | 4.54E-02 | 110 | | | | |
| E2f4Tam | 4.54E-02 | 110 | | | | |
| Egr1 | 4.54E-02 | 110 | | | | |
| Hdac1 | 4.54E-02 | 110 | | | | |
| Pol2b | 4.54E-02 | 110 | | | | |
| Tblr1 | 4.54E-02 | 110 | | | | |
| Tr4 | 4.54E-02 | 110 | | | | |
| Ets1 | 4.61E-02 | 117 | | | | |
| Rbbp5 | 4.61E-02 | 117 | | | | |
| Nfatc1 | 4.78E-02 | 119 | | | | |
| Irf1Ifng30 | 4.81E-02 | 120 | | | | |
| eGFP-Gata2 | 4.86E-02 | 121 | | | | |

## Supplementary Table 16: Lung function eSNP regulated probesets regression on COPD

Beta: beta coefficient from the logistic regression of probeset levels on COPD status. SE: standard error. P value: P value for probeset regression on COPD. FDR: False Discovery Rate.

| eSNP-regulated genes association results with COPD | | | | | | |
|---|---|---|---|---|---|---|
| **Gene Symbol** | **Gene Name** | **probeset** | **Beta** | **SE** | **P value** | **FDR** |
| ITIH5 | inter-alpha (globulin) inhibitor H5 | 100132638_TGI_at | -1.146 | 0.296 | 1.07E-04 | 0.042761 |
| TTC19 | tetratricopeptide repeat domain 19 | 100132808_TGI_at | -0.659 | 0.169 | 9.96E-05 | 0.042761 |
| AI417595 | cDNA clone that maps to EMCN | 100130355_TGI_at | -0.603 | 0.195 | 1.94E-03 | 0.173672 |
| AK026718 | cDNA clone that maps to SNX2 | 100145444_TGI_at | -9.052 | 2.898 | 1.79E-03 | 0.173672 |
| AK056784 | cDNA clone that maps to SH3PXD2A | 100157818_TGI_at | -12.403 | 3.957 | 1.72E-03 | 0.173672 |
| C3orf26 | chromosome 3 open reading frame 26 | 100159492_TGI_at | 1.122 | 0.343 | 1.09E-03 | 0.173672 |
| CCBE1 | collagen and calcium binding EGF domains 1 | 100312458_TGI_at | -0.424 | 0.137 | 1.96E-03 | 0.173672 |
| NR3C1 | "nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)" | 100122984_TGI_at | -0.367 | 0.115 | 1.43E-03 | 0.173672 |
| PABPC4 | "poly(A) binding protein, cytoplasmic 4 (inducible form)" | 100302787_TGI_at | 0.383 | 0.123 | 1.79E-03 | 0.173672 |
| CCBE1 | collagen and calcium binding EGF domains 1 | 100129234_TGI_at | -1.762 | 0.579 | 2.35E-03 | 0.18817 |
| ITIH5 | inter-alpha (globulin) inhibitor H5 | 100159682_TGI_at | -0.388 | 0.131 | 3.14E-03 | 0.209944 |
| TRIM63 | tripartite motif-containing 63 | 100137694_TGI_at | 5.472 | 1.853 | 3.15E-03 | 0.209944 |
| ALDH2 | aldehyde dehydrogenase 2 family (mitochondrial) | 100308316_TGI_at | -1.130 | 0.388 | 3.53E-03 | 0.217168 |
| NR0B2 | "nuclear receptor subfamily 0, group B, member 2" | 100149978_TGI_at | -1.600 | 0.553 | 3.81E-03 | 0.217757 |
| C3orf26 | chromosome 3 open reading frame 26 | 100304176_TGI_at | 1.500 | 0.530 | 4.62E-03 | 0.230572 |
| CLDN23 | claudin 23 | 100135523_TGI_at | -0.399 | 0.140 | 4.50E-03 | 0.230572 |
| CCBE1 | collagen and calcium binding EGF domains 1 | 100129585_TGI_at | -1.826 | 0.650 | 4.95E-03 | 0.232861 |
| NPNT | nephronectin | 100129915_TGI_at | -0.098 | 0.035 | 5.28E-03 | 0.23431 |
| BC019888 | cDNA clone that maps to ZKSCAN3 | 100140600_TGI_at | -2.292 | 0.847 | 6.83E-03 | 0.259807 |
| NTN4 | netrin 4 | 100137266_TGI_at | -0.377 | 0.139 | 6.77E-03 | 0.259807 |
| SLC6A4 | "solute carrier family 6 (neurotransmitter transporter, serotonin), member 4" | 100136626_TGI_at | -0.262 | 0.096 | 6.68E-03 | 0.259807 |
| ATF6 | activating transcription factor 6 | 100155887_TGI_at | 0.528 | 0.197 | 7.49E-03 | 0.260405 |
| LTK | leukocyte receptor tyrosine kinase | 100154412_TGI_at | -1.177 | 0.439 | 7.42E-03 | 0.260405 |
| NA | FGF receptor activating protein 1 | 100124148_TGI_at | -0.841 | 0.317 | 8.00E-03 | 0.266384 |
| AGER | advanced glycosylation end product-specific receptor | 100313510_TGI_at | -0.058 | 0.022 | 8.41E-03 | 0.268743 |
| AY102072 | cDNA clone that maps to ACTR3C | 100157804_TGI_at | -1.818 | 0.705 | 9.89E-03 | 0.282271 |

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|---|---|---|---|---|---|---|
| C21orf82 | chromosome 21 open reading frame 82 | 100128165_TGI_at | 7.912 | 3.046 | 9.38E-03 | 0.282271 |
| ZNF436 | zinc finger protein 436 | 100310881_TGI_at | -2.002 | 0.776 | 9.89E-03 | 0.282271 |
| SDK1 | "sidekick homolog 1, cell adhesion molecule (chicken)" | 100132261_TGI_at | 0.714 | 0.278 | 1.03E-02 | 0.283933 |
| SLC35A1 | "solute carrier family 35 (CMP-sialic acid transporter), member A1" | 100306590_TGI_at | -0.481 | 0.190 | 1.14E-02 | 0.302476 |
| FAM63A | "family with sequence similarity 63, member A" | 100313509_TGI_at | -0.438 | 0.174 | 1.20E-02 | 0.310629 |
| NA | NA | 100142556_TGI_at | 2.195 | 0.892 | 1.38E-02 | 0.345439 |
| BRWD1 | bromodomain and WD repeat domain containing 1 | 100300682_TGI_at | -3.105 | 1.288 | 1.59E-02 | 0.353056 |
| CCNT2 | cyclin T2 | 100306705_TGI_at | -0.495 | 0.204 | 1.51E-02 | 0.353056 |
| PADI2 | "peptidyl arginine deiminase, type II" | 100143443_TGI_at | 0.160 | 0.066 | 1.56E-02 | 0.353056 |
| RPS5 | ribosomal protein S5 | 100139275_TGI_at | 0.092 | 0.038 | 1.59E-02 | 0.353056 |
| AZGP1 | "alpha-2-glycoprotein 1, zinc-binding" | 100151170_TGI_at | 0.093 | 0.039 | 1.73E-02 | 0.36202 |
| EPS15 | epidermal growth factor receptor pathway substrate 15 | 100140992_TGI_at | -0.364 | 0.153 | 1.77E-02 | 0.36202 |
| NA | NA | 100149604_TGI_at | 18.689 | 7.829 | 1.70E-02 | 0.36202 |
| AGER | advanced glycosylation end product-specific receptor | 100143779_TGI_at | -0.065 | 0.028 | 1.89E-02 | 0.368955 |
| VEZT | "vezatin, adherens junctions transmembrane protein" | 100302084_TGI_at | -2.590 | 1.102 | 1.88E-02 | 0.368955 |
| NR3C1 | "nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)" | 100129487_TGI_at | -0.334 | 0.144 | 2.05E-02 | 0.390406 |
| BAG5 | BCL2-associated athanogene 5 | 100126588_TGI_at | -0.516 | 0.227 | 2.29E-02 | 0.405396 |
| C10orf58 | chromosome 10 open reading frame 58 | 100161068_TGI_at | 0.393 | 0.176 | 2.52E-02 | 0.405396 |
| FBXO38 | F-box protein 38 | 100134215_TGI_at | -0.494 | 0.217 | 2.27E-02 | 0.405396 |
| MCM6 | minichromosome maintenance complex component 6 | 100305043_TGI_at | 0.739 | 0.329 | 2.48E-02 | 0.405396 |
| NA | hypothetical protein LOC729082 | 100309540_TGI_at | 1.337 | 0.590 | 2.36E-02 | 0.405396 |
| NA | NA | 100129852_TGI_at | -4.085 | 1.822 | 2.49E-02 | 0.405396 |
| NA | "similar to amyloid beta (A4) precursor protein-binding, family B, member 1 interacting protein" | 100300305_TGI_at | 5.415 | 2.422 | 2.54E-02 | 0.405396 |
| TGFB2 | "transforming growth factor, beta 2" | 100303767_TGI_at | -0.826 | 0.362 | 2.27E-02 | 0.405396 |
| GGT7 | gamma-glutamyltransferase 7 | 100300977_TGI_at | 1.351 | 0.607 | 2.60E-02 | 0.407845 |
| RPS5 | ribosomal protein S5 | 100307917_TGI_at | 0.079 | 0.036 | 2.67E-02 | 0.410209 |
| NA | NA | 100142471_TGI_at | -0.986 | 0.449 | 2.82E-02 | 0.417104 |
| TOM1L2 | target of myb1-like 2 (chicken) | 100153419_TGI_at | 2.296 | 1.045 | 2.81E-02 | 0.417104 |
| ARHGAP27 | Rho GTPase activating protein 27 | 100133349_TGI_at | -1.004 | 0.464 | 3.06E-02 | 0.423096 |
| ARHGEF19 | Rho guanine nucleotide exchange factor (GEF) 19 | 100313238_TGI_at | -1.518 | 0.703 | 3.07E-02 | 0.423096 |
| PID1 | phosphotyrosine interaction domain containing 1 | 100307074_TGI_at | 1.614 | 0.747 | 3.07E-02 | 0.423096 |
| PIP4K2B | "phosphatidylinositol-5-phosphate 4-kinase, type II, beta" | 100123137_TGI_at | -0.395 | 0.183 | 3.11E-02 | 0.423096 |
| ZRANB3 | "zinc finger, RAN-binding domain containing 3" | 100133530_TGI_at | 7.168 | 3.328 | 3.12E-02 | 0.423096 |
| ARHGEF19 | Rho guanine nucleotide exchange factor (GEF) 19 | 100122367_TGI_at | -2.314 | 1.096 | 3.48E-02 | 0.431674 |
| NA | NA | 100304704_TGI_at | 1.144 | 0.537 | 3.31E-02 | 0.431674 |

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|---|---|---|---|---|---|---|
| NA | NA | 100128463_TGI_at | -1.397 | 0.662 | 3.49E-02 | 0.431674 |
| SLC22A5 | "solute carrier family 22 (organic cation/carnitine transporter), member 5" | 100123073_TGI_at | -0.841 | 0.398 | 3.46E-02 | 0.431674 |
| SPINK5 | "serine peptidase inhibitor, Kazal type 5" | 100305138_TGI_at | 0.875 | 0.409 | 3.24E-02 | 0.431674 |
| ZRANB3 | "zinc finger, RAN-binding domain containing 3" | 100310941_TGI_at | 5.020 | 2.383 | 3.51E-02 | 0.431674 |
| PSMB3 | "proteasome (prosome, macropain) subunit, beta type, 3" | 100134576_TGI_at | 0.245 | 0.117 | 3.60E-02 | 0.436223 |
| RPS6KL1 | ribosomal protein S6 kinase-like 1 | 100151794_TGI_at | 2.849 | 1.371 | 3.77E-02 | 0.450151 |
| NA | hypothetical LOC646719 | 100310722_TGI_at | -0.607 | 0.297 | 4.08E-02 | 0.455542 |
| NA | NA | 100136516_TGI_at | 4.995 | 2.444 | 4.10E-02 | 0.455542 |
| NA | NA | 100130789_TGI_at | -2.137 | 1.046 | 4.10E-02 | 0.455542 |
| UBE2Q1 | ubiquitin-conjugating enzyme E2Q family member 1 | 100162507_TGI_at | -2.348 | 1.140 | 3.95E-02 | 0.455542 |
| ZADH2 | zinc binding alcohol dehydrogenase domain containing 2 | 100306063_TGI_at | -0.977 | 0.476 | 4.01E-02 | 0.455542 |
| LONP2 | "lon peptidase 2, peroxisomal" | 100134381_TGI_at | 1.353 | 0.665 | 4.18E-02 | 0.456652 |
| PIP4K2B | "phosphatidylinositol-5-phosphate 4-kinase, type II, beta" | 100304243_TGI_at | -0.698 | 0.344 | 4.23E-02 | 0.456652 |
| HLA-DQB1 | "major histocompatibility complex, class II, DQ beta 1" | 100311704_TGI_at | 3.721 | 1.845 | 4.38E-02 | 0.466537 |
| SVEP1 | "sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1" | 100160095_TGI_at | 11.846 | 5.903 | 4.48E-02 | 0.471009 |
| ATF6 | activating transcription factor 6 | 100304092_TGI_at | 0.488 | 0.247 | 4.80E-02 | 0.479158 |
| C21orf82 | chromosome 21 open reading frame 82 | 100301107_TGI_at | 3.617 | 1.827 | 4.77E-02 | 0.479158 |
| MRPS6 | mitochondrial ribosomal protein S6 | 100145031_TGI_at | 0.211 | 0.106 | 4.62E-02 | 0.479158 |
| NA | NA | 100307733_TGI_at | -0.583 | 0.295 | 4.79E-02 | 0.479158 |
| NA | hypothetical protein LOC256273 | 100130569_TGI_at | -1.019 | 0.518 | 4.91E-02 | 0.479158 |
| NA | NA | 100313618_TGI_at | 7.118 | 3.622 | 4.94E-02 | 0.479158 |
| ZSWIM7 | "zinc finger, SWIM-type containing 7" | 100125319_TGI_at | -0.693 | 0.353 | 4.98E-02 | 0.479158 |
| EIF2B2 | "eukaryotic translation initiation factor 2B, subunit 2 beta, 39kDa" | 100127661_TGI_at | 1.120 | 0.573 | 5.05E-02 | 0.479627 |
| MCM6 | minichromosome maintenance complex component 6 | 100148961_TGI_at | 1.025 | 0.526 | 5.14E-02 | 0.479627 |
| NUDT5 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 | 100154198_TGI_at | 0.468 | 0.241 | 5.16E-02 | 0.479627 |
| C9orf95 | chromosome 9 open reading frame 95 | 100125670_TGI_at | -0.438 | 0.226 | 5.24E-02 | 0.48007 |
| SNRPF | small nuclear ribonucleoprotein polypeptide F | 100310201_TGI_at | 0.387 | 0.200 | 5.29E-02 | 0.48007 |
| TMED10 | transmembrane emp24-like trafficking protein 10 (yeast) | 100152363_TGI_at | -2.839 | 1.481 | 5.52E-02 | 0.495627 |
| CNKSR1 | connector enhancer of kinase suppressor of Ras 1 | 100154120_TGI_at | -0.559 | 0.294 | 5.70E-02 | 0.503127 |
| HOXC12 | homeobox C12 | 100137986_TGI_at | 35.637 | 18.833 | 5.84E-02 | 0.503127 |
| PDDC1 | Parkinson disease 7 domain containing 1 | 100132055_TGI_at | -0.236 | 0.124 | 5.75E-02 | 0.503127 |
| S100A14 | S100 calcium binding protein A14 | 100310151_TGI_at | -0.257 | 0.136 | 5.85E-02 | 0.503127 |
| CCBE1 | collagen and calcium binding EGF domains 1 | 100136733_TGI_at | -0.658 | 0.350 | 6.03E-02 | 0.513148 |
| ARNT | aryl hydrocarbon receptor nuclear translocator | 100138305_TGI_at | -0.264 | 0.144 | 6.61E-02 | 0.517073 |

