
Epigenome-wide Association Study of Body Mass Index in African American populations from InterGEN and GENOA

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Study Importance:

What is already known?

- Despite existing research on the effects of obesity on DNA methylation among some populations, there is an immediate need for more research among Black/AA women.
- Black/AA populations have a younger age of mortality and onset of cardiometabolic disorders than other ethnic groups.
- The incidence and prevalence of obesity has grown to pandemic proportions, with approximately 1.5 billion people worldwide exceeding obese or overweight criteria.

What does this study add?

- 25 CpG sites were found to be hypomethylated with higher BMI and 3 were found hypermethylated.
- Of the 28 CpG sites from our discovery cohort of all Black/AA women, we identified 12 novel CpG sites not previously associated with BMI in previous BMI analyses and replicated among a second all Black/AA cohort.
- Some of the sites identified may be unique to Black/AA populations, specifically women.

How might these results change the direction of research or the focus of clinical practice?

- Epigenomic studies can be utilized to develop individual healthcare plans and identify needs for the individual and community.

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Abstract:

Background Obesity is a significant public health concern across the globe. Research investigating epigenetic mechanisms related to obesity and obesity-associated conditions have identified differences that may contribute to cellular dysregulation that accelerates the development of disease. However, few studies include Black/African American women, who experience the highest incidence of obesity and early onset of cardiometabolic disorders.

Methods We examined the association of body mass index (BMI) with epigenome-wide DNA methylation (DNAm) using the 850K EPIC Illumina Beadchip in two Black/African American populations [Intergenerational Impact of Genetic and Psychological Factors on Blood Pressure (InterGEN), $n = 239$; and The Genetic Epidemiology Network of Arteriopathy (GENOA) study, $n = 961$] using linear mixed-effects regression models adjusted for batch effects, cell-type heterogeneity, population stratification, and confounding factors.

Results Cross-sectional analysis of the InterGEN discovery cohort identified 28 DNAm sites significantly associated with BMI, 24 of which had not been previously reported. Of these, 17 were replicated using the GENOA study. We also conducted a meta-analysis, including both the InterGEN and GENOA cohorts, and identified 658 DNAm sites associated with BMI with false discovery rate less than 0.05. In a meta-analysis of Black/African American women, we identified 628 DNAm sites significantly associated with BMI. Using a more stringent significance threshold hold of Bonferroni correct p -value of 0.05, we identify 65 and 61 DNAm sites associated with BMI from the combined sex, and female-only meta-analysis, respectively.

Conclusion Our study suggests that BMI is associated with differences in DNA methylation among women that can be identified with DNA extracted from salivary (discovery) and peripheral blood (replication) samples among Black/African American populations across 2 cohorts.

Keywords: DNA methylation, obesity, BMI, African American

1. Introduction

The incidence and prevalence of obesity has grown to pandemic proportions, with approximately 1.5 billion people worldwide exceeding obese or overweight criteria.¹⁻³ By 2030, obese or overweight adults are expected to account for approximately 58% of the world's population.⁴ Body Mass Index (BMI) is an important quantitative measure of adiposity.^{1, 5-9} Lifestyle, behavior, and environmental influences on the development of obesity include over consumption of calories, lack of physical activity, medications, and quality of food available.^{5, 8} Health consequences due to obesity include hypertension, dyslipidemia, type 2 diabetes, coronary heart disease, stroke, and mortality.^{5, 7, 8} However, beyond external lifestyle and environmental factors, genome-wide association studies (GWAS) have shown significant association of genes with adiposity, particularly among minority populations.^{4, 7, 10} However, literature is lacking on epigenome wide association studies (EWAS) among Black/African American (AA) populations, who are disproportionately affected by obesity.

Black/AA populations have a younger age of mortality and onset of cardiometabolic disorders than other ethnic groups.^{11, 12} The age of mortality and risk for cardiometabolic disorders can be strongly influenced by environmental factors.^{11, 12} Some of these factors include discrimination and socioeconomic status (SES), which can contribute to poor mental and physical health.^{11, 13} Over time, environmental factors such as experiencing discrimination can contribute to differences in DNA methylation patterns.¹⁴ DNA methylation is an epigenetic mark that is involved in the regulation of gene expression.¹⁵ Environmental (i.e. climate) and lifestyle factors (i.e. diet/obesity), as well as time (i.e. aging), are some of the known influences on DNA methylation patterns and gene expression.^{4, 5, 10, 15} Obesity has been shown to be associated with DNA methylation, particularly at genes involved in physiologic pathways such as inflammation, which can trigger damaging immune and oxidative stress responses.^{6, 16} Some changes in DNA methylation have been shown to causally influence obesity, while others are more likely to be a consequence, or biomarker, of the disease process.^{1, 17, 18} However, alterations in DNA methylation resulting from various exposures may be reversible and amenable to interventions.¹⁰

Despite existing research on the effects of obesity on DNA methylation among some populations, there is an immediate need for more research among Black/AA women.^{7, 16} Ancestry and sex are two known influences of obesity related changes in DNA methylation.¹⁷ Previous EWAS studies focused on evaluating DNA methylation related to BMI and obesity have been conducted primarily among European and South Asian populations, with limited representation

of populations with African ancestry.^{1,7,16-20} Because women tend to have a higher BMI than men, and Black/AA women have among the highest incidence of obesity,⁵ it is important to better understand the influence of obesity on features that can alter physiology, such as DNA methylation, in order to better address this health disparity and attenuate the development of cardiometabolic disorders. The purpose of this study is to conduct an EWAS among Black/AA women in the well characterized InterGEN cohort and replicate in the GENOA cohort to identify differences in DNA methylation associated with obesity.

2. Materials and Methods

Discovery Cohort

The InterGEN study is a longitudinal cohort study in Connecticut that examined the effects of genetic, epigenetic, and psychological factors on blood pressure in mother/child dyads. Recruitment began in April 2015 and follow-up completed in 2019. Eligibility criteria included: mothers (≥ 21 years old) who self-identify as Black/AA, speak English, and have no mental illness that could interfere with psychological measurements. Women enrolled with a biological child (3-5 years old) who lived with her most of the time and could provide a saliva sample. More information on the cohort and psychological measures can be found in previous reports.^{9,21,35,42,43} During the baseline visit, study personnel collected clinical measurements of blood pressure, height, weight, percent body fat, percent body water (mothers only) and saliva for DNA analysis from both mother and child. Demographic information, health history and psychological measures (including parenting, experiences of perceived racism and discrimination, and depression) were collected through mother's report using Audio Computer-Assisted Self-Interview (ACASI) software. The present study only included InterGEN mothers (Table 1). Yale University and Columbia University's Institutional Review Board (IRB) approved the study procedures.

DNA Methylation

Researchers collected saliva samples for DNA using the Oragene (OG)-500 format tubes,^{3,43,45} which required participants to spit into the tube until the contents reached the fill line per collection instructions (2 mL). Detailed DNA collection and analysis procedures have been described elsewhere.^{42,45} Samples were transported from the field to the research laboratory where they were refrigerated at 4°C until DNA extraction and analysis were completed. Standard protocol for DNA extraction and purification was conducted as indicated in the standard operating procedures guidelines using ReliaPrep kits, and the Illumina Infinium Methylation EPIC (850K) BeadChip was used for epigenome-wide DNAm measurement. We used a quantile normalization approach in the R package "*minfi*" for processing EPIC data to correct for methylation signals, and to generate adjusted β -values for the associated analyses⁴⁶. All individual samples passed laboratory-based quality-control procedures (missing rate $< 10\%$ and no sex mismatch). After merging with phenotypic data at baseline visit, 239 participants were included in the EWAS of BMI. CpG sites were excluded if they had a missing rate greater than 10% ($n = 3,264$), overlapped with SNPs ($n = 87,074$), or were listed in the recent Illumina product quality [notice](#). Quality control procedures and all analyses were uniformly performed among autosomal sites. A total of 756,544 autosomal CpG sites were included in the association analyses as previously described.^{42,47} The CpG sites measured by the EPIC BeadChip were mapped to Genome Research Consortium human build 37 (GRCh37).

Replication Study

Replication of these findings was conducting using a sample of 961 Black/AA participants from the GENOA study also using the Illumina Infinium Methylation EPIC (850K) BeadChip. In addition to all GENOA participants, replication was also conducted in women only ($N=685$, see Figures 1-4, table 2 and supplementary tables 1).

GENOA sample: The Genetic Epidemiology Network of Arteriopathy (GENOA) is a multi-phase, community-based, prospective study of sibships with two or more siblings diagnosed with primary hypertension before the age of 60. Participants self-identified as Black/AA, all siblings with a sibship were invited to participate regardless of hypertension status, and recruitment took place in Jackson, Mississippi. A total of $N=1,854$ Black/AA participants were recruited in Phase I (1995-2000) from 683 sibships, and $N=1,482$ returned in Phase II (2000-2005). Most participants (71%) in GENOA were women. In each phase, demographics, medical history, clinical characteristics, lifestyle factors, and fasting blood samples were collected.^{42,48} Sample characteristics for both InterGEN and GENOA can be found in Table 1. In Phase I, DNA methylation was measured from peripheral blood samples, and BMI and smoking status was also assessed. Smoking status was assessed through questions regarding whether the individual smokes, frequency and type of cigarettes used (i.e. filtered, unfiltered, e-cigarettes, other). Institutional Review Board approval was received for the GENOA study protocol through the University of Mississippi Medical Center and the University of Michigan IRBs.

Genomic DNA was extracted from stored peripheral blood leukocytes that was collected at Phase 1 (N=1106) or Phase 2 (N=304) using AutoGen FlexStar (AutoGen, Holliston, MA). Bisulfite conversion was performed with the EZ DNA Methylation Kit (Zymo Research, Irvine, CA), and methylation was assessed using the Illumina EPIC (850K) BeadChip. After obtaining the raw intensity data, the shinyMethyl R package⁴⁸ was used to generate the density plot to identify sex mismatch or sample outliers.⁴¹ Sample identity was further checked using 59 SNP probes implemented in the EPIC chip, and mismatched samples were removed. Samples with incomplete bisulfite conversion identified using the QCinfo() function in the ENmix R package⁴⁹ were also removed. The *minfi* R package was used to perform background correction and normalization.^{41, 50} The regression on correlated probes (RCP) method⁵¹ was used to adjust probe-type bias. Principal Variance Component Analysis (PVCA)⁵² was used to quantify the corresponding effect of each batch factor (sample plate, chip, and row), and ComBat⁵³ was used to adjust for batch effects. The effects of GENOA Phase, age and gender were preserved when adjusting for batch effects. Sample plate, chip and row were adjusted for sequentially, until the weighted proportion of variation explained by any batch factor in the first PCs (containing 60% of the variation) in the methylation was below 5%. Detection p-value for each sample at each probe was obtained, and individual probes with detection p-value $<10^{-16}$ were considered successfully detected. Samples and probes with detection rate $<10\%$ were removed. After merging with phenotypic data, 857,121 CpG sites for 961 Black/AA participants were used for this analysis. Cell counts were estimated and adjusted using the Houseman method.^{23, 41}

Statistical Analysis

We conducted an EWAS of BMI among women enrolled in the InterGEN study. DNA methylation beta-value was modeled as the dependent variable using linear mixed effects model. Age and smoking status were controlled for as potential confounders. To control for potential heterogeneity in cell proportions from saliva, we implemented a reference-free deconvolution method to estimate putative cell type proportions and included them as covariates.^{41, 46} We also adjusted for batch effects as random intercepts in the analysis. False discovery rate (FDR) was used to correct for multiple comparisons. We applied the Benjamini and Hochberg method to calculate the FDR-corrected p-value.^{41, 52} CpG sites with FDR-corrected p-value < 0.05 were considered as statistically significant in the discovery EWAS to pursue replication. In GENOA, linear mixed effect models were implemented to assess the association between DNAm and BMI adjusting for age, sex, smoking status, cell type proportions and the top 10 genetic PCs. Family ID was included as a random effect to account for relatedness. We performed inverse-variance weighted fixed-effects meta-analysis among DNAm sites available from both InterGEN and GENOA studies using a computationally efficient software METAL.²³ We reported the epigenome-wide significant (Bonferroni p-value <0.05 , nominal p-value $< 6.50 \times 10^{-8}$) DNAm sites considering a total of 749,801 tests and their heterogeneity between two Black/AA EWAS. All statistical analyses were performed in the R statistical environment version 3.4.1 (<http://www.r-project.org/>). We conducted pathway enrichment analysis based on annotated genes from the top DNAm sites from meta-analysis results. The analysis was completed using the Analysis35R package missMethyl which correct for the distribution of the DNAm sites on the array.⁵

3. Results

InterGEN EWAS

The descriptive statistics can be found in Table 1. In the discovery EWAS using the InterGEN sample, 28 CpG sites were significantly associated with BMI after adjusting for age and smoking status (FDR corrected $p < 0.05$). (Table 2, Figures 1&2) These CpG sites were mapped to the *SOCS3*, *LOC100996291*, *RALGDS*, *PSKH1*, *IWS1*, *SH3RF2*, *RNF144B*, *FGD2*, *BMP6*, *PLCH1*, *FAM47E*, *LOC101928674*, *TSLP*, *ABCC1*, *SH3BP1*, and *LIMD1* genes. 25 CpG sites were found to be hypomethylated with higher BMI and 3 were found hypermethylated (Table 2). Among the 28 significant CpGs, we identified gap signals of cg19679801 (3.64% and 96.36% in groups 1 and 2) using GapHunter (R package minfi) after excluding outlier signals with $<1\%$ of study samples. The association of cg19679801 might be affected by an underlying genetic effect with low minor allele frequency. GapHunter was run on the GENOA sample and there was no signal gap.

GENOA Replication

A total of 17 out of 28 CpG sites in the InterGEN EWAS replicated in the GENOA full sample EWAS with consistent directionality and statistical significance after Bonferroni correction ($p < 0.0018 = 0.05/28$), (Table 2). 12 CpG sites were novel compared to the previous reports,^{1, 16, 17} of which 11 were new to the Illumina arrays (that is, they were not available on earlier arrays including the 450K). Genes mapped by these newly identified EPIC-850K array specific CpG sites include *SOCS3*, *RALGDS*, *PSKH1*, *FGD2*, *BMP6*, *TSLP* (Table 2).

Meta-analysis

To maximize the statistical power, we also conducted a fixed-effects meta-analysis combining EWAS results from the InterGen and GENOA cohort studies (Figure 3). Using a stringent significance threshold of Bonferroni corrected $p < 0.05$ to reduce false positive rate, sixty-five CpG sites were significantly associated with BMI (Table S2S). Among those, 48 were not significant in the discovery analysis, mapping to genes including *VASN*, *CPT1A*, *MAFG*, *SNTB1* (Table S2S). The beta coefficients among 65 genome-wide significant DNA methylation (DNAm) sites between InterGen and GENOA were highly correlated with correlation coefficient of 0.93 (p -value $< 2.2 \times 10^{-16}$, Figure 3C). We also conducted a fixed-effect meta-analysis combining female-only EWAS results from the two studies ($n=239$ for InterGen and $n=685$ for GENOA, Figure 4). 61 CpG sites were significantly associated with BMI (Bonferroni corrected meta-analysis $p < 0.05$, Supplementary Tables 1 & 2). Similarly, the beta coefficients among 61 genome-wide significant DNAm sites between InterGen and GENOA were highly correlated with correlation coefficient of 0.93 (p -value $< 2.2 \times 10^{-16}$, Figure 4C). Of those CpG sites in the meta-analysis, most BMI-associated DNAm sites were consistent between two meta-analyses. However, 12 DNAm sites were only genome-wide significant (p -value $< 6.50 \times 10^{-8}$) in the female-only meta-analysis, but not genome-wide significant in the meta-analysis including both men and women (Table S2). Because some DNAm sites are correlated, the Bonferroni correction for multiple testing can increase the false negative rate. Thus, we also reported BMI-associated DNAm sites from the sex-combined meta-analysis (658 sites, Table S3) and the female only meta-analysis (626 sites, Table S4).

Pathway Enrichment Analysis

We tested pathway enrichment using two sets of top associations, 65 Bonferroni significant CpG sites (42 unique genes) and 154 CpG sites with nominal p -value $< 10^{-6}$ (124 unique genes). After multiple testing correction using FDR 0.05, no pathway was significantly enriched among BMI-associated CpG sites.

3. Discussion

We completed cross-sectional epigenome-wide analysis of BMI and DNA methylation from 2 cohorts of Black/AA individuals in the United States. Of the 28 CpG sites from our discovery cohort of all Black/AA women, we identified 12 novel CpG sites not previously associated with BMI in previous BMI analyses and replicated among a second all Black/AA cohort.^{1, 16, 17} Although other EWAS's were conducted, they were primarily white cohorts and did not conduct any stratified analyses.^{1, 10, 19-10, 21} Our findings are notable in that we were able to identify differences in DNA methylation associated with BMI in saliva samples and replicate our findings in a separate cohort using peripheral blood samples. Most previous work has conducted EWAS studies utilizing peripheral blood samples, and our study supports that less invasive saliva samples can be used to evaluate or replicate previously identified differences in DNA methylation associated with BMI. The New England Family Study used adipose tissue, rather than blood, to examine sex-specific methylation associated with obesity.²² A majority of CpG sites that were associated with BMI were hypomethylated and the direction of change was consistent across both cohorts using different tissue types. Results from our meta-analysis identified 17 CpG sites previously reported in BMI EWAS studies. We identified DNA methylation differences within 19 genes of which previous BMI EWAS observed significant DNA methylation differences at different CpG sites.

Of the 12 novel CpG sites from our discovery and replication cohorts, 2 CpG sites (cg110473253, cg13343932) are located in the cytokine signaling 3 (*SOCS3*) gene. Two additional CpG sites (cg18181703, cg09349128) were also significant in *SOCS3* in our meta-analysis, and differential methylation at these sites has been associated with BMI in previous EWAS studies.^{1, 17, 23-25} Hypomethylation of the *SOCS3* mapped CpG sites were consistently found for all studies. In addition to evaluating the relationship between BMI and DNA methylation, Li and colleagues²³ evaluated the change in DNA methylation over time related to BMI. When they evaluated the change in BMI and DNA methylation across identical twin pairs, the association was only significant when BMI was used as the predictor and DNA methylation as the outcome variable. Further, their results suggest that hypomethylation at the *SOCS3* site (cg18181703) is the result of increased BMI. In murine models, expression of *SOCS3* improves leptin and insulin sensitivity.²⁶ Ali and colleagues also observed hypomethylation at *SOCS3* cg18181703 was associated with increased BMI, waist to height ratio, triglycerides, and metabolic syndrome.²⁷ Interestingly, in multivariate analysis, Chamber et al noted that DNA methylation differences at the *SOCS3* site was not significantly associated with type 2 diabetes after adjusting for BMI and suggests that DNA methylation at these sites may serve as a biomarker for insulin resistance and risk for metabolic disease.²¹ Therefore, loss of methylation across *SOCS3* could contribute to the development of obesity induced metabolic syndrome and type 2 diabetes if associated with decreased gene expression.

A previous study of Norwegian lean and obese young women ($N=120$, mean age 27.2), identified 10 CpG sites across 8 genes associated with obesity (appendix- table S5).²⁵ We identified significantly different methylation at CpG sites in 3 of the same genes in our discovery cohort (*SOCS3*, *SBNO2*, and *FGD2*) and 3 CpG sites located in the gene bodies of *SOCS3* (cg18181703) and *SBNO2* (cg12170787, cg18608055). Similar to Kvaløy and colleagues, we observed

that more differentially methylated sites were associated with hypomethylation versus hypermethylation²⁶⁻²⁹. Many of the CpGs identified in Kvaløy's study were also associated with serum C-reactive protein (CRP) levels²⁹. Among sites identified in our meta-analysis, 5 of the CpG sites were consistent with differential DNA methylation among Black/AA CRP-EWAS results with consistent directionality [hypomethylation: *SNOB2* (cg18608055), *SOCS3* (cg18181703), *PIK3IP1* (cg08548559), *GPRIN3* (cg02734358), and hypermethylation: *MYO5C* (cg06192883)].²⁹ Some of the sites in the Ligthart study [*SNOB2* (cg18608055), *SOCS3* (cg18181703), *MYO5C* (cg06192883)] were also associated with other cardiometabolic traits, including total cholesterol, incidence of coronary heart disease, triglycerides, and fasting glucose and insulin levels. Although this study was not designed to assess these long-term outcomes, replication of these sites suggests that differential DNA methylation associated with BMI can be detected via saliva samples of women prior to the development of other cardiometabolic complications. Further work in this area could illuminate whether differential DNA methylation at these sites could serve as a biomarker for increased risk of developing obesity-induced cardiometabolic disorders.

A large proportion of the GENOA sample had hypertension, which may influence methylation.²⁸ None of the CpGs identified in the InterGEN discovery cohort were significantly associated with systolic or diastolic blood pressure (BP) in the largest EWAS of BP to date.⁹ However, one CpG site that was identified only in the InterGEN/GENOA meta-analysis, cg00574958, was also identified in the BP EWAS.^{9, 28} Differential DNA methylation has consistently been reported in cg00574958 carnitine palmitoyltransferase 1A (*CPT1A*) in EWAS studies for BMI and other cardiometabolic disorders.^{1, 17, 28-33} Although we did not observe significant differences in cg00574958 of *CPT1A* in our discovery cohort, we did observe significant hypomethylation at this site in our meta-analysis and in the GENOA cohort. The site in the InterGEN cohort was directionally congruent, but did not reach statistical significance after multiple corrections. Differences in *CPT1A* methylation are likely to influence biosynthesis of cholesterol and triglyceride metabolism¹⁷ and may be moderated by dietary intake of fats and carbohydrates.³¹ Lai and colleagues determined that *CPT1A* methylation is induced by carbohydrate and reduced by fat.³¹ Although the mechanism is unknown, they hypothesize that methylation at *CPT1A* could mediate the influence of fat intake on BMI and increase risk of developing cardiometabolic disease.

To better characterize the function of the CpGs identified in the InterGEN study and the meta-analysis, (Table 2, Supplemental Tables 1 and 2), we looked them up in databases that report associations between CpGs and transcripts of nearby genes (i.e., identify methylation sites associated with transcript expression, or cis-eQTM). We considered a CpG and a transcript to be associated using the significance criteria reported in the original publication for each database.³⁴⁻³⁶ In monocytes from the Multi-Ethnic Sample of Atherosclerosis (MESA, n=1264), the following pairs of CpGs and transcripts were associated (FDR<0.001): cg12367539 with *HNRNPH1* (p=4.85e-07), cg21650866 with *PTP4A3* (p=8.84e-08), and cg00926657 with *BAIAP2* (p=2.72e-06). In whole blood from the Framingham Heart Study (FHS, N=4170), following pairs of CpGs and transcripts were associated (FDR<0.05): cg12367539 with *RUFY1* (p=1.38e-14), cg00574958 with *CPT1A* (p=5.89e-26), cg08548559 with *PISD* (2.51e-21), cg17901584 with *DHCR24* (3.98e-18), and cg21650866 with *PTP4A3* (p=6.76e-09).³⁴⁻³⁶ In peripheral blood mononuclear cells from the iMETHYL database, the following pairs of CpGs and transcripts were associated (FDR<0.05): cg17901584 with *DHCR24* (p=1.027e-13) and *RP11-67L3* (p=0.0058), cg07458272 with *KIAA0355* (p=0.0054), and cg09349128 with *ALG12* (p=0.0064).³⁴⁻³⁶ Methylation at these CpGs decreased gene expression for all associations noted, with the exception of cg07458272 with *KIAA0355* and cg09349128 with *ALG12*.³⁴⁻³⁶ The following significant cpG sites and associated genes from MESA or FHS noted above were also replicated in the InterGEN and GENOA analyses for this study (cg12367539 with *HNRNPH1*, cg12367539 with *RUFY1*, cg09349128 with *ALG12*) and can be found in table 2 with additional data in Supplemental Tables 1A and 2A).

