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Epigenome-Wide Association Study of DNA Methylation and Adult Asthma in the Agricultural Lung Health Study

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Take Home Message

We found distinct methylation signals in non-atopic and atopic asthma. Most were related to gene expression and replicated in asthma-relevant tissues, confirming the value of blood DNA methylation for identifying novel genes linked in asthma pathogenesis.

Abstract

Epigenome-wide studies of methylation in children support a role for epigenetic mechanisms in asthma. Studies in adults are rare, and few have examined non-atopic asthma. We conducted the largest epigenome-wide association study of blood DNA methylation in adults in relation to non-atopic and atopic asthma.

We measured DNA methylation in blood using the Illumina MethylationEPIC array among 2,286 participants in a case-control study of current adult asthma nested within a U.S. agricultural cohort. Atopy was defined by serum specific immunoglobulin E. Participants were categorized as atopy without asthma (n=185), non-atopic asthma (n=673), atopic asthma (n=271), or a reference group of neither atopy nor asthma (n=1,157). Analyses were conducted using logistic regression.

No associations were observed with atopy without asthma. Numerous CpGs were differentially methylated in non-atopic asthma (8 at family-wise error rate [FWER] $p<9\times10^{-8}$; 524 at False Discovery Rate [FDR]<0.05) and implicated 382 novel genes. More CpGs were identified in atopic asthma (181 at FWER; 1,086 at FDR) and implicated 569 novel genes. 104 FDR CpGs overlapped. 35% of CpGs in non-atopic asthma and 91% in atopic asthma replicated in studies of whole blood, eosinophils, airway epithelium, or nasal epithelium. Implicated genes were enriched in pathways related to the nervous system or inflammation.

We identified numerous, distinct differentially methylated CpGs in non-atopic and atopic asthma. Many CpGs from blood replicated in asthma-relevant tissues. These circulating biomarkers reflect risk and sequelae of disease and implicate novel genes associated with non-atopic and atopic asthma.

Introduction

Asthma is a heterogeneous, chronic disease of the airways, affecting over 300 million people worldwide (1). Although asthma has a substantial familial component, only a small portion of the variation in disease risk and heritability is explained despite large genome-wide association studies (2, 3). Epigenetic mechanisms may contribute to the unexplained variation. The best-studied epigenetic modification is DNA methylation.

Most epigenome-wide association studies (EWAS) of methylation in relation to asthma have been conducted in children (4). However, asthma risk factors and pathogenetic mechanisms vary between children and adults (3). Compared to childhood asthma, a higher proportion of adult asthma is non-atopic and pathogenesis of asthma may differ by atopy status. The few published EWAS in adults have fewer than 80 asthma cases, measured DNA methylation using the older Illumina Infinium 27K BeadChip or 450K BeadChip, or did not stratify by atopy status.

Using DNA from blood, we conducted the largest EWAS of DNA methylation and adult asthma to date, using the more comprehensive Illumina Infinium MethylationEPIC BeadChip, which assesses methylation at over 850K C-phosphate-G sites (CpGs). To better elucidate the pathogenesis of asthma, we stratified by atopy, objectively defined by specific immunoglobulin E (IgE). We assessed the potential functional impact of the differentially methylated CpGs through enrichment of functional genomic features, pathway analyses, associations with gene expression, and identification of druggable targets. We replicated our differentially methylated CpGs in blood using existing studies with methylation assessed in whole blood, purified eosinophils, nasal epithelium, or bronchial airway epithelium.

Methods

Study Population

Participants were enrolled in the Agricultural Lung Health Study (ALHS), a case-control study of adult current asthma nested within the Agricultural Health Study (AHS). The AHS is a cohort of farmers and their spouses from Iowa and North Carolina. Details of the AHS and ALHS have been described previously (5, 6). The ALHS enrolled 3,301 participants in 2009-2013.

Based on responses to an AHS questionnaire administered in 2005-2010 (data version P3REL201209.00), the ALHS enrolled asthma cases using three definitions: 1) self-reported current diagnosed asthma without any self-reported diagnosis of chronic obstructive pulmonary disease (COPD) or emphysema (n=876); 2) potential undiagnosed asthma identified by self-report of current asthma symptoms or use of asthma medication without COPD or emphysema diagnosis among never or light, former smokers (≤10 pack-years) (n=309); or 3) current self-reported diagnosed asthma with COPD or emphysema diagnosis among never or light, former smokers (≤10 pack years) (n=38). Controls (n=2,078) were randomly selected from the AHS participants without the above criteria. Full description of the methods is in the appendix.

All participants provided informed consent. The Institutional Review Board at the National Institutes of Health approved this study.

Stratification by Atopy

Atopy was determined by a positive blood IgE, based on IgE ≥0·70 IU/mL (7) to at least one of ten common antigens: Bermuda grass, ragweed, Timothy grass, mountain cedar, *Alternaria*, dust mite, cat dander, milk, egg, and wheat. IgE was measured at ImmuneTech (Foster City, CA) using the Luminex platform (Luminex Corporation, Austin, TX). Asthma case-control status was stratified by atopy to categorize individuals into one of four mutually exclusive groups: atopy alone (i.e., individuals without asthma but have atopy), non-atopic asthma (i.e., individuals with asthma but no atopy), atopic asthma (i.e., individuals with asthma and atopy), or non-cases (i.e., individuals with neither asthma nor atopy).

DNA Methylation and Quality Control

The DNA was bisulfite converted using the EZ-96 DNA Methylation kit (Zymo Research Corporation, Irvine, CA). Methylation was assessed for 2,391 ALHS participants using the Infinium MethylationEPIC BeadChip, following Illumina's protocol.

Sample level quality control excluded 102 participants with either >5% of CpGs with detection p-values $>1{\cdot}0\times10^{-10}$ or intensity values less than three standard deviations below the mean bisulfite control intensities and 1 participant with sex mismatch. CpGs were removed if >5% of samples had detection p-values $>1{\cdot}0\times10^{-10}$ (# CpGs = 31,533). Background and dye-bias correction were done using "Relic" in ENmix (8, 9). Data were normalized using inter-array (quantile) normalization (8). Probe-type bias adjustment was conducted using the "Rcp" function in ENmix (10). We corrected for batch effect (i.e., plate effect) using "ComBat" in sva (11). We used "gaphunter" in minfi to trim extreme methylation outliers at individual CpGs (threshold=0·3, outCutoff = 0·0025) (12). We analyzed 817,235 autosomal CpGs.

Among the 2,286 participants with methylation data passing quality control and complete information on smoking history, there were 185 with atopy alone, 673 with non-atopic asthma, 271 with atopic asthma, and 1,157 non-cases (Figure E1).

Cell Type Proportions

Details of the peripheral blood smears have been previously described (13) and were available in 1,894 participants. Monocytes, lymphocytes, neutrophils, and eosinophils were counted in smears without platelet clumping and <20% smudged cells. Cell type proportions were calculated from counts for 1,658 participants. For individuals without cell counts, cell type proportions were estimated from methylation data using the Houseman method (14) with the Reinius et al. reference panel (15).

Identification of Differentially Methylated CpGs

Epigenome-wide analyses were conducted using logistic regression separately for three outcomes: atopy alone, non-atopic asthma, and atopic asthma. Non-cases were the referent group. Untransformed beta methylation values were used as the predictor. All analyses were adjusted for age (continuous), sex, body mass index (continuous), smoking status (never, former, current), pack-years of cigarette smoking (continuous), state (North Carolina or Iowa), and four cell type proportions (monocyte, lymphocyte, neutrophil, and eosinophil). Because farmers were less likely to be enrolled in the busy fall harvest season, we also adjusted for fall enrollment (yes/no). We assessed significance using a family-wise error rate (FWER) of $p<9\times10^{-8}$ (16), as well as Benjamini-Hochberg false discovery rate (FDR<0·05) (17).

Several sensitivity analyses were conducted. To evaluate possible influences of asthma-related genotypes on the associations, we calculated a weighted polygenic risk score for asthma using the results from a large genome-wide meta-analysis of asthma (2). Single nucleotide polymorphisms with $p<5\times10^{-8}$ were clumped using PLINK ($r^2 = 0·5$) to identify independent loci within ±250 kb (18). Methylation analyses were repeated adjusting for the polygenic risk score of asthma. We also repeated the analyses adjusting for current farming (i.e., currently farming crops, working with farm animals, or working with pesticides). Analyses were conducted using the seven Houseman estimated cell types (monocyte, NK, B cell, CD4+, CD8+, neutrophil, eosinophil) instead of the four measured cell types. Because we used a stricter threshold to classify atopy than some previous studies, we conducted methylation analyses after re-stratifying asthma case-control status with an atopy cutoff ≥0·35 IU/mL. Analyses were conducted in R v3.4.0.

Examination of polymorphic probes and additional filtering

We excluded cross-reactive probes (19), probes with SNPs at the extension base (minor allele frequency >1%) (20), and “ch” probes from downstream analyses (i.e., enrichment of functional genomic features, pathway analyses, expression quantitative trait methylation, druggable targets, and replication look-ups). We visually inspected distributions of significant CpGs for departure from unimodality.

Enrichment of functional genomic features

We localized CpGs to four genomic features: CpG islands, CpG island shores, promoters, and transcription factor binding sites. We evaluated enrichment or depletion for these features among FDR-significant CpGs using two-sided Fisher's exact test and applied a Bonferroni threshold ($p<0.05/4 = 0.0125$). Enrichment of transcription factor motifs was identified using eFORGE TF (21). We used eFORGE v2.0 to identify tissue- and cell type-specific enrichment in blood, lung, and fetal lung for the following functionally relevant genomic features: DNase I hypersensitive sites, 15 chromatin states, and five histone marks (21).

Pathway Analyses

We conducted pathway analyses using the "gsameth" function in the missMethyl package in R (22), which accounts for the differing number of probes per gene. Pathways within the Kyoto Encyclopedia of Genes and Genomes (KEGG) gene sets from the Gene Set Enrichment Analysis Molecular Signatures Database (GSEA MSigDB) (23-25) were evaluated. We reported pathways with a nominal p-value <0·05.

Expression Quantitative Trait Methylation (eQTM) analyses

We evaluated associations of significant CpGs with expression of nearby genes. We found no studies with both gene expression and methylation in blood based on the EPIC array. Therefore, we evaluated eQTMs for the significant CpGs present on the 450K array. Illumina 450K methylation and gene expression data from RNA-seq were available in blood samples from 3,075 adults in the Biobank-based integrative omics study (BIOS) consortium (26). We evaluated *cis*-eQTMs using expression transcripts within ±250 kb of each significant CpG. Significance was assessed at FDR<0·05.

Search for Druggable Targets among Novel Asthma Genes

A previous systematic literature review identified asthma-related genes from EWAS or a large asthma genome-wide association study (GWAS) (27). We updated their search to incorporate more recent studies. Genes not previously associated with asthma were annotated to the ChEMBL database (v25, released on January 2, 2019) to identify approved or in development drugs that target novel genes implicated by our significant CpGs (28).

Replication of Findings in Blood, Eosinophils, Nasal, and Bronchial Epithelium

We looked-up our FDR significant CpGs identified in atopic asthma in two studies with blood methylation: Swiss Cohort Study on Air Pollution and Lung and Heart Diseases in Adults (SAPALDIA), Pregnancy and Childhood Epigenetics Consortium (PACE) meta-analysis (27), four studies with nasal methylation: Epigenetic Variation and Childhood Asthma in Puerto Ricans (EVA-PR) (29), Inner-City Asthma Consortium (ICAC) (30), Prevention and Incidence of Asthma and Mite Allergy (PIAMA) (29), Project Viva (31), one study with eosinophils methylation: Saguenay-Lac-Saint-Jean (SLSJ) (32, 33), and one study with bronchial epithelium methylation (34). FDR significant CpGs identified in non-atopic asthma were looked-up in SAPALDIA, PACE meta-analysis, EVA-PR, Project Viva, and SLSJ.

Results

Table 1 includes descriptive characteristics of the study population. The median age across the four outcome groups ranged from 60-63 years. Atopic asthmatics were more likely to have adequately controlled asthma than non-atopic asthmatics (58% vs 45%).

Atopy alone

No CpGs were differentially methylated among individuals with atopy without asthma (n=185) compared to non-cases (neither atopy nor asthma) (n=1,157) at FWER ($p<9\times10^{-8}$) or FDR<0.05 (λ=0·97) (Appendix, Figure E2). Using a lower atopy cutoff (≥0·35 IU/mL), we compared 528 with atopy alone to 814 non-cases, and no CpGs were significant. No additional analyses were conducted.

Non-atopic asthma

For non-atopic asthma (n=673) compared to non-cases (n=1,157), eight CpGs were differentially methylated using FWER ($p<9\times10^{-8}$) and 524 at FDR<0·05 (Figure 1; top 30 CpGs in Table 2; all FDR CpGs in Appendix, Table E1). In 516 of the 524 differentially methylated CpGs, methylation was lower in non-atopic asthmatics compared to non-cases. Systematic inflation was minimal (λ=1·14) (Appendix, Figure E3). All differentially methylated CpGs had a unimodal methylation distribution.

Results were not appreciably altered after adjusting for the polygenic risk score of asthma or current farming (Appendix, Table E2). Repeating analyses using the seven estimated cell types, instead of the four measured and estimated cell types, resulted in greater inflation (λ=1·66) (127 CpGs significant at FWER; 2,243 CpGs FDR<0·05) (Appendix, Table E2). When individuals were recategorized using the less stringent atopy cutoff (≥0·35 IU/mL) (483 non-atopic asthmatics versus 814 non-cases), the number of associations decreased (9 CpGs FDR<0·05) (Appendix, Table E2).

In case-only analyses (i.e., restricted to non-atopic asthmatics), we calculated adjusted odds ratios for the 524 differentially methylated CpGs, comparing 278 inhaled corticosteroid users to 395 non-users, and found no significant associations (FDR<0·05). Adjusted odds ratios comparing 131 non-atopic asthmatics with inadequately controlled asthma to 305 with controlled asthma identified differential methylation (FDR<0·05) by asthma control at 17 of the 524 CpGs (range ORs: 0.63-0.95) (Appendix, Table E3).

Functional Enrichment. Removing 15 potentially cross-reactive CpGs (19) left 509 for downstream analyses. These CpGs were depleted for CpG islands ($p=5·4\times10^{-27}$), CpG island shores (p=0·0004), and promoters ($p=1·7\times10^{-18}$) (Appendix, Table E4), enriched for transcription factor binding sites ($p=1·4\times10^{-13}$), and enriched (FDR<0.05) for two transcription factor motifs: V_FOXO3A_Q1 and V_AIRE_01 (Appendix, Table E5). Enrichment of DNase I hypersensitivity was observed in blood, fetal lung, and lung (Appendix, Figure E4). Of the 15 chromatin states, we observed enrichment for active transcription start sites in blood, as well as enrichment for enhancers, weak transcription, and strong transcription in blood and lung (Appendix, Figure E4). Among histone marks, we found enrichment for H3K4me1 in blood, fetal lung, and lung, for H3K4me3 in blood and fetal lung, and for H3K36me3 in blood (Appendix, Figure E4).

Pathway Analyses. Nine pathways showed enrichment (p<0.05), including Alzheimer's disease, amyotrophic lateral sclerosis, long-term potentiation, vascular smooth muscle contraction, and calcium signaling (Appendix, Table E6, Figures E5-E6). Two asthma relevant pathways had p-values between 0.05 and 0.10: asthma (p=0.08) and sphingolipid metabolism (p=0.055).

cis-eQTM. Of the 509 CpGs associated with non-atopic asthma, 169 CpGs on the 450K and 168 were available in BIOS (26). 120 CpGs (71·4%) were significantly (FDR<0·05) associated with 377 gene expressions in *cis* (Appendix, Table E7).

Druggable targets. The 509 differentially methylated CpGs annotated to 479 genes. After excluding genes identified from previous asthma EWAS and GWAS (Appendix, Table E8), 382 genes were novel, including *AZU1* and *PDE4B*. In ChEMBL (28), *PDE4B* is a target of several approved drugs related to asthma or other respiratory diseases (e.g., Roflumilast, Dyphylline, Theophylline) (Appendix, Table E9).

Replication. Five replication studies assessed methylation in either blood, nasal epithelium, or eosinophils. Replication studies generally had smaller sample sizes and not all stratified on atopy (Table 4). Of the 509 differentially methylated CpGs identified in non-atopic asthma, 169 CpGs were on the 450K array and 84 CpGs (50%) replicated (p<0·05 and same direction of association) in at least one study (Appendix, Table E10). Project Viva used the EPIC array, which had an additional 314 CpGs, of which 56 replicated (Appendix, Table E10).

Atopic asthma

Comparing atopic asthma (n=271) to non-cases (n=1,157), we identified 181 differentially methylated CpGs using FWER ($p<9\times10^{-8}$) and 1,086 at FDR<0·05 (Figure 2; Top 30 CpGs in Table 3; all FDR CpGs in Appendix, Table E11). In 99·5% of the 1,086 differentially methylated CpGs, methylation was lower in atopic asthmatics than non-cases. All differentially methylated CpGs had a unimodal methylation distribution. Systematic inflation was not observed (λ=0·98) (Appendix, Figure E7). Of the 1,086 CpGs, 104 (9.6%) were significant in non-atopic asthma (Appendix, Table E12).

Adjustment for the polygenic risk score of asthma or current farming did not materially alter the results (Appendix, Table E2). When we adjusted for the seven estimated cell types instead of the four cell types, the lambda increased to 1.21 (407 CpGs significant using FWER; 2,947 CpGs FDR<0·05, including 1,076 of the original 1,086 CpGs (Appendix, Table E11). When we classified atopy using ≥0·35 IU/mL (461 atopic asthmatics versus 814 non-cases), the number of associations decreased (124 CpGs significant using FWER, 847 CpGs FDR<0·05, including 669 of the original 1,086 CpGs (Appendix, Table E2)).

Conducting adjusted logistic regression analyses restricted to atopic asthmatics, none of the 1,086 significant CpGs were differentially methylated (FDR<0·05) in relation to inhaled corticosteroid use (103 users versus 168 non-users) nor asthma control (44 with inadequately controlled asthma versus 156 with adequately controlled asthma).

Functional enrichment. Removing 16 potentially cross-reactive probes (19) left 1,070 differentially methylated CpGs for downstream analyses. We found depletion for CpG islands ($p=4{\cdot}3\times10^{-66}$), CpG island shores ($p=1{\cdot}3\times10^{-6}$), and promoters ($p=1{\cdot}0\times10^{-46}$), enrichment for transcription factor binding sites (p=0·0057) (Appendix, Table E4), and enrichment for eight transcription factor motifs, including GATA3_primary and MA0029.1-Evi1 (Appendix, Table E5). Among the 15 chromatin states, we identified enrichment of enhancers, genic enhancers, weak transcription, and strong transcription in blood and lung (Appendix, Figure E8). The FDR significant CpGs were enriched for H3K4me1 and H3K36me3 in blood, fetal lung, and lung (Appendix, Figure E8).

Pathway analyses. Ten KEGG pathways had $p<0.05$, including insulin signaling, type II diabetes, starch and sucrose metabolism, and valine, leucine, and isoleucine degradation (Appendix, Table E6, Figure E5-E6). The asthma pathway was marginally significant ($p=0.055$). Figure 3 shows a network plot of 9 disease and biological processes implicated by genes identified in our non-atopic and atopic asthma analyses.

cis-eQTM. Of the 1,070 CpGs associated with atopic asthma, 349 were present in the 450K array and 346 were available in BIOS. 242 CpGs (69·9%) were significantly associated with 671 gene expressions in *cis* (Appendix, Table E13).

Druggable targets. The 1,070 CpGs annotated to 885 genes, of which, 569 have not been reported in previous asthma EWAS or GWAS, including *PDE4B* and *PPARG*. In ChEMBL (28), *PPARG* is a target of a candidate asthma drug, Rosiglitazone (35, 36) (Appendix, Table E14).

Replication. Eight replication studies assessed methylation in blood, nasal epithelium, bronchial epithelium, or eosinophils (Table 4). The 1,076 CpGs identified in atopic asthma included 349 CpGs on the 450K array, and 341 (98%) replicated in at least one study (Appendix, Table E15). An additional 684 CpGs were available in Project Viva, which assessed nasal methylation using the EPIC array, and 595 (87%) replicated (Appendix, Table E15).

Discussion

Several hundred CpGs in blood were differentially methylated in blood DNA from adults with non-atopic or atopic asthma compared to adults with neither asthma nor atopy. Many more CpGs were differentially methylated in relation to atopic than non-atopic asthma, and about 10% of differentially methylated CpGs for atopic asthma overlapped with non-atopic asthma. Our findings highlight the importance of distinguishing between non-atopic and atopic asthma to improve our understanding of asthma and show that differential methylation in atopic asthma is not driven by atopy *per se*.

We performed several analyses to further evaluate our findings. Results were similar after adjustment for the polygenic risk score of asthma, suggesting that our findings are not influenced by known genetic variations for asthma. In most participants, we directly measured differential blood counts for monocytes, lymphocytes, neutrophils, and eosinophils. Adjustment instead for all seven estimated cell types (which disaggregates lymphocytes into NK, B cell, CD4+, and CD8+) resulted in some inflation, but results were similar. Eosinophils are higher in asthmatics than the general population (37). Estimation of eosinophils from a small reference panel of healthy participants may not be highly accurate, as suggested in our data (Spearman correlation between measured and estimated = 0·09). Using a less stringent atopy cutoff (≥0.35 IU/mL) yielded fewer significant findings, consistent with previous evidence that the lower threshold is less discriminant (7). Further, results for atopic asthma were more robust to the threshold change (more CpGs remained significant) than the results for non-atopic asthma.

A substantial proportion of our differentially methylated CpGs replicated in at least one published study. A higher proportion replicated in atopic than non-atopic asthma, probably reflecting the much larger quantity of studies available, and thus higher power, for atopic asthma. Most CpGs that replicated in non-atopic asthma overlapped with our findings in atopic asthma (Table 4), suggesting that these are asthma-related CpGs independent of atopy status. Our results in atopic asthma were highly consistent in a small cohort of patients with methylation measured in isolated eosinophils, a critical cell type of atopic asthma. Nasal epithelium is a good surrogate for lower respiratory epithelium (38). 89% of our findings in atopic asthma replicated in nasal tissue, suggesting that methylation in blood is a good surrogate for nasal tissue in methylation studies of atopic asthma. This is an important observation, given the wide availability of stored blood for methylation analyses.

In our study and most of the replication studies, methylation at significant CpGs tended to be lower in asthmatics than non-asthmatics. We hypothesize that the lower methylation in asthmatics reflects a combination of the cell type composition of cells displaying lower methylation at these CpGs (39) and the activation of cell types related to disease processes. For example, there might be a shift from naïve T cells to effector memory CD8T cells and NK cells (39) or activation of basal cells (40). Mechanistic studies are needed to investigate why methylation is generally lower among asthmatics than non-asthmatics at differentially methylated CpGs across the studied tissues.

This study provides substantial replication of prior studies. Our analysis of non-atopic asthmatics implicated 479 genes, including 96 identified in previous asthma GWAS or EWAS (Appendix, Table E16). Of 885 genes implicated in our analysis of atopic asthma, 315 were identified in GWAS or EWAS of asthma (Appendix, Table E17). We also identified many novel asthma-related genes not previously implicated in GWAS or EWAS. For example, high expression of *AZU1*, an inflammatory mediator that regulates neutrophils, is correlated with poor asthma control (41). Additionally, *DEGS2* is involved in sphingolipid metabolism, which has been implicated in respiratory outcomes (42) including asthma (39).

Enrichment of functional genomic features and pathway analyses provides biological insight into our differentially methylated CpGs. Our results highlighted certain genomic features, histone marks in blood, lung, and fetal lung, and transcription factor motifs that might be biologically relevant to asthma. For example, transcription factor FOXO3A and GATA3 help regulate type 2 helper T cells (43, 44), an important cell type in asthma. EVI-1 interacts with *SMAD3* (45), a known asthma gene. The differentially methylated CpGs in non-atopic asthma were enriched in signaling pathways related to the nervous system (e.g., sphingolipid metabolism, calcium signaling, and vascular smooth muscle contraction). Sphingolipids and calcium are signaling molecules involved in vascular smooth muscle contraction (46-49), suggesting that mechanisms related to innervation of the airways may play a greater role in non-atopic versus atopic asthma. Atopic asthma CpGs were enriched in pathways involved in inflammatory response (i.e., insulin signaling) (50) or characterized by chronic inflammation (i.e., diabetes) (51), consistent with the inflammatory nature of atopic asthma.

Previous studies have identified CpGs differentially methylated in relation to total serum IgE (33, 43, 52, 53), atopy (29, 54, 55), and allergies (54, 56). In our study, no CpGs were differentially methylated in relation to atopy alone. Because previous studies have been conducted in children or a combination of children and adults and our study is comprised of older adults (median age 62 years), it is possible that differential methylation related to atopy in children may not persist into adulthood.

This study has some limitations. Our population was rural and may differ in environmental factors compared to urban populations (e.g., air pollution). However, we found high levels of replication across geographically distinct populations from published studies. Heterogeneity in disease phenotypes likely remains even though we stratified asthma by atopy status. Because the study is cross-sectional, we cannot determine if findings reflect the pathogenesis or consequences of asthma.

This study has several strengths. It is the largest EWAS of adult asthma. The substantial replication in nasal epithelium and purified eosinophils suggests that methylation in blood is a good proxy for asthma-relevant tissues in discovering novel differential methylation in atopic asthma. Pathway analyses support the biological plausibility of our findings. The CpGs implicated in blood are enriched for localization to functional genomic elements in blood and lung. Many CpGs were associated with gene expression in both non-atopic and atopic asthma, further supporting the potential functional impact of the differential methylation we identified at these loci. Different findings for non-atopic and atopic asthma confirm the importance of separating forms of asthma to discover novel associations, which may better inform disease etiology and lead to improved treatment strategies.

Declaration of interests

All other authors declare no competing interests.

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Table 1. Characteristics of participants in the Agricultural Lung Health Study by asthma and atopy status (n=2,286)

	Non-cases[1] N = 1,157	**Atopy alone** N = 185	**Non-atopic asthma** N = 673	**Atopic asthma** N = 271
	N (%)	N (%)	N (%)	N (%)
Gender				
Male	625 (54.0)	110 (59.5)	300 (44.6)	138 (50.9)
Female	532 (46.0)	75 (40.5)	373 (55.4)	133 (49.1)
Smoking Status				
Never	754 (65.2)	121 (65.4)	456 (67.8)	192 (70.9)
Former	342 (29.6)	56 (30.3)	201 (29.9)	68 (25.1)
Current	61 (5.3)	8 (4.3)	16 (2.4)	11 (4.1)
State				
Iowa	839 (72.5)	114 (61.6)	502 (74.6)	179 (66.1)
North Carolina	318 (27.5)	71 (38.4)	171 (25.4)	92 (33.4)
Fall Enrollment				
Yes	219 (18.9)	45 (24.3)	179 (26.6)	75 (27.7)
No	938 (81.1)	140 (75.7)	494 (73.4)	196 (72.3)
Current Farming				
Yes	797 (68.9)	130 (70.3)	440 (65.4)	180 (66.4)
No	360 (31.1)	55 (29.7)	233 (34.6)	91 (33.6)
Asthma Control				
Adequately controlled	–	–	305 (45.3)	156 (57.6)
Inadequately controlled	–	–	131 (19.5)	44 (16.2)
Missing	–	–	237 (35.2)	71 (26.2)
Inhaled Corticosteriod Use				
Yes	–	–	278 (41.3)	103 (38.0)
No	–	–	395 (58.7)	168 (62.0)
	Median (IQR)	Median (IQR)	Median (IQR)	Median (IQR)
Age at home visit (y)	63 (55 - 72)	60 (55 - 68)	62 (55 - 71)	60 (52 - 68)
Packyears[2] (y)	14.5 (2.3 - 35)	7.3 (0.9 - 25)	6 (1.5 - 19)	7.7 (1.5 - 21.3)
Body Mass Index (kg/m^2)	28.8 (25.6-32.6)	29.0 (25.3-32.5)	30.5 (26.9-35.1)	29.6 (26.1-33.9)
Cell Type				
Monocyte	0.08 (0.06-0.10)	0.08 (0.06-0.11)	0.07 (0.05-0.10)	0.08 (0.06-0.10)
Neutrophil	0.56 (0.48-0.63)	0.56 (0.47-0.63)	0.57 (0.48-0.65)	0.57 (0.50-0.65)
Eosinophil	0.01 (0.00-0.03)	0.02 (0.00-0.05)	0.02 (0.00-0.04)	0.02 (0.00-0.04)
Lymphocyte	0.34 (0.27-0.42)	0.34 (0.26-0.40)	0.33 (0.25-0.40)	0.32 (0.25-0.40)

IQR: interquartile range

[1] Non-cases are participants with neither asthma nor atopy

[2] Among former and current smokers

Table 2. Top 30 significant CpG sites in non-atopic asthma

chromosome	position[1]	CpG	Gene Name[2]	N	OR[3]	CI	P	FDR	Coef.[4]
16	68804850	cg06085527		1829	0.93	(0.91, 0.95)	1.62E-08	7.76E-03	-0.0093
14	100610407	cg14084609	*DEGS2*	1830	0.82	(0.76, 0.88)	2.99E-08	7.76E-03	-0.0033
1	26091858	cg08028384	*SELENON*	1829	0.93	(0.90, 0.95)	3.73E-08	7.76E-03	-0.0099
2	234608559	cg10180919	*UGT1A6*	1829	0.89	(0.85, 0.93)	4.52E-08	7.76E-03	-0.006
10	22743835	cg15737719	*LOC100499489*	1829	0.76	(0.68, 0.84)	4.75E-08	7.76E-03	-0.0023
1	6341287	cg09249800	*GPR153*	1828	0.93	(0.90, 0.95)	7.16E-08	8.81E-03	-0.0085
14	55603874	cg23575099	*LGALS3*	1830	0.81	(0.76, 0.88)	8.46E-08	8.81E-03	-0.0029
13	41631052	cg07908654	*WBP4*	1830	0.86	(0.81, 0.91)	8.62E-08	8.81E-03	-0.0036
11	93456334	cg23338316	*SCARNA9*	1828	0.87	(0.82, 0.91)	1.13E-07	1.03E-02	-0.0048
3	152215571	cg07952576	*TMEM14EP*	1828	0.97	(0.96, 0.98)	1.87E-07	1.31E-02	-0.026
6	149450585	cg09639771	*TAB2*	1830	0.95	(0.93, 0.97)	1.90E-07	1.31E-02	-0.0128
1	59543930	cg18581916	*LINC01358*	1830	0.95	(0.93, 0.97)	1.93E-07	1.31E-02	-0.0126
13	97846783	cg23933458	*LINC00456*	1829	0.96	(0.94, 0.97)	2.33E-07	1.46E-02	-0.0158
17	56269767	cg01955639	*EPX*	1830	0.88	(0.84, 0.92)	3.18E-07	1.58E-02	-0.0038
16	21831372	cg07611887	*RRN3P1*	1829	0.88	(0.84, 0.92)	3.26E-07	1.58E-02	-0.0053
15	85186517	cg17194668	*WDR73*	1830	0.86	(0.81, 0.91)	3.76E-07	1.58E-02	-0.0037
7	150773709	cg06807926	*FASTK*	1828	0.96	(0.94, 0.98)	3.91E-07	1.58E-02	-0.0141
9	95800911	cg03234093	*SUSD3*	1829	0.95	(0.94, 0.97)	3.99E-07	1.58E-02	-0.013
4	38110810	cg07456972	*TBC1D1*	1825	0.81	(0.75, 0.88)	4.13E-07	1.58E-02	-0.0025
16	68804845	cg21468244		1827	0.95	(0.93, 0.97)	4.14E-07	1.58E-02	-0.0133
10	45495435	cg01614759	*ZNF22*	1829	0.87	(0.82, 0.92)	4.17E-07	1.58E-02	-0.0037
15	31505024	cg08884974	*LINC02352*	1829	0.88	(0.83, 0.92)	4.26E-07	1.58E-02	-0.0043
7	36077237	cg24598141	*LOC101928618*	1827	0.97	(0.95, 0.98)	4.59E-07	1.63E-02	-0.0175
14	68713369	cg01171954	*LOC100996664*	1828	0.94	(0.92, 0.96)	5.04E-07	1.66E-02	-0.0102
4	159969044	cg15834151	*C4orf45*	1830	0.93	(0.91, 0.96)	5.08E-07	1.66E-02	-0.0076
2	74612222	cg17988187	*DCTN1-AS1*	1830	0.89	(0.85, 0.93)	5.62E-07	1.70E-02	-0.0051
1	6341230	cg21220721	*GPR153*	1828	0.94	(0.92, 0.97)	5.62E-07	1.70E-02	-0.009
15	81623226	cg25466522	*TMC3-AS1*	1828	0.82	(0.76, 0.89)	6.02E-07	1.76E-02	-0.0024
3	159847104	cg17991030	*IL12A-AS1*	1829	0.97	(0.95, 0.98)	6.46E-07	1.82E-02	-0.019
3	14708144	cg15106081	*C3orf20*	1827	0.76	(0.68, 0.85)	7.20E-07	1.93E-02	-0.0017

[1] Genome build GRCh37/hg19

[2] Annotated using HOMER v4.9.1 and their human genome database (hg19, 5v.10) (57)

[3] Logistic regression model adjusted for age, sex, body mass index, smoking status, packyears, state of residence, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil). ORs indicate the multiplicative change in the odds of having non-atopic asthma in relation to an increase in DNA methylation.

[4] Adjusted mean methylation difference based on non-atopic asthma status. The coefficient is from a linear regression model with robust standard error estimation, where methylation is the outcome and non-atopic asthma status is the predictor, adjusting for the same covariates that was used in the logistic regression. Coefficient of -0.01 means that the mean methylation value is 0.01 lower in non-atopic asthmatics compared to non-cases. Possible methylation values range from 0 to 1.

Table 3. Top 30 significant CpG sites in atopic asthma

chromosome	position[1]	CpG	Gene Name[2]	N	OR[3]	CI	P	FDR	Coef.[4]
2	31302644	cg26382374	*GALNT14*	1425	0.76	(0.71, 0.82)	2.27E-14	1.86E-08	-0.0101
15	31248701	cg16606719	*MTMR10*	1428	0.72	(0.66, 0.79)	5.51E-13	2.25E-07	-0.0066
9	126497597	cg01745810	*DENND1A*	1428	0.76	(0.71, 0.82)	8.29E-13	2.26E-07	-0.0082
17	79851485	cg12380988	*ANAPC11*	1428	0.74	(0.68, 0.80)	1.40E-12	2.86E-07	-0.0075
3	33112660	cg26396322	*TMPPE*	1428	0.72	(0.66, 0.79)	2.32E-12	3.79E-07	-0.006
1	6341287	cg09249800	*GPR153*	1428	0.88	(0.85, 0.91)	6.80E-12	9.26E-07	-0.0161
15	81623226	cg25466522	*TMC3-AS1*	1426	0.70	(0.63, 0.78)	1.75E-11	2.04E-06	-0.0051
11	65546210	cg05300717	*AP5B1*	1421	0.87	(0.84, 0.91)	2.32E-11	2.37E-06	-0.0121
7	65439512	cg04290133	*GUSB*	1422	0.81	(0.75, 0.86)	3.61E-11	3.09E-06	-0.008
1	6341327	cg11699125	*GPR153*	1426	0.90	(0.87, 0.93)	3.78E-11	3.09E-06	-0.0191
1	180940378	cg11649969	*STX6*	1428	0.60	(0.51, 0.70)	5.10E-11	3.49E-06	-0.0032
10	135061670	cg12227660	*MIR202HG*	1419	0.88	(0.84, 0.91)	5.13E-11	3.49E-06	-0.0158
12	6342778	cg20560376	*CD9*	1427	0.71	(0.64, 0.79)	6.03E-11	3.79E-06	-0.0056
1	160309220	cg09332506	*NCSTN*	1428	0.53	(0.44, 0.64)	7.96E-11	4.15E-06	-0.0027
18	8720395	cg27550672	*MTCL1*	1428	0.68	(0.61, 0.76)	8.37E-11	4.15E-06	-0.0038
16	16143033	cg24304533	*ABCC1*	1426	0.73	(0.67, 0.81)	8.52E-11	4.15E-06	-0.0057
16	11709855	cg24517604	*LITAF*	1425	0.77	(0.71, 0.83)	8.64E-11	4.15E-06	-0.0068
7	149543136	cg05184016	*ZNF862*	1427	0.68	(0.61, 0.76)	1.01E-10	4.59E-06	-0.0048
14	95615731	cg01901579	*DICER1*	1428	0.78	(0.72, 0.84)	1.07E-10	4.60E-06	-0.0074
3	195974300	cg02803925	*SLC51A*	1424	0.77	(0.71, 0.83)	1.13E-10	4.62E-06	-0.0051
15	52427175	cg05853552	*BCL2L10*	1428	0.74	(0.67, 0.81)	1.28E-10	4.87E-06	-0.0063
17	55190679	cg13947225	*AKAP1*	1424	0.81	(0.76, 0.87)	1.31E-10	4.87E-06	-0.0083
7	99507261	cg17717565	*TRIM4*	1421	0.84	(0.79, 0.88)	1.43E-10	5.08E-06	-0.0103
13	41631052	cg07908654	*WBP4*	1428	0.78	(0.73, 0.84)	1.53E-10	5.21E-06	-0.0068
2	96965099	cg01923915	*SNRNP200*	1428	0.73	(0.67, 0.81)	2.07E-10	6.54E-06	-0.005
8	22169041	cg16427256	*PIWIL2*	1428	0.76	(0.69, 0.82)	2.08E-10	6.54E-06	-0.0052
16	616212	cg04497992	*NHLRC4*	1428	0.87	(0.83, 0.91)	2.75E-10	8.32E-06	-0.0127
17	25897247	cg06127160	*LGALS9*	1428	0.87	(0.83, 0.91)	3.08E-10	8.65E-06	-0.0114
15	40093898	cg18852698	*LOC105370941*	1427	0.82	(0.77, 0.87)	3.20E-10	8.65E-06	-0.007
2	32946576	cg18399629	*MIR4765*	1428	0.69	(0.62, 0.78)	3.28E-10	8.65E-06	-0.004

[1] Genome build GRCh37/hg19

[2] Annotated using HOMER v4.9.1 and their human genome database (hg19, 5v.10) (57)

[3] Logistic regression model adjusted for age, sex, body mass index, smoking status, packyears, state of residence, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil). ORs indicate the multiplicative change in the odds of having atopic asthma in relation to an increase in DNA methylation.

[4] Adjusted mean methylation difference based on atopic asthma status. The coefficient is from a linear regression model with robust standard error estimation, where methylation is the outcome and atopic asthma status is the predictor, adjusting for the same covariates that was used in the logistic regression. Coefficient of -0.01 means that the mean methylation value is 0.01 lower in atopic asthmatics compared to non-cases. Possible methylation values range from 0 to 1.

Table 4. Summary of Look-up Replication

	Tissue	Study Population	Methylation Array	Stratify by Atopy?	# asthma cases	# controls	# overlap with ALHS FDR results (%)[1]	# replicated (%)[2]	# replicated and overlap in ALHS AA
Non-atopic Asthma									
SAPALDIA	blood	adults	450K	Non-atopic	70	134	169 (100)	0 (0)	0
PACE meta-analysis	blood	children	450K	Did not stratify	631	2,862	168 (99.4)	68 (40.5)	41
EVA-PR	nasal	children	450K	Non-atopic	66	104	146 (86.4)	8 (5.5)	5
Project Viva	nasal	children	EPIC	Did not stratify	65	398	471 (92.5)	143 (30.4)	86
SLSJ	eosinophil	both	450K	Did not stratify	16	8	168 (99.4)	49 (29.2)	39
Atopic Asthma									**# replicated and overlap in ALHS NA**
SAPALDIA	blood	adults	450K	Atopic	91	134	349 (100)	0 (0)	0
PACE meta-analysis	blood	children	450K	Did not stratify	631	2,862	347 (99.4)	288 (83.0)	41
EVA-PR	nasal	children	450K	Atopic	169	104	299 (83.3)	235 (78.6)	28
ICAC	nasal	children	450K	Atopic	36	36	349 (100)	222 (63.6)	26
PIAMA	nasal	children	450K	Atopic	27	219	349 (100)	63 (18.1)	16
Project Viva	nasal	children	EPIC	Atopic	36	265	1,008 (94.2)	875 (86.8)	86
SLSJ	eosinophil	both	450K	Did not stratify	16	8	338 (96.8)	274 (81.1)	39
Bronchial epithelium	airway epithelial	adults	450K	Did not stratify	74	41	254 (72.8)	49 (19.3)	4

AA: atopic asthma; NA: non-atopic asthma

[1] For 450K, percentages based on 169 CpGs for non-atopic asthma and 349 CpGs for atopic asthma. For EPIC, percentages based on 509 CpGs for non-atopic asthma and 1,070 CpGs for atopic asthma

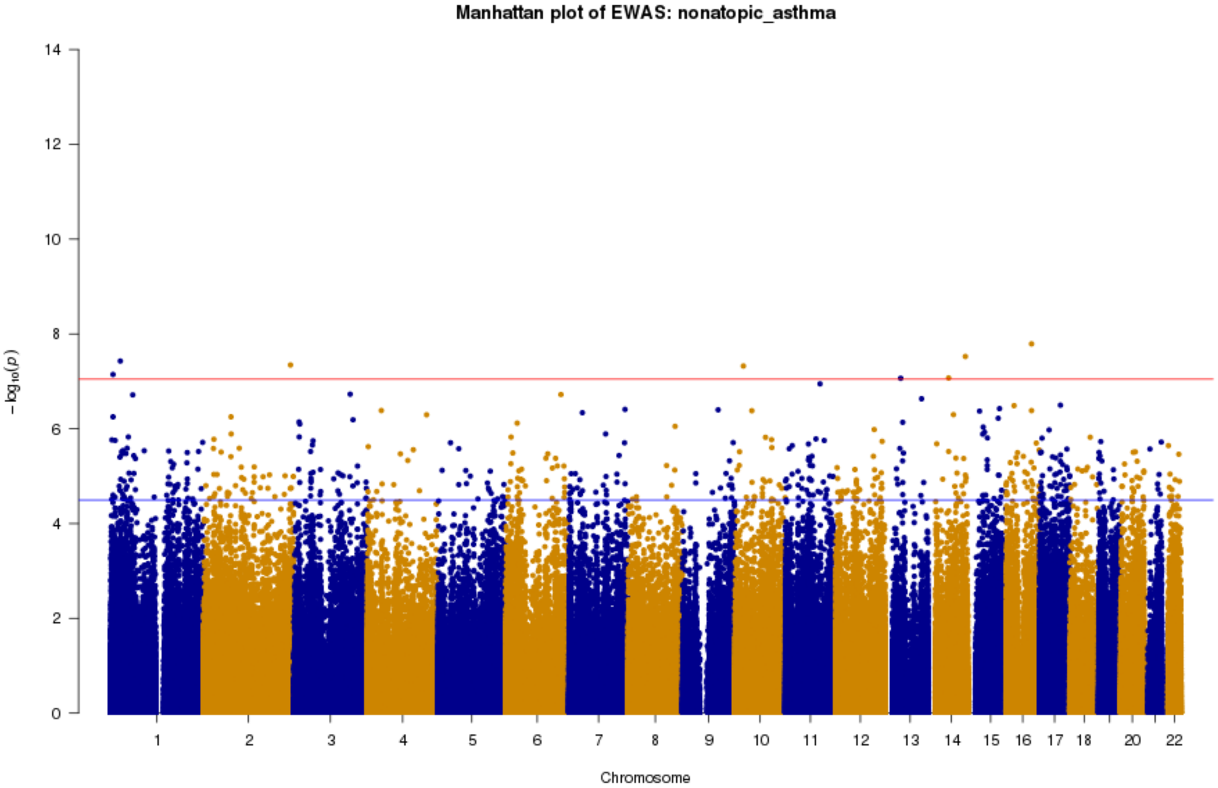
[2] CpGs in replication study with $p<0.05$ and same direction of association as observed in the ALHS. Percentages based on the number of CpGs that overlap with the replication study

Figure legend

Figure 1. Manhattan plot of epigenome-wide analysis of non-atopic asthma. Red line represents the family-wise error threshold and the blue line represents the false discovery rate threshold. Analyses adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil).

Figure 2. Manhattan plot of epigenome-wide analysis of atopic asthma. Red line represents the family-wise error threshold and the blue line represents the false discovery rate threshold. Analyses adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil).

Figure 3. Network plot of 9 enriched pathways (squares), connecting implicated genes (circles) from non-atopic and/or atopic asthma. Blue represent genes or pathways implicated in non-atopic asthma. Orange represent genes or pathways implicated in atopic asthma.


Manhattan plot of EWAS: nonatopic_asthma
−log10(p)
0
2
4
6
8
10
12
14
Chromosome
1
2
3
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6
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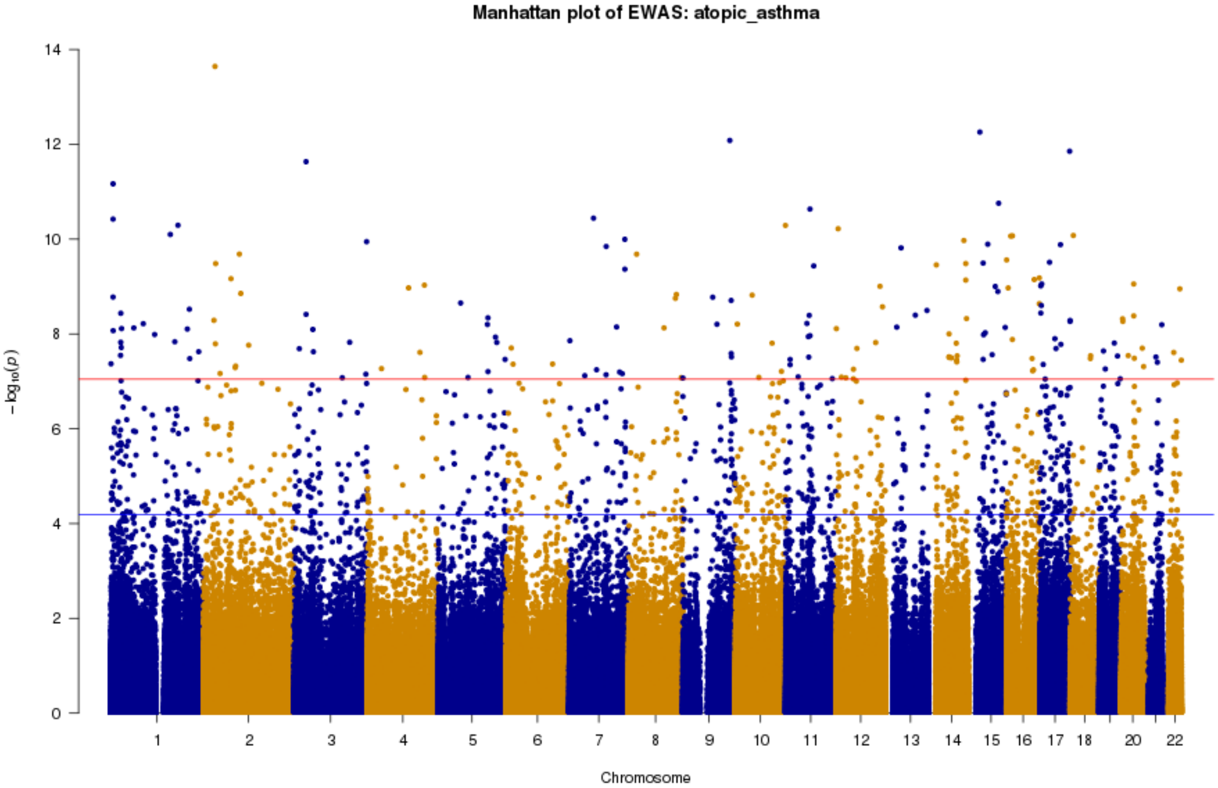
15
16
17
18
20
22


Manhattan plot of EWAS: atopic_asthma
−log10(p)
0
2
4
6
8
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Chromosome
1
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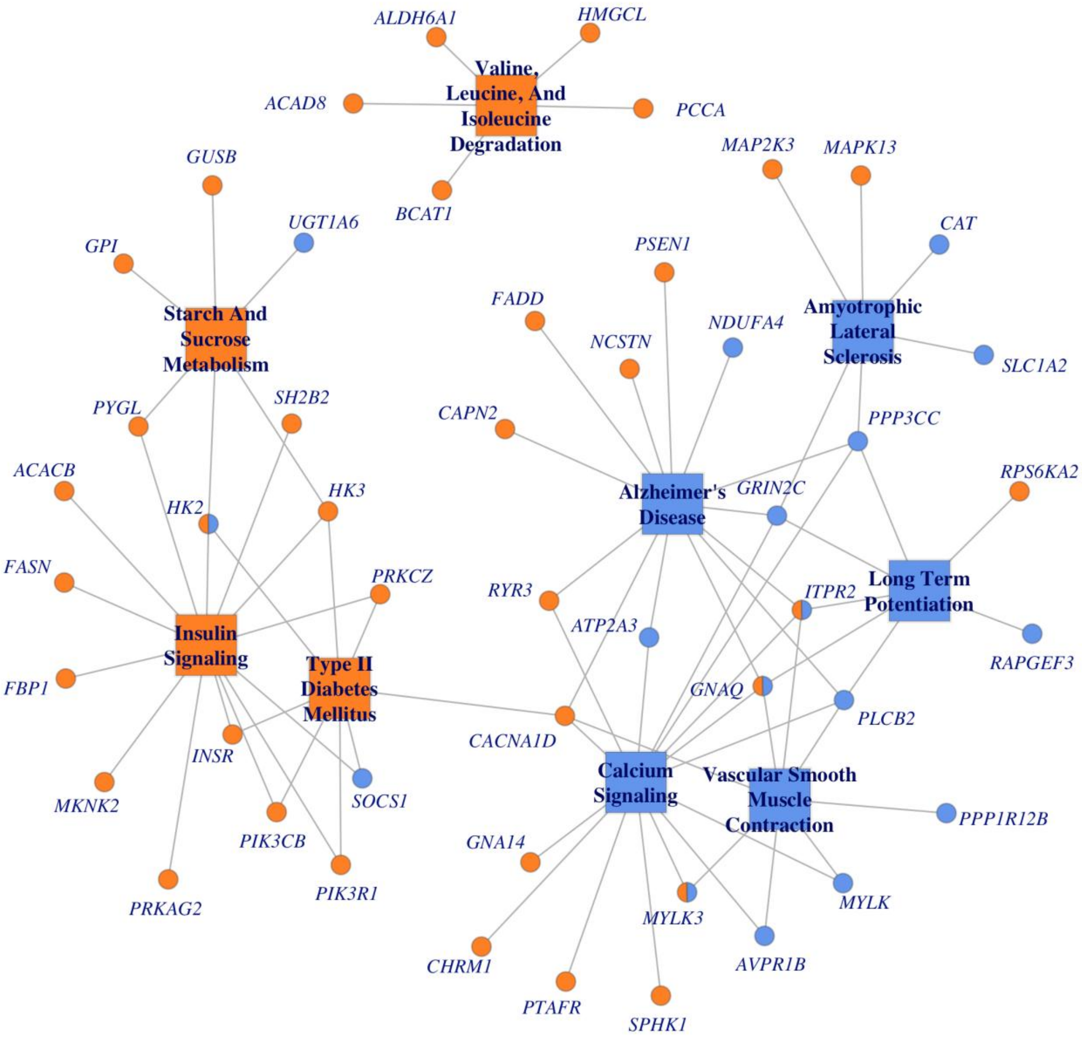


ALDH6A1
HMGCL
Valine, Leucine, And Isoleucine Degradation
ACAD8
PCCA
BCAT1
MAP2K3
MAPK13
GUSB
UGT1A6
CAT
GPI
PSEN1
FADD
Starch And Sucrose Metabolism
Amyotrophic Lateral Sclerosis
NCSTN
NDUFA4
SLC1A2
PYGL
SH2B2
CAPN2
PPP3CC
ACACB
HK3
RPS6KA2
HK2
Alzheimer's Disease
GRIN2C
FASN
PRKCZ
RYR3
ITPR2
Long Term Potentiation
Insulin Signaling
ATP2A3
RAPGEF3
Type II Diabetes Mellitus
FBP1
GNAQ
PLCB2
CACNA1D
INSR
Calcium Signaling
Vascular Smooth Muscle Contraction
SOCS1
MKNK2
PPP1R12B
PIK3CB
GNA14
MYLK
PIK3R1
PRKAG2
MYLK3
AVPR1B
CHRM1
PTAFR
SPHK1

Methods

Data Collection

Some demographic information was collected via questionnaires from the Agricultural Health Study (AHS) (e.g., sex, smoking history, site [i.e., Iowa, North Carolina]). In the Agricultural Lung Health Study (ALHS), field technicians visited individuals' home to collect blood samples and measure height and weight to calculate body mass index (kg/m2). A computer-assisted telephone interview (CATI) was conducted after the home visit. The CATI collected information on oral corticosteroid use, asthma control, as well as smoking history, which was used to update their smoking status (never, former, current) and packyear from the AHS. Date of enrollment was used to categorize participants to a season of enrollment: spring (enrolled March 21 to June 20), summer (enrolled June 21 to September 20), fall (enrolled September 21 to December 21), or winter (enrolled December 22 to March 20).

Asthma Control

Individuals with asthma were asked to complete the Asthma Control Questionnaire (ACQ), a six-item questionnaire about their asthma severity during the past two weeks (frequency of night-time waking, symptoms of night-time waking, activity limitation, shortness of breath, wheezing, and use of bronchodilator) (1). Individuals provided responses on a 7-point scale from 0 (no impairment) to 6 (maximum impairment). Pre-bronchodilator percent predicted FEV1 collected by the field technicians during the home visit was also categorized on a 7-point scale from 0 to 6. For those who responded to the six questions and had a percent predicted FEV1, a mean ACQ score was calculated. Individuals with an ACQ score < 1.5 were considered to have controlled asthma, whereas individuals with an ACQ score ≥ 1.5 were considered to have uncontrolled asthma.

Asthma Polygenic Risk Score

A weighted polygenic risk score was calculated using the results from the multi-ancestry, fixed-effects model from the largest genome-wide meta-analysis of asthma (2). SNPs with p-values $<5\times10^{-8}$ were clumped using PLINK ($r^2 = 0.5$) to identify independent loci within ±250 kb (3). 98 SNPs remained after clumping to calculate the polygenic risk score.

Post-hoc Analyses of Differentially Methylated CpGs

Additional analyses were conducted for FDR significant CpG sites. Because sex may contribute to the pathogenesis of asthma, we repeated the analyses and added an interaction term between sex and the methylation value at each differentially methylated CpG site. To examine if methylation differs by use of oral inhaled corticosteroid (yes versus no), we conducted case-only analyses, modeling use of oral inhaled corticosteroid as the outcome and adjusted for the covariates used in the main model. Similar analyses were conducted with asthma control (uncontrolled versus controlled) as the outcome.

Gene Annotation

Because Illumina does not update the annotation in their manifest file, CpG sites were mapped to genes using HOMER v4.9.1 and the human genome database (hg19, v5.10) provided by HOMER (4). Each CpG site was mapped to the closest transcription start site (TSS) based on the RefSeq annotation, using the "annotatePeaks.pl" script with default setting. CpG sites within 100 kb from the TSS were annotated to the gene from the Gene Symbol column.

Enrichment of functional genomic features

CpG sites were localized to four genomic features: CpG islands, CpG island shores, promoters, and transcription factor binding sites. The genomic locations for CpG islands were obtained from the CpG islands track in the regulation section of the University of California, Santa Cruz (UCSC) Genome Browser. CpG island shores were defined as 2 kb regions adjacent to the CpG islands. Promoters were defined as the regions 1 kb upstream and downstream of all RefSeq protein-coding genes.

We obtained the transcription factor binding sites from the transcription factor ChIP track within the ENCODE regulation super-track in the regulation section of the UCSC Genome Browser, based on Factorbook Motifs and

ENCODE data for 161 factors in 91 cell types. Enrichment was tested using a two-sided Fisher's exact test. A genomic feature was considered significant using a Bonferroni threshold ($p<0.0125$). An enrichment score was calculated as the log2 ratio of the percentage of significant CpG sites in a feature over the percentage of total CpG sites in the feature.

Using the summary mode option in eFORGE TF, we uploaded the FDR significant CpG sites (Sample = fLung) to identify enriched transcription factor motifs (FDR<0.05). Because eFORGE TF reads a maximum of 1,000 probes, the top 1,000 significant CpG sites were uploaded if the epigenome-wide analyses identified over 1,000 FDR significant CpG sites.

In eFORGE v2.0, data were analyzed from the Consolidated Roadmap Epigenomics consortium.

Expression Quantitative Trait Methylation (eQTM)

Because studies with methylation from the EPIC array and gene expression data are currently unavailable, eQTMs were conducted for differentially methylated CpG sites that are in the 450K array. Methylation from the Illumina 450K array and gene expression data were available in 3,075 samples in the Biobank-based integrative omics study (BIOS) consortium from the following cohorts: Leiden Longevity Study, LifeLines Study, Rotterdam Study, and Netherland Twin Study (5). cis-eQTMs were conducted for gene expression transcripts within ±250 kb of each CpG site (168 CpGs for non-atopic asthma, 346 CpGs for atopic asthma). In each cohort, the gene expression was regressed on methylation M value (log2 ratio of methylated versus unmethylated probe intensities), using the limma package in R. Analyses were adjusted for age, sex, lymphocyte proportion, monocyte proportion, and RNA flow cell number. Model inflation was corrected using the "bacon" method (6). The results from each cohort were meta-analyzed using an inverse variance-weighted fixed-effects model in METAL (7).

Identify Genes Implicated with Asthma in Previous EWAS or GWAS

Reese et al. performed a literature review up to January 12, 2018 to identify genes that have been reported to be differentially methylated in relation to asthma (8). A list of these genes is available in a supplemental table [Appendix, Table E8]. Their list also includes genes from a large GWAS of asthma.

We updated Reese et al.'s list of genes by running their PubMed search to identify studies published between January 12, 2018 to August 9, 2019. The following search terms were used:

(((((("Asthma"[Majr]))) OR (((((airways hyper responsiveness[Title/Abstract]) OR airway reactivity[Title/Abstract]) OR bronchodilator response[Title/Abstract]) OR asthma[Title/Abstract]) OR wheez*[Title/Abstract] OR FENO[Title/Abstract]))) AND (((("Methylation"[Majr]) OR "DNA Methylation"[Majr])) OR ((methylation[Title/Abstract]) OR DNA methylation[Title/Abstract])))

We included the reported asthma genes downloaded from the GWAS Catalog on October 11, 2019.

Search for Druggable Targets

Genes that had not been previous been associated with asthma (i.e., novel genes) were annotated to the ChEMBL database (v25, released on January 2, 2019) to identify approved drugs or drugs in development that target the gene (9).

Replication of Findings in Other Studies

Chicago

This study recruited asthmatic and non-asthmatic adults (mean age 39 and 38 years, respectively) undergoing bronchoscopy between March 2010 and March 2014 at the University of Chicago (10). Asthma cases had to have a current doctor's diagnosis of asthma, no conflicting pulmonary diagnoses, and were using asthma medications. Controls did not have current or previous asthma diagnosis and had normal spirometry and methacholine challenge tests.

Methylation was measured in endobronchial brushings obtained during bronchoscopy, using the Infinium HumanMethylation 450K BeadChip. Probes meeting the following criteria were excluded: 1) probes located on the sex chromosome, 2) probes with a detection p-value >0.01 in 75% of samples, 3) probes mapping to more than one location in a bisulfite-converted genome, or 4) probes overlapping with location of known SNPs. Methylation data were processed using minfi (11). Probe-type bias was corrected using the SWAN method (12). Chip-level effects were regressed out using COMBAT (13). Residual methylation β values were used in the analyses.

Analyses were conducted using limma, adjusting for gender, age, current smoker (yes/no), and ethnicity (African-American, European-American, other). There were 74 asthmatics and 41 non-asthmatics with methylation data. The analyses for have been published (10).

Epigenetic Variation and Childhood Asthma in Puerto Ricans (EVA-PR)

EVA-PR is a case-control study of subjects aged 9-20 years from San Juan, Puerto Rico (14). Cases were considered to have asthma if they had physician-diagnosed asthma and at least 1 episode of wheeze in the previous year. Methylation was measured from nasal epithelial samples. Serum allergen-specific IgE was measured for 5 common aeroallergens in Puerto Rico: house dust mite, cockroach, cat dander, dog dander, and mouse urinary protein. Participants were considered to have atopy if they had at least one specific IgE ≥0.35 IU/mL. In their analyses, EVA-PR had 67 non-atopic asthmatics and 169 atopic asthmatics. The referent group was non-atopic, non-asthmatic controls (n=104).

Methylation was measured using the HumanMethylation 450K BeadChip. DNA was bisulfite-converted using EZ-96 Bisulfite DNA Clean-up Kit (Zymo Research, Orange, CA). Methylation data was processed using minifi (11). We removed samples with low detection values (>10 CpG sites with detection p-value >0.01). The β-values were calculated for each CpG site. ENmix was used for background correction and normalization (15). The following criteria were used to exclude CpG probes: probes with a multimodal distribution, cross-reactive and SNP-containing probes, probes in the sex chromosome, low-quality probes (>10% samples with detection p-value >0.01), probes with a mean β-value <0.1 or >0.9 or extreme β-values in >80% samples.

Methylation was modeled using M values ($M = log2(\frac{\beta}{1-\beta})$). The following logistic regression models were used for their analyses.

Atopic asthma = methylation + age + sex + latent factors + A
Non-atopic asthma = methylation + age + sex + latent factors + A

Where:

- latent factors are from the surrogate variable analysis (sva package) to capture unknown data heterogeneity
- A = top 5 principal components from genotype data

The results from the atopic asthma model have been previously published (14). The same model was applied for non-atopic asthma.

Inner-City Asthma Consortium (ICAC)

The ICAC recruited children ages 10-12 years across 6 sites from which census tracts contained ≥20% of households at less than US government poverty level. Methylation from nasal brushings were measured from samples with ≥80% ciliated epithelial cells.

Methylation measured in 36 cases with asthma and with atopy and 36 controls (i.e., no asthma and no atopy), using the HumanMethylation 450K BeadChip. Methylation data were processed using minfi (11) and normalized using SWAN (12). Probes with localized to known SNPs in European and African populations were excluded (16). Normalized M values were used in the linear regression model, using limma.

Methylation = asthma + age + sex + race/ethnicity + technical variables + batch effects

The results of this study have previously been published (17).

Pregnancy and Childhood Epigenetic (PACE) Consortium
The PACE consortium conducted a meta-analysis of childhood asthma in relation to DNA methylation in blood from children ages 7-17 years. The meta-analysis consisted of 6 studies (BAMSE EpiGene, BAMSE MeDALL, CHOP, GALA II, ICAC, NFBC 1986, PIAMA, Raine study, and STOPPA). A total of 631 asthmatic cases and 2,862 non-cases were analyzed. Studies did not differentiate by atopy status. All studies used untransformed β values for the methylation values. Generally, the cohorts used the following logistic regression model:

Childhood asthma = methylation + maternal age + sustained maternal smoking during pregnancy + maternal asthma + maternal socioeconomic status + child's sex + 7 cell type proportions (monocyte, NK, B cell, CD4, CD8, eosinophil, neutrophil)

Cohorts adjusted for batch effects using ComBat, sva, or including a batch variable in their models. Replication look-up was performed using the results of this PACE meta-analysis paper (8).

Prevention and Incidence of Asthma and Mite Allergy (PIAMA)
PIAMA is a birth cohort of children born in 1996-1997 in the Netherlands (18). Details of the cohort have been published previously (18). The recruitment took place in prenatal clinics. In total, 10,232 pregnant women completed a validated screening questionnaire at their prenatal health care clinic (n=52 clinics). Based on this screening, 7,862 women were invited to participate, of whom 4,146 women agreed and gave informed consent. The study started with 3,963 newborns. Questionnaire based follow-up of the children took place at 3 months of age, annually from 1 to 8 years of age, and at 12, 14, and 16 or 17 years of age. The Medical Ethical Committees of the participating institutes approved the study, and all participants gave written informed consent. Nasal epithelial cells were collected at age 16 years.

Children were considered to have asthma if they had ever been diagnosed with asthma and either wheezed in the last 12 months or used medication for respiratory or lung problems. Serum specific IgE were measured for the following aeroallergens: house dust mite, cat, dactylis (grass), and birch. Atopy was defined as having at least one specific IgE ≥0.35 IU/mL.

Methylation was measured using the Infinium HumanMethylation 450K BeadChip. Methylation data were pre-processed using minfi (11). Samples with call rate <99% were removed. We used the 65 SNP probes to check the concordance between paired DNA samples (samples with blood and nasal methylation from the same participant). Paired samples with Pearson correlation <0.90 were excluded. Probes were also excluded for following criteria: probes on the sex chromosomes, probes mapping to multiple loci, 65 SNP probes, or probes containing SNPs at the target CpG sites with a MAF>5%. Background correction and normalization was conducted using DASEN (19). Trimmed M-values were used in the analyses.

The following model was used for the analysis:

Methylation = atopic asthma + age + center of brushing + gender + batch

Project Viva
Project Viva is a prospective cohort study where mothers were recruited between 1999 and 2002 at their first prenatal visit at Atrius Harvard Vanguard Medical Associates. Mothers were eligible to participate if they were fluent in English, gestational age <22 weeks at first prenatal visit, and singleton pregnancy. Nasal swabs were collected at mean age 12.9 years.

Children had current asthma if the mother reported a doctor's diagnosis of asthma since birth on the early teen questionnaire plus report of wheeze or asthma medication in the past year on early teen follow-up. Children without asthma had no asthma diagnosis, no wheeze, and no asthma medication use.

Total IgE was measured using ImmunoCAP assay (Phadia, Uppsala, Sweden) for common indoor allergens (*Dermatophagoides farinae*, cat and dog dander), mold allergens (*Alternaria* or *Aspergillus* species), and outdoor allergens (rye grass, ragweed, oak, and silver birch). Children with any specific IgE level > 0.35 IU/mL were sensitive to environmental allergens.

DNA methylation was measured in DNA extracted from nasal samples, using the Infinium MethylationEPIC BeadChip. Sample plates and chips were randomized to ensure balance by sex, current asthma status, current allergic rhinitis, and race. Methylation data were pre-processed using minfi (11). Samples were excluded for the following criteria: low-quality samples (intensities <10.5), mismatch recorded sex, mixed genotype distributions on the measured SNP probes), and technical duplicates. Probes were excluded if detection p-value was >0.05 for 5% or more of the samples, probes on the sex chromosomes, non-CpG probes, probes with SNPs at the single base extension (minor allele frequency [MAF] ≥ 5%), probes containing an SNP (MAF ≥ 5%), probes with a SNP at the CpG site (MAF ≥ 5%), and cross-reactive probes (20). Data were preprocessed using the functional normalization with 3 PCs from the control probes to adjust for technical variability (21). Probe-type bias was adjusted using RELIC from the ENmix package (22). Sample plate batch effects were adjusted using ComBat (13).

Project Viva ran two separate asthma analyses. One analysis compared 65 asthmatic children to 398 non-asthmatic children. The other analysis compared 36 asthmatic children with environment IgE sensitization to 265 non-asthmatic children without environmental IgE sensitization.

All analyses adjusted for child's race/ethnicity, sex, age at sample collection, BMI z-sore, maternal education, smokers living in the house, sine and cosine of season at sample collection, and cellular heterogeneity (10 PCs from ReFACToR (23)).

The analyses for asthma and atopic asthma were have been published (24). The full results were downloaded from https://figshare.com/articles/The_Nasal_Methylome_as_a_Biomarker_of_Asthma_and_Airway_Inflammation_in_Children/8285612/1.

Saguenay–Lac-Saint-Jean (SLSJ) asthma familial cohort
The families (1394 individuals distributed in 271 families) included in the SLSJ asthma cohort were recruited through probands with documented allergic asthma (25). To be included in the study, a family needs to fulfill these criteria: the two parents must be available for clinical assessment, one parent must be unaffected and all grand-parents must be of French-Canadian origin. Clinical evaluation (measures of lung function: forced expiratory volume in 1 s (FEV_1) and methacholine challenge (PC_{20})), white blood cell counts, skin prick test for allergy and a standardized questionnaire were completed for all individuals. New blood sampling was performed on 24 individuals, 16 individuals with asthma and eight individuals without asthma, in order to isolate eosinophils to measure methylation profile.

Isolation of eosinophils from blood samples

Eosinophils were isolated from 200ml blood samples from 24 samples, a subset of the SLSJ asthma cohort, following protocols already described (26, 27). The first step was to remove platelet-rich plasma by centrifugation and to use dextran to remove the erythrocytes by sedimentation. A lymphocyte separation medium was used to withdraw mononuclear cells by density gradient. After separation of mononuclear and granulocyte cells, hypotonic lysis with water was performed to remove remaining erythrocytes from the granulocyte cells and negative selection with anti-CD16 MicroBeads and magnetic cell sorter allowed to isolate the eosinophils (Miltenyi Biotec, Auburn, CA, USA). DNA were extracted using the DNeasy Blood and Tissue kit following the company's instruction (QIAGEN, Toronto, Canada).

Methylation analysis

Methylation levels were obtained from Illumina Human Methylation 450k BeadChip. Data filtering and normalization were performed with RnBeads package in R. Probes with low signals considering detection p value > 0.01 as threshold and probes located on SNP were first removed from analysis. Normalization was performed using the "swan" method and background subtraction was done using "methylumi.noob" method.

Covariates and statistical model

Logistic regressions were performed in R using glm (family = binomial) with sex as covariate.

asthma ~ methylation + sex

Asthma is defined as: Present or past documented clinical history of asthma and was coded as 0 = unaffected and 1 = affected.

These analyses were conducted for a previous paper (8).

SAPALDIA

The Swiss Cohort Study on Air Pollution and Lung and Heart Diseases in Adults (SAPALDIA) is a prospective cohort study, enrolling participants from eight regions in 1991. Followed-up occurred in 2001-2003 and 2010-2011. A nested case-control study of adult asthma was conducted in participants who were followed-up in 2010-2011.

Cases had self-reported asthma, self-reported age of onset later than 16 years, never reported having chronic obstructive pulmonary disease (COPD), and were non-smokers for at least 10 years before the blood draw and interview. Controls were randomly selected among participants who never reported having asthma, never used asthma medication, never wheezed without a cold in the last 1 months, and never had 3 or more asthma-related symptoms in the last 12 months.

Atopy was defined using skin prick test against nine common inhalant allergens (Phazet, Pharmacia®, Uppsala, Sweden) performed at baseline examination (28). Subjects with positive skin prick response to at least one allergen (cat, mould (*Cladosporium*), timothy grass pollen, Parietaria pollen, house dust mite, mould (*Alternaria*), birch pollen and dog) were classified as atopic.

Height and weight were measured to compute body mass index. Participants reported their highest education level and categorized into low (primary school), middle (secondary/middle school or apprenticeship), or high (college/university). Packyears was calculated from the self-reported number of cigarettes smoked per day and smoking history.

Methylation was measured in DNA from peripheral blood that was collected in 2010-2011, using the Infinium HumanMethylation 450K BeadChip. Each chip had a similar proportion of samples from different centers, case-control status, and confounding factors to minimize batch effects. Methylation data were preprocessed using minfi (11). Samples with sex mismatches and call rate <0.95 were excluded. We used Noob for background correction and dye-bias correction (29). Methylation levels were expressed as β values. β values were set to missing if the detection p-value was $>10^{-16}$. Probes were excluded if they were on the sex chromosome, had a call rate <0.95, hybridized to multiple genomic locations or overlap with known SNPs with a MAF >1%. Probe-type bias was corrected using beta-mixture quantile normalization (BMIQ) (30). Principal component analysis was conducted on the 220 control probes to obtain the first 30 principal components to adjust for batch effects (31).

Houseman estimated cell types were calculated using the Reinius reference panel (32, 33). Analyses were conducted using logistic regression for non-atopic and atopic asthma, separately.

$$\text{Non-atopic asthma} = \text{Methylation} + \text{BMI} + \text{Age} + \text{Sex} + \text{Education} + \text{Area} + \text{Packyear} + \text{Benchtime} + \text{Bcell} \\ + \text{CD4T} + \text{CD8T} + \text{NK} + \text{Mono} + \text{Eos} + \text{PC1-30}$$

$$\text{Atopic asthma} = \text{Methylation} + \text{BMI} + \text{Age} + \text{Sex} + \text{Education} + \text{Area} + \text{Packyear} + \text{Benchtime} + \text{Bcell} \\ + \text{CD4T} + \text{CD8T} + \text{NK} + \text{Mono} + \text{Eos} + \text{PC1-30}$$

Figure E1. Workflow of epigenome-wide association study of adult asthma

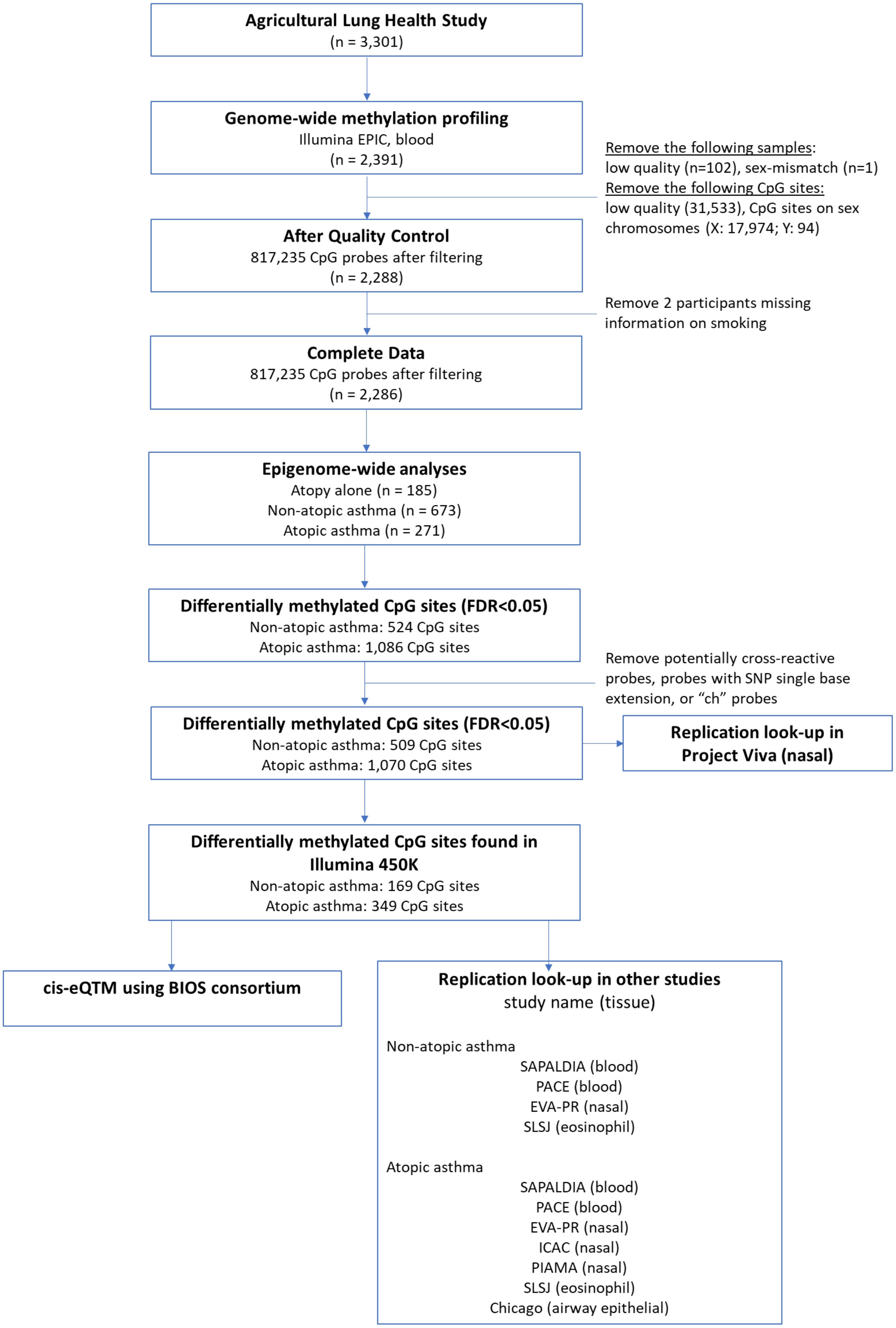
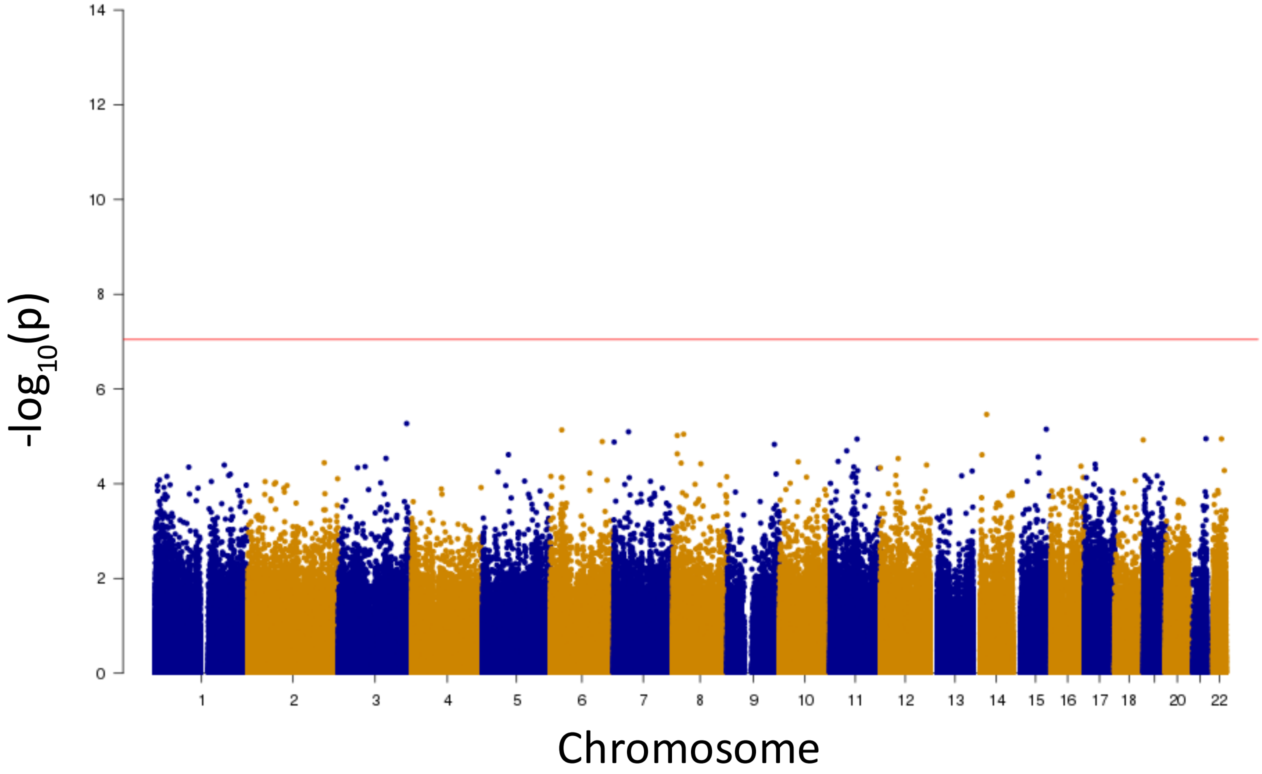


Figure E2. Manhattan plot of epigenome-wide analyses of atopy alone.

(a) Manhattan plot shows that none of the CpG sites were significant using FWER (red line).



(b) QQ-plot showing the observed -log$_{10}$ p-value versus the expected -log$_{10}$ p-value for atopy alone. Lambda = 0.97

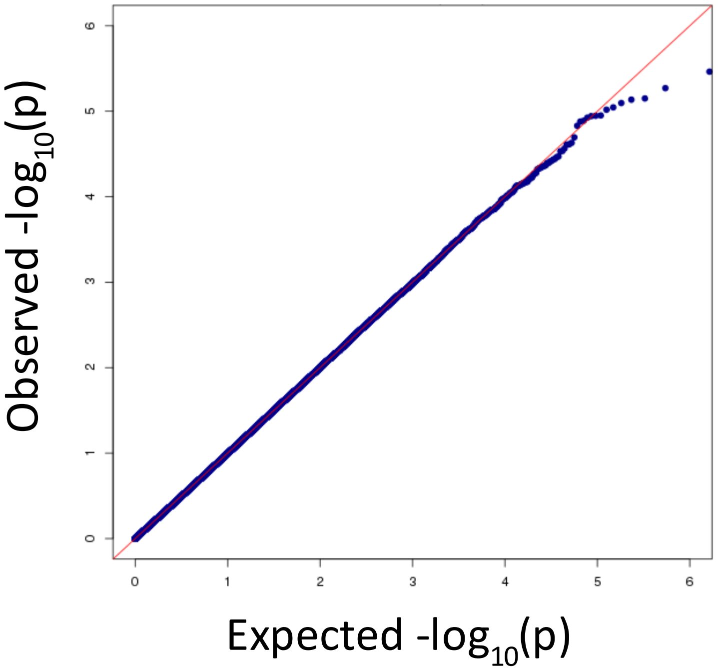
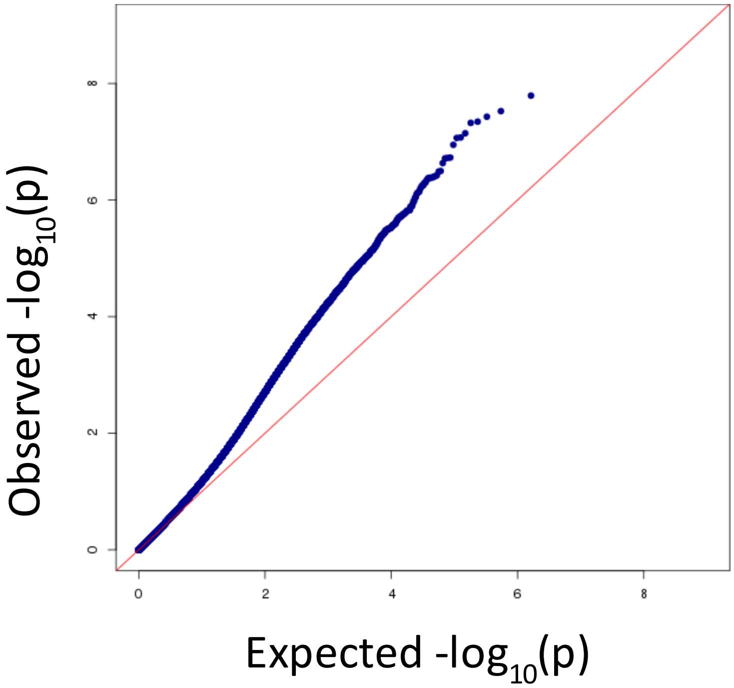


Figure E3. QQ-plot and volcano plot for the epigenome-wide analysis of non-atopic asthma.

(a) QQ-plot of the observed -log10 p-value versus the expected -log10 p-value for non-atopic asthma. Lambda = 1.14



(b) Volcano plot of the observed -log10 p-value versus beta coefficient for non-atopic asthma. Points above the red line are FWER significant. Points above the blue line are FDR significant.

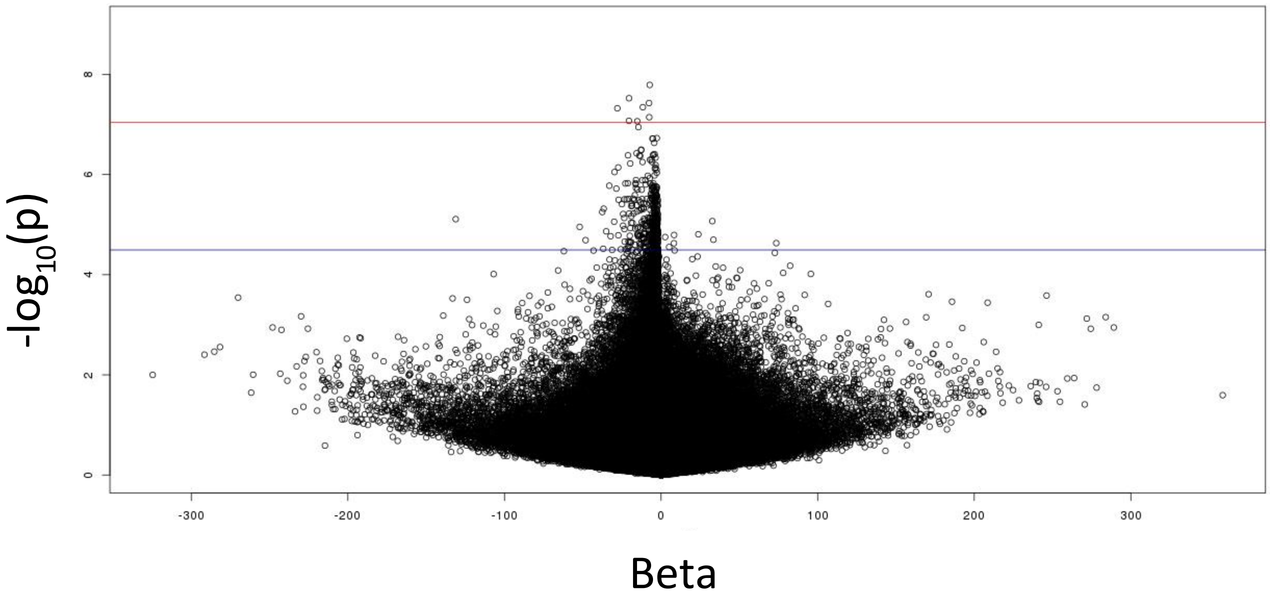
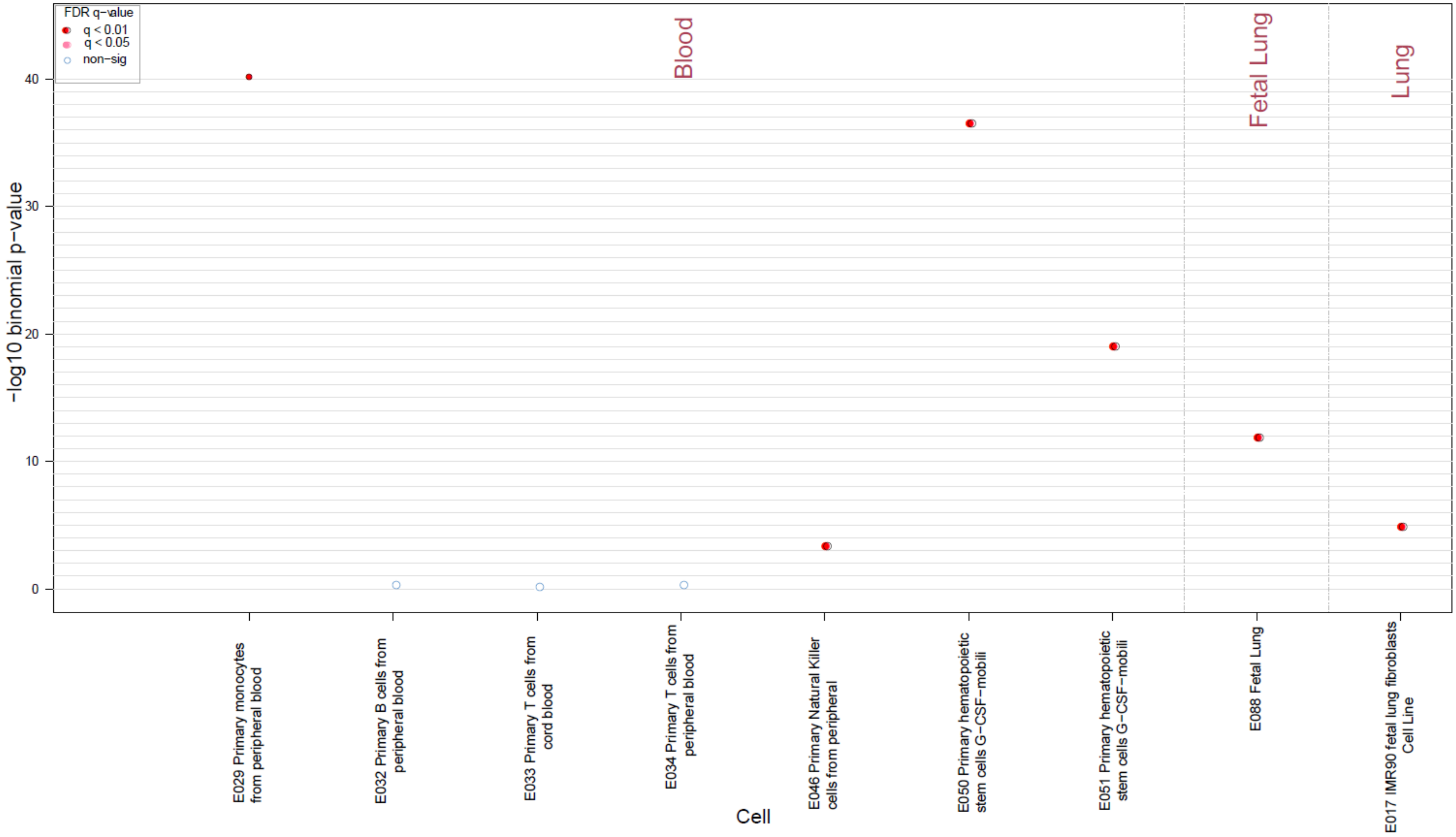
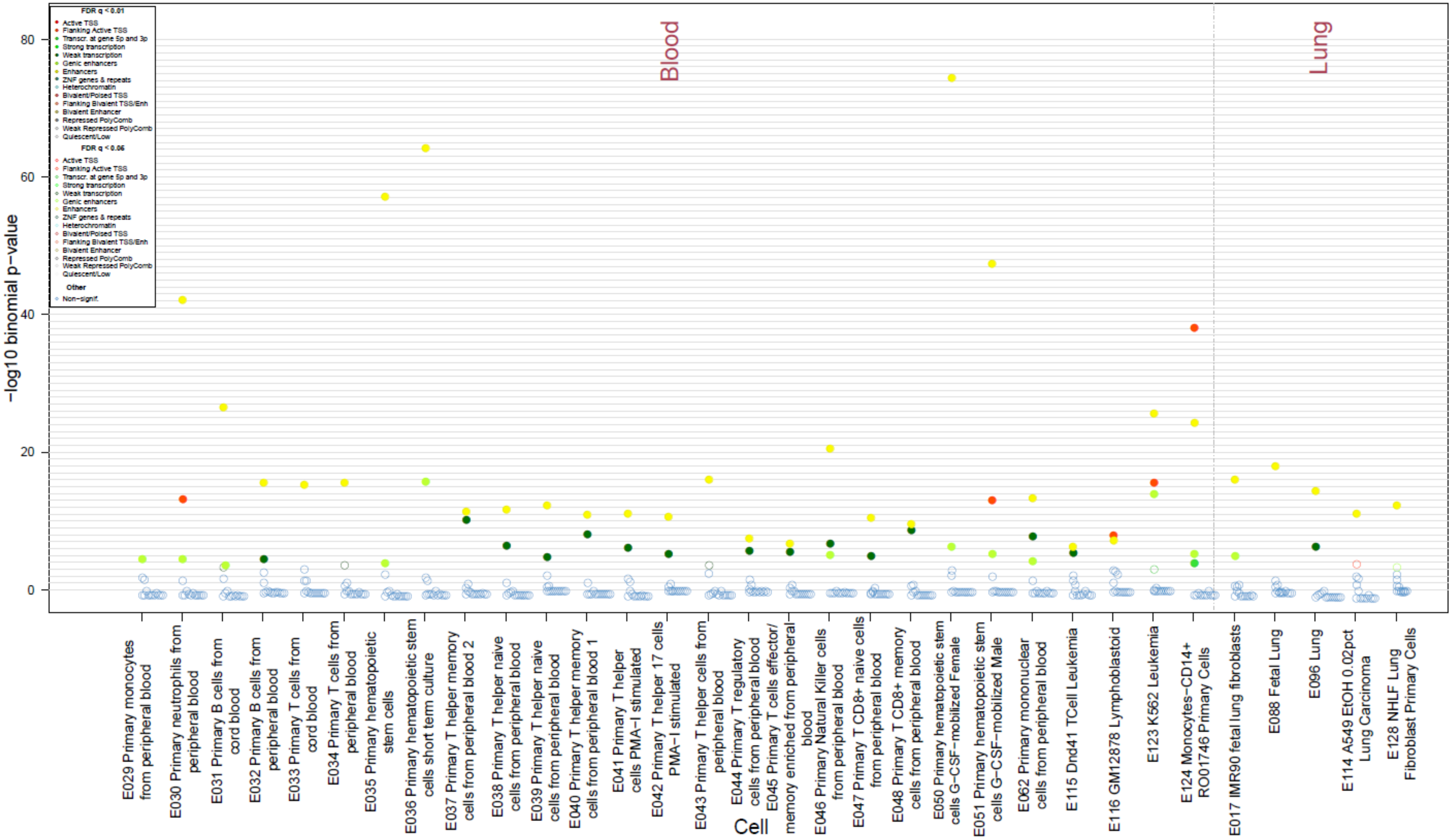


Figure E4. Tissue- and cell-specific enrichment pattern in CpG sites significantly associated (FDR<0.05) with non-atopic asthma, using eFORGE

(a) DNase I hypersensitive sites (probably transcription factor binding sites) enrichment in cell lines from the Roadmap Epigenomics consortium



(b) Chromatin state enrichment in cell lines from the Roadmap Epigenomics consortium



(c) Histone mark enrichment in cell lines from the Roadmap Epigenomics consortium

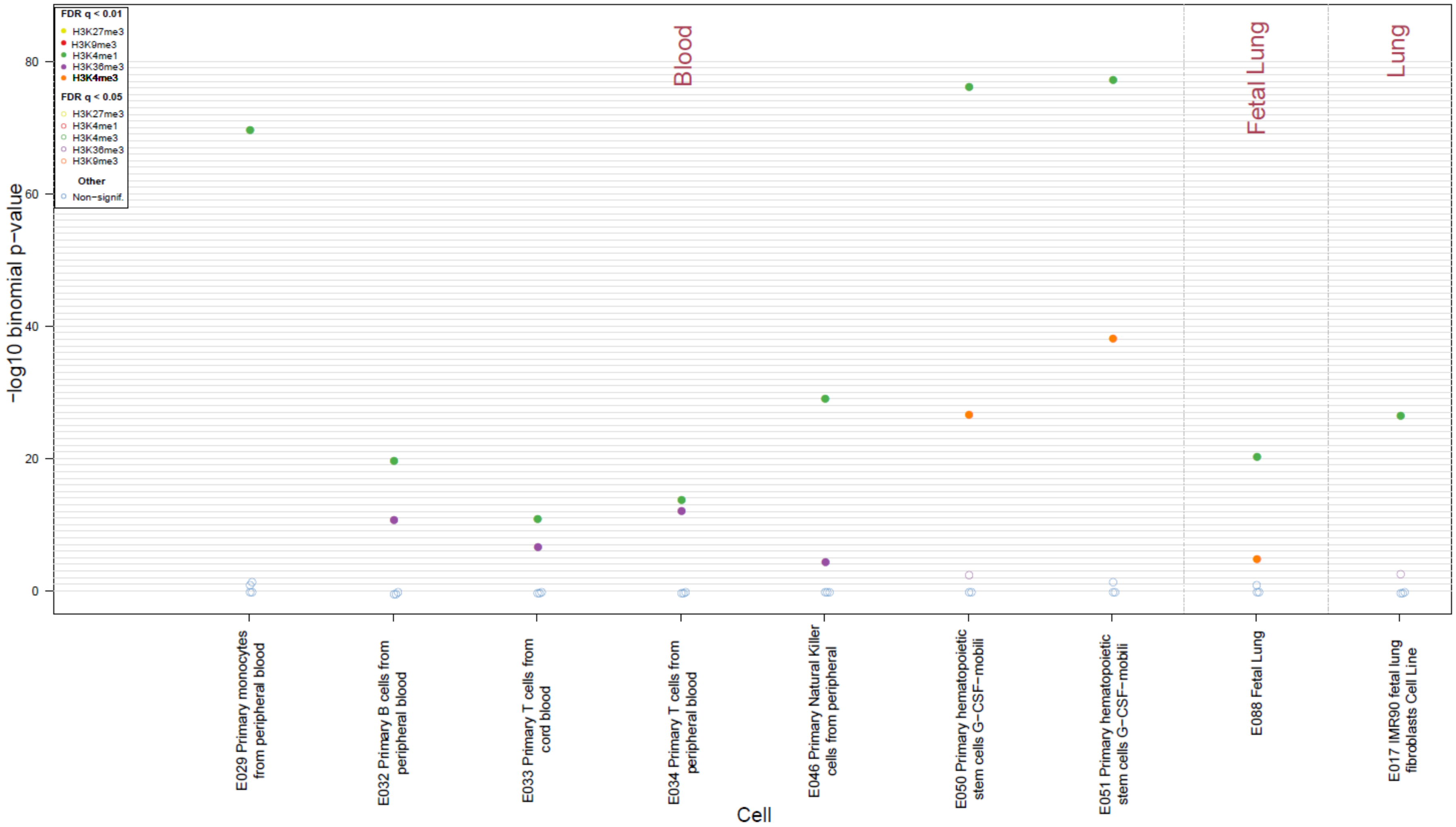


Figure E5. Heatmap of potentially biologically relevant pathways by atopic and non-atopic asthma.

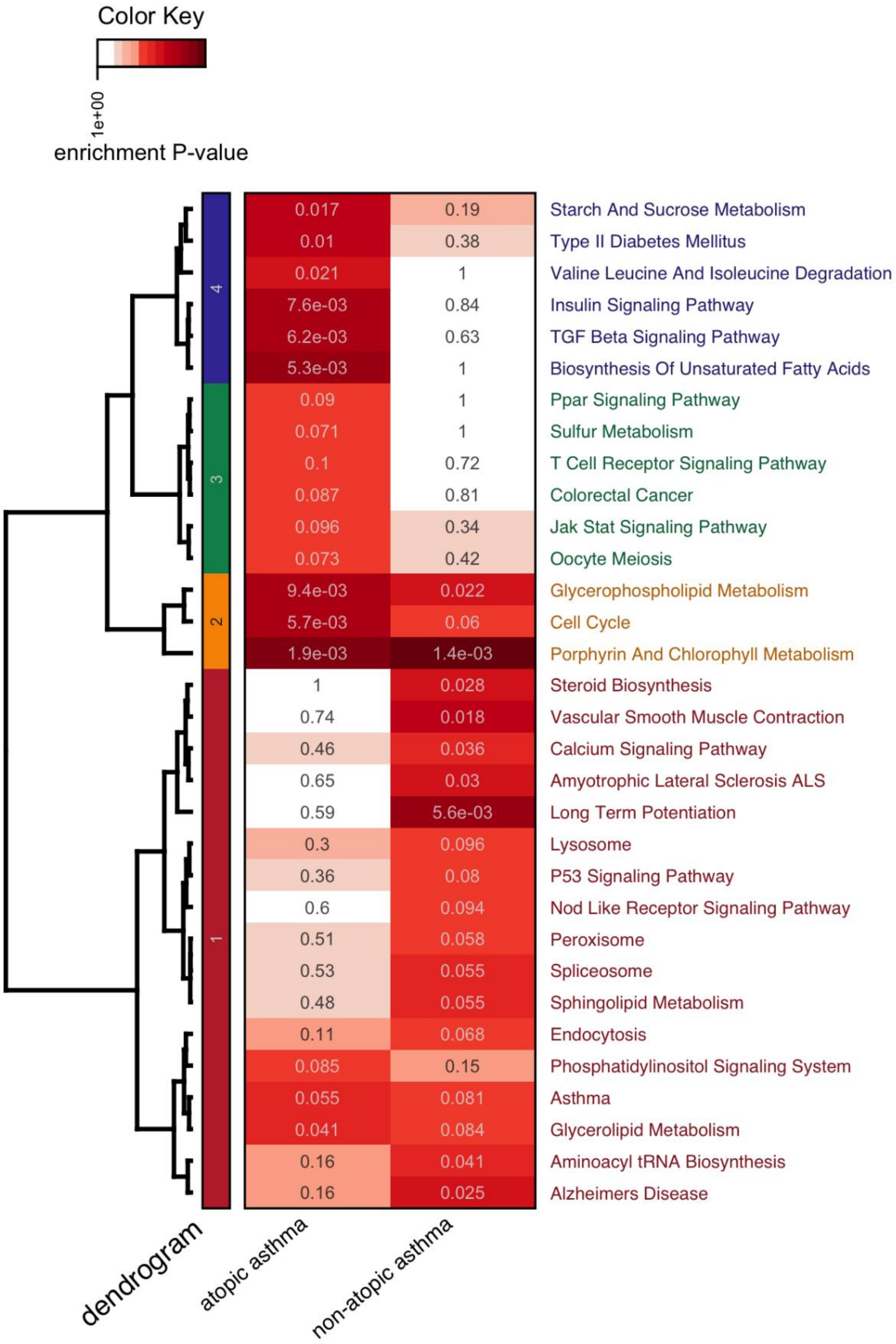


Figure E6. Heatmap of potentially biologically relevant pathways by significant genes and atopic and non-atopic asthma.

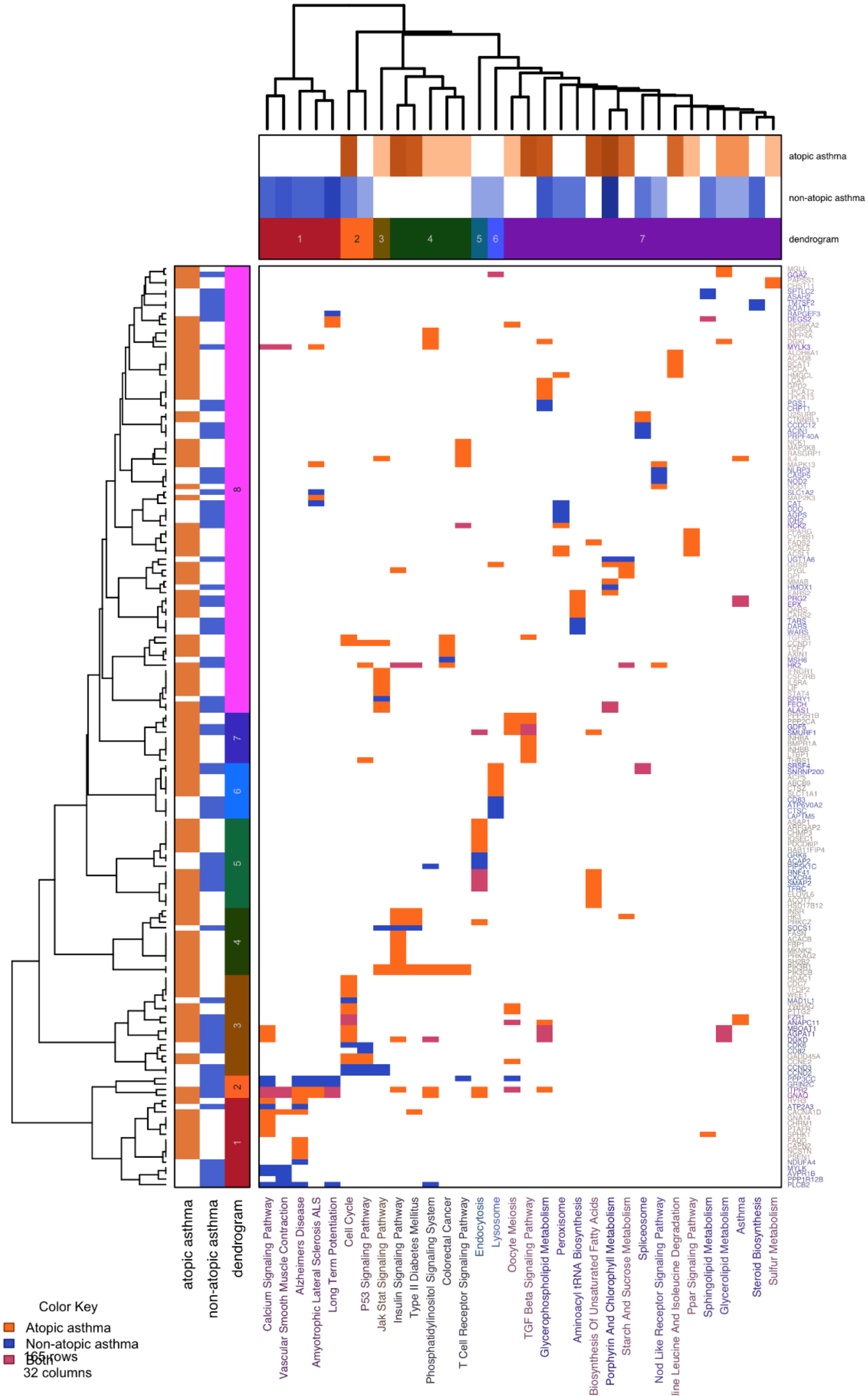
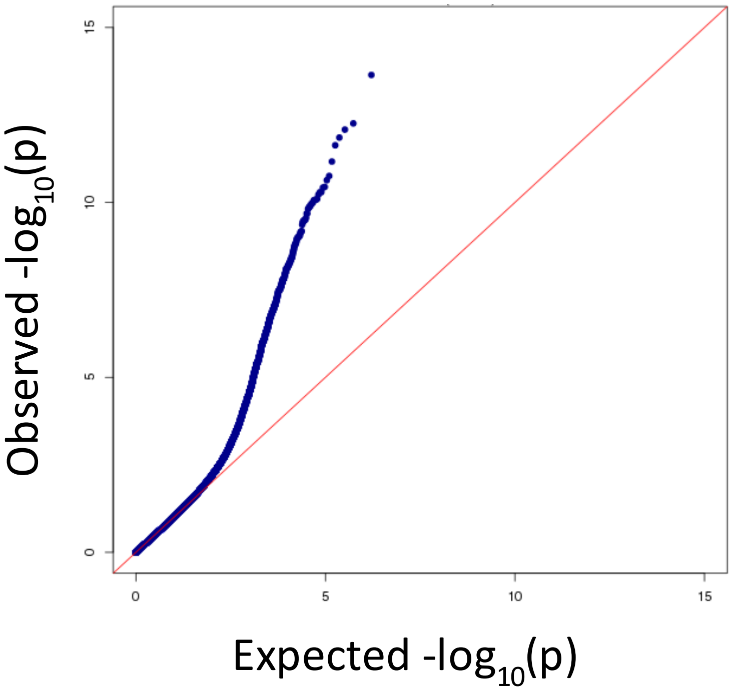


Figure E7. QQ-plot and volcano plot for the epigenome-wide analysis of atopic asthma.

(a) QQ-plot of the observed -log10 p-value versus the expected -log10 p-value in atopic asthma. Lambda = 0.98.



(b) Volcano plot of the observed -log10 p-value versus beta coefficient in atopic asthma. Points above the red line are FWER significant. Points above the blue line are FDR significant.