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|---|---|---|---|---|---|---|
| CCDC53 | coiled-coil domain containing 53 | 100151519_TGI_at | -0.360 | 0.193 | 6.24E-02 | 0.517073 |
| CEP192 | centrosomal protein 192kDa | 100154727_TGI_at | -6.254 | 3.497 | 7.37E-02 | 0.517073 |
| CLEC2D | "C-type lectin domain family 2, member D" | 100304233_TGI_at | 0.250 | 0.140 | 7.37E-02 | 0.517073 |
| FGD6 | "FYVE, RhoGEF and PH domain containing 6" | 100151388_TGI_at | -0.589 | 0.318 | 6.39E-02 | 0.517073 |
| HOXC6 | homeobox C6 | 100144365_TGI_at | 0.605 | 0.333 | 6.92E-02 | 0.517073 |
| MON1B | MON1 homolog B (yeast) | 100307707_TGI_at | -0.605 | 0.338 | 7.37E-02 | 0.517073 |
| NA | NA | 100140380_TGI_at | -6.597 | 3.543 | 6.27E-02 | 0.517073 |
| NA | NA | 100160039_TGI_at | -6.267 | 3.394 | 6.48E-02 | 0.517073 |
| NA | NA | 100145604_TGI_at | -6.384 | 3.500 | 6.81E-02 | 0.517073 |
| NA | hypothetical FLJ44796 | 100149872_TGI_at | -0.514 | 0.283 | 6.95E-02 | 0.517073 |
| NA | hypothetical FLJ44796 | 100307273_TGI_at | -0.528 | 0.292 | 7.08E-02 | 0.517073 |
| NA | NA | 100151793_TGI_at | 8.189 | 4.539 | 7.12E-02 | 0.517073 |
| NA | NA | 100306620_TGI_at | -1.449 | 0.807 | 7.25E-02 | 0.517073 |
| NA | NA | 100136594_TGI_at | -1.311 | 0.731 | 7.27E-02 | 0.517073 |
| NPHP3 | nephronophthisis 3 (adolescent) | 100143326_TGI_at | -1.406 | 0.772 | 6.83E-02 | 0.517073 |
| NUDT5 | nudix (nucleoside diphosphate linked moiety X)-type motif 5 | 100303975_TGI_at | 0.420 | 0.228 | 6.56E-02 | 0.517073 |
| RHOA | "ras homolog gene family, member A" | 100138300_TGI_at | -0.109 | 0.060 | 6.71E-02 | 0.517073 |
| SPTBN5 | "spectrin, beta, non-erythrocytic 5" | 100134750_TGI_at | 3.019 | 1.649 | 6.71E-02 | 0.517073 |
| YLPM1 | YLP motif containing 1 | 100160610_TGI_at | -6.631 | 3.636 | 6.82E-02 | 0.517073 |
| ADAM19 | ADAM metallopeptidase domain 19 (meltrin beta) | 100132327_TGI_at | 0.391 | 0.222 | 7.86E-02 | 0.518998 |
| AMT | aminomethyltransferase | 100124708_TGI_at | -0.515 | 0.296 | 8.16E-02 | 0.518998 |
| CLEC2D | "C-type lectin domain family 2, member D" | 100309845_TGI_at | 0.252 | 0.145 | 8.09E-02 | 0.518998 |
| ERP29 | endoplasmic reticulum protein 29 | 100300653_TGI_at | -9.905 | 5.636 | 7.89E-02 | 0.518998 |
| FGD6 | "FYVE, RhoGEF and PH domain containing 6" | 100146416_TGI_at | -0.947 | 0.548 | 8.42E-02 | 0.518998 |
| MAPT | microtubule-associated protein tau | 100161408_TGI_at | 1.688 | 0.957 | 7.78E-02 | 0.518998 |
| NA | NA | 100161122_TGI_at | 1.001 | 0.567 | 7.72E-02 | 0.518998 |
| NA | NA | 100311757_TGI_at | -3.058 | 1.738 | 7.85E-02 | 0.518998 |
| NA | NA | 100307519_TGI_at | -0.506 | 0.289 | 8.01E-02 | 0.518998 |
| NA | NA | 100132347_TGI_at | 1.513 | 0.870 | 8.21E-02 | 0.518998 |
| NA | hypothetical protein LOC285835 | 100155331_TGI_at | -0.937 | 0.544 | 8.51E-02 | 0.518998 |
| NOTCH4 | Notch homolog 4 (Drosophila) | 100148822_TGI_at | -0.174 | 0.098 | 7.68E-02 | 0.518998 |
| NUDT14 | nudix (nucleoside diphosphate linked moiety X)-type motif 14 | 100151496_TGI_at | -0.392 | 0.227 | 8.45E-02 | 0.518998 |
| RUNX2 | runt-related transcription factor 2 | 100122981_TGI_at | -1.738 | 1.003 | 8.31E-02 | 0.518998 |
| SIAH1 | seven in absentia homolog 1 (Drosophila) | 100139154_TGI_at | -0.490 | 0.282 | 8.21E-02 | 0.518998 |
| ZNF323 | zinc finger protein 323 | 100143968_TGI_at | -0.404 | 0.230 | 7.96E-02 | 0.518998 |
| ZNF323 | zinc finger protein 323 | 100301615_TGI_at | -0.355 | 0.205 | 8.37E-02 | 0.518998 |

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| GPC5 | glypican 5 | 100129443_TGI_at | -4.158 | 2.428 | 8.68E-02 | 0.521146 |
| ZNF436 | zinc finger protein 436 | 100127649_TGI_at | -1.359 | 0.795 | 8.74E-02 | 0.521146 |
| ZNF639 | zinc finger protein 639 | 100302139_TGI_at | -3.976 | 2.324 | 8.71E-02 | 0.521146 |
| SLC22A5 | "solute carrier family 22 (organic cation/carnitine transporter), member 5" | 100309997_TGI_at | -4.655 | 2.737 | 8.90E-02 | 0.527209 |
| FLOT1 | flotillin 1 | 100313972_TGI_at | 4.419 | 2.611 | 9.05E-02 | 0.531991 |
| CKM | "creatine kinase, muscle" | 100148378_TGI_at | 9.873 | 5.859 | 9.20E-02 | 0.536589 |
| RBP2 | "retinol binding protein 2, cellular" | 100309242_TGI_at | -0.560 | 0.334 | 9.32E-02 | 0.539883 |
| HSD17B12 | hydroxysteroid (17-beta) dehydrogenase 12 | 100308139_TGI_at | -0.326 | 0.197 | 9.81E-02 | 0.552667 |
| IQGAP3 | IQ motif containing GTPase activating protein 3 | 100307611_TGI_at | 5.484 | 3.323 | 9.89E-02 | 0.552667 |
| NA | NA | 100157337_TGI_at | -0.603 | 0.365 | 9.86E-02 | 0.552667 |
| PNPO | pyridoxamine 5';-phosphate oxidase | 100129691_TGI_at | 0.695 | 0.420 | 9.78E-02 | 0.552667 |
| SEC61A2 | Sec61 alpha 2 subunit (S. cerevisiae) | 100305260_TGI_at | -1.239 | 0.747 | 9.70E-02 | 0.552667 |
| ATF6B | activating transcription factor 6 beta | 100302735_TGI_at | -0.311 | 0.190 | 1.02E-01 | 0.562102 |
| SIAH1 | seven in absentia homolog 1 (Drosophila) | 100305657_TGI_at | -0.637 | 0.389 | 1.02E-01 | 0.562102 |
| ZFP57 | zinc finger protein 57 homolog (mouse) | 100303994_TGI_at | 1.530 | 0.939 | 1.03E-01 | 0.565819 |
| WWOX | WW domain containing oxidoreductase | 100143315_TGI_at | 2.818 | 1.736 | 1.04E-01 | 0.567886 |
| DST | dystonin | 100138535_TGI_at | -0.364 | 0.226 | 1.07E-01 | 0.570381 |
| NA | NA | 100311980_TGI_at | -0.236 | 0.146 | 1.07E-01 | 0.570381 |
| NA | NA | 100304001_TGI_at | -0.244 | 0.151 | 1.07E-01 | 0.570381 |
| NA | NA | 100155895_TGI_at | 15.626 | 9.764 | 1.10E-01 | 0.572148 |
| S100A1 | S100 calcium binding protein A1 | 100126124_TGI_at | 1.507 | 0.941 | 1.09E-01 | 0.572148 |
| ZNF322A | zinc finger protein 322A | 100148923_TGI_at | -0.469 | 0.293 | 1.09E-01 | 0.572148 |
| NA | NA | 100134209_TGI_at | -3.294 | 2.063 | 1.10E-01 | 0.572905 |
| ATP8B3 | "ATPase, class I, type 8B, member 3" | 100139929_TGI_at | -5.768 | 3.638 | 1.13E-01 | 0.577655 |
| PTCH1 | patched homolog 1 (Drosophila) | 100141529_TGI_at | -1.686 | 1.063 | 1.13E-01 | 0.577655 |
| TPM1 | tropomyosin 1 (alpha) | 100304832_TGI_at | 0.201 | 0.127 | 1.13E-01 | 0.577655 |
| TMEM163 | transmembrane protein 163 | 100311300_TGI_at | -0.140 | 0.089 | 1.15E-01 | 0.580598 |
| C1orf113 | chromosome 1 open reading frame 113 | 100312774_TGI_at | -40.983 | 26.582 | 1.23E-01 | 0.582349 |
| CEACAM4 | carcinoembryonic antigen-related cell adhesion molecule 4 | 100141551_TGI_at | 1.721 | 1.148 | 1.34E-01 | 0.582349 |
| DST | dystonin | 100306458_TGI_at | -0.286 | 0.183 | 1.19E-01 | 0.582349 |
| EHHADH | "enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase" | 100147399_TGI_at | -0.913 | 0.587 | 1.20E-01 | 0.582349 |
| GRK4 | G protein-coupled receptor kinase 4 | 100134728_TGI_at | 3.576 | 2.334 | 1.25E-01 | 0.582349 |
| HORMAD1 | HORMA domain containing 1 | 100135055_TGI_at | 11.354 | 7.520 | 1.31E-01 | 0.582349 |
| HSD17B12 | hydroxysteroid (17-beta) dehydrogenase 12 | 100148450_TGI_at | -0.134 | 0.088 | 1.27E-01 | 0.582349 |
| IQGAP3 | IQ motif containing GTPase activating protein 3 | 100131939_TGI_at | 8.191 | 5.342 | 1.25E-01 | 0.582349 |

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|---|---|---|---|---|---|---|
| JUB | "jub, ajuba homolog (Xenopus laevis)" | 100301474_TGI_at | -0.502 | 0.335 | 1.34E-01 | 0.582349 |
| KCNE2 | "potassium voltage-gated channel, Isk-related family, member 2" | 100309078_TGI_at | 3.865 | 2.571 | 1.33E-01 | 0.582349 |
| LASS2 | "LAG1 homolog, ceramide synthase 2" | 100151271_TGI_at | -0.291 | 0.186 | 1.18E-01 | 0.582349 |
| LASS2 | "LAG1 homolog, ceramide synthase 2" | 100302368_TGI_at | -0.258 | 0.169 | 1.27E-01 | 0.582349 |
| NA | hypothetical LOC553103 | 100158314_TGI_at | -5.952 | 3.846 | 1.22E-01 | 0.582349 |
| NA | NA | 100160204_TGI_at | -0.477 | 0.312 | 1.26E-01 | 0.582349 |
| NA | NA | 100139132_TGI_at | -4.063 | 2.687 | 1.31E-01 | 0.582349 |
| NOP16 | NOP16 nucleolar protein homolog (yeast) | 100141815_TGI_at | 0.262 | 0.174 | 1.31E-01 | 0.582349 |
| OR13C3 | "olfactory receptor, family 13, subfamily C, member 3" | 100122819_TGI_at | 12.968 | 8.649 | 1.34E-01 | 0.582349 |
| PCM1 | pericentriolar material 1 | 100312395_TGI_at | -0.194 | 0.129 | 1.34E-01 | 0.582349 |
| PGBD1 | piggyBac transposable element derived 1 | 100161813_TGI_at | -2.966 | 1.967 | 1.32E-01 | 0.582349 |
| SLMO2 | slowmo homolog 2 (Drosophila) | 100152090_TGI_at | 0.752 | 0.479 | 1.17E-01 | 0.582349 |
| SNORA24 | "small nucleolar RNA, H/ACA box 24" | 100149386_TGI_at | 0.778 | 0.507 | 1.25E-01 | 0.582349 |
| STAT6 | "signal transducer and activator of transcription 6, interleukin-4 induced" | 100305452_TGI_at | -0.243 | 0.159 | 1.28E-01 | 0.582349 |
| TMEM163 | transmembrane protein 163 | 100158135_TGI_at | -0.230 | 0.148 | 1.19E-01 | 0.582349 |
| ZNF25 | zinc finger protein 25 | 100154037_TGI_at | -0.988 | 0.640 | 1.23E-01 | 0.582349 |
| ZNF28 | zinc finger protein 28 | 100302468_TGI_at | -0.919 | 0.613 | 1.34E-01 | 0.582349 |
| ZNRD1 | zinc ribbon domain containing 1 | 100158228_TGI_at | 0.982 | 0.638 | 1.23E-01 | 0.582349 |
| NA | NA | 100121683_TGI_at | 6.682 | 4.500 | 1.38E-01 | 0.594113 |
| RAD50 | RAD50 homolog (S. cerevisiae) | 100132153_TGI_at | -0.791 | 0.534 | 1.38E-01 | 0.594113 |
| ANAPC4 | anaphase promoting complex subunit 4 | 100130614_TGI_at | -0.226 | 0.152 | 1.39E-01 | 0.594314 |
| NA | ubiquinol-cytochrome c reductase complex (7.2 kD) | 100141331_TGI_at | -0.904 | 0.612 | 1.40E-01 | 0.594687 |
| C1QL3 | "complement component 1, q subcomponent-like 3" | 100123512_TGI_at | -3.272 | 2.267 | 1.49E-01 | 0.59675 |
| C6orf173 | chromosome 6 open reading frame 173 | 100121877_TGI_at | 0.491 | 0.336 | 1.44E-01 | 0.59675 |
| CPD | carboxypeptidase D | 100139113_TGI_at | 0.549 | 0.378 | 1.47E-01 | 0.59675 |
| CTSS | cathepsin S | 100125530_TGI_at | 0.066 | 0.046 | 1.51E-01 | 0.59675 |
| HLA-DQB2 | "major histocompatibility complex, class II, DQ beta 2" | 100311684_TGI_at | 10.271 | 7.101 | 1.48E-01 | 0.59675 |
| NA | hypothetical LOC554223 | 100304197_TGI_at | -1.070 | 0.727 | 1.41E-01 | 0.59675 |
| NA | NA | 100161388_TGI_at | 7.360 | 5.049 | 1.45E-01 | 0.59675 |
| NA | NA | 100155522_TGI_at | -0.074 | 0.051 | 1.48E-01 | 0.59675 |
| NA | NA | 100305324_TGI_at | -0.215 | 0.149 | 1.49E-01 | 0.59675 |
| NPHP3 | nephronophthisis 3 (adolescent) | 100311821_TGI_at | -1.993 | 1.384 | 1.50E-01 | 0.59675 |
| RBP2 | "retinol binding protein 2, cellular" | 100161662_TGI_at | -0.452 | 0.309 | 1.43E-01 | 0.59675 |
| SFTA2 | surfactant associated 2 | 100125489_TGI_at | -0.057 | 0.039 | 1.47E-01 | 0.59675 |
| TRIM4 | tripartite motif-containing 4 | 100301456_TGI_at | -0.991 | 0.680 | 1.45E-01 | 0.59675 |
| XRCC3 | X-ray repair complementing defective repair in Chinese | 100305763_TGI_at | -0.279 | 0.194 | 1.51E-01 | 0.59675 |