The potential for mediation and/or pleiotropic effects of BMI-associated DNA methylation differences with other BMI related traits have been reported across the spectrum. For example, many of the previous works cited here have found differential DNA methylation associations with other traits, including *SOCS3* with type 2 diabetes,^{27, 33} *CPT1A* with type 2 diabetes²¹ and lipid profiles,^{37, 38} and *ABCG1* with blood pressure.³⁹ However, the fact that many of these CpG sites have replicated specifically for BMI across multiple studies with different cardiometabolic phenotypes, populations, and sample characteristics such as sex suggests a consistent association signal with BMI. Additional evidence is provided by the difference between the InterGEN and GENOA cohort tissue types (saliva vs blood), age range, sex, and geographic locations with replication remaining significant for many CpG sites.

We note that this study was unable to determine whether the DNA methylation changes associated with BMI are causal or a consequence of BMI. Previous studies have suggested that, for the most part, associated tend to follow BMI changes, and are thus methylation differences may be biomarkers of adiposity.¹ Previous studies that included Mendelian randomization or mediation analysis suggest that many of the observed epigenetic changes associated with BMI may also be precursors to the development of cardiometabolic traits that are associated with differences at these loci.^{1, 17, 23, 25, 33, 40} Future work investigating mechanistic underpinnings of DNA methylation conversion at these sites could lead to novel targets for preventative measure and interventions to reduce and/or prevent the development of BMI-associated cardiometabolic disease. Research increasingly illustrates the potential influence of sex on the association of

SES and obesity, while education was only a significant (negative) factor among women. Ultimately, recent findings demonstrate that epigenetic mediation pathways linking SES to obesity are stronger for women.^{22, 41}

In conclusion, we were able to identify differential DNA methylation at a number of loci, some within genes that have previously been associated with obesity and cardiometabolic disorders. Some of the sites identified may be unique to Black/AA populations, specifically women. Given our results, it is notable that considering sex differences and diverse racial/ethnic groups can improve EWAS discovery. Further replication studies among larger cohorts of Black/AA populations and women (as the results were significantly replicated in women only, but not men and women in GEONA) will help identify the generalizability of these results and whether they represent a consistent epigenetic signature associated with BMI.

Strengths and Limitations

This study included data from two well established and well characterized Black/AA study cohorts. The InterGEN study included healthy Black/AA women and children, and collected weight and height for BMI calculation, % body fat, and % body water (mother only) at 4 time points. Findings from the study were significantly replicated with the GENOA dataset. Study samples were de-identified and replication was conducted to prevent bias. De-identification ensures the amenity between those who provided the samples and those conducting the data analyses. Therefore, assumptions or biases amongst participants will not impact the analyses process. The InterGEN and GENOA study protocols established methods that ensured rigor in recruitment, data collection, and statistical analyses. Rigor for the studies were enhanced through ongoing training and supervision of research staff and use of robust and reproducible methods that have been published. For instance, all research staff received intensive initial and ongoing training in data collection and in distress protocols. We enhanced reproducibility in several ways: 1) published 2 methods papers (cited previously), 2) made study data available on DbGaP, 3) and disseminating findings through more 30 publications and publicly via our study website.

The focus of this paper was on BMI and not other potential comorbidities. The snapshot that our results give us provide both valuable information for methodologies that could be applied to other at-risk populations. The analysis methods outlined here may have utility for future studies evaluating epigenetic risks related to cardiometabolic outcomes. Another limitation of the study is that we did not evaluate any downstream protein products that may result from DNAm sites identified as significant. Future studies we have planned may include other methods such as metabolomics and nutritional data to obtain a more complete picture of the participants' environment and all us to determine how DNAm may influence physiology. Despite higher incidence of obesity and cardiometabolic disorders, Black/AA women have been underrepresented in research studies focused on EWAS of BMI. Including minority populations in epigenomic studies is important and can be utilized to develop individual healthcare plans and identify needs for the individual and community. The InterGEN and GENOA cohort studies were pre-existing datasets that did not include data on lifestyle choices, dietary intake, nutritional habits, and physical activity. Therefore, this information could not be assessed in the analysis.⁷

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Data Availability Statement: InterGEN genotype and phenotype data are available through the Database of Genotypes and Phenotypes (dbGaP accession number phs001792.v1.p1). DNA methylation data are available with a Data Use Agreement upon reasonable request to the InterGEN study investigators, J.Y. Taylor (jyt2116@cumc.columbia.edu) and Y.V. Sun (yan.v.sun@emory.edu). GENOA genotype and phenotype data are available through the Database of Genotypes and Phenotypes (dbGaP accession number phs001238.v2.p1). Methylation data is from the Gene Expression Omnibus (GEO): GSE157131. Due to IRB restriction, mapping of the sample IDs between genotype data (dbGaP) and DNA methylation data (GEO) cannot be provided publicly but is available upon written request to the study investigators, J. Smith (smjenn@umich.edu) and S. Kardia (skardia@umich.edu).

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Table 1. Participant characteristics, InterGEN study (n=239) and GENOA study (N=961).

	InterGEN Women (N=239)	GENOA	
		Total Sample (N=961)	Women (N=685)
Mean Age in years (SD)**	31.3 (5.8)	57.5 (10.3)	57.1 (10.4)
Education, N (%) **			
High school or less	100 (41.8)	587 (61.1)	421 (65.5)
Some college or Associates degree	105 (44)	157 (16.3)	111 (16.2)
Bachelor's degree or higher	34 (14.2)	217 (22.6)	153 (22.3)
BMI Category, N (%) **			
Underweight (<18.5 kg/m ²)	13 (5.4)	4 (0.4)	3 (0.4)
Normal (18.5-24.9 kg/m ²)	58 (24.3)	140 (14.6)	79 (11.5)
Overweight (25-29.9 kg/m ²)	59 (24.7)	319 (33.2)	197 (28.8)
Obese (≥30 kg/m ²)	109 (45.6)	498 (51.8)	406 (59.3)
Mean BMI kg/m² (SD)*	29.7 (8.3)	31.3 (6.5)	32.3 (6.8)
Current Smoker, N (%) *			
Yes	52 (21.8)	161 (16.8)	92 (13.4)
No	187 (78.2)	800 (83.2)	593 (86.6)

Note. Participants were given the option not to respond to any of the questions, so all number may not add up to total N; *: p-value<0.01; **: p-value<0.001 from either t-test for continuous variables or chi-squared test for categorical variables.

Table 2. Discovery of 28 Epigenome-wide Significant Associations in InterGEN (FDR-q < 0.05), with Replication in GENOA Full Sample and Females Only.

CpG	CHR	BP	Gene	Genomic Region	Relation to UCSC CpG Island	InterGEN (Discovery, n = 239)			GENOA (Replication, n = 961)			GENOA (Replication, Female Only, n = 685)		
						Beta	SE	P	Beta	SE	P	Beta	SE	P
cg18181703	17	76354621	<i>SOCS3</i>	Body	N Shore	-0.28	3.58E-02	1.02E-12	-1.60E-03	2.91E-04	5.13E-08	-0.0016	3.07E-04	1.85E-07
cg11047325	17	76354934	<i>SOCS3</i>	Body	Island	-0.50	6.49E-02	2.03E-12	-2.28E-03	4.75E-04	1.82E-06	-0.0024	5.13E-04	2.37E-06
cg03067296	17	76274577	<i>LOC100996291</i>	TSS200		-0.27	3.59E-02	7.99E-12	-1.54E-03	2.24E-04	1.15E-11	-0.0016	2.46E-04	5.60E-11
cg13343932	17	76355061	<i>SOCS3</i>	Body	Island	-0.41	5.90E-02	6.69E-11	-1.95E-03	4.12E-04	2.51E-06	-0.0021	4.35E-04	1.48E-06
cg19748455	17	76274856	<i>LOC100996291</i>	TSS1500		-0.23	3.73E-02	4.11E-09	-1.44E-03	2.49E-04	9.89E-09	-0.0017	2.62E-04	3.13E-10
cg09349128	22	50327986	Intergenic		N Shore	-0.22	3.70E-02	1.28E-08	-1.07E-03	1.73E-04	9.87E-10	-0.0013	1.90E-04	3.37E-11
cg03770138	9	136009651	<i>RALGDS</i>	Body		-0.13	2.25E-02	6.72E-08	-1.05E-03	2.42E-04	1.66E-05	-0.0012	2.62E-04	6.06E-06
cg24382141	16	67944348	<i>PSKHI</i>	Body	S Shore	-0.13	2.33E-02	1.16E-07	-6.91E-04	1.77E-04	9.69E-05	-0.0006	1.97E-04	1.06E-03
cg02398240	2	128256334	<i>IWS1</i>	Body		-0.16	2.94E-02	1.41E-07	-6.65E-04	2.45E-04	6.71E-03	-0.0007	2.70E-04	7.60E-03
cg11917181	5	14108303	Intergenic			-0.11	2.05E-02	1.53E-07	-1.66E-05	1.21E-04	8.91E-01	0.0001	1.31E-04	4.35E-01
cg16843099	5	178956830	Intergenic		N Shore	-0.24	4.41E-02	1.73E-07	-6.94E-05	2.36E-04	7.69E-01	-0.0002	2.71E-04	4.26E-01
cg19758958	11	62319222	Intergenic			-0.13	2.37E-02	1.88E-07	-1.03E-03	2.12E-04	1.42E-06	-0.0010	2.30E-04	1.05E-05
cg19679801	5	145422431	<i>SH3RF2</i>	Body		-0.19	3.43E-02	2.40E-07	4.95E-05	1.28E-04	6.98E-01	3.38E-06	1.38E-04	9.80E-01
cg12367539	5	178956838	Intergenic		N Shore	-0.25	4.70E-02	2.55E-07	1.14E-04	2.21E-04	6.05E-01	-4.57E-05	2.51E-04	8.56E-01
cg19494100	6	18387313	<i>RNF144B</i>	TSS1500	N Shore	-0.08	1.45E-02	3.88E-07	-1.23E-04	1.48E-04	4.05E-01	-0.0001	1.58E-04	4.01E-01
cg15781610	6	36992554	<i>FGD2</i>	Body		-0.17	3.22E-02	4.09E-07	-9.34E-04	2.31E-04	5.65E-05	-0.0009	2.55E-04	3.22E-04
cg00840791	19	16453259	Intergenic			-0.38	7.14E-02	4.70E-07	-3.47E-03	7.12E-04	1.31E-06	-0.0038	7.76E-04	1.24E-06
cg17936938	6	7866213	<i>BMP6</i>	Body		0.18	3.39E-02	4.96E-07	9.37E-04	2.49E-04	1.74E-04	0.0009	2.75E-04	1.23E-03
cg10508317	17	76355146	<i>SOCS3</i>	Body	Island	-0.08	1.57E-02	5.66E-07	-4.16E-04	1.09E-04	1.42E-04	-0.0004	1.11E-04	6.24E-05
cg01671681	3	155421735	<i>PLCH1</i>	5UTR		-0.14	2.69E-02	5.69E-07	-6.78E-04	2.21E-04	2.27E-03	-0.0007	2.35E-04	2.59E-03
cg03578005	4	77170672	<i>FAM47E</i>	Body	N Shore	-0.06	1.07E-02	6.25E-07	-2.76E-05	3.29E-05	4.03E-01	-2.34E-05	3.65E-05	5.22E-01
cg04610187	17	76360794	<i>LOC101928674</i>	Body	S Shelf	-0.14	2.77E-02	7.43E-07	-4.97E-04	3.03E-04	1.02E-01	-0.0003	3.20E-04	3.14E-01
cg20710777	5	110411740	<i>TSLP</i>	Body	S Shelf	-0.17	3.31E-02	8.70E-07	-5.19E-04	1.12E-04	3.96E-06	-0.0005	1.25E-04	2.19E-04
cg04730825	16	16116191	<i>ABCCI</i>	Body		-0.07	1.29E-02	9.31E-07	8.72E-05	1.55E-04	5.74E-01	7.56E-05	1.72E-04	6.60E-01
cg13258453	6	25180502	Intergenic			-0.19	3.73E-02	1.18E-06	-3.76E-04	2.45E-04	1.26E-01	-0.0003	2.73E-04	2.12E-01
cg20803896	12	99006941	Intergenic			0.11	2.15E-02	1.20E-06	6.98E-04	1.95E-04	3.72E-04	0.0008	2.08E-04	2.58E-04
cg15227014	22	38037179	<i>SH3BP1</i>	Body	S Shore	0.12	2.43E-02	1.23E-06	2.50E-04	2.19E-04	2.55E-01	0.0003	2.37E-04	2.72E-01
cg20647087	3	45709608	<i>LMND1</i>	Body		-0.11	2.19E-02	1.69E-06	-1.16E-04	1.67E-04	4.86E-01	-5.19E-05	1.73E-04	7.64E-01

Note: The CpG sites were mapped to Genome Research Consortium human build 37 (GRCh37). The genes mapped to each CpG site were identified according to Illumina's annotation file of the EPIC BeadChip. Body: gene body; TSS: transcription start site; 5UTR: 5'-untranslated region; 3UTR: 3'-untranslated region.

Supplementary Tables & Figures

Table S1. Epigenome-wide associations of 61 significant (Bonferroni corrected $p < 0.05$) CpG sites with BMI from the meta-analysis of InterGEN and GENOA. Female only.

CpG	CHR	BP	Gene	Genomic Region	Relation to UCSC CpG Island	Meta-analysis			InterGEN			GENOA		
						Effect	StdErr	P.value	BETA	SE	P	BETA	SE	P
12 Unique CpG sites														
cg16531578	6	42370098	TRERF1	5UTR		-1.80E-03	3.00E-04	4.37E-09	-2.61E-03	5.92E-04	2.02E-05	-1.53E-03	3.66E-04	3.30E-05
cg14970975	12	6444675	TNFRSF1A	Body		-5.00E-04	1.00E-04	1.46E-08	-6.29E-04	1.43E-04	1.94E-05	-4.27E-04	1.15E-04	2.11E-04
cg01355089	1	93495018	Intergenic			1.10E-03	2.00E-04	2.66E-08	1.17E-03	2.93E-04	9.79E-05	1.03E-03	2.67E-04	1.15E-04
cg26470501	19	45252955	BCL3	Body	S Shore	-9.00E-04	2.00E-04	3.24E-08	-1.14E-03	2.58E-04	1.73E-05	-7.91E-04	2.29E-04	5.91E-04
cg07458272	19	34744396	KIAA0355	TSS1500	N Shore	9.00E-04	2.00E-04	3.24E-08	1.30E-03	2.94E-04	1.86E-05	7.60E-04	2.09E-04	2.93E-04
cg20959703	19	17959783	JAK3	TSS1500	S Shore	-1.00E-03	2.00E-04	3.44E-08	-1.29E-03	2.80E-04	8.32E-06	-7.51E-04	2.22E-04	7.56E-04
cg23545556	6	6928585	Intergenic			1.00E-03	2.00E-04	3.97E-08	8.63E-04	2.38E-04	3.88E-04	1.36E-03	3.15E-04	1.89E-05
cg09831562	3	181327125	SOX2-OT	TSS1500		7.00E-04	1.00E-04	4.07E-08	7.84E-04	2.60E-04	2.98E-03	6.66E-04	1.45E-04	5.06E-06
cg25428009	8	126304221	NSMCE2	Body		9.00E-04	2.00E-04	4.33E-08	6.98E-04	2.69E-04	1.05E-02	1.07E-03	2.16E-04	9.83E-07
cg24575378	1	24583120	Intergenic			1.20E-03	2.00E-04	5.47E-08	1.49E-03	3.92E-04	2.20E-04	1.04E-03	2.59E-04	6.63E-05
cg07913959	6	46627552	PLA2G7	Body		3.00E-04	1.00E-04	5.56E-08	3.31E-04	1.66E-04	4.76E-02	3.21E-04	6.36E-05	5.69E-07
cg16626764	14	91077172	TTC7B	Body		1.00E-03	2.00E-04	5.95E-08	9.16E-04	3.04E-04	3.01E-03	1.06E-03	2.35E-04	7.33E-06
Common with results from meta of InterGEN and GENOA combined														
cg03067296	17	76274577	LOC100996291	TSS200		-2.00E-03	2.00E-04	3.48E-22	-2.66E-03	3.59E-04	7.99E-12	-1.64E-03	2.46E-04	5.60E-11
cg18181703	17	76354621	SOC3	Body	N Shore	-2.10E-03	2.00E-04	1.31E-19	-2.78E-03	3.58E-04	1.02E-12	-1.62E-03	3.07E-04	1.85E-07
cg19748455	17	76274856	LOC100996291	TSS1500		-1.90E-03	2.00E-04	1.21E-18	-2.33E-03	3.73E-04	4.11E-09	-1.68E-03	2.62E-04	3.13E-10
cg09349128	22	50327986	Intergenic		N Shore	-1.50E-03	2.00E-04	2.13E-18	-2.22E-03	3.70E-04	1.28E-08	-1.28E-03	1.90E-04	3.37E-11
cg11047325	17	76354934	SOC3	Body	Island	-3.40E-03	4.00E-04	2.27E-17	-4.96E-03	6.49E-04	2.03E-12	-2.44E-03	5.13E-04	2.37E-06
cg13343932	17	76355061	SOC3	Body	Island	-2.80E-03	3.00E-04	6.79E-16	-4.14E-03	5.90E-04	6.69E-11	-2.11E-03	4.35E-04	1.48E-06
cg03770138	9	136099651	RALGDS	Body		-1.20E-03	2.00E-04	3.40E-13	-1.28E-03	2.25E-04	6.72E-08	-1.19E-03	2.62E-04	6.06E-06
cg00840791	19	16453259	Intergenic			-3.80E-03	5.00E-04	6.66E-13	-3.76E-03	7.14E-04	4.70E-07	-3.80E-03	7.76E-04	1.24E-06
cg18608055	19	1130866	SBN2	Body		-1.30E-03	2.00E-04	1.54E-12	-1.78E-03	3.64E-04	2.40E-06	-1.18E-03	2.24E-04	1.71E-07
cg12170787	19	1130965	SBN2	Body		-9.00E-04	1.00E-04	2.36E-12	-1.56E-03	3.31E-04	5.86E-06	-8.27E-04	1.48E-04	3.51E-08
cg19758958	11	62319222	Intergenic			-1.20E-03	2.00E-04	2.76E-12	-1.29E-03	2.37E-04	1.88E-07	-1.02E-03	2.30E-04	1.05E-05
cg02370334	19	17955786	JAK3	5UTR	S Shelf	-1.60E-03	2.00E-04	7.78E-12	-1.53E-03	3.38E-04	1.10E-05	-1.60E-03	3.13E-04	4.08E-07
cg08548559	22	31686097	PIK3P1	Body	N Shore	-1.60E-03	3.00E-04	6.38E-11	-1.85E-03	4.34E-04	3.56E-05	-1.55E-03	3.10E-04	7.79E-07
cg09536368	6	149461319	Intergenic			-5.00E-04	1.00E-04	1.63E-10	-4.88E-04	1.61E-04	2.85E-03	-5.30E-04	9.42E-05	2.66E-08
cg10508317	17	76355146	SOC3;LOC101928674	Body	Island	-6.00E-04	1.00E-04	2.88E-10	-8.21E-04	1.57E-04	5.66E-07	-4.48E-04	1.11E-04	6.24E-05
cg10288525	13	33455187	LINC00423	Body		9.00E-04	1.00E-04	5.64E-10	4.82E-04	2.20E-04	2.97E-02	1.21E-03	1.92E-04	4.95E-10
cg01198738	8	121597619	SNTB1	Body		-1.70E-03	3.00E-04	6.53E-10	-1.29E-03	4.46E-04	4.46E-03	-1.91E-03	3.42E-04	3.67E-08
cg20803896	12	99006941	Intergenic			9.00E-04	1.00E-04	7.46E-10	1.09E-03	2.15E-04	1.20E-06	7.63E-04	2.08E-04	2.58E-04
cg15781610	6	36992554	FGD2	Body		-1.20E-03	2.00E-04	9.23E-10	-1.70E-03	3.22E-04	4.09E-07	-9.23E-04	2.55E-04	3.22E-04
cg24382141	16	67944348	PSKH1	Body	S Shore	-9.00E-04	2.00E-04	1.06E-09	-1.29E-03	2.33E-04	1.16E-07	-6.47E-04	1.97E-04	1.06E-03
cg16291589	20	6023178	LRRN4	Body	S Shore	1.20E-03	2.00E-04	1.12E-09	1.26E-03	3.19E-04	1.14E-04	1.10E-03	2.75E-04	4.14E-06
cg15721584	3	181326755	SOX2-OT	Body		2.20E-03	4.00E-04	1.18E-09	1.63E-03	5.35E-04	2.70E-03	2.67E-03	4.90E-04	6.96E-08
cg09063556	16	66653795	CTM14	Body		7.00E-04	1.00E-04	1.50E-09	6.38E-04	1.78E-04	4.62E-04	6.60E-04	1.35E-04	1.40E-06
cg24993990	2	166428802	CSRN3	5UTR		1.30E-03	2.00E-04	2.70E-09	1.50E-03	3.36E-04	1.49E-05	1.11E-03	2.75E-04	6.51E-05
cg00926657	17	79880822	MAFG	Body	Island	9.00E-04	2.00E-04	2.71E-09	5.46E-04	2.44E-04	2.66E-02	1.12E-03	1.92E-04	1.01E-08
cg00160670	21	35320599	LINC00649	Body		-1.50E-03	3.00E-04	3.67E-09	-1.55E-03	3.31E-04	6.43E-06	-1.45E-03	4.04E-04	3.39E-04
cg19957386	17	47836122	FAM117A	Body		-1.00E-03	2.00E-04	4.64E-09	-1.09E-03	2.51E-04	2.37E-05	-9.01E-04	2.28E-04	8.45E-05
cg17936938	6	7866213	BMP6	Body		1.20E-03	2.00E-04	5.65E-09	1.78E-03	3.39E-04	4.96E-07	8.92E-04	2.75E-04	1.23E-03
cg06898549	12	41083590	Intergenic		N Shelf	1.20E-03	2.00E-04	6.05E-09	1.06E-03	3.74E-04	5.24E-03	1.28E-03	2.50E-04	4.42E-07
cg09832683	17	15013038	Intergenic			1.30E-03	2.00E-04	6.17E-09	1.71E-03	3.48E-04	2.25E-06	9.71E-04	2.76E-04	4.59E-04
cg03260624	1	91970722	CDC7	Body	S Shelf	8.00E-04	1.00E-04	6.99E-09	6.39E-04	2.06E-04	2.26E-03	8.76E-04	1.76E-04	8.76E-07
cg26402346	12	101864876	Intergenic			1.60E-03	3.00E-04	7.04E-09	1.45E-03	4.51E-04	1.62E-03	1.63E-03	3.38E-04	1.70E-06
cg02734358	4	90227074	GPRIN3	5UTR	N Shore	-1.20E-03	2.00E-04	7.69E-09	-1.58E-03	3.55E-04	1.66E-05	-1.04E-03	2.67E-04	1.14E-04
cg20090157	17	76274606	LOC100996291	TSS200		-1.10E-03	2.00E-04	8.57E-09	-1.34E-03	3.38E-04	1.11E-04	-9.79E-04	2.30E-04	2.31E-05
cg00574958	11	68607622	CPT1A	5UTR	S Shore	-4.00E-04	1.00E-04	1.00E-08	-2.70E-04	1.32E-04	4.27E-02	-5.13E-04	9.22E-05	3.89E-08
cg01671681	3	155421735	PLCH1	5UTR		-1.00E-03	2.00E-04	1.11E-08	-1.40E-03	2.69E-04	5.69E-07	-7.10E-04	2.35E-04	2.59E-03
cg02398240	2	128256334	IWS1	Body		-1.10E-03	2.00E-04	1.16E-08	-1.62E-03	2.94E-04	1.41E-07	-7.22E-04	2.70E-04	7.60E-03
cg01364674	1	24348512	Intergenic			4.00E-04	1.00E-04	1.47E-08	3.75E-04	1.11E-04	8.93E-04	4.46E-04	9.77E-05	5.99E-06
cg08309687	21	35320596	LINC00649	Body		-1.40E-03	2.00E-04	1.71E-08	-1.27E-03	3.35E-04	2.21E-04	-1.58E-03	3.74E-04	2.69E-05
cg14728380	17	80280330	SECTM1	Body	S Shelf	1.30E-03	2.00E-04	1.82E-08	1.09E-03	3.61E-04	2.90E-03	1.39E-03	2.91E-04	2.08E-06
cg01101459	1	234871477	Intergenic			9.00E-04	2.00E-04	2.00E-08	1.55E-03	4.32E-04	4.49E-04	8.41E-04	1.84E-04	5.79E-06
cg21650866	8	142297256	Intergenic		S Shore	1.30E-03	2.00E-04	3.10E-08	1.16E-03	2.89E-04	9.27E-05	1.52E-03	3.92E-04	1.14E-04
cg09310636	14	90760903	NR2E2	Body		8.00E-04	1.00E-04	3.16E-08	7.82E-04	2.14E-04	3.45E-04	7.47E-04	1.80E-04	3.80E-05
cg19157500	13	31271994	Intergenic			1.00E-03	2.00E-04	3.35E-08	1.27E-03	3.35E-04	2.16E-04	9.43E-04	2.30E-04	4.71E-05
cg22652934	21	36180035	RUNX1	Body		-1.20E-03	2.00E-04	3.85E-08	-2.04E-03	4.93E-04	5.64E-05	-9.99E-04	2.45E-04	5.07E-05
cg00014380	16	4424290	VASN; CORO7- PAM16; CORO7	Body		6.00E-04	1.00E-04	4.39E-08	8.92E-04	2.40E-04	2.77E-04	5.37E-04	1.27E-04	2.76E-05
cg17457241	16	8814411	ABAT	5UTR		7.00E-04	1.00E-04	4.71E-08	3.96E-04	2.09E-04	6.05E-02	9.07E-04	1.66E-04	6.41E-08
cg09613192	2	181388538	Intergenic			1.20E-03	2.00E-04	4.82E-08	1.17E-03	3.56E-04	1.20E-03	1.18E-03	2.72E-04	1.60E-05
cg03295554	11	128395450	LOC101929517 ETS1	Body	S Shelf	-1.70E-03	3.00E-04	5.80E-08	-1.26E-03	4.32E-04	3.91E-03	-2.06E-03	4.34E-04	2.56E-06

Figure S1A. Volcano plot of the meta-analysis of BMI EWAS.