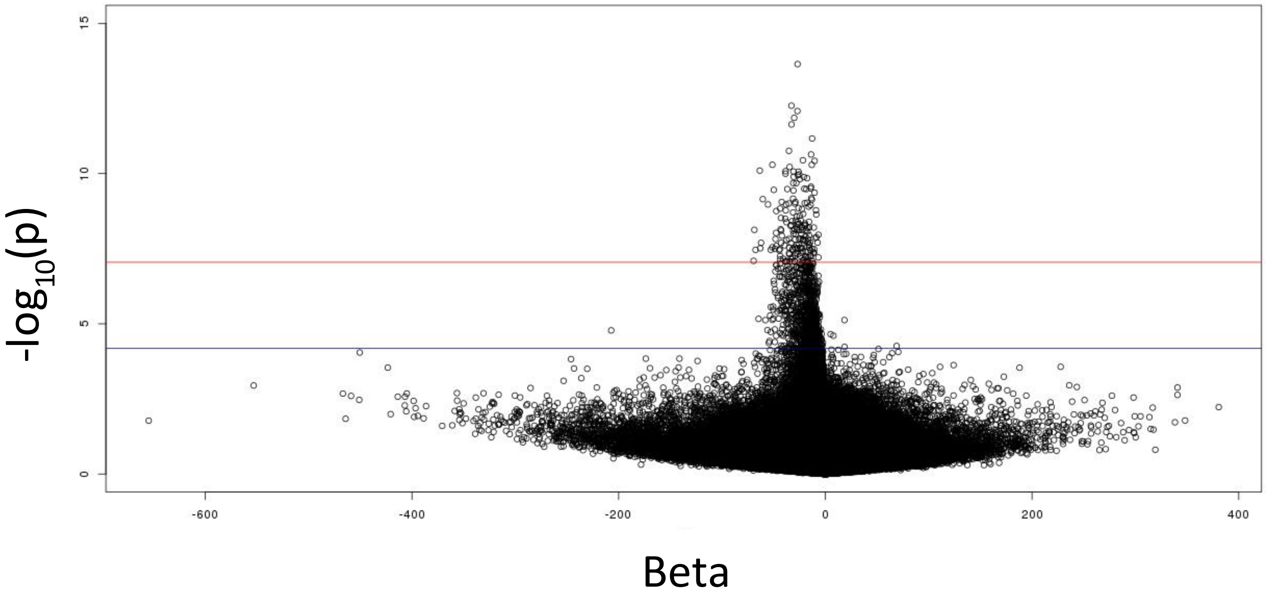
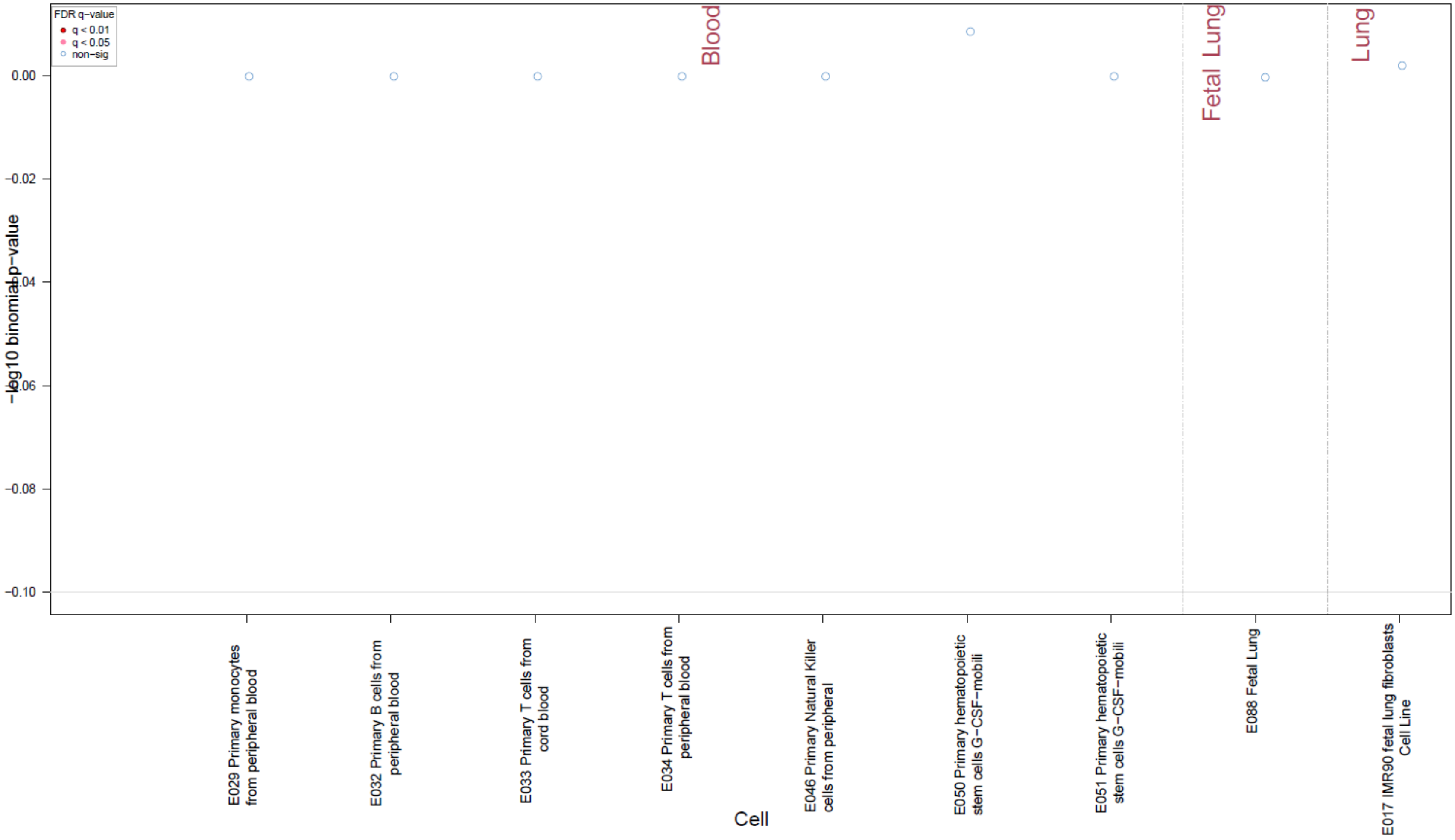
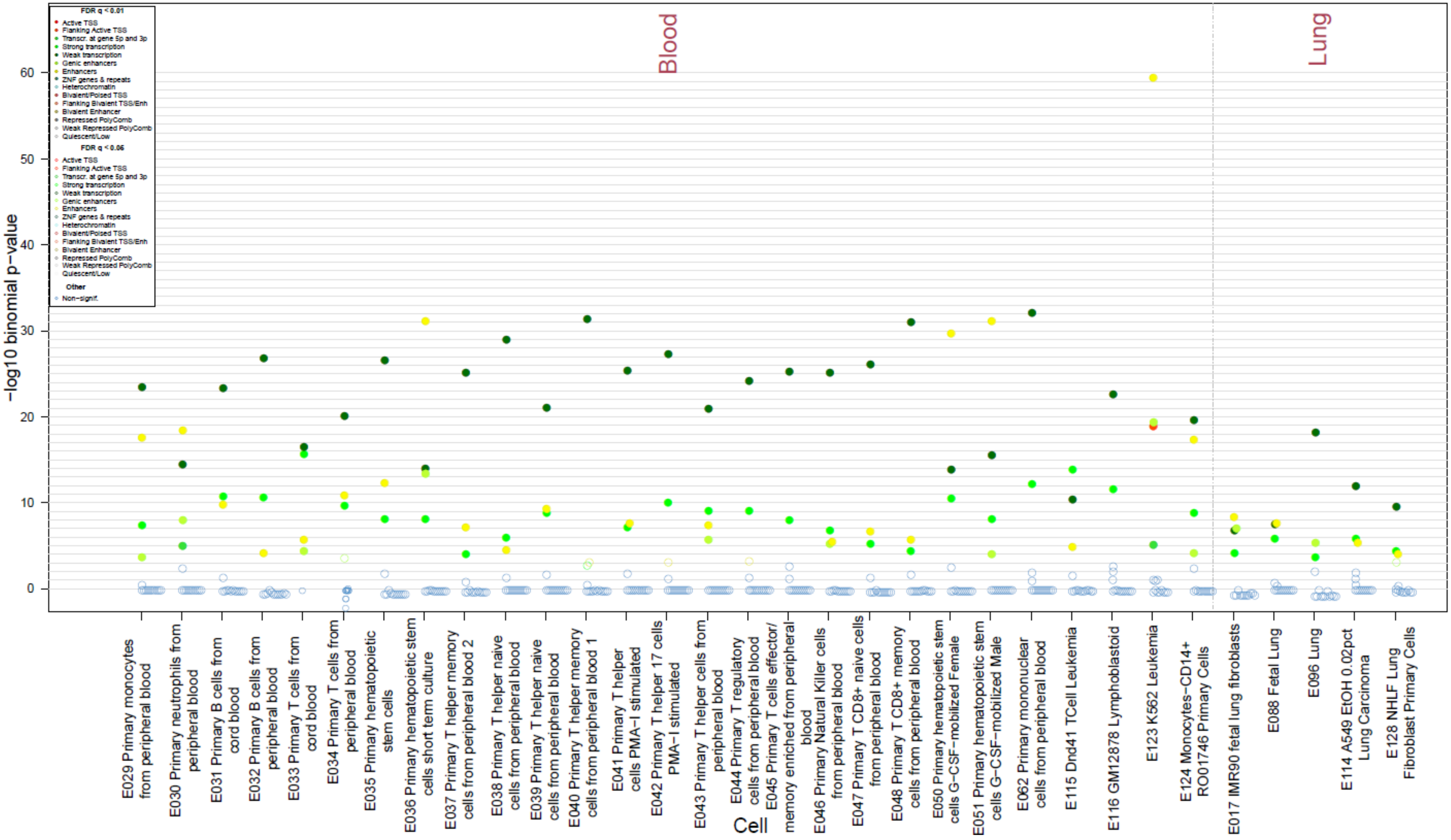


Figure E8. Tissue- and cell-specific enrichment pattern in CpG sites significantly associated (FDR<0.05) with atopic asthma, using eFORGE

(a) DNase I hypersensitive sites (probably transcription factor binding sites) enrichment in cell lines from the Roadmap Epigenomics consortium



(b) Chromatin state enrichment in cell lines from the Roadmap Epigenomics consortium



(c) Histone mark enrichment in cell lines from the Roadmap Epigenomics consortium

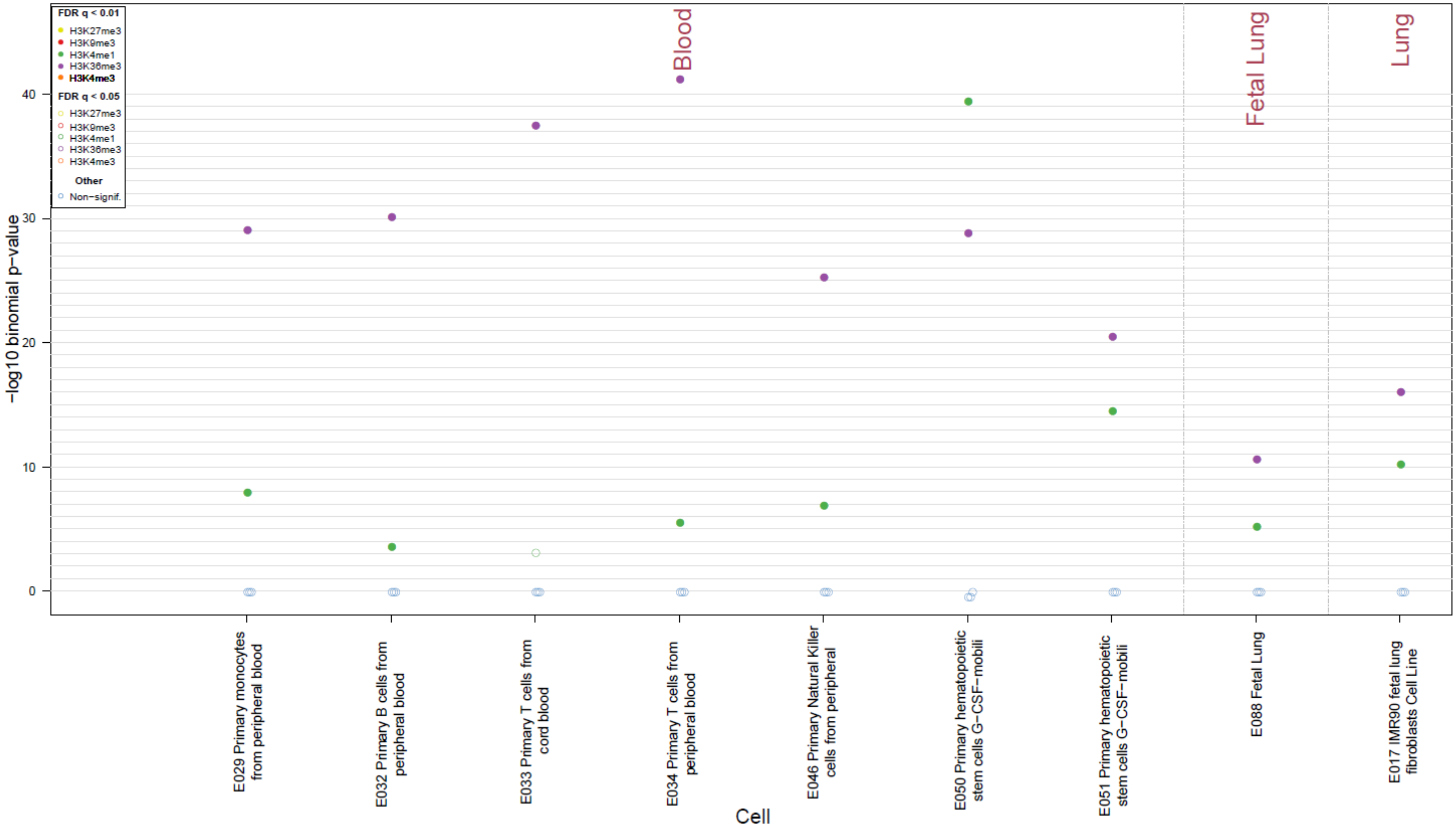


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Table E1. Differentially methylated CpG sites (FDR<0.05) in Non-atopic Asthma[1]

chromosome	position[2]	CpG	crossreactive[3]	N	Beta	SE	P	FDR	OR (CI)	Gene.Name	Distance.to.TSS
16	68804850	cg06085527		1829	-7.25	1.28	1.62E-08	7.76E-03	0.93 (0.91, 0.95)		28432
14	100610407	cg14084609		1830	-20.45	3.69	2.99E-08	7.76E-03	0.82 (0.76, 0.88)	DEGS2	15604
1	26091858	cg08028384		1829	-7.69	1.4	3.73E-08	7.76E-03	0.93 (0.9, 0.95)	SELENON	-34808
2	234608559	cg10180919		1829	-11.61	2.12	4.52E-08	7.76E-03	0.89 (0.85, 0.93)	UGT1A6	7048
10	22743835	cg15737719		1829	-27.91	5.11	4.75E-08	7.76E-03	0.76 (0.68, 0.84)	LOC100499489	-16978
1	6341287	cg09249800	1	1828	-7.56	1.4	7.16E-08	8.81E-03	0.93 (0.9, 0.95)	GPR153	-20253
14	55603874	cg23575099		1830	-20.51	3.83	8.46E-08	8.81E-03	0.81 (0.76, 0.88)	LGALS3	174
13	41631052	cg07908654		1830	-15.21	2.84	8.62E-08	8.81E-03	0.86 (0.81, 0.91)	WBP4	-4644
11	93456334	cg23338316		1828	-14.47	2.73	1.13E-07	1.03E-02	0.87 (0.82, 0.91)	SCARNA9	1655
3	152215571	cg07952576		1828	-2.73	0.52	1.87E-07	1.31E-02	0.97 (0.96, 0.98)	TMEM14EP	-156793
6	149450585	cg09639771	1	1830	-5.45	1.05	1.90E-07	1.31E-02	0.95 (0.93, 0.97)	TAB2	-88474
1	59543930	cg18581916		1830	-5.3	1.02	1.93E-07	1.31E-02	0.95 (0.93, 0.97)	LINC01358	57783
13	97846783	cg23933458		1829	-4.36	0.84	2.33E-07	1.46E-02	0.96 (0.94, 0.97)	LINC00456	-14908
17	56269767	cg01955639		1830	-12.67	2.48	3.18E-07	1.58E-02	0.88 (0.84, 0.92)	EPX	-317
16	21831372	cg07611887	1	1829	-12.75	2.5	3.26E-07	1.58E-02	0.88 (0.84, 0.92)	RRN3P1	-878
15	85186517	cg17194668		1830	-15.6	3.07	3.76E-07	1.58E-02	0.86 (0.81, 0.91)	WDR73	10959
7	150773709	cg06807926		1828	-4.11	0.81	3.91E-07	1.58E-02	0.96 (0.94, 0.98)	FASTK	4260
9	95800911	cg03234093		1829	-4.84	0.95	3.99E-07	1.58E-02	0.95 (0.94, 0.97)	SUSD3	-20058
4	38110810	cg07456972		1825	-21.11	4.17	4.13E-07	1.58E-02	0.81 (0.75, 0.88)	TBC1D1	-991
16	68804845	cg21468244		1827	-5.14	1.02	4.14E-07	1.58E-02	0.95 (0.93, 0.97)		28427
10	45495435	cg01614759		1829	-13.89	2.74	4.17E-07	1.58E-02	0.87 (0.82, 0.92)	ZNF22	-837
15	31505024	cg08884974		1829	-13.35	2.64	4.26E-07	1.58E-02	0.88 (0.83, 0.92)	LINC02352	-3199
7	36077237	cg24598141		1827	-3.54	0.7	4.59E-07	1.63E-02	0.97 (0.95, 0.98)	LOC101928618	-57682
14	68713369	cg01171954		1828	-6.09	1.21	5.04E-07	1.66E-02	0.94 (0.92, 0.96)	LOC100996664	382134
4	159969044	cg15834151		1830	-7.13	1.42	5.08E-07	1.66E-02	0.93 (0.91, 0.96)	C4orf45	-12712
2	74612222	cg17988187		1830	-11.85	2.37	5.62E-07	1.70E-02	0.89 (0.85, 0.93)	DCTN1-AS1	-622
1	6341230	cg21220721		1828	-5.71	1.14	5.62E-07	1.70E-02	0.94 (0.92, 0.97)	GPR153	-20196
15	81623226	cg25466522		1828	-19.68	3.94	6.02E-07	1.76E-02	0.82 (0.76, 0.89)	TMC3-AS1	6553
3	159847104	cg17991030		1829	-3.5	0.7	6.46E-07	1.82E-02	0.97 (0.95, 0.98)	IL12A-AS1	77774
3	14708144	cg15106081		1827	-27.35	5.52	7.20E-07	1.93E-02	0.76 (0.68, 0.85)	C3orf20	-8461
13	47161427	cg09131500		1830	-3.54	0.72	7.31E-07	1.93E-02	0.97 (0.95, 0.98)	LRCH1	34132
6	31680144	cg20133890		1822	-3.99	0.81	7.62E-07	1.95E-02	0.96 (0.95, 0.98)	LY6G6E	1697
3	16545999	cg08091497		1829	-2.85	0.58	7.96E-07	1.97E-02	0.97 (0.96, 0.98)	RFTN1	9222
8	126445744	cg26472183		1788	-29.7	6.04	8.91E-07	2.14E-02	0.74 (0.66, 0.84)	TRIB1	1294
15	41309253	cg21953058		1827	-2.73	0.56	9.22E-07	2.15E-02	0.97 (0.96, 0.98)	CHAC1	63907
12	104276789	cg11098795		1827	-4.19	0.86	1.04E-06	2.34E-02	0.96 (0.94, 0.98)	NT5DC3	-41815
17	25897247	cg06127160		1830	-8.5	1.74	1.06E-06	2.34E-02	0.92 (0.89, 0.95)	LGALS9	-60926
15	45028161	cg15022400		1830	-7.22	1.49	1.18E-06	2.54E-02	0.93 (0.9, 0.96)	TRIM69	-398
2	75089669	cg12077754		1830	-10.09	2.08	1.29E-06	2.59E-02	0.90 (0.87, 0.94)	HK2	29888
7	98722470	cg14769121		1828	-16.03	3.31	1.29E-06	2.59E-02	0.85 (0.8, 0.91)	SMURF1	19272
15	40093898	cg18852698		1829	-12.02	2.48	1.30E-06	2.59E-02	0.89 (0.84, 0.93)	LOC105370941	18792
1	47746081	cg13789639		1828	-16.23	3.37	1.49E-06	2.61E-02	0.85 (0.8, 0.91)	STIL	33737
3	15066613	cg16499536		1828	-21.2	4.41	1.49E-06	2.61E-02	0.81 (0.74, 0.88)	MRPS25	40230
6	15364953	cg15123849		1828	-4.9	1.02	1.50E-06	2.61E-02	0.95 (0.93, 0.97)	JARID2	115868
18	55250579	cg06592575		1829	-22.78	4.74	1.51E-06	2.61E-02	0.80 (0.73, 0.87)	FECH	3389
10	82251396	cg24699150		1826	-6.96	1.45	1.52E-06	2.61E-02	0.93 (0.91, 0.96)	TSPAN14	37359
15	52427175	cg05853552		1830	-16.24	3.38	1.56E-06	2.61E-02	0.85 (0.8, 0.91)	BCL2L10	-22204
17	6658198	cg14321269		1829	-9.76	2.03	1.58E-06	2.61E-02	0.91 (0.87, 0.94)		-957
11	82503066	cg17746899		1830	-5.7	1.19	1.64E-06	2.61E-02	0.94 (0.92, 0.97)	FAM181B	-58161
2	28564231	cg09468422		1830	-33.07	6.9	1.67E-06	2.61E-02	0.72 (0.63, 0.82)	LOC100505716	-30906
10	98408203	cg18498503		1828	-4.41	0.92	1.70E-06	2.61E-02	0.96 (0.94, 0.97)	TM9SF3	-61395
1	3282449	cg03337482		1830	-3.4	0.71	1.72E-06	2.61E-02	0.97 (0.95, 0.98)	ARHGEF16	-88697
11	104898835	cg10220988		1830	-2.69	0.56	1.77E-06	2.61E-02	0.97 (0.96, 0.98)	CASP5	-4941
1	12185845	cg22123711		1830	-5.9	1.23	1.77E-06	2.61E-02	0.94 (0.92, 0.97)	MIR7846	-41154
3	52223131	cg03881379		1830	-5.12	1.07	1.80E-06	2.61E-02	0.95 (0.93, 0.97)	ALAS1	-8967
12	125589647	cg26964704		1830	-16.06	3.37	1.85E-06	2.61E-02	0.85 (0.8, 0.91)	AACS	39735
19	5851504	cg09001777		1829	-4.82	1.01	1.87E-06	2.61E-02	0.95 (0.93, 0.97)	FUT3	-20
21	46496180	cg05516004		1830	-28.57	6	1.91E-06	2.61E-02	0.75 (0.67, 0.85)	ADARB1	1215
1	247581408	cg00448525		1828	-2.83	0.6	1.94E-06	2.61E-02	0.97 (0.96, 0.98)	NLRP3	58
9	136341915	cg13410614		1829	-3.11	0.65	1.96E-06	2.61E-02	0.97 (0.96, 0.98)	SLC2A6	2360
7	149543165	cg07970948		1827	-5.95	1.25	1.98E-06	2.61E-02	0.94 (0.92, 0.97)	ZNF862	7710

5	33205501	cg10291951		1830	-14.94	3.14	1.98E-06	2.61E-02	0.86 (0.81, 0.92)	TARS	-235300
16	81517665	cg05499338		1830	-12.37	2.6	2.01E-06	2.61E-02	0.88 (0.84, 0.93)	CMIP	-11288
14	23548087	cg14060758		1830	-3.89	0.82	2.08E-06	2.64E-02	0.96 (0.95, 0.98)	ACIN1	-7309
11	62269149	cg25465557		1829	-4.69	0.99	2.10E-06	2.64E-02	0.95 (0.94, 0.97)	AHNAK	44009
3	50650322	cg05186879		1825	-4.44	0.94	2.21E-06	2.72E-02	0.96 (0.94, 0.97)	MAPKAPK3	1030
11	18637603	cg09098714		1829	-3.16	0.67	2.27E-06	2.72E-02	0.97 (0.96, 0.98)	SPTY2D1OS	16253
22	17583333	cg15931859		1829	-4.04	0.85	2.27E-06	2.72E-02	0.96 (0.94, 0.98)	IL17RA	17485
4	3084890	cg03914277		1829	-6.34	1.34	2.39E-06	2.72E-02	0.94 (0.91, 0.96)	HTT	8483
10	99223744	cg12182708		1829	-3.07	0.65	2.50E-06	2.72E-02	0.97 (0.96, 0.98)	ZDHHC16	17857
1	44411569	cg02835421		1827	-6.59	1.4	2.57E-06	2.72E-02	0.94 (0.91, 0.96)	IPO13	-908
2	96965099	cg01923915		1830	-16.77	3.57	2.58E-06	2.72E-02	0.85 (0.79, 0.91)	SNRNP200	6207
13	39614547	cg06095753		1830	-3.04	0.65	2.61E-06	2.72E-02	0.97 (0.96, 0.98)	NHLRC3	2100
2	27473369	cg23635560		1830	-5.52	1.17	2.61E-06	2.72E-02	0.95 (0.92, 0.97)	SLC30A3	12590
5	55419860	cg24442367		1827	-3.27	0.7	2.64E-06	2.72E-02	0.97 (0.95, 0.98)	ANKRD55	109325
11	10525508	cg11199798		1827	-2.77	0.59	2.65E-06	2.72E-02	0.97 (0.96, 0.98)	MIR4485	4364
21	15964265	cg20090759		1828	-2.49	0.53	2.68E-06	2.72E-02	0.98 (0.97, 0.99)	SAMSN1	-8543
17	73641675	cg14934396		1829	-3.82	0.81	2.69E-06	2.72E-02	0.96 (0.95, 0.98)	SMIM6	-970
4	124165382	cg03326609		1828	-5.06	1.08	2.78E-06	2.72E-02	0.95 (0.93, 0.97)	SPRY1	-152567
16	89392503	cg09668022		1828	-4.53	0.97	2.82E-06	2.72E-02	0.96 (0.94, 0.97)	LOC100287036	4963
1	33227555	cg03125875		1829	-6.11	1.31	2.89E-06	2.72E-02	0.94 (0.92, 0.97)	KIAA1522	-3679
1	90354310	cg15791719		1830	-3.2	0.68	2.91E-06	2.72E-02	0.97 (0.96, 0.98)	LRRC8D	66831
1	156221551	cg13585073		1830	-6.06	1.3	2.95E-06	2.72E-02	0.94 (0.92, 0.97)	PAQR6	-3644
14	55583041	cg00336912		1830	-17.82	3.82	3.02E-06	2.72E-02	0.84 (0.78, 0.9)	LGALS3	-12893
1	236518104	cg17464069		1826	-3.76	0.8	3.02E-06	2.72E-02	0.96 (0.95, 0.98)	EDARADD	-39575
3	45687594	cg19967449	1	1830	-3.53	0.76	3.02E-06	2.72E-02	0.97 (0.95, 0.98)	LIMD1-AS1	42779
10	12371568	cg24317972		1827	-20.66	4.43	3.06E-06	2.72E-02	0.81 (0.75, 0.89)	CAMK1D	-19973
20	39704724	cg05026674		1830	-9.31	2	3.08E-06	2.72E-02	0.91 (0.88, 0.95)	TOP1	47267
1	29523841	cg16263722		1830	-12.11	2.6	3.08E-06	2.72E-02	0.89 (0.84, 0.93)	SRSF4	-15205
2	48031924	cg25117333		1830	-2.2	0.47	3.11E-06	2.72E-02	0.98 (0.97, 0.99)	MSH6	20831
17	4795410	cg11625476		1830	-23.4	5.02	3.12E-06	2.72E-02	0.79 (0.72, 0.87)	C17orf107	-7537
20	34018983	cg15532312		1826	-21.97	4.71	3.14E-06	2.72E-02	0.80 (0.73, 0.88)	GDF5	6986
19	1173241	cg08408668		1829	-4.14	0.89	3.16E-06	2.72E-02	0.96 (0.94, 0.98)	SBNO2	1040
1	206109139	cg13672080	1	1830	-27.09	5.81	3.19E-06	2.72E-02	0.76 (0.68, 0.85)	FAM72A	-28125
16	31210736	cg27646484		1829	-5.22	1.12	3.20E-06	2.72E-02	0.95 (0.93, 0.97)	PYCARD-AS1	-2469
17	2287284	cg17105176		1827	-17.05	3.66	3.22E-06	2.72E-02	0.84 (0.78, 0.91)	MNT	16973
6	20034134	cg10011040		1829	-14.24	3.06	3.25E-06	2.72E-02	0.87 (0.82, 0.92)	MBOAT1	178560
13	49175326	cg15338967		1826	-7.05	1.52	3.26E-06	2.72E-02	0.93 (0.9, 0.96)	LINC00462	-20290
1	41005302	cg16948651		1828	-3.59	0.77	3.33E-06	2.72E-02	0.96 (0.95, 0.98)	ZNF684	8070
4	89446409	cg03340036		1830	-2.11	0.45	3.39E-06	2.72E-02	0.98 (0.97, 0.99)	LOC101929134	1449
6	114016878	cg06052655		1829	-2.8	0.6	3.39E-06	2.72E-02	0.97 (0.96, 0.98)	LINC02541	-45602
1	31251307	cg21810778		1830	-4.05	0.87	3.39E-06	2.72E-02	0.96 (0.94, 0.98)	LAPTM5	-20625
22	45555611	cg21211039		1830	-3.97	0.86	3.45E-06	2.74E-02	0.96 (0.95, 0.98)	NUP50-DT	4050
17	56274480	cg08105265		1830	-13.3	2.87	3.58E-06	2.81E-02	0.88 (0.83, 0.93)	EPX	4396
7	134854291	cg08177041		1830	-3.35	0.72	3.67E-06	2.85E-02	0.97 (0.95, 0.98)	CYREN	-66
1	62209607	cg10704177		1829	-11.22	2.42	3.71E-06	2.85E-02	0.89 (0.85, 0.94)	PATJ	1459
19	3521502	cg00477633		1829	-18.72	4.05	3.76E-06	2.85E-02	0.83 (0.77, 0.9)	FZR1	-1451
11	71786271	cg00893849		1830	-7.15	1.55	3.80E-06	2.85E-02	0.93 (0.9, 0.96)	MIR3165	-2924
12	102090601	cg17430986		1827	-4.83	1.05	3.82E-06	2.85E-02	0.95 (0.93, 0.97)	CHPT1	-815
16	46776932	cg16064932		1829	-9.32	2.02	3.83E-06	2.85E-02	0.91 (0.88, 0.95)	MYLK3	5288
2	74375903	cg26529864		1803	-24.98	5.41	3.89E-06	2.85E-02	0.78 (0.7, 0.87)	BOLA3-AS1	796
17	34946860	cg23218859		1830	-2.29	0.5	3.91E-06	2.85E-02	0.98 (0.97, 0.99)	DHRS11	-1365
1	25059454	cg11966720		1827	-4.72	1.02	3.97E-06	2.86E-02	0.95 (0.94, 0.97)	CLIC4	-12305
16	27299412	cg23771052		1830	-2.99	0.65	4.05E-06	2.86E-02	0.97 (0.96, 0.98)	NSMCE1	-19300
11	63466987	cg07636225		1828	-15.55	3.38	4.08E-06	2.86E-02	0.86 (0.8, 0.91)	RTN3	18066
17	43472435	cg18410271		1829	-5.15	1.12	4.13E-06	2.86E-02	0.95 (0.93, 0.97)	ARHGAP27	30576
14	75069041	cg12258670		1830	-18.54	4.03	4.16E-06	2.86E-02	0.83 (0.77, 0.9)	LTBP2	9992
6	108910710	cg16775629		1829	-6	1.3	4.20E-06	2.86E-02	0.94 (0.92, 0.97)	FOXO3	28642
6	134956367	cg05920921		1826	-2.15	0.47	4.21E-06	2.86E-02	0.98 (0.97, 0.99)	LOC101928304	-95225
19	827739	cg14663914		1829	-3.93	0.85	4.25E-06	2.86E-02	0.96 (0.95, 0.98)	AZU1	-86
14	95991371	cg23661721		1829	-2.19	0.48	4.25E-06	2.86E-02	0.98 (0.97, 0.99)	SCARNA13	8594
1	66777579	cg24058805		1830	-18.94	4.12	4.27E-06	2.86E-02	0.83 (0.76, 0.9)	PDE4B	-20211
11	62164435	cg02974089		1824	-4.65	1.02	4.56E-06	3.01E-02	0.95 (0.94, 0.97)	SCGB1A1	-22071
15	52030746	cg07177867		1830	-11.28	2.46	4.56E-06	3.01E-02	0.89 (0.85, 0.94)	LYSMD2	-427
11	65239080	cg23299484		1829	-4.29	0.94	4.67E-06	3.03E-02	0.96 (0.94, 0.98)	MALAT1	-26128
4	109282481	cg25642315		1829	-4.61	1.01	4.67E-06	3.03E-02	0.95 (0.94, 0.97)	LEF1-AS1	189206
9	126497597	cg01745810		1830	-12.69	2.77	4.76E-06	3.04E-02	0.88 (0.83, 0.93)	DENND1A	194819
13	46927146	cg16872030		1830	-3.25	0.71	4.77E-06	3.04E-02	0.97 (0.95, 0.98)	RUBCNL	34488
19	8634583	cg23720822		1829	-36.63	8.01	4.81E-06	3.04E-02	0.69 (0.59, 0.81)	MYO1F	7747

17	56283901	cg11112605		1830	-11.19	2.45	4.87E-06	3.04E-02	0.89 (0.85, 0.94)	MKS1	12764
20	44465613	cg20337696		1829	-12.47	2.73	4.87E-06	3.04E-02	0.88 (0.84, 0.93)	SNX21	3144
1	161698821	cg06734380		1830	-2.62	0.57	4.92E-06	3.05E-02	0.97 (0.96, 0.99)	FCRLB	6379
16	67906415	cg09584899		1829	-6.85	1.5	5.08E-06	3.12E-02	0.93 (0.91, 0.96)	EDC4	-510
16	11709855	cg24517604		1829	-13.47	2.96	5.19E-06	3.17E-02	0.87 (0.82, 0.93)	LITAF	-28534
1	205225282	cg24407546		1829	-4.38	0.96	5.23E-06	3.17E-02	0.96 (0.94, 0.98)	TMCC2	-46
6	14758733	cg08470588		1829	-3.34	0.73	5.47E-06	3.27E-02	0.97 (0.95, 0.98)	LINC01108	-473049
16	29822365	cg05918326		1828	-15.42	3.39	5.49E-06	3.27E-02	0.86 (0.8, 0.92)	PRRT2	-1043
20	10534496	cg05232481		1829	-2.46	0.54	5.55E-06	3.29E-02	0.98 (0.97, 0.99)	MIR6870	95846
1	169525950	cg08653021		1829	-37.54	8.27	5.60E-06	3.29E-02	0.69 (0.58, 0.81)	F5	29818
17	62075151	cg03554335		1830	-3.95	0.87	5.70E-06	3.33E-02	0.96 (0.95, 0.98)	PRR29	-559
11	66276941	cg22406869	1	1829	-4.06	0.9	5.89E-06	3.39E-02	0.96 (0.94, 0.98)	BBS1	-1177
10	11799636	cg04765471		1828	-5.71	1.26	5.96E-06	3.39E-02	0.94 (0.92, 0.97)	ECHDC3	15281
15	52135487	cg12402318		1830	-17.54	3.87	5.97E-06	3.39E-02	0.84 (0.78, 0.91)	TMOD3	13663
8	103603330	cg17245251		1830	-20.36	4.5	5.98E-06	3.39E-02	0.82 (0.75, 0.89)	ODF1	39483
11	72983405	cg04099543		1829	-4.27	0.94	6.08E-06	3.39E-02	0.96 (0.94, 0.98)	P2RY6	219
6	139656042	cg02432022		1829	-2.04	0.45	6.10E-06	3.39E-02	0.98 (0.97, 0.99)	CITED2	39307
6	157516126	cg18812843		1830	-24.24	5.36	6.13E-06	3.39E-02	0.78 (0.71, 0.87)	TMEM242	229164
3	171858472	cg19980260		1830	-3.08	0.68	6.14E-06	3.39E-02	0.97 (0.96, 0.98)	FNDC3B	100129
2	137080313	cg00344572		1829	-3.6	0.8	6.39E-06	3.49E-02	0.96 (0.95, 0.98)	CXCR4	-204589
2	102151048	cg07014573		1813	-3.83	0.85	6.46E-06	3.49E-02	0.96 (0.95, 0.98)	RFX8	-59884
17	73305193	cg26978762		1829	-4.41	0.98	6.49E-06	3.49E-02	0.96 (0.94, 0.98)	SLC25A19	-19664
18	47815588	cg15053869		1830	-3.08	0.68	6.50E-06	3.49E-02	0.97 (0.96, 0.98)	CXXC1	-897
12	4312337	cg23428738		1830	-2.23	0.5	6.61E-06	3.53E-02	0.98 (0.97, 0.99)	CCND2	-70564
1	165826270	cg09277749		1814	-3.19	0.71	6.69E-06	3.54E-02	0.97 (0.96, 0.98)	UCK2	29539
16	75145843	cg05820066		1829	-2.95	0.66	6.73E-06	3.54E-02	0.97 (0.96, 0.98)	LDHD	4826
6	126375816	cg27341747		1827	-18.96	4.21	6.76E-06	3.54E-02	0.83 (0.76, 0.9)	MIR5695	67945
13	30307238	cg02480174		1823	-3.62	0.8	7.01E-06	3.58E-02	0.96 (0.95, 0.98)	LOC102723345	85409
17	27884154	cg13578165	1	1829	-3.53	0.79	7.04E-06	3.58E-02	0.97 (0.95, 0.98)	ABHD15	9887
18	22040005	cg14997111		1830	-2.26	0.5	7.08E-06	3.58E-02	0.98 (0.97, 0.99)	HRH4	-587
1	234841610	cg08427005		1830	-4.16	0.93	7.13E-06	3.58E-02	0.96 (0.94, 0.98)	LINC01132	-18178
6	43445012	cg14009632		1830	-3.33	0.74	7.14E-06	3.58E-02	0.97 (0.95, 0.98)	TJAP1	-248
3	13457267	cg04992150		1830	-4.61	1.03	7.19E-06	3.58E-02	0.95 (0.94, 0.97)	NUP210	4551
15	52028433	cg04804748		1830	-7.24	1.61	7.25E-06	3.58E-02	0.93 (0.9, 0.96)	LYSMD2	1886
3	72340184	cg21156580		1825	-8.49	1.89	7.25E-06	3.58E-02	0.92 (0.89, 0.95)	LINC00870	139777
12	52404134	cg14242936		1827	-3.61	0.8	7.26E-06	3.58E-02	0.96 (0.95, 0.98)	GRASP	-141
19	39742656	cg00717259		1826	-5.24	1.17	7.35E-06	3.58E-02	0.95 (0.93, 0.97)	IFNL4	-3161
17	74242643	cg13117318		1825	-23.51	5.24	7.37E-06	3.58E-02	0.79 (0.71, 0.88)	RNF157	-6252
12	105043367	cg04814136		1829	-2.34	0.52	7.38E-06	3.58E-02	0.98 (0.97, 0.99)	MIR3922	57957
10	6238080	cg20712856		1830	-3.52	0.79	7.42E-06	3.58E-02	0.97 (0.95, 0.98)	PFKFB3	-6759
8	125557455	cg04353863	1	1824	-2.31	0.52	7.45E-06	3.58E-02	0.98 (0.97, 0.99)	NDUFB9	6113
18	43641560	cg19322743		1827	-6.19	1.38	7.49E-06	3.58E-02	0.94 (0.91, 0.97)	PSTPIP2	10689
5	10560140	cg23856600		1830	-7.28	1.63	7.55E-06	3.59E-02	0.93 (0.9, 0.96)	ANKRD33B	-4294
5	74342697	cg14390854		1830	-10.88	2.43	7.63E-06	3.60E-02	0.90 (0.86, 0.94)	LINC01336	5770
6	36318881	cg04924375		1825	-5.68	1.27	7.72E-06	3.63E-02	0.94 (0.92, 0.97)	C6orf222	-14220
18	33553117	cg00663686		1828	-131.15	29.33	7.77E-06	3.63E-02	0.27 (0.15, 0.48)	C18orf21	530
20	62538983	cg17477733		1829	-3.46	0.77	7.81E-06	3.63E-02	0.97 (0.95, 0.98)	MIR941-1	-11818
5	140261930	cg22150440	1	1829	-2.16	0.48	7.87E-06	3.63E-02	0.98 (0.97, 0.99)	PCDHA13	77
11	34230092	cg21876760		1828	-3.56	0.8	7.92E-06	3.64E-02	0.97 (0.95, 0.98)	NAT10	102982
16	50748861	cg16834953		1826	-2.32	0.52	8.12E-06	3.71E-02	0.98 (0.97, 0.99)	NOD2	15601
17	55190679	cg13947225		1826	-10.68	2.4	8.21E-06	3.72E-02	0.90 (0.86, 0.94)	AKAP1	27545
3	52271724	cg12985905		1828	-3.67	0.82	8.30E-06	3.72E-02	0.96 (0.95, 0.98)	TWF2	1458
20	62372541	cg20626587		1828	-5.11	1.15	8.38E-06	3.72E-02	0.95 (0.93, 0.97)	SLC2A4RG	1331
12	123459749	cg00795535		1830	32.72	7.35	8.51E-06	3.72E-02	1.39 (1.2, 1.6)	OGFOD2	0
3	119498870	cg09113950		1828	-2.6	0.59	8.57E-06	3.72E-02	0.97 (0.96, 0.99)	NR1I2	-460
14	78105289	cg17753773		1820	-7.84	1.76	8.62E-06	3.72E-02	0.92 (0.89, 0.96)	SPTLC2	-22180
1	49317683	cg04976987		1819	-3.01	0.68	8.66E-06	3.72E-02	0.97 (0.96, 0.98)	BEND5	-75043
16	16195619	cg03392077		1829	-5.47	1.23	8.74E-06	3.72E-02	0.95 (0.92, 0.97)	ABCC6	121708
1	62437936	cg15672644		1830	-29.96	6.74	8.75E-06	3.72E-02	0.74 (0.65, 0.85)	MIR3116-1	-106521
3	46142638	cg16171189		1827	-2.28	0.51	8.78E-06	3.72E-02	0.98 (0.97, 0.99)	XCR1	-73660
9	117157871	cg14260530		1828	-5.39	1.21	8.80E-06	3.72E-02	0.95 (0.93, 0.97)	AKNA	-1187
7	17192401	cg17991808		1828	-5.63	1.27	8.84E-06	3.72E-02	0.95 (0.92, 0.97)	AHR	-145874
9	35755346	cg01499988		1830	-12.31	2.77	8.86E-06	3.72E-02	0.88 (0.84, 0.93)	MSMP	-1073
7	5710286	cg18401534		1830	-2.9	0.65	8.87E-06	3.72E-02	0.97 (0.96, 0.98)	RNF216-IT1	9805
16	57833579	cg26819611		1830	-7.16	1.61	8.94E-06	3.72E-02	0.93 (0.9, 0.96)	KIFC3	-1651
17	45754000	cg19791728		1829	-4.43	1	8.98E-06	3.72E-02	0.96 (0.94, 0.98)	TBKBP1	-18629
19	1948987	cg01014987		1829	-3.12	0.7	9.04E-06	3.72E-02	0.97 (0.96, 0.98)	CSNK1G2-AS1	5560
11	18299633	cg01247459		1829	-2.94	0.66	9.07E-06	3.72E-02	0.97 (0.96, 0.98)	SAA1	11862

7	128899554	cg03822873		1829	-7.28	1.64	9.08E-06	3.72E-02	0.93 (0.9, 0.96)	AHCYL2	34700
22	21921269	cg06850285		1830	-6.19	1.39	9.08E-06	3.72E-02	0.94 (0.91, 0.97)	UBE2L3	-566
2	28550757	cg05642098		1829	-19.12	4.31	9.21E-06	3.72E-02	0.83 (0.76, 0.9)	LOC100505716	-17432
3	125980095	cg16945415		1830	-3.9	0.88	9.22E-06	3.72E-02	0.96 (0.95, 0.98)	ALDH1L1	-80067
21	40467185	cg20833901		1827	-4.38	0.99	9.23E-06	3.72E-02	0.96 (0.94, 0.98)	PSMG1	88254
2	37007179	cg18197869		1829	-18.21	4.11	9.24E-06	3.72E-02	0.83 (0.77, 0.9)	VIT	83347
17	41172412	cg02190078		1830	-3.35	0.75	9.32E-06	3.73E-02	0.97 (0.95, 0.98)	VAT1	2046
2	178270267	cg07325407		1830	-4.25	0.96	9.39E-06	3.73E-02	0.96 (0.94, 0.98)	AGPS	12797
20	11758521	cg02844688		1830	-3.59	0.81	9.43E-06	3.73E-02	0.96 (0.95, 0.98)	LINC00687	92841
14	100610570	cg18550847		1830	-9.95	2.25	9.48E-06	3.73E-02	0.91 (0.87, 0.95)	DEGS2	15441
15	82234347	cg25228737		1830	-3.32	0.75	9.49E-06	3.73E-02	0.97 (0.95, 0.98)	MEX3B	104136
15	83732582	cg23499392		1830	-2.73	0.62	9.63E-06	3.77E-02	0.97 (0.96, 0.98)	MIR4515	-3504
17	81055722	cg13054523		1830	-11.56	2.61	9.77E-06	3.78E-02	0.89 (0.85, 0.94)	METRNL	18156
17	7863010	cg13905385		1830	-2.33	0.53	9.79E-06	3.78E-02	0.98 (0.97, 0.99)	CNTROB	27569
3	132831676	cg02274033		1830	-2.34	0.53	9.85E-06	3.78E-02	0.98 (0.97, 0.99)	TMEM108	-11988
2	220115026	cg02961280		1827	-8.98	2.03	9.86E-06	3.78E-02	0.91 (0.88, 0.95)		-2938
11	119486443	cg23575688		1828	-3.37	0.76	9.91E-06	3.78E-02	0.97 (0.95, 0.98)	NECTIN1	112991
5	86375384	cg01611175		1830	-4.07	0.92	1.00E-05	3.79E-02	0.96 (0.94, 0.98)	MIR4280	35386
7	99728544	cg07786412		1822	-4.5	1.02	1.02E-05	3.79E-02	0.96 (0.94, 0.98)	MBLAC1	4228
11	128562297	cg19296671		1813	-3.54	0.8	1.02E-05	3.79E-02	0.97 (0.95, 0.98)	FLI1	-1513
2	242294423	cg21450154		1829	-6.01	1.36	1.02E-05	3.79E-02	0.94 (0.92, 0.97)	FARP2	-1240
17	81040906	cg22503106		1814	-10.74	2.43	1.02E-05	3.79E-02	0.90 (0.86, 0.94)	METRNL	3340
2	136777134	cg06569561		1830	-2.68	0.61	1.03E-05	3.79E-02	0.97 (0.96, 0.99)	DARS	-33881
2	160896165	cg14169284		1829	-3.16	0.72	1.03E-05	3.79E-02	0.97 (0.96, 0.98)	PLA2R1	22960
3	151297861	cg15159044		1813	-3.26	0.74	1.03E-05	3.79E-02	0.97 (0.95, 0.98)	MIR5186	-14079
18	61557735	cg20875821		1830	-2.71	0.61	1.04E-05	3.81E-02	0.97 (0.96, 0.98)	SERPINB2	2797
1	156221285	cg05699320		1829	-4.6	1.04	1.05E-05	3.81E-02	0.96 (0.94, 0.97)	PAQR6	-3378
20	43590115	cg13792581		1828	-24.26	5.51	1.05E-05	3.81E-02	0.78 (0.7, 0.87)	TOMM34	-1002
12	113330801	cg04662947		1830	-9.66	2.19	1.06E-05	3.82E-02	0.91 (0.87, 0.95)	OAS1	-13780
2	102952956	cg17555715		1830	-9.37	2.13	1.07E-05	3.82E-02	0.91 (0.87, 0.95)	IL1RL1	-753
14	102667161	cg11968273		1820	-5.01	1.14	1.09E-05	3.82E-02	0.95 (0.93, 0.97)	MOK	39796
16	11328957	cg23386939		1828	-2.69	0.61	1.10E-05	3.82E-02	0.97 (0.96, 0.99)	SOCS1	21081
6	33255400	cg10966235		1798	-51.99	11.83	1.11E-05	3.82E-02	0.59 (0.47, 0.75)	MIR6873	-335
9	130859606	cg14612966		1827	-14.35	3.26	1.11E-05	3.82E-02	0.87 (0.81, 0.92)	SLC25A25	-1154
20	52238380	cg14613901		1829	-3.47	0.79	1.11E-05	3.82E-02	0.97 (0.95, 0.98)	LOC105372672	13488
19	827715	cg02147126		1829	-3.47	0.79	1.12E-05	3.82E-02	0.97 (0.95, 0.98)	AZU1	-110
11	44578801	cg14780449		1826	-4.48	1.02	1.12E-05	3.82E-02	0.96 (0.94, 0.98)	CD82	-8339
3	46996484	cg19114543		1830	-3.78	0.86	1.12E-05	3.82E-02	0.96 (0.95, 0.98)	CCDC12	21506
12	5851581	cg20378408		1830	-3.3	0.75	1.12E-05	3.82E-02	0.97 (0.95, 0.98)	ANO2	202843
11	64878218	cg26311703		1830	-5.58	1.27	1.12E-05	3.82E-02	0.95 (0.92, 0.97)	TM7SF2	-1107
19	827821	cg15610437		1829	-3.77	0.86	1.13E-05	3.82E-02	0.96 (0.95, 0.98)	AZU1	-4
12	106621388	cg19785826		1829	-5.85	1.33	1.13E-05	3.82E-02	0.94 (0.92, 0.97)	CKAP4	20324
3	107836286	cg05209272		1829	-3.39	0.77	1.14E-05	3.82E-02	0.97 (0.95, 0.98)	LINC01215	-7624
6	158564873	cg07137115		1829	-2.41	0.55	1.14E-05	3.82E-02	0.98 (0.97, 0.99)	SERAC1	24438
13	31295237	cg26272008		1830	-5.49	1.25	1.14E-05	3.82E-02	0.95 (0.92, 0.97)	ALOX5AP	7623
1	206226009	cg15677434		1830	-4.97	1.13	1.15E-05	3.82E-02	0.95 (0.93, 0.97)	AVPR1B	1727
19	40837284	cg21664942		1830	-13	2.96	1.15E-05	3.82E-02	0.88 (0.83, 0.93)	C19orf47	17031
14	39643445	cg02543556		1827	-15.09	3.44	1.16E-05	3.82E-02	0.86 (0.8, 0.92)	PNN	-941
11	2848310	cg21130221		1828	-3.53	0.8	1.16E-05	3.82E-02	0.97 (0.95, 0.98)	KCNQ1-AS1	34488
2	109204230	cg24936095		1827	-3.73	0.85	1.16E-05	3.82E-02	0.96 (0.95, 0.98)	LIMS1	-526
6	41996600	cg02024241		1830	-4.14	0.95	1.17E-05	3.82E-02	0.96 (0.94, 0.98)	CCND3	20031
17	64940745	cg07432111		1829	-3.24	0.74	1.17E-05	3.82E-02	0.97 (0.95, 0.98)	CACNG4	-20234
1	27060511	cg09849688		1829	-19.6	4.47	1.17E-05	3.82E-02	0.82 (0.75, 0.9)	ARID1A	37990
10	75677011	cg04084348		1828	-3.74	0.85	1.18E-05	3.83E-02	0.96 (0.95, 0.98)	C10orf55	5523
22	35773941	cg12165656		1818	-4.15	0.95	1.19E-05	3.83E-02	0.96 (0.94, 0.98)	HMOX1	-3118
7	29304984	cg15030712		1829	-4.2	0.96	1.19E-05	3.83E-02	0.96 (0.94, 0.98)	LOC102724484	-56399
11	65543903	cg25887955		1827	-3.71	0.85	1.19E-05	3.83E-02	0.96 (0.95, 0.98)	AP5B1	4158
1	55012926	cg11715991		1830	-3.72	0.85	1.20E-05	3.83E-02	0.96 (0.95, 0.98)	ACOT11	-880
12	56600222	cg17116500		1830	-16.51	3.77	1.20E-05	3.83E-02	0.85 (0.79, 0.91)	RNF41	15262
6	42716310	cg26069291		1828	-3.56	0.81	1.22E-05	3.87E-02	0.97 (0.95, 0.98)	BICRAL	1615
11	70165870	cg14569513		1830	-23.41	5.35	1.23E-05	3.87E-02	0.79 (0.71, 0.88)	MIR548K	35810
16	18591891	cg05676915	1	1829	-3.29	0.75	1.24E-05	3.87E-02	0.97 (0.95, 0.98)	ABCC6P1	9322
6	47012342	cg26667462		1828	-3.08	0.71	1.24E-05	3.87E-02	0.97 (0.96, 0.98)	ADGRF1	-2244
20	30793354	cg26744554		1829	-3.13	0.72	1.24E-05	3.87E-02	0.97 (0.96, 0.98)	PLAGL2	2191
6	110720501	cg00847453		1830	-3.58	0.82	1.25E-05	3.87E-02	0.96 (0.95, 0.98)	DDO	16251
16	68334619	cg04304036		1828	-2.47	0.57	1.25E-05	3.87E-02	0.98 (0.96, 0.99)	SLC7A6OS	10248
3	46269741	cg07519863		1829	-4.52	1.03	1.25E-05	3.87E-02	0.96 (0.94, 0.98)	CCR3	-14130
10	93998677	cg24238409		1828	-2.25	0.51	1.26E-05	3.89E-02	0.98 (0.97, 0.99)	CPEB3	4358

11	503283	cg05567377		1830	-3.28	0.75	1.27E-05	3.90E-02	0.97 (0.95, 0.98)	RNH1	3537
1	36352279	cg05873271		1826	-6.64	1.52	1.28E-05	3.91E-02	0.94 (0.91, 0.96)	AGO1	3484
22	47303273	cg12998731		1826	-4.16	0.95	1.29E-05	3.91E-02	0.96 (0.94, 0.98)	TBC1D22A-AS1	8664
14	100820846	cg13147461		1827	-7.81	1.79	1.30E-05	3.91E-02	0.92 (0.89, 0.96)	WARS	21080
6	13462275	cg23215701		1830	-3.42	0.78	1.31E-05	3.91E-02	0.97 (0.95, 0.98)	GFOD1	10019
10	81034149	cg13250178		1824	-3.78	0.87	1.32E-05	3.91E-02	0.96 (0.95, 0.98)	PPIF	-73070
3	47023603	cg15157945		1830	-3.82	0.88	1.33E-05	3.91E-02	0.96 (0.95, 0.98)	CCDC12	-104
12	56120970	cg15338098		1829	-3.14	0.72	1.33E-05	3.91E-02	0.97 (0.96, 0.98)	CD63	601
11	102327308	cg18118893		1826	-3.36	0.77	1.33E-05	3.91E-02	0.97 (0.95, 0.98)	TMEM123	-3534
16	50701499	cg00921350		1830	-4.92	1.13	1.34E-05	3.91E-02	0.95 (0.93, 0.97)	LOC101927272	-1266
7	129266958	cg02041484		1828	-2.34	0.54	1.34E-05	3.91E-02	0.98 (0.97, 0.99)	NRF1	-2960
2	136781306	cg04052546		1829	-2.16	0.5	1.34E-05	3.91E-02	0.98 (0.97, 0.99)	DARS	-38053
17	3706841	cg11902347		1830	-1.99	0.46	1.34E-05	3.91E-02	0.98 (0.97, 0.99)	ITGAE	-2305
3	194899199	cg12784307		1828	-2.94	0.68	1.34E-05	3.91E-02	0.97 (0.96, 0.98)	XXYLT1-AS2	30600
10	45900112	cg25136646		1829	-4.61	1.06	1.35E-05	3.91E-02	0.95 (0.94, 0.97)	ALOX5	30499
13	103509167	cg01555198		1829	-3.64	0.84	1.36E-05	3.91E-02	0.96 (0.95, 0.98)	ERCC5	10977
13	47274074	cg11015284		1830	-35.03	8.05	1.36E-05	3.91E-02	0.70 (0.6, 0.82)	ESD	97292
16	1715613	cg16710434		1829	-3.2	0.74	1.36E-05	3.91E-02	0.97 (0.95, 0.98)	JPT2	-12664
3	16491130	cg24171689		1830	-5.47	1.26	1.36E-05	3.91E-02	0.95 (0.92, 0.97)	RFTN1	64091
17	41172326	cg20334877		1830	-3.12	0.72	1.38E-05	3.94E-02	0.97 (0.96, 0.98)	VAT1	2132
3	171205319	cg20804243		1829	-10.71	2.46	1.38E-05	3.94E-02	0.90 (0.86, 0.94)	TNIK	-27123
9	35834279	cg15818306		1827	-3.8	0.87	1.39E-05	3.96E-02	0.96 (0.95, 0.98)	TMEM8B	4785
5	132577108	cg12828656		1829	-3.19	0.73	1.40E-05	3.96E-02	0.97 (0.95, 0.98)	MIR1289-2	186289
19	6067328	cg22748479		1830	-3.09	0.71	1.40E-05	3.96E-02	0.97 (0.96, 0.98)	RFX2	43335
12	124221672	cg26802802		1830	-5.01	1.15	1.42E-05	4.00E-02	0.95 (0.93, 0.97)	ATP6V0A2	24808
1	206257829	cg00136106		1829	-2.64	0.61	1.43E-05	4.01E-02	0.97 (0.96, 0.99)	RHEX	30817
5	76248749	cg16545105		1830	-3.72	0.86	1.44E-05	4.01E-02	0.96 (0.95, 0.98)	CRHBP	70
7	151011113	cg03381616		1829	-3.16	0.73	1.45E-05	4.01E-02	0.97 (0.96, 0.98)	NUB1	-27733
1	154293494	cg06181069		1830	-4.79	1.1	1.46E-05	4.01E-02	0.95 (0.93, 0.97)	AQP10	-97
4	40178593	cg09719750		1830	-10.46	2.41	1.46E-05	4.01E-02	0.90 (0.86, 0.94)	RHOH	-14037
21	36341223	cg27195131		1828	-5.08	1.17	1.46E-05	4.01E-02	0.95 (0.93, 0.97)	RUNX1-IT1	70499
1	159859638	cg04954249		1829	-3.95	0.91	1.48E-05	4.01E-02	0.96 (0.94, 0.98)	MIR4259	10230
13	33788523	cg15442959		1827	-6	1.39	1.48E-05	4.01E-02	0.94 (0.92, 0.97)	STARD13	-8337
18	13302729	cg02006119		1830	-4.4	1.02	1.50E-05	4.01E-02	0.96 (0.94, 0.98)	LDLRAD4	24626
1	181097559	cg06289919		1830	-2.53	0.58	1.50E-05	4.01E-02	0.98 (0.96, 0.99)	IER5	39922
12	56425944	cg19254378		1829	-2.38	0.55	1.50E-05	4.01E-02	0.98 (0.97, 0.99)	LOC105369781	-7070
5	176856845	cg19459094		1830	-10.65	2.46	1.50E-05	4.01E-02	0.90 (0.86, 0.94)	GRK6	3159
17	56355362	cg22331200		1830	-3.84	0.89	1.50E-05	4.01E-02	0.96 (0.95, 0.98)	MPO	2933
16	72088457	cg25008015	1	1830	-1.99	0.46	1.50E-05	4.01E-02	0.98 (0.97, 0.99)	HP	-33
4	71503456	cg07538578		1829	-3.04	0.7	1.51E-05	4.01E-02	0.97 (0.96, 0.98)	ENAM	8996
18	72548725	cg15034807		1827	-4.96	1.15	1.51E-05	4.01E-02	0.95 (0.93, 0.97)	ZNF407	205807
5	55444106	cg21124310		1825	-3.07	0.71	1.51E-05	4.01E-02	0.97 (0.96, 0.98)	ANKRD55	85079
11	34486306	cg00127788		1830	-6.13	1.42	1.53E-05	4.01E-02	0.94 (0.91, 0.97)	CAT	25835
10	119167795	cg01086527		1830	-14.9	3.45	1.53E-05	4.01E-02	0.86 (0.81, 0.92)	PDZD8	-32818
16	616212	cg04497992		1830	-6.78	1.57	1.54E-05	4.01E-02	0.93 (0.91, 0.96)	NHLRC4	-782
9	132600788	cg13953978		1830	-11.05	2.56	1.54E-05	4.01E-02	0.90 (0.85, 0.94)	USP20	3093
16	392274	cg14977769	1	1825	-2.01	0.47	1.54E-05	4.01E-02	0.98 (0.97, 0.99)	AXIN1	10401
9	125589222	cg19210893		1828	-10.48	2.42	1.54E-05	4.01E-02	0.90 (0.86, 0.94)	PDCL	1712
17	80190054	cg19284277		1829	-5.45	1.26	1.54E-05	4.01E-02	0.95 (0.92, 0.97)	SLC16A3	-53
7	92456994	cg20675152		1830	-3.17	0.73	1.55E-05	4.02E-02	0.97 (0.96, 0.98)	CDK6	6236
8	117059957	cg04962865		1827	23.81	5.51	1.56E-05	4.03E-02	1.27 (1.14, 1.41)	LINC00536	277339
17	70710636	cg10741887		1830	-2.18	0.5	1.57E-05	4.05E-02	0.98 (0.97, 0.99)	LINC00511	-74026
2	7027871	cg02589986		1830	-6.26	1.45	1.59E-05	4.05E-02	0.94 (0.91, 0.97)	RSAD2	10076
12	100866309	cg09313442		1829	-2.19	0.51	1.59E-05	4.05E-02	0.98 (0.97, 0.99)	NR1H4	-1241
14	91436403	cg11148876		1829	-3.75	0.87	1.59E-05	4.05E-02	0.96 (0.95, 0.98)	RPS6KA5	90074
2	86830411	cg25493477		1830	-14.99	3.47	1.59E-05	4.05E-02	0.86 (0.8, 0.92)	RNF103	20588
6	53791988	cg00273658		1827	-4.85	1.12	1.61E-05	4.05E-02	0.95 (0.93, 0.97)	LOC101927189	-2791
3	159532265	cg02342367		1827	8.32	1.93	1.61E-05	4.05E-02	1.09 (1.05, 1.13)	SCHIP1	-25384
17	27388119	cg11942358		1829	-4.13	0.96	1.61E-05	4.05E-02	0.96 (0.94, 0.98)	TIAF1	14507
1	172425816	cg17946525		1830	-12.87	2.99	1.62E-05	4.05E-02	0.88 (0.83, 0.93)	C1orf105	3784
16	88558237	cg05958985		1829	-7.73	1.79	1.63E-05	4.05E-02	0.93 (0.89, 0.96)	MIR5189	22912
1	23072310	cg19851810		1825	-27.28	6.33	1.63E-05	4.05E-02	0.76 (0.67, 0.86)	MIR4684	26301
14	72050329	cg02414559		1828	-2.36	0.55	1.64E-05	4.05E-02	0.98 (0.97, 0.99)	SIPA1L1	-2668
20	47013919	cg20845336	1	1824	-3.25	0.76	1.64E-05	4.05E-02	0.97 (0.95, 0.98)	LINC00494	25266
16	22009450	cg22747707		1826	-2.35	0.54	1.64E-05	4.05E-02	0.98 (0.97, 0.99)	PDZD9	2980
20	3788428	cg26350671		1828	-3.76	0.87	1.64E-05	4.05E-02	0.96 (0.95, 0.98)	LINC01730	-712
7	2116512	cg03116466		1828	-3.46	0.8	1.65E-05	4.05E-02	0.97 (0.95, 0.98)	MAD1L1	-136327
1	43880657	cg16572910		1830	-5.06	1.18	1.65E-05	4.05E-02	0.95 (0.93, 0.97)	SZT2	25102

11	10543456	cg07565042	1829	-7.04	1.64	1.66E-05	4.05E-02	0.93 (0.9, 0.96)	MTRNR2L8	-12734
20	4072430	cg09194810	1829	-14.82	3.44	1.66E-05	4.05E-02	0.86 (0.81, 0.92)	SMOX	-56995
17	33426885	cg08154963	1830	-2.98	0.69	1.67E-05	4.05E-02	0.97 (0.96, 0.98)	RFFL	-10538
6	32141591	cg09597192	1830	-19.99	4.64	1.67E-05	4.05E-02	0.82 (0.75, 0.9)	AGPAT1	2324
17	79851485	cg12380988	1830	-13.69	3.18	1.68E-05	4.06E-02	0.87 (0.82, 0.93)	ANAPC11	1683
1	179261588	cg20999663	1829	-4.68	1.09	1.69E-05	4.07E-02	0.95 (0.93, 0.97)	SOAT1	-1260
6	159477416	cg06445384	1828	-32.22	7.49	1.70E-05	4.07E-02	0.72 (0.63, 0.84)	TAGAP	-11233
16	57662165	cg24099727	1830	-7.07	1.64	1.70E-05	4.07E-02	0.93 (0.9, 0.96)	ADGRG1	28
22	19953712	cg18731680	1829	-2.71	0.63	1.72E-05	4.11E-02	0.97 (0.96, 0.99)	MIR4761	2437
18	2986172	cg06308882	1829	-2.58	0.6	1.74E-05	4.11E-02	0.97 (0.96, 0.99)	LPIN2	25772
17	4741523	cg06449385	1823	-14.48	3.37	1.74E-05	4.11E-02	0.87 (0.81, 0.92)	MINK1	4889
10	74069493	cg07828833	1829	-3.78	0.88	1.76E-05	4.11E-02	0.96 (0.95, 0.98)	DDIT4	35817
2	153440054	cg13047724	1829	-4.04	0.94	1.76E-05	4.11E-02	0.96 (0.94, 0.98)	PRPF40A	133920
7	22395972	cg09698506	1828	2.61	0.61	1.77E-05	4.11E-02	1.03 (1.01, 1.04)	RAPGEF5	560
20	31306896	cg15698538	1827	-2.51	0.59	1.78E-05	4.11E-02	0.98 (0.96, 0.99)	COMMD7	24917
2	236636037	cg16672147	1829	-3.27	0.76	1.78E-05	4.11E-02	0.97 (0.95, 0.98)	AGAP1-IT1	221643
9	102342539	cg23522962	1830	-3.3	0.77	1.78E-05	4.11E-02	0.97 (0.95, 0.98)	NAMA	-205001
11	3145609	cg01418188	1828	-3.44	0.8	1.79E-05	4.11E-02	0.97 (0.95, 0.98)	OSBPL5	40972
3	46131480	cg00005461	1829	-3.16	0.74	1.80E-05	4.11E-02	0.97 (0.95, 0.98)	XCR1	-62502
2	173940277	cg19579160	1830	-6.23	1.45	1.80E-05	4.11E-02	0.94 (0.91, 0.97)	MAP3K20	-287
12	125201422	cg21279677	1828	-3.22	0.75	1.80E-05	4.11E-02	0.97 (0.95, 0.98)	SCARB1	147096
5	135336741	cg22788906	1830	-2.84	0.66	1.80E-05	4.11E-02	0.97 (0.96, 0.98)	TGFBI	-27842
10	126040305	cg25715278	1830	-4.92	1.15	1.80E-05	4.11E-02	0.95 (0.93, 0.97)	OAT	67239
2	234246583	cg05724080	1828	-8.01	1.87	1.81E-05	4.11E-02	0.92 (0.89, 0.96)	DGKD	-16569
17	47411420	cg06005163	1827	-2.67	0.62	1.81E-05	4.11E-02	0.97 (0.96, 0.99)	LOC102724596	-27106
12	122884585	cg12315900	1829	-3.02	0.7	1.81E-05	4.11E-02	0.97 (0.96, 0.98)	CLIP1-AS1	4497
3	195782538	cg14352263	1830	-3.9	0.91	1.81E-05	4.11E-02	0.96 (0.94, 0.98)	TFRC	26422
11	44578725	cg06169291	1830	-11.18	2.61	1.82E-05	4.11E-02	0.89 (0.85, 0.94)	CD82	-8415
2	43440068	cg13254847	1829	-5.46	1.27	1.82E-05	4.11E-02	0.95 (0.92, 0.97)	ZFP36L2	13676
1	243634599	cg09912228	1830	-2.21	0.52	1.84E-05	4.13E-02	0.98 (0.97, 0.99)	MIR4677	125122
9	134206000	cg14031473	1827	-2.9	0.68	1.84E-05	4.13E-02	0.97 (0.96, 0.98)	PLPP7	40920
12	62644785	cg21061310	1830	-10.96	2.56	1.87E-05	4.19E-02	0.90 (0.85, 0.94)	USP15	-9335
21	37536817	cg07834490	1823	-3.88	0.91	1.88E-05	4.19E-02	0.96 (0.94, 0.98)	DOPEY2	-21
1	202545589	cg24376793	1828	-11.38	2.66	1.88E-05	4.19E-02	0.89 (0.85, 0.94)	PPP1R12B	36348
1	40861980	cg24395217	1828	-2.44	0.57	1.89E-05	4.20E-02	0.98 (0.97, 0.99)	SMAP2	-491
7	10747735	cg22954819	1826	-2.99	0.7	1.90E-05	4.21E-02	0.97 (0.96, 0.98)	NDUFA4	232077
17	3880229	cg10132304	1830	-4.14	0.97	1.91E-05	4.21E-02	0.96 (0.94, 0.98)	ATP2A3	-12472
11	111716149	cg15072057	1827	-2.75	0.64	1.91E-05	4.21E-02	0.97 (0.96, 0.99)	ALG9	25854
22	26873008	cg04701118	1830	-2.36	0.55	1.92E-05	4.22E-02	0.98 (0.97, 0.99)	HPS4	2638
1	66736380	cg00849335	1829	-1.86	0.44	1.93E-05	4.22E-02	0.98 (0.97, 0.99)	PDE4B	-61410
12	65021536	cg10426838	1828	-7.14	1.67	1.94E-05	4.22E-02	0.93 (0.9, 0.96)	MIR548Z	-5152
2	106360709	cg14131038	1830	-2.45	0.57	1.94E-05	4.22E-02	0.98 (0.96, 0.99)	NCK2	-810
6	7145478	cg20893838	1828	-3.27	0.77	1.94E-05	4.22E-02	0.97 (0.95, 0.98)	RREB1	37393
11	57157632	cg12819873	1829	-12.54	2.94	1.97E-05	4.25E-02	0.88 (0.83, 0.93)	PRG2	497
1	172790731	cg26873486	1823	-3.72	0.87	1.97E-05	4.25E-02	0.96 (0.95, 0.98)	FASLG	162584
15	90597964	cg22948672	1827	-4.35	1.02	1.98E-05	4.25E-02	0.96 (0.94, 0.98)	IDH2	45888
11	110318240	cg27623075	1827	-3.93	0.92	1.98E-05	4.25E-02	0.96 (0.94, 0.98)	FDX1	17580
5	137521998	cg08621659	1829	-2.28	0.54	1.99E-05	4.25E-02	0.98 (0.97, 0.99)	KIF20A	7582
17	72838819	cg12190341	1830	-4.42	1.04	1.99E-05	4.25E-02	0.96 (0.94, 0.98)	GRIN2C	17187
1	25015150	cg16257804	1827	-4.68	1.1	1.99E-05	4.25E-02	0.95 (0.93, 0.98)	SRRM1	45101
7	100224557	cg11751434	1828	33.45	7.84	2.00E-05	4.26E-02	1.40 (1.2, 1.63)	TFR2	6715
20	35422703	cg21045547	1830	-11.17	2.62	2.01E-05	4.27E-02	0.89 (0.85, 0.94)	DSN1	-20474
12	32669224	cg11175241	1830	-3.26	0.76	2.02E-05	4.27E-02	0.97 (0.95, 0.98)	FGD4	14248
4	140697658	cg13120180	1830	-4.18	0.98	2.03E-05	4.27E-02	0.96 (0.94, 0.98)	MGST2	110737
7	36301103	cg22940815	1830	-4.89	1.15	2.03E-05	4.27E-02	0.95 (0.93, 0.97)	KIAA0895	105678
16	69535862	cg16863862	1830	-2.78	0.65	2.04E-05	4.27E-02	0.97 (0.96, 0.99)	MIR1538	63908
17	66622811	cg16933977	1830	-48.18	11.31	2.04E-05	4.27E-02	0.62 (0.49, 0.77)	LINC01482	-1483
3	119069258	cg23938511	1825	-4.19	0.98	2.05E-05	4.28E-02	0.96 (0.94, 0.98)	ARHGAP31-AS1	-27652
19	14397583	cg05962003	1825	-4.76	1.12	2.08E-05	4.33E-02	0.95 (0.93, 0.97)	LINC01842	-46971
12	18964297	cg18481322	1825	-2.88	0.68	2.08E-05	4.33E-02	0.97 (0.96, 0.98)	CAPZA3	73253
16	23508779	cg21145387	1820	-3.68	0.87	2.09E-05	4.34E-02	0.96 (0.95, 0.98)	GGA2	13035
11	88078288	cg23579490	1829	-2.19	0.51	2.10E-05	4.34E-02	0.98 (0.97, 0.99)	CTSC	-7334
4	25789390	cg04349839	1830	-2.76	0.65	2.11E-05	4.34E-02	0.97 (0.96, 0.99)	SEL1L3	75262
3	72704361	cg27316598	1829	-2.92	0.69	2.11E-05	4.34E-02	0.97 (0.96, 0.98)	LOC105377162	9038
4	2275801	cg12674840	1827	-5.12	1.2	2.13E-05	4.36E-02	0.95 (0.93, 0.97)	MXD4	-12063
12	58210716	cg26620147	1829	-3.32	0.78	2.13E-05	4.36E-02	0.97 (0.95, 0.98)	AVIL	-865
15	101798908	cg03666966	1829	-20.85	4.91	2.16E-05	4.38E-02	0.81 (0.74, 0.89)	CHSY1	-6772
20	35504371	cg09241885	1829	-9.39	2.21	2.16E-05	4.38E-02	0.91 (0.87, 0.95)	TLDC2	-152

16	2176722	cg17546493	1	1829	-5.87	1.38	2.18E-05	4.38E-02	0.94 (0.92, 0.97)	MIR4516	-6397
12	48152204	cg21166775		1830	-3.67	0.86	2.18E-05	4.38E-02	0.96 (0.95, 0.98)	RAPGEF3	-24
12	27025721	cg24684972		1830	-2.5	0.59	2.18E-05	4.38E-02	0.98 (0.96, 0.99)	ITPR2	-39591
7	72277651	cg25322146		1830	-2.52	0.59	2.18E-05	4.38E-02	0.98 (0.96, 0.99)	TYW1B	21161
7	5523691	cg11554295		1828	-3.93	0.92	2.19E-05	4.38E-02	0.96 (0.94, 0.98)	MIR589	11856
2	65173818	cg12967579		1828	-23.25	5.48	2.19E-05	4.38E-02	0.79 (0.71, 0.88)	LINC02245	-14238
12	11877740	cg24279017		1830	-3.14	0.74	2.19E-05	4.38E-02	0.97 (0.96, 0.98)	ETV6	74953
12	6233657	cg27347104		1829	-5.92	1.39	2.19E-05	4.38E-02	0.94 (0.92, 0.97)	VWF	183
9	80602527	cg25348163		1829	-20.1	4.74	2.20E-05	4.39E-02	0.82 (0.75, 0.9)	GNAQ	43837
11	94336029	cg01887834		1829	-2.24	0.53	2.22E-05	4.40E-02	0.98 (0.97, 0.99)	PIWIL4	35556
6	159541084	cg11759930		1830	-2.42	0.57	2.22E-05	4.40E-02	0.98 (0.97, 0.99)	FNDC1	-49344
12	51322158	cg10487714		1824	-5.74	1.35	2.23E-05	4.40E-02	0.94 (0.92, 0.97)	METTL7A	3625
2	132291050	cg02575307	1	1830	-6.35	1.5	2.24E-05	4.40E-02	0.94 (0.91, 0.97)	CCDC74A	5644
12	27027924	cg10220104		1830	-19	4.48	2.24E-05	4.40E-02	0.83 (0.76, 0.9)	ITPR2	-41794
6	38061902	cg12604858		1828	-10.68	2.52	2.24E-05	4.40E-02	0.90 (0.86, 0.94)	ZFAND3	274596
1	167520305	cg17936236		1830	-5.15	1.21	2.25E-05	4.40E-02	0.95 (0.93, 0.97)	CREG1	2750
19	2594841	cg26569937		1824	-19.77	4.66	2.25E-05	4.40E-02	0.82 (0.75, 0.9)	MIR7850	-35871
14	75162215	cg06984345		1830	-9.02	2.13	2.27E-05	4.43E-02	0.91 (0.88, 0.95)	AREL1	17591
10	73946374	cg14261336		1827	-2.32	0.55	2.28E-05	4.44E-02	0.98 (0.97, 0.99)	ANAPC16	-29383
2	113380344	cg01469583		1828	-2.48	0.59	2.30E-05	4.45E-02	0.98 (0.96, 0.99)	FLJ42351	21412
7	30184490	cg22066020		1826	-5.93	1.4	2.30E-05	4.45E-02	0.94 (0.92, 0.97)	MTURN	9939
2	69430731	cg16381477		1830	-2.75	0.65	2.31E-05	4.45E-02	0.97 (0.96, 0.99)	MIR3126	99918
5	142504382	cg20350272		1823	-3.25	0.77	2.31E-05	4.45E-02	0.97 (0.95, 0.98)	ARHGAP26-IT1	-67682
7	1650459	cg03489907		1818	73.58	17.39	2.34E-05	4.49E-02	2.09 (1.48, 2.93)	TFAMP1	-3646
2	31302644	cg26382374		1828	-10.91	2.58	2.34E-05	4.49E-02	0.90 (0.85, 0.94)	GALNT14	49861
14	95615731	cg01901579		1830	-12.78	3.02	2.35E-05	4.49E-02	0.88 (0.83, 0.93)	DICER1	8027
16	88838368	cg26603047		1830	8.23	1.95	2.35E-05	4.49E-02	1.09 (1.05, 1.13)	PIEZO1	13259
1	31958245	cg04552418		1829	-2.17	0.51	2.36E-05	4.50E-02	0.98 (0.97, 0.99)	LINC01225	-13593
2	65100535	cg23057699		1830	-3.5	0.83	2.37E-05	4.50E-02	0.97 (0.95, 0.98)	LINC01800	-9771
11	62164451	cg11205545		1830	-13.88	3.29	2.38E-05	4.50E-02	0.87 (0.82, 0.93)	SCGB1A1	-22055
21	43723461	cg17051407		1828	-2.83	0.67	2.38E-05	4.50E-02	0.97 (0.96, 0.98)	TFF3	12244
17	9939929	cg15357334		1829	-3.41	0.81	2.40E-05	4.53E-02	0.97 (0.95, 0.98)	GAS7	134
3	123371420	cg07638500		1829	-4.41	1.04	2.41E-05	4.54E-02	0.96 (0.94, 0.98)	MYLK	-31967
16	2863919	cg10194884		1830	-4.54	1.08	2.42E-05	4.54E-02	0.96 (0.94, 0.98)	PRSS21	-3244
2	218113120	cg16299559		1827	-4.78	1.13	2.42E-05	4.54E-02	0.95 (0.93, 0.97)	DIRC3-AS1	-34335
7	30467544	cg27543741		1829	-3.29	0.78	2.44E-05	4.56E-02	0.97 (0.95, 0.98)	LINC01176	37044
13	47161752	cg01953813		1829	-3.43	0.81	2.46E-05	4.59E-02	0.97 (0.95, 0.98)	LRCH1	34457
3	71256044	cg09589331		1829	-2.26	0.54	2.48E-05	4.59E-02	0.98 (0.97, 0.99)	FOXP1	38271
11	109956144	cg11810303		1830	-5.31	1.26	2.48E-05	4.59E-02	0.95 (0.93, 0.97)	ZC3H12C	-7942
16	1988449	cg13728275		1830	-3.22	0.76	2.49E-05	4.59E-02	0.97 (0.95, 0.98)	MSRB1	4877
12	105683461	cg17998403		1829	-3.11	0.74	2.49E-05	4.59E-02	0.97 (0.96, 0.98)	KCCAT198	37333
7	101007603	cg27109461		1828	-4.44	1.05	2.49E-05	4.59E-02	0.96 (0.94, 0.98)	COL26A1	1503
11	75114223	cg05122026		1830	-6.44	1.53	2.51E-05	4.60E-02	0.94 (0.91, 0.97)	SNORD15B	-1241
1	6341327	cg11699125		1827	-4.94	1.17	2.51E-05	4.60E-02	0.95 (0.93, 0.97)	GPR153	-20293
15	48116584	cg24372191		1828	-3.72	0.88	2.51E-05	4.60E-02	0.96 (0.95, 0.98)	LINC01491	21848
11	65489884	cg08589455		1817	-13.06	3.1	2.52E-05	4.61E-02	0.88 (0.83, 0.93)	RNASEH2C	-1476
1	150967828	cg07479786		1829	-16.69	3.96	2.53E-05	4.62E-02	0.85 (0.78, 0.91)	MINDY1	11444
15	40601467	cg02240622		1830	-3.31	0.79	2.54E-05	4.62E-02	0.97 (0.95, 0.98)	PLCB2	-1294
17	4383882	cg12856590		1809	-3.64	0.86	2.55E-05	4.63E-02	0.96 (0.95, 0.98)	SPNS2	-18255
13	95923665	cg16464329		1824	-4.89	1.16	2.57E-05	4.66E-02	0.95 (0.93, 0.97)	ABCC4	30034
15	40633232	cg14287557		1829	-3.38	0.8	2.59E-05	4.68E-02	0.97 (0.95, 0.98)	CCDC9B	-65
3	45688760	cg00780501		1830	-2.7	0.64	2.62E-05	4.73E-02	0.97 (0.96, 0.99)	LIMD1-AS1	41613
17	49025289	cg13617202		1830	-4.91	1.17	2.63E-05	4.73E-02	0.95 (0.93, 0.97)	TOB1	-79951
22	27014116	cg02455383		1830	-3.62	0.86	2.66E-05	4.74E-02	0.96 (0.95, 0.98)	CRYBB1	-126
12	14999304	cg03634089		1830	-5.01	1.19	2.67E-05	4.74E-02	0.95 (0.93, 0.97)	ART4	-2892
17	518485	cg15186355		1830	-3.13	0.74	2.67E-05	4.74E-02	0.97 (0.96, 0.98)	VPS53	99610
2	65131556	cg17786894		1829	-2.8	0.67	2.68E-05	4.74E-02	0.97 (0.96, 0.99)	LINC02245	28024
1	35920054	cg23091723		1830	-2.72	0.65	2.68E-05	4.74E-02	0.97 (0.96, 0.99)	KIAA0319L	102982
22	43490246	cg11807649		1829	-3.87	0.92	2.69E-05	4.74E-02	0.96 (0.94, 0.98)	TTLL1	-4813
17	58155376	cg01248878		1830	-4.36	1.04	2.70E-05	4.74E-02	0.96 (0.94, 0.98)	HEATR6	915
5	173199528	cg05150185		1829	-3.14	0.75	2.70E-05	4.74E-02	0.97 (0.95, 0.98)	LINC01485	18416
2	28578984	cg09763039		1826	-4	0.95	2.70E-05	4.74E-02	0.96 (0.94, 0.98)	FOSL2	-36794
22	21123428	cg16617564		1827	-3.79	0.9	2.70E-05	4.74E-02	0.96 (0.95, 0.98)	SERPIND1	-4954
10	52127425	cg25372176		1828	-9.92	2.36	2.70E-05	4.74E-02	0.91 (0.86, 0.95)	ASAH2	-119056
2	192701514	cg15074047		1830	-5.23	1.25	2.71E-05	4.74E-02	0.95 (0.93, 0.97)	CAVIN2	10491
6	31582837	cg24211388		1829	-2.7	0.64	2.71E-05	4.74E-02	0.97 (0.96, 0.99)	AIF1	-148
8	22288224	cg18042586		1830	-2.81	0.67	2.73E-05	4.75E-02	0.97 (0.96, 0.99)	PPP3CC	-10258
10	74080727	cg24374476		1798	-4.35	1.04	2.73E-05	4.75E-02	0.96 (0.94, 0.98)	DNAJB12	34179

20	60709957	cg13197551	1830	-20.93	4.99	2.74E-05	4.75E-02	0.81 (0.74, 0.89)	PSMA7	8556
8	103990730	cg23511239	1826	-3.18	0.76	2.74E-05	4.75E-02	0.97 (0.95, 0.98)	ATP6V1C1	-42517
20	31067881	cg00280111	1827	-3.27	0.78	2.76E-05	4.75E-02	0.97 (0.95, 0.98)	NOL4L	3503
6	7167468	cg14919455	1830	-2.92	0.7	2.77E-05	4.75E-02	0.97 (0.96, 0.98)	RREB1	59383
1	117114916	cg21167563	1829	-4.27	1.02	2.77E-05	4.75E-02	0.96 (0.94, 0.98)	CD58	-1202
15	89020059	cg26025224	1830	-3.47	0.83	2.77E-05	4.75E-02	0.97 (0.95, 0.98)	MRPS11	9376
10	53005907	cg04905364	1830	-10.62	2.53	2.78E-05	4.75E-02	0.90 (0.86, 0.94)	MIR605	-53425
1	11901487	cg07532960	1830	-3.48	0.83	2.78E-05	4.75E-02	0.97 (0.95, 0.98)	NPPA-AS1	1112
10	30685417	cg17120616	1828	-3.5	0.84	2.78E-05	4.75E-02	0.97 (0.95, 0.98)	GOLGA2P6	-24582
12	50262986	cg04920032	1830	-3.9	0.93	2.80E-05	4.77E-02	0.96 (0.94, 0.98)	BCDIN3D	-26075
6	157948630	cg08794018	1829	5.13	1.23	2.80E-05	4.77E-02	1.05 (1.03, 1.08)	MIR3692	-1533
12	120528783	cg10336036	1829	-13.19	3.15	2.84E-05	4.81E-02	0.88 (0.82, 0.93)	RAB35	25859
10	135061670	cg12227660	1810	-5.82	1.39	2.85E-05	4.81E-02	0.94 (0.92, 0.97)	MIR202HG	-282
14	81883595	cg04316096	1829	-4.66	1.11	2.86E-05	4.81E-02	0.95 (0.93, 0.98)	STON2	9960
9	132044732	cg04395593	1829	-3.56	0.85	2.86E-05	4.81E-02	0.97 (0.95, 0.98)	LOC101929331	38
5	179200573	cg10113951	1830	-20.7	4.95	2.86E-05	4.81E-02	0.81 (0.74, 0.9)	LTC4S	-20412
11	35325601	cg14282386	1830	-2.7	0.64	2.86E-05	4.81E-02	0.97 (0.96, 0.99)	SLC1A2	115503
1	53834451	cg25567227	1830	-4.1	0.98	2.88E-05	4.83E-02	0.96 (0.94, 0.98)	LINC01771	40547
16	73019173	cg10298741	1830	-11.01	2.63	2.91E-05	4.86E-02	0.90 (0.85, 0.94)	ZFHX3	63100
3	194856863	cg18521725	1830	-4.01	0.96	2.91E-05	4.86E-02	0.96 (0.94, 0.98)	MIR3137	-1555
9	115147327	cg17141163	1802	-2.05	0.49	2.92E-05	4.86E-02	0.98 (0.97, 0.99)	HSDL2	5139
1	208040253	cg24315421	1830	-4.38	1.05	2.92E-05	4.86E-02	0.96 (0.94, 0.98)	MIR29B2CHG	-44206
6	125919706	cg04161328	1827	-2.64	0.63	2.93E-05	4.86E-02	0.97 (0.96, 0.99)	LINC02523	-75792
3	195106547	cg16032884	1829	-2.29	0.55	2.93E-05	4.86E-02	0.98 (0.97, 0.99)	ACAP2	57269
2	17042926	cg12997777	1824	-2.7	0.65	2.95E-05	4.86E-02	0.97 (0.96, 0.99)	FAM49A	-195793
11	107710989	cg18976159	1830	-3.1	0.74	2.95E-05	4.86E-02	0.97 (0.96, 0.98)	SLC35F2	18924
15	70492278	cg05219896	1830	-4.4	1.05	2.96E-05	4.86E-02	0.96 (0.94, 0.98)	TLE3	-102023
2	129200109	cg08790890	1830	-3.72	0.89	2.96E-05	4.86E-02	0.96 (0.95, 0.98)	HS6ST1	-123939
1	32410585	cg15535138	1830	-6.35	1.52	2.97E-05	4.86E-02	0.94 (0.91, 0.97)	PTP4A2	-6598
17	9862873	cg26996616	1830	-4.19	1	2.97E-05	4.86E-02	0.96 (0.94, 0.98)	GAS7	-108
16	75050761	cg11271052	1828	-2.11	0.51	2.99E-05	4.88E-02	0.98 (0.97, 0.99)	ZNRF1	17847
12	58210661	cg04046364	1830	-2.98	0.72	3.01E-05	4.88E-02	0.97 (0.96, 0.98)	AVIL	-810
17	76409193	cg18787963	1829	-3.92	0.94	3.01E-05	4.88E-02	0.96 (0.94, 0.98)	PGS1	34495
10	99168386	cg01541570	1829	-3.42	0.82	3.02E-05	4.88E-02	0.97 (0.95, 0.98)	RRP12	-7260
5	159743203	cg02441833	1828	-21.5	5.15	3.02E-05	4.88E-02	0.81 (0.73, 0.89)	CCNJL	-3597
1	220965460	cg25967384	1813	-1.96	0.47	3.02E-05	4.88E-02	0.98 (0.97, 0.99)	MARC1	5422
17	33885049	cg00397422	1830	-10.33	2.48	3.03E-05	4.88E-02	0.90 (0.86, 0.95)	SLFN14	60
5	106830005	cg14118059	1826	-36.92	8.85	3.03E-05	4.88E-02	0.69 (0.58, 0.82)	EFNA5	176590
19	3670246	cg17820448	1830	-4.38	1.05	3.04E-05	4.89E-02	0.96 (0.94, 0.98)	PIP5K1C	30230
1	37239629	cg19032328	1828	-2.8	0.67	3.05E-05	4.90E-02	0.97 (0.96, 0.99)	GRIK3	260214
8	11623360	cg14306688	1830	-3.16	0.76	3.07E-05	4.91E-02	0.97 (0.95, 0.98)	NEIL2	-3811
7	1914073	cg18650626	1816	-5.65	1.35	3.07E-05	4.91E-02	0.95 (0.92, 0.97)	MIR4655	-30185
1	3100956	cg23689722	1830	-2.58	0.62	3.08E-05	4.92E-02	0.97 (0.96, 0.99)	MIR4251	56418
12	15124659	cg00390941	1826	-22.75	5.46	3.10E-05	4.92E-02	0.80 (0.72, 0.89)	PDE6H	-1296
16	81552233	cg17577640	1830	-3.31	0.79	3.10E-05	4.92E-02	0.97 (0.95, 0.98)	MIR7854	-15273
6	33382557	cg02305757	1830	-4.55	1.09	3.11E-05	4.92E-02	0.96 (0.94, 0.98)	CUTA	3507
18	2980515	cg07616376	1829	-25.73	6.18	3.11E-05	4.92E-02	0.77 (0.68, 0.87)	LPIN2	31429
12	118577239	cg13346427	1828	-2.43	0.58	3.12E-05	4.92E-02	0.98 (0.96, 0.99)	PEBP1	3551
12	15091395	cg22106221	1828	-3.4	0.82	3.12E-05	4.92E-02	0.97 (0.95, 0.98)	ERP27	87
1	167198727	cg05121010	1829	-6.02	1.45	3.14E-05	4.94E-02	0.94 (0.92, 0.97)	POU2F1	8605
4	16871911	cg06646410	1830	-4.36	1.05	3.15E-05	4.95E-02	0.96 (0.94, 0.98)	LDB2	28520
19	39353395	cg17679548	1830	-4.1	0.98	3.16E-05	4.96E-02	0.96 (0.94, 0.98)	HNRNPL	-10417
1	182231752	cg12040931	1828	-4.07	0.98	3.19E-05	4.98E-02	0.96 (0.94, 0.98)	LINC01344	51443
11	2241568	cg13638867	1828	-4.6	1.1	3.19E-05	4.98E-02	0.96 (0.93, 0.98)	MIR4686	47276
16	75037584	cg16660617	1830	-31.26	7.52	3.20E-05	4.99E-02	0.73 (0.63, 0.85)	ZNRF1	4670

[1] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)

[2] Genome build GRCh37/hg19

[3] Removed from down stream analyses because Pidsley et al identified to be cross-reactive probe

Table E2. Summary of epigenome-wide association analyses, across different models

Original model (Atopy ≥0.70)[1]

	N	# FWER < 9E-08 CpGs	# FDR Sig CpGs	Lambda
Non-cases	1157	Ref	Ref	Ref
Atopy Only	185	0	0	0.97
Non-Atopic Asthma	673	8	524	1.14
Atopic Asthma	271	181	1,086	0.98

Include asthma polygenetic risk score[1]

	N	# FWER < 9E-08 CpGs	# FDR Sig CpGs	Lambda	Corr$_{\text{beta values}}$ (P)[2]
Non-cases	1157	Ref	Ref	Ref	-
Atopy Only	185	-	-	-	-
Non-Atopic Asthma	673	4	66	1.14	0.99 (<0.001)
Atopic Asthma	271	150	954	0.96	0.98 (<0.001)

Include current farming[1]

	N	# FWER < 9E-08 CpGs	# FDR Sig CpGs	Lambda	Corr$_{\text{beta values}}$ (P)[2]
Non-cases	1157	Ref	Ref	Ref	-
Atopy Only	185	-	-	-	-
Non-Atopic Asthma	673	8	520	1.14	1.0(<0.001)
Atopic Asthma	271	174	1,068	0.97	1.0(<0.001)

Using Houseman's 7 estimated cell types[3]

	N	# FWER < 9E-08 CpGs	# FDR Sig CpGs	Lambda	Corr$_{\text{beta values}}$ (P)[2]
Non-cases	1157	Ref	Ref	Ref	-
Atopy Only	185	-	-	-	0.98 (<0.001)
Non-Atopic Asthma	673	127	2243	1.66	0.86 (<0.001)
Atopic Asthma	271	407	2947	1.21	0.92 (<0.001)

Atopy cutoff ≥0.35[1]

	N	# FWER < 9E-08 CpGs	# FDR Sig CpGs	Lambda	Corr$_{\text{beta values}}$ (P)[2]
Non-cases	814	Ref	Ref	Ref	-
Atopy Only	528	0	0	0.91	0.47 (<0.001)
Non-Atopic Asthma	483	1	9	1.15	0.80 (<0.001)
Atopic Asthma	461	124	847	1.07	0.69 (<0.001)

[1] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)

[2] Spearman correlation comparing the p-values from the specified model to the original model. P-value provided in parentheses.

[3] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and 7 cell types (monocyte, NK, B cell, CD4+, CD8+, neutrophil, eosinophil)

Table E3. Among non-atopic asthma, 17 CpG sites are significantly (FDR<0.05) different between uncontrolled versus controlled asthma[1]

chromosome	position[2]	CpG	N	Beta	SE	P	FDR	OR (CI)	Gene
chr18	13302729	cg02006119	436	-7.42121	2.280738	1.14E-03	4.21E-02	0.93 (0.89, 0.97)	LDLRAD4
chr9	95800911	cg03234093	435	-8.25712	2.399795	5.80E-04	3.38E-02	0.92 (0.88, 0.97)	SUSD3
chr1	159859638	cg04954249	436	-7.64356	2.166053	4.17E-04	3.38E-02	0.93 (0.89, 0.97)	MIR4259
chr12	104276789	cg11098795	436	-8.92065	2.211467	5.49E-05	2.88E-02	0.91 (0.88, 0.96)	NT5DC3
chr7	5523691	cg11554295	436	-6.77194	2.091586	1.20E-03	4.21E-02	0.93 (0.9, 0.97)	MIR589
chr17	74242643	cg13117318	435	-46.7934	14.72375	1.48E-03	4.57E-02	0.63 (0.47, 0.84)	RNF157
chr1	32410585	cg15535138	436	-13.2424	3.930185	7.53E-04	3.59E-02	0.88 (0.81, 0.95)	PTP4A2
chr20	31306896	cg15698538	435	-4.62007	1.340293	5.67E-04	3.38E-02	0.95 (0.93, 0.98)	COMMD7
chr1	25015150	cg16257804	436	-9.36477	2.705173	5.37E-04	3.38E-02	0.91 (0.86, 0.96)	SRRM1
chr5	176856845	cg19459094	436	-23.7124	7.000783	7.06E-04	3.59E-02	0.79 (0.69, 0.9)	GRK6
chr6	7145478	cg20893838	435	-6.00748	1.829473	1.02E-03	4.13E-02	0.94 (0.91, 0.98)	RREB1
chr12	62644785	cg21061310	436	-18.7677	5.269891	3.69E-04	3.38E-02	0.83 (0.75, 0.92)	USP15
chr8	103990730	cg23511239	435	-5.99985	1.796146	8.37E-04	3.65E-02	0.94 (0.91, 0.98)	ATP6V1C1
chr10	126040305	cg25715278	436	-9.13546	2.52237	2.93E-04	3.38E-02	0.91 (0.87, 0.96)	OAT
chr15	89020059	cg26025224	436	-7.27187	1.961574	2.10E-04	3.38E-02	0.93 (0.89, 0.97)	MRPS11
chr11	64878218	cg26311703	436	-10.548	3.276963	1.29E-03	4.22E-02	0.90 (0.84, 0.96)	TM7SF2
chr16	57833579	cg26819611	436	-15.4077	4.027296	1.30E-04	3.38E-02	0.86 (0.79, 0.93)	KIFC3

[1] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)

[2] Genome build GRCh37/hg19

Table E4. Enrichment Analyses of Four Genomic Features

(A) Non-atopic asthma

Feature	Enrichment	P_Value
CpG Islands	-2.53	5.40E-27
CpG Island Shores	-0.56	4.43E-04
Promoters	-1.48	1.74E-18
TF Binding	0.35	1.36E-13

(B) Atopic asthma

Feature	Enrichment	P_Value
CpG Islands	-3.10	4.29E-66
CpG Island Shores	-0.52	1.26E-06
Promoters	-1.78	1.00E-46
TF Binding	0.10	5.72E-03

Table E5. Enriched Transcription Factor Motifs Using eFORGE TF

Transcription Factor	Database	q-value
Non-atopic asthma		
V_FOXO3A_Q1	TRANSFAC	1.47E-02
V_AIRE_01	TRANSFAC	4.70E-02
Atopic asthma		
Gata3_primary	UniProbe	6.95E-05
MA0140.1-Tal1::Gata1	JASPAR	6.95E-05
MA0029.1-Evi1	JASPAR	2.13E-04
V_GATA2_02	TRANSFAC	1.54E-03
V_IPF1_02	TRANSFAC	1.23E-02
V_ATF_01	TRANSFAC	1.32E-02
V_EVI1_05	TRANSFAC	1.32E-02
V_EVI1_03	TRANSFAC	1.61E-02

Table E8. Genes Associated with Asthma in Previous EWAS or GWAS

	Xu_2018	Forno_2018_top30	Kogan_2019	Lund_2018	Zhang_2019	Everson_2019	Popovic	Wang
PMID	29496485	30584054	30669148	29729188	30762239	26292806	30681197	31187518
	LOC339524	PDE6A	LHX6	PTGDS	OR2B11	HK1	PM20D1	IL12B
	SERPINC1	METTL1	SCARNA18	SMAD3	DEFB104BDEFB104A	APTX		MYOD1
	PROK1	CES4A	STC1	ABLIM1	LAMA5	LITAF		OAZ3
	MXD3	GJA4	LOC101928523	CYTIP	ATP9B			CORT
	AMD1	SPP2		ELN	TET1			CENPS
	RAPGEF1	CDHR3		LINC00676				HTRA3
	MED27	GRK5		IRS2				ANKRD13A
	STX3	FBXL7		TBX20				C1QL1
	MRPL16	LINC00704		SRD5A2				DDAH1
	CHTF8	ANKRD31		DPEP1				SH3BGRL2
	TRIB2	C22orf31		FOXK2				NEUROGI
	LPIN1	SUCNR1		ZNF561				ADARB2
	CHTF8	NTRK1		RABGEF1				MAP9
	CIRH1A	PLEC		COX19				PSMCI
	PPP1R26	PCSK6		ADAP1				MRPL9
	OLFM1	CAPN14		ADAM6				
	SLC25A25	SYNPO		GRAMD1B				
	PTGES2	TSHR		CR936796				
	VPS37B	NCF2		HLA-G				
	ABCB9	PCSK6		HLA-H				
	DICER1	NUP98		DDO				
	CLMN	BANF2		METTL24				
	MSI2	EFNA5		PLAGL1				
	AKAP1	C15orf54		PRDM16				
		LRRFIP1		GNG7				
		ZPLD1		ZC3HAV1				
		CDH26		ABCA13				
		DUOX1		WDR27				
		ADCK1		ADRBK1				
				PARD6G-AS1				
				E2F3				
				LOC102723709				
				LINC00955				
				CWH43				

	Asthma Genes Identified In Literature By Reese et al.	Reese_2019	Reese_2019_DMR	Cardenas_Asthma_UCSC	Cardenas_OtherNearestGene_Asthma	Cardenas_DMR_AtopicAsthma	Cardenas_AtopicAsthma_UCSC	Cardenas_OtherNearestGene_AtopicAsthma	GWAS Catalog
PMID	30579849	30579849	30579849	31300640	31300640	31300640	31300640	31300640	
	ADAM17	PRKCZ	HSPA7	NADK	SEPT2	EPX	NADK	NADK	MARCH11
	ADRB2	ACOT7	IRF6	PRKCZ	SEPT7	LINC01140	MEGF6	MEGF6	SEPT7
	AHR	SLC25A33	PRKCZ	LOC388588	ABHD17C	RASSF2	LOC388588	SMIM1	A4GALT
	AK5	CATSPER4	LINC01140	ACOT7	ACCS	GABBR1	ACOT7	ACOT7	AAGAB
	AKAP6	NR0B2	KIF5C	ZBTB48	ACKR3	ZBTB48	ZBTB48	ZBTB48	ABCB5
	ALOX12	MECR	LPIN1	MAN1C1	ACOT7	RGS3	RERE	RERE	ABI3BP
	ARG1	ERMAP	PCYT1A	ARID1A	ADA	COL15A1	SLC25A33	H6PD	ACMSD
	ARG2	DMAP1	IL5RA	NR0B2	ADGRL1		C1orf127	SPSB1	ACO1
	ARMC10	ERI3	EGFLAM	KIAA1522	ADORA3		TMEM51	SLC25A33	ACTL9
	BRD2	NFIA	IL4	FOXJ3	ANAPC1		IFFO2	C1orf127	ACVR2A
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	CDK2	ADCY3	PPP1R26-AS1	ADORA3	C10orf71		GNL2	AHDC1	AKAP6
	CHI3L1	LOC100189589	SLC25A25	TMIGD3	C1orf105		CAP1	PTAFR	ALDH1A2
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	COL12A1	TMEM131	LINC01488	C1orf204	CACNA1S		FOXJ3	EPB41	ALLC
	CRB1	STEAP3	MS4A2	NOS1AP	CACUL1		CCDC30	MECR	ALPK2
	CRNN	RALB	PDE6H	C1orf105	CCDC127		ERMAP	KIAA0319L	ANAPC1
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	FCER2	FOXP1	RPTOR	LOC285033	CHGA		KANK4	ST3GAL3	ARHGAP21
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	STK38	PAPSS1	HERPUD1
	TREM2	EXOSC9	HGC18
	NCR2	SPATA5	HGMA1
	TRERF1	MAML3	HIST3H2A
	TNFRSF21	ZNF827	HLA
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	SYTL3	PTGER4	HLA-DRB1
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	EZR	PIK3R1	HLA-DRB6
	EZR-AS1	ARHGEF28	HLA-DRB9
	EZR	GCNT4	HNF1A
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	RAPGEF5	FAM151B	HRNR
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	JAZF1-AS1	LINC01554	HSPA9P
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	CCM2	IL3	IAPP
	ABCA13	IL13	ID2
	IKZF1	IL4	IFI44
	DDC	VDAC1	IFNA14
	GRB10	CDKL3	IFNA22P
	GUSB	C5orf66	IFT122
	AUTS2	TIFAB	IGFN1
	HIP1	TMEM173	IGH
	RHBDD2	CD14	IGSF3

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IL6
IL6R
IL7R
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IRF4
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MYL9
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CXADR
MAP3K7CL
BACH1
MRAP

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PNN
NA
ATG14
DAAM1
PRKCH
PPP2R5E
ACTN1
EXD2
GALNT16
SLC39A9
SUSD6
SLC10A1
DPF3
BBOF1
ABCD4
LTBP2
AREL1
LINC01220
TGFB3
CEP128
TSHR
GALC
LINC01146
TTC7B
GPR68
CHGA
BTBD7
EVL
WDR25
DYNC1H1
HSP90AA1
WDR20
RYR3
RASGRP1
GPR176
PHGR1
CCDC32
CHAC1
CHP1
UBR1
ELL3
SORD
LYSMD2
ARPP19
NEDD4
LINC00926
LIPC
MYO1E
RORA

RPL32P3
RPL41
RPL41P2
RPL5
RPS26
RPTN
RTEL1
RTEL1-TNFRSF6B
RTF1
RTN4RL1
RUNX1
RUNX3
RYR1
S100A11
SAMD12
SAMD5
SARDH
SBNO2
SCG3
SCGN
SCHIP1
SCUBE3
SDHAP1
SDK2
SDR9C7
SEC31A
SEMA3E
SEMA6D
SEMG2
SERPINB11
SERPINB2
SERPINB7
SETD4
SFMBT2
SFTA1P
SGCG
SH2B3
SH3PXD2A
SIK2
SIM2
SLC16A7
SLC18A3
SLC19A3
SLC22A4
SLC22A5
SLC24A2
SLC25A46
SLC29A3
SLC2A10
SLC2A4RG
SLC30A8
SLC48A1
SLC4A11
SLC5A12
SLC6A11
SLC6A12
SLC6A13
SLC6A15
SLC7A10
SLC7A2
SLC8A1
SLC9A2
SLC9A4
SLCO1A2
SLCO1B1
SLP1
SMAD3
SMAD4
SMAD6
SMARCA2
SMARCE1
SMCP
SMPD1
SNORA66
SNORD21
SNX20
SOCS
SOCS1
SOX1
SPATS2L
SPEF2
SPPL3
SPRR1A
SPRR1B
SPRR2A
SPRR2B
SPRR2D
SPRR2E
SPRR2F
SPRR3
SPRR4
SPRY2
SPRY4

PAXBP1
RCAN1
DOPEY2
KCNJ6
C2CD2
PDE9A
HSF2BP
ADARB1
PI4KA
MAPK1
CABIN1
CRYBB1
CCDC117
KREMEN1
LIMK2
HMGXB4
JOSD1
CENPM
UPK3A
C22orf34

DAPK2
MAP2K1
SKOR1
PIAS1
ANP32A
CELF6
CYP11A1
ARID3B
SCAMP2
C15orf39
PEAK1
CIB2
RASGRF1
TMED3
MTHFS
FAH
ABHD17C
IL16
TMC3
SEMA4B
CRTC3
SV2B
IGF1R
PCSK6
NPRL3
AXIN1
RAB11FIP3
MGRN1
ANKS3
USP7
CLEC16A
RMI2
LITAF
C16orf45
ABCC1
VPS35L
KNOP1
ACSM1
METTL9
POLR3E
EARS2
PRKCB
XPO6
NFATC2IP
PAGR1
BOLA2
FBRS
CCDC189
SETD1A
TGFB1I1
GPT2
ABCC11
LONP2
RBL2
FTO
AMFR
ADGRG1
ZNF319
NDRG4
CKLF
RIPOR1
DDX28
SLC7A6
SF3B3
IL34
PMFBP1
WDR59
WFDC1
COTL1
KLHL36
ZFPM1
ZC3H18
ANKRD11
RPH3AL
VPS53
RPA1
MNT
ATP2A3
ANKFY1
ALOX15
ALOX12P2
ALOX12-AS1
PIK3R6
COX10
CDRT7
PMP22
COPS3
ATPAF2
KSR1
RAB11FIP4
CCL2
CCL18
LASP1

SPSB1
SQRDL
SRBD1
SRIL
SSR3
STAC
STARD3
STARD4
STAT5A
STAT5B
STAT6
STK11
STMN3
SUOX
SYNPO2
TAC3
TACR1
TAF4B
TAP2
TATDN1
TAX1BP1
TBCD
TBKBP1
TBL1XR1
TBX21
TCAP
TCHH
TCHHL1
TCL6
TCP11
TDRKH
TEAD1
TEK
TESPA1
TEX41
TFCP2L1
TFRC
THAP12
THPO
THRB
TIPARP-AS1
TLE4
TLN1
TLR1
TLR10
TLR6
TLSP
TM9SF2
TMEM132B
TMEM132D
TMEM133
TMEM163
TMEM194A
TMEM232
TMEM75
TMEM9
TMPPE
TMPRSS15
TMSB4X
TMTC2
TNFRSF11A
TNFRSF11B
TNFRSF6B
TNFSF11
TNFSF18
TNFSF4
TNKS
TNS1
TNSF18
TOMM7
TPD52
TPD52L3
TRAF3
TRAM2
TRIB2
TRIM15
TRIM26
TRIM27
TRIM39
TRIM71
TRIO
TRPA1
TRPM8
TRPS1
TSG1
TSHZ2
TSLP
TSPAN8
TWIST1
TXNDC8
UBAC2
UGT3A1
UHRF2

MED1
IKZF3
KRT13
NKIRAS2
RAB5C
DHX8
KANSL1
NPEPPS
ABCC3
MMD
MSI2
EPX
MKS1
MIR21
TUBD1
10-Mar
CYB561
ARHGAP27P1
PITPNC1
ARSG
CPSF4L
RAB37
TMEM104
ARMC7
MIF4GD
RNF157
DNAH17
EIF4A3
RPTOR
NPLOC4
CCDC57
NARF
METRNL
LPIN2
DLGAP1
EPB41L3
MTCL1
RAB31
VAPA
APCDD1
MIB1
CABLES1
TMEM241
INO80C
PIK3C3
ZBTB7C
FECH
SERPINB3
KCNG2
PRTN3
ELANE
ARID3A
DAZAP1
NFIC
TNFAIP8L1
PTPRS
SAFB2
RFX2
MLLT1
HNRNPM
ZNF653
ZNF833P
C19orf53
ADGRL1
EPS15L1
CPAMD8
MVB12A
GATAD2A
LRP3
CEBPA
KCTD15
GPI
LINC01531
HAUS5
ZBTB32
SIPA1L3
LGALS4
MED29
CLC
BCKDHA
DEDD2
STRN4
SIGLEC8
LOC100289473
RNF24
SMOX
RASSF2
SLC23A2
RRBP1
SLC24A3
LINC00656
SYNDIG1
HM13

UNC5B
UNC79
UTRN
VAV3
VCAN
VDR
VPS13C
WBSCR17
WDR36
WDR72
WNT11
XKR6
XPR1
XRCC4
YEATS4
YWHAZP3
ZBP2
ZBTB10
ZBTB16
ZBTB38
ZBTB39
ZBTB46
ZC3H10
ZCCHC2
ZCCHC6
ZFF36L1
ZFPM1
ZFYVE26
ZGPAT
ZIC4
ZMYND19
ZNF217
ZNF365
ZNF366
ZNF432
ZNF608
ZNF614
ZNF652
ZNF665
ZNF71
ZNF80
ZNF841
ZPBP2

BCL2L1
MAPRE1
NCOA6
GDF5
PHF20
MYL9
CTNNBL1
SERINC3
ADA
TOMM34
SLPI
LINC01270
RIPOR3
BCAS4
NFATC2
SUMO1P1
CYP24A1
LSM14B
CXADR
MAP3K7CL
BACH1
MRAP
PAXBP1
LINC01548
RCAN1
RUNX1
DOP1B
KCNJ6
PSMG1
C2CD2
PDE9A
HSF2BP
ADARB1
PI4KA
MAPK1
CABIN1
CRYBB1
MIAT
MN1
CCDC117
KREMEN1
LIF
LIMK2
HMGXB4
MYH9
CSF2RB
MPST
JOSD1
MGAT3
MIR1281
CENPM
NFAM1
UPK3A
RIBC2
C22orf34
BRD1

Table E6. Pathways Enriched (p<0.10) based on Epigenome-Wide Analyses for Non-atopic and Atopic Asthma

	Non-atopic Asthma		Atopic Asthma	
Pathway	**P**	**Genes**	**P**	**Genes**
KEGG_PORPHYRIN_AND_CHLOROPHYLL_METABOLISM	1.42E-03	ALAS1,FECH,HMOX1,UGT1A6	1.91E-03	ALAS1,EARS2,FECH,GUSB,MMAB
KEGG_LONG_TERM_POTENTIATION	5.62E-03	GNAQ,GRIN2C,ITPR2,PLCB2,PPP3CC,RAPGEF3	5.93E-01	GNAQ,ITPR2,RPS6KA2
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTION	1.76E-02	AVPR1B,GNAQ,ITPR2,MYLK,MYLK3,PLCB2,PPP1R12B	7.38E-01	CACNA1D,GNAQ,ITPR2,MYLK3
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	2.21E-02	AGPAT1,CHPT1,DGKD,MBOAT1,PGS1	9.39E-03	AGPAT1,DGKD,DGKI,GPD2,LCAT,LPCAT2,LPCAT3,MBOAT1
KEGG_ALZHEIMERS_DISEASE	2.46E-02	ATP2A3,GNAQ,GRIN2C,ITPR2,NDUFA4,PLCB2,PPP3CC	1.61E-01	CACNA1D,CAPN2,FADD,GNAQ,ITPR2,NCSTN,PSEN1,RYR3
KEGG_STEROID_BIOSYNTHESIS	2.81E-02	SOAT1,TM7SF2	1	
KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	3.02E-02	CAT,GRIN2C,PPP3CC,SLC1A2	6.52E-01	MAP2K3,MAPK13
KEGG_CALCIUM_SIGNALING_PATHWAY	3.59E-02	ATP2A3,AVPR1B,GNAQ,GRIN2C,ITPR2,MYLK,MYLK3,PLCB2,PPP3CC	4.60E-01	CACNA1D,CHRM1,GNA14,GNAQ,ITPR2,MYLK3,PTAFR,RYR3,SPHK1
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	4.06E-02	DARS,TARS,WARS	1.64E-01	CARS2,EARS2,QARS
KEGG_SPHINGOLIPID_METABOLISM	5.46E-02	ASAH2,DEGS2,SPTLC2	4.84E-01	DEGS2,SPHK1
KEGG_SPLICEOSOME	5.52E-02	ACIN1,CCDC12,PRPF40A,SNRNP200,SRSF4	5.32E-01	CTNNBL1,SNRNP200,SRSF4,U2SURP
KEGG_PEROXISOME	5.82E-02	AGPS,CAT,DDO,IDH2	5.11E-01	ACSL1,ACSL5,HMGCL
KEGG_CELL_CYCLE	5.99E-02	ANAPC11,CCND2,CCND3,CDK6,FZR1,MAD1L1	5.73E-03	ANAPC11,CCND1,CCNE2,CDC7,FZR1,GADD45A,HDAC1,PTTG2,TFDP2,TGFB3,WEE1,YWHAQ
KEGG_ENDOCYTOSIS	6.83E-02	ACAP2,CXCR4,GRK6,PIP5K1C,RNF41,SMAP2,SMURF1,TFRC	1.06E-01	ARFGAP2,ASAP1,CHMP3,CXCR4,IQSEC1,PDCD6IP,PRKCZ,RAB11FIP4,RNF41,SMAP2,SMURF1,TFRC
KEGG_P53_SIGNALING_PATHWAY	8.00E-02	CCND2,CCND3,CD82,CDK6	3.57E-01	CCND1,CCNE2,GADD45A,THBS1
KEGG_ASTHMA	8.05E-02	EPX,PRG2	5.49E-02	EPX,IL4,PRG2
KEGG_GLYCEROLIPID_METABOLISM	8.36E-02	AGPAT1,DGKD,MBOAT1	4.14E-02	AGPAT1,DGKD,DGKI,MBOAT1,MGLL
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	9.43E-02	CASP5,NLRP3,NOD2	6.04E-01	MAPK13,NOD1
KEGG_LYSOSOME	9.57E-02	ATP6V0A2,CD63,CTSC,GGA2,LAPTM5	3.01E-01	ABCB9,ACP5,CTSZ,GGA2,GUSB,SLC11A1
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	1.48E-01	DGKD,ITPR2,PIP5K1C,PLCB2	8.47E-02	DGKD,DGKI,INPP4A,INPP5A,ITPR2,PIK3CB,PIK3R1
KEGG_STARCH_AND_SUCROSE_METABOLISM	1.95E-01	HK2,UGT1A6	1.66E-02	GPI,GUSB,HK2,HK3,PYGL
KEGG_JAK_STAT_SIGNALING_PATHWAY	3.37E-01	CCND2,CCND3,SOCS1,SPRY1	9.58E-02	CCND1,CSF2RB,IFNGR1,IL4,IL5RA,LIF,PIK3CB,PIK3R1,STAT4
KEGG_TYPE_II_DIABETES_MELLITUS	3.83E-01	HK2,SOCS1	1.04E-02	CACNA1D,HK2,HK3,INSR,PIK3CB,PIK3R1,PRKCZ
KEGG_OOCYTE_MEIOSIS	4.18E-01	ANAPC11,ITPR2,PPP3CC	7.27E-02	ANAPC11,CCNE2,ITPR2,PPP2CA,PPP2R1B,PTTG2,RPS6KA2,YWHAQ
KEGG_TGF_BETA_SIGNALING_PATHWAY	6.34E-01	GDF5,SMURF1	6.18E-03	BMPR1A,GDF5,INHBA,INHBB,LTBP1,PPP2CA,PPP2R1B,SMURF1,TGFB3,THBS1
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	7.24E-01	NCK2,PPP3CC	9.95E-02	IL4,MAP3K8,MAPK13,NCK1,NCK2,PIK3CB,PIK3R1,RASGRP1
KEGG_COLORECTAL_CANCER	8.14E-01	MSH6	8.74E-02	AXIN1,CCND1,PIK3CB,PIK3R1,TCF7,TGFB3
KEGG_INSULIN_SIGNALING_PATHWAY	8.40E-01	HK2,SOCS1	7.63E-03	ACACB,FASN,FBP1,HK2,HK3,INSR,MKNK2,PIK3CB,PIK3R1,PRKAG2,PRKCZ,PYGL,SH2B2
KEGG_BIOSYNTHESIS_OF_UNSATURATED_FATTY_ACIDS	1		5.31E-03	ACOT7,ELOVL6,FADS2,HSD17B12
KEGG_VALINE_LEUCINE_AND_ISOLEUCINE_DEGRADATION	1		2.14E-02	ACAD8,ALDH6A1,BCAT1,HMGCL,PCCA
KEGG_SULFUR_METABOLISM	1		7.14E-02	CHST11,PAPSS1
KEGG_PPAR_SIGNALING_PATHWAY	1		8.99E-02	ACSL1,ACSL5,CYP8B1,FADS2,PPARG