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|---|---|---|---|---|---|---|
| | hamster cells 3 | | | | | |
| SRD5A3 | steroid 5 alpha-reductase 3 | 100130701_TGI_at | 0.276 | 0.193 | 1.52E-01 | 0.598514 |
| NPHP3 | nephronophthisis 3 (adolescent) | 100159303_TGI_at | -0.536 | 0.377 | 1.55E-01 | 0.605303 |
| ROCK2 | "Rho-associated, coiled-coil containing protein kinase 2" | 100311377_TGI_at | -0.273 | 0.192 | 1.55E-01 | 0.605303 |
| C6orf162 | chromosome 6 open reading frame 162 | 100144708_TGI_at | 1.320 | 0.932 | 1.57E-01 | 0.608388 |
| ZNF292 | zinc finger protein 292 | 100139965_TGI_at | -0.280 | 0.199 | 1.59E-01 | 0.614241 |
| B4GALT4 | "UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 4" | 100145663_TGI_at | 0.320 | 0.230 | 1.65E-01 | 0.631228 |
| ROCK2 | "Rho-associated, coiled-coil containing protein kinase 2" | 100306938_TGI_at | -0.949 | 0.684 | 1.65E-01 | 0.631228 |
| FSTL4 | follistatin-like 4 | 100143365_TGI_at | -0.783 | 0.567 | 1.67E-01 | 0.635531 |
| KCNE2 | "potassium voltage-gated channel, Isk-related family, member 2" | 100155146_TGI_at | 5.383 | 3.909 | 1.68E-01 | 0.635626 |
| NA | NA | 100130540_TGI_at | 0.423 | 0.308 | 1.69E-01 | 0.635626 |
| PILRB | paired immunoglobin-like type 2 receptor beta | 100300966_TGI_at | -0.064 | 0.046 | 1.70E-01 | 0.638361 |
| HCG8 | HLA complex group 8 | 100138253_TGI_at | -1.644 | 1.217 | 1.77E-01 | 0.640269 |
| MRPS21 | mitochondrial ribosomal protein S21 | 100307575_TGI_at | 0.288 | 0.213 | 1.76E-01 | 0.640269 |
| NA | interferon induced transmembrane protein pseudogene | 100158197_TGI_at | 5.480 | 4.024 | 1.73E-01 | 0.640269 |
| OXCT2 | 3-oxoacid CoA transferase 2 | 100148761_TGI_at | 2.708 | 1.996 | 1.75E-01 | 0.640269 |
| PADI2 | "peptidyl arginine deiminase, type II" | 100135390_TGI_at | 5.457 | 4.043 | 1.77E-01 | 0.640269 |
| PSORS1C1 | psoriasis susceptibility 1 candidate 1 | 100121628_TGI_at | 2.740 | 2.015 | 1.74E-01 | 0.640269 |
| ZNF25 | zinc finger protein 25 | 100304014_TGI_at | -0.982 | 0.721 | 1.73E-01 | 0.640269 |
| ZNF271 | zinc finger protein 271 | 100304878_TGI_at | 1.382 | 1.020 | 1.75E-01 | 0.640269 |
| NA | NA | 100309227_TGI_at | -0.070 | 0.052 | 1.78E-01 | 0.640393 |
| ASAH1 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 | 100307977_TGI_at | -0.238 | 0.178 | 1.82E-01 | 0.642877 |
| HHIP | hedgehog interacting protein | 100311674_TGI_at | 0.229 | 0.171 | 1.82E-01 | 0.642877 |
| PPA2 | pyrophosphatase (inorganic) 2 | 100160580_TGI_at | 0.957 | 0.713 | 1.79E-01 | 0.642877 |
| SH3PXD2A | SH3 and PX domains 2A | 100150425_TGI_at | 0.765 | 0.572 | 1.81E-01 | 0.642877 |
| C6orf66 | chromosome 6 open reading frame 66 | 100133695_TGI_at | 0.420 | 0.321 | 1.90E-01 | 0.64875 |
| CCDC77 | coiled-coil domain containing 77 | 100134025_TGI_at | -0.581 | 0.442 | 1.88E-01 | 0.64875 |
| CNGA1 | cyclic nucleotide gated channel alpha 1 | 100163169_TGI_at | 5.694 | 4.376 | 1.93E-01 | 0.64875 |
| DDR1 | discoidin domain receptor tyrosine kinase 1 | 100161807_TGI_at | -0.109 | 0.084 | 1.92E-01 | 0.64875 |
| FMO2 | flavin containing monooxygenase 2 (non-functional) | 100162242_TGI_at | -0.219 | 0.167 | 1.89E-01 | 0.64875 |
| LRRC37A4 | "leucine rich repeat containing 37, member A4 (pseudogene)" | 100308628_TGI_at | -0.233 | 0.179 | 1.94E-01 | 0.64875 |
| NA | NA | 100154936_TGI_at | -0.367 | 0.277 | 1.85E-01 | 0.64875 |
| NA | NA | 100155944_TGI_at | -10.836 | 8.324 | 1.93E-01 | 0.64875 |
| PCBP2 | poly(rC) binding protein 2 | 100311439_TGI_at | -0.180 | 0.137 | 1.90E-01 | 0.64875 |
| RBM23 | RNA binding motif protein 23 | 100135911_TGI_at | -0.201 | 0.152 | 1.87E-01 | 0.64875 |

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| RPS19 | ribosomal protein S19 | 100127522_TGI_at | 0.064 | 0.049 | 1.91E-01 | 0.64875 |
| SETX | senataxin | 100310831_TGI_at | -1.983 | 1.519 | 1.92E-01 | 0.64875 |
| SPINK5 | "serine peptidase inhibitor, Kazal type 5" | 100160780_TGI_at | 0.137 | 0.104 | 1.87E-01 | 0.64875 |
| PIGV | "phosphatidylinositol glycan anchor biosynthesis, class V" | 100137081_TGI_at | -0.457 | 0.354 | 1.96E-01 | 0.653599 |
| HCG4P6 | HLA complex group 4 pseudogene 6 | 100123483_TGI_at | 6.324 | 4.913 | 1.98E-01 | 0.6541 |
| TRIM26 | tripartite motif-containing 26 | 100153401_TGI_at | -3.697 | 2.872 | 1.98E-01 | 0.6541 |
| C18orf10 | chromosome 18 open reading frame 10 | 100308899_TGI_at | -3.084 | 2.409 | 2.00E-01 | 0.657669 |
| LYSMD4 | "LysM, putative peptidoglycan-binding, domain containing 4" | 100138194_TGI_at | -0.908 | 0.710 | 2.01E-01 | 0.657669 |
| MRPS21 | mitochondrial ribosomal protein S21 | 100156777_TGI_at | 1.050 | 0.824 | 2.03E-01 | 0.658705 |
| NA | NA | 100157269_TGI_at | -5.274 | 4.152 | 2.04E-01 | 0.658705 |
| PILRB | paired immunoglobin-like type 2 receptor beta | 100133464_TGI_at | -0.057 | 0.045 | 2.04E-01 | 0.658705 |
| RP3-377H14.5 | hypothetical protein FLJ35429 | 100311825_TGI_at | 1.428 | 1.123 | 2.04E-01 | 0.658705 |
| TXNDC11 | thioredoxin domain containing 11 | 100140312_TGI_at | -0.133 | 0.105 | 2.08E-01 | 0.668969 |
| RPUSD4 | RNA pseudouridylate synthase domain containing 4 | 100143437_TGI_at | 0.473 | 0.378 | 2.10E-01 | 0.670285 |
| RREB1 | ras responsive element binding protein 1 | 100307951_TGI_at | -0.420 | 0.336 | 2.10E-01 | 0.670285 |
| C6orf162 | chromosome 6 open reading frame 162 | 100311360_TGI_at | 1.189 | 0.953 | 2.12E-01 | 0.673979 |
| PQLC3 | PQ loop repeat containing 3 | 100124316_TGI_at | -0.171 | 0.138 | 2.14E-01 | 0.676525 |
| HCG18 | HLA complex group 18 | 100131217_TGI_at | 0.900 | 0.729 | 2.17E-01 | 0.678677 |
| RAD50 | RAD50 homolog (S. cerevisiae) | 100304804_TGI_at | -1.932 | 1.564 | 2.17E-01 | 0.678677 |
| ROCK2 | "Rho-associated, coiled-coil containing protein kinase 2" | 100160466_TGI_at | -0.512 | 0.415 | 2.16E-01 | 0.678677 |
| C15orf57 | chromosome 15 open reading frame 57 | 100307916_TGI_at | 1.511 | 1.229 | 2.19E-01 | 0.680532 |
| GIT2 | G protein-coupled receptor kinase interacting ArfGAP 2 | 100309959_TGI_at | 0.991 | 0.811 | 2.22E-01 | 0.682204 |
| MRPL43 | mitochondrial ribosomal protein L43 | 100148949_TGI_at | -1.827 | 1.492 | 2.21E-01 | 0.682204 |
| NA | ichthyin protein | 100141348_TGI_at | 2.529 | 2.070 | 2.22E-01 | 0.682204 |
| SPINK6 | "serine peptidase inhibitor, Kazal type 6" | 100137671_TGI_at | 9.565 | 7.845 | 2.23E-01 | 0.682204 |
| ANXA6 | annexin A6 | 100129059_TGI_at | 1.069 | 0.894 | 2.32E-01 | 0.683494 |
| CEP192 | centrosomal protein 192kDa | 100142718_TGI_at | -0.425 | 0.351 | 2.27E-01 | 0.683494 |
| GOSR1 | golgi SNAP receptor complex member 1 | 100136117_TGI_at | 0.456 | 0.386 | 2.37E-01 | 0.683494 |
| HCG22 | HLA complex group 22 | 100129279_TGI_at | 7.381 | 6.166 | 2.31E-01 | 0.683494 |
| HLA-C | "major histocompatibility complex, class I, C" | 100309484_TGI_at | 0.037 | 0.031 | 2.32E-01 | 0.683494 |
| HLA-C | "major histocompatibility complex, class I, C" | 100302942_TGI_at | 0.040 | 0.034 | 2.38E-01 | 0.683494 |
| HOXC6 | homeobox C6 | 100309835_TGI_at | 10.154 | 8.388 | 2.26E-01 | 0.683494 |
| KPNA3 | karyopherin alpha 3 (importin alpha 4) | 100141096_TGI_at | -1.037 | 0.868 | 2.32E-01 | 0.683494 |
| NA | hypothetical protein LOC644246 | 100134593_TGI_at | 0.099 | 0.083 | 2.30E-01 | 0.683494 |
| NA | NA | 100309580_TGI_at | -1.869 | 1.573 | 2.35E-01 | 0.683494 |
| NA | hypothetical protein LOC644246 | 100310659_TGI_at | 0.121 | 0.102 | 2.36E-01 | 0.683494 |

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| PIGL | "phosphatidylinositol glycan anchor biosynthesis, class L" | 100158126_TGI_at | -2.106 | 1.783 | 2.37E-01 | 0.683494 |
| RBM6 | RNA binding motif protein 6 | 100124865_TGI_at | -0.257 | 0.214 | 2.29E-01 | 0.683494 |
| STAT6 | "signal transducer and activator of transcription 6, interleukin-4 induced" | 100310285_TGI_at | -0.203 | 0.171 | 2.34E-01 | 0.683494 |
| TIGD2 | tigger transposable element derived 2 | 100148014_TGI_at | -0.814 | 0.691 | 2.39E-01 | 0.683494 |
| TPM1 | tropomyosin 1 (alpha) | 100156621_TGI_at | 0.729 | 0.619 | 2.39E-01 | 0.683494 |
| TUBB | "tubulin, beta" | 100300978_TGI_at | 0.075 | 0.062 | 2.30E-01 | 0.683494 |
| VTA1 | Vps20-associated 1 homolog (S. cerevisiae) | 100153205_TGI_at | -0.505 | 0.421 | 2.31E-01 | 0.683494 |
| IREB2 | iron-responsive element binding protein 2 | 100129239_TGI_at | 1.830 | 1.558 | 2.40E-01 | 0.684621 |
| NA | NA | 100136084_TGI_at | 0.991 | 0.844 | 2.41E-01 | 0.684621 |
| NA | hypothetical protein LOC729082 | 100141553_TGI_at | -0.108 | 0.093 | 2.42E-01 | 0.687262 |
| G3BP1 | GTPase activating protein (SH3 domain) binding protein 1 | 100300564_TGI_at | 0.408 | 0.357 | 2.53E-01 | 0.693792 |
| LRRC37A4 | "leucine rich repeat containing 37, member A4 (pseudogene)" | 100135158_TGI_at | -1.015 | 0.882 | 2.50E-01 | 0.693792 |
| NA | hypothetical LOC554223 | 100141210_TGI_at | -1.220 | 1.055 | 2.48E-01 | 0.693792 |
| NA | NA | 100310523_TGI_at | -0.737 | 0.639 | 2.48E-01 | 0.693792 |
| NA | NA | 100144981_TGI_at | 4.392 | 3.814 | 2.50E-01 | 0.693792 |
| NA | NA | 100136210_TGI_at | 11.887 | 10.376 | 2.52E-01 | 0.693792 |
| NICN1 | nicolin 1 | 100129450_TGI_at | -0.524 | 0.453 | 2.47E-01 | 0.693792 |
| NMU | neuromedin U | 100137237_TGI_at | 0.612 | 0.533 | 2.51E-01 | 0.693792 |
| TMEM108 | transmembrane protein 108 | 100157152_TGI_at | -0.700 | 0.610 | 2.52E-01 | 0.693792 |
| VEZT | "vezatin, adherens junctions transmembrane protein" | 100305406_TGI_at | -1.171 | 1.024 | 2.53E-01 | 0.693792 |
| NA | hypothetical protein FLJ32810 | 100304225_TGI_at | -1.045 | 0.919 | 2.55E-01 | 0.696954 |
| ANXA6 | annexin A6 | 100300070_TGI_at | 0.070 | 0.063 | 2.71E-01 | 0.697283 |
| AP3B2 | "adaptor-related protein complex 3, beta 2 subunit" | 100141670_TGI_at | 4.332 | 3.908 | 2.68E-01 | 0.697283 |
| C1GALT1 | "core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1" | 100154998_TGI_at | 0.459 | 0.412 | 2.65E-01 | 0.697283 |
| FAM13A1 | "family with sequence similarity 13, member A1" | 100312038_TGI_at | 0.193 | 0.170 | 2.57E-01 | 0.697283 |
| HOXB7 | homeobox B7 | 100154282_TGI_at | 0.759 | 0.686 | 2.69E-01 | 0.697283 |
| HOXC6 | homeobox C6 | 100148000_TGI_at | 6.852 | 6.201 | 2.69E-01 | 0.697283 |
| KIAA1267 | KIAA1267 | 100160728_TGI_at | 4.269 | 3.878 | 2.71E-01 | 0.697283 |
| MFAP2 | microfibrillar-associated protein 2 | 100133163_TGI_at | 0.412 | 0.371 | 2.66E-01 | 0.697283 |
| NA | nuclear DNA-binding protein | 100162510_TGI_at | -0.202 | 0.179 | 2.58E-01 | 0.697283 |
| NA | sterile alpha motif and leucine zipper containing kinase AZK | 100305328_TGI_at | 0.651 | 0.580 | 2.62E-01 | 0.697283 |
| NA | NA | 100158666_TGI_at | 0.755 | 0.678 | 2.65E-01 | 0.697283 |
| NA | NA | 100160114_TGI_at | -2.648 | 2.381 | 2.66E-01 | 0.697283 |

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|---|---|---|---|---|---|---|
| NA | similar to RIKEN cDNA C630028N24 gene | 100132425_TGI_at | -2.492 | 2.246 | 2.67E-01 | 0.697283 |
| NA | NA | 100129603_TGI_at | -11.758 | 10.672 | 2.71E-01 | 0.697283 |
| PPA2 | pyrophosphatase (inorganic) 2 | 100307499_TGI_at | 0.673 | 0.597 | 2.60E-01 | 0.697283 |
| ZADH2 | zinc binding alcohol dehydrogenase domain containing 2 | 100134955_TGI_at | -1.198 | 1.063 | 2.60E-01 | 0.697283 |
| ZMAT3 | "zinc finger, matrin type 3" | 100142264_TGI_at | 0.201 | 0.179 | 2.61E-01 | 0.697283 |
| ZNF389 | zinc finger protein 389 | 100145476_TGI_at | -5.265 | 4.740 | 2.67E-01 | 0.697283 |
| NA | NA | 100135728_TGI_at | 0.874 | 0.798 | 2.74E-01 | 0.701053 |
| NA | NA | 100157433_TGI_at | 1.641 | 1.507 | 2.76E-01 | 0.705101 |
| HLA-A | "major histocompatibility complex, class I, A" | 100303756_TGI_at | 0.055 | 0.051 | 2.79E-01 | 0.709073 |
| PCGF2 | polycomb group ring finger 2 | 100140755_TGI_at | -0.584 | 0.540 | 2.80E-01 | 0.709073 |
| ROCK2 | "Rho-associated, coiled-coil containing protein kinase 2" | 100159613_TGI_at | -0.302 | 0.279 | 2.80E-01 | 0.709073 |
| PCM1 | pericentriolar material 1 | 100134179_TGI_at | -0.141 | 0.131 | 2.82E-01 | 0.71192 |
| HLA-DPA1 | "major histocompatibility complex, class II, DP alpha 1" | 100305836_TGI_at | 0.108 | 0.101 | 2.85E-01 | 0.715389 |
| USP4 | ubiquitin specific peptidase 4 (proto-oncogene) | 100162155_TGI_at | -0.106 | 0.099 | 2.85E-01 | 0.715389 |
| ERP29 | endoplasmic reticulum protein 29 | 100161262_TGI_at | -1.604 | 1.516 | 2.90E-01 | 0.723459 |
| FGFBP3 | fibroblast growth factor binding protein 3 | 100128225_TGI_at | -1.148 | 1.091 | 2.92E-01 | 0.723459 |
| JMJD7-PLA2G4B | JMJD7-PLA2G4B readthrough transcript | 100150740_TGI_at | -0.426 | 0.404 | 2.92E-01 | 0.723459 |
| MEST | mesoderm specific transcript homolog (mouse) | 100127501_TGI_at | 0.099 | 0.094 | 2.91E-01 | 0.723459 |
| RHOBTB3 | Rho-related BTB domain containing 3 | 100126558_TGI_at | -0.217 | 0.207 | 2.95E-01 | 0.728611 |
| hCG_2039148 | hypothetical protein LOC100132356 | 100155226_TGI_at | -0.888 | 0.852 | 2.97E-01 | 0.730062 |
| FBXO38 | F-box protein 38 | 100313079_TGI_at | -0.296 | 0.286 | 2.99E-01 | 0.73023 |
| NA | NA | 100148878_TGI_at | 3.115 | 2.995 | 2.98E-01 | 0.73023 |
| NA | NA | 100137632_TGI_at | 0.568 | 0.549 | 3.01E-01 | 0.73023 |
| TDRD10 | tudor domain containing 10 | 100158499_TGI_at | -0.195 | 0.188 | 3.00E-01 | 0.73023 |
| FAM62B | family with sequence similarity 62 (C2 domain containing) member B | 100301867_TGI_at | -0.148 | 0.144 | 3.02E-01 | 0.731633 |
| FGD6 | "FYVE, RhoGEF and PH domain containing 6" | 100306202_TGI_at | 3.222 | 3.136 | 3.04E-01 | 0.734605 |
| MRPL43 | mitochondrial ribosomal protein L43 | 100152029_TGI_at | 0.247 | 0.244 | 3.11E-01 | 0.747192 |
| NA | NA | 100162932_TGI_at | -3.064 | 3.023 | 3.11E-01 | 0.747192 |
| CROCC | "ciliary rootlet coiled-coil, rootletin" | 100310898_TGI_at | -0.277 | 0.278 | 3.19E-01 | 0.748105 |
| GPATCH2 | G patch domain containing 2 | 100132932_TGI_at | -0.645 | 0.647 | 3.19E-01 | 0.748105 |
| MPP6 | "membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)" | 100136557_TGI_at | 0.451 | 0.455 | 3.22E-01 | 0.748105 |
| NA | hypothetical protein MGC16291 | 100123769_TGI_at | -1.367 | 1.358 | 3.14E-01 | 0.748105 |
| NA | hypothetical LOC648987 | 100309522_TGI_at | -2.257 | 2.279 | 3.22E-01 | 0.748105 |
| NA | FKSG49 | 100162323_TGI_at | 0.111 | 0.113 | 3.23E-01 | 0.748105 |
| NA | NA | 100307218_TGI_at | 1.430 | 1.448 | 3.23E-01 | 0.748105 |