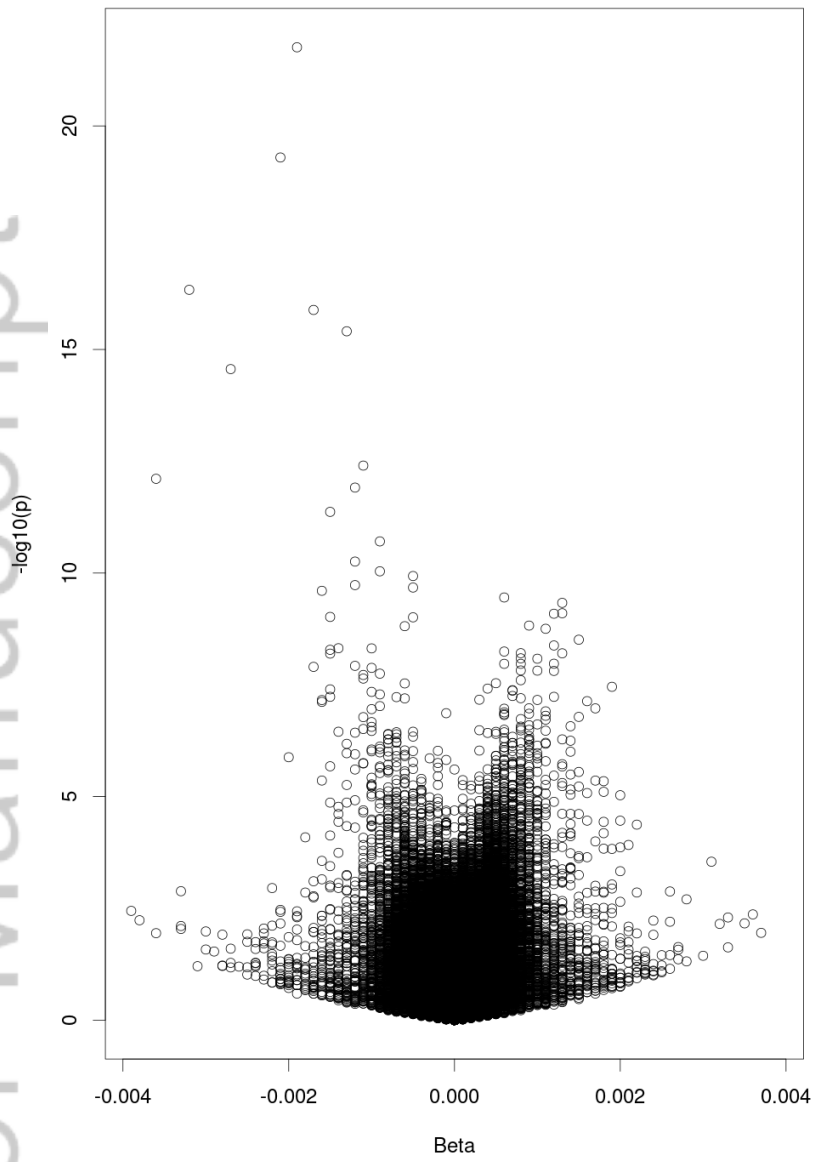


Figure S1B. Volcano plot of the female-only meta-analysis of BMI EWAS.

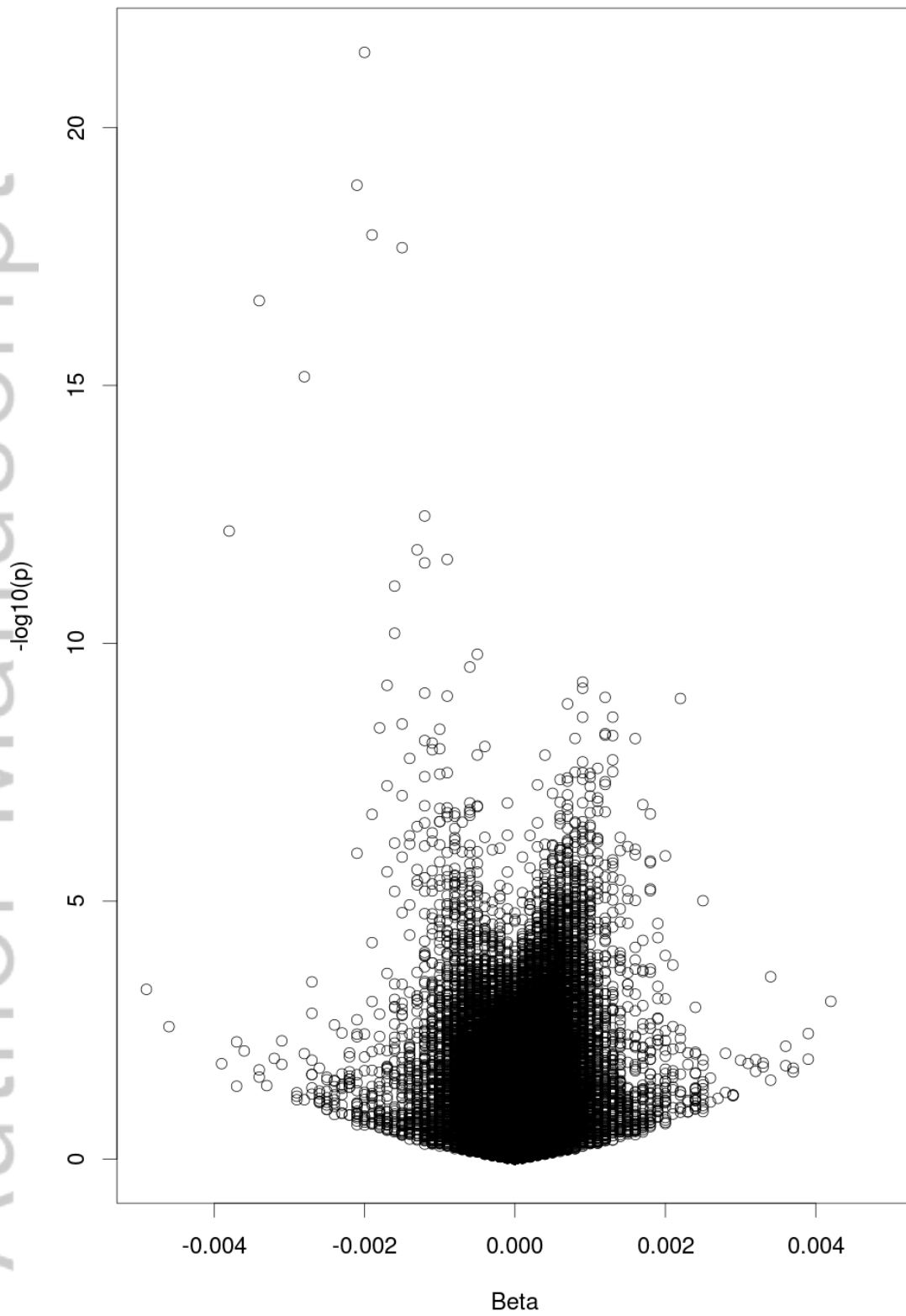


Table S2. Epigenome-wide associations of 65 significant (Bonferroni corrected $p < 0.05$) CpG sites with BMI from the meta-analysis of InterGEN and GENOA.

CpG	CHR	BP	Gene	Relation to UCSC CpG Island	Meta-analysis				InterGEN			GENOA		
					Genomic Region	Effect	StdErr	P-value	BETA	SE	P	BETA	SE	P
cg03067296	17	76274577	LOC100996291		TSS200	-1.90E-03	2.00E-04	1.70E-22	-2.70E-03	3.60E-04	8.00E-12	-1.50E-03	2.20E-04	1.10E-11
cg18181703	17	76354621	SOCS3	N Shore	Body	-2.10E-03	2.00E-04	5.10E-20	-2.80E-03	3.60E-04	1.00E-12	-1.60E-03	2.90E-04	5.10E-08
cg11047325	17	76354934	SOCS3	Island	Body	-3.20E-03	4.00E-04	4.60E-17	-5.00E-03	6.50E-04	2.00E-12	-2.30E-03	4.80E-04	1.80E-06
cg19748455	17	76274856	LOC100996291		TSS1500	-1.70E-03	2.00E-04	1.30E-16	-2.30E-03	3.70E-04	4.10E-09	-1.40E-03	2.50E-04	9.90E-09
cg09349128	22	50327986	Intergenic	N Shore		-1.30E-03	2.00E-04	3.90E-16	-2.20E-03	3.70E-04	1.30E-08	-1.10E-03	1.70E-04	9.90E-10
cg13343932	17	76355061	SOCS3	Island	Body	-2.70E-03	3.00E-04	2.70E-15	-4.10E-03	5.90E-04	6.70E-11	-2.00E-03	4.10E-04	2.50E-06
cg19758958	11	62319222	Intergenic			-1.10E-03	2.00E-04	4.00E-13	-1.30E-03	2.40E-04	1.90E-07	-1.00E-03	2.10E-04	1.40E-06
cg00840791	19	16453259	Intergenic			-3.60E-03	5.00E-04	7.80E-13	-3.80E-03	7.10E-04	4.70E-07	-3.50E-03	7.10E-04	1.30E-06
cg03770138	9	136009651	RALGDS		Body	-1.20E-03	2.00E-04	1.20E-12	-1.30E-03	2.30E-04	6.70E-08	-1.00E-03	2.40E-04	1.70E-05
cg02370334	19	17955786	JAK3	S Shelf	5UTR	-1.50E-03	2.00E-04	4.30E-12	-1.50E-03	3.40E-04	1.10E-05	-1.50E-03	2.80E-04	2.10E-07
cg12170787	19	1130965	SBNO2		Body	-9.00E-04	1.00E-04	2.00E-11	-1.60E-03	3.30E-04	5.90E-06	-7.40E-04	1.40E-04	1.50E-07
cg18608055	19	1130866	SBNO2		Body	-1.20E-03	2.00E-04	5.50E-11	-1.80E-03	3.60E-04	2.40E-06	-9.90E-04	2.10E-04	2.40E-06
cg24382141	16	67944348	PSKH1	S Shore	Body	-9.00E-04	1.00E-04	9.20E-11	-1.30E-03	2.30E-04	1.20E-07	-6.90E-04	1.80E-04	9.70E-05
cg09536368	6	149461319	Intergenic			-5.00E-04	1.00E-04	1.20E-10	-4.90E-04	1.60E-04	2.80E-03	-4.70E-04	8.30E-05	1.70E-08
cg15781610	6	36992554	FGD2		Body	-1.20E-03	2.00E-04	1.90E-10	-1.70E-03	3.20E-04	4.10E-07	-9.30E-04	2.30E-04	5.70E-05
cg00574958	11	68607622	CPT1A	S Shore	5UTR	-5.00E-04	1.00E-04	2.10E-10	-2.70E-04	1.30E-04	4.30E-02	-5.30E-04	8.40E-05	6.90E-10
cg00160670	21	35320599	LINC00649		Body	-1.60E-03	2.00E-04	2.50E-10	-1.50E-03	3.30E-04	6.40E-06	-1.60E-03	3.70E-04	2.20E-05
cg09063556	16	66653795	CMTM4		Body	6.00E-04	1.00E-04	3.50E-10	6.40E-04	1.80E-04	4.60E-04	6.30E-04	1.20E-04	3.10E-07
cg09832683	17	15013038	Intergenic			1.30E-03	2.00E-04	4.60E-10	1.70E-03	3.50E-04	2.30E-06	1.00E-03	2.50E-04	4.00E-05
cg24993990	2	166428802	CSRP3		5UTR	1.30E-03	2.00E-04	7.90E-10	1.50E-03	3.40E-04	1.50E-05	1.10E-03	2.60E-04	1.80E-05
cg17936938	6	7866213	BMP6		Body	1.20E-03	2.00E-04	8.10E-10	1.80E-03	3.40E-04	5.00E-07	9.40E-04	2.50E-04	1.70E-04
cg08548559	22	31686097	PIK3IP1	N Shore	Body	-1.50E-03	2.00E-04	9.60E-10	-1.80E-03	4.30E-04	3.60E-05	-1.30E-03	3.00E-04	7.60E-06
cg10508317	17	76355146	SOCS3	Island	Body	-5.00E-04	1.00E-04	9.80E-10	-8.20E-04	1.60E-04	5.70E-07	-4.20E-04	1.10E-04	1.40E-04
cg20803896	12	99006941	Intergenic			9.00E-04	1.00E-04	1.50E-09	1.10E-03	2.20E-04	1.20E-06	7.00E-04	2.00E-04	3.70E-04
cg20710777	5	110411740	TSLP	S Shelf	Body	-6.00E-04	1.00E-04	1.50E-09	-1.70E-03	3.30E-04	8.70E-07	-5.20E-04	1.10E-04	4.00E-06
cg19157500	13	31271994	Intergenic			1.10E-03	2.00E-04	1.80E-09	1.30E-03	3.40E-04	2.20E-04	1.00E-03	2.20E-04	2.70E-06
cg26402346	12	101864876	Intergenic			1.50E-03	3.00E-04	3.10E-09	1.40E-03	4.50E-04	1.60E-03	1.50E-03	3.10E-04	7.40E-07
cg06898549	12	41083590	Intergenic	N Shelf		1.20E-03	2.00E-04	4.20E-09	1.10E-03	3.70E-04	5.20E-03	1.20E-03	2.30E-04	3.00E-07
cg08309687	21	35320596	LINC00649		TSS1500	-1.40E-03	2.00E-04	4.80E-09	-1.30E-03	3.40E-04	2.20E-04	-1.60E-03	3.50E-04	7.40E-06
cg20090157	17	76274606	LOC100996291		TSS200	-1.00E-03	2.00E-04	4.80E-09	-1.30E-03	3.40E-04	1.10E-04	-9.30E-04	2.10E-04	1.10E-05
cg01198738	8	121597619	SNTB1		Body	-1.50E-03	3.00E-04	5.20E-09	-1.30E-03	4.50E-04	4.50E-03	-1.60E-03	3.20E-04	3.70E-07
cg00014380	16	4424290	VASN	S Shelf	5UTR	6.00E-04	1.00E-04	5.70E-09	8.90E-04	2.40E-04	2.80E-04	5.40E-04	1.20E-04	3.50E-06
cg03260624	1	91970722	CDC7	S Shelf	Body	8.00E-04	1.00E-04	6.20E-09	6.40E-04	2.10E-04	2.30E-03	8.60E-04	1.70E-04	7.60E-07
cg21650866	8	142297256	Intergenic	S Shore		1.30E-03	2.00E-04	6.20E-09	1.20E-03	2.90E-04	9.30E-05	1.50E-03	3.50E-04	2.20E-05

cg14369893	21	46501109	ADARB1		5UTR	-1.50E-03	3.00E-04	6.30E-09	-1.70E-03	3.80E-04	2.00E-05	-1.40E-03	3.70E-04	1.40E-04
cg16740586	21	43655919	ABCG1	S Shore	Body	8.00E-04	1.00E-04	8.10E-09	4.40E-04	2.50E-04	8.30E-02	8.80E-04	1.50E-04	1.70E-08
cg06192883	15	52554171	MYO5C		Body	1.00E-03	2.00E-04	8.20E-09	1.30E-03	3.50E-04	4.30E-04	9.50E-04	2.10E-04	5.60E-06
cg08373547	14	52794541	PTGER2		3UTR	1.20E-03	2.00E-04	1.10E-08	9.30E-04	3.20E-04	4.10E-03	1.40E-03	2.70E-04	5.90E-07
cg00926657	17	79880822	MAFG	Island	Body	8.00E-04	1.00E-04	1.10E-08	5.50E-04	2.40E-04	2.70E-02	9.60E-04	1.80E-04	6.80E-08
cg18840187	4	169608898	PALLD		Body	6.00E-04	1.00E-04	1.10E-08	5.60E-04	1.70E-04	1.40E-03	5.60E-04	1.20E-04	2.90E-06
cg22652934	21	36180035	RUNX1		Body	-1.20E-03	2.00E-04	1.20E-08	-2.00E-03	4.90E-04	5.60E-05	-1.00E-03	2.30E-04	1.40E-05
cg03295554	11	128395450	LOC101929517	S Shelf	TSS1500	-1.70E-03	3.00E-04	1.30E-08	-1.30E-03	4.30E-04	3.90E-03	-2.00E-03	3.90E-04	5.80E-07
cg01671681	3	155421735	PLCH1		5UTR	-1.00E-03	2.00E-04	1.30E-08	-1.40E-03	2.70E-04	5.70E-07	-6.80E-04	2.20E-04	2.30E-03
cg10288525	13	33455187	LINC00423		Body	8.00E-04	1.00E-04	1.50E-08	4.80E-04	2.20E-04	3.00E-02	1.00E-03	1.90E-04	3.60E-08
cg16291589	20	6023178	LRRN4	S Shore	Body	1.00E-03	2.00E-04	1.50E-08	1.30E-03	3.20E-04	1.10E-04	9.20E-04	2.20E-04	3.80E-05
cg09613192	2	181388538	Intergenic			1.20E-03	2.00E-04	1.50E-08	1.20E-03	3.60E-04	1.20E-03	1.20E-03	2.60E-04	5.00E-06
cg19957386	17	47836122	FAM117A		Body	-9.00E-04	2.00E-04	1.80E-08	-1.10E-03	2.50E-04	2.40E-05	-7.70E-04	2.10E-04	2.30E-04
cg02398240	2	128256334	IWS1		Body	-1.10E-03	2.00E-04	1.90E-08	-1.60E-03	2.90E-04	1.40E-07	-6.70E-04	2.40E-04	6.70E-03
cg02734358	4	90227074	GPRIN3	N Shore	5UTR	-1.10E-03	2.00E-04	2.30E-08	-1.60E-03	3.60E-04	1.70E-05	-9.10E-04	2.40E-04	2.10E-04
cg20493906	4	106113303	TET2		5UTR	8.00E-04	1.00E-04	2.50E-08	6.60E-04	2.20E-04	3.80E-03	8.10E-04	1.70E-04	2.10E-06
cg21313072	18	43640508	PSTPIP2		Body	5.00E-04	1.00E-04	2.90E-08	3.80E-04	1.50E-04	1.40E-02	5.70E-04	1.10E-04	5.10E-07
cg14377972	15	99356110	IGF1R		Body	-6.00E-04	1.00E-04	2.90E-08	-4.40E-04	2.50E-04	7.50E-02	-6.30E-04	1.20E-04	1.50E-07
cg15721584	3	181326755	SOX2-OT		TSS1500	1.90E-03	4.00E-04	3.50E-08	1.60E-03	5.30E-04	2.70E-03	2.20E-03	4.70E-04	3.70E-06
cg01364674	1	24348512	Intergenic			4.00E-04	1.00E-04	3.80E-08	3.80E-04	1.10E-04	8.90E-04	3.90E-04	9.10E-05	1.60E-05
cg17901584	1	55353706	DHCR24	S Shore	TSS1500	-1.50E-03	3.00E-04	4.00E-08	-2.50E-03	5.30E-04	8.30E-06	-1.10E-03	3.10E-04	2.70E-04
cg17457241	16	8814411	ABAT		5UTR	7.00E-04	1.00E-04	4.20E-08	4.00E-04	2.10E-04	6.10E-02	8.20E-04	1.50E-04	8.30E-08
cg15183129	1	160759781	Intergenic			7.00E-04	1.00E-04	4.30E-08	8.70E-04	1.90E-04	1.20E-05	5.50E-04	1.60E-04	8.40E-04
cg09152259	2	128156114	Intergenic	N Shelf		-1.00E-03	2.00E-04	4.60E-08	-1.70E-03	3.80E-04	2.40E-05	-7.80E-04	2.00E-04	1.10E-04
cg25705792	21	35320017	LINC00649		TSS1500	-9.00E-04	2.00E-04	5.20E-08	-1.10E-03	2.60E-04	7.10E-05	-8.30E-04	2.30E-04	2.60E-04
cg09310636	14	90760903	NRDE2		Body	7.00E-04	1.00E-04	5.60E-08	7.80E-04	2.10E-04	3.50E-04	6.70E-04	1.70E-04	6.00E-05
cg02233071	21	36181046	RUNX1		Body	-1.50E-03	3.00E-04	5.90E-08	-1.30E-03	4.80E-04	5.90E-03	-1.50E-03	3.30E-04	3.60E-06
cg14728380	17	80280330	SECTM1	S Shelf	Body	1.20E-03	2.00E-04	5.90E-08	1.10E-03	3.60E-04	2.90E-03	1.20E-03	2.70E-04	7.40E-06
cg22413912	7	2255758	MAD1L1		Body	-7.00E-04	1.00E-04	6.00E-08	-6.00E-04	2.40E-04	1.40E-02	-8.10E-04	1.70E-04	1.40E-06
cg01101459	1	234871477	Intergenic			8.00E-04	2.00E-04	6.30E-08	1.50E-03	4.30E-04	4.50E-04	7.40E-04	1.70E-04	1.10E-05
cg08350157	3	131219430	MRPL3	N Shelf	Body	-6.00E-04	1.00E-04	6.40E-08	-4.00E-04	2.00E-04	4.60E-02	-6.80E-04	1.30E-04	3.10E-07

Table S3. Epigenome-wide associations of 658 significant (FDR 0.05 threshold) CpG sites with BMI from the meta-analysis of InterGEN and GENOA.