Table E7. Significant methylation^{1} and cis-gene expression associations from the BIOS consortium^{2}, based on non-atopic asthma results

chromsome: position^{3}	CpG	Genename	N	Zscore^{4}	P.value^{4}	FDR p	Direction	HGNC_Gene_Name
chr1: 117114916	cg21167563	ENSG00000225079	3075	-3.386	7.08E-04	3.19E-03	+---	FTH1P22
chr1: 117114916	cg21167563	ENSG00000163399	3075	3.753	1.75E-04	1.57E-03	-+++	ATP1A1
chr1: 12185845	cg22123711	ENSG00000120949	3075	-4.197	2.71E-05	2.16E-04	----	TNFRSF8
chr1: 154293494	cg06181069	ENSG00000228013	3075	3.031	2.44E-03	1.04E-02	-+++	
chr1: 154293494	cg06181069	ENSG00000143549	3075	-4.893	9.91E-07	8.43E-06	----	TPM3
chr1: 154293494	cg06181069	ENSG00000143515	3075	10.924	8.82E-28	1.50E-26	++++	ATP8B2
chr1: 154293494	cg06181069	ENSG00000169291	3075	-3.032	2.43E-03	1.04E-02	----	SHE
chr1: 165826270	cg09277749	ENSG00000143179	3075	-6.269	3.62E-10	2.17E-09	----	UCK2
chr1: 167520305	cg17936236	ENSG00000143162	3075	-7.425	1.13E-13	9.05E-13	----	CREG1
chr1: 169525950	cg08653021	ENSG00000188404	3075	2.838	4.54E-03	4.09E-02	++++	SELL
chr1: 27060511	cg09849688	ENSG00000117676	3075	-2.917	3.54E-03	1.94E-02	----	RPS6KA1
chr1: 27060511	cg09849688	ENSG00000060642	3075	-4.406	1.05E-05	1.16E-04	----	PIGV
chr1: 29523841	cg16263722	ENSG00000060656	3075	-3.852	1.17E-04	5.85E-04	----	PTPRU
chr1: 43880657	cg16572910	ENSG00000066322	3075	-2.97	2.98E-03	3.88E-02	----	ELOVL1
chr1: 44411569	cg02835421	ENSG00000117411	3075	-3.728	1.93E-04	1.93E-03	----	B4GALT2
chr1: 44411569	cg02835421	ENSG00000237950	3075	-3.075	2.10E-03	1.05E-02	----	
chr1: 44411569	cg02835421	ENSG00000117410	3075	-2.815	4.88E-03	1.63E-02	----	ATP6V0B
chr1: 62209607	cg10704177	ENSG00000132849	3075	-5.302	1.15E-07	2.29E-07	----	INADL
chr1: 62209607	cg10704177	ENSG00000162604	3075	-3.667	2.45E-04	2.45E-04	--+-	TM2D1
chr1: 6341230	cg21220721	ENSG00000215788	3075	-2.247	2.46E-02	4.32E-02	--+-	TNFRSF25
chr1: 6341230	cg21220721	ENSG00000158292	3075	-3.243	1.18E-03	4.34E-03	+---	GPR153
chr1: 6341230	cg21220721	ENSG00000116237	3075	-2.104	3.54E-02	4.87E-02	----	ICMT
chr1: 6341230	cg21220721	ENSG00000097021	3075	-3.481	4.99E-04	2.75E-03	----	ACOT7
chr1: 6341230	cg21220721	ENSG00000162408	3075	-3.96	7.50E-05	8.24E-04	--+-	NOL9
chr1: 6341230	cg21220721	ENSG00000116254	3075	-2.511	1.21E-02	2.65E-02	-+--	CHD5
chr1: 6341230	cg21220721	ENSG00000187017	3075	-2.84	4.51E-03	1.24E-02	----	ESPN
chr1: 6341230	cg21220721	ENSG00000158286	3075	-2.205	2.75E-02	4.32E-02	---+	RNF207
chr1: 6341327	cg11699125	ENSG00000158292	3075	-4	6.34E-05	3.49E-04	----	GPR153
chr1: 6341327	cg11699125	ENSG00000116237	3075	-2.312	2.08E-02	3.26E-02	----	ICMT
chr1: 6341327	cg11699125	ENSG00000097021	3075	-4.244	2.19E-05	2.41E-04	----	ACOT7
chr1: 6341327	cg11699125	ENSG00000162408	3075	-3.417	6.34E-04	2.32E-03	--+-	NOL9
chr1: 6341327	cg11699125	ENSG00000116254	3075	-3.159	1.58E-03	4.35E-03	----	CHD5
chr1: 6341327	cg11699125	ENSG00000187017	3075	-2.542	1.10E-02	2.42E-02	-+--	ESPN
chr1: 6341327	cg11699125	ENSG00000158286	3075	-2.351	1.87E-02	3.26E-02	----	RNF207
chr1: 66777579	cg24058805	ENSG00000184588	3075	3.544	3.94E-04	7.88E-04	++++	PDE4B
chr2: 129200109	cg08790890	ENSG00000136720	3075	-3.181	1.47E-03	2.94E-03	----	HS6ST1
chr2: 173940277	cg19579160	ENSG00000091436	3075	-3.155	1.60E-03	1.60E-03	----	
chr2: 220115026	cg02961280	ENSG00000127824	3075	-2.899	3.75E-03	2.12E-02	----	TUBA4A
chr2: 220115026	cg02961280	ENSG00000144567	3075	-3.004	2.66E-03	2.12E-02	----	FAM134A
chr2: 220115026	cg02961280	ENSG00000115661	3075	-2.924	3.46E-03	2.12E-02	----	STK16
chr2: 27473369	cg23635560	ENSG00000138073	3075	-3.244	1.18E-03	3.06E-02	----	PREB
chr2: 65131556	cg17786894	ENSG00000011523	3075	-2.851	4.36E-03	1.02E-02	----	CEP68
chr2: 65131556	cg17786894	ENSG00000115902	3075	6.464	1.02E-10	7.15E-10	++++	SLC1A4
chr2: 65131556	cg17786894	ENSG00000237638	3075	-2.737	6.19E-03	1.08E-02	----	
chr2: 65131556	cg17786894	ENSG00000138069	3075	-4.002	6.29E-05	2.20E-04	----	RAB1A
chr2: 74375903	cg26529864	ENSG00000188687	3075	2.413	1.58E-02	4.11E-02	++++	SLC4A5
chr2: 74375903	cg26529864	ENSG00000225439	3075	-4.435	9.20E-06	5.98E-05	----	BOLA3-AS1
chr2: 74375903	cg26529864	ENSG00000163170	3075	-2.927	3.42E-03	1.11E-02	--+-	BOLA3
chr2: 74375903	cg26529864	ENSG00000187605	3075	4.058	4.96E-05	2.15E-04	++++	TET3
chr2: 74375903	cg26529864	ENSG00000114956	3075	-4.615	3.94E-06	5.12E-05	----	DGUOK
chr2: 74612222	cg17988187	ENSG00000188687	3075	2.708	6.77E-03	4.38E-02	++++	SLC4A5
chr2: 74612222	cg17988187	ENSG00000115289	3075	-3.18	1.47E-03	1.84E-02	----	PCGF1
chr2: 74612222	cg17988187	ENSG00000225439	3075	-3.745	1.80E-04	4.51E-03	----	BOLA3-AS1

chr2: 74612222	cg17988187	ENSG00000115274	3075	-2.696	7.02E-03	4.38E-02	----	INO80B
chr2: 75089669	cg12077754	ENSG00000159399	3075	-4.919	8.70E-07	3.48E-06	----	HK2
chr3: 13457267	cg04992150	ENSG00000163517	3075	-4.498	6.85E-06	2.05E-05	---+	HDAC11
chr3: 13457267	cg04992150	ENSG00000163520	3075	3.484	4.95E-04	7.42E-04	++++	FBLN2
chr3: 16491130	cg24171689	ENSG00000131378	3075	-6.571	5.00E-11	1.50E-10	----	RFTN1
chr3: 46996484	cg19114543	ENSG00000181585	3075	2.369	1.78E-02	3.70E-02	-+++	TMIE
chr3: 46996484	cg19114543	ENSG00000160796	3075	-5.842	5.16E-09	3.09E-08	----	NBEAL2
chr3: 46996484	cg19114543	ENSG00000181555	3075	-2.355	1.85E-02	3.70E-02	-+--	SETD2
chr3: 47023603	cg15157945	ENSG00000160796	3075	-8.822	1.13E-18	6.76E-18	----	NBEAL2
chr3: 47023603	cg15157945	ENSG00000236409	3075	-3.336	8.50E-04	2.55E-03	----	NRADDP
chr4: 109282481	cg25642315	ENSG00000138795	3075	3.322	8.94E-04	2.68E-03	-+++	LEF1
chr4: 109282481	cg25642315	ENSG00000232021	3075	2.454	1.41E-02	2.12E-02	+++-	LEF1-AS1
chr4: 2275801	cg12674840	ENSG00000185818	3075	-7.131	1.00E-12	1.00E-11	----	NAT8L
chr4: 25789390	cg04349839	ENSG00000250317	3075	2.142	3.22E-02	3.22E-02	++-+	SMIM20
chr4: 25789390	cg04349839	ENSG00000091490	3075	3.031	2.44E-03	4.88E-03	++++	SEL1L3
chr5: 132577108	cg12828656	ENSG00000053108	3075	-2.483	1.31E-02	3.92E-02	--+-	FSTL4
chr5: 132577108	cg12828656	ENSG00000170606	3075	-2.157	3.10E-02	4.65E-02	--+-	HSPA4
chr5: 159743203	cg02441833	ENSG00000164611	3075	-3.14	1.69E-03	1.35E-02	+---	PTTG1
chr5: 176856845	cg19459094	ENSG00000131183	3075	-8.455	2.79E-17	5.86E-16	----	SLC34A1
chr5: 176856845	cg19459094	ENSG00000113758	3075	-5.88	4.10E-09	4.30E-08	----	DBN1
chr5: 176856845	cg19459094	ENSG00000247679	3075	4.472	7.73E-06	5.41E-05	++++	
chr5: 176856845	cg19459094	ENSG00000184840	3075	-3.532	4.12E-04	1.73E-03	----	TMED9
chr5: 176856845	cg19459094	ENSG00000169223	3075	-3.667	2.45E-04	1.29E-03	----	LMAN2
chr5: 176856845	cg19459094	ENSG00000246596	2182	3.033	2.43E-03	8.49E-03	+++?	
chr5: 176856845	cg19459094	ENSG00000169228	3075	-2.432	1.50E-02	3.50E-02	+---	RAB24
chr5: 176856845	cg19459094	ENSG00000169230	3075	-2.461	1.39E-02	3.50E-02	----	PRELID1
chr5: 176856845	cg19459094	ENSG00000213347	3075	-2.512	1.20E-02	3.50E-02	----	MXD3
chr5: 76248749	cg16545105	ENSG00000132846	3075	-3.125	1.78E-03	1.42E-02	-+--	ZBED3
chr6: 110720501	cg00847453	ENSG00000203797	3075	2.969	2.99E-03	1.79E-02	+++-	DDO
chr6: 31582837	cg24211388	ENSG00000226979	3075	2.865	4.18E-03	2.04E-02	+-++	LTA
chr6: 31582837	cg24211388	ENSG00000204387	3075	3.171	1.52E-03	1.35E-02	+-++	C6orf48
chr6: 31582837	cg24211388	ENSG00000204439	3075	-3.06	2.21E-03	1.35E-02	--+-	C6orf47
chr6: 31582837	cg24211388	ENSG00000204386	3075	-4.36	1.30E-05	5.08E-04	----	NEU1
chr6: 31582837	cg24211388	ENSG00000213719	3075	-3.828	1.29E-04	2.52E-03	----	CLIC1
chr6: 31582837	cg24211388	ENSG00000204438	3075	-3.038	2.38E-03	1.35E-02	----	GPANK1
chr6: 31582837	cg24211388	ENSG00000204482	3075	-3.174	1.50E-03	1.35E-02	----	LST1
chr6: 31582837	cg24211388	ENSG00000204472	3075	-3.032	2.43E-03	1.35E-02	----	AIF1
chr6: 31680144	cg20133890	ENSG00000226979	3075	6.778	1.22E-11	5.24E-10	++++	LTA
chr6: 31680144	cg20133890	ENSG00000227507	3075	4.171	3.03E-05	4.34E-04	++++	LTB
chr6: 31680144	cg20133890	ENSG00000204387	3075	5.777	7.62E-09	1.64E-07	++++	C6orf48
chr6: 31680144	cg20133890	ENSG00000204475	3075	-2.997	2.72E-03	1.84E-02	----	NCR3
chr6: 31680144	cg20133890	ENSG00000204396	3075	-3.063	2.19E-03	1.84E-02	----	VWA7
chr6: 31680144	cg20133890	ENSG00000204386	3075	-3.466	5.28E-04	5.67E-03	----	NEU1
chr6: 31680144	cg20133890	ENSG00000204428	3075	-2.969	2.99E-03	1.84E-02	----	LY6G5C
chr6: 32141591	cg09597192	ENSG00000204314	3075	-2.719	6.54E-03	2.88E-02	----	PRRT1
chr6: 32141591	cg09597192	ENSG00000204308	3075	-3.92	8.85E-05	1.95E-03	----	RNF5
chr6: 32141591	cg09597192	ENSG00000221988	3075	-2.878	4.00E-03	2.20E-02	----	PPT2
chr6: 32141591	cg09597192	ENSG00000204344	3075	3.37	7.50E-04	8.25E-03	++++	STK19
chr6: 32141591	cg09597192	ENSG00000204304	3075	3.12	1.81E-03	1.33E-02	++++	PBX2
chr6: 33255400	cg10966235	ENSG00000236104	3075	-3.591	3.30E-04	8.24E-03	----	ZBTB22
chr6: 33382557	cg02305757	ENSG00000197283	3075	7.51	5.93E-14	1.42E-12	++++	SYNGAP1
chr6: 33382557	cg02305757	ENSG00000204248	3075	2.749	5.98E-03	4.78E-02	++++	COL11A2
chr6: 33382557	cg02305757	ENSG00000231500	3075	2.975	2.93E-03	3.52E-02	+-++	RPS18
chr7: 100224557	cg11751434	ENSG00000236305	2182	2.823	4.76E-03	4.06E-02	+++?	
chr7: 100224557	cg11751434	ENSG00000078487	3075	3.191	1.42E-03	3.12E-02	++++	ZCWPW1
chr7: 100224557	cg11751434	ENSG00000160813	3075	2.774	5.53E-03	4.06E-02	++++	PPP1R35
chr7: 128899554	cg03822873	ENSG00000128602	3075	-2.774	5.53E-03	4.98E-02	----	SMO
chr7: 149543165	cg07970948	ENSG00000106479	3075	3.435	5.93E-04	1.38E-03	++-+	ZNF862
chr7: 149543165	cg07970948	ENSG00000171130	3075	-4.217	2.47E-05	1.73E-04	----	ATP6V0E2
chr7: 149543165	cg07970948	ENSG00000181444	3075	3.683	2.31E-04	8.08E-04	++++	ZNF467
chr7: 150773709	cg06807926	ENSG00000181652	3075	5.958	2.55E-09	4.08E-08	++++	ATG9B

chr7: 150773709	cg06807926	ENSG00000164867	3075	4.247	2.16E-05	1.47E-04	++++	NOS3
chr7: 150773709	cg06807926	ENSG00000213199	3075	4.193	2.76E-05	1.47E-04	++++	ASIC3
chr7: 150773709	cg06807926	ENSG00000133612	3075	3.278	1.05E-03	4.18E-03	++++	AGAP3
chr7: 1650459	cg03489907	ENSG00000230487	3075	3.647	2.65E-04	2.12E-03	-+++	PSMG3-AS1
chr7: 1914073	cg18650626	ENSG00000002822	3075	-4.326	1.52E-05	1.52E-05	----	MAD1L1
chr7: 29304984	cg15030712	ENSG00000106069	3075	-4.923	8.54E-07	1.71E-06	----	CHN2
chr7: 29304984	cg15030712	ENSG00000106066	3075	-4.378	1.20E-05	1.20E-05	----	CPVL
chr7: 5523691	cg11554295	ENSG00000182095	3075	-3.463	5.34E-04	5.87E-03	----	TNRC18
chr7: 98722470	cg14769121	ENSG00000198742	3075	-3.085	2.03E-03	1.02E-02	---+	SMURF1
chr8: 22288224	cg18042586	ENSG00000120910	3075	-4.974	6.57E-07	8.54E-06	----	PPP3CC
chr8: 22288224	cg18042586	ENSG00000120896	3075	2.974	2.94E-03	9.55E-03	++++	SORBS3
chr8: 22288224	cg18042586	ENSG00000197181	3075	2.875	4.04E-03	1.05E-02	-+++	PIWIL2
chr8: 22288224	cg18042586	ENSG00000254064	3075	3.311	9.29E-04	4.03E-03	++++	
chr8: 22288224	cg18042586	ENSG00000147439	3075	-2.275	2.29E-02	4.97E-02	----	BIN3
chr8: 22288224	cg18042586	ENSG00000168495	3075	-3.799	1.46E-04	9.46E-04	----	POLR3D
chr9: 117157871	cg14260530	ENSG00000196739	3075	-2.729	6.35E-03	1.69E-02	---+	COL27A1
chr9: 117157871	cg14260530	ENSG00000095397	3075	3.686	2.28E-04	9.11E-04	++++	DFNB31
chr9: 117157871	cg14260530	ENSG00000228278	3075	4.092	4.27E-05	3.41E-04	++++	ORM2
chr9: 132600788	cg13953978	ENSG00000136878	3075	-7.351	1.97E-13	1.08E-12	----	USP20
chr9: 132600788	cg13953978	ENSG00000136816	3075	-4.622	3.81E-06	1.40E-05	----	TOR1B
chr9: 132600788	cg13953978	ENSG00000148358	3075	2.721	6.50E-03	1.43E-02	++++	GPR107
chr9: 132600788	cg13953978	ENSG00000136827	3075	-4.227	2.37E-05	6.51E-05	----	TOR1A
chr9: 132600788	cg13953978	ENSG00000136819	3075	-11.027	2.83E-28	3.11E-27	----	C9orf78
chr9: 134206000	cg14031473	ENSG00000050555	3075	9.773	1.47E-22	1.62E-21	++++	LAMC3
chr9: 134206000	cg14031473	ENSG00000107263	3075	-4.9	9.57E-07	5.26E-06	-+--	RAPGEF1
chr9: 134206000	cg14031473	ENSG00000130714	3075	2.599	9.35E-03	2.57E-02	++++	POMT1
chr9: 134206000	cg14031473	ENSG00000130723	3075	3.664	2.49E-04	9.12E-04	++++	PRRC2B
chr9: 136341915	cg13410614	ENSG00000148248	3075	-5.358	8.41E-08	2.86E-07	----	SURF4
chr9: 136341915	cg13410614	ENSG00000123453	3075	8.745	2.22E-18	3.78E-17	++++	SARDH
chr9: 136341915	cg13410614	ENSG00000225756	3075	8.218	2.08E-16	1.76E-15	++++	DBH-AS1
chr9: 136341915	cg13410614	ENSG00000123454	3075	6.521	6.98E-11	3.95E-10	++++	DBH
chr9: 136341915	cg13410614	ENSG00000197859	3075	6.038	1.56E-09	6.64E-09	++++	ADAMTSL2
chr9: 136341915	cg13410614	ENSG00000198870	3075	2.769	5.62E-03	1.36E-02	++++	C9orf96
chr9: 136341915	cg13410614	ENSG00000148297	3075	-2.578	9.93E-03	2.11E-02	----	MED22
chr9: 136341915	cg13410614	ENSG00000160326	3075	-4.086	4.39E-05	1.24E-04	----	SLC2A6
chr9: 136341915	cg13410614	ENSG00000148290	3075	-2.24	2.51E-02	4.74E-02	---+	SURF1
chr10: 135061670	cg12227660	ENSG00000151651	3075	-6.582	4.63E-11	7.40E-10	----	ADAM8
chr10: 135061670	cg12227660	ENSG00000235245	3075	3.296	9.81E-04	5.23E-03	++-+	
chr10: 135061670	cg12227660	ENSG00000127884	3075	-2.89	3.85E-03	1.23E-02	--+-	ECHS1
chr10: 135061670	cg12227660	ENSG00000198546	3075	-3.714	2.04E-04	1.63E-03	+---	ZNF511
chr10: 135061670	cg12227660	ENSG00000151650	3075	-3.141	1.69E-03	6.74E-03	----	VENTX
chr10: 45495435	cg01614759	ENSG00000165511	3075	-3.369	7.53E-04	3.01E-03	+---	C10orf25
chr10: 74069493	cg07828833	ENSG00000166295	3075	6.551	5.72E-11	2.00E-10	++++	ANAPC16
chr10: 74069493	cg07828833	ENSG00000107745	3075	-2.065	3.89E-02	3.89E-02	+---	MICU1
chr10: 74069493	cg07828833	ENSG00000107742	3075	9.084	1.04E-19	7.30E-19	++++	SPOCK2
chr10: 74069493	cg07828833	ENSG00000138303	3075	-2.393	1.67E-02	1.95E-02	--+-	ASCC1
chr10: 74069493	cg07828833	ENSG00000168209	3075	-2.482	1.31E-02	1.83E-02	-+-+	DDIT4
chr10: 74069493	cg07828833	ENSG00000200170	3075	2.511	1.21E-02	1.83E-02	++++	
chr10: 74069493	cg07828833	ENSG00000148719	3075	-2.767	5.65E-03	1.32E-02	----	DNAJB12
chr10: 75677011	cg04084348	ENSG00000196968	3075	-12.432	1.75E-35	3.16E-34	----	FUT11
chr10: 75677011	cg04084348	ENSG00000176986	3075	-10.186	2.29E-24	2.06E-23	----	SEC24C
chr10: 75677011	cg04084348	ENSG00000035403	3075	-4.907	9.26E-07	4.17E-06	-+--	VCL
chr10: 75677011	cg04084348	ENSG00000214655	3075	-7.736	1.03E-14	6.17E-14	----	ZSWIM8
chr10: 75677011	cg04084348	ENSG00000156110	3075	3.084	2.04E-03	6.13E-03	++++	ADK
chr10: 75677011	cg04084348	ENSG00000185009	3075	-3.379	7.28E-04	2.62E-03	-+--	AP3M1
chr10: 99223744	cg12182708	ENSG00000171314	3075	-5.017	5.24E-07	9.43E-06	----	PGAM1
chr10: 99223744	cg12182708	ENSG00000155229	3075	3.925	8.67E-05	3.94E-04	+-++	MMS19
chr10: 99223744	cg12182708	ENSG00000119986	3075	-2.637	8.36E-03	2.15E-02	----	AVPI1
chr10: 99223744	cg12182708	ENSG00000165879	3075	-4.043	5.27E-05	3.94E-04	----	FRAT1
chr10: 99223744	cg12182708	ENSG00000165886	3075	-3.261	1.11E-03	4.00E-03	--+-	UBTD1
chr10: 99223744	cg12182708	ENSG00000181274	3075	-3.923	8.76E-05	3.94E-04	----	FRAT2

chr10: 99223744	cg12182708	ENSG00000155254	3075	-3.09	2.00E-03	6.00E-03	----	MARVELD1
chr10: 99223744	cg12182708	ENSG00000213390	3075	-2.59	9.59E-03	2.16E-02	-+--	ARHGAP19
chr11: 119486443	cg23575688	ENSG00000110400	3075	-2.462	1.38E-02	1.38E-02	-+--	PVRL1
chr11: 2848310	cg21130221	ENSG00000110619	3075	-3.136	1.71E-03	8.56E-03	----	CARS
chr11: 2848310	cg21130221	ENSG00000269821	3075	-2.56	1.05E-02	3.49E-02	----	KCNQ1OT1
chr11: 2848310	cg21130221	ENSG00000254827	3075	-2.361	1.82E-02	4.55E-02	----	SLC22A18AS
chr11: 2848310	cg21130221	ENSG00000205531	3075	4.259	2.05E-05	2.05E-04	++++	NAP1L4
chr11: 3145609	cg01418188	ENSG00000110619	3075	-4.129	3.65E-05	4.01E-04	----	CARS
chr11: 3145609	cg01418188	ENSG00000183562	2182	2.904	3.69E-03	1.35E-02	+++?	
chr11: 3145609	cg01418188	ENSG00000205531	3075	3.703	2.13E-04	1.17E-03	++++	NAP1L4
chr11: 44578801	cg14780449	ENSG00000157570	3075	4.294	1.76E-05	5.27E-05	++++	TSPAN18
chr11: 44578801	cg14780449	ENSG00000085117	3075	-3.841	1.23E-04	1.84E-04	----	CD82
chr11: 57157632	cg12819873	ENSG00000149136	3075	-3.031	2.44E-03	2.20E-02	-+--	SSRP1
chr11: 63466987	cg07636225	ENSG00000168004	3075	-15.592	8.20E-55	1.07E-53	----	HRASLS5
chr11: 63466987	cg07636225	ENSG00000133317	3075	-12.587	2.49E-36	1.62E-35	----	LGALS12
chr11: 63466987	cg07636225	ENSG00000256280	3075	-2.926	3.43E-03	1.49E-02	----	
chr11: 65239080	cg23299484	ENSG00000168056	3075	-5.252	1.50E-07	3.76E-06	----	LTBP3
chr11: 72983405	cg04099543	ENSG00000054967	3075	-4.951	7.37E-07	6.63E-06	----	RELT
chr11: 72983405	cg04099543	ENSG00000256448	3075	-3.411	6.46E-04	2.91E-03	----	
chr11: 72983405	cg04099543	ENSG00000054965	3075	-2.989	2.80E-03	8.39E-03	-+--	FAM168A
chr11: 75114223	cg05122026	ENSG00000158555	3075	-5.351	8.73E-08	6.11E-07	----	GDPD5
chr11: 75114223	cg05122026	ENSG00000149243	3075	-3.008	2.63E-03	9.21E-03	----	KLHL35
chr12: 125589647	cg26964704	ENSG00000184992	3075	-5.035	4.78E-07	2.39E-06	----	BRI3BP
chr12: 125589647	cg26964704	ENSG00000081760	3075	-3.42	6.26E-04	1.57E-03	----	AACS
chr12: 48152204	cg21166775	ENSG00000134291	3075	4.989	6.06E-07	3.03E-06	+-++	TMEM106C
chr12: 48152204	cg21166775	ENSG00000111405	2182	-3.48	5.02E-04	1.25E-03	---?	ENDOU
chr12: 48152204	cg21166775	ENSG00000111424	3075	-3.164	1.56E-03	3.11E-03	-+--	VDR
chr12: 48152204	cg21166775	ENSG00000257433	3075	-4.383	1.17E-05	3.91E-05	----	
chr12: 48152204	cg21166775	ENSG00000079337	3075	-10.164	2.86E-24	2.86E-23	----	RAPGEF3
chr12: 50262986	cg04920032	ENSG00000139644	3075	-2.901	3.72E-03	3.25E-02	----	TMBIM6
chr12: 50262986	cg04920032	ENSG00000178449	3075	2.752	5.92E-03	3.25E-02	+-++	COX14
chr12: 50262986	cg04920032	ENSG00000167566	3075	-2.611	9.03E-03	3.31E-02	----	NCKAP5L
chr12: 52404134	cg14242936	ENSG00000170442	3075	-3.444	5.74E-04	4.42E-03	----	KRT86
chr12: 52404134	cg14242936	ENSG00000139567	3075	-3.368	7.58E-04	4.42E-03	----	ACVRL1
chr12: 52404134	cg14242936	ENSG00000123358	3075	-3.051	2.28E-03	6.85E-03	----	NR4A1
chr12: 52404134	cg14242936	ENSG00000135503	3075	-3.262	1.11E-03	4.42E-03	-+--	ACVR1B
chr12: 56600222	cg17116500	ENSG00000139579	3075	-3.458	5.44E-04	4.21E-03	----	NABP2
chr12: 56600222	cg17116500	ENSG00000139641	3075	-3.785	1.54E-04	1.59E-03	----	ESYT1
chr12: 56600222	cg17116500	ENSG00000062485	3075	-5.361	8.25E-08	2.56E-06	----	CS
chr12: 56600222	cg17116500	ENSG00000139531	3075	-3.944	8.02E-05	1.24E-03	----	SUOX
chr12: 58210661	cg04046364	ENSG00000139266	3075	5.823	5.78E-09	1.21E-07	+-++	MARCH9
chr12: 58210661	cg04046364	ENSG00000155980	3075	2.555	1.06E-02	4.46E-02	++++	KIF5A
chr12: 58210661	cg04046364	ENSG00000135506	3075	-3.347	8.18E-04	4.29E-03	--+-	OS9
chr12: 58210661	cg04046364	ENSG00000178498	3075	3.509	4.50E-04	3.30E-03	++++	DTX3
chr12: 58210661	cg04046364	ENSG00000175215	3075	-3.497	4.71E-04	3.30E-03	-+--	CTDSP2
chr12: 58210716	cg26620147	ENSG00000139266	3075	4.872	1.10E-06	2.31E-05	+-++	MARCH9
chr12: 58210716	cg26620147	ENSG00000175215	3075	-3.634	2.79E-04	2.93E-03	-+--	CTDSP2
chr12: 6233657	cg27347104	ENSG00000010278	3075	2.971	2.96E-03	1.48E-02	++-+	CD9
chr13: 41631052	cg07908654	ENSG00000120662	3075	3.418	6.30E-04	2.52E-03	++++	MTRF1
chr13: 41631052	cg07908654	ENSG00000165572	3075	3.277	1.05E-03	3.15E-03	+-++	KBTBD6
chr13: 41631052	cg07908654	ENSG00000120696	3075	4.157	3.22E-05	2.45E-04	++++	KBTBD7
chr13: 41631052	cg07908654	ENSG00000120688	3075	2.396	1.66E-02	3.97E-02	++++	WBP4
chr13: 41631052	cg07908654	ENSG00000120690	3075	4.103	4.08E-05	2.45E-04	++++	ELF1
chr13: 49175326	cg15338967	ENSG00000152207	3075	-7.019	2.24E-12	1.12E-11	----	CYSLTR2
chr14: 100610407	cg14084609	ENSG00000140105	3075	-2.678	7.40E-03	3.70E-02	-+--	WARS
chr14: 100610407	cg14084609	ENSG00000168350	3075	-2.938	3.30E-03	3.30E-02	-+--	DEGS2
chr14: 95615731	cg01901579	ENSG00000235706	3075	2.521	1.17E-02	2.34E-02	++++	DICER1-AS1
chr14: 95615731	cg01901579	ENSG00000259143	3075	2.848	4.39E-03	1.76E-02	++++	
chr14: 95615731	cg01901579	ENSG00000165959	3075	2.269	2.32E-02	3.10E-02	++++	CLMN
chr14: 95991371	cg23661721	ENSG00000165959	3075	-3.623	2.91E-04	2.91E-03	----	CLMN
chr15: 40601467	cg02240622	ENSG00000137843	3075	-2.563	1.04E-02	2.52E-02	----	PAK6

chr15: 40601467	cg02240622	ENSG00000248508	3075	3.184	1.45E-03	4.93E-03	++++	SRP14-AS1
chr15: 40601467	cg02240622	ENSG00000140320	3075	3.856	1.15E-04	6.53E-04	++++	BAHD1
chr15: 40601467	cg02240622	ENSG00000137841	3075	-5.154	2.55E-07	2.16E-06	----	PLCB2
chr15: 40601467	cg02240622	ENSG00000128944	3075	-3.295	9.85E-04	4.19E-03	----	KNSTRN
chr15: 40601467	cg02240622	ENSG00000259330	3075	-2.942	3.26E-03	9.23E-03	----	LINC00984
chr15: 40601467	cg02240622	ENSG00000104081	3075	-5.418	6.02E-08	1.02E-06	----	BMF
chr15: 41309253	cg21953058	ENSG00000104142	3075	-2.553	1.07E-02	4.27E-02	--+-	VPS18
chr15: 41309253	cg21953058	ENSG00000187446	3075	-5.01	5.43E-07	6.52E-06	----	CHP1
chr15: 41309253	cg21953058	ENSG00000166145	3075	-3.518	4.35E-04	2.61E-03	----	SPINT1
chr15: 45028161	cg15022400	ENSG00000229474	3075	-10.228	1.48E-24	7.40E-24	----	PATL2
chr15: 45028161	cg15022400	ENSG00000104133	3075	-2.413	1.58E-02	3.73E-02	-+--	SPG11
chr15: 45028161	cg15022400	ENSG00000179523	3075	-2.353	1.86E-02	3.73E-02	+---	EIF3J-AS1
chr15: 45028161	cg15022400	ENSG00000185880	3075	-11.539	8.40E-31	8.40E-30	----	TRIM69
chr15: 45028161	cg15022400	ENSG00000166710	3075	-6.143	8.11E-10	2.70E-09	----	B2M
chr15: 85186517	cg17194668	ENSG00000176700	3075	3.237	1.21E-03	1.33E-02	+++-	SCAND2P
chr15: 89020059	cg26025224	ENSG00000172183	3075	-3.75	1.77E-04	8.85E-04	+---	ISG20
chr16: 2863919	cg10194884	ENSG00000172460	3075	-12.674	8.21E-37	1.27E-35	----	PRSS30P
chr16: 2863919	cg10194884	ENSG00000103355	3075	-5.215	1.84E-07	1.14E-06	----	PRSS33
chr16: 2863919	cg10194884	ENSG00000215148	3075	-4.293	1.76E-05	9.09E-05	----	PRSS41
chr16: 2863919	cg10194884	ENSG00000007038	3075	-19.335	2.71E-83	8.39E-82	----	PRSS21
chr16: 2863919	cg10194884	ENSG00000167977	3075	-3.31	9.33E-04	3.21E-03	----	KCTD5
chr16: 2863919	cg10194884	ENSG00000005001	3075	-8.748	2.18E-18	2.25E-17	----	PRSS22
chr16: 2863919	cg10194884	ENSG00000162078	3075	-6.872	6.32E-12	4.90E-11	----	ZG16B
chr16: 2863919	cg10194884	ENSG00000140992	3075	-3.41	6.50E-04	2.52E-03	+---	PDPK1
chr16: 2863919	cg10194884	ENSG00000059122	3075	-3.765	1.67E-04	7.39E-04	----	FLYWCH1
chr16: 31210736	cg27646484	ENSG00000099365	3075	4.157	3.23E-05	7.43E-04	++++	STX1B
chr16: 50701499	cg00921350	ENSG00000167208	3075	-4.882	1.05E-06	9.43E-06	----	SNX20
chr16: 50701499	cg00921350	ENSG00000167207	3075	2.807	4.99E-03	1.86E-02	++++	NOD2
chr16: 50701499	cg00921350	ENSG00000270120	3075	2.737	6.20E-03	1.86E-02	+-++	
chr16: 57833579	cg26819611	ENSG00000166188	3075	-4.762	1.92E-06	1.25E-05	----	ZNF319
chr16: 57833579	cg26819611	ENSG00000103005	3075	-5.277	1.31E-07	1.70E-06	----	USB1
chr16: 57833579	cg26819611	ENSG00000182885	3075	-3.834	1.26E-04	5.46E-04	----	GPR97
chr16: 57833579	cg26819611	ENSG00000260467	3075	-2.725	6.43E-03	2.09E-02	----	
chr16: 616212	cg04497992	ENSG00000127585	3075	-3.087	2.02E-03	1.81E-02	----	FBXL16
chr16: 616212	cg04497992	ENSG00000103126	3075	-4.763	1.91E-06	6.10E-05	----	AXIN1
chr16: 616212	cg04497992	ENSG00000086504	3075	-3.374	7.41E-04	1.18E-02	--+-	MRPL28
chr16: 616212	cg04497992	ENSG00000103254	3075	-2.719	6.55E-03	2.99E-02	+---	FAM173A
chr16: 616212	cg04497992	ENSG00000161999	3075	2.754	5.89E-03	2.99E-02	++++	JMJD8
chr16: 616212	cg04497992	ENSG00000127586	3075	-3.054	2.26E-03	1.81E-02	----	CHTF18
chr16: 616212	cg04497992	ENSG00000007376	3075	-2.77	5.61E-03	2.99E-02	----	RPUSD1
chr16: 68334619	cg04304036	ENSG00000103064	3075	7.73	1.08E-14	1.40E-13	++++	SLC7A6
chr16: 68334619	cg04304036	ENSG00000103056	3075	3.488	4.87E-04	2.11E-03	++++	SMPD3
chr16: 68334619	cg04304036	ENSG00000072736	3075	3.363	7.72E-04	2.51E-03	++++	NFATC3
chr16: 68334619	cg04304036	ENSG00000132600	3075	3.852	1.17E-04	7.62E-04	+-++	PRMT7
chr16: 68334619	cg04304036	ENSG00000103067	3075	2.529	1.14E-02	2.12E-02	++++	ESRP2
chr16: 68334619	cg04304036	ENSG00000103066	3075	-2.745	6.06E-03	1.31E-02	----	PLA2G15
chr16: 68334619	cg04304036	ENSG00000167264	3075	-3.066	2.17E-03	5.64E-03	----	DUS2
chr16: 88558237	cg05958985	ENSG00000158717	3075	-2.56	1.05E-02	3.66E-02	----	RNF166
chr16: 88558237	cg05958985	ENSG00000179588	3075	-4.34	1.43E-05	9.99E-05	----	ZFPM1
chr16: 88558237	cg05958985	ENSG00000103335	3075	-4.351	1.36E-05	9.99E-05	----	PIEZO1
chr16: 88558237	cg05958985	ENSG00000225614	3075	-3.373	7.45E-04	3.47E-03	---+	ZNF469
chr16: 88838368	cg26603047	ENSG00000158717	3075	7.231	4.81E-13	1.11E-11	++++	RNF166
chr16: 88838368	cg26603047	ENSG00000179588	3075	5.257	1.47E-07	1.69E-06	++++	ZFPM1
chr16: 88838368	cg26603047	ENSG00000103335	3075	3.601	3.17E-04	1.82E-03	--++	PIEZO1
chr16: 88838368	cg26603047	ENSG00000261744	2182	3.157	1.59E-03	7.33E-03	+++?	
chr16: 88838368	cg26603047	ENSG00000167515	3075	-2.968	2.99E-03	1.15E-02	----	TRAPPC2L
chr16: 88838368	cg26603047	ENSG00000260121	3075	2.506	1.22E-02	4.01E-02	++++	
chr16: 88838368	cg26603047	ENSG00000129993	3075	-3.751	1.76E-04	1.35E-03	----	CBFA2T3
chr17: 33426885	cg08154963	ENSG00000092871	3075	-3.732	1.90E-04	2.09E-03	-+--	RFFL
chr17: 33885049	cg00397422	ENSG00000129270	3075	6.162	7.16E-10	1.72E-08	++++	MMP28
chr17: 33885049	cg00397422	ENSG00000267364	3075	-4.55	5.36E-06	6.43E-05	----	

chr17: 43472435	cg18410271	ENSG00000204650	3075	9.633	5.79E-22	1.10E-20	++++	CRHR1-IT1
chr17: 43472435	cg18410271	ENSG00000131484	1525	-2.56	1.05E-02	3.98E-02	?--?	
chr17: 43472435	cg18410271	ENSG00000264070	3075	8.007	1.18E-15	7.45E-15	++++	DND1P1
chr17: 43472435	cg18410271	ENSG00000214425	3075	-8.035	9.38E-16	7.45E-15	----	LRRC37A4P
chr17: 43472435	cg18410271	ENSG00000159314	3075	-3.677	2.36E-04	1.12E-03	----	ARHGAP27
chr17: 56274480	cg08105265	ENSG00000121053	3075	-3.884	1.03E-04	1.54E-03	----	EPX
chr17: 56355362	cg22331200	ENSG00000108375	3075	2.674	7.49E-03	4.90E-02	++++	RNF43
chr17: 56355362	cg22331200	ENSG00000265148	3075	2.672	7.54E-03	4.90E-02	++++	BZRAP1-AS1
chr17: 58155376	cg01248878	ENSG00000261040	3075	-2.868	4.13E-03	1.13E-02	-+--	
chr17: 58155376	cg01248878	ENSG00000068097	3075	-15.48	4.71E-54	5.18E-53	----	HEATR6
chr17: 58155376	cg01248878	ENSG00000170832	3075	-3.664	2.48E-04	1.36E-03	-+--	USP32
chr17: 58155376	cg01248878	ENSG00000062716	3075	-3.499	4.67E-04	1.71E-03	----	VMP1
chr17: 62075151	cg03554335	ENSG00000007312	3075	4.341	1.42E-05	1.14E-04	++++	CD79B
chr17: 62075151	cg03554335	ENSG00000199753	3075	2.873	4.07E-03	1.30E-02	++++	SNORD104
chr17: 62075151	cg03554335	ENSG00000266402	3075	3.317	9.10E-04	4.85E-03	++++	SNORA76
chr17: 62075151	cg03554335	ENSG00000178607	3075	-3.132	1.74E-03	6.95E-03	-+--	ERN1
chr17: 62075151	cg03554335	ENSG00000224383	3075	-11.584	4.94E-31	7.91E-30	----	C17orf72
chr17: 6658198	cg14321269	ENSG00000132530	3075	-4.853	1.22E-06	1.46E-05	----	XAF1
chr17: 72838819	cg12190341	ENSG00000170190	3075	-2.791	5.26E-03	4.21E-02	----	SLC16A5
chr17: 72838819	cg12190341	ENSG00000161509	3075	2.993	2.76E-03	4.21E-02	++++	GRIN2C
chr17: 80190054	cg19284277	ENSG00000173762	3075	6.086	1.16E-09	1.08E-08	+-++	CD7
chr17: 80190054	cg19284277	ENSG00000169683	3075	-4.112	3.92E-05	2.20E-04	----	LRRC45
chr17: 80190054	cg19284277	ENSG00000169727	3075	-2.822	4.78E-03	1.67E-02	---+	GPS1
chr17: 80190054	cg19284277	ENSG00000141574	3075	-3.254	1.14E-03	4.54E-03	----	SECTM1
chr17: 80190054	cg19284277	ENSG00000141551	3075	-4.464	8.04E-06	5.63E-05	----	CSNK1D
chr17: 80190054	cg19284277	ENSG00000178927	3075	-3.326	8.80E-04	4.11E-03	+---	C17orf62
chr17: 80190054	cg19284277	ENSG00000169710	3075	6.373	1.86E-10	2.60E-09	++++	FASN
chr17: 80190054	cg19284277	ENSG00000141526	3075	-8.431	3.44E-17	9.62E-16	----	SLC16A3
chr17: 81040906	cg22503106	ENSG00000261888	3075	-13.641	2.29E-42	1.38E-41	----	
chr17: 81040906	cg22503106	ENSG00000141556	3075	-3.969	7.21E-05	1.44E-04	----	TBCD
chr17: 81040906	cg22503106	ENSG00000176845	3075	-6.571	5.00E-11	1.50E-10	----	METRNL
chr17: 81040906	cg22503106	ENSG00000175711	3075	2.23	2.58E-02	3.87E-02	++++	B3GNTL1
chr17: 81055722	cg13054523	ENSG00000261888	3075	-12.664	9.36E-37	5.62E-36	----	
chr17: 81055722	cg13054523	ENSG00000141556	3075	-2.875	4.04E-03	6.06E-03	----	TBCD
chr17: 81055722	cg13054523	ENSG00000176845	3075	-6.41	1.46E-10	4.37E-10	----	METRNL
chr17: 81055722	cg13054523	ENSG00000175711	3075	4.65	3.32E-06	6.64E-06	++++	B3GNTL1
chr17: 9862873	cg26996616	ENSG00000007237	3075	2.796	5.18E-03	1.55E-02	++++	GAS7
chr18: 61557735	cg20875821	ENSG00000242550	3075	7.957	1.77E-15	5.30E-15	++++	SERPINB10
chr18: 61557735	cg20875821	ENSG00000197632	3075	-3.546	3.91E-04	3.91E-04	----	SERPINB2
chr18: 61557735	cg20875821	ENSG00000166401	3075	-7.742	9.77E-15	1.47E-14	----	SERPINB8
chr19: 1173241	cg08408668	ENSG00000248015	2182	3.417	6.34E-04	4.86E-03	+++?	
chr19: 1173241	cg08408668	ENSG00000130005	3075	5.069	4.00E-07	9.21E-06	+-++	GAMT
chr19: 1173241	cg08408668	ENSG00000167470	3075	-3.25	1.15E-03	6.64E-03	----	MIDN
chr19: 1173241	cg08408668	ENSG00000116017	3075	-3.926	8.62E-05	9.92E-04	----	ARID3A
chr19: 1173241	cg08408668	ENSG00000064932	3075	-2.948	3.20E-03	1.47E-02	--+-	SBNO2
chr19: 5851504	cg09001777	ENSG00000105519	3075	3.53	4.16E-04	2.08E-03	+-++	CAPS
chr19: 5851504	cg09001777	ENSG00000167733	3075	3.662	2.51E-04	1.88E-03	++++	HSD11B1L
chr19: 5851504	cg09001777	ENSG00000130255	3075	4.266	1.99E-05	2.98E-04	+-++	RPL36
chr19: 5851504	cg09001777	ENSG00000266983	2182	3.072	2.13E-03	7.98E-03	+++?	
chr19: 827715	cg02147126	ENSG00000172270	3075	-3.548	3.89E-04	4.47E-03	--+-	BSG
chr19: 827715	cg02147126	ENSG00000116017	3075	-4.243	2.21E-05	5.08E-04	----	ARID3A
chr19: 827739	cg14663914	ENSG00000172270	3075	-3.325	8.83E-04	9.05E-03	----	BSG
chr19: 827739	cg14663914	ENSG00000099821	3075	3.243	1.18E-03	9.05E-03	+-++	POLRMT
chr19: 827739	cg14663914	ENSG00000116017	3075	-3.967	7.29E-05	1.68E-03	----	ARID3A
chr19: 827821	cg15610437	ENSG00000172270	3075	-3.518	4.35E-04	5.00E-03	----	BSG
chr19: 827821	cg15610437	ENSG00000116017	3075	-3.786	1.53E-04	3.52E-03	----	ARID3A
chr20: 35422703	cg21045547	ENSG00000101084	3075	3.265	1.09E-03	1.31E-02	++++	C20orf24
chr20: 35504371	cg09241885	ENSG00000101342	3075	2.693	7.08E-03	2.71E-02	++++	TLDC2
chr20: 35504371	cg09241885	ENSG00000080839	3075	3.483	4.95E-04	3.96E-03	+-++	RBL1
chr20: 35504371	cg09241885	ENSG00000101347	3075	2.57	1.02E-02	2.71E-02	-+++	SAMHD1
chr20: 43590115	cg13792581	ENSG00000101104	3075	4.441	8.95E-06	6.26E-05	++++	PABPC1L

chr20: 43590115	cg13792581	ENSG00000124233	3075	-3.767	1.65E-04	3.85E-04	----	SEMG1
chr20: 43590115	cg13792581	ENSG00000025772	3075	-3.929	8.53E-05	2.99E-04	----	TOMM34
chr20: 60709957	cg13197551	ENSG00000149657	3075	-7.965	1.66E-15	1.66E-14	----	LSM14B
chr22: 19953712	cg18731680	ENSG00000215012	3075	7.353	1.94E-13	1.55E-12	++++	C22orf29
chr22: 19953712	cg18731680	ENSG00000099889	3075	-8.73	2.55E-18	4.08E-17	----	ARVCF
chr22: 19953712	cg18731680	ENSG00000093010	3075	-4.02	5.83E-05	3.11E-04	----	COMT
chr22: 19953712	cg18731680	ENSG00000183597	3075	-3.469	5.22E-04	2.09E-03	----	TANGO2
chr22: 21921269	cg06850285	ENSG00000100027	3075	-2.658	7.85E-03	1.57E-02	-+--	YPEL1
chr22: 21921269	cg06850285	ENSG00000169635	3075	4.555	5.24E-06	2.70E-05	++++	HIC2
chr22: 21921269	cg06850285	ENSG00000183506	3075	3.626	2.87E-04	9.58E-04	+-++	PI4KAP2
chr22: 21921269	cg06850285	ENSG00000100030	3075	-4.548	5.40E-06	2.70E-05	-+--	MAPK1
chr22: 21921269	cg06850285	ENSG00000161179	3075	2.371	1.77E-02	2.95E-02	+-++	YDJC
chr22: 21921269	cg06850285	ENSG00000161180	3075	-3.148	1.65E-03	4.12E-03	----	CCDC116
chr22: 27014116	cg02455383	ENSG00000100099	3075	4.795	1.63E-06	1.06E-05	++++	HPS4
chr22: 27014116	cg02455383	ENSG00000223704	3075	5.325	1.01E-07	1.31E-06	++++	
chr22: 27014116	cg02455383	ENSG00000128203	3075	-3.545	3.92E-04	1.70E-03	--+-	ASPHD2
chr22: 45555611	cg21211039	ENSG00000100364	3075	-3.621	2.94E-04	1.03E-03	----	KIAA0930
chr22: 45555611	cg21211039	ENSG00000093000	3075	-2.918	3.52E-03	8.22E-03	----	NUP50
chr22: 45555611	cg21211039	ENSG00000226328	3075	-10.408	2.29E-25	1.60E-24	----	

[1] Analyses are restricted to the 169 differentially methylated CpG sites identified in non-atopic asthma that are found in the 450K

[2] BIOS was able to conduct cis-eQTM analyses for 168 CpG sites. 120 CpG sites were associated with gene expression.

[3] Genome build GRCh37/hg19

[4] Adjusted for for age, sex, lymphocyte proportion, monocyte proportion, and RNA flow cell number

Table E9. Druggable Targets of Novel Asthma Genes Identified in Non-atopic Asthma

chromosome	position	CpG	Gene	ChEMBL Drug Target	ChEMBL_25 database released on 01/02/2019	Approved drugs and clinical candidates
1	220965460	cg25967384	MARC1	CHEMBL3706559	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3706559/	No
12	5851581	cg20378408	ANO2	CHEMBL4105767	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105767/	No
10	52127425	cg25372176	ASAH2	CHEMBL2021754	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2021754/	No
11	104898835	cg10220988	CASP5	CHEMBL3131	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3131/	No
11	104898835	cg10220988	CASP5	CHEMBL3831289	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3831289/	EMRICASAN
12	4312337	cg23428738	CCND2	CHEMBL2095942	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3301385/	No
12	4312337	cg23428738	CCND2	CHEMBL3301386	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3301386/	No
12	4312337	cg23428738	CCND2	CHEMBL2095942	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095942/	No
6	41996600	cg02024241	CCND3	CHEMBL2422	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2422/	No
6	41996600	cg02024241	CCND3	CHEMBL3038472	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3038472/	No
6	41996600	cg02024241	CCND3	CHEMBL2111448	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111448/	No
6	41996600	cg02024241	CCND3	CHEMBL2095942	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095942/	No
12	56120970	cg15338098	CD63	CHEMBL3713303	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3713303/	No
5	76248749	cg16545105	CRHBP	CHEMBL5930	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5930/	No
5	76248749	cg16545105	CRHBP	CHEMBL3885546	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3885546/	No
2	234246583	cg05724080	DGKD	CHEMBL1075120	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1075120/	No
13	103509167	cg01555198	ERCC5	CHEMBL4736	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4736/	No
11	128562297	cg19296671	FLI1	CHEMBL3885568	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3885568/	No
6	108910710	cg16775629	FOXO3	CHEMBL5778	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5778/	No
19	5851504	cg09001777	FUT3	CHEMBL3269	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3269/	No
9	80602527	cg25348163	GNAQ	CHEMBL3286079	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3286079/	No
1	37239629	cg19032328	GRIK3	CHEMBL3684	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3684/	No
1	37239629	cg19032328	GRIK3	CHEMBL2109241	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2109241/	No
5	176856845	cg19459094	GRK6	CHEMBL6144	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL6144/	No
22	35773941	cg12165656	HMOX1	CHEMBL2823	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2823/	No
18	22040005	cg14997111	HRH4	CHEMBL3759	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3759/	TOREFORANT, PF-03893787, UR-63325
18	22040005	cg14997111	HRH4	CHEMBL2111378	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111378/	No
16	57833579	cg26819611	KIFC3	CHEMBL1075119	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1075119/	No
5	179200573	cg10113951	LTC4S	CHEMBL1743183	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1743183/	No
4	140697658	cg13120180	MGST2	CHEMBL1743185	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1743185/	No
17	4741523	cg06449385	MINK1	CHEMBL5518	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5518/	No
17	4741523	cg06449385	MINK1	CHEMBL3430890	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430890/	No

3	123371420	cg07638500	MYLK	CHEMBL2428	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2428/	No
16	46776932	cg16064932	MYLK3	CHEMBL4627	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4627/	No
11	34230092	cg21876760	NAT10	CHEMBL4105935	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105935/	No
1	247581408	cg00448525	NLRP3	CHEMBL1741208	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1741208/	No
12	100866309	cg09313442	NR1H4	CHEMBL2047	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2047/	PX-102, TUROFEXORATE ISOPROPYL, CHENODIOL, URSODIOL, OBETICHOLIC ACID
3	119498870	cg09113950	NR1I2	CHEMBL3401	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3401/	No
10	126040305	cg25715278	OAT	CHEMBL5954	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5954/	No
11	72983405	cg04099543	P2RY6	CHEMBL4714	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4714/	No
1	66777579	cg24058805	PDE4B	CHEMBL275	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL275/	No
1	66777579	cg24058805	PDE4B	CHEMBL2093863	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2093863/	ROFLUMILAST, AMLEXANOX, DYPHYLLINE, APREMILAST, THEOPHYLLINE GLYCINATE, CRISABOROLE, THEOPHYLLINE, FLAVOXATE
1	66777579	cg24058805	PDE4B	CHEMBL2095153	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095153/	No
1	66777579	cg24058805	PDE4B	CHEMBL2111340	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111340/	No
1	66777579	cg24058805	PDE4B	CHEMBL2363066	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2363066/	DIPYRIDAMOLE, PENTOXIFYLLINE
1	66736380	cg00849335	PDE4B	CHEMBL275	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL275/	No
1	66736380	cg00849335	PDE4B	CHEMBL2093863	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2093863/	ROFLUMILAST, AMLEXANOX, DYPHYLLINE, APREMILAST, THEOPHYLLINE GLYCINATE, CRISABOROLE, THEOPHYLLINE, FLAVOXATE
1	66736380	cg00849335	PDE4B	CHEMBL2095153	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095153/	No
1	66736380	cg00849335	PDE4B	CHEMBL2111340	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111340/	No
1	66736380	cg00849335	PDE4B	CHEMBL2363066	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2363066/	DIPYRIDAMOLE, PENTOXIFYLLINE
12	118577239	cg13346427	PEBP1	CHEMBL4105856	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105856/	No
10	81034149	cg13250178	PPIF	CHEMBL3325306	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3325306/	No
11	503283	cg05567377	RNH1	CHEMBL5893	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5893/	No
1	179261588	cg20999663	SOAT1	CHEMBL2782	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2782/	BENFLUOREX
20	39704724	cg05026674	TOP1	CHEMBL1781	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1781/	BECATECARIN, IRINOTECAN SUCROSOFATE, ETIRINOTECAN PEGOL, IRINOTECAN
1	165826270	cg09277749	UCK2	CHEMBL2469	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2469/	No
1	165826270	cg09277749	UCK2	CHEMBL3542438	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3542438/	No
12	6233657	cg27347104	VWF	CHEMBL2021748	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2021748/	CAPLACIZUMAB
3	46131480	cg00005461	XCR1	CHEMBL4339	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4339/	No
3	46142638	cg16171189	XCR1	CHEMBL4339	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4339/	No

Table E10. Replication Look-up Results of Non-atopic Asthma

				ALHS				In 450K Array?	PACE			EVA-PR		SAPALDIA			Project Viva		SLSJ		
chromosome	position^1	CpG	Gene Name	Beta	SE	P	FDR		Beta	SE	P	Beta	P	Beta	SE	P	Beta	P	Beta	SE	P
3	46131480	cg00005461	XCR1	-3.1635	0.73773364	1.80E-05	0.041037429		-	-	-	-	-	-	-	-	-0.0005	0.855567	-	-	-
11	34486306	cg00127788	CAT	-6.1289	1.417274728	1.53E-05	0.040190712		-	-	-	-	-	-	-	-	0.004531	0.026213	-	-	-
1	206257829	cg00136106	C1orf186	-2.638	0.60804858	1.43E-05	0.040190712		-	-	-	-	-	-	-	-	0.010125	0.254309	-	-	-
6	53791988	cg00273658	LOC1019271	-4.8454	1.123471626	1.61E-05	0.040501315		-	-	-	-	-	-	-	-	-0.00164	0.616855	-	-	-
20	31067881	cg00280111	NOL4L	-3.2723	0.780499216	2.76E-05	0.047496804		-	-	-	-	-	-	-	-	-0.0018	0.672652	-	-	-
14	55583041	cg00336912	LGALS3	-17.816	3.815257505	3.02E-06	0.027181247		-	-	-	-	-	-	-	-	-0.01726	0.003313	-	-	-
2	137080313	cg00344572	CXCR4	-3.602	0.798140928	6.39E-06	0.034956921		-	-	-	-	-	-	-	-	-0.00246	0.313965	-	-	-
12	15124659	cg00390941	PDE6H	-22.747	5.459791827	3.10E-05	0.049213288	1	-9.4594	3.1526	0.002696	-0.69477	0.029349	0.416539	0.283547	0.141825	-0.01026	0.001716	-12.098	5.206	0.02
17	33885049	cg00397422	SLFN14	-10.334	2.477499487	3.03E-05	0.048886141	1	-4.6987	2.5948	0.07017	0.109807	0.7601	-0.12217	0.318339	0.701157	-0.01326	0.006207	-7.678	3.786	0.043
1	247581408	cg00448525	NLRP3	-2.8349	0.595575769	1.94E-06	0.026069972		-	-	-	-	-	-	-	-	0.000599	0.844414	-	-	-
19	3521502	cg00477633	FZR1	-18.72	4.0483412	3.76E-06	0.028467711		-	-	-	-	-	-	-	-	-0.01415	0.007951	-	-	-
18	33553117	cg00663686	C18orf21	-131.15	29.33068303	7.77E-06	0.036283428	1	-9.4633	5.5893	0.09043	0.201713	0.591605	0.278638	0.236991	0.239702	0.000143	0.645349	0.501	106.488	0.996
19	39742656	cg00717259	IFNL4	-5.2375	1.168253705	7.35E-06	0.035817794		-	-	-	-	-	-	-	-	-0.0039	0.39312	-	-	-
3	45688760	cg00780501	LIMD1-AS1	-2.7009	0.64242683	2.62E-05	0.04726483		-	-	-	-	-	-	-	-	-0.00143	0.177695	-	-	-
12	123459749	cg00795535	OGFOD2	32.7232	7.350334605	8.51E-06	0.037178678	1	-8.5189	4.5345	0.06029	0.306453	0.350928	0.155615	0.228816	0.496449	0.002537	0.016391	-18.164	52.947	0.732
6	110720501	cg00847453	DDO	-3.5797	0.81934664	1.25E-05	0.038716406	1	-0.1587	1.6375	0.9228	0.803688	0.092477	0.057595	0.226117	0.798946	0.000167	0.978992	0.172	6.675	0.979
1	66736380	cg00849335	PDE4B	-1.8627	0.435971441	1.93E-05	0.042250758		-	-	-	-	-	-	-	-	0.004506	0.424714	-	-	-
11	71786271	cg00893849	MIR3165	-7.1518	1.547376777	3.80E-06	0.028467711		-	-	-	-	-	-	-	-	-0.00356	0.453486	-	-	-
16	50701499	cg00921350	LOC1019272	-4.9197	1.130003953	1.34E-05	0.039250229	1	-5.4937	2.0177	0.006475	-0.09793	0.896255	0.21383	0.218052	0.326771	-0.01388	0.005333	-11.96	8.09	0.139
19	1948987	cg01014987	CSNK1G2-AS	-3.115	0.701755939	9.04E-06	0.037178678		-	-	-	-	-	-	-	-	0.001236	0.79688	-	-	-
10	119167795	cg01086527	PDZD8	-14.904	3.446660759	1.53E-05	0.040190712		-	-	-	-	-	-	-	-	-0.01992	9.41E-05	-	-	-
14	68713369	cg01171954	LOC1009966	-6.0851	1.211003233	5.04E-07	0.01660328		-	-	-	-	-	-	-	-	-0.01395	0.050017	-	-	-
11	18299633	cg01247459	SAA1	-2.9354	0.661404813	9.07E-06	0.037178678		-	-	-	-	-	-	-	-	0.004468	0.150109	-	-	-
17	58155376	cg01248878	HEATR6	-4.3594	1.038515419	2.70E-05	0.047443003	1	-1.6265	1.872	0.3849	-1.12915	0.019904	-0.03284	0.419262	0.937559	0.003656	0.061826	-2.199	6.24	0.724
11	3145609	cg01418188	OSBPL5	-3.4366	0.801089183	1.79E-05	0.041037429	1	2.146	2.7741	0.4392	0.197808	0.742201	0.598286	0.499636	0.231133	0.005102	0.050394	0.581	5.57	0.917
2	113380344	cg01469583	FLJ42351	-2.482	0.586322453	2.30E-05	0.044582402		-	-	-	-	-	-	-	-	-0.00073	0.663549	-	-	-
9	35755346	cg01499988	MSMP	-12.313	2.771238534	8.86E-06	0.037178678	1	-12.469	2.6238	2.01E-06	-0.61544	0.087221	0.328273	0.277951	0.237584	-0.01334	0.014485	-7.224	3.458	0.037
10	99168386	cg01541570	RRP12	-3.4218	0.820129932	3.02E-05	0.048867467		-	-	-	-	-	-	-	-	-0.00121	0.386855	-	-	-
13	103509167	cg01555198	ERCC5	-3.6448	0.837786465	1.36E-05	0.039250229		-	-	-	-	-	-	-	-	-0.01233	0.251356	-	-	-
5	86375384	cg01611175	MIR4280	-4.0694	0.921365729	1.00E-05	0.037915742		-	-	-	-	-	-	-	-	-0.01224	0.027176	-	-	-
10	45495435	cg01614759	ZNF22	-13.89	2.744496175	4.17E-07	0.015811056	1	-9.3123	2.3643	8.19E-05	-0.18464	0.551395	0.101461	0.241191	0.674	-0.0236	3.21E-05	-5.805	2.789	0.037
9	126497597	cg01745810	DENND1A	-12.695	2.774732133	4.76E-06	0.030406268		-	-	-	-	-	-	-	-	-	-	-	-	-
11	94336029	cg01887834	PIWIL4	-2.2395	0.527987549	2.22E-05	0.044011775		-	-	-	-	-	-	-	-	0.000893	0.88313	-	-	-
14	95615731	cg01901579	DICER1	-12.783	3.022785731	2.35E-05	0.044925686	1	-9.286	2.0492	5.86E-06	-0.74362	0.061919	0.281885	0.291456	0.333464	-0.02147	0.000589	-7.337	3.493	0.036
2	96965099	cg01923915	SNRNP200	-16.775	3.567638666	2.58E-06	0.027181247		-	-	-	-	-	-	-	-	-0.01906	0.000939	-	-	-
13	47161752	cg01953813	LRCH1	-3.4276	0.812558957	2.46E-05	0.045935495		-	-	-	-	-	-	-	-	0.005333	0.460959	-	-	-
17	56269767	cg01955639	EPX	-12.668	2.477710126	3.18E-07	0.015811056		-	-	-	-	-	-	-	-	-0.02277	1.55E-05	-	-	-
18	13302729	cg02006119	LDLRAD4	-4.4029	1.017067101	1.50E-05	0.040190712		-	-	-	-	-	-	-	-	-0.00649	0.099619	-	-	-
6	41996600	cg02024241	CCND3	-4.143	0.945057627	1.17E-05	0.038178101		-	-	-	-	-	-	-	-	0.006243	0.309456	-	-	-
7	129266958	cg02041484	NRF1	-2.3437	0.538390094	1.34E-05	0.039250229	1	-3.7904	1.9088	0.04706	-	-	1.081459	0.618567	0.080407	0.008825	0.067463	-1.858	2.838	0.513
19	827715	cg02147126	AZU1	-3.4722	0.790420884	1.12E-05	0.038178101	1	-5.5719	2.055	0.006701	-0.06501	0.861069	0.797204	0.568466	0.160803	-0.00303	0.163843	-1.221	3.219	0.705
17	41172412	cg02190078	VAT1	-3.3455	0.754799635	9.32E-06	0.037291968		-	-	-	-	-	-	-	-	0.000816	0.824272	-	-	-
15	40601467	cg02240622	PLCB2	-3.307	0.78537171	2.54E-05	0.046317494	1	-4.731	2.3504	0.04413	-	-	-0.0243	0.656918	0.970491	-0.00153	0.567423	-2.111	3.728	0.571
3	132831676	cg02274033	TMEM108	-2.3432	0.530083261	9.85E-06	0.037840547		-	-	-	-	-	-	-	-	0.015237	0.120164	-	-	-
6	33382557	cg02305757	CUTA	-4.5547	1.093447509	3.11E-05	0.049213288	1	-0.9771	2.8815	0.7345	0.440981	0.695803	-0.01981	0.251042	0.937103	-0.00343	0.437684	-14.544	9.551	0.128
3	159532265	cg02342367	SCHIP1	8.32017	1.928823433	1.61E-05	0.040501315		-	-	-	-	-	-	-	-	0.003105	0.339809	-	-	-
14	72050329	cg02414559	SIPA1L1	-2.3632	0.548450143	1.64E-05	0.040501315		-	-	-	-	-	-	-	-	-0.00264	0.52569	-	-	-
6	139656042	cg02432022	CITED2	-2.0389	0.450778005	6.10E-06	0.033920223		-	-	-	-	-	-	-	-	-	-	-	-	-
5	159743203	cg02441833	CCNJL	-21.497	5.152801576	3.02E-05	0.048867467	1	-4.1776	3.6425	0.2514	0.643278	0.084987	0.425126	0.300483	0.157124	0.002376	0.331837	-17.988	16.133	0.265

22	27014116	cg02455383	CRYBB1	-3.6207	0.861868637	2.66E-05	0.047443003	1	-2.0618	2.3048	0.371	-	-	0.338817	0.458217	0.459649	-0.00576	0.084972	-3.469	4.18	0.407
13	30307238	cg02480174	LOC1027233	-3.616	0.804734971	7.01E-06	0.035817794		-	-	-	-	-	-	-	-	-0.00584	0.380696	-	-	-
14	39643445	cg02543556	PNN	-15.087	3.440666417	1.16E-05	0.038178101		-	-	-	-	-	-	-	-	-0.01824	0.000249	-	-	-
2	7027871	cg02589986	RSAD2	-6.2571	1.449708801	1.59E-05	0.040501315		-	-	-	-	-	-	-	-	-0.02074	0.000333	-	-	-
1	44411569	cg02835421	IPO13	-6.5897	1.401223678	2.57E-06	0.027181247	1	-4.3593	2.8167	0.1217	-0.36478	0.50857	0.208981	0.409854	0.610127	0.002743	0.153429	-4.336	7.895	0.583
20	11758521	cg02844688	LINC00687	-3.5878	0.809923958	9.43E-06	0.037291968		-	-	-	-	-	-	-	-	0.003428	0.716535	-	-	-
2	220115026	cg02961280	TUBA4B	-8.9757	2.030621518	9.86E-06	0.037840547	1	-1.9726	1.9187	0.3039	-	-	0.438603	0.395877	0.267892	0.001532	0.288594	-9.144	8.201	0.265
11	62164435	cg02974089	SCGB1A1	-4.6543	1.015288396	4.56E-06	0.030038603		-	-	-	-	-	-	-	-	-0.02188	0.003747	-	-	-
7	2116512	cg03116466	MAD1L1	-3.4583	0.802845321	1.65E-05	0.040515973	1	-7.1861	2.6298	0.006284	-	-	0.198413	0.483605	0.681602	-0.00647	0.184566	-1.827	4.621	0.693
1	33227555	cg03125875	KIAA1522	-6.1115	1.306265281	2.89E-06	0.027181247		-	-	-	-	-	-	-	-	-0.01328	0.005624	-	-	-
9	95800911	cg03234093	SUSD3	-4.8395	0.954641773	3.99E-07	0.015811056		-	-	-	-	-	-	-	-	3.22E-06	0.998905	-	-	-
4	124165382	cg03326609	SPRY1	-5.0601	1.079787581	2.78E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00953	0.119434	-	-	-
1	3282449	cg03337482	ARHGEF16	-3.4049	0.711681676	1.72E-06	0.026069972	1	-2.9162	1.4975	0.05149	0.487219	0.233328	-0.03787	0.248839	0.879024	-0.00806	0.167641	-12.333	6.489	0.057
4	89446409	cg03340036	LOC1019291	-2.1082	0.453819855	3.39E-06	0.027181247	1	-1.512	1.7205	0.3795	-	-	0.819406	0.73997	0.268142	-0.00636	0.112681	-1.812	2.128	0.394
7	151011113	cg03381616	NUB1	-3.157	0.728082724	1.45E-05	0.040190712		-	-	-	-	-	-	-	-	-0.00612	0.436753	-	-	-
16	16195619	cg03392077	ABCC6	-5.4653	1.229179406	8.74E-06	0.037178678		-	-	-	-	-	-	-	-	-0.0159	0.022775	-	-	-
7	1650459	cg03489907	TFAMP1	73.5763	17.39499323	2.34E-05	0.044912444	1	1.2399	6.6522	0.8521	-0.05845	0.869811	-0.07476	0.241961	0.757342	0.001926	0.252722	-238.701	153.18	0.119
17	62075151	cg03554335	PRR29	-3.9544	0.871533009	5.70E-06	0.033268202	1	-1.2145	1.8552	0.5127	0.297583	0.546147	0.109226	0.335444	0.744715	0.011118	0.021331	-0.682	6.107	0.911
12	14999304	cg03634089	ART4	-5.014	1.193933784	2.67E-05	0.047443003		-	-	-	-	-	-	-	-	0.00081	0.559955	-	-	-
15	101798908	cg03666966	CHSY1	-20.847	4.907606237	2.16E-05	0.043837662		-	-	-	-	-	-	-	-	-	-	-	-	-
7	128899554	cg03822873	AHCYL2	-7.2777	1.639846255	9.08E-06	0.037178678	1	-1.8333	1.906	0.3361	0.224811	0.490325	0.678605	0.386588	0.079195	0.000295	0.902235	-7.302	5.862	0.213
3	52223131	cg03881379	ALAS1	-5.1193	1.072071326	1.80E-06	0.026069972		-	-	-	-	-	-	-	-	-0.00101	0.746962	-	-	-
4	3084890	cg03914277	HTT	-6.3368	1.343264516	2.39E-06	0.027181247		-	-	-	-	-	-	-	-	-0.01405	0.003906	-	-	-
12	58210661	cg04046364	AVIL	-2.9838	0.715051215	3.01E-05	0.048867467	1	-1.1666	2.0248	0.5645	-0.28838	0.396542	0.603948	0.689575	0.381124	0.000394	0.894348	-1.623	2.94	0.581
2	136781306	cg04052546	DARS	-2.1564	0.495369158	1.34E-05	0.039250229		-	-	-	-	-	-	-	-	-	-	-	-	-
10	75677011	cg04084348	C10orf55	-3.7439	0.854710171	1.18E-05	0.038353842	1	-4.6609	2.76	0.09127	-0.25306	0.483683	0.396276	0.514604	0.441264	0.000715	0.780375	-2.166	4.163	0.603
11	72983405	cg04099543	P2RY6	-4.266	0.943026677	6.08E-06	0.033920223	1	-6.09	2.9067	0.03616	-	-	0.25743	0.592718	0.664055	0.004554	0.375785	5.659	6.44	0.38
6	125919706	cg04161328	LOC643623	-2.6439	0.632643349	2.93E-05	0.048597685		-	-	-	-	-	-	-	-	-0.00029	0.714491	-	-	-
16	68334619	cg04304036	SLC7A6OS	-2.4691	0.565109428	1.25E-05	0.038716406	1	-4.582	1.9293	0.01755	-0.11863	0.676859	1.750598	0.692324	0.011452	0.005811	0.158036	-2.45	2.636	0.353
14	81883595	cg04316096	STON2	-4.6635	1.114583305	2.86E-05	0.048161332		-	-	-	-	-	-	-	-	-0.00292	0.283667	-	-	-
4	25789390	cg04349839	SEL1L3	-2.7552	0.647845911	2.11E-05	0.043458285	1	0.07	1.6866	0.9669	0.122585	0.696096	0.265845	0.495568	0.59165	-0.00556	0.375301	-4.404	4.189	0.293
9	132044732	cg04395593	LOC1019293	-3.5552	0.849704091	2.86E-05	0.048161332		-	-	-	-	-	-	-	-	0.000141	0.936023	-	-	-
16	616212	cg04497992	NHLRC4	-6.7792	1.568041863	1.54E-05	0.040190712	1	-10.133	2.128	1.92E-06	0.212269	0.71443	0.137039	0.281907	0.626886	-0.0161	0.007584	-9.761	4.778	0.041
1	31958245	cg04552418	LINC01225	-2.1713	0.513557793	2.36E-05	0.044940396	1	-2.6956	1.8286	0.1404	0.304507	0.270909	1.807041	0.708114	0.010714	-0.00053	0.784111	-1.059	2.469	0.668
12	113330801	cg04662947	OAS1	-9.6606	2.193592412	1.06E-05	0.038178101		-	-	-	-	-	-	-	-	-0.0009	0.658132	-	-	-
22	26873008	cg04701118	HPS4	-2.3604	0.552221922	1.92E-05	0.04209883		-	-	-	-	-	-	-	-	-0.00409	0.167584	-	-	-
10	11799636	cg04765471	ECHDC3	-5.7132	1.26180654	5.96E-06	0.033920223		-	-	-	-	-	-	-	-	-0.02244	0.001533	-	-	-
15	52028433	cg04804748	LYSMD2	-7.2361	1.612918065	7.25E-06	0.035817794		-	-	-	-	-	-	-	-	-0.00237	0.518714	-	-	-
12	105043367	cg04814136	MIR3922	-2.3381	0.521599146	7.38E-06	0.035817794		-	-	-	-	-	-	-	-	-0.00285	0.466323	-	-	-
10	53005907	cg04905364	MIR605	-10.62	2.53391279	2.78E-05	0.047496804		-	-	-	-	-	-	-	-	-0.00339	0.357608	-	-	-
12	50262986	cg04920032	BCDIN3D	-3.8986	0.930713148	2.80E-05	0.047743066	1	-2.0845	2.4538	0.3956	-0.05218	0.943738	-0.21776	0.454578	0.631906	-0.01521	0.002957	-7.188	4.626	0.12
6	36318881	cg04924375	C6orf222	-5.6804	1.270016505	7.72E-06	0.036278845		-	-	-	-	-	-	-	-	-0.00488	0.158055	-	-	-
1	159859638	cg04954249	MIR4259	-3.9463	0.911124834	1.48E-05	0.040190712		-	-	-	-	-	-	-	-	0.008709	0.00225	-	-	-
8	117059957	cg04962865	LINC00536	23.8065	5.509922645	1.56E-05	0.040233061	1	-0.9227	2.9775	0.7567	-0.14324	0.659904	-0.14918	0.215008	0.487775	-0.00018	0.868511	-16.444	31.081	0.597
1	49317683	cg04976987	BEND5	-3.0141	0.677609567	8.66E-06	0.037178678		-	-	-	-	-	-	-	-	-	-	-	-	-
3	13457267	cg04992150	NUP210	-4.6094	1.027081656	7.19E-06	0.035817794	1	0.4221	2.6181	0.8719	0.782914	0.355114	0.698578	0.421851	0.097725	0.003746	0.061256	-3.857	4.415	0.382
20	39704724	cg05026674	TOP1	-9.3071	1.995052814	3.08E-06	0.027181247		-	-	-	-	-	-	-	-	-0.02295	0.001098	-	-	-
1	167198727	cg05121010	POU2F1	-6.025	1.447314161	3.14E-05	0.049488072		-	-	-	-	-	-	-	-	-0.0047	0.290847	-	-	-
11	75114223	cg05122026	SNORD15B	-6.4437	1.529204823	2.51E-05	0.045984376	1	-0.5523	2.3924	0.8174	0.482409	0.536136	-0.0032	0.264824	0.990363	0.002585	0.52025	-49.974	20.841	0.016
5	173199528	cg05150185	LINC01485	-3.1415	0.748422455	2.70E-05	0.047443003		-	-	-	-	-	-	-	-	-0.00538	0.189243	-	-	-
3	50650322	cg05186879	MAPKAPK3	-4.4448	0.939064429	2.21E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00958	0.122756	-	-	-
3	107836286	cg05209272	LINC01215	-3.388	0.772046262	1.14E-05	0.038178101		-	-	-	-	-	-	-	-	-0.00047	0.936286	-	-	-
15	70492278	cg05219896	TLE3	-4.3959	1.052610134	2.96E-05	0.048683157		-	-	-	-	-	-	-	-	-0.01659	0.004278	-	-	-

20	10534496	cg05232481	MIR6870	-2.4592	0.541311643	5.55E-06	0.032848739		-	-	-	-	-	-	-	-	0.001815	0.504572	-	-	-
16	81517665	cg05499338	CMIP	-12.372	2.603330945	2.01E-06	0.026069972	1	-5.5279	2.3839	0.0204	-0.00913	0.97555	0.08069	0.244607	0.741494	-0.0193	4.13E-05	-5.789	3.075	0.06
21	46496180	cg05516004	ADARB1	-28.566	5.997826038	1.91E-06	0.026069972	1	-1.0069	3.1535	0.7495	-0.29935	0.416424	0.386346	0.278486	0.165347	-0.00551	0.003344	-23.007	10.542	0.029
11	503283	cg05567377	RNH1	-3.2763	0.750454203	1.27E-05	0.038930229		-	-	-	-	-	-	-	-	0.007107	0.075741	-	-	-
2	28550757	cg05642098	LOC1005057	-19.123	4.311817242	9.21E-06	0.037178678		-	-	-	-	-	-	-	-	-0.02162	0.001251	-	-	-
1	156221285	cg05699320	PAQR6	-4.5971	1.043145428	1.05E-05	0.03807844		-	-	-	-	-	-	-	-	-0.00698	0.214867	-	-	-
2	234246583	cg05724080	DGKD	-8.0132	1.86916157	1.81E-05	0.041037429		-	-	-	-	-	-	-	-	-0.02212	8.60E-05	-	-	-
16	75145843	cg05820066	LDHD	-2.9547	0.656302589	6.73E-06	0.035404611	1	-0.8826	2.0138	0.6612	0.900105	0.017793	-0.01073	0.392278	0.978186	0.002796	0.686231	-0.187	4.06	0.963
15	52427175	cg05853552	BCL2L10	-16.238	3.38035606	1.56E-06	0.026069972		-	-	-	-	-	-	-	-	-0.01408	0.001468	-	-	-
1	36352279	cg05873271	AGO1	-6.6364	1.520814316	1.28E-05	0.03913888		-	-	-	-	-	-	-	-	-0.00208	0.421182	-	-	-
16	29822365	cg05918326	PRRT2	-15.423	3.393296596	5.49E-06	0.032740109		-	-	-	-	-	-	-	-	0.002535	0.113773	-	-	-
6	134956367	cg05920921	LOC1019283	-2.1503	0.467379686	4.21E-06	0.028624856		-	-	-	-	-	-	-	-	-0.00225	0.571663	-	-	-
16	88558237	cg05958985	MIR5189	-7.7346	1.794540174	1.63E-05	0.040501315	1	-4.088	2.0771	0.04905	0.338032	0.468255	0.135926	0.239779	0.570795	-0.01465	0.000718	-11.132	5.554	0.045
19	14397583	cg05962003	LINC01842	-4.7578	1.117722924	2.08E-05	0.043260494		-	-	-	-	-	-	-	-	-0.01505	0.049685	-	-	-
17	47411420	cg06005163	LOC1027245	-2.6717	0.623162299	1.81E-05	0.041037429		-	-	-	-	-	-	-	-	0.002191	0.638089	-	-	-
6	114016878	cg06052655	LOC1019276	-2.7963	0.601933591	3.39E-06	0.027181247		-	-	-	-	-	-	-	-	0.001874	0.595437	-	-	-
16	68804850	cg06085527	MIR7641-2	-7.2478	1.283145444	1.62E-08	0.007760824		-	-	-	-	-	-	-	-	-0.02106	0.003065	-	-	-
13	39614547	cg06095753	NHLRC3	-3.038	0.646488849	2.61E-06	0.027181247		-	-	-	-	-	-	-	-	0.004632	0.159772	-	-	-
17	25897247	cg06127160	LGALS9	-8.5037	1.74268139	1.06E-06	0.023468934		-	-	-	-	-	-	-	-	-0.03447	1.20E-05	-	-	-
11	44578725	cg06169291	CD82	-11.184	2.609348833	1.82E-05	0.041037429		-	-	-	-	-	-	-	-	0.000457	0.803848	-	-	-
1	154293494	cg06181069	AQP10	-4.787	1.104359068	1.46E-05	0.040190712	1	-2.4867	2.7023	0.3575	-0.20432	0.680852	0.554489	0.536597	0.301443	-0.00432	0.022489	-5.011	6.235	0.422
1	181097559	cg06289919	IER5	-2.5268	0.583818099	1.50E-05	0.040190712		-	-	-	-	-	-	-	-	-0.00208	0.607419	-	-	-
18	2986172	cg06308882	LPIN2	-2.5763	0.599755867	1.74E-05	0.041037429		-	-	-	-	-	-	-	-	-	-	-	-	-
6	159477416	cg06445384	TAGAP	-32.224	7.493087843	1.70E-05	0.040849532		-	-	-	-	-	-	-	-	0.0036	0.357609	-	-	-
17	4741523	cg06449385	MINK1	-14.483	3.371733089	1.74E-05	0.041037429		-	-	-	-	-	-	-	-	-0.01499	0.018207	-	-	-
2	136777134	cg06569561	DARS	-2.6797	0.607527271	1.03E-05	0.037915742		-	-	-	-	-	-	-	-	-	-	-	-	-
18	55250579	cg06592575	FECH	-22.784	4.737128342	1.51E-06	0.026069972		-	-	-	-	-	-	-	-	-0.01629	0.000174	-	-	-
4	16871911	cg06646410	LDB2	-4.3613	1.047868173	3.15E-05	0.049524937		-	-	-	-	-	-	-	-	-0.00327	0.666668	-	-	-
1	161698821	cg06734380	FCRLB	-2.622	0.573976036	4.92E-06	0.030459237		-	-	-	-	-	-	-	-	-	-	-	-	-
7	150773709	cg06807926	FASTK	-4.1121	0.810509691	3.91E-07	0.015811056	1	0.3386	2.0065	0.866	0.973764	0.211453	-0.31984	0.339394	0.345995	0.004072	0.548198	-1.345	6.595	0.838
22	21921269	cg06850285	UBE2L3	-6.187	1.394134853	9.08E-06	0.037178678	1	-0.4246	1.9995	0.8318	-0.48752	0.338201	1.245359	0.565797	0.027731	-	-	-3.947	5.643	0.484
14	75162215	cg06984345	AREL1	-9.0249	2.130022024	2.27E-05	0.044179218		-	-	-	-	-	-	-	-	-0.0232	0.00012	-	-	-
2	102151048	cg07014573	RFX8	-3.83	0.849081391	6.46E-06	0.034956921		-	-	-	-	-	-	-	-	-0.00062	0.822613	-	-	-
6	158564873	cg07137115	SERAC1	-2.4079	0.548573839	1.14E-05	0.038178101		-	-	-	-	-	-	-	-	-0.00116	0.889868	-	-	-
15	52030746	cg07177867	LYSMD2	-11.282	2.461134693	4.56E-06	0.030038603	1	-10.621	2.4352	1.29E-05	-0.32955	0.491581	0.150159	0.258389	0.56115	-0.01973	5.15E-05	-7.012	3.282	0.033
2	178270267	cg07325407	AGPS	-4.2537	0.960026537	9.39E-06	0.037291968		-	-	-	-	-	-	-	-	-0.00703	0.418454	-	-	-
17	64940745	cg07432111	CACNG4	-3.2405	0.739219771	1.17E-05	0.038178101	1	-0.6937	1.2448	0.5773	0.004484	0.99343	-0.01642	0.229552	0.94299	-	-	-10.735	8.805	0.223
4	38110810	cg07456972	TBC1D1	-21.109	4.169276587	4.13E-07	0.015811056		-	-	-	-	-	-	-	-	-0.01928	0.000649	-	-	-
1	150967828	cg07479786	FAM63A	-16.694	3.962999012	2.53E-05	0.046098892	1	10.5648	5.6383	0.06096	-	-	0.235478	0.265567	0.375241	8.82E-06	0.997738	-64.26	58.597	0.273
3	46269741	cg07519863	CCR3	-4.5193	1.034499055	1.25E-05	0.038716406		-	-	-	-	-	-	-	-	-0.01556	0.004387	-	-	-
1	11901487	cg07532960	NPPA-AS1	-3.4807	0.830521088	2.78E-05	0.047496804		-	-	-	-	-	-	-	-	0.000862	0.768006	-	-	-
4	71503456	cg07538578	ENAM	-3.043	0.70314262	1.51E-05	0.040190712		-	-	-	-	-	-	-	-	0.002222	0.722973	-	-	-
11	10543456	cg07565042	MTRNR2L8	-7.0436	1.63563401	1.66E-05	0.040599872	1	-5.5987	2.2987	0.01487	-0.62843	0.136073	0.348227	0.301432	0.247991	-0.01295	0.051647	-6.432	3.1	0.038
18	2980515	cg07616376	LPIN2	-25.733	6.177618654	3.11E-05	0.049213288		-	-	-	-	-	-	-	-	0.002076	0.499943	-	-	-
11	63466987	cg07636225	RTN3	-15.55	3.375146888	4.08E-06	0.028624856	1	-9.7145	2.517	0.000114	-1.48665	0.02395	0.115287	0.274472	0.674463	-0.01625	0.002169	-5.567	2.745	0.043
3	123371420	cg07638500	MYLK	-4.4107	1.044322311	2.41E-05	0.045290749	1	1.292	2.5015	0.6055	-0.08418	0.797044	0.089639	0.477672	0.851145	-0.00216	0.625192	-3.819	4.362	0.381
7	99728544	cg07786412	MBLAC1	-4.4967	1.01914061	1.02E-05	0.037915742		-	-	-	-	-	-	-	-	-0.00382	0.611094	-	-	-
10	74069493	cg07828833	DDIT4	-3.784	0.881309938	1.76E-05	0.041037429	1	-2.9611	2.1854	0.1754	-0.56772	0.215893	-0.19417	0.373082	0.602745	-	-	-7.208	5.042	0.153
21	37536817	cg07834490	DOPEY2	-3.8822	0.907418255	1.88E-05	0.04187031		-	-	-	-	-	-	-	-	-0.01578	0.020078	-	-	-
13	41631052	cg07908654	WBP4	-15.207	2.840435454	8.62E-08	0.008802394	1	-11.465	2.2261	2.60E-07	0.064568	0.823419	0.265149	0.274348	0.33381	-0.02302	0.000784	-5.015	2.438	0.04
3	152215571	cg07952576	TMEM14EP	-2.7288	0.523580415	1.87E-07	0.01316747		-	-	-	-	-	-	-	-	0.001741	0.742458	-	-	-
7	149543165	cg07970948	ZNF862	-5.9494	1.251050973	1.98E-06	0.026069972	1	-9.4111	1.7403	6.39E-08	-0.15648	0.541137	0.170355	0.245997	0.488618	-0.0374	5.42E-06	-8.724	4.037	0.031
1	26091858	cg08028384	SELENON	-7.692	1.397687167	3.73E-08	0.007760824		-	-	-	-	-	-	-	-	-	-	-	-	-

3	16545999	cg08091497	RFTN1	-2.8513	0.577625563	7.96E-07	0.019716136		-	-	-	-	-	-	-	-	0.00364	0.432905	-	-	-
17	56274480	cg08105265	EPX	-13.297	2.869327338	3.58E-06	0.028151074	1	-5.4295	1.7672	0.002123	-0.17754	0.589791	0.278077	0.242099	0.250718	-0.01997	5.05E-06	-10.249	4.444	0.021
17	33426885	cg08154963	RFFL	-2.9774	0.691598346	1.67E-05	0.040601873	1	-4.6677	2.4519	0.05694	-	-	0.617425	0.853783	0.469579	-0.00291	0.241387	-1.877	3.094	0.544
7	134854291	cg08177041	C7orf49	-3.3528	0.724284211	3.67E-06	0.028467711		-	-	-	-	-	-	-	-	-0.00021	0.941539	-	-	-
19	1173241	cg08408668	SBNO2	-4.1431	0.889061972	3.16E-06	0.027181247	1	-1.442	2.1255	0.4975	-1.84187	0.004252	0.666273	0.52351	0.203123	-0.00143	0.525417	-1.246	3.949	0.752
1	234841610	cg08427005	LINC01132	-4.1633	0.927267076	7.13E-06	0.035817794		-	-	-	-	-	-	-	-	0.006332	0.482688	-	-	-
6	14758733	cg08470588	LINC01108	-3.3398	0.734698843	5.47E-06	0.032740109		-	-	-	-	-	-	-	-	-0.00268	0.163815	-	-	-
11	65489884	cg08589455	RNASEH2C	-13.057	3.098893309	2.52E-05	0.045984376		-	-	-	-	-	-	-	-	-0.02002	0.000249	-	-	-
5	137521998	cg08621659	KIF20A	-2.2849	0.535620017	1.99E-05	0.042547094		-	-	-	-	-	-	-	-	-0.00359	0.261728	-	-	-
1	169525950	cg08653021	F5	-37.541	8.267466401	5.60E-06	0.032953606	1	-12.59	3.7187	0.000711	-0.42079	0.175373	-0.24681	0.25379	0.33081	-0.00595	0.004876	-22.595	10.429	0.03
2	129200109	cg08790890	HS6ST1	-3.7229	0.891312049	2.96E-05	0.048683157	1	-1.1309	2.2609	0.6169	-0.15454	0.634954	0.582243	0.350742	0.096908	-0.00288	0.449256	-6.052	5.162	0.241
6	157948630	cg08794018	MIR3692	5.13449	1.225679634	2.80E-05	0.047743066		-	-	-	-	-	-	-	-	0.001945	0.702899	-	-	-
15	31505024	cg08884974	LOC1027250	-13.353	2.640522919	4.26E-07	0.015811056	1	-5.7143	2.562	0.02572	-0.18638	0.517924	0.300093	0.332269	0.36644	-0.01	0.112653	-7.769	3.987	0.051
19	5851504	cg09001777	FUT3	-4.8246	1.012188924	1.87E-06	0.026069972	1	-2.8147	2.8427	0.3221	0.117653	0.791605	0.443196	0.526974	0.400336	0.000654	0.613008	-2.903	5.131	0.572
11	18637603	cg09098714	SPTY2D1-AS	-3.1644	0.669279096	2.27E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00369	0.394221	-	-	-
3	119498870	cg09113950	NR1I2	-2.6046	0.585223281	8.57E-06	0.037178678		-	-	-	-	-	-	-	-	-0.00335	0.55571	-	-	-
13	47161427	cg09131500	LRCH1	-3.5444	0.715615668	7.31E-07	0.019267287		-	-	-	-	-	-	-	-	-0.01741	0.035717	-	-	-
20	4072430	cg09194810	SMOX	-14.823	3.442499704	1.66E-05	0.040599872		-	-	-	-	-	-	-	-	-0.02342	2.15E-05	-	-	-
20	35504371	cg09241885	TLDC2	-9.389	2.210267914	2.16E-05	0.043837662	1	-6.7807	2.2077	0.002131	-	-	0.31768	0.242645	0.190453	-0.01515	0.000295	-11.956	5.081	0.019
1	165826270	cg09277749	UCK2	-3.1919	0.708760092	6.69E-06	0.035404611	1	0.3325	1.3269	0.8021	0.060912	0.811156	-0.32214	0.259474	0.214421	-0.00577	0.536829	1.066	3.929	0.786
12	100866309	cg09313442	NR1H4	-2.1921	0.507954386	1.59E-05	0.040501315		-	-	-	-	-	-	-	-	-	-	-	-	-
2	28564231	cg09468422	LOC1005057	-33.065	6.903397832	1.67E-06	0.026069972		-	-	-	-	-	-	-	-	-0.00405	0.088585	-	-	-
16	67906415	cg09584899	EDC4	-6.8492	1.501564693	5.08E-06	0.031224358		-	-	-	-	-	-	-	-	0.004217	0.090679	-	-	-
3	71256044	cg09589331	FOXP1	-2.2592	0.535787329	2.48E-05	0.045984376		-	-	-	-	-	-	-	-	-0.02621	0.003135	-	-	-
6	32141591	cg09597192	AGPAT1	-19.991	4.644352868	1.67E-05	0.040601873	1	-12.529	2.7256	4.29E-06	0.130076	0.696888	0.273218	0.261409	0.295943	-0.0147	0.002885	-9.054	3.884	0.02
16	89392503	cg09668022	LOC1002870	-4.5332	0.967905454	2.82E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00103	0.703081	-	-	-
7	22395972	cg09698506	RAPGEF5	2.61448	0.609202804	1.77E-05	0.041037429		-	-	-	-	-	-	-	-	0.00088	0.88514	-	-	-
4	40178593	cg09719750	RHOH	-10.457	2.412167429	1.46E-05	0.040190712	1	4.7387	3.1762	0.1357	-0.24533	0.55322	0.293073	0.207464	0.15776	0.00041	0.872659	-25.724	27.825	0.355
2	28578984	cg09763039	FOSL2	-4.0001	0.953018116	2.70E-05	0.047443003		-	-	-	-	-	-	-	-	-0.00755	0.137629	-	-	-
1	27060511	cg09849688	ARID1A	-19.6	4.47140077	1.17E-05	0.038178101	1	-1.0862	1.725	0.5289	-0.11524	0.64981	0.385496	0.269826	0.153095	-0.00081	0.768897	-0.983	9.115	0.914
1	243634599	cg09912228	MIR4677	-2.2067	0.515135395	1.84E-05	0.041319395		-	-	-	-	-	-	-	-	-0.00213	0.572427	-	-	-
6	20034134	cg10011040	MBOAT1	-14.235	3.05854842	3.25E-06	0.027181247		-	-	-	-	-	-	-	-	-	-	-	-	-
5	179200573	cg10113951	LTC4S	-20.697	4.946708189	2.86E-05	0.048161332		-	-	-	-	-	-	-	-	-0.00885	0.006329	-	-	-
17	3880229	cg10132304	ATP2A3	-4.1392	0.968319845	1.91E-05	0.04209883		-	-	-	-	-	-	-	-	-	-	-	-	-
2	234608559	cg10180919	UGT1A6	-11.614	2.123557672	4.52E-08	0.007760824		-	-	-	-	-	-	-	-	-0.01694	0.001072	-	-	-
16	2863919	cg10194884	PRSS21	-4.5449	1.076326662	2.42E-05	0.045317311	1	-2.332	1.907	0.2214	-0.79695	0.359113	-0.26002	0.273627	0.341966	-0.00914	0.086855	-9.329	5.833	0.11
12	27027924	cg10220104	ITPR2	-19.001	4.482075754	2.24E-05	0.044011775		-	-	-	-	-	-	-	-	-	-	-	-	-
11	104898835	cg10220988	CASP5	-2.6884	0.562705962	1.77E-06	0.026069972		-	-	-	-	-	-	-	-	-0.01515	0.07647	-	-	-
5	33205501	cg10291951	TARS	-14.935	3.140906834	1.98E-06	0.026069972		-	-	-	-	-	-	-	-	-0.01579	0.005277	-	-	-
16	73019173	cg10298741	ZFHX3	-11.01	2.633821992	2.91E-05	0.048597685	1	-6.7531	2.4541	0.005928	0.402518	0.382476	0.372043	0.28095	0.185427	-0.01436	0.006099	-8.08	3.706	0.029
12	120528783	cg10336036	RAB35	-13.185	3.150010549	2.84E-05	0.048161332		-	-	-	-	-	-	-	-	-0.00269	0.137749	-	-	-
12	65021536	cg10426838	MIR548Z	-7.1393	1.671178619	1.94E-05	0.042250758		-	-	-	-	-	-	-	-	-0.01616	0.002199	-	-	-
12	51322158	cg10487714	METTL7A	-5.7378	1.352936793	2.23E-05	0.044011775		-	-	-	-	-	-	-	-	-0.00651	0.282002	-	-	-
1	62209607	cg10704177	PATJ	-11.215	2.423970044	3.71E-06	0.028467711	1	-10.418	2.0121	2.25E-07	-0.31281	0.698753	0.257987	0.25133	0.304663	-0.02009	0.001908	-6.067	2.894	0.036
17	70710636	cg10741887	LINC00511	-2.176	0.50382778	1.57E-05	0.040431271		-	-	-	-	-	-	-	-	-0.00385	0.55139	-	-	-
6	33255400	cg10966235	MIR6873	-51.994	11.83027683	1.11E-05	0.038178101	1	-4.8046	4.2886	0.2626	-0.37481	0.36343	-0.06737	0.232305	0.771797	-	-	-37.084	16.802	0.027
13	47274074	cg11015284	ESD	-35.029	8.052444338	1.36E-05	0.039250229		-	-	-	-	-	-	-	-	-0.00815	0.00012	-	-	-
12	104276789	cg11098795	NT5DC3	-4.1875	0.857413665	1.04E-06	0.023468934		-	-	-	-	-	-	-	-	-0.00126	0.467557	-	-	-
17	56283901	cg11112605	MKS1	-11.19	2.448536428	4.87E-06	0.030406268		-	-	-	-	-	-	-	-	-0.02344	2.68E-05	-	-	-
14	91436403	cg11148876	RPS6KA5	-3.7456	0.867852246	1.59E-05	0.040501315		-	-	-	-	-	-	-	-	-0.00593	0.26501	-	-	-
12	32669224	cg11175241	FGD4	-3.2582	0.764445883	2.02E-05	0.042745205		-	-	-	-	-	-	-	-	-0.00885	0.146766	-	-	-
11	10525508	cg11199798	MIR4485	-2.7701	0.58985745	2.65E-06	0.027181247		-	-	-	-	-	-	-	-	0.003114	0.542924	-	-	-
11	62164451	cg11205545	SCGB1A1	-13.884	3.285468288	2.38E-05	0.045076793		-	-	-	-	-	-	-	-	-0.01594	0.000162	-	-	-

16	75050761	cg11271052	ZNRF1	-2.1119	0.505974063	2.99E-05	0.048867467		-	-	-	-	-	-	-	-	0.005188	0.414804	-	-	-
7	5523691	cg11554295	MIR589	-3.9254	0.924719865	2.19E-05	0.043837662	1	-3.5646	2.5245	0.158	-	-	0.813082	0.607221	0.180564	-0.00105	0.744268	-1.592	4.298	0.711
17	4795410	cg11625476	C17orf107	-23.396	5.017849279	3.12E-06	0.027181247	1	-4.9967	4.421	0.2584	0.031497	0.932889	-0.07985	0.213765	0.708761	-0.00178	0.189271	-40.367	56.516	0.475
1	6341327	cg11699125	GPR153	-4.9382	1.171856061	2.51E-05	0.045984376	1	-10.235	1.663	7.54E-10	-0.23843	0.333101	0.265831	0.250838	0.289248	-0.03696	3.53E-06	-8.651	4.368	0.048
1	55012926	cg11715991	ACOT11	-3.7248	0.85094104	1.20E-05	0.038353842		-	-	-	-	-	-	-	-	-	-	-	-	-
7	100224557	cg11751434	TFR2	33.4532	7.843972622	2.00E-05	0.042576019	1	0.723	1.9045	0.7042	0.338883	0.143722	-0.1429	0.246232	0.561681	0.0028	0.134318	10.793	8.139	0.185
6	159541084	cg11759930	FNDC1	-2.4211	0.570756363	2.22E-05	0.044011775		-	-	-	-	-	-	-	-	-0.00263	0.394398	-	-	-
22	43490246	cg11807649	TTLL1	-3.8743	0.922761783	2.69E-05	0.047443003		-	-	-	-	-	-	-	-	0.000605	0.692345	-	-	-
11	109956144	cg11810303	ZC3H12C	-5.3103	1.259325252	2.48E-05	0.045984376		-	-	-	-	-	-	-	-	-0.0152	0.042075	-	-	-
17	3706841	cg11902347	ITGAE	-1.992	0.457529953	1.34E-05	0.039250229		-	-	-	-	-	-	-	-	-0.00243	0.613802	-	-	-
17	27388119	cg11942358	TIAF1	-4.1257	0.956644865	1.61E-05	0.040501315		-	-	-	-	-	-	-	-	0.003005	0.558943	-	-	-
1	25059454	cg11966720	CLIC4	-4.7205	1.023296801	3.97E-06	0.028624856		-	-	-	-	-	-	-	-	-0.0218	8.96E-05	-	-	-
14	102667161	cg11968273	MOK	-5.0094	1.138958968	1.09E-05	0.038178101		-	-	-	-	-	-	-	-	-0.00321	0.107157	-	-	-
1	182231752	cg12040931	LINC01344	-4.0701	0.978512423	3.19E-05	0.049846963		-	-	-	-	-	-	-	-	-0.00407	0.236544	-	-	-
2	75089669	cg12077754	HK2	-10.094	2.084605574	1.29E-06	0.025946281	1	-7.8985	1.7231	4.56E-06	0.138238	0.627504	0.301677	0.261972	0.249502	-0.02267	0.000385	-6.48	3.052	0.034
22	35773941	cg12165656	HMOX1	-4.1485	0.947377238	1.19E-05	0.038353842		-	-	-	-	-	-	-	-	-0.00424	0.403786	-	-	-
10	99223744	cg12182708	ZDHHC16	-3.0714	0.652333851	2.50E-06	0.027181247	1	-6.7167	2.1357	0.001661	0.201254	0.587741	1.248139	0.75267	0.097261	-0.00092	0.546934	-1.176	2.751	0.669
17	72838819	cg12190341	GRIN2C	-4.4181	1.035753239	1.99E-05	0.042547094	1	-2.2337	2.4045	0.3529	0.158727	0.815252	-0.01594	0.238575	0.946738	-0.00209	0.699984	-25.279	16.663	0.129
10	135061670	cg12227660	MIR202HG	-5.8161	1.389788822	2.85E-05	0.048161332	1	-7.6486	2.0431	0.000181	-	-	0.036638	0.255954	0.886176	-0.017	0.003694	-	-	-
14	75069041	cg12258670	LTBP2	-18.538	4.027033927	4.16E-06	0.028624856		-	-	-	-	-	-	-	-	-0.0187	0.000462	-	-	-
12	122884585	cg12315900	CLIP1-AS1	-3.0161	0.703422399	1.81E-05	0.041037429		-	-	-	-	-	-	-	-	0.000618	0.580256	-	-	-
17	79851485	cg12380988	ANAPC11	-13.688	3.180846312	1.68E-05	0.040708156		-	-	-	-	-	-	-	-	-0.01638	0.002596	-	-	-
15	52135487	cg12402318	TMOD3	-17.539	3.874087198	5.97E-06	0.033920223	1	-9.528	2.8359	0.00078	-0.38868	0.274932	0.424046	0.294894	0.150445	-0.01266	0.002299	-10.516	4.599	0.022
6	38061902	cg12604858	ZFAND3	-10.677	2.518420435	2.24E-05	0.044011775	1	-2.7933	2.5515	0.2736	0.099838	0.763769	0.091863	0.251382	0.714791	-0.00169	0.618612	-15.378	8.67	0.076
4	2275801	cg12674840	MXD4	-5.1211	1.204717371	2.13E-05	0.043655818	1	2.0928	1.4079	0.1372	-0.06298	0.879789	0.141381	0.184628	0.443817	0.005245	0.491193	-24.41	17.437	0.162
3	194899199	cg12784307	XXYLT1-AS2	-2.939	0.67503027	1.34E-05	0.039250229		-	-	-	-	-	-	-	-	-0.01677	0.049221	-	-	-
11	57157632	cg12819873	PRG2	-12.539	2.937613306	1.97E-05	0.042547094	1	-10.829	2.446	9.55E-06	0.232084	0.439048	0.19104	0.253392	0.450889	-0.02081	8.89E-05	-6.389	3.161	0.043
5	132577108	cg12828656	MIR1289-2	-3.1914	0.734687323	1.40E-05	0.039584095	1	-2.6507	2.6245	0.3125	-	-	0.369981	0.69302	0.593433	-0.00136	0.633043	-1.349	3.604	0.708
17	4383882	cg12856590	SPNS2	-3.6369	0.863900377	2.55E-05	0.046394477		-	-	-	-	-	-	-	-	-0.00095	0.823078	-	-	-
2	65173818	cg12967579	LOC400958	-23.248	5.477717534	2.19E-05	0.043837662		-	-	-	-	-	-	-	-	0.003478	0.220929	-	-	-
3	52271724	cg12985905	TWF2	-3.6658	0.82242924	8.30E-06	0.037178678		-	-	-	-	-	-	-	-	-0.00222	0.132817	-	-	-
2	17042926	cg12997777	FAM49A	-2.6952	0.645184247	2.95E-05	0.048683157		-	-	-	-	-	-	-	-	0.000377	0.656244	-	-	-
22	47303273	cg12998731	TBC1D22A-A	-4.161	0.954061267	1.29E-05	0.039250229		-	-	-	-	-	-	-	-	-0.0005	0.904746	-	-	-
2	153440054	cg13047724	PRPF40A	-4.0436	0.941919557	1.76E-05	0.041037429		-	-	-	-	-	-	-	-	-0.00514	0.29213	-	-	-
17	81055722	cg13054523	METRNL	-11.558	2.613738697	9.77E-06	0.037840547	1	-13.94	2.446	1.20E-08	-0.03038	0.925818	0.154219	0.254377	0.544341	-0.01178	0.01247	-16.264	7.03	0.021
17	74242643	cg13117318	RNF157	-23.506	5.243818114	7.37E-06	0.035817794		-	-	-	-	-	-	-	-	-	-	-	-	-
4	140697658	cg13120180	MGST2	-4.175	0.97957351	2.03E-05	0.042745205		-	-	-	-	-	-	-	-	-0.00924	0.109621	-	-	-
14	100820846	cg13147461	WARS	-7.8123	1.791927124	1.30E-05	0.039250229		-	-	-	-	-	-	-	-	-0.01776	0.000951	-	-	-
20	60709957	cg13197551	PSMA7	-20.93	4.989970084	2.74E-05	0.047485135	1	-15.397	3.1376	9.23E-07	-0.75141	0.02545	0.075718	0.283647	0.789512	-0.01312	0.000111	-10.23	4.487	0.023
10	81034149	cg13250178	PPIF	-3.7772	0.866887249	1.32E-05	0.039250229		-	-	-	-	-	-	-	-	-0.00226	0.736769	-	-	-
2	43440068	cg13254847	ZFP36L2	-5.4624	1.274372123	1.82E-05	0.041037429		-	-	-	-	-	-	-	-	-0.00636	0.064196	-	-	-
12	118577239	cg13346427	PEBP1	-2.427	0.582755824	3.12E-05	0.049213288		-	-	-	-	-	-	-	-	0.010383	0.010736	-	-	-
9	136341915	cg13410614	SLC2A6	-3.1117	0.654035102	1.96E-06	0.026069972	1	-2.2426	2.3694	0.3439	-0.13549	0.780218	0.858729	0.629027	0.1722	0.00317	0.241397	-1.535	3.54	0.665
1	156221551	cg13585073	PAQR6	-6.0636	1.297237639	2.95E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00086	0.850365	-	-	-
17	49025289	cg13617202	TOB1	-4.9127	1.168828584	2.63E-05	0.047393854		-	-	-	-	-	-	-	-	-0.01604	0.001074	-	-	-
11	2241568	cg13638867	MIR4686	-4.5954	1.104767318	3.19E-05	0.049846963	1	-2.8987	1.6327	0.07583	0.174918	0.612407	0.341975	0.245832	0.164198	-0.00454	0.518967	-7.041	3.316	0.034
16	1988449	cg13728275	MSRB1	-3.2191	0.763529079	2.49E-05	0.045984376		-	-	-	-	-	-	-	-	0.001975	0.596766	-	-	-
1	47746081	cg13789639	STIL	-16.225	3.371155855	1.49E-06	0.026069972		-	-	-	-	-	-	-	-	-0.01793	0.001272	-	-	-
20	43590115	cg13792581	TOMM34	-24.264	5.505047956	1.05E-05	0.03807844	1	-13.711	3.1498	1.34E-05	-0.00742	0.982277	0.497117	0.3074	0.105842	-0.01642	7.49E-06	-9.152	4.158	0.028
17	7863010	cg13905385	CNTROB	-2.3282	0.52653736	9.79E-06	0.037840547		-	-	-	-	-	-	-	-	0.000351	0.91541	-	-	-
17	55190679	cg13947225	AKAP1	-10.684	2.395715227	8.21E-06	0.037178678		-	-	-	-	-	-	-	-	-0.0207	0.003558	-	-	-
9	132600788	cg13953978	USP20	-11.048	2.555818765	1.54E-05	0.040190712	1	-5.4284	1.9059	0.004396	0.212412	0.507532	-0.0246	0.235432	0.916791	-0.01903	0.00039	-5.729	2.69	0.033
6	43445012	cg14009632	TJAP1	-3.3283	0.741349558	7.14E-06	0.035817794	1	0.2947	1.3741	0.8302	0.184185	0.425861	-0.00735	0.202551	0.971057	0.00596	0.27973	2.2	7.015	0.754

9	134206000	cg14031473	PLPP7	-2.8965	0.67620774	1.84E-05	0.041319395	1	-3.3638	1.8538	0.06959	-0.64818	0.042287	0.12841	0.244188	0.598983	-0.00245	0.724548	-9.383	6.191	0.13
14	23548087	cg14060758	ACIN1	-3.8905	0.819821534	2.08E-06	0.026401093		-	-	-	-	-	-	-	-	0.000653	0.734218	-	-	-
14	100610407	cg14084609	DEGS2	-20.454	3.690772998	2.99E-08	0.007760824	1	-12.034	2.0281	2.96E-09	-0.37747	0.276885	0.346286	0.25836	0.18014	-0.02182	1.52E-06	-7.163	3.34	0.032
5	106830005	cg14118059	EFNA5	-36.92	8.850387901	3.03E-05	0.048867467	1	1.6631	4.7621	0.7269	0.543251	0.088226	-0.12138	0.235209	0.605825	-	-	-27.359	32.46	0.399
2	106360709	cg14131038	NCK2	-2.4475	0.573021149	1.94E-05	0.042250758	1	1.6215	1.5925	0.3086	0.247129	0.38671	1.008212	0.534718	0.059362	-	-	-2.358	3.17	0.457
2	160896165	cg14169284	PLA2R1	-3.1587	0.715998811	1.03E-05	0.037915742		-	-	-	-	-	-	-	-	0.003045	0.764212	-	-	-
12	52404134	cg14242936	GRASP	-3.6083	0.804345205	7.26E-06	0.035817794	1	0.8256	1.646	0.616	0.953151	0.091517	-0.71103	0.437747	0.104314	-0.00605	0.476325	0.103	5.713	0.986
9	117157871	cg14260530	AKNA	-5.3874	1.212088337	8.80E-06	0.037178678	1	2.6791	1.8305	0.1433	-0.51472	0.37103	0.308799	0.213714	0.148481	-0.00455	0.29993	-5.452	10.367	0.599
10	73946374	cg14261336	ANAPC16	-2.3158	0.546733629	2.28E-05	0.044337415		-	-	-	-	-	-	-	-	-0.00152	0.868129	-	-	-
11	35325601	cg14282386	SLC1A2	-2.6984	0.644839327	2.86E-05	0.048161332		-	-	-	-	-	-	-	-	0.001174	0.613052	-	-	-
15	40633232	cg14287557	C15orf52	-3.3807	0.803678506	2.59E-05	0.046893025		-	-	-	-	-	-	-	-	-0.00155	0.369487	-	-	-
8	11623360	cg14306688	NEIL2	-3.1605	0.758232064	3.07E-05	0.049091263		-	-	-	-	-	-	-	-	0.000473	0.933768	-	-	-
17	6658198	cg14321269	XAF1	-9.7619	2.033525954	1.58E-06	0.026069972	1	-4.8707	2.1314	0.0223	0.254417	0.520529	0.436866	0.25006	0.08063	-0.01446	0.029626	-9.268	4.552	0.042
3	195782538	cg14352263	TFRC	-3.9004	0.909832546	1.81E-05	0.041037429		-	-	-	-	-	-	-	-	0.001888	0.515795	-	-	-
5	74342697	cg14390854	LINC01336	-10.877	2.430471151	7.63E-06	0.036051842		-	-	-	-	-	-	-	-	-0.02483	0.000304	-	-	-
11	70165870	cg14569513	MIR548K	-23.406	5.353478552	1.23E-05	0.038716406		-	-	-	-	-	-	-	-	-0.0117	0.000278	-	-	-
9	130859606	cg14612966	SLC25A25	-14.348	3.264270783	1.11E-05	0.038178101	1	-10.601	2.5939	4.37E-05	0.573911	0.060734	0.181965	0.288457	0.528158	-0.0203	3.50E-05	-7.365	3.436	0.032
20	52238380	cg14613901	LOC1053726	-3.4687	0.789382542	1.11E-05	0.038178101		-	-	-	-	-	-	-	-	-0.00393	0.49333	-	-	-
19	827739	cg14663914	AZU1	-3.9281	0.854123418	4.25E-06	0.028624856	1	-3.1813	2.1388	0.1369	-0.22544	0.558732	1.034382	0.559484	0.064485	-0.00377	0.017132	-1.079	3.238	0.739
7	98722470	cg14769121	SMURF1	-16.026	3.309737496	1.29E-06	0.025946281	1	-9.4902	2.4316	9.50E-05	-0.33976	0.288066	0.278831	0.276614	0.313447	-0.0238	0.000482	-6.45	3.109	0.038
11	44578801	cg14780449	CD82	-4.4754	1.018693478	1.12E-05	0.038178101	1	2.953	2.3962	0.2178	-0.55805	0.156323	0.671618	0.444755	0.131021	0.002445	0.598083	1.492	6.198	0.81
6	7167468	cg14919455	RREB1	-2.9185	0.696348827	2.77E-05	0.047496804	1	-1.7646	2.4184	0.4656	-	-	-0.09698	0.727307	0.893927	-0.00163	0.594293	-1.499	2.737	0.584
17	73641675	cg14934396	SMIM6	-3.82	0.814002719	2.69E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00393	0.669296	-	-	-
18	22040005	cg14997111	HRH4	-2.2613	0.503501625	7.08E-06	0.035817794		-	-	-	-	-	-	-	-	-0.008	0.031568	-	-	-
15	45028161	cg15022400	TRIM69	-7.2208	1.486066468	1.18E-06	0.025370613	1	0.3651	1.8123	0.8403	-	-	0.1362	0.23501	0.562217	-0.00308	0.255542	-3.597	5.693	0.527
7	29304984	cg15030712	LOC1027244	-4.2006	0.959153207	1.19E-05	0.038353842	1	-1.7075	1.9794	0.3883	-0.04635	0.887031	0.523926	0.422621	0.215084	0.001024	0.608615	-0.92	4.527	0.839
18	72548725	cg15034807	ZNF407	-4.9601	1.146289614	1.51E-05	0.040190712		-	-	-	-	-	-	-	-	-0.00072	0.894032	-	-	-
18	47815588	cg15053869	CXXC1	-3.0796	0.682936246	6.50E-06	0.034956921		-	-	-	-	-	-	-	-	-0.00354	0.272485	-	-	-
11	111716149	cg15072057	ALG9	-2.7474	0.642600384	1.91E-05	0.04209883		-	-	-	-	-	-	-	-	-0.00297	0.444563	-	-	-
2	192701514	cg15074047	SDPR	-5.2346	1.247322905	2.71E-05	0.047443003	1	-5.7163	2.2943	0.01272	0.196323	0.686104	0.164662	0.298336	0.580994	-0.00427	0.394818	-10.012	5.167	0.053
3	14708144	cg15106081	C3orf20	-27.347	5.518067542	7.20E-07	0.019267287		-	-	-	-	-	-	-	-	-0.01885	0.000218	-	-	-
6	15364953	cg15123849	JARID2	-4.8969	1.017695701	1.50E-06	0.026069972		-	-	-	-	-	-	-	-	-0.01416	0.072719	-	-	-
3	47023603	cg15157945	CCDC12	-3.815	0.876049015	1.33E-05	0.039250229	1	1.6596	2.6002	0.5233	0.018323	0.965847	0.013604	0.525871	0.979362	0.002952	0.052117	0.724	4.854	0.881
3	151297861	cg15159044	MIR5186	-3.2615	0.739342687	1.03E-05	0.037915742		-	-	-	-	-	-	-	-	-0.0124	0.120635	-	-	-
17	518485	cg15186355	VPS53	-3.1269	0.744479732	2.67E-05	0.047443003		-	-	-	-	-	-	-	-	-0.00049	0.77613	-	-	-
12	56120970	cg15338098	CD63	-3.1423	0.721410068	1.33E-05	0.039250229		-	-	-	-	-	-	-	-	0.002608	0.50529	-	-	-
13	49175326	cg15338967	LINC00462	-7.0507	1.515076154	3.26E-06	0.027181247	1	-5.8534	2.0116	0.003617	-0.85571	0.17423	-0.11235	0.24109	0.641205	-0.01424	0.00685	-7.343	3.589	0.041
17	9939929	cg15357334	GAS7	-3.4089	0.807104089	2.40E-05	0.045290749		-	-	-	-	-	-	-	-	-0.00501	0.05022	-	-	-
13	33788523	cg15442959	STARD13	-6.0024	1.385497399	1.48E-05	0.040190712		-	-	-	-	-	-	-	-	-0.00928	0.110782	-	-	-
20	34018983	cg15532312	GDF5	-21.968	4.712562777	3.14E-06	0.027181247		-	-	-	-	-	-	-	-	-0.01941	0.000185	-	-	-
1	32410585	cg15535138	PTP4A2	-6.3458	1.519713592	2.97E-05	0.048683157		-	-	-	-	-	-	-	-	-0.00158	0.106506	-	-	-
19	827821	cg15610437	AZU1	-3.7712	0.859098922	1.13E-05	0.038178101	1	-0.7169	2.2967	0.7549	-0.30741	0.576311	0.471078	0.509211	0.354907	-0.00248	0.326617	-0.19	3.741	0.959
1	62437936	cg15672644	MIR3116-1	-29.958	6.738100105	8.75E-06	0.037178678		-	-	-	-	-	-	-	-	-0.0079	7.17E-05	-	-	-
1	206226009	cg15677434	AVPR1B	-4.9685	1.132397807	1.15E-05	0.038178101	1	-3.9246	1.8906	0.03791	0.185081	0.570324	-0.08079	0.387552	0.834873	-0.00248	0.555471	-4.909	4.623	0.288
20	31306896	cg15698538	COMMD7	-2.5147	0.586064735	1.78E-05	0.041037429		-	-	-	-	-	-	-	-	-0.0136	0.171635	-	-	-
10	22743835	cg15737719	LOC1004994	-27.915	5.112108413	4.75E-08	0.007760824		-	-	-	-	-	-	-	-	-0.01413	0.000145	-	-	-
1	90354310	cg15791719	LRRC8D	-3.1951	0.6831399	2.91E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00105	0.915915	-	-	-
9	35834279	cg15818306	TMEM8B	-3.7993	0.874407162	1.39E-05	0.039584095		-	-	-	-	-	-	-	-	-0.00189	0.643709	-	-	-
4	159969044	cg15834151	C4orf45	-7.1312	1.419622611	5.08E-07	0.01660328		-	-	-	-	-	-	-	-	-	-	-	-	-
22	17583333	cg15931859	IL17RA	-4.0371	0.853883857	2.27E-06	0.027181247		-	-	-	-	-	-	-	-	-0.0061	0.200339	-	-	-
3	195106547	cg16032884	ACAP2	-2.2948	0.549190462	2.93E-05	0.048634554		-	-	-	-	-	-	-	-	-0.00033	0.934485	-	-	-
16	46776932	cg16064932	MYLK3	-9.3168	2.016500519	3.83E-06	0.028467711		-	-	-	-	-	-	-	-	-0.01823	0.001144	-	-	-
3	46142638	cg16171189	XCR1	-2.2787	0.51262015	8.78E-06	0.037178678		-	-	-	-	-	-	-	-	-0.0034	0.389868	-	-	-

1	25015150	cg16257804	SRRM1	-4.6808	1.097112759	1.99E-05	0.042547094		-	-	-	-	-	-	-	-	-	-	-	-	-
1	29523841	cg16263722	SRSF4	-12.107	2.595019696	3.08E-06	0.027181247	1	-11.154	2.1505	2.14E-07	-0.83987	0.09155	0.433654	0.244401	0.076005	-0.02147	3.65E-05	-9.024	4.208	0.032
2	218113120	cg16299559	DIRC3-AS1	-4.7801	1.132089133	2.42E-05	0.045317311		-	-	-	-	-	-	-	-	-0.0057	0.208384	-	-	-
2	69430731	cg16381477	MIR3126	-2.7539	0.650692008	2.31E-05	0.044582402		-	-	-	-	-	-	-	-	0.001472	0.797502	-	-	-
13	95923665	cg16464329	ABCC4	-4.8857	1.160951219	2.57E-05	0.046614038		-	-	-	-	-	-	-	-	-	-	-	-	-
3	15066613	cg16499536	MRPS25	-21.2	4.405064732	1.49E-06	0.026069972		-	-	-	-	-	-	-	-	-	-	-	-	-
5	76248749	cg16545105	CRHBP	-3.7242	0.858464709	1.44E-05	0.040190712	1	-4.418	1.982	0.02581	-0.39655	0.371619	-0.10835	0.390463	0.781397	-0.00137	0.778903	-6.145	5.561	0.269
1	43880657	cg16572910	SZT2	-5.0615	1.175005124	1.65E-05	0.040515973	1	-2.6522	2.4896	0.2867	-1.63136	0.15071	-0.02184	0.261312	0.933406	-0.0021	0.568148	-4.291	11.381	0.706
22	21123428	cg16617564	SERPIND1	-3.7902	0.903007683	2.70E-05	0.047443003		-	-	-	-	-	-	-	-	0.001887	0.588813	-	-	-
16	75037584	cg16660617	ZNRF1	-31.264	7.517657607	3.20E-05	0.049919095		-	-	-	-	-	-	-	-	-0.01499	0.004946	-	-	-
2	236636037	cg16672147	AGAP1-IT1	-3.2734	0.762787471	1.78E-05	0.041037429		-	-	-	-	-	-	-	-	0.004423	0.230635	-	-	-
16	1715613	cg16710434	HN1L	-3.2014	0.735871685	1.36E-05	0.039250229		-	-	-	-	-	-	-	-	-0.00288	0.218195	-	-	-
6	108910710	cg16775629	FOXO3	-5.9994	1.303870736	4.20E-06	0.028624856		-	-	-	-	-	-	-	-	0.0009	0.723734	-	-	-
16	50748861	cg16834953	NOD2	-2.3163	0.519115324	8.12E-06	0.037073808		-	-	-	-	-	-	-	-	-0.00283	0.440609	-	-	-
16	69535862	cg16863862	MIR1538	-2.7754	0.651430576	2.04E-05	0.042745205		-	-	-	-	-	-	-	-	-0.00371	0.627527	-	-	-
13	46927146	cg16872030	RUBCNL	-3.2517	0.710844995	4.77E-06	0.030406268		-	-	-	-	-	-	-	-	-0.00027	0.937717	-	-	-
17	66622811	cg16933977	LINC01482	-48.18	11.30863391	2.04E-05	0.042745205		-	-	-	-	-	-	-	-	0.000108	0.944284	-	-	-
3	125980095	cg16945415	ALDH1L1	-3.9042	0.880386038	9.22E-06	0.037178678	1	-0.2907	3.2021	0.9277	-0.63072	0.411417	0.928068	0.620194	0.134545	0.003313	0.250882	0.709	5.074	0.889
1	41005302	cg16948651	ZNF684	-3.5888	0.771924899	3.33E-06	0.027181247		-	-	-	-	-	-	-	-	-0.0011	0.73332	-	-	-
21	43723461	cg17051407	TFF3	-2.8328	0.670377107	2.38E-05	0.045076793		-	-	-	-	-	-	-	-	-	-	-	-	-
17	2287284	cg17105176	MNT	-17.053	3.662429435	3.22E-06	0.027181247		-	-	-	-	-	-	-	-	-0.02428	1.71E-05	-	-	-
12	56600222	cg17116500	RNF41	-16.51	3.771637916	1.20E-05	0.038353842	1	-8.7936	2.9591	0.002961	-0.72172	0.049231	0.475432	0.258512	0.065899	-0.01007	0.002232	-10.284	5.242	0.04824
10	30685417	cg17120616	GOLGA2P6	-3.502	0.835571148	2.78E-05	0.047496804		-	-	-	-	-	-	-	-	0.000857	0.77861	-	-	-
9	115147327	cg17141163	HSDL2	-2.0493	0.490287166	2.92E-05	0.048597685		-	-	-	-	-	-	-	-	-0.00657	0.56692	-	-	-
15	85186517	cg17194668	WDR73	-15.604	3.071181738	3.76E-07	0.015811056	1	-8.8908	3.3751	0.008432	0.433961	0.210012	0.416914	0.284809	0.143238	-0.0109	0.000642	-18.312	7.95	0.021
8	103603330	cg17245251	ODF1	-20.357	4.49686622	5.98E-06	0.033920223		-	-	-	-	-	-	-	-	-0.01813	0.000202	-	-	-
12	102090601	cg17430986	CHPT1	-4.8305	1.045379325	3.82E-06	0.028467711		-	-	-	-	-	-	-	-	-0.00282	0.170315	-	-	-
1	236518104	cg17464069	EDARADD	-3.7585	0.804946162	3.02E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00708	0.08099	-	-	-
20	62538983	cg17477733	MIR941-1	-3.4577	0.773502299	7.81E-06	0.036283428		-	-	-	-	-	-	-	-	-0.00222	0.364714	-	-	-
2	102952956	cg17555715	IL1RL1	-9.3727	2.129248231	1.07E-05	0.038178101		-	-	-	-	-	-	-	-	-0.01377	0.009557	-	-	-
16	81552233	cg17577640	MIR7854	-3.3057	0.793496823	3.10E-05	0.049213288		-	-	-	-	-	-	-	-	0.002759	0.205851	-	-	-
19	39353395	cg17679548	HNRNPL	-4.0966	0.984323864	3.16E-05	0.049524937		-	-	-	-	-	-	-	-	-0.00615	0.32126	-	-	-
11	82503066	cg17746899	FAM181B	-5.6964	1.188305389	1.64E-06	0.026069972		-	-	-	-	-	-	-	-	-0.02174	0.002012	-	-	-
14	78105289	cg17753773	SPTLC2	-7.8368	1.761434306	8.62E-06	0.037178678		-	-	-	-	-	-	-	-	-0.00323	0.375855	-	-	-
2	65131556	cg17786894	LOC400958	-2.8028	0.6674633	2.68E-05	0.047443003	1	0.2879	0.877	0.7427	0.435782	0.317703	-0.29106	0.261952	0.266525	-	-	-1.786	3.344	0.593
19	3670246	cg17820448	PIP5K1C	-4.3832	1.051096187	3.04E-05	0.048965624		-	-	-	-	-	-	-	-	0.00085	0.822386	-	-	-
1	167520305	cg17936236	CREG1	-5.1495	1.214814641	2.25E-05	0.044011775	1	-2.7765	2.1129	0.1888	-0.02433	0.966329	0.224626	0.281413	0.424751	-0.01147	0.014006	-10.295	5.337	0.054
1	172425816	cg17946525	C1orf105	-12.873	2.98561805	1.62E-05	0.040501315		-	-	-	-	-	-	-	-	-0.02491	1.92E-05	-	-	-
2	74612222	cg17988187	DCTN1-AS1	-11.853	2.36877744	5.62E-07	0.017024549	1	-11.042	2.2745	1.21E-06	0.472781	0.227721	0.217668	0.259545	0.401665	-0.01721	0.00206	-7.982	3.585	0.026
3	159847104	cg17991030	IL12A-AS1	-3.4998	0.703194554	6.46E-07	0.018204397		-	-	-	-	-	-	-	-	0.000482	0.935467	-	-	-
7	17192401	cg17991808	AHR	-5.6286	1.266621227	8.84E-06	0.037178678		-	-	-	-	-	-	-	-	-0.01118	0.007533	-	-	-
12	105683461	cg17998403	KCCAT198	-3.1083	0.737370891	2.49E-05	0.045984376		-	-	-	-	-	-	-	-	0.001936	0.628268	-	-	-
8	22288224	cg18042586	PPP3CC	-2.811	0.670054156	2.73E-05	0.047485135	1	-0.0343	1.8644	0.9853	0.181238	0.389368	0.427912	0.217079	0.048698	-	-	-12.374	8.697	0.155
11	102327308	cg18118893	TMEM123	-3.3638	0.772406119	1.33E-05	0.039250229		-	-	-	-	-	-	-	-	-0.00191	0.201701	-	-	-
2	37007179	cg18197869	VIT	-18.208	4.10611241	9.24E-06	0.037178678		-	-	-	-	-	-	-	-	-0.00518	0.158983	-	-	-
7	5710286	cg18401534	RNF216-IT1	-2.9027	0.653309714	8.87E-06	0.037178678		-	-	-	-	-	-	-	-	0.001028	0.685	-	-	-
17	43472435	cg18410271	ARHGAP27	-5.1454	1.117388461	4.13E-06	0.028624856	1	-4.9216	2.8843	0.08794	-0.92357	0.43226	-0.24436	0.368139	0.506831	0.001264	0.717621	-10.709	10.049	0.287
12	18964297	cg18481322	CAPZA3	-2.8815	0.677039321	2.08E-05	0.043283027		-	-	-	-	-	-	-	-	-0.00296	0.567145	-	-	-
10	98408203	cg18498503	TM9SF3	-4.406	0.920554814	1.70E-06	0.026069972		-	-	-	-	-	-	-	-	0.006432	0.069991	-	-	-
3	194856863	cg18521725	MIR3137	-4.0084	0.958931433	2.91E-05	0.048597685		-	-	-	-	-	-	-	-	-0.00184	0.713462	-	-	-
14	100610570	cg18550847	DEGS2	-9.9473	2.246089967	9.48E-06	0.037291968	1	-9.3774	1.8912	7.10E-07	-0.08361	0.781455	0.311565	0.252448	0.217138	-0.02502	9.27E-06	-9.173	4.182	0.028
1	59543930	cg18581916	LINC01358	-5.3032	1.018753409	1.93E-07	0.01316747		-	-	-	-	-	-	-	-	-0.01674	0.004098	-	-	-
7	1914073	cg18650626	MIR4655	-5.6463	1.354518146	3.07E-05	0.049091263	1	-3.7581	0.9653	9.89E-05	-0.21057	0.51644	-0.01391	0.204559	0.945782	-	-	-7.92	4.327	0.067