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|---|---|---|---|---|---|---|
| NA | NA | 100159186_TGI_at | -9.125 | 9.246 | 3.24E-01 | 0.748105 |
| PCM1 | pericentriolar material 1 | 100303798_TGI_at | -0.153 | 0.153 | 3.19E-01 | 0.748105 |
| RPRD2 | regulation of nuclear pre-mRNA domain containing 2 | 100129463_TGI_at | -0.386 | 0.387 | 3.18E-01 | 0.748105 |
| SEC61A2 | Sec61 alpha 2 subunit (S. cerevisiae) | 100129724_TGI_at | -1.013 | 1.009 | 3.15E-01 | 0.748105 |
| TPM1 | tropomyosin 1 (alpha) | 100145725_TGI_at | 0.049 | 0.050 | 3.24E-01 | 0.748105 |
| VTA1 | Vps20-associated 1 homolog (S. cerevisiae) | 100311276_TGI_at | -0.373 | 0.370 | 3.13E-01 | 0.748105 |
| CLOCK | clock homolog (mouse) | 100307345_TGI_at | -0.850 | 0.882 | 3.35E-01 | 0.756474 |
| ESR1 | estrogen receptor 1 | 100303655_TGI_at | 0.244 | 0.251 | 3.30E-01 | 0.756474 |
| HBS1L | HBS1-like (S. cerevisiae) | 100133258_TGI_at | -0.782 | 0.807 | 3.32E-01 | 0.756474 |
| HLA-DQB1 | "major histocompatibility complex, class II, DQ beta 1" | 100302941_TGI_at | 0.020 | 0.021 | 3.34E-01 | 0.756474 |
| MAPT | microtubule-associated protein tau | 100306395_TGI_at | 6.778 | 7.025 | 3.35E-01 | 0.756474 |
| NA | NA | 100151558_TGI_at | 0.492 | 0.505 | 3.30E-01 | 0.756474 |
| NA | NA | 100307969_TGI_at | -1.515 | 1.579 | 3.37E-01 | 0.756474 |
| NCAPG2 | "non-SMC condensin II complex, subunit G2" | 100136204_TGI_at | 0.319 | 0.328 | 3.31E-01 | 0.756474 |
| PPP1R3B | "protein phosphatase 1, regulatory (inhibitor) subunit 3B" | 100136365_TGI_at | 0.567 | 0.589 | 3.36E-01 | 0.756474 |
| SNRPC | small nuclear ribonucleoprotein polypeptide C | 100159916_TGI_at | -0.194 | 0.202 | 3.38E-01 | 0.756474 |
| TOM1L2 | target of myb1-like 2 (chicken) | 100301274_TGI_at | 6.486 | 6.754 | 3.37E-01 | 0.756474 |
| HIGD2A | "HIG1 domain family, member 2A" | 100153252_TGI_at | 0.238 | 0.252 | 3.44E-01 | 0.767301 |
| CDC42SE1 | CDC42 small effector 1 | 100140105_TGI_at | -0.371 | 0.393 | 3.45E-01 | 0.768395 |
| JARID1A | "jumonji, AT rich interactive domain 1A" | 100313404_TGI_at | -0.581 | 0.617 | 3.46E-01 | 0.768395 |
| NA | NA | 100305045_TGI_at | -0.814 | 0.867 | 3.47E-01 | 0.769277 |
| NAPRT1 | nicotinate phosphoribosyltransferase domain containing 1 | 100154661_TGI_at | 0.456 | 0.489 | 3.51E-01 | 0.774092 |
| ACP6 | "acid phosphatase 6, lysophosphatidic" | 100128577_TGI_at | -0.437 | 0.500 | 3.82E-01 | 0.775721 |
| ADAM17 | ADAM metallopeptidase domain 17 | 100307726_TGI_at | -3.062 | 3.393 | 3.67E-01 | 0.775721 |
| ADORA2B | adenosine A2b receptor | 100146347_TGI_at | 0.427 | 0.508 | 4.00E-01 | 0.775721 |
| AMOTL1 | angiomotin like 1 | 100136633_TGI_at | 0.248 | 0.306 | 4.19E-01 | 0.775721 |
| ANKRD13B | ankyrin repeat domain 13B | 100159312_TGI_at | 0.279 | 0.307 | 3.64E-01 | 0.775721 |
| ARID1A | AT rich interactive domain 1A (SWI-like) | 100136478_TGI_at | -0.278 | 0.342 | 4.16E-01 | 0.775721 |
| ASAH1 | N-acylsphingosine amidohydrolase (acid ceramidase) 1 | 100308495_TGI_at | -3.420 | 3.833 | 3.72E-01 | 0.775721 |
| BAT2 | HLA-B associated transcript 2 | 100139818_TGI_at | 0.417 | 0.476 | 3.81E-01 | 0.775721 |
| BAT4 | HLA-B associated transcript 4 | 100138357_TGI_at | -0.420 | 0.497 | 3.99E-01 | 0.775721 |
| BSCL2 | Bernardinelli-Seip congenital lipodystrophy 2 (seipin) | 100155082_TGI_at | -0.096 | 0.115 | 4.07E-01 | 0.775721 |
| C16orf63 | chromosome 16 open reading frame 63 | 100148972_TGI_at | -0.199 | 0.230 | 3.87E-01 | 0.775721 |
| C1orf89 | chromosome 1 open reading frame 89 | 100143670_TGI_at | 1.840 | 2.201 | 4.03E-01 | 0.775721 |
| C2 | complement component 2 | 100161625_TGI_at | -0.047 | 0.053 | 3.82E-01 | 0.775721 |
| C6orf191 | chromosome 6 open reading frame 191 | 100150758_TGI_at | 10.785 | 12.565 | 3.91E-01 | 0.775721 |
| CACNA2D4 | "calcium channel, voltage-dependent, alpha 2/delta subunit 4" | 100301072_TGI_at | -1.168 | 1.437 | 4.16E-01 | 0.775721 |

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|---|---|---|---|---|---|---|
| CCBL2 | cysteine conjugate-beta lyase 2 | 100303452_TGI_at | 0.190 | 0.229 | 4.06E-01 | 0.775721 |
| CCDC91 | coiled-coil domain containing 91 | 100124630_TGI_at | -0.325 | 0.386 | 3.99E-01 | 0.775721 |
| CDSN | corneodesmosin | 100303039_TGI_at | -1.594 | 1.964 | 4.17E-01 | 0.775721 |
| CLEC2D | "C-type lectin domain family 2, member D" | 100303868_TGI_at | 1.767 | 1.967 | 3.69E-01 | 0.775721 |
| CLOCK | clock homolog (mouse) | 100147633_TGI_at | -0.724 | 0.887 | 4.15E-01 | 0.775721 |
| CPD | carboxypeptidase D | 100305644_TGI_at | 0.360 | 0.395 | 3.61E-01 | 0.775721 |
| CROCCL1 | "ciliary rootlet coiled-coil, rootletin-like 1" | 100124110_TGI_at | -0.093 | 0.110 | 3.95E-01 | 0.775721 |
| FMO2 | flavin containing monooxygenase 2 (non-functional) | 100310951_TGI_at | -0.029 | 0.035 | 4.17E-01 | 0.775721 |
| FSTL4 | follistatin-like 4 | 100145132_TGI_at | -5.914 | 6.652 | 3.74E-01 | 0.775721 |
| FZD7 | frizzled homolog 7 (Drosophila) | 100122090_TGI_at | 0.588 | 0.637 | 3.56E-01 | 0.775721 |
| GRB2 | growth factor receptor-bound protein 2 | 100140717_TGI_at | 0.207 | 0.230 | 3.66E-01 | 0.775721 |
| HCG27 | HLA complex group 27 | 100128894_TGI_at | -1.082 | 1.199 | 3.67E-01 | 0.775721 |
| HLA-DQB1 | "major histocompatibility complex, class II, DQ beta 1" | 100300398_TGI_at | 0.019 | 0.021 | 3.77E-01 | 0.775721 |
| HLA-DQB1 | "major histocompatibility complex, class II, DQ beta 1" | 100304009_TGI_at | 0.017 | 0.021 | 4.02E-01 | 0.775721 |
| IFNGR2 | interferon gamma receptor 2 (interferon gamma transducer 1) | 100308980_TGI_at | -4.553 | 5.266 | 3.87E-01 | 0.775721 |
| IFNGR2 | interferon gamma receptor 2 (interferon gamma transducer 1) | 100310797_TGI_at | -2.120 | 2.469 | 3.91E-01 | 0.775721 |
| KIAA0802 | KIAA0802 | 100300284_TGI_at | -0.530 | 0.594 | 3.73E-01 | 0.775721 |
| KLC1 | kinesin light chain 1 | 100142037_TGI_at | 0.628 | 0.755 | 4.06E-01 | 0.775721 |
| KTELC1 | KTEL (Lys-Tyr-Glu-Leu) containing 1 | 100157247_TGI_at | 0.411 | 0.461 | 3.72E-01 | 0.775721 |
| LDHC | lactate dehydrogenase C | 100142627_TGI_at | 3.593 | 3.959 | 3.64E-01 | 0.775721 |
| MAPKBP1 | mitogen-activated protein kinase binding protein 1 | 100306182_TGI_at | -3.578 | 4.253 | 4.00E-01 | 0.775721 |
| MEIG1 | meiosis expressed gene 1 homolog (mouse) | 100149806_TGI_at | -2.964 | 3.393 | 3.82E-01 | 0.775721 |
| MTMR3 | myotubularin related protein 3 | 100308994_TGI_at | -0.373 | 0.414 | 3.67E-01 | 0.775721 |
| NA | NA | 100144443_TGI_at | 2.280 | 2.529 | 3.67E-01 | 0.775721 |
| NA | NA | 100145578_TGI_at | -0.772 | 0.871 | 3.75E-01 | 0.775721 |
| NA | NA | 100151676_TGI_at | -3.016 | 3.431 | 3.79E-01 | 0.775721 |
| NA | peptidylprolyl isomerase E pseudogene | 100133670_TGI_at | -0.439 | 0.505 | 3.86E-01 | 0.775721 |
| NA | NA | 100133629_TGI_at | 0.288 | 0.336 | 3.91E-01 | 0.775721 |
| NA | NA | 100129276_TGI_at | -1.665 | 1.992 | 4.03E-01 | 0.775721 |
| NA | FLJ33360 protein | 100303540_TGI_at | -2.484 | 3.028 | 4.12E-01 | 0.775721 |
| NA | NA | 100307171_TGI_at | -0.231 | 0.282 | 4.13E-01 | 0.775721 |
| NA | sterile alpha motif and leucine zipper containing kinase AZK | 100122720_TGI_at | 0.952 | 1.165 | 4.14E-01 | 0.775721 |
| NA | hypothetical LOC648987 | 100123880_TGI_at | -1.421 | 1.744 | 4.15E-01 | 0.775721 |
| NA | FLJ33360 protein | 100138705_TGI_at | -2.489 | 3.066 | 4.17E-01 | 0.775721 |
| NA | NA | 100130704_TGI_at | -0.395 | 0.488 | 4.19E-01 | 0.775721 |

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|---|---|---|---|---|---|---|
| NA | hypothetical LOC648987 | 100129380_TGI_at | -1.353 | 1.678 | 4.20E-01 | 0.775721 |
| PCBP2 | poly(rC) binding protein 2 | 100302664_TGI_at | 0.075 | 0.090 | 4.08E-01 | 0.775721 |
| PCGF2 | polycomb group ring finger 2 | 100150055_TGI_at | -0.527 | 0.617 | 3.93E-01 | 0.775721 |
| PIGU | "phosphatidylinositol glycan anchor biosynthesis, class U" | 100138660_TGI_at | 0.580 | 0.697 | 4.05E-01 | 0.775721 |
| PIP4K2B | "phosphatidylinositol-5-phosphate 4-kinase, type II, beta" | 100301317_TGI_at | -1.551 | 1.708 | 3.64E-01 | 0.775721 |
| PLA2G5 | "phospholipase A2, group V" | 100311695_TGI_at | -0.639 | 0.695 | 3.58E-01 | 0.775721 |
| RBM23 | RNA binding motif protein 23 | 100310197_TGI_at | -0.145 | 0.175 | 4.09E-01 | 0.775721 |
| RP3-377H14.5 | hypothetical protein FLJ35429 | 100141578_TGI_at | 4.406 | 5.330 | 4.08E-01 | 0.775721 |
| RPS19 | ribosomal protein S19 | 100314018_TGI_at | 0.021 | 0.024 | 3.85E-01 | 0.775721 |
| SGCD | "sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)" | 100156891_TGI_at | -0.526 | 0.617 | 3.94E-01 | 0.775721 |
| SGCD | "sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)" | 100142964_TGI_at | 1.331 | 1.587 | 4.02E-01 | 0.775721 |
| SMPDL3B | "sphingomyelin phosphodiesterase, acid-like 3B" | 100145066_TGI_at | 0.478 | 0.538 | 3.74E-01 | 0.775721 |
| STRA13 | stimulated by retinoic acid 13 homolog (mouse) | 100151685_TGI_at | -0.193 | 0.216 | 3.72E-01 | 0.775721 |
| TRIM26 | tripartite motif-containing 26 | 100126192_TGI_at | -0.358 | 0.444 | 4.20E-01 | 0.775721 |
| UBXN6 | UBX domain protein 6 | 100310092_TGI_at | 0.133 | 0.164 | 4.18E-01 | 0.775721 |
| VDAC2 | voltage-dependent anion channel 2 | 100153741_TGI_at | 0.128 | 0.155 | 4.08E-01 | 0.775721 |
| VEZT | "vezatin, adherens junctions transmembrane protein" | 100302085_TGI_at | -0.229 | 0.274 | 4.03E-01 | 0.775721 |
| ZNF165 | zinc finger protein 165 | 100312805_TGI_at | 0.885 | 1.014 | 3.83E-01 | 0.775721 |
| ZNF187 | zinc finger protein 187 | 100139670_TGI_at | -0.481 | 0.596 | 4.20E-01 | 0.775721 |
| ZNF271 | zinc finger protein 271 | 100304943_TGI_at | 0.323 | 0.375 | 3.89E-01 | 0.775721 |
| ZNF600 | zinc finger protein 600 | 100157946_TGI_at | -0.321 | 0.352 | 3.62E-01 | 0.775721 |
| PGM2L1 | phosphoglucomutase 2-like 1 | 100156557_TGI_at | 0.383 | 0.478 | 4.23E-01 | 0.778878 |
| TAP2 | "transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)" | 100129037_TGI_at | 1.454 | 1.822 | 4.25E-01 | 0.780527 |
| C17orf57 | chromosome 17 open reading frame 57 | 100306281_TGI_at | 0.743 | 0.934 | 4.27E-01 | 0.782006 |
| SLC27A5 | "solute carrier family 27 (fatty acid transporter), member 5" | 100150898_TGI_at | 0.903 | 1.139 | 4.28E-01 | 0.783017 |
| NA | NA | 100313840_TGI_at | -0.998 | 1.264 | 4.30E-01 | 0.784047 |
| NA | NA | 100159981_TGI_at | 1.606 | 2.044 | 4.32E-01 | 0.786447 |
| NA | NA | 100162706_TGI_at | -0.576 | 0.736 | 4.34E-01 | 0.786855 |
| RNF5 | ring finger protein 5 | 100158927_TGI_at | -0.128 | 0.164 | 4.33E-01 | 0.786855 |
| ARNT | aryl hydrocarbon receptor nuclear translocator | 100309723_TGI_at | -0.188 | 0.246 | 4.46E-01 | 0.788803 |
| C12orf48 | chromosome 12 open reading frame 48 | 100162004_TGI_at | 1.789 | 2.313 | 4.39E-01 | 0.788803 |
| CDK5RAP3 | CDK5 regulatory subunit associated protein 3 | 100139309_TGI_at | -0.087 | 0.115 | 4.47E-01 | 0.788803 |
| DCXR | dicarbonyl/L-xylulose reductase | 100124485_TGI_at | 0.117 | 0.152 | 4.44E-01 | 0.788803 |
| FLOT1 | flotillin 1 | 100304636_TGI_at | 0.803 | 1.042 | 4.41E-01 | 0.788803 |