CpG	CHR	POS	UCSC RefGene Name	UCSC RefGene Group	Relation to UCSC CpG Island	META			InterGEN			GENOA		
						BETA	SE	P	BETA	SE	P	BETA	SE	PF
cg03067296	17	762745 77	LOC100996291	TSS200		-2.00E-03	2.00E-04	3.48E-22	-2.66E-03	3.59E-04	7.99E-12	-1.64E-03	2.46E-04	5.60E-11
cg18181703	17	763546 21	SOCS3	Body		-2.10E-03	2.00E-04	1.31E-19	-2.78E-03	3.58E-04	1.02E-12	-1.62E-03	3.07E-04	1.85E-07
cg19748455	17	762748 56	LOC100996291	TSS1500		-1.90E-03	2.00E-04	1.21E-18	-2.33E-03	3.73E-04	4.11E-09	-1.68E-03	2.62E-04	3.13E-10
cg09349128	22	503279 86			N Shore	-1.50E-03	2.00E-04	2.13E-18	-2.22E-03	3.70E-04	1.28E-08	-1.28E-03	1.90E-04	3.37E-11
cg11047325	17	763549 34	SOCS3	Body		-3.40E-03	4.00E-04	2.27E-17	-4.96E-03	6.49E-04	2.03E-12	-2.44E-03	5.13E-04	2.37E-06
cg13343932	17	763550 61	SOCS3;LOC101928 674;LOC101928674	Body;TSS150 0;TSS1500		-2.80E-03	3.00E-04	6.79E-16	-4.14E-03	5.90E-04	6.69E-11	-2.11E-03	4.35E-04	1.48E-06
cg03770138	9	136009 651	RALGDS	Body		-1.20E-03	2.00E-04	3.40E-13	-1.28E-03	2.25E-04	6.72E-08	-1.19E-03	2.62E-04	6.06E-06
cg00840791	19	164532 59			N Shore	-3.80E-03	5.00E-04	6.66E-13	-3.76E-03	7.14E-04	4.70E-07	-3.80E-03	7.76E-04	1.24E-06
cg18608055	19	113086 6	SBNO2;SBNO2	Body;Body		-1.30E-03	2.00E-04	1.54E-12	-1.78E-03	3.64E-04	2.40E-06	-1.18E-03	2.24E-04	1.71E-07
cg12170787	19	113096 5	SBNO2;SBNO2	Body;Body	Island	-9.00E-04	1.00E-04	2.36E-12	-1.56E-03	3.31E-04	5.86E-06	-8.27E-04	1.48E-04	3.51E-08
cg19758958	11	623192 22				-1.20E-03	2.00E-04	2.76E-12	-1.29E-03	2.37E-04	1.88E-07	-1.02E-03	2.30E-04	1.05E-05
cg02370334	19	179557 86	JAK3	5URT	Island	-1.60E-03	2.00E-04	7.78E-12	-1.53E-03	3.38E-04	1.10E-05	-1.60E-03	3.13E-04	4.08E-07
cg08548559	22	316860 97	PIK3IP1;PIK3IP1	Body;Body		-1.60E-03	3.00E-04	6.38E-11	-1.85E-03	4.34E-04	3.56E-05	-1.55E-03	3.10E-04	7.79E-07
cg09536368	6	149461 319				-5.00E-04	1.00E-04	1.63E-10	-4.88E-04	1.61E-04	2.85E-03	-5.30E-04	9.42E-05	2.66E-08
cg10508317	17	763551 46	SOCS3;LOC101928 674;LOC101928674	Body;TSS150 0;TSS1500		-6.00E-04	1.00E-04	2.88E-10	-8.21E-04	1.57E-04	5.66E-07	-4.48E-04	1.11E-04	6.24E-05
cg10288525	13	334551 87	LINC00423	Body		9.00E-04	1.00E-04	5.64E-10	4.82E-04	2.20E-04	2.97E-02	1.21E-03	1.92E-04	4.95E-10
cg01198738	8	121597 619	SNTB1	Body		-1.70E-03	3.00E-04	6.53E-10	-1.29E-03	4.46E-04	4.46E-03	-1.91E-03	3.42E-04	3.67E-08

cg20803896	12	990069 41				9.00E-04	1.00E-04	7.46E-10	1.09E-03	2.15E-04	1.20E-06	7.63E-04	2.08E-04	2.58E-04
cg15781610	6	369925 54	FGD2	Body		-1.20E-03	2.00E-04	9.23E-10	-1.70E-03	3.22E-04	4.09E-07	-9.23E-04	2.55E-04	3.22E-04
cg24382141	16	679443 48	PSKH1	Body		-9.00E-04	2.00E-04	1.06E-09	-1.29E-03	2.33E-04	1.16E-07	-6.47E-04	1.97E-04	1.06E-03
cg16291589	20	602317 8	LRRN4	Body		1.20E-03	2.00E-04	1.12E-09	1.26E-03	3.19E-04	1.14E-04	1.10E-03	2.37E-04	4.14E-06
cg15721584	3	181326 755	SOX2-OT;SOX2-OT;SOX2-OT;SOX2-OT;SOX2-OT	TSS1500;TSS1500;TSS1500;Body;Body;Body		2.20E-03	4.00E-04	1.18E-09	1.63E-03	5.35E-04	2.70E-03	2.67E-03	4.90E-04	6.96E-08
cg09063556	16	666537 95	CMTM4;CMTM4	3UTR;Body		7.00E-04	1.00E-04	1.50E-09	6.38E-04	1.78E-04	4.62E-04	6.60E-04	1.35E-04	1.40E-06
cg24993990	2	166428 802	CSRNP3;CSRNP3	T	S Shelf	1.30E-03	2.00E-04	2.70E-09	1.50E-03	3.36E-04	1.49E-05	1.11E-03	2.77E-04	6.51E-05
cg00926657	17	798808 22	MAFG;MAFG	Body;Body		9.00E-04	2.00E-04	2.71E-09	5.46E-04	2.44E-04	2.66E-02	1.12E-03	1.92E-04	1.01E-08
cg00160670	21	353205 99	LINC00649;LINC0649	TSS1500;Body	N Shore	-1.50E-03	3.00E-04	3.67E-09	-1.55E-03	3.31E-04	6.43E-06	-1.45E-03	4.04E-04	3.39E-04
cg16531578	6	423700 98	TRERF1;TRERF1	5URT;5URT		-1.80E-03	3.00E-04	4.37E-09	-2.61E-03	5.92E-04	2.02E-05	-1.53E-03	3.66E-04	3.30E-05
cg19957386	17	478361 22	FAM117A	Body		-1.00E-03	2.00E-04	4.64E-09	-1.09E-03	2.51E-04	2.37E-05	-9.01E-04	2.28E-04	8.45E-05
cg17936938	6	786621 3	BMP6	Body		1.20E-03	2.00E-04	5.65E-09	1.78E-03	3.39E-04	4.96E-07	8.92E-04	2.75E-04	1.23E-03
cg06898549	12	410835 90			Island	1.20E-03	2.00E-04	6.05E-09	1.06E-03	3.74E-04	5.24E-03	1.28E-03	2.50E-04	4.42E-07
cg09832683	17	150130 38				1.30E-03	2.00E-04	6.17E-09	1.71E-03	3.48E-04	2.25E-06	9.71E-04	2.76E-04	4.59E-04
cg03260624	1	919707 22	CDC7;CDC7;CDC7	Body;Body;Body		8.00E-04	1.00E-04	6.99E-09	6.39E-04	2.06E-04	2.26E-03	8.76E-04	1.76E-04	8.76E-07
cg26402346	12	101864 876				1.60E-03	3.00E-04	7.04E-09	1.45E-03	4.51E-04	1.62E-03	1.63E-03	3.38E-04	1.70E-06
cg02734358	4	902270 74	GPRIN3	5URT		-1.20E-03	2.00E-04	7.69E-09	-1.58E-03	3.55E-04	1.66E-05	-1.04E-03	2.67E-04	1.14E-04
cg20090157	17	762746 06	LOC100996291	TSS200		-1.10E-03	2.00E-04	8.57E-09	-1.34E-03	3.38E-04	1.11E-04	-9.79E-04	2.30E-04	2.31E-05
cg00574958	11	686076 22	CPT1A;CPT1A	5URT;5URT		-4.00E-04	1.00E-04	1.00E-08	-2.70E-04	1.32E-04	4.27E-02	-5.13E-04	9.22E-05	3.89E-08
cg01671681	3	155421 735	PLCH1	5URT		-1.00E-03	2.00E-04	1.11E-08	-1.40E-03	2.69E-04	5.69E-07	-7.10E-04	2.35E-04	2.59E-03

cg02398240	2	128256 334	IWS1	Body		-1.10E-03	2.00E-04	1.16E-08	-1.62E-03	2.94E-04	1.41E-07	-7.22E-04	2.70E-04	7.60E-03
cg14970975	12	64467 5	TNFRSF1A	Body		-5.00E-04	1.00E-04	1.46E-08	-6.29E-04	1.43E-04	1.94E-05	-4.27E-04	1.15E-04	2.11E-04
cg01364674	1	243485 12			S Shore	4.00E-04	1.00E-04	1.47E-08	3.75E-04	1.11E-04	8.93E-04	4.46E-04	9.77E-05	5.99E-06
cg08309687	21	353205 96	LINC00649;LINC0649	TSS1500;Body		-1.40E-03	2.00E-04	1.71E-08	-1.27E-03	3.35E-04	2.21E-04	-1.58E-03	3.74E-04	2.69E-05
cg14728380	17	802803 30	SECTM1	Body	S Shore	1.30E-03	2.00E-04	1.82E-08	1.09E-03	3.61E-04	2.90E-03	1.39E-03	2.91E-04	2.08E-06
cg01101459	1	234871 477				9.00E-04	2.00E-04	2.00E-08	1.55E-03	4.32E-04	4.49E-04	8.41E-04	1.84E-04	5.79E-06
cg01355089	1	934950 18				1.10E-03	2.00E-04	2.66E-08	1.17E-03	2.93E-04	9.79E-05	1.03E-03	2.67E-04	1.15E-04
cg21650866	8	142297 256				1.30E-03	2.00E-04	3.10E-08	1.16E-03	2.89E-04	9.27E-05	1.52E-03	3.92E-04	1.14E-04
cg09310636	14	907609 03	NRDE2	Body		8.00E-04	1.00E-04	3.16E-08	7.82E-04	2.14E-04	3.45E-04	7.47E-04	1.80E-04	3.80E-05
cg26470501	19	452529 55	BCL3	Body		-9.00E-04	2.00E-04	3.24E-08	-1.14E-03	2.58E-04	1.73E-05	-7.91E-04	2.29E-04	5.91E-04
cg07458272	19	347443 96	KIAA0355	TSS1500		9.00E-04	2.00E-04	3.24E-08	1.30E-03	2.94E-04	1.86E-05	7.60E-04	2.09E-04	2.93E-04
cg19157500	13	312719 94				1.00E-03	2.00E-04	3.35E-08	1.27E-03	3.35E-04	2.16E-04	9.43E-04	2.30E-04	4.71E-05
cg20959703	19	179597 83	JAK3	TSS1500	Island	-1.00E-03	2.00E-04	3.44E-08	-1.29E-03	2.80E-04	8.32E-06	-7.51E-04	2.22E-04	7.56E-04
cg22652934	21	361800 35	RUNX1;RUNX1	Body;Body		-1.20E-03	2.00E-04	3.85E-08	-2.04E-03	4.93E-04	5.64E-05	-9.99E-04	2.45E-04	5.07E-05
cg23545556	6	692858 5				1.00E-03	2.00E-04	3.97E-08	8.63E-04	2.38E-04	3.88E-04	1.36E-03	3.15E-04	1.89E-05
cg09831562	3	181327 125	SOX2-OT;SOX2-OT;SOX2-OT;SOX2-OT;SOX2-OT	TSS1500;TSS1500;TSS1500;Body;Body;Body		7.00E-04	1.00E-04	4.07E-08	7.84E-04	2.60E-04	2.98E-03	6.66E-04	1.45E-04	5.06E-06
cg25428009	8	126304 221	NSMCE2	Body		9.00E-04	2.00E-04	4.33E-08	6.98E-04	2.69E-04	1.05E-02	1.07E-03	2.16E-04	9.83E-07
cg00014380	16	442429 0	VASN;CORO7-PAM16;CORO7;CORO7;CORO7	5URT;Body;Body;Body;Body		6.00E-04	1.00E-04	4.39E-08	8.92E-04	2.40E-04	2.77E-04	5.37E-04	1.27E-04	2.76E-05
cg17457241	16	881441 1	ABAT;ABAT;ABAT	TSS200;5URT;5URT		7.00E-04	1.00E-04	4.71E-08	3.96E-04	2.09E-04	6.05E-02	9.07E-04	1.66E-04	6.41E-08

cg09613192	2	181388 538				1.20E-03	2.00E-04	4.82E-08	1.17E-03	3.56E-04	1.20E-03	1.18E-03	2.72E-04	1.60E-05
cg24575378	1	245831 20				1.20E-03	2.00E-04	5.47E-08	1.49E-03	3.92E-04	2.20E-04	1.04E-03	2.59E-04	6.63E-05
cg07913959	6	466725 52	PLA2G7;PLA2C7	Body;Body		3.00E-04	1.00E-04	5.56E-08	3.31E-04	1.66E-04	4.76E-02	3.21E-04	6.36E-05	5.69E-07
cg03295554	11	128395 450	LOC101929517;ETS	TSS1500;Body	N Shelf	-1.70E-03	3.00E-04	5.80E-08	-1.26E-03	4.32E-04	3.91E-03	-2.06E-03	4.34E-04	2.56E-06
cg16626764	14	910771 72	TTC7B;TTC7B	Ex- onBnd;Body		1.00E-03	2.00E-04	5.95E-08	9.16E-04	3.04E-04	3.01E-03	1.06E-03	2.35E-04	7.33E-06
cg18840187	4	169608 898	PALLD;PALLD;PAL LLD	Body;Body;B ody		5.00E-04	1.00E-04	8.12E-08	5.64E-04	1.73E-04	1.42E-03	5.18E-04	1.21E-04	2.23E-05
cg15183129	1	160759 781				7.00E-04	1.00E-04	8.68E-08	8.74E-04	1.93E-04	1.21E-05	5.50E-04	1.76E-04	1.89E-03
cg14369893	21	465011 09	ADARB1;ADARB1 ;ADARB1;ADARB 1;ADARB1;ADAR B1;ADARB1;ADA RB1	5URT;5URT; 5URT;5URT; Body;Body;B ody;Body	S Shelf	-1.50E-03	3.00E-04	8.99E-08	-1.67E-03	3.79E-04	2.00E-05	-1.25E-03	4.00E-04	1.84E-03
cg06192883	15	525541 71	MYO5C	Body		1.00E-03	2.00E-04	9.15E-08	1.26E-03	3.51E-04	4.32E-04	9.40E-04	2.34E-04	6.39E-05
cg08016417	4	153588 259	TMEM154	Body		1.10E-03	2.00E-04	9.98E-08	1.20E-03	3.34E-04	4.64E-04	1.04E-03	2.63E-04	8.25E-05
cg05304729	1	158800 024	MNDA	TSS1500		1.10E-03	2.00E-04	1.16E-07	1.49E-03	3.91E-04	1.96E-04	8.99E-04	2.30E-04	1.05E-04
cg14624311	16	859425 38	IRF8	Body	N Shore	6.00E-04	1.00E-04	1.21E-07	9.53E-04	1.94E-04	2.17E-06	4.31E-04	1.49E-04	4.03E-03
cg12962778	12	547783 12	ZNF385A;ZNF385 A;ZNF385A;ZNF3 85A;ZNF385A;ZNF 385A;ZNF385A;Z NF385A;LOC10272 4050;LOC10272405	1stExon;1stE xon;5URT;5 URT;5URT;5 URT;Body;B ody;Body;Bo dy		9.00E-04	2.00E-04	1.24E-07	6.93E-04	2.92E-04	1.89E-02	1.08E-03	2.23E-04	1.63E-06
cg20710777	5	110411 740	TSLP;TSLP;TSLP	Body;Body;B ody		-6.00E-04	1.00E-04	1.25E-07	-1.70E-03	3.31E-04	8.70E-07	-4.63E-04	1.25E-04	2.19E-04
cg26002437	10	454732 31	C10orf10;RASSF4	Body;Body		-1.00E-04	0.00E+00	1.25E-07	-2.49E-04	9.07E-05	6.76E-03	-1.13E-04	2.38E-05	2.56E-06
cg15218293	16	777712 84	NUDT7;NUDT7;N UDT7;NUDT7	Body;Body;B ody;Body	S Shore	1.70E-03	3.00E-04	1.35E-07	2.38E-03	6.83E-04	6.58E-04	1.47E-03	3.55E-04	4.03E-05
cg20646219	17	384902 28	RARA;RARA;RAR A	Body;Body;B ody		7.00E-04	1.00E-04	1.37E-07	7.79E-04	1.99E-04	1.32E-04	6.23E-04	1.75E-04	3.86E-04

cg19572574	10	635927 31				-1.20E-03	2.00E-04	1.41E-07	-1.49E-03	3.71E-04	9.66E-05	-9.86E-04	2.75E-04	3.65E-04
cg10452282	4	166136 676	KLHL2;KLHL2;KLHL2	5URT;Body; Body		-5.00E-04	1.00E-04	1.42E-07	-7.21E-04	1.99E-04	4.00E-04	-4.84E-04	1.23E-04	8.65E-05
cg03276602	7	150451 580				-5.00E-04	1.00E-04	1.48E-07	-7.52E-04	1.83E-04	6.29E-05	-4.20E-04	1.16E-04	3.30E-04
cg15001240	12	276154 08				-9.00E-04	2.00E-04	1.55E-07	-1.16E-03	2.63E-04	1.84E-05	-7.03E-04	2.26E-04	1.90E-03
cg25705792	21	353200 17 0649	LINC00649;LINC00649	TSS1500;Bod y		-1.00E-03	2.00E-04	1.60E-07	-1.07E-03	2.62E-04	7.09E-05	-8.40E-04	2.51E-04	8.70E-04
cg12808636	1	119879 86				7.00E-04	1.00E-04	1.65E-07	6.16E-04	1.87E-04	1.22E-03	6.93E-04	1.70E-04	5.11E-05
cg22460123	12	526382 94	KRT7	Body		-6.00E-04	1.00E-04	1.69E-07	-7.78E-04	1.60E-04	2.87E-06	-3.85E-04	1.45E-04	8.06E-03
cg26663590	16	289593 10				1.10E-03	2.00E-04	1.78E-07	1.12E-03	3.55E-04	1.87E-03	1.15E-03	2.78E-04	3.73E-05
cg12129908	3	529077 61 0	TMEM110- MUSTN1;TMEM110	Body;Body		1.20E-03	2.00E-04	1.86E-07	1.46E-03	3.82E-04	1.90E-04	1.02E-03	2.79E-04	2.70E-04
cg09897881	15	861958 08	AKAP13;AKAP13; AKAP13	Body;Body;B ody		-6.00E-04	1.00E-04	1.89E-07	-9.55E-04	2.32E-04	6.45E-05	-5.25E-04	1.47E-04	3.91E-04
cg00437879	10	926192 95			S Shelf	-9.00E-04	2.00E-04	1.93E-07	-1.11E-03	3.42E-04	1.41E-03	-7.99E-04	1.93E-04	3.88E-05
cg16809457	6	903996 77	MDN1	Body		1.00E-03	2.00E-04	1.93E-07	9.59E-04	3.47E-04	6.36E-03	1.08E-03	2.44E-04	1.16E-05
cg00307819	17	478179 38	FAM117A	Body		-8.00E-04	2.00E-04	1.96E-07	-6.21E-04	2.16E-04	4.57E-03	-9.84E-04	2.19E-04	8.47E-06
cg19488267	14	857630 19				1.80E-03	4.00E-04	2.04E-07	1.96E-03	5.41E-04	4.09E-04	1.74E-03	4.63E-04	1.95E-04
cg16936953	17	579156 65	VMP1;VMP1	Ex- onBnd;Body		-1.90E-03	4.00E-04	2.08E-07	-2.63E-03	6.13E-04	3.11E-05	-1.53E-03	4.73E-04	1.23E-03
cg19640090	12	119751 55	ETV6;RNU6-19P	Body;Body		-6.00E-04	1.00E-04	2.17E-07	-6.38E-04	2.43E-04	9.65E-03	-6.53E-04	1.46E-04	9.11E-06
cg15553397	1	766951 86	ST6GAL- NAC3;ST6GAL- NAC3	Body;Body	S Shore	6.00E-04	1.00E-04	2.23E-07	5.89E-04	1.88E-04	2.08E-03	5.90E-04	1.43E-04	4.20E-05
cg11155434	11	128358 527	ETS1;ETS1;ETS1	Body;Body;B ody		-8.00E-04	1.00E-04	2.26E-07	-1.10E-03	2.84E-04	1.59E-04	-6.29E-04	1.69E-04	2.16E-04
cg16740586	21	436559 19	ABCG1;ABCG1;ABCG1; ABCG1;ABCG1;ABCG1	Body;Body;B ody;Body;Bo dy;Body		7.00E-04	1.00E-04	2.26E-07	4.44E-04	2.54E-04	8.31E-02	8.53E-04	1.69E-04	5.64E-07
cg11902329	2	228253 636				-9.00E-04	2.00E-04	2.30E-07	-1.27E-03	5.51E-04	2.26E-02	-8.87E-04	1.90E-04	3.55E-06

cg05330318	6	301841 79			S Shore	6.00E-04	1.00E-04	2.53E-07	5.67E-04	2.00E-04	5.11E-03	5.91E-04	1.37E-04	1.94E-05
cg10780778	6	263519 15				-1.00E-03	2.00E-04	2.86E-07	-1.61E-03	4.62E-04	6.49E-04	-8.75E-04	2.17E-04	6.13E-05
cg15730234	1	101759 418			N Shore	-1.00E-03	2.00E-04	2.87E-07	-9.84E-04	2.45E-04	9.31E-05	-1.02E-03	3.18E-04	1.45E-03
cg27579586	20	451965 29	SLC13A3;SLC13A3 ;SLC13A3;SLC13A3 3;SLC13A3	Body;Body;B ody;Body;Bo dy		9.00E-04	2.00E-04	2.87E-07	3.97E-04	2.77E-04	1.54E-01	1.34E-03	2.41E-04	4.00E-08
cg22679812	16	706262 13	IL34;IL34	5URT;5URT		8.00E-04	2.00E-04	2.92E-07	6.38E-04	2.39E-04	8.27E-03	9.23E-04	2.07E-04	9.33E-06
cg07120889	1	150535 935	ADAMTSL4-AS1	Body		-7.00E-04	1.00E-04	2.94E-07	-8.60E-04	2.07E-04	5.31E-05	-5.58E-04	1.74E-04	1.44E-03
cg10192877	21	436416 90	ABCG1;ABCG1;AB CG1;ABCG1;ABC G1;ABCG1	5URT;Body; Body;Body;B ody;Body	S Shore	3.00E-04	1.00E-04	3.03E-07	2.39E-04	1.04E-04	2.33E-02	3.75E-04	7.98E-05	3.29E-06
cg08726900	16	895504 74	ANKRD11;ANKR D11;ANKRD11;A NKRD11	Body;5URT;5 URT;5URT		-1.20E-03	2.00E-04	3.04E-07	-7.23E-04	3.84E-04	6.16E-02	-1.49E-03	2.96E-04	6.87E-07
cg07021906	16	878668 33	SLC7A5	Body		8.00E-04	2.00E-04	3.08E-07	1.03E-03	3.75E-04	6.55E-03	7.82E-04	1.80E-04	1.55E-05
cg06566477	20	610785 02				6.00E-04	1.00E-04	3.13E-07	7.88E-04	2.03E-04	1.59E-04	5.27E-04	1.51E-04	5.01E-04
cg09138892	17	790056 62	BAIAP2-AS1	Body		1.00E-03	2.00E-04	3.36E-07	1.41E-03	3.90E-04	3.82E-04	8.19E-04	2.14E-04	1.42E-04
cg01641754	5	983559 83				-1.30E-03	2.00E-04	3.58E-07	-1.67E-03	3.59E-04	7.06E-06	-8.82E-04	3.37E-04	9.12E-03
cg16305292	8	142219 965	SLC45A4;SLC45A4	3UTR;3UTR		9.00E-04	2.00E-04	3.67E-07	1.21E-03	2.88E-04	4.62E-05	6.84E-04	2.12E-04	1.31E-03
cg12378285	2	136808 729				1.00E-03	2.00E-04	3.68E-07	1.09E-03	3.16E-04	7.59E-04	9.92E-04	2.64E-04	1.89E-04
cg20493906	4	106113 303	TET2;TET2;TET2- AS1	5URT;5URT; Body		7.00E-04	1.00E-04	3.88E-07	6.56E-04	2.23E-04	3.85E-03	7.76E-04	1.86E-04	3.62E-05
cg22356061	1	227954 102	SNAP47	Body		-8.00E-04	2.00E-04	3.90E-07	-6.45E-04	2.52E-04	1.14E-02	-9.20E-04	2.06E-04	9.58E-06
cg24830274	7	418267 34			S Shelf	9.00E-04	2.00E-04	4.43E-07	7.53E-04	3.13E-04	1.74E-02	9.41E-04	2.11E-04	9.29E-06
cg05241923	9	136010 810	RALGDS	Body		-1.10E-03	2.00E-04	4.74E-07	-1.36E-03	3.02E-04	1.43E-05	-7.78E-04	2.91E-04	7.60E-03
cg02417857	3	181326 706	SOX2-OT;SOX2- OT;SOX2- OT;SOX2-	TSS1500;TSS 1500;TSS1500 ;Body;Body; Body		9.00E-04	2.00E-04	4.97E-07	1.39E-03	3.76E-04	2.95E-04	7.40E-04	1.98E-04	2.09E-04