22	19953712	cg18731680	MIR4761	-2.7058	0.629422567	1.72E-05	0.041017216	1	-3.0975	1.8561	0.09515	-0.48832	0.182017	1.416419	0.621365	0.022636	-0.00184	0.623577	-0.167	3.028	0.956
17	76409193	cg18787963	PGS1	-3.9224	0.94007207	3.01E-05	0.048867467		-	-	-	-	-	-	-	-	9.49E-05	0.982321	-	-	-
6	157516126	cg18812843	TMEM242	-24.24	5.360651281	6.13E-06	0.033920223		-	-	-	-	-	-	-	-	-0.00875	0.004266	-	-	-
15	40093898	cg18852698	LOC1053709	-12.018	2.483261858	1.30E-06	0.025946281		-	-	-	-	-	-	-	-	-0.02795	7.07E-05	-	-	-
11	107710989	cg18976159	SLC35F2	-3.1002	0.742133113	2.95E-05	0.048683157		-	-	-	-	-	-	-	-	-0.00115	0.100108	-	-	-
1	37239629	cg19032328	GRIK3	-2.8047	0.672685438	3.05E-05	0.049048642		-	-	-	-	-	-	-	-	-0.00285	0.391637	-	-	-
3	46996484	cg19114543	CCDC12	-3.7798	0.860562363	1.12E-05	0.038178101	1	-0.8911	2.0456	0.6631	-	-	0.341469	0.471612	0.469038	-	-	-2.167	3.933	0.582
9	125589222	cg19210893	PDCL	-10.48	2.424276612	1.54E-05	0.040190712		-	-	-	-	-	-	-	-	-0.01739	0.000267	-	-	-
12	56425944	cg19254378	LOC1053697	-2.3789	0.549659743	1.50E-05	0.040190712		-	-	-	-	-	-	-	-	0.001268	0.7962	-	-	-
17	80190054	cg19284277	SLC16A3	-5.4543	1.261518536	1.54E-05	0.040190712	1	0.255	1.833	0.8894	-0.16733	0.605883	-0.00592	0.327034	0.985558	-0.00182	0.561864	-4.282	5.041	0.396
11	128562297	cg19296671	FLI1	-3.538	0.801764999	1.02E-05	0.037915742	1	2.4557	1.526	0.1076	0.660206	0.043841	0.328508	0.32398	0.310594	-0.00031	0.949202	-0.828	6.882	0.904
18	43641560	cg19322743	PSTPIP2	-6.1911	1.382201561	7.49E-06	0.035817794		-	-	-	-	-	-	-	-	-0.01945	0.002655	-	-	-
5	176856845	cg19459094	GRK6	-10.648	2.459986402	1.50E-05	0.040190712	1	-2.8995	2.9187	0.3205	-0.31396	0.596675	0.456171	0.285126	0.109623	0.000853	0.728428	-9.995	9.348	0.285
2	173940277	cg19579160	MAP3K20	-6.2334	1.45366271	1.80E-05	0.041037429	1	-3.4994	2.9422	0.2343	-0.23042	0.626484	0.591057	0.449184	0.188225	0.000405	0.726847	-1.535	8.708	0.86
12	106621388	cg19785826	CKAP4	-5.8546	1.333481811	1.13E-05	0.038178101		-	-	-	-	-	-	-	-	-0.00074	0.487829	-	-	-
17	45754000	cg19791728	TBKBP1	-4.4324	0.998192577	8.98E-06	0.037178678		-	-	-	-	-	-	-	-	-0.01194	0.018179	-	-	-
1	23072310	cg19851810	MIR4684	-27.275	6.327860828	1.63E-05	0.040501315		-	-	-	-	-	-	-	-	-0.01182	0.008247	-	-	-
3	171858472	cg19980260	FNDC3B	-3.0756	0.680237756	6.14E-06	0.033920223	1	-4.2154	2.2494	0.06093	0.826158	0.032967	0.687702	0.646336	0.287328	0.000415	0.820491	-1.179	3.203	0.713
21	15964265	cg20090759	SAMSN1	-2.4942	0.531347167	2.68E-06	0.027181247		-	-	-	-	-	-	-	-	0.000684	0.866675	-	-	-
6	31680144	cg20133890	LY6G6E	-3.988	0.806508063	7.62E-07	0.019466768	1	-3.7856	1.6571	0.02234	-0.01791	0.952818	0.518392	0.247625	0.036308	-0.0173	0.003968	-4.587	4.314	0.288
17	41172326	cg20334877	VAT1	-3.1163	0.716881572	1.38E-05	0.039520425		-	-	-	-	-	-	-	-	-0.0025	0.452755	-	-	-
20	44465613	cg20337696	SNX21	-12.474	2.729310377	4.87E-06	0.030406268		-	-	-	-	-	-	-	-	-0.00736	0.194658	-	-	-
5	142504382	cg20350272	ARHGAP26-I	-3.2535	0.768642011	2.31E-05	0.044582402		-	-	-	-	-	-	-	-	-2.6E-05	0.992889	-	-	-
12	5851581	cg20378408	ANO2	-3.3036	0.751957466	1.12E-05	0.038178101		-	-	-	-	-	-	-	-	0.006116	0.366274	-	-	-
20	62372541	cg20626587	SLC2A4RG	-5.1106	1.147095246	8.38E-06	0.037178678		-	-	-	-	-	-	-	-	-0.00354	0.242095	-	-	-
7	92456994	cg20675152	CDK6	-3.1677	0.733060474	1.55E-05	0.040233061		-	-	-	-	-	-	-	-	-0.00016	0.947702	-	-	-
10	6238080	cg20712856	PFKFB3	-3.5227	0.786100055	7.42E-06	0.035817794		-	-	-	-	-	-	-	-	-0.00137	0.794131	-	-	-
3	171205319	cg20804243	TNIK	-10.71	2.463942379	1.38E-05	0.039520425		-	-	-	-	-	-	-	-	-0.02496	1.46E-05	-	-	-
21	40467185	cg20833901	PSMG1	-4.38	0.987702515	9.23E-06	0.037178678		-	-	-	-	-	-	-	-	-0.00783	0.157794	-	-	-
18	61557735	cg20875821	SERPINB2	-2.7067	0.614050478	1.04E-05	0.03807844	1	-3.1131	2.0434	0.1276	0.739338	0.068013	0.217945	0.548882	0.691315	-0.01249	0.066421	-2.264	2.906	0.436
6	7145478	cg20893838	RREB1	-3.2711	0.765782739	1.94E-05	0.042250758	1	2.4014	1.8304	0.1895	-0.60277	0.162712	1.306017	0.596461	0.028553	-0.00443	0.09129	-1.524	3.805	0.689
1	179261588	cg20999663	SOAT1	-4.6803	1.087803088	1.69E-05	0.040708156		-	-	-	-	-	-	-	-	-0.00099	0.806649	-	-	-
20	35422703	cg21045547	DSN1	-11.174	2.620812175	2.01E-05	0.04271626	1	-11.708	2.5722	5.32E-06	-0.49685	0.187504	0.457847	0.236053	0.052429	-	-	-14.308	6.552	0.029
12	62644785	cg21061310	USP15	-10.965	2.561570004	1.87E-05	0.041760602		-	-	-	-	-	-	-	-	-0.00391	0.563918	-	-	-
5	55444106	cg21124310	ANKRD55	-3.0741	0.710322786	1.51E-05	0.040190712		-	-	-	-	-	-	-	-	-0.00024	0.934106	-	-	-
11	2848310	cg21130221	KCNQ1-AS1	-3.5265	0.80404728	1.16E-05	0.038178101	1	-0.9021	2.276	0.6918	-	-	-0.01606	0.505433	0.974647	-0.00241	0.556719	-4.033	4.492	0.369
16	23508779	cg21145387	GGA2	-3.6808	0.865132346	2.09E-05	0.043445622		-	-	-	-	-	-	-	-	0.001668	0.322159	-	-	-
3	72340184	cg21156580	LINC00870	-8.4932	1.893204455	7.25E-06	0.035817794		-	-	-	-	-	-	-	-	-0.01755	0.000654	-	-	-
12	48152204	cg21166775	RAPGEF3	-3.671	0.864732583	2.18E-05	0.043837662	1	2.5728	2.9192	0.3781	2.024301	0.005951	0.403637	0.671353	0.547688	-0.00013	0.926982	-0.723	4.938	0.884
1	117114916	cg21167563	CD58	-4.2742	1.019777116	2.77E-05	0.047496804	1	-4.0648	2.0817	0.05087	-0.02498	0.932391	-0.0348	0.338647	0.91816	-0.0138	0.012	-8.05	4	0.044
22	45555611	cg21211039	NUP50-AS1	-3.9713	0.855565647	3.45E-06	0.027409634	1	-6.2842	1.8994	0.000938	0.202968	0.513249	-0.05638	0.326362	0.86284	-0.0176	0.074859	-5.207	2.86	0.069
1	6341230	cg21220721	GPR153	-5.7111	1.141339306	5.62E-07	0.017024549	1	-6.3237	1.1042	1.02E-08	-0.51098	0.042636	0.170893	0.224002	0.445518	-0.03489	1.71E-05	-19.088	8.07	0.018
12	125201422	cg21279677	SCARB1	-3.2188	0.750496728	1.80E-05	0.041037429		-	-	-	-	-	-	-	-	0.001225	0.434308	-	-	-
2	242294423	cg21450154	FARP2	-6.0148	1.363255148	1.02E-05	0.037915742		-	-	-	-	-	-	-	-	-0.00089	0.842057	-	-	-
16	68804845	cg21468244	MIR7641-2	-5.1391	1.015185108	4.14E-07	0.015811056		-	-	-	-	-	-	-	-	-0.02518	0.001786	-	-	-
19	40837284	cg21664942	C19orf47	-13.004	2.964586253	1.15E-05	0.038178101		-	-	-	-	-	-	-	-	-0.01762	0.004072	-	-	-
1	31251307	cg21810778	LAPTM5	-4.0485	0.871448946	3.39E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00639	0.206094	-	-	-
11	34230092	cg21876760	NAT10	-3.5644	0.797872166	7.92E-06	0.036344598		-	-	-	-	-	-	-	-	0.002438	0.420751	-	-	-
15	41309253	cg21953058	CHAC1	-2.733	0.556875993	9.22E-07	0.021522725	1	-1.21	1.5171	0.4251	0.016479	0.957884	0.375991	0.423996	0.375197	-0.00447	0.462952	-1.339	4.012	0.739
7	30184490	cg22066020	MTURN	-5.9329	1.401496152	2.30E-05	0.044582402		-	-	-	-	-	-	-	-	-0.01135	0.039741	-	-	-
12	15091395	cg22106221	ERP27	-3.3965	0.815567312	3.12E-05	0.049213288		-	-	-	-	-	-	-	-	0.000942	0.66039	-	-	-
1	12185845	cg22123711	MIR7846	-5.8964	1.234108486	1.77E-06	0.026069972	1	-4.5619	2.1763	0.03607	-0.71216	0.092143	0.574201	0.349538	0.100436	-0.00806	0.047303	-15.449	7.576	0.041
17	56355362	cg22331200	MPO	-3.84	0.886971645	1.50E-05	0.040190712	1	-3.9353	2.64	0.1361	0.335855	0.654071	0.305998	0.531626	0.564893	-0.00711	0.010652	-0.877	3.567	0.806

17	81040906	cg22503106	METRNL	-10.743	2.434760168	1.02E-05	0.037915742	1	-7.5342	1.9856	0.000148	-0.27734	0.353952	0.143737	0.335894	0.668706	-0.0254	0.003641	-4.899	2.353	0.037
16	22009450	cg22747707	PDZD9	-2.3479	0.544849187	1.64E-05	0.040501315		-	-	-	-	-	-	-	-	0.004683	0.559674	-	-	-
19	6067328	cg22748479	RFX2	-3.0853	0.710151998	1.40E-05	0.039584095		-	-	-	-	-	-	-	-	-0.00098	0.392609	-	-	-
5	135336741	cg22788906	TGFBI	-2.844	0.663099597	1.80E-05	0.041037429		-	-	-	-	-	-	-	-	-0.00435	0.202744	-	-	-
7	36301103	cg22940815	KIAA0895	-4.8853	1.14638237	2.03E-05	0.042745205		-	-	-	-	-	-	-	-	-	-	-	-	-
15	90597964	cg22948672	IDH2	-4.3494	1.019175505	1.98E-05	0.042547094		-	-	-	-	-	-	-	-	-0.0108	0.067561	-	-	-
7	10747735	cg22954819	NDUFA4	-2.986	0.698331864	1.90E-05	0.04209883		-	-	-	-	-	-	-	-	-0.00118	0.808245	-	-	-
2	65100535	cg23057699	LINC01800	-3.5033	0.828734451	2.37E-05	0.04495932		-	-	-	-	-	-	-	-	-0.00148	0.752797	-	-	-
1	35920054	cg23091723	KIAA0319L	-2.7203	0.647841233	2.68E-05	0.047443003		-	-	-	-	-	-	-	-	0.001965	0.66243	-	-	-
6	13462275	cg23215701	GFOD1	-3.4183	0.784414739	1.31E-05	0.039250229		-	-	-	-	-	-	-	-	-3.4E-05	0.991198	-	-	-
17	34946860	cg23218859	DHRS11	-2.2892	0.495935518	3.91E-06	0.028565299		-	-	-	-	-	-	-	-	-0.01897	0.015437	-	-	-
11	65239080	cg23299484	MALAT1	-4.2932	0.937588404	4.67E-06	0.030310201	1	-6.8878	2.5424	0.006746	-0.62615	0.257212	0.446608	0.394871	0.258046	-0.0006	0.874012	-0.97	7.57	0.898
11	93456334	cg23338316	SCARNA9	-14.471	2.727959788	1.13E-07	0.010245468		-	-	-	-	-	-	-	-	-0.01608	0.001981	-	-	-
16	11328957	cg23386939	SOCS1	-2.6891	0.611762312	1.10E-05	0.038178101		-	-	-	-	-	-	-	-	-0.00016	0.96356	-	-	-
12	4312337	cg23428738	CCND2	-2.2333	0.495649265	6.61E-06	0.035328474	1	-2.8959	1.829	0.1133	0.025598	0.92726	1.005662	0.579779	0.082818	-0.01127	0.129044	-2.27	2.237	0.31
15	83732582	cg23499392	MIR4515	-2.7294	0.616782318	9.63E-06	0.037671641		-	-	-	-	-	-	-	-	0.005177	0.367059	-	-	-
8	103990730	cg23511239	ATP6V1C1	-3.1823	0.758697403	2.74E-05	0.047485135		-	-	-	-	-	-	-	-	0.000823	0.746316	-	-	-
9	102342539	cg23522962	NAMA	-3.2967	0.768366078	1.78E-05	0.041037429		-	-	-	-	-	-	-	-	0.001563	0.646639	-	-	-
14	55603874	cg23575099	LGALS3	-20.507	3.828093064	8.46E-08	0.008802394	1	-7.796	3.0211	0.009866	-	-	0.648503	0.325442	0.046296	-0.01574	0.106966	-9.763	4.849	0.044
11	119486443	cg23575688	NECTIN1	-3.3661	0.761719098	9.91E-06	0.037853399	1	-0.7443	1.9898	0.7084	0.02096	0.952496	1.330541	0.55211	0.015956	0.003133	0.077128	-2.403	3.28	0.464
11	88078288	cg23579490	CTSC	-2.1879	0.514363674	2.10E-05	0.043458285		-	-	-	-	-	-	-	-	-0.00083	0.86278	-	-	-
2	27473369	cg23635560	SLC30A3	-5.5158	1.173717694	2.61E-06	0.027181247	1	-5.2345	2.1664	0.01568	0.67688	0.302429	0.030864	0.276895	0.911247	-0.0096	0.049611	-8.853	5.491	0.107
14	95991371	cg23661721	SCARNA13	-2.1935	0.476982767	4.25E-06	0.028624856	1	-1.4403	1.7579	0.4126	0.30248	0.287493	-0.05316	0.675059	0.937233	-0.00387	0.410189	-2.732	2.632	0.299
1	3100956	cg23689722	MIR4251	-2.5785	0.618709324	3.08E-05	0.049139909	1	-3.1201	1.8326	0.08866	-	-	0.548866	0.371531	0.139593	-0.00043	0.934366	-3.689	5.216	0.479
19	8634583	cg23720822	MYO1F	-36.63	8.01026134	4.81E-06	0.030406268		-	-	-	-	-	-	-	-	0.001322	0.454749	-	-	-
16	27299412	cg23771052	NSMCE1	-2.985	0.64771264	4.05E-06	0.028624856		-	-	-	-	-	-	-	-	-0.00195	0.634481	-	-	-
5	10560140	cg23856600	ANKRD33B	-7.2829	1.626565373	7.55E-06	0.035890549		-	-	-	-	-	-	-	-	-0.01289	0.078509	-	-	-
13	97846783	cg23933458	LINC00456	-4.3633	0.843891924	2.33E-07	0.014676242		-	-	-	-	-	-	-	-	-0.0072	0.177213	-	-	-
3	119069258	cg23938511	ARHGAP31-A	-4.1919	0.984033538	2.05E-05	0.042745205		-	-	-	-	-	-	-	-	0.003945	0.503503	-	-	-
1	66777579	cg24058805	PDE4B	-18.942	4.119849583	4.27E-06	0.028624856	1	-10.56	3.0107	0.000453	0.191527	0.576878	0.445508	0.305466	0.144716	-0.01135	0.000447	-11.514	5.504	0.036
16	57662165	cg24099727	ADGRG1	-7.0737	1.644480031	1.70E-05	0.040776663		-	-	-	-	-	-	-	-	0.002843	0.46399	-	-	-
3	16491130	cg24171689	RFTN1	-5.4738	1.258477563	1.36E-05	0.039250229	1	-1.0117	1.789	0.5717	-0.12606	0.755136	0.001431	0.247541	0.995387	0.00308	0.552534	-17.002	10.961	0.121
6	31582837	cg24211388	AIF1	-2.6954	0.642295453	2.71E-05	0.047443003	1	-5.4275	2.0724	0.008819	-	-	0.947744	0.746682	0.204343	-0.00367	0.190193	-0.938	3.446	0.785
10	93998677	cg24238409	CPEB3	-2.2462	0.51446292	1.26E-05	0.038930229	1	-1.611	1.7831	0.3663	-0.05278	0.851156	0.281931	0.420612	0.502675	-0.01544	0.093529	-2.841	2.951	0.336
12	11877740	cg24279017	ETV6	-3.1378	0.739306734	2.19E-05	0.043837662	1	-3.673	1.838	0.04567	0.267224	0.50758	0.246807	0.331962	0.457192	-0.01131	0.213465	-6.136	3.803	0.107
1	208040253	cg24315421	C1orf132	-4.382	1.04850885	2.92E-05	0.048597685	1	-1.321	1.7525	0.451	0.195463	0.538687	0.845486	0.497114	0.088982	-0.00017	0.864241	-8.403	6.595	0.203
10	12371568	cg24317972	CAMK1D	-20.663	4.427787707	3.06E-06	0.027181247		-	-	-	-	-	-	-	-	-0.01193	0.014208	-	-	-
15	48116584	cg24372191	LINC01491	-3.7152	0.88168273	2.51E-05	0.045984376		-	-	-	-	-	-	-	-	-0.00511	0.333753	-	-	-
10	74080727	cg24374476	DNAJB12	-4.3516	1.037254853	2.73E-05	0.047485135		-	-	-	-	-	-	-	-	0.001908	0.419034	-	-	-
1	202545589	cg24376793	PPP1R12B	-11.382	2.660530718	1.88E-05	0.04187031	1	-6.2098	2.2404	0.005576	-0.54543	0.160116	0.394041	0.294054	0.180236	-0.01691	0.005312	-4.715	2.421	0.051
1	40861980	cg24395217	SMAP2	-2.4383	0.569960526	1.89E-05	0.04187031		-	-	-	-	-	-	-	-	-0.00554	0.047793	-	-	-
1	205225282	cg24407546	TMCC2	-4.3784	0.961142376	5.23E-06	0.031646949		-	-	-	-	-	-	-	-	-0.01862	0.003661	-	-	-
5	55419860	cg24442367	ANKRD55	-3.2698	0.696184507	2.64E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00722	0.391483	-	-	-
16	11709855	cg24517604	LITAF	-13.467	2.955231622	5.19E-06	0.031630099		-	-	-	-	-	-	-	-	-0.02132	0.000162	-	-	-
7	36077237	cg24598141	LOC1019286	-3.5416	0.702321411	4.59E-07	0.016308829		-	-	-	-	-	-	-	-	-	-	-	-	-
12	27025721	cg24684972	ITPR2	-2.5026	0.58947627	2.18E-05	0.043837662		-	-	-	-	-	-	-	-	-0.0002	0.962525	-	-	-
10	82251396	cg24699150	TSPAN14	-6.9647	1.448538364	1.52E-06	0.026069972		-	-	-	-	-	-	-	-	0.003502	0.310914	-	-	-
2	109204230	cg24936095	LIMS1	-3.7346	0.851814338	1.16E-05	0.038178101	1	-1.5358	2.253	0.4954	0.052677	0.926197	0.507787	0.425993	0.233258	0.002835	0.545721	-3.889	4.638	0.402
2	48031924	cg25117333	MSH6	-2.2033	0.472492707	3.11E-06	0.027181247		-	-	-	-	-	-	-	-	-0.00306	0.503815	-	-	-
10	45900112	cg25136646	ALOX5	-4.6101	1.059500068	1.35E-05	0.039250229		-	-	-	-	-	-	-	-	-0.00445	0.332552	-	-	-
15	82234347	cg25228737	MEX3B	-3.3211	0.7499361	9.49E-06	0.037291968	1	-2.9789	1.8854	0.1141	-	-	-0.18255	0.405861	0.652866	-0.00848	0.124006	-6.621	4.18	0.113
7	72277651	cg25322146	TYW1B	-2.5171	0.592913351	2.18E-05	0.043837662		-	-	-	-	-	-	-	-	-0.01076	0.111963	-	-	-
9	80602527	cg25348163	GNAQ	-20.101	4.736899399	2.20E-05	0.043881202		-	-	-	-	-	-	-	-	-0.01468	0.001259	-	-	-

10	52127425	cg25372176	ASAH2	-9.9216	2.363566064	2.70E-05	0.047443003		-	-	-	-	-	-	-	-	0.001306	0.679487	-	-	-
11	62269149	cg25465557	AHNAK	-4.6893	0.988558223	2.10E-06	0.026401093		-	-	-	-	-	-	-	-	-	-	-	-	-
15	81623226	cg25466522	TMC3-AS1	-19.679	3.943261768	6.02E-07	0.017582361		-	-	-	-	-	-	-	-	-0.02248	7.01E-05	-	-	-
2	86830411	cg25493477	RNF103	-14.994	3.474431654	1.59E-05	0.040501315		-	-	-	-	-	-	-	-	-0.02328	5.37E-05	-	-	-
1	53834451	cg25567227	LINC01771	-4.0966	0.979420443	2.88E-05	0.048350754		-	-	-	-	-	-	-	-	-0.00779	0.181517	-	-	-
4	109282481	cg25642315	LEF1-AS1	-4.6087	1.006439595	4.67E-06	0.030310201	1	-2.3665	1.8309	0.1962	0.035473	0.942218	-0.04075	0.24485	0.867826	-0.02057	0.010947	-7.396	3.596	0.04
10	126040305	cg25715278	OAT	-4.9245	1.148243277	1.80E-05	0.041037429		-	-	-	-	-	-	-	-	-0.00409	0.185226	-	-	-
11	65543903	cg25887955	AP5B1	-3.7081	0.84663639	1.19E-05	0.038353842		-	-	-	-	-	-	-	-	0.007579	0.080768	-	-	-
1	220965460	cg25967384	MARC1	-1.9573	0.469131655	3.02E-05	0.048867467		-	-	-	-	-	-	-	-	-	-	-	-	-
15	89020059	cg26025224	MRPS11	-3.4675	0.827268478	2.77E-05	0.047496804	1	1.5679	2.0018	0.4335	0.720798	0.193867	0.317218	0.263757	0.229095	-0.00732	0.252909	-3.788	6.991	0.588
6	42716310	cg26069291	GLTSCR1L	-3.5554	0.812994116	1.22E-05	0.038716406	1	-3.7014	1.6951	0.02899	0.076358	0.858401	0.485073	0.299669	0.105512	-0.00024	0.970564	-5.448	3.378	0.107
13	31295237	cg26272008	ALOX5AP	-5.4928	1.251702864	1.14E-05	0.038178101		-	-	-	-	-	-	-	-	-0.01139	0.025734	-	-	-
11	64878218	cg26311703	TM7SF2	-5.5781	1.270114412	1.12E-05	0.038178101		-	-	-	-	-	-	-	-	0.001509	0.186109	-	-	-
20	3788428	cg26350671	LINC01730	-3.7573	0.871959723	1.64E-05	0.040501315		-	-	-	-	-	-	-	-	-0.00076	0.834539	-	-	-
2	31302644	cg26382374	GALNT14	-10.907	2.57883061	2.34E-05	0.044912444		-	-	-	-	-	-	-	-	-	-	-	-	-
8	126445744	cg26472183	TRIB1	-29.701	6.04372345	8.91E-07	0.021406755		-	-	-	-	-	-	-	-	-0.01184	3.59E-06	-	-	-
2	74375903	cg26529864	BOLA3-AS1	-24.983	5.411044034	3.89E-06	0.028565299	1	-10.711	5.0624	0.03436	0.112115	0.747443	0.343333	0.31006	0.268159	-0.00601	0.028298	-16.822	7.755	0.03
19	2594841	cg26569937	MIR7850	-19.769	4.664511912	2.25E-05	0.044078761		-	-	-	-	-	-	-	-	-0.01013	0.024355	-	-	-
16	88838368	cg26603047	PIEZO1	8.22922	1.946144584	2.35E-05	0.044925686	1	-	-	-	-	-	-0.24682	0.348966	0.479392	-	-	-5.049	16.21	0.755
12	58210716	cg26620147	AVIL	-3.3192	0.780861545	2.13E-05	0.043655818	1	-3.5588	2.0765	0.08656	-0.63792	0.076229	1.393157	0.664258	0.035966	-0.00058	0.744288	-2.267	3.621	0.531
6	47012342	cg26667462	ADGRF1	-3.0824	0.705268565	1.24E-05	0.038716406		-	-	-	-	-	-	-	-	6.29E-05	0.955693	-	-	-
20	30793354	cg26744554	PLAGL2	-3.134	0.717072132	1.24E-05	0.038716406		-	-	-	-	-	-	-	-	-0.00152	0.635471	-	-	-
12	124221672	cg26802802	ATP6V0A2	-5.0076	1.153436494	1.42E-05	0.039889106		-	-	-	-	-	-	-	-	-0.00857	0.116799	-	-	-
16	57833579	cg26819611	KIFC3	-7.1597	1.612061032	8.94E-06	0.037178678	1	-4.5147	2.9322	0.1236	-	-	0.525788	0.412465	0.202399	0.001824	0.447604	-4.586	7.088	0.518
1	172790731	cg26873486	FASLG	-3.7221	0.872143336	1.97E-05	0.042547094		-	-	-	-	-	-	-	-	-0.00484	0.27431	-	-	-
12	125589647	cg26964704	AACS	-16.055	3.366145131	1.85E-06	0.026069972	1	-6.9894	2.7894	0.01222	-0.3651	0.380404	0.320044	0.243053	0.187918	-0.01153	0.002274	-9.288	4.261	0.029
17	73305193	cg26978762	SLC25A19	-4.4059	0.976943484	6.49E-06	0.034956921		-	-	-	-	-	-	-	-	-0.00081	0.763101	-	-	-
17	9862873	cg26996616	GAS7	-4.1852	1.00229953	2.97E-05	0.048683157	1	-2.5236	1.6355	0.1228	0.623153	0.119372	0.008558	0.329581	0.979285	0.000428	0.886002	-6.882	6.126	0.261
7	101007603	cg27109461	COL26A1	-4.4417	1.053621961	2.49E-05	0.045984376	1	-4.3178	2.1927	0.04893	0.834516	0.430608	0.310711	0.297287	0.295952	-0.00627	0.268781	-14.299	7.594	0.06
21	36341223	cg27195131	RUNX1-IT1	-5.0821	1.172404523	1.46E-05	0.040190712		-	-	-	-	-	-	-	-	0.005444	0.353272	-	-	-
3	72704361	cg27316598	LOC1053771	-2.9211	0.686779605	2.11E-05	0.043458285	1	-1.1179	1.4124	0.4286	0.073563	0.796839	-0.19663	0.194905	0.313056	-0.00469	0.41439	-3.888	7.333	0.596
6	126375816	cg27341747	MIR5695	-18.956	4.211299084	6.76E-06	0.035404611		-	-	-	-	-	-	-	-	-0.01817	0.000644	-	-	-
12	6233657	cg27347104	VWF	-5.9201	1.394609645	2.19E-05	0.043837662	1	-5.0545	2.2308	0.02347	0.297726	0.463029	-0.30859	0.31587	0.328588	-0.00736	0.107636	-18.123	9.978	0.069
7	30467544	cg27543741	LINC01176	-3.2944	0.780573562	2.44E-05	0.045586609		-	-	-	-	-	-	-	-	-	-	-	-	-
11	110318240	cg27623075	FDX1	-3.9302	0.921106901	1.98E-05	0.042547094		-	-	-	-	-	-	-	-	-0.01042	0.077348	-	-	-
16	31210736	cg27646484	PYCARD-AS1	-5.2153	1.119768768	3.20E-06	0.027181247	1	0.1451	2.1864	0.9471	-0.07094	0.901276	-0.27506	0.251622	0.274332	0.002785	0.538236	-13.655	9	0.129

[1] Genome build GRCh37/hg19

Table E11. Differentially methylated CpG sites (FDR<0.05) in Atopic Asthma[1]

chromosome	position[2]	CpG	crossreactive[3]	N	Beta	SE	P	FDR	OR (CI)	Gene.Name	Distance.to.TSS
2	31302644	cg26382374		1425	-26.89	3.52	2.27E-14	1.86E-08	0.76 (0.71, 0.82)	GALNT14	49861
15	31248701	cg16606719		1428	-32.81	4.55	5.51E-13	2.25E-07	0.72 (0.66, 0.79)	MTMR10	35105
9	126497597	cg01745810		1428	-27.03	3.78	8.29E-13	2.26E-07	0.76 (0.71, 0.82)	DENND1A	194819
17	79851485	cg12380988		1428	-30.15	4.26	1.40E-12	2.86E-07	0.74 (0.68, 0.8)	ANAPC11	1683
3	33112660	cg26396322		1428	-32.73	4.67	2.32E-12	3.79E-07	0.72 (0.66, 0.79)	TMPPE	25632
1	6341287	cg09249800	1	1428	-12.82	1.87	6.80E-12	9.26E-07	0.88 (0.85, 0.91)	GPR153	-20253
15	81623226	cg25466522		1426	-35.21	5.24	1.75E-11	2.04E-06	0.70 (0.63, 0.78)	TMC3-AS1	6553
11	65546210	cg05300717		1421	-13.79	2.06	2.32E-11	2.37E-06	0.87 (0.84, 0.91)	AP5B1	1851
7	65439512	cg04290133		1422	-21.69	3.28	3.61E-11	3.09E-06	0.81 (0.75, 0.86)	GUSB	7788
1	6341327	cg11699125		1426	-10.34	1.56	3.78E-11	3.09E-06	0.90 (0.87, 0.93)	GPR153	-20293
1	180940378	cg11649969		1428	-51.25	7.8	5.10E-11	3.49E-06	0.60 (0.51, 0.7)	STX6	51878
10	135061670	cg12227660		1419	-13.1	2	5.13E-11	3.49E-06	0.88 (0.84, 0.91)	MIR202HG	-282
12	6342778	cg20560376		1427	-34.55	5.28	6.03E-11	3.79E-06	0.71 (0.64, 0.79)	CD9	33297
1	160309220	cg09332506		1428	-63.43	9.76	7.96E-11	4.15E-06	0.53 (0.44, 0.64)	NCSTN	-3842
18	8720395	cg27550672		1428	-38.46	5.92	8.37E-11	4.15E-06	0.68 (0.61, 0.76)	MTCL1	3027
16	16143033	cg24304533		1426	-30.81	4.75	8.52E-11	4.15E-06	0.73 (0.67, 0.81)	ABCC1	99600
16	11709855	cg24517604		1425	-25.96	4	8.64E-11	4.15E-06	0.77 (0.71, 0.83)	LITAF	-28534
7	149543136	cg05184016		1427	-38.5	5.96	1.01E-10	4.59E-06	0.68 (0.61, 0.76)	ZNF862	7681
14	95615731	cg01901579		1428	-25.25	3.91	1.07E-10	4.60E-06	0.78 (0.72, 0.84)	DICER1	8027
3	195974300	cg02803925		1424	-26.6	4.12	1.13E-10	4.62E-06	0.77 (0.71, 0.83)	SLC51A	30918
15	52427175	cg05853552		1428	-30.63	4.76	1.28E-10	4.87E-06	0.74 (0.67, 0.81)	BCL2L10	-22204
17	55190679	cg13947225		1424	-20.83	3.24	1.31E-10	4.87E-06	0.81 (0.76, 0.87)	AKAP1	27545
7	99507261	cg17717565		1421	-17.65	2.75	1.43E-10	5.08E-06	0.84 (0.79, 0.88)	TRIM4	9961
13	41631052	cg07908654		1428	-24.56	3.84	1.53E-10	5.21E-06	0.78 (0.73, 0.84)	WBP4	-4644
2	96965099	cg01923915		1428	-31.04	4.88	2.07E-10	6.54E-06	0.73 (0.67, 0.81)	SNRNP200	6207
8	22169041	cg16427256		1428	-28.09	4.42	2.08E-10	6.54E-06	0.76 (0.69, 0.82)	PIWIL2	35962
16	616212	cg04497992		1428	-13.86	2.2	2.75E-10	8.32E-06	0.87 (0.83, 0.91)	NHLRC4	-782
17	25897247	cg06127160		1428	-14.15	2.25	3.08E-10	8.65E-06	0.87 (0.83, 0.91)	LGALS9	-60926

15	40093898	cg18852698	1427	-20.4	3.24	3.20E-10	8.65E-06	0.82 (0.77, 0.87)	LOC105370941	18792
2	32946576	cg18399629	1428	-36.82	5.86	3.28E-10	8.65E-06	0.69 (0.62, 0.78)	MIR4765	86255
14	100610570	cg18550847	1428	-18.39	2.93	3.28E-10	8.65E-06	0.83 (0.79, 0.88)	DEGS2	15441
14	21456512	cg11442986	1428	-49.83	7.94	3.50E-10	8.94E-06	0.61 (0.52, 0.71)	METTL17	-1452
11	75550064	cg02046836	1428	-30.85	4.92	3.67E-10	9.09E-06	0.73 (0.67, 0.81)	UVRAG	23853
7	149543165	cg07970948	1425	-10.42	1.67	4.31E-10	1.04E-05	0.90 (0.87, 0.93)	ZNF862	7710
16	88540241	cg08940169	1427	-13.69	2.22	6.59E-10	1.54E-05	0.87 (0.83, 0.91)	MIR5189	4916
2	74311093	cg04100865	1427	-31.22	5.06	6.83E-10	1.55E-05	0.73 (0.66, 0.81)	BOLA3	63945
16	75037584	cg16660617	1428	-60.5	9.82	7.13E-10	1.57E-05	0.55 (0.45, 0.66)	ZNRF1	4670
14	100610667	cg01000631	1428	-13.01	2.11	7.32E-10	1.57E-05	0.88 (0.84, 0.92)	DEGS2	15344
17	4741523	cg06449385	1422	-28.97	4.73	8.82E-10	1.80E-05	0.75 (0.68, 0.82)	MINK1	4889
20	33927324	cg12548730	1426	-42.19	6.88	8.83E-10	1.80E-05	0.66 (0.57, 0.75)	FAM83C	-47100
4	153499517	cg04459751	1428	-17.61	2.88	9.37E-10	1.85E-05	0.84 (0.79, 0.89)	MIR4453	41938
17	2287008	cg14511746	1426	-19.96	3.26	9.69E-10	1.85E-05	0.82 (0.77, 0.87)	MNT	17249
12	118832042	cg23699170	1421	-35.35	5.78	9.91E-10	1.85E-05	0.70 (0.63, 0.79)	SUDS3	17685
15	72636405	cg11668148	1428	-29.48	4.82	9.98E-10	1.85E-05	0.74 (0.68, 0.82)	CELF6	-23881
4	111049852	cg05555563	1428	-38.15	6.26	1.07E-09	1.90E-05	0.68 (0.6, 0.77)	ELOVL6	69918
16	4884192	cg08348441	1428	-55.48	9.1	1.07E-09	1.90E-05	0.57 (0.48, 0.69)	GLYR1	13110
22	46992206	cg14849880	1428	-14.25	2.34	1.12E-09	1.95E-05	0.87 (0.83, 0.91)	GRAMD4	-24092
15	79609419	cg00527937	1427	-16.03	2.64	1.27E-09	2.16E-05	0.85 (0.81, 0.9)	TMED3	6016
2	100673005	cg10794399	1428	-26.01	4.3	1.40E-09	2.33E-05	0.77 (0.71, 0.84)	AFF3	49039
8	129152449	cg08338792	1428	-43.74	7.23	1.47E-09	2.40E-05	0.65 (0.56, 0.74)	MIR1208	-9912
10	45495435	cg01614759	1427	-22.65	3.75	1.52E-09	2.44E-05	0.80 (0.74, 0.86)	ZNF22	-837
1	6341230	cg21220721	1426	-9.07	1.5	1.67E-09	2.59E-05	0.91 (0.89, 0.94)	GPR153	-20196
9	80602527	cg25348163	1428	-38.25	6.35	1.68E-09	2.59E-05	0.68 (0.6, 0.77)	GNAQ	43837
8	126445744	cg26472183	1398	-47.48	7.89	1.77E-09	2.68E-05	0.62 (0.53, 0.73)	TRIB1	1294
9	130158080	cg02137883	1425	-31.23	5.2	1.97E-09	2.93E-05	0.73 (0.66, 0.81)	SLC2A8	-1336
5	59980902	cg14963970	1428	-21.4	3.58	2.22E-09	3.24E-05	0.81 (0.75, 0.87)	DEPDC1B	15090
16	88558223	cg04983687	1428	-8.81	1.47	2.30E-09	3.30E-05	0.92 (0.89, 0.94)	MIR5189	22898
17	3655775	cg22668931	1416	-24.79	4.16	2.51E-09	3.54E-05	0.78 (0.72, 0.85)	HASPIN	28579
12	125589647	cg26964704	1428	-27.82	4.68	2.68E-09	3.71E-05	0.76 (0.69, 0.83)	AACS	39735
1	211667682	cg12483927	1425	-42.93	7.24	3.01E-09	4.10E-05	0.65 (0.56, 0.75)	RD3	-1424
13	111316234	cg19745810	1422	-38.86	6.56	3.20E-09	4.29E-05	0.68 (0.6, 0.77)	CARS2	42292

17	2287284	cg17105176		1425	-28.7	4.87	3.63E-09	4.75E-05	0.75 (0.68, 0.83)	MNT	16973
1	27240694	cg01942646		1428	-23.71	4.02	3.66E-09	4.75E-05	0.79 (0.73, 0.85)	NR0B2	-128
3	33114261	cg24113459		1428	-32.37	5.5	3.86E-09	4.93E-05	0.72 (0.65, 0.81)	TMPPE	24031
13	80066032	cg11770323		1428	-15.78	2.68	4.02E-09	5.03E-05	0.85 (0.81, 0.9)	NDFIP2-AS1	-10667
11	63466987	cg07636225		1428	-26.67	4.53	4.06E-09	5.03E-05	0.77 (0.7, 0.84)	RTN3	18066
20	34018983	cg15532312		1424	-37.58	6.39	4.16E-09	5.07E-05	0.69 (0.61, 0.78)	GDF5	6986
5	133443229	cg06651549		1426	-19.72	3.36	4.57E-09	5.49E-05	0.82 (0.77, 0.88)	TCF7	-7159
14	102656363	cg11081261		1427	-25.5	4.35	4.74E-09	5.60E-05	0.77 (0.71, 0.84)	WDR20	50175
20	4072430	cg09194810		1427	-26.72	4.57	4.80E-09	5.60E-05	0.77 (0.7, 0.84)	SMOX	-56995
2	28550757	cg05642098		1427	-32.99	5.65	5.16E-09	5.90E-05	0.72 (0.64, 0.8)	LOC100505716	-17432
17	81040906	cg22503106		1414	-19.55	3.35	5.20E-09	5.90E-05	0.82 (0.77, 0.88)	METRNL	3340
20	4764277	cg01613077		1428	-33.67	5.77	5.44E-09	6.01E-05	0.71 (0.64, 0.8)	RASSF2	31491
17	81055722	cg13054523		1428	-19.97	3.42	5.44E-09	6.01E-05	0.82 (0.77, 0.88)	METRNL	18156
11	57157632	cg12819873		1428	-22.66	3.9	6.00E-09	6.54E-05	0.80 (0.74, 0.86)	PRG2	497
1	87596049	cg20654602		1426	-15.62	2.69	6.09E-09	6.54E-05	0.86 (0.81, 0.9)	LINC01140	602
10	5578539	cg15642638		1428	-23.2	3.99	6.21E-09	6.54E-05	0.79 (0.73, 0.86)	CALML3-AS1	-10331
9	91994786	cg03492094		1428	-11.08	1.91	6.25E-09	6.54E-05	0.90 (0.86, 0.93)	SECISBP2	61021
5	132008525	cg26787239		1428	-27.56	4.75	6.32E-09	6.54E-05	0.76 (0.69, 0.83)	IL4	-1152
21	46506629	cg19582046		1426	-17.22	2.97	6.40E-09	6.54E-05	0.84 (0.79, 0.89)	ADARB1	11664
7	127527862	cg01009225		1426	-43.24	7.47	7.13E-09	7.18E-05	0.65 (0.56, 0.75)	SND1-IT1	-109699
13	30143971	cg19928703		1428	-29.58	5.11	7.20E-09	7.18E-05	0.74 (0.67, 0.82)	SLC7A1	25853
15	99444730	cg08538069		1427	-27.69	4.79	7.30E-09	7.19E-05	0.76 (0.69, 0.83)	PGPEP1L	104154
8	95865949	cg25161908		1428	-68.67	11.88	7.46E-09	7.19E-05	0.50 (0.4, 0.64)	INTS8	30432
1	62209607	cg10704177		1427	-18.82	3.26	7.48E-09	7.19E-05	0.83 (0.78, 0.88)	PATJ	1459
1	29229403	cg12645785		1428	-22.23	3.85	7.71E-09	7.26E-05	0.80 (0.74, 0.86)	EPB41	-11684
12	1413681	cg19260922		1427	-25.64	4.44	7.73E-09	7.26E-05	0.77 (0.71, 0.84)	LINC00942	-195975
1	206109139	cg13672080	1	1428	-42.68	7.4	7.89E-09	7.33E-05	0.65 (0.56, 0.75)	FAM72A	-28125
3	51449240	cg06571036		1428	-31.13	5.4	8.03E-09	7.37E-05	0.73 (0.66, 0.81)	RBM15B	20542
1	6645171	cg20267283		1426	-17.27	3	8.55E-09	7.76E-05	0.84 (0.79, 0.89)	ZBTB48	5121
15	45709844	cg06863152		1426	-47.64	8.3	9.44E-09	8.48E-05	0.62 (0.53, 0.73)	C15orf48	-12882
14	55603874	cg23575099		1428	-30.87	5.39	9.99E-09	8.87E-05	0.73 (0.66, 0.82)	LGALS3	174
1	118153944	cg02290349		1421	-23.24	4.06	1.03E-08	9.04E-05	0.79 (0.73, 0.86)	TENT5C	5341
15	41246346	cg01437709		1425	-28.95	5.06	1.04E-08	9.04E-05	0.75 (0.68, 0.83)	CHAC1	1000

11	65547172	cg03695871	1428	-6.67	1.17	1.09E-08	9.38E-05	0.94 (0.91, 0.96)	AP5B1	889
11	61033076	cg02487088	1426	-15.7	2.75	1.14E-08	9.70E-05	0.85 (0.81, 0.9)	PGA5	24429
5	153664745	cg17138920	1428	-42.1	7.38	1.17E-08	9.86E-05	0.66 (0.57, 0.76)	MIR1294	-61920
17	40168331	cg00823480	1427	-19.32	3.4	1.26E-08	1.05E-04	0.82 (0.77, 0.88)	DNAJC7	851
16	16195619	cg03392077	1427	-8.72	1.53	1.31E-08	1.08E-04	0.92 (0.89, 0.94)	ABCC6	121708
7	1914073	cg18650626	1416	-9.95	1.75	1.39E-08	1.14E-04	0.91 (0.87, 0.94)	MIR4655	-30185
1	172425816	cg17946525	1428	-23.91	4.22	1.46E-08	1.18E-04	0.79 (0.72, 0.86)	C1orf105	3784
3	150447687	cg15053244	1428	-35.15	6.21	1.50E-08	1.18E-04	0.70 (0.62, 0.79)	LOC101928105	9084
1	27048589	cg19375767	1428	-16.71	2.95	1.50E-08	1.18E-04	0.85 (0.8, 0.9)	ARID1A	26068
5	157159820	cg13576217	1428	-48.27	8.53	1.51E-08	1.18E-04	0.62 (0.52, 0.73)	THG1L	1000
12	107273455	cg12916632	1427	-25.32	4.47	1.52E-08	1.18E-04	0.78 (0.71, 0.85)	TMEM263	-76044
19	40837284	cg21664942	1428	-22.01	3.89	1.56E-08	1.19E-04	0.80 (0.74, 0.87)	C19orf47	17031
10	99057649	cg08871283	1428	-21.19	3.75	1.57E-08	1.19E-04	0.81 (0.75, 0.87)	ARHGAP19-SLIT1	-5220
14	75069041	cg12258670	1428	-29.27	5.18	1.57E-08	1.19E-04	0.75 (0.67, 0.83)	LTBP2	9992
2	32299042	cg22717723	1426	-37.45	6.63	1.62E-08	1.21E-04	0.69 (0.6, 0.78)	SPAST	10363
17	56283901	cg11112605	1428	-19.25	3.41	1.66E-08	1.23E-04	0.82 (0.77, 0.88)	MKS1	12764
2	121816646	cg22982094	1426	-21.4	3.8	1.73E-08	1.27E-04	0.81 (0.75, 0.87)	TFCP2L1	226131
1	28484534	cg12154164	1428	-16.99	3.02	1.93E-08	1.41E-04	0.84 (0.8, 0.9)	PTAFR	18920
6	15364953	cg15123849	1427	-7.54	1.34	1.98E-08	1.43E-04	0.93 (0.9, 0.95)	JARID2	115868
20	56949432	cg06794913	1424	-14.82	2.64	2.00E-08	1.43E-04	0.86 (0.82, 0.91)	VAPB	-14742
12	56694932	cg24028828	1428	-62.22	11.09	2.02E-08	1.43E-04	0.54 (0.43, 0.67)	CS	-758
17	43111632	cg18176312	1428	-42.79	7.63	2.03E-08	1.43E-04	0.65 (0.56, 0.76)	DCAKD	17252
3	15066613	cg16499536	1426	-33.17	5.92	2.05E-08	1.43E-04	0.72 (0.64, 0.81)	MRPS25	40230
19	11687621	cg10644885	1428	-15.78	2.82	2.29E-08	1.59E-04	0.85 (0.81, 0.9)	ACP5	934
1	236715049	cg22087490	1428	-25.58	4.58	2.37E-08	1.62E-04	0.77 (0.71, 0.85)	LGALS8-AS1	-27242
3	52809942	cg09469170	1428	-27.76	4.97	2.38E-08	1.62E-04	0.76 (0.69, 0.84)	ITIH1	-1659
4	141536591	cg26713832	1425	-39.39	7.06	2.45E-08	1.65E-04	0.67 (0.59, 0.77)	TNRC18P1	27642
22	30650471	cg02645272	1428	-15.97	2.86	2.46E-08	1.65E-04	0.85 (0.81, 0.9)	LIF	-7632
9	130217517	cg25221180	1420	-47.44	8.52	2.59E-08	1.72E-04	0.62 (0.53, 0.74)	LRSAM1	2984
15	64275810	cg13645296	1428	-18.18	3.27	2.74E-08	1.81E-04	0.83 (0.78, 0.89)	LOC101928988	55338
1	26517586	cg02171825	1428	-51.26	9.24	2.84E-08	1.85E-04	0.60 (0.5, 0.72)	CATSPER4	468
20	19222240	cg11929042	1428	-29.79	5.37	2.87E-08	1.85E-04	0.74 (0.67, 0.82)	SLC24A3	28951
18	55250579	cg06592575	1427	-35.01	6.31	2.88E-08	1.85E-04	0.70 (0.62, 0.8)	FECH	3389

14	77419754	cg04933530		1428	-15.62	2.82	2.90E-08	1.85E-04	0.86 (0.81, 0.9)	LINC01629	-6226
19	49469965	cg22027879	1	1428	-23.8	4.29	2.92E-08	1.85E-04	0.79 (0.72, 0.86)	FTL	1400
14	55583041	cg00336912		1427	-26.96	4.87	3.04E-08	1.89E-04	0.76 (0.69, 0.84)	LGALS3	-12893
9	130859606	cg14612966		1428	-24.23	4.38	3.06E-08	1.89E-04	0.78 (0.72, 0.86)	SLC25A25	-1154
21	30699368	cg08094347		1427	-62.96	11.37	3.07E-08	1.89E-04	0.53 (0.43, 0.67)	BACH1	21844
11	62164451	cg11205545		1428	-22.41	4.05	3.08E-08	1.89E-04	0.80 (0.74, 0.87)	SCGB1A1	-22055
14	55850801	cg00978517		1428	-28.26	5.11	3.14E-08	1.92E-04	0.75 (0.68, 0.83)	ATG14	27774
14	62001072	cg08077807		1428	-48.77	8.82	3.20E-08	1.94E-04	0.61 (0.52, 0.73)	LINC01303	35839
20	35504511	cg00414077		1428	-10.86	1.97	3.26E-08	1.95E-04	0.90 (0.86, 0.93)	TLDC2	-12
16	69170548	cg08085199		1428	-12.59	2.28	3.30E-08	1.95E-04	0.88 (0.84, 0.92)	UTP4	4050
18	54558018	cg20813763		1428	-44.1	7.98	3.30E-08	1.95E-04	0.64 (0.55, 0.75)	LINC-ROR	181331
1	212612526	cg17078207		1427	-31.48	5.7	3.31E-08	1.95E-04	0.73 (0.65, 0.82)	NENF	6298
15	40094043	cg14329961		1428	-31.91	5.78	3.44E-08	1.99E-04	0.73 (0.65, 0.81)	LOC105370941	18937
5	179413374	cg22775585		1427	-52.8	9.57	3.45E-08	1.99E-04	0.59 (0.49, 0.71)	MIR340	29022
11	12180609	cg15579574		1428	-67.52	12.24	3.46E-08	1.99E-04	0.51 (0.4, 0.65)	MICAL2	-3016
14	75890874	cg00658852		1428	-44.56	8.09	3.57E-08	2.03E-04	0.64 (0.55, 0.75)	JDP2	-3634
22	50984822	cg14496081		1428	-14.29	2.59	3.58E-08	2.03E-04	0.87 (0.82, 0.91)	KLHDC7B	-1639
14	76447643	cg08922698		1427	-21.61	3.93	3.90E-08	2.20E-04	0.81 (0.75, 0.87)	TGFB3	721
21	34570139	cg11606229		1428	-19.01	3.46	3.96E-08	2.22E-04	0.83 (0.77, 0.88)	LINC01548	-27599
1	872235	cg00582671		1428	-11.74	2.14	4.27E-08	2.37E-04	0.89 (0.85, 0.93)	SAMD11	11115
6	126377786	cg11115840		1428	-10.82	1.98	4.31E-08	2.38E-04	0.90 (0.86, 0.93)	MIR5695	65975
6	20034134	cg10011040		1427	-22.9	4.18	4.35E-08	2.39E-04	0.80 (0.73, 0.86)	MBOAT1	178560
17	8765911	cg06223015		1428	-35.18	6.43	4.40E-08	2.40E-04	0.70 (0.62, 0.8)	PIK3R6	5082
11	12136405	cg23044178		1428	-28.71	5.25	4.46E-08	2.41E-04	0.75 (0.68, 0.83)	MICAL2	4283
2	86830411	cg25493477		1428	-26.36	4.83	4.77E-08	2.56E-04	0.77 (0.7, 0.84)	RNF103	20588
20	60709957	cg13197551		1428	-34.75	6.37	4.88E-08	2.61E-04	0.71 (0.62, 0.8)	PSMA7	8556
2	85625138	cg14947564		1428	-14.21	2.61	5.14E-08	2.73E-04	0.87 (0.82, 0.91)	CAPG	11816
4	38110810	cg07456972		1424	-29.02	5.34	5.39E-08	2.84E-04	0.75 (0.67, 0.83)	TBC1D1	-991
19	16578633	cg16597993		1428	-24.57	4.52	5.49E-08	2.88E-04	0.78 (0.72, 0.85)	EPS15L1	4189
12	47427791	cg06996254		1424	-43.6	8.03	5.56E-08	2.89E-04	0.65 (0.55, 0.76)	PCED1B	-45594
7	73650354	cg04650104		1425	-13.98	2.58	5.71E-08	2.95E-04	0.87 (0.83, 0.91)	RFC2	18433
16	73019173	cg10298741		1428	-19.49	3.59	5.73E-08	2.95E-04	0.82 (0.77, 0.88)	ZFHX3	63100
16	70648377	cg03837359		1428	-18.16	3.35	6.01E-08	3.07E-04	0.83 (0.78, 0.89)	IL34	-9517

10	124303676	cg07066120	1425	-6.74	1.24	6.17E-08	3.13E-04	0.93 (0.91, 0.96)	DMBT1	-16504
5	133563532	cg08969102	1428	-16.36	3.02	6.24E-08	3.15E-04	0.85 (0.8, 0.9)	PPP2CA	-1583
7	135541567	cg01119571	1428	-31.81	5.88	6.38E-08	3.20E-04	0.73 (0.65, 0.82)	FAM180A	-107974
2	44968238	cg13299425	1428	-40.79	7.56	6.83E-08	3.40E-04	0.67 (0.57, 0.77)	SIX3-AS1	200407
7	142659425	cg17784922	1421	-33.16	6.15	6.90E-08	3.42E-04	0.72 (0.64, 0.81)	KEL	77
3	193974031	cg06566952	1428	-20.1	3.73	7.07E-08	3.48E-04	0.82 (0.76, 0.88)	LINC02036	-6090
7	99081553	cg24869851	1427	-43.73	8.12	7.27E-08	3.56E-04	0.65 (0.55, 0.76)	ZNF789	11039
7	41914145	cg20178107	1428	-21.67	4.03	7.58E-08	3.69E-04	0.81 (0.74, 0.87)	INHBA	-171440
11	33731839	cg18814289	1427	-69.4	12.93	8.04E-08	3.89E-04	0.50 (0.39, 0.64)	C11orf91	-9554
12	15124659	cg00390941	1422	-38.45	7.17	8.15E-08	3.91E-04	0.68 (0.59, 0.78)	PDE6H	-1296
10	63507455	cg07356438	1428	-37.38	6.97	8.25E-08	3.91E-04	0.69 (0.6, 0.79)	CABCOCO1	84737
4	154269418	cg12614529	1425	-12.49	2.33	8.27E-08	3.91E-04	0.88 (0.84, 0.92)	MND1	3618
5	79782956	cg15434896	1428	-29.7	5.54	8.27E-08	3.91E-04	0.74 (0.67, 0.83)	FAM151B	-843
8	142238794	cg23911543	1428	-17.64	3.29	8.37E-08	3.91E-04	0.84 (0.79, 0.89)	SLC45A4	-122
3	130616293	cg20263733	1428	-34.5	6.44	8.39E-08	3.91E-04	0.71 (0.62, 0.8)	ATP2C1	2860
12	27027924	cg10220104	1427	-29.89	5.58	8.43E-08	3.91E-04	0.74 (0.66, 0.83)	ITPR2	-41794
9	456725	cg10051213	1427	-32.03	5.98	8.51E-08	3.93E-04	0.73 (0.65, 0.82)	KANK1	-13568
11	125464650	cg24106568	1427	-38.32	7.16	8.76E-08	4.02E-04	0.68 (0.59, 0.78)	STT3A	1961
19	56833959	cg08058756	1422	-19.08	3.57	8.85E-08	4.02E-04	0.83 (0.77, 0.89)	ZSCAN5A	-7664
12	47477069	cg03210018	1427	-17.39	3.25	8.86E-08	4.02E-04	0.84 (0.79, 0.9)	AMIGO2	-3336
17	14112661	cg07643489	1428	-22.07	4.13	8.95E-08	4.04E-04	0.80 (0.74, 0.87)	CDRT15	27488
14	100610407	cg14084609	1428	-25.2	4.72	9.50E-08	4.27E-04	0.78 (0.71, 0.85)	DEGS2	15604
1	27869474	cg24541864	1423	-11.46	2.15	9.72E-08	4.32E-04	0.89 (0.85, 0.93)	WASF2	-52777
1	234835623	cg00851361	1427	-14.32	2.69	9.73E-08	4.32E-04	0.87 (0.82, 0.91)	LINC01132	-24165
10	129172573	cg26865494	1428	-12.48	2.34	9.78E-08	4.32E-04	0.88 (0.84, 0.92)	NPS	-175039
12	55072835	cg10828236	1427	-43.96	8.25	9.94E-08	4.37E-04	0.64 (0.55, 0.76)	DCD	-30559
10	119167795	cg01086527	1428	-24.56	4.62	1.07E-07	4.67E-04	0.78 (0.71, 0.86)	PDZD8	-32818
9	126312322	cg02202133	1426	-14.96	2.82	1.08E-07	4.67E-04	0.86 (0.81, 0.91)	MIR7150	-64422
22	39850774	cg05541460	1427	-19.84	3.73	1.08E-07	4.67E-04	0.82 (0.76, 0.88)	MGAT3	-2550
2	157295032	cg05786348	1428	-23.08	4.35	1.10E-07	4.69E-04	0.79 (0.73, 0.86)	GPD2	2133
6	36108416	cg27508506	1428	-47.57	8.96	1.10E-07	4.69E-04	0.62 (0.52, 0.74)	MAPK13	10156
3	195974349	cg01139080	1427	-14.8	2.79	1.11E-07	4.69E-04	0.86 (0.82, 0.91)	SLC51A	30967
19	50323562	cg09080248	1428	-23.57	4.44	1.12E-07	4.69E-04	0.79 (0.72, 0.86)	MED25	2027

6	144968704	cg23948955	1427	-18.44	3.47	1.12E-07	4.69E-04	0.83 (0.78, 0.89)	SNORA98	241914
10	100140714	cg26633168	1427	-47.33	8.92	1.12E-07	4.69E-04	0.62 (0.52, 0.74)	MIR1287	14349
11	43760352	cg02233915	1423	-36.52	6.89	1.15E-07	4.80E-04	0.69 (0.61, 0.79)	HSD17B12	58210
22	31643111	cg10105512	1428	-16.03	3.03	1.18E-07	4.90E-04	0.85 (0.8, 0.9)	LIMK2	-1236
3	49522836	cg00742276	1428	-18.34	3.46	1.20E-07	4.90E-04	0.83 (0.78, 0.89)	DAG1	15272
2	62515892	cg13073332	1428	-15.08	2.85	1.20E-07	4.90E-04	0.86 (0.81, 0.91)	B3GNT2	73237
11	93456334	cg23338316	1427	-19.37	3.66	1.20E-07	4.90E-04	0.82 (0.77, 0.89)	SCARNA9	1655
19	11610822	cg10491532	1427	-16.94	3.21	1.27E-07	5.15E-04	0.84 (0.79, 0.9)	MIR7974	-4386
20	35943761	cg03812149	1420	-13.96	2.64	1.28E-07	5.15E-04	0.87 (0.83, 0.92)	MANBAL	25711
17	17156930	cg16145720	1424	-27.78	5.26	1.28E-07	5.15E-04	0.76 (0.68, 0.84)	FLCN	-16429
17	6658198	cg14321269	1427	-14.92	2.83	1.30E-07	5.21E-04	0.86 (0.81, 0.91)		-957
2	11917623	cg10142874	1418	-13.88	2.63	1.33E-07	5.28E-04	0.87 (0.83, 0.92)	MIR548S	10054
8	26243601	cg22816343	1428	-28.07	5.32	1.33E-07	5.28E-04	0.76 (0.68, 0.84)	BNIP3L	3079
11	85781719	cg02503303	1428	-12.38	2.35	1.35E-07	5.30E-04	0.88 (0.84, 0.93)	PICALM	-797
17	81043782	cg26749306	1427	-25.89	4.91	1.35E-07	5.30E-04	0.77 (0.7, 0.85)	METRNL	6216
11	43779382	cg21259720	1426	-34.35	6.53	1.41E-07	5.51E-04	0.71 (0.62, 0.81)	HSD17B12	77240
17	76623418	cg08481694	1428	-19.38	3.68	1.42E-07	5.53E-04	0.82 (0.77, 0.89)	LINC02081	4720
7	139427635	cg03369382	1428	-42.76	8.13	1.44E-07	5.55E-04	0.65 (0.56, 0.76)	HIPK2	50057
6	45812853	cg26219449	1427	-15.36	2.92	1.44E-07	5.55E-04	0.86 (0.81, 0.91)	CLIC5	92480
2	200787960	cg14108285	1428	-45.95	8.74	1.47E-07	5.64E-04	0.63 (0.53, 0.75)	C2orf69	11982
4	103750639	cg02436083	1428	-23.07	4.39	1.49E-07	5.69E-04	0.79 (0.73, 0.87)	LOC105377348	169
17	41472748	cg10433549	1428	-23.08	4.4	1.51E-07	5.74E-04	0.79 (0.73, 0.87)	ARL4D	-3604
3	66489480	cg09012511	1428	-14.22	2.71	1.52E-07	5.75E-04	0.87 (0.82, 0.91)	LRIG1	61364
16	23491546	cg23746329	1428	-23.49	4.47	1.53E-07	5.76E-04	0.79 (0.72, 0.86)	COG7	-27035
2	86157952	cg17218818	1427	-35.56	6.78	1.54E-07	5.77E-04	0.70 (0.61, 0.8)	ST3GAL5-AS1	41550
9	130866500	cg02361196	1426	-15.11	2.88	1.57E-07	5.86E-04	0.86 (0.81, 0.91)	SLC25A25	5740
2	74612222	cg17988187	1428	-16.37	3.12	1.59E-07	5.91E-04	0.85 (0.8, 0.9)	DCTN1-AS1	-622
5	138875768	cg07718085	1427	-29.75	5.68	1.61E-07	5.95E-04	0.74 (0.66, 0.83)	TMEM173	-13394
5	20576898	cg05883445	1428	-37.76	7.21	1.65E-07	6.07E-04	0.69 (0.6, 0.79)	CDH18	-917
1	29523841	cg16263722	1428	-18.19	3.48	1.70E-07	6.23E-04	0.83 (0.78, 0.89)	SRSF4	-15205
15	101798908	cg03666966	1427	-31.64	6.05	1.74E-07	6.35E-04	0.73 (0.65, 0.82)	CHSY1	-6772
17	56269767	cg01955639	1428	-18.56	3.55	1.76E-07	6.36E-04	0.83 (0.77, 0.89)	EPX	-317
14	75162215	cg06984345	1428	-15.07	2.88	1.76E-07	6.36E-04	0.86 (0.81, 0.91)	AREL1	17591

3	44381576	cg04385523	1428	-48.35	9.26	1.80E-07	6.48E-04	0.62 (0.51, 0.74)	TCAIM	1633
8	131454686	cg04308301	1428	-17.24	3.3	1.82E-07	6.52E-04	0.84 (0.79, 0.9)	ASAP1	1219
16	195133	cg23079735	1428	-16.66	3.19	1.83E-07	6.53E-04	0.85 (0.8, 0.9)	NPRL3	-6437
9	130859520	cg26150475	1426	-40.2	7.72	1.88E-07	6.65E-04	0.67 (0.58, 0.78)	SLC25A25	-1240
15	101920222	cg26197665	1427	-18.16	3.48	1.88E-07	6.65E-04	0.83 (0.78, 0.89)	PCSK6-AS1	45581
5	43523547	cg07944332	1427	-32.23	6.19	1.93E-07	6.78E-04	0.72 (0.64, 0.82)	C5orf34	-8275
17	55167149	cg06483820	1425	-20.23	3.89	1.94E-07	6.78E-04	0.82 (0.76, 0.88)	AKAP1	4015
13	113825954	cg12172163	1428	-14.01	2.69	1.94E-07	6.78E-04	0.87 (0.82, 0.92)	PROZ	12987
17	72709731	cg21640749	1428	-17.07	3.28	1.97E-07	6.85E-04	0.84 (0.79, 0.9)	CD300LF	-593
2	47242277	cg06528816	1428	-15.99	3.07	2.00E-07	6.93E-04	0.85 (0.8, 0.91)	MCFD2	-73284
17	15137304	cg20315954	1428	-24.5	4.72	2.03E-07	7.00E-04	0.78 (0.71, 0.86)	MIR4731	17708
9	365007	cg05178561	1428	-20.12	3.88	2.09E-07	7.15E-04	0.82 (0.76, 0.88)	DOCK8	91960
11	60623918	cg25087851	1425	-11.94	2.3	2.09E-07	7.15E-04	0.89 (0.85, 0.93)	PTGDR2	-475
10	94837967	cg15767361	1426	-27.17	5.24	2.13E-07	7.25E-04	0.76 (0.69, 0.84)	CYP26A1	4321
1	40532772	cg15881027	1426	-25.1	4.84	2.14E-07	7.26E-04	0.78 (0.71, 0.86)	CAP1	26518
10	114437682	cg03756297	1428	-39.26	7.57	2.17E-07	7.33E-04	0.68 (0.58, 0.78)	MIR4295	43754
1	47746081	cg13789639	1428	-22.76	4.4	2.31E-07	7.77E-04	0.80 (0.73, 0.87)	STIL	33737
19	5592815	cg12104982	1427	-15.45	2.99	2.44E-07	8.17E-04	0.86 (0.81, 0.91)	TINCR	-24771
4	146800380	cg25799589	1426	-30.91	5.99	2.45E-07	8.17E-04	0.73 (0.65, 0.83)	ZNF827	59731
9	138362327	cg14011077	1426	-20	3.88	2.47E-07	8.21E-04	0.82 (0.76, 0.88)	PPP1R26-AS1	1767
21	37536817	cg07834490	1423	-6.73	1.31	2.51E-07	8.30E-04	0.93 (0.91, 0.96)	DOPEY2	-21
6	126375816	cg27341747	1424	-29.02	5.63	2.59E-07	8.53E-04	0.75 (0.67, 0.84)	MIR5695	67945
11	2696198	cg01439230	1427	-43.54	8.46	2.65E-07	8.66E-04	0.65 (0.55, 0.76)	KCNQ1OT1	25029
11	126279702	cg20037145	1424	-10.39	2.02	2.65E-07	8.66E-04	0.90 (0.87, 0.94)	ST3GAL4	3626
12	68056168	cg19968199	1428	-44.51	8.65	2.70E-07	8.75E-04	0.64 (0.54, 0.76)	DYRK2	13657
8	128981622	cg02133716	1427	-32.82	6.38	2.71E-07	8.75E-04	0.72 (0.64, 0.82)	MIR1205	8744
6	107272133	cg13118684	1427	-21.12	4.11	2.71E-07	8.75E-04	0.81 (0.75, 0.88)	LINC02532	-36834
7	97908505	cg02985445	1428	-13.46	2.62	2.73E-07	8.75E-04	0.87 (0.83, 0.92)	BRI3	-2473
3	136618139	cg14184646	1427	-41.86	8.14	2.73E-07	8.75E-04	0.66 (0.56, 0.77)	NCK1	-31177
20	34364813	cg16122287	1423	-36.05	7.02	2.77E-07	8.84E-04	0.70 (0.61, 0.8)	PHF20	4891
11	112149745	cg22972893	1428	-20.01	3.9	2.88E-07	9.15E-04	0.82 (0.76, 0.88)	LOC283140	8274
14	62068941	cg08061334	1428	-19.8	3.86	2.89E-07	9.15E-04	0.82 (0.76, 0.88)	LINC01303	-31571
9	134883788	cg13628444	1427	-19.74	3.85	2.91E-07	9.18E-04	0.82 (0.76, 0.89)	MED27	71485

2	234246583	cg05724080		1428	-12.29	2.4	3.00E-07	9.39E-04	0.88 (0.84, 0.93)	DGKD	-16569
15	67802577	cg27335233		1428	-13.8	2.69	3.00E-07	9.39E-04	0.87 (0.83, 0.92)	IQCH-AS1	10733
9	97403129	cg13576859		1428	-14.83	2.9	3.10E-07	9.67E-04	0.86 (0.81, 0.91)	FBP1	-599
3	181897670	cg09596645		1428	-34.87	6.82	3.19E-07	9.91E-04	0.71 (0.62, 0.81)	LINC01206	227519
7	75511298	cg15952483		1424	-29.21	5.72	3.32E-07	1.03E-03	0.75 (0.67, 0.84)	RHBDD2	2989
15	33717344	cg15314908		1426	-35.73	7.01	3.38E-07	1.04E-03	0.70 (0.61, 0.8)	RYR3	114182
17	36452075	cg17519037	1	1428	-29.62	5.81	3.46E-07	1.06E-03	0.74 (0.66, 0.83)	MRPL45	-913
1	33221514	cg03092343		1428	-16.03	3.15	3.49E-07	1.07E-03	0.85 (0.8, 0.91)	KIAA1522	-9720
17	26793673	cg22146772		1426	-20.81	4.09	3.64E-07	1.11E-03	0.81 (0.75, 0.88)	SLC13A2	-6990
7	2683257	cg01978458		1428	-11.02	2.17	3.66E-07	1.11E-03	0.90 (0.86, 0.93)	TTYH3	11655
1	90344715	cg17256681		1426	-49.93	9.82	3.71E-07	1.12E-03	0.61 (0.5, 0.74)	LRRC8D	57236
9	140308660	cg13562011		1427	-20.94	4.12	3.75E-07	1.13E-03	0.81 (0.75, 0.88)	EXD3	9053
7	75592134	cg16182457		1426	-24.36	4.79	3.75E-07	1.13E-03	0.78 (0.71, 0.86)	SNORA14A	19034
1	175136705	cg17804141		1419	-12.32	2.42	3.78E-07	1.13E-03	0.88 (0.84, 0.93)	KIAA0040	25243
1	175772135	cg04031158		1428	-29.72	5.85	3.81E-07	1.14E-03	0.74 (0.66, 0.83)	TNR	-59384
3	14708144	cg15106081		1425	-36.59	7.21	3.83E-07	1.14E-03	0.69 (0.6, 0.8)	C3orf20	-8461
1	154581658	cg23475294		1428	-19.31	3.81	3.95E-07	1.17E-03	0.82 (0.77, 0.89)	ADAR	-935
3	72509222	cg10279452		1428	-21.68	4.28	3.96E-07	1.17E-03	0.81 (0.74, 0.88)	RYBP	-13449
9	130608923	cg13458609		1423	-10.08	1.99	3.98E-07	1.17E-03	0.90 (0.87, 0.94)	ENG	522
20	47731131	cg23498922		1428	-24.11	4.76	3.99E-07	1.17E-03	0.79 (0.72, 0.86)	CSE1L	68349
7	50861834	cg13459606		1426	-15.62	3.08	4.00E-07	1.17E-03	0.86 (0.81, 0.91)	GRB10	-676
16	55542668	cg03471593		1426	-6.11	1.21	4.03E-07	1.17E-03	0.94 (0.92, 0.96)	LPCAT2	-244
19	7291221	cg19696679		1428	-34.33	6.78	4.07E-07	1.18E-03	0.71 (0.62, 0.81)	INSR	3091
17	17843585	cg22508829		1428	-26.85	5.31	4.23E-07	1.22E-03	0.76 (0.69, 0.85)	TOM1L2	32198
13	111316145	cg12075669		1428	-11.8	2.33	4.26E-07	1.23E-03	0.89 (0.85, 0.93)	CARS2	42381
8	141046469	cg09377531		1421	-16.07	3.18	4.28E-07	1.23E-03	0.85 (0.8, 0.91)	PEG13	64164
17	1047567	cg26235490		1428	-16.65	3.3	4.51E-07	1.29E-03	0.85 (0.79, 0.9)	ABR	-17668
3	171205319	cg20804243		1428	-16.79	3.33	4.56E-07	1.29E-03	0.85 (0.79, 0.9)	TNIK	-27123
17	21103728	cg12060026		1427	-18.83	3.73	4.59E-07	1.29E-03	0.83 (0.77, 0.89)	TMEM11	14179
15	64024116	cg26337091		1424	-14.77	2.93	4.60E-07	1.29E-03	0.86 (0.81, 0.91)	HERC1	102030
5	177613806	cg05473599		1427	-12.59	2.5	4.61E-07	1.29E-03	0.88 (0.84, 0.93)		626
11	123429280	cg15158069		1427	-7.33	1.45	4.61E-07	1.29E-03	0.93 (0.9, 0.96)	GRAMD1B	-1689
10	114437552	cg02698198		1427	-17.35	3.44	4.62E-07	1.29E-03	0.84 (0.79, 0.9)	MIR4295	43624

11	44092987	cg17879351		1428	-20.08	3.99	4.70E-07	1.31E-03	0.82 (0.76, 0.88)	ACCS	5176
6	7199401	cg13863638		1426	-49.5	9.83	4.71E-07	1.31E-03	0.61 (0.5, 0.74)	RREB1	91316
16	85655007	cg02124524		1426	-39.07	7.77	4.95E-07	1.37E-03	0.68 (0.58, 0.79)	GSE1	8166
15	52135487	cg12402318		1428	-26.4	5.25	4.98E-07	1.37E-03	0.77 (0.69, 0.85)	TMOD3	13663
3	3152201	cg23582054		1428	-10.57	2.1	5.01E-07	1.38E-03	0.90 (0.86, 0.94)	IL5RA	-144
6	116781307	cg25488567		1428	-17.64	3.51	5.03E-07	1.38E-03	0.84 (0.78, 0.9)	CALHM6	-1225
3	124646526	cg17365440		1427	-18.39	3.66	5.07E-07	1.39E-03	0.83 (0.77, 0.89)	MUC13	7068
10	102277130	cg21867373		1428	-17.89	3.56	5.12E-07	1.39E-03	0.84 (0.78, 0.9)	SEC31B	2464
1	112045886	cg19686029		1425	-28.73	5.72	5.13E-07	1.39E-03	0.75 (0.67, 0.84)	ADORA3	856
5	149293098	cg10521603		1427	-37.8	7.53	5.24E-07	1.42E-03	0.69 (0.59, 0.79)	LOC644762	19441
1	177907297	cg17971251		1428	-16.43	3.28	5.32E-07	1.43E-03	0.85 (0.8, 0.9)	SEC16B	31752
4	185712241	cg18182820		1428	-27.49	5.48	5.34E-07	1.44E-03	0.76 (0.68, 0.85)	SLED1	7958
5	74342697	cg14390854		1428	-16.23	3.24	5.36E-07	1.44E-03	0.85 (0.8, 0.91)	LINC01336	5770
9	130222969	cg14012059		1417	-7.17	1.43	5.57E-07	1.49E-03	0.93 (0.91, 0.96)	LRSAM1	8436
16	53120120	cg01137366		1425	-10.21	2.04	5.59E-07	1.49E-03	0.90 (0.87, 0.94)	CHD9	31176
19	3521502	cg00477633		1426	-27.5	5.5	5.61E-07	1.49E-03	0.76 (0.68, 0.85)	FZR1	-1451
5	112541553	cg09565310		1428	-19.93	3.98	5.63E-07	1.49E-03	0.82 (0.76, 0.89)	MCC	89058
17	55191754	cg16438366		1427	-12.16	2.43	5.64E-07	1.49E-03	0.89 (0.84, 0.93)	AKAP1	28620
12	113642799	cg04806741		1428	-21.62	4.32	5.73E-07	1.51E-03	0.81 (0.74, 0.88)	IQCD	16099
7	98722470	cg14769121		1428	-22.11	4.42	5.79E-07	1.52E-03	0.80 (0.74, 0.87)	SMURF1	19272
14	77381159	cg23825347		1428	-8.99	1.8	5.85E-07	1.53E-03	0.91 (0.88, 0.95)	LINC01629	-44821
12	123201189	cg18830042	1	1428	-18.82	3.77	5.96E-07	1.55E-03	0.83 (0.77, 0.89)	HCAR3	249
9	5587802	cg04825341		1426	-27.59	5.53	5.99E-07	1.55E-03	0.76 (0.68, 0.85)	RIC1	-41316
14	88502505	cg01295798		1428	-35.29	7.07	6.06E-07	1.57E-03	0.70 (0.61, 0.81)	LOC101928791	-9850
13	31308509	cg24380653		1427	-24.45	4.9	6.20E-07	1.60E-03	0.78 (0.71, 0.86)	ALOX5AP	-1135
2	8472503	cg06773230		1428	-21.98	4.41	6.30E-07	1.62E-03	0.80 (0.74, 0.88)	LINC00299	-3955
12	8201975	cg20818756		1427	-18.47	3.71	6.42E-07	1.64E-03	0.83 (0.77, 0.89)	FOXJ2	16617
1	43290834	cg11987455		1428	-17.58	3.53	6.44E-07	1.64E-03	0.84 (0.78, 0.9)	ERMAP	-414
17	17939419	cg20885063		1427	-22.35	4.49	6.53E-07	1.66E-03	0.80 (0.73, 0.87)	ATPAF2	3060
9	139701021	cg04883329		1425	-7.53	1.51	6.59E-07	1.67E-03	0.93 (0.9, 0.96)	RABL6	-1352
20	35422703	cg21045547		1428	-17.58	3.54	6.71E-07	1.70E-03	0.84 (0.78, 0.9)	DSN1	-20474
14	67983363	cg08778580		1428	-16.29	3.28	6.84E-07	1.73E-03	0.85 (0.8, 0.91)	TMEM229B	-1343
22	37296313	cg09339568		1428	-9.17	1.85	6.89E-07	1.73E-03	0.91 (0.88, 0.95)	CSF2RB	-13361

9	131355483	cg05072637		1428	-15.97	3.22	6.90E-07	1.73E-03	0.85 (0.8, 0.91)	SPTAN1	40647
7	29382450	cg20831584		1428	-20.84	4.2	6.94E-07	1.73E-03	0.81 (0.75, 0.88)	LOC102724484	-133865
1	19467440	cg23087931		1427	-48.65	9.81	7.13E-07	1.78E-03	0.61 (0.51, 0.75)	UBR4	69305
7	151501146	cg12736613		1427	-16.4	3.31	7.23E-07	1.80E-03	0.85 (0.8, 0.91)	PRKAG2	10810
20	36340388	cg20893283		1426	-16.03	3.24	7.25E-07	1.80E-03	0.85 (0.8, 0.91)	CTNNBL1	18032
4	185744331	cg17718238		1427	-24.42	4.93	7.42E-07	1.83E-03	0.78 (0.71, 0.86)	ACSL1	2936
21	34130201	cg07778428		1428	-17.1	3.46	7.60E-07	1.87E-03	0.84 (0.79, 0.9)	PAXBP1	13967
5	37668810	cg07879720		1423	-13.65	2.76	7.66E-07	1.87E-03	0.87 (0.83, 0.92)	GDNF	166113
15	63495110	cg21067343		1427	-24.51	4.96	7.66E-07	1.87E-03	0.78 (0.71, 0.86)	RAB8B	13383
19	15436097	cg02068052		1427	-17.74	3.59	7.69E-07	1.88E-03	0.84 (0.78, 0.9)	BRD4	7256
17	62255234	cg09335712		1427	-19.48	3.94	7.84E-07	1.90E-03	0.82 (0.76, 0.89)	SNORA50C	31536
2	75089669	cg12077754		1428	-13.53	2.74	7.84E-07	1.90E-03	0.87 (0.83, 0.92)	HK2	29888
1	172507360	cg24039962		1427	-26.14	5.29	7.90E-07	1.91E-03	0.77 (0.69, 0.85)	SUCO	5103
17	25833338	cg00460843		1428	-14.68	2.97	8.05E-07	1.94E-03	0.86 (0.81, 0.92)	KSR1	34303
2	8676902	cg03119191		1427	-10.78	2.19	8.06E-07	1.94E-03	0.90 (0.86, 0.94)	LINC01814	47019
11	57156050	cg15700636		1424	-15.43	3.13	8.32E-07	1.99E-03	0.86 (0.81, 0.91)	PRG2	2079
5	173285792	cg26817086		1428	-10.12	2.06	8.50E-07	2.03E-03	0.90 (0.87, 0.94)	CPEB4	-29538
5	137812320	cg22905973		1428	-41.57	8.45	8.56E-07	2.04E-03	0.66 (0.56, 0.78)	EGR1	11140
15	64275853	cg11266582		1422	-7.5	1.52	8.59E-07	2.04E-03	0.93 (0.9, 0.96)	LOC101928988	55381
16	31484722	cg11215870		1423	-13.42	2.73	8.79E-07	2.08E-03	0.87 (0.83, 0.92)	TGFB1I1	197
19	35950799	cg17062760		1428	-14.3	2.91	8.81E-07	2.08E-03	0.87 (0.82, 0.92)	FFAR2	10183
11	8717586	cg10224250		1426	-11.44	2.33	8.83E-07	2.08E-03	0.89 (0.85, 0.93)	SNORA3B	10601
11	47937934	cg18367488		1427	-17.62	3.59	8.91E-07	2.09E-03	0.84 (0.78, 0.9)	PTPRJ	-64175
5	179203369	cg09031958		1427	-18.95	3.86	8.98E-07	2.09E-03	0.83 (0.77, 0.89)	LTC4S	-17616
11	119507838	cg12359648		1426	-26.23	5.34	8.98E-07	2.09E-03	0.77 (0.69, 0.85)	NECTIN1	91596
2	38812997	cg06755692		1427	-14.49	2.95	9.02E-07	2.09E-03	0.87 (0.82, 0.92)	HNRNPLL	17180
3	12269362	cg04399631		1428	-7.53	1.53	9.04E-07	2.09E-03	0.93 (0.9, 0.96)	PPARG	-59986
17	17156056	cg00321711		1423	-13.1	2.67	9.06E-07	2.09E-03	0.88 (0.83, 0.92)	FLCN	-15555
8	8702053	cg12077460		1426	-9.08	1.85	9.09E-07	2.09E-03	0.91 (0.88, 0.95)	MFHAS1	49077
2	28550531	cg17862837		1428	-48.34	9.84	9.09E-07	2.09E-03	0.62 (0.51, 0.75)	LOC100505716	-17206
19	41925187	cg02447557		1428	-34.35	7	9.11E-07	2.09E-03	0.71 (0.62, 0.81)	B3GNT8	9447
9	101595635	cg04148640		1423	-37.63	7.67	9.23E-07	2.11E-03	0.69 (0.59, 0.8)	GALNT12	25655
7	150648840	cg24836822	1	1428	-14.76	3.01	9.26E-07	2.11E-03	0.86 (0.81, 0.92)	KCNH2	4076

10	91262748	cg24600621		1428	-31.58	6.44	9.27E-07	2.11E-03	0.73 (0.64, 0.83)	SLC16A12	32564
15	52030746	cg07177867		1428	-16.04	3.27	9.40E-07	2.13E-03	0.85 (0.8, 0.91)	LYSMD2	-427
6	158994509	cg27279839		1418	-19.7	4.02	9.40E-07	2.13E-03	0.82 (0.76, 0.89)	MIR7161	-36229
13	99991345	cg10145411		1428	-24.28	4.95	9.43E-07	2.13E-03	0.78 (0.71, 0.86)	FKSG29	-12328
5	150486801	cg23172995		1428	-25.46	5.19	9.44E-07	2.13E-03	0.78 (0.7, 0.86)	TNIP1	-19581
2	74612706	cg13774539		1428	-12.19	2.49	9.62E-07	2.16E-03	0.89 (0.84, 0.93)	DCTN1-AS1	-138
19	44175158	cg26058544		1426	-16.08	3.28	9.65E-07	2.16E-03	0.85 (0.8, 0.91)	PLAUR	-661
10	104414965	cg19002713		1428	-28.99	5.92	9.69E-07	2.16E-03	0.75 (0.67, 0.84)	TRIM8	10714
1	118139009	cg11558387		1427	-16.26	3.32	9.70E-07	2.16E-03	0.85 (0.8, 0.91)	LOC100996263	9382
1	9599067	cg18783781		1428	-16.26	3.32	9.74E-07	2.16E-03	0.85 (0.8, 0.91)	SLC25A33	-460
14	75153307	cg26103369		1428	-41.72	8.52	9.77E-07	2.16E-03	0.66 (0.56, 0.78)	AREL1	26499
2	30414835	cg19376906		1428	-10.34	2.11	9.83E-07	2.17E-03	0.90 (0.87, 0.94)	LBH	-39561
14	88656128	cg08652605		1426	-14.46	2.96	9.87E-07	2.17E-03	0.87 (0.82, 0.92)	KCNK10	81126
11	69418951	cg16549727		1420	-22.8	4.66	9.98E-07	2.19E-03	0.80 (0.73, 0.87)	CCND1	-36921
1	204370262	cg21142557		1427	-31.21	6.39	1.02E-06	2.23E-03	0.73 (0.65, 0.83)	PPP1R15B	10682
11	65547049	cg05257275		1427	-8.21	1.68	1.03E-06	2.24E-03	0.92 (0.89, 0.95)	AP5B1	1012
8	103603330	cg17245251		1428	-27.52	5.63	1.03E-06	2.24E-03	0.76 (0.68, 0.85)	ODF1	39483
7	30505269	cg07299810		1422	-25.94	5.31	1.05E-06	2.28E-03	0.77 (0.7, 0.86)	NOD1	13123
17	21119381	cg23149707		1428	-12.75	2.61	1.05E-06	2.28E-03	0.88 (0.84, 0.93)	TMEM11	-1474
1	26624534	cg19296400		1427	-13.78	2.82	1.06E-06	2.29E-03	0.87 (0.82, 0.92)	UBXN11	8660
1	167512106	cg14617280		1428	-33.76	6.92	1.07E-06	2.31E-03	0.71 (0.62, 0.82)	CREG1	10949
12	92431524	cg02142455		1425	-39.7	8.14	1.08E-06	2.32E-03	0.67 (0.57, 0.79)	LINC01619	103964
6	25608913	cg03784596		1427	-30.79	6.31	1.09E-06	2.34E-03	0.73 (0.65, 0.83)	SCGN	-43515
19	45427880	cg24712122	1	1425	-9.95	2.04	1.10E-06	2.35E-03	0.91 (0.87, 0.94)	APOC1P1	-2179
1	61607055	cg26252077		1423	-13.5	2.77	1.12E-06	2.39E-03	0.87 (0.83, 0.92)	NFIA	59076
10	43911124	cg22080845		1427	-46.17	9.49	1.14E-06	2.43E-03	0.63 (0.52, 0.76)	HNRNPF	-6429
1	66777579	cg24058805		1428	-26.99	5.55	1.15E-06	2.44E-03	0.76 (0.68, 0.85)	PDE4B	-20211
3	52810259	cg07730263		1428	-12.18	2.51	1.18E-06	2.50E-03	0.89 (0.84, 0.93)	ITIH1	-1342
22	38386904	cg15352551		1428	-10.75	2.21	1.19E-06	2.51E-03	0.90 (0.86, 0.94)	MIR4534	2104
8	128972681	cg05480350		1428	-14.78	3.04	1.21E-06	2.54E-03	0.86 (0.81, 0.92)	MIR1205	-197
1	10516255	cg07361747		1426	-8.48	1.75	1.21E-06	2.54E-03	0.92 (0.89, 0.95)	CORT	6480
16	67075173	cg03850588		1426	-18.81	3.88	1.23E-06	2.57E-03	0.83 (0.77, 0.89)	CBFB	12124
10	70531163	cg21553305		1427	-35.84	7.39	1.23E-06	2.57E-03	0.70 (0.6, 0.81)		12089

13	34446325	cg18544612	1428	-15.74	3.25	1.24E-06	2.59E-03	0.85 (0.8, 0.91)	RFC3	54120
10	104227113	cg10897344	1421	-16.26	3.35	1.25E-06	2.60E-03	0.85 (0.8, 0.91)	MFSD13A	5944
15	58572140	cg04979283	1426	-32.93	6.8	1.26E-06	2.60E-03	0.72 (0.63, 0.82)	AQP9	141746
1	182308249	cg07579327	1428	-13.63	2.81	1.26E-06	2.60E-03	0.87 (0.83, 0.92)	LINC01344	-25054
7	37434016	cg11422446	1426	-14.39	2.97	1.26E-06	2.60E-03	0.87 (0.82, 0.92)	ELMO1	-40745
9	130859454	cg13835688	1428	-13.97	2.89	1.28E-06	2.63E-03	0.87 (0.82, 0.92)	SLC25A25	-1306
2	69828510	cg10054763	1428	-33.02	6.83	1.34E-06	2.75E-03	0.72 (0.63, 0.82)	ANXA4	-42426
6	167189272	cg03329755	1416	-19	3.93	1.37E-06	2.81E-03	0.83 (0.77, 0.89)	RPS6KA2	86766
11	62678778	cg03448301	1426	-34.44	7.13	1.38E-06	2.81E-03	0.71 (0.62, 0.81)	CHRM1	10233
12	9486204	cg15964898	1428	-45.77	9.48	1.38E-06	2.81E-03	0.63 (0.53, 0.76)	LINC02367	-33855
15	80142016	cg17934955	1428	-25.14	5.21	1.39E-06	2.83E-03	0.78 (0.7, 0.86)	MTHFS	47322
1	23072310	cg19851810	1423	-38.84	8.05	1.41E-06	2.86E-03	0.68 (0.58, 0.79)	MIR4684	26301
17	26973493	cg06608224	1424	-14.36	2.98	1.46E-06	2.95E-03	0.87 (0.82, 0.92)	KIAA0100	-1317
19	51961666	cg17521120	1428	-14.2	2.95	1.47E-06	2.97E-03	0.87 (0.82, 0.92)	SIGLEC8	41
11	70053254	cg15482717	1428	-12.07	2.51	1.49E-06	2.99E-03	0.89 (0.84, 0.93)	FADD	3986
22	30549748	cg16465403	1428	-14.09	2.93	1.49E-06	2.99E-03	0.87 (0.82, 0.92)	HORMAD2-AS1	-73280
22	37299905	cg05808227	1428	-16.83	3.5	1.50E-06	3.00E-03	0.85 (0.79, 0.91)	CSF2RB	-9769
12	109971517	cg05076510	1428	-13.09	2.72	1.51E-06	3.02E-03	0.88 (0.83, 0.93)	MMAB	39840
20	35475630	cg07589211	1422	-8.55	1.78	1.53E-06	3.05E-03	0.92 (0.89, 0.95)	SOGA1	12645
4	148635716	cg00006459	1426	-23.76	4.95	1.59E-06	3.15E-03	0.79 (0.72, 0.87)	ARHGAP10	-17736
8	105599835	cg10815420	1426	-34.5	7.19	1.59E-06	3.15E-03	0.71 (0.62, 0.82)	LRP12	1416
17	39686628	cg21723861	1416	-22.1	4.6	1.59E-06	3.15E-03	0.80 (0.73, 0.88)	KRT19	-1988
1	115032585	cg23779286	1428	-14	2.92	1.63E-06	3.22E-03	0.87 (0.82, 0.92)	TRIM33	21195
8	129152499	cg08089777	1426	-39.6	8.27	1.68E-06	3.30E-03	0.67 (0.57, 0.79)	MIR1208	-9862
3	36974725	cg11014921	1428	-40.34	8.43	1.68E-06	3.30E-03	0.67 (0.57, 0.79)	TRANK1	11822
9	101595573	cg24818060	1428	-42.7	8.93	1.72E-06	3.37E-03	0.65 (0.55, 0.78)	GALNT12	25593
10	129799166	cg01325448	1428	-13.56	2.84	1.78E-06	3.48E-03	0.87 (0.83, 0.92)	PTPRE	2777
6	135482465	cg15202169	1428	-14.5	3.04	1.80E-06	3.51E-03	0.87 (0.81, 0.92)	MYB	-19987
9	128107984	cg14556243	1427	-10.48	2.2	1.81E-06	3.52E-03	0.90 (0.86, 0.94)	GAPVD1	46816
1	47157809	cg06824199	1427	-33.35	6.99	1.84E-06	3.57E-03	0.72 (0.62, 0.82)	EFCAB14-AS1	18102
15	68146684	cg14209284	1428	-23.75	4.98	1.87E-06	3.62E-03	0.79 (0.72, 0.87)	RNU6-2	-14302
6	137544615	cg00638845	1428	-23.57	4.94	1.88E-06	3.63E-03	0.79 (0.72, 0.87)	IFNGR1	-4049
7	127528039	cg09696385	1428	-34.42	7.23	1.89E-06	3.64E-03	0.71 (0.62, 0.82)	SND1-IT1	-109522

8	68109236	cg12168006		1428	-42.24	8.87	1.90E-06	3.65E-03	0.66 (0.55, 0.78)	CSPP1	113154
8	95918378	cg13279458		1424	-9.86	2.07	1.92E-06	3.68E-03	0.91 (0.87, 0.94)	CCNE2	-10897
11	12136467	cg01450133		1426	-26.45	5.56	1.93E-06	3.69E-03	0.77 (0.69, 0.86)	MICAL2	4345
15	94408646	cg18991231		1428	-14.02	2.95	1.95E-06	3.72E-03	0.87 (0.82, 0.92)	LINC02207	8858
14	100066736	cg12773397		1424	-21.92	4.61	1.98E-06	3.76E-03	0.80 (0.73, 0.88)	CCDC85C	3990
1	27241913	cg19787060		1427	-13.39	2.82	1.98E-06	3.76E-03	0.87 (0.83, 0.92)	NR0B2	-1347
10	86096789	cg04546473		1428	-19.57	4.12	2.05E-06	3.87E-03	0.82 (0.76, 0.89)	CCSER2	8445
17	80419874	cg05613273		1428	-31.01	6.53	2.05E-06	3.87E-03	0.73 (0.65, 0.83)	NARF	3335
1	27868615	cg27508623		1424	-12.02	2.53	2.05E-06	3.87E-03	0.89 (0.84, 0.93)	WASF2	-51918
9	35755346	cg01499988		1428	-18.28	3.85	2.06E-06	3.88E-03	0.83 (0.77, 0.9)	MSMP	-1073
7	139896924	cg15203376		1428	-17.06	3.59	2.07E-06	3.89E-03	0.84 (0.79, 0.9)	KDM7A-DT	19864
7	73208138	cg17982734		1423	-9.63	2.03	2.08E-06	3.90E-03	0.91 (0.87, 0.95)	CLDN3	-23539
13	48876919	cg13221796		1428	-11.02	2.32	2.13E-06	3.98E-03	0.90 (0.86, 0.94)	RB1-DT	877
1	19675581	cg11495942		1428	-26.53	5.6	2.18E-06	4.07E-03	0.77 (0.69, 0.86)	PQLC2	36842
1	28459201	cg25960268		1428	-10.97	2.32	2.21E-06	4.11E-03	0.90 (0.86, 0.94)	EYA3	-44054
12	113713802	cg04524109	1	1428	-18.47	3.9	2.22E-06	4.12E-03	0.83 (0.77, 0.9)	MIR6762	-15525
21	46955647	cg00714531		1428	-15.67	3.31	2.24E-06	4.15E-03	0.85 (0.8, 0.91)	SLC19A1	-1106
20	43590115	cg13792581		1426	-35.77	7.57	2.29E-06	4.23E-03	0.70 (0.6, 0.81)	TOMM34	-1002
20	35504064	cg19448292		1428	-13.93	2.95	2.30E-06	4.24E-03	0.87 (0.82, 0.92)	TLDC2	-459
1	43290841	cg04377912		1425	-32.98	6.98	2.32E-06	4.26E-03	0.72 (0.63, 0.82)	ERMAP	-407
19	44220148	cg20673965		1425	-11.28	2.39	2.32E-06	4.26E-03	0.89 (0.85, 0.94)	IRGC	-65
17	59297117	cg00961073		1426	-37.35	7.91	2.33E-06	4.26E-03	0.69 (0.59, 0.8)	LOC101927855	147947
19	34860339	cg02359181		1428	-19.21	4.07	2.33E-06	4.26E-03	0.83 (0.76, 0.89)	GPI	4315
6	139841523	cg18190876		1428	-22.44	4.75	2.35E-06	4.29E-03	0.80 (0.73, 0.88)	LINC01625	-45791
13	113305704	cg25479097		1426	-19.04	4.04	2.38E-06	4.33E-03	0.83 (0.76, 0.89)	ATP11AUN	4347
2	233076983	cg01224965		1428	-17.29	3.67	2.41E-06	4.37E-03	0.84 (0.78, 0.9)	ALPP	-166260
5	172227661	cg21237481		1427	-16.69	3.54	2.41E-06	4.37E-03	0.85 (0.79, 0.91)	DUSP1	-29459
11	61607741	cg13764085		1428	-11.75	2.49	2.42E-06	4.38E-03	0.89 (0.85, 0.93)	FADS2	12237
15	52157096	cg26997652		1428	-31.36	6.66	2.45E-06	4.42E-03	0.73 (0.64, 0.83)	TMOD3	35272
3	195835467	cg06144471		1426	-21.52	4.57	2.48E-06	4.46E-03	0.81 (0.74, 0.88)	TFRC	-26436
18	33021980	cg12734151		1426	-31.8	6.76	2.54E-06	4.56E-03	0.73 (0.64, 0.83)	INO80C	55632
1	2036398	cg06315149		1428	-16.44	3.49	2.55E-06	4.56E-03	0.85 (0.79, 0.91)	PRKCZ	244
5	149295369	cg09486450		1428	-36.27	7.71	2.55E-06	4.56E-03	0.70 (0.6, 0.81)	LOC644762	17170

7	150651937	cg18666454		1427	-15.09	3.21	2.56E-06	4.57E-03	0.86 (0.81, 0.92)	KCNH2	979
6	143014942	cg25602071		1428	-22.15	4.71	2.59E-06	4.61E-03	0.80 (0.73, 0.88)	LOC153910	-55917
3	66428294	cg04217850		1427	-20.9	4.45	2.60E-06	4.62E-03	0.81 (0.74, 0.89)	LRIG1	122550
16	23511855	cg03935956		1428	-9.21	1.96	2.68E-06	4.74E-03	0.91 (0.88, 0.95)	GGA2	9959
13	47274074	cg11015284		1428	-50.46	10.75	2.68E-06	4.74E-03	0.60 (0.49, 0.75)	ESD	97292
9	130158144	cg00114012		1427	-15.67	3.34	2.69E-06	4.74E-03	0.85 (0.8, 0.91)	SLC2A8	-1272
11	63272225	cg05380077		1425	-10.51	2.24	2.69E-06	4.74E-03	0.90 (0.86, 0.94)	LGALS12	-1298
10	15194066	cg21994464		1424	-15.36	3.27	2.70E-06	4.75E-03	0.86 (0.8, 0.91)	PPIAP30	3279
22	32873926	cg01976243		1428	-13.62	2.9	2.73E-06	4.79E-03	0.87 (0.82, 0.92)	FBXO7	2703
16	31135265	cg02869730		1428	-52.72	11.25	2.77E-06	4.84E-03	0.59 (0.47, 0.74)	KAT8	6281
17	74708216	cg15769653		1427	-40.5	8.64	2.77E-06	4.84E-03	0.67 (0.56, 0.79)	MXRA7	-1130
2	70736862	cg05316492		1428	-24.94	5.32	2.78E-06	4.84E-03	0.78 (0.7, 0.86)	TGFA-IT1	-28091
1	27240812	cg16868031		1427	-15.74	3.36	2.87E-06	4.99E-03	0.85 (0.8, 0.91)	NR0B2	-246
17	47590272	cg26102082		1425	-19.88	4.25	2.88E-06	5.00E-03	0.82 (0.75, 0.89)	MIR6165	2094
10	114437523	cg26724455		1427	-23.52	5.03	2.89E-06	5.00E-03	0.79 (0.72, 0.87)	MIR4295	43595
9	84249091	cg02227075		1426	-18.17	3.89	2.98E-06	5.15E-03	0.83 (0.77, 0.9)	TLE1	55358
9	32426874	cg22022320		1428	-42.48	9.09	2.99E-06	5.16E-03	0.65 (0.55, 0.78)	ACO1	42274
3	13069838	cg19344749		1424	-9.96	2.13	3.00E-06	5.16E-03	0.91 (0.87, 0.94)	IQSEC1	-41303
7	150649655	cg23147443	1	1428	-12.06	2.58	3.04E-06	5.22E-03	0.89 (0.84, 0.93)	KCNH2	3261
14	69650830	cg02170785		1427	-13.94	2.99	3.05E-06	5.23E-03	0.87 (0.82, 0.92)	EXD2	-7363
17	13996337	cg01927901		1428	-26.02	5.58	3.13E-06	5.35E-03	0.77 (0.69, 0.86)	COX10-AS1	-23563
20	24630818	cg27028878		1427	-8.61	1.85	3.17E-06	5.41E-03	0.92 (0.88, 0.95)	SYNDIG1	180377
5	40674971	cg17939602		1427	-11.34	2.43	3.19E-06	5.43E-03	0.89 (0.85, 0.94)	PTGER4	-5060
8	6360436	cg12074090		1425	-15.21	3.27	3.22E-06	5.47E-03	0.86 (0.81, 0.92)	ANGPT2	60347
19	3521450	cg06734854		1428	-11.57	2.49	3.28E-06	5.56E-03	0.89 (0.85, 0.94)	FZR1	-1503
3	11522965	cg02228403		1428	-26.56	5.71	3.29E-06	5.56E-03	0.77 (0.69, 0.86)	VGLL4	87432
1	17751974	cg21932513		1428	-12.44	2.68	3.29E-06	5.56E-03	0.88 (0.84, 0.93)	RCC2	13084
12	93798975	cg26584983		1428	-39.14	8.42	3.31E-06	5.58E-03	0.68 (0.57, 0.8)	NUDT4	26650
17	71224314	cg27046434	1	1426	-24.31	5.23	3.36E-06	5.65E-03	0.78 (0.71, 0.87)	FAM104A	-459
22	32873859	cg06866757		1427	-13.14	2.83	3.39E-06	5.68E-03	0.88 (0.83, 0.93)	FBXO7	2636
6	11383319	cg14879823		1428	-50.48	10.87	3.39E-06	5.68E-03	0.60 (0.49, 0.75)	NEDD9	-739
3	170948986	cg14265474		1428	-30.2	6.5	3.42E-06	5.72E-03	0.74 (0.65, 0.84)	MIR569	-124439
5	139597203	cg16953142		1428	-43.04	9.27	3.44E-06	5.74E-03	0.65 (0.54, 0.78)	CYSTM1	42551

19	12997997	cg08679013	1425	-11.39	2.45	3.46E-06	5.75E-03	0.89 (0.85, 0.94)	KLF1	19
2	12553424	cg24323626	1427	-11.91	2.57	3.46E-06	5.75E-03	0.89 (0.84, 0.93)	MIR3681	214169
6	157313826	cg16677621	1409	-21.44	4.62	3.47E-06	5.75E-03	0.81 (0.74, 0.88)	MIR4466	-212962
2	191300784	cg15998761	1428	-20.46	4.41	3.49E-06	5.77E-03	0.81 (0.75, 0.89)	MFSD6	27704
2	43516267	cg00758214	1428	-32.92	7.1	3.50E-06	5.77E-03	0.72 (0.63, 0.83)	LINC01126	61918
13	110350537	cg03189469	1428	-16.44	3.54	3.50E-06	5.77E-03	0.85 (0.79, 0.91)	LINC00676	-30083
1	120821493	cg07827820	1428	-44.33	9.56	3.53E-06	5.79E-03	0.64 (0.53, 0.77)	FAM72B	-17511
6	25609068	cg23131680	1428	-22.97	4.95	3.53E-06	5.79E-03	0.79 (0.72, 0.88)	SCGN	-43360
8	38007025	cg01047262	1428	-41.58	8.97	3.54E-06	5.79E-03	0.66 (0.55, 0.79)	STAR	1574
8	135747178	cg13064897	1426	-18.04	3.89	3.55E-06	5.79E-03	0.83 (0.77, 0.9)	ZFAT	-21887
12	1890975	cg18135530	1427	-39.28	8.47	3.55E-06	5.79E-03	0.68 (0.57, 0.8)	LRTM2	-38457
17	58459590	cg02979987	1428	-33.62	7.25	3.58E-06	5.82E-03	0.71 (0.62, 0.82)	USP32	9995
6	7043141	cg18455414	1426	-11.6	2.5	3.58E-06	5.82E-03	0.89 (0.85, 0.94)	RREB1	-64688
2	217120630	cg01970030	1427	-33.21	7.17	3.59E-06	5.82E-03	0.72 (0.62, 0.83)	LINC01963	39019
3	42942410	cg04992471	1428	-15.18	3.28	3.61E-06	5.83E-03	0.86 (0.81, 0.92)	ZNF662	-4991
1	68163609	cg26145152	1428	-17.14	3.7	3.61E-06	5.83E-03	0.84 (0.78, 0.91)	GADD45A	12750
18	8801435	cg13174688	1423	-15.04	3.25	3.63E-06	5.85E-03	0.86 (0.81, 0.92)	MTCL1	84067
3	3152374	cg01310029	1427	-11.96	2.58	3.64E-06	5.86E-03	0.89 (0.84, 0.93)	IL5RA	-317
14	105352991	cg23584308	1428	-16.02	3.46	3.66E-06	5.88E-03	0.85 (0.8, 0.91)	CEP170B	21342
21	38751589	cg13051367	1428	-21.41	4.63	3.72E-06	5.95E-03	0.81 (0.74, 0.88)	DYRK1A	11731
10	102276804	cg23904266	1428	-12.15	2.63	3.72E-06	5.95E-03	0.89 (0.84, 0.93)	SEC31B	2790
22	36841223	cg22883080	1428	-8.32	1.8	3.73E-06	5.95E-03	0.92 (0.89, 0.95)	TXN2	36463
8	21670177	cg10055846	1427	-14.45	3.12	3.76E-06	5.99E-03	0.87 (0.81, 0.92)	GFRA2	-23832
17	76565232	cg09705784	1428	-8.75	1.89	3.80E-06	6.03E-03	0.92 (0.88, 0.95)	DNAH17	8243
1	40878936	cg20035380	1428	-10.34	2.24	3.80E-06	6.03E-03	0.90 (0.86, 0.94)	SMAP2	16465
16	46776932	cg16064932	1427	-13.02	2.82	3.81E-06	6.03E-03	0.88 (0.83, 0.93)	MYLK3	5288
19	41255444	cg02402423	1428	-17.7	3.83	3.82E-06	6.04E-03	0.84 (0.78, 0.9)	C19orf54	383
20	24630982	cg11841710	1428	-28.7	6.21	3.83E-06	6.04E-03	0.75 (0.66, 0.85)	SYNDIG1	180541
10	6645837	cg16306670	1427	-38.63	8.36	3.87E-06	6.09E-03	0.68 (0.58, 0.8)	LOC101928150	-14840
15	43387093	cg06437892	1426	-21.23	4.6	3.92E-06	6.16E-03	0.81 (0.74, 0.89)	UBR1	11192
14	100610186	cg16409452	1428	-22.72	4.92	3.94E-06	6.18E-03	0.80 (0.72, 0.88)	DEGS2	15825
11	46579500	cg00766820	1424	-24.76	5.37	3.97E-06	6.22E-03	0.78 (0.7, 0.87)	AMBRA1	33413
17	45708176	cg04681520	1428	-46.34	10.05	3.98E-06	6.22E-03	0.63 (0.52, 0.77)	KPNB1	-19027

17	29837074	cg11238327	1428	-11.12	2.41	4.03E-06	6.29E-03	0.89 (0.85, 0.94)	RAB11FIP4	22056
15	42456971	cg20378916	1428	-26.89	5.84	4.08E-06	6.34E-03	0.76 (0.68, 0.86)	PLA2G4F	-8133
12	53994642	cg15279186	1427	-10.67	2.32	4.09E-06	6.34E-03	0.90 (0.86, 0.94)	ATF7	25137
5	132009352	cg25368824	1427	-11.04	2.4	4.09E-06	6.34E-03	0.90 (0.85, 0.94)	IL4	-325
1	6342888	cg12740725	1427	-25.36	5.51	4.11E-06	6.36E-03	0.78 (0.7, 0.86)	GPR153	-21854
15	64856362	cg24536162	1428	-28.47	6.18	4.14E-06	6.40E-03	0.75 (0.67, 0.85)	ZNF609	64744
9	20692704	cg13298043	1428	-8.24	1.79	4.27E-06	6.57E-03	0.92 (0.89, 0.95)	FOCAD-AS1	-7956
9	101705161	cg16680864	1427	-8.97	1.95	4.27E-06	6.57E-03	0.91 (0.88, 0.95)	COL15A1	-833
4	185734335	cg25877465	1425	-12.5	2.72	4.32E-06	6.64E-03	0.88 (0.84, 0.93)	ACSL1	-923
9	130521313	cg25470919	1425	-15.87	3.45	4.35E-06	6.67E-03	0.85 (0.8, 0.91)	SH2D3C	3383
8	33421410	cg23205629	1427	-11.2	2.44	4.40E-06	6.73E-03	0.89 (0.85, 0.94)	RNF122	3235
11	6257262	cg12492850	1422	-10.6	2.31	4.51E-06	6.89E-03	0.90 (0.86, 0.94)	FAM160A2	-1322
9	132600788	cg13953978	1428	-16.09	3.51	4.55E-06	6.94E-03	0.85 (0.79, 0.91)	USP20	3093
2	74531615	cg17660709	1426	-13.2	2.88	4.66E-06	7.09E-03	0.88 (0.83, 0.93)	SLC4A5	10536
9	91919480	cg17542165	1423	-31.38	6.86	4.71E-06	7.15E-03	0.73 (0.64, 0.84)	CKS2	-6629
9	114957571	cg03757043	1428	-17.44	3.81	4.78E-06	7.25E-03	0.84 (0.78, 0.91)	SUSD1	-19995
21	43786727	cg19247032	1428	-23.26	5.09	4.82E-06	7.29E-03	0.79 (0.72, 0.88)	TFF1	-84
21	37536923	cg00673191	1426	-5.47	1.2	4.90E-06	7.40E-03	0.95 (0.92, 0.97)	DOPEY2	85
18	33159713	cg03318414	1428	-13.98	3.06	4.92E-06	7.40E-03	0.87 (0.82, 0.92)	MIR3975	-11987
19	16561197	cg11939550	1424	-6.63	1.45	4.92E-06	7.40E-03	0.94 (0.91, 0.96)	EPS15L1	21625
16	30967493	cg01191788	1428	-19.37	4.24	4.94E-06	7.42E-03	0.82 (0.76, 0.9)	SETD1A	-1121
16	69928821	cg18617819	1427	-9.95	2.18	4.95E-06	7.42E-03	0.91 (0.87, 0.94)	WWP2	-30064
3	195965369	cg22221575	1427	-10.1	2.21	4.99E-06	7.47E-03	0.90 (0.87, 0.94)	SLC51A	21987
1	25351284	cg00158128	1428	-8.88	1.95	5.01E-06	7.49E-03	0.92 (0.88, 0.95)	MIR4425	1291
1	151449494	cg06513960	1426	-32.83	7.19	5.04E-06	7.52E-03	0.72 (0.63, 0.83)	POGZ	-17554
11	1828746	cg21992676	1428	-18.19	3.99	5.09E-06	7.58E-03	0.83 (0.77, 0.9)	SYT8	-26793
7	140102460	cg15244874	1418	-6.31	1.38	5.12E-06	7.61E-03	0.94 (0.91, 0.96)	RAB19	-1382
16	85654213	cg04847043	1427	-26.95	5.91	5.15E-06	7.64E-03	0.76 (0.68, 0.86)	GSE1	7372
17	73972367	cg08423755	1428	-38.74	8.5	5.16E-06	7.64E-03	0.68 (0.57, 0.8)	TEN1-CDK3	-2930
6	7119942	cg15634144	1427	-9.82	2.16	5.18E-06	7.66E-03	0.91 (0.87, 0.95)	RREB1	11857
10	73936754	cg25854298	1428	-23.08	5.06	5.19E-06	7.66E-03	0.79 (0.72, 0.88)	ANAPC16	-39003
15	99443249	cg23990557	1428	-7.61	1.67	5.22E-06	7.69E-03	0.93 (0.9, 0.96)	PGPEP1L	105635
17	74402188	cg05056419	1428	-20.53	4.51	5.24E-06	7.70E-03	0.81 (0.75, 0.89)	SPHK1	20900

17	40724562	cg00170714		1428	-12.16	2.67	5.32E-06	7.81E-03	0.89 (0.84, 0.93)	PSMC3IP	5171
6	32141591	cg09597192		1427	-28.14	6.18	5.33E-06	7.81E-03	0.75 (0.67, 0.85)	AGPAT1	2324
16	68325153	cg17300669		1426	-53.46	11.75	5.34E-06	7.81E-03	0.59 (0.47, 0.74)	SLC7A6OS	19714
3	186193874	cg02423065		1428	-25.87	5.69	5.46E-06	7.97E-03	0.77 (0.69, 0.86)	LINC02052	17575
15	39697356	cg04997452		1427	-40.02	8.8	5.47E-06	7.97E-03	0.67 (0.56, 0.8)	C15orf54	154487
20	33606115	cg07332540		1427	-11.03	2.43	5.52E-06	8.00E-03	0.90 (0.85, 0.94)	MIR499B	-27841
5	43081709	cg26425190		1426	-37.23	8.19	5.53E-06	8.00E-03	0.69 (0.59, 0.81)	LOC648987	-14169
1	33473905	cg11202380		1427	-18.69	4.11	5.54E-06	8.00E-03	0.83 (0.77, 0.9)	AK2	28606
1	210704772	cg11844053		1426	-8.95	1.97	5.54E-06	8.00E-03	0.91 (0.88, 0.95)	HHAT	202133
10	103923333	cg23516680		1427	-17.74	3.9	5.54E-06	8.00E-03	0.84 (0.78, 0.9)	NOLC1	11401
3	66404129	cg07410597		1428	-22.44	4.94	5.55E-06	8.00E-03	0.80 (0.73, 0.88)	SLC25A26	132962
3	119355809	cg05045380		1427	-10.77	2.37	5.58E-06	8.03E-03	0.90 (0.86, 0.94)	POPDC2	23627
12	7104184	cg19434937		1428	-11.95	2.63	5.61E-06	8.06E-03	0.89 (0.84, 0.93)	LPCAT3	21657
3	148711966	cg07447194		1423	-10.61	2.34	5.75E-06	8.24E-03	0.90 (0.86, 0.94)	GYG1	2772
21	36608456	cg17532497		1428	-19.59	4.32	5.83E-06	8.33E-03	0.82 (0.76, 0.89)	RUNX1	-186862
19	2594841	cg26569937		1421	-28.81	6.36	5.83E-06	8.33E-03	0.75 (0.66, 0.85)	MIR7850	-35871
13	100188895	cg17139328		1426	-24.95	5.51	5.87E-06	8.37E-03	0.78 (0.7, 0.87)	TM9SF2	35268
9	131648836	cg12450789		1427	-20.23	4.46	5.90E-06	8.40E-03	0.82 (0.75, 0.89)	LRRC8A	4056
6	36108112	cg03502211		1428	-18.08	3.99	5.91E-06	8.40E-03	0.83 (0.77, 0.9)	MAPK13	9852
13	46709790	cg09245115		1426	-10.14	2.24	5.93E-06	8.41E-03	0.90 (0.86, 0.94)	CPB2	-30580
14	24745117	cg16714237		1427	-13.34	2.94	5.94E-06	8.41E-03	0.88 (0.83, 0.93)	RABGGTA	-4285
12	122826219	cg04236871		1428	-16.9	3.73	5.96E-06	8.41E-03	0.84 (0.78, 0.91)	CLIP1-AS1	-53869
1	52130680	cg14378743	1	1428	-35.06	7.74	5.96E-06	8.41E-03	0.70 (0.61, 0.82)	OSBPL9	48135
6	143022065	cg25852061		1428	-5.3	1.17	6.00E-06	8.45E-03	0.95 (0.93, 0.97)	LOC153910	-63040
16	55542709	cg01998785		1428	-9.66	2.13	6.03E-06	8.48E-03	0.91 (0.87, 0.95)	LPCAT2	-203
20	35504403	cg09227119		1427	-12.89	2.85	6.05E-06	8.50E-03	0.88 (0.83, 0.93)	TLDC2	-120
17	66443040	cg02243624		1428	-27.67	6.13	6.29E-06	8.82E-03	0.76 (0.67, 0.86)	WIPI1	10624
12	68764080	cg16950658		1424	-8.17	1.81	6.30E-06	8.82E-03	0.92 (0.89, 0.95)	MDM1	-37920
13	52198723	cg14118054		1428	-23.45	5.19	6.36E-06	8.88E-03	0.79 (0.71, 0.88)	WDFY2	40240
19	2059698	cg19475270		1428	-11.8	2.61	6.38E-06	8.90E-03	0.89 (0.84, 0.94)	MKNK2	-8456
4	77906103	cg09040200		1428	-30.04	6.66	6.40E-06	8.91E-03	0.74 (0.65, 0.84)	SEPT11	35237
19	30432108	cg11392833		1428	-34.22	7.59	6.45E-06	8.96E-03	0.71 (0.61, 0.82)	URI1	-1037
1	167595191	cg24714082		1428	-10.85	2.4	6.47E-06	8.98E-03	0.90 (0.86, 0.94)	RCSD1	-4238