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| NA | hypothetical protein LOC643977 | 100157324_TGI_at | -0.713 | 0.920 | 4.38E-01 | 0.788803 |
| NA | NA | 100139549_TGI_at | -0.794 | 1.034 | 4.42E-01 | 0.788803 |
| NA | NA | 100136066_TGI_at | 2.702 | 3.537 | 4.45E-01 | 0.788803 |
| PELI2 | pellino homolog 2 (Drosophila) | 100146392_TGI_at | -4.552 | 5.962 | 4.45E-01 | 0.788803 |
| PIGV | "phosphatidylinositol glycan anchor biosynthesis, class V" | 100306509_TGI_at | -0.774 | 1.018 | 4.47E-01 | 0.788803 |
| TRIM66 | tripartite motif-containing 66 | 100145297_TGI_at | -0.766 | 0.999 | 4.43E-01 | 0.788803 |
| YEATS4 | YEATS domain containing 4 | 100125980_TGI_at | -0.595 | 0.767 | 4.37E-01 | 0.788803 |
| TMEM77 | transmembrane protein 77 | 100306966_TGI_at | 0.165 | 0.218 | 4.48E-01 | 0.788887 |
| ADORA2B | adenosine A2b receptor | 100300365_TGI_at | 0.443 | 0.589 | 4.53E-01 | 0.790158 |
| CACNA2D4 | "calcium channel, voltage-dependent, alpha 2/delta subunit 4" | 100307865_TGI_at | -2.434 | 3.278 | 4.58E-01 | 0.790158 |
| FAM168A | "family with sequence similarity 168, member A" | 100305819_TGI_at | -0.375 | 0.501 | 4.53E-01 | 0.790158 |
| HLA-DOB | "major histocompatibility complex, class II, DO beta" | 100133511_TGI_at | 0.229 | 0.306 | 4.55E-01 | 0.790158 |
| NA | NA | 100126167_TGI_at | -1.825 | 2.425 | 4.52E-01 | 0.790158 |
| NA | NA | 100127527_TGI_at | -1.640 | 2.187 | 4.53E-01 | 0.790158 |
| NA | NA | 100135910_TGI_at | -2.796 | 3.755 | 4.56E-01 | 0.790158 |
| NA | NA | 100145206_TGI_at | -2.304 | 3.099 | 4.57E-01 | 0.790158 |
| NA | FLJ45422 protein | 100137319_TGI_at | 1.573 | 2.118 | 4.58E-01 | 0.790158 |
| MRPL10 | mitochondrial ribosomal protein L10 | 100309376_TGI_at | -0.155 | 0.209 | 4.60E-01 | 0.791675 |
| ANGPT1 | angiopoietin 1 | 100129666_TGI_at | -0.064 | 0.088 | 4.62E-01 | 0.79448 |
| "MARCH5" | membrane-associated ring finger (C3HC4) 5 | 100148133_TGI_at | -0.183 | 0.253 | 4.68E-01 | 0.795483 |
| BTN3A2 | "butyrophilin, subfamily 3, member A2" | 100161253_TGI_at | -0.086 | 0.119 | 4.68E-01 | 0.795483 |
| HLA-G | "major histocompatibility complex, class I, G" | 100160221_TGI_at | 1.523 | 2.107 | 4.70E-01 | 0.795483 |
| ITPKA | "inositol 1,4,5-trisphosphate 3-kinase A" | 100124857_TGI_at | 3.026 | 4.160 | 4.67E-01 | 0.795483 |
| MLF1 | myeloid leukemia factor 1 | 100301782_TGI_at | 0.095 | 0.130 | 4.65E-01 | 0.795483 |
| NA | NA | 100130314_TGI_at | 0.965 | 1.319 | 4.64E-01 | 0.795483 |
| WDR32 | WD repeat domain 32 | 100146140_TGI_at | -0.592 | 0.819 | 4.70E-01 | 0.795483 |
| GRK4 | G protein-coupled receptor kinase 4 | 100303520_TGI_at | 1.710 | 2.398 | 4.76E-01 | 0.796473 |
| HSD17B7P2 | hydroxysteroid (17-beta) dehydrogenase 7 pseudogene 2 | 100300887_TGI_at | -6.632 | 9.263 | 4.74E-01 | 0.796473 |
| LSM11 | "LSM11, U7 small nuclear RNA associated" | 100149905_TGI_at | 2.519 | 3.521 | 4.74E-01 | 0.796473 |
| MMP15 | matrix metallopeptidase 15 (membrane-inserted) | 100142706_TGI_at | -0.118 | 0.165 | 4.75E-01 | 0.796473 |
| SEMA3A | "sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A" | 100158468_TGI_at | 2.161 | 3.041 | 4.77E-01 | 0.796473 |
| THSD4 | "thrombospondin, type I, domain containing 4" | 100310339_TGI_at | -0.232 | 0.326 | 4.77E-01 | 0.796473 |
| WNT3 | "wingless-type MMTV integration site family, member 3" | 100138516_TGI_at | -0.360 | 0.505 | 4.77E-01 | 0.796473 |
| CLOCK | clock homolog (mouse) | 100129781_TGI_at | 1.043 | 1.477 | 4.80E-01 | 0.799185 |
| CYP21A2 | "cytochrome P450, family 21, subfamily A, polypeptide | 100303617_TGI_at | 2.388 | 3.390 | 4.81E-01 | 0.799185 |

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| | 2" | | | | | |
| GOLPH3L | golgi phosphoprotein 3-like | 100143466_TGI_at | 1.034 | 1.470 | 4.82E-01 | 0.799185 |
| ARL17P1 | ADP-ribosylation factor-like 17 pseudogene 1 | 100312557_TGI_at | 11.258 | 16.178 | 4.87E-01 | 0.80105 |
| C5orf35 | chromosome 5 open reading frame 35 | 100131401_TGI_at | 0.661 | 0.954 | 4.88E-01 | 0.80105 |
| KCNMB3 | "potassium large conductance calcium-activated channel, subfamily M beta member 3" | 100313107_TGI_at | -0.637 | 0.915 | 4.86E-01 | 0.80105 |
| NA | NA | 100150316_TGI_at | -2.091 | 2.994 | 4.85E-01 | 0.80105 |
| PCBP2 | poly(rC) binding protein 2 | 100137523_TGI_at | 0.047 | 0.068 | 4.88E-01 | 0.80105 |
| RHOBTB3 | Rho-related BTB domain containing 3 | 100154919_TGI_at | -0.148 | 0.213 | 4.89E-01 | 0.80105 |
| AGPAT1 | "1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)" | 100135327_TGI_at | -1.237 | 1.808 | 4.94E-01 | 0.80512 |
| NA | hypothetical protein BC014011 | 100146413_TGI_at | 1.664 | 2.432 | 4.94E-01 | 0.80512 |
| NA | NA | 100313880_TGI_at | 0.329 | 0.482 | 4.95E-01 | 0.80512 |
| WDR60 | WD repeat domain 60 | 100129573_TGI_at | -0.151 | 0.223 | 4.99E-01 | 0.810638 |
| FAM71F2 | "family with sequence similarity 71, member F2" | 100153459_TGI_at | -4.439 | 6.665 | 5.05E-01 | 0.811215 |
| GALNT6 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) | 100150083_TGI_at | 0.507 | 0.757 | 5.03E-01 | 0.811215 |
| NA | hypothetical protein LOC285540 | 100307638_TGI_at | -0.811 | 1.208 | 5.02E-01 | 0.811215 |
| PCBP2 | poly(rC) binding protein 2 | 100131043_TGI_at | 0.068 | 0.102 | 5.02E-01 | 0.811215 |
| TYRO3 | TYRO3 protein tyrosine kinase | 100129019_TGI_at | 0.531 | 0.794 | 5.04E-01 | 0.811215 |
| ZNF391 | zinc finger protein 391 | 100150625_TGI_at | -3.255 | 4.883 | 5.05E-01 | 0.811215 |
| THEX1 | three prime histone mRNA exonuclease 1 | 100152809_TGI_at | 0.649 | 0.979 | 5.08E-01 | 0.813115 |
| MAP3K12 | mitogen-activated protein kinase kinase kinase 12 | 100302531_TGI_at | -0.105 | 0.159 | 5.10E-01 | 0.815548 |
| MLH3 | mutL homolog 3 (E. coli) | 100302585_TGI_at | -0.511 | 0.781 | 5.13E-01 | 0.818107 |
| MLH3 | mutL homolog 3 (E. coli) | 100146446_TGI_at | 0.411 | 0.633 | 5.17E-01 | 0.820823 |
| NA | NA | 100136812_TGI_at | 0.530 | 0.817 | 5.16E-01 | 0.820823 |
| COL21A1 | "collagen, type XXI, alpha 1" | 100149189_TGI_at | -0.120 | 0.189 | 5.25E-01 | 0.821948 |
| LYZ | lysozyme (renal amyloidosis) | 100303765_TGI_at | 0.031 | 0.048 | 5.23E-01 | 0.821948 |
| NA | Kazal type serine protease inhibitor 5-like 2 | 100147290_TGI_at | -7.133 | 11.090 | 5.20E-01 | 0.821948 |
| NA | NA | 100123597_TGI_at | -4.800 | 7.468 | 5.20E-01 | 0.821948 |
| NA | hypothetical LOC100131053 | 100162335_TGI_at | -1.535 | 2.418 | 5.25E-01 | 0.821948 |
| PSMA4 | "proteasome (prosome, macropain) subunit, alpha type, 4" | 100148404_TGI_at | 0.061 | 0.095 | 5.22E-01 | 0.821948 |
| TRIM38 | tripartite motif-containing 38 | 100127556_TGI_at | 0.123 | 0.193 | 5.24E-01 | 0.821948 |
| TTC35 | tetratricopeptide repeat domain 35 | 100139300_TGI_at | -0.131 | 0.204 | 5.21E-01 | 0.821948 |
| ATP5O | "ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit" | 100136800_TGI_at | 0.051 | 0.082 | 5.30E-01 | 0.823392 |
| HLA-G | "major histocompatibility complex, class I, G" | 100136412_TGI_at | -0.292 | 0.465 | 5.30E-01 | 0.823392 |
| NA | NA | 100153916_TGI_at | 0.600 | 0.952 | 5.29E-01 | 0.823392 |

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| NA | NA | 100132397_TGI_at | -0.284 | 0.452 | 5.30E-01 | 0.823392 |
| HLA-F | "major histocompatibility complex, class I, F" | 100311606_TGI_at | 0.628 | 1.004 | 5.32E-01 | 0.823939 |
| C10orf55 | chromosome 10 open reading frame 55 | 100160231_TGI_at | -3.240 | 5.339 | 5.44E-01 | 0.823944 |
| C14orf94 | chromosome 14 open reading frame 94 | 100146509_TGI_at | 0.101 | 0.165 | 5.39E-01 | 0.823944 |
| CCBL2 | cysteine conjugate-beta lyase 2 | 100135988_TGI_at | 0.187 | 0.300 | 5.33E-01 | 0.823944 |
| CNGA1 | cyclic nucleotide gated channel alpha 1 | 100124251_TGI_at | 2.266 | 3.690 | 5.39E-01 | 0.823944 |
| GEN1 | "Gen homolog 1, endonuclease (Drosophila)" | 100136657_TGI_at | 0.996 | 1.643 | 5.44E-01 | 0.823944 |
| ITIH4 | inter-alpha (globulin) inhibitor H4 (plasma Kallikrein-sensitive glycoprotein) | 100132374_TGI_at | -0.344 | 0.553 | 5.34E-01 | 0.823944 |
| MON1B | MON1 homolog B (yeast) | 100122211_TGI_at | 0.341 | 0.560 | 5.43E-01 | 0.823944 |
| NA | NA | 100124649_TGI_at | 7.741 | 12.670 | 5.41E-01 | 0.823944 |
| NA | NA | 100312826_TGI_at | -0.410 | 0.675 | 5.44E-01 | 0.823944 |
| NIPSNAP1 | nipsnap homolog 1 (C. elegans) | 100131090_TGI_at | 0.277 | 0.454 | 5.41E-01 | 0.823944 |
| NPHP3 | nephronophthisis 3 (adolescent) | 100313479_TGI_at | -0.269 | 0.437 | 5.38E-01 | 0.823944 |
| RHOBTB3 | Rho-related BTB domain containing 3 | 100306800_TGI_at | -0.322 | 0.530 | 5.43E-01 | 0.823944 |
| ABT1 | activator of basal transcription 1 | 100302369_TGI_at | 0.808 | 1.351 | 5.50E-01 | 0.827871 |
| IKZF2 | IKAROS family zinc finger 2 (Helios) | 100306345_TGI_at | -0.132 | 0.220 | 5.50E-01 | 0.827871 |
| NA | NA | 100303991_TGI_at | -6.615 | 11.075 | 5.50E-01 | 0.827871 |
| SRD5A3 | steroid 5 alpha-reductase 3 | 100301711_TGI_at | -1.453 | 2.437 | 5.51E-01 | 0.827871 |
| C1orf77 | chromosome 1 open reading frame 77 | 100308400_TGI_at | 8.809 | 14.819 | 5.52E-01 | 0.828127 |
| NA | similar to FLJ43276 protein | 100155121_TGI_at | -0.319 | 0.539 | 5.54E-01 | 0.828723 |
| CLTB | "clathrin, light chain (Lcb)" | 100134693_TGI_at | 0.056 | 0.097 | 5.61E-01 | 0.829168 |
| CYFIP2 | cytoplasmic FMR1 interacting protein 2 | 100125704_TGI_at | -0.211 | 0.362 | 5.59E-01 | 0.829168 |
| DARS | aspartyl-tRNA synthetase | 100138467_TGI_at | 0.085 | 0.148 | 5.64E-01 | 0.829168 |
| ENSA | endosulfine alpha | 100161206_TGI_at | -0.052 | 0.088 | 5.59E-01 | 0.829168 |
| HCG18 | HLA complex group 18 | 100139688_TGI_at | -0.180 | 0.312 | 5.63E-01 | 0.829168 |
| MAPRE2 | "microtubule-associated protein, RP/EB family, member 2" | 100161482_TGI_at | -0.189 | 0.323 | 5.58E-01 | 0.829168 |
| MGA | MAX gene associated | 100306577_TGI_at | -0.722 | 1.229 | 5.57E-01 | 0.829168 |
| NA | NA | 100136326_TGI_at | -0.690 | 1.187 | 5.61E-01 | 0.829168 |
| NA | NA | 100308684_TGI_at | -9.513 | 16.457 | 5.63E-01 | 0.829168 |
| VDAC2 | voltage-dependent anion channel 2 | 100305257_TGI_at | 0.115 | 0.198 | 5.64E-01 | 0.829168 |
| CLN5 | "ceroid-lipofuscinosis, neuronal 5" | 100146692_TGI_at | -0.167 | 0.292 | 5.67E-01 | 0.829988 |
| MEST | mesoderm specific transcript homolog (mouse) | 100308753_TGI_at | 0.507 | 0.883 | 5.66E-01 | 0.829988 |
| SLC4A8 | "solute carrier family 4, sodium bicarbonate cotransporter, member 8" | 100130519_TGI_at | 1.891 | 3.314 | 5.68E-01 | 0.830346 |
| NA | NA | 100150806_TGI_at | 0.648 | 1.148 | 5.73E-01 | 0.833085 |
| RHOBTB3 | Rho-related BTB domain containing 3 | 100143194_TGI_at | 0.116 | 0.206 | 5.72E-01 | 0.833085 |