			OT;SOX2- OT;SOX2-OT											
cg14115749	19	44	195964 GATAD2A;GA- TAD2A	Body;Body		8.00E-04	2.00E-04	5.09E-07	7.85E-04	2.55E-04	2.43E-03	7.97E-04	2.01E-04	8.15E-05
cg21586215	12	13	227779 ETNK1;ETNK1	TSS200;TSS2 00		-1.00E-04	0.00E+00	5.27E-07	-1.46E-04	6.89E-05	3.54E-02	-1.22E-04	2.68E-05	6.35E-06
cg10581989	16	86	119643 GSPT1;GSPT1;GSP T1	3UTR;3UTR; 3UTR		1.00E-03	2.00E-04	5.28E-07	1.42E-03	3.45E-04	6.11E-05	7.91E-04	2.45E-04	1.33E-03
cg20378147	1	27	320506 TINAGL1;TINAGL 1;TINAGL1;TINA GL1;TINAGL1;TIN AGL1	ExonBnd;Ex- onBnd;Ex- onBnd;Body; Body;Body		2.00E-04	0.00E+00	5.33E-07	3.76E-04	1.06E-04	4.80E-04	1.41E-04	3.42E-05	4.39E-05
cg17901584	1	06	553537 DHCR24	TSS1500		-1.40E-03	3.00E-04	5.41E-07	-2.46E-03	5.34E-04	8.32E-06	-1.01E-03	3.31E-04	2.49E-03
cg04809899	2	915	223824			8.00E-04	2.00E-04	5.59E-07	6.77E-04	2.38E-04	5.06E-03	8.92E-04	2.14E-04	3.43E-05
cg05613192	2	416	223912			1.00E-03	2.00E-04	5.64E-07	1.21E-03	3.56E-04	8.50E-04	9.29E-04	2.50E-04	2.12E-04
cg26935416	12	18	482023 HDAC7;HDAC7;H DAC7	Body;Body;B ody	S Shelf	-4.00E-04	1.00E-04	5.79E-07	-3.06E-04	1.39E-04	2.91E-02	-4.39E-04	9.63E-05	6.25E-06
cg17256791	15	64	855477 PDE8A;PDE8A;PD E8A	5URT;Body; Body		1.40E-03	3.00E-04	5.82E-07	1.01E-03	4.90E-04	4.17E-02	1.56E-03	3.35E-04	4.02E-06
cg24531955	8	91	231546 LOXL2	3UTR		-8.00E-04	2.00E-04	5.89E-07	-7.31E-04	2.56E-04	4.88E-03	-7.79E-04	1.90E-04	4.66E-05
cg07717661	15	27	643820 FAM96A;FAM96A; FAM96A;FAM96A	Body;Body;B ody;Body		1.10E-03	2.00E-04	5.98E-07	1.24E-03	3.56E-04	6.66E-04	1.05E-03	2.92E-04	3.33E-04
cg26236214	13	078	111867 ARHGEF7;ARHGE F7;ARHGEF7;ARH GEF7;ARHGEF7	5URT;5URT; Body;Body;B ody		9.00E-04	2.00E-04	6.04E-07	1.30E-03	3.33E-04	1.42E-04	7.48E-04	2.20E-04	7.08E-04
cg08857797	17	99	409276 VPS25	Body		1.10E-03	2.00E-04	6.37E-07	1.43E-03	3.31E-04	2.90E-05	8.00E-04	2.77E-04	4.04E-03
cg10785394	1	006	178993			7.00E-04	1.00E-04	6.56E-07	7.91E-04	1.98E-04	9.97E-05	6.57E-04	2.19E-04	2.83E-03
cg05708512	5	91	317313			-8.00E-04	2.00E-04	6.58E-07	-7.00E-04	2.18E-04	1.59E-03	-9.60E-04	2.48E-04	1.18E-04
cg21575225	1	485	156073 LMNA	5URT		-1.10E-03	2.00E-04	6.88E-07	-1.41E-03	3.46E-04	7.20E-05	-8.84E-04	2.89E-04	2.29E-03
cg22028323	10	58	984867			9.00E-04	2.00E-04	6.96E-07	6.97E-04	3.15E-04	2.85E-02	1.05E-03	2.31E-04	6.94E-06
cg21506763	3	29	380603 PLCD1;PLCD1;PL CD1	Body;Body;B ody		7.00E-04	1.00E-04	7.02E-07	9.83E-04	2.83E-04	6.74E-04	6.43E-04	1.74E-04	2.44E-04

cg08373547	14	527945 41	PTGER2	3UTR		1.10E-03	2.00E-04	7.13E-07	9.31E-04	3.20E-04	4.13E-03	1.19E-03	2.94E-04	5.55E-05
cg04401764	12	547773 96	ZNF385A;ZNF385A; ZNF385A;ZNF385A; ZNF385A;LOC102724050;LOC102724050	Body;Body;Body; Body;Body;Body; Body;Body;Body		8.00E-04	2.00E-04	7.19E-07	7.54E-04	2.86E-04	9.26E-03	8.95E-04	2.12E-04	2.84E-05
cg18942579	17	579157 73	VMP1;VMP1	Ex-onBnd;Body		-1.60E-03	3.00E-04	7.50E-07	-1.99E-03	4.81E-04	5.58E-05	-1.24E-03	4.19E-04	3.27E-03
cg19822755	16	301082 59	YPEL3;YPEL3	TSS1500;TSS1500		7.00E-04	1.00E-04	7.50E-07	5.94E-04	2.88E-04	4.10E-02	7.39E-04	1.63E-04	7.39E-06
cg03351508	21	165915 98				-1.40E-03	3.00E-04	7.81E-07	-2.03E-03	5.77E-04	5.67E-04	-1.23E-03	3.35E-04	2.64E-04
cg13139542	2	824281 5	LINC00299	Body		4.00E-04	1.00E-04	7.91E-07	7.91E-04	2.44E-04	1.44E-03	3.75E-04	9.25E-05	5.75E-05
cg21733150	1	670293 21	SGIP1;SGIP1	Body;Body		-1.00E-03	2.00E-04	8.08E-07	-9.91E-04	2.66E-04	2.76E-04	-9.35E-04	2.88E-04	1.26E-03
cg17871993	7	656730 56	TPST1	5URT		5.00E-04	1.00E-04	8.08E-07	4.65E-04	1.70E-04	6.96E-03	6.02E-04	1.45E-04	3.76E-05
cg17680767	5	736232 08	LINC01333	Body		-8.00E-04	2.00E-04	8.09E-07	-6.92E-04	2.62E-04	9.03E-03	-9.20E-04	2.18E-04	2.82E-05
cg07190151	5	583385 74	PDE4D;PDE4D;PDE4D;PDE4D;PDE4D	Body;Body;Body;Body;Body	S Shelf	-6.00E-04	1.00E-04	8.27E-07	-8.36E-04	1.89E-04	1.82E-05	-4.68E-04	1.81E-04	9.90E-03
cg08640498	12	578285 15	INHBC;INHBC	5URT;1stExon		5.00E-04	1.00E-04	8.51E-07	5.80E-04	1.63E-04	5.07E-04	4.89E-04	1.42E-04	6.31E-04
cg02040103	4	224751 52	ADGRA3	Body	S Shelf	-1.20E-03	2.00E-04	8.52E-07	-1.79E-03	4.38E-04	6.77E-05	-9.29E-04	2.91E-04	1.50E-03
cg12256648	3	143752 097				1.50E-03	3.00E-04	8.75E-07	1.56E-03	3.84E-04	7.79E-05	1.44E-03	5.19E-04	5.57E-03
cg07124045	10	103595 509	KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2	Body;Body;Body;Body;Body		3.00E-04	1.00E-04	8.80E-07	5.61E-04	2.01E-04	5.88E-03	2.63E-04	6.13E-05	2.08E-05
cg09018739	16	571801 07	CPNE2	Body		8.00E-04	2.00E-04	8.98E-07	1.06E-03	2.92E-04	3.77E-04	6.97E-04	2.01E-04	5.75E-04
cg19432644	1	156165 820	SLC25A44;SLC25A44;SLC25A44;SLC25A44	5URT;5URT;Ex-onBnd;Body;Body;Body		6.00E-04	1.00E-04	9.26E-07	7.00E-04	1.66E-04	4.15E-05	4.43E-04	1.62E-04	6.34E-03
cg02650017	17	473016 14	PHOSPHO1;PHOSPHO1	Body;Body		-2.00E-04	0.00E+00	9.42E-07	-4.20E-04	1.47E-04	4.75E-03	-2.03E-04	4.80E-05	2.80E-05

cg02112168	14	455795 61	SNORD127;PRPF3	TSS1500;Body		1.00E-03	2.00E-04	9.49E-07	1.13E-03	3.23E-04	6.03E-04	9.70E-04	2.81E-04	5.96E-04
cg00094538	7	142505 684				-8.00E-04	2.00E-04	9.55E-07	-6.53E-04	2.51E-04	1.02E-02	-1.01E-03	2.37E-04	2.12E-05
cg24392515	14	245784 15				7.00E-04	1.00E-04	9.56E-07	7.60E-04	2.03E-04	2.57E-04	6.99E-04	2.21E-04	1.60E-03
cg13093111	17	663085 77	ARSG;ARSG	Body;Body		1.60E-03	3.00E-04	9.86E-07	1.87E-03	5.10E-04	3.44E-04	1.40E-03	4.21E-04	9.34E-04
cg02108045	12	939620 28	SOCS2-AS1	Body		6.00E-04	1.00E-04	1.01E-06	3.89E-04	1.80E-04	3.19E-02	8.94E-04	1.86E-04	2.00E-06
cg08505450	17	478360 75	FAM117A	Body		-3.00E-04	1.00E-04	1.01E-06	-2.27E-04	1.84E-04	2.19E-01	-2.59E-04	5.47E-05	2.72E-06
cg06373268	2	790415 85				6.00E-04	1.00E-04	1.01E-06	7.82E-04	2.91E-04	8.08E-03	5.22E-04	1.25E-04	3.47E-05
cg01995927	1	242578 39				9.00E-04	2.00E-04	1.02E-06	8.86E-04	3.01E-04	3.69E-03	9.95E-04	2.54E-04	1.03E-04
cg15043602	17	170794 54	MPRIP;MPRIP	Body;Body		6.00E-04	1.00E-04	1.04E-06	7.81E-04	2.09E-04	2.68E-04	5.45E-04	1.67E-04	1.12E-03
cg20426042	8	977787 09	CPQ	5URT		1.40E-03	3.00E-04	1.05E-06	1.34E-03	4.00E-04	1.04E-03	1.58E-03	4.40E-04	3.66E-04
cg02535555	3	121990 376	CASR;CASR	Body;Body	S Shore	-5.00E-04	1.00E-04	1.10E-06	-4.28E-04	1.58E-04	7.58E-03	-6.28E-04	1.51E-04	3.70E-05
cg13053471	1	235147 039				-7.00E-04	1.00E-04	1.11E-06	-7.83E-04	2.09E-04	2.61E-04	-5.97E-04	1.87E-04	1.48E-03
cg19818308	14	759467 45			N Shore	9.00E-04	2.00E-04	1.13E-06	1.06E-03	2.74E-04	1.54E-04	8.20E-04	2.73E-04	2.76E-03
cg08108165	15	574104 18	TCF12;TCF12;TCF1 2;TCF12	Body;Body;B ody;Body		-9.00E-04	2.00E-04	1.14E-06	-1.03E-03	2.73E-04	2.28E-04	-7.47E-04	2.36E-04	1.60E-03
cg08350157	3	131219 430	MRPL3	Body	N Shelf	-6.00E-04	1.00E-04	1.14E-06	-4.00E-04	1.99E-04	4.59E-02	-6.48E-04	1.43E-04	6.55E-06
cg16097041	1	154965 544	LE- NEP;FLAD1;FLAD 1;FLAD1	TSS1500;3UT R;3UTR;3UT R		7.00E-04	1.00E-04	1.14E-06	4.97E-04	2.11E-04	1.97E-02	7.92E-04	1.80E-04	1.34E-05
cg26248007	13	487307 82				7.00E-04	1.00E-04	1.15E-06	8.57E-04	3.05E-04	5.68E-03	6.66E-04	1.66E-04	6.74E-05
cg19377661	3	142605 811	PCOLCE2	Body		-2.10E-03	4.00E-04	1.18E-06	-1.20E-03	6.47E-04	6.56E-02	-2.79E-03	5.74E-04	1.54E-06
cg21134922	5	605869 09				7.00E-04	1.00E-04	1.18E-06	3.59E-04	2.13E-04	9.38E-02	8.47E-04	1.73E-04	1.27E-06
cg03413355	15	565375 79				1.10E-03	2.00E-04	1.19E-06	8.84E-04	3.30E-04	8.08E-03	1.31E-03	3.16E-04	3.68E-05
cg09495478	3	449381 02	TGM4	Body	S Shore	4.00E-04	1.00E-04	1.24E-06	4.58E-04	1.27E-04	4.18E-04	3.77E-04	1.15E-04	1.12E-03

cg18522582	2	223915 743	KCNE4	TSS1500		1.60E-03	3.00E-04	1.26E-06	1.15E-03	5.70E-04	4.53E-02	1.89E-03	4.18E-04	7.01E-06
cg10937494	17	801951 01	SLC16A3;SLC16A3 ;SLC16A3;SLC16A 3;SLC16A3;SLC16 A3	Body;Body;B ody;Body;Bo dy;Body		6.00E-04	1.00E-04	1.31E-06	7.99E-04	2.17E-04	3.28E-04	5.17E-04	1.56E-04	9.54E-04
cg23830794	14	944761 86	LINC00521	Body		2.00E-03	4.00E-04	1.33E-06	1.16E-03	5.80E-04	4.75E-02	2.80E-03	5.79E-04	1.64E-06
cg10969521	21	363555 37	RUNX1	Body		-1.50E-03	3.00E-04	1.40E-06	-1.52E-03	4.60E-04	1.19E-03	-1.42E-03	4.03E-04	4.60E-04
cg05948408	5	881785 72	MEF2C;MEF2C;M EF2C;MEF2C;MEF 2C-AS1	5URT;5URT; 5URT;5URT; TSS1500		1.00E-04	0.00E+00	1.40E-06	1.26E-04	8.30E-05	1.30E-01	1.30E-04	2.85E-05	5.56E-06
cg00379740	17	385075 18	RARA;RARA;RAR A;RARA	Body;Body;B ody;Body		6.00E-04	1.00E-04	1.40E-06	6.71E-04	1.74E-04	1.67E-04	4.79E-04	1.59E-04	2.75E-03
cg12769615	4	956531 56				7.00E-04	1.00E-04	1.44E-06	5.60E-04	2.55E-04	3.00E-02	7.92E-04	1.82E-04	1.54E-05
cg00994936	19	142390 2	DAZAP1;DAZAP1	Body;Body		5.00E-04	1.00E-04	1.50E-06	7.25E-04	2.05E-04	5.25E-04	3.91E-04	1.10E-04	3.98E-04
cg16197636	8	422347 24	DKK4	TSS200		1.30E-03	3.00E-04	1.59E-06	1.00E-03	3.63E-04	6.56E-03	1.72E-03	4.16E-04	3.89E-05
cg23006541	11	680756 47				1.00E-03	2.00E-04	1.59E-06	4.36E-04	3.15E-04	1.67E-01	1.33E-03	2.61E-04	4.75E-07
cg13264822	7	137565 290	CREB3L2	Body		5.00E-04	1.00E-04	1.59E-06	9.38E-04	3.18E-04	3.71E-03	4.13E-04	1.01E-04	4.61E-05
cg11804293	4	900562 55				7.00E-04	2.00E-04	1.59E-06	6.56E-04	2.59E-04	1.23E-02	7.91E-04	1.93E-04	4.77E-05
cg03866862	6	334015 42	SYNGAP1	Body		8.00E-04	2.00E-04	1.66E-06	6.69E-04	2.93E-04	2.36E-02	8.73E-04	2.05E-04	2.47E-05
cg26120813	12	133000 792				1.10E-03	2.00E-04	1.66E-06	3.29E-04	4.40E-04	4.55E-01	1.31E-03	2.57E-04	4.21E-07
cg04211591	2	230159 830				1.80E-03	4.00E-04	1.67E-06	2.34E-03	6.23E-04	2.38E-04	1.53E-03	4.87E-04	1.78E-03
cg21786446	2	160462 426	BAZ2B;BAZ2B	5URT;5URT	S Shore	1.00E-03	2.00E-04	1.68E-06	8.32E-04	2.36E-04	5.49E-04	1.40E-03	4.04E-04	5.88E-04
cg22513955	17	166512 3	SERPINF1	TSS200		5.00E-04	1.00E-04	1.70E-06	6.76E-04	1.58E-04	3.17E-05	3.78E-04	1.49E-04	1.16E-02
cg03741348	1	327122 37	FAM167B	TSS1500		7.00E-04	1.00E-04	1.72E-06	7.88E-04	2.03E-04	1.56E-04	5.92E-04	2.05E-04	4.06E-03
cg08673945	9	204906 77	MLLT3;MLLT3	Body;Body		-1.00E-03	2.00E-04	1.74E-06	-1.44E-03	3.50E-04	6.25E-05	-7.96E-04	2.82E-04	4.87E-03
cg20978247	6	329050 85	HLA-DMB	Body	S Shore	1.80E-03	4.00E-04	1.79E-06	2.07E-03	6.02E-04	7.48E-04	1.65E-03	4.91E-04	8.34E-04

cg23098236	4	397160 40	UBE2K;UBE2K;UB E2K	Body;Body;B ody		1.30E-03	3.00E-04	1.83E-06	1.21E-03	3.68E-04	1.26E-03	1.38E-03	3.96E-04	5.47E-04
cg09041527	8	116594 97	1	5URT;5URT; FDFT1;FDFT1;FDF T1;FDFT1;FDFT1;F DFT1;FDFT1;FDFT ;TSS1500;TSS 1500;TSS1500 1500;5URT		-5.00E-04	1.00E-04	1.86E-06	-5.67E-04	1.53E-04	2.90E-04	-3.88E-04	1.24E-04	1.83E-03
cg11793449	17	763138 72				-6.00E-04	1.00E-04	1.87E-06	-7.14E-04	1.73E-04	6.08E-05	-4.46E-04	1.69E-04	8.63E-03
cg23998749	1	154968 781				5.00E-04	1.00E-04	1.88E-06	3.94E-04	1.67E-04	1.93E-02	6.40E-04	1.50E-04	2.13E-05
cg12989718	16	473935 2	MGRN1;MGRN1; MGRN1;MGRN1; MGRN1	3UTR;3UTR; 3UTR;3UTR; Body		4.00E-04	1.00E-04	1.91E-06	3.96E-04	1.23E-04	1.55E-03	3.48E-04	9.89E-05	4.63E-04
cg18091083	17	788190 92	RPTOR;RPTOR	Body;Body		1.20E-03	2.00E-04	1.99E-06	1.35E-03	3.65E-04	2.91E-04	1.04E-03	3.42E-04	2.45E-03
cg03808896	5	132160 489	SHROOM1;SHRO OM1	Body;Body		8.00E-04	2.00E-04	2.02E-06	8.56E-04	2.84E-04	3.00E-03	8.14E-04	2.21E-04	2.60E-04
cg12712122	6	884353 12				9.00E-04	2.00E-04	2.11E-06	7.04E-04	2.75E-04	1.13E-02	1.08E-03	2.63E-04	4.46E-05
cg10183965	17	382449 7				7.00E-04	1.00E-04	2.13E-06	8.93E-04	2.71E-04	1.24E-03	5.70E-04	1.60E-04	3.96E-04
cg26943120	4	547211 6	STK32B;STK32B	Body;Body	S Shore	1.30E-03	3.00E-04	2.13E-06	1.35E-03	4.30E-04	2.06E-03	1.20E-03	3.37E-04	3.89E-04
cg17980786	3	329336 37	TRIM71	3UTR		6.00E-04	1.00E-04	2.15E-06	7.11E-04	2.00E-04	5.15E-04	5.91E-04	1.86E-04	1.59E-03
cg23886355	13	113662 042	MCF2L;MCF2L	Body;Body	S Shore	6.00E-04	1.00E-04	2.20E-06	5.46E-04	1.95E-04	5.70E-03	6.53E-04	1.70E-04	1.37E-04
cg04695090	22	386095 08	MAFF;MAFF;MAF F;MAFF	5URT;5URT; 5URT;5URT		6.00E-04	1.00E-04	2.24E-06	4.56E-04	1.90E-04	1.74E-02	7.11E-04	1.69E-04	3.10E-05
cg19695507	10	135261 93	BEND7;BEND7	Body;Body		6.00E-04	1.00E-04	2.25E-06	1.29E-03	2.66E-04	3.00E-06	3.99E-04	1.46E-04	6.42E-03
cg01790438	5	103321 17				2.00E-04	1.00E-04	2.27E-06	2.77E-04	1.02E-04	7.13E-03	2.25E-04	5.77E-05	1.11E-04
cg22690339	6	382490 61	BTBD9;BTBD9;BTB D9;BTBD9	Body;Body;B ody;Body		8.00E-04	2.00E-04	2.29E-06	9.04E-04	2.78E-04	1.41E-03	7.97E-04	2.31E-04	6.14E-04

cg02688432	1	919707 45	CDC7;CDC7;CDC7	Body;Body;B ody		8.00E-04	2.00E-04	2.92E-06	6.06E-04	2.78E-04	3.08E-02	9.88E-04	2.31E-04	2.23E-05
cg20360704	4	113739 170	ANK2	TSS200		4.00E-04	1.00E-04	3.03E-06	5.10E-04	1.79E-04	5.05E-03	4.03E-04	1.08E-04	2.03E-04
cg17868815	16	814767 31				9.00E-04	2.00E-04	3.07E-06	7.66E-04	2.80E-04	7.06E-03	9.14E-04	2.40E-04	1.55E-04
cg23508887	18	135020 53	LDLRAD4;LDLRA D4	Body;Body		9.00E-04	2.00E-04	3.10E-06	1.18E-03	3.32E-04	5.02E-04	7.79E-04	2.46E-04	1.59E-03
cg12489028	2	325681 46			N Shore	-8.00E-04	2.00E-04	3.13E-06	-1.04E-03	2.29E-04	1.02E-05	-5.09E-04	2.97E-04	8.66E-02
cg14458725	2	143621 423				3.00E-04	1.00E-04	3.14E-06	3.12E-04	2.13E-04	1.45E-01	3.36E-04	7.60E-05	1.14E-05
cg12042252	2	735960 96				8.00E-04	2.00E-04	3.17E-06	5.45E-04	2.54E-04	3.34E-02	1.04E-03	2.37E-04	1.43E-05
cg26315985	1	653638 70	JAK1	5URT		-8.00E-04	2.00E-04	3.23E-06	-8.45E-04	3.45E-04	1.55E-02	-7.27E-04	1.83E-04	7.99E-05
cg13518625	8	295228 38			N Shore	-6.00E-04	1.00E-04	3.28E-06	-5.34E-04	2.84E-04	6.22E-02	-5.60E-04	1.32E-04	2.38E-05
cg10457997	17	647965 07	PRKCA	Body		8.00E-04	2.00E-04	3.32E-06	7.37E-04	2.80E-04	9.48E-03	9.23E-04	2.38E-04	1.19E-04
cg09837467	1	183523 933			S Shore	9.00E-04	2.00E-04	3.36E-06	9.68E-04	2.86E-04	9.03E-04	8.70E-04	2.72E-04	1.47E-03
cg14634473	10	231054 37				-9.00E-04	2.00E-04	3.36E-06	-8.89E-04	2.66E-04	1.06E-03	-8.35E-04	2.58E-04	1.27E-03
cg01433332	16	854075 75				4.00E-04	1.00E-04	3.40E-06	3.17E-04	1.99E-04	1.13E-01	3.74E-04	8.56E-05	1.47E-05
cg02191659	17	101546 29				6.00E-04	1.00E-04	3.40E-06	7.94E-04	2.24E-04	5.31E-04	5.46E-04	1.74E-04	1.81E-03
cg12239530	22	320249 63	PISD	5URT		1.20E-03	3.00E-04	3.41E-06	1.28E-03	5.06E-04	1.28E-02	1.23E-03	3.16E-04	1.05E-04
cg12776836	9	123268 2				1.00E-03	2.00E-04	3.44E-06	9.34E-04	3.63E-04	1.10E-02	1.05E-03	2.71E-04	1.19E-04
cg26403843	5	158634 085	RNF145;RNF145;R NF145;RNF145;RN F145	5URT;Body; Body;Body;B ody		1.30E-03	3.00E-04	3.45E-06	7.38E-04	4.17E-04	7.85E-02	1.86E-03	3.94E-04	2.96E-06
cg27023597	17	579182 62	MIR21	TSS1500		-1.20E-03	3.00E-04	3.53E-06	-1.14E-03	4.00E-04	4.87E-03	-1.20E-03	3.27E-04	2.78E-04
cg22413912	7	225575 8	MAD1L1;MAD1L1 ;MAD1L1;MAD1L 1;MAD1L1	Body;Body;B ody;Body;Bo dy		-7.00E-04	1.00E-04	3.53E-06	-6.03E-04	2.42E-04	1.37E-02	-7.04E-04	1.79E-04	9.63E-05
cg06469895	16	694182 06	TERF2	Body		7.00E-04	2.00E-04	3.67E-06	1.16E-03	2.68E-04	2.71E-05	4.92E-04	1.88E-04	8.90E-03