2	129236825	cg00785978	1427	-11.84	2.63	6.50E-06	9.00E-03	0.89 (0.84, 0.94)	HS6ST1	-160655
16	80653966	cg07428892	1427	-14.3	3.17	6.56E-06	9.07E-03	0.87 (0.81, 0.92)	LINC01227	-47262
15	40851643	cg19069027	1426	-10.24	2.27	6.57E-06	9.07E-03	0.90 (0.86, 0.94)	CCDC32	5612
10	93786975	cg12119581	1424	-50.41	11.19	6.63E-06	9.12E-03	0.60 (0.49, 0.75)	BTAF1	103240
6	138098613	cg18341600	1426	-9.45	2.1	6.63E-06	9.12E-03	0.91 (0.87, 0.95)	LINC02539	-38440
17	4743324	cg07307484	1428	-32.24	7.16	6.66E-06	9.15E-03	0.72 (0.63, 0.83)	MINK1	6690
21	19072007	cg14654849	1428	-45.28	10.06	6.73E-06	9.23E-03	0.64 (0.52, 0.77)	BTG3	-86740
7	102630100	cg17459348	1428	-21.72	4.83	6.80E-06	9.31E-03	0.80 (0.73, 0.88)	LRRC17	76757
17	70694204	cg10466699	1425	-64.6	14.36	6.87E-06	9.37E-03	0.52 (0.4, 0.69)	LINC00511	-57594
5	10560140	cg23856600	1428	-9.47	2.11	6.87E-06	9.37E-03	0.91 (0.87, 0.95)	ANKRD33B	-4294
19	35894520	cg16191278	1425	-13.45	2.99	6.93E-06	9.44E-03	0.87 (0.82, 0.93)	LINC01531	-1988
19	30456228	cg14140268	1426	-13.07	2.91	6.96E-06	9.46E-03	0.88 (0.83, 0.93)	URI1	23083
17	29837057	cg15209998	1425	-9.57	2.13	7.05E-06	9.57E-03	0.91 (0.87, 0.95)	RAB11FIP4	22039
21	43771120	cg18879389	1428	-23.36	5.21	7.27E-06	9.85E-03	0.79 (0.71, 0.88)	TFF2	87
2	179989225	cg11000869	1427	-36.76	8.2	7.34E-06	9.93E-03	0.69 (0.59, 0.81)	CCDC141	-74440
11	66118897	cg17751391	1428	-9.59	2.14	7.36E-06	9.94E-03	0.91 (0.87, 0.95)	LOC102724064	3436
13	52301946	cg07818422	1427	-51.28	11.44	7.42E-06	1.00E-02	0.60 (0.48, 0.75)	DHRS12	76351
18	77703051	cg06592918	1428	-9.14	2.04	7.43E-06	1.00E-02	0.91 (0.88, 0.95)	PQLC1	8601
7	100230770	cg13732043	1424	18.53	4.14	7.53E-06	1.01E-02	1.20 (1.11, 1.31)	TFR2	502
1	234791553	cg08553585	1427	-58.05	12.97	7.56E-06	1.01E-02	0.56 (0.43, 0.72)	LOC101927787	9519
20	42355376	cg16829505	1427	-27.34	6.11	7.61E-06	1.02E-02	0.76 (0.67, 0.86)	GTSF1L	265
11	10499641	cg17022365	1427	-18.8	4.2	7.71E-06	1.03E-02	0.83 (0.76, 0.9)	AMPD3	16964
11	65489884	cg08589455	1418	-18	4.02	7.76E-06	1.04E-02	0.84 (0.77, 0.9)	RNASEH2C	-1476
15	72646210	cg10387956	1428	-13.96	3.12	7.78E-06	1.04E-02	0.87 (0.82, 0.92)	HEXA-AS1	-22243
16	68049958	cg21092930	1427	-8.11	1.81	7.79E-06	1.04E-02	0.92 (0.89, 0.96)	DPEP2NB	-145
1	6645165	cg26819549	1425	-10.09	2.26	7.85E-06	1.04E-02	0.90 (0.86, 0.94)	ZBTB48	5115
12	56600222	cg17116500	1428	-23.24	5.2	7.88E-06	1.05E-02	0.79 (0.72, 0.88)	RNF41	15262
3	194862233	cg25926955	1427	-13.56	3.04	8.01E-06	1.06E-02	0.87 (0.82, 0.93)	XXYLT1-AS2	-6366
3	5193472	cg14415107	1427	-20.96	4.7	8.12E-06	1.07E-02	0.81 (0.74, 0.89)	ARL8B	29543
17	74298896	cg05042038	1428	-11.52	2.58	8.17E-06	1.08E-02	0.89 (0.85, 0.94)	QRICH2	4864
20	33416959	cg11988722	1428	-6.46	1.45	8.22E-06	1.08E-02	0.94 (0.91, 0.96)	NCOA6	-3508
12	121130587	cg02324015	1427	-35.56	7.98	8.25E-06	1.09E-02	0.70 (0.6, 0.82)	MLEC	4475
12	8975309	cg27653134	1428	-28.18	6.32	8.30E-06	1.09E-02	0.75 (0.67, 0.85)	A2ML1	242

11	840407	cg13806461	1427	-25.08	5.63	8.35E-06	1.10E-02	0.78 (0.7, 0.87)	POLR2L	2121
21	34124445	cg15301710	1424	-26.14	5.87	8.38E-06	1.10E-02	0.77 (0.69, 0.86)	PAXBP1	19723
17	506008	cg22252112	1428	-11.47	2.57	8.39E-06	1.10E-02	0.89 (0.85, 0.94)	VPS53	112087
7	117581709	cg00746666	1425	-16.6	3.73	8.48E-06	1.11E-02	0.85 (0.79, 0.91)	CTTNBP2	-68149
8	68022262	cg14783123	1427	-20.18	4.53	8.49E-06	1.11E-02	0.82 (0.75, 0.89)	CSPP1	26180
20	35504198	cg14613878	1425	-8.56	1.92	8.54E-06	1.11E-02	0.92 (0.88, 0.95)	TLDC2	-325
16	88558237	cg05958985	1427	-10.58	2.38	8.62E-06	1.12E-02	0.90 (0.86, 0.94)	MIR5189	22912
6	44193413	cg25738218	1411	-16.4	3.69	8.66E-06	1.12E-02	0.85 (0.79, 0.91)	SLC29A1	2051
3	71295684	cg06391412	1427	-16.85	3.79	8.67E-06	1.12E-02	0.84 (0.78, 0.91)	FOXP1	-1369
5	132114623	cg07828169	1428	-18.48	4.16	8.68E-06	1.12E-02	0.83 (0.77, 0.9)	SEPT8	-1063
9	138362321	cg13850063	1427	-17.66	3.97	8.80E-06	1.14E-02	0.84 (0.78, 0.91)	PPP1R26-AS1	1773
7	150646704	cg16107105	1427	-19.77	4.45	8.81E-06	1.14E-02	0.82 (0.75, 0.9)	KCNH2	6212
12	31453901	cg18805734	1428	-9.93	2.23	8.86E-06	1.14E-02	0.91 (0.87, 0.95)	FLJ13224	-23348
22	30612925	cg24447018	1428	-8.45	1.9	8.86E-06	1.14E-02	0.92 (0.89, 0.95)	LIF	29914
14	74532925	cg23472776	1427	-28.07	6.32	8.97E-06	1.15E-02	0.76 (0.67, 0.85)	ALDH6A1	18270
22	45820349	cg27131881	1428	-9.46	2.13	8.99E-06	1.15E-02	0.91 (0.87, 0.95)	RIBC2	10778
6	53057849	cg23054654	1428	-14.15	3.19	9.04E-06	1.16E-02	0.87 (0.82, 0.92)	GCM1	-44226
3	128134845	cg03278639	1428	-15.02	3.39	9.14E-06	1.17E-02	0.86 (0.81, 0.92)	DNAJB8-AS1	-47591
17	10747298	cg26985528	1428	-8.36	1.88	9.22E-06	1.18E-02	0.92 (0.89, 0.95)	PIRT	-5881
17	41400661	cg17378535	1427	-10.52	2.37	9.37E-06	1.19E-02	0.90 (0.86, 0.94)	LINC00854	-19600
1	173496518	cg21568193	1427	-18.95	4.28	9.38E-06	1.19E-02	0.83 (0.76, 0.9)	PRDX6	50033
1	61437380	cg09247486	1428	-21.59	4.87	9.42E-06	1.19E-02	0.81 (0.73, 0.89)	NFIA-AS2	-933
5	157159916	cg14254530	1427	-37.71	8.51	9.42E-06	1.19E-02	0.69 (0.58, 0.81)	THG1L	1096
11	70165886	cg15643933	1426	-16.76	3.78	9.42E-06	1.19E-02	0.85 (0.79, 0.91)	MIR548K	35826
3	49148220	cg26323242	1428	-9.57	2.16	9.45E-06	1.19E-02	0.91 (0.87, 0.95)	QARS	-5659
12	12887740	cg09444226	1427	-15.6	3.53	9.72E-06	1.23E-02	0.86 (0.8, 0.92)	APOLD1	8890
12	15126020	cg09447105	1428	-18.88	4.27	9.73E-06	1.23E-02	0.83 (0.76, 0.9)	PDE6H	65
12	64961489	cg20992317	1422	-8.56	1.94	9.85E-06	1.24E-02	0.92 (0.88, 0.95)	RASSF3	-42803
8	21670183	cg03475216	1428	-17.47	3.95	9.91E-06	1.24E-02	0.84 (0.78, 0.91)	GFRA2	-23838
9	113530240	cg14226212	1428	-12.2	2.76	1.00E-05	1.25E-02	0.89 (0.84, 0.93)	MUSK	99190
16	23563601	cg05261121	1426	-28.53	6.46	1.01E-05	1.26E-02	0.75 (0.66, 0.85)	EARS2	5094
12	117463293	cg12383160	1428	-22.61	5.12	1.01E-05	1.26E-02	0.80 (0.72, 0.88)	LOC100506551	-38152
4	148735567	cg12396412	1428	-36.23	8.21	1.01E-05	1.26E-02	0.70 (0.59, 0.82)	MIR4799	31822

4	1578163	cg05470179	1428	-16.11	3.65	1.02E-05	1.27E-02	0.85 (0.79, 0.91)	FAM53A	107554
7	150653449	cg08900098	1428	-9.53	2.16	1.04E-05	1.29E-02	0.91 (0.87, 0.95)	KCNH2	-533
9	130859191	cg07459967	1417	-23.11	5.25	1.06E-05	1.31E-02	0.79 (0.72, 0.88)	SLC25A25	-1569
11	118083942	cg14190451	1427	-8.86	2.01	1.06E-05	1.31E-02	0.92 (0.88, 0.95)	JAML	131
10	22743835	cg15737719	1426	-28.79	6.54	1.06E-05	1.31E-02	0.75 (0.66, 0.85)	LOC100499489	-16978
8	59564316	cg02212711	1423	-21.97	4.99	1.07E-05	1.32E-02	0.80 (0.73, 0.89)	NSMAF	7649
5	95124396	cg05596757	1426	-29.29	6.65	1.07E-05	1.32E-02	0.75 (0.65, 0.85)	GLRX	34180
3	66500703	cg05543520	1426	-14.05	3.19	1.08E-05	1.33E-02	0.87 (0.82, 0.92)	LRIG1	50141
9	140470011	cg20758387	1428	-8.68	1.97	1.08E-05	1.33E-02	0.92 (0.88, 0.95)	DPH7	3066
6	89693712	cg08820720	1428	-40.99	9.32	1.09E-05	1.34E-02	0.66 (0.55, 0.8)	RNGTT	-20365
14	21436271	cg18368116	1428	-19.17	4.36	1.09E-05	1.34E-02	0.83 (0.76, 0.9)	RNASE2	12642
12	6984857	cg12003079	1428	-10.74	2.45	1.12E-05	1.37E-02	0.90 (0.86, 0.94)	SPSB2	-2337
7	50626298	cg26365969	1427	-13.28	3.02	1.14E-05	1.39E-02	0.88 (0.83, 0.93)	DDC	2469
14	21508987	cg13072730	1427	-15.59	3.55	1.15E-05	1.40E-02	0.86 (0.8, 0.92)	RNASE7	-1397
17	34344758	cg08584457	1428	-16.59	3.78	1.16E-05	1.41E-02	0.85 (0.79, 0.91)	CCL23	246
3	141682388	cg19294517	1426	-9.6	2.19	1.16E-05	1.41E-02	0.91 (0.87, 0.95)	TFDP2	36840
17	179947	cg19456763	1428	-11.17	2.55	1.16E-05	1.41E-02	0.89 (0.85, 0.94)	LOC100506388	-1048
12	113723004	cg09908050	1426	-19.45	4.44	1.17E-05	1.42E-02	0.82 (0.75, 0.9)	MIR6762	-6323
20	17659317	cg00990977	1428	-31.26	7.14	1.18E-05	1.43E-02	0.73 (0.64, 0.84)	RRBP1	3610
12	113697418	cg16147002	1427	-10.25	2.34	1.18E-05	1.43E-02	0.90 (0.86, 0.94)	TPCN1	15353
2	231583339	cg05447875	1426	-12.94	2.95	1.20E-05	1.45E-02	0.88 (0.83, 0.93)	CAB39	5077
2	99124870	cg18455616	1428	-6.45	1.47	1.20E-05	1.45E-02	0.94 (0.91, 0.96)	INPP4A	63550
5	179333851	cg14362073	1427	-18.73	4.28	1.23E-05	1.48E-02	0.83 (0.76, 0.9)	TBC1D9B	1004
2	161798364	cg02494549	1427	-27.74	6.35	1.24E-05	1.49E-02	0.76 (0.67, 0.86)	TANK	-195101
6	34245341	cg22797971	1426	-8.69	1.99	1.24E-05	1.49E-02	0.92 (0.88, 0.95)	SMIM29	-28457
6	6971749	cg06394964	1425	-12.1	2.77	1.25E-05	1.50E-02	0.89 (0.84, 0.94)	RREB1	-136080
3	42923116	cg13531735	1428	-32.55	7.45	1.25E-05	1.50E-02	0.72 (0.62, 0.84)	CYP8B1	-5484
3	15066608	cg21419012	1421	-21.52	4.93	1.25E-05	1.50E-02	0.81 (0.73, 0.89)	MRPS25	40235
9	138701748	cg13423371	1424	-15.2	3.48	1.26E-05	1.51E-02	0.86 (0.8, 0.92)	CAMSAP1	97256
1	146503900	cg13951007	1427	-14.9	3.41	1.27E-05	1.51E-02	0.86 (0.81, 0.92)	LOC728989	10698
17	78662780	cg22994495	1428	-17.34	3.97	1.27E-05	1.51E-02	0.84 (0.78, 0.91)	LOC101928855	116651
9	5436224	cg14025883	1423	-15.24	3.49	1.28E-05	1.52E-02	0.86 (0.8, 0.92)	PLGRKT	1712
1	11786594	cg07453055	1424	-13.26	3.04	1.29E-05	1.53E-02	0.88 (0.83, 0.93)	AGTRAP	-9547

15	75054510	cg20385913		1425	-16.16	3.71	1.30E-05	1.54E-02	0.85 (0.79, 0.91)	CYP1A2	13327
16	69567173	cg03501393		1427	-6.57	1.51	1.31E-05	1.55E-02	0.94 (0.91, 0.96)	MIR1538	32597
7	36067955	cg15873326		1405	-20.26	4.65	1.32E-05	1.56E-02	0.82 (0.75, 0.89)	LOC101928618	-66964
2	131126377	cg17334945		1428	-13.84	3.18	1.33E-05	1.57E-02	0.87 (0.82, 0.93)	PTPN18	12798
13	27837816	cg08302053		1428	-10.13	2.33	1.34E-05	1.58E-02	0.90 (0.86, 0.95)	RASL11A	-6647
3	33837694	cg00381391		1428	-18.51	4.25	1.35E-05	1.59E-02	0.83 (0.76, 0.9)	PDCD6IP	-2368
19	39303993	cg04420917		1428	-13.42	3.09	1.37E-05	1.61E-02	0.87 (0.82, 0.93)	LGALS4	-254
22	32860440	cg11495812		1427	-16.08	3.7	1.37E-05	1.61E-02	0.85 (0.79, 0.92)	BPIFC	-7068
11	65545808	cg24009118		1427	-20.28	4.67	1.40E-05	1.64E-02	0.82 (0.75, 0.89)	AP5B1	2253
16	11729131	cg08776942		1421	-11.65	2.68	1.41E-05	1.65E-02	0.89 (0.84, 0.94)	SNN	-33157
10	932509	cg14644626		1428	-17.92	4.13	1.42E-05	1.66E-02	0.84 (0.77, 0.91)	LARP4B	45135
22	30342424	cg16899419		1428	-8.99	2.07	1.43E-05	1.67E-02	0.91 (0.88, 0.95)	MIR6818	-60613
18	19334381	cg00924612		1426	-35.71	8.24	1.46E-05	1.70E-02	0.70 (0.6, 0.82)	MIB1	13092
5	172271228	cg08886771		1425	-18.62	4.3	1.46E-05	1.70E-02	0.83 (0.76, 0.9)	ERGIC1	10006
13	22105010	cg18010432	1	1428	-35.06	8.09	1.47E-05	1.71E-02	0.70 (0.6, 0.83)	ZDHHC20	-71502
6	158994407	cg26774971		1423	-7.63	1.76	1.47E-05	1.71E-02	0.93 (0.9, 0.96)	MIR7161	-36331
10	31987694	cg17384357		1427	-18.15	4.19	1.49E-05	1.72E-02	0.83 (0.77, 0.91)	ARHGAP12	210159
12	120970625	cg23434083		1428	-18.7	4.32	1.49E-05	1.72E-02	0.83 (0.76, 0.9)	RNF10	-1506
5	179200573	cg10113951		1427	-29.52	6.82	1.50E-05	1.73E-02	0.74 (0.65, 0.85)	LTC4S	-20412
22	37280288	cg21306887		1427	-41.84	9.67	1.51E-05	1.74E-02	0.66 (0.54, 0.8)	NCF4	23259
6	42363749	cg20840540		1427	-13.82	3.19	1.52E-05	1.75E-02	0.87 (0.82, 0.93)	TRERF1	56039
17	56269818	cg02970679		1427	-19.97	4.62	1.53E-05	1.76E-02	0.82 (0.75, 0.9)	EPX	-266
10	86097061	cg15732078		1428	-13.45	3.11	1.53E-05	1.76E-02	0.87 (0.82, 0.93)	CCSER2	8717
4	95183565	cg18456722		1425	-48.9	11.31	1.54E-05	1.77E-02	0.61 (0.49, 0.77)	SMARCAD1	9121
21	30722759	cg23557612		1425	-25.72	5.95	1.54E-05	1.77E-02	0.77 (0.69, 0.87)	BACH1-IT2	-22061
9	140273055	cg11619782		1427	-23.3	5.39	1.56E-05	1.78E-02	0.79 (0.71, 0.88)	EXD3	44658
22	32150934	cg16160637		1426	-4.25	0.98	1.56E-05	1.78E-02	0.96 (0.94, 0.98)	DEPDC5	87
2	120937418	cg23196129		1428	-11.35	2.63	1.58E-05	1.80E-02	0.89 (0.85, 0.94)	TMEM185B	43565
7	137501840	cg26703587		1428	-13.12	3.04	1.58E-05	1.80E-02	0.88 (0.83, 0.93)	DGKI	29237
3	39243826	cg07465458		1426	-9.52	2.21	1.59E-05	1.81E-02	0.91 (0.87, 0.95)	XIRP1	-9740
2	113465627	cg13205244		1427	-10.57	2.45	1.59E-05	1.81E-02	0.90 (0.86, 0.94)	CKAP2L	56626
19	19599547	cg20493175		1427	-9.68	2.24	1.61E-05	1.83E-02	0.91 (0.87, 0.95)	GATAD2A	23399
3	4355431	cg07733260		1428	-55.98	12.98	1.62E-05	1.84E-02	0.57 (0.44, 0.74)	SETMAR	10444

17	73331630	cg03653158		1428	-13.87	3.22	1.64E-05	1.85E-02	0.87 (0.82, 0.93)	SLC25A19	-46101
22	35652215	cg05358754		1428	-26.23	6.09	1.64E-05	1.85E-02	0.77 (0.68, 0.87)	HMGXB4	-1229
1	6377509	cg07906050		1428	-16.74	3.89	1.64E-05	1.85E-02	0.85 (0.78, 0.91)	ACOT7	41494
11	68816453	cg27481141		1412	-207.2	48.11	1.66E-05	1.87E-02	0.13 (0.05, 0.32)	TPCN2	104
12	7862691	cg15075897		1427	-29.33	6.82	1.68E-05	1.89E-02	0.75 (0.65, 0.85)	DPPA3	-1358
12	56404209	cg06612119		1427	-6	1.4	1.69E-05	1.90E-02	0.94 (0.92, 0.97)	IKZF4	-10479
14	23466659	cg23993677		1427	-13.19	3.07	1.69E-05	1.90E-02	0.88 (0.83, 0.93)	C14orf93	3586
3	42948626	cg15146567		1428	-8.72	2.03	1.71E-05	1.92E-02	0.92 (0.88, 0.95)	ZNF662	969
14	39643445	cg02543556		1428	-19.55	4.55	1.72E-05	1.92E-02	0.82 (0.75, 0.9)	PNN	-941
1	24143366	cg26389822		1428	-17.95	4.18	1.72E-05	1.92E-02	0.84 (0.77, 0.91)	HMGCL	8582
18	71910225	cg02951831		1428	-6.08	1.41	1.73E-05	1.93E-02	0.94 (0.92, 0.97)	CYB5A	49025
6	148830438	cg09980470		1428	-10.01	2.33	1.73E-05	1.93E-02	0.90 (0.86, 0.95)	SASH1	152
10	12448959	cg18715410		1427	-16.82	3.91	1.73E-05	1.93E-02	0.85 (0.78, 0.91)	CAMK1D	57418
14	76337892	cg24829718		1427	-21.98	5.12	1.74E-05	1.93E-02	0.80 (0.73, 0.89)	TGFB3	110472
17	56274597	cg03519593		1426	-14.24	3.32	1.75E-05	1.94E-02	0.87 (0.81, 0.93)	EPX	4513
3	127543047	cg04721651		1425	-10.31	2.4	1.75E-05	1.94E-02	0.90 (0.86, 0.95)	MGLL	-955
5	176327783	cg19791262		1428	-7.93	1.85	1.77E-05	1.96E-02	0.92 (0.89, 0.96)	HK3	-1451
11	6552435	cg01482779		1424	-7.92	1.85	1.78E-05	1.97E-02	0.92 (0.89, 0.96)	DNHD1	33910
5	176774729	cg15344640		1428	-24.55	5.72	1.78E-05	1.97E-02	0.78 (0.7, 0.88)	LMAN2	4155
2	86789025	cg10354401		1428	-32.46	7.57	1.79E-05	1.97E-02	0.72 (0.62, 0.84)	CHMP3	1594
13	100761701	cg05306459		1428	-15.51	3.62	1.80E-05	1.98E-02	0.86 (0.8, 0.92)	PCCA	20433
3	53513310	cg17941143		1425	-6.75	1.57	1.81E-05	1.99E-02	0.93 (0.91, 0.96)	CACNA1D	-15765
2	217120445	cg00427854		1428	-27.56	6.43	1.82E-05	2.00E-02	0.76 (0.67, 0.86)	LINC01963	38834
11	3170821	cg02332678		1428	-9.53	2.23	1.84E-05	2.02E-02	0.91 (0.87, 0.95)	OSBPL5	15760
4	912549	cg23855365	1	1427	-5.77	1.35	1.85E-05	2.02E-02	0.94 (0.92, 0.97)	TMEM175	-13625
5	134818031	cg27308490		1426	-10.85	2.53	1.85E-05	2.02E-02	0.90 (0.85, 0.94)	TIFAB	-29943
17	59296188	cg00359030		1427	-52.76	12.33	1.86E-05	2.03E-02	0.59 (0.46, 0.75)	LOC101927855	148876
10	18550623	cg21505451		1427	-10.86	2.54	1.87E-05	2.04E-02	0.90 (0.85, 0.94)	CACNB2	1040
11	111570978	cg24368962		1426	-23.17	5.41	1.87E-05	2.04E-02	0.79 (0.71, 0.88)	PPP2R1B	66190
3	52220370	cg17074037		1427	-10.61	2.48	1.88E-05	2.05E-02	0.90 (0.86, 0.94)	ALAS1	-11728
15	92078200	cg14622604		1428	-15.66	3.66	1.89E-05	2.05E-02	0.86 (0.8, 0.92)	CRAT37	71632
15	92005188	cg05110389		1428	-11.82	2.77	1.93E-05	2.09E-02	0.89 (0.84, 0.94)	CRAT37	-1380
10	5576480	cg03651219		1427	-21.28	4.98	1.94E-05	2.10E-02	0.81 (0.73, 0.89)	CALML3-AS1	-8272

11	63997324	cg21234134	1425	-9.89	2.32	1.94E-05	2.10E-02	0.91 (0.87, 0.95)	DNAJC4	-428
17	76565091	cg15284593	1427	-14.75	3.45	1.95E-05	2.11E-02	0.86 (0.81, 0.92)	DNAH17	8384
9	123969395	cg00381516	1424	-35.69	8.36	1.96E-05	2.11E-02	0.70 (0.59, 0.82)	RAB14	-5031
8	19341295	cg08922108	1427	-10.97	2.57	1.96E-05	2.11E-02	0.90 (0.85, 0.94)	CSGALNACT1	118760
22	37173159	cg09247945	1427	-30.83	7.22	1.96E-05	2.11E-02	0.73 (0.64, 0.85)	IFT27	-983
3	197239695	cg18161208	1427	-12.92	3.03	1.97E-05	2.12E-02	0.88 (0.83, 0.93)	BDH1	43162
9	126319516	cg08649376	1427	-12.1	2.83	1.98E-05	2.13E-02	0.89 (0.84, 0.94)	MIR7150	-71616
3	128442438	cg06019933	1428	-13.62	3.19	2.00E-05	2.14E-02	0.87 (0.82, 0.93)	RAB7A	-2540
17	56288205	cg08222787	1428	-24.5	5.75	2.02E-05	2.16E-02	0.78 (0.7, 0.88)	MKS1	8460
17	58717993	cg14697045	1427	-11.9	2.79	2.02E-05	2.16E-02	0.89 (0.84, 0.94)	BCAS3	-37142
12	132464955	cg00764582	1424	-14.27	3.35	2.03E-05	2.16E-02	0.87 (0.81, 0.93)	EP400	30491
14	55604454	cg01051098	1427	-43.51	10.21	2.03E-05	2.16E-02	0.65 (0.53, 0.79)	LGALS3	754
8	129023431	cg25401182	1425	-6.48	1.52	2.03E-05	2.16E-02	0.94 (0.91, 0.97)	MIR1206	2288
15	65904714	cg15988632	1425	-28.4	6.67	2.04E-05	2.17E-02	0.75 (0.66, 0.86)	SLC24A1	972
12	131310417	cg21575634	1425	-21.04	4.94	2.05E-05	2.18E-02	0.81 (0.74, 0.89)	STX2	13401
5	81159782	cg25518040	1427	-31.4	7.37	2.05E-05	2.18E-02	0.73 (0.63, 0.84)	ATG10	-108061
11	73714778	cg15903936	1428	-38.91	9.14	2.06E-05	2.18E-02	0.68 (0.57, 0.81)	UCP3	5503
10	98425110	cg16508714	1428	-8.86	2.08	2.08E-05	2.20E-02	0.92 (0.88, 0.95)	PIK3AP1	55168
22	36837152	cg24278615	1425	-9.95	2.34	2.08E-05	2.20E-02	0.91 (0.86, 0.95)	TXN2	40534
17	9838988	cg04202435	1428	-14.85	3.49	2.09E-05	2.20E-02	0.86 (0.81, 0.92)	GAS7	23777
11	134128612	cg18278420	1421	-30.36	7.14	2.09E-05	2.20E-02	0.74 (0.64, 0.85)	ACAD8	5179
6	24877462	cg12213680	1418	-12.14	2.85	2.10E-05	2.21E-02	0.89 (0.84, 0.94)	RIPOR2	130
19	40227949	cg18254848	1428	-20.45	4.81	2.11E-05	2.22E-02	0.82 (0.74, 0.9)	CLC	719
1	179016233	cg24108508	1428	-10.4	2.44	2.11E-05	2.22E-02	0.90 (0.86, 0.95)	FAM20B	20975
3	16889869	cg08288503	1428	-10.17	2.39	2.12E-05	2.22E-02	0.90 (0.86, 0.95)	PLCL2	-36582
2	9752386	cg02473287	1428	-14.51	3.41	2.15E-05	2.25E-02	0.86 (0.81, 0.92)	YWHAQ	18797
16	3246099	cg04931493	1428	-3.55	0.84	2.16E-05	2.26E-02	0.97 (0.95, 0.98)	OR1F1	-8147
16	85654157	cg07098502	1428	-29.53	6.95	2.17E-05	2.26E-02	0.74 (0.65, 0.85)	GSE1	7316
1	203255003	cg14991022	1427	-24.03	5.66	2.17E-05	2.26E-02	0.79 (0.7, 0.88)	LINC01353	-1276
10	11291279	cg05219423	1427	-13.24	3.12	2.21E-05	2.30E-02	0.88 (0.82, 0.93)	CELF2	84287
11	34827586	cg20387860	1427	-29.68	7	2.21E-05	2.30E-02	0.74 (0.65, 0.85)	PDHX	-110090
10	81004884	cg07056602	1427	5.06	1.19	2.22E-05	2.31E-02	1.05 (1.03, 1.08)	PPIF	-102335
21	36689434	cg18099556	1428	-19.93	4.7	2.22E-05	2.31E-02	0.82 (0.75, 0.9)	LOC100506403	263627

3	69812798	cg06070625		1428	-17.89	4.22	2.23E-05	2.31E-02	0.84 (0.77, 0.91)	MITF	92
2	74375903	cg26529864		1408	-31.18	7.35	2.23E-05	2.31E-02	0.73 (0.63, 0.85)	BOLA3-AS1	796
16	3843133	cg13135255		1428	-8.98	2.12	2.26E-05	2.34E-02	0.91 (0.88, 0.95)	TRAP1	-75536
1	2036283	cg16599817		1428	-9.76	2.3	2.27E-05	2.34E-02	0.91 (0.87, 0.95)	PRKCZ	129
7	4727742	cg19396390		1427	-18.62	4.39	2.27E-05	2.34E-02	0.83 (0.76, 0.9)	FOXK1	5813
14	73061991	cg10933988		1428	-23.26	5.49	2.29E-05	2.36E-02	0.79 (0.71, 0.88)	MIR7843	78464
10	45494806	cg06958964		1428	-33.04	7.81	2.31E-05	2.38E-02	0.72 (0.62, 0.84)	ZNF22	-1466
16	66597367	cg14248318		1428	-17.07	4.03	2.32E-05	2.38E-02	0.84 (0.78, 0.91)	CMTM1	-2926
18	59733858	cg14263230		1424	-20.38	4.82	2.34E-05	2.40E-02	0.82 (0.74, 0.9)	PIGN	120430
2	11926291	cg19993461		1428	-41.98	9.92	2.34E-05	2.40E-02	0.66 (0.54, 0.8)	MIR548S	18722
21	43928228	cg23003220		1425	-9.49	2.25	2.35E-05	2.41E-02	0.91 (0.87, 0.95)	SLC37A1	-5734
1	3807168	cg16349667		1424	-5.73	1.36	2.36E-05	2.41E-02	0.94 (0.92, 0.97)	C1orf174	9688
14	73614098	cg05981968		1427	-20.67	4.89	2.40E-05	2.45E-02	0.81 (0.74, 0.9)	PSEN1	10956
3	14420209	cg17338225		1428	-13.64	3.23	2.41E-05	2.46E-02	0.87 (0.82, 0.93)	SLC6A6	-23866
1	180940271	cg02683853		1428	-23.3	5.52	2.42E-05	2.46E-02	0.79 (0.71, 0.88)	STX6	51985
2	192043611	cg02856510		1428	-16.12	3.82	2.42E-05	2.46E-02	0.85 (0.79, 0.92)	STAT4	-27290
2	99122909	cg02420943		1427	-7.62	1.8	2.43E-05	2.47E-02	0.93 (0.89, 0.96)	INPP4A	61589
14	50780168	cg15998596		1424	-14.44	3.42	2.43E-05	2.47E-02	0.87 (0.81, 0.93)	ATP5S	1122
11	43403482	cg16450797		1427	-7.31	1.73	2.44E-05	2.47E-02	0.93 (0.9, 0.96)	TTC17	23048
12	89637744	cg27143027		1428	-7.29	1.73	2.44E-05	2.47E-02	0.93 (0.9, 0.96)	DUSP6	108891
2	48340131	cg21672758		1425	-30.29	7.18	2.46E-05	2.49E-02	0.74 (0.64, 0.85)	FOXN2	-201663
17	80200741	cg02765363		1428	-9.06	2.15	2.50E-05	2.52E-02	0.91 (0.88, 0.95)	MIR6787	6198
4	908952	cg14140403	1	1377	7.84	1.86	2.50E-05	2.52E-02	1.08 (1.04, 1.12)	TMEM175	-17222
11	122901047	cg11514604		1427	-40.49	9.61	2.51E-05	2.53E-02	0.67 (0.55, 0.81)	LOC341056	12774
14	60662291	cg24062598		1427	-47.51	11.27	2.51E-05	2.53E-02	0.62 (0.5, 0.78)	DHRS7	-25710
18	61550142	cg04765589		1427	-28.28	6.71	2.53E-05	2.54E-02	0.75 (0.66, 0.86)	SERPINB2	-4796
1	151818600	cg01200145		1428	-6.16	1.46	2.55E-05	2.56E-02	0.94 (0.91, 0.97)	C2CD4D	-5568
12	6332058	cg08559734		1428	-26.57	6.31	2.55E-05	2.56E-02	0.77 (0.68, 0.87)	CD9	22577
10	120495050	cg23414568		1428	-12.42	2.95	2.59E-05	2.59E-02	0.88 (0.83, 0.94)	CACUL1	19707
12	123446272	cg03131767		1428	-16.29	3.87	2.61E-05	2.61E-02	0.85 (0.79, 0.92)	ABCB9	4783
10	116447282	cg23464586		1427	-16.93	4.03	2.62E-05	2.61E-02	0.84 (0.78, 0.91)	ABLIM1	-2869
10	12371568	cg24317972		1424	-24.64	5.86	2.62E-05	2.61E-02	0.78 (0.7, 0.88)	CAMK1D	-19973
3	188001192	cg19198938		1428	-15.95	3.8	2.66E-05	2.65E-02	0.85 (0.79, 0.92)	LPP	58000

3	39217727	cg04404773	1428	-9.44	2.25	2.67E-05	2.65E-02	0.91 (0.87, 0.95)	XIRP1	16349
2	48806774	cg27016609	1428	-6.74	1.61	2.67E-05	2.65E-02	0.93 (0.91, 0.96)	STON1-GTF2A1L	-951
2	99193996	cg15929700	1427	-18.08	4.3	2.68E-05	2.66E-02	0.83 (0.77, 0.91)	COA5	30984
14	77425779	cg16270995	1425	-8.19	1.95	2.69E-05	2.67E-02	0.92 (0.89, 0.96)	LINC01629	-201
10	134373103	cg08014024	1428	-13.51	3.22	2.71E-05	2.68E-02	0.87 (0.82, 0.93)	INPP5A	21821
6	167135251	cg03512256	1428	-30.19	7.2	2.73E-05	2.70E-02	0.74 (0.64, 0.85)	RPS6KA2	-94487
19	32864762	cg08256839	1425	-10.68	2.55	2.73E-05	2.70E-02	0.90 (0.85, 0.94)	ZNF507	28249
10	114437411	cg00329570	1428	-25.87	6.17	2.75E-05	2.71E-02	0.77 (0.68, 0.87)	MIR4295	43483
1	223899685	cg08439122	1428	-6.88	1.64	2.76E-05	2.72E-02	0.93 (0.9, 0.96)	CAPN2	-433
11	59525449	cg17030380	1426	-27.21	6.49	2.76E-05	2.72E-02	0.76 (0.67, 0.87)	STX3	2918
20	57585940	cg15402265	1428	-8.97	2.14	2.77E-05	2.72E-02	0.91 (0.88, 0.95)	CTSZ	-3632
6	73623666	cg22418084	1428	-5.33	1.27	2.79E-05	2.74E-02	0.95 (0.92, 0.97)	MIR4282	53809
3	45914188	cg10650214	1428	-11.68	2.79	2.82E-05	2.77E-02	0.89 (0.84, 0.94)	CCR9	-13807
7	1577697	cg23871276	1428	-10.75	2.57	2.84E-05	2.78E-02	0.90 (0.85, 0.94)	MAFK	7330
13	43355514	cg24818699	1428	-18.32	4.38	2.84E-05	2.78E-02	0.83 (0.76, 0.91)	FAM216B	-171
2	7027871	cg02589986	1428	-8.31	1.99	2.85E-05	2.78E-02	0.92 (0.89, 0.96)	RSAD2	10076
1	211647456	cg06418837	1428	-13.56	3.24	2.85E-05	2.78E-02	0.87 (0.82, 0.93)	RD3	18802
2	106475496	cg17558817	1427	-9.5	2.27	2.86E-05	2.79E-02	0.91 (0.87, 0.95)	NCK2	7293
20	3989981	cg01908419	1428	-9.9	2.37	2.90E-05	2.82E-02	0.91 (0.86, 0.95)	RNF24	6256
19	41129881	cg24872571	1428	-18.27	4.37	2.91E-05	2.83E-02	0.83 (0.76, 0.91)	LTBP4	22605
4	3240754	cg01542143	1426	-14.06	3.37	2.94E-05	2.85E-02	0.87 (0.81, 0.93)	MSANTD1	-5341
5	153836180	cg17558547	1427	-18.33	4.39	2.94E-05	2.85E-02	0.83 (0.76, 0.91)	SAP30L	10664
2	85944732	cg13353793	1428	-20.48	4.9	2.95E-05	2.85E-02	0.81 (0.74, 0.9)	GNLY	23319
1	6341901	cg14879885	1428	-15.34	3.67	2.95E-05	2.85E-02	0.86 (0.8, 0.92)	GPR153	-20867
19	12998426	cg26136776	1428	-13.58	3.25	2.95E-05	2.85E-02	0.87 (0.82, 0.93)	KLF1	-410
11	47092992	cg01258949	1424	-28.15	6.74	2.96E-05	2.86E-02	0.75 (0.66, 0.86)	ARFGAP2	105683
11	123616411	cg06633463	1428	-24.2	5.79	2.97E-05	2.87E-02	0.79 (0.7, 0.88)	ZNF202	-4021
15	31505024	cg08884974	1427	-14.51	3.48	2.98E-05	2.87E-02	0.86 (0.81, 0.93)	LINC02352	-3199
16	15698882	cg02374401	1428	-15.41	3.69	2.99E-05	2.88E-02	0.86 (0.8, 0.92)	MIR6506	6069
1	179843111	cg10100117	1428	-11.88	2.85	3.00E-05	2.88E-02	0.89 (0.84, 0.94)	TOR1AIP2	3829
9	35537849	cg12629001	1427	-21.21	5.08	3.00E-05	2.88E-02	0.81 (0.73, 0.89)	RUSC2	-779
17	25805881	cg17651926	1428	-23.6	5.66	3.02E-05	2.90E-02	0.79 (0.71, 0.88)	KSR1	6846
11	85884166	cg12667152	1426	-7.58	1.82	3.03E-05	2.90E-02	0.93 (0.89, 0.96)	EED	-71259

10	5487127	cg01808470	1428	-36.13	8.66	3.04E-05	2.91E-02	0.70 (0.59, 0.83)	NET1	-1386
11	72925008	cg05999592	1424	-6.91	1.66	3.09E-05	2.95E-02	0.93 (0.9, 0.96)	P2RY2	-4334
1	44716058	cg16710124	1428	-24.55	5.89	3.10E-05	2.96E-02	0.78 (0.7, 0.88)	SNORA110	2172
3	183631176	cg01291780	1427	-25.04	6.01	3.13E-05	2.98E-02	0.78 (0.69, 0.88)	PARL	-28481
22	24550935	cg20182202	1428	-8.92	2.14	3.13E-05	2.98E-02	0.91 (0.88, 0.95)	SUSD2	-26508
14	62235205	cg24076840	1428	-17.75	4.26	3.14E-05	2.99E-02	0.84 (0.77, 0.91)	SNAPC1	6131
3	195974258	cg07641926	1426	-6.82	1.64	3.19E-05	3.03E-02	0.93 (0.9, 0.96)	SLC51A	30876
1	1690811	cg11296110	1423	-9.19	2.21	3.19E-05	3.03E-02	0.91 (0.87, 0.95)	NADK	-731
19	16553751	cg05194248	1427	-7.25	1.74	3.20E-05	3.03E-02	0.93 (0.9, 0.96)	EPS15L1	29071
11	10543456	cg07565042	1427	-8.93	2.15	3.21E-05	3.03E-02	0.91 (0.88, 0.95)	MTRNR2L8	-12734
8	142305640	cg20216313	1426	-3.77	0.91	3.21E-05	3.03E-02	0.96 (0.95, 0.98)	SLC45A4	-40913
11	368638	cg26461944	1408	-8.47	2.04	3.21E-05	3.03E-02	0.92 (0.88, 0.96)	B4GALNT4	-1156
7	150649807	cg24491618	1427	-12.91	3.11	3.23E-05	3.05E-02	0.88 (0.83, 0.93)	KCNH2	3109
11	12747546	cg14179258	1427	-3.49	0.84	3.27E-05	3.08E-02	0.97 (0.95, 0.98)	TEAD1	51578
2	121949349	cg06516790	1427	-13.79	3.32	3.29E-05	3.10E-02	0.87 (0.82, 0.93)	TFCP2L1	93428
15	38881520	cg06290138	1425	-20.37	4.91	3.30E-05	3.10E-02	0.82 (0.74, 0.9)	RASGRP1	-24514
1	115594714	cg09863265	1427	-7.1	1.71	3.31E-05	3.11E-02	0.93 (0.9, 0.96)	TSHB	18148
11	57163587	cg14999724	1427	-10.02	2.41	3.31E-05	3.11E-02	0.90 (0.86, 0.95)	PRG2	-5458
9	115184285	cg02874537	1428	-5.67	1.37	3.33E-05	3.12E-02	0.94 (0.92, 0.97)	HSDL2	42097
5	179131225	cg26245101	1428	-25.62	6.17	3.33E-05	3.12E-02	0.77 (0.69, 0.87)	CANX	5296
7	45038259	cg14131691	1428	-10.32	2.49	3.35E-05	3.13E-02	0.90 (0.86, 0.95)	CCM2	-1085
14	51446038	cg14354244	1428	-12.14	2.93	3.37E-05	3.15E-02	0.89 (0.84, 0.94)	PYGL	-34791
10	129172535	cg11791710	1427	-14.83	3.58	3.38E-05	3.15E-02	0.86 (0.8, 0.92)	NPS	-175077
20	48806066	cg02930951	1428	-14.97	3.61	3.40E-05	3.16E-02	0.86 (0.8, 0.92)	CEBPB	-1053
10	97624495	cg04587103	1428	-10.37	2.5	3.40E-05	3.16E-02	0.90 (0.86, 0.95)	CC2D2B	-43226
7	1913918	cg06864151	1428	-22.16	5.35	3.42E-05	3.18E-02	0.80 (0.72, 0.89)	MIR4655	-30030
1	212312063	cg25159046	1428	-11.81	2.85	3.43E-05	3.18E-02	0.89 (0.84, 0.94)	MIR3122	61109
1	17448350	cg12561552	1427	-12.31	2.97	3.44E-05	3.18E-02	0.88 (0.83, 0.94)	PADI2	-2403
10	1108248	cg15331937	1428	-8.49	2.05	3.44E-05	3.18E-02	0.92 (0.88, 0.96)	WDR37	5473
10	129860424	cg16330225	1428	-20.43	4.93	3.44E-05	3.18E-02	0.82 (0.74, 0.9)	AS-PTPRE	264
17	79824551	cg25475273	1425	-9.86	2.38	3.45E-05	3.19E-02	0.91 (0.86, 0.95)	ARHGDIA	4298
17	80188275	cg03722757	1427	-6.75	1.63	3.46E-05	3.20E-02	0.93 (0.91, 0.97)	SLC16A3	1389
20	34479717	cg19960458	1427	-15.73	3.8	3.47E-05	3.20E-02	0.85 (0.79, 0.92)	SCAND1	62830

15	101719523	cg24254196	1428	-10.35	2.5	3.47E-05	3.20E-02	0.90 (0.86, 0.95)	CHSY1	72613
1	201520863	cg24014587	1428	-11.06	2.67	3.48E-05	3.20E-02	0.90 (0.85, 0.94)	RPS10P7	31832
16	75625311	cg23975326	1426	-18.97	4.58	3.50E-05	3.22E-02	0.83 (0.76, 0.9)	GABARAPL2	25063
7	107876312	cg24358891	1421	-16.15	3.9	3.51E-05	3.22E-02	0.85 (0.79, 0.92)	NRCAM	4301
2	2712909	cg27014783	1428	-12.64	3.06	3.51E-05	3.22E-02	0.88 (0.83, 0.94)	MYT1L	-377825
16	30409908	cg01304182	1427	-7.03	1.7	3.52E-05	3.22E-02	0.93 (0.9, 0.96)	ZNF48	3169
6	140053824	cg04170495	1427	-8.09	1.96	3.53E-05	3.22E-02	0.92 (0.89, 0.96)	FILNC1	-38385
17	40288533	cg09778927	1428	-8	1.93	3.53E-05	3.22E-02	0.92 (0.89, 0.96)	HSPB9	13778
10	12456489	cg20072505	1428	-15.44	3.73	3.53E-05	3.22E-02	0.86 (0.8, 0.92)	CAMK1D	64948
7	128868265	cg14755690	1427	-17.99	4.35	3.54E-05	3.23E-02	0.84 (0.77, 0.91)	AHCYL2	3411
8	126591840	cg05879394	1427	-8.96	2.17	3.55E-05	3.23E-02	0.91 (0.88, 0.95)	TRIB1	147390
3	171865257	cg06304167	1428	-19.38	4.69	3.55E-05	3.23E-02	0.82 (0.75, 0.9)	FNDC3B	106914
17	56270828	cg17374802	1428	-12.06	2.92	3.55E-05	3.23E-02	0.89 (0.84, 0.94)	EPX	744
20	62700725	cg00390694	1428	-14.72	3.56	3.56E-05	3.23E-02	0.86 (0.8, 0.93)	TCEA2	6716
2	69831408	cg22059413	1427	-14.71	3.56	3.57E-05	3.24E-02	0.86 (0.81, 0.93)	ANXA4	-39528
4	2368055	cg03035271	1424	-4.01	0.97	3.58E-05	3.24E-02	0.96 (0.94, 0.98)	ZFYVE28	-1452
11	72136395	cg19791780	1422	-15.58	3.77	3.58E-05	3.24E-02	0.86 (0.79, 0.92)	CLPB	9332
16	69901132	cg18693924	1427	-12.34	2.99	3.59E-05	3.25E-02	0.88 (0.83, 0.94)	WWP2	28493
15	39823154	cg01284182	1426	-11.12	2.69	3.60E-05	3.25E-02	0.89 (0.85, 0.94)	THBS1	-50125
8	25847266	cg26804299	1427	-3.82	0.92	3.60E-05	3.25E-02	0.96 (0.95, 0.98)	EBF2	55373
1	222086992	cg05934594	1428	-11.1	2.69	3.61E-05	3.25E-02	0.89 (0.85, 0.94)	LINC01655	-72985
7	139948872	cg01116541	1428	-6.65	1.61	3.64E-05	3.28E-02	0.94 (0.91, 0.97)	KDM7A-DT	71812
16	85593560	cg06475513	1428	-17.1	4.14	3.66E-05	3.29E-02	0.84 (0.78, 0.91)	GSE1	-51468
2	74265933	cg08334830	1428	-17.88	4.33	3.66E-05	3.29E-02	0.84 (0.77, 0.91)	TET3	52403
17	7648108	cg01330991	1427	-19.62	4.75	3.67E-05	3.29E-02	0.82 (0.75, 0.9)	RPL29P2	-9529
2	8466005	cg26955963	1428	-7.71	1.87	3.68E-05	3.29E-02	0.93 (0.89, 0.96)	LINC00299	2543
1	224444519	cg13360526	1425	-14.7	3.56	3.69E-05	3.29E-02	0.86 (0.81, 0.93)	MIR320B2	323
9	124042257	cg18655410	1427	-9.29	2.25	3.69E-05	3.29E-02	0.91 (0.87, 0.95)	GSN-AS1	5550
1	24172120	cg20317437	1427	-14.17	3.43	3.69E-05	3.29E-02	0.87 (0.81, 0.93)	HMGCL	-20172
6	36311062	cg21576315	1428	-9.77	2.37	3.69E-05	3.29E-02	0.91 (0.87, 0.95)	C6orf222	-6401
10	31289208	cg23260901	1428	-7.96	1.93	3.69E-05	3.29E-02	0.92 (0.89, 0.96)	ZNF438	-763
17	4112498	cg17526357	1428	-13.38	3.24	3.71E-05	3.30E-02	0.87 (0.82, 0.93)	ANKFY1	54643
20	35504371	cg09241885	1427	-12.64	3.07	3.72E-05	3.30E-02	0.88 (0.83, 0.94)	TLDC2	-152

18	74253340	cg20936755	1427	-7.71	1.87	3.72E-05	3.30E-02	0.93 (0.89, 0.96)	LINC00908	12729
11	73897097	cg04484304	1427	-32.1	7.78	3.73E-05	3.31E-02	0.73 (0.62, 0.84)	PPME1	14990
10	88477842	cg04259566	1428	-17.88	4.34	3.74E-05	3.31E-02	0.84 (0.77, 0.91)	BMPR1A	-38553
3	125181706	cg04569594	1427	-34.73	8.42	3.74E-05	3.31E-02	0.71 (0.6, 0.83)	SNX4	57351
1	234667087	cg00123090	1428	-9.43	2.29	3.75E-05	3.31E-02	0.91 (0.87, 0.95)	LINC01354	437
12	109568238	cg01671341	1426	-17.77	4.31	3.75E-05	3.31E-02	0.84 (0.77, 0.91)	ACACB	-8963
9	91979711	cg09684929	1427	-7.74	1.88	3.75E-05	3.31E-02	0.93 (0.89, 0.96)	SECISBP2	45946
17	80075917	cg14832684	1428	-54.08	13.12	3.75E-05	3.31E-02	0.58 (0.45, 0.75)	FASN	-19812
5	67715050	cg21931263	1428	-10.35	2.51	3.77E-05	3.32E-02	0.90 (0.86, 0.95)	PIK3R1	126655
2	219254588	cg00634542	1427	-6.43	1.56	3.86E-05	3.40E-02	0.94 (0.91, 0.97)	SLC11A1	7837
16	2863919	cg10194884	1428	-6.17	1.5	3.88E-05	3.41E-02	0.94 (0.91, 0.97)	PRSS21	-3244
2	127461631	cg16856131	1426	-8.08	1.96	3.88E-05	3.41E-02	0.92 (0.89, 0.96)	GYPC	48121
17	49241518	cg25665831	1428	-9.73	2.36	3.89E-05	3.41E-02	0.91 (0.87, 0.95)	NME2	-1277
12	51782847	cg10590350	1428	-8.19	1.99	3.93E-05	3.44E-02	0.92 (0.89, 0.96)	SLC4A8	-2253
1	19547855	cg05698970	1426	-17.69	4.3	3.95E-05	3.45E-02	0.84 (0.77, 0.91)	LOC101927895	10976
3	72644845	cg23076894	1427	-10.81	2.63	3.95E-05	3.45E-02	0.90 (0.85, 0.95)	LOC105377162	68554
12	52995634	cg00793181	1427	-13.21	3.21	3.96E-05	3.45E-02	0.88 (0.82, 0.93)	KRT72	-313
6	150400090	cg11230866	1427	-9.02	2.19	3.96E-05	3.45E-02	0.91 (0.88, 0.95)	ULBP3	-9808
2	231661317	cg09458420	1427	-12.7	3.09	4.00E-05	3.49E-02	0.88 (0.83, 0.94)	ITM2C	-67995
14	74547881	cg12605076	1426	-48.88	11.91	4.04E-05	3.51E-02	0.61 (0.49, 0.77)	ALDH6A1	3314
12	50441815	cg20649656	1424	-23.73	5.78	4.04E-05	3.51E-02	0.79 (0.7, 0.88)	ASIC1	-9604
1	91992292	cg11799283	1426	-6.35	1.55	4.07E-05	3.53E-02	0.94 (0.91, 0.97)	CDC7	25628
1	203763352	cg24343524	1428	-16.97	4.14	4.08E-05	3.54E-02	0.84 (0.78, 0.92)	ZC3H11A	-1312
14	69801210	cg02095988	1427	-18.35	4.47	4.09E-05	3.54E-02	0.83 (0.76, 0.91)	ERH	63810
10	30793024	cg09532994	1426	-10.24	2.5	4.10E-05	3.54E-02	0.90 (0.86, 0.95)	MAP3K8	69461
3	141900424	cg10141168	1425	-11.71	2.86	4.10E-05	3.54E-02	0.89 (0.84, 0.94)	TFDP2	-32039
14	22886075	cg23612739	1427	-14.17	3.45	4.10E-05	3.54E-02	0.87 (0.81, 0.93)	DAD1	172067
6	36584993	cg22069559	1428	-11.69	2.85	4.12E-05	3.56E-02	0.89 (0.84, 0.94)	MIR3925	5295
6	167177613	cg20774312	1422	-13.15	3.21	4.19E-05	3.61E-02	0.88 (0.82, 0.93)	RPS6KA2	98425
10	114133657	cg14930775	1428	-13.26	3.24	4.20E-05	3.62E-02	0.88 (0.82, 0.93)	ACSL5	-258
11	6225537	cg00286717	1424	-20.04	4.89	4.21E-05	3.62E-02	0.82 (0.74, 0.9)	C11orf42	-1260
2	33437478	cg23985372	1428	-9.13	2.23	4.22E-05	3.63E-02	0.91 (0.87, 0.95)	LTBP1	77815
11	118892305	cg14931486	1385	-2.29	0.56	4.23E-05	3.63E-02	0.98 (0.97, 0.99)		2652

3	12918528	cg25224369		1428	-11.84	2.89	4.23E-05	3.63E-02	0.89 (0.84, 0.94)	LINC02022	8181
11	75409605	cg01167694		1427	-20.35	4.97	4.25E-05	3.64E-02	0.82 (0.74, 0.9)	MOGAT2	-19258
15	68476905	cg13077072		1427	-15.96	3.9	4.31E-05	3.69E-02	0.85 (0.79, 0.92)	CALML4	21542
17	66437754	cg17354333		1428	-7.22	1.77	4.34E-05	3.71E-02	0.93 (0.9, 0.96)	WIPI1	15910
14	69154547	cg04564998		1427	-54.62	13.36	4.36E-05	3.72E-02	0.58 (0.45, 0.75)	LOC100996664	-59044
3	171091657	cg08698681		1428	-17.69	4.33	4.37E-05	3.72E-02	0.84 (0.77, 0.91)	TNIK	86539
3	3152530	cg10159529		1428	-12.83	3.14	4.37E-05	3.72E-02	0.88 (0.83, 0.94)	IL5RA	-473
1	84744762	cg17772438		1418	-18.63	4.56	4.37E-05	3.72E-02	0.83 (0.76, 0.91)	SAMD13	-19286
11	72932079	cg14655553		1419	-9.6	2.35	4.43E-05	3.76E-02	0.91 (0.87, 0.95)	P2RY2	2578
15	91136869	cg23875532		1427	-13.36	3.27	4.43E-05	3.76E-02	0.87 (0.82, 0.93)	CRTC3	63752
17	21176463	cg11522179		1428	-12.89	3.16	4.45E-05	3.77E-02	0.88 (0.83, 0.94)	MAP2K3	-11504
17	57948101	cg13491003		1428	-7.62	1.87	4.45E-05	3.77E-02	0.93 (0.89, 0.96)	TUBD1	22204
16	85568407	cg03983220		1426	-4.49	1.1	4.49E-05	3.80E-02	0.96 (0.94, 0.98)	GSE1	-76621
5	10708717	cg16362140		1428	-9.6	2.35	4.49E-05	3.80E-02	0.91 (0.87, 0.95)	DAP	52669
12	53567662	cg09357175		1427	-9.81	2.4	4.51E-05	3.81E-02	0.91 (0.86, 0.95)	CSAD	6767
17	41400541	cg13726456		1426	-6.39	1.57	4.60E-05	3.88E-02	0.94 (0.91, 0.97)	LINC00854	-19480
19	51961735	cg18536198	1	1428	-9.24	2.27	4.62E-05	3.90E-02	0.91 (0.87, 0.95)	SIGLEC8	-28
7	24965657	cg25270424		1426	-21.85	5.36	4.63E-05	3.90E-02	0.80 (0.72, 0.89)	OSBPL3	-33418
11	70165870	cg14569513		1427	-28.66	7.04	4.64E-05	3.91E-02	0.75 (0.65, 0.86)	MIR548K	35810
19	30432160	cg01627992		1428	-20.3	4.98	4.65E-05	3.91E-02	0.82 (0.74, 0.9)	URI1	-985
11	70166022	cg10120159		1427	-22.93	5.63	4.67E-05	3.92E-02	0.80 (0.71, 0.89)	MIR548K	35962
6	111920032	cg21140167		1428	-34.6	8.5	4.67E-05	3.92E-02	0.71 (0.6, 0.84)	TRAF3IP2	7121
20	61923909	cg01051200		1428	-16.22	3.98	4.68E-05	3.92E-02	0.85 (0.79, 0.92)	COL20A1	-628
19	5093491	cg24823679		1428	-13.32	3.27	4.71E-05	3.94E-02	0.88 (0.82, 0.93)	KDM4B	124368
15	52861754	cg25003924		1427	-7.04	1.73	4.72E-05	3.95E-02	0.93 (0.9, 0.96)	ARPP19	-112
5	141909727	cg03079679		1428	-9.35	2.3	4.76E-05	3.97E-02	0.91 (0.87, 0.95)	FGF1	83998
15	99443339	cg26272088		1428	-13.89	3.41	4.76E-05	3.97E-02	0.87 (0.81, 0.93)	PGPEP1L	105545
8	145643626	cg20259557		1428	-12.01	2.95	4.78E-05	3.99E-02	0.89 (0.84, 0.94)	SLC39A4	-1348
15	44070538	cg26024852		1426	-33.11	8.14	4.79E-05	3.99E-02	0.72 (0.61, 0.84)	ELL3	-1037
12	121861616	cg19998289		1428	-11.56	2.84	4.80E-05	3.99E-02	0.89 (0.84, 0.94)	MIR7107	20538
3	3151679	cg25308597		1426	-4.02	0.99	4.81E-05	4.00E-02	0.96 (0.94, 0.98)	IL5RA	378
13	41935735	cg07769280		1425	-7.58	1.87	4.82E-05	4.00E-02	0.93 (0.89, 0.96)	NAA16	50395
1	167520305	cg17936236		1428	-6.84	1.68	4.85E-05	4.02E-02	0.93 (0.9, 0.97)	CREG1	2750

19	930871	cg18337287		1428	-21.35	5.25	4.85E-05	4.02E-02	0.81 (0.73, 0.9)	ARID3A	4835
15	43309540	cg00092426		1428	-20.29	5	4.86E-05	4.02E-02	0.82 (0.74, 0.9)	UBR1	88745
7	26450563	cg10667267		1426	-27.72	6.83	4.90E-05	4.05E-02	0.76 (0.66, 0.87)	LOC441204	7456
18	12411141	cg17844602		1428	-12.17	3	4.90E-05	4.05E-02	0.89 (0.83, 0.94)	PRELID3A	3247
11	68035071	cg27094581		1428	-14.44	3.56	4.91E-05	4.05E-02	0.87 (0.81, 0.93)	C11orf24	4397
8	96420384	cg05159759		1425	-9.77	2.41	4.97E-05	4.09E-02	0.91 (0.87, 0.95)	C8orf37	-138923
5	58654193	cg08761605		1428	-16.59	4.09	4.97E-05	4.09E-02	0.85 (0.78, 0.92)	PDE4D	-1467
17	9923599	cg17040893		1423	-8.9	2.2	5.02E-05	4.13E-02	0.91 (0.88, 0.96)	GAS7	6023
18	46570302	cg06208130		1427	-32.45	8	5.04E-05	4.14E-02	0.72 (0.62, 0.85)	MIR4744	5835
16	2589773	cg01979270	1	1427	-8.24	2.03	5.05E-05	4.15E-02	0.92 (0.88, 0.96)	PDPK1	1809
14	21089395	cg02864713		1428	-20.34	5.02	5.07E-05	4.16E-02	0.82 (0.74, 0.9)	OR6S1	20454
16	67978450	cg06839111		1428	-13.01	3.21	5.08E-05	4.16E-02	0.88 (0.82, 0.94)	LCAT	-436
1	6074441	cg13123771		1426	-10.51	2.59	5.08E-05	4.16E-02	0.90 (0.86, 0.95)	KCNAB2	-11631
14	55849528	cg12192145		1428	-18.94	4.67	5.09E-05	4.16E-02	0.83 (0.76, 0.91)	ATG14	29047
1	100234313	cg26592446		1428	-17.77	4.39	5.10E-05	4.17E-02	0.84 (0.77, 0.91)	FRRS1	-2965
6	28843296	cg09191776		1427	-21.53	5.31	5.12E-05	4.18E-02	0.81 (0.73, 0.89)	LINC01623	-11843
4	37953726	cg20911897		1425	-3.4	0.84	5.13E-05	4.18E-02	0.97 (0.95, 0.98)	PTTG2	-8329
9	366070	cg08531949		1428	-7.24	1.79	5.14E-05	4.19E-02	0.93 (0.9, 0.96)	DOCK8	93023
5	176920990	cg02996630		1428	-7.25	1.79	5.15E-05	4.19E-02	0.93 (0.9, 0.96)	PDLIM7	3615
22	39848852	cg00827939		1423	-9.21	2.28	5.16E-05	4.20E-02	0.91 (0.87, 0.95)	MGAT3	-4472
2	137135606	cg10114537		1427	-16.86	4.16	5.17E-05	4.20E-02	0.84 (0.78, 0.92)	CXCR4	-259882
2	38806109	cg20619340		1428	-19.23	4.75	5.18E-05	4.20E-02	0.83 (0.75, 0.91)	HNRNPLL	24068
8	120599284	cg07236691		1428	-12.74	3.15	5.21E-05	4.22E-02	0.88 (0.83, 0.94)	ENPP2	5963
22	39869399	cg01315054		1428	-14	3.46	5.23E-05	4.24E-02	0.87 (0.81, 0.93)	MGAT3-AS1	3427
17	47372126	cg07050712		1428	-11.79	2.92	5.24E-05	4.24E-02	0.89 (0.84, 0.94)	MIR6129	-6311
10	32160635	cg25916167		1428	-12.6	3.12	5.24E-05	4.24E-02	0.88 (0.83, 0.94)	ARHGAP12	37218
12	123872423	cg02053425		1426	-7.19	1.78	5.25E-05	4.24E-02	0.93 (0.9, 0.96)	KMT5A	-3398
16	30488321	cg06972908		1428	-8.68	2.15	5.25E-05	4.24E-02	0.92 (0.88, 0.96)	ITGAL	4339
1	179005979	cg03698182		1428	-15.55	3.85	5.26E-05	4.24E-02	0.86 (0.79, 0.92)	FAM20B	10721
22	23885362	cg27060510		1428	-2.62	0.65	5.26E-05	4.24E-02	0.97 (0.96, 0.99)	IGLL1	37132
7	101829270	cg11644402		1403	-42.85	10.6	5.29E-05	4.25E-02	0.65 (0.53, 0.8)	SH2B2	-99082
10	73906532	cg23468453		1428	-28.32	7.01	5.29E-05	4.25E-02	0.75 (0.66, 0.86)	SPOCK2	-57743
1	95358601	cg01633282		1426	-40.23	9.96	5.34E-05	4.29E-02	0.67 (0.55, 0.81)	CNN3	32762

6	7154703	cg17446528	1426	-5.69	1.41	5.36E-05	4.30E-02	0.94 (0.92, 0.97)	RREB1	46618
9	71561785	cg15713581	1425	-13.22	3.27	5.37E-05	4.30E-02	0.88 (0.82, 0.93)	LOC101927069	28971
2	183513961	cg16195942	1427	-16.74	4.14	5.37E-05	4.30E-02	0.85 (0.78, 0.92)	DNAJC10	-66806
3	50338171	cg08574671	1425	-7.21	1.78	5.38E-05	4.30E-02	0.93 (0.9, 0.96)	HYAL3	-1273
17	57925800	cg08744877	1427	-26.32	6.52	5.38E-05	4.30E-02	0.77 (0.68, 0.87)	MIR21	7174
9	2810737	cg01750299	1426	-14.27	3.53	5.40E-05	4.31E-02	0.87 (0.81, 0.93)	PUM3	33392
17	81040724	cg20290167	1427	-9.3	2.3	5.40E-05	4.31E-02	0.91 (0.87, 0.95)	METRNL	3158
15	40173065	cg25939647	1423	-7.39	1.83	5.41E-05	4.31E-02	0.93 (0.9, 0.96)	GPR176	40027
12	104808575	cg09800745	1428	-16.75	4.15	5.47E-05	4.35E-02	0.85 (0.78, 0.92)	CHST11	-42116
3	47742869	cg11540119	1426	-15.12	3.75	5.47E-05	4.35E-02	0.86 (0.8, 0.93)	SMARCC1	80535
12	25103501	cg25984364	1428	-17.89	4.43	5.48E-05	4.35E-02	0.84 (0.77, 0.91)	BCAT1	-1109
17	78389106	cg12432898	1428	68.95	17.09	5.49E-05	4.36E-02	1.99 (1.43, 2.79)	LOC100294362	-139
19	44124896	cg02668270	1415	-10.26	2.54	5.50E-05	4.36E-02	0.90 (0.86, 0.95)	ZNF428	-883
16	57103772	cg12928479	1423	-8.74	2.17	5.50E-05	4.36E-02	0.92 (0.88, 0.96)	CPNE2	-22682
1	43291088	cg04036011	1420	-7.18	1.78	5.51E-05	4.36E-02	0.93 (0.9, 0.96)	ERMAP	-160
17	40810559	cg10180165	1428	-18.99	4.71	5.52E-05	4.36E-02	0.83 (0.75, 0.91)	TUBG2	-706
3	9929455	cg19227526	1428	-9.45	2.35	5.60E-05	4.42E-02	0.91 (0.87, 0.95)	JAGN1	-2815
12	104484062	cg07100454	1428	-34.88	8.66	5.61E-05	4.43E-02	0.71 (0.6, 0.84)	HCFC2	25827
14	103436387	cg18505004	1427	-18.88	4.69	5.67E-05	4.47E-02	0.83 (0.76, 0.91)	AMN	47395
3	57064082	cg03069832	1428	-15.82	3.93	5.68E-05	4.47E-02	0.85 (0.79, 0.92)	SPATA12	-30386
16	3055636	cg07961282	1427	-21.87	5.43	5.69E-05	4.48E-02	0.80 (0.72, 0.89)	LOC101929613	6681
2	121155673	cg06525046	1426	-11.87	2.95	5.72E-05	4.49E-02	0.89 (0.84, 0.94)	INHBB	51956
4	108615003	cg00587765	1427	-19.87	4.94	5.73E-05	4.49E-02	0.82 (0.74, 0.9)	PAPSS1	26415
4	1577971	cg19901381	1428	-15.69	3.9	5.73E-05	4.49E-02	0.85 (0.79, 0.92)	FAM53A	107746
1	52442668	cg07142936	1427	-24.06	5.98	5.74E-05	4.50E-02	0.79 (0.7, 0.88)	RAB3B	13767
11	9632897	cg26938803	1427	-8.98	2.23	5.75E-05	4.50E-02	0.91 (0.88, 0.95)	WEE1	36664
9	80189185	cg08635575	1428	-11.55	2.87	5.78E-05	4.52E-02	0.89 (0.84, 0.94)	GNA14	74046
3	142724451	cg01375248	1428	-7.34	1.82	5.79E-05	4.52E-02	0.93 (0.9, 0.96)	U2SURP	4080
10	95200513	cg13827101	1428	-24.14	6	5.79E-05	4.52E-02	0.79 (0.7, 0.88)	MYOF	41560
4	148733880	cg20866785	1428	-10.43	2.6	5.80E-05	4.52E-02	0.90 (0.86, 0.95)	MIR4799	30135
11	64216380	cg03074692	1376	18.62	4.64	5.88E-05	4.58E-02	1.20 (1.1, 1.32)	LOC100996455	-148
17	47590237	cg12561474	1425	-23.15	5.76	5.88E-05	4.58E-02	0.79 (0.71, 0.89)	MIR6165	2059
16	11709899	cg06743426	1428	-7.39	1.84	5.89E-05	4.58E-02	0.93 (0.9, 0.96)	LITAF	-28578

2	136901306	cg06725108	1426	-7.99	1.99	5.92E-05	4.60E-02	0.92 (0.89, 0.96)	CXCR4	-25582
2	187420032	cg27609375	1428	-4.1	1.02	5.93E-05	4.60E-02	0.96 (0.94, 0.98)	ITGAV	-34757
12	44228244	cg00491149	1428	-21.54	5.37	5.95E-05	4.61E-02	0.81 (0.73, 0.9)	TMEM117	-1419
18	61559440	cg14884379	1428	-13.45	3.35	5.96E-05	4.62E-02	0.87 (0.82, 0.93)	SERPINB2	4502
4	6782128	cg06231269	1428	-6.84	1.7	5.98E-05	4.63E-02	0.93 (0.9, 0.97)	KIAA0232	-2330
2	28877884	cg22304799	1428	-41.63	10.37	6.00E-05	4.64E-02	0.66 (0.54, 0.81)	PLB1	88661
15	57519802	cg21831937	1425	-23.86	5.95	6.02E-05	4.65E-02	0.79 (0.7, 0.89)	TCF12	8148
3	138478129	cg16050349	1428	-8.62	2.15	6.03E-05	4.65E-02	0.92 (0.88, 0.96)	PIK3CB	71
2	28373887	cg27514107	1427	-18.13	4.52	6.03E-05	4.65E-02	0.83 (0.76, 0.91)	LOC100505736	55940
5	179751794	cg04459091	1427	-22.99	5.73	6.07E-05	4.68E-02	0.79 (0.71, 0.89)	GFPT2	28592
1	242351909	cg04763288	1428	-18.74	4.68	6.13E-05	4.71E-02	0.83 (0.76, 0.91)	MAP1LC3C	-189525
9	103278557	cg13783924	1428	-13.57	3.39	6.13E-05	4.71E-02	0.87 (0.82, 0.93)	TMEFF1	43038
1	155741125	cg21211696	1428	-29.62	7.39	6.15E-05	4.72E-02	0.74 (0.64, 0.86)	SCARNA26B	12497
8	57885566	cg01279789	1427	-36.37	9.08	6.16E-05	4.72E-02	0.70 (0.58, 0.83)	IMPAD1	20863
11	63011231	cg16239613	1428	-4.86	1.21	6.16E-05	4.72E-02	0.95 (0.93, 0.98)	SLC22A25	-14108
5	131770410	cg16587582	1422	-17.39	4.34	6.19E-05	4.74E-02	0.84 (0.77, 0.91)		23946
21	38574170	cg12100242	1428	-31.24	7.8	6.21E-05	4.75E-02	0.73 (0.63, 0.85)	DSCR9	-6633
5	53520049	cg15581007	1425	-6.17	1.54	6.21E-05	4.75E-02	0.94 (0.91, 0.97)	ARL15	86353
16	57683565	cg16725301	1427	-14.1	3.52	6.22E-05	4.75E-02	0.87 (0.81, 0.93)	ADGRG1	10359
1	184709731	cg09741958	1424	-5.23	1.31	6.26E-05	4.77E-02	0.95 (0.92, 0.97)	EDEM3	14309
1	32761824	cg14975122	1428	-10.56	2.64	6.26E-05	4.77E-02	0.90 (0.85, 0.95)	HDAC1	4117
18	9521949	cg01048814	1428	-30.33	7.58	6.28E-05	4.78E-02	0.74 (0.64, 0.86)	RALBP1	46420
8	67967170	cg20454670	1427	-34.95	8.74	6.30E-05	4.79E-02	0.71 (0.59, 0.84)	COPS5	7391
6	42109176	cg24627621	1427	-13.07	3.27	6.33E-05	4.81E-02	0.88 (0.82, 0.94)	C6orf132	1538
20	35422698	cg16046667	1428	-10.13	2.53	6.36E-05	4.83E-02	0.90 (0.86, 0.95)	DSN1	-20469
17	33885049	cg00397422	1428	-13.36	3.34	6.39E-05	4.84E-02	0.87 (0.82, 0.93)	SLFN14	60
16	78782477	cg02236679	1427	-22.41	5.61	6.39E-05	4.84E-02	0.80 (0.72, 0.89)	WWOX	649168
15	57603845	cg15335273	1427	-24.01	6.01	6.39E-05	4.84E-02	0.79 (0.7, 0.88)	LINC01413	-7490
1	236715069	cg22976779	1428	-14.09	3.53	6.40E-05	4.84E-02	0.87 (0.81, 0.93)	LGALS8-AS1	-27262
18	33046000	cg24629258	1427	-27.59	6.9	6.41E-05	4.84E-02	0.76 (0.66, 0.87)	INO80C	31612
11	65482056	cg10093679	1428	-13.83	3.46	6.42E-05	4.84E-02	0.87 (0.81, 0.93)	KAT5	2584
16	79644995	cg10696524	1423	-18.55	4.64	6.42E-05	4.84E-02	0.83 (0.76, 0.91)	MAF	-10374
21	46709748	cg04992921	1425	-18.33	4.59	6.45E-05	4.86E-02	0.83 (0.76, 0.91)	LOC642852	1782

16	387629	cg22158603	1427	-11.57	2.9	6.45E-05	4.86E-02	0.89 (0.84, 0.94)	AXIN1	15046
7	28228530	cg14298642	1425	-34.78	8.71	6.54E-05	4.92E-02	0.71 (0.6, 0.84)	JAZF1	-8094

[1] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)

[2] Genome build GRCh37/hg19

[3] Removed from down stream analyses because Pidsley et al identified to be cross-reactive probe

Table E12. 104 CpGs that were FDR Significant in Both Non-atopic and Atopic Asthma[1]

probe	chr	position[2]	Gene.Name	crossreactive	Beta_NA	SE_NA	P_NA	N_NA	OR.CI_NA	FDR_NA	Beta_AA	SE_AA	P_AA	N_AA	OR.CI_AA	FDR_AA
cg21220721	1	6341230	GPR153		-5.711107508	1.141339306	5.62E-07	1828	0.94 (0.92, 0.97)	0.017010595	-9.06845	1.504746	1.67E-09	1426	0.91 (0.89, 0.94)	2.59E-05
cg09249800	1	6341287	GPR153		-7.557365165	1.402832584	7.16E-08	1828	0.93 (0.9, 0.95)	0.008805707	-12.8227	1.868696	6.80E-12	1428	0.88 (0.85, 0.91)	9.26E-07
cg11699125	1	6341327	GPR153		-4.93823042	1.17185606	2.51E-05	1827	0.95 (0.93, 0.97)	0.045992373	-10.3405	1.563758	3.78E-11	1426	0.90 (0.87, 0.93)	3.09E-06
cg19851810	1	23072310	MIR4684		-27.27547273	6.327860828	1.63E-05	1825	0.76 (0.67, 0.86)	0.040491402	-38.8425	8.05322	1.41E-06	1423	0.68 (0.58, 0.79)	0.002859
cg16263722	1	29523841	SRSF4		-12.10690521	2.595019696	3.08E-06	1830	0.89 (0.84, 0.93)	0.027161046	-18.1919	3.478806	1.70E-07	1428	0.83 (0.78, 0.89)	0.000623
cg13789639	1	47746081	STIL		-16.22535891	3.371155855	1.49E-06	1828	0.85 (0.8, 0.91)	0.026073688	-22.7598	4.400395	2.31E-07	1428	0.80 (0.73, 0.87)	0.000777
cg10704177	1	62209607	PATJ		-11.21529982	2.423970044	3.71E-06	1829	0.89 (0.85, 0.94)	0.028454637	-18.8164	3.25551	7.48E-09	1427	0.83 (0.78, 0.88)	7.19E-05
cg24058805	1	66777579	PDE4B		-18.94154622	4.119849583	4.27E-06	1830	0.83 (0.76, 0.9)	0.028603225	-26.9858	5.547552	1.15E-06	1428	0.76 (0.68, 0.85)	0.002441
cg17936236	1	167520305	CREG1		-5.149531761	1.214814641	2.25E-05	1830	0.95 (0.93, 0.97)	0.043989922	-6.84283	1.684317	4.85E-05	1428	0.93 (0.9, 0.97)	0.040199
cg17946525	1	172425816	C1orf105		-12.87254138	2.98561805	1.62E-05	1830	0.88 (0.83, 0.93)	0.040491402	-23.9063	4.218942	1.46E-08	1428	0.79 (0.72, 0.86)	0.000118
cg13672080	1	206109139	FAM72A	1	-27.08609873	5.814655977	3.19E-06	1830	0.76 (0.68, 0.85)	0.027161046	-42.6826	7.396223	7.89E-09	1428	0.65 (0.56, 0.75)	7.33E-05
cg02589986	2	7027871	RSAD2		-6.257080611	1.449708801	1.59E-05	1830	0.94 (0.91, 0.97)	0.040479864	-8.3139	1.986432	2.85E-05	1428	0.92 (0.89, 0.96)	0.027827
cg05642098	2	28550757	LOC100505716		-19.12276099	4.311817242	9.21E-06	1829	0.83 (0.76, 0.9)	0.037198283	-32.9946	5.648041	5.16E-09	1427	0.72 (0.64, 0.8)	5.90E-05
cg26382374	2	31302644	GALNT14		-10.9074025	2.57883061	2.34E-05	1828	0.90 (0.85, 0.94)	0.044871548	-26.8875	3.522003	2.27E-14	1425	0.76 (0.71, 0.82)	1.86E-08
cg26529864	2	74375903	BOLA3-AS1		-24.9827352	5.411044034	3.89E-06	1803	0.78 (0.7, 0.87)	0.028530258	-31.1792	7.353147	2.23E-05	1408	0.73 (0.63, 0.85)	0.023098
cg17988187	2	74612222	DCTN1-AS1		-11.85260428	2.36877744	5.62E-07	1830	0.89 (0.85, 0.93)	0.017010595	-16.3745	3.12404	1.59E-07	1428	0.85 (0.8, 0.9)	0.000591
cg12077754	2	75089669	HK2		-10.09373363	2.084605574	1.29E-06	1830	0.90 (0.87, 0.94)	0.025912329	-13.534	2.739994	7.84E-07	1428	0.87 (0.83, 0.92)	0.001901
cg25493477	2	86830411	RNF103		-14.99411859	3.474431654	1.59E-05	1830	0.86 (0.8, 0.92)	0.040479864	-26.3604	4.828243	4.77E-08	1428	0.77 (0.7, 0.84)	0.000256
cg01923915	2	96965099	SNRNP200		-16.77478053	3.567638666	2.58E-06	1830	0.85 (0.79, 0.91)	0.027161046	-31.0387	4.883559	2.07E-10	1428	0.73 (0.67, 0.81)	6.54E-06
cg05724080	2	234246583	DGKD		-8.013228845	1.86916157	1.81E-05	1828	0.92 (0.89, 0.96)	0.041087506	-12.2933	2.399558	3.00E-07	1428	0.88 (0.84, 0.93)	0.000939
cg15106081	3	14708144	C3orf20		-27.346914	5.518067542	7.20E-07	1827	0.76 (0.68, 0.85)	0.019270929	-36.5854	7.206113	3.83E-07	1425	0.69 (0.6, 0.8)	0.001138
cg16499536	3	15066613	MRPS25		-21.20048221	4.405064732	1.49E-06	1828	0.81 (0.74, 0.88)	0.026073688	-33.1712	5.915514	2.05E-08	1426	0.72 (0.64, 0.81)	0.000143
cg20804243	3	171205319	TNIK		-10.70960827	2.463942379	1.38E-05	1829	0.90 (0.86, 0.94)	0.039433017	-16.7872	3.32823	4.56E-07	1428	0.85 (0.79, 0.9)	0.001293
cg07456972	4	38110810	TBC1D1		-21.10926848	4.169276587	4.13E-07	1825	0.81 (0.75, 0.88)	0.015824641	-29.0247	5.337545	5.39E-08	1424	0.75 (0.67, 0.83)	0.000284
cg23856600	5	10560140	ANKRD33B		-7.282877033	1.626565373	7.55E-06	1830	0.93 (0.9, 0.96)	0.035872815	-9.47152	2.105886	6.87E-06	1428	0.91 (0.87, 0.95)	0.009373
cg14390854	5	74342697	LINC01336		-10.87699338	2.430471151	7.63E-06	1830	0.90 (0.86, 0.94)	0.03604337	-16.2281	3.237331	5.36E-07	1428	0.85 (0.8, 0.91)	0.001436
cg10113951	5	179200573	LTC4S		-20.6970834	4.946708189	2.86E-05	1830	0.81 (0.74, 0.9)	0.04809243	-29.5195	6.819139	1.50E-05	1427	0.74 (0.65, 0.85)	0.017339
cg15123849	6	15364953	JARID2		-4.896929516	1.017695701	1.50E-06	1828	0.95 (0.93, 0.97)	0.026073688	-7.53633	1.342545	1.98E-08	1427	0.93 (0.9, 0.95)	0.000143
cg10011040	6	20034134	MBOAT1		-14.23512765	3.05854842	3.25E-06	1829	0.87 (0.82, 0.92)	0.027161046	-22.8977	4.181409	4.35E-08	1427	0.80 (0.73, 0.86)	0.000239
cg09597192	6	32141591	AGPAT1		-19.99121726	4.644352868	1.67E-05	1830	0.82 (0.75, 0.9)	0.040497996	-28.1413	6.182916	5.33E-06	1427	0.75 (0.67, 0.85)	0.007806
cg27341747	6	126375816	MIR5695		-18.95573901	4.211299084	6.76E-06	1827	0.83 (0.76, 0.9)	0.035413517	-29.0175	5.633191	2.59E-07	1424	0.75 (0.67, 0.84)	0.000853
cg18650626	7	1914073	MIR4655		-5.646315199	1.354518146	3.07E-05	1816	0.95 (0.92, 0.97)	0.049098071	-9.94841	1.752979	1.39E-08	1416	0.91 (0.87, 0.94)	0.000114
cg14769121	7	98722470	SMURF1		-16.02592268	3.309737496	1.29E-06	1828	0.85 (0.8, 0.91)	0.025912329	-22.1059	4.422862	5.79E-07	1428	0.80 (0.74, 0.87)	0.001517
cg07970948	7	149543165	ZNF862		-5.949395353	1.251050973	1.98E-06	1827	0.94 (0.92, 0.97)	0.026073688	-10.4206	1.669317	4.31E-10	1425	0.90 (0.87, 0.93)	1.04E-05
cg17245251	8	103603330	ODF1		-20.35732793	4.49686622	5.98E-06	1830	0.82 (0.75, 0.89)	0.033904209	-27.5245	5.633811	1.03E-06	1428	0.76 (0.68, 0.85)	0.002245
cg26472183	8	126445744	TRIB1		-29.70120461	6.04372345	8.91E-07	1788	0.74 (0.66, 0.84)	0.021416364	-47.482	7.890437	1.77E-09	1398	0.62 (0.53, 0.73)	2.68E-05
cg01499988	9	35755346	MSMP		-12.31318965	2.771238534	8.86E-06	1830	0.88 (0.84, 0.93)	0.037198283	-18.2785	3.849856	2.06E-06	1428	0.83 (0.77, 0.9)	0.003879
cg25348163	9	80602527	GNAQ		-20.10060796	4.736899399	2.20E-05	1829	0.82 (0.75, 0.9)	0.043851634	-38.2544	6.348392	1.68E-09	1428	0.68 (0.6, 0.77)	2.59E-05
cg01745810	9	126497597	DENND1A		-12.69484151	2.774732133	4.76E-06	1830	0.88 (0.83, 0.93)	0.030381179	-27.0298	3.77709	8.29E-13	1428	0.76 (0.71, 0.82)	2.26E-07

cg14612966	9	130859606	SLC25A25	-14.34761942	3.264270782	1.11E-05	1827	0.87 (0.81, 0.92)	0.038246598	-24.2278	4.375016	3.06E-08	1428	0.78 (0.72, 0.86)	0.000189
cg13953978	9	132600788	USP20	-11.04782903	2.555818764	1.54E-05	1830	0.90 (0.85, 0.94)	0.040080952	-16.0882	3.5093	4.55E-06	1428	0.85 (0.79, 0.91)	0.006937
cg24317972	10	12371568	CAMK1D	-20.66278981	4.427787707	3.06E-06	1827	0.81 (0.75, 0.89)	0.027161046	-24.6403	5.861406	2.62E-05	1424	0.78 (0.7, 0.88)	0.026144
cg15737719	10	22743835	LOC100499489	-27.91461717	5.112108413	4.75E-08	1829	0.76 (0.68, 0.84)	0.007763733	-28.7891	6.53615	1.06E-05	1426	0.75 (0.66, 0.85)	0.013125
cg01614759	10	45495435	ZNF22	-13.88951618	2.744496175	4.17E-07	1829	0.87 (0.82, 0.92)	0.015824641	-22.6514	3.749055	1.52E-09	1427	0.80 (0.74, 0.86)	2.44E-05
cg01086527	10	119167795	PDZD8	-14.90399222	3.446660759	1.53E-05	1830	0.86 (0.81, 0.92)	0.040080952	-24.5569	4.621223	1.07E-07	1428	0.78 (0.71, 0.86)	0.000467
cg12227660	10	135061670	MIR202HG	-5.816055349	1.389788822	2.85E-05	1810	0.94 (0.92, 0.97)	0.04809243	-13.1034	1.995269	5.13E-11	1419	0.88 (0.84, 0.91)	3.49E-06
cg07565042	11	10543456	MTRNR2L8	-7.043627546	1.63563401	1.66E-05	1829	0.93 (0.9, 0.96)	0.040495824	-8.9307	2.147899	3.21E-05	1427	0.91 (0.88, 0.95)	0.030327
cg12819873	11	57157632	PRG2	-12.53869278	2.937613306	1.97E-05	1829	0.88 (0.83, 0.93)	0.04246208	-22.6624	3.895973	6.00E-09	1428	0.80 (0.74, 0.86)	6.54E-05
cg11205545	11	62164451	SCGB1A1	-13.88376228	3.285468288	2.38E-05	1830	0.87 (0.82, 0.93)	0.045023595	-22.4054	4.046714	3.08E-08	1428	0.80 (0.74, 0.87)	0.000189
cg07636225	11	63466987	RTN3	-15.5503938	3.375146888	4.08E-06	1828	0.86 (0.8, 0.91)	0.028603225	-26.6674	4.53402	4.06E-09	1428	0.77 (0.7, 0.84)	5.03E-05
cg08589455	11	65489884	RNASEH2C	-13.05697707	3.098893309	2.52E-05	1817	0.88 (0.83, 0.93)	0.046072309	-17.9979	4.024724	7.76E-06	1418	0.84 (0.77, 0.9)	0.010362
cg14569513	11	70165870	MIR548K	-23.40611115	5.353478551	1.23E-05	1830	0.79 (0.71, 0.88)	0.038694839	-28.6611	7.036459	4.64E-05	1427	0.75 (0.65, 0.86)	0.039052
cg23338316	11	93456334	SCARNA9	-14.47113057	2.727959788	1.13E-07	1828	0.87 (0.82, 0.91)	0.010260839	-19.3701	3.65932	1.20E-07	1427	0.82 (0.77, 0.89)	0.00049
cg00390941	12	15124659	PDE6H	-22.74735787	5.459791827	3.10E-05	1826	0.80 (0.72, 0.89)	0.049223421	-38.4514	7.168657	8.15E-08	1422	0.68 (0.59, 0.78)	0.000391
cg10220104	12	27027924	ITPR2	-19.00116813	4.482075754	2.24E-05	1830	0.83 (0.76, 0.9)	0.043989922	-29.8912	5.57917	8.43E-08	1427	0.74 (0.66, 0.83)	0.000391
cg17116500	12	56600222	RNF41	-16.51028034	3.771637916	1.20E-05	1830	0.85 (0.79, 0.91)	0.038307891	-23.237	5.200342	7.88E-06	1428	0.79 (0.72, 0.88)	0.010454
cg26964704	12	125589647	AACS	-16.05531226	3.366145131	1.85E-06	1830	0.85 (0.8, 0.91)	0.026073688	-27.8229	4.676225	2.68E-09	1428	0.76 (0.69, 0.83)	3.71E-05
cg07908654	13	41631052	WBP4	-15.20687578	2.840435454	8.62E-08	1830	0.86 (0.81, 0.91)	0.008805707	-24.5627	3.836765	1.53E-10	1428	0.78 (0.73, 0.84)	5.21E-06
cg11015284	13	47274074	ESD	-35.0292798	8.052444338	1.36E-05	1830	0.70 (0.6, 0.82)	0.039135197	-50.4649	10.75149	2.68E-06	1428	0.60 (0.49, 0.75)	0.004738
cg02543556	14	39643445	PNN	-15.08701157	3.440666417	1.16E-05	1827	0.86 (0.8, 0.92)	0.038246598	-19.547	4.548059	1.72E-05	1428	0.82 (0.75, 0.9)	0.019229
cg00336912	14	55583041	LGALS3	-17.81607544	3.815257505	3.02E-06	1830	0.84 (0.78, 0.9)	0.027161046	-26.9644	4.867955	3.04E-08	1427	0.76 (0.69, 0.84)	0.000189
cg23575099	14	55603874	LGALS3	-20.50704797	3.828093064	8.46E-08	1830	0.81 (0.76, 0.88)	0.008805707	-30.8665	5.385949	9.99E-09	1428	0.73 (0.66, 0.82)	8.87E-05
cg12258670	14	75069041	LTBP2	-18.53776593	4.027033927	4.16E-06	1830	0.83 (0.77, 0.9)	0.028603225	-29.2717	5.177687	1.57E-08	1428	0.75 (0.67, 0.83)	0.000119
cg06984345	14	75162215	AREL1	-9.024939923	2.130022024	2.27E-05	1830	0.91 (0.88, 0.95)	0.044275023	-15.068	2.884683	1.76E-07	1428	0.86 (0.81, 0.91)	0.000636
cg01901579	14	95615731	DICER1	-12.78278896	3.022785731	2.35E-05	1830	0.88 (0.83, 0.93)	0.044871548	-25.251	3.910467	1.07E-10	1428	0.78 (0.72, 0.84)	4.60E-06
cg14084609	14	100610407	DEGS2	-20.4536536	3.690772998	2.99E-08	1830	0.82 (0.76, 0.88)	0.007763733	-25.203	4.723183	9.50E-08	1428	0.78 (0.71, 0.85)	0.000427
cg18550847	14	100610570	DEGS2	-9.947297596	2.246089967	9.48E-06	1830	0.91 (0.87, 0.95)	0.037286347	-18.3945	2.926844	3.28E-10	1428	0.83 (0.79, 0.88)	8.65E-06
cg08884974	15	31505024	LOC102725022	-13.35344261	2.640522919	4.26E-07	1829	0.87 (0.83, 0.92)	0.015824641	-14.5084	3.475378	2.98E-05	1427	0.86 (0.81, 0.93)	0.028719
cg18852698	15	40093898	LOC105370941	-12.01773006	2.483261858	1.30E-06	1829	0.89 (0.84, 0.93)	0.025912329	-20.3974	3.243514	3.20E-10	1427	0.82 (0.77, 0.87)	8.65E-06
cg07177867	15	52030746	LYSMD2	-11.2822758	2.461134692	4.56E-06	1830	0.89 (0.85, 0.94)	0.030053158	-16.0386	3.270672	9.40E-07	1428	0.85 (0.8, 0.91)	0.002125
cg12402318	15	52135487	TMOD3	-17.53908055	3.874087198	5.97E-06	1830	0.84 (0.78, 0.91)	0.033904209	-26.3956	5.250847	4.98E-07	1428	0.77 (0.69, 0.85)	0.001375
cg05853552	15	52427175	BCL2L10	-16.23842854	3.38035606	1.56E-06	1830	0.85 (0.8, 0.91)	0.026073688	-30.6259	4.763122	1.28E-10	1428	0.74 (0.67, 0.81)	4.87E-06
cg25466522	15	81623226	TMC3-AS1	-19.67862964	3.943261768	6.02E-07	1828	0.82 (0.76, 0.89)	0.017570553	-35.2136	5.235663	1.75E-11	1426	0.70 (0.63, 0.78)	2.04E-06
cg03666966	15	101798908	CHSY1	-20.84731877	4.907606237	2.16E-05	1829	0.81 (0.74, 0.89)	0.043759038	-31.6381	6.054374	1.74E-07	1427	0.73 (0.65, 0.82)	0.000635
cg04497992	16	616212	NHLRC4	-6.779153104	1.568041863	1.54E-05	1830	0.93 (0.91, 0.96)	0.040080952	-13.8592	2.195685	2.75E-10	1428	0.87 (0.83, 0.91)	8.32E-06
cg10194884	16	2863919	PRSS21	-4.54489445	1.076326662	2.42E-05	1830	0.96 (0.94, 0.98)	0.045360291	-6.17374	1.500569	3.88E-05	1428	0.94 (0.91, 0.97)	0.034059
cg24517604	16	11709855	LITAF	-13.46730572	2.955231622	5.19E-06	1829	0.87 (0.82, 0.93)	0.031652609	-25.9579	4.000253	8.64E-11	1425	0.77 (0.71, 0.83)	4.15E-06
cg03392077	16	16195619	ABCC6	-5.465304943	1.229179406	8.74E-06	1829	0.95 (0.92, 0.97)	0.037198283	-8.7247	1.534697	1.31E-08	1427	0.92 (0.89, 0.94)	0.000108
cg16064932	16	46776932	MYLK3	-9.316847816	2.016500519	3.83E-06	1829	0.91 (0.88, 0.95)	0.028454637	-13.0179	2.816701	3.81E-06	1427	0.88 (0.83, 0.93)	0.006034
cg10298741	16	73019173	ZFHX3	-11.01011794	2.633821992	2.91E-05	1830	0.90 (0.85, 0.94)	0.04856995	-19.4911	3.591488	5.73E-08	1428	0.82 (0.77, 0.88)	0.000295
cg16660617	16	75037584	ZNRF1	-31.26362612	7.517657607	3.20E-05	1830	0.73 (0.63, 0.85)	0.049907481	-60.4956	9.81568	7.13E-10	1428	0.55 (0.45, 0.66)	1.57E-05

cg05958985	16	88558237	MIR5189	-7.734557745	1.794540174	1.63E-05	1829	0.93 (0.89, 0.96)	0.040491402	-10.5759	2.377026	8.62E-06	1427	0.90 (0.86, 0.94)	0.0112
cg17105176	17	2287284	MNT	-17.05322113	3.662429435	3.22E-06	1827	0.84 (0.78, 0.91)	0.027161046	-28.7048	4.865134	3.63E-09	1425	0.75 (0.68, 0.83)	4.75E-05
cg06449385	17	4741523	MINK1	-14.48298983	3.371733089	1.74E-05	1823	0.87 (0.81, 0.92)	0.041087506	-28.9685	4.726159	8.82E-10	1422	0.75 (0.68, 0.82)	1.80E-05
cg14321269	17	6658198	XAF1	-9.761873533	2.033525954	1.58E-06	1829	0.91 (0.87, 0.94)	0.026073688	-14.9163	2.82574	1.30E-07	1427	0.86 (0.82, 0.91)	0.000521
cg06127160	17	25897247	LGALS9	-8.503738562	1.74268139	1.06E-06	1830	0.92 (0.89, 0.95)	0.023412678	-14.148	2.247641	3.08E-10	1428	0.87 (0.83, 0.91)	8.65E-06
cg00397422	17	33885049	SLFN14	-10.33362017	2.477499487	3.03E-05	1830	0.90 (0.86, 0.95)	0.048840672	-13.3595	3.341656	6.39E-05	1428	0.87 (0.82, 0.93)	0.048398
cg13947225	17	55190679	AKAP1	-10.6841835	2.395715227	8.21E-06	1826	0.90 (0.86, 0.94)	0.037198283	-20.8308	3.241721	1.31E-10	1424	0.81 (0.76, 0.87)	4.87E-06
cg01955639	17	56269767	EPX	-12.66773261	2.477710126	3.18E-07	1830	0.88 (0.84, 0.92)	0.015824641	-18.5615	3.553808	1.76E-07	1428	0.83 (0.77, 0.89)	0.000636
cg11112605	17	56283901	MKS1	-11.19015042	2.448536428	4.87E-06	1830	0.89 (0.85, 0.94)	0.030381179	-19.2519	3.410928	1.66E-08	1428	0.82 (0.77, 0.88)	0.000123
cg12380988	17	79851485	ANAPC11	-13.6875558	3.180846312	1.68E-05	1830	0.87 (0.82, 0.93)	0.040619964	-30.1455	4.255343	1.40E-12	1428	0.74 (0.68, 0.8)	2.86E-07
cg22503106	17	81040906	METRNL	-10.74312778	2.434760167	1.02E-05	1814	0.90 (0.86, 0.94)	0.037916759	-19.5451	3.346353	5.20E-09	1414	0.82 (0.77, 0.88)	5.90E-05
cg13054523	17	81055722	METRNL	-11.55832781	2.613738697	9.77E-06	1830	0.89 (0.85, 0.94)	0.037830691	-19.974	3.424264	5.44E-09	1428	0.82 (0.77, 0.88)	6.01E-05
cg06592575	18	55250579	FECH	-22.78443698	4.737128342	1.51E-06	1829	0.80 (0.73, 0.87)	0.026073688	-35.0096	6.309313	2.88E-08	1427	0.70 (0.62, 0.8)	0.000185
cg26569937	19	2594841	MIR7850	-19.7685052	4.664511912	2.25E-05	1824	0.82 (0.75, 0.9)	0.043989922	-28.8123	6.356819	5.83E-06	1421	0.75 (0.66, 0.85)	0.00833
cg00477633	19	3521502	FZR1	-18.71977976	4.0483412	3.76E-06	1829	0.83 (0.77, 0.9)	0.028454637	-27.5037	5.496189	5.61E-07	1426	0.76 (0.68, 0.85)	0.001487
cg21664942	19	40837284	C19orf47	-13.00410184	2.964586253	1.15E-05	1830	0.88 (0.83, 0.93)	0.038246598	-22.0079	3.892018	1.56E-08	1428	0.80 (0.74, 0.87)	0.000119
cg09194810	20	4072430	SMOX	-14.8225175	3.442499704	1.66E-05	1829	0.86 (0.81, 0.92)	0.040495824	-26.7247	4.565158	4.80E-09	1427	0.77 (0.7, 0.84)	5.60E-05
cg15532312	20	34018983	GDF5	-21.96753702	4.712562777	3.14E-06	1826	0.80 (0.73, 0.88)	0.027161046	-37.5769	6.393225	4.16E-09	1424	0.69 (0.61, 0.78)	5.07E-05
cg21045547	20	35422703	DSN1	-11.17387021	2.620812175	2.01E-05	1830	0.89 (0.85, 0.94)	0.042666035	-17.5758	3.536644	6.71E-07	1428	0.84 (0.78, 0.9)	0.001698
cg09241885	20	35504371	TLDC2	-9.389006036	2.210267914	2.16E-05	1829	0.91 (0.87, 0.95)	0.043759038	-12.6437	3.065881	3.72E-05	1427	0.88 (0.83, 0.94)	0.033045
cg13792581	20	43590115	TOMM34	-24.2641343	5.505047956	1.05E-05	1828	0.78 (0.7, 0.87)	0.038137633	-35.7675	7.56824	2.29E-06	1426	0.70 (0.6, 0.81)	0.004234
cg13197551	20	60709957	PSMA7	-20.92960816	4.989970084	2.74E-05	1830	0.81 (0.74, 0.89)	0.047529567	-34.7465	6.369028	4.88E-08	1428	0.71 (0.62, 0.8)	0.000261
cg07834490	21	37536817	DOPEY2	-3.882234284	0.907418255	1.88E-05	1823	0.96 (0.94, 0.98)	0.041863809	-6.73078	1.305238	2.51E-07	1423	0.93 (0.91, 0.96)	0.00083

[1] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)

[2] Genome build GRCh37/hg19

Table E13. Significant methylation[1] and cis-gene expression associations from the BIOS consortium[2], based on atopic asthma results

chromsome: position[3]	CpG	Genename	N	Zscore[4]	P.value[4]	FDR p	Direction	HGNC_Gene_Name
chr1: 151449494	cg06513960	ENSG00000232671	3075	-3.271	1.07E-03	4.09E-03	--+-	
chr1: 151449494	cg06513960	ENSG00000159377	3075	-3.122	1.80E-03	4.68E-03	----	PSMB4
chr1: 151449494	cg06513960	ENSG00000159352	3075	-3.225	1.26E-03	4.09E-03	----	PSMD4
chr1: 151449494	cg06513960	ENSG00000143442	3075	4.228	2.36E-05	1.53E-04	++++	POGZ
chr1: 151449494	cg06513960	ENSG00000143398	3075	2.514	1.19E-02	2.58E-02	-+++	PIP5K1A
chr1: 151449494	cg06513960	ENSG00000143376	3075	4.522	6.13E-06	7.97E-05	++++	SNX27
chr1: 167520305	cg17936236	ENSG00000143162	3075	-7.425	1.13E-13	9.05E-13	----	CREG1
chr1: 17751974	cg21932513	ENSG00000256049	3075	-7.096	1.28E-12	6.40E-12	----	PADI6
chr1: 177907297	cg17971251	ENSG00000242193	3075	-2.274	2.30E-02	4.59E-02	----	
chr1: 179016233	cg24108508	ENSG00000116199	3075	-3.593	3.27E-04	5.44E-04	----	FAM20B
chr1: 179016233	cg24108508	ENSG00000186283	3075	4.181	2.90E-05	7.26E-05	++++	TOR3A
chr1: 179016233	cg24108508	ENSG00000143322	3075	7.156	8.31E-13	4.16E-12	++++	ABL2
chr1: 2036283	cg16599817	ENSG00000116151	3075	3.307	9.44E-04	9.44E-03	++++	MORN1
chr1: 2036283	cg16599817	ENSG00000067606	3075	-2.745	6.05E-03	3.02E-02	----	PRKCZ
chr1: 2036398	cg06315149	ENSG00000078369	3075	2.591	9.57E-03	4.79E-02	-+++	GNB1
chr1: 2036398	cg06315149	ENSG00000067606	3075	-3.843	1.22E-04	1.22E-03	----	PRKCZ
chr1: 223899685	cg08439122	ENSG00000162909	3075	-8.732	2.50E-18	7.50E-18	----	CAPN2
chr1: 24172120	cg20317437	ENSG00000197880	3075	7.982	1.44E-15	1.88E-14	++++	MDS2
chr1: 24172120	cg20317437	ENSG00000188822	3075	-6.755	1.43E-11	9.27E-11	----	CNR2
chr1: 26517586	cg02171825	ENSG00000176083	3075	-6.104	1.04E-09	5.18E-09	----	ZNF683
chr1: 26517586	cg02171825	ENSG00000158006	3075	-7.881	3.24E-15	3.24E-14	----	PAFAH2
chr1: 26517586	cg02171825	ENSG00000142675	3075	4.385	1.16E-05	2.90E-05	++++	CNKSR1
chr1: 26517586	cg02171825	ENSG00000142669	3075	-3.911	9.19E-05	1.84E-04	-+--	SH3BGRL3
chr1: 26517586	cg02171825	ENSG00000175087	3075	2.596	9.42E-03	1.35E-02	+-++	PDIK1L
chr1: 26517586	cg02171825	ENSG00000169442	3075	-3.517	4.36E-04	7.26E-04	----	CD52
chr1: 26517586	cg02171825	ENSG00000130695	3075	-4.962	6.99E-07	2.33E-06	----	CEP85
chr1: 27240694	cg01942646	ENSG00000158246	3075	-10.333	4.99E-25	6.49E-24	----	FAM46B
chr1: 27240694	cg01942646	ENSG00000204160	3075	3.675	2.38E-04	1.55E-03	++++	ZDHHC18
chr1: 29523841	cg16263722	ENSG00000060656	3075	-3.852	1.17E-04	5.85E-04	----	PTPRU
chr1: 32761824	cg14975122	ENSG00000160058	3075	-5.823	5.78E-09	1.16E-07	-+--	BSDC1
chr1: 32761824	cg14975122	ENSG00000175130	3075	-3.732	1.90E-04	1.90E-03	-+--	MARCKSL1
chr1: 33473905	cg11202380	ENSG00000239670	2182	-3.024	2.49E-03	9.97E-03	---?	
chr1: 33473905	cg11202380	ENSG00000267885	3075	-4.205	2.62E-05	3.14E-04	----	
chr1: 33473905	cg11202380	ENSG00000004455	3075	-3.273	1.07E-03	6.39E-03	----	AK2
chr1: 3807168	cg16349667	ENSG00000227372	3075	7.313	2.62E-13	1.31E-12	++++	TP73-AS1
chr1: 3807168	cg16349667	ENSG00000198912	3075	-14.371	7.84E-47	7.84E-46	----	C1orf174
chr1: 3807168	cg16349667	ENSG00000169598	3075	-3.804	1.42E-04	2.84E-04	----	DFFB
chr1: 3807168	cg16349667	ENSG00000116213	3075	-2.264	2.36E-02	3.36E-02	----	WRAP73
chr1: 3807168	cg16349667	ENSG00000236423	3075	-3.189	1.43E-03	2.38E-03	+---	LINC01134
chr1: 3807168	cg16349667	ENSG00000116198	3075	-6.634	3.27E-11	1.09E-10	----	CEP104
chr1: 3807168	cg16349667	ENSG00000235169	3075	4.974	6.56E-07	1.64E-06	++++	SMIM1
chr1: 43290834	cg11987455	ENSG00000171960	3075	-3.97	7.20E-05	8.64E-04	----	PPIH
chr1: 47157809	cg06824199	ENSG00000269956	3075	3.191	1.42E-03	4.96E-03	++++	MKNK1-AS1
chr1: 47157809	cg06824199	ENSG00000079277	3075	5.406	6.44E-08	4.51E-07	++++	MKNK1
chr1: 61607055	cg26252077	ENSG00000162599	3075	-2.501	1.24E-02	1.24E-02	----	NFIA
chr1: 62209607	cg10704177	ENSG00000132849	3075	-5.302	1.15E-07	2.29E-07	----	INADL
chr1: 62209607	cg10704177	ENSG00000162604	3075	-3.667	2.45E-04	2.45E-04	--+-	TM2D1
chr1: 6341230	cg21220721	ENSG00000215788	3075	-2.247	2.46E-02	4.32E-02	--+-	TNFRSF25
chr1: 6341230	cg21220721	ENSG00000158292	3075	-3.243	1.18E-03	4.34E-03	+---	GPR153
chr1: 6341230	cg21220721	ENSG00000116237	3075	-2.104	3.54E-02	4.87E-02	----	ICMT
chr1: 6341230	cg21220721	ENSG00000097021	3075	-3.481	4.99E-04	2.75E-03	----	ACOT7
chr1: 6341230	cg21220721	ENSG00000162408	3075	-3.96	7.50E-05	8.24E-04	--+-	NOL9

chr1: 6341230	cg21220721	ENSG00000116254	3075	-2.511	1.21E-02	2.65E-02	-+--	CHD5
chr1: 6341230	cg21220721	ENSG00000187017	3075	-2.84	4.51E-03	1.24E-02	----	ESPN
chr1: 6341230	cg21220721	ENSG00000158286	3075	-2.205	2.75E-02	4.32E-02	---+	RNF207
chr1: 6341327	cg11699125	ENSG00000158292	3075	-4	6.34E-05	3.49E-04	----	GPR153
chr1: 6341327	cg11699125	ENSG00000116237	3075	-2.312	2.08E-02	3.26E-02	----	ICMT
chr1: 6341327	cg11699125	ENSG00000097021	3075	-4.244	2.19E-05	2.41E-04	----	ACOT7
chr1: 6341327	cg11699125	ENSG00000162408	3075	-3.417	6.34E-04	2.32E-03	--+-	NOL9
chr1: 6341327	cg11699125	ENSG00000116254	3075	-3.159	1.58E-03	4.35E-03	----	CHD5
chr1: 6341327	cg11699125	ENSG00000187017	3075	-2.542	1.10E-02	2.42E-02	-+--	ESPN
chr1: 6341327	cg11699125	ENSG00000158286	3075	-2.351	1.87E-02	3.26E-02	----	RNF207
chr1: 66777579	cg24058805	ENSG00000184588	3075	3.544	3.94E-04	7.88E-04	++++	PDE4B
chr1: 872235	cg00582671	ENSG00000228794	3075	5.789	7.08E-09	1.32E-07	++++	LINC01128
chr1: 872235	cg00582671	ENSG00000187583	3075	-2.465	1.37E-02	4.01E-02	---+	PLEKHN1
chr1: 872235	cg00582671	ENSG00000187961	3075	-3.003	2.67E-03	1.27E-02	+---	KLHL17
chr1: 872235	cg00582671	ENSG00000223823	3075	2.438	1.48E-02	4.01E-02	-++-	
chr1: 872235	cg00582671	ENSG00000188290	3075	-5.674	1.39E-08	1.32E-07	----	HES4
chr1: 872235	cg00582671	ENSG00000187642	3075	-2.382	1.72E-02	4.09E-02	----	C1orf170
chr1: 872235	cg00582671	ENSG00000240618	3075	3.615	3.01E-04	1.91E-03	++-+	
chr1: 872235	cg00582671	ENSG00000224956	3075	-2.456	1.41E-02	4.01E-02	----	
chr1: 91992292	cg11799283	ENSG00000069702	3075	-3.345	8.24E-04	1.65E-03	----	TGFBR3
chr1: 9599067	cg18783781	ENSG00000171621	3075	-3.437	5.88E-04	2.65E-03	----	SPSB1
chr1: 9599067	cg18783781	ENSG00000171603	3075	-2.885	3.91E-03	1.17E-02	-+--	CLSTN1
chr1: 9599067	cg18783781	ENSG00000171608	3075	3.582	3.41E-04	2.65E-03	-+++	PIK3CD
chr2: 120937418	cg23196129	ENSG00000088179	3075	3.192	1.42E-03	9.79E-03	+-++	PTPN4
chr2: 120937418	cg23196129	ENSG00000144118	3075	3.03	2.45E-03	9.79E-03	++++	RALB
chr2: 161798364	cg02494549	ENSG00000136560	3075	3.128	1.76E-03	1.76E-03	++++	TANK
chr2: 191300784	cg15998761	ENSG00000151689	3075	-9.607	7.49E-22	4.50E-21	----	INPP1
chr2: 219254588	cg00634542	ENSG00000144579	3075	-3.324	8.88E-04	2.84E-03	----	CTDSP1
chr2: 219254588	cg00634542	ENSG00000135926	3075	-3.817	1.35E-04	7.22E-04	-+--	TMBIM1
chr2: 219254588	cg00634542	ENSG00000179921	3075	-4.34	1.43E-05	1.14E-04	----	GPBAR1
chr2: 219254588	cg00634542	ENSG00000018280	3075	-3.435	5.93E-04	2.37E-03	----	SLC11A1
chr2: 219254588	cg00634542	ENSG00000127831	3075	-2.849	4.38E-03	1.17E-02	----	VIL1
chr2: 219254588	cg00634542	ENSG00000163464	3075	-4.526	6.00E-06	9.60E-05	----	CXCR1
chr2: 231661317	cg09458420	ENSG00000238062	3075	-3.634	2.79E-04	6.52E-04	----	SPATA3-AS1
chr2: 231661317	cg09458420	ENSG00000135898	3075	-4.938	7.89E-07	2.76E-06	----	GPR55
chr2: 231661317	cg09458420	ENSG00000135916	3075	-7.085	1.39E-12	9.71E-12	----	ITM2C
chr2: 231661317	cg09458420	ENSG00000135932	3075	3.11	1.87E-03	3.28E-03	+-++	CAB39
chr2: 28550531	cg17862837	ENSG00000158019	3075	-3.43	6.04E-04	3.02E-03	-+--	BRE
chr2: 47242277	cg06528816	ENSG00000068724	3075	-3.472	5.16E-04	4.13E-03	----	TTC7A
chr2: 48806774	cg27016609	ENSG00000243244	3075	7.285	3.23E-13	9.69E-13	++++	STON1
chr2: 69831408	cg22059413	ENSG00000198380	3075	2.739	6.16E-03	2.03E-02	++++	GFPT1
chr2: 69831408	cg22059413	ENSG00000169599	3075	2.709	6.75E-03	2.03E-02	++++	NFU1
chr2: 74375903	cg26529864	ENSG00000188687	3075	2.413	1.58E-02	4.11E-02	++++	SLC4A5
chr2: 74375903	cg26529864	ENSG00000225439	3075	-4.435	9.20E-06	5.98E-05	----	BOLA3-AS1
chr2: 74375903	cg26529864	ENSG00000163170	3075	-2.927	3.42E-03	1.11E-02	--+-	BOLA3
chr2: 74375903	cg26529864	ENSG00000187605	3075	4.058	4.96E-05	2.15E-04	++++	TET3
chr2: 74375903	cg26529864	ENSG00000114956	3075	-4.615	3.94E-06	5.12E-05	----	DGUOK
chr2: 74612222	cg17988187	ENSG00000188687	3075	2.708	6.77E-03	4.38E-02	++++	SLC4A5
chr2: 74612222	cg17988187	ENSG00000115289	3075	-3.18	1.47E-03	1.84E-02	----	PCGF1
chr2: 74612222	cg17988187	ENSG00000225439	3075	-3.745	1.80E-04	4.51E-03	----	BOLA3-AS1
chr2: 74612222	cg17988187	ENSG00000115274	3075	-2.696	7.02E-03	4.38E-02	----	INO80B
chr2: 74612706	cg13774539	ENSG00000225439	3075	-3.864	1.11E-04	2.67E-03	-+--	BOLA3-AS1
chr2: 75089669	cg12077754	ENSG00000159399	3075	-4.919	8.70E-07	3.48E-06	----	HK2
chr2: 99124870	cg18455616	ENSG00000183513	3075	6.195	5.84E-10	2.33E-09	++++	COA5
chr2: 99124870	cg18455616	ENSG00000071073	3075	3.296	9.80E-04	1.31E-03	++++	MGAT4A
chr2: 99124870	cg18455616	ENSG00000115446	3075	-4.634	3.58E-06	7.16E-06	----	UNC50
chr3: 12269362	cg04399631	ENSG00000132170	3075	-3.56	3.70E-04	1.11E-03	----	PPARG
chr3: 128134845	cg03278639	ENSG00000244300	2182	-3.581	3.42E-04	6.83E-04	---?	