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| TMEM110 | transmembrane protein 110 | 100133810_TGI_at | 0.173 | 0.306 | 5.73E-01 | 0.833085 |
| LRRC37A | leucine rich repeat containing 37A | 100304816_TGI_at | 17.054 | 30.362 | 5.74E-01 | 0.833188 |
| ITGA2 | "integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)" | 100135535_TGI_at | -0.113 | 0.203 | 5.79E-01 | 0.838167 |
| C18orf10 | chromosome 18 open reading frame 10 | 100305245_TGI_at | -0.124 | 0.229 | 5.87E-01 | 0.838811 |
| CYP2C9 | "cytochrome P450, family 2, subfamily C, polypeptide 9" | 100123290_TGI_at | -6.468 | 11.758 | 5.82E-01 | 0.838811 |
| GEN1 | "Gen homolog 1, endonuclease (Drosophila)" | 100158297_TGI_at | -0.258 | 0.474 | 5.86E-01 | 0.838811 |
| HLA-C | "major histocompatibility complex, class I, C" | 100313121_TGI_at | -0.018 | 0.033 | 5.88E-01 | 0.838811 |
| HOXA1 | homeobox A1 | 100300632_TGI_at | -1.743 | 3.214 | 5.88E-01 | 0.838811 |
| NA | NA | 100123120_TGI_at | -1.085 | 2.000 | 5.87E-01 | 0.838811 |
| PGBD1 | piggyBac transposable element derived 1 | 100135231_TGI_at | -0.357 | 0.656 | 5.86E-01 | 0.838811 |
| TMEM50B | transmembrane protein 50B | 100127382_TGI_at | -0.075 | 0.136 | 5.82E-01 | 0.838811 |
| MUC21 | "mucin 21, cell surface associated" | 100309111_TGI_at | 0.180 | 0.334 | 5.90E-01 | 0.839466 |
| VARS2 | "valyl-tRNA synthetase 2, mitochondrial (putative)" | 100151371_TGI_at | 0.209 | 0.388 | 5.90E-01 | 0.839466 |
| NA | NA | 100308581_TGI_at | -0.120 | 0.228 | 5.97E-01 | 0.845812 |
| PDPN | podoplanin | 100311884_TGI_at | 0.318 | 0.602 | 5.97E-01 | 0.845812 |
| ATP6V1G2 | "ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G2" | 100142732_TGI_at | 0.268 | 0.522 | 6.07E-01 | 0.847528 |
| BCAR1 | breast cancer anti-estrogen resistance 1 | 100307330_TGI_at | 1.427 | 2.857 | 6.18E-01 | 0.847528 |
| CYP2C9 | "cytochrome P450, family 2, subfamily C, polypeptide 9" | 100303586_TGI_at | -1.656 | 3.229 | 6.08E-01 | 0.847528 |
| GOLPH3L | golgi phosphoprotein 3-like | 100159164_TGI_at | 0.683 | 1.334 | 6.09E-01 | 0.847528 |
| GOLPH3L | golgi phosphoprotein 3-like | 100308717_TGI_at | 1.014 | 1.988 | 6.10E-01 | 0.847528 |
| MTMR3 | myotubularin related protein 3 | 100160585_TGI_at | -0.268 | 0.533 | 6.16E-01 | 0.847528 |
| NA | hypothetical STGC3 | 100156808_TGI_at | 1.254 | 2.405 | 6.02E-01 | 0.847528 |
| NA | NA | 100146746_TGI_at | 0.090 | 0.176 | 6.08E-01 | 0.847528 |
| NA | NA | 100130228_TGI_at | -0.185 | 0.365 | 6.12E-01 | 0.847528 |
| NA | NA | 100150862_TGI_at | -12.532 | 25.022 | 6.16E-01 | 0.847528 |
| NBPF1 | "neuroblastoma breakpoint family, member 1" | 100158208_TGI_at | 0.765 | 1.477 | 6.05E-01 | 0.847528 |
| NCKIPSD | NCK interacting protein with SH3 domain | 100130226_TGI_at | 0.170 | 0.332 | 6.08E-01 | 0.847528 |
| NIPSNAP1 | nipsnap homolog 1 (C. elegans) | 100302806_TGI_at | 0.175 | 0.342 | 6.08E-01 | 0.847528 |
| RBM23 | RNA binding motif protein 23 | 100306484_TGI_at | -0.164 | 0.323 | 6.12E-01 | 0.847528 |
| SGCD | "sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)" | 100154320_TGI_at | -0.351 | 0.690 | 6.11E-01 | 0.847528 |
| SLMO2 | slowmo homolog 2 (Drosophila) | 100130622_TGI_at | -0.182 | 0.364 | 6.18E-01 | 0.847528 |
| SUPT3H | suppressor of Ty 3 homolog (S. cerevisiae) | 100300937_TGI_at | -0.899 | 1.794 | 6.17E-01 | 0.847528 |
| WDR52 | WD repeat domain 52 | 100157274_TGI_at | 0.327 | 0.655 | 6.18E-01 | 0.847528 |
| ZFAND2A | "zinc finger, AN1-type domain 2A" | 100151722_TGI_at | 0.073 | 0.145 | 6.16E-01 | 0.847528 |
| SYTL2 | synaptotagmin-like 2 | 100123986_TGI_at | -0.181 | 0.365 | 6.21E-01 | 0.849928 |

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| SMPDL3B | "sphingomyelin phosphodiesterase, acid-like 3B" | 100303445_TGI_at | 0.342 | 0.695 | 6.23E-01 | 0.851122 |
| GFM1 | "G elongation factor, mitochondrial 1" | 100301664_TGI_at | -0.131 | 0.268 | 6.25E-01 | 0.852529 |
| NA | similar to hCG2042473 | 100152956_TGI_at | -2.264 | 4.653 | 6.27E-01 | 0.853208 |
| C14orf153 | chromosome 14 open reading frame 153 | 100306300_TGI_at | 0.324 | 0.694 | 6.40E-01 | 0.855812 |
| C7orf46 | chromosome 7 open reading frame 46 | 100305640_TGI_at | -0.619 | 1.310 | 6.37E-01 | 0.855812 |
| FN3K | fructosamine 3 kinase | 100139631_TGI_at | 2.918 | 6.156 | 6.36E-01 | 0.855812 |
| HLA-DQA2 | "major histocompatibility complex, class II, DQ alpha 2" | 100313766_TGI_at | 0.010 | 0.021 | 6.42E-01 | 0.855812 |
| HLA-F | "major histocompatibility complex, class I, F" | 100303129_TGI_at | 0.046 | 0.099 | 6.41E-01 | 0.855812 |
| MICB | MHC class I polypeptide-related sequence B | 100161520_TGI_at | 0.109 | 0.232 | 6.40E-01 | 0.855812 |
| NA | NA | 100151492_TGI_at | -0.079 | 0.166 | 6.32E-01 | 0.855812 |
| NA | NA | 100305399_TGI_at | 0.073 | 0.153 | 6.35E-01 | 0.855812 |
| NDUFA12 | "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12" | 100148776_TGI_at | 0.051 | 0.108 | 6.40E-01 | 0.855812 |
| PDGFD | platelet derived growth factor D | 100132001_TGI_at | 0.290 | 0.610 | 6.34E-01 | 0.855812 |
| PLEKHM1 | "pleckstrin homology domain containing, family M (with RUN domain) member 1" | 100159134_TGI_at | 0.165 | 0.353 | 6.41E-01 | 0.855812 |
| RPL27A | ribosomal protein L27a | 100162298_TGI_at | 0.644 | 1.377 | 6.40E-01 | 0.855812 |
| THSD4 | "thrombospondin, type I, domain containing 4" | 100142979_TGI_at | -0.171 | 0.356 | 6.31E-01 | 0.855812 |
| CDC123 | cell division cycle 123 homolog (S. cerevisiae) | 100149333_TGI_at | -0.088 | 0.192 | 6.48E-01 | 0.857199 |
| HIST1H2BL | "histone cluster 1, H2bl" | 100302815_TGI_at | 21.870 | 47.827 | 6.47E-01 | 0.857199 |
| NA | NA | 100147343_TGI_at | -0.231 | 0.502 | 6.46E-01 | 0.857199 |
| TRIM4 | tripartite motif-containing 4 | 100126573_TGI_at | -0.184 | 0.408 | 6.51E-01 | 0.858629 |
| USP4 | ubiquitin specific peptidase 4 (proto-oncogene) | 100155972_TGI_at | -0.043 | 0.096 | 6.51E-01 | 0.858629 |
| NA | NA | 100306708_TGI_at | 0.597 | 1.336 | 6.55E-01 | 0.862436 |
| MLH3 | mutL homolog 3 (E. coli) | 100129848_TGI_at | 0.414 | 0.934 | 6.58E-01 | 0.863044 |
| THEX1 | three prime histone mRNA exonuclease 1 | 100122765_TGI_at | 0.243 | 0.547 | 6.58E-01 | 0.863044 |
| GRB2 | growth factor receptor-bound protein 2 | 100304907_TGI_at | 0.269 | 0.612 | 6.60E-01 | 0.863213 |
| NA | hypothetical LOC65996 | 100127780_TGI_at | 0.118 | 0.267 | 6.59E-01 | 0.863213 |
| FMO2 | flavin containing monooxygenase 2 (non-functional) | 100132596_TGI_at | -0.016 | 0.036 | 6.63E-01 | 0.865461 |
| ARL6IP1 | ADP-ribosylation factor-like 6 interacting protein 1 | 100149583_TGI_at | 2.475 | 5.964 | 6.78E-01 | 0.865954 |
| C6orf12 | chromosome 6 open reading frame 12 | 100125007_TGI_at | -0.647 | 1.541 | 6.75E-01 | 0.865954 |
| CHRNA5 | "cholinergic receptor, nicotinic, alpha 5" | 100156434_TGI_at | -1.570 | 3.758 | 6.76E-01 | 0.865954 |
| HLA-G | "major histocompatibility complex, class I, G" | 100138030_TGI_at | 1.212 | 2.910 | 6.77E-01 | 0.865954 |
| INTS5 | integrator complex subunit 5 | 100135147_TGI_at | 0.231 | 0.554 | 6.77E-01 | 0.865954 |
| NA | hypothetical protein LOC100133205 | 100129291_TGI_at | 1.171 | 2.706 | 6.65E-01 | 0.865954 |
| NA | NA | 100124184_TGI_at | 0.589 | 1.379 | 6.69E-01 | 0.865954 |
| NA | mesenchymal stem cell protein DSCD28 | 100147593_TGI_at | 1.201 | 2.839 | 6.72E-01 | 0.865954 |
| NA | NA | 100143280_TGI_at | 0.130 | 0.310 | 6.76E-01 | 0.865954 |

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| NA | hypothetical protein LOC283587 | 100132831_TGI_at | -0.680 | 1.638 | 6.78E-01 | 0.865954 |
| RNF144B | ring finger 144B | 100152113_TGI_at | 0.389 | 0.921 | 6.73E-01 | 0.865954 |
| SGCD | "sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)" | 100144469_TGI_at | 0.495 | 1.182 | 6.75E-01 | 0.865954 |
| SON | SON DNA binding protein | 100130835_TGI_at | 0.251 | 0.593 | 6.72E-01 | 0.865954 |
| WDR52 | WD repeat domain 52 | 100126013_TGI_at | 0.159 | 0.374 | 6.70E-01 | 0.865954 |
| C19orf6 | chromosome 19 open reading frame 6 | 100158347_TGI_at | 1.314 | 3.191 | 6.80E-01 | 0.866132 |
| MAP3K12 | mitogen-activated protein kinase kinase kinase 12 | 100306859_TGI_at | -0.174 | 0.422 | 6.80E-01 | 0.866132 |
| DMPK | dystrophia myotonica-protein kinase | 100148527_TGI_at | -0.084 | 0.208 | 6.87E-01 | 0.868957 |
| EHHADH | "enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A dehydrogenase" | 100135841_TGI_at | -1.034 | 2.558 | 6.86E-01 | 0.868957 |
| KCNMB3 | "potassium large conductance calcium-activated channel, subfamily M beta member 3" | 100133838_TGI_at | -0.483 | 1.190 | 6.85E-01 | 0.868957 |
| MAPT | microtubule-associated protein tau | 100136496_TGI_at | 0.298 | 0.740 | 6.87E-01 | 0.868957 |
| HCG27 | HLA complex group 27 | 100300925_TGI_at | -0.471 | 1.186 | 6.91E-01 | 0.870406 |
| MAP1LC3A | microtubule-associated protein 1 light chain 3 alpha | 100143040_TGI_at | -0.124 | 0.311 | 6.91E-01 | 0.870406 |
| TRIM10 | tripartite motif-containing 10 | 100133405_TGI_at | -1.222 | 3.061 | 6.90E-01 | 0.870406 |
| C16orf5 | chromosome 16 open reading frame 5 | 100159519_TGI_at | 0.144 | 0.371 | 6.98E-01 | 0.874863 |
| MBNL1 | muscleblind-like (Drosophila) | 100305792_TGI_at | 0.103 | 0.266 | 6.98E-01 | 0.874863 |
| VDAC2 | voltage-dependent anion channel 2 | 100309207_TGI_at | 0.069 | 0.177 | 6.96E-01 | 0.874863 |
| CLUAP1 | clusterin associated protein 1 | 100313559_TGI_at | 0.099 | 0.267 | 7.11E-01 | 0.876887 |
| GALC | galactosylceramidase | 100307819_TGI_at | -0.099 | 0.260 | 7.04E-01 | 0.876887 |
| HOXB2 | homeobox B2 | 100147773_TGI_at | 0.291 | 0.762 | 7.03E-01 | 0.876887 |
| ITPR3 | "inositol 1,4,5-triphosphate receptor, type 3" | 100131760_TGI_at | -3.217 | 8.658 | 7.10E-01 | 0.876887 |
| KIAA1267 | KIAA1267 | 100148039_TGI_at | -0.037 | 0.098 | 7.08E-01 | 0.876887 |
| NA | NA | 100127813_TGI_at | 2.795 | 7.379 | 7.05E-01 | 0.876887 |
| NA | NA | 100311952_TGI_at | -0.068 | 0.185 | 7.11E-01 | 0.876887 |
| PLA2G5 | "phospholipase A2, group V" | 100130289_TGI_at | -0.324 | 0.872 | 7.10E-01 | 0.876887 |
| RAB6A | "RAB6A, member RAS oncogene family" | 100309263_TGI_at | 0.143 | 0.382 | 7.07E-01 | 0.876887 |
| WDR52 | WD repeat domain 52 | 100309898_TGI_at | 0.149 | 0.388 | 7.01E-01 | 0.876887 |
| C1orf113 | chromosome 1 open reading frame 113 | 100149702_TGI_at | -1.097 | 3.005 | 7.15E-01 | 0.877853 |
| CAMK1D | calcium/calmodulin-dependent protein kinase ID | 100139207_TGI_at | 0.084 | 0.228 | 7.14E-01 | 0.877853 |
| NA | hypothetical protein LOC285540 | 100148345_TGI_at | -0.533 | 1.455 | 7.14E-01 | 0.877853 |
| PDGFD | platelet derived growth factor D | 100306816_TGI_at | 0.954 | 2.633 | 7.17E-01 | 0.877853 |
| PTER | phosphotriesterase related | 100132235_TGI_at | -0.479 | 1.322 | 7.17E-01 | 0.877853 |
| NA | NA | 100124262_TGI_at | -0.188 | 0.527 | 7.21E-01 | 0.878801 |
| NA | NA | 100161240_TGI_at | 0.616 | 1.727 | 7.21E-01 | 0.878801 |
| PM20D1 | peptidase M20 domain containing 1 | 100155586_TGI_at | 1.805 | 5.037 | 7.20E-01 | 0.878801 |