cg25124889	13	243270 15	MIPEP	Body		8.00E-04	2.00E-04	3.78E-06	7.90E-04	2.28E-04	6.71E-04	7.16E-04	2.34E-04	2.30E-03
cg04595884	17	588700 64	BCAS3;BCAS3	Body;Body		9.00E-04	2.00E-04	3.80E-06	5.18E-04	3.24E-04	1.12E-01	1.08E-03	2.37E-04	6.21E-06
cg03068437	1	170037 915	KIFAP3;KIFAP3;KIFAP3;KIFAP3;KIFAP3	1stExon;5UR T;5URT;Body	N Shelf	-1.00E-03	2.00E-04	3.89E-06	-1.07E-03	2.95E-04	3.77E-04	-8.71E-04	3.02E-04	4.04E-03
cg04585778	17	543952 92	ANKFN1	Body		6.00E-04	1.00E-04	3.89E-06	6.20E-04	2.16E-04	4.74E-03	6.63E-04	1.83E-04	3.14E-04
cg23204398	8	126365 081	NSMCE2	Body		1.40E-03	3.00E-04	3.90E-06	7.82E-04	4.34E-04	7.34E-02	1.87E-03	4.03E-04	4.47E-06
cg17418742	11	156020 30				5.00E-04	1.00E-04	3.94E-06	7.28E-04	2.64E-04	6.60E-03	4.96E-04	1.31E-04	1.68E-04
cg24913868	10	101296 069	NKX2-3	3UTR		-6.00E-04	1.00E-04	3.99E-06	-5.65E-04	1.98E-04	4.91E-03	-5.97E-04	1.65E-04	3.13E-04
cg20301125	5	130975 565				9.00E-04	2.00E-04	4.00E-06	1.24E-03	2.89E-04	3.06E-05	6.28E-04	2.76E-04	2.33E-02
cg04725636	8	670045 38	DNAJC5B	Body	N Shore	-1.30E-03	3.00E-04	4.05E-06	-1.84E-03	4.81E-04	1.90E-04	-9.95E-04	3.38E-04	3.34E-03
cg16011130	4	856032 17	WDFY3	Body		8.00E-04	2.00E-04	4.15E-06	8.91E-04	2.47E-04	4.26E-04	6.58E-04	2.23E-04	3.29E-03
cg01820374	12	688208 3	LAG3	Body		-8.00E-04	2.00E-04	4.23E-06	-9.81E-04	2.38E-04	5.99E-05	-5.47E-04	2.26E-04	1.56E-02
cg22246215	1	203118 486	ADORA1;ADORA1	Body;Body		6.00E-04	1.00E-04	4.24E-06	5.40E-04	1.89E-04	4.87E-03	5.79E-04	1.60E-04	3.33E-04
cg18062721	3	116434 27	VGLL4;VGLL4;VGLL4;VGLL4	5URT;Body;Body;Body		1.10E-03	2.00E-04	4.25E-06	1.34E-03	3.72E-04	4.40E-04	9.70E-04	3.27E-04	3.14E-03
cg14946327	9	969185 29				4.00E-04	1.00E-04	4.26E-06	4.31E-04	1.40E-04	2.54E-03	4.65E-04	1.36E-04	6.45E-04
cg07328569	1	615244 38				-7.00E-04	2.00E-04	4.31E-06	-1.19E-03	3.07E-04	1.59E-04	-5.33E-04	1.72E-04	2.02E-03
cg16766623	2	218812 908				3.00E-04	1.00E-04	4.36E-06	4.98E-04	1.45E-04	7.83E-04	2.73E-04	8.17E-05	8.79E-04
cg22530144	2	463008 69	PRKCE	Body		-8.00E-04	2.00E-04	4.42E-06	-7.86E-04	2.62E-04	3.13E-03	-9.03E-04	2.59E-04	5.20E-04
cg16416819	9	127022 538	NEK6;NEK6;NEK6;NEK6	Body;5URT;5URT;5URT		8.00E-04	2.00E-04	4.46E-06	1.18E-03	2.91E-04	8.04E-05	5.58E-04	2.01E-04	5.62E-03
cg02485044	13	502343 43				6.00E-04	1.00E-04	4.49E-06	3.09E-04	2.26E-04	1.73E-01	6.73E-04	1.47E-04	5.50E-06
cg19543782	10	357754 90	CCNY;CCNY;CCNY;CCNY	Body;Body;5URT;Body;Body		5.00E-04	1.00E-04	4.55E-06	8.74E-04	2.15E-04	7.63E-05	3.95E-04	1.40E-04	4.87E-03

cg10705487	5	179108 352	CBY3	TSS1500		5.00E-04	1.00E-04	4.55E-06	5.24E-04	1.86E-04	5.38E-03	5.55E-04	1.54E-04	3.25E-04
cg01409343	17	579157 40	VMP1;VMP1	Ex- onBnd;Body		-1.10E-03	2.00E-04	4.64E-06	-1.76E-03	3.76E-04	6.28E-06	-6.45E-04	3.10E-04	3.77E-02
cg01538166	17	177439 87				-9.00E-04	2.00E-04	4.69E-06	-1.17E-03	3.37E-04	6.46E-04	-7.85E-04	2.52E-04	1.94E-03
cg16954329	5	103239 87				1.00E-03	2.00E-04	4.70E-06	1.17E-03	3.98E-04	3.71E-03	9.13E-04	2.58E-04	4.21E-04
cg19750024	8	220681 89	BMP1;BMP1	Body;Body	S Shore	-8.00E-04	2.00E-04	4.78E-06	-1.24E-03	2.97E-04	5.27E-05	-5.75E-04	2.20E-04	9.25E-03
cg02233071	21	361810 46	RUNX1;RUNX1	Body;Body		-1.30E-03	3.00E-04	4.82E-06	-1.33E-03	4.78E-04	5.95E-03	-1.32E-03	3.65E-04	3.13E-04
cg23467004	19	129122 44	PRDX2	5URT		-2.00E-04	1.00E-04	4.92E-06	-3.16E-04	8.54E-05	3.01E-04	-1.93E-04	6.63E-05	3.72E-03
cg16029189	1	201504 437				-7.00E-04	1.00E-04	4.93E-06	-5.87E-04	2.43E-04	1.69E-02	-7.10E-04	1.82E-04	1.07E-04
cg27438980	15	991951 43	IRAIN;JGF1R;JGF1 R	TSS1500;Bod y;Body		-8.00E-04	2.00E-04	5.03E-06	-8.17E-04	3.26E-04	1.31E-02	-7.60E-04	1.99E-04	1.49E-04
cg04610187	17	763607 94	LOC101928674;LO C101928674;LOC10 1928674	Body;Body;B ody		-1.00E-03	2.00E-04	5.05E-06	-1.43E-03	2.77E-04	7.43E-07	-3.23E-04	3.20E-04	3.14E-01
cg03936075	6	113704 79	NEDD9;NEDD9	5URT;Body		8.00E-04	2.00E-04	5.18E-06	6.53E-04	3.18E-04	4.16E-02	8.88E-04	2.16E-04	4.40E-05
cg00607627	16	289959 94	LAT;LAT;LAT;LA T	TSS1500;TSS 1500;TSS1500 ;TSS200		-5.00E-04	1.00E-04	5.20E-06	-3.96E-04	1.82E-04	3.11E-02	-5.67E-04	1.39E-04	5.25E-05
cg00218090	14	100485 810			S Shelf	5.00E-04	1.00E-04	5.21E-06	4.24E-04	2.59E-04	1.03E-01	5.42E-04	1.27E-04	2.24E-05
cg26326160	20	419210 81				1.20E-03	3.00E-04	5.41E-06	1.74E-03	4.12E-04	4.26E-05	8.37E-04	3.51E-04	1.74E-02
cg21313072	18	436405 08	PSTPIP2	Body		4.00E-04	1.00E-04	5.43E-06	3.81E-04	1.53E-04	1.40E-02	4.50E-04	1.18E-04	1.44E-04
cg27285287	2	234094 884	INPP5D;INPP5D	Body;Body		1.10E-03	2.00E-04	5.45E-06	1.27E-03	3.64E-04	6.50E-04	9.04E-04	2.99E-04	2.59E-03
cg09057405	14	248209 50			S Shelf	8.00E-04	2.00E-04	5.61E-06	5.94E-04	2.51E-04	1.91E-02	9.33E-04	2.33E-04	7.11E-05
cg01867298	11	117689 143				-5.00E-04	1.00E-04	5.62E-06	-4.06E-04	1.95E-04	3.87E-02	-5.01E-04	1.23E-04	5.66E-05
cg18333255	2	203686 636	ICA1L;ICA1L;ICA 1L;ICA1L	Body;Body;B ody;Body		6.00E-04	1.00E-04	5.70E-06	3.15E-04	2.13E-04	1.40E-01	8.91E-04	1.88E-04	2.57E-06
cg15357118	2	128927 972	UGGT1;UGGT1;U GGT1;UGGT1	ExonBnd;Ex- onBnd;Body; Body		7.00E-04	2.00E-04	5.71E-06	7.81E-04	2.17E-04	4.21E-04	6.09E-04	2.16E-04	5.09E-03

cg11635053	3	184055 217	FAM131A;FAM131 A	TSS200;5UR T		-1.00E-04	0.00E+00	5.75E-06	-8.36E-05	1.51E-04	5.80E-01	-8.31E-05	1.85E-05	8.14E-06
cg09530861	6	107776 494	PDSS2	Body		4.00E-04	1.00E-04	5.76E-06	5.92E-04	2.21E-04	8.34E-03	3.81E-04	1.01E-04	1.82E-04
cg27662789	12	436662 81				1.80E-03	4.00E-04	5.80E-06	1.74E-03	8.54E-04	4.36E-02	1.75E-03	4.33E-04	5.69E-05
cg05284742	14	935521 28	ITPK1;ITPK1;ITPK 1	Body;Body;B ody		4.00E-04	1.00E-04	5.83E-06	3.30E-04	1.63E-04	4.52E-02	4.31E-04	1.05E-04	4.86E-05
cg03523676	14	245402 35	CPNE6;CPNE6	TSS1500;1stE xon		8.00E-04	2.00E-04	5.84E-06	9.21E-04	2.82E-04	1.32E-03	6.64E-04	2.06E-04	1.34E-03
cg11121826	17	751059 57	SEC14L1;SEC14L1	5URT;5URT		4.00E-04	1.00E-04	5.85E-06	3.13E-04	1.77E-04	8.01E-02	4.50E-04	1.07E-04	2.70E-05
cg05778424	17	551695 08	AKAP1;AKAP1;A KAP1	5URT;5URT; 5URT		9.00E-04	2.00E-04	5.89E-06	9.47E-04	3.26E-04	4.21E-03	8.48E-04	2.43E-04	5.26E-04
cg17739917	17	384775 72	RARA;RARA;RAR A	5URT;5URT; 5URT		1.30E-03	3.00E-04	5.90E-06	5.82E-04	4.25E-04	1.73E-01	2.03E-03	4.09E-04	8.57E-07
cg07235958	1	155974 953			S Shore	-7.00E-04	2.00E-04	5.94E-06	-4.47E-04	2.01E-04	2.77E-02	-9.94E-04	2.29E-04	1.69E-05
cg08298283	10	725398 36	TBATA	Body		9.00E-04	2.00E-04	6.16E-06	9.94E-04	3.39E-04	3.89E-03	8.98E-04	2.60E-04	5.99E-04
cg22688566	17	274598 35	MYO18A;MYO18A	Body;Body	Island	7.00E-04	2.00E-04	6.21E-06	5.14E-04	2.35E-04	3.01E-02	9.71E-04	2.32E-04	3.20E-05
cg10381071	15	703910 35	TLE3;TLE3;TLE3;T LE3;TLE3	TSS1500;TSS 1500;TSS1500 ;TSS1500;TSS 1500		-5.00E-04	1.00E-04	6.26E-06	-5.55E-04	1.73E-04	1.63E-03	-5.02E-04	1.57E-04	1.50E-03
cg27529460	11	278788 75				1.80E-03	4.00E-04	6.28E-06	4.92E-04	6.27E-04	4.34E-01	2.62E-03	5.07E-04	3.02E-07
cg05948127	7	107577 779	LAMB1	Body		1.50E-03	3.00E-04	6.30E-06	1.35E-03	5.41E-04	1.37E-02	1.67E-03	4.40E-04	1.63E-04
cg12972064	3	171887 393	FNDC3B;FNDC3B	Body;Body		-1.10E-03	2.00E-04	6.33E-06	-1.49E-03	3.80E-04	1.36E-04	-7.91E-04	2.96E-04	7.66E-03
cg17075888	7	952253 39	PDK4	Body		-1.20E-03	3.00E-04	6.40E-06	-6.83E-04	3.42E-04	4.77E-02	-1.87E-03	4.05E-04	4.40E-06
cg02119938	15	785050 51	ACSBG1;ACSBG1	Body;Body		-6.00E-04	1.00E-04	6.40E-06	-6.46E-04	2.88E-04	2.64E-02	-5.76E-04	1.47E-04	9.72E-05
cg22045206	21	447523 69	LINC00322	TSS1500		3.00E-04	1.00E-04	6.46E-06	6.92E-04	1.57E-04	2.00E-05	2.19E-04	7.61E-05	4.12E-03
cg15985580	10	121111 744	GRK5	Body		-1.60E-03	4.00E-04	6.47E-06	-2.54E-03	8.66E-04	3.86E-03	-1.43E-03	3.94E-04	3.17E-04
cg17808676	2	182332 122	ITGA4	Body		1.00E-03	2.00E-04	6.48E-06	1.11E-03	3.61E-04	2.50E-03	9.92E-04	3.00E-04	9.84E-04

cg24597457	7	641	129028 AHCYL2;AHCYL2 ;AHCYL2;AHCYL	Body;Body;B ody;Body	N Shore	8.00E-04	2.00E-04	6.64E-06	1.17E-03	3.62E-04	1.56E-03	6.99E-04	2.09E-04	8.78E-04
cg27216853	2	72	102056 CYS1	Body		8.00E-04	2.00E-04	6.81E-06	1.25E-03	3.02E-04	5.86E-05	5.57E-04	2.16E-04	1.03E-02
cg21414092	15	54	812482 MESDC2;MESDC2	Body;Body		-8.00E-04	2.00E-04	6.85E-06	-1.23E-03	2.89E-04	3.73E-05	-5.19E-04	2.10E-04	1.35E-02
cg05013695	10	98	990797 FRAT1	1stExon		1.00E-04	0.00E+00	6.86E-06	5.53E-05	8.91E-05	5.36E-01	7.36E-05	1.65E-05	9.64E-06
cg00010572	2	3	834501 LINC00299	Body		5.00E-04	1.00E-04	6.88E-06	5.35E-04	3.12E-04	8.86E-02	4.61E-04	1.11E-04	3.54E-05
cg04136321	6	33	320939 ATF6B;ATF6B	Body;Body		6.00E-04	1.00E-04	6.90E-06	5.23E-04	2.08E-04	1.30E-02	5.88E-04	1.57E-04	2.02E-04
cg14052997	10	46	895755 ATAD1	5URT		3.00E-04	1.00E-04	6.99E-06	3.69E-04	1.04E-04	5.28E-04	2.80E-04	9.85E-05	4.70E-03
cg16956116	6	76	824568 FAM46A	3UTR		1.00E-03	2.00E-04	7.03E-06	1.31E-03	3.55E-04	3.15E-04	8.28E-04	2.99E-04	5.76E-03
cg06096336	2	800	231989 HTR2B;HTR2B;PS MD1;PSMD1;PSM D1	5URT;1stExo n;Body;Body ;Body		1.10E-03	3.00E-04	7.06E-06	1.47E-03	3.46E-04	3.64E-05	7.42E-04	3.62E-04	4.06E-02
cg11847601	16	54	571800 CPNE2	Body		4.00E-04	1.00E-04	7.07E-06	5.86E-04	1.59E-04	3.20E-04	3.30E-04	1.14E-04	4.04E-03
cg19603202	22	26	384317 POLR2F;POLR2F	Body;Body		4.00E-04	1.00E-04	7.13E-06	3.93E-04	1.17E-04	1.02E-03	3.25E-04	1.08E-04	2.61E-03
cg22256420	10	6	406036			6.00E-04	1.00E-04	7.19E-06	4.52E-04	1.70E-04	8.78E-03	7.42E-04	1.96E-04	1.66E-04
cg18520125	13	26	289039 FLT1	Body		7.00E-04	1.00E-04	7.38E-06	9.65E-04	2.95E-04	1.31E-03	5.50E-04	1.67E-04	1.03E-03
cg11378135	12	51	765476			1.00E-03	2.00E-04	7.41E-06	1.29E-03	3.66E-04	5.57E-04	8.46E-04	2.89E-04	3.55E-03
cg01155138	2	43	863062 POLR1A	Body		6.00E-04	1.00E-04	7.63E-06	5.71E-04	1.76E-04	1.44E-03	6.03E-04	1.95E-04	2.13E-03
cg06710464	17	95	790476 BAIAP2;BAIAP2;B AIAP2;BAIAP2	Body;Body;B ody;Body		6.00E-04	1.00E-04	7.64E-06	6.15E-04	2.61E-04	1.97E-02	6.26E-04	1.65E-04	1.56E-04
cg19494100	6	13	183873 RNF144B	TSS1500		-5.00E-04	1.00E-04	7.69E-06	-7.71E-04	1.45E-04	3.88E-07	-1.33E-04	1.58E-04	4.01E-01
cg02571142	8	03	422348 DKK4	TSS200		1.00E-03	2.00E-04	7.70E-06	1.14E-03	3.75E-04	2.71E-03	9.79E-04	2.97E-04	1.05E-03
cg27087650	19	96	452557 BCL3	Body		-6.00E-04	1.00E-04	7.74E-06	-3.20E-04	2.27E-04	1.61E-01	-7.16E-04	1.60E-04	8.90E-06
cg12269535	6	14	431420 SRF;SRF	Body;Body		-9.00E-04	2.00E-04	7.78E-06	-1.14E-03	2.76E-04	6.31E-05	-6.44E-04	3.04E-04	3.42E-02

cg06926961	12	798491 13			N Shelf	7.00E-04	1.00E-04	7.88E-06	8.28E-04	3.34E-04	1.42E-02	6.29E-04	1.68E-04	1.90E-04
cg09035925	20	199157 69	RIN2;RIN2	Body;Body		8.00E-04	2.00E-04	7.94E-06	8.69E-04	2.38E-04	3.55E-04	6.70E-04	2.55E-04	8.66E-03
cg04557677	19	179590 82	JAK3	TSS1500		-2.00E-04	0.00E+00	7.96E-06	-5.81E-04	1.58E-04	3.30E-04	-1.82E-04	5.22E-05	5.17E-04
cg26460720	20	572640 51	NPEPL1;NPEPL1,S TX16-NPEPL1	TSS200;TSS2 00;Body		9.00E-04	2.00E-04	7.98E-06	1.13E-03	3.25E-04	6.74E-04	7.19E-04	2.41E-04	2.92E-03
cg09741846	10	754137 75	SYNPO2L	Body		8.00E-04	2.00E-04	8.05E-06	7.68E-04	3.03E-04	1.21E-02	7.76E-04	2.11E-04	2.60E-04
cg05713943	13	979123 52	MBNL2;MBNL2;M BNL2	5URT;5URT; 5URT		-6.00E-04	1.00E-04	8.06E-06	-9.41E-04	2.56E-04	3.22E-04	-5.01E-04	1.73E-04	3.85E-03
cg24723465	1	246843 900			N Shore	2.00E-04	1.00E-04	8.08E-06	4.04E-04	1.41E-04	4.90E-03	2.00E-04	5.44E-05	2.50E-04
cg16755922	17	805362 14	FOXX2	Body		8.00E-04	2.00E-04	8.17E-06	1.60E-03	4.61E-04	6.86E-04	6.88E-04	2.06E-04	8.98E-04
cg02451866	10	712516 04	TSPAN15	Body		5.00E-04	1.00E-04	8.28E-06	2.86E-04	1.75E-04	1.04E-01	5.87E-04	1.34E-04	1.49E-05
cg13415859	6	341468 0	SLC22A23;SLC22A 23;SLC22A23;SLC2 2A23;SLC22A23	5URT;5URT; Body;Body;B ody		9.00E-04	2.00E-04	8.32E-06	8.58E-04	2.88E-04	3.31E-03	8.97E-04	2.71E-04	9.76E-04
cg00701951	10	124228 478	HTRA1	Body	S Shore	-8.00E-04	2.00E-04	8.35E-06	-2.44E-03	5.59E-04	2.42E-05	-5.89E-04	1.79E-04	1.08E-03
cg12407462	5	761127 76				9.00E-04	2.00E-04	8.48E-06	9.58E-04	3.02E-04	1.82E-03	9.41E-04	3.01E-04	1.87E-03
cg17077319	3	149886 667				1.20E-03	3.00E-04	8.50E-06	7.42E-04	4.17E-04	7.73E-02	1.60E-03	3.67E-04	1.47E-05
cg13747876	17	801954 02	SLC16A3;SLC16A3 ;SLC16A3;SLC16A 3;SLC16A3;SLC16 A3	Body;Body;B ody;Body;Bo dy;Body		6.00E-04	1.00E-04	8.57E-06	7.67E-04	2.20E-04	6.41E-04	4.80E-04	1.62E-04	3.19E-03
cg16625765	16	298384 13	MVP;MVP	5URT;5URT	N Shore	8.00E-04	2.00E-04	8.57E-06	1.01E-03	2.95E-04	7.45E-04	7.17E-04	2.45E-04	3.55E-03
cg25651593	16	881450 1	ABAT;ABAT;ABA T	TSS200;5UR T;5URT		6.00E-04	1.00E-04	8.60E-06	4.05E-04	2.43E-04	9.76E-02	6.20E-04	1.48E-04	3.11E-05
cg01883759	7	282205 76	JAZF1;JAZF1-AS1	TSS200;Body	Island	-4.00E-04	1.00E-04	8.71E-06	-1.58E-04	1.80E-04	3.81E-01	-4.48E-04	9.77E-05	5.46E-06
cg18149207	1	151805 634	RORC	TSS1500		4.00E-04	1.00E-04	8.76E-06	2.05E-04	1.27E-04	1.07E-01	5.51E-04	1.20E-04	5.35E-06
cg25392060	8	142297 121				7.00E-04	2.00E-04	8.84E-06	9.74E-04	2.64E-04	3.05E-04	5.39E-04	1.92E-04	5.19E-03