chr3: 128134845	cg03278639	ENSG00000179348	3075	-7.317	2.54E-13	1.02E-12	----	GATA2
chr3: 12918528	cg25224369	ENSG00000144712	3075	2.736	6.22E-03	1.56E-02	+-++	CAND2
chr3: 12918528	cg25224369	ENSG00000132155	3075	3.874	1.07E-04	5.37E-04	++-+	RAF1
chr3: 171091657	cg08698681	ENSG00000154310	3075	-3.87	1.09E-04	3.26E-04	----	TNIK
chr3: 195965369	cg22221575	ENSG00000163959	3075	3.173	1.51E-03	1.66E-02	++++	SLC51A
chr3: 195974258	cg07641926	ENSG00000163958	3075	-4.049	5.14E-05	5.14E-04	----	ZDHHC19
chr3: 195974300	cg02803925	ENSG00000163958	3075	-3.889	1.01E-04	1.01E-03	----	ZDHHC19
chr3: 3152374	cg01310029	ENSG00000091181	3075	-16.716	1.01E-62	3.03E-62	----	IL5RA
chr3: 3152374	cg01310029	ENSG00000072756	3075	-4.235	2.28E-05	3.42E-05	----	TRNT1
chr3: 3152374	cg01310029	ENSG00000113851	3075	-3.295	9.85E-04	9.85E-04	----	CRBN
chr3: 3152530	cg10159529	ENSG00000091181	3075	-23.08	7.34E-118	2.20E-117	----	IL5RA
chr3: 33837694	cg00381391	ENSG00000170248	3075	-3.358	7.85E-04	1.57E-03	----	PDCD6IP
chr3: 42923116	cg13531735	ENSG00000144648	3075	-3.668	2.45E-04	2.69E-03	----	ACKR2
chr3: 42923116	cg13531735	ENSG00000230084	3075	2.63	8.53E-03	3.13E-02	++++	
chr3: 42923116	cg13531735	ENSG00000144649	2182	-2.652	8.01E-03	3.13E-02	---?	FAM198A
chr3: 44381576	cg04385523	ENSG00000144792	3075	-2.968	2.99E-03	2.39E-02	----	ZNF660
chr3: 66428294	cg04217850	ENSG00000144749	3075	-3.986	6.72E-05	1.34E-04	----	LRIG1
chr3: 71295684	cg06391412	ENSG00000114861	3075	-3.103	1.92E-03	1.92E-03	----	FOXP1
chr4: 148635716	cg00006459	ENSG00000071205	3075	-5.957	2.57E-09	7.71E-09	----	ARHGAP10
chr4: 148733880	cg20866785	ENSG00000071205	3075	-4.236	2.27E-05	6.82E-05	----	ARHGAP10
chr4: 154269418	cg12614529	ENSG00000109654	3075	-2.332	1.97E-02	1.97E-02	---+	TRIM2
chr4: 154269418	cg12614529	ENSG00000121210	3075	2.619	8.83E-03	1.77E-02	-+++	KIAA0922
chr4: 1577971	cg19901381	ENSG00000168924	3075	-3.01	2.62E-03	1.31E-02	----	LETM1
chr4: 1577971	cg19901381	ENSG00000218422	3075	3.954	7.68E-05	7.68E-04	++++	
chr4: 1578163	cg05470179	ENSG00000218422	3075	2.927	3.42E-03	3.42E-02	++++	
chr5: 10708717	cg16362140	ENSG00000251196	3075	-2.939	3.29E-03	2.63E-02	----	
chr5: 112541553	cg09565310	ENSG00000171444	3075	3.097	1.95E-03	3.91E-03	++++	MCC
chr5: 112541553	cg09565310	ENSG00000172795	3075	2.011	4.43E-02	4.43E-02	+-++	DCP2
chr5: 132008525	cg26787239	ENSG00000197536	3075	-3.24	1.20E-03	9.58E-03	----	C5orf56
chr5: 132008525	cg26787239	ENSG00000113520	3075	-5.071	3.97E-07	6.35E-06	----	IL4
chr5: 132009352	cg25368824	ENSG00000164402	3075	-3.526	4.22E-04	6.20E-03	---+	SEPT8
chr5: 132009352	cg25368824	ENSG00000113520	3075	-2.612	9.01E-03	4.81E-02	----	IL4
chr5: 132009352	cg25368824	ENSG00000238160	3075	3.362	7.75E-04	6.20E-03	++++	
chr5: 132114623	cg07828169	ENSG00000164402	3075	3.045	2.33E-03	2.79E-02	++++	SEPT8
chr5: 150486801	cg23172995	ENSG00000197043	3075	-2.487	1.29E-02	3.14E-02	-+--	ANXA6
chr5: 150486801	cg23172995	ENSG00000145908	3075	2.472	1.34E-02	3.14E-02	+-++	ZNF300
chr5: 150486801	cg23172995	ENSG00000211445	3075	2.525	1.16E-02	3.14E-02	+++-	GPX3
chr5: 176774729	cg15344640	ENSG00000184840	3075	-2.848	4.39E-03	3.15E-02	--+-	TMED9
chr5: 176774729	cg15344640	ENSG00000131187	3075	-4.294	1.75E-05	3.33E-04	----	F12
chr5: 176774729	cg15344640	ENSG00000246334	3075	2.576	1.00E-02	4.75E-02	++++	PRR7-AS1
chr5: 176774729	cg15344640	ENSG00000183258	3075	-2.809	4.97E-03	3.15E-02	----	DDX41
chr6: 116781307	cg25488567	ENSG00000187189	3075	4.164	3.13E-05	3.75E-04	++++	TSPYL4
chr6: 116781307	cg25488567	ENSG00000196911	3075	2.556	1.06E-02	3.66E-02	++++	KPNA5
chr6: 116781307	cg25488567	ENSG00000240050	722	2.506	1.22E-02	3.66E-02	??+?	
chr6: 116781307	cg25488567	ENSG00000188820	3075	3.199	1.38E-03	8.27E-03	+++-	FAM26F
chr6: 167135251	cg03512256	ENSG00000071242	3075	-7.929	2.22E-15	1.11E-14	----	RPS6KA2
chr6: 167135251	cg03512256	ENSG00000026297	3075	-3.062	2.20E-03	5.49E-03	----	RNASET2
chr6: 167177613	cg20774312	ENSG00000227598	3075	5.391	7.01E-08	2.10E-07	++++	
chr6: 167177613	cg20774312	ENSG00000071242	3075	-5.689	1.28E-08	7.67E-08	----	RPS6KA2
chr6: 167177613	cg20774312	ENSG00000197146	3075	5.288	1.23E-07	2.47E-07	++++	
chr6: 167177613	cg20774312	ENSG00000026297	3075	2.616	8.90E-03	1.34E-02	++++	RNASET2
chr6: 167189272	cg03329755	ENSG00000071242	3075	-17.434	4.56E-68	2.74E-67	----	RPS6KA2
chr6: 167189272	cg03329755	ENSG00000197146	3075	-3.116	1.83E-03	3.66E-03	---+	
chr6: 167189272	cg03329755	ENSG00000026297	3075	-5.775	7.68E-09	2.30E-08	----	RNASET2
chr6: 24877462	cg12213680	ENSG00000217083	2182	4.242	2.22E-05	1.33E-04	+++?	
chr6: 24877462	cg12213680	ENSG00000260286	3075	2.401	1.63E-02	2.80E-02	-+++	C6orf229
chr6: 24877462	cg12213680	ENSG00000214975	3075	2.493	1.27E-02	2.53E-02	+++-	PPIAP29
chr6: 24877462	cg12213680	ENSG00000137261	3075	3.894	9.88E-05	2.96E-04	++++	KIAA0319

chr6: 24877462	cg12213680	ENSG00000112308	3075	3.423	6.19E-04	1.49E-03	++++	C6orf62
chr6: 24877462	cg12213680	ENSG00000111913	3075	3.967	7.27E-05	2.91E-04	-+++	FAM65B
chr6: 24877462	cg12213680	ENSG00000111802	3075	5.444	5.20E-08	6.24E-07	+-++	TDP2
chr6: 28843296	cg09191776	ENSG00000204713	3075	2.902	3.70E-03	7.40E-03	++++	TRIM27
chr6: 32141591	cg09597192	ENSG00000204314	3075	-2.719	6.54E-03	2.88E-02	----	PRRT1
chr6: 32141591	cg09597192	ENSG00000204308	3075	-3.92	8.85E-05	1.95E-03	----	RNF5
chr6: 32141591	cg09597192	ENSG00000221988	3075	-2.878	4.00E-03	2.20E-02	----	PPT2
chr6: 32141591	cg09597192	ENSG00000204344	3075	3.37	7.50E-04	8.25E-03	++++	STK19
chr6: 32141591	cg09597192	ENSG00000204304	3075	3.12	1.81E-03	1.33E-02	++++	PBX2
chr6: 42109176	cg24627621	ENSG00000124496	3075	-8.189	2.64E-16	2.64E-15	----	TRERF1
chr6: 42109176	cg24627621	ENSG00000112599	3075	3.256	1.13E-03	5.64E-03	++++	GUCA1B
chr6: 42363749	cg20840540	ENSG00000124496	3075	-6.111	9.92E-10	3.97E-09	----	TRERF1
chr6: 42363749	cg20840540	ENSG00000112599	3075	2.507	1.22E-02	2.44E-02	++++	GUCA1B
chr7: 127528039	cg09696385	ENSG00000197157	3075	-3.424	6.18E-04	1.22E-03	-++-	SND1
chr7: 127528039	cg09696385	ENSG00000128594	3075	3.234	1.22E-03	1.22E-03	-+++	LRRC4
chr7: 142659425	cg17784922	ENSG00000106123	3075	5.382	7.37E-08	1.33E-06	++++	EPHB6
chr7: 142659425	cg17784922	ENSG00000232869	3075	2.99	2.79E-03	1.67E-02	++++	TRBV29-1
chr7: 142659425	cg17784922	ENSG00000165125	3075	3.218	1.29E-03	1.16E-02	++++	TRPV6
chr7: 149543136	cg05184016	ENSG00000106479	3075	3.145	1.66E-03	5.81E-03	-+++	ZNF862
chr7: 149543136	cg05184016	ENSG00000171130	3075	-3.989	6.63E-05	4.64E-04	----	ATP6V0E2
chr7: 149543165	cg07970948	ENSG00000106479	3075	3.435	5.93E-04	1.38E-03	++-+	ZNF862
chr7: 149543165	cg07970948	ENSG00000171130	3075	-4.217	2.47E-05	1.73E-04	----	ATP6V0E2
chr7: 149543165	cg07970948	ENSG00000181444	3075	3.683	2.31E-04	8.08E-04	++++	ZNF467
chr7: 150646704	cg16107105	ENSG00000181652	3075	6.293	3.12E-10	2.96E-09	++++	ATG9B
chr7: 150646704	cg16107105	ENSG00000164867	3075	2.312	2.08E-02	4.23E-02	+-+-	NOS3
chr7: 150646704	cg16107105	ENSG00000213199	3075	3.14	1.69E-03	6.42E-03	+-++	ASIC3
chr7: 150646704	cg16107105	ENSG00000177590	3075	2.561	1.04E-02	2.84E-02	++++	
chr7: 150646704	cg16107105	ENSG00000213203	3075	3.409	6.52E-04	4.13E-03	++++	GIMAP1
chr7: 150646704	cg16107105	ENSG00000196329	3075	2.286	2.23E-02	4.23E-02	+++-	GIMAP5
chr7: 150646704	cg16107105	ENSG00000002726	3075	-6.892	5.50E-12	1.05E-10	----	AOC1
chr7: 150646704	cg16107105	ENSG00000164897	3075	-3.171	1.52E-03	6.42E-03	----	TMUB1
chr7: 150646704	cg16107105	ENSG00000164885	3075	-2.827	4.70E-03	1.49E-02	--+-	CDK5
chr7: 150646704	cg16107105	ENSG00000133612	3075	-2.31	2.09E-02	4.23E-02	--+-	AGAP3
chr7: 150649807	cg24491618	ENSG00000181652	3075	10.565	4.34E-26	8.24E-25	++++	ATG9B
chr7: 150649807	cg24491618	ENSG00000164867	3075	6.58	4.72E-11	4.48E-10	++++	NOS3
chr7: 150649807	cg24491618	ENSG00000213199	3075	4.93	8.20E-07	3.12E-06	++++	ASIC3
chr7: 150649807	cg24491618	ENSG00000177590	3075	5.02	5.16E-07	2.45E-06	++++	
chr7: 150649807	cg24491618	ENSG00000213203	3075	2.985	2.83E-03	8.97E-03	++++	GIMAP1
chr7: 150649807	cg24491618	ENSG00000196329	3075	2.833	4.61E-03	1.25E-02	++++	GIMAP5
chr7: 150649807	cg24491618	ENSG00000002726	3075	-6.044	1.50E-09	9.49E-09	-+--	AOC1
chr7: 150651937	cg18666454	ENSG00000181652	3075	6.678	2.42E-11	2.30E-10	++++	ATG9B
chr7: 150651937	cg18666454	ENSG00000164867	3075	5.265	1.40E-07	8.86E-07	++++	NOS3
chr7: 150651937	cg18666454	ENSG00000213199	3075	2.804	5.05E-03	1.20E-02	++++	ASIC3
chr7: 150651937	cg18666454	ENSG00000177590	3075	4.221	2.43E-05	1.15E-04	++++	
chr7: 150651937	cg18666454	ENSG00000002726	3075	-9.568	1.09E-21	2.08E-20	----	AOC1
chr7: 150651937	cg18666454	ENSG00000164897	3075	-3.432	5.99E-04	2.28E-03	-+--	TMUB1
chr7: 150651937	cg18666454	ENSG00000164885	3075	-3.12	1.81E-03	5.72E-03	-+--	CDK5
chr7: 150651937	cg18666454	ENSG00000133612	3075	-2.948	3.20E-03	8.69E-03	-+--	AGAP3
chr7: 1577697	cg23871276	ENSG00000164855	2182	-3.524	4.25E-04	2.97E-03	---?	TMEM184A
chr7: 1914073	cg18650626	ENSG00000002822	3075	-4.326	1.52E-05	1.52E-05	----	MAD1L1
chr7: 24965657	cg25270424	ENSG00000105926	3075	2.66	7.81E-03	3.91E-02	++++	MPP6
chr7: 50861834	cg13459606	ENSG00000106078	3075	-2.128	3.34E-02	3.34E-02	+--+	COBL
chr7: 50861834	cg13459606	ENSG00000106070	3075	-3.994	6.50E-05	1.30E-04	----	GRB10
chr7: 65439512	cg04290133	ENSG00000169919	3075	-5.2	1.99E-07	1.39E-06	----	GUSB
chr7: 65439512	cg04290133	ENSG00000126522	3075	-5.025	5.03E-07	1.76E-06	----	ASL
chr7: 97908505	cg02985445	ENSG00000205356	3075	7.133	9.83E-13	5.90E-12	++++	TECPR1
chr7: 97908505	cg02985445	ENSG00000180535	3075	-2.671	7.55E-03	2.04E-02	----	BHLHA15
chr7: 97908505	cg02985445	ENSG00000164713	3075	2.569	1.02E-02	2.04E-02	++--	BRI3

chr7: 98722470	cg14769121	ENSG00000198742	3075	-3.085	2.03E-03	1.02E-02	---+	SMURF1
chr8: 105599835	cg10815420	ENSG00000147650	3075	-6.018	1.76E-09	1.76E-09	----	LRP12
chr8: 128972681	cg05480350	ENSG00000136997	3075	-8.167	3.15E-16	4.72E-16	----	MYC
chr8: 128972681	cg05480350	ENSG00000249859	3075	-11.672	1.77E-31	5.31E-31	----	PVT1
chr8: 128972681	cg05480350	ENSG00000207110	3075	-5.845	5.06E-09	5.06E-09	----	RNU1-106P
chr8: 141046469	cg09377531	ENSG00000167632	3075	-3.156	1.60E-03	1.60E-03	-+--	TRAPPC9
chr8: 145643626	cg20259557	ENSG00000160948	3075	-7.311	2.65E-13	6.10E-12	----	VPS28
chr8: 145643626	cg20259557	ENSG00000071894	3075	4.187	2.82E-05	3.24E-04	++++	CPSF1
chr8: 26243601	cg22816343	ENSG00000221914	3075	2.536	1.12E-02	2.80E-02	+-++	PPP2R2A
chr8: 26243601	cg22816343	ENSG00000104765	3075	4.26	2.05E-05	1.02E-04	++++	BNIP3L
chr8: 33421410	cg23205629	ENSG00000198042	3075	-3.77	1.63E-04	3.26E-04	----	MAK16
chr8: 33421410	cg23205629	ENSG00000172728	3075	-21.984	4.11E-107	1.64E-106	----	FUT10
chr8: 33421410	cg23205629	ENSG00000133874	3075	-2.895	3.79E-03	5.06E-03	----	RNF122
chr8: 6360436	cg12074090	ENSG00000147316	3075	-3.936	8.27E-05	2.07E-04	----	MCPH1
chr8: 6360436	cg12074090	ENSG00000246089	3075	-4.746	2.08E-06	1.04E-05	----	
chr8: 6360436	cg12074090	ENSG00000249898	3075	-2.672	7.54E-03	1.26E-02	----	
chr8: 8702053	cg12077460	ENSG00000233609	3075	-2.915	3.56E-03	3.56E-03	---+	
chr8: 8702053	cg12077460	ENSG00000147324	3075	-8.884	6.46E-19	1.94E-18	----	MFHAS1
chr8: 8702053	cg12077460	ENSG00000104626	3075	-3.146	1.65E-03	2.48E-03	----	ERI1
chr9: 113530240	cg14226212	ENSG00000198121	3075	-3.314	9.20E-04	9.20E-04	----	LPAR1
chr9: 130158144	cg00114012	ENSG00000197958	3075	3.451	5.59E-04	1.86E-03	++++	RPL12
chr9: 130158144	cg00114012	ENSG00000148356	3075	-3.472	5.16E-04	1.86E-03	-+--	LRSAM1
chr9: 130158144	cg00114012	ENSG00000196152	3075	-5.016	5.26E-07	5.26E-06	----	ZNF79
chr9: 130222969	cg14012059	ENSG00000136856	3075	-6.361	2.01E-10	2.21E-09	----	SLC2A8
chr9: 130222969	cg14012059	ENSG00000197958	3075	4.615	3.93E-06	2.16E-05	+++-	RPL12
chr9: 130222969	cg14012059	ENSG00000148356	3075	-4.221	2.43E-05	8.91E-05	----	LRSAM1
chr9: 130608923	cg13458609	ENSG00000160404	3075	-4.044	5.26E-05	9.98E-04	----	TOR2A
chr9: 130608923	cg13458609	ENSG00000136877	3075	-3.493	4.78E-04	4.54E-03	----	FPGS
chr9: 130859454	cg13835688	ENSG00000232850	2182	3.859	1.14E-04	2.96E-03	+++?	
chr9: 132600788	cg13953978	ENSG00000136878	3075	-7.351	1.97E-13	1.08E-12	----	USP20
chr9: 132600788	cg13953978	ENSG00000136816	3075	-4.622	3.81E-06	1.40E-05	----	TOR1B
chr9: 132600788	cg13953978	ENSG00000148358	3075	2.721	6.50E-03	1.43E-02	++++	GPR107
chr9: 132600788	cg13953978	ENSG00000136827	3075	-4.227	2.37E-05	6.51E-05	----	TOR1A
chr9: 132600788	cg13953978	ENSG00000136819	3075	-11.027	2.83E-28	3.11E-27	----	C9orf78
chr9: 134883788	cg13628444	ENSG00000160563	3075	-4.914	8.92E-07	1.78E-06	----	MED27
chr9: 138362321	cg13850063	ENSG00000196422	3075	-13.427	4.21E-41	2.11E-40	----	PPP1R26
chr9: 138362327	cg14011077	ENSG00000196422	3075	-17.05	3.47E-65	1.73E-64	----	PPP1R26
chr9: 138362327	cg14011077	ENSG00000122140	3075	-2.904	3.69E-03	9.21E-03	--+-	MRPS2
chr9: 138701748	cg13423371	ENSG00000107147	3075	-2.945	3.23E-03	1.61E-02	---+	KCNT1
chr9: 140273055	cg11619782	ENSG00000198113	3075	-3.922	8.80E-05	2.20E-03	----	TOR4A
chr9: 140308660	cg13562011	ENSG00000188986	3075	-3.247	1.17E-03	7.29E-03	----	NELFB
chr9: 140308660	cg13562011	ENSG00000165724	3075	-2.667	7.65E-03	3.82E-02	+-+-	ZMYND19
chr9: 140308660	cg13562011	ENSG00000197070	3075	-3.638	2.75E-04	2.29E-03	--+-	ARRDC1
chr9: 140308660	cg13562011	ENSG00000187713	3075	-3.952	7.74E-05	1.94E-03	+---	TMEM203
chr9: 140308660	cg13562011	ENSG00000198113	3075	-3.781	1.56E-04	1.95E-03	----	TOR4A
chr9: 91994786	cg03492094	ENSG00000225460	3075	-3.141	1.68E-03	5.62E-03	---+	
chr9: 91994786	cg03492094	ENSG00000130222	3075	-3.11	1.87E-03	5.62E-03	----	GADD45G
chr9: 97403129	cg13576859	ENSG00000165140	3075	-9.453	3.31E-21	9.92E-21	----	FBP1
chr10: 103923333	cg23516680	ENSG00000166189	3075	-3.782	1.55E-04	1.55E-03	----	HPS6
chr10: 135061670	cg12227660	ENSG00000151651	3075	-6.582	4.63E-11	7.40E-10	----	ADAM8
chr10: 135061670	cg12227660	ENSG00000235245	3075	3.296	9.81E-04	5.23E-03	++-+	
chr10: 135061670	cg12227660	ENSG00000127884	3075	-2.89	3.85E-03	1.23E-02	--+-	ECHS1
chr10: 135061670	cg12227660	ENSG00000198546	3075	-3.714	2.04E-04	1.63E-03	+---	ZNF511
chr10: 135061670	cg12227660	ENSG00000151650	3075	-3.141	1.69E-03	6.74E-03	----	VENTX
chr10: 45495435	cg01614759	ENSG00000165511	3075	-3.369	7.53E-04	3.01E-03	+---	C10orf25
chr10: 5576480	cg03651219	ENSG00000173848	3075	3.968	7.26E-05	3.63E-04	+-++	NET1
chr10: 5576480	cg03651219	ENSG00000215267	2182	-3.44	5.81E-04	1.45E-03	---?	AKR1C7P
chr10: 5576480	cg03651219	ENSG00000108021	3075	2.629	8.57E-03	1.43E-02	--++	FAM208B

chr10: 73906532	cg23468453	ENSG00000166295	3075	3.044	2.34E-03	1.64E-02	+-++	ANAPC16
chr10: 98425110	cg16508714	ENSG00000236552	3075	3.07	2.14E-03	8.58E-03	++++	RPL13AP5
chr11: 111570978	cg24368962	ENSG00000137720	3075	2.994	2.75E-03	1.10E-02	++++	C11orf1
chr11: 111570978	cg24368962	ENSG00000150764	3075	-5.272	1.35E-07	1.08E-06	----	DIXDC1
chr11: 118083942	cg14190451	ENSG00000110324	3075	-3.291	9.99E-04	6.50E-03	----	IL10RA
chr11: 118083942	cg14190451	ENSG00000160593	3075	-3.462	5.35E-04	6.50E-03	----	AMICA1
chr11: 12136405	cg23044178	ENSG00000170242	3075	2.942	3.26E-03	1.30E-02	++++	USP47
chr11: 123616411	cg06633463	ENSG00000023171	3075	-2.164	3.05E-02	3.05E-02	----	GRAMD1B
chr11: 123616411	cg06633463	ENSG00000166261	3075	2.961	3.06E-03	6.13E-03	++++	ZNF202
chr11: 368638	cg26461944	ENSG00000023191	3075	-3.632	2.81E-04	9.83E-03	----	RNH1
chr11: 47092992	cg01258949	ENSG00000134575	3075	-2.934	3.34E-03	3.01E-02	----	ACP2
chr11: 57156050	cg15700636	ENSG00000134802	3075	-2.951	3.17E-03	2.85E-02	--+-	SLC43A3
chr11: 57157632	cg12819873	ENSG00000149136	3075	-3.031	2.44E-03	2.20E-02	-+--	SSRP1
chr11: 60623918	cg25087851	ENSG00000110108	3075	-5.489	4.04E-08	2.02E-07	----	TMEM109
chr11: 60623918	cg25087851	ENSG00000183134	3075	-20.307	1.12E-91	1.12E-90	----	PTGDR2
chr11: 6225537	cg00286717	ENSG00000051009	3075	-2.963	3.04E-03	2.74E-02	----	FAM160A2
chr11: 62678778	cg03448301	ENSG00000162194	3075	-2.642	8.23E-03	3.79E-02	+---	C11orf48
chr11: 62678778	cg03448301	ENSG00000185475	3075	-2.783	5.38E-03	3.09E-02	----	TMEM179B
chr11: 62678778	cg03448301	ENSG00000168002	3075	-3.073	2.12E-03	1.63E-02	+---	POLR2G
chr11: 62678778	cg03448301	ENSG00000214753	3075	-4.375	1.21E-05	2.79E-04	----	HNRNPUL2
chr11: 62678778	cg03448301	ENSG00000185670	3075	-3.587	3.35E-04	3.85E-03	----	ZBTB3
chr11: 63466987	cg07636225	ENSG00000168004	3075	-15.592	8.20E-55	1.07E-53	----	HRASLS5
chr11: 63466987	cg07636225	ENSG00000133317	3075	-12.587	2.49E-36	1.62E-35	----	LGALS12
chr11: 63466987	cg07636225	ENSG00000256280	3075	-2.926	3.43E-03	1.49E-02	----	
chr11: 64216380	cg03074692	ENSG00000173511	3075	3.623	2.92E-04	1.53E-03	++++	VEGFB
chr11: 64216380	cg03074692	ENSG00000162302	3075	-3.368	7.57E-04	3.18E-03	----	RPS6KA4
chr11: 64216380	cg03074692	ENSG00000231680	3075	-10.293	7.62E-25	1.60E-23	----	
chr11: 64216380	cg03074692	ENSG00000236935	3075	5.199	2.01E-07	1.40E-06	++++	
chr11: 64216380	cg03074692	ENSG00000181908	3075	-5.624	1.86E-08	1.96E-07	----	
chr11: 65482056	cg10093679	ENSG00000172732	3075	-3.143	1.67E-03	1.04E-02	----	MUS81
chr11: 65482056	cg10093679	ENSG00000251562	3075	3.822	1.32E-04	2.05E-03	++++	MALAT1
chr11: 65482056	cg10093679	ENSG00000175550	3075	-3.012	2.60E-03	1.15E-02	--+-	DRAP1
chr11: 65482056	cg10093679	ENSG00000172500	3075	-3.199	1.38E-03	1.04E-02	----	FIBP
chr11: 65482056	cg10093679	ENSG00000173465	3075	-2.772	5.58E-03	1.94E-02	----	SSSCA1
chr11: 65482056	cg10093679	ENSG00000255557	3075	2.692	7.11E-03	1.94E-02	++++	
chr11: 65482056	cg10093679	ENSG00000173727	3075	2.674	7.49E-03	1.94E-02	++++	
chr11: 65482056	cg10093679	ENSG00000172638	3075	-2.675	7.47E-03	1.94E-02	----	EFEMP2
chr11: 65482056	cg10093679	ENSG00000176973	3075	-3.049	2.30E-03	1.15E-02	+---	FAM89B
chr11: 65482056	cg10093679	ENSG00000175602	3075	-2.673	7.52E-03	1.94E-02	----	CCDC85B
chr11: 65482056	cg10093679	ENSG00000175573	3075	-3.713	2.05E-04	2.11E-03	----	C11orf68
chr11: 65482056	cg10093679	ENSG00000254470	3075	3.943	8.04E-05	2.05E-03	++++	AP5B1
chr11: 65546210	cg05300717	ENSG00000172757	3075	-3.989	6.64E-05	2.66E-04	--+-	CFL1
chr11: 65546210	cg05300717	ENSG00000260233	3075	3.345	8.23E-04	1.65E-03	++++	SSSCA1-AS1
chr11: 65546210	cg05300717	ENSG00000172732	3075	-4.927	8.34E-07	5.34E-06	----	MUS81
chr11: 65546210	cg05300717	ENSG00000175550	3075	-5.138	2.78E-07	2.97E-06	--+-	DRAP1
chr11: 65546210	cg05300717	ENSG00000172500	3075	-5.217	1.82E-07	2.91E-06	----	FIBP
chr11: 65546210	cg05300717	ENSG00000175376	3075	-3.745	1.81E-04	4.82E-04	----	EIF1AD
chr11: 65546210	cg05300717	ENSG00000175294	3075	-3.864	1.12E-04	3.57E-04	----	CATSPER1
chr11: 65546210	cg05300717	ENSG00000173465	3075	-3.92	8.84E-05	3.14E-04	--+-	SSSCA1
chr11: 65546210	cg05300717	ENSG00000172638	3075	-3.54	4.01E-04	9.15E-04	----	EFEMP2
chr11: 65546210	cg05300717	ENSG00000173338	3075	-3.35	8.08E-04	1.65E-03	--+-	KCNK7
chr11: 65546210	cg05300717	ENSG00000175467	3075	-3.604	3.14E-04	7.72E-04	-++-	SART1
chr11: 65546210	cg05300717	ENSG00000142186	3075	-2.531	1.14E-02	2.02E-02	----	SCYL1
chr11: 65546210	cg05300717	ENSG00000176973	3075	-4.875	1.09E-06	5.79E-06	--+-	FAM89B
chr11: 65546210	cg05300717	ENSG00000175602	3075	-2.772	5.57E-03	1.05E-02	--+-	CCDC85B
chr11: 65546210	cg05300717	ENSG00000175573	3075	-4.81	1.51E-06	6.91E-06	--+-	C11orf68
chr11: 65546210	cg05300717	ENSG00000175334	3075	-4.941	7.77E-07	5.34E-06	--+-	BANF1
chr11: 65546210	cg05300717	ENSG00000172977	3075	-3.78	1.57E-04	4.57E-04	----	KAT5

chr11: 65546210	cg05300717	ENSG00000172922	3075	-2.475	1.33E-02	2.24E-02	--+-	RNASEH2C
chr11: 65546210	cg05300717	ENSG00000254470	3075	7.17	7.48E-13	2.39E-11	++++	AP5B1
chr11: 65547049	cg05257275	ENSG00000172803	3075	-4.648	3.34E-06	1.07E-04	----	SNX32
chr11: 65547172	cg03695871	ENSG00000172803	3075	-4.852	1.22E-06	3.90E-05	----	SNX32
chr11: 65547172	cg03695871	ENSG00000173338	3075	-4.277	1.89E-05	3.03E-04	--+-	KCNK7
chr11: 65547172	cg03695871	ENSG00000173327	3075	-3.438	5.87E-04	6.26E-03	----	MAP3K11
chr11: 840407	cg13806461	ENSG00000177697	3075	3.27	1.07E-03	1.45E-02	++++	CD151
chr11: 840407	cg13806461	ENSG00000214063	3075	-6.116	9.58E-10	2.59E-08	----	TSPAN4
chr12: 121861616	cg19998289	ENSG00000256742	3075	2.21	2.71E-02	4.52E-02	++++	
chr12: 121861616	cg19998289	ENSG00000139714	3075	2.83	4.65E-03	1.16E-02	+-++	MORN3
chr12: 121861616	cg19998289	ENSG00000261827	3075	-3.489	4.86E-04	1.62E-03	-+--	
chr12: 121861616	cg19998289	ENSG00000135124	3075	-3.791	1.50E-04	7.52E-04	----	P2RX4
chr12: 121861616	cg19998289	ENSG00000110931	3075	-5.483	4.18E-08	4.18E-07	----	CAMKK2
chr12: 121861616	cg19998289	ENSG00000089041	3075	-2.578	9.95E-03	1.99E-02	-+--	P2RX7
chr12: 123446272	cg03131767	ENSG00000090975	3075	5.183	2.18E-07	1.31E-06	++++	PITPNM2
chr12: 123446272	cg03131767	ENSG00000130787	3075	5.825	5.72E-09	6.86E-08	++++	HIP1R
chr12: 123446272	cg03131767	ENSG00000130783	3075	3.478	5.06E-04	2.02E-03	++++	CCDC62
chr12: 125589647	cg26964704	ENSG00000184992	3075	-5.035	4.78E-07	2.39E-06	----	BRI3BP
chr12: 125589647	cg26964704	ENSG00000081760	3075	-3.42	6.26E-04	1.57E-03	----	AACS
chr12: 12887740	cg09444226	ENSG00000178878	3075	-5.721	1.06E-08	1.17E-07	----	APOLD1
chr12: 15126020	cg09447105	ENSG00000111341	3075	2.989	2.80E-03	2.80E-02	++++	MGP
chr12: 15126020	cg09447105	ENSG00000139055	3075	-2.699	6.97E-03	3.48E-02	+---	ERP27
chr12: 31453901	cg18805734	ENSG00000013573	3075	2.841	4.50E-03	2.70E-02	++++	DDX11
chr12: 52995634	cg00793181	ENSG00000257495	3075	5.476	4.35E-08	3.48E-07	++++	
chr12: 52995634	cg00793181	ENSG00000170486	3075	-4.077	4.57E-05	1.83E-04	----	KRT72
chr12: 52995634	cg00793181	ENSG00000172867	3075	2.75	5.96E-03	1.59E-02	++++	KRT2
chr12: 56600222	cg17116500	ENSG00000139579	3075	-3.458	5.44E-04	4.21E-03	----	NABP2
chr12: 56600222	cg17116500	ENSG00000139641	3075	-3.785	1.54E-04	1.59E-03	----	ESYT1
chr12: 56600222	cg17116500	ENSG00000062485	3075	-5.361	8.25E-08	2.56E-06	----	CS
chr12: 56600222	cg17116500	ENSG00000139531	3075	-3.944	8.02E-05	1.24E-03	----	SUOX
chr12: 56694932	cg24028828	ENSG00000139641	3075	-7.726	1.11E-14	1.49E-13	----	ESYT1
chr12: 56694932	cg24028828	ENSG00000062485	3075	-9.206	3.38E-20	9.12E-19	----	CS
chr12: 7104184	cg19434937	ENSG00000089692	3075	-4.581	4.64E-06	3.36E-05	----	LAG3
chr12: 7104184	cg19434937	ENSG00000159335	3075	-5.46	4.76E-08	6.91E-07	----	PTMS
chr12: 7104184	cg19434937	ENSG00000110811	3075	2.749	5.97E-03	1.92E-02	++++	LEPREL2
chr12: 7104184	cg19434937	ENSG00000111664	3075	3.373	7.43E-04	3.59E-03	++++	GNB3
chr12: 7104184	cg19434937	ENSG00000248593	3075	-8.443	3.10E-17	8.98E-16	----	DSTNP2
chr12: 7104184	cg19434937	ENSG00000111669	3075	-3.424	6.16E-04	3.57E-03	-+--	TPI1
chr12: 7104184	cg19434937	ENSG00000111678	3075	2.685	7.26E-03	2.11E-02	+-+-	C12orf57
chr12: 7104184	cg19434937	ENSG00000240370	3075	-4.995	5.90E-07	5.70E-06	---+	RPL13P5
chr12: 7104184	cg19434937	ENSG00000111679	3075	-3.088	2.02E-03	8.35E-03	-+--	PTPN6
chr12: 7104184	cg19434937	ENSG00000111676	3075	-2.864	4.19E-03	1.52E-02	-+--	ATN1
chr12: 7862691	cg15075897	ENSG00000059804	3075	3.472	5.16E-04	2.58E-03	++++	SLC2A3
chr12: 8975309	cg27653134	ENSG00000139187	3075	-4.688	2.75E-06	3.03E-05	----	KLRG1
chr12: 8975309	cg27653134	ENSG00000111752	3075	2.978	2.90E-03	1.60E-02	++++	PHC1
chr13: 113305704	cg25479097	ENSG00000126217	3075	5.435	5.48E-08	1.64E-07	++++	MCF2L
chr13: 113305704	cg25479097	ENSG00000068650	3075	2.612	9.01E-03	1.35E-02	++++	ATP11A
chr13: 30143971	cg19928703	ENSG00000139514	3075	-2.415	1.57E-02	3.14E-02	---+	SLC7A1
chr13: 41631052	cg07908654	ENSG00000120662	3075	3.418	6.30E-04	2.52E-03	++++	MTRF1
chr13: 41631052	cg07908654	ENSG00000165572	3075	3.277	1.05E-03	3.15E-03	+-++	KBTBD6
chr13: 41631052	cg07908654	ENSG00000120696	3075	4.157	3.22E-05	2.45E-04	++++	KBTBD7
chr13: 41631052	cg07908654	ENSG00000120688	3075	2.396	1.66E-02	3.97E-02	++++	WBP4
chr13: 41631052	cg07908654	ENSG00000120690	3075	4.103	4.08E-05	2.45E-04	++++	ELF1
chr13: 48876919	cg13221796	ENSG00000238086	2182	2.726	6.40E-03	3.84E-02	+++?	PPP1R26P1
chr13: 52301946	cg07818422	ENSG00000102796	3075	3.87	1.09E-04	5.44E-04	++++	DHRS12
chr13: 80066032	cg11770323	ENSG00000227354	3075	-2.948	3.20E-03	3.63E-03	----	RBM26-AS1
chr13: 80066032	cg11770323	ENSG00000139746	3075	-2.909	3.63E-03	3.63E-03	+---	RBM26
chr13: 80066032	cg11770323	ENSG00000102471	3075	-6.871	6.38E-12	1.91E-11	----	NDFIP2

chr14: 100610186	cg16409452	ENSG00000140105	3075	-2.884	3.92E-03	1.96E-02	-+--	WARS
chr14: 100610186	cg16409452	ENSG00000168350	3075	-4.26	2.05E-05	2.05E-04	----	DEGS2
chr14: 100610407	cg14084609	ENSG00000140105	3075	-2.678	7.40E-03	3.70E-02	-+--	WARS
chr14: 100610407	cg14084609	ENSG00000168350	3075	-2.938	3.30E-03	3.30E-02	-+--	DEGS2
chr14: 100610667	cg01000631	ENSG00000140105	3075	-3.594	3.26E-04	3.26E-03	-+--	WARS
chr14: 103436387	cg18505004	ENSG00000198752	3075	3.6	3.18E-04	1.91E-03	-+++	CDC42BPB
chr14: 105352991	cg23584308	ENSG00000170779	3075	-4.231	2.33E-05	1.75E-04	----	CDCA4
chr14: 105352991	cg23584308	ENSG00000099814	3075	4.056	4.98E-05	2.49E-04	++++	CEP170B
chr14: 105352991	cg23584308	ENSG00000183484	3075	-2.739	6.16E-03	1.85E-02	---+	GPR132
chr14: 105352991	cg23584308	ENSG00000179627	3075	-8.093	5.82E-16	8.73E-15	----	ZBTB42
chr14: 105352991	cg23584308	ENSG00000166428	3075	-3.374	7.42E-04	2.78E-03	----	PLD4
chr14: 21436271	cg18368116	ENSG00000258810	3075	5.07	3.97E-07	1.72E-06	++++	
chr14: 21436271	cg18368116	ENSG00000169385	3075	-8.501	1.87E-17	2.43E-16	----	RNASE2
chr14: 21436271	cg18368116	ENSG00000169397	3075	-6.986	2.84E-12	1.84E-11	----	RNASE3
chr14: 21436271	cg18368116	ENSG00000165792	3075	-4.297	1.73E-05	5.62E-05	----	METTL17
chr14: 21436271	cg18368116	ENSG00000169413	3075	3.143	1.67E-03	4.34E-03	+++-	RNASE6
chr14: 21436271	cg18368116	ENSG00000165801	3075	2.815	4.88E-03	1.06E-02	++-+	ARHGEF40
chr14: 55849528	cg12192145	ENSG00000186615	3075	-2.86	4.24E-03	2.97E-02	----	KTN1-AS1
chr14: 62001072	cg08077807	ENSG00000250548	3075	-13.989	1.83E-44	1.28E-43	----	
chr14: 62068941	cg08061334	ENSG00000250548	3075	-8.559	1.14E-17	6.84E-17	----	
chr14: 69650830	cg02170785	ENSG00000259062	3075	2.822	4.77E-03	2.86E-02	++++	ACTN1-AS1
chr14: 75153307	cg26103369	ENSG00000198208	3075	2.616	8.91E-03	3.63E-02	++++	RPS6KL1
chr14: 75153307	cg26103369	ENSG00000119689	3075	-5.617	1.94E-08	2.91E-07	----	DLST
chr14: 75153307	cg26103369	ENSG00000119681	3075	-2.587	9.68E-03	3.63E-02	-+--	LTBP2
chr14: 75153307	cg26103369	ENSG00000119596	3075	-2.588	9.65E-03	3.63E-02	----	YLPM1
chr14: 95615731	cg01901579	ENSG00000235706	3075	2.521	1.17E-02	2.34E-02	++++	DICER1-AS1
chr14: 95615731	cg01901579	ENSG00000259143	3075	2.848	4.39E-03	1.76E-02	++++	
chr14: 95615731	cg01901579	ENSG00000165959	3075	2.269	2.32E-02	3.10E-02	++++	CLMN
chr15: 101719523	cg24254196	ENSG00000259755	3075	5.599	2.16E-08	4.86E-08	++++	
chr15: 101719523	cg24254196	ENSG00000259182	3075	6.055	1.40E-09	4.21E-09	++++	
chr15: 101719523	cg24254196	ENSG00000259376	3075	8.112	5.00E-16	2.25E-15	++++	
chr15: 101719523	cg24254196	ENSG00000131873	3075	9.904	4.00E-23	3.60E-22	++++	CHSY1
chr15: 40173065	cg25939647	ENSG00000248508	3075	5.708	1.14E-08	6.86E-08	++++	SRP14-AS1
chr15: 52861754	cg25003924	ENSG00000128989	3075	-2.824	4.74E-03	1.18E-02	----	ARPP19
chr15: 52861754	cg25003924	ENSG00000197535	3075	-2.889	3.87E-03	1.18E-02	----	MYO5A
chr15: 64275810	cg13645296	ENSG00000035664	3075	-7.469	8.08E-14	6.46E-13	----	DAPK2
chr15: 64275853	cg11266582	ENSG00000035664	3075	-6.865	6.63E-12	5.30E-11	----	DAPK2
chr15: 64275853	cg11266582	ENSG00000166794	3075	-2.916	3.55E-03	1.42E-02	--+-	PPIB
chr15: 64275853	cg11266582	ENSG00000259351	2182	-2.441	1.47E-02	3.91E-02	---?	
chr15: 99443339	cg26272088	ENSG00000182253	3075	-6.402	1.53E-10	4.60E-10	----	SYNM
chr15: 99443339	cg26272088	ENSG00000140443	3075	5.829	5.59E-09	8.39E-09	++++	IGF1R
chr16: 11729131	cg08776942	ENSG00000189067	3075	4.115	3.88E-05	1.90E-04	++++	LITAF
chr16: 11729131	cg08776942	ENSG00000184602	3075	4.048	5.17E-05	1.90E-04	++++	SNN
chr16: 11729131	cg08776942	ENSG00000188897	3075	4.443	8.86E-06	9.75E-05	++++	
chr16: 23511855	cg03935956	ENSG00000166847	3075	10.795	3.64E-27	4.36E-26	++++	DCTN5
chr16: 23511855	cg03935956	ENSG00000166851	3075	3.543	3.96E-04	1.19E-03	++++	PLK1
chr16: 23511855	cg03935956	ENSG00000103356	3075	-2.413	1.58E-02	2.71E-02	----	EARS2
chr16: 23511855	cg03935956	ENSG00000260136	2182	4.1	4.13E-05	2.48E-04	+++?	
chr16: 23511855	cg03935956	ENSG00000259806	3075	2.953	3.15E-03	6.29E-03	++++	
chr16: 23511855	cg03935956	ENSG00000103365	3075	-3.666	2.46E-04	9.85E-04	----	GGA2
chr16: 23511855	cg03935956	ENSG00000260482	3075	2.232	2.56E-02	3.85E-02	++++	
chr16: 23511855	cg03935956	ENSG00000168434	3075	3.373	7.43E-04	1.78E-03	++++	COG7
chr16: 2863919	cg10194884	ENSG00000172460	3075	-12.674	8.21E-37	1.27E-35	----	PRSS30P
chr16: 2863919	cg10194884	ENSG00000103355	3075	-5.215	1.84E-07	1.14E-06	----	PRSS33
chr16: 2863919	cg10194884	ENSG00000215148	3075	-4.293	1.76E-05	9.09E-05	----	PRSS41
chr16: 2863919	cg10194884	ENSG00000007038	3075	-19.335	2.71E-83	8.39E-82	----	PRSS21
chr16: 2863919	cg10194884	ENSG00000167977	3075	-3.31	9.33E-04	3.21E-03	----	KCTD5
chr16: 2863919	cg10194884	ENSG00000005001	3075	-8.748	2.18E-18	2.25E-17	----	PRSS22

chr16: 2863919	cg10194884	ENSG00000162078	3075	-6.872	6.32E-12	4.90E-11	----	ZG16B
chr16: 2863919	cg10194884	ENSG00000140992	3075	-3.41	6.50E-04	2.52E-03	+---	PDPK1
chr16: 2863919	cg10194884	ENSG00000059122	3075	-3.765	1.67E-04	7.39E-04	----	FLYWCH1
chr16: 30409908	cg01304182	ENSG00000005844	3075	-3.064	2.18E-03	1.36E-02	----	ITGAL
chr16: 30409908	cg01304182	ENSG00000261346	3075	-2.735	6.24E-03	3.12E-02	----	
chr16: 30409908	cg01304182	ENSG00000169217	3075	-3.323	8.92E-04	1.36E-02	----	CD2BP2
chr16: 30409908	cg01304182	ENSG00000102879	3075	-3.256	1.13E-03	1.36E-02	----	CORO1A
chr16: 30409908	cg01304182	ENSG00000261416	3075	-3.135	1.72E-03	1.36E-02	----	
chr16: 30488321	cg06972908	ENSG00000005844	3075	-9.676	3.80E-22	9.49E-21	----	ITGAL
chr16: 30488321	cg06972908	ENSG00000197162	3075	4.273	1.93E-05	1.61E-04	++++	ZNF785
chr16: 30488321	cg06972908	ENSG00000261346	3075	-3.189	1.43E-03	4.65E-03	-+--	
chr16: 30488321	cg06972908	ENSG00000169957	3075	4.103	4.08E-05	2.55E-04	+++-	ZNF768
chr16: 30488321	cg06972908	ENSG00000260487	2182	-2.47	1.35E-02	3.38E-02	---?	
chr16: 30488321	cg06972908	ENSG00000261840	3075	3.177	1.49E-03	4.65E-03	++++	
chr16: 30488321	cg06972908	ENSG00000169955	3075	3.984	6.77E-05	2.82E-04	++++	ZNF747
chr16: 30488321	cg06972908	ENSG00000080603	3075	2.903	3.70E-03	1.03E-02	-+++	SRCAP
chr16: 30488321	cg06972908	ENSG00000179918	3075	3.991	6.59E-05	2.82E-04	++-+	SEPHS2
chr16: 30488321	cg06972908	ENSG00000156860	3075	4.484	7.33E-06	9.16E-05	++++	FBRS
chr16: 55542668	cg03471593	ENSG00000087253	3075	4.543	5.56E-06	8.34E-06	++++	LPCAT2
chr16: 55542668	cg03471593	ENSG00000261997	3075	-5.407	6.40E-08	1.92E-07	----	
chr16: 55542668	cg03471593	ENSG00000256812	3075	-2.051	4.03E-02	4.03E-02	--+-	CAPNS2
chr16: 616212	cg04497992	ENSG00000127585	3075	-3.087	2.02E-03	1.81E-02	----	FBXL16
chr16: 616212	cg04497992	ENSG00000103126	3075	-4.763	1.91E-06	6.10E-05	----	AXIN1
chr16: 616212	cg04497992	ENSG00000086504	3075	-3.374	7.41E-04	1.18E-02	--+-	MRPL28
chr16: 616212	cg04497992	ENSG00000103254	3075	-2.719	6.55E-03	2.99E-02	+---	FAM173A
chr16: 616212	cg04497992	ENSG00000161999	3075	2.754	5.89E-03	2.99E-02	++++	JMJD8
chr16: 616212	cg04497992	ENSG00000127586	3075	-3.054	2.26E-03	1.81E-02	----	CHTF18
chr16: 616212	cg04497992	ENSG00000007376	3075	-2.77	5.61E-03	2.99E-02	----	RPUSD1
chr16: 67978450	cg06839111	ENSG00000167261	3075	-3.302	9.59E-04	9.59E-03	----	DPEP2
chr16: 67978450	cg06839111	ENSG00000167264	3075	-6.328	2.48E-10	4.96E-09	----	DUS2
chr16: 69170548	cg08085199	ENSG00000168807	3075	-4.204	2.62E-05	1.08E-04	---+	SNTB2
chr16: 69170548	cg08085199	ENSG00000132603	3075	-2.418	1.56E-02	3.12E-02	+--+	NIP7
chr16: 69170548	cg08085199	ENSG00000103044	3075	4.157	3.23E-05	1.08E-04	++++	HAS3
chr16: 69170548	cg08085199	ENSG00000141076	3075	5.949	2.70E-09	2.70E-08	++++	CIRH1A
chr16: 69170548	cg08085199	ENSG00000157315	3075	3.831	1.28E-04	3.19E-04	++++	TMED6
chr16: 78782477	cg02236679	ENSG00000186153	3075	-2.266	2.34E-02	2.34E-02	-+--	WWOX
chr16: 85654213	cg04847043	ENSG00000131149	3075	-2.819	4.82E-03	4.34E-02	-+--	GSE1
chr16: 85655007	cg02124524	ENSG00000131149	3075	-3.651	2.61E-04	1.68E-03	---+	GSE1
chr16: 85655007	cg02124524	ENSG00000270124	3075	-2.859	4.25E-03	1.28E-02	----	
chr16: 85655007	cg02124524	ENSG00000131148	3075	-3.558	3.74E-04	1.68E-03	----	EMC8
chr16: 85655007	cg02124524	ENSG00000131143	3075	-2.352	1.87E-02	4.20E-02	+---	COX4I1
chr16: 88540241	cg08940169	ENSG00000179588	3075	-3.586	3.35E-04	2.18E-03	----	ZFPM1
chr16: 88540241	cg08940169	ENSG00000103335	3075	-3.897	9.75E-05	1.27E-03	---+	PIEZO1
chr16: 88540241	cg08940169	ENSG00000225614	3075	-3.351	8.05E-04	3.49E-03	---+	ZNF469
chr16: 88558223	cg04983687	ENSG00000179588	3075	-6.476	9.39E-11	1.31E-09	----	ZFPM1
chr16: 88558223	cg04983687	ENSG00000103335	3075	-4.979	6.40E-07	2.99E-06	---+	PIEZO1
chr16: 88558223	cg04983687	ENSG00000051523	3075	-2.787	5.32E-03	9.30E-03	-+--	CYBA
chr16: 88558223	cg04983687	ENSG00000167508	3075	-3.756	1.73E-04	4.83E-04	----	MVD
chr16: 88558223	cg04983687	ENSG00000261744	2182	-2.875	4.04E-03	8.08E-03	---?	
chr16: 88558223	cg04983687	ENSG00000225614	3075	-5.913	3.37E-09	2.36E-08	---+	ZNF469
chr16: 88558223	cg04983687	ENSG00000174177	3075	-4.168	3.07E-05	1.07E-04	----	CTU2
chr16: 88558223	cg04983687	ENSG00000185669	3075	-3.538	4.03E-04	9.40E-04	----	SNAI3
chr16: 88558237	cg05958985	ENSG00000158717	3075	-2.56	1.05E-02	3.66E-02	----	RNF166
chr16: 88558237	cg05958985	ENSG00000179588	3075	-4.34	1.43E-05	9.99E-05	----	ZFPM1
chr16: 88558237	cg05958985	ENSG00000103335	3075	-4.351	1.36E-05	9.99E-05	----	PIEZO1
chr16: 88558237	cg05958985	ENSG00000225614	3075	-3.373	7.45E-04	3.47E-03	---+	ZNF469
chr17: 15137304	cg20315954	ENSG00000109099	3075	-18.024	1.26E-72	3.77E-72	----	PMP22
chr17: 15137304	cg20315954	ENSG00000175106	3075	-3.293	9.90E-04	1.48E-03	----	TVP23C

chr17: 33885049	cg00397422	ENSG00000129270	3075	6.162	7.16E-10	1.72E-08	++++	MMP28
chr17: 33885049	cg00397422	ENSG00000267364	3075	-4.55	5.36E-06	6.43E-05	----	
chr17: 39686628	cg21723861	ENSG00000173801	3075	-2.915	3.56E-03	1.78E-02	--+-	JUP
chr17: 40724562	cg00170714	ENSG00000141699	3075	-3.751	1.76E-04	2.03E-03	----	FAM134C
chr17: 40724562	cg00170714	ENSG00000108785	3075	4.227	2.37E-05	5.44E-04	++++	HSD17B1P1
chr17: 40724562	cg00170714	ENSG00000108786	3075	2.598	9.37E-03	4.31E-02	++++	HSD17B1
chr17: 40724562	cg00170714	ENSG00000183978	3075	-3.435	5.93E-04	4.42E-03	--+-	COA3
chr17: 40724562	cg00170714	ENSG00000131475	3075	-3.364	7.69E-04	4.42E-03	----	VPS25
chr17: 40810559	cg10180165	ENSG00000108797	3075	-3.584	3.39E-04	9.14E-03	----	CNTNAP1
chr17: 41400541	cg13726456	ENSG00000067596	3075	-2.23	2.57E-02	4.29E-02	---+	DHX8
chr17: 41400541	cg13726456	ENSG00000267681	3075	6.353	2.11E-10	1.58E-09	++++	
chr17: 41400541	cg13726456	ENSG00000108830	3075	6.062	1.35E-09	4.04E-09	++++	RND2
chr17: 41400541	cg13726456	ENSG00000175906	3075	6.25	4.10E-10	1.62E-09	++++	ARL4D
chr17: 41400541	cg13726456	ENSG00000267002	3075	-3.128	1.76E-03	3.30E-03	----	
chr17: 41400541	cg13726456	ENSG00000198496	3075	18.804	7.01E-79	1.05E-77	++++	NBR2
chr17: 41400541	cg13726456	ENSG00000188554	3075	4.552	5.31E-06	1.14E-05	++++	NBR1
chr17: 41400541	cg13726456	ENSG00000236383	3075	6.242	4.33E-10	1.62E-09	++++	LINC00854
chr17: 41400541	cg13726456	ENSG00000108828	3075	6.004	1.92E-09	4.81E-09	++++	VAT1
chr17: 41400661	cg17378535	ENSG00000267681	3075	5.303	1.14E-07	8.57E-07	++++	
chr17: 41400661	cg17378535	ENSG00000108830	3075	2.808	4.99E-03	1.25E-02	+++-	RND2
chr17: 41400661	cg17378535	ENSG00000267002	3075	-2.361	1.82E-02	3.42E-02	----	
chr17: 41400661	cg17378535	ENSG00000198496	3075	12.839	9.95E-38	1.49E-36	++++	NBR2
chr17: 41400661	cg17378535	ENSG00000188554	3075	4.042	5.31E-05	1.99E-04	++++	NBR1
chr17: 41400661	cg17378535	ENSG00000012048	3075	2.398	1.65E-02	3.42E-02	+--+	BRCA1
chr17: 41400661	cg17378535	ENSG00000236383	3075	4.19	2.79E-05	1.39E-04	++++	LINC00854
chr17: 41400661	cg17378535	ENSG00000188825	3075	-3.554	3.80E-04	1.14E-03	----	LINC00910
chr17: 41472748	cg10433549	ENSG00000198496	3075	3.62	2.95E-04	3.54E-03	++++	NBR2
chr17: 41472748	cg10433549	ENSG00000012048	3075	2.701	6.91E-03	2.76E-02	-+++	BRCA1
chr17: 41472748	cg10433549	ENSG00000188825	3075	-2.956	3.12E-03	1.87E-02	----	LINC00910
chr17: 43111632	cg18176312	ENSG00000172992	3075	3.229	1.24E-03	1.18E-02	++++	DCAKD
chr17: 43111632	cg18176312	ENSG00000161714	3075	-4.502	6.74E-06	1.28E-04	-+--	PLCD3
chr17: 47372126	cg07050712	ENSG00000064300	3075	-3.015	2.57E-03	2.82E-02	----	NGFR
chr17: 4743324	cg07307484	ENSG00000161905	3075	-11.12	9.99E-29	2.70E-27	----	ALOX15
chr17: 47590237	cg12561474	ENSG00000064300	3075	-2.927	3.43E-03	3.77E-02	--+-	NGFR
chr17: 47590272	cg26102082	ENSG00000064300	3075	-5.35	8.79E-08	9.67E-07	----	NGFR
chr17: 47590272	cg26102082	ENSG00000198740	3075	-4.05	5.13E-05	2.82E-04	-+--	ZNF652
chr17: 47590272	cg26102082	ENSG00000121067	3075	2.693	7.09E-03	2.60E-02	++++	SPOP
chr17: 55167149	cg06483820	ENSG00000121057	3075	4.917	8.77E-07	7.89E-06	++++	AKAP1
chr17: 55167149	cg06483820	ENSG00000121064	3075	-3.385	7.13E-04	3.21E-03	----	SCPEP1
chr17: 56269818	cg02970679	ENSG00000176160	3075	2.603	9.25E-03	4.63E-02	+-++	HSF5
chr17: 56269818	cg02970679	ENSG00000265206	3075	-2.61	9.06E-03	4.63E-02	-+--	MIR142
chr17: 56269818	cg02970679	ENSG00000121053	3075	-4.327	1.51E-05	2.27E-04	----	EPX
chr17: 56270828	cg17374802	ENSG00000121053	3075	-5.614	1.98E-08	2.97E-07	----	EPX
chr17: 56274597	cg03519593	ENSG00000121053	3075	-3.465	5.30E-04	7.95E-03	----	EPX
chr17: 6658198	cg14321269	ENSG00000132530	3075	-4.853	1.22E-06	1.46E-05	----	XAF1
chr17: 72709731	cg21640749	ENSG00000109062	3075	-2.8	5.11E-03	2.73E-02	----	SLC9A3R1
chr17: 72709731	cg21640749	ENSG00000172794	3075	-5.186	2.15E-07	1.72E-06	----	RAB37
chr17: 72709731	cg21640749	ENSG00000186074	3075	-6.937	4.01E-12	6.41E-11	----	CD300LF
chr17: 7648108	cg01330991	ENSG00000239697	3075	-3.665	2.47E-04	6.42E-03	----	TNFSF12
chr17: 7648108	cg01330991	ENSG00000170043	3075	-3.064	2.19E-03	2.84E-02	----	TRAPPC1
chr17: 76565232	cg09705784	ENSG00000267123	3075	-2.491	1.27E-02	4.24E-02	----	
chr17: 76565232	cg09705784	ENSG00000087157	3075	4.053	5.06E-05	2.53E-04	++++	PGS1
chr17: 76565232	cg09705784	ENSG00000187775	3075	4.161	3.18E-05	2.53E-04	++++	DNAH17
chr17: 81040724	cg20290167	ENSG00000261888	3075	-9.432	4.01E-21	2.40E-20	----	
chr17: 81040724	cg20290167	ENSG00000176845	3075	-4.883	1.04E-06	2.62E-06	----	METRNL
chr17: 81040724	cg20290167	ENSG00000175711	3075	4.838	1.31E-06	2.62E-06	++++	B3GNTL1
chr17: 81040906	cg22503106	ENSG00000261888	3075	-13.641	2.29E-42	1.38E-41	----	
chr17: 81040906	cg22503106	ENSG00000141556	3075	-3.969	7.21E-05	1.44E-04	----	TBCD

chr17: 81040906	cg22503106	ENSG00000176845	3075	-6.571	5.00E-11	1.50E-10	----	METRNL
chr17: 81040906	cg22503106	ENSG00000175711	3075	2.23	2.58E-02	3.87E-02	++++	B3GNTL1
chr17: 81043782	cg26749306	ENSG00000261888	3075	-10.508	7.91E-26	4.74E-25	----	
chr17: 81043782	cg26749306	ENSG00000176845	3075	-2.348	1.89E-02	3.78E-02	----	METRNL
chr17: 81043782	cg26749306	ENSG00000175711	3075	4.676	2.93E-06	8.78E-06	++++	B3GNTL1
chr17: 81055722	cg13054523	ENSG00000261888	3075	-12.664	9.36E-37	5.62E-36	----	
chr17: 81055722	cg13054523	ENSG00000141556	3075	-2.875	4.04E-03	6.06E-03	----	TBCD
chr17: 81055722	cg13054523	ENSG00000176845	3075	-6.41	1.46E-10	4.37E-10	----	METRNL
chr17: 81055722	cg13054523	ENSG00000175711	3075	4.65	3.32E-06	6.64E-06	++++	B3GNTL1
chr18: 46570302	cg06208130	ENSG00000101665	3075	-2.466	1.37E-02	3.46E-02	-+--	SMAD7
chr18: 46570302	cg06208130	ENSG00000267764	2182	-2.381	1.73E-02	3.46E-02	---?	
chr19: 11687621	cg10644885	ENSG00000102575	3075	-5.516	3.47E-08	7.97E-07	----	ACP5
chr19: 11687621	cg10644885	ENSG00000205517	3075	4.087	4.36E-05	3.34E-04	++++	RGL3
chr19: 11687621	cg10644885	ENSG00000197933	3075	-3.761	1.69E-04	9.72E-04	----	ZNF823
chr19: 11687621	cg10644885	ENSG00000187266	3075	2.853	4.33E-03	1.66E-02	++++	EPOR
chr19: 11687621	cg10644885	ENSG00000105520	3075	4.263	2.02E-05	2.32E-04	++++	
chr19: 11687621	cg10644885	ENSG00000105514	3075	3.691	2.24E-04	1.03E-03	++++	RAB3D
chr19: 16578633	cg16597993	ENSG00000269399	3075	-3.109	1.88E-03	1.54E-02	----	
chr19: 16578633	cg16597993	ENSG00000072954	3075	-3.75	1.77E-04	3.01E-03	----	TMEM38A
chr19: 16578633	cg16597993	ENSG00000072958	3075	-2.997	2.73E-03	1.54E-02	----	AP1M1
chr19: 2059698	cg19475270	ENSG00000130270	3075	-3.262	1.11E-03	2.87E-02	----	ATP8B3
chr19: 34860339	cg02359181	ENSG00000105220	3075	-6.907	4.96E-12	4.47E-11	----	GPI
chr19: 39303993	cg04420917	ENSG00000104814	3075	-5.84	5.21E-09	9.38E-08	----	MAP4K1
chr19: 39303993	cg04420917	ENSG00000130402	3075	-2.806	5.01E-03	1.29E-02	-+--	ACTN4
chr19: 39303993	cg04420917	ENSG00000068903	3075	-2.909	3.63E-03	1.09E-02	-+--	SIRT2
chr19: 39303993	cg04420917	ENSG00000196218	3075	-3.735	1.88E-04	1.12E-03	----	RYR1
chr19: 39303993	cg04420917	ENSG00000104825	3075	-3.423	6.18E-04	2.78E-03	----	NFKBIB
chr19: 39303993	cg04420917	ENSG00000171747	3075	2.616	8.89E-03	2.00E-02	-+++	LGALS4
chr19: 39303993	cg04420917	ENSG00000104823	3075	-3.118	1.82E-03	6.56E-03	----	ECH1
chr19: 39303993	cg04420917	ENSG00000269050	2182	2.423	1.54E-02	3.08E-02	+++?	
chr19: 39303993	cg04420917	ENSG00000182472	3075	-4.597	4.28E-06	3.85E-05	----	CAPN12
chr19: 40227949	cg18254848	ENSG00000226025	2182	-5.805	6.42E-09	3.53E-08	---?	
chr19: 40227949	cg18254848	ENSG00000268088	2182	-3.627	2.87E-04	1.05E-03	---?	
chr19: 40227949	cg18254848	ENSG00000105205	3075	-14.524	8.50E-48	9.34E-47	----	CLC
chr19: 40227949	cg18254848	ENSG00000176396	3075	-2.476	1.33E-02	3.66E-02	-+--	EID2
chr19: 41129881	cg24872571	ENSG00000105223	3075	-3.233	1.22E-03	2.57E-02	-+--	PLD3
chr19: 41255444	cg02402423	ENSG00000261857	2182	-3.55	3.85E-04	3.08E-03	---?	MIA
chr19: 41255444	cg02402423	ENSG00000233622	3075	4.176	2.97E-05	4.75E-04	++++	CYP2T2P
chr19: 44220148	cg20673965	ENSG00000176222	3075	2.963	3.05E-03	3.02E-02	++++	ZNF404
chr19: 44220148	cg20673965	ENSG00000105755	3075	-3.744	1.81E-04	3.80E-03	----	ETHE1
chr19: 44220148	cg20673965	ENSG00000159905	2182	2.855	4.31E-03	3.02E-02	-++?	ZNF221
chr19: 44220148	cg20673965	ENSG00000073050	3075	-2.72	6.54E-03	3.43E-02	----	XRCC1
chr19: 51961666	cg17521120	ENSG00000105374	3075	-6.709	1.96E-11	1.64E-10	----	NKG7
chr19: 51961666	cg17521120	ENSG00000160318	3075	-5.815	6.06E-09	3.79E-08	----	CLDND2
chr19: 51961666	cg17521120	ENSG00000269403	3075	-4.086	4.39E-05	2.20E-04	----	
chr19: 51961666	cg17521120	ENSG00000105366	3075	-16.387	2.36E-60	5.91E-59	----	SIGLEC8
chr19: 51961666	cg17521120	ENSG00000105379	3075	-2.831	4.64E-03	1.29E-02	+---	ETFB
chr19: 51961666	cg17521120	ENSG00000105497	3075	2.868	4.13E-03	1.29E-02	++++	ZNF175
chr19: 51961666	cg17521120	ENSG00000142512	3075	-6.774	1.25E-11	1.56E-10	----	SIGLEC10
chr19: 51961666	cg17521120	ENSG00000167765	2182	3.635	2.79E-04	9.95E-04	+++?	
chr19: 51961666	cg17521120	ENSG00000254760	3075	-3.713	2.05E-04	8.54E-04	----	
chr19: 930871	cg18337287	ENSG00000185198	3075	-3.837	1.24E-04	1.31E-03	----	PRSS57
chr19: 930871	cg18337287	ENSG00000064932	3075	5.117	3.10E-07	6.51E-06	++++	SBNO2
chr20: 17659317	cg00990977	ENSG00000125868	3075	-3.189	1.43E-03	4.28E-03	----	DSTN
chr20: 17659317	cg00990977	ENSG00000125844	3075	-2.681	7.35E-03	1.10E-02	-+--	RRBP1
chr20: 33416959	cg11988722	ENSG00000131067	3075	4.714	2.43E-06	1.94E-05	++++	GGT7
chr20: 33416959	cg11988722	ENSG00000078814	3075	4.542	5.57E-06	2.23E-05	++++	MYH7B
chr20: 35422703	cg21045547	ENSG00000101084	3075	3.265	1.09E-03	1.31E-02	++++	C20orf24

chr20: 35504064	cg19448292	ENSG00000149639	3075	-4.284	1.83E-05	1.47E-04	----	SOGA1
chr20: 35504198	cg14613878	ENSG00000101342	3075	2.781	5.43E-03	2.17E-02	+-++	TLDC2
chr20: 35504198	cg14613878	ENSG00000101347	3075	3.236	1.21E-03	9.71E-03	++++	SAMHD1
chr20: 35504371	cg09241885	ENSG00000101342	3075	2.693	7.08E-03	2.71E-02	++++	TLDC2
chr20: 35504371	cg09241885	ENSG00000080839	3075	3.483	4.95E-04	3.96E-03	+-++	RBL1
chr20: 35504371	cg09241885	ENSG00000101347	3075	2.57	1.02E-02	2.71E-02	-+++	SAMHD1
chr20: 35504403	cg09227119	ENSG00000101342	3075	4.24	2.24E-05	8.96E-05	++++	TLDC2
chr20: 35504403	cg09227119	ENSG00000101347	3075	4.647	3.36E-06	2.69E-05	++++	SAMHD1
chr20: 35504511	cg00414077	ENSG00000101347	3075	3.22	1.28E-03	1.03E-02	-+++	SAMHD1
chr20: 43590115	cg13792581	ENSG00000101104	3075	4.441	8.95E-06	6.26E-05	++++	PABPC1L
chr20: 43590115	cg13792581	ENSG00000124233	3075	-3.767	1.65E-04	3.85E-04	----	SEMG1
chr20: 43590115	cg13792581	ENSG00000025772	3075	-3.929	8.53E-05	2.99E-04	----	TOMM34
chr20: 4764277	cg01613077	ENSG00000101265	3075	2.777	5.49E-03	1.65E-02	+-++	RASSF2
chr20: 47731131	cg23498922	ENSG00000124214	3075	3.873	1.08E-04	5.92E-04	++++	STAU1
chr20: 47731131	cg23498922	ENSG00000124201	3075	3.071	2.14E-03	7.84E-03	++++	ZNFX1
chr20: 47731131	cg23498922	ENSG00000177410	3075	-2.445	1.45E-02	3.98E-02	+---	ZFAS1
chr20: 47731131	cg23498922	ENSG00000124198	3075	4.153	3.28E-05	3.60E-04	++++	ARFGEF2
chr20: 48806066	cg02930951	ENSG00000240849	3075	-4.369	1.25E-05	1.13E-04	----	TMEM189
chr20: 60709957	cg13197551	ENSG00000149657	3075	-7.965	1.66E-15	1.66E-14	----	LSM14B
chr20: 62700725	cg00390694	ENSG00000196700	3075	3.253	1.14E-03	1.35E-02	++++	ZNF512B
chr20: 62700725	cg00390694	ENSG00000171700	3075	-2.52	1.17E-02	4.40E-02	----	RGS19
chr20: 62700725	cg00390694	ENSG00000196421	3075	2.82	4.81E-03	2.40E-02	++++	LINC00176
chr20: 62700725	cg00390694	ENSG00000198276	3075	-3.121	1.80E-03	1.35E-02	----	UCKL1
chr21: 37536923	cg00673191	ENSG00000236830	3075	3.863	1.12E-04	1.23E-03	++++	CBR3-AS1
chr21: 43771120	cg18879389	ENSG00000160183	3075	-3.187	1.44E-03	5.89E-03	-+--	TMPRSS3
chr21: 43771120	cg18879389	ENSG00000160180	3075	-16.342	4.96E-60	4.46E-59	----	TFF3
chr21: 43771120	cg18879389	ENSG00000160190	3075	-3.096	1.96E-03	5.89E-03	----	SLC37A1
chr21: 43786727	cg19247032	ENSG00000160183	3075	-3.031	2.44E-03	1.10E-02	----	TMPRSS3
chr21: 43786727	cg19247032	ENSG00000160180	3075	-13.572	5.86E-42	5.27E-41	----	TFF3
chr21: 43786727	cg19247032	ENSG00000160185	3075	2.674	7.50E-03	2.25E-02	++++	UBASH3A
chr21: 43786727	cg19247032	ENSG00000160190	3075	-2.328	1.99E-02	4.49E-02	----	SLC37A1
chr21: 46955647	cg00714531	ENSG00000182871	3075	-4.392	1.13E-05	6.75E-05	----	COL18A1
chr22: 32150934	cg16160637	ENSG00000198089	3075	8.212	2.18E-16	1.53E-15	++++	SFI1
chr22: 32150934	cg16160637	ENSG00000128245	3075	-3.632	2.81E-04	4.92E-04	----	YWHAH
chr22: 32150934	cg16160637	ENSG00000100150	3075	-4.798	1.60E-06	5.61E-06	----	DEPDC5
chr22: 32150934	cg16160637	ENSG00000183530	3075	-3.134	1.72E-03	2.41E-03	----	PRR14L
chr22: 32150934	cg16160637	ENSG00000241878	3075	-3.716	2.03E-04	4.73E-04	----	PISD
chr22: 39850774	cg05541460	ENSG00000100346	3075	5.752	8.85E-09	4.42E-08	++++	CACNA1I
chr22: 39850774	cg05541460	ENSG00000128268	3075	-9.12	7.50E-20	7.50E-19	----	MGAT3

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[1] Analyses are restricted to the 349 differentially methylated CpG sites identified in atopic asthma that are found in the 450K array

[2] BIOS was able to conduct cis-eQTM analyses for 346 CpG sites. Only 242 CpG sites were associated with gene expression.

[3] Genome build GRCh37/hg19

[4] Adjusted for for age, sex, lymphocyte proportion, monocyte proportion, and RNA flow cell number

Table E14. Druggable Targets of Novel Asthma Genes Identified in Atopic Asthma

chromosome	position	CpG	Gene	Durg target (ChEMBL)	# ChEMBL_25 database released on 01/02/2019	Approved drugs and clinical candidates
10	114133657	cg14930775	ACSL5	CHEMBL4105818	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105818/	No
11	10499641	cg17022365	AMPD3	CHEMBL2912	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2912/	No
12	50441815	cg20649656	ASIC1	CHEMBL1628477	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1628477/	No
19	15436097	cg02068052	BRD4	CHEMBL1163125	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1163125/	No
19	15436097	cg02068052	BRD4	CHEMBL4106143	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4106143/	No
8	95918378	cg13279458	CCNE2	CHEMBL2111444	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111444/	No
8	95918378	cg13279458	CCNE2	CHEMBL2094126	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2094126/	No
3	45914188	cg10650214	CCR9	CHEMBL5815	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5815/	VERCIRNON, MLN3126
1	91992292	cg11799283	CDC7	CHEMBL5443	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5443/	BMS-863233, RXDX-103, NMS-1116354
1	91992292	cg11799283	CDC7	CHEMBL2111377	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111377/	BMS-863233, RXDX-103, NMS-1116354
16	23491546	cg23746329	COG7	CHEMBL4105843	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105843/	No
3	49522836	cg00742276	DAG1	CHEMBL3714399	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3714399/	No
2	234246583	cg05724080	DGKD	CHEMBL1075120	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1075120/	No
11	85884166	cg12667152	EED	CHEMBL2189117	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2189117/	No
11	85884166	cg12667152	EED	CHEMBL3137286	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3137286/	No
11	85884166	cg12667152	EED	CHEMBL3137287	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3137287/	No
11	85884166	cg12667152	EED	CHEMBL3301388	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3301388/	No
5	137812320	cg22905973	EGR1	CHEMBL3616355	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3616355/	No
8	120599284	cg07236691	ENPP2	CHEMBL3691	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3691/	No
19	35950799	cg17062760	FFAR2	CHEMBL5493	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5493/	No
5	141909727	cg03079679	FGF1	CHEMBL2120	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2120/	MUPARFOSTAT, SURAMIN
9	80602527	cg25348163	GNAQ	CHEMBL3286079	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3286079/	No
1	32761824	cg14975122	HDAC1	CHEMBL325	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL325/	MOCETINOSTAT, VORINOSTAT
1	32761824	cg14975122	HDAC1	CHEMBL3885590	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3885590/	No
1	32761824	cg14975122	HDAC1	CHEMBL4106143	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4106143/	No
1	32761824	cg14975122	HDAC1	CHEMBL2111429	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111429/	No
1	32761824	cg14975122	HDAC1	CHEMBL3430897	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430897/	No
1	32761824	cg14975122	HDAC1	CHEMBL3885589	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3885589/	No
1	32761824	cg14975122	HDAC1	CHEMBL4106187	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4106187/	No
1	32761824	cg14975122	HDAC1	CHEMBL3430896	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430896/	No
1	32761824	cg14975122	HDAC1	CHEMBL3038483	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3038483/	No
1	32761824	cg14975122	HDAC1	CHEMBL2093865	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2093865/	BELINOSTAT, ENTINOSTAT, ROMIDEPSIN, FIMEPINOSTAT, TACEDINALINE, CUDC-101, PANOBINOSTAT
7	41914145	cg20178107	INHBA	CHEMBL3588735	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3588735/	SOTATERCEPT

19	7291221	cg19696679	INSR	CHEMBL1981	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1981/	BMS-754807, INSULIN PURIFIED BEEF, INSULIN ZINC SUSP PURIFIED BEEF/PORK, INSULIN ZINC SUSP RECOMBINANT HUMAN, INSULIN SUSP ISOPHANE PURIFIED BEEF, LINSITINIB, INSULIN PORK, INSULIN SUSP ISOPHANE RECOMBINANT HUMAN, INSULIN SUSP ISOPHANE BEEF/PORK, INSULIN SUSP PROTAMINE ZINC BEEF/PORK, INSULIN ZINC SUSP SEMISYNTHETIC PURIFIED HUMAN, INSULIN GLULISINE, INSULIN HUMAN, INSULIN ZINC SUSP PROMPT PURIFIED PORK, INSULIN ZINC SUSP EXTENDED PURIFIED BEEF, INSULIN ZINC SUSP BEEF, INSULIN ZINC SUSP PURIFIED PORK, INSULIN SUSP ISOPHANE PURIFIED PORK, INSULIN ZINC SUSP PURIFIED BEEF, INSULIN ZINC SUSP PROMPT BEEF
11	65482056	cg10093679	KAT5	CHEMBL5750	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5750/	No
16	31135265	cg02869730	KAT8	CHEMBL1932912	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1932912/	No
19	5093491	cg24823679	KDM4B	CHEMBL3313832	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3313832/	No
19	5093491	cg24823679	KDM4B	CHEMBL3430889	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430889/	No
19	12998426	cg26136776	KLF1	CHEMBL3407313	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3407313/	No
19	12997997	cg08679013	KLF1	CHEMBL3407313	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3407313/	No
12	123872423	cg02053425	KMT5A	CHEMBL1795176	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1795176/	No
16	67978450	cg06839111	LCAT	CHEMBL5942	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5942/	No
5	179200573	cg10113951	LTC4S	CHEMBL1743183	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1743183/	No
5	179203369	cg09031958	LTC4S	CHEMBL1743183	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1743183/	No
7	1577697	cg23871276	MAFK	CHEMBL2346484	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2346484/	No
3	127543047	cg04721651	MGLL	CHEMBL4191	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4191/	No
17	4741523	cg06449385	MINK1	CHEMBL5518	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5518/	No
17	4743324	cg07307484	MINK1	CHEMBL3430890	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430890/	No
19	2059698	cg19475270	MKNK2	CHEMBL4204	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4204/	No
19	2059698	cg19475270	MKNK2	CHEMBL3883293	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3883293/	No
9	113530240	cg14226212	MUSK	CHEMBL5684	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5684/	No
16	46776932	cg16064932	MYLK3	CHEMBL4627	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4627/	No
13	41935735	cg07769280	NAA16	CHEMBL3430873	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430873/	No
7	30505269	cg07299810	NOD1	CHEMBL1293222	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3430873/	No
10	129172535	cg11791710	NPS	CHEMBL3596086	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3596086/	No
10	129172573	cg26865494	NPS	CHEMBL3596086	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3596086/	No
11	72925008	cg05999592	P2RY2	CHEMBL4398	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4398/	No
11	72932079	cg14655553	P2RY2	CHEMBL4398	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4398/	No
1	17448350	cg12561552	PADI2	CHEMBL1909487	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1909487/	No
1	66777579	cg24058805	PDE4B	CHEMBL275	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL275/	No
1	66777579	cg24058805	PDE4B	CHEMBL2093863	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2093863/	ROFLUMILAST, AMLEXANOX, DYPHYLLINE, APREMILAST, THEOPHYLLINE GLYCINATE, CRISABOROLE, THEOPHYLLINE, FLAVOXATE

1	66777579	cg24058805	PDE4B	CHEMBL2095153	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095153/	No
1	66777579	cg24058805	PDE4B	CHEMBL2111340	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111340/	No
1	66777579	cg24058805	PDE4B	CHEMBL2363066	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2363066/	DIPYRIDAMOLE, PENTOXIFYLLINE
3	12269362	cg04399631	PPARG	CHEMBL235	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL235/	ARHALOFENATE, MURAGLITAZAR, ATX08-001, MBX-2044, TROGLITAZONE, MK-0533, EFATUTAZONE, IMIGLITAZAR, CLX-0921, NETOGLITAZONE, OMS405, AVE0847, PIOGLITAZONE, BALAGLITAZONE, BARDOXOLONE METHYL, BALSALAZIDE, TESAGLITAZAR, RIVOGLITAZONE, INT131, ROSIGLITAZONE
3	12269362	cg04399631	PPARG	CHEMBL3559683	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3559683/	SODELGLITAZAR, INDEGLITAZAR, BEZAFIBRATE
3	12269362	cg04399631	PPARG	CHEMBL2095162	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095162/	No
3	12269362	cg04399631	PPARG	CHEMBL2095163	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095163/	No
3	12269362	cg04399631	PPARG	CHEMBL2096976	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2096976/	No
3	12269362	cg04399631	PPARG	CHEMBL2095161	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2095161/	No
3	12269362	cg04399631	PPARG	CHEMBL2111325	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111325/	No
3	12269362	cg04399631	PPARG	CHEMBL2111371	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111371/	No
3	12269362	cg04399631	PPARG	CHEMBL2111394	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2111394/	No
10	81004884	cg07056602	PPIF	CHEMBL3325306	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3325306/	No
11	73897097	cg04484304	PPME1	CHEMBL1293320	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1293320/	No
14	51446038	cg14354244	PYGL	CHEMBL2568	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL2568/	No
3	128442438	cg06019933	RAB7A	CHEMBL4105784	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105784/	No
17	74402188	cg05056419	SPHK1	CHEMBL4394	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4394/	No
12	6984857	cg12003079	SPSB2	CHEMBL3325308	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3325308/	No
5	133443229	cg06651549	TCF7	CHEMBL3885542	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL3885542/	No
3	141900424	cg10141168	TFDP2	CHEMBL4105986	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105986/	No
3	141682388	cg19294517	TFDP2	CHEMBL4105986	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL4105986/	No
16	3843133	cg13135255	TRAP1	CHEMBL1075132	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL1075132/	No
11	9632897	cg26938803	WEE1	CHEMBL5491	https://www.ebi.ac.uk/chembl/target_report_card/CHEMBL5491/	No

Table E15. Replication Look-up Results of Atopic Asthma

				ALHS				In 450K Array?	SLSJ			PIAMA			PACE			EVA-PR		Bronchial Epithelium		ICAC		SAPALDIA			Project Viva	
chromosome	position[1]	CpG	Gene Name	Beta	SE	P	FDR		Beta	SE	P	Beta	SE	P	Beta	SE	P	Beta	P	T-value	P	T-value	P	Beta	SE	P	Beta	P
4	148635716	cg00006459	ARHGAP10	-23.76	4.95	1.59E-06	3.16E-03	1	-4.45	2.31	5.40E-02	0.66	0.67	3.26E-01	-6.59	2.67	1.36E-02	-0.42	3.52E-02	-	-	-4.27	6.12E-05	0.45	0.25	7.36E-02	-0.02	1.30E-02
15	43309540	cg00092426	UBR1	-20.29	5.00	4.86E-05	4.03E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.07E-05
9	130158144	cg00114012	SLC2A8	-15.67	3.34	2.69E-06	4.74E-03	1	-6.22	2.93	3.38E-02	-0.92	0.47	4.94E-02	-8.03	1.99	5.69E-05	-0.30	2.69E-01	1.22	2.26E-01	-1.19	2.39E-01	0.30	0.23	1.99E-01	-0.03	1.39E-03
1	234667087	cg00123090	LINC01354	-9.43	2.29	3.75E-05	3.31E-02	1	-13.36	5.64	1.79E-02	-0.45	0.46	3.29E-01	-6.84	2.08	1.03E-03	-2.17	4.33E-05	-	-	-0.85	3.98E-01	-0.07	0.23	7.62E-01	-	-
1	25351284	cg00158128	MIR4425	-8.88	1.95	5.01E-06	7.48E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.08E-05
17	40724562	cg00170714	PSMC3IP	-12.16	2.67	5.32E-06	7.80E-03	1	-6.23	2.96	3.56E-02	0.21	0.99	8.35E-01	-12.13	2.24	6.15E-08	-1.03	8.31E-05	2.81	5.93E-03	-1.92	5.88E-02	0.37	0.26	1.58E-01	-0.03	8.55E-04
11	6225537	cg00286717	C11orf42	-20.04	4.89	4.21E-05	3.62E-02	1	-6.01	2.83	3.40E-02	-0.61	0.55	2.69E-01	-4.10	2.23	6.56E-02	-0.75	3.88E-03	2.44	1.64E-02	-2.09	4.01E-02	0.65	0.30	3.04E-02	-0.02	1.58E-03
17	17156056	cg00321711	FLCN	-13.10	2.67	9.06E-07	2.09E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.84E-05
10	114437411	cg00329570	MIR4295	-25.87	6.17	2.75E-05	2.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.94E-02
14	55583041	cg00336912	LGALS3	-26.96	4.87	3.04E-08	1.89E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.32E-03
17	59296188	cg00359030	LOC1019278	-52.76	12.33	1.86E-05	2.04E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.17E-02
3	33837694	cg00381391	PDCD6IP	-18.51	4.25	1.35E-05	1.59E-02	1	-5.55	2.72	4.10E-02	-0.63	0.77	4.16E-01	-9.44	2.31	4.25E-05	-0.49	8.37E-03	-2.99	3.47E-03	-4.60	1.83E-05	0.16	0.24	4.98E-01	-0.03	3.06E-04
9	123969395	cg00381516	RAB14	-35.69	8.36	1.96E-05	2.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	9.72E-05
20	62700725	cg00390694	TCEA2	-14.72	3.56	3.56E-05	3.23E-02	1	-19.25	9.09	3.42E-02	-0.27	0.54	6.11E-01	-12.66	3.94	1.30E-03	-	-	-0.38	7.04E-01	-2.71	8.58E-03	0.58	0.24	1.37E-02	-0.01	2.73E-03
12	15124659	cg00390941	PDE6H	-38.45	7.17	8.15E-08	3.91E-04	1	-12.22	5.30	2.10E-02	-1.19	0.95	2.14E-01	-9.46	3.15	2.70E-03	-0.60	7.89E-03	0.85	3.98E-01	-2.24	2.86E-02	0.40	0.24	9.70E-02	-0.02	1.60E-03
17	33885049	cg00397422	SLFN14	-13.36	3.34	6.39E-05	4.84E-02	1	-7.73	3.82	4.32E-02	-1.08	0.68	1.14E-01	-4.70	2.59	7.02E-02	-0.48	4.10E-02	-2.35	2.06E-02	-3.15	2.41E-03	0.16	0.30	5.87E-01	-0.02	7.98E-03
20	35504511	cg00414077	TLDC2	-10.86	1.97	3.26E-08	1.94E-04	1	-13.87	5.81	1.71E-02	-0.21	0.46	6.46E-01	-7.60	2.18	4.92E-04	-0.13	7.55E-01	2.39	1.85E-02	-0.88	3.84E-01	0.42	0.24	8.07E-02	-0.01	4.08E-02
2	217120445	cg00427854	LINC01963	-27.56	6.43	1.82E-05	2.00E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.81E-04
17	25833338	cg00460843	KSR1	-14.68	2.97	8.05E-07	1.94E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.41E-02
19	3521502	cg00477633	FZR1	-27.50	5.50	5.61E-07	1.49E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.17E-03
12	44228244	cg00491149	TMEM117	-21.54	5.37	5.95E-05	4.62E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.75E-02
15	79609419	cg00527937	TMED3	-16.03	2.64	1.27E-09	2.17E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.79E-05
1	872235	cg00582671	SAMD11	-11.74	2.14	4.27E-08	2.37E-04	1	-9.19	4.35	3.47E-02	0.30	0.68	6.58E-01	-6.37	1.87	6.56E-04	-1.04	3.30E-03	-	-	-1.97	5.27E-02	0.13	0.24	5.69E-01	-0.02	8.75E-03
4	108615003	cg00587765	PAPSS1	-19.87	4.94	5.73E-05	4.49E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.22E-05
2	219254588	cg00634542	SLC11A1	-6.43	1.56	3.86E-05	3.40E-02	1	-7.18	4.00	7.25E-02	0.10	0.36	7.79E-01	-2.75	1.78	1.23E-01	-0.95	7.38E-04	-	-	-0.79	4.32E-01	0.08	0.23	7.39E-01	-0.01	5.06E-01
6	137544615	cg00638845	IFNGR1	-23.57	4.94	1.88E-06	3.63E-03	1	-6.73	3.11	3.06E-02	0.24	0.77	7.60E-01	-8.46	2.71	1.77E-03	-0.16	4.18E-01	-3.08	2.59E-03	-0.93	3.54E-01	0.38	0.25	1.32E-01	-0.02	5.27E-03
14	75890874	cg00658852	JDP2	-44.56	8.09	3.57E-08	2.03E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.44E-03
21	37536923	cg00673191	DOPEY2	-5.47	1.20	4.90E-06	7.40E-03	1	-6.24	3.52	7.59E-02	-1.53	0.59	9.22E-03	-3.13	1.85	9.03E-02	-0.99	6.07E-05	1.87	6.40E-02	-0.71	4.80E-01	0.23	0.43	5.92E-01	-0.01	1.23E-01
21	46955647	cg00714531	SLC19A1	-15.67	3.31	2.24E-06	4.14E-03	1	-7.95	3.56	2.54E-02	0.29	0.64	6.52E-01	-9.26	2.20	2.63E-05	-0.64	3.32E-03	-	-	-2.40	1.90E-02	0.15	0.24	5.34E-01	-0.02	4.94E-03
3	49522836	cg00742276	DAG1	-18.34	3.46	1.20E-07	4.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.05E-03
7	117581709	cg00746666	CTTNBP2	-16.60	3.73	8.48E-06	1.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.70E-04
2	43516267	cg00758214	LINC01126	-32.92	7.10	3.50E-06	5.77E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.57E-03
12	132464955	cg00764582	EP400	-14.27	3.35	2.03E-05	2.17E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.74E-02
11	46579500	cg00766820	AMBRA1	-24.76	5.37	3.97E-06	6.21E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.11E-02
2	129236825	cg00785978	HS6ST1	-11.84	2.63	6.50E-06	9.00E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.69E-04
12	52995634	cg00793181	KRT72	-13.21	3.21	3.96E-05	3.46E-02	1	-16.53	7.32	2.40E-02	-0.13	0.55	8.18E-01	-7.95	2.38	8.41E-04	-0.76	4.62E-03	-	-	-2.49	1.50E-02	0.03	0.22	8.99E-01	-0.02	1.54E-03
17	40168331	cg00823480	D-JC7	-19.32	3.40	1.26E-08	1.05E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.21E-04
22	39848852	cg00827939	MGAT3	-9.21	2.28	5.16E-05	4.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.47E-04
1	234835623	cg00851361	LINC01132	-14.32	2.69	9.73E-08	4.32E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	9.19E-02
18	19334381	cg00924612	MIB1	-35.71	8.24	1.46E-05	1.70E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.13E-05
17	59297117	cg00961073	LOC1019278	-37.35	7.91	2.33E-06	4.27E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.65E-03
14	55850801	cg00978517	ATG14	-28.26	5.11	3.14E-08	1.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.96E-05
20	17659317	cg00990977	RRBP1	-31.26	7.14	1.18E-05	1.43E-02	1	-15.01	7.06	3.36E-02	1.03	0.83	2.14E-01	-10.40	3.18	1.07E-03	-0.62	7.45E-03	-	-	-3.25	1.76E-03	0.27	0.25	2.76E-01	-0.02	1.03E-05
14	100610667	cg01000631	DEGS2	-13.01	2.11	7.32E-10	1.57E-05	1	-8.15	3.71	2.80E-02	-1.02	0.82	2.16E-01	-9.86	1.81	4.88E-08	-0.88	3.93E-05	-	-	-2.26	2.70E-02	0.06	0.21	7.76E-01	-0.04	3.86E-06
7	127527862	cg01009225	SND1-IT1	-43.24	7.47	7.13E-09	7.18E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.85E-04
8	38007025	cg01047262	STAR	-41.58	8.97	3.54E-06	5.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.56E-05
18	9521949	cg01048814	RALBP1	-30.33	7.58	6.28E-05	4.79E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	9.08E-04
14	55604454	cg01051098	LGALS3	-43.51	10.21	2.03E-05	2.17E-02	1	-25.84	11.83	2.89E-02	-0.44	0.49	3.65E-01	-11.50	4.82	1.71E-02	-1.28	7.45E-05	3.05	2.87E-03	-3.28	1.62E-03	0.14	0.21	5.04E-01	-0.01	3.76E-02
20	61923909	cg01051200	COL20A1	-16.22	3.98	4.68E-05	3.92E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.44E-03
10	119167795	cg01086527	PDZD8	-24.56	4.62	1.07E-07	4.69E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.03E-04
7	139948872	cg01116541	JHDM1D-AS1	-6.65	1.61	3.64E-05	3.28E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.12E-03
7	135541567	cg01119571	FAM180A	-31.81	5.88	6.38E-08	3.20E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.85E-05
16	53120120	cg01137366	CHD9	-10.21	2.04	5.59E-07	1.49E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.73E-02
3	195974349	cg01139080	SLC51A	-14.80	2.79	1.11E-07	4.70E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.17E-06
11	75409605	cg01167694	MOGAT2	-20.35	4.97	4.25E-05	3.64E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.52E-03
16	30967493	cg01191788	SETD1A	-19.37	4.24	4.94E-06	7.42E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.30E-06
1	151818600	cg01200145	C2CD4D	-6.16	1.46	2.55E-05	2.56E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.36E-03
2	233076983	cg01224965	ALPP	-17.29	3.67	2.41E-06	4.36E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.89E-06
11	47092992	cg01258949	ARFGAP2	-28.15	6.74	2.96E-05	2.86E-02	1	-5.01	3.13	1.09E-01	-0.19	0.28	4.90E-01	-4.54	2.69	9.07E-02	-0.47	2.03E-02	1.28	2.04E-01	-1.64	1.05E-01	0.25	0.28	3.71E-01	-0.03	2.09E-03
8	57885566	cg01279789	IMPAD1	-36.37	9.08	6.16E-05	4.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.89E-04
15	39823154	cg01284182	THBS1	-11.12	2.69	3.60E-05	3.25E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.42E-04
3	183631176	cg01291780	PARL	-25.04	6.01	3.13E-05	2.99E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.19E-03

14	88502505	cg01295798	LOC1019287	-35.29	7.07	6.06E-07	1.57E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.83E-05
16	30409908	cg01304182	ZNF48	-7.03	1.70	3.52E-05	3.22E-02	1	-15.56	6.86	2.33E-02	0.03	0.44	9.53E-01	-7.21	2.03	3.68E-04	-1.43	1.53E-05	1.68	9.52E-02	-1.66	1.01E-01	0.12	0.25	6.51E-01	-0.02	9.27E-03
3	3152374	cg01310029	IL5RA	-11.96	2.58	3.64E-06	5.85E-03	1	-6.07	2.92	3.76E-02	-1.45	0.53	5.69E-03	-11.12	2.42	4.18E-06	-1.71	3.59E-10	-	-	-3.59	6.09E-04	0.35	0.24	1.44E-01	-0.04	6.97E-07
22	39869399	cg01315054	MGAT3-AS1	-14.00	3.46	5.23E-05	4.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.51E-03
10	129799166	cg01325448	PTPRE	-13.56	2.84	1.78E-06	3.47E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.39E-04
17	7648108	cg01330991	RPL29P2	-19.62	4.75	3.67E-05	3.29E-02	1	-6.05	2.98	4.25E-02	0.00	0.52	9.94E-01	-8.11	2.36	5.98E-04	-0.74	1.64E-03	-0.65	5.16E-01	-1.85	6.87E-02	0.44	0.27	1.01E-01	-0.02	5.89E-03
3	142724451	cg01375248	U2SURP	-7.34	1.82	5.79E-05	4.52E-02	1	-9.45	4.58	3.92E-02	0.57	0.60	3.43E-01	-3.22	1.98	1.04E-01	-0.02	9.31E-01	1.43	1.55E-01	-0.94	3.53E-01	0.37	0.21	7.80E-02	-0.03	3.86E-02
15	41246346	cg01437709	CHAC1	-28.95	5.06	1.04E-08	9.04E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.58E-05
11	2696198	cg01439230	KCNQ1OT1	-43.54	8.46	2.65E-07	8.68E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.37E-02
11	12136467	cg01450133	MICAL2	-26.45	5.56	1.93E-06	3.70E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.92E-06
11	6552435	cg01482779	DNHD1	-7.92	1.85	1.78E-05	1.97E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.77E-02
9	35755346	cg01499988	MSMP	-18.28	3.85	2.06E-06	3.87E-03	1	-7.33	3.51	3.65E-02	-1.84	0.88	3.70E-02	-12.47	2.62	2.01E-06	-0.78	6.86E-04	-2.67	8.73E-03	-2.95	4.30E-03	0.49	0.25	4.51E-02	-0.02	3.26E-02
4	3240754	cg01542143	MSANTD1	-14.06	3.37	2.94E-05	2.85E-02	1	-11.78	4.78	1.37E-02	-0.14	0.75	8.55E-01	-8.37	2.72	2.05E-03	-1.06	2.13E-04	2.51	1.34E-02	-1.22	2.27E-01	0.24	0.22	2.73E-01	-0.02	2.84E-04
20	4764277	cg01613077	RASSF2	-33.67	5.77	5.44E-09	6.01E-05	1	-12.16	4.83	1.18E-02	0.36	0.83	6.66E-01	-9.97	2.88	5.27E-04	-0.45	2.29E-02	-0.40	6.90E-01	-3.80	3.06E-04	0.50	0.24	3.80E-02	-0.03	4.51E-06
10	45495435	cg01614759	ZNF22	-22.65	3.75	1.52E-09	2.44E-05	1	-5.84	2.80	3.73E-02	-1.20	0.67	7.48E-02	-9.31	2.36	8.19E-05	-0.75	1.91E-04	-0.07	9.47E-01	-3.01	3.61E-03	0.23	0.24	3.53E-01	-0.03	1.56E-05
19	30432160	cg01627992	URI1	-20.30	4.98	4.65E-05	3.91E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.79E-03
1	95358601	cg01633282	CNN3	-40.23	9.96	5.34E-05	4.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.61E-02
12	109568238	cg01671341	ACACB	-17.77	4.31	3.75E-05	3.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.41E-05
9	126497597	cg01745810	DENND1A	-27.03	3.78	8.29E-13	2.26E-07		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	2810737	cg01750299	PUM3	-14.27	3.53	5.40E-05	4.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.49E-02
10	5487127	cg01808470	NET1	-36.13	8.66	3.04E-05	2.91E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.60E-03
14	95615731	cg01901579	DICER1	-25.25	3.91	1.07E-10	4.58E-06	1	-7.41	3.52	3.53E-02	-3.39	0.93	2.62E-04	-9.29	2.05	5.86E-06	-0.65	3.60E-03	1.43	1.55E-01	-1.06	2.91E-01	0.21	0.27	4.33E-01	-0.03	1.34E-04
20	3989981	cg01908419	RNF24	-9.90	2.37	2.90E-05	2.82E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.72E-04
2	96965099	cg01923915	SNRNP200	-31.04	4.88	2.07E-10	6.55E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.16E-03
17	13996337	cg01927901	COX10-AS1	-26.02	5.58	3.13E-06	5.35E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.32E-04
1	27240694	cg01942646	NR0B2	-23.71	4.02	3.66E-09	4.75E-05	1	-5.88	2.83	3.75E-02	-0.31	0.66	6.41E-01	-13.02	2.70	1.45E-06	-1.25	8.21E-05	3.77	2.69E-04	-1.84	6.98E-02	0.27	0.25	2.71E-01	-0.04	3.30E-06
17	56269767	cg01955639	EPX	-18.56	3.55	1.76E-07	6.37E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.63E-06
2	217120630	cg01970030	LINC01963	-33.21	7.17	3.59E-06	5.82E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.64E-04
22	32873926	cg01976243	FBXO7	-13.62	2.90	2.73E-06	4.78E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.50E-03
7	2683257	cg01978458	TTYH3	-11.02	2.17	3.66E-07	1.11E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.84E-04
16	55542709	cg01998785	LPCAT2	-9.66	2.13	6.03E-06	8.49E-03	1	-7.34	3.48	3.48E-02	-0.92	0.80	2.50E-01	-9.91	1.99	6.17E-07	-1.49	1.07E-06	0.28	7.81E-01	-3.01	3.60E-03	0.36	0.24	1.41E-01	-0.03	3.15E-04
11	75550064	cg02046836	UVRAG	-30.85	4.92	3.67E-10	9.08E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.22E-03
12	123872423	cg02053425	KMT5A	-7.19	1.78	5.25E-05	4.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.85E-02
19	15436097	cg02068052	BRD4	-17.74	3.59	7.69E-07	1.88E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.66E-03
14	69801210	cg02095988	ERH	-18.35	4.47	4.09E-05	3.54E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.76E-08
16	85655007	cg02124524	GSE1	-39.07	7.77	4.95E-07	1.37E-03	1	-11.70	5.34	2.85E-02	-2.79	0.78	3.49E-04	-12.66	3.25	9.91E-05	-	-	-	-	-5.33	1.15E-06	0.44	0.25	7.92E-02	-	-
8	128981622	cg02133716	MIR1205	-32.82	6.38	2.71E-07	8.75E-04	1	-11.43	5.12	2.55E-02	-1.53	0.95	1.08E-01	-16.57	3.37	8.64E-07	-0.87	1.39E-04	-2.46	1.53E-02	-3.76	3.47E-04	0.30	0.24	2.05E-01	-0.02	1.81E-06
9	130158080	cg02137883	SLC2A8	-31.23	5.20	1.97E-09	2.93E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.60E-04
12	92431524	cg02142455	LINC01619	-39.70	8.14	1.08E-06	2.32E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.84E-04
14	69650830	cg02170785	EXD2	-13.94	2.99	3.05E-06	5.22E-03	1	-5.46	2.73	4.57E-02	-0.69	0.55	2.15E-01	-9.79	2.50	9.20E-05	-0.82	1.37E-04	-	-	-3.80	3.13E-04	0.14	0.24	5.47E-01	-0.03	4.78E-05
1	26517586	cg02171825	CATSPER4	-51.26	9.24	2.84E-08	1.85E-04	1	-11.31	4.99	2.34E-02	-0.55	0.89	5.34E-01	-13.19	2.97	9.01E-06	-	-	-0.68	4.99E-01	-3.24	1.82E-03	0.47	0.37	2.03E-01	-0.01	2.32E-02
9	126312322	cg02202133	MIR7150	-14.96	2.82	1.08E-07	4.69E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	9.79E-02
8	59564316	cg02212711	NSMAF	-21.97	4.99	1.07E-05	1.32E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.28E-03
9	84249091	cg02227075	TLE1	-18.17	3.89	2.98E-06	5.14E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.01E-04
3	11522965	cg02228403	VGLL4	-26.56	5.71	3.29E-06	5.56E-03	1	-4.68	2.40	5.12E-02	-0.53	0.72	4.61E-01	-9.84	2.63	1.79E-04	0.31	1.13E-01	0.85	3.95E-01	-1.38	1.71E-01	0.25	0.25	3.23E-01	-0.03	1.01E-05
11	43760352	cg02233915	HSD17B12	-36.52	6.89	1.15E-07	4.80E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.25E-04
16	78782477	cg02236679	WWOX	-22.41	5.61	6.39E-05	4.84E-02	1	-19.25	8.99	3.22E-02	-0.30	0.28	2.81E-01	-7.68	3.40	2.38E-02	-	-	1.79	7.58E-02	-2.62	1.09E-02	0.43	0.24	7.26E-02	0.00	5.55E-01
17	66443040	cg02243624	WIPI1	-27.67	6.13	6.29E-06	8.81E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.66E-04
1	118153944	cg02290349	FAM46C	-23.24	4.06	1.03E-08	9.04E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.39E-03
12	121130587	cg02324015	MLEC	-35.56	7.98	8.25E-06	1.09E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.19E-02
11	3170821	cg02332678	OSBPL5	-9.53	2.23	1.84E-05	2.02E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.99E-05
19	34860339	cg02359181	GPI	-19.21	4.07	2.33E-06	4.27E-03	1	-6.39	3.12	4.04E-02	-1.46	0.77	5.82E-02	-12.75	2.72	2.68E-06	-1.36	2.74E-07	-2.85	5.27E-03	-3.61	5.69E-04	0.12	0.25	6.30E-01	-0.03	7.14E-05
9	130866500	cg02361196	SLC25A25	-15.11	2.88	1.57E-07	5.87E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.02E-03
16	15698882	cg02374401	MIR6506	-15.41	3.69	2.99E-05	2.88E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.62E-01
19	41255444	cg02402423	C19orf54	-17.70	3.83	3.82E-06	6.04E-03	1	-12.83	5.34	1.63E-02	-0.23	0.60	7.02E-01	-8.73	2.10	3.29E-05	-0.92	9.76E-03	3.76	2.75E-04	-2.38	1.99E-02	-0.11	0.21	6.08E-01	-0.02	1.37E-02
2	99122909	cg02420943	INPP4A	-7.62	1.80	2.43E-05	2.47E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.27E-05
3	186193874	cg02423065	LINC02052	-25.87	5.69	5.46E-06	7.97E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
4	103750639	cg02436083	LOC1053773	-23.07	4.39	1.49E-07	5.70E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.44E-03
19	41925187	cg02447557	B3GNT8	-34.35	7.00	9.11E-07	2.09E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.41E-05
2	9752386	cg02473287	YWHAQ	-14.51	3.41	2.15E-05	2.25E-02	1	-8.25	3.83	3.14E-02	-0.58	0.51	2.59E-01	-10.99	2.46	8.00E-06	-0.79	4.79E-04	-1.82	7.12E-02	-2.52	1.39E-02	0.19	0.28	5.00E-01	-0.02	7.41E-04
11	61033076	cg02487088	PGA5	-15.70	2.75	1.14E-08	9.73E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.05E-03
2	161798364	cg02494549	TANK	-27.74	6.35	1.24E-05	1.49E-02	1	-4.51	2.35	5.48E-02	-1.72	0.91	5.84E-02	-14.66	2.80	1.56E-07	-0.85	3.75E-04	-1.11	2.68E-01	-4.51	2.56E-05	0.30	0.25	2.31E-01	-0.01	3.92E-02
11	85781719	cg02503303	PICALM	-12.38	2.35	1.35E-07	5.32E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.47E-05
14	39643445	cg02543556	PNN	-19.55	4.55	1.72E-05	1.93E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.71E-05
2	7027871	cg02589986	RSAD2	-8.31	1.99	2.85E-05	2.78E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.69E-04
22	30650471	cg02645272	LIF	-15.97	2.86	2.46E-08	1.65E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.31E-05
19	44124896	cg02668270	ZNF428	-10.26	2.54	5.50E-05	4.35E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.96E-03

1	180940271	cg02683853	STX6	-23.30	5.52	2.42E-05	2.46E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.55E-05
10	114437552	cg02698198	MIR4295	-17.35	3.44	4.62E-07	1.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.62E-03
17	80200741	cg02765363	MIR6787	-9.06	2.15	2.50E-05	2.52E-02	1	-19.23	8.84	2.97E-02	0.14	0.49	7.72E-01	-3.16	2.45	1.97E-01	-	-	2.39	1.84E-02	-1.63	1.08E-01	0.20	0.23	3.94E-01	-0.02	1.90E-02
3	195974300	cg02803925	SLC51A	-26.60	4.12	1.13E-10	4.62E-06	1	-5.76	2.78	3.82E-02	-0.13	0.39	7.32E-01	-14.57	2.97	9.27E-07	-	-	-2.15	3.34E-02	-3.32	1.45E-03	0.46	0.31	1.45E-01	-0.04	6.92E-05
2	192043611	cg02856510	STAT4	-16.12	3.82	2.42E-05	2.46E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.68E-04
14	21089395	cg02864713	OR6S1	-20.34	5.02	5.07E-05	4.16E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.49E-02
16	31135265	cg02869730	KAT8	-52.72	11.25	2.77E-06	4.84E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.43E-03
9	115184285	cg02874537	HSDL2	-5.67	1.37	3.33E-05	3.12E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01	6.31E-01
20	48806066	cg02930951	CEBPB	-14.97	3.61	3.40E-05	3.16E-02	1	-12.62	5.73	2.77E-02	0.45	0.76	5.51E-01	-5.18	2.37	2.87E-02	-0.74	3.54E-03	-4.60	1.15E-05	-1.89	6.29E-02	0.08	0.25	7.36E-01	-0.01	8.21E-02
18	71910225	cg02951831	CYB5A	-6.08	1.41	1.73E-05	1.93E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.58E-02
17	56269818	cg02970679	EPX	-19.97	4.62	1.53E-05	1.76E-02	1	-8.44	3.73	2.37E-02	-0.26	0.96	7.88E-01	-13.35	2.73	9.99E-07	-0.99	9.57E-06	-1.04	3.03E-01	-3.26	1.74E-03	0.18	0.22	4.08E-01	-0.03	6.25E-06
17	58459590	cg02979987	USP32	-33.62	7.25	3.58E-06	5.81E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.22E-03
7	97908505	cg02985445	BRI3	-13.46	2.62	2.73E-07	8.76E-04	1	-10.05	4.34	2.05E-02	-0.43	0.44	3.25E-01	-6.54	2.16	2.44E-03	0.86	6.51E-02	5.86	5.02E-08	0.59	5.59E-01	0.20	0.21	3.35E-01	-0.02	8.08E-04
5	176920990	cg02996630	PDLIM7	-7.25	1.79	5.15E-05	4.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.10E-05
4	2368055	cg03035271	ZFYVE28	-4.01	0.97	3.58E-05	3.24E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	7.63E-01
3	57064082	cg03069832	SPATA12	-15.82	3.93	5.68E-05	4.47E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	64216380	cg03074692	LOC1009964	18.62	4.64	5.88E-05	4.58E-02	1	1.85	3.40	5.86E-01	-0.43	0.71	5.42E-01	2.45	3.07	4.24E-01	-	-	-	-	0.81	4.19E-01	0.15	0.20	4.57E-01	-	-
5	141909727	cg03079679	FGF1	-9.35	2.30	4.76E-05	3.98E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.03E-02
1	33221514	cg03092343	KIAA1522	-16.03	3.15	3.49E-07	1.07E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.28E-04
2	8676902	cg03119191	LINC01814	-10.78	2.19	8.06E-07	1.94E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.03E-02
12	123446272	cg03131767	ABCB9	-16.29	3.87	2.61E-05	2.61E-02	1	-6.82	3.17	3.11E-02	-0.11	0.61	8.58E-01	-11.72	2.36	7.21E-07	0.66	1.73E-03	5.99	2.66E-08	1.75	8.41E-02	0.28	0.25	2.69E-01	-0.02	1.82E-02
13	110350537	cg03189469	LINC00676	-16.44	3.54	3.50E-06	5.77E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.01E-06
12	47477069	cg03210018	AMIGO2	-17.39	3.25	8.86E-08	4.02E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.49E-05
3	128134845	cg03278639	D-JB8-AS1	-15.02	3.39	9.14E-06	1.17E-02	1	-10.25	4.51	2.30E-02	-0.52	0.89	5.60E-01	-5.81	2.21	8.55E-03	-0.92	4.53E-04	-3.52	6.20E-04	-3.27	1.69E-03	0.05	0.22	8.29E-01	-0.02	1.70E-05
18	33159713	cg03318414	MIR3975	-13.98	3.06	4.92E-06	7.40E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.74E-04
6	167189272	cg03329755	RPS6KA2	-19.00	3.93	1.37E-06	2.82E-03	1	-9.55	4.41	3.04E-02	-0.86	0.41	3.77E-02	-8.91	1.97	6.14E-06	-	-	-	-	-2.24	2.81E-02	0.16	0.20	4.26E-01	-0.03	8.69E-04
7	139427635	cg03369382	HIPK2	-42.76	8.13	1.44E-07	5.55E-04	1	-11.49	5.26	2.90E-02	0.21	0.59	7.28E-01	-4.92	3.05	1.07E-01	-0.47	1.40E-02	-6.56	1.86E-09	-1.65	1.04E-01	-0.04	0.23	8.69E-01	-0.01	1.21E-02
16	16195619	cg03392077	ABCC6	-8.72	1.53	1.31E-08	1.08E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.51E-02
11	62678778	cg03448301	CHRM1	-34.44	7.13	1.38E-06	2.82E-03	1	-6.28	3.16	4.69E-02	-1.43	0.93	1.21E-01	-11.97	2.97	5.69E-05	-0.93	1.21E-05	-1.17	2.43E-01	-3.88	2.37E-04	0.31	0.25	2.18E-01	-0.02	1.54E-04
16	55542668	cg03471593	LPCAT2	-6.11	1.21	4.03E-07	1.17E-03	1	-6.78	3.64	6.24E-02	-0.66	0.41	1.08E-01	-4.46	1.31	6.72E-04	-0.80	8.72E-06	-	-	-1.81	7.48E-02	0.20	0.23	3.70E-01	-0.01	4.40E-01
8	21670183	cg03475216	GFRA2	-17.47	3.95	9.91E-06	1.24E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.18E-04
9	91994786	cg03492094	SECISBP2	-11.08	1.91	6.25E-09	6.54E-05	1	-9.83	4.51	2.93E-02	-0.14	0.53	7.97E-01	-7.12	1.97	3.13E-04	-1.21	1.11E-04	-3.01	3.29E-03	-3.15	2.44E-03	0.42	0.25	9.66E-02	-0.03	8.07E-05
16	69567173	cg03501393	MIR1538	-6.57	1.51	1.31E-05	1.56E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.17E-02
6	36108112	cg03502211	MAPK13	-18.08	3.99	5.91E-06	8.40E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.07E-04
6	167135251	cg03512256	RPS6KA2	-30.19	7.20	2.73E-05	2.70E-02	1	-22.42	10.59	3.42E-02	0.19	0.85	8.25E-01	-9.81	2.86	6.15E-04	-0.07	7.43E-01	-	-	-2.40	1.91E-02	0.38	0.25	1.26E-01	-0.02	7.26E-07
17	56274597	cg03519593	EPX	-14.24	3.32	1.75E-05	1.94E-02	1	-11.34	4.76	1.71E-02	0.07	0.90	9.39E-01	-8.29	2.53	1.07E-03	-0.63	2.37E-03	0.90	3.71E-01	-0.99	3.27E-01	0.13	0.20	5.12E-01	-0.02	1.19E-02
10	5576480	cg03651219	CALML3-AS1	-21.28	4.98	1.94E-05	2.10E-02	1	-9.22	5.09	6.99E-02	-0.17	0.25	4.99E-01	-11.23	2.85	8.18E-05	-	-	1.38	1.71E-01	-2.21	3.04E-02	0.37	0.22	9.35E-02	-0.02	1.36E-03
17	73331630	cg03653158	SLC25A19	-13.87	3.22	1.64E-05	1.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.96E-04
15	101798908	cg03666966	CHSY1	-31.64	6.05	1.74E-07	6.33E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	65547172	cg03695871	AP5B1	-6.67	1.17	1.09E-08	9.41E-05	1	-11.29	5.91	5.60E-02	-0.14	0.28	6.09E-01	-5.64	1.43	7.81E-05	-1.13	2.94E-08	-2.25	2.64E-02	-2.16	3.40E-02	0.73	0.31	1.90E-02	-0.02	7.37E-02
1	179005979	cg03698182	FAM20B	-15.55	3.85	5.26E-05	4.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.19E-03
17	80188275	cg03722757	SLC16A3	-6.75	1.63	3.46E-05	3.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.66E-02
10	114437682	cg03756297	MIR4295	-39.26	7.57	2.17E-07	7.31E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.05E-03
9	114957571	cg03757043	SUSD1	-17.44	3.81	4.78E-06	7.25E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.30E-04
6	25608913	cg03784596	SCGN	-30.79	6.31	1.09E-06	2.33E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.44E-05
20	35943761	cg03812149	MANBAL	-13.96	2.64	1.28E-07	5.16E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.37E-03
16	70648377	cg03837359	IL34	-18.16	3.35	6.01E-08	3.07E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.37E-05
16	67075173	cg03850588	CBFB	-18.81	3.88	1.23E-06	2.58E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.63E-04
16	23511855	cg03935956	GGA2	-9.21	1.96	2.68E-06	4.74E-03	1	-9.21	4.36	3.49E-02	-0.29	0.55	5.95E-01	-6.40	1.86	5.74E-04	-0.26	2.46E-01	-3.85	1.98E-04	-2.25	2.80E-02	0.17	0.25	4.81E-01	-0.02	4.42E-02
16	85568407	cg03983220	GSE1	-4.49	1.10	4.49E-05	3.80E-02	1	-7.58	3.89	5.15E-02	-0.26	0.42	5.40E-01	-4.86	1.75	5.51E-03	-0.59	6.61E-03	-1.81	7.32E-02	-2.61	1.11E-02	0.14	0.23	5.52E-01	-0.02	7.90E-02
1	175772135	cg04031158	TNR	-29.72	5.85	3.81E-07	1.14E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.10E-05
1	43291088	cg04036011	ERMAP	-7.18	1.78	5.51E-05	4.36E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.88E-04
2	74311093	cg04100865	BOLA3	-31.22	5.06	6.83E-10	1.55E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.87E-04
9	101595635	cg04148640	GALNT12	-37.63	7.67	9.23E-07	2.11E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.65E-05
6	140053824	cg04170495	LOC1001327	-8.09	1.96	3.53E-05	3.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.05E-05
17	9838988	cg04202435	GAS7	-14.85	3.49	2.09E-05	2.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.10E-02
3	66428294	cg04217850	LRIG1	-20.90	4.45	2.60E-06	4.61E-03	1	-11.58	5.79	4.57E-02	0.10	1.09	9.25E-01	-13.23	2.80	2.35E-06	-0.97	1.65E-04	-0.92	3.58E-01	-2.67	9.42E-03	0.16	0.24	4.88E-01	-0.03	3.66E-07
12	122826219	cg04236871	CLIP1-AS1	-16.90	3.73	5.96E-06	8.42E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.84E-05
10	88477842	cg04259566	BMPR1A	-17.88	4.34	3.74E-05	3.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.61E-03
7	65439512	cg04290133	GUSB	-21.69	3.28	3.61E-11	3.09E-06	1	-9.59	4.20	2.25E-02	-1.27	0.65	5.07E-02	-8.18	2.11	1.07E-04	-	-	-1.38	1.71E-01	-4.07	1.25E-04	0.33	0.24	1.63E-01	-0.03	4.34E-05
8	131454686	cg04308301	ASAP1	-17.24	3.30	1.82E-07	6.52E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.34E-02
1	43290841	cg04377912	ERMAP	-32.98	6.98	2.32E-06	4.27E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.76E-05
3	44381576	cg04385523	TCAIM	-48.35	9.26	1.80E-07	6.49E-04	1	-10.65	4.66	2.22E-02	-1.31	0.81	1.07E-01	-6.45	3.06	3.52E-02	-0.65	6.19E-03	1.90	6.05E-02	-4.13	1.01E-04	0.41	0.28	1.33E-01	-0.01	2.27E-03
3	12269362	cg04399631	PPARG	-7.53	1.53	9.04E-07	2.09E-03	1	-4.99	2.72	6.68E-02	-0.77	0.48	1.08E-01	-3.30	1.79	6.41E-02	-0.27	1.47E-01	2.08	4.02E-02	-0.94	3.53E-01	0.31	0.24	1.93E-01	-0.02	8.39E-02
3	39217727	cg04404773	XIRP1	-9.44	2.25	2.67E-05	2.65E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.64E-05
19	39303993	cg04420917	LGALS4	-13.42	3.09	1.37E-05	1.61E-02	1	-11.60	5.27	2.79E-02	-0.53	0.80	5.10E-01	-6.21	2.44	1.11E-02	0.48	8.25E-02	2.23	2.79E-02	1.64	1.07E-01	0.31	0.24	1.86E-01	-0.02	8.02E-04
5	179751794	cg04459091	GFPT2	-22.99	5.73	6.07E-05	4.68E-02	1	-15.17	6.84	2.65E-02	-1.05	0.76	1.68E-01	-10.45	3.20	1.11E-03	-0.82	1.92E-05	0.63	5.31E-01	-3.97	1.76E-04	0.13	0.21	5.37E-01	-0.03	1.34E-08