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| ARIH2 | ariadne homolog 2 (Drosophila) | 100314021_TGI_at | 0.132 | 0.386 | 7.32E-01 | 0.882101 |
| C6orf138 | chromosome 6 open reading frame 138 | 100121858_TGI_at | -1.004 | 2.904 | 7.30E-01 | 0.882101 |
| HCP5 | HLA complex P5 | 100144394_TGI_at | -0.043 | 0.126 | 7.33E-01 | 0.882101 |
| HDAC9 | histone deacetylase 9 | 100146735_TGI_at | -0.878 | 2.551 | 7.31E-01 | 0.882101 |
| HLA-DOA | "major histocompatibility complex, class II, DO alpha" | 100126591_TGI_at | -0.013 | 0.038 | 7.27E-01 | 0.882101 |
| HLA-DRB5 | "major histocompatibility complex, class II, DR beta 5" | 100302940_TGI_at | 0.003 | 0.010 | 7.29E-01 | 0.882101 |
| MRPL43 | mitochondrial ribosomal protein L43 | 100134957_TGI_at | -0.075 | 0.217 | 7.31E-01 | 0.882101 |
| RHOBTB3 | Rho-related BTB domain containing 3 | 100153237_TGI_at | -0.095 | 0.276 | 7.31E-01 | 0.882101 |
| C11orf83 | chromosome 11 open reading frame 83 | 100153773_TGI_at | 0.392 | 1.157 | 7.35E-01 | 0.882199 |
| NA | NA | 100149004_TGI_at | 0.049 | 0.145 | 7.35E-01 | 0.882199 |
| AMIGO3 | adhesion molecule with Ig-like domain 3 | 100137568_TGI_at | -0.513 | 1.653 | 7.56E-01 | 0.884324 |
| BTN2A2 | "butyrophilin, subfamily 2, member A2" | 100141839_TGI_at | -0.092 | 0.296 | 7.56E-01 | 0.884324 |
| C10orf11 | chromosome 10 open reading frame 11 | 100144009_TGI_at | -1.393 | 4.532 | 7.59E-01 | 0.884324 |
| CAMK1D | calcium/calmodulin-dependent protein kinase ID | 100142010_TGI_at | 0.066 | 0.208 | 7.50E-01 | 0.884324 |
| CCNT2 | cyclin T2 | 100144954_TGI_at | -0.175 | 0.540 | 7.46E-01 | 0.884324 |
| EYA3 | eyes absent homolog 3 (Drosophila) | 100122866_TGI_at | -0.127 | 0.388 | 7.44E-01 | 0.884324 |
| HLA-DPB1 | "major histocompatibility complex, class II, DP beta 1" | 100145052_TGI_at | -0.055 | 0.181 | 7.61E-01 | 0.884324 |
| LST1 | leukocyte specific transcript 1 | 100149313_TGI_at | -0.011 | 0.035 | 7.44E-01 | 0.884324 |
| MCART1 | mitochondrial carrier triple repeat 1 | 100155123_TGI_at | 0.282 | 0.899 | 7.54E-01 | 0.884324 |
| MUC21 | "mucin 21, cell surface associated" | 100159175_TGI_at | 0.045 | 0.135 | 7.41E-01 | 0.884324 |
| NA | NA | 100149241_TGI_at | 0.135 | 0.411 | 7.42E-01 | 0.884324 |
| NA | NA | 100309243_TGI_at | -0.219 | 0.680 | 7.47E-01 | 0.884324 |
| NA | hypothetical protein FLJ11151 | 100311790_TGI_at | -0.149 | 0.468 | 7.50E-01 | 0.884324 |
| NA | NA | 100151362_TGI_at | 0.439 | 1.391 | 7.53E-01 | 0.884324 |
| NA | NA | 100150849_TGI_at | 3.710 | 11.912 | 7.55E-01 | 0.884324 |
| RABAC1 | Rab acceptor 1 (prenylated) | 100306969_TGI_at | 0.047 | 0.152 | 7.56E-01 | 0.884324 |
| RABEP1 | "rabaptin, RAB GTPase binding effector protein 1" | 100135777_TGI_at | -0.094 | 0.309 | 7.60E-01 | 0.884324 |
| SNAPIN | SNAP-associated protein | 100154603_TGI_at | -0.128 | 0.414 | 7.58E-01 | 0.884324 |
| SPATA1 | spermatogenesis associated 1 | 100151666_TGI_at | -0.366 | 1.187 | 7.57E-01 | 0.884324 |
| TAP2 | "transporter 2, ATP-binding cassette, sub-family B (MDR/TAP)" | 100161395_TGI_at | 0.020 | 0.059 | 7.40E-01 | 0.884324 |
| TSEN54 | tRNA splicing endonuclease 54 homolog (S. cerevisiae) | 100159529_TGI_at | 0.201 | 0.647 | 7.56E-01 | 0.884324 |
| UHRF1BP1 | UHRF1 binding protein 1 | 100149686_TGI_at | 0.544 | 1.786 | 7.61E-01 | 0.884324 |
| NA | peptidylprolyl isomerase E pseudogene | 100313726_TGI_at | -0.090 | 0.299 | 7.62E-01 | 0.8846 |
| NA | NA | 100139086_TGI_at | 0.118 | 0.394 | 7.64E-01 | 0.8854 |
| NLRC3 | "NLR family, CARD domain containing 3" | 100125900_TGI_at | -0.067 | 0.227 | 7.69E-01 | 0.889047 |
| UHRF1BP1 | UHRF1 binding protein 1 | 100128579_TGI_at | 0.074 | 0.254 | 7.72E-01 | 0.891366 |
| GFM1 | "G elongation factor, mitochondrial 1" | 100150755_TGI_at | 0.077 | 0.266 | 7.74E-01 | 0.89202 |

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|---|---|---|---|---|---|---|
| MAPKBP1 | mitogen-activated protein kinase binding protein 1 | 100302252_TGI_at | -0.966 | 3.390 | 7.76E-01 | 0.89202 |
| NA | NA | 100161847_TGI_at | 0.384 | 1.346 | 7.75E-01 | 0.89202 |
| KLC1 | kinesin light chain 1 | 100310380_TGI_at | 0.185 | 0.662 | 7.80E-01 | 0.894471 |
| WWOX | WW domain containing oxidoreductase | 100138939_TGI_at | 0.166 | 0.594 | 7.80E-01 | 0.894471 |
| HLA-DQA2 | "major histocompatibility complex, class II, DQ alpha 2" | 100125191_TGI_at | -0.550 | 2.002 | 7.84E-01 | 0.896187 |
| HLA-DRB1 | "major histocompatibility complex, class II, DR beta 1" | 100125275_TGI_at | 0.013 | 0.046 | 7.83E-01 | 0.896187 |
| C3orf70 | chromosome 3 open reading frame 70 | 100155000_TGI_at | -0.089 | 0.326 | 7.86E-01 | 0.897284 |
| NA | hypothetical protein LOC284581 | 100300216_TGI_at | 0.124 | 0.461 | 7.87E-01 | 0.897284 |
| NA | sterile alpha motif and leucine zipper containing kinase AZK | 100129209_TGI_at | 0.116 | 0.433 | 7.89E-01 | 0.897284 |
| PSMD7 | "proteasome (prosome, macropain) 26S subunit, non-ATPase, 7" | 100303831_TGI_at | -0.092 | 0.342 | 7.88E-01 | 0.897284 |
| HCG18 | HLA complex group 18 | 100308127_TGI_at | -0.142 | 0.549 | 7.96E-01 | 0.903829 |
| C4BPB | "complement component 4 binding protein, beta" | 100159322_TGI_at | -0.143 | 0.559 | 7.98E-01 | 0.904487 |
| ARNT | aryl hydrocarbon receptor nuclear translocator | 100310890_TGI_at | 0.316 | 1.296 | 8.07E-01 | 0.907694 |
| C18orf10 | chromosome 18 open reading frame 10 | 100135353_TGI_at | -0.226 | 0.930 | 8.08E-01 | 0.907694 |
| C22orf34 | chromosome 22 open reading frame 34 | 100129499_TGI_at | -0.091 | 0.382 | 8.11E-01 | 0.907694 |
| CCDC38 | coiled-coil domain containing 38 | 100140090_TGI_at | 3.212 | 12.927 | 8.04E-01 | 0.907694 |
| CFDP1 | craniofacial development protein 1 | 100147953_TGI_at | 0.030 | 0.129 | 8.20E-01 | 0.907694 |
| EFCAB5 | EF-hand calcium binding domain 5 | 100305934_TGI_at | 3.414 | 14.543 | 8.14E-01 | 0.907694 |
| FAM103A1 | "family with sequence similarity 103, member A1" | 100301598_TGI_at | -0.077 | 0.340 | 8.20E-01 | 0.907694 |
| HLA-A | "major histocompatibility complex, class I, A" | 100129349_TGI_at | 0.003 | 0.015 | 8.18E-01 | 0.907694 |
| HLA-DRB3 | "major histocompatibility complex, class II, DR beta 3" | 100139572_TGI_at | 0.003 | 0.013 | 8.11E-01 | 0.907694 |
| NA | NA | 100149232_TGI_at | 4.396 | 18.627 | 8.13E-01 | 0.907694 |
| NCR3 | natural cytotoxicity triggering receptor 3 | 100125842_TGI_at | -0.224 | 0.940 | 8.11E-01 | 0.907694 |
| NUP85 | nucleoporin 85kDa | 100143655_TGI_at | -0.069 | 0.296 | 8.15E-01 | 0.907694 |
| PDXDC2 | pyridoxal-dependent decarboxylase domain containing 2 | 100310948_TGI_at | -0.087 | 0.380 | 8.20E-01 | 0.907694 |
| PSORS1C3 | psoriasis susceptibility 1 candidate 3 | 100304000_TGI_at | -0.642 | 2.814 | 8.20E-01 | 0.907694 |
| PTER | phosphotriesterase related | 100124216_TGI_at | -0.123 | 0.512 | 8.11E-01 | 0.907694 |
| QSOX2 | quiescin Q6 sulfhydryl oxidase 2 | 100124395_TGI_at | -0.139 | 0.582 | 8.12E-01 | 0.907694 |
| ZSCAN12L1 | zinc finger and SCAN domain containing 12-like 1 | 100148250_TGI_at | -1.475 | 5.917 | 8.03E-01 | 0.907694 |
| "MARCH5" | membrane-associated ring finger (C3HC4) 5 | 100305748_TGI_at | -0.051 | 0.247 | 8.36E-01 | 0.908959 |
| ARL5C | ADP-ribosylation factor-like 5C | 100300166_TGI_at | 6.387 | 31.003 | 8.37E-01 | 0.908959 |
| C18orf10 | chromosome 18 open reading frame 10 | 100122767_TGI_at | -0.096 | 0.458 | 8.34E-01 | 0.908959 |
| C4BPA | "complement component 4 binding protein, alpha" | 100122178_TGI_at | -0.003 | 0.015 | 8.51E-01 | 0.908959 |
| GATAD2B | GATA zinc finger domain containing 2B | 100155432_TGI_at | 0.031 | 0.149 | 8.35E-01 | 0.908959 |
| HCG2P7 | HLA complex group 2 pseudogene 7 | 100143227_TGI_at | -0.341 | 1.799 | 8.50E-01 | 0.908959 |
| KIAA0317 | KIAA0317 | 100126667_TGI_at | -0.094 | 0.493 | 8.50E-01 | 0.908959 |

| | | | | | | |
|---|---|---|---|---|---|---|
| KIAA0562 | KIAA0562 | 100141567_TGI_at | -0.188 | 0.947 | 8.42E-01 | 0.908959 |
| KPNA3 | karyopherin alpha 3 (importin alpha 4) | 100162913_TGI_at | -0.142 | 0.655 | 8.28E-01 | 0.908959 |
| MAPKBP1 | mitogen-activated protein kinase binding protein 1 | 100156388_TGI_at | -0.361 | 1.674 | 8.29E-01 | 0.908959 |
| MLF1 | myeloid leukemia factor 1 | 100304858_TGI_at | 0.276 | 1.326 | 8.35E-01 | 0.908959 |
| MPP6 | "membrane protein, palmitoylated 6 (MAGUK p55 subfamily member 6)" | 100128819_TGI_at | -0.664 | 3.113 | 8.31E-01 | 0.908959 |
| NA | NA | 100138417_TGI_at | -1.248 | 5.662 | 8.26E-01 | 0.908959 |
| NA | fructosamine-3-kinase-related protein | 100159829_TGI_at | -0.122 | 0.575 | 8.31E-01 | 0.908959 |
| NA | NA | 100151213_TGI_at | -0.923 | 4.364 | 8.32E-01 | 0.908959 |
| NA | nuclear DNA-binding protein | 100152575_TGI_at | -0.082 | 0.414 | 8.43E-01 | 0.908959 |
| NA | NA | 100123914_TGI_at | -0.049 | 0.260 | 8.49E-01 | 0.908959 |
| NDUFAF1 | "NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1" | 100132051_TGI_at | -0.108 | 0.567 | 8.49E-01 | 0.908959 |
| PTER | phosphotriesterase related | 100305949_TGI_at | -0.093 | 0.491 | 8.50E-01 | 0.908959 |
| RABAC1 | Rab acceptor 1 (prenylated) | 100124297_TGI_at | 0.041 | 0.186 | 8.24E-01 | 0.908959 |
| RAD1 | RAD1 homolog (S. pombe) | 100309539_TGI_at | -0.153 | 0.798 | 8.47E-01 | 0.908959 |
| STAT6 | "signal transducer and activator of transcription 6, interleukin-4 induced" | 100156721_TGI_at | -0.009 | 0.046 | 8.49E-01 | 0.908959 |
| TCP11 | t-complex 11 homolog (mouse) | 100304633_TGI_at | 1.061 | 5.389 | 8.44E-01 | 0.908959 |
| TREM1 | triggering receptor expressed on myeloid cells 1 | 100135979_TGI_at | -0.008 | 0.041 | 8.46E-01 | 0.908959 |
| WWP2 | WW domain containing E3 ubiquitin protein ligase 2 | 100300793_TGI_at | 0.091 | 0.473 | 8.48E-01 | 0.908959 |
| ZNF132 | zinc finger protein 132 | 100125493_TGI_at | -0.240 | 1.104 | 8.28E-01 | 0.908959 |
| AGPAT1 | "1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)" | 100126665_TGI_at | 0.041 | 0.254 | 8.72E-01 | 0.910334 |
| B3GNTL1 | "UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1" | 100312006_TGI_at | -0.106 | 0.922 | 9.09E-01 | 0.910334 |
| C1orf113 | chromosome 1 open reading frame 113 | 100129400_TGI_at | -0.100 | 0.627 | 8.73E-01 | 0.910334 |
| C22orf34 | chromosome 22 open reading frame 34 | 100307496_TGI_at | 0.097 | 0.564 | 8.63E-01 | 0.910334 |
| C2CD3 | C2 calcium-dependent domain containing 3 | 100145368_TGI_at | 0.076 | 0.461 | 8.69E-01 | 0.910334 |
| C6orf164 | chromosome 6 open reading frame 164 | 100147499_TGI_at | 0.926 | 7.821 | 9.06E-01 | 0.910334 |
| CAMK1D | calcium/calmodulin-dependent protein kinase ID | 100301887_TGI_at | 0.397 | 2.913 | 8.92E-01 | 0.910334 |
| CCNT2 | cyclin T2 | 100304349_TGI_at | -0.064 | 0.488 | 8.96E-01 | 0.910334 |
| CLUAP1 | clusterin associated protein 1 | 100312853_TGI_at | -0.031 | 0.273 | 9.10E-01 | 0.910334 |
| EXOC2 | exocyst complex component 2 | 100139548_TGI_at | -0.080 | 0.586 | 8.91E-01 | 0.910334 |
| FAM13A1 | "family with sequence similarity 13, member A1" | 100160946_TGI_at | 0.023 | 0.138 | 8.69E-01 | 0.910334 |
| GFM1 | "G elongation factor, mitochondrial 1" | 100141104_TGI_at | 0.133 | 1.027 | 8.97E-01 | 0.910334 |
| GTF3C5 | "general transcription factor IIIC, polypeptide 5, 63kDa" | 100157332_TGI_at | -0.050 | 0.367 | 8.91E-01 | 0.910334 |
| HCG2P7 | HLA complex group 2 pseudogene 7 | 100300348_TGI_at | -0.318 | 2.553 | 9.01E-01 | 0.910334 |
| HLA-DQB2 | "major histocompatibility complex, class II, DQ beta 2" | 100157567_TGI_at | 0.021 | 0.151 | 8.90E-01 | 0.910334 |

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|---|---|---|---|---|---|---|
| HLA-DRB4 | "major histocompatibility complex, class II, DR beta 4" | 100127159_TGI_at | -0.001 | 0.010 | 8.90E-01 | 0.910334 |
| JMJD7-PLA2G4B | JMJD7-PLA2G4B readthrough transcript | 100147021_TGI_at | 0.062 | 0.409 | 8.80E-01 | 0.910334 |
| KIAA0317 | KIAA0317 | 100308140_TGI_at | 0.110 | 0.943 | 9.07E-01 | 0.910334 |
| LY6G5C | "lymphocyte antigen 6 complex, locus G5C" | 100126781_TGI_at | 0.111 | 0.747 | 8.82E-01 | 0.910334 |
| MAPT | microtubule-associated protein tau | 100123425_TGI_at | 0.219 | 1.835 | 9.05E-01 | 0.910334 |
| MLH3 | mutL homolog 3 (E. coli) | 100151060_TGI_at | -0.284 | 2.119 | 8.93E-01 | 0.910334 |
| NA | NA | 100304931_TGI_at | -0.283 | 1.598 | 8.60E-01 | 0.910334 |
| NA | NA | 100311514_TGI_at | -0.016 | 0.099 | 8.70E-01 | 0.910334 |
| NA | NA | 100123896_TGI_at | 0.037 | 0.232 | 8.75E-01 | 0.910334 |
| NA | NA | 100304754_TGI_at | -0.535 | 3.507 | 8.79E-01 | 0.910334 |
| NA | NA | 100306689_TGI_at | -0.170 | 1.148 | 8.82E-01 | 0.910334 |
| NA | NA | 100151178_TGI_at | -0.178 | 1.215 | 8.83E-01 | 0.910334 |
| NA | NA | 100313804_TGI_at | -0.266 | 1.836 | 8.85E-01 | 0.910334 |
| NA | NA | 100160131_TGI_at | -0.287 | 2.050 | 8.89E-01 | 0.910334 |
| NA | hypothetical protein FLJ11151 | 100151120_TGI_at | 0.050 | 0.364 | 8.90E-01 | 0.910334 |
| NA | NA | 100143321_TGI_at | -0.157 | 1.274 | 9.02E-01 | 0.910334 |
| NA | NA | 100152779_TGI_at | 0.169 | 1.440 | 9.06E-01 | 0.910334 |
| NA | hypothetical LOC648987 | 100157820_TGI_at | -0.108 | 0.948 | 9.09E-01 | 0.910334 |
| NUP210L | nucleoporin 210kDa-like | 100136037_TGI_at | -0.603 | 5.196 | 9.08E-01 | 0.910334 |
| OPN5 | opsin 5 | 100304757_TGI_at | -0.601 | 3.454 | 8.62E-01 | 0.910334 |
| PAAF1 | proteasomal ATPase-associated factor 1 | 100150651_TGI_at | -0.052 | 0.332 | 8.76E-01 | 0.910334 |
| PILRB | paired immunoglobin-like type 2 receptor beta | 100162662_TGI_at | 0.088 | 0.593 | 8.81E-01 | 0.910334 |
| PRG4 | proteoglycan 4 | 100302581_TGI_at | 0.040 | 0.350 | 9.10E-01 | 0.910334 |
| PRKD3 | protein kinase D3 | 100145697_TGI_at | 0.066 | 0.511 | 8.97E-01 | 0.910334 |
| RNF39 | ring finger protein 39 | 100135776_TGI_at | -0.157 | 1.040 | 8.80E-01 | 0.910334 |
| SGCD | "sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)" | 100313731_TGI_at | -0.229 | 1.326 | 8.63E-01 | 0.910334 |
| SLC30A10 | "solute carrier family 30, member 10" | 100159938_TGI_at | 0.552 | 4.432 | 9.01E-01 | 0.910334 |
| SREBF1 | sterol regulatory element binding transcription factor 1 | 100136519_TGI_at | 0.263 | 1.696 | 8.77E-01 | 0.910334 |
| TCF19 | transcription factor 19 (SC1) | 100142285_TGI_at | -0.126 | 0.889 | 8.87E-01 | 0.910334 |
| TH1L | TH1-like (Drosophila) | 100306923_TGI_at | 0.117 | 0.634 | 8.54E-01 | 0.910334 |
| TH1L | TH1-like (Drosophila) | 100126253_TGI_at | 0.038 | 0.273 | 8.91E-01 | 0.910334 |
| THSD4 | "thrombospondin, type I, domain containing 4" | 100308491_TGI_at | 0.085 | 0.580 | 8.84E-01 | 0.910334 |
| TMEM87A | transmembrane protein 87A | 100305514_TGI_at | 0.914 | 6.037 | 8.80E-01 | 0.910334 |
| TNS1 | tensin 1 | 100145096_TGI_at | -0.102 | 0.732 | 8.89E-01 | 0.910334 |
| VAMP4 | vesicle-associated membrane protein 4 | 100156028_TGI_at | 0.105 | 0.864 | 9.04E-01 | 0.910334 |
| ZNF584 | zinc finger protein 584 | 100127553_TGI_at | -0.085 | 0.632 | 8.93E-01 | 0.910334 |