cg22770295	20	8	CDC25B;CDC25B; CDC25B;CDC25B; CDC25B;CDC25B; CDC25B;CDC25B; CDC25B;CDC25B	TSS1500;Body; y;Body;Body; ;Body;Body; Body;Body;B ody;Body		-2.00E-04	0.00E+00	8.93E-06	-1.06E-04	7.47E-05	1.58E-01	-2.70E-04	5.94E-05	6.51E-06	
cg17367948	17	34	718633			5.00E-04	1.00E-04	8.97E-06	6.14E-04	1.88E-04	1.35E-03	4.68E-04	1.52E-04	2.22E-03	
cg24263062	20	1	273019	EBF4	Body	1.50E-03	3.00E-04	8.99E-06	2.20E-03	5.03E-04	2.15E-05	9.19E-04	4.54E-04	4.35E-02	
cg11918171	3	495	111314	ZBED2;CD96;CD96	y;Body	N Shore	1.10E-03	2.00E-04	9.02E-06	1.35E-03	3.54E-04	2.06E-04	8.71E-04	3.51E-04	1.33E-02
cg04510454	15	21	759705	CSPG4	Body		5.00E-04	1.00E-04	9.20E-06	4.68E-04	1.42E-04	1.23E-03	4.65E-04	1.57E-04	3.08E-03
cg13507563	11	83	179524	SERGEF;SERGEF;S ERGEF	Body;Body;B ody		5.00E-04	1.00E-04	9.22E-06	1.15E-03	2.75E-04	4.83E-05	3.90E-04	1.35E-04	4.02E-03
cg14237301	16	77	285064	APOBR	Body		7.00E-04	2.00E-04	9.31E-06	8.93E-04	2.79E-04	1.69E-03	6.17E-04	1.94E-04	1.56E-03
cg07452625	16	68	895985	SPG7;SPG7	Body;Body		5.00E-04	1.00E-04	9.37E-06	9.86E-04	2.38E-04	5.50E-05	3.49E-04	1.23E-04	4.59E-03
cg25015371	6	950	108874				7.00E-04	1.00E-04	9.44E-06	8.19E-04	2.15E-04	2.06E-04	5.10E-04	2.04E-04	1.27E-02
cg07788575	8	44	430184	HGSNAT	Body	Island	5.00E-04	1.00E-04	9.48E-06	4.43E-04	1.81E-04	1.55E-02	4.74E-04	1.28E-04	2.40E-04
cg26440042	22	10	375901				1.30E-03	3.00E-04	9.52E-06	9.91E-04	4.04E-04	1.53E-02	1.53E-03	4.01E-04	1.55E-04
cg07078732	2	65	305051				5.00E-04	1.00E-04	9.57E-06	5.88E-04	1.55E-04	2.12E-04	3.48E-04	1.36E-04	1.06E-02
cg16696202	3	49	939450				6.00E-04	1.00E-04	9.57E-06	7.32E-04	2.24E-04	1.32E-03	5.35E-04	1.75E-04	2.30E-03
cg23426431	12	855	107767	BTBD11	Body		6.00E-04	1.00E-04	9.59E-06	6.83E-04	2.13E-04	1.61E-03	5.81E-04	1.90E-04	2.25E-03
cg21762610	2	030	210655	UNC80;UNC80	Body;Body		1.60E-03	4.00E-04	9.67E-06	1.39E-03	4.88E-04	4.96E-03	1.86E-03	5.39E-04	6.11E-04
cg07004907	11	733086					1.00E-03	2.00E-04	9.74E-06	6.88E-04	4.06E-04	9.25E-02	1.06E-03	2.56E-04	3.60E-05
cg05825244	20	8	273048	EBF4;EBF4	Ex- onBnd;Body		2.50E-03	6.00E-04	9.80E-06	3.30E-03	7.85E-04	4.51E-05	1.62E-03	7.97E-04	4.21E-02
cg01004980	3	69	488830	PRKAR2A	Body		7.00E-04	2.00E-04	9.86E-06	9.80E-04	2.92E-04	9.93E-04	5.67E-04	1.82E-04	1.92E-03
cg01928516	17	7	220837	SMG6;SRR;SRR	TSS1500;SUR T;SUR		8.00E-04	2.00E-04	1.00E-05	6.03E-04	2.82E-04	3.39E-02	1.00E-03	2.50E-04	6.85E-05

cg05555876	8	15	549359 TCEA1;TCEA1;TC EA1;TCEA1	TSS1500;TSS 1500;TSS1500 ;TSS1500		7.00E-04	2.00E-04	1.01E-05	1.24E-03	3.28E-04	2.17E-04	5.54E-04	1.91E-04	3.84E-03
cg22488164	12	10	147169 PLBD1	Body		6.00E-04	1.00E-04	1.02E-05	8.59E-04	2.86E-04	3.07E-03	5.40E-04	1.60E-04	7.88E-04
cg03957124	6	69	370168		S Shore	-6.00E-04	1.00E-04	1.02E-05	-4.91E-04	1.61E-04	2.78E-03	-6.53E-04	2.00E-04	1.17E-03
cg10992736	6	370	158036 ZDHHC14;ZDHH C14	Body;Body		-7.00E-04	1.00E-04	1.02E-05	-1.07E-03	2.56E-04	5.03E-05	-4.46E-04	1.82E-04	1.45E-02
cg11441879	1	295	169074			3.00E-04	1.00E-04	1.02E-05	3.97E-04	1.48E-04	8.11E-03	2.63E-04	7.31E-05	3.50E-04
cg08163193	9	51	346920 CCL19	TSS1500		6.00E-04	1.00E-04	1.02E-05	3.19E-04	1.77E-04	7.41E-02	8.37E-04	1.86E-04	7.84E-06
cg04169527	11	5	975980 SWAP70;SWAP70	Body;Body		7.00E-04	2.00E-04	1.03E-05	4.16E-04	2.67E-04	1.22E-01	9.68E-04	2.19E-04	1.12E-05
cg11230523	2	98	747657 LOXL3;LOXL3;LO XL3	Body;Body;5 URT		-3.00E-04	1.00E-04	1.04E-05	-4.76E-04	2.29E-04	3.93E-02	-3.22E-04	8.17E-05	9.07E-05
cg24054032	1	99	681188			5.00E-04	1.00E-04	1.04E-05	3.63E-04	2.24E-04	1.08E-01	5.39E-04	1.30E-04	3.65E-05
cg18652923	2	344	109745 SH3RF3- AS1;SH3RF3	Body;TSS150 0		1.00E-04	0.00E+00	1.05E-05	1.47E-04	1.09E-04	1.78E-01	1.23E-04	2.94E-05	3.05E-05
cg25536676	1	27	553533 DHCR24	TSS1500	N Shore	-5.00E-04	1.00E-04	1.06E-05	-6.35E-04	1.75E-04	3.76E-04	-3.60E-04	1.29E-04	5.42E-03
cg19541622	4	56180	ZNF718;ZNF595;Z NF595;ZNF595;Z F595;ZNF718;ZNF 718	TSS1500;5UR T;5URT;Bod y;Body;Body ;Body		1.00E-03	2.00E-04	1.07E-05	1.14E-03	3.55E-04	1.65E-03	9.56E-04	3.14E-04	2.44E-03
cg06373167	1	044	203278 BTG2	3UTR		-8.00E-04	2.00E-04	1.08E-05	-7.00E-04	2.50E-04	5.69E-03	-1.02E-03	2.91E-04	5.14E-04
cg13300580	1	39	274405 SLC9A1;SLC9A1	Body;Body		5.00E-04	1.00E-04	1.09E-05	2.59E-04	1.84E-04	1.61E-01	6.07E-04	1.37E-04	1.07E-05
cg07855221	17	14	798773 MAFG;MAFG;SIR T7	3UTR;3UTR; TSS1500		8.00E-04	2.00E-04	1.10E-05	2.31E-04	2.92E-04	4.30E-01	1.23E-03	2.43E-04	5.46E-07
cg15370819	19	97	543793 MYADM;MY- ADM;MY- ADM;MY- ADM;MY- ADM;MY- ADM;MY- ADM;MY- ADM;MY-	3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR		7.00E-04	2.00E-04	1.10E-05	6.40E-04	2.49E-04	1.10E-02	7.92E-04	2.20E-04	3.53E-04

			ADM;MY- ADM;MY- ADM;MYADM											
cg11612905	2	234359 654	DGKD;DGKD	Body;Body		5.00E-04	1.00E-04	1.10E-05	7.98E-04	1.89E-04	4.07E-05	3.55E-04	1.66E-04	3.27E-02
cg03825390	6	332608 51	RGL2;RGL2	Body;Body		2.00E-04	0.00E+00	1.12E-05	1.93E-04	9.78E-05	4.99E-02	1.68E-04	4.27E-05	9.50E-05
cg16105303	10	147913 42	FAM107B;FAM107 B	Body;5URT	N Shore	6.00E-04	1.00E-04	1.13E-05	7.30E-04	2.82E-04	1.06E-02	5.39E-04	1.50E-04	3.47E-04
cg20941062	5	132299 811	AFF4	TSS1500		-9.00E-04	2.00E-04	1.13E-05	-9.70E-04	2.61E-04	2.77E-04	-7.07E-04	2.92E-04	1.56E-02
cg22714777	2	119605 229	EN1;EN1	1stExon;5UR T	S Shelf	4.00E-04	1.00E-04	1.14E-05	2.41E-04	1.58E-04	1.31E-01	4.91E-04	1.14E-04	1.88E-05
cg00799144	22	312172 30	OSBP2;OSBP2;OSB P2;OSBP2;OSBP2	TSS1500;Bod y;Body;Body ;5URT		2.00E-04	0.00E+00	1.15E-05	2.32E-04	7.38E-05	1.99E-03	2.02E-04	6.57E-05	2.21E-03
cg20779663	10	135699 95			N Shelf	-8.00E-04	2.00E-04	1.16E-05	-1.26E-03	2.71E-04	6.69E-06	-4.14E-04	2.40E-04	8.51E-02
cg25922935	3	156747 491	LEKR1	Body		9.00E-04	2.00E-04	1.16E-05	7.96E-04	2.90E-04	6.76E-03	9.76E-04	2.83E-04	6.01E-04
cg03990261	11	101188 33	SBF2	Body	N Shelf	1.00E-03	2.00E-04	1.17E-05	1.33E-03	3.90E-04	8.53E-04	7.95E-04	2.66E-04	2.94E-03
cg14578060	7	764347 89				-1.00E-03	2.00E-04	1.17E-05	-1.19E-03	2.92E-04	7.38E-05	-6.77E-04	3.42E-04	4.82E-02
cg11303839	7	754059 67	CCL26	5URT	S Shore	-1.40E-03	3.00E-04	1.18E-05	-1.54E-03	4.60E-04	1.05E-03	-1.32E-03	4.62E-04	4.45E-03
cg07821355	6	116706 621	DSE;DSE	5URT;5URT		-6.00E-04	1.00E-04	1.19E-05	-6.04E-04	2.02E-04	3.25E-03	-5.94E-04	1.86E-04	1.44E-03
cg26453543	16	189433 48			S Shore	8.00E-04	2.00E-04	1.20E-05	8.57E-04	2.25E-04	1.97E-04	7.61E-04	3.52E-04	3.12E-02
cg09664445	17	261240 6	CLUH	5URT		6.00E-04	1.00E-04	1.22E-05	4.96E-04	1.88E-04	9.38E-03	6.01E-04	1.71E-04	4.66E-04
cg00410534	16	672325 57	ELMO3;E2F4	TSS1500;3UT R		4.00E-04	1.00E-04	1.23E-05	3.96E-04	1.48E-04	8.20E-03	3.76E-04	1.09E-04	5.85E-04
cg19089201	7	450022 87	MYO1G	3UTR		-9.00E-04	2.00E-04	1.24E-05	-8.13E-04	3.67E-04	2.83E-02	-9.27E-04	2.45E-04	1.72E-04
cg08836972	6	265329 14			N Shelf	1.00E-03	2.00E-04	1.24E-05	9.90E-04	2.87E-04	7.23E-04	1.06E-03	3.95E-04	7.39E-03

cg04381163	22	318520 77	EIF4ENIF1;EIF4ENIF1	Body;Body;Body		4.00E-04	1.00E-04	1.24E-05	7.07E-04	2.01E-04	5.55E-04	3.12E-04	9.99E-05	1.85E-03
cg07930159	8	809648 82	TPD52;TPD52;TPD52;TPD52;TPD52;TPD52;TPD52;TPD52;TPD52;TPD52	Body;Body;Body;Body;Body;Body;Body;Body;Body		9.00E-04	2.00E-04	1.24E-05	2.29E-04	2.92E-04	4.34E-01	1.44E-03	2.74E-04	2.00E-07
cg26802813	3	470141 28	CCDC12;CCDC12;CCDC12	Body;Body;Body		-7.00E-04	2.00E-04	1.25E-05	-8.20E-04	2.04E-04	8.94E-05	-4.69E-04	2.29E-04	4.06E-02
cg10585586	1	853621 20				8.00E-04	2.00E-04	1.26E-05	1.12E-03	3.07E-04	3.37E-04	6.17E-04	2.27E-04	6.73E-03
cg04444771	10	454737 12	C10orf10;RASSF4	5URT;Body		-4.00E-04	1.00E-04	1.27E-05	-3.00E-04	1.61E-04	6.44E-02	-4.76E-04	1.18E-04	5.91E-05
cg06540722	13	341119 66	STARD13	5URT	N Shelf	1.00E-03	2.00E-04	1.28E-05	7.25E-04	3.40E-04	3.44E-02	1.17E-03	2.97E-04	9.41E-05
cg04842352	16	499073 68				4.00E-04	1.00E-04	1.28E-05	2.70E-04	2.07E-04	1.94E-01	5.00E-04	1.17E-04	2.23E-05
cg05973262	6	321918 95	NOTCH4	TSS200	N Shore	9.00E-04	2.00E-04	1.28E-05	8.15E-04	3.32E-04	1.52E-02	9.26E-04	2.56E-04	3.23E-04
cg12848614	14	701934 96				-8.00E-04	2.00E-04	1.30E-05	-1.61E-03	3.54E-04	1.08E-05	-4.92E-04	2.04E-04	1.63E-02
cg23722790	1	674676 02	SLC35D1	3UTR		5.00E-04	1.00E-04	1.31E-05	4.83E-04	2.14E-04	2.53E-02	5.78E-04	1.54E-04	1.96E-04
cg16655795	19	428972 38				5.00E-04	1.00E-04	1.31E-05	7.74E-04	2.39E-04	1.51E-03	4.39E-04	1.39E-04	1.62E-03
cg08959230	16	304092 61	ZNF48;ZNF48;ZNF48;ZNF48	Body;Body;Body;Body	N Shore	4.00E-04	1.00E-04	1.32E-05	5.58E-04	1.64E-04	8.45E-04	3.06E-04	1.02E-04	2.66E-03
cg13373351	14	245396 01	CPNE6;CPNE6	TSS1500;TSS1500		7.00E-04	2.00E-04	1.33E-05	7.93E-04	2.68E-04	3.60E-03	6.89E-04	2.14E-04	1.38E-03
cg09767524	13	676225 49	PCDH9;PCDH9	Body;Body		-7.00E-04	2.00E-04	1.34E-05	-7.53E-04	2.09E-04	4.16E-04	-6.33E-04	2.57E-04	1.40E-02
cg25997480	10	908339 94				8.00E-04	2.00E-04	1.38E-05	4.48E-04	3.25E-04	1.70E-01	9.10E-04	2.12E-04	2.05E-05
cg10437839	11	647019 10	PPP2R5B	3UTR	N Shelf	7.00E-04	2.00E-04	1.38E-05	4.98E-04	2.55E-04	5.27E-02	9.21E-04	2.26E-04	5.15E-05
cg09702859	1	198901 839	MIR181A1HG	Body		1.40E-03	3.00E-04	1.41E-05	1.43E-03	5.17E-04	6.42E-03	1.43E-03	4.26E-04	8.59E-04
cg08867908	1	228417 9	LOC100129534;MO RN1	TSS200;Body		-1.00E-04	0.00E+00	1.42E-05	-8.09E-05	1.69E-04	6.32E-01	-8.01E-05	1.86E-05	1.87E-05
cg25037165	11	128242 83	TEAD1	Body		-7.00E-04	2.00E-04	1.42E-05	-9.25E-04	2.93E-04	1.94E-03	-6.14E-04	1.97E-04	1.94E-03

cg07814318	15	316245 84	KLF13;KLF13	Body;Body	N Shelf	9.00E-04	2.00E-04	1.42E-05	7.61E-04	3.18E-04	1.78E-02	1.03E-03	2.80E-04	2.57E-04
cg19998073	14	890784 43	ZC3H14;ZC3H14;Z C3H14;ZC3H14;ZC 3H14;ZC3H14	3UTR;3UTR; 3UTR;3UTR; 3UTR;3UTR		5.00E-04	1.00E-04	1.43E-05	4.00E-04	1.64E-04	1.62E-02	5.59E-04	1.53E-04	2.68E-04
cg15051432	3	999296 90				-8.00E-04	2.00E-04	1.43E-05	-1.24E-03	3.17E-04	1.37E-04	-5.59E-04	2.16E-04	9.99E-03
cg08686039	1	204175 429	GOLT1A	Body		8.00E-04	2.00E-04	1.43E-05	2.51E-04	2.93E-04	3.93E-01	1.30E-03	2.59E-04	6.41E-07
cg13810931	11	672646 77	PITPNM1;PIT- PNM1	Body;Body		6.00E-04	1.00E-04	1.45E-05	8.78E-04	2.27E-04	1.67E-04	4.54E-04	1.86E-04	1.47E-02
cg22515589	17	794264 32	BAHCC1	Body		5.00E-04	1.00E-04	1.45E-05	7.10E-04	2.33E-04	2.70E-03	4.34E-04	1.33E-04	1.21E-03
cg08635575	9	801891 85	GNA14	Body	S Shore	4.00E-04	1.00E-04	1.45E-05	5.43E-04	1.59E-04	8.27E-04	3.37E-04	1.17E-04	4.20E-03
cg12508994	14	820011 97	SEL1L;SEL1L	TSS1500;TSS 1500		2.00E-04	1.00E-04	1.47E-05	3.06E-04	1.19E-04	1.10E-02	2.09E-04	5.87E-05	3.98E-04
cg21081097	19	454586 10	CLPTM1;CLPTM1; CLPTM1;CLPTM1	5URT;1stExo n;5URT;Bod y		2.00E-04	0.00E+00	1.47E-05	2.16E-04	6.93E-05	2.14E-03	1.58E-04	5.13E-05	2.17E-03
cg20003499	7	977557 92	LMTK2	Body		8.00E-04	2.00E-04	1.47E-05	1.42E-03	4.04E-04	5.91E-04	6.29E-04	2.04E-04	2.16E-03
cg13195276	5	127203 128				7.00E-04	2.00E-04	1.48E-05	7.39E-04	3.11E-04	1.86E-02	6.87E-04	1.90E-04	3.13E-04
cg08018468	1	437680 48	TIE1;TIE1	Body;Body		5.00E-04	1.00E-04	1.48E-05	4.79E-04	1.53E-04	2.04E-03	4.80E-04	1.61E-04	2.92E-03
cg12259187	9	822387 85	TLE4;TLE4;TLE4;T LE4;TLE4;TLE4	5URT;Body; Body;Body;B ody;Body		6.00E-04	1.00E-04	1.49E-05	5.02E-04	1.77E-04	5.06E-03	6.57E-04	1.98E-04	9.59E-04
cg16315329	3	506487 06	CISH;MAP- KAPK3;CISH	Body;TSS150 0;5URT		-3.00E-04	1.00E-04	1.49E-05	-2.15E-04	1.78E-04	2.30E-01	-3.72E-04	8.78E-05	2.65E-05
cg20938047	14	253570 32	STXBP6;STXBP6;S TXBP6	Body;Body;B ody		7.00E-04	2.00E-04	1.51E-05	7.98E-04	4.10E-04	5.32E-02	6.49E-04	1.67E-04	1.15E-04
cg01676795	7	755863 48	POR	Body		1.00E-03	2.00E-04	1.51E-05	1.34E-03	4.71E-04	5.09E-03	9.31E-04	2.78E-04	8.64E-04
cg18931885	10	112100 739				7.00E-04	2.00E-04	1.51E-05	7.27E-04	2.50E-04	4.13E-03	6.58E-04	2.05E-04	1.40E-03
cg12633968	18	124923 03	SPIRE1;SPIRE1;SPI RE1	Body;Body;B ody		1.00E-03	2.00E-04	1.53E-05	8.93E-04	3.93E-04	2.45E-02	1.11E-03	2.98E-04	2.29E-04
cg02809553	14	752829 66	YLP1M1;YLP1M1	Ex- onBnd;Body		5.00E-04	1.00E-04	1.53E-05	6.66E-04	1.74E-04	1.87E-04	4.13E-04	1.84E-04	2.53E-02

cg19741548	8	749633				6.00E-04	1.00E-04	1.53E-05	4.31E-04	1.89E-04	2.44E-02	8.52E-04	2.15E-04	8.27E-05
cg12470493	3	149865				9.00E-04	2.00E-04	1.53E-05	2.28E-04	2.79E-04	4.16E-01	1.48E-03	2.79E-04	1.58E-07
cg11540855	3	116435	VGLL4;VGLL4;VGLL4;VGLL4;VGLL4	5URT;Ex-onBnd;Ex-onBnd;Ex-onBnd;Ex-onBnd;Body;Body		5.00E-04	1.00E-04	1.54E-05	5.14E-04	1.52E-04	9.00E-04	4.25E-04	1.56E-04	6.75E-03
cg18545915	14	248672	NYNRIN	TSS1500		7.00E-04	2.00E-04	1.56E-05	6.64E-04	2.29E-04	4.25E-03	6.43E-04	2.01E-04	1.44E-03
cg20664313	12	133071	FBRSL1	Body		7.00E-04	2.00E-04	1.58E-05	2.32E-04	2.92E-04	4.29E-01	9.14E-04	1.96E-04	3.76E-06
cg11738389	6	566214	DST;DST;DST	Body;Body;Body		1.00E-03	2.00E-04	1.59E-05	7.96E-04	3.52E-04	2.52E-02	1.26E-03	3.31E-04	1.58E-04
cg19542445	12	259622	CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C;CACNA1C	Body;Body;Body;Body;Body;Body;Body;Body;Body;Body;Body;Body;Body		6.00E-04	1.00E-04	1.60E-05	5.06E-04	2.08E-04	1.63E-02	7.47E-04	2.04E-04	2.72E-04
cg27397830	11	606798				6.00E-04	1.00E-04	1.60E-05	6.99E-04	1.87E-04	2.65E-04	4.27E-04	1.77E-04	1.64E-02
cg15227014	22	380371	SH3BP1;SH3BP1	Ex-onBnd;Body		7.00E-04	2.00E-04	1.61E-05	1.23E-03	2.43E-04	1.23E-06	2.60E-04	2.37E-04	2.72E-01
cg16406078	20	825634	FAM110A;FAM110A;FAM110A;FAM110A	1stExon;Body;Body;Body		-9.00E-04	2.00E-04	1.61E-05	-1.02E-03	3.08E-04	1.09E-03	-8.40E-04	3.03E-04	5.70E-03
cg16909660	8	145855	DLGAP2;DLGAP2	5URT;5URT		4.00E-04	1.00E-04	1.62E-05	3.50E-04	1.39E-04	1.28E-02	3.65E-04	1.04E-04	4.99E-04
cg00949930	2	179916	CCDC141	TSS1500	N Shore	8.00E-04	2.00E-04	1.65E-05	1.21E-03	2.92E-04	5.84E-05	5.02E-04	2.21E-04	2.31E-02