4	153499517	cg04459751	MIR4453	-17.61	2.88	9.37E-10	1.85E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	8.28E-06
11	73897097	cg04484304	PPME1	-32.10	7.78	3.73E-05	3.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.27E-03
16	616212	cg04497992	NHLRC4	-13.86	2.20	2.75E-10	8.34E-06	1	-9.64	4.73	4.14E-02	-0.32	0.56	5.70E-01	-10.13	2.13	1.92E-06	-1.61	1.81E-04	-	-	-1.58	1.20E-01	0.14	0.23	5.59E-01	-0.02	3.61E-03
10	86096789	cg04546473	CCSER2	-19.57	4.12	2.05E-06	3.87E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.59E-03
14	69154547	cg04564998	LOC1009966	-54.62	13.36	4.36E-05	3.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01	7.37E-02
3	125181706	cg04569594	SNX4	-34.73	8.42	3.74E-05	3.31E-02	1	-6.45	3.15	4.09E-02	-0.24	0.76	7.52E-01	-11.10	3.07	2.98E-04	-1.09	1.15E-05	1.74	8.53E-02	-2.92	4.72E-03	0.41	0.22	6.26E-02	-0.02	5.82E-04
10	97624495	cg04587103	C10orf131	-10.37	2.50	3.40E-05	3.16E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.31E-04
7	73650354	cg04650104	RFC2	-13.98	2.58	5.71E-08	2.95E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.27E-02
17	45708176	cg04681520	KPNB1	-46.34	10.05	3.98E-06	6.23E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.11E-05
3	127543047	cg04721651	MGLL	-10.31	2.40	1.75E-05	1.94E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.11E-03
1	242351909	cg04763288	MAP1LC3C	-18.74	4.68	6.13E-05	4.71E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.03E-03
18	61550142	cg04765589	SERPINB2	-28.28	6.71	2.53E-05	2.55E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.80E-04
12	113642799	cg04806741	IQCD	-21.62	4.32	5.73E-07	1.50E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	5587802	cg04825341	RIC1	-27.59	5.53	5.99E-07	1.55E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.58E-04
16	85654213	cg04847043	GSE1	-26.95	5.91	5.15E-06	7.63E-03	1	-10.06	4.45	2.36E-02	-0.69	0.85	4.17E-01	-10.92	2.99	2.66E-04	-0.86	9.02E-05	-	-	-3.91	2.13E-04	0.45	0.24	6.14E-02	-	-
9	139701021	cg04883329	RABL6	-7.53	1.51	6.59E-07	1.67E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.42E-01
16	3246099	cg04931493	OR1F1	-3.55	0.84	2.16E-05	2.26E-02	1	10.17	9.29	2.74E-01	-0.17	1.02	8.65E-01	-0.09	1.59	9.57E-01	-1.14	4.02E-02	3.02	3.19E-03	0.56	5.80E-01	0.18	0.17	3.03E-01	0.00	7.05E-01
14	77419754	cg04933530	LINC01629	-15.62	2.82	2.90E-08	1.85E-04	1	-7.86	3.55	2.68E-02	-0.38	0.34	2.63E-01	-11.70	2.20	1.02E-07	-2.61	9.51E-09	1.56	1.22E-01	-3.49	8.35E-04	0.48	0.23	3.44E-02	-0.02	3.06E-03
15	58572140	cg04979283	AQP9	-32.93	6.80	1.26E-06	2.61E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.11E-04
16	88558223	cg04983687	MIR5189	-8.81	1.47	2.30E-09	3.30E-05	1	-11.27	5.31	3.37E-02	-2.02	0.36	1.44E-08	-7.76	1.21	1.33E-10	-	-	-4.01	1.09E-04	-7.22	5.27E-10	0.28	0.21	1.90E-01	-0.07	1.16E-07
3	42942410	cg04992471	ZNF662	-15.18	3.28	3.61E-06	5.83E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.61E-03
21	46709748	cg04992921	LOC642852	-18.33	4.59	6.45E-05	4.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.95E-02
15	39697356	cg04997452	C15orf54	-40.02	8.80	5.47E-06	7.97E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.67E-03
17	74298896	cg05042038	QRICH2	-11.52	2.58	8.17E-06	1.08E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.17E-04
3	119355809	cg05045380	POPDC2	-10.77	2.37	5.58E-06	8.03E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.66E-06
17	74402188	cg05056419	SPHK1	-20.53	4.51	5.24E-06	7.70E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.88E-04
9	131355483	cg05072637	SPTAN1	-15.97	3.22	6.90E-07	1.73E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.20E-05
12	109971517	cg05076510	MMAB	-13.09	2.72	1.51E-06	3.02E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.11E-04
15	92005188	cg05110389	CRAT37	-11.82	2.77	1.93E-05	2.10E-02	1	-4.60	2.73	9.20E-02	0.32	0.60	5.94E-01	-2.25	1.89	2.34E-01	-0.30	1.06E-01	3.04	2.93E-03	-4.60	1.88E-05	0.11	0.23	6.24E-01	-0.03	3.13E-03
8	96420384	cg05159759	C8orf37	-9.77	2.41	4.97E-05	4.10E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.25E-02
9	365007	cg05178561	DOCK8	-20.12	3.88	2.09E-07	7.15E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.27E-06
7	149543136	cg05184016	ZNF862	-38.50	5.96	1.01E-10	4.58E-06	1	-6.48	3.24	4.55E-02	-2.67	0.79	7.59E-04	-16.07	2.89	2.74E-08	-	-	-2.82	5.71E-03	-5.29	1.38E-06	0.33	0.26	1.89E-01	-0.03	4.24E-06
19	16553751	cg05194248	EPS15L1	-7.25	1.74	3.20E-05	3.03E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.64E-01
10	11291279	cg05219423	CELF2	-13.24	3.12	2.21E-05	2.30E-02	1	-7.30	3.31	2.75E-02	-0.03	1.05	9.76E-01	-9.83	2.33	2.44E-05	-1.05	3.54E-06	-2.12	3.62E-02	-4.00	1.57E-04	0.20	0.23	3.90E-01	-0.04	4.97E-06
11	65547049	cg05257275	AP5B1	-8.21	1.68	1.03E-06	2.24E-03	1	-9.28	5.40	8.58E-02	0.24	0.35	4.94E-01	-3.89	1.83	3.35E-02	-0.51	5.28E-02	-2.35	2.04E-02	-1.58	1.20E-01	0.45	0.34	1.81E-01	0.00	9.98E-01
16	23563601	cg05261121	EARS2	-28.53	6.46	1.01E-05	1.26E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.51E-06
11	65546210	cg05300717	AP5B1	-13.79	2.06	2.32E-11	2.37E-06	1	-16.12	6.45	1.25E-02	-1.39	0.64	3.03E-02	-15.35	2.48	6.51E-10	-	-	-2.33	2.16E-02	-3.33	1.41E-03	0.43	0.24	7.96E-02	-0.04	1.79E-05
13	100761701	cg05306459	PCCA	-15.51	3.62	1.80E-05	1.98E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.75E-04
2	70736862	cg05316492	TGFA-IT1	-24.94	5.32	2.78E-06	4.85E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.09E-06
22	35652215	cg05358754	HMGXB4	-26.23	6.09	1.64E-05	1.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.55E-05
11	63272225	cg05380077	LGALS12	-10.51	2.24	2.69E-06	4.74E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.06E-04
2	231583339	cg05447875	CAB39	-12.94	2.95	1.20E-05	1.44E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.07E-04
4	1578163	cg05470179	FAM53A	-16.11	3.65	1.02E-05	1.28E-02	1	-15.77	6.77	1.98E-02	-0.58	0.78	4.53E-01	-4.24	2.45	8.40E-02	-1.88	1.88E-06	-	-	-1.75	8.39E-02	0.09	0.21	6.78E-01	-	-
5	177613806	cg05473599	GMCL1P1	-12.59	2.50	4.61E-07	1.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	9.35E-02
8	128972681	cg05480350	MIR1205	-14.78	3.04	1.21E-06	2.55E-03	1	-11.13	5.45	4.11E-02	-1.06	0.93	2.54E-01	-7.00	2.43	4.04E-03	-1.15	3.45E-06	-	-	-3.40	1.11E-03	-0.14	0.20	5.08E-01	-	-
22	39850774	cg05541460	MGAT3	-19.84	3.73	1.08E-07	4.69E-04	1	-5.04	2.33	3.06E-02	-1.11	0.73	1.26E-01	-7.61	1.90	6.30E-05	-0.72	2.19E-04	7.06	1.59E-10	-2.19	3.17E-02	0.88	0.32	5.64E-03	-0.04	1.34E-05
3	66500703	cg05543520	LRIG1	-14.05	3.19	1.08E-05	1.33E-02	1	-16.06	7.33	2.85E-02	-0.35	0.39	3.64E-01	-3.09	2.68	2.48E-01	-	-	-	-	-0.26	7.92E-01	0.00	0.23	9.86E-01	-0.01	3.40E-01
4	111049852	cg05555563	ELOVL6	-38.15	6.26	1.07E-09	1.91E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.72E-04
5	95124396	cg05596757	GLRX	-29.29	6.65	1.07E-05	1.32E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.34E-04
17	80419874	cg05613273	-RF	-31.01	6.53	2.05E-06	3.87E-03	1	-5.59	2.84	4.88E-02	-0.29	0.37	4.34E-01	-12.84	3.03	2.31E-05	-0.12	5.36E-01	-0.49	6.23E-01	-0.27	7.91E-01	0.55	0.26	3.82E-02	-0.03	7.10E-05
2	28550757	cg05642098	LOC1005057	-32.99	5.65	5.16E-09	5.90E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.47E-04
1	19547855	cg05698970	LOC1019278	-17.69	4.30	3.95E-05	3.45E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.37E-03
2	234246583	cg05724080	DGKD	-12.29	2.40	3.00E-07	9.41E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.56E-06
2	157295032	cg05786348	GPD2	-23.08	4.35	1.10E-07	4.70E-04	1	-6.52	3.07	3.35E-02	-0.58	0.96	5.41E-01	-7.63	2.17	4.38E-04	0.07	7.86E-01	0.98	3.31E-01	-1.13	2.64E-01	0.39	0.23	8.53E-02	-0.03	1.70E-03
22	37299905	cg05808227	CSF2RB	-16.83	3.50	1.50E-06	3.00E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.99E-04
15	52427175	cg05853552	BCL2L10	-30.63	4.76	1.28E-10	4.87E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.25E-03
8	126591840	cg05879394	TRIB1	-8.96	2.17	3.55E-05	3.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.02E-03
5	20576898	cg05883445	CDH18	-37.76	7.21	1.65E-07	6.06E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.12E-03
1	222086992	cg05934594	LINC01655	-11.10	2.69	3.61E-05	3.25E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.11E-04
16	88558237	cg05958985	MIR5189	-10.58	2.38	8.62E-06	1.12E-02	1	-11.03	5.54	4.66E-02	-0.33	0.71	6.41E-01	-4.09	2.08	4.91E-02	-1.03	5.17E-04	-1.10	2.73E-01	-2.21	3.02E-02	0.06	0.24	8.03E-01	-0.02	3.63E-04
14	73614098	cg05981968	PSEN1	-20.67	4.89	2.40E-05	2.45E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.47E-03
11	72925008	cg05999592	P2RY2	-6.91	1.66	3.09E-05	2.96E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.84E-03
3	128442438	cg06019933	RAB7A	-13.62	3.19	2.00E-05	2.14E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.16E-03
3	69812798	cg06070625	MITF	-17.89	4.22	2.23E-05	2.31E-02	1	-7.20	3.30	2.94E-02	-1.02	0.48	3.46E-02	-10.54	2.32	5.36E-06	-1.25	3.51E-04	-	-	-1.07	2.88E-01	0.13	0.23	5.60E-01	-0.03	4.62E-05
17	25897247	cg06127160	LGALS9	-14.15	2.25	3.08E-10	8.66E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.05	4.76E-06
3	195835467	cg06144471	TFRC	-21.52	4.57	2.48E-06	4.46E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
18	46570302	cg06208130	MIR4744	-32.45	8.00	5.04E-05	4.14E-02	1	-27.06	11.14	1.51E-02	-1.08	0.82	1.89E-01	-4.99	3.20	1.19E-01	-0.65	4.29E-03	0.62	5.39E-01	-3.36	1.29E-03	0.54	0.23	1.79E-02	-0.01	1.04E-02

17	8765911	cg06223015	PIK3R6	-35.18	6.43	4.40E-08	2.39E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.95E-04
4	6782128	cg06231269	KIAA0232	-6.84	1.70	5.98E-05	4.62E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.07E-01
15	38881520	cg06290138	RASGRP1	-20.37	4.91	3.30E-05	3.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.94E-06
3	171865257	cg06304167	FNDC3B	-19.38	4.69	3.55E-05	3.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.94E-05
1	2036398	cg06315149	PRKCZ	-16.44	3.49	2.55E-06	4.57E-03	1	-10.29	4.58	2.46E-02	-0.06	0.47	8.93E-01	-11.88	2.63	6.08E-06	0.35	2.32E-01	5.15	1.14E-06	-0.96	3.40E-01	0.27	0.23	2.48E-01	-0.02	1.30E-03
3	71295684	cg06391412	FOXP1	-16.85	3.79	8.67E-06	1.12E-02	1	-6.87	3.11	2.74E-02	-0.64	0.37	8.57E-02	-13.39	2.26	3.00E-09	-	-	-	-	0.05	9.59E-01	0.29	0.21	1.78E-01	-0.03	6.88E-05
6	6971749	cg06394964	RREB1	-12.10	2.77	1.25E-05	1.49E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.01E-05
1	211647456	cg06418837	RD3	-13.56	3.24	2.85E-05	2.79E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.55E-02
15	43387093	cg06437892	UBR1	-21.23	4.60	3.92E-06	6.17E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.64E-03
17	4741523	cg06449385	MINK1	-28.97	4.73	8.82E-10	1.80E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.17E-03
16	85593560	cg06475513	GSE1	-17.10	4.14	3.66E-05	3.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.59E-02
17	55167149	cg06483820	AKAP1	-20.23	3.89	1.94E-07	6.79E-04	1	-	-	-	0.41	0.66	5.37E-01	-	-	-	-0.91	1.60E-05	-	-	-2.34	2.21E-02	-0.06	0.23	8.07E-01	-	-
1	151449494	cg06513960	POGZ	-32.83	7.19	5.04E-06	7.51E-03	1	-13.89	7.14	5.17E-02	0.20	1.09	8.58E-01	-5.77	3.19	7.07E-02	-0.50	3.80E-02	-2.02	4.54E-02	-2.42	1.83E-02	-0.01	0.22	9.55E-01	-0.02	1.12E-04
2	121949349	cg06516790	TFCP2L1	-13.79	3.32	3.29E-05	3.09E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.81E-04
2	121155673	cg06525046	INHBB	-11.87	2.95	5.72E-05	4.49E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.35E-04
2	47242277	cg06528816	MCFD2	-15.99	3.07	2.00E-07	6.94E-04	1	-7.84	3.63	3.07E-02	0.30	0.55	5.86E-01	-8.48	2.00	2.17E-05	-0.87	1.29E-03	-2.15	3.41E-02	-0.31	7.58E-01	0.30	0.24	2.25E-01	-0.03	2.36E-03
3	193974031	cg06566952	LINC02036	-20.10	3.73	7.07E-08	3.48E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.91E-05
3	51449240	cg06571036	RBM15B	-31.13	5.40	8.03E-09	7.37E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.39E-03
18	55250579	cg06592575	FECH	-35.01	6.31	2.88E-08	1.85E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.94E-05
18	77703051	cg06592918	PQLC1	-9.14	2.04	7.43E-06	1.00E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.13E-02
17	26973493	cg06608224	KIAA0100	-14.36	2.98	1.46E-06	2.95E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.03E-02
12	56404209	cg06612119	IKZF4	-6.00	1.40	1.69E-05	1.90E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.77E-02
11	123616411	cg06633463	ZNF202	-24.20	5.79	2.97E-05	2.86E-02	1	-6.12	3.07	4.63E-02	-0.86	0.67	2.03E-01	-11.01	2.85	1.10E-04	-1.21	1.37E-06	-	-	-3.14	2.46E-03	0.59	0.25	1.81E-02	-	-
5	133443229	cg06651549	TCF7	-19.72	3.36	4.57E-09	5.49E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.65E-05
2	136901306	cg06725108	CXCR4	-7.99	1.99	5.92E-05	4.60E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.36E-05
19	3521450	cg06734854	FZR1	-11.57	2.49	3.28E-06	5.56E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.37E-03
16	11709899	cg06743426	LITAF	-7.39	1.84	5.89E-05	4.58E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.09E-01
2	38812997	cg06755692	HNRNPLL	-14.49	2.95	9.02E-07	2.09E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.26E-04
2	8472503	cg06773230	LINC00299	-21.98	4.41	6.30E-07	1.62E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.80E-05
20	56949432	cg06794913	VAPB	-14.82	2.64	2.00E-08	1.43E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.74E-03
1	47157809	cg06824199	EFCAB14-AS	-33.35	6.99	1.84E-06	3.57E-03	1	-6.50	3.30	4.90E-02	-1.43	0.75	5.76E-02	-10.82	2.70	6.07E-05	-0.52	5.56E-02	1.90	6.00E-02	-0.32	7.51E-01	0.41	0.24	8.40E-02	-0.03	1.57E-05
16	67978450	cg06839111	LCAT	-13.01	3.21	5.08E-05	4.16E-02	1	-14.41	7.30	4.85E-02	0.56	0.70	4.27E-01	-2.50	2.60	3.36E-01	-1.48	1.39E-02	-	-	-1.65	1.04E-01	0.41	0.25	9.68E-02	-0.01	1.09E-01
15	45709844	cg06863152	C15orf48	-47.64	8.30	9.44E-09	8.48E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.65E-04
7	1913918	cg06864151	MIR4655	-22.16	5.35	3.42E-05	3.18E-02	1	-14.72	7.62	5.34E-02	-0.72	0.79	3.63E-01	-9.78	2.80	4.76E-04	-0.30	1.37E-01	0.18	8.55E-01	-2.70	8.78E-03	0.35	0.20	8.24E-02	-	-
22	32873859	cg06866757	FBXO7	-13.14	2.83	3.39E-06	5.68E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.28E-03
10	45494806	cg06958964	ZNF22	-33.04	7.81	2.31E-05	2.37E-02	1	-9.79	4.79	4.08E-02	0.16	0.97	8.70E-01	-15.96	3.42	2.97E-06	-1.20	4.17E-06	-1.80	7.54E-02	-2.25	2.79E-02	-0.01	0.22	9.55E-01	-0.02	3.97E-04
16	30488321	cg06972908	ITGAL	-8.68	2.15	5.25E-05	4.23E-02	1	-5.05	2.46	3.97E-02	-1.01	0.70	1.49E-01	-8.70	2.09	3.27E-05	-1.52	2.79E-06	1.85	6.75E-02	-2.16	3.45E-02	0.45	0.27	9.40E-02	-0.03	6.42E-04
14	75162215	cg06984345	AREL1	-15.07	2.88	1.76E-07	6.37E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.69E-04
12	47427791	cg06996254	PCED1B	-43.60	8.03	5.56E-08	2.90E-04	1	-12.39	5.74	3.08E-02	-0.62	0.39	1.10E-01	-13.67	3.23	2.29E-05	-1.48	1.04E-08	-1.14	2.56E-01	-2.53	1.36E-02	0.20	0.23	3.97E-01	-0.03	3.25E-06
17	47372126	cg07050712	MIR6129	-11.79	2.92	5.24E-05	4.23E-02	1	-6.46	3.24	4.59E-02	0.57	0.55	3.06E-01	-1.71	2.10	4.13E-01	-0.27	1.51E-01	-2.66	8.95E-03	-1.77	8.07E-02	0.17	0.20	4.07E-01	0.00	6.26E-01
10	81004884	cg07056602	PPIF	5.06	1.19	2.22E-05	2.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.03	6.00E-04
10	124303676	cg07066120	DMBT1	-6.74	1.24	6.17E-08	3.13E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	85654157	cg07098502	GSE1	-29.53	6.95	2.17E-05	2.27E-02	1	-8.54	3.91	2.89E-02	0.87	0.74	2.40E-01	-5.51	2.57	3.18E-02	-0.64	5.20E-03	-	-	-3.09	2.85E-03	0.24	0.25	3.45E-01	-0.01	7.26E-03
12	104484062	cg07100454	HCFC2	-34.88	8.66	5.61E-05	4.43E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.64E-02
1	52442668	cg07142936	RAB3B	-24.06	5.98	5.74E-05	4.50E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.65E-04
15	52030746	cg07177867	LYSMD2	-16.04	3.27	9.40E-07	2.13E-03	1	-7.06	3.30	3.26E-02	-3.20	1.12	4.24E-03	-10.62	2.44	1.29E-05	-0.89	2.09E-03	-0.17	8.64E-01	-2.10	3.93E-02	0.37	0.23	1.13E-01	-0.03	4.64E-05
8	120599284	cg07236691	ENPP2	-12.74	3.15	5.21E-05	4.23E-02	1	-7.16	3.31	3.03E-02	-1.11	0.80	1.65E-01	-7.09	2.12	8.13E-04	-0.30	1.93E-01	3.60	4.87E-04	-0.55	5.84E-01	0.22	0.25	3.86E-01	-0.03	5.25E-03
7	30505269	cg07299810	NOD1	-25.94	5.31	1.05E-06	2.27E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.48E-02
17	4743324	cg07307484	MINK1	-32.24	7.16	6.66E-06	9.15E-03	1	-24.33	9.71	1.22E-02	0.71	1.02	4.87E-01	-6.58	3.36	5.04E-02	-0.70	3.06E-03	2.35	2.08E-02	-3.70	4.35E-04	-0.21	0.22	3.34E-01	-0.01	1.16E-01
20	33606115	cg07332540	MIR499B	-11.03	2.43	5.52E-06	8.00E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	6.29E-02
10	63507455	cg07356438	C10orf107	-37.38	6.97	8.25E-08	3.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.31E-04
1	10516255	cg07361747	CORT	-8.48	1.75	1.21E-06	2.55E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	66404129	cg07410597	SLC25A26	-22.44	4.94	5.55E-06	8.00E-03	1	-5.96	2.76	3.09E-02	-1.80	0.83	3.07E-02	-12.48	2.43	2.70E-07	-0.82	2.92E-04	3.74	2.93E-04	-1.75	8.38E-02	0.23	0.24	3.37E-01	-0.03	1.62E-04
16	80653966	cg07428892	LINC01227	-14.30	3.17	6.56E-06	9.07E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.91E-03
3	148711966	cg07447194	GYG1	-10.61	2.34	5.75E-06	8.24E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.79E-04
1	11786594	cg07453055	AGTRAP	-13.26	3.04	1.29E-05	1.53E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	8.15E-07
4	38110810	cg07456972	TBC1D1	-29.02	5.34	5.39E-08	2.84E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.63E-04
9	130859191	cg07459967	SLC25A25	-23.11	5.25	1.06E-05	1.32E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	8.49E-01
3	39243826	cg07465458	XIRP1	-9.52	2.21	1.59E-05	1.81E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.52E-05
11	10543456	cg07565042	MTRNR2L8	-8.93	2.15	3.21E-05	3.03E-02	1	-6.46	3.13	3.90E-02	-0.58	0.39	1.39E-01	-5.60	2.30	1.49E-02	-0.66	1.53E-02	1.29	2.00E-01	-0.41	6.84E-01	0.40	0.28	1.55E-01	-0.02	5.01E-02
1	182308249	cg07579327	LINC01344	-13.63	2.81	1.26E-06	2.61E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.09E-04
20	35475630	cg07589211	SOGA1	-8.55	1.78	1.53E-06	3.06E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.18E-03
11	63466987	cg07636225	RTN3	-26.67	4.53	4.06E-09	5.03E-05	1	-5.62	2.77	4.25E-02	-0.42	0.29	1.45E-01	-9.71	2.52	1.14E-04	-2.02	5.28E-08	1.47	1.44E-01	-3.24	1.83E-03	0.24	0.26	3.51E-01	-0.02	3.97E-03
3	195974258	cg07641926	SLC51A	-6.82	1.64	3.19E-05	3.03E-02	1	-9.57	4.16	2.14E-02	-0.19	0.36	6.01E-01	-5.45	1.84	3.10E-03	-0.63	6.77E-03	-1.04	2.99E-01	-2.65	9.89E-03	0.18	0.28	5.31E-01	-0.02	2.06E-02
17	14112661	cg07643489	CDRT15	-22.07	4.13	8.95E-08	4.04E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.17E-05
5	138875768	cg07718085	TMEM173	-29.75	5.68	1.61E-07	5.95E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.74E-03
3	52810259	cg07730263	ITIH1	-12.18	2.51	1.18E-06	2.50E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.72E-03

3	4355431	cg07733260	SETMAR	-55.98	12.98	1.62E-05	1.83E-02	1	-13.85	6.55	3.46E-02	0.20	0.98	8.38E-01	-10.48	4.20	1.26E-02	-	-	-	-	-2.27	2.65E-02	0.08	0.20	6.86E-01	-0.01	8.13E-03
13	41935735	cg07769280	NAA16	-7.58	1.87	4.82E-05	4.00E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.90E-03
21	34130201	cg07778428	PAXBP1	-17.10	3.46	7.60E-07	1.87E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.07E-05
13	52301946	cg07818422	DHRS12	-51.28	11.44	7.42E-06	1.00E-02	1	-19.67	9.00	2.89E-02	-0.38	0.88	6.67E-01	-4.16	3.33	2.11E-01	-0.23	3.09E-01	-0.69	4.91E-01	-3.35	1.30E-03	0.35	0.20	8.03E-02	0.00	3.10E-01
1	120821493	cg07827820	FAM72B	-44.33	9.56	3.53E-06	5.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.72E-05
5	132114623	cg07828169	SEPT8	-18.48	4.16	8.68E-06	1.12E-02	1	-6.39	3.17	4.37E-02	-0.14	0.53	7.88E-01	-8.93	2.72	1.03E-03	-0.76	2.70E-03	-2.01	4.66E-02	-3.71	4.21E-04	0.37	0.27	1.73E-01	-0.02	1.03E-02
21	37536817	cg07834490	DOPEY2	-6.73	1.31	2.51E-07	8.31E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.38E-02
5	37668810	cg07879720	GDNF	-13.65	2.76	7.66E-07	1.87E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.45E-03
1	6377509	cg07906050	ACOT7	-16.74	3.89	1.64E-05	1.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.19E-05
13	41631052	cg07908654	WBP4	-24.56	3.84	1.53E-10	5.22E-06	1	-5.00	2.45	4.11E-02	-1.92	0.78	1.45E-02	-11.47	2.23	2.60E-07	-0.76	1.67E-04	-0.88	3.81E-01	-3.94	1.89E-04	0.38	0.25	1.26E-01	-0.03	7.75E-04
5	43523547	cg07944332	C5orf34	-32.23	6.19	1.93E-07	6.79E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.28E-02
16	3055636	cg07961282	LOC1019296	-21.87	5.43	5.69E-05	4.47E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.18E-02
7	149543165	cg07970948	ZNF862	-10.42	1.67	4.31E-10	1.04E-05	1	-8.62	4.00	3.09E-02	-1.86	0.49	1.66E-04	-9.41	1.74	6.39E-08	-	-	0.42	6.78E-01	-5.26	1.51E-06	0.27	0.22	2.34E-01	-0.06	1.41E-06
10	134373103	cg08014024	INPP5A	-13.51	3.22	2.71E-05	2.68E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.10E-06
19	56833959	cg08058756	ZSCAN5A	-19.08	3.57	8.85E-08	4.02E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.69E-03
14	62068941	cg08061334	LOC1019277	-19.80	3.86	2.89E-07	9.17E-04	1	-5.75	3.00	5.56E-02	-0.36	0.46	4.38E-01	-7.64	2.60	3.25E-03	-0.15	5.14E-01	1.97	5.17E-02	-1.87	6.54E-02	0.11	0.27	6.93E-01	-0.02	6.20E-03
14	62001072	cg08077807	LOC1019277	-48.77	8.82	3.20E-08	1.94E-04	1	-4.80	2.41	4.60E-02	-0.24	0.89	7.90E-01	-16.27	3.08	1.29E-07	-0.75	5.36E-04	-1.95	5.41E-02	-3.64	5.21E-04	0.35	0.30	2.40E-01	-0.03	7.01E-05
16	69170548	cg08085199	UTP4	-12.59	2.28	3.30E-08	1.94E-04	1	-6.87	3.27	3.57E-02	-0.12	0.61	8.40E-01	-5.12	1.88	6.49E-03	-0.83	6.58E-04	-	-	-2.10	3.90E-02	0.19	0.22	3.93E-01	-	-
8	129152499	cg08089777	MIR1208	-39.60	8.27	1.68E-06	3.31E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.44E-06
21	30699368	cg08094347	BACH1	-62.96	11.37	3.07E-08	1.89E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.08E-06
17	56288205	cg08222787	MKS1	-24.50	5.75	2.02E-05	2.16E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	6.16E-05
19	32864762	cg08256839	ZNF507	-10.68	2.55	2.73E-05	2.70E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	16889869	cg08288503	PLCL2	-10.17	2.39	2.12E-05	2.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.27E-05
13	27837816	cg08302053	RASL11A	-10.13	2.33	1.34E-05	1.58E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	7.93E-04
2	74265933	cg08334830	TET3	-17.88	4.33	3.66E-05	3.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	6.08E-02
8	129152449	cg08338792	MIR1208	-43.74	7.23	1.47E-09	2.40E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.79E-07
16	4884192	cg08348441	GLYR1	-55.48	9.10	1.07E-09	1.91E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.61E-03
17	73972367	cg08423755	TEN1	-38.74	8.50	5.16E-06	7.63E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.99E-04
1	223899685	cg08439122	CAPN2	-6.88	1.64	2.76E-05	2.72E-02	1	-6.05	2.92	3.84E-02	0.81	0.72	2.65E-01	-3.70	1.90	5.13E-02	-0.44	1.74E-02	-3.90	1.69E-04	-0.24	8.10E-01	0.37	0.23	1.09E-01	-0.01	2.88E-01
17	76623418	cg08481694	LINC02081	-19.38	3.68	1.42E-07	5.52E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.46E-04
9	366070	cg08531949	DOCK8	-7.24	1.79	5.14E-05	4.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.10E-04
15	99444730	cg08538069	PGPEP1L	-27.69	4.79	7.30E-09	7.19E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.42E-03
1	234791553	cg08553585	LOC1019277	-58.05	12.97	7.56E-06	1.01E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.47E-06
12	6332058	cg08559734	CD9	-26.57	6.31	2.55E-05	2.56E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.19E-04
3	50338171	cg08574671	HYAL3	-7.21	1.78	5.38E-05	4.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.05E-03
17	34344758	cg08584457	CCL23	-16.59	3.78	1.16E-05	1.41E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.50E-03
11	65489884	cg08589455	R-SEH2C	-18.00	4.02	7.76E-06	1.04E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.10E-04
9	80189185	cg08635575	G-14	-11.55	2.87	5.78E-05	4.52E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.34E-05
9	126319516	cg08649376	MIR7150	-12.10	2.83	1.98E-05	2.12E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.96E-02
14	88656128	cg08652605	KCNK10	-14.46	2.96	9.87E-07	2.18E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	7.86E-02
19	12997997	cg08679013	KLF1	-11.39	2.45	3.46E-06	5.75E-03	1	-22.77	9.37	1.51E-02	0.23	1.00	8.21E-01	-7.68	2.44	1.68E-03	-1.79	5.56E-04	1.92	5.79E-02	-1.56	1.24E-01	0.34	0.24	1.60E-01	-0.02	6.91E-03
3	171091657	cg08698681	TNIK	-17.69	4.33	4.37E-05	3.72E-02	1	-10.84	4.67	2.01E-02	-1.26	0.92	1.72E-01	-12.14	2.67	5.52E-06	-0.72	6.11E-04	-0.39	6.97E-01	-2.86	5.54E-03	0.19	0.23	4.01E-01	-0.03	8.49E-06
17	57925800	cg08744877	MIR21	-26.32	6.52	5.38E-05	4.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.47E-05
5	58654193	cg08761605	PDE4D	-16.59	4.09	4.97E-05	4.10E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	11729131	cg08776942	SNN	-11.65	2.68	1.41E-05	1.65E-02	1	-6.13	2.98	3.98E-02	-1.91	0.78	1.43E-02	-9.03	2.12	2.06E-05	-0.91	4.21E-05	-0.17	8.67E-01	-3.71	4.17E-04	0.45	0.27	9.59E-02	-0.03	4.63E-04
14	67983363	cg08778580	TMEM229B	-16.29	3.28	6.84E-07	1.72E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.99E-04
6	89693712	cg08820720	RNGTT	-40.99	9.32	1.09E-05	1.33E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.29E-02
10	99057649	cg08871283	ARHGAP19	-21.19	3.75	1.57E-08	1.19E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.26E-05
15	31505024	cg08884974	LOC1027250	-14.51	3.48	2.98E-05	2.88E-02	1	-7.92	4.10	5.35E-02	-0.15	0.39	6.97E-01	-5.71	2.56	2.57E-02	-0.39	4.48E-02	5.28	6.61E-07	-1.29	2.03E-01	0.00	0.26	9.93E-01	-0.01	1.13E-01
5	172271228	cg08886771	ERGIC1	-18.62	4.30	1.46E-05	1.70E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.02E-05
7	150653449	cg08900098	KCNH2	-9.53	2.16	1.04E-05	1.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.20E-04
8	19341295	cg08922108	CSGAL-CT1	-10.97	2.57	1.96E-05	2.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.48E-02
14	76447643	cg08922698	TGFB3	-21.61	3.93	3.90E-08	2.20E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.11E-06
16	88540241	cg08940169	MIR5189	-13.69	2.22	6.59E-10	1.54E-05	1	-16.13	7.56	3.29E-02	-2.00	0.46	1.53E-05	-9.73	1.90	2.93E-07	-	-	-3.35	1.12E-03	-4.56	2.18E-05	0.30	0.21	1.58E-01	-0.05	1.50E-06
5	133563532	cg08969102	PPP2CA	-16.36	3.02	6.24E-08	3.15E-04	1	-7.36	3.44	3.23E-02	-1.60	0.75	3.27E-02	-8.91	2.06	1.54E-05	-0.80	1.68E-03	-1.03	3.04E-01	-2.99	3.90E-03	0.47	0.26	7.17E-02	-0.02	2.14E-02
3	66489480	cg09012511	LRIG1	-14.22	2.71	1.52E-07	5.74E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.77E-03
5	179203369	cg09031958	LTC4S	-18.95	3.86	8.98E-07	2.09E-03	1	-8.84	4.12	3.19E-02	0.12	0.54	8.26E-01	-3.83	2.29	9.35E-02	-0.31	1.41E-01	-	-	-0.61	5.41E-01	0.32	0.25	1.93E-01	-0.02	1.90E-02
4	77906103	cg09040200	SEPT11	-30.04	6.66	6.40E-06	8.91E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
19	50323562	cg09080248	MED25	-23.57	4.44	1.12E-07	4.70E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.07E-03
6	28843296	cg09191776	LINC01623	-21.53	5.31	5.12E-05	4.18E-02	1	-	-	-	-2.78	0.94	3.24E-03	-6.39	3.63	7.86E-02	-0.34	8.41E-02	-	-	-1.85	6.88E-02	0.21	0.23	3.53E-01	-0.03	1.24E-05
20	4072430	cg09194810	SMOX	-26.72	4.57	4.80E-09	5.60E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.46E-05
20	35504403	cg09227119	TLDC2	-12.89	2.85	6.05E-06	8.50E-03	1	-9.70	4.33	2.51E-02	-0.30	0.33	3.61E-01	-7.54	2.20	6.03E-04	-1.43	2.73E-03	1.45	1.50E-01	-1.17	2.45E-01	0.22	0.22	3.06E-01	-0.02	1.06E-02
20	35504371	cg09241885	TLDC2	-12.64	3.07	3.72E-05	3.31E-02	1	-11.94	5.07	1.85E-02	0.07	0.35	8.47E-01	-6.78	2.21	2.13E-03	-	-	2.06	4.17E-02	0.59	5.56E-01	0.29	0.22	1.86E-01	-0.01	2.72E-02
13	46709790	cg09245115	CPB2	-10.14	2.24	5.93E-06	8.42E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.88E-04
1	61437380	cg09247486	NFIA-AS2	-21.59	4.87	9.42E-06	1.19E-02	1	-11.25	5.03	2.54E-02	-0.83	0.92	3.64E-01	-7.82	2.07	1.56E-04	-0.56	7.22E-03	1.05	2.95E-01	-3.12	2.66E-03	0.22	0.21	2.89E-01	-0.03	6.46E-07
22	37173159	cg09247945	IFT27	-30.83	7.22	1.96E-05	2.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.05E-02
1	160309220	cg09332506	NCSTN	-63.43	9.76	7.96E-11	4.15E-06	1	-8.59	3.88	2.68E-02	-2.56	0.97	8.15E-03	-15.15	3.10	1.00E-06	-0.56	6.35E-03	-	-	-3.12	2.64E-03	0.46	0.25	6.08E-02	-0.02	1.39E-04

17	62255234	cg09335712	SNORA50C	-19.48	3.94	7.84E-07	1.90E-03	1	-6.38	3.01	3.41E-02	-0.88	0.66	1.84E-01	-8.74	2.50	4.74E-04	-0.54	1.82E-02	0.27	7.84E-01	-2.99	3.89E-03	0.39	0.29	1.70E-01	-0.02	1.66E-04
22	37296313	cg09339568	CSF2RB	-9.17	1.85	6.89E-07	1.73E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.34E-06
12	53567662	cg09357175	CSAD	-9.81	2.40	4.51E-05	3.81E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.35E-03
8	141046469	cg09377531	PEG13	-16.07	3.18	4.28E-07	1.23E-03	1	-5.82	2.85	4.12E-02	-1.63	0.60	6.47E-03	-10.41	1.83	1.23E-08	-1.27	7.93E-08	-1.69	9.40E-02	-4.46	3.13E-05	0.35	0.22	1.23E-01	-0.05	2.75E-06
12	12887740	cg09444226	APOLD1	-15.60	3.53	9.72E-06	1.22E-02	1	-21.35	10.90	5.02E-02	0.20	0.54	7.05E-01	-3.87	2.72	1.55E-01	-0.58	4.84E-02	-3.10	2.44E-03	-2.13	3.68E-02	0.23	0.21	2.78E-01	0.00	5.57E-01
12	15126020	cg09447105	PDE6H	-18.88	4.27	9.73E-06	1.22E-02	1	-10.27	4.73	3.00E-02	-5.62	1.28	1.21E-05	-13.27	2.68	7.60E-07	-1.43	4.45E-05	-1.52	1.32E-01	-1.87	6.53E-02	0.20	0.23	3.72E-01	-0.03	1.53E-06
2	231661317	cg09458420	ITM2C	-12.70	3.09	4.00E-05	3.49E-02	1	-6.91	3.10	2.57E-02	-0.36	0.29	2.08E-01	-10.13	2.46	3.79E-05	-1.23	5.37E-05	-1.65	1.02E-01	-3.83	2.75E-04	0.52	0.23	2.38E-02	-0.03	8.43E-05
3	52809942	cg09469170	ITIH1	-27.76	4.97	2.38E-08	1.62E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.61E-05
5	149295369	cg09486450	LOC644762	-36.27	7.71	2.55E-06	4.57E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.15E-05
10	30793024	cg09532994	MAP3K8	-10.24	2.50	4.10E-05	3.54E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.30E-04
5	112541553	cg09565310	MCC	-19.93	3.98	5.63E-07	1.49E-03	1	-5.99	2.77	3.04E-02	-0.51	0.38	1.75E-01	-11.68	2.50	3.10E-06	-0.37	5.50E-02	2.93	4.18E-03	-1.50	1.39E-01	0.36	0.24	1.35E-01	-0.02	3.18E-02
3	181897670	cg09596645	LINC01206	-34.87	6.82	3.19E-07	9.90E-04	1	-5.35	2.57	3.74E-02	-0.34	0.28	2.27E-01	-10.06	2.37	2.24E-05	-2.04	1.74E-08	1.82	7.20E-02	-3.41	1.09E-03	0.36	0.24	1.36E-01	-0.04	1.11E-06
6	32141591	cg09597192	AGPAT1	-28.14	6.18	5.33E-06	7.80E-03	1	-9.08	3.89	1.96E-02	-3.37	1.16	3.81E-03	-12.53	2.73	4.29E-06	-1.08	1.98E-06	-1.36	1.77E-01	-2.82	6.25E-03	0.34	0.23	1.48E-01	-0.02	1.59E-03
9	91979711	cg09684929	SECISBP2	-7.74	1.88	3.75E-05	3.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.83E-02
7	127528039	cg09696385	SND1-IT1	-34.42	7.23	1.89E-06	3.65E-03	1	-4.35	2.30	5.89E-02	-0.62	0.86	4.68E-01	-11.03	2.70	4.33E-05	-0.74	1.82E-03	0.23	8.22E-01	-2.72	8.33E-03	0.39	0.31	2.00E-01	-0.03	4.86E-05
17	76565232	cg09705784	D-H17	-8.75	1.89	3.80E-06	6.03E-03	1	-5.82	2.68	3.00E-02	-2.30	0.96	1.63E-02	-9.15	1.74	1.50E-07	-0.81	4.14E-05	-	-	-3.00	3.80E-03	0.33	0.24	1.65E-01	-0.04	5.95E-04
1	184709731	cg09741958	EDEM3	-5.23	1.31	6.26E-05	4.77E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.13E-03
17	40288533	cg09778927	HSPB9	-8.00	1.93	3.53E-05	3.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.51E-05
12	104808575	cg09800745	CHST11	-16.75	4.15	5.47E-05	4.35E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.50E-04
1	115594714	cg09863265	TSHB	-7.10	1.71	3.31E-05	3.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.16E-01
12	113723004	cg09908050	MIR6762	-19.45	4.44	1.17E-05	1.42E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.05E-03
6	148830438	cg09980470	SASH1	-10.01	2.33	1.73E-05	1.93E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.85E-04
6	20034134	cg10011040	MBOAT1	-22.90	4.18	4.35E-08	2.39E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	456725	cg10051213	KANK1	-32.03	5.98	8.51E-08	3.93E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.37E-04
2	69828510	cg10054763	ANXA4	-33.02	6.83	1.34E-06	2.75E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.89E-02
8	21670177	cg10055846	GFRA2	-14.45	3.12	3.76E-06	5.98E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.17E-04
11	65482056	cg10093679	KAT5	-13.83	3.46	6.42E-05	4.84E-02	1	-18.08	9.00	4.46E-02	-0.65	0.68	3.38E-01	-5.86	3.30	7.59E-02	-	-	0.04	9.67E-01	-2.06	4.27E-02	0.25	0.26	3.43E-01	-0.01	1.09E-02
1	179843111	cg10100117	TOR1AIP2	-11.88	2.85	3.00E-05	2.88E-02	1	-	-	-	-0.21	0.45	6.37E-01	-1.05	2.60	6.87E-01	-	-	-	-	-2.83	6.16E-03	0.14	0.26	5.83E-01	-0.02	3.57E-02
22	31643111	cg10105512	LIMK2	-16.03	3.03	1.18E-07	4.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.30E-05
5	179200573	cg10113951	LTC4S	-29.52	6.82	1.50E-05	1.73E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.13E-02
2	137135606	cg10114537	CXCR4	-16.86	4.16	5.17E-05	4.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.79E-05
11	70166022	cg10120159	MIR548K	-22.93	5.63	4.67E-05	3.92E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.91E-05
3	141900424	cg10141168	TFDP2	-11.71	2.86	4.10E-05	3.54E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.58E-01
2	11917623	cg10142874	MIR548S	-13.88	2.63	1.33E-07	5.29E-04	1	-8.33	4.02	3.84E-02	-0.68	0.42	1.08E-01	-11.55	2.36	1.04E-06	-	-	-1.11	2.68E-01	-3.64	5.26E-04	0.49	0.25	5.08E-02	-0.03	1.69E-05
13	99991345	cg10145411	FKSG29	-24.28	4.95	9.43E-07	2.13E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.38E-04
3	3152530	cg10159529	IL5RA	-12.83	3.14	4.37E-05	3.72E-02	1	-6.21	2.87	3.07E-02	-0.43	0.36	2.31E-01	-10.82	2.36	4.48E-06	-1.44	7.95E-08	-	-	-2.12	3.77E-02	0.20	0.23	3.97E-01	-	-
17	40810559	cg10180165	TUBG2	-18.99	4.71	5.52E-05	4.36E-02	1	-10.22	4.94	3.85E-02	0.44	0.88	6.17E-01	-2.54	3.20	4.28E-01	-0.19	3.91E-01	-0.42	6.79E-01	-1.31	1.95E-01	0.26	0.23	2.57E-01	-0.01	1.01E-01
16	2863919	cg10194884	PRSS21	-6.17	1.50	3.88E-05	3.41E-02	1	-9.42	5.90	1.10E-01	-0.70	1.16	5.49E-01	-2.33	1.91	2.21E-01	0.43	4.16E-01	-1.01	3.13E-01	0.66	5.09E-01	0.22	0.24	3.54E-01	-0.01	1.07E-01
12	27027924	cg10220104	ITPR2	-29.89	5.58	8.43E-08	3.92E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	8717586	cg10224250	SNORA3B	-11.44	2.33	8.83E-07	2.08E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.32E-03
3	72509222	cg10279452	RYBP	-21.68	4.28	3.96E-07	1.17E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	73019173	cg10298741	ZFHX3	-19.49	3.59	5.73E-08	2.95E-04	1	-8.11	3.73	2.95E-02	-1.20	0.64	5.91E-02	-6.75	2.45	5.93E-03	-0.10	7.63E-01	4.70	7.75E-06	-1.18	2.44E-01	-0.03	0.24	8.98E-01	-0.03	2.59E-04
2	86789025	cg10354401	CHMP3	-32.46	7.57	1.79E-05	1.97E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.50E-06
15	72646210	cg10387956	HEXA-AS1	-13.96	3.12	7.78E-06	1.04E-02	1	-4.37	2.24	5.10E-02	-0.51	0.77	5.02E-01	-9.63	2.05	2.72E-06	-0.37	6.65E-02	-1.18	2.42E-01	-3.28	1.64E-03	0.52	0.27	5.32E-02	-0.04	7.40E-06
17	41472748	cg10433549	ARL4D	-23.08	4.40	1.51E-07	5.74E-04	1	-8.37	3.84	2.91E-02	-0.50	1.10	6.45E-01	-7.73	2.33	9.06E-04	-1.23	7.07E-07	-4.47	1.88E-05	-2.22	2.94E-02	-0.16	0.22	4.54E-01	-0.02	9.83E-03
17	70694204	cg10466699	LINC00511	-64.60	14.36	6.87E-06	9.38E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	6.07E-01
19	11610822	cg10491532	MIR7974	-16.94	3.21	1.27E-07	5.15E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.84E-05
5	149293098	cg10521603	LOC644762	-37.80	7.53	5.24E-07	1.42E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
12	51782847	cg10590350	SLC4A8	-8.19	1.99	3.93E-05	3.44E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	5.65E-01
19	11687621	cg10644885	ACP5	-15.78	2.82	2.29E-08	1.58E-04	1	-9.90	4.21	1.86E-02	-1.29	0.64	4.33E-02	-15.00	2.29	5.77E-11	-1.08	6.44E-07	-	-	-3.21	2.03E-03	0.28	0.23	2.12E-01	-0.03	3.85E-03
3	45914188	cg10650214	CCR9	-11.68	2.79	2.82E-05	2.76E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	9.40E-06
7	26450563	cg10667267	LOC441204	-27.72	6.83	4.90E-05	4.05E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.37E-03
16	79644995	cg10696524	MAF	-18.55	4.64	6.42E-05	4.84E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.00E-02
1	62209607	cg10704177	PATJ	-18.82	3.26	7.48E-09	7.19E-05	1	-6.09	2.91	3.64E-02	-0.38	0.38	3.10E-01	-10.42	2.01	2.25E-07	-2.57	2.82E-06	-	-	-2.43	1.77E-02	0.30	0.22	1.76E-01	-0.03	1.78E-03
2	100673005	cg10794399	AFF3	-26.01	4.30	1.40E-09	2.34E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.06E-03
8	105599835	cg10815420	LRP12	-34.50	7.19	1.59E-06	3.16E-03	1	-6.20	3.67	9.14E-02	-0.66	0.44	1.30E-01	-15.10	2.93	2.66E-07	-0.40	4.31E-02	1.69	9.32E-02	-1.16	2.51E-01	0.12	0.23	6.05E-01	-0.02	7.98E-03
12	55072835	cg10828236	DCD	-43.96	8.25	9.94E-08	4.37E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.35E-04
10	104227113	cg10897344	MFSD13A	-16.26	3.35	1.25E-06	2.60E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	7.58E-06
14	73061991	cg10933988	MIR7843	-23.26	5.49	2.29E-05	2.36E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.89E-05
2	179989225	cg11000869	CCDC141	-36.76	8.20	7.34E-06	9.93E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.27E-04
3	36974725	cg11014921	TRANK1	-40.34	8.43	1.68E-06	3.31E-03	1	-5.57	2.74	4.20E-02	-0.73	1.00	4.67E-01	-8.35	2.90	4.04E-03	-0.79	4.70E-04	2.82	5.76E-03	-2.52	1.40E-02	0.55	0.28	4.72E-02	-0.02	3.12E-04
13	47274074	cg11015284	ESD	-50.46	10.75	2.68E-06	4.74E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.06E-05
14	102656363	cg11081261	WDR20	-25.50	4.35	4.74E-09	5.60E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.09E-05
17	56283901	cg11112605	MKS1	-19.25	3.41	1.66E-08	1.23E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.17E-05
6	126377786	cg11115840	MIR5695	-10.82	1.98	4.31E-08	2.38E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.58E-04
1	33473905	cg11202380	AK2	-18.69	4.11	5.54E-06	8.00E-03	1	-13.44	5.89	2.25E-02	0.12	0.82	8.86E-01	-10.18	2.56	6.81E-05	-0.91	3.67E-05	2.18	3.17E-02	-3.20	2.06E-03	0.57	0.26	3.06E-02	-0.02	3.50E-04
11	62164451	cg11205545	SCGB1A1	-22.41	4.05	3.08E-08	1.89E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.36E-03

16	31484722	cg11215870	TGFB1I1	-13.42	2.73	8.79E-07	2.08E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.45E-05
6	150400090	cg11230866	ULBP3	-9.02	2.19	3.96E-05	3.46E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.81E-05
17	29837074	cg11238327	RAB11FIP4	-11.12	2.41	4.03E-06	6.28E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.18E-06
15	64275853	cg11266582	LOC1019289	-7.50	1.52	8.59E-07	2.04E-03	1	-10.49	4.72	2.63E-02	0.43	0.85	6.10E-01	-11.58	2.68	1.52E-05	-	-	-	-	-3.29	1.57E-03	0.60	0.25	1.70E-02	-0.03	3.33E-03
1	1690811	cg11296110	-DK	-9.19	2.21	3.19E-05	3.03E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.75E-05
19	30432108	cg11392833	URI1	-34.22	7.59	6.45E-06	8.97E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.54E-03
7	37434016	cg11422446	ELMO1	-14.39	2.97	1.26E-06	2.61E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.70E-04
14	21456512	cg11442986	METTL17	-49.83	7.94	3.50E-10	8.94E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.40E-04
22	32860440	cg11495812	BPIFC	-16.08	3.70	1.37E-05	1.61E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.79E-01
1	19675581	cg11495942	PQLC2	-26.53	5.60	2.18E-06	4.06E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	122901047	cg11514604	LOC341056	-40.49	9.61	2.51E-05	2.52E-02	1	-57.65	26.16	2.76E-02	-0.93	0.98	3.45E-01	-3.16	4.01	4.30E-01	-0.16	5.50E-01	2.66	8.93E-03	-1.29	2.02E-01	0.52	0.23	2.37E-02	0.00	5.83E-02
17	21176463	cg11522179	MAP2K3	-12.89	3.16	4.45E-05	3.77E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.20E-04
3	47742869	cg11540119	SMARCC1	-15.12	3.75	5.47E-05	4.35E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.19E-04
1	118139009	cg11558387	LOC1009962	-16.26	3.32	9.70E-07	2.16E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.19E-04
21	34570139	cg11606229	LINC01548	-19.01	3.46	3.96E-08	2.22E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.21E-05
9	140273055	cg11619782	EXD3	-23.30	5.39	1.56E-05	1.78E-02	1	-18.88	7.89	1.68E-02	0.23	0.85	7.84E-01	-9.03	3.49	9.81E-03	-0.51	4.15E-02	-0.79	4.32E-01	-2.88	5.35E-03	0.31	0.24	2.00E-01	-0.01	2.83E-03
7	101829270	cg11644402	SH2B2	-42.85	10.60	5.29E-05	4.25E-02	1	-25.97	12.86	4.34E-02	0.20	0.71	7.74E-01	-6.79	4.60	1.40E-01	-	-	-	-	-3.14	2.52E-03	-0.05	0.22	8.27E-01	0.00	4.97E-02
1	180940378	cg11649969	STX6	-51.25	7.80	5.10E-11	3.49E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.90E-05
15	72636405	cg11668148	CELF6	-29.48	4.82	9.98E-10	1.85E-05	1	-4.68	2.38	4.90E-02	0.17	0.84	8.43E-01	-8.41	2.28	2.22E-04	-0.43	3.21E-02	-0.61	5.45E-01	-2.57	1.22E-02	0.25	0.24	2.99E-01	-0.04	2.60E-05
1	6341327	cg11699125	GPR153	-10.34	1.56	3.78E-11	3.09E-06	1	-8.53	4.32	4.83E-02	-3.36	0.67	6.19E-07	-10.23	1.66	7.54E-10	-	-	-	-	-4.08	1.19E-04	0.26	0.23	2.68E-01	-0.06	1.07E-06
13	80066032	cg11770323	NDFIP2-AS1	-15.78	2.68	4.02E-09	5.03E-05	1	-5.91	2.84	3.78E-02	-0.51	0.30	9.28E-02	-9.41	2.08	5.86E-06	-2.19	5.53E-09	1.55	1.23E-01	-3.95	1.85E-04	0.24	0.26	3.51E-01	-0.04	9.07E-05
10	129172535	cg11791710	NPS	-14.83	3.58	3.38E-05	3.15E-02	1	-8.07	3.91	3.90E-02	0.39	1.01	6.98E-01	-10.01	2.69	1.96E-04	-0.61	7.40E-03	-2.73	7.45E-03	-3.51	7.83E-04	0.41	0.32	1.94E-01	-0.03	2.16E-04
1	91992292	cg11799283	CDC7	-6.35	1.55	4.07E-05	3.54E-02	1	-5.01	3.37	1.37E-01	-0.09	0.56	8.67E-01	-3.02	1.93	1.19E-01	-0.32	6.99E-02	-	-	-0.79	4.32E-01	0.71	0.24	2.80E-03	-0.02	1.00E-01
20	24630982	cg11841710	SYNDIG1	-28.70	6.21	3.83E-06	6.04E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.42E-05
1	210704772	cg11844053	HHAT	-8.95	1.97	5.54E-06	8.00E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.79E-05
20	19222240	cg11929042	SLC24A3	-29.79	5.37	2.87E-08	1.85E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
19	16561197	cg11939550	EPS15L1	-6.63	1.45	4.92E-06	7.40E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.04E-04
1	43290834	cg11987455	ERMAP	-17.58	3.53	6.44E-07	1.64E-03	1	-5.30	2.60	4.21E-02	-0.63	0.54	2.43E-01	-11.98	2.42	7.55E-07	-1.04	1.36E-05	-1.92	5.74E-02	-3.46	9.29E-04	0.25	0.28	3.77E-01	-0.03	3.14E-04
20	33416959	cg11988722	NCOA6	-6.46	1.45	8.22E-06	1.08E-02	1	-6.37	2.90	2.80E-02	-2.84	1.18	1.60E-02	-7.34	1.91	1.23E-04	-0.92	1.82E-04	-	-	-2.52	1.40E-02	0.16	0.20	4.18E-01	-0.04	2.74E-05
12	6984857	cg12003079	SPSB2	-10.74	2.45	1.12E-05	1.37E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.28E-02
17	21103728	cg12060026	TMEM11	-18.83	3.73	4.59E-07	1.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.78E-03
8	6360436	cg12074090	ANGPT2	-15.21	3.27	3.22E-06	5.47E-03	1	-8.26	3.49	1.78E-02	-1.33	0.88	1.29E-01	-7.27	2.49	3.47E-03	-0.56	4.60E-03	-0.86	3.90E-01	-2.51	1.45E-02	0.03	0.26	9.06E-01	-0.04	1.02E-05
13	111316145	cg12075669	CARS2	-11.80	2.33	4.26E-07	1.23E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.11E-05
8	8702053	cg12077460	MFHAS1	-9.08	1.85	9.09E-07	2.09E-03	1	-5.65	2.69	3.58E-02	-0.56	0.53	2.86E-01	-8.32	2.08	6.20E-05	-0.92	7.18E-04	1.81	7.32E-02	-2.53	1.36E-02	0.23	0.21	2.74E-01	-0.03	9.03E-03
2	75089669	cg12077754	HK2	-13.53	2.74	7.84E-07	1.90E-03	1	-6.53	3.08	3.40E-02	-0.88	0.60	1.40E-01	-7.90	1.72	4.56E-06	-1.23	1.17E-08	-	-	-4.11	1.08E-04	0.27	0.22	2.24E-01	-0.03	1.94E-04
21	38574170	cg12100242	DSCR9	-31.24	7.80	6.21E-05	4.75E-02	1	-5.18	2.92	7.64E-02	-0.15	0.57	7.87E-01	-4.89	3.22	1.30E-01	-0.59	1.15E-03	-	-	-1.95	5.48E-02	0.20	0.23	4.03E-01	-	-
19	5592815	cg12104982	TINCR	-15.45	2.99	2.44E-07	8.16E-04	1	-25.72	10.62	1.54E-02	-4.13	0.85	1.31E-06	-15.43	2.91	1.13E-07	-	-	-	-	-4.01	1.49E-04	0.28	0.23	2.23E-01	-0.03	1.49E-05
10	93786975	cg12119581	BTAF1	-50.41	11.19	6.63E-06	9.13E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.53E-04
1	28484534	cg12154164	PTAFR	-16.99	3.02	1.93E-08	1.41E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.75E-04
8	68109236	cg12168006	CSPP1	-42.24	8.87	1.90E-06	3.66E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.60E-02
13	113825954	cg12172163	PROZ	-14.01	2.69	1.94E-07	6.79E-04	1	-9.97	4.40	2.35E-02	-1.12	0.69	1.03E-01	-7.63	2.11	3.01E-04	-0.78	2.16E-02	1.69	9.40E-02	-0.44	6.64E-01	0.25	0.21	2.29E-01	-0.03	7.53E-04
14	55849528	cg12192145	ATG14	-18.94	4.67	5.09E-05	4.16E-02	1	-5.05	2.51	4.37E-02	-0.07	0.74	9.21E-01	-7.26	2.08	4.75E-04	-0.63	4.23E-03	1.74	8.55E-02	-3.61	5.84E-04	0.43	0.26	9.66E-02	-0.03	1.01E-05
6	24877462	cg12213680	FAM65B	-12.14	2.85	2.10E-05	2.22E-02	1	-5.57	2.55	2.91E-02	-0.60	0.38	1.13E-01	-8.73	2.39	2.62E-04	-1.28	3.61E-07	-	-	-3.37	1.22E-03	0.81	0.29	5.32E-03	-0.04	5.74E-05
10	135061670	cg12227660	MIR202HG	-13.10	2.00	5.13E-11	3.49E-06	1	-	-	-	-0.75	0.36	3.63E-02	-7.65	2.04	1.81E-04	-	-	-	-	-3.74	3.74E-04	0.10	0.25	6.73E-01	-0.03	1.36E-04
14	75069041	cg12258670	LTBP2	-29.27	5.18	1.57E-08	1.19E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.84E-05
11	119507838	cg12359648	NECTIN1	-26.23	5.34	8.98E-07	2.09E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.82E-06
17	79851485	cg12380988	A-PC11	-30.15	4.26	1.40E-12	2.86E-07		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.39E-03
12	117463293	cg12383160	LOC1005065	-22.61	5.12	1.01E-05	1.26E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.55E-03
4	148735567	cg12396412	MIR4799	-36.23	8.21	1.01E-05	1.26E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
15	52135487	cg12402318	TMOD3	-26.40	5.25	4.98E-07	1.38E-03	1	-10.51	4.60	2.23E-02	0.49	0.85	5.65E-01	-9.53	2.84	7.80E-04	-0.19	4.59E-01	-1.26	2.11E-01	1.02	3.13E-01	0.50	0.26	5.60E-02	-0.02	1.57E-03
17	78389106	cg12432898	LOC1002943	68.95	17.09	5.49E-05	4.35E-02	1	-39.87	52.84	4.50E-01	-0.80	0.67	2.36E-01	-0.17	5.71	9.76E-01	-	-	-	-	0.88	3.83E-01	-0.03	0.17	8.70E-01	0.00	7.23E-01
9	131648836	cg12450789	LRRC8A	-20.23	4.46	5.90E-06	8.40E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.19E-03
1	211667682	cg12483927	RD3	-42.93	7.24	3.01E-09	4.10E-05	1	-11.52	5.60	3.96E-02	-1.16	0.89	1.95E-01	-10.21	3.20	1.40E-03	-0.55	1.05E-02	0.71	4.77E-01	-2.56	1.27E-02	0.44	0.24	6.64E-02	-0.01	5.14E-02
11	6257262	cg12492850	FAM160A2	-10.60	2.31	4.51E-06	6.89E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	7.32E-04
20	33927324	cg12548730	FAM83C	-42.19	6.88	8.83E-10	1.80E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.65E-03
17	47590237	cg12561474	MIR6165	-23.15	5.76	5.88E-05	4.58E-02	1	-15.29	7.92	5.35E-02	0.29	0.36	4.20E-01	-5.23	4.44	2.39E-01	-	-	-	-	-1.11	2.72E-01	0.08	0.26	7.55E-01	0.00	4.77E-01
1	17448350	cg12561552	PADI2	-12.31	2.97	3.44E-05	3.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.80E-03
14	74547881	cg12605076	ALDH6A1	-48.88	11.91	4.04E-05	3.52E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.48E-03
4	154269418	cg12614529	MND1	-12.49	2.33	8.27E-08	3.91E-04	1	-7.90	3.74	3.47E-02	-2.43	1.02	1.71E-02	-8.07	2.01	5.77E-05	-1.41	4.62E-06	-1.74	8.38E-02	-2.99	3.82E-03	0.03	0.20	8.64E-01	-0.03	2.41E-04
9	35537849	cg12629001	RUSC2	-21.21	5.08	3.00E-05	2.88E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.47E-02
1	29229403	cg12645785	EPB41	-22.23	3.85	7.71E-09	7.26E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.26E-05
11	85884166	cg12667152	EED	-7.58	1.82	3.03E-05	2.91E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.73E-01
18	33021980	cg12734151	INO80C	-31.80	6.76	2.54E-06	4.57E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.04E-03
7	151501146	cg12736613	PRKAG2	-16.40	3.31	7.23E-07	1.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.59E-05
1	6342888	cg12740725	GPR153	-25.36	5.51	4.11E-06	6.36E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.37E-02
14	100066736	cg12773397	CCDC85C	-21.92	4.61	1.98E-06	3.76E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.32E-03
11	57157632	cg12819873	PRG2	-22.66	3.90	6.00E-09	6.53E-05	1	-6.43	3.18	4.32E-02	-2.43	1.05	2.10E-02	-10.83	2.45	9.55E-06	-0.78	3.19E-04	0.73	4.65E-01	-2.70	8.70E-03	0.26	0.23	2.60E-01	-0.03	5.77E-05

12	107273455	cg12916632	TMEM263	-25.32	4.47	1.52E-08	1.18E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.79E-03
16	57103772	cg12928479	CPNE2	-8.74	2.17	5.50E-05	4.35E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.48E-04
21	38751589	cg13051367	DYRK1A	-21.41	4.63	3.72E-06	5.95E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.43E-03
17	81055722	cg13054523	METRNL	-19.97	3.42	5.44E-09	6.01E-05	1	-16.32	7.05	2.06E-02	-0.59	0.60	3.27E-01	-13.94	2.45	1.20E-08	-0.36	1.06E-01	1.77	7.94E-02	-0.78	4.40E-01	0.10	0.22	6.40E-01	-0.02	6.60E-04
8	135747178	cg13064897	ZFAT	-18.04	3.89	3.55E-06	5.80E-03	1	-11.90	5.49	3.01E-02	-0.28	0.29	3.34E-01	-10.21	2.71	1.67E-04	-2.12	3.09E-07	1.16	2.48E-01	-2.80	6.68E-03	0.13	0.23	5.76E-01	-0.02	4.63E-04
14	21508987	cg13072730	R-SE7	-15.59	3.55	1.15E-05	1.40E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.03E-05
2	62515892	cg13073332	B3GNT2	-15.08	2.85	1.20E-07	4.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.69E-06
15	68476905	cg13077072	CALML4	-15.96	3.90	4.31E-05	3.69E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.18E-03
6	107272133	cg13118684	LOC1004227	-21.12	4.11	2.71E-07	8.75E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.18E-03
1	6074441	cg13123771	KC-B2	-10.51	2.59	5.08E-05	4.16E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.16E-03
16	3843133	cg13135255	TRAP1	-8.98	2.12	2.26E-05	2.34E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.72E-04
18	8801435	cg13174688	MTCL1	-15.04	3.25	3.63E-06	5.84E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.72E-02
20	60709957	cg13197551	PSMA7	-34.75	6.37	4.88E-08	2.61E-04	1	-10.49	4.61	2.28E-02	-2.05	1.02	4.42E-02	-15.40	3.14	9.23E-07	-0.75	2.05E-03	-	-	-1.57	1.21E-01	0.29	0.28	3.13E-01	-0.02	2.76E-05
2	113465627	cg13205244	CKAP2L	-10.57	2.45	1.59E-05	1.81E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
13	48876919	cg13221796	LINC00441	-11.02	2.32	2.13E-06	3.98E-03	1	-6.87	3.63	5.88E-02	-0.60	0.93	5.18E-01	-9.25	2.19	2.47E-05	-0.29	2.99E-01	0.13	8.98E-01	-1.21	2.30E-01	0.22	0.26	4.06E-01	-0.02	5.40E-02
8	95918378	cg13279458	CCNE2	-9.86	2.07	1.92E-06	3.69E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.94E-01
9	20692704	cg13298043	FOCAD-AS1	-8.24	1.79	4.27E-06	6.57E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.30E-01
2	44968238	cg13299425	SIX3-AS1	-40.79	7.56	6.83E-08	3.40E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.71E-03
2	85944732	cg13353793	GNLY	-20.48	4.90	2.95E-05	2.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.71E-06
1	224444519	cg13360526	MIR320B2	-14.70	3.56	3.69E-05	3.29E-02	1	-13.67	6.65	3.98E-02	-0.43	0.34	2.02E-01	-11.13	3.75	3.00E-03	-	-	4.53	1.51E-05	-2.48	1.56E-02	0.27	0.24	2.55E-01	0.00	3.82E-01
9	138701748	cg13423371	CAMSAP1	-15.20	3.48	1.26E-05	1.51E-02	1	-8.91	4.07	2.83E-02	-0.58	0.79	4.65E-01	-4.07	2.52	1.07E-01	-0.64	1.97E-03	-	-	-1.88	6.48E-02	0.11	0.22	6.23E-01	-0.03	9.86E-04
9	130608923	cg13458609	ENG	-10.08	1.99	3.98E-07	1.17E-03	1	-6.47	3.18	4.20E-02	-0.26	0.28	3.58E-01	-12.05	2.22	5.74E-08	-	-	-	-	-4.28	5.87E-05	0.34	0.24	1.69E-01	-0.02	3.73E-03
7	50861834	cg13459606	GRB10	-15.62	3.08	4.00E-07	1.17E-03	1	-10.18	5.01	4.22E-02	-2.68	0.98	6.15E-03	-4.17	1.83	2.27E-02	-0.74	5.56E-04	-	-	-0.03	9.79E-01	0.35	0.22	1.21E-01	-0.03	1.61E-04
17	57948101	cg13491003	TUBD1	-7.62	1.87	4.45E-05	3.77E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.54E-02
3	42923116	cg13531735	CYP8B1	-32.55	7.45	1.25E-05	1.50E-02	1	-10.78	4.64	2.01E-02	-0.79	0.72	2.68E-01	-6.77	3.01	2.42E-02	-0.57	1.05E-02	-0.74	4.60E-01	-2.14	3.62E-02	0.77	0.29	8.23E-03	-0.01	1.06E-03
9	140308660	cg13562011	EXD3	-20.94	4.12	3.75E-07	1.13E-03	1	-13.58	5.49	1.34E-02	-0.12	1.18	9.20E-01	-9.83	2.45	6.12E-05	-1.05	2.45E-05	-2.44	1.63E-02	-3.34	1.37E-03	0.19	0.22	3.84E-01	-0.02	1.21E-03
5	157159820	cg13576217	THG1L	-48.27	8.53	1.51E-08	1.18E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.07E-02
9	97403129	cg13576859	FBP1	-14.83	2.90	3.10E-07	9.66E-04	1	-13.95	6.19	2.42E-02	-0.31	0.73	6.74E-01	-8.69	2.00	1.37E-05	-0.99	7.38E-05	-1.63	1.07E-01	-3.15	2.39E-03	0.32	0.25	2.09E-01	-0.04	1.16E-05
9	134883788	cg13628444	MED27	-19.74	3.85	2.91E-07	9.19E-04	1	-7.08	3.37	3.56E-02	-3.01	0.94	1.37E-03	-12.04	2.44	7.76E-07	-1.94	4.59E-08	-1.30	1.95E-01	-2.15	3.48E-02	0.46	0.28	1.00E-01	-0.03	3.36E-04
15	64275810	cg13645296	LOC1019289	-18.18	3.27	2.74E-08	1.81E-04	1	-13.69	6.10	2.48E-02	-0.86	0.57	1.33E-01	-7.13	1.91	1.92E-04	-1.15	9.98E-07	0.75	4.57E-01	-3.28	1.60E-03	0.31	0.23	1.70E-01	-0.03	7.11E-05
17	41400541	cg13726456	LINC00854	-6.39	1.57	4.60E-05	3.88E-02	1	-25.94	11.65	2.60E-02	-4.68	1.44	1.20E-03	-3.36	2.01	9.47E-02	-3.30	4.57E-07	-0.51	6.13E-01	-2.40	1.92E-02	0.06	0.21	7.96E-01	-	-
7	100230770	cg13732043	TFR2	18.53	4.14	7.53E-06	1.01E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.03	1.12E-05
11	61607741	cg13764085	FADS2	-11.75	2.49	2.42E-06	4.38E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.00E-03
2	74612706	cg13774539	DCTN1-AS1	-12.19	2.49	9.62E-07	2.16E-03	1	-	-	-	-2.35	0.82	4.11E-03	-7.45	2.41	1.97E-03	-0.90	2.67E-02	1.62	1.08E-01	-1.33	1.89E-01	0.51	0.27	5.62E-02	-0.03	1.39E-04
9	103278557	cg13783924	TMEFF1	-13.57	3.39	6.13E-05	4.71E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.92E-03
1	47746081	cg13789639	STIL	-22.76	4.40	2.31E-07	7.78E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.98E-03
20	43590115	cg13792581	TOMM34	-35.77	7.57	2.29E-06	4.23E-03	1	-9.27	4.21	2.76E-02	-2.90	1.11	9.27E-03	-13.71	3.15	1.34E-05	-0.71	5.08E-04	-1.81	7.38E-02	-3.80	3.10E-04	0.58	0.28	3.47E-02	-0.02	4.27E-06
11	840407	cg13806461	POLR2L	-25.08	5.63	8.35E-06	1.10E-02	1	-211.11	93.04	2.33E-02	0.13	0.56	8.17E-01	5.09	5.18	3.26E-01	0.25	3.47E-01	-	-	-0.86	3.92E-01	0.30	0.17	8.53E-02	-	-
10	95200513	cg13827101	MYOF	-24.14	6.00	5.79E-05	4.52E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.09E-03
9	130859454	cg13835688	SLC25A25	-13.97	2.89	1.28E-06	2.65E-03	1	-7.69	3.46	2.63E-02	-3.31	0.99	8.29E-04	-11.63	1.97	3.33E-09	-1.04	1.61E-06	-	-	-3.44	9.77E-04	0.25	0.22	2.68E-01	-0.04	1.10E-04
9	138362321	cg13850063	PPP1R26-AS	-17.66	3.97	8.80E-06	1.14E-02	1	-22.15	10.21	3.01E-02	-0.15	0.42	7.15E-01	-24.77	4.56	5.49E-08	-0.15	4.99E-01	-	-	-0.37	7.10E-01	0.42	0.20	4.15E-02	-0.01	6.99E-02
6	7199401	cg13863638	RREB1	-49.50	9.83	4.71E-07	1.31E-03	1	-6.58	3.62	6.90E-02	0.61	0.78	4.35E-01	-8.69	3.10	5.01E-03	-0.56	1.84E-02	-0.47	6.39E-01	-1.88	6.41E-02	0.29	0.30	3.34E-01	-0.02	2.42E-06
17	55190679	cg13947225	AKAP1	-20.83	3.24	1.31E-10	4.87E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.76E-04
1	146503900	cg13951007	LOC728989	-14.90	3.41	1.27E-05	1.51E-02	1	-10.16	5.04	4.39E-02	-0.62	0.51	2.26E-01	-8.23	2.52	1.09E-03	-0.92	1.29E-04	2.97	3.63E-03	-2.12	3.77E-02	0.56	0.26	3.30E-02	-0.02	7.19E-03
9	132600788	cg13953978	USP20	-16.09	3.51	4.55E-06	6.94E-03	1	-5.73	2.70	3.38E-02	-0.53	1.00	5.94E-01	-5.43	1.91	4.40E-03	-0.62	4.78E-03	-	-	-0.72	4.77E-01	0.07	0.21	7.23E-01	-0.03	1.39E-03
9	138362327	cg14011077	PPP1R26-AS	-20.00	3.88	2.47E-07	8.21E-04	1	-16.82	7.96	3.46E-02	-0.48	0.48	3.13E-01	-15.12	2.61	7.02E-09	-0.41	3.69E-02	2.83	5.50E-03	-0.80	4.25E-01	0.27	0.19	1.48E-01	-0.02	8.30E-04
9	130222969	cg14012059	LRSAM1	-7.17	1.43	5.57E-07	1.49E-03	1	-12.75	6.33	4.41E-02	-0.12	0.33	7.26E-01	-4.09	1.73	1.82E-02	-2.00	3.14E-08	-	-	-3.20	2.05E-03	0.22	0.25	3.87E-01	-0.03	6.11E-03
9	5436224	cg14025883	PLGRKT	-15.24	3.49	1.28E-05	1.52E-02	1	-6.12	2.83	3.05E-02	-1.12	0.64	8.08E-02	-11.76	2.39	8.42E-07	-1.80	8.97E-09	-4.88	3.67E-06	-4.32	5.17E-05	0.07	0.22	7.53E-01	-0.04	1.13E-05
14	100610407	cg14084609	DEGS2	-25.20	4.72	9.50E-08	4.27E-04	1	-7.21	3.36	3.19E-02	-0.93	0.56	9.61E-02	-12.03	2.03	2.96E-09	-0.24	2.40E-01	1.18	2.39E-01	-0.41	6.81E-01	0.26	0.23	2.68E-01	-0.03	1.11E-05
2	200787960	cg14108285	C2orf69	-45.95	8.74	1.47E-07	5.63E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.79E-03
13	52198723	cg14118054	WDFY2	-23.45	5.19	6.36E-06	8.89E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.23E-05
7	45038259	cg14131691	CCM2	-10.32	2.49	3.35E-05	3.13E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.45E-04
19	30456228	cg14140268	URI1	-13.07	2.91	6.96E-06	9.47E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.40E-04
11	12747546	cg14179258	TEAD1	-3.49	0.84	3.27E-05	3.08E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.18E-01
3	136618139	cg14184646	NCK1	-41.86	8.14	2.73E-07	8.76E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.30E-04
11	118083942	cg14190451	JAML	-8.86	2.01	1.06E-05	1.32E-02	1	-	-	-	-0.08	0.31	8.04E-01	-	-	-	-	-	-	-	0.99	3.25E-01	-0.19	0.37	6.13E-01	-0.04	9.82E-03
15	68146684	cg14209284	RNU6-2	-23.75	4.98	1.87E-06	3.62E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.49E-05
9	113530240	cg14226212	MUSK	-12.20	2.76	1.00E-05	1.26E-02	1	-5.89	2.99	4.91E-02	-0.29	0.38	4.35E-01	-6.02	2.21	6.44E-03	-0.01	9.83E-01	-	-	-0.26	7.93E-01	0.10	0.28	7.16E-01	-0.03	2.38E-04
16	66597367	cg14248318	CMTM1	-17.07	4.03	2.32E-05	2.39E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.13E-05
5	157159916	cg14254530	THG1L	-37.71	8.51	9.42E-06	1.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.40E-04
18	59733858	cg14263230	PIGN	-20.38	4.82	2.34E-05	2.40E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.79E-04
3	170948986	cg14265474	MIR569	-30.20	6.50	3.42E-06	5.72E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.42E-04
7	28228530	cg14298642	JAZF1	-34.78	8.71	6.54E-05	4.92E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.26E-04
17	6658198	cg14321269	XAF1	-14.92	2.83	1.30E-07	5.21E-04	1	-9.27	4.56	4.18E-02	0.41	0.58	4.82E-01	-4.87	2.13	2.23E-02	1.39	5.59E-06	-	-	-0.01	9.90E-01	0.28	0.24	2.37E-01	-0.01	1.41E-01
15	40094043	cg14329961	LOC1053709	-31.91	5.78	3.44E-08	1.99E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.74E-05
14	51446038	cg14354244	PYGL	-12.14	2.93	3.37E-05	3.15E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.14E-04
5	179333851	cg14362073	TBC1D9B	-18.73	4.28	1.23E-05	1.49E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-

5	74342697	cg14390854	LINC01336	-16.23	3.24	5.36E-07	1.44E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.86E-06
3	5193472	cg14415107	ARL8B	-20.96	4.70	8.12E-06	1.07E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.31E-03
22	50984822	cg14496081	KLHDC7B	-14.29	2.59	3.58E-08	2.03E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.31E-04
17	2287008	cg14511746	MNT	-19.96	3.26	9.69E-10	1.85E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.05	5.78E-06
9	128107984	cg14556243	GAPVD1	-10.48	2.20	1.81E-06	3.53E-03	1	-4.53	2.36	5.45E-02	-0.51	0.41	2.21E-01	-5.05	1.73	3.47E-03	-0.47	2.28E-02	1.99	4.87E-02	-2.85	5.76E-03	0.21	0.23	3.63E-01	-0.03	8.40E-04
11	70165870	cg14569513	MIR548K	-28.66	7.04	4.64E-05	3.90E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.68E-05
9	130859606	cg14612966	SLC25A25	-24.23	4.38	3.06E-08	1.89E-04	1	-7.37	3.45	3.27E-02	-2.05	0.97	3.52E-02	-10.60	2.59	4.37E-05	-0.58	4.77E-03	-2.37	1.97E-02	-3.38	1.18E-03	0.03	0.23	8.80E-01	-0.03	3.77E-05
20	35504198	cg14613878	TLDC2	-8.56	1.92	8.54E-06	1.11E-02	1	-7.29	3.28	2.61E-02	0.56	0.93	5.42E-01	-8.57	2.04	2.70E-05	-0.79	2.07E-03	0.03	9.75E-01	-2.97	4.12E-03	0.27	0.22	2.20E-01	-0.03	2.95E-04
1	167512106	cg14617280	CREG1	-33.76	6.92	1.07E-06	2.32E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.65E-03
15	92078200	cg14622604	CRAT37	-15.66	3.66	1.89E-05	2.05E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.27E-05
10	932509	cg14644626	LARP4B	-17.92	4.13	1.42E-05	1.66E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	7.96E-03
21	19072007	cg14654849	BTG3	-45.28	10.06	6.73E-06	9.23E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
11	72932079	cg14655553	P2RY2	-9.60	2.35	4.43E-05	3.76E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.01E-03
17	58717993	cg14697045	BCAS3	-11.90	2.79	2.02E-05	2.16E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	8.23E-01
7	128868265	cg14755690	AHCYL2	-17.99	4.35	3.54E-05	3.23E-02	1	-6.23	2.99	3.71E-02	-0.13	0.40	7.48E-01	-6.15	2.45	1.20E-02	0.58	4.03E-03	-	-	1.18	2.41E-01	0.55	0.26	3.10E-02	-0.03	2.52E-03
7	98722470	cg14769121	SMURF1	-22.11	4.42	5.79E-07	1.52E-03	1	-6.50	3.13	3.76E-02	-0.23	0.79	7.72E-01	-9.49	2.43	9.50E-05	-0.51	1.65E-02	3.18	1.93E-03	-0.82	4.16E-01	0.26	0.25	2.90E-01	-0.03	1.55E-03
8	68022262	cg14783123	CSPP1	-20.18	4.53	8.49E-06	1.11E-02	1	-4.63	2.41	5.42E-02	-0.91	0.39	2.01E-02	-3.59	2.13	9.09E-02	-1.09	1.09E-09	-2.05	4.30E-02	-5.34	1.10E-06	-0.13	0.29	6.64E-01	-0.03	2.15E-04
17	80075917	cg14832684	FASN	-54.08	13.12	3.75E-05	3.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.09E-03
22	46992206	cg14849880	GRAMD4	-14.25	2.34	1.12E-09	1.95E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.25E-02
6	11383319	cg14879823	NEDD9	-50.48	10.87	3.39E-06	5.68E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.92E-03
1	6341901	cg14879885	GPR153	-15.34	3.67	2.95E-05	2.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.85E-05
18	61559440	cg14884379	SERPINB2	-13.45	3.35	5.96E-05	4.62E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.34E-03
10	114133657	cg14930775	ACSL5	-13.26	3.24	4.20E-05	3.61E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.47E-03
11	118892305	cg14931486	MIR3656	-2.29	0.56	4.23E-05	3.63E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.01	6.93E-01
2	85625138	cg14947564	CAPG	-14.21	2.61	5.14E-08	2.73E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.23E-03
5	59980902	cg14963970	DEPDC1B	-21.40	3.58	2.22E-09	3.24E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.11E-03
1	32761824	cg14975122	HDAC1	-10.56	2.64	6.26E-05	4.77E-02	1	-7.39	3.65	4.30E-02	-0.25	0.53	6.38E-01	-7.93	2.28	5.13E-04	-0.89	1.26E-03	-0.05	9.60E-01	-1.88	6.40E-02	0.42	0.29	1.41E-01	-0.02	1.13E-03
1	203255003	cg14991022	LINC01353	-24.03	5.66	2.17E-05	2.27E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.71E-01
11	57163587	cg14999724	PRG2	-10.02	2.41	3.31E-05	3.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.92E-03
3	150447687	cg15053244	LOC1019281	-35.15	6.21	1.50E-08	1.18E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.47E-05
12	7862691	cg15075897	DPPA3	-29.33	6.82	1.68E-05	1.90E-02	1	-11.11	5.02	2.69E-02	-0.30	0.66	6.48E-01	-12.14	2.88	2.56E-05	-0.99	1.20E-04	1.11	2.68E-01	-1.48	1.43E-01	0.35	0.23	1.38E-01	-0.02	3.72E-04
3	14708144	cg15106081	C3orf20	-36.59	7.21	3.83E-07	1.14E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.70E-05
6	15364953	cg15123849	JARID2	-7.54	1.34	1.98E-08	1.43E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.88E-01
3	42948626	cg15146567	ZNF662	-8.72	2.03	1.71E-05	1.92E-02	1	-9.62	4.80	4.50E-02	-0.54	0.59	3.58E-01	-3.37	1.79	6.00E-02	-1.03	1.07E-03	2.36	2.01E-02	-1.60	1.15E-01	0.43	0.24	7.42E-02	-0.03	1.50E-03
11	123429280	cg15158069	GRAMD1B	-7.33	1.45	4.61E-07	1.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6	135482465	cg15202169	MYB	-14.50	3.04	1.80E-06	3.51E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.26E-03
7	139896924	cg15203376	JHDM1D-AS1	-17.06	3.59	2.07E-06	3.89E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.55E-04
17	29837057	cg15209998	RAB11FIP4	-9.57	2.13	7.05E-06	9.58E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.90E-05
7	140102460	cg15244874	RAB19	-6.31	1.38	5.12E-06	7.61E-03	1	-4.46	2.64	9.12E-02	-1.53	0.58	8.02E-03	-1.45	1.69	3.89E-01	-0.81	3.34E-06	-2.59	1.09E-02	-2.31	2.40E-02	0.13	0.23	5.79E-01	-0.04	4.13E-03
12	53994642	cg15279186	ATF7	-10.67	2.32	4.09E-06	6.35E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	9.75E-01
17	76565091	cg15284593		-14.75	3.45	1.95E-05	2.11E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.29E-03
21	34124445	cg15301710	PAXBP1	-26.14	5.87	8.38E-06	1.10E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
15	33717344	cg15314908	RYR3	-35.73	7.01	3.38E-07	1.04E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.93E-06
10	1108248	cg15331937	WDR37	-8.49	2.05	3.44E-05	3.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.15E-04
15	57603845	cg15335273	LINC01413	-24.01	6.01	6.39E-05	4.84E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.88E-06
5	176774729	cg15344640	LMAN2	-24.55	5.72	1.78E-05	1.97E-02	1	-5.72	2.88	4.71E-02	-1.63	0.77	3.48E-02	-12.14	3.05	6.93E-05	-0.86	2.43E-04	-1.97	5.18E-02	-3.71	4.16E-04	0.41	0.25	1.04E-01	-0.03	1.70E-05
22	38386904	cg15352551	MIR4534	-10.75	2.21	1.19E-06	2.50E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.32E-03
20	57585940	cg15402265	CTSZ	-8.97	2.14	2.77E-05	2.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.81E-03
5	79782956	cg15434896	FAM151B	-29.70	5.54	8.27E-08	3.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.59E-05
11	70053254	cg15482717	FADD	-12.07	2.51	1.49E-06	2.99E-03	1	-10.46	4.55	2.15E-02	0.35	0.70	6.19E-01	-7.89	2.42	1.10E-03	-1.21	1.20E-04	-	-	-1.37	1.76E-01	0.32	0.22	1.41E-01	-0.02	1.71E-03
20	34018983	cg15532312	GDF5	-37.58	6.39	4.16E-09	5.08E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.09E-05
11	12180609	cg15579574	MICAL2	-67.52	12.24	3.46E-08	1.99E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.15E-04
5	53520049	cg15581007	ARL15	-6.17	1.54	6.21E-05	4.75E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.64E-02
6	7119942	cg15634144	RREB1	-9.82	2.16	5.18E-06	7.65E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.49E-02
10	5578539	cg15642638	CALML3-AS1	-23.20	3.99	6.21E-09	6.54E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.49E-04
11	70165886	cg15643933	MIR548K	-16.76	3.78	9.42E-06	1.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.11E-02
11	57156050	cg15700636	PRG2	-15.43	3.13	8.32E-07	1.99E-03	1	-7.34	3.40	3.08E-02	-1.24	0.95	1.92E-01	-11.65	2.25	2.35E-07	-0.95	1.06E-05	-1.26	2.11E-01	-2.47	1.59E-02	0.12	0.22	5.82E-01	-0.04	4.01E-06
9	71561785	cg15713581	LOC1019270	-13.22	3.27	5.37E-05	4.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.42E-05
10	86097061	cg15732078	CCSER2	-13.45	3.11	1.53E-05	1.76E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.57E-01
10	22743835	cg15737719	LOC1004994	-28.79	6.54	1.06E-05	1.32E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.39E-04
10	94837967	cg15767361	CYP26A1	-27.17	5.24	2.13E-07	7.25E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.26E-03
17	74708216	cg15769653	MXRA7	-40.50	8.64	2.77E-06	4.84E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.66E-03
7	36067955	cg15873326	LOC1019286	-20.26	4.65	1.32E-05	1.56E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.30E-05
1	40532772	cg15881027	CAP1	-25.10	4.84	2.14E-07	7.25E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.11E-05
11	73714778	cg15903936	UCP3	-38.91	9.14	2.06E-05	2.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.26E-06
2	99193996	cg15929700	COA5	-18.08	4.30	2.68E-05	2.66E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.73E-05
7	75511298	cg15952483	RHBDD2	-29.21	5.72	3.32E-07	1.03E-03	1	-18.56	10.74	8.40E-02	-0.35	0.66	5.94E-01	-11.71	5.23	2.52E-02	-	-	-2.55	1.20E-02	-2.58	1.19E-02	-0.11	0.24	6.61E-01	-0.01	3.11E-04

12	9486204	cg15964898	LOC1019304	-45.77	9.48	1.38E-06	2.82E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.28E-04
15	65904714	cg15988632	SLC24A1	-28.40	6.67	2.04E-05	2.17E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	5.34E-01
14	50780168	cg15998596	ATP5S	-14.44	3.42	2.43E-05	2.47E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.35E-01
2	191300784	cg15998761	MFSD6	-20.46	4.41	3.49E-06	5.77E-03	1	-5.32	2.64	4.40E-02	-3.89	0.86	5.36E-06	-9.29	2.39	1.04E-04	-0.82	2.09E-05	-3.09	2.52E-03	-2.67	9.50E-03	0.40	0.25	1.19E-01	-0.03	3.33E-05
20	35422698	cg16046667	DSN1	-10.13	2.53	6.36E-05	4.83E-02	1	-	-	-	-0.17	0.77	8.26E-01	-6.68	2.39	5.25E-03	-	-	-	-	-0.36	7.17E-01	0.17	0.22	4.29E-01	-	-
3	138478129	cg16050349	PIK3CB	-8.62	2.15	6.03E-05	4.65E-02	1	-5.88	2.83	3.78E-02	0.16	0.48	7.34E-01	-5.87	2.08	4.67E-03	-0.56	9.81E-03	-3.89	1.71E-04	-1.91	5.99E-02	0.73	0.32	2.05E-02	-0.03	1.35E-04
16	46776932	cg16064932	MYLK3	-13.02	2.82	3.81E-06	6.03E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.86E-04
7	150646704	cg16107105	KCNH2	-19.77	4.45	8.81E-06	1.14E-02	1	-6.16	2.93	3.56E-02	-2.26	1.03	2.89E-02	-5.58	2.74	4.17E-02	-0.51	1.81E-02	-0.07	9.48E-01	-2.91	4.87E-03	0.48	0.25	5.79E-02	-0.02	8.64E-04
20	34364813	cg16122287	PHF20	-36.05	7.02	2.77E-07	8.84E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.13E-03
17	17156930	cg16145720	FLCN	-27.78	5.26	1.28E-07	5.16E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.20E-04
12	113697418	cg16147002	TPCN1	-10.25	2.34	1.18E-05	1.43E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.88E-02
22	32150934	cg16160637	DEPDC5	-4.25	0.98	1.56E-05	1.78E-02	1	-5.57	2.80	4.68E-02	-0.43	0.58	4.52E-01	-5.28	1.81	3.56E-03	-0.37	8.24E-02	1.96	5.20E-02	-0.79	4.35E-01	0.02	0.26	9.31E-01	-0.01	2.85E-01
7	75592134	cg16182457	SNORA14A	-24.36	4.79	3.75E-07	1.13E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.92E-03
19	35894520	cg16191278	LINC01531	-13.45	2.99	6.93E-06	9.44E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.17E-05
2	183513961	cg16195942	D-JC10	-16.74	4.14	5.37E-05	4.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	6.57E-02
11	63011231	cg16239613	SLC22A25	-4.86	1.21	6.16E-05	4.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	29523841	cg16263722	SRSF4	-18.19	3.48	1.70E-07	6.23E-04	1	-9.11	4.25	3.19E-02	-1.74	0.95	6.89E-02	-11.15	2.15	2.14E-07	-1.76	1.11E-06	2.09	3.86E-02	-3.09	2.92E-03	0.25	0.22	2.55E-01	-0.03	5.46E-06
14	77425779	cg16270995	LINC01629	-8.19	1.95	2.69E-05	2.67E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.33E-03
10	6645837	cg16306670	LOC1019281	-38.63	8.36	3.87E-06	6.09E-03	1	-14.40	6.56	2.81E-02	-1.35	0.71	5.85E-02	-2.97	2.89	3.05E-01	-0.20	2.87E-01	0.27	7.87E-01	-2.56	1.28E-02	0.28	0.23	2.20E-01	-0.01	3.55E-02
10	129860424	cg16330225	AS-PTPRE	-20.43	4.93	3.44E-05	3.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.23E-03
1	3807168	cg16349667	C1orf174	-5.73	1.36	2.36E-05	2.42E-02	1	-11.49	5.87	5.02E-02	0.15	0.44	7.26E-01	-5.66	1.79	1.57E-03	-1.20	6.77E-04	-1.53	1.28E-01	-2.37	2.08E-02	0.17	0.19	3.76E-01	-0.03	1.65E-02
5	10708717	cg16362140	DAP	-9.60	2.35	4.49E-05	3.80E-02	1	-6.64	3.17	3.61E-02	-1.86	0.78	1.78E-02	-10.14	2.09	1.17E-06	-0.95	7.90E-06	-1.56	1.22E-01	-3.56	6.81E-04	0.37	0.23	1.11E-01	-0.04	2.56E-06
14	100610186	cg16409452	DEGS2	-22.72	4.92	3.94E-06	6.19E-03	1	-8.48	3.69	2.14E-02	-1.39	0.80	8.51E-02	-9.84	1.96	4.89E-07	-0.71	5.63E-04	0.34	7.34E-01	-2.86	5.53E-03	0.56	0.25	2.68E-02	-0.03	3.28E-05
8	22169041	cg16427256	PIWIL2	-28.09	4.42	2.08E-10	6.55E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17	55191754	cg16438366	AKAP1	-12.16	2.43	5.64E-07	1.49E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.77E-04
11	43403482	cg16450797	TTC17	-7.31	1.73	2.44E-05	2.47E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
22	30549748	cg16465403	HORMAD2-AS	-14.09	2.93	1.49E-06	2.99E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.59E-04
3	15066613	cg16499536	MRPS25	-33.17	5.92	2.05E-08	1.43E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
10	98425110	cg16508714	PIK3AP1	-8.86	2.08	2.08E-05	2.20E-02	1	-4.09	2.87	1.54E-01	-0.21	0.64	7.47E-01	-1.44	2.17	5.08E-01	-0.20	3.91E-01	-	-	-1.59	1.17E-01	0.44	0.25	8.33E-02	-0.02	4.02E-02
11	69418951	cg16549727	CCND1	-22.80	4.66	9.98E-07	2.19E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.49E-05
5	131770410	cg16587582	C5orf56	-17.39	4.34	6.19E-05	4.74E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.34E-02
19	16578633	cg16597993	EPS15L1	-24.57	4.52	5.49E-08	2.87E-04	1	-	-	-	-1.90	0.99	5.59E-02	-11.47	3.38	6.82E-04	-	-	-	-	-3.85	2.64E-04	0.29	0.23	2.11E-01	-0.03	3.61E-06
1	2036283	cg16599817	PRKCZ	-9.76	2.30	2.27E-05	2.34E-02	1	-10.23	4.54	2.42E-02	-0.20	0.60	7.39E-01	-6.03	1.92	1.67E-03	0.50	1.10E-01	4.11	7.55E-05	-0.77	4.42E-01	0.16	0.23	5.05E-01	-0.03	5.14E-03
15	31248701	cg16606719	MTMR10	-32.81	4.55	5.51E-13	2.25E-07		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
16	75037584	cg16660617	ZNRF1	-60.50	9.82	7.13E-10	1.57E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.84E-02
6	157313826	cg16677621	MIR4466	-21.44	4.62	3.47E-06	5.75E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.68E-01
9	101705161	cg16680864	COL15A1	-8.97	1.95	4.27E-06	6.57E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.49E-06
1	44716058	cg16710124	SNORA110	-24.55	5.89	3.10E-05	2.96E-02	1	-19.45	9.20	3.45E-02	-0.70	0.91	4.40E-01	-6.60	3.35	4.90E-02	-0.76	9.50E-04	4.52	1.57E-05	-2.82	6.24E-03	0.11	0.22	6.27E-01	-0.01	8.73E-03
14	24745117	cg16714237	RABGGTA	-13.34	2.94	5.94E-06	8.42E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.35E-03
16	57683565	cg16725301	ADGRG1	-14.10	3.52	6.22E-05	4.75E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.73E-06
20	42355376	cg16829505	GTSF1L	-27.34	6.11	7.61E-06	1.02E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	1.66E-01
2	127461631	cg16856131	GYPC	-8.08	1.96	3.88E-05	3.41E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	6.20E-01
1	27240812	cg16868031	NR0B2	-15.74	3.36	2.87E-06	4.99E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.62E-04
22	30342424	cg16899419	MIR6818	-8.99	2.07	1.43E-05	1.66E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
12	68764080	cg16950658	MDM1	-8.17	1.81	6.30E-06	8.82E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.32E-01
5	139597203	cg16953142	CYSTM1	-43.04	9.27	3.44E-06	5.74E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.19E-04
11	10499641	cg17022365	AMPD3	-18.80	4.20	7.71E-06	1.03E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.91E-03
11	59525449	cg17030380	STX3	-27.21	6.49	2.76E-05	2.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.59E-04
17	9923599	cg17040893	GAS7	-8.90	2.20	5.02E-05	4.13E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	1.32E-01
19	35950799	cg17062760	FFAR2	-14.30	2.91	8.81E-07	2.08E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.60E-04
3	52220370	cg17074037	ALAS1	-10.61	2.48	1.88E-05	2.04E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	6.38E-02
1	212612526	cg17078207	NENF	-31.48	5.70	3.31E-08	1.94E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.59E-04
17	2287284	cg17105176	MNT	-28.70	4.87	3.63E-09	4.75E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.11E-04
12	56600222	cg17116500	RNF41	-23.24	5.20	7.88E-06	1.05E-02	1	-10.46	5.29	4.82E-02	-1.02	0.88	2.50E-01	-8.79	2.96	2.96E-03	-1.00	1.64E-04	-	-	-2.96	4.23E-03	0.23	0.20	2.39E-01	-0.01	2.89E-03
5	153664745	cg17138920	MIR1294	-42.10	7.38	1.17E-08	9.82E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.10E-05
13	100188895	cg17139328	TM9SF2	-24.95	5.51	5.87E-06	8.38E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.80E-02
2	86157952	cg17218818	ST3GAL5-AS	-35.56	6.78	1.54E-07	5.79E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.99E-02
8	103603330	cg17245251	ODF1	-27.52	5.63	1.03E-06	2.25E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.34E-05
1	90344715	cg17256681	LRRC8D	-49.93	9.82	3.71E-07	1.12E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.94E-04
16	68325153	cg17300669	SLC7A6OS	-53.46	11.75	5.34E-06	7.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.42E-05
2	131126377	cg17334945	PTPN18	-13.84	3.18	1.33E-05	1.57E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.56E-03
3	14420209	cg17338225	SLC6A6	-13.64	3.23	2.41E-05	2.46E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.66E-04
17	66437754	cg17354333	WIPI1	-7.22	1.77	4.34E-05	3.71E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.18E-01
3	124646526	cg17365440	MUC13	-18.39	3.66	5.07E-07	1.39E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.81E-03
17	56270828	cg17374802	EPX	-12.06	2.92	3.55E-05	3.23E-02	1	-7.73	3.48	2.63E-02	-1.06	1.01	2.96E-01	-10.55	2.22	2.05E-06	-0.99	1.71E-04	0.76	4.48E-01	-2.15	3.47E-02	0.28	0.21	1.80E-01	-0.03	1.34E-06
17	41400661	cg17378535	LINC00854	-10.52	2.37	9.37E-06	1.19E-02	1	-29.65	13.13	2.39E-02	-1.48	0.79	5.92E-02	-7.35	2.11	4.87E-04	-	-	0.90	3.68E-01	-1.72	9.00E-02	0.01	0.22	9.61E-01	-0.02	3.60E-03
10	31987694	cg17384357	ARHGAP12	-18.15	4.19	1.49E-05	1.73E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	9.13E-02

6	7154703	cg17446528	RREB1	-5.69	1.41	5.36E-05	4.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.30E-02
7	102630100	cg17459348	LRRC17	-21.72	4.83	6.80E-06	9.31E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.37E-05
19	51961666	cg17521120	SIGLEC8	-14.20	2.95	1.47E-06	2.97E-03	1	-6.88	3.47	4.71E-02	-1.89	1.04	6.88E-02	-8.79	2.34	1.68E-04	-1.98	1.78E-06	-0.51	6.14E-01	-3.20	2.05E-03	0.31	0.23	1.77E-01	-0.03	6.54E-07
17	4112498	cg17526357	ANKFY1	-13.38	3.24	3.71E-05	3.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.30E-05
21	36608456	cg17532497	RUNX1	-19.59	4.32	5.83E-06	8.33E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.79E-05
9	91919480	cg17542165	CKS2	-31.38	6.86	4.71E-06	7.16E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.86E-04
5	153836180	cg17558547	SAP30L	-18.33	4.39	2.94E-05	2.85E-02	1	-6.74	3.16	3.30E-02	-0.23	0.54	6.75E-01	-6.41	2.52	1.10E-02	-0.60	5.76E-03	-2.13	3.51E-02	-2.01	4.89E-02	0.50	0.26	5.84E-02	-0.03	8.35E-05
2	106475496	cg17558817	NCK2	-9.50	2.27	2.86E-05	2.79E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.32E-05
17	25805881	cg17651926	KSR1	-23.60	5.66	3.02E-05	2.90E-02	1	-	-	-	0.37	0.63	5.51E-01	0.74	4.27	8.63E-01	-	-	-	-	-1.54	1.27E-01	-0.19	0.24	4.39E-01	0.00	3.13E-01
2	74531615	cg17660709	SLC4A5	-13.20	2.88	4.66E-06	7.09E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.75E-05
7	99507261	cg17717565	TRIM4	-17.65	2.75	1.43E-10	5.09E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.37E-04
4	185744331	cg17718238	ACSL1	-24.42	4.93	7.42E-07	1.83E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.79E-04
11	66118897	cg17751391	LOC1027240	-9.59	2.14	7.36E-06	9.94E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.46E-02
1	84744762	cg17772438	SAMD13	-18.63	4.56	4.37E-05	3.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.72E-04
7	142659425	cg17784922	KEL	-33.16	6.15	6.90E-08	3.42E-04	1	-14.11	6.59	3.22E-02	-1.00	0.96	2.96E-01	-13.70	3.29	3.16E-05	-0.31	1.79E-01	5.45	3.14E-07	-1.99	5.07E-02	0.20	0.23	3.79E-01	-0.01	9.99E-03
1	175136705	cg17804141	KIAA0040	-12.32	2.42	3.78E-07	1.13E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.08E-03
18	12411141	cg17844602	PRELID3A	-12.17	3.00	4.90E-05	4.05E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.12E-03
2	28550531	cg17862837	LOC1005057	-48.34	9.84	9.09E-07	2.09E-03	1	-10.53	5.26	4.55E-02	-0.89	0.69	1.98E-01	-11.78	3.60	1.09E-03	-0.80	1.32E-04	-2.12	3.63E-02	-3.30	1.54E-03	-0.02	0.25	9.47E-01	-0.01	4.36E-01
11	44092987	cg17879351	ACCS	-20.08	3.99	4.70E-07	1.31E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.91E-07
15	80142016	cg17934955	MTHFS	-25.14	5.21	1.39E-06	2.83E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.72E-01
1	167520305	cg17936236	CREG1	-6.84	1.68	4.85E-05	4.02E-02	1	-10.42	5.39	5.33E-02	-0.12	0.48	8.03E-01	-2.78	2.11	1.89E-01	-0.72	7.34E-02	-	-	-1.59	1.17E-01	0.45	0.27	9.51E-02	-0.02	4.19E-03
5	40674971	cg17939602	PTGER4	-11.34	2.43	3.19E-06	5.43E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
3	53513310	cg17941143	CAC-1D	-6.75	1.57	1.81E-05	1.99E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	172425816	cg17946525	C1orf105	-23.91	4.22	1.46E-08	1.18E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.53E-06
1	177907297	cg17971251	SEC16B	-16.43	3.28	5.32E-07	1.43E-03	1	-7.07	3.33	3.38E-02	-1.13	0.61	6.41E-02	-14.63	2.55	9.52E-09	-0.41	3.87E-02	-1.48	1.42E-01	-2.86	5.66E-03	0.29	0.23	1.95E-01	-0.03	1.55E-04
7	73208138	cg17982734	CLDN3	-9.63	2.03	2.08E-06	3.91E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.92E-03
2	74612222	cg17988187	DCTN1-AS1	-16.37	3.12	1.59E-07	5.92E-04	1	-8.01	3.60	2.62E-02	-1.09	0.68	1.09E-01	-11.04	2.27	1.21E-06	-1.02	9.69E-05	1.23	2.21E-01	-3.06	3.17E-03	0.18	0.23	4.43E-01	-0.03	2.89E-04
21	36689434	cg18099556	LOC1005064	-19.93	4.70	2.22E-05	2.31E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.28E-04
12	1890975	cg18135530	LRTM2	-39.28	8.47	3.55E-06	5.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.63E-04
3	197239695	cg18161208	BDH1	-12.92	3.03	1.97E-05	2.12E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.86E-02
17	43111632	cg18176312	DCAKD	-42.79	7.63	2.03E-08	1.43E-04	1	-19.86	8.61	2.11E-02	1.02	0.86	2.36E-01	-5.62	3.52	1.10E-01	-0.84	4.15E-04	0.08	9.34E-01	-3.90	2.20E-04	-0.15	0.22	4.87E-01	0.00	2.98E-01
4	185712241	cg18182820	SLED1	-27.49	5.48	5.34E-07	1.43E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	9.35E-05
6	139841523	cg18190876	LINC01625	-22.44	4.75	2.35E-06	4.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.02E-05
19	40227949	cg18254848	CLC	-20.45	4.81	2.11E-05	2.22E-02	1	-5.42	2.73	4.70E-02	-0.74	0.84	3.78E-01	-7.59	2.68	4.55E-03	-0.58	5.30E-03	-0.11	9.11E-01	-3.46	9.17E-04	0.22	0.24	3.74E-01	-0.03	2.58E-05
11	134128612	cg18278420	ACAD8	-30.36	7.14	2.09E-05	2.21E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	6.67E-01
19	930871	cg18337287	ARID3A	-21.35	5.25	4.85E-05	4.02E-02	1	-6.79	3.22	3.50E-02	-1.50	0.85	7.69E-02	-15.13	2.81	7.21E-08	-1.15	7.45E-07	-	-	-4.18	8.52E-05	0.30	0.25	2.32E-01	-0.03	7.37E-05
6	138098613	cg18341600	LOC1005074	-9.45	2.10	6.63E-06	9.13E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.81E-04
11	47937934	cg18367488	PTPRJ	-17.62	3.59	8.91E-07	2.09E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.27E-02
14	21436271	cg18368116	R-SE2	-19.17	4.36	1.09E-05	1.34E-02	1	-7.58	3.32	2.23E-02	-0.39	0.68	5.60E-01	-11.80	2.58	4.93E-06	-0.89	1.82E-04	1.08	2.82E-01	-2.82	6.19E-03	0.47	0.24	4.52E-02	-0.03	2.57E-04
2	32946576	cg18399629	MIR4765	-36.82	5.86	3.28E-10	8.66E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.64E-05
6	7043141	cg18455414	RREB1	-11.60	2.50	3.58E-06	5.81E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.93E-05
2	99124870	cg18455616	INPP4A	-6.45	1.47	1.20E-05	1.45E-02	1	-6.83	3.44	4.69E-02	-0.83	0.48	8.34E-02	-1.84	1.45	2.03E-01	-0.46	1.33E-02	-	-	-3.12	2.65E-03	-0.06	0.21	7.57E-01	-0.05	8.50E-07
4	95183565	cg18456722	SMARCAD1	-48.90	11.31	1.54E-05	1.77E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.01E-04
14	103436387	cg18505004	AMN	-18.88	4.69	5.67E-05	4.47E-02	1	-6.62	3.38	5.03E-02	-0.46	0.60	4.41E-01	-8.10	2.70	2.66E-03	-0.14	4.49E-01	-0.73	4.68E-01	-1.41	1.64E-01	0.34	0.22	1.19E-01	-0.02	4.48E-03
13	34446325	cg18544612	RFC3	-15.74	3.25	1.24E-06	2.58E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.97E-04
14	100610570	cg18550847	DEGS2	-18.39	2.93	3.28E-10	8.66E-06	1	-9.24	4.21	2.84E-02	-1.25	0.76	9.92E-02	-9.38	1.89	7.10E-07	-0.78	1.79E-04	-1.22	2.24E-01	-2.32	2.36E-02	0.37	0.23	1.18E-01	-0.03	3.72E-05
16	69928821	cg18617819	WWP2	-9.95	2.18	4.95E-06	7.43E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.00E-02
7	1914073	cg18650626	MIR4655	-9.95	1.75	1.39E-08	1.13E-04	1	-7.88	4.30	6.69E-02	-3.19	0.78	4.21E-05	-3.76	0.97	9.89E-05	-	-	-0.66	5.11E-01	-4.83	7.88E-06	0.29	0.20	1.40E-01	-	-
9	124042257	cg18655410	GSN-AS1	-9.29	2.25	3.69E-05	3.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.46E-04
7	150651937	cg18666454	KCNH2	-15.09	3.21	2.56E-06	4.57E-03	1	-7.10	3.18	2.55E-02	-1.17	0.81	1.49E-01	-11.32	2.15	1.46E-07	-0.94	3.41E-05	-2.46	1.54E-02	-3.61	5.80E-04	0.33	0.24	1.76E-01	-0.04	2.54E-06
16	69901132	cg18693924	WWP2	-12.34	2.99	3.59E-05	3.25E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.03E-03
10	12448959	cg18715410	CAMK1D	-16.82	3.91	1.73E-05	1.93E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.30E-05
1	9599067	cg18783781	SLC25A33	-16.26	3.32	9.74E-07	2.16E-03	1	-6.02	2.98	4.31E-02	-0.19	1.10	8.64E-01	-10.56	2.36	7.45E-06	-0.89	1.13E-04	-1.41	1.62E-01	-2.17	3.33E-02	0.26	0.24	2.76E-01	-0.02	8.50E-03
12	31453901	cg18805734	FLJ13224	-9.93	2.23	8.86E-06	1.14E-02	1	-6.30	3.21	4.99E-02	-0.38	0.50	4.41E-01	-6.97	2.17	1.33E-03	-0.31	1.81E-01	1.14	2.58E-01	-1.35	1.83E-01	0.29	0.26	2.64E-01	-0.02	2.01E-03
11	33731839	cg18814289	C11orf91	-69.40	12.93	8.04E-08	3.89E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.95E-04
15	40093898	cg18852698	LOC1053709	-20.40	3.24	3.20E-10	8.66E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.05	9.81E-06
21	43771120	cg18879389	TFF2	-23.36	5.21	7.27E-06	9.86E-03	1	-5.08	3.60	1.58E-01	-0.90	0.52	8.37E-02	-13.79	2.84	1.21E-06	-0.52	8.22E-02	3.90	1.63E-04	-1.65	1.03E-01	0.13	0.21	5.24E-01	-0.02	2.52E-04
15	94408646	cg18991231	LOC1019271	-14.02	2.95	1.95E-06	3.72E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.46E-01
10	104414965	cg19002713	TRIM8	-28.99	5.92	9.69E-07	2.16E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.90E-02
15	40851643	cg19069027	C15orf57	-10.24	2.27	6.57E-06	9.07E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.29E-06
3	188001192	cg19198938	LPP	-15.95	3.80	2.66E-05	2.65E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.93E-03
3	9929455	cg19227526	JAGN1	-9.45	2.35	5.60E-05	4.42E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.28E-04
21	43786727	cg19247032	TFF1	-23.26	5.09	4.82E-06	7.30E-03	1	-8.91	4.32	3.90E-02	-0.32	0.35	3.67E-01	-9.21	2.92	1.62E-03	-1.00	2.08E-03	3.52	6.32E-04	-1.21	2.29E-01	0.32	0.22	1.47E-01	-0.02	1.71E-02
12	1413681	cg19260922	LINC00942	-25.64	4.44	7.73E-09	7.26E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.99E-04
3	141682388	cg19294517	TFDP2	-9.60	2.19	1.16E-05	1.41E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.23E-03
1	26624534	cg19296400	UBXN11	-13.78	2.82	1.06E-06	2.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.55E-02
3	13069838	cg19344749	IQSEC1	-9.96	2.13	3.00E-06	5.16E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.34E-02

1	27048589	cg19375767	ARID1A	-16.71	2.95	1.50E-08	1.18E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.56E-06
2	30414835	cg19376906	LBH	-10.34	2.11	9.83E-07	2.17E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.05	1.63E-06
7	4727742	cg19396390	FOXK1	-18.62	4.39	2.27E-05	2.34E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.60E-03
12	7104184	cg19434937	LPCAT3	-11.95	2.63	5.61E-06	8.05E-03	1	-7.64	3.68	3.79E-02	-0.37	0.43	3.99E-01	-8.95	1.86	1.55E-06	-2.24	1.59E-05	-1.95	5.42E-02	-2.42	1.82E-02	0.11	0.21	5.93E-01	-0.03	1.66E-03
20	35504064	cg19448292	TLDC2	-13.93	2.95	2.30E-06	4.25E-03	1	-5.79	2.75	3.51E-02	-0.42	0.76	5.80E-01	-8.59	2.22	1.11E-04	-0.21	3.97E-01	1.55	1.23E-01	-0.28	7.84E-01	0.09	0.24	7.24E-01	-0.02	2.14E-02
17	179947	cg19456763	LOC1005063	-11.17	2.55	1.16E-05	1.41E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.03E-05
19	2059698	cg19475270	MKNK2	-11.80	2.61	6.38E-06	8.90E-03	1	-17.39	7.41	1.89E-02	-0.34	0.42	4.14E-01	-4.23	2.14	4.82E-02	-2.44	1.46E-05	1.92	5.69E-02	-2.13	3.66E-02	0.48	0.23	3.79E-02	-0.01	1.23E-03
21	46506629	cg19582046	ADARB1	-17.22	2.97	6.40E-09	6.54E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.21E-05
1	112045886	cg19686029	ADORA3	-28.73	5.72	5.13E-07	1.39E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.30E-06
19	7291221	cg19696679	INSR	-34.33	6.78	4.07E-07	1.18E-03	1	-	-	-	-0.07	0.99	9.40E-01	-2.48	3.68	5.01E-01	-	-	-	-	0.55	5.84E-01	0.05	0.22	8.33E-01	-0.03	1.87E-04
13	111316234	cg19745810	CARS2	-38.86	6.56	3.20E-09	4.28E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.43E-04
1	27241913	cg19787060	NR0B2	-13.39	2.82	1.98E-06	3.76E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.89E-05
5	176327783	cg19791262	HK3	-7.93	1.85	1.77E-05	1.96E-02	1	-6.86	3.54	5.30E-02	-0.62	0.92	4.95E-01	-5.87	2.08	4.76E-03	-0.80	1.54E-02	1.20	2.31E-01	-0.41	6.87E-01	0.20	0.25	4.27E-01	-0.02	2.94E-03
11	72136395	cg19791780	CLPB	-15.58	3.77	3.58E-05	3.24E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.45E-02
1	23072310	cg19851810	MIR4684	-38.84	8.05	1.41E-06	2.86E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.53E-03
4	1577971	cg19901381	FAM53A	-15.69	3.90	5.73E-05	4.49E-02	1	-8.35	3.78	2.74E-02	0.09	0.45	8.50E-01	-8.49	2.41	4.21E-04	-0.58	6.43E-03	1.01	3.17E-01	-0.63	5.32E-01	0.27	0.20	1.80E-01	-0.02	6.17E-04
13	30143971	cg19928703	SLC7A1	-29.58	5.11	7.20E-09	7.18E-05	1	-10.45	4.76	2.81E-02	-0.31	0.27	2.63E-01	-11.71	2.68	1.21E-05	-	-	-0.10	9.21E-01	-3.03	3.45E-03	0.39	0.23	8.88E-02	-0.03	7.19E-05
20	34479717	cg19960458	SCAND1	-15.73	3.80	3.47E-05	3.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
12	68056168	cg19968199	DYRK2	-44.51	8.65	2.70E-07	8.75E-04	1	-5.49	2.87	5.60E-02	-0.45	0.81	5.82E-01	-6.32	2.66	1.75E-02	-0.79	5.40E-04	0.21	8.37E-01	-3.16	2.37E-03	0.25	0.27	3.51E-01	-0.03	6.51E-05
2	11926291	cg19993461	MIR548S	-41.98	9.92	2.34E-05	2.40E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.07E-03
12	121861616	cg19998289	MIR7107	-11.56	2.84	4.80E-05	4.00E-02	1	-8.92	3.87	2.12E-02	-2.59	1.01	1.01E-02	-5.75	1.88	2.27E-03	-0.56	1.72E-02	-0.31	7.55E-01	-2.14	3.57E-02	0.09	0.22	6.67E-01	-0.03	6.99E-06
1	40878936	cg20035380	SMAP2	-10.34	2.24	3.80E-06	6.03E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	9.58E-01
11	126279702	cg20037145	ST3GAL4	-10.39	2.02	2.65E-07	8.68E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.02E-02
10	12456489	cg20072505	CAMK1D	-15.44	3.73	3.53E-05	3.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.57E-03
7	41914145	cg20178107	INHBA	-21.67	4.03	7.58E-08	3.69E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.79E-06
22	24550935	cg20182202	SUSD2	-8.92	2.14	3.13E-05	2.98E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.60E-05
8	142305640	cg20216313	SLC45A4	-3.77	0.91	3.21E-05	3.03E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	8.67E-01
8	145643626	cg20259557	SLC39A4	-12.01	2.95	4.78E-05	3.99E-02	1	-13.34	5.64	1.80E-02	-0.44	0.69	5.24E-01	-4.66	1.92	1.56E-02	-1.44	3.16E-07	-	-	-3.55	6.89E-04	0.20	0.20	3.20E-01	-0.01	1.44E-01
3	130616293	cg20263733	ATP2C1	-34.50	6.44	8.39E-08	3.92E-04	1	-5.16	2.66	5.21E-02	-4.23	1.13	1.73E-04	-14.20	2.81	4.26E-07	-0.91	3.36E-05	-1.51	1.35E-01	-3.74	3.80E-04	0.50	0.27	6.55E-02	-0.03	4.20E-04
1	6645171	cg20267283	ZBTB48	-17.27	3.00	8.55E-09	7.77E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	8.41E-06
17	81040724	cg20290167	METRNL	-9.30	2.30	5.40E-05	4.31E-02	1	-11.91	5.06	1.85E-02	-0.06	0.68	9.26E-01	-6.09	2.14	4.38E-03	-1.85	4.99E-10	-	-	-2.24	2.85E-02	0.26	0.21	2.30E-01	-0.02	3.68E-03
17	15137304	cg20315954	MIR4731	-24.50	4.72	2.03E-07	6.99E-04	1	-9.73	4.15	1.90E-02	-0.43	0.83	6.04E-01	-12.65	2.73	3.58E-06	-0.80	4.69E-04	-	-	-2.39	1.95E-02	0.30	0.24	2.17E-01	-	-
1	24172120	cg20317437	HMGCL	-14.17	3.43	3.69E-05	3.29E-02	1	-5.36	2.85	6.02E-02	0.78	0.97	4.18E-01	-8.55	2.46	4.99E-04	-0.74	1.68E-03	-2.11	3.75E-02	-2.79	6.79E-03	0.20	0.24	4.08E-01	-0.03	3.28E-05
15	42456971	cg20378916	PLA2G4F	-26.89	5.84	4.08E-06	6.34E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	6.24E-02
15	75054510	cg20385913	CYP1A2	-16.16	3.71	1.30E-05	1.54E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.76E-02
11	34827586	cg20387860	PDHX	-29.68	7.00	2.21E-05	2.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8	67967170	cg20454670	COPS5	-34.95	8.74	6.30E-05	4.79E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.58E-03
19	19599547	cg20493175	GATAD2A	-9.68	2.24	1.61E-05	1.83E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	3.85E-01
12	6342778	cg20560376	CD9	-34.55	5.28	6.03E-11	3.79E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.16E-05
2	38806109	cg20619340	HNRNPLL	-19.23	4.75	5.18E-05	4.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.01E-06
12	50441815	cg20649656	ASIC1	-23.73	5.78	4.04E-05	3.52E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.22E-02
1	87596049	cg20654602	LINC01140	-15.62	2.69	6.09E-09	6.54E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	7.25E-05
19	44220148	cg20673965	IRGC	-11.28	2.39	2.32E-06	4.27E-03	1	-8.98	4.31	3.74E-02	-0.48	1.12	6.67E-01	-11.06	2.43	5.54E-06	-1.58	5.44E-05	1.47	1.44E-01	-2.18	3.27E-02	0.36	0.25	1.48E-01	-0.02	3.33E-04
9	140470011	cg20758387	DPH7	-8.68	1.97	1.08E-05	1.33E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.23E-02
6	167177613	cg20774312	RPS6KA2	-13.15	3.21	4.19E-05	3.61E-02	1	-19.55	8.62	2.33E-02	-0.57	0.76	4.53E-01	-5.15	2.55	4.37E-02	-0.40	4.47E-02	1.74	8.44E-02	-1.04	3.04E-01	0.09	0.19	6.31E-01	-0.02	3.74E-03
3	171205319	cg20804243	TNIK	-16.79	3.33	4.56E-07	1.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.25E-05
18	54558018	cg20813763	LINC-ROR	-44.10	7.98	3.30E-08	1.94E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.61E-03
12	8201975	cg20818756	FOXJ2	-18.47	3.71	6.42E-07	1.64E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.48E-05
7	29382450	cg20831584	LOC1027244	-20.84	4.20	6.94E-07	1.73E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.23E-03
6	42363749	cg20840540	TRERF1	-13.82	3.19	1.52E-05	1.75E-02	1	-12.74	5.32	1.65E-02	-1.53	0.77	4.60E-02	-9.47	2.50	1.54E-04	-0.51	1.09E-02	-2.28	2.45E-02	-2.15	3.54E-02	0.45	0.23	4.72E-02	-0.03	1.21E-06
4	148733880	cg20866785	MIR4799	-10.43	2.60	5.80E-05	4.52E-02	1	-5.42	2.96	6.66E-02	-0.02	0.44	9.65E-01	-9.27	2.16	1.70E-05	-0.69	2.36E-03	-3.18	1.89E-03	-2.91	4.87E-03	0.03	0.28	9.27E-01	-0.04	1.13E-06
17	17939419	cg20885063	ATPAF2	-22.35	4.49	6.53E-07	1.66E-03	1	-7.44	3.45	3.13E-02	-2.29	0.83	5.84E-03	-10.94	2.24	1.06E-06	-0.60	2.62E-03	-	-	-2.65	9.97E-03	0.36	0.24	1.32E-01	-0.03	1.72E-04
20	36340388	cg20893283	CTNNBL1	-16.03	3.24	7.25E-07	1.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	9.66E-03
4	37953726	cg20911897	PTTG2	-3.40	0.84	5.13E-05	4.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.60E-01
18	74253340	cg20936755	LINC00908	-7.71	1.87	3.72E-05	3.30E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.91E-04
12	64961489	cg20992317	RASSF3	-8.56	1.94	9.85E-06	1.24E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.92E-05
20	35422703	cg21045547	DSN1	-17.58	3.54	6.71E-07	1.70E-03	1	-14.30	6.54	2.86E-02	-0.02	0.99	9.84E-01	-11.71	2.57	5.32E-06	-1.42	1.08E-07	-	-	-2.05	4.39E-02	0.04	0.23	8.65E-01	-	-
15	63495110	cg21067343	RAB8B	-24.51	4.96	7.66E-07	1.87E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	9.10E-02
16	68049958	cg21092930	LOC1001313	-8.11	1.81	7.79E-06	1.04E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.38E-04
6	111920032	cg21140167	TRAF3IP2	-34.60	8.50	4.67E-05	3.92E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.43E-03
1	204370262	cg21142557	PPP1R15B	-31.21	6.39	1.02E-06	2.24E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.49E-03
1	155741125	cg21211696	SCAR-26B	-29.62	7.39	6.15E-05	4.72E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.50E-04
1	6341230	cg21220721	GPR153	-9.07	1.50	1.67E-09	2.59E-05	1	-19.07	8.06	1.80E-02	-2.49	0.49	4.13E-07	-6.32	1.10	1.02E-08	-	-	-4.00	1.16E-04	-4.73	1.14E-05	0.26	0.21	2.22E-01	-0.06	9.14E-07
11	63997324	cg21234134	D-JC4	-9.89	2.32	1.94E-05	2.10E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	4.56E-01
5	172227661	cg21237481	DUSP1	-16.69	3.54	2.41E-06	4.36E-03	1	-4.46	2.46	7.00E-02	-0.23	0.44	5.93E-01	-5.12	2.26	2.32E-02	-0.25	2.22E-01	-1.95	5.33E-02	-1.19	2.40E-01	0.38	0.26	1.41E-01	-0.02	1.87E-03
11	43779382	cg21259720	HSD17B12	-34.35	6.53	1.41E-07	5.50E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.71E-05
22	37280288	cg21306887	NCF4	-41.84	9.67	1.51E-05	1.74E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.28E-03