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|---|---|---|---|---|---|---|
| BRUNOL4 | "bruno-like 4, RNA binding protein (Drosophila)" | 100146695_TGI_at | -0.212 | 2.087 | 9.19E-01 | 0.914564 |
| C6orf162 | chromosome 6 open reading frame 162 | 100143632_TGI_at | 0.196 | 1.860 | 9.16E-01 | 0.914564 |
| NA | NA | 100126219_TGI_at | 0.111 | 1.073 | 9.18E-01 | 0.914564 |
| NA | NA | 100150988_TGI_at | 0.665 | 6.617 | 9.20E-01 | 0.914564 |
| RPAP1 | RNA polymerase II associated protein 1 | 100154811_TGI_at | -0.058 | 0.554 | 9.17E-01 | 0.914564 |
| MLF1 | myeloid leukemia factor 1 | 100123606_TGI_at | 0.031 | 0.311 | 9.22E-01 | 0.915047 |
| NA | NA | 100129584_TGI_at | 1.365 | 14.288 | 9.24E-01 | 0.916261 |
| MN1 | meningioma (disrupted in balanced translocation) 1 | 100307164_TGI_at | 0.013 | 0.134 | 9.25E-01 | 0.916356 |
| ANGPTL6 | angiopoietin-like 6 | 100132449_TGI_at | -0.331 | 4.339 | 9.39E-01 | 0.916765 |
| ATF6 | activating transcription factor 6 | 100305118_TGI_at | 0.534 | 6.908 | 9.38E-01 | 0.916765 |
| CCDC51 | coiled-coil domain containing 51 | 100313943_TGI_at | 0.018 | 0.204 | 9.31E-01 | 0.916765 |
| FGFR1OP2 | FGFR1 oncogene partner 2 | 100311305_TGI_at | -0.020 | 0.272 | 9.40E-01 | 0.916765 |
| FMO2 | flavin containing monooxygenase 2 (non-functional) | 100129207_TGI_at | 0.004 | 0.050 | 9.43E-01 | 0.916765 |
| HLA-DRB1 | "major histocompatibility complex, class II, DR beta 1" | 100312946_TGI_at | -0.001 | 0.016 | 9.27E-01 | 0.916765 |
| IGSF11 | "immunoglobulin superfamily, member 11" | 100146385_TGI_at | 0.263 | 3.086 | 9.32E-01 | 0.916765 |
| NA | NA | 100303672_TGI_at | -0.204 | 2.331 | 9.30E-01 | 0.916765 |
| NA | NA | 100155445_TGI_at | -0.022 | 0.283 | 9.39E-01 | 0.916765 |
| NA | NA | 100158823_TGI_at | -0.980 | 13.620 | 9.43E-01 | 0.916765 |
| RAB3IP | RAB3A interacting protein (rabin3) | 100160044_TGI_at | -0.011 | 0.148 | 9.40E-01 | 0.916765 |
| RELT | RELT tumor necrosis factor receptor | 100301195_TGI_at | -0.027 | 0.355 | 9.39E-01 | 0.916765 |
| STK32C | serine/threonine kinase 32C | 100158065_TGI_at | 0.094 | 1.140 | 9.34E-01 | 0.916765 |
| SYTL2 | synaptotagmin-like 2 | 100301468_TGI_at | 0.031 | 0.338 | 9.28E-01 | 0.916765 |
| TNC | tenascin C | 100161091_TGI_at | -0.037 | 0.476 | 9.38E-01 | 0.916765 |
| ARNT | aryl hydrocarbon receptor nuclear translocator | 100306322_TGI_at | 0.037 | 0.629 | 9.53E-01 | 0.916826 |
| BAG5 | BCL2-associated athanogene 5 | 100311425_TGI_at | -0.075 | 1.309 | 9.55E-01 | 0.916826 |
| DCBLD2 | "discoidin, CUB and LCCL domain containing 2" | 100308435_TGI_at | -0.989 | 14.875 | 9.47E-01 | 0.916826 |
| HLA-B | "major histocompatibility complex, class I, B" | 100300038_TGI_at | -0.002 | 0.028 | 9.51E-01 | 0.916826 |
| KATNAL2 | katanin p60 subunit A-like 2 | 100311198_TGI_at | -0.280 | 4.562 | 9.51E-01 | 0.916826 |
| NA | NA | 100133899_TGI_at | -0.003 | 0.041 | 9.45E-01 | 0.916826 |
| NA | NA | 100144299_TGI_at | -0.064 | 1.106 | 9.54E-01 | 0.916826 |
| NT5C | "5'; 3';-nucleotidase, cytosolic" | 100158391_TGI_at | -0.020 | 0.365 | 9.55E-01 | 0.916826 |
| OTUD4 | OTU domain containing 4 | 100302095_TGI_at | 0.265 | 4.375 | 9.52E-01 | 0.916826 |
| RPRD2 | regulation of nuclear pre-mRNA domain containing 2 | 100144721_TGI_at | 0.024 | 0.391 | 9.51E-01 | 0.916826 |
| TSPAN14 | tetraspanin 14 | 100304251_TGI_at | -0.016 | 0.240 | 9.46E-01 | 0.916826 |
| MLF1 | myeloid leukemia factor 1 | 100312821_TGI_at | -0.312 | 5.937 | 9.58E-01 | 0.918248 |
| LRRC16A | leucine rich repeat containing 16A | 100311443_TGI_at | -0.066 | 1.317 | 9.60E-01 | 0.918994 |
| NA | NA | 100155899_TGI_at | -0.072 | 1.473 | 9.61E-01 | 0.918994 |

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|---|---|---|---|---|---|---|
| CACNA2D4 | "calcium channel, voltage-dependent, alpha 2/delta subunit 4" | 100131579_TGI_at | -0.136 | 2.926 | 9.63E-01 | 0.919564 |
| ADAM17 | ADAM metallopeptidase domain 17 | 100126288_TGI_at | -0.002 | 0.237 | 9.92E-01 | 0.91973 |
| AIF1 | allograft inflammatory factor 1 | 100151160_TGI_at | 0.000 | 0.038 | 9.96E-01 | 0.91973 |
| APOM | apolipoprotein M | 100126143_TGI_at | -0.009 | 1.419 | 9.95E-01 | 0.91973 |
| CGN | cingulin | 100156369_TGI_at | -0.022 | 0.521 | 9.67E-01 | 0.91973 |
| CLUAP1 | clusterin associated protein 1 | 100152540_TGI_at | -0.006 | 0.252 | 9.82E-01 | 0.91973 |
| EIF3E | "eukaryotic translation initiation factor 3, subunit E" | 100152431_TGI_at | -0.025 | 0.956 | 9.79E-01 | 0.91973 |
| FAM177A1 | "family with sequence similarity 177, member A1" | 100121711_TGI_at | 0.010 | 2.285 | 9.96E-01 | 0.91973 |
| GBP3 | guanylate binding protein 3 | 100126116_TGI_at | 0.002 | 0.103 | 9.87E-01 | 0.91973 |
| HHIP | hedgehog interacting protein | 100148028_TGI_at | 0.006 | 0.362 | 9.87E-01 | 0.91973 |
| HLA-DRB6 | "major histocompatibility complex, class II, DR beta 6 (pseudogene)" | 100160430_TGI_at | -0.033 | 1.797 | 9.85E-01 | 0.91973 |
| ITCH | itchy E3 ubiquitin protein ligase homolog (mouse) | 100307620_TGI_at | 0.006 | 0.197 | 9.74E-01 | 0.91973 |
| LONP2 | "lon peptidase 2, peroxisomal" | 100300599_TGI_at | 0.011 | 1.311 | 9.93E-01 | 0.91973 |
| NA | NA | 100142307_TGI_at | -0.319 | 7.560 | 9.66E-01 | 0.91973 |
| NA | 60S ribosomal pseudogene | 100304214_TGI_at | -0.027 | 1.213 | 9.82E-01 | 0.91973 |
| NA | NA | 100305428_TGI_at | 0.013 | 0.804 | 9.87E-01 | 0.91973 |
| NA | NA | 100145017_TGI_at | 0.104 | 6.364 | 9.87E-01 | 0.91973 |
| P4HA3 | "procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III" | 100133960_TGI_at | -0.029 | 1.476 | 9.84E-01 | 0.91973 |
| PDXDC2 | pyridoxal-dependent decarboxylase domain containing 2 | 100122963_TGI_at | 0.002 | 0.041 | 9.69E-01 | 0.91973 |
| PID1 | phosphotyrosine interaction domain containing 1 | 100157087_TGI_at | -0.002 | 0.074 | 9.80E-01 | 0.91973 |
| RABEP1 | "rabaptin, RAB GTPase binding effector protein 1" | 100155542_TGI_at | 0.006 | 0.542 | 9.91E-01 | 0.91973 |
| ROM1 | retinal outer segment membrane protein 1 | 100122809_TGI_at | 0.031 | 1.397 | 9.82E-01 | 0.91973 |
| RPUSD4 | RNA pseudouridylate synthase domain containing 4 | 100310631_TGI_at | -0.213 | 9.950 | 9.83E-01 | 0.91973 |
| SLITRK5 | "SLIT and NTRK-like family, member 5" | 100149341_TGI_at | 0.013 | 2.017 | 9.95E-01 | 0.91973 |
| SNRPF | small nuclear ribonucleoprotein polypeptide F | 100145491_TGI_at | -0.005 | 0.697 | 9.94E-01 | 0.91973 |
| TMEM108 | transmembrane protein 108 | 100139628_TGI_at | 0.009 | 0.274 | 9.74E-01 | 0.91973 |
| TRIM66 | tripartite motif-containing 66 | 100136729_TGI_at | -0.049 | 6.321 | 9.94E-01 | 0.91973 |
| TSPAN14 | tetraspanin 14 | 100150788_TGI_at | -0.005 | 0.224 | 9.82E-01 | 0.91973 |
| ZNF131 | zinc finger protein 131 | 100147117_TGI_at | 0.040 | 1.493 | 9.78E-01 | 0.91973 |
| ZSWIM7 | "zinc finger, SWIM-type containing 7" | 100162676_TGI_at | -0.001 | 0.136 | 9.91E-01 | 0.91973 |
| NA | NA | 100124335_TGI_at | 0.000 | 0.757 | 1.00E+00 | 0.921622 |

**Supplementary Table 17: Connectivity Map results for drugs that could reverse or induce the COPD gene expression signature *in silico*.**

Enrichment: The similarity metric between the COPD gene signature and the reference transcriptional profiles. This ranges from -1 to +1 to reflect the similarity or dissimilarity of the expression profiles. P value: An estimate of the likelihood that the enrichment of COPD gene signature would be observed by chance. This value is determined empirically by computing the enrichment of one hundred thousand sets of expression profiles selected at random from the set of all profiles in the result.

| **Compounds that induce COPD signature** | | | | |
|---|---|---|---|---|
| **Rank** | **Compound** | **Enrichment** | **P value** | **Use/mechanism of action** |
| 1 | Alsterpaullone | 0•995 | <2•2e-16 | Act as glycogen synthase kinase-3 (GSK3) inhibitor, Cyclin-Dependent Kinase Inhibitor (31)• Also act as Wnt signaling agonist (32), and down-regulates vascular endothelial growth factor (VEGF) and fibroblast growth factor (FGF) (33)• Alsterpaullone has also been studied as an antimanic therapeutic for the acute manic phase of bipolar disorder (34)• |
| 2 | H-7 | 0•969 | <2•2e-16 | protein kinase A and C (PKA/PKC) inhibitor (35) |
| 3 | Vorinostat | 0•832 | <2•2e-16 | Histone Deacetylase (HDAC) inhibitor (36) |
| 4 | Trichostatin A | 0•514 | <2•2e-16 | Histone Deacetylase (HDAC) inhibitor (37) |
| 5 | Doxorubicin | 0•982 | 0•00004 | An anthracycline antibiotic and used in cancer chemotherapy (38) |
| 6 | Camptothecin | 0•971 | 0•00004 | Cytotoxic quinoline alkaloid which inhibits the DNA enzyme topoisomerase I (topo I) and used in chemotherapy(39) |
| 7 | Mitoxantrone | 0•965 | 0•00006 | Anthracenedione antineoplastic agent (40), and used in multiple sclerosis (41)• |
| 8 | Gw-8510 | 0•908 | 0•00008 | Inhibitor of cyclin kinase 2 (CDK2) (42) |
| 9 | Procaine | 0•756 | 0•00202 | Local anesthetic which acts mainly as a sodium channel blocker, and has been used to treat dementia (43) |
| 10 | Tiabendazole | 0•786 | 0•00408 | Fungicide and parasiticide, used to treat strongyloidiasis (44) |
| **Compounds that reverse COPD gene signature** | | | | |
| 1 | Adiphenine | -0•74 | 0•00242 | Local anesthetic that act as inhibitor of nicotinic receptors (45, 46) |
| 2 | Hexetidine | -0•81 | 0•00257 | Anti-bacterial and anti-fungal agent• Also act as a local anesthetic, astringent and deodorant and has antiplaque effects (47)• |
| 3 | Disulfiram | -0•717 | 0•00401 | Acetaldehyde dehydrogenase inhibitor, used to support the treatment of chronic alcoholism (48)• Disulfiram is also being studied as a treatment for cocaine dependence since it inhibits dopamine β-hydroxylase (DβH), which converts dopamine to norepinephrine (49) |
| 4 | Metixene | -0•777 | 0•00511 | Discontinued. Muscarinic anticholinergic used as an antiparkinsonian agent (50) |

| | | | | |
|---|---|---|---|---|
| 5 | Gabazine SR-95531 | -0•765 | 0•00621 | Antagonist of gamma-aminobutyric acid class A (GABAA) receptors (51)• |
| 6 | Perphenazine | -0•689 | 0•00661 | Perphenazine is a typical antipsychotic drug (52) Acts as inhibitor of dopamine D1 and dopamine D2 receptors (53) and also binds the alpha adrenergic receptor (54) |
| 7 | Colchicine | -0•629 | 0•0081 | Drug used to treat gout, work by arresting microtubule assembly and inhibition of neutrophil and endothelial cell adhesion molecules (55) |
| 8 | Metaraminol | -0•743 | 0•00869 | Alpha-1 adrenergic receptor agonist, acts through peripheral vasoconstriction used in the prevention and treatment of hypotension (56) |
| 9 | Hecogenin | -0•728 | 0•01112 | Hecogenin is the steroidal saponin aglycone (or sapogenin) present in the leaves of species from the *Agave* genus• It has antioxidant and anti-inflammatory properties (57) |
| 10 | Withaferin A | -0•707 | 0•01516 | A steroidal lectone that exhibits anti-inflammatory, immunomodulatory, and anti-angiogenic properties (58, 59)• Withaferin A inhibits both NF-κB (60) and down regulates VEGF gene expression (61) |

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