3	15066608	cg21419012	MRPS25	-21.52	4.93	1.25E-05	1.50E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.12E-08
10	18550623	cg21505451	CACNB2	-10.86	2.54	1.87E-05	2.04E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.14E-02
10	70531163	cg21553305	MIR1254-1	-35.84	7.39	1.23E-06	2.58E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.80E-03
1	173496518	cg21568193	PRDX6	-18.95	4.28	9.38E-06	1.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.12E-05
12	131310417	cg21575634	STX2	-21.04	4.94	2.05E-05	2.18E-02	1	-	-	-	-0.75	0.68	2.69E-01	-7.68	2.29	7.84E-04	-0.49	8.25E-03	-2.70	8.01E-03	-2.98	3.95E-03	0.80	0.57	1.62E-01	-0.03	1.39E-04
6	36311062	cg21576315	C6orf222	-9.77	2.37	3.69E-05	3.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.64E-03
17	72709731	cg21640749	CD300LF	-17.07	3.28	1.97E-07	6.87E-04	1	-12.28	5.36	2.20E-02	-0.11	0.74	8.78E-01	-7.32	2.34	1.77E-03	-0.76	1.39E-02	-	-	-1.95	5.53E-02	0.53	0.27	5.38E-02	-	-
19	40837284	cg21664942	C19orf47	-22.01	3.89	1.56E-08	1.19E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.68E-03
2	48340131	cg21672758	FOXN2	-30.29	7.18	2.46E-05	2.49E-02	1	-14.59	5.86	1.27E-02	-0.30	0.85	7.24E-01	-10.93	3.08	3.81E-04	-0.42	7.72E-02	0.47	6.40E-01	-2.47	1.62E-02	0.39	0.24	1.01E-01	-0.03	6.83E-06
17	39686628	cg21723861	KRT19	-22.10	4.60	1.59E-06	3.16E-03	1	-9.90	4.46	2.63E-02	-0.19	0.44	6.66E-01	-14.05	2.68	1.59E-07	-1.17	1.02E-04	-	-	-3.36	1.26E-03	0.23	0.23	3.04E-01	-	-
15	57519802	cg21831937	TCF12	-23.86	5.95	6.02E-05	4.65E-02	1	-9.82	5.17	5.74E-02	0.77	0.53	1.50E-01	-2.44	2.62	3.52E-01	-0.49	3.31E-02	0.32	7.51E-01	-1.73	8.87E-02	0.33	0.35	3.53E-01	-0.01	2.17E-02
10	102277130	cg21867373	SEC31B	-17.89	3.56	5.12E-07	1.39E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.65E-04
5	67715050	cg21931263	PIK3R1	-10.35	2.51	3.77E-05	3.32E-02	1	-6.29	2.99	3.55E-02	0.04	0.35	9.04E-01	-4.40	2.09	3.52E-02	-0.70	1.79E-03	-0.42	6.78E-01	-1.97	5.28E-02	0.18	0.30	5.44E-01	-0.02	3.74E-02
1	17751974	cg21932513	RCC2	-12.44	2.68	3.29E-06	5.56E-03	1	-9.82	4.34	2.37E-02	0.10	0.52	8.46E-01	-7.64	2.06	2.08E-04	-1.10	1.95E-05	-	-	-2.94	4.43E-03	0.41	0.25	1.08E-01	-0.01	6.19E-02
11	1828746	cg21992676	SYT8	-18.19	3.99	5.09E-06	7.57E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.09E-04
10	15194066	cg21994464	PPIAP30	-15.36	3.27	2.70E-06	4.75E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.76E-04
9	32426874	cg22022320	ACO1	-42.48	9.09	2.99E-06	5.15E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.98E-04
2	69831408	cg22059413	ANXA4	-14.71	3.56	3.57E-05	3.24E-02	1	-4.52	2.57	7.82E-02	-2.47	0.75	9.66E-04	-7.94	2.29	5.15E-04	-1.27	4.97E-10	-	-	-3.57	6.56E-04	0.19	0.23	3.96E-01	-	-
6	36584993	cg22069559	MIR3925	-11.69	2.85	4.12E-05	3.56E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.46E-04
10	43911124	cg22080845	HNRNPF	-46.17	9.49	1.14E-06	2.43E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.69E-03
1	236715049	cg22087490	LGALS8-AS1	-25.58	4.58	2.37E-08	1.62E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.63E-04
17	26793673	cg22146772	SLC13A2	-20.81	4.09	3.64E-07	1.11E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.35E-04
16	387629	cg22158603	AXIN1	-11.57	2.90	6.45E-05	4.86E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.63E-05
3	195965369	cg22221575	SLC51A	-10.10	2.21	4.99E-06	7.47E-03	1	-4.51	2.29	4.86E-02	0.27	0.57	6.30E-01	-7.15	1.83	9.60E-05	-0.92	1.02E-05	3.41	9.06E-04	-1.28	2.05E-01	0.20	0.23	3.93E-01	-0.05	5.04E-06
17	506008	cg22252112	VPS53	-11.47	2.57	8.39E-06	1.10E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.68E-04
2	28877884	cg22304799	PLB1	-41.63	10.37	6.00E-05	4.64E-02	1	-19.20	9.46	4.25E-02	-0.20	0.26	4.37E-01	-6.79	3.81	7.47E-02	-0.10	6.04E-01	1.76	8.17E-02	0.93	3.55E-01	0.45	0.25	7.81E-02	-0.01	3.89E-02
6	73623666	cg22418084	MIR4282	-5.33	1.27	2.79E-05	2.74E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.92E-02
17	81040906	cg22503106	METRNL	-19.55	3.35	5.20E-09	5.90E-05	1	-4.92	2.36	3.73E-02	-0.83	0.51	1.06E-01	-7.53	1.99	1.48E-04	-0.88	3.90E-05	-	-	-2.19	3.16E-02	0.01	0.27	9.68E-01	-0.03	1.41E-02
17	17843585	cg22508829	TOM1L2	-26.85	5.31	4.23E-07	1.22E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.71E-05
17	3655775	cg22668931	GSG2	-24.79	4.16	2.51E-09	3.54E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.81E-02
2	32299042	cg22717723	SPAST	-37.45	6.63	1.62E-08	1.22E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.56E-06
5	179413374	cg22775585	MIR340	-52.80	9.57	3.45E-08	1.99E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.53E-03
6	34245341	cg22797971	C6orf1	-8.69	1.99	1.24E-05	1.49E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.73E-03
8	26243601	cg22816343	BNIP3L	-28.07	5.32	1.33E-07	5.29E-04	1	-4.60	2.41	5.66E-02	-0.60	0.79	4.47E-01	-11.80	2.49	2.12E-06	-0.61	6.57E-03	4.48	1.82E-05	-4.64	1.59E-05	0.26	0.26	3.23E-01	-0.03	3.86E-05
22	36841223	cg22883080	TXN2	-8.32	1.80	3.73E-06	5.95E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.57E-02
5	137812320	cg22905973	EGR1	-41.57	8.45	8.56E-07	2.04E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.06E-04
11	112149745	cg22972893	LOC283140	-20.01	3.90	2.88E-07	9.15E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.77E-05
1	236715069	cg22976779	LGALS8-AS1	-14.09	3.53	6.40E-05	4.84E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.06E-05
2	121816646	cg22982094	TFCP2L1	-21.40	3.80	1.73E-08	1.27E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.36E-05
17	78662780	cg22994495	LOC1019288	-17.34	3.97	1.27E-05	1.51E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.41E-06
21	43928228	cg23003220	SLC37A1	-9.49	2.25	2.35E-05	2.40E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.58E-03
11	12136405	cg23044178	MICAL2	-28.71	5.25	4.46E-08	2.41E-04	1	-3.89	2.91	1.81E-01	-0.48	0.73	5.08E-01	-9.34	2.34	6.61E-05	-0.22	2.64E-01	-	-	-3.86	2.52E-04	0.38	0.25	1.28E-01	-0.03	5.85E-04
6	53057849	cg23054654	GCM1	-14.15	3.19	9.04E-06	1.16E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.60E-04
3	72644845	cg23076894	LOC1053771	-10.81	2.63	3.95E-05	3.45E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.28E-04
16	195133	cg23079735	NPRL3	-16.66	3.19	1.83E-07	6.52E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	5.81E-05
1	19467440	cg23087931	UBR4	-48.65	9.81	7.13E-07	1.78E-03	1	-13.91	6.50	3.23E-02	-0.24	0.89	7.87E-01	0.11	3.15	9.72E-01	0.22	3.31E-01	2.27	2.54E-02	-3.53	7.53E-04	0.53	0.21	1.22E-02	0.00	3.39E-01
6	25609068	cg23131680	SCGN	-22.97	4.95	3.53E-06	5.80E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.41E-03
17	21119381	cg23149707	TMEM11	-12.75	2.61	1.05E-06	2.27E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.80E-01
5	150486801	cg23172995	TNIP1	-25.46	5.19	9.44E-07	2.13E-03	1	-4.96	2.41	3.95E-02	-0.48	0.29	9.27E-02	-6.56	2.57	1.08E-02	-0.91	2.23E-04	1.39	1.67E-01	-4.19	8.19E-05	0.41	0.25	9.60E-02	-0.03	1.24E-04
2	120937418	cg23196129	TMEM185B	-11.35	2.63	1.58E-05	1.80E-02	1	-6.73	3.26	3.88E-02	-0.17	0.36	6.25E-01	-3.68	2.16	8.93E-02	-1.00	1.20E-05	-1.31	1.92E-01	-3.36	1.28E-03	0.29	0.26	2.77E-01	-0.02	4.24E-03
8	33421410	cg23205629	RNF122	-11.20	2.44	4.40E-06	6.74E-03	1	-5.64	2.91	5.23E-02	-2.07	0.99	3.77E-02	-9.10	2.05	9.28E-06	-0.72	7.30E-04	5.22	8.47E-07	-0.59	5.57E-01	0.22	0.21	2.87E-01	-0.03	8.85E-05
10	31289208	cg23260901	ZNF438	-7.96	1.93	3.69E-05	3.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.73E-02
11	93456334	cg23338316	SCAR-9	-19.37	3.66	1.20E-07	4.91E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.21E-03
10	120495050	cg23414568	CACUL1	-12.42	2.95	2.59E-05	2.60E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.58E-03
12	120970625	cg23434083	RNF10	-18.70	4.32	1.49E-05	1.73E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.28E-05
10	116447282	cg23464586	ABLIM1	-16.93	4.03	2.62E-05	2.62E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.99E-03
10	73906532	cg23468453	SPOCK2	-28.32	7.01	5.29E-05	4.25E-02	1	-11.70	5.35	2.86E-02	0.31	0.78	6.89E-01	-7.65	2.72	4.95E-03	-0.54	2.02E-02	-3.47	7.50E-04	-2.92	4.74E-03	0.27	0.22	2.36E-01	-0.01	3.00E-03
14	74532925	cg23472776	ALDH6A1	-28.07	6.32	8.97E-06	1.15E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.11E-04
1	154581658	cg23475294	ADAR	-19.31	3.81	3.95E-07	1.17E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.40E-05
20	47731131	cg23498922	CSE1L	-24.11	4.76	3.99E-07	1.17E-03	1	-7.74	4.03	5.49E-02	-1.12	1.18	3.45E-01	-7.48	2.42	2.00E-03	-0.85	6.04E-04	-	-	-2.69	9.06E-03	0.40	0.24	9.33E-02	-0.02	7.11E-04
10	103923333	cg23516680	NOLC1	-17.74	3.90	5.54E-06	8.00E-03	1	-5.58	2.83	4.88E-02	-0.41	0.64	5.19E-01	-9.02	2.42	1.91E-04	-0.89	4.57E-05	-0.51	6.13E-01	-2.89	5.08E-03	0.26	0.25	2.96E-01	-0.02	1.43E-03
21	30722759	cg23557612	BACH1-IT2	-25.72	5.95	1.54E-05	1.77E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.76E-04
14	55603874	cg23575099	LGALS3	-30.87	5.39	9.99E-09	8.87E-05	1	-9.79	4.86	4.39E-02	-1.12	0.84	1.83E-01	-7.80	3.02	9.87E-03	-	-	-	-	-1.03	3.05E-01	0.22	0.29	4.50E-01	-0.02	1.31E-01
3	3152201	cg23582054	IL5RA	-10.57	2.10	5.01E-07	1.38E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	7.77E-06
14	105352991	cg23584308	CEP170B	-16.02	3.46	3.66E-06	5.87E-03	1	-12.92	5.78	2.53E-02	1.27	1.02	2.13E-01	-5.32	2.50	3.33E-02	-0.86	4.14E-03	1.31	1.92E-01	-2.62	1.07E-02	0.18	0.22	4.00E-01	-0.01	5.63E-03
14	22886075	cg23612739	DAD1	-14.17	3.45	4.10E-05	3.54E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.97E-03
12	118832042	cg23699170	SUDS3	-35.35	5.78	9.91E-10	1.85E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.96E-02

16	23491546	cg23746329	COG7	-23.49	4.47	1.53E-07	5.75E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.94E-04
1	115032585	cg23779286	TRIM33	-14.00	2.92	1.63E-06	3.21E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.32E-04
14	77381159	cg23825347	LINC01629	-8.99	1.80	5.85E-07	1.53E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	7.81E-02
5	10560140	cg23856600	ANKRD33B	-9.47	2.11	6.87E-06	9.38E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.83E-02
7	1577697	cg23871276	MAFK	-10.75	2.57	2.84E-05	2.78E-02	1	-56.94	24.91	2.23E-02	-0.25	0.38	5.08E-01	-6.76	2.66	1.10E-02	-3.10	3.73E-07	2.28	2.46E-02	-2.61	1.11E-02	0.59	0.24	1.52E-02	-0.01	1.91E-01
15	91136869	cg23875532	CRTC3	-13.36	3.27	4.43E-05	3.76E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.85E-03
10	102276804	cg23904266	SEC31B	-12.15	2.63	3.72E-06	5.95E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	3.81E-06
8	142238794	cg23911543	SLC45A4	-17.64	3.29	8.37E-08	3.92E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.44E-03
6	144968704	cg23948955	SNORA98	-18.44	3.47	1.12E-07	4.70E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.97E-02
16	75625311	cg23975326	GABARAPL2	-18.97	4.58	3.50E-05	3.22E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.98E-01
2	33437478	cg23985372	LTBP1	-9.13	2.23	4.22E-05	3.63E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.32E-04
15	99443249	cg23990557	PGPEP1L	-7.61	1.67	5.22E-06	7.68E-03	1	-6.72	3.54	5.77E-02	-0.18	0.29	5.38E-01	-4.94	2.04	1.54E-02	-0.59	7.60E-03	-	-	-2.90	5.06E-03	0.49	0.32	1.21E-01	-	-
14	23466659	cg23993677	C14orf93	-13.19	3.07	1.69E-05	1.90E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.02E-03
11	65545808	cg24009118	AP5B1	-20.28	4.67	1.40E-05	1.64E-02	1	-15.86	6.63	1.67E-02	0.00	0.59	9.99E-01	-6.65	2.45	6.72E-03	-0.81	6.03E-04	0.68	4.99E-01	-2.55	1.31E-02	0.54	0.23	1.83E-02	-0.01	3.52E-02
1	201520863	cg24014587	RPS10P7	-11.06	2.67	3.48E-05	3.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.37E-03
12	56694932	cg24028828	CS	-62.22	11.09	2.02E-08	1.43E-04	1	-7.74	3.39	2.24E-02	-0.55	0.73	4.47E-01	-13.71	2.88	1.99E-06	-0.61	4.26E-03	-1.27	2.06E-01	-3.84	2.71E-04	0.45	0.29	1.28E-01	-0.02	4.86E-04
1	172507360	cg24039962	SUCO	-26.14	5.29	7.90E-07	1.91E-03	1	-7.62	4.07	6.14E-02	-0.82	0.66	2.15E-01	-4.64	2.55	6.88E-02	-0.85	3.03E-04	3.77	2.68E-04	-2.78	6.96E-03	0.20	0.25	4.32E-01	-0.02	1.22E-03
1	66777579	cg24058805	PDE4B	-26.99	5.55	1.15E-06	2.44E-03	1	-11.49	5.48	3.60E-02	-0.58	0.47	2.11E-01	-10.56	3.01	4.53E-04	-	-	-	-	-2.20	3.13E-02	0.15	0.24	5.15E-01	-0.02	1.84E-04
14	60662291	cg24062598	DHRS7	-47.51	11.27	2.51E-05	2.53E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.84E-02
14	62235205	cg24076840	S-PC1	-17.75	4.26	3.14E-05	2.99E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.60E-04
11	125464650	cg24106568	STT3A	-38.32	7.16	8.76E-08	4.02E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.92E-04
1	179016233	cg24108508	FAM20B	-10.40	2.44	2.11E-05	2.22E-02	1	-6.91	3.13	2.74E-02	0.19	0.43	6.52E-01	-5.71	1.79	1.40E-03	-0.84	6.71E-05	-1.14	2.56E-01	-2.70	8.71E-03	0.28	0.22	1.97E-01	-0.03	1.22E-03
3	33114261	cg24113459	TMPPE	-32.37	5.50	3.86E-09	4.92E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.34E-07
15	101719523	cg24254196	CHSY1	-10.35	2.50	3.47E-05	3.20E-02	1	-7.59	3.89	5.11E-02	-0.75	0.45	9.42E-02	-1.65	1.56	2.92E-01	-0.67	2.09E-04	1.12	2.63E-01	-1.20	2.35E-01	0.23	0.19	2.37E-01	-0.02	1.17E-01
22	36837152	cg24278615	TXN2	-9.95	2.34	2.08E-05	2.20E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.15E-01
16	16143033	cg24304533	ABCC1	-30.81	4.75	8.52E-11	4.15E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	8.41E-05
10	12371568	cg24317972	CAMK1D	-24.64	5.86	2.62E-05	2.62E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.95E-03
2	12553424	cg24323626	MIR3681	-11.91	2.57	3.46E-06	5.75E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	4.14E-03
1	203763352	cg24343524	ZC3H11A	-16.97	4.14	4.08E-05	3.54E-02	1	-9.34	4.61	4.27E-02	-1.28	0.76	9.32E-02	-8.37	2.69	1.83E-03	-0.62	5.55E-03	-1.44	1.52E-01	0.17	8.64E-01	0.37	0.27	1.83E-01	-0.02	1.81E-02
7	107876312	cg24358891	NRCAM	-16.15	3.90	3.51E-05	3.22E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.81E-06
11	111570978	cg24368962	PPP2R1B	-23.17	5.41	1.87E-05	2.04E-02	1	-8.38	3.97	3.48E-02	-0.34	0.93	7.10E-01	-15.79	3.26	1.28E-06	-	-	-0.94	3.51E-01	-3.78	3.32E-04	0.25	0.26	3.28E-01	-0.03	3.07E-06
13	31308509	cg24380653	ALOX5AP	-24.45	4.90	6.20E-07	1.60E-03	1	-14.34	6.19	2.05E-02	-0.45	0.87	6.06E-01	-7.16	3.09	2.04E-02	-1.12	1.96E-05	3.11	2.37E-03	-2.04	4.53E-02	0.49	0.24	4.55E-02	-0.02	7.70E-04
22	30612925	cg24447018	LIF	-8.45	1.90	8.86E-06	1.14E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.05	9.67E-07
7	150649807	cg24491618	KCNH2	-12.91	3.11	3.23E-05	3.05E-02	1	-6.72	3.26	3.91E-02	-1.43	0.82	8.10E-02	-7.53	2.07	2.78E-04	-1.05	3.07E-06	0.81	4.23E-01	-2.62	1.08E-02	0.33	0.22	1.25E-01	-0.02	8.58E-05
16	11709855	cg24517604	LITAF	-25.96	4.00	8.64E-11	4.15E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.21E-04
15	64856362	cg24536162	ZNF609	-28.47	6.18	4.14E-06	6.40E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	27869474	cg24541864	WASF2	-11.46	2.15	9.72E-08	4.32E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.92E-05
10	91262748	cg24600621	SLC16A12	-31.58	6.44	9.27E-07	2.11E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.12E-01
6	42109176	cg24627621	C6orf132	-13.07	3.27	6.33E-05	4.81E-02	1	-6.66	3.17	3.56E-02	-0.29	0.33	3.72E-01	-8.64	2.30	1.69E-04	-2.98	3.81E-08	1.72	8.85E-02	-2.85	5.81E-03	0.33	0.24	1.72E-01	-0.03	9.60E-04
18	33046000	cg24629258	INO80C	-27.59	6.90	6.41E-05	4.84E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	5.43E-02
1	167595191	cg24714082	RCSD1	-10.85	2.40	6.47E-06	8.97E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.39E-02
9	101595573	cg24818060	GALNT12	-42.70	8.93	1.72E-06	3.36E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.10E-04
13	43355514	cg24818699	FAM216B	-18.32	4.38	2.84E-05	2.78E-02	1	-6.39	3.70	8.39E-02	0.93	0.99	3.49E-01	-13.92	3.13	8.53E-06	-0.53	1.68E-02	2.84	5.35E-03	-2.26	2.73E-02	0.25	0.22	2.63E-01	-0.02	1.33E-04
19	5093491	cg24823679	KDM4B	-13.32	3.27	4.71E-05	3.95E-02	1	-15.93	7.13	2.55E-02	-0.88	0.70	2.12E-01	-7.73	2.34	9.41E-04	-1.72	2.54E-04	4.35	3.07E-05	-0.51	6.12E-01	0.29	0.22	1.97E-01	-0.02	3.58E-03
14	76337892	cg24829718	TGFB3	-21.98	5.12	1.74E-05	1.94E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.46E-04
7	99081553	cg24869851	ZNF789	-43.73	8.12	7.27E-08	3.56E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.29E-04
19	41129881	cg24872571	LTBP4	-18.27	4.37	2.91E-05	2.83E-02	1	-12.86	5.93	3.00E-02	-0.04	0.37	9.18E-01	-6.22	3.14	4.75E-02	0.02	9.55E-01	1.79	7.60E-02	0.36	7.18E-01	0.14	0.24	5.60E-01	-0.01	1.37E-01
15	52861754	cg25003924	ARPP19	-7.04	1.73	4.72E-05	3.95E-02	1	-7.18	3.93	6.79E-02	0.04	0.35	9.19E-01	-4.22	2.12	4.67E-02	-0.52	4.76E-02	-0.34	7.32E-01	-0.58	5.64E-01	0.84	0.35	1.50E-02	-0.02	4.26E-02
11	60623918	cg25087851	PTGDR2	-11.94	2.30	2.09E-07	7.15E-04	1	-6.85	3.19	3.17E-02	-1.81	0.94	5.42E-02	-11.86	2.10	1.69E-08	-1.00	1.08E-04	1.31	1.93E-01	-2.09	4.03E-02	0.51	0.25	3.82E-02	-0.04	6.89E-07
1	212312063	cg25159046	MIR3122	-11.81	2.85	3.43E-05	3.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.03E-02
8	95865949	cg25161908	INTS8	-68.67	11.88	7.46E-09	7.19E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.45E-03
9	130217517	cg25221180	LRSAM1	-47.44	8.52	2.59E-08	1.72E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.63E-05
3	12918528	cg25224369	LINC02022	-11.84	2.89	4.23E-05	3.63E-02	1	-7.10	3.56	4.60E-02	-0.76	0.76	3.21E-01	-10.53	2.36	7.75E-06	-1.35	3.63E-06	-1.22	2.27E-01	-3.07	3.03E-03	0.39	0.23	9.75E-02	-0.03	1.64E-05
7	24965657	cg25270424	OSBPL3	-21.85	5.36	4.64E-05	3.90E-02	1	-4.98	2.53	4.90E-02	-2.06	0.81	1.10E-02	-14.53	2.88	4.75E-07	-1.13	2.68E-07	-	-	-1.96	5.42E-02	0.46	0.27	8.48E-02	-0.02	1.35E-04
3	3151679	cg25308597	IL5RA	-4.02	0.99	4.81E-05	4.00E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.08E-02
9	80602527	cg25348163	G-Q	-38.25	6.35	1.68E-09	2.59E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.03E-03
5	132009352	cg25368824	IL4	-11.04	2.40	4.09E-06	6.35E-03	1	-4.63	2.47	6.04E-02	-0.85	0.88	3.32E-01	-9.51	2.32	4.20E-05	-0.20	3.20E-01	-0.78	4.38E-01	0.51	6.09E-01	0.26	0.24	2.66E-01	-0.03	9.00E-05
8	129023431	cg25401182	MIR1206	-6.48	1.52	2.03E-05	2.17E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.52E-01
15	81623226	cg25466522	TMC3-AS1	-35.21	5.24	1.75E-11	2.04E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.07E-04
9	130521313	cg25470919	SH2D3C	-15.87	3.45	4.35E-06	6.67E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	2.11E-04
17	79824551	cg25475273	ARHGDIA	-9.86	2.38	3.45E-05	3.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.32E-04
13	113305704	cg25479097	ATP11AUN	-19.04	4.04	2.38E-06	4.33E-03	1	-7.00	3.13	2.52E-02	0.38	0.58	5.10E-01	-12.19	2.48	9.11E-07	-0.64	1.51E-03	-	-	-2.62	1.07E-02	0.11	0.22	6.27E-01	-0.03	2.06E-02
6	116781307	cg25488567	FAM26F	-17.64	3.51	5.03E-07	1.38E-03	1	-4.35	2.19	4.75E-02	-0.59	0.65	3.60E-01	-7.63	2.21	5.45E-04	-0.94	3.11E-05	-2.71	7.83E-03	-3.07	3.06E-03	0.12	0.21	5.82E-01	-0.03	2.53E-04
2	86830411	cg25493477	RNF103	-26.36	4.83	4.77E-08	2.57E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.71E-05
5	81159782	cg25518040	ATG10	-31.40	7.37	2.05E-05	2.18E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.96E-03
6	143014942	cg25602071	LOC153910	-22.15	4.71	2.59E-06	4.61E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.32E-02
17	49241518	cg25665831	NME2	-9.73	2.36	3.89E-05	3.41E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.70E-03

6	44193413	cg25738218	SLC29A1	-16.40	3.69	8.66E-06	1.12E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	6.63E-04
4	146800380	cg25799589	ZNF827	-30.91	5.99	2.45E-07	8.19E-04	1	-7.26	3.59	4.31E-02	-0.31	0.26	2.25E-01	-10.74	2.52	2.06E-05	-0.51	1.13E-02	-0.49	6.23E-01	-1.74	8.65E-02	0.52	0.23	2.35E-02	-0.03	2.49E-04
6	143022065	cg25852061	LOC153910	-5.30	1.17	6.00E-06	8.45E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.62E-01
10	73936754	cg25854298	A-PC16	-23.08	5.06	5.19E-06	7.65E-03	1	-7.45	3.35	2.61E-02	-2.71	1.01	7.20E-03	-11.91	2.68	8.74E-06	-1.40	7.02E-09	3.19	1.88E-03	-3.23	1.91E-03	0.32	0.23	1.56E-01	-0.03	1.09E-04
4	185734335	cg25877465	ACSL1	-12.50	2.72	4.32E-06	6.63E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.78E-03
10	32160635	cg25916167	ARHGAP12	-12.60	3.12	5.24E-05	4.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.18E-01
3	194862233	cg25926955	XXYLT1-AS2	-13.56	3.04	8.01E-06	1.06E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.25E-03
15	40173065	cg25939647	GPR176	-7.39	1.83	5.41E-05	4.31E-02	1	-8.08	3.68	2.81E-02	-1.41	1.03	1.72E-01	-9.35	1.96	1.91E-06	-1.06	9.32E-05	-2.79	6.19E-03	-3.18	2.18E-03	0.30	0.24	2.10E-01	-0.04	3.37E-04
1	28459201	cg25960268	EYA3	-10.97	2.32	2.21E-06	4.11E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	1.79E-05
12	25103501	cg25984364	BCAT1	-17.89	4.43	5.48E-05	4.35E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	9.87E-04
15	44070538	cg26024852	ELL3	-33.11	8.14	4.79E-05	3.99E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	8.24E-05
19	44175158	cg26058544	PLAUR	-16.08	3.28	9.65E-07	2.16E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.27E-02
17	47590272	cg26102082	MIR6165	-19.88	4.25	2.88E-06	4.99E-03	1	-14.97	6.65	2.43E-02	-0.10	0.37	7.82E-01	-8.05	2.52	1.37E-03	-	-	-	-	-2.87	5.47E-03	0.25	0.24	2.90E-01	-0.02	6.93E-03
14	75153307	cg26103369	AREL1	-41.72	8.52	9.77E-07	2.16E-03	1	-4.05	2.21	6.65E-02	-1.40	0.92	1.27E-01	-11.01	3.06	3.21E-04	-0.91	1.99E-04	0.17	8.63E-01	-3.11	2.73E-03	0.55	0.33	9.20E-02	-0.03	1.02E-04
19	12998426	cg26136776	KLF1	-13.58	3.25	2.95E-05	2.86E-02	1	-8.68	4.42	4.99E-02	-2.06	1.19	8.17E-02	-9.18	2.69	6.38E-04	-0.41	8.70E-02	1.13	2.60E-01	-2.17	3.37E-02	0.40	0.24	9.83E-02	-0.02	5.02E-04
1	68163609	cg26145152	GADD45A	-17.14	3.70	3.61E-06	5.83E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.42E-03
9	130859520	cg26150475	SLC25A25	-40.20	7.72	1.88E-07	6.66E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.14E-04
15	101920222	cg26197665	PCSK6-AS1	-18.16	3.48	1.88E-07	6.66E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.94E-05
6	45812853	cg26219449	CLIC5	-15.36	2.92	1.44E-07	5.55E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
17	1047567	cg26235490	ABR	-16.65	3.30	4.51E-07	1.29E-03	1	-7.98	3.92	4.21E-02	-1.77	0.79	2.43E-02	-9.48	2.51	1.60E-04	-0.96	1.52E-03	-	-	-1.73	8.87E-02	0.16	0.22	4.65E-01	-0.02	1.23E-03
5	179131225	cg26245101	CANX	-25.62	6.17	3.33E-05	3.12E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	5.95E-04
1	61607055	cg26252077	NFIA	-13.50	2.77	1.12E-06	2.39E-03	1	-5.57	2.71	3.94E-02	-0.42	0.32	1.93E-01	-12.78	2.28	2.18E-08	-0.87	8.49E-04	-	-	-2.23	2.89E-02	0.23	0.21	2.89E-01	-	-
15	99443339	cg26272088	PGPEP1L	-13.89	3.41	4.76E-05	3.98E-02	1	-6.51	3.12	3.71E-02	-1.98	0.89	2.64E-02	-8.39	2.43	5.66E-04	-0.84	4.68E-04	0.68	5.00E-01	-1.23	2.24E-01	0.21	0.23	3.52E-01	-0.03	3.75E-03
3	49148220	cg26323242	QARS	-9.57	2.16	9.45E-06	1.19E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.38E-03
15	64024116	cg26337091	HERC1	-14.77	2.93	4.60E-07	1.29E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	1.44E-02
7	50626298	cg26365969	DDC	-13.28	3.02	1.14E-05	1.39E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.99E-05
2	31302644	cg26382374	GALNT14	-26.89	3.52	2.27E-14	1.86E-08		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
1	24143366	cg26389822	HMGCL	-17.95	4.18	1.72E-05	1.93E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.53E-03
3	33112660	cg26396322	TMPPE	-32.73	4.67	2.32E-12	3.79E-07		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.02E-04
5	43081709	cg26425190	LOC648987	-37.23	8.19	5.53E-06	8.00E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	4.35E-02
11	368638	cg26461944	B4GALNT4	-8.47	2.04	3.21E-05	3.03E-02	1	-2.66	18.72	8.87E-01	-0.16	0.49	7.44E-01	-1.79	1.92	3.53E-01	-0.31	3.68E-01	-1.74	8.41E-02	0.02	9.87E-01	-0.06	0.18	7.52E-01	-0.01	3.41E-01
8	126445744	cg26472183	TRIB1	-47.48	7.89	1.77E-09	2.68E-05		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.74E-06
2	74375903	cg26529864	BOLA3-AS1	-31.18	7.35	2.23E-05	2.31E-02	1	-16.62	7.64	2.96E-02	-2.77	0.88	1.72E-03	-10.71	5.06	3.44E-02	-	-	-	-	-1.60	1.14E-01	0.36	0.24	1.35E-01	-0.01	1.10E-01
19	2594841	cg26569937	MIR7850	-28.81	6.36	5.83E-06	8.33E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	7.98E-03
12	93798975	cg26584983	NUDT4	-39.14	8.42	3.31E-06	5.57E-03	1	-11.79	5.07	2.01E-02	0.72	0.97	4.57E-01	-10.27	3.20	1.34E-03	-0.36	1.11E-01	4.42	2.34E-05	-3.41	1.08E-03	-0.05	0.26	8.54E-01	-0.01	7.08E-03
1	100234313	cg26592446	FRRS1	-17.77	4.39	5.10E-05	4.17E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.05E-05
10	100140714	cg26633168	MIR1287	-47.33	8.92	1.12E-07	4.70E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.71E-04
7	137501840	cg26703587	DGKI	-13.12	3.04	1.58E-05	1.81E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.44E-04
4	141536591	cg26713832	TNRC18P1	-39.39	7.06	2.45E-08	1.65E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.42E-04
10	114437523	cg26724455	MIR4295	-23.52	5.03	2.89E-06	5.01E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	2.97E-05
17	81043782	cg26749306	METRNL	-25.89	4.91	1.35E-07	5.32E-04	1	-4.95	2.65	6.14E-02	-2.71	0.93	3.53E-03	-12.03	2.96	4.86E-05	-0.40	6.58E-02	-	-	-3.06	3.12E-03	0.10	0.25	6.84E-01	-0.03	3.11E-05
6	158994407	cg26774971	MIR7161	-7.63	1.76	1.47E-05	1.70E-02	1	-12.37	5.73	3.10E-02	-0.17	0.84	8.42E-01	-10.23	2.39	1.88E-05	-	-	1.13	2.62E-01	-3.31	1.50E-03	0.34	0.23	1.42E-01	-0.03	1.66E-03
5	132008525	cg26787239	IL4	-27.56	4.75	6.32E-09	6.54E-05	1	-8.70	3.94	2.73E-02	-0.58	0.99	5.63E-01	-8.45	2.82	2.75E-03	-0.35	1.12E-01	-0.82	4.14E-01	-2.56	1.25E-02	0.48	0.24	4.70E-02	-0.02	1.09E-03
8	25847266	cg26804299	EBF2	-3.82	0.92	3.60E-05	3.25E-02	1	-20.20	14.98	1.78E-01	-2.01	0.78	9.82E-03	2.87	1.34	3.27E-02	-0.04	8.55E-01	-	-	-1.20	2.33E-01	-0.03	0.17	8.52E-01	-	-
5	173285792	cg26817086	CPEB4	-10.12	2.06	8.50E-07	2.03E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	6.34E-05
1	6645165	cg26819549	ZBTB48	-10.09	2.26	7.85E-06	1.04E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	1.06E-04
10	129172573	cg26865494	NPS	-12.48	2.34	9.78E-08	4.32E-04	1	-7.70	3.62	3.36E-02	-2.11	0.93	2.31E-02	-7.75	2.49	1.86E-03	-	-	-2.02	4.55E-02	-2.12	3.77E-02	0.36	0.24	1.27E-01	-0.04	9.75E-06
11	9632897	cg26938803	WEE1	-8.98	2.23	5.75E-05	4.50E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	6.37E-01
2	8466005	cg26955963	LINC00299	-7.71	1.87	3.68E-05	3.29E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	5.54E-03
12	125589647	cg26964704	AACS	-27.82	4.68	2.68E-09	3.72E-05	1	-9.36	4.31	2.99E-02	-4.62	1.30	4.02E-04	-6.99	2.79	1.22E-02	-0.71	2.34E-02	4.28	4.07E-05	-1.50	1.38E-01	0.15	0.22	4.86E-01	-0.02	2.05E-03
17	10747298	cg26985528	PIRT	-8.36	1.88	9.22E-06	1.18E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.58E-03
15	52157096	cg26997652	TMOD3	-31.36	6.66	2.45E-06	4.43E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.47E-04
2	2712909	cg27014783	MYT1L	-12.64	3.06	3.51E-05	3.22E-02	1	-19.14	8.58	2.56E-02	-0.67	1.01	5.06E-01	-1.09	2.28	6.31E-01	-1.25	2.18E-03	-	-	-2.31	2.41E-02	-0.04	0.21	8.37E-01	-	-
2	48806774	cg27016609	STON1-GTF2	-6.74	1.61	2.67E-05	2.66E-02	1	-8.34	3.90	3.26E-02	-1.42	0.92	1.25E-01	-3.63	1.76	3.98E-02	-1.78	3.90E-05	0.89	3.77E-01	-1.75	8.45E-02	0.38	0.24	1.22E-01	-0.03	1.60E-03
20	24630818	cg27028878	SYNDIG1	-8.61	1.85	3.17E-06	5.41E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.04	4.08E-05
22	23885362	cg27060510	IGLL1	-2.62	0.65	5.26E-05	4.23E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.00	9.69E-01
11	68035071	cg27094581	C11orf24	-14.44	3.56	4.91E-05	4.05E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	6.14E-05
22	45820349	cg27131881	RIBC2	-9.46	2.13	8.99E-06	1.15E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	3.59E-02
12	89637744	cg27143027	DUSP6	-7.29	1.73	2.44E-05	2.47E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	9.96E-04
6	158994509	cg27279839	MIR7161	-19.70	4.02	9.40E-07	2.13E-03	1	-10.95	6.61	9.79E-02	-2.05	0.90	2.27E-02	-2.56	3.54	4.69E-01	-	-	-3.34	1.16E-03	-2.35	2.18E-02	0.23	0.22	2.91E-01	-0.01	5.47E-03
5	134818031	cg27308490	TIFAB	-10.85	2.53	1.85E-05	2.03E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	4.65E-06
15	67802577	cg27335233	IQCH-AS1	-13.80	2.69	3.00E-07	9.41E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
6	126375816	cg27341747	MIR5695	-29.02	5.63	2.59E-07	8.53E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	2.01E-03
11	68816453	cg27481141	TPCN2	-207.20	48.11	1.66E-05	1.87E-02	1	50.24	84.81	5.54E-01	0.28	1.16	8.08E-01	-4.55	6.12	4.57E-01	-	-	-2.64	9.41E-03	1.01	3.15E-01	-0.21	0.25	4.00E-01	0.00	2.81E-01
6	36108416	cg27508506	MAPK13	-47.57	8.96	1.10E-07	4.70E-04		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.02	1.85E-05
1	27868615	cg27508623	WASF2	-12.02	2.53	2.05E-06	3.87E-03		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	2.02E-01
2	28373887	cg27514107	LOC1005057	-18.13	4.52	6.03E-05	4.65E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.01	8.64E-02

18	8720395	cg27550672	MTCL1	-38.46	5.92	8.37E-11	4.15E-06		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	7.75E-05
2	187420032	cg27609375	ITGAV	-4.10	1.02	5.93E-05	4.60E-02		-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-0.03	3.69E-03
12	8975309	cg27653134	A2ML1	-28.18	6.32	8.30E-06	1.09E-02	1	-22.75	11.23	4.28E-02	-0.39	0.33	2.27E-01	-4.14	3.39	2.22E-01	-0.51	1.75E-01	0.70	4.85E-01	-2.10	3.91E-02	0.08	0.24	7.30E-01	-0.02	2.00E-03

[1] Genome build GRCh37/hg19

Table E16. 96 Implicated Genes in Non-atopic Asthma Reported in Previous Asthma GWAS or EWAS

probe	chromosome	position[1]	Gene.Name	Distance.to.TSS	N	Beta[2]	SE[2]	P[2]	FDR	OR.CI	crossreactive
cg00344572	2	137080313	CXCR4	-204589	1829	-3.6	0.8	6.39E-06	0.034948	0.96 (0.95, 0.98)	
cg00390941	12	15124659	PDE6H	-1296	1826	-22.75	5.46	3.10E-05	0.049223	0.80 (0.72, 0.89)	
cg00847453	6	110720501	DDO	16251	1830	-3.58	0.82	1.25E-05	0.038695	0.96 (0.95, 0.98)	
cg01418188	11	3145609	OSBPL5	40972	1828	-3.44	0.8	1.79E-05	0.041088	0.97 (0.95, 0.98)	
cg01499988	9	35755346	MSMP	-1073	1830	-12.31	2.77	8.86E-06	0.037198	0.88 (0.84, 0.93)	
cg01614759	10	45495435	ZNF22	-837	1829	-13.89	2.74	4.17E-07	0.015825	0.87 (0.82, 0.92)	
cg01887834	11	94336029	PIWIL4	35556	1829	-2.24	0.53	2.22E-05	0.04399	0.98 (0.97, 0.99)	
cg01901579	14	95615731	DICER1	8027	1830	-12.78	3.02	2.35E-05	0.044872	0.88 (0.83, 0.93)	
cg01953813	13	47161752	LRCH1	34457	1829	-3.43	0.81	2.46E-05	0.0459	0.97 (0.95, 0.98)	
cg01955639	17	56269767	EPX	-317	1830	-12.67	2.48	3.18E-07	0.015825	0.88 (0.84, 0.92)	
cg02342367	3	159532265	SCHIP1	-25384	1827	8.32	1.93	1.61E-05	0.040491	1.09 (1.05, 1.13)	
cg02432022	6	139656042	CITED2	39307	1829	-2.04	0.45	6.10E-06	0.033904	0.98 (0.97, 0.99)	
cg02455383	22	27014116	CRYBB1	-126	1830	-3.62	0.86	2.66E-05	0.047424	0.96 (0.95, 0.98)	
cg02543556	14	39643445	PNN	-941	1827	-15.09	3.44	1.16E-05	0.038247	0.86 (0.8, 0.92)	
cg03125875	1	33227555	KIAA1522	-3679	1829	-6.11	1.31	2.89E-06	0.027161	0.94 (0.92, 0.97)	
cg03881379	3	52223131	ALAS1	-8967	1830	-5.12	1.07	1.80E-06	0.026074	0.95 (0.93, 0.97)	
cg03914277	4	3084890	HTT	8483	1829	-6.34	1.34	2.39E-06	0.027161	0.94 (0.91, 0.96)	
cg04804748	15	52028433	LYSMD2	1886	1830	-7.24	1.61	7.25E-06	0.035796	0.93 (0.9, 0.96)	
cg04962865	8	117059957	LINC00536	277339	1827	23.81	5.51	1.56E-05	0.040345	1.27 (1.14, 1.41)	
cg05516004	21	46496180	ADARB1	1215	1830	-28.57	6	1.91E-06	0.026074	0.75 (0.67, 0.85)	
cg05920921	6	134956367	LOC101928304	-95225	1826	-2.15	0.47	4.21E-06	0.028603	0.98 (0.97, 0.99)	
cg06308882	18	2986172	LPIN2	25772	1829	-2.58	0.6	1.74E-05	0.041088	0.97 (0.96, 0.99)	
cg06592575	18	55250579	FECH	3389	1829	-22.78	4.74	1.51E-06	0.026074	0.80 (0.73, 0.87)	
cg06984345	14	75162215	AREL1	17591	1830	-9.02	2.13	2.27E-05	0.044275	0.91 (0.88, 0.95)	
cg07177867	15	52030746	LYSMD2	-427	1830	-11.28	2.46	4.56E-06	0.030053	0.89 (0.85, 0.94)	
cg07519863	3	46269741	CCR3	-14130	1829	-4.52	1.03	1.25E-05	0.038695	0.96 (0.94, 0.98)	
cg07616376	18	2980515	LPIN2	31429	1829	-25.73	6.18	3.11E-05	0.049223	0.77 (0.68, 0.87)	
cg07636225	11	63466987	RTN3	18066	1828	-15.55	3.38	4.08E-06	0.028603	0.86 (0.8, 0.91)	
cg07828833	10	74069493	DDIT4	35817	1829	-3.78	0.88	1.76E-05	0.041088	0.96 (0.95, 0.98)	
cg07834490	21	37536817	DOPEY2	-21	1823	-3.88	0.91	1.88E-05	0.041864	0.96 (0.94, 0.98)	
cg07970948	7	149543165	ZNF862	7710	1827	-5.95	1.25	1.98E-06	0.026074	0.94 (0.92, 0.97)	
cg08105265	17	56274480	EPX	4396	1830	-13.3	2.87	3.58E-06	0.028132	0.88 (0.83, 0.93)	
cg08408668	19	1173241	SBNO2	1040	1829	-4.14	0.89	3.16E-06	0.027161	0.96 (0.94, 0.98)	

cg08427005	1	234841610	LINC01132	-18178	1830	-4.16	0.93	7.13E-06	0.035796	0.96 (0.94, 0.98)
cg09131500	13	47161427	LRCH1	34132	1830	-3.54	0.72	7.31E-07	0.019271	0.97 (0.95, 0.98)
cg09194810	20	4072430	SMOX	-56995	1829	-14.82	3.44	1.66E-05	0.040496	0.86 (0.81, 0.92)
cg09241885	20	35504371	TLDC2	-152	1829	-9.39	2.21	2.16E-05	0.043759	0.91 (0.87, 0.95)
cg09589331	3	71256044	FOXP1	38271	1829	-2.26	0.54	2.48E-05	0.045935	0.98 (0.97, 0.99)
cg09698506	7	22395972	RAPGEF5	560	1828	2.61	0.61	1.77E-05	0.041088	1.03 (1.01, 1.04)
cg09849688	1	27060511	ARID1A	37990	1829	-19.6	4.47	1.17E-05	0.038247	0.82 (0.75, 0.9)
cg10132304	17	3880229	ATP2A3	-12472	1830	-4.14	0.97	1.91E-05	0.042073	0.96 (0.94, 0.98)
cg10220104	12	27027924	ITPR2	-41794	1830	-19	4.48	2.24E-05	0.04399	0.83 (0.76, 0.9)
cg10704177	1	62209607	PATJ	1459	1829	-11.22	2.42	3.71E-06	0.028455	0.89 (0.85, 0.94)
cg11098795	12	104276789	NT5DC3	-41815	1827	-4.19	0.86	1.04E-06	0.023413	0.96 (0.94, 0.98)
cg11112605	17	56283901	MKS1	12764	1830	-11.19	2.45	4.87E-06	0.030381	0.89 (0.85, 0.94)
cg11751434	7	100224557	TFR2	6715	1828	33.45	7.84	2.00E-05	0.042564	1.40 (1.2, 1.63)
cg12077754	2	75089669	HK2	29888	1830	-10.09	2.08	1.29E-06	0.025912	0.90 (0.87, 0.94)
cg12258670	14	75069041	LTBP2	9992	1830	-18.54	4.03	4.16E-06	0.028603	0.83 (0.77, 0.9)
cg12819873	11	57157632	PRG2	497	1829	-12.54	2.94	1.97E-05	0.042462	0.88 (0.83, 0.93)
cg12997777	2	17042926	FAM49A	-195793	1824	-2.7	0.65	2.95E-05	0.048641	0.97 (0.96, 0.99)
cg13054523	17	81055722	METRNL	18156	1830	-11.56	2.61	9.77E-06	0.037831	0.89 (0.85, 0.94)
cg13117318	17	74242643	RNF157	-6252	1825	-23.51	5.24	7.37E-06	0.035796	0.79 (0.71, 0.88)
cg13792581	20	43590115	TOMM34	-1002	1828	-24.26	5.51	1.05E-05	0.038138	0.78 (0.7, 0.87)
cg13947225	17	55190679	AKAP1	27545	1826	-10.68	2.4	8.21E-06	0.037198	0.90 (0.86, 0.94)
cg14118059	5	106830005	EFNA5	176590	1826	-36.92	8.85	3.03E-05	0.048841	0.69 (0.58, 0.82)
cg14131038	2	106360709	NCK2	-810	1830	-2.45	0.57	1.94E-05	0.042166	0.98 (0.96, 0.99)
cg14352263	3	195782538	TFRC	26422	1830	-3.9	0.91	1.81E-05	0.041088	0.96 (0.94, 0.98)
cg14612966	9	130859606	SLC25A25	-1154	1827	-14.35	3.26	1.11E-05	0.038247	0.87 (0.81, 0.92)
cg14919455	6	7167468	RREB1	59383	1830	-2.92	0.7	2.77E-05	0.04753	0.97 (0.96, 0.98)
cg15072057	11	111716149	ALG9	25854	1827	-2.75	0.64	1.91E-05	0.042073	0.97 (0.96, 0.99)
cg15123849	6	15364953	JARID2	115868	1828	-4.9	1.02	1.50E-06	0.026074	0.95 (0.93, 0.97)
cg15186355	17	518485	VPS53	99610	1830	-3.13	0.74	2.67E-05	0.047424	0.97 (0.96, 0.98)
cg15532312	20	34018983	GDF5	6986	1826	-21.97	4.71	3.14E-06	0.027161	0.80 (0.73, 0.88)
cg16032884	3	195106547	ACAP2	57269	1829	-2.29	0.55	2.93E-05	0.04857	0.98 (0.97, 0.99)
cg16834953	16	50748861	NOD2	15601	1826	-2.32	0.52	8.12E-06	0.037072	0.98 (0.97, 0.99)
cg17105176	17	2287284	MNT	16973	1827	-17.05	3.66	3.22E-06	0.027161	0.84 (0.78, 0.91)
cg17245251	8	103603330	ODF1	39483	1830	-20.36	4.5	5.98E-06	0.033904	0.82 (0.75, 0.89)
cg17555715	2	102952956	IL1RL1	-753	1830	-9.37	2.13	1.07E-05	0.038247	0.91 (0.87, 0.95)
cg17946525	1	172425816	C1orf105	3784	1830	-12.87	2.99	1.62E-05	0.040491	0.88 (0.83, 0.93)

cg17991808	7	17192401	AHR	-145874	1828	-5.63	1.27	8.84E-06	0.037198	0.95 (0.92, 0.97)
cg18410271	17	43472435	ARHGAP27	30576	1829	-5.15	1.12	4.13E-06	0.028603	0.95 (0.93, 0.97)
cg19210893	9	125589222	PDCL	1712	1828	-10.48	2.42	1.54E-05	0.040081	0.90 (0.86, 0.94)
cg19791728	17	45754000	TBKBP1	-18629	1829	-4.43	1	8.98E-06	0.037198	0.96 (0.94, 0.98)
cg19980260	3	171858472	FNDC3B	100129	1830	-3.08	0.68	6.14E-06	0.033904	0.97 (0.96, 0.98)
cg20626587	20	62372541	SLC2A4RG	1331	1828	-5.11	1.15	8.38E-06	0.037198	0.95 (0.93, 0.97)
cg20675152	7	92456994	CDK6	6236	1830	-3.17	0.73	1.55E-05	0.040213	0.97 (0.96, 0.98)
cg20712856	10	6238080	PFKFB3	-6759	1830	-3.52	0.79	7.42E-06	0.035796	0.97 (0.95, 0.98)
cg20804243	3	171205319	TNIK	-27123	1829	-10.71	2.46	1.38E-05	0.039433	0.90 (0.86, 0.94)
cg20833901	21	40467185	PSMG1	88254	1827	-4.38	0.99	9.23E-06	0.037198	0.96 (0.94, 0.98)
cg20875821	18	61557735	SERPINB2	2797	1830	-2.71	0.61	1.04E-05	0.038113	0.97 (0.96, 0.98)
cg20893838	6	7145478	RREB1	37393	1828	-3.27	0.77	1.94E-05	0.042166	0.97 (0.95, 0.98)
cg21156580	3	72340184	LINC00870	139777	1825	-8.49	1.89	7.25E-06	0.035796	0.92 (0.89, 0.95)
cg21167563	1	117114916	CD58	-1202	1829	-4.27	1.02	2.77E-05	0.04753	0.96 (0.94, 0.98)
cg21279677	12	125201422	SCARB1	147096	1828	-3.22	0.75	1.80E-05	0.041088	0.97 (0.95, 0.98)
cg21953058	15	41309253	CHAC1	63907	1827	-2.73	0.56	9.22E-07	0.021528	0.97 (0.96, 0.98)
cg22503106	17	81040906	METRNL	3340	1814	-10.74	2.43	1.02E-05	0.037917	0.90 (0.86, 0.94)
cg22748479	19	6067328	RFX2	43335	1830	-3.09	0.71	1.40E-05	0.039589	0.97 (0.96, 0.98)
cg23091723	1	35920054	KIAA0319L	102982	1830	-2.72	0.65	2.68E-05	0.047424	0.97 (0.96, 0.99)
cg23215701	6	13462275	GFOD1	10019	1830	-3.42	0.78	1.31E-05	0.039135	0.97 (0.95, 0.98)
cg23386939	16	11328957	SOCS1	21081	1828	-2.69	0.61	1.10E-05	0.038247	0.97 (0.96, 0.99)
cg23575688	11	119486443	NECTIN1	112991	1828	-3.37	0.76	9.91E-06	0.037845	0.97 (0.95, 0.98)
cg23856600	5	10560140	ANKRD33B	-4294	1830	-7.28	1.63	7.55E-06	0.035873	0.93 (0.9, 0.96)
cg24099727	16	57662165	ADGRG1	28	1830	-7.07	1.64	1.70E-05	0.040742	0.93 (0.9, 0.96)
cg24279017	12	11877740	ETV6	74953	1830	-3.14	0.74	2.19E-05	0.043759	0.97 (0.96, 0.98)
cg24317972	10	12371568	CAMK1D	-19973	1827	-20.66	4.43	3.06E-06	0.027161	0.81 (0.75, 0.89)
cg24407546	1	205225282	TMCC2	-46	1829	-4.38	0.96	5.23E-06	0.03166	0.96 (0.94, 0.98)
cg24517604	16	11709855	LITAF	-28534	1829	-13.47	2.96	5.19E-06	0.031653	0.87 (0.82, 0.93)
cg24684972	12	27025721	ITPR2	-39591	1830	-2.5	0.59	2.18E-05	0.043759	0.98 (0.96, 0.99)
cg25466522	15	81623226	TMC3-AS1	6553	1828	-19.68	3.94	6.02E-07	0.017571	0.82 (0.76, 0.89)
cg25887955	11	65543903	AP5B1	4158	1827	-3.71	0.85	1.19E-05	0.038288	0.96 (0.95, 0.98)
cg26472183	8	126445744	TRIB1	1294	1788	-29.7	6.04	8.91E-07	0.021416	0.74 (0.66, 0.84)
cg26873486	1	172790731	FASLG	162584	1823	-3.72	0.87	1.97E-05	0.042462	0.96 (0.95, 0.98)
cg26964704	12	125589647	AACS	39735	1830	-16.06	3.37	1.85E-06	0.026074	0.85 (0.8, 0.91)

[1] Genome build GRCh37/hg19

[2] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)

Table E17. 315 Implicated Genes in Atopic Asthma Reported in Previous Asthma GWAS or EWAS

probe	chromosome	position[1]	Gene.Name	Distance.to.TSS	Beta[2]	SE[2]	P[2]	N	FDR	OR.CI	crossreactive
cg00006459	4	148635716	ARHGAP10	-17736	-23.76	4.95	1.59E-06	1426	0.003146	0.79 (0.72, 0.87)	
cg00092426	15	43309540	UBR1	88745	-20.29	5	4.86E-05	1428	0.040241	0.82 (0.74, 0.9)	
cg00170714	17	40724562	PSMC3IP	5171	-12.16	2.67	5.32E-06	1428	0.007806	0.89 (0.84, 0.93)	
cg00286717	11	6225537	C11orf42	-1260	-20.04	4.89	4.21E-05	1424	0.036216	0.82 (0.74, 0.9)	
cg00390941	12	15124659	PDE6H	-1296	-38.45	7.17	8.15E-08	1422	0.000391	0.68 (0.59, 0.78)	
cg00414077	20	35504511	TLDC2	-12	-10.86	1.97	3.26E-08	1428	0.000195	0.90 (0.86, 0.93)	
cg00460843	17	25833338	KSR1	34303	-14.68	2.97	8.05E-07	1428	0.001937	0.86 (0.81, 0.92)	
cg00527937	15	79609419	TMED3	6016	-16.03	2.64	1.27E-09	1427	2.16E-05	0.85 (0.81, 0.9)	
cg00587765	4	108615003	PAPSS1	26415	-19.87	4.94	5.73E-05	1427	0.04494	0.82 (0.74, 0.9)	
cg00673191	21	37536923	DOPEY2	85	-5.47	1.2	4.90E-06	1426	0.007402	0.95 (0.92, 0.97)	
cg00827939	22	39848852	MGAT3	-4472	-9.21	2.28	5.16E-05	1423	0.04196	0.91 (0.87, 0.95)	
cg00851361	1	234835623	LINC01132	-24165	-14.32	2.69	9.73E-08	1427	0.000432	0.87 (0.82, 0.91)	
cg00924612	18	19334381	MIB1	13092	-35.71	8.24	1.46E-05	1426	0.016997	0.70 (0.6, 0.82)	
cg00978517	14	55850801	ATG14	27774	-28.26	5.11	3.14E-08	1428	0.000192	0.75 (0.68, 0.83)	
cg00990977	20	17659317	RRBP1	3610	-31.26	7.14	1.18E-05	1428	0.014286	0.73 (0.64, 0.84)	
cg01009225	7	127527862	SND1-IT1	-109699	-43.24	7.47	7.13E-09	1426	7.18E-05	0.65 (0.56, 0.75)	
cg01047262	8	38007025	STAR	1574	-41.58	8.97	3.54E-06	1428	0.005791	0.66 (0.55, 0.79)	
cg01191788	16	30967493	SETD1A	-1121	-19.37	4.24	4.94E-06	1428	0.007421	0.82 (0.76, 0.9)	
cg01310029	3	3152374	IL5RA	-317	-11.96	2.58	3.64E-06	1427	0.005856	0.89 (0.84, 0.93)	
cg01325448	10	129799166	PTPRE	2777	-13.56	2.84	1.78E-06	1428	0.00348	0.87 (0.83, 0.92)	
cg01437709	15	41246346	CHAC1	1000	-28.95	5.06	1.04E-08	1425	9.04E-05	0.75 (0.68, 0.83)	
cg01450133	11	12136467	MICAL2	4345	-26.45	5.56	1.93E-06	1426	0.003694	0.77 (0.69, 0.86)	
cg01499988	9	35755346	MSMP	-1073	-18.28	3.85	2.06E-06	1428	0.003879	0.83 (0.77, 0.9)	
cg01542143	4	3240754	MSANTD1	-5341	-14.06	3.37	2.94E-05	1426	0.028531	0.87 (0.81, 0.93)	
cg01613077	20	4764277	RASSF2	31491	-33.67	5.77	5.44E-09	1428	6.01E-05	0.71 (0.64, 0.8)	
cg01614759	10	45495435	ZNF22	-837	-22.65	3.75	1.52E-09	1427	2.44E-05	0.80 (0.74, 0.86)	
cg01671341	12	109568238	ACACB	-8963	-17.77	4.31	3.75E-05	1426	0.03306	0.84 (0.77, 0.91)	
cg01901579	14	95615731	DICER1	8027	-25.25	3.91	1.07E-10	1428	4.60E-06	0.78 (0.72, 0.84)	
cg01908419	20	3989981	RNF24	6256	-9.9	2.37	2.90E-05	1428	0.028248	0.91 (0.86, 0.95)	
cg01942646	1	27240694	NR0B2	-128	-23.71	4.02	3.66E-09	1428	4.75E-05	0.79 (0.73, 0.85)	
cg01955639	17	56269767	EPX	-317	-18.56	3.55	1.76E-07	1428	0.000636	0.83 (0.77, 0.89)	

cg01998785	16	55542709	LPCAT2	-203	-9.66	2.13	6.03E-06	1428	0.008482	0.91 (0.87, 0.95)
cg02124524	16	85655007	GSE1	8166	-39.07	7.77	4.95E-07	1426	0.001371	0.68 (0.58, 0.79)
cg02133716	8	128981622	MIR1205	8744	-32.82	6.38	2.71E-07	1427	0.000875	0.72 (0.64, 0.82)
cg02142455	12	92431524	LINC01619	103964	-39.7	8.14	1.08E-06	1425	0.002323	0.67 (0.57, 0.79)
cg02170785	14	69650830	EXD2	-7363	-13.94	2.99	3.05E-06	1427	0.005226	0.87 (0.82, 0.92)
cg02171825	1	26517586	CATSPER4	468	-51.26	9.24	2.84E-08	1428	0.000185	0.60 (0.5, 0.72)
cg02228403	3	11522965	VGLL4	87432	-26.56	5.71	3.29E-06	1428	0.005555	0.77 (0.69, 0.86)
cg02233915	11	43760352	HSD17B12	58210	-36.52	6.89	1.15E-07	1423	0.00048	0.69 (0.61, 0.79)
cg02332678	11	3170821	OSBPL5	15760	-9.53	2.23	1.84E-05	1428	0.020184	0.91 (0.87, 0.95)
cg02359181	19	34860339	GPI	4315	-19.21	4.07	2.33E-06	1428	0.00426	0.83 (0.76, 0.89)
cg02361196	9	130866500	SLC25A25	5740	-15.11	2.88	1.57E-07	1426	0.000586	0.86 (0.81, 0.91)
cg02420943	2	99122909	INPP4A	61589	-7.62	1.8	2.43E-05	1427	0.024669	0.93 (0.89, 0.96)
cg02473287	2	9752386	YWHAQ	18797	-14.51	3.41	2.15E-05	1428	0.022526	0.86 (0.81, 0.92)
cg02494549	2	161798364	TANK	-195101	-27.74	6.35	1.24E-05	1427	0.014903	0.76 (0.67, 0.86)
cg02503303	11	85781719	PICALM	-797	-12.38	2.35	1.35E-07	1428	0.00053	0.88 (0.84, 0.93)
cg02543556	14	39643445	PNN	-941	-19.55	4.55	1.72E-05	1428	0.019229	0.82 (0.75, 0.9)
cg02645272	22	30650471	LIF	-7632	-15.97	2.86	2.46E-08	1428	0.000165	0.85 (0.81, 0.9)
cg02683853	1	180940271	STX6	51985	-23.3	5.52	2.42E-05	1428	0.024629	0.79 (0.71, 0.88)
cg02856510	2	192043611	STAT4	-27290	-16.12	3.82	2.42E-05	1428	0.024629	0.85 (0.79, 0.92)
cg02930951	20	48806066	CEBPB	-1053	-14.97	3.61	3.40E-05	1428	0.031647	0.86 (0.8, 0.92)
cg02970679	17	56269818	EPX	-266	-19.97	4.62	1.53E-05	1427	0.017586	0.82 (0.75, 0.9)
cg02996630	5	176920990	PDLIM7	3615	-7.25	1.79	5.15E-05	1428	0.04192	0.93 (0.9, 0.96)
cg03069832	3	57064082	SPATA12	-30386	-15.82	3.93	5.68E-05	1428	0.04472	0.85 (0.79, 0.92)
cg03092343	1	33221514	KIAA1522	-9720	-16.03	3.15	3.49E-07	1428	0.001068	0.85 (0.8, 0.91)
cg03131767	12	123446272	ABCB9	4783	-16.29	3.87	2.61E-05	1428	0.026108	0.85 (0.79, 0.92)
cg03189469	13	110350537	LINC00676	-30083	-16.44	3.54	3.50E-06	1428	0.005767	0.85 (0.79, 0.91)
cg03210018	12	47477069	AMIGO2	-3336	-17.39	3.25	8.86E-08	1427	0.000402	0.84 (0.79, 0.9)
cg03329755	6	167189272	RPS6KA2	86766	-19	3.93	1.37E-06	1416	0.002806	0.83 (0.77, 0.89)
cg03369382	7	139427635	HIPK2	50057	-42.76	8.13	1.44E-07	1428	0.000555	0.65 (0.56, 0.76)
cg03448301	11	62678778	CHRM1	10233	-34.44	7.13	1.38E-06	1426	0.002812	0.71 (0.62, 0.81)
cg03471593	16	55542668	LPCAT2	-244	-6.11	1.21	4.03E-07	1426	0.001172	0.94 (0.92, 0.96)
cg03475216	8	21670183	GFRA2	-23838	-17.47	3.95	9.91E-06	1428	0.012441	0.84 (0.78, 0.91)
cg03492094	9	91994786	SECISBP2	61021	-11.08	1.91	6.25E-09	1428	6.54E-05	0.90 (0.86, 0.93)

cg03502211	6	36108112	MAPK13	9852	-18.08	3.99	5.91E-06	1428	0.0084	0.83 (0.77, 0.9)
cg03512256	6	167135251	RPS6KA2	-94487	-30.19	7.2	2.73E-05	1428	0.026978	0.74 (0.64, 0.85)
cg03519593	17	56274597	EPX	4513	-14.24	3.32	1.75E-05	1426	0.019405	0.87 (0.81, 0.93)
cg03695871	11	65547172	AP5B1	889	-6.67	1.17	1.09E-08	1428	9.38E-05	0.94 (0.91, 0.96)
cg03757043	9	114957571	SUSD1	-19995	-17.44	3.81	4.78E-06	1428	0.007247	0.84 (0.78, 0.91)
cg03784596	6	25608913	SCGN	-43515	-30.79	6.31	1.09E-06	1427	0.002338	0.73 (0.65, 0.83)
cg03837359	16	70648377	IL34	-9517	-18.16	3.35	6.01E-08	1428	0.000307	0.83 (0.78, 0.89)
cg03983220	16	85568407	GSE1	-76621	-4.49	1.1	4.49E-05	1426	0.037985	0.96 (0.94, 0.98)
cg04031158	1	175772135	TNR	-59384	-29.72	5.85	3.81E-07	1428	0.001136	0.74 (0.66, 0.83)
cg04036011	1	43291088	ERMAP	-160	-7.18	1.78	5.51E-05	1420	0.043591	0.93 (0.9, 0.96)
cg04148640	9	101595635	GALNT12	25655	-37.63	7.67	9.23E-07	1423	0.00211	0.69 (0.59, 0.8)
cg04170495	6	140053824	FILNC1	-38385	-8.09	1.96	3.53E-05	1427	0.032233	0.92 (0.89, 0.96)
cg04217850	3	66428294	LRIG1	122550	-20.9	4.45	2.60E-06	1427	0.004619	0.81 (0.74, 0.89)
cg04290133	7	65439512	GUSB	7788	-21.69	3.28	3.61E-11	1422	3.09E-06	0.81 (0.75, 0.86)
cg04308301	8	131454686	ASAP1	1219	-17.24	3.3	1.82E-07	1428	0.000652	0.84 (0.79, 0.9)
cg04377912	1	43290841	ERMAP	-407	-32.98	6.98	2.32E-06	1425	0.00426	0.72 (0.63, 0.82)
cg04404773	3	39217727	XIRP1	16349	-9.44	2.25	2.67E-05	1428	0.026545	0.91 (0.87, 0.95)
cg04420917	19	39303993	LGALS4	-254	-13.42	3.09	1.37E-05	1428	0.016086	0.87 (0.82, 0.93)
cg04459091	5	179751794	GFPT2	28592	-22.99	5.73	6.07E-05	1427	0.046754	0.79 (0.71, 0.89)
cg04763288	1	242351909	MAP1LC3C	-189525	-18.74	4.68	6.13E-05	1428	0.047127	0.83 (0.76, 0.91)
cg04765589	18	61550142	SERPINB2	-4796	-28.28	6.71	2.53E-05	1427	0.025432	0.75 (0.66, 0.86)
cg04847043	16	85654213	GSE1	7372	-26.95	5.91	5.15E-06	1427	0.007638	0.76 (0.68, 0.86)
cg04992471	3	42942410	ZNF662	-4991	-15.18	3.28	3.61E-06	1428	0.00583	0.86 (0.81, 0.92)
cg04997452	15	39697356	C15orf54	154487	-40.02	8.8	5.47E-06	1427	0.007968	0.67 (0.56, 0.8)
cg05045380	3	119355809	POPDC2	23627	-10.77	2.37	5.58E-06	1427	0.008028	0.90 (0.86, 0.94)
cg05072637	9	131355483	SPTAN1	40647	-15.97	3.22	6.90E-07	1428	0.00173	0.85 (0.8, 0.91)
cg05178561	9	365007	DOCK8	91960	-20.12	3.88	2.09E-07	1428	0.000715	0.82 (0.76, 0.88)
cg05184016	7	149543136	ZNF862	7681	-38.5	5.96	1.01E-10	1427	4.59E-06	0.68 (0.61, 0.76)
cg05194248	19	16553751	EPS15L1	29071	-7.25	1.74	3.20E-05	1427	0.030327	0.93 (0.9, 0.96)
cg05219423	10	11291279	CELF2	84287	-13.24	3.12	2.21E-05	1427	0.023008	0.88 (0.82, 0.93)
cg05257275	11	65547049	AP5B1	1012	-8.21	1.68	1.03E-06	1427	0.002245	0.92 (0.89, 0.95)
cg05261121	16	23563601	EARS2	5094	-28.53	6.46	1.01E-05	1426	0.012602	0.75 (0.66, 0.85)
cg05300717	11	65546210	AP5B1	1851	-13.79	2.06	2.32E-11	1421	2.37E-06	0.87 (0.84, 0.91)

cg05306459	13	100761701	PCCA	20433	-15.51	3.62	1.80E-05	1428	0.019825	0.86 (0.8, 0.92)
cg05358754	22	35652215	HMGXB4	-1229	-26.23	6.09	1.64E-05	1428	0.018512	0.77 (0.68, 0.87)
cg05447875	2	231583339	CAB39	5077	-12.94	2.95	1.20E-05	1426	0.014486	0.88 (0.83, 0.93)
cg05480350	8	128972681	MIR1205	-197	-14.78	3.04	1.21E-06	1428	0.002542	0.86 (0.81, 0.92)
cg05541460	22	39850774	MGAT3	-2550	-19.84	3.73	1.08E-07	1427	0.000467	0.82 (0.76, 0.88)
cg05543520	3	66500703	LRIG1	50141	-14.05	3.19	1.08E-05	1426	0.013292	0.87 (0.82, 0.92)
cg05613273	17	80419874	NARF	3335	-31.01	6.53	2.05E-06	1428	0.003869	0.73 (0.65, 0.83)
cg05786348	2	157295032	GPD2	2133	-23.08	4.35	1.10E-07	1428	0.000469	0.79 (0.73, 0.86)
cg05808227	22	37299905	CSF2RB	-9769	-16.83	3.5	1.50E-06	1428	0.003005	0.85 (0.79, 0.91)
cg05879394	8	126591840	TRIB1	147390	-8.96	2.17	3.55E-05	1427	0.032271	0.91 (0.88, 0.95)
cg06070625	3	69812798	MITF	92	-17.89	4.22	2.23E-05	1428	0.023098	0.84 (0.77, 0.91)
cg06144471	3	195835467	TFRC	-26436	-21.52	4.57	2.48E-06	1426	0.004464	0.81 (0.74, 0.88)
cg06223015	17	8765911	PIK3R6	5082	-35.18	6.43	4.40E-08	1428	0.00024	0.70 (0.62, 0.8)
cg06290138	15	38881520	RASGRP1	-24514	-20.37	4.91	3.30E-05	1425	0.031034	0.82 (0.74, 0.9)
cg06304167	3	171865257	FNDC3B	106914	-19.38	4.69	3.55E-05	1428	0.032271	0.82 (0.75, 0.9)
cg06315149	1	2036398	PRKCZ	244	-16.44	3.49	2.55E-06	1428	0.00456	0.85 (0.79, 0.91)
cg06391412	3	71295684	FOXP1	-1369	-16.85	3.79	8.67E-06	1427	0.011224	0.84 (0.78, 0.91)
cg06394964	6	6971749	RREB1	-136080	-12.1	2.77	1.25E-05	1425	0.014957	0.89 (0.84, 0.94)
cg06437892	15	43387093	UBR1	11192	-21.23	4.6	3.92E-06	1426	0.006161	0.81 (0.74, 0.89)
cg06475513	16	85593560	GSE1	-51468	-17.1	4.14	3.66E-05	1428	0.032869	0.84 (0.78, 0.91)
cg06483820	17	55167149	AKAP1	4015	-20.23	3.89	1.94E-07	1425	0.000678	0.82 (0.76, 0.88)
cg06516790	2	121949349	TFCP2L1	93428	-13.79	3.32	3.29E-05	1427	0.030976	0.87 (0.82, 0.93)
cg06525046	2	121155673	INHBB	51956	-11.87	2.95	5.72E-05	1426	0.04494	0.89 (0.84, 0.94)
cg06592575	18	55250579	FECH	3389	-35.01	6.31	2.88E-08	1427	0.000185	0.70 (0.62, 0.8)
cg06592918	18	77703051	PQLC1	8601	-9.14	2.04	7.43E-06	1428	0.010003	0.91 (0.88, 0.95)
cg06612119	12	56404209	IKZF4	-10479	-6	1.4	1.69E-05	1427	0.018972	0.94 (0.92, 0.97)
cg06725108	2	136901306	CXCR4	-25582	-7.99	1.99	5.92E-05	1426	0.045989	0.92 (0.89, 0.96)
cg06743426	16	11709899	LITAF	-28578	-7.39	1.84	5.89E-05	1428	0.045799	0.93 (0.9, 0.96)
cg06755692	2	38812997	HNRNPLL	17180	-14.49	2.95	9.02E-07	1427	0.002091	0.87 (0.82, 0.92)
cg06773230	2	8472503	LINC00299	-3955	-21.98	4.41	6.30E-07	1428	0.001619	0.80 (0.74, 0.88)
cg06958964	10	45494806	ZNF22	-1466	-33.04	7.81	2.31E-05	1428	0.023776	0.72 (0.62, 0.84)
cg06984345	14	75162215	AREL1	17591	-15.07	2.88	1.76E-07	1428	0.000636	0.86 (0.81, 0.91)
cg06996254	12	47427791	PCED1B	-45594	-43.6	8.03	5.56E-08	1424	0.000289	0.65 (0.55, 0.76)

cg07098502	16	85654157	GSE1	7316	-29.53	6.95	2.17E-05	1428	0.022649	0.74 (0.65, 0.85)
cg07177867	15	52030746	LYSMD2	-427	-16.04	3.27	9.40E-07	1428	0.002125	0.85 (0.8, 0.91)
cg07361747	1	10516255	CORT	6480	-8.48	1.75	1.21E-06	1426	0.002542	0.92 (0.89, 0.95)
cg07410597	3	66404129	SLC25A26	132962	-22.44	4.94	5.55E-06	1428	0.007999	0.80 (0.73, 0.88)
cg07459967	9	130859191	SLC25A25	-1569	-23.11	5.25	1.06E-05	1417	0.013125	0.79 (0.72, 0.88)
cg07465458	3	39243826	XIRP1	-9740	-9.52	2.21	1.59E-05	1426	0.018072	0.91 (0.87, 0.95)
cg07636225	11	63466987	RTN3	18066	-26.67	4.53	4.06E-09	1428	5.03E-05	0.77 (0.7, 0.84)
cg07718085	5	138875768	TMEM173	-13394	-29.75	5.68	1.61E-07	1427	0.000595	0.74 (0.66, 0.83)
cg07730263	3	52810259	ITIH1	-1342	-12.18	2.51	1.18E-06	1428	0.002498	0.89 (0.84, 0.93)
cg07778428	21	34130201	PAXBP1	13967	-17.1	3.46	7.60E-07	1428	0.001871	0.84 (0.79, 0.9)
cg07827820	1	120821493	FAM72B	-17511	-44.33	9.56	3.53E-06	1428	0.005791	0.64 (0.53, 0.77)
cg07828169	5	132114623	SEPT8	-1063	-18.48	4.16	8.68E-06	1428	0.011224	0.83 (0.77, 0.9)
cg07834490	21	37536817	DOPEY2	-21	-6.73	1.31	2.51E-07	1423	0.00083	0.93 (0.91, 0.96)
cg07879720	5	37668810	GDNF	166113	-13.65	2.76	7.66E-07	1423	0.001874	0.87 (0.83, 0.92)
cg07906050	1	6377509	ACOT7	41494	-16.74	3.89	1.64E-05	1428	0.018512	0.85 (0.78, 0.91)
cg07970948	7	149543165	ZNF862	7710	-10.42	1.67	4.31E-10	1425	1.04E-05	0.90 (0.87, 0.93)
cg08014024	10	134373103	INPP5A	21821	-13.51	3.22	2.71E-05	1428	0.026845	0.87 (0.82, 0.93)
cg08089777	8	129152499	MIR1208	-9862	-39.6	8.27	1.68E-06	1426	0.0033	0.67 (0.57, 0.79)
cg08094347	21	30699368	BACH1	21844	-62.96	11.37	3.07E-08	1427	0.000189	0.53 (0.43, 0.67)
cg08222787	17	56288205	MKS1	8460	-24.5	5.75	2.02E-05	1428	0.021608	0.78 (0.7, 0.88)
cg08288503	3	16889869	PLCL2	-36582	-10.17	2.39	2.12E-05	1428	0.022241	0.90 (0.86, 0.95)
cg08334830	2	74265933	TET3	52403	-17.88	4.33	3.66E-05	1428	0.032869	0.84 (0.77, 0.91)
cg08338792	8	129152449	MIR1208	-9912	-43.74	7.23	1.47E-09	1428	2.40E-05	0.65 (0.56, 0.74)
cg08531949	9	366070	DOCK8	93023	-7.24	1.79	5.14E-05	1428	0.04188	0.93 (0.9, 0.96)
cg08553585	1	234791553	LOC101927787	9519	-58.05	12.97	7.56E-06	1427	0.010145	0.56 (0.43, 0.72)
cg08559734	12	6332058	CD9	22577	-26.57	6.31	2.55E-05	1428	0.02557	0.77 (0.68, 0.87)
cg08635575	9	80189185	GNA14	74046	-11.55	2.87	5.78E-05	1428	0.045194	0.89 (0.84, 0.94)
cg08698681	3	171091657	TNIK	86539	-17.69	4.33	4.37E-05	1428	0.037201	0.84 (0.77, 0.91)
cg08744877	17	57925800	MIR21	7174	-26.32	6.52	5.38E-05	1427	0.042979	0.77 (0.68, 0.87)
cg08761605	5	58654193	PDE4D	-1467	-16.59	4.09	4.97E-05	1428	0.040944	0.85 (0.78, 0.92)
cg08886771	5	172271228	ERGIC1	10006	-18.62	4.3	1.46E-05	1425	0.016997	0.83 (0.76, 0.9)
cg08900098	7	150653449	KCNH2	-533	-9.53	2.16	1.04E-05	1428	0.012936	0.91 (0.87, 0.95)
cg08922698	14	76447643	TGFB3	721	-21.61	3.93	3.90E-08	1427	0.00022	0.81 (0.75, 0.87)

cg08969102	5	133563532	PPP2CA	-1583	-16.36	3.02	6.24E-08	1428	0.000315	0.85 (0.8, 0.9)
cg09012511	3	66489480	LRIG1	61364	-14.22	2.71	1.52E-07	1428	0.000575	0.87 (0.82, 0.91)
cg09191776	6	28843296	LINC01623	-11843	-21.53	5.31	5.12E-05	1427	0.041801	0.81 (0.73, 0.89)
cg09194810	20	4072430	SMOX	-56995	-26.72	4.57	4.80E-09	1427	5.60E-05	0.77 (0.7, 0.84)
cg09227119	20	35504403	TLDC2	-120	-12.89	2.85	6.05E-06	1427	0.008495	0.88 (0.83, 0.93)
cg09241885	20	35504371	TLDC2	-152	-12.64	3.07	3.72E-05	1427	0.033045	0.88 (0.83, 0.94)
cg09332506	1	160309220	NCSTN	-3842	-63.43	9.76	7.96E-11	1428	4.15E-06	0.53 (0.44, 0.64)
cg09339568	22	37296313	CSF2RB	-13361	-9.17	1.85	6.89E-07	1428	0.00173	0.91 (0.88, 0.95)
cg09447105	12	15126020	PDE6H	65	-18.88	4.27	9.73E-06	1428	0.012252	0.83 (0.76, 0.9)
cg09469170	3	52809942	ITIH1	-1659	-27.76	4.97	2.38E-08	1428	0.000162	0.76 (0.69, 0.84)
cg09565310	5	112541553	MCC	89058	-19.93	3.98	5.63E-07	1428	0.001487	0.82 (0.76, 0.89)
cg09684929	9	91979711	SECISBP2	45946	-7.74	1.88	3.75E-05	1427	0.03306	0.93 (0.89, 0.96)
cg09696385	7	127528039	SND1-IT1	-109522	-34.42	7.23	1.89E-06	1428	0.003643	0.71 (0.62, 0.82)
cg09705784	17	76565232	DNAH17	8243	-8.75	1.89	3.80E-06	1428	0.00603	0.92 (0.88, 0.95)
cg09800745	12	104808575	CHST11	-42116	-16.75	4.15	5.47E-05	1428	0.043485	0.85 (0.78, 0.92)
cg10054763	2	69828510	ANXA4	-42426	-33.02	6.83	1.34E-06	1428	0.002751	0.72 (0.63, 0.82)
cg10055846	8	21670177	GFRA2	-23832	-14.45	3.12	3.76E-06	1427	0.00599	0.87 (0.81, 0.92)
cg10105512	22	31643111	LIMK2	-1236	-16.03	3.03	1.18E-07	1428	0.00049	0.85 (0.8, 0.9)
cg10114537	2	137135606	CXCR4	-259882	-16.86	4.16	5.17E-05	1427	0.041999	0.84 (0.78, 0.92)
cg10159529	3	3152530	IL5RA	-473	-12.83	3.14	4.37E-05	1428	0.037201	0.88 (0.83, 0.94)
cg10220104	12	27027924	ITPR2	-41794	-29.89	5.58	8.43E-08	1427	0.000391	0.74 (0.66, 0.83)
cg10279452	3	72509222	RYBP	-13449	-21.68	4.28	3.96E-07	1428	0.001167	0.81 (0.74, 0.88)
cg10354401	2	86789025	CHMP3	1594	-32.46	7.57	1.79E-05	1428	0.019742	0.72 (0.62, 0.84)
cg10644885	19	11687621	ACP5	934	-15.78	2.82	2.29E-08	1428	0.000159	0.85 (0.81, 0.9)
cg10704177	1	62209607	PATJ	1459	-18.82	3.26	7.48E-09	1427	7.19E-05	0.83 (0.78, 0.88)
cg10794399	2	100673005	AFF3	49039	-26.01	4.3	1.40E-09	1428	2.33E-05	0.77 (0.71, 0.84)
cg10815420	8	105599835	LRP12	1416	-34.5	7.19	1.59E-06	1426	0.003146	0.71 (0.62, 0.82)
cg10897344	10	104227113	MFSD13A	5944	-16.26	3.35	1.25E-06	1421	0.002599	0.85 (0.8, 0.91)
cg11081261	14	102656363	WDR20	50175	-25.5	4.35	4.74E-09	1427	5.60E-05	0.77 (0.71, 0.84)
cg11112605	17	56283901	MKS1	12764	-19.25	3.41	1.66E-08	1428	0.000123	0.82 (0.77, 0.88)
cg11215870	16	31484722	TGFB1I1	197	-13.42	2.73	8.79E-07	1423	0.00208	0.87 (0.83, 0.92)
cg11230866	6	150400090	ULBP3	-9808	-9.02	2.19	3.96E-05	1427	0.034538	0.91 (0.88, 0.95)
cg11238327	17	29837074	RAB11FIP4	22056	-11.12	2.41	4.03E-06	1428	0.006285	0.89 (0.85, 0.94)

cg11296110	1	1690811	NADK	-731	-9.19	2.21	3.19E-05	1423	0.030279	0.91 (0.87, 0.95)
cg11422446	7	37434016	ELMO1	-40745	-14.39	2.97	1.26E-06	1426	0.0026	0.87 (0.82, 0.92)
cg11606229	21	34570139	LINC01548	-27599	-19.01	3.46	3.96E-08	1428	0.000222	0.83 (0.77, 0.88)
cg11649969	1	180940378	STX6	51878	-51.25	7.8	5.10E-11	1428	3.49E-06	0.60 (0.51, 0.7)
cg11668148	15	72636405	CELF6	-23881	-29.48	4.82	9.98E-10	1428	1.85E-05	0.74 (0.68, 0.82)
cg11841710	20	24630982	SYNDIG1	180541	-28.7	6.21	3.83E-06	1428	0.006042	0.75 (0.66, 0.85)
cg11844053	1	210704772	HHAT	202133	-8.95	1.97	5.54E-06	1426	0.007999	0.91 (0.88, 0.95)
cg11929042	20	19222240	SLC24A3	28951	-29.79	5.37	2.87E-08	1428	0.000185	0.74 (0.67, 0.82)
cg11939550	19	16561197	EPS15L1	21625	-6.63	1.45	4.92E-06	1424	0.007405	0.94 (0.91, 0.96)
cg11987455	1	43290834	ERMAP	-414	-17.58	3.53	6.44E-07	1428	0.001645	0.84 (0.78, 0.9)
cg11988722	20	33416959	NCOA6	-3508	-6.46	1.45	8.22E-06	1428	0.010835	0.94 (0.91, 0.96)
cg12074090	8	6360436	ANGPT2	60347	-15.21	3.27	3.22E-06	1425	0.005471	0.86 (0.81, 0.92)
cg12075669	13	111316145	CARS2	42381	-11.8	2.33	4.26E-07	1428	0.001226	0.89 (0.85, 0.93)
cg12077754	2	75089669	HK2	29888	-13.53	2.74	7.84E-07	1428	0.001901	0.87 (0.83, 0.92)
cg12119581	10	93786975	BTAF1	103240	-50.41	11.19	6.63E-06	1424	0.009122	0.60 (0.49, 0.75)
cg12154164	1	28484534	PTAFR	18920	-16.99	3.02	1.93E-08	1428	0.000141	0.84 (0.8, 0.9)
cg12192145	14	55849528	ATG14	29047	-18.94	4.67	5.09E-05	1428	0.041639	0.83 (0.76, 0.91)
cg12213680	6	24877462	RIPOR2	130	-12.14	2.85	2.10E-05	1418	0.022116	0.89 (0.84, 0.94)
cg12258670	14	75069041	LTBP2	9992	-29.27	5.18	1.57E-08	1428	0.000119	0.75 (0.67, 0.83)
cg12359648	11	119507838	NECTIN1	91596	-26.23	5.34	8.98E-07	1426	0.002091	0.77 (0.69, 0.85)
cg12605076	14	74547881	ALDH6A1	3314	-48.88	11.91	4.04E-05	1426	0.035124	0.61 (0.49, 0.77)
cg12629001	9	35537849	RUSC2	-779	-21.21	5.08	3.00E-05	1427	0.02881	0.81 (0.73, 0.89)
cg12645785	1	29229403	EPB41	-11684	-22.23	3.85	7.71E-09	1428	7.26E-05	0.80 (0.74, 0.86)
cg12734151	18	33021980	INO80C	55632	-31.8	6.76	2.54E-06	1426	0.00456	0.73 (0.64, 0.83)
cg12736613	7	151501146	PRKAG2	10810	-16.4	3.31	7.23E-07	1427	0.001795	0.85 (0.8, 0.91)
cg12819873	11	57157632	PRG2	497	-22.66	3.9	6.00E-09	1428	6.54E-05	0.80 (0.74, 0.86)
cg13054523	17	81055722	METRNL	18156	-19.97	3.42	5.44E-09	1428	6.01E-05	0.82 (0.77, 0.88)
cg13064897	8	135747178	ZFAT	-21887	-18.04	3.89	3.55E-06	1426	0.005791	0.83 (0.77, 0.9)
cg13072730	14	21508987	RNASE7	-1397	-15.59	3.55	1.15E-05	1427	0.014048	0.86 (0.8, 0.92)
cg13073332	2	62515892	B3GNT2	73237	-15.08	2.85	1.20E-07	1428	0.00049	0.86 (0.81, 0.91)
cg13174688	18	8801435	MTCL1	84067	-15.04	3.25	3.63E-06	1423	0.005851	0.86 (0.81, 0.92)
cg13353793	2	85944732	GNLY	23319	-20.48	4.9	2.95E-05	1428	0.028531	0.81 (0.74, 0.9)
cg13458609	9	130608923	ENG	522	-10.08	1.99	3.98E-07	1423	0.001167	0.90 (0.87, 0.94)

cg13459606	7	50861834	GRB10	-676	-15.62	3.08	4.00E-07	1426	0.001167	0.86 (0.81, 0.91)
cg13491003	17	57948101	TUBD1	22204	-7.62	1.87	4.45E-05	1428	0.037725	0.93 (0.89, 0.96)
cg13576859	9	97403129	FBP1	-599	-14.83	2.9	3.10E-07	1428	0.000967	0.86 (0.81, 0.91)
cg13628444	9	134883788	MED27	71485	-19.74	3.85	2.91E-07	1427	0.000918	0.82 (0.76, 0.89)
cg13732043	7	100230770	TFR2	502	18.53	4.14	7.53E-06	1424	0.010121	1.20 (1.11, 1.31)
cg13764085	11	61607741	FADS2	12237	-11.75	2.49	2.42E-06	1428	0.004375	0.89 (0.85, 0.93)
cg13792581	20	43590115	TOMM34	-1002	-35.77	7.57	2.29E-06	1426	0.004234	0.70 (0.6, 0.81)
cg13835688	9	130859454	SLC25A25	-1306	-13.97	2.89	1.28E-06	1428	0.002635	0.87 (0.82, 0.92)
cg13850063	9	138362321	PPP1R26-AS1	1773	-17.66	3.97	8.80E-06	1427	0.011356	0.84 (0.78, 0.91)
cg13863638	6	7199401	RREB1	91316	-49.5	9.83	4.71E-07	1426	0.001309	0.61 (0.5, 0.74)
cg13947225	17	55190679	AKAP1	27545	-20.83	3.24	1.31E-10	1424	4.87E-06	0.81 (0.76, 0.87)
cg14011077	9	138362327	PPP1R26-AS1	1767	-20	3.88	2.47E-07	1426	0.000821	0.82 (0.76, 0.88)
cg14012059	9	130222969	LRSAM1	8436	-7.17	1.43	5.57E-07	1417	0.001487	0.93 (0.91, 0.96)
cg14025883	9	5436224	PLGRKT	1712	-15.24	3.49	1.28E-05	1423	0.015227	0.86 (0.8, 0.92)
cg14118054	13	52198723	WDFY2	40240	-23.45	5.19	6.36E-06	1428	0.008885	0.79 (0.71, 0.88)
cg14131691	7	45038259	CCM2	-1085	-10.32	2.49	3.35E-05	1428	0.031324	0.90 (0.86, 0.95)
cg14179258	11	12747546	TEAD1	51578	-3.49	0.84	3.27E-05	1427	0.030823	0.97 (0.95, 0.98)
cg14184646	3	136618139	NCK1	-31177	-41.86	8.14	2.73E-07	1427	0.000875	0.66 (0.56, 0.77)
cg14298642	7	28228530	JAZF1	-8094	-34.78	8.71	6.54E-05	1425	0.049215	0.71 (0.6, 0.84)
cg14511746	17	2287008	MNT	17249	-19.96	3.26	9.69E-10	1426	1.85E-05	0.82 (0.77, 0.87)
cg14612966	9	130859606	SLC25A25	-1154	-24.23	4.38	3.06E-08	1428	0.000189	0.78 (0.72, 0.86)
cg14613878	20	35504198	TLDC2	-325	-8.56	1.92	8.54E-06	1425	0.011113	0.92 (0.88, 0.95)
cg14884379	18	61559440	SERPINB2	4502	-13.45	3.35	5.96E-05	1428	0.046168	0.87 (0.82, 0.93)
cg14991022	1	203255003	LINC01353	-1276	-24.03	5.66	2.17E-05	1427	0.022649	0.79 (0.7, 0.88)
cg14999724	11	57163587	PRG2	-5458	-10.02	2.41	3.31E-05	1427	0.031057	0.90 (0.86, 0.95)
cg15123849	6	15364953	JARID2	115868	-7.54	1.34	1.98E-08	1427	0.000143	0.93 (0.9, 0.95)
cg15146567	3	42948626	ZNF662	969	-8.72	2.03	1.71E-05	1428	0.01917	0.92 (0.88, 0.95)
cg15158069	11	123429280	GRAMD1B	-1689	-7.33	1.45	4.61E-07	1427	0.001293	0.93 (0.9, 0.96)
cg15209998	17	29837057	RAB11FIP4	22039	-9.57	2.13	7.05E-06	1425	0.009571	0.91 (0.87, 0.95)
cg15284593	17	76565091	DNAH17	8384	-14.75	3.45	1.95E-05	1427	0.021079	0.86 (0.81, 0.92)
cg15301710	21	34124445	PAXBP1	19723	-26.14	5.87	8.38E-06	1424	0.010971	0.77 (0.69, 0.86)
cg15314908	15	33717344	RYR3	114182	-35.73	7.01	3.38E-07	1426	0.001042	0.70 (0.61, 0.8)
cg15344640	5	176774729	LMAN2	4155	-24.55	5.72	1.78E-05	1428	0.019658	0.78 (0.7, 0.88)

cg15434896	5	79782956	FAM151B	-843	-29.7	5.54	8.27E-08	1428	0.000391	0.74 (0.67, 0.83)
cg15532312	20	34018983	GDF5	6986	-37.58	6.39	4.16E-09	1424	5.07E-05	0.69 (0.61, 0.78)
cg15579574	11	12180609	MICAL2	-3016	-67.52	12.24	3.46E-08	1428	0.000199	0.51 (0.4, 0.65)
cg15634144	6	7119942	RREB1	11857	-9.82	2.16	5.18E-06	1427	0.007655	0.91 (0.87, 0.95)
cg15700636	11	57156050	PRG2	2079	-15.43	3.13	8.32E-07	1424	0.001994	0.86 (0.81, 0.91)
cg15881027	1	40532772	CAP1	26518	-25.1	4.84	2.14E-07	1426	0.000726	0.78 (0.71, 0.86)
cg15903936	11	73714778	UCP3	5503	-38.91	9.14	2.06E-05	1428	0.021835	0.68 (0.57, 0.81)
cg15952483	7	75511298	RHBDD2	2989	-29.21	5.72	3.32E-07	1424	0.001028	0.75 (0.67, 0.84)
cg15998761	2	191300784	MFSD6	27704	-20.46	4.41	3.49E-06	1428	0.005767	0.81 (0.75, 0.89)
cg16107105	7	150646704	KCNH2	6212	-19.77	4.45	8.81E-06	1427	0.011356	0.82 (0.75, 0.9)
cg16122287	20	34364813	PHF20	4891	-36.05	7.02	2.77E-07	1423	0.000884	0.70 (0.61, 0.8)
cg16147002	12	113697418	TPCN1	15353	-10.25	2.34	1.18E-05	1427	0.014286	0.90 (0.86, 0.94)
cg16191278	19	35894520	LINC01531	-1988	-13.45	2.99	6.93E-06	1425	0.009439	0.87 (0.82, 0.93)
cg16362140	5	10708717	DAP	52669	-9.6	2.35	4.49E-05	1428	0.037985	0.91 (0.87, 0.95)
cg16438366	17	55191754	AKAP1	28620	-12.16	2.43	5.64E-07	1427	0.001487	0.89 (0.84, 0.93)
cg16508714	10	98425110	PIK3AP1	55168	-8.86	2.08	2.08E-05	1428	0.02199	0.92 (0.88, 0.95)
cg16549727	11	69418951	CCND1	-36921	-22.8	4.66	9.98E-07	1420	0.002192	0.80 (0.73, 0.87)
cg16597993	19	16578633	EPS15L1	4189	-24.57	4.52	5.49E-08	1428	0.000288	0.78 (0.72, 0.85)
cg16599817	1	2036283	PRKCZ	129	-9.76	2.3	2.27E-05	1428	0.023423	0.91 (0.87, 0.95)
cg16680864	9	101705161	COL15A1	-833	-8.97	1.95	4.27E-06	1427	0.006572	0.91 (0.88, 0.95)
cg16725301	16	57683565	ADGRG1	10359	-14.1	3.52	6.22E-05	1427	0.047507	0.87 (0.81, 0.93)
cg16868031	1	27240812	NR0B2	-246	-15.74	3.36	2.87E-06	1427	0.00499	0.85 (0.8, 0.91)
cg17030380	11	59525449	STX3	2918	-27.21	6.49	2.76E-05	1426	0.027176	0.76 (0.67, 0.87)
cg17074037	3	52220370	ALAS1	-11728	-10.61	2.48	1.88E-05	1427	0.020458	0.90 (0.86, 0.94)
cg17105176	17	2287284	MNT	16973	-28.7	4.87	3.63E-09	1425	4.75E-05	0.75 (0.68, 0.83)
cg17139328	13	100188895	TM9SF2	35268	-24.95	5.51	5.87E-06	1426	0.008372	0.78 (0.7, 0.87)
cg17245251	8	103603330	ODF1	39483	-27.52	5.63	1.03E-06	1428	0.002245	0.76 (0.68, 0.85)
cg17334945	2	131126377	PTPN18	12798	-13.84	3.18	1.33E-05	1428	0.015707	0.87 (0.82, 0.93)
cg17374802	17	56270828	EPX	744	-12.06	2.92	3.55E-05	1428	0.032271	0.89 (0.84, 0.94)
cg17446528	6	7154703	RREB1	46618	-5.69	1.41	5.36E-05	1426	0.042979	0.94 (0.92, 0.97)
cg17521120	19	51961666	SIGLEC8	41	-14.2	2.95	1.47E-06	1428	0.002966	0.87 (0.82, 0.92)
cg17526357	17	4112498	ANKFY1	54643	-13.38	3.24	3.71E-05	1428	0.033028	0.87 (0.82, 0.93)
cg17532497	21	36608456	RUNX1	-186862	-19.59	4.32	5.83E-06	1428	0.00833	0.82 (0.76, 0.89)

cg17558547	5	153836180	SAP30L	10664	-18.33	4.39	2.94E-05	1427	0.028531	0.83 (0.76, 0.91)
cg17558817	2	106475496	NCK2	7293	-9.5	2.27	2.86E-05	1427	0.027891	0.91 (0.87, 0.95)
cg17651926	17	25805881	KSR1	6846	-23.6	5.66	3.02E-05	1428	0.028968	0.79 (0.71, 0.88)
cg17660709	2	74531615	SLC4A5	10536	-13.2	2.88	4.66E-06	1426	0.007092	0.88 (0.83, 0.93)
cg17879351	11	44092987	ACCS	5176	-20.08	3.99	4.70E-07	1428	0.001309	0.82 (0.76, 0.88)
cg17934955	15	80142016	MTHFS	47322	-25.14	5.21	1.39E-06	1428	0.002826	0.78 (0.7, 0.86)
cg17939602	5	40674971	PTGER4	-5060	-11.34	2.43	3.19E-06	1427	0.005431	0.89 (0.85, 0.94)
cg17941143	3	53513310	CACNA1D	-15765	-6.75	1.57	1.81E-05	1425	0.019908	0.93 (0.91, 0.96)
cg17946525	1	172425816	C1orf105	3784	-23.91	4.22	1.46E-08	1428	0.000118	0.79 (0.72, 0.86)
cg17971251	1	177907297	SEC16B	31752	-16.43	3.28	5.32E-07	1428	0.001435	0.85 (0.8, 0.9)
cg18254848	19	40227949	CLC	719	-20.45	4.81	2.11E-05	1428	0.022164	0.82 (0.74, 0.9)
cg18337287	19	930871	ARID3A	4835	-21.35	5.25	4.85E-05	1428	0.040199	0.81 (0.73, 0.9)
cg18367488	11	47937934	PTPRJ	-64175	-17.62	3.59	8.91E-07	1427	0.002091	0.84 (0.78, 0.9)
cg18368116	14	21436271	RNASE2	12642	-19.17	4.36	1.09E-05	1428	0.013375	0.83 (0.76, 0.9)
cg18455414	6	7043141	RREB1	-64688	-11.6	2.5	3.58E-06	1426	0.005817	0.89 (0.85, 0.94)
cg18455616	2	99124870	INPP4A	63550	-6.45	1.47	1.20E-05	1428	0.014486	0.94 (0.91, 0.96)
cg18666454	7	150651937	KCNH2	979	-15.09	3.21	2.56E-06	1427	0.004568	0.86 (0.81, 0.92)
cg18715410	10	12448959	CAMK1D	57418	-16.82	3.91	1.73E-05	1427	0.019262	0.85 (0.78, 0.91)
cg18783781	1	9599067	SLC25A33	-460	-16.26	3.32	9.74E-07	1428	0.002163	0.85 (0.8, 0.91)
cg18879389	21	43771120	TFF2	87	-23.36	5.21	7.27E-06	1428	0.009853	0.79 (0.71, 0.88)
cg19069027	15	40851643	CCDC32	5612	-10.24	2.27	6.57E-06	1426	0.00907	0.90 (0.86, 0.94)
cg19198938	3	188001192	LPP	58000	-15.95	3.8	2.66E-05	1428	0.02651	0.85 (0.79, 0.92)
cg19344749	3	13069838	IQSEC1	-41303	-9.96	2.13	3.00E-06	1424	0.005161	0.91 (0.87, 0.94)
cg19375767	1	27048589	ARID1A	26068	-16.71	2.95	1.50E-08	1428	0.000118	0.85 (0.8, 0.9)
cg19448292	20	35504064	TLDC2	-459	-13.93	2.95	2.30E-06	1428	0.004243	0.87 (0.82, 0.92)
cg19456763	17	179947	LOC100506388	-1048	-11.17	2.55	1.16E-05	1428	0.014107	0.89 (0.85, 0.94)
cg19582046	21	46506629	ADARB1	11664	-17.22	2.97	6.40E-09	1426	6.54E-05	0.84 (0.79, 0.89)
cg19686029	1	112045886	ADORA3	856	-28.73	5.72	5.13E-07	1425	0.001393	0.75 (0.67, 0.84)
cg19696679	19	7291221	INSR	3091	-34.33	6.78	4.07E-07	1428	0.001179	0.71 (0.62, 0.81)
cg19745810	13	111316234	CARS2	42292	-38.86	6.56	3.20E-09	1422	4.29E-05	0.68 (0.6, 0.77)
cg19787060	1	27241913	NR0B2	-1347	-13.39	2.82	1.98E-06	1427	0.003763	0.87 (0.83, 0.92)
cg19928703	13	30143971	SLC7A1	25853	-29.58	5.11	7.20E-09	1428	7.18E-05	0.74 (0.67, 0.82)
cg19968199	12	68056168	DYRK2	13657	-44.51	8.65	2.70E-07	1428	0.000875	0.64 (0.54, 0.76)

cg20072505	10	12456489	CAMK1D	64948	-15.44	3.73	3.53E-05	1428	0.032233	0.86 (0.8, 0.92)
cg20178107	7	41914145	INHBA	-171440	-21.67	4.03	7.58E-08	1428	0.000369	0.81 (0.74, 0.87)
cg20216313	8	142305640	SLC45A4	-40913	-3.77	0.91	3.21E-05	1426	0.030327	0.96 (0.95, 0.98)
cg20263733	3	130616293	ATP2C1	2860	-34.5	6.44	8.39E-08	1428	0.000391	0.71 (0.62, 0.8)
cg20267283	1	6645171	ZBTB48	5121	-17.27	3	8.55E-09	1426	7.76E-05	0.84 (0.79, 0.89)
cg20290167	17	81040724	METRNL	3158	-9.3	2.3	5.40E-05	1427	0.043054	0.91 (0.87, 0.95)
cg20493175	19	19599547	GATAD2A	23399	-9.68	2.24	1.61E-05	1427	0.018274	0.91 (0.87, 0.95)
cg20560376	12	6342778	CD9	33297	-34.55	5.28	6.03E-11	1427	3.79E-06	0.71 (0.64, 0.79)
cg20619340	2	38806109	HNRNPLL	24068	-19.23	4.75	5.18E-05	1428	0.042039	0.83 (0.75, 0.91)
cg20654602	1	87596049	LINC01140	602	-15.62	2.69	6.09E-09	1426	6.54E-05	0.86 (0.81, 0.9)
cg20673965	19	44220148	IRGC	-65	-11.28	2.39	2.32E-06	1425	0.00426	0.89 (0.85, 0.94)
cg20774312	6	167177613	RPS6KA2	98425	-13.15	3.21	4.19E-05	1422	0.03612	0.88 (0.82, 0.93)
cg20804243	3	171205319	TNIK	-27123	-16.79	3.33	4.56E-07	1428	0.001293	0.85 (0.79, 0.9)
cg20818756	12	8201975	FOXJ2	16617	-18.47	3.71	6.42E-07	1427	0.001645	0.83 (0.77, 0.89)
cg20840540	6	42363749	TRERF1	56039	-13.82	3.19	1.52E-05	1427	0.01752	0.87 (0.82, 0.93)
cg20885063	17	17939419	ATPAF2	3060	-22.35	4.49	6.53E-07	1427	0.001662	0.80 (0.73, 0.87)
cg20893283	20	36340388	CTNNBL1	18032	-16.03	3.24	7.25E-07	1426	0.001795	0.85 (0.8, 0.91)
cg20992317	12	64961489	RASSF3	-42803	-8.56	1.94	9.85E-06	1422	0.012384	0.92 (0.88, 0.95)
cg21259720	11	43779382	HSD17B12	77240	-34.35	6.53	1.41E-07	1426	0.000551	0.71 (0.62, 0.81)
cg21568193	1	173496518	PRDX6	50033	-18.95	4.28	9.38E-06	1427	0.011917	0.83 (0.76, 0.9)
cg21575634	12	131310417	STX2	13401	-21.04	4.94	2.05E-05	1425	0.021758	0.81 (0.74, 0.89)
cg21672758	2	48340131	FOXN2	-201663	-30.29	7.18	2.46E-05	1425	0.024881	0.74 (0.64, 0.85)
cg21723861	17	39686628	KRT19	-1988	-22.1	4.6	1.59E-06	1416	0.003146	0.80 (0.73, 0.88)
cg21867373	10	102277130	SEC31B	2464	-17.89	3.56	5.12E-07	1428	0.001393	0.84 (0.78, 0.9)
cg21931263	5	67715050	PIK3R1	126655	-10.35	2.51	3.77E-05	1428	0.0332	0.90 (0.86, 0.95)
cg22022320	9	32426874	ACO1	42274	-42.48	9.09	2.99E-06	1428	0.005155	0.65 (0.55, 0.78)
cg22059413	2	69831408	ANXA4	-39528	-14.71	3.56	3.57E-05	1427	0.032381	0.86 (0.81, 0.93)
cg22158603	16	387629	AXIN1	15046	-11.57	2.9	6.45E-05	1427	0.048582	0.89 (0.84, 0.94)
cg22252112	17	506008	VPS53	112087	-11.47	2.57	8.39E-06	1428	0.010971	0.89 (0.85, 0.94)
cg22503106	17	81040906	METRNL	3340	-19.55	3.35	5.20E-09	1414	5.90E-05	0.82 (0.77, 0.88)
cg22717723	2	32299042	SPAST	10363	-37.45	6.63	1.62E-08	1426	0.000121	0.69 (0.6, 0.78)
cg22816343	8	26243601	BNIP3L	3079	-28.07	5.32	1.33E-07	1428	0.000528	0.76 (0.68, 0.84)
cg22972893	11	112149745	LOC283140	8274	-20.01	3.9	2.88E-07	1428	0.000915	0.82 (0.76, 0.88)

cg22982094	2	121816646	TFCP2L1	226131	-21.4	3.8	1.73E-08	1426	0.000127	0.81 (0.75, 0.87)
cg23044178	11	12136405	MICAL2	4283	-28.71	5.25	4.46E-08	1428	0.000241	0.75 (0.68, 0.83)
cg23079735	16	195133	NPRL3	-6437	-16.66	3.19	1.83E-07	1428	0.000653	0.85 (0.8, 0.9)
cg23131680	6	25609068	SCGN	-43360	-22.97	4.95	3.53E-06	1428	0.005791	0.79 (0.72, 0.88)
cg23205629	8	33421410	RNF122	3235	-11.2	2.44	4.40E-06	1427	0.006734	0.89 (0.85, 0.94)
cg23414568	10	120495050	CACUL1	19707	-12.42	2.95	2.59E-05	1428	0.025939	0.88 (0.83, 0.94)
cg23434083	12	120970625	RNF10	-1506	-18.7	4.32	1.49E-05	1428	0.017248	0.83 (0.76, 0.9)
cg23464586	10	116447282	ABLIM1	-2869	-16.93	4.03	2.62E-05	1427	0.026144	0.84 (0.78, 0.91)
cg23472776	14	74532925	ALDH6A1	18270	-28.07	6.32	8.97E-06	1427	0.011508	0.76 (0.67, 0.85)
cg23475294	1	154581658	ADAR	-935	-19.31	3.81	3.95E-07	1428	0.001167	0.82 (0.77, 0.89)
cg23582054	3	3152201	IL5RA	-144	-10.57	2.1	5.01E-07	1428	0.001379	0.90 (0.86, 0.94)
cg23856600	5	10560140	ANKRD33B	-4294	-9.47	2.11	6.87E-06	1428	0.009373	0.91 (0.87, 0.95)
cg23875532	15	91136869	CRTC3	63752	-13.36	3.27	4.43E-05	1427	0.037634	0.87 (0.82, 0.93)
cg23904266	10	102276804	SEC31B	2790	-12.15	2.63	3.72E-06	1428	0.005949	0.89 (0.84, 0.93)
cg23911543	8	142238794	SLC45A4	-122	-17.64	3.29	8.37E-08	1428	0.000391	0.84 (0.79, 0.89)
cg23985372	2	33437478	LTBP1	77815	-9.13	2.23	4.22E-05	1428	0.036264	0.91 (0.87, 0.95)
cg24009118	11	65545808	AP5B1	2253	-20.28	4.67	1.40E-05	1427	0.016415	0.82 (0.75, 0.89)
cg24028828	12	56694932	CS	-758	-62.22	11.09	2.02E-08	1428	0.000143	0.54 (0.43, 0.67)
cg24113459	3	33114261	TMPPE	24031	-32.37	5.5	3.86E-09	1428	4.93E-05	0.72 (0.65, 0.81)
cg24304533	16	16143033	ABCC1	99600	-30.81	4.75	8.52E-11	1426	4.15E-06	0.73 (0.67, 0.81)
cg24317972	10	12371568	CAMK1D	-19973	-24.64	5.86	2.62E-05	1424	0.026144	0.78 (0.7, 0.88)
cg24358891	7	107876312	NRCAM	4301	-16.15	3.9	3.51E-05	1421	0.032194	0.85 (0.79, 0.92)
cg24368962	11	111570978	PPP2R1B	66190	-23.17	5.41	1.87E-05	1426	0.020376	0.79 (0.71, 0.88)
cg24447018	22	30612925	LIF	29914	-8.45	1.9	8.86E-06	1428	0.011385	0.92 (0.89, 0.95)
cg24491618	7	150649807	KCNH2	3109	-12.91	3.11	3.23E-05	1427	0.030481	0.88 (0.83, 0.93)
cg24517604	16	11709855	LITAF	-28534	-25.96	4	8.64E-11	1425	4.15E-06	0.77 (0.71, 0.83)
cg24629258	18	33046000	INO80C	31612	-27.59	6.9	6.41E-05	1427	0.048446	0.76 (0.66, 0.87)
cg24818060	9	101595573	GALNT12	25593	-42.7	8.93	1.72E-06	1428	0.003371	0.65 (0.55, 0.78)
cg24829718	14	76337892	TGFB3	110472	-21.98	5.12	1.74E-05	1427	0.019347	0.80 (0.73, 0.89)
cg25003924	15	52861754	ARPP19	-112	-7.04	1.73	4.72E-05	1427	0.039482	0.93 (0.9, 0.96)
cg25087851	11	60623918	PTGDR2	-475	-11.94	2.3	2.09E-07	1425	0.000715	0.89 (0.85, 0.93)
cg25221180	9	130217517	LRSAM1	2984	-47.44	8.52	2.59E-08	1420	0.000172	0.62 (0.53, 0.74)
cg25270424	7	24965657	OSBPL3	-33418	-21.85	5.36	4.63E-05	1426	0.039008	0.80 (0.72, 0.89)

cg25308597	3	3151679	IL5RA	378	-4.02	0.99	4.81E-05	1426	0.039989	0.96 (0.94, 0.98)
cg25368824	5	132009352	IL4	-325	-11.04	2.4	4.09E-06	1427	0.006342	0.90 (0.85, 0.94)
cg25466522	15	81623226	TMC3-AS1	6553	-35.21	5.24	1.75E-11	1426	2.04E-06	0.70 (0.63, 0.78)
cg25799589	4	146800380	ZNF827	59731	-30.91	5.99	2.45E-07	1426	0.000817	0.73 (0.65, 0.83)
cg25939647	15	40173065	GPR176	40027	-7.39	1.83	5.41E-05	1423	0.043092	0.93 (0.9, 0.96)
cg25984364	12	25103501	BCAT1	-1109	-17.89	4.43	5.48E-05	1428	0.043522	0.84 (0.77, 0.91)
cg26024852	15	44070538	ELL3	-1037	-33.11	8.14	4.79E-05	1426	0.039904	0.72 (0.61, 0.84)
cg26103369	14	75153307	AREL1	26499	-41.72	8.52	9.77E-07	1428	0.002164	0.66 (0.56, 0.78)
cg26150475	9	130859520	SLC25A25	-1240	-40.2	7.72	1.88E-07	1426	0.000665	0.67 (0.58, 0.78)
cg26252077	1	61607055	NFIA	59076	-13.5	2.77	1.12E-06	1423	0.00239	0.87 (0.83, 0.92)
cg26365969	7	50626298	DDC	2469	-13.28	3.02	1.14E-05	1427	0.013947	0.88 (0.83, 0.93)
cg26396322	3	33112660	TMPPE	25632	-32.73	4.67	2.32E-12	1428	3.79E-07	0.72 (0.66, 0.79)
cg26472183	8	126445744	TRIB1	1294	-47.48	7.89	1.77E-09	1398	2.68E-05	0.62 (0.53, 0.73)
cg26592446	1	100234313	FRRS1	-2965	-17.77	4.39	5.10E-05	1428	0.041679	0.84 (0.77, 0.91)
cg26749306	17	81043782	METRNL	6216	-25.89	4.91	1.35E-07	1427	0.00053	0.77 (0.7, 0.85)
cg26787239	5	132008525	IL4	-1152	-27.56	4.75	6.32E-09	1428	6.54E-05	0.76 (0.69, 0.83)
cg26817086	5	173285792	CPEB4	-29538	-10.12	2.06	8.50E-07	1428	0.002031	0.90 (0.87, 0.94)
cg26819549	1	6645165	ZBTB48	5115	-10.09	2.26	7.85E-06	1425	0.010431	0.90 (0.86, 0.94)
cg26955963	2	8466005	LINC00299	2543	-7.71	1.87	3.68E-05	1428	0.032885	0.93 (0.89, 0.96)
cg26964704	12	125589647	AACS	39735	-27.82	4.68	2.68E-09	1428	3.71E-05	0.76 (0.69, 0.83)
cg27028878	20	24630818	SYNDIG1	180377	-8.61	1.85	3.17E-06	1427	0.005408	0.92 (0.88, 0.95)
cg27094581	11	68035071	C11orf24	4397	-14.44	3.56	4.91E-05	1428	0.040532	0.87 (0.81, 0.93)
cg27131881	22	45820349	RIBC2	10778	-9.46	2.13	8.99E-06	1428	0.011516	0.91 (0.87, 0.95)
cg27308490	5	134818031	TIFAB	-29943	-10.85	2.53	1.85E-05	1426	0.020239	0.90 (0.85, 0.94)
cg27508506	6	36108416	MAPK13	10156	-47.57	8.96	1.10E-07	1428	0.000469	0.62 (0.52, 0.74)
cg27550672	18	8720395	MTCL1	3027	-38.46	5.92	8.37E-11	1428	4.15E-06	0.68 (0.61, 0.76)

[1] Genome build GRCh37/hg19

[2] Model adjusted for age, sex, body mass index, smoking status, packyears, state, fall enrollment, and four cell types (monocyte, lymphocyte, neutrophil, and eosinophil)