cg23509526	2	982950 80	LINC01125	Body		9.00E-04	2.00E-04	1.65E-05	6.06E-04	3.64E-04	9.76E-02	1.03E-03	2.52E-04	4.96E-05
cg21327712	1	111744 503	DENND2D;DENND2D	TSS1500;Body	S Shore	9.00E-04	2.00E-04	1.66E-05	9.36E-04	3.58E-04	9.86E-03	9.24E-04	2.70E-04	6.57E-04
cg04927537	17	769760 91	LGALS3BP	TSS200		1.30E-03	3.00E-04	1.66E-05	1.19E-03	4.23E-04	5.65E-03	1.44E-03	4.38E-04	1.04E-03
cg26931608	1	170036 455	KIFAP3;KIFAP3;KIFAP3	5URT;5URT;Body;Body	S Shelf	-1.50E-03	4.00E-04	1.68E-05	-2.26E-03	5.31E-04	3.63E-05	-9.38E-04	4.78E-04	5.03E-02
cg15242769	22	436709 35	SCUBE1	Body		7.00E-04	2.00E-04	1.68E-05	5.67E-04	2.33E-04	1.61E-02	7.44E-04	2.07E-04	3.48E-04
cg10964502	21	447521 05	LINC00322	TSS200		8.00E-04	2.00E-04	1.70E-05	6.83E-04	3.39E-04	4.55E-02	8.33E-04	2.18E-04	1.48E-04
cg13520904	18	330390 43				-5.00E-04	1.00E-04	1.70E-05	-6.59E-04	1.67E-04	1.18E-04	-3.35E-04	1.50E-04	2.61E-02
cg02648692	22	450642 43	PRR5;PRR5	TSS200;TSS200	N Shore	0.00E+00	0.00E+00	1.70E-05	1.83E-05	3.65E-05	6.17E-01	-2.85E-05	6.40E-06	9.89E-06
cg09568899	19	460675 96	OPA3;OPA3	Body;Body		4.00E-04	1.00E-04	1.71E-05	5.27E-04	1.53E-04	7.60E-04	3.66E-04	1.36E-04	7.06E-03
cg16277071	17	755373 17			S Shelf	7.00E-04	2.00E-04	1.72E-05	5.07E-04	2.36E-04	3.30E-02	7.98E-04	2.08E-04	1.38E-04
cg23226831	1	115700 937				-2.00E-04	0.00E+00	1.72E-05	-1.72E-04	2.09E-04	4.11E-01	-1.93E-04	4.57E-05	2.82E-05
cg08036259	1	169081 528	ATP1B1	Body		-6.00E-04	1.00E-04	1.72E-05	-4.33E-04	2.00E-04	3.18E-02	-6.43E-04	1.69E-04	1.60E-04
cg20902443	10	133871 98	SEPHS1;SEPHS1;SEPHS1	5URT;5URT;5URT		7.00E-04	2.00E-04	1.72E-05	5.20E-04	2.13E-04	1.56E-02	8.60E-04	2.33E-04	2.38E-04
cg13218558	1	116311 21				7.00E-04	2.00E-04	1.73E-05	6.49E-04	2.30E-04	5.43E-03	7.17E-04	2.21E-04	1.22E-03
cg10919522	14	742274 41	ELMSAN1;ELMSAN1	TSS1500;5URT		-9.00E-04	2.00E-04	1.73E-05	-6.98E-04	3.32E-04	3.73E-02	-9.46E-04	2.49E-04	1.61E-04
cg01337593	3	151443 95				6.00E-04	1.00E-04	1.73E-05	3.88E-04	2.05E-04	6.00E-02	6.98E-04	1.73E-04	6.37E-05
cg11204177	7	829190 52				-6.00E-04	1.00E-04	1.73E-05	-9.32E-04	2.08E-04	1.43E-05	-3.28E-04	1.95E-04	9.18E-02
cg14485110	2	703504 37				5.00E-04	1.00E-04	1.74E-05	3.46E-04	2.02E-04	8.84E-02	5.29E-04	1.32E-04	6.73E-05
cg06290506	4	769772 36	ART3	5URT		3.00E-04	1.00E-04	1.74E-05	5.12E-04	1.82E-04	5.50E-03	3.08E-04	9.08E-05	7.29E-04
cg00113074	3	323450 52	CMTM8	Body		-1.20E-03	3.00E-04	1.75E-05	-9.37E-04	3.25E-04	4.45E-03	-1.74E-03	5.05E-04	5.93E-04
cg27086356	3	170627 562	EIF5A2	TSS1500		-1.10E-03	3.00E-04	1.77E-05	-1.34E-03	4.02E-04	1.09E-03	-9.07E-04	3.20E-04	4.74E-03

cg07747616	6	772979	4	BMP6	Body			-8.00E-04	2.00E-04	1.78E-05	-1.09E-03	2.79E-04	1.39E-04	-5.93E-04	2.72E-04	2.95E-02
cg08782002	17	618478	85	CCDC47	5URT			-6.00E-04	1.00E-04	1.79E-05	-6.14E-04	2.18E-04	5.53E-03	-5.78E-04	1.78E-04	1.26E-03
cg03118376	6	134891	92	GFOD1;GFOD1	1500	TSS1500;TSS		5.00E-04	1.00E-04	1.80E-05	5.94E-04	1.72E-04	6.95E-04	4.18E-04	1.58E-04	8.47E-03
cg09152259	2	128156	114					-8.00E-04	2.00E-04	1.81E-05	-1.66E-03	3.82E-04	2.41E-05	-5.39E-04	2.22E-04	1.55E-02
cg24033280	14	457122	90	MIS18BP1	Body			4.00E-04	1.00E-04	1.82E-05	1.22E-04	2.40E-04	6.13E-01	4.00E-04	9.11E-05	1.33E-05
cg00045592	1	160714	299	SLAMF7;SLAMF7; SLAMF7;SLAMF7; SLAMF7;SLAMF7; SLAMF7;SLAMF7	5URT;Body; Body;Body;B ody;Body;Bo dy;Body;Bod y;Body			1.00E-03	2.00E-04	1.82E-05	7.48E-04	3.20E-04	2.07E-02	1.15E-03	3.10E-04	2.31E-04
cg16395997	1	356279	8	WRAP73	Body	Island		9.00E-04	2.00E-04	1.83E-05	1.30E-03	4.42E-04	3.90E-03	8.06E-04	2.46E-04	1.12E-03
cg10922280	16	680342	27	DPEP2	TSS1500			6.00E-04	1.00E-04	1.83E-05	4.78E-04	1.92E-04	1.39E-02	7.14E-04	1.99E-04	3.55E-04
cg09857555	7	142026	829					-8.00E-04	2.00E-04	1.85E-05	-8.90E-04	2.87E-04	2.30E-03	-7.71E-04	2.60E-04	3.08E-03
cg13819988	17	174871	94	PEMT;PEMT;PEM T;PEMT	TSS1500;Bod y;Body;Body			5.00E-04	1.00E-04	1.85E-05	6.22E-04	2.17E-04	4.65E-03	4.76E-04	1.47E-04	1.32E-03
cg04598105	19	981293	8	ZNF812	TSS1500	N Shore		-5.00E-04	1.00E-04	1.85E-05	-4.71E-04	1.81E-04	1.02E-02	-5.36E-04	1.57E-04	6.90E-04
cg07836518	6	132452	453					6.00E-04	1.00E-04	1.86E-05	4.01E-04	2.64E-04	1.31E-01	6.28E-04	1.54E-04	5.28E-05
cg21481630	2	727702	78	EXOC6B	Body			3.00E-04	1.00E-04	1.91E-05	4.42E-04	1.71E-04	1.07E-02	2.33E-04	6.48E-05	3.55E-04
cg14390798	6	565365	32	RNU6- 71P;DST;DST;DST	Body;Body;B ody;Body			8.00E-04	2.00E-04	1.93E-05	7.81E-04	3.24E-04	1.70E-02	8.31E-04	2.35E-04	4.46E-04
cg26955383	10	105218	660	CALHM1	TSS200	N Shelf		6.00E-04	1.00E-04	1.94E-05	6.36E-04	2.34E-04	7.21E-03	5.84E-04	1.77E-04	1.03E-03
cg17822325	1	318964	62	SERINC2;SERINC2 ;SERINC2;SERINC 2;SERINC2	5URT;Body; Body;Body;B ody			8.00E-04	2.00E-04	1.96E-05	7.69E-04	2.28E-04	9.39E-04	8.32E-04	3.17E-04	8.95E-03
cg09752132	19	140836	29	RFX1	Body			5.00E-04	1.00E-04	1.97E-05	7.58E-05	3.17E-04	8.11E-01	5.29E-04	1.19E-04	9.40E-06
cg16302903	8	822585	39					-5.00E-04	1.00E-04	1.98E-05	-2.13E-04	2.92E-04	4.67E-01	-5.95E-04	1.36E-04	1.46E-05
cg04437067	6	110817	319					6.00E-04	1.00E-04	2.00E-05	4.55E-04	1.95E-04	2.10E-02	7.40E-04	1.99E-04	2.22E-04

cg10380546	11	942218	AP2A2;AP2A2	Body;Body		9.00E-04	2.00E-04	2.00E-05	1.62E-04	3.17E-04	6.10E-01	1.30E-03	2.57E-04	5.14E-07
cg07203167	1	183551 326	NCF2;NCF2;NCF2; NCF2	Body;Body;B ody;Body	N Shore	4.00E-04	1.00E-04	2.00E-05	4.21E-04	1.41E-04	3.34E-03	4.64E-04	1.52E-04	2.34E-03
cg04010915	12	110547 053				3.00E-04	1.00E-04	2.02E-05	3.77E-04	1.54E-04	1.57E-02	2.92E-04	8.27E-05	4.51E-04
cg12144681	8	142220 329	SLC45A4;SLC45A4	3UTR;3UTR		3.00E-04	1.00E-04	2.04E-05	3.08E-04	1.34E-04	2.28E-02	2.74E-04	7.61E-05	3.53E-04
cg18120259	6	438946 39	LINC01512	Body		-8.00E-04	2.00E-04	2.06E-05	-1.35E-03	3.50E-04	1.74E-04	-5.54E-04	2.08E-04	7.83E-03
cg13078565	17	375411 6				4.00E-04	1.00E-04	2.06E-05	4.08E-04	1.43E-04	5.00E-03	4.45E-04	1.40E-04	1.59E-03
cg08949269	20	314432 98				8.00E-04	2.00E-04	2.08E-05	8.01E-04	2.74E-04	4.04E-03	7.34E-04	2.37E-04	2.00E-03
cg27019594	3	127892 866	EEFSEC	Body		6.00E-04	1.00E-04	2.10E-05	6.46E-04	2.12E-04	2.71E-03	5.43E-04	1.82E-04	2.90E-03
cg26038971	3	141857 74				-7.00E-04	2.00E-04	2.12E-05	-4.25E-04	2.38E-04	7.58E-02	-8.15E-04	2.01E-04	5.59E-05
cg09627709	7	977557 19	LMTK2	Body		8.00E-04	2.00E-04	2.13E-05	8.25E-04	3.45E-04	1.81E-02	8.00E-04	2.28E-04	4.66E-04
cg09964698	3	712354 48	FOXP1;FOXP1;FO XP1;FOXP1;FOXP1 ;FOXP1	Body;Body;B ody;Body;Bo dy;Body		-1.10E-03	3.00E-04	2.13E-05	-9.37E-04	4.00E-04	2.04E-02	-1.32E-03	3.64E-04	3.22E-04
cg23025447	10	708830 43	VPS26A;VPS26A	TSS1500;TSS 1500		9.00E-04	2.00E-04	2.13E-05	9.30E-04	3.05E-04	2.68E-03	8.72E-04	2.95E-04	3.17E-03
cg07467649	7	728564 62	BAZ1B	3UTR		7.00E-04	2.00E-04	2.13E-05	1.25E-03	2.54E-04	2.47E-06	3.11E-04	2.05E-04	1.30E-01
cg27555390	19	453178 10	BCAM;BCAM	Body;Body		3.00E-04	1.00E-04	2.14E-05	2.72E-04	1.05E-04	1.04E-02	2.60E-04	7.72E-05	8.08E-04
cg18473335	14	245401 74	CPNE6;CPNE6;CP NE6	TSS1500;5UR T ₁ stExon		1.20E-03	3.00E-04	2.14E-05	1.02E-03	4.16E-04	1.50E-02	1.35E-03	3.83E-04	4.76E-04
cg14069726	5	165513 101			N Shelf	-1.00E-04	0.00E+00	2.15E-05	-1.28E-04	9.03E-05	1.57E-01	-8.09E-05	2.01E-05	6.07E-05
cg05776323	1	161165 053	ADAMTS4	Body		6.00E-04	1.00E-04	2.17E-05	6.53E-04	2.24E-04	4.15E-03	5.44E-04	1.75E-04	1.91E-03
cg20651995	2	695254 71				-6.00E-04	2.00E-04	2.18E-05	-1.11E-03	2.65E-04	4.79E-05	-4.17E-04	1.84E-04	2.40E-02
cg06629453	2	988529 10	VWA3B	Body		4.00E-04	1.00E-04	2.19E-05	2.93E-04	1.35E-04	3.10E-02	5.12E-04	1.34E-04	1.46E-04
cg14352682	6	306141 68	C6orf136;C6orf136; C6orf136;ATAT1	TSS1500;TSS 1500;TSS1500 ;Body		4.00E-04	1.00E-04	2.22E-05	3.71E-04	1.33E-04	6.11E-03	4.46E-04	1.38E-04	1.31E-03

cg02385309	22	366093 71	MAFF;MAFF;MAF F;MAFF	5URT;5URT; 5URT;5URT		8.00E-04	2.00E-04	2.23E-05	6.96E-04	2.60E-04	8.20E-03	8.72E-04	2.63E-04	9.44E-04
cg10570276	20	368107 54				8.00E-04	2.00E-04	2.23E-05	5.31E-04	3.06E-04	8.43E-02	8.77E-04	2.21E-04	7.84E-05
cg03169557	16	895989 50	SPG7;SPG7	Body;Body		7.00E-04	2.00E-04	2.25E-05	1.27E-03	3.38E-04	2.48E-04	5.27E-04	1.92E-04	6.22E-03
cg05785686	2	201015 06	TTC32	1stExon	N Shore	0.00E+00	0.00E+00	2.27E-05	4.95E-05	2.62E-05	6.05E-02	2.30E-05	5.86E-06	9.87E-05
cg13296238	3	127323 965	MCM2;MCM2	Body;Body		4.00E-04	1.00E-04	2.28E-05	5.34E-04	1.57E-04	8.41E-04	3.75E-04	1.43E-04	8.80E-03
cg02919794	17	802031 12	CSNK1D;CSNK1D; CSNK1D	3UTR;Body; Body		1.00E-04	0.00E+00	2.30E-05	1.78E-04	8.93E-05	4.81E-02	9.45E-05	2.46E-05	1.33E-04
cg08521187	2	757094 8	LOC100506274	Body		5.00E-04	1.00E-04	2.31E-05	3.79E-04	1.46E-04	1.07E-02	8.22E-04	2.19E-04	1.94E-04
cg13274938	17	384938 22	RARA;RARA;RAR A	Body;Body;B ody		4.00E-04	1.00E-04	2.32E-05	3.43E-04	1.50E-04	2.31E-02	3.78E-04	1.06E-04	3.98E-04
cg20728490	10	980641 75	DNTT;DNTT;DNT T;DNTT	5URT;5URT; 1stExon;1stE xon		-1.00E-03	2.00E-04	2.33E-05	-8.55E-04	3.90E-04	2.97E-02	-1.06E-03	2.92E-04	2.91E-04
cg14114804	14	776069 90	ZDHHC22	5URT		5.00E-04	1.00E-04	2.33E-05	4.63E-04	1.68E-04	6.46E-03	4.57E-04	1.42E-04	1.42E-03
cg01864395	17	762741 40	LOC100996291	Body		-4.00E-04	1.00E-04	2.35E-05	-5.87E-04	1.41E-04	4.99E-05	-2.50E-04	1.34E-04	6.28E-02
cg09092525	20	585701 33	CDH26;CDH26	TSS150;Bod y		-9.00E-04	2.00E-04	2.36E-05	-1.33E-03	2.96E-04	1.48E-05	-4.45E-04	2.90E-04	1.25E-01
cg21946195	2	860122 25	MIR6071;ATOH8	TSS150;Bod y		-7.00E-04	2.00E-04	2.37E-05	-8.50E-04	2.25E-04	2.31E-04	-5.41E-04	2.56E-04	3.50E-02
cg18904875	2	202818 188				-4.00E-04	1.00E-04	2.40E-05	-5.25E-04	1.44E-04	3.64E-04	-3.44E-04	1.49E-04	2.14E-02
cg16896911	19	338956 90	PEPD;PEPD;PEPD	Body;Body;B ody		8.00E-04	2.00E-04	2.43E-05	5.66E-04	2.99E-04	6.01E-02	9.36E-04	2.40E-04	1.09E-04
cg21349939	18	529670 8	ZBTB14;ZBTB14; BTB14;ZBTB14	5URT;TSS15 00;TSS150;T SS1500		0.00E+00	0.00E+00	2.44E-05	-8.63E-05	6.16E-05	1.63E-01	-4.12E-05	1.02E-05	5.83E-05
cg14017402	2	862256 02				6.00E-04	1.00E-04	2.46E-05	4.16E-04	1.85E-04	2.58E-02	7.95E-04	2.08E-04	1.46E-04
cg10201857	17	384861 51	RARA;RARA;RAR A	5URT;5URT; 5URT	S Shore	8.00E-04	2.00E-04	2.46E-05	5.57E-04	2.43E-04	2.32E-02	1.01E-03	2.69E-04	1.89E-04
cg02504211	3	194815 434	XXYLT1- AS1;XXYLT1;XXYL T1	Body;Body;B ody		6.00E-04	1.00E-04	2.49E-05	3.56E-04	2.61E-04	1.74E-01	6.65E-04	1.62E-04	4.37E-05

cg14265604	1	244557 871				8.00E-04	2.00E-04	2.50E-05	9.35E-04	2.60E-04	4.30E-04	6.22E-04	2.65E-04	1.91E-02
cg19060760	12	188703 8	ADIPOR2;ADI- POR2	Ex- onBnd;Body		8.00E-04	2.00E-04	2.51E-05	1.16E-03	4.01E-04	4.51E-03	7.40E-04	2.31E-04	1.42E-03
cg15626919	16	696474 19	NFAT5;NFAT5;NF AT5;NFAT5;NFAT 5;NFAT5	5URT;5URT; 5URT;Body; Body;Body		5.00E-04	1.00E-04	2.51E-05	6.25E-04	1.61E-04	1.57E-04	3.53E-04	1.75E-04	4.46E-02
cg12061886	14	757467 93	FOS	Body		1.00E-03	2.00E-04	2.51E-05	7.97E-04	3.75E-04	3.49E-02	1.22E-03	3.27E-04	2.05E-04
cg03318904	22	398015 22	TAB1;TAB1	Body;Body	S Shore	4.00E-04	1.00E-04	2.52E-05	2.18E-04	1.77E-04	2.20E-01	5.43E-04	1.26E-04	2.01E-05
cg05151709	1	846155				-1.00E-03	2.00E-04	2.52E-05	-1.11E-03	4.38E-04	1.25E-02	-9.49E-04	2.80E-04	7.58E-04
cg04253214	1	789420 99				1.40E-03	3.00E-04	2.53E-05	1.03E-03	6.70E-04	1.28E-01	1.50E-03	3.79E-04	7.91E-05
cg03080569	12	578283 96	INHBC	TSS200		5.00E-04	1.00E-04	2.53E-05	5.28E-04	1.66E-04	1.80E-03	4.00E-04	1.41E-04	4.84E-03
cg07465699	14	104263 793	PPP1R13B	Body	Island	6.00E-04	1.00E-04	2.56E-05	1.09E-03	2.39E-04	1.02E-05	3.28E-04	1.74E-04	6.03E-02
cg21425838	14	101151 668				3.00E-04	1.00E-04	2.57E-05	3.99E-04	1.97E-04	4.47E-02	2.89E-04	7.74E-05	2.11E-04
cg26690891	2	150294 943	LYPD6;LYPD6	Body;Body		1.20E-03	3.00E-04	2.57E-05	1.10E-03	3.80E-04	4.24E-03	1.40E-03	4.55E-04	2.10E-03
cg20098659	12	101833 64	LOC102724020;CL EC9A;CLEC9A	TSS200;1stEx on;5URT		1.10E-03	3.00E-04	2.58E-05	2.28E-03	5.21E-04	2.20E-05	7.10E-04	3.10E-04	2.22E-02
cg03500056	16	881450 7	ABAT;ABAT;ABA T	TSS200;5UR T;5URT		8.00E-04	2.00E-04	2.58E-05	4.20E-04	3.38E-04	2.16E-01	9.37E-04	2.22E-04	2.81E-05
cg03102881	16	811308 02	GCSH;GCSH	TSS1500;TSS 1500		3.00E-04	1.00E-04	2.59E-05	5.23E-04	2.23E-04	2.05E-02	2.32E-04	6.24E-05	2.23E-04
cg07247797	1	417461 50				7.00E-04	2.00E-04	2.60E-05	7.85E-04	2.45E-04	1.63E-03	5.66E-04	2.02E-04	5.17E-03
cg26362368	1	106756 23	PEX14	Body		6.00E-04	1.00E-04	2.61E-05	9.54E-04	2.14E-04	1.58E-05	3.17E-04	1.97E-04	1.07E-01
cg13059136	11	298654 1 4	SNORA54;NAP1L 4	TSS1500;Bod y	Island	9.00E-04	2.00E-04	2.62E-05	1.15E-03	3.86E-04	3.50E-03	8.02E-04	2.61E-04	2.23E-03
cg05895018	14	103400 237	CDC42BPB	Body		5.00E-04	1.00E-04	2.62E-05	5.39E-04	2.06E-04	9.89E-03	4.41E-04	1.33E-04	9.55E-04
cg01067538	10	950037 70			N Shelf	4.00E-04	1.00E-04	2.63E-05	5.17E-04	1.67E-04	2.33E-03	3.20E-04	1.06E-04	2.70E-03
cg08862479	5	177889 945	COL23A1	Body		9.00E-04	2.00E-04	2.64E-05	1.55E-03	3.79E-04	7.16E-05	6.19E-04	2.80E-04	2.76E-02
cg24418947	1	468360 23			S Shore	1.50E-03	4.00E-04	2.68E-05	2.28E-03	7.12E-04	1.62E-03	1.25E-03	4.19E-04	2.96E-03

cg00504599	17	794280 36	BAHCC1	Body		8.00E-04	2.00E-04	2.71E-05	1.35E-03	3.65E-04	3.01E-04	5.94E-04	2.23E-04	8.09E-03
cg05889085	8	357185 61			S Shelf	1.90E-03	5.00E-04	2.71E-05	1.03E-03	7.92E-04	1.93E-01	2.33E-03	5.53E-04	2.95E-05
cg05245822	18	375501 41				1.00E-03	2.00E-04	2.72E-05	2.63E-04	4.44E-04	5.54E-01	1.21E-03	2.67E-04	6.66E-06
cg02218675	16	777429 43				5.00E-04	1.00E-04	2.72E-05	6.05E-04	2.20E-04	6.60E-03	5.16E-04	1.62E-04	1.53E-03
cg25763292	10	115442 231	CASP7;CASP7;CA SP7;CASP7;CASP7; CASP7	5URT;5URT; 5URT;5URT; 5URT;Body		5.00E-04	1.00E-04	2.74E-05	5.10E-04	1.80E-04	5.13E-03	4.92E-04	1.59E-04	2.11E-03
cg04466503	14	621106 70	FLJ22447	Body		1.00E-03	2.00E-04	2.74E-05	9.41E-04	3.56E-04	9.12E-03	9.72E-04	2.98E-04	1.18E-03
cg26468779	14	599580 11	JKAMP;JKAMP;K AMP;JKAMP;KA MP;JKAMP	Body;Body;B ody;Body;Bo dy;Body		-3.00E-04	1.00E-04	2.79E-05	-2.79E-04	1.50E-04	6.59E-02	-2.46E-04	6.52E-05	1.82E-04
cg09176736	20	377958 4	CDC25B;CDC25B; CDC25B;CDC25B; CDC25B;CDC25B; CDC25B;CDC25B; CDC25B;CDC25B	TSS1500;Bod y;Body;Body ;Body;Body; Body;Body;B ody;Body		-2.00E-04	0.00E+00	2.79E-05	-1.04E-04	6.01E-05	8.54E-02	-2.77E-04	6.45E-05	2.07E-05
cg02011576	3	380602 65	PLCD1;PLCD1;PL CD1	Body;Body;B ody		8.00E-04	2.00E-04	2.79E-05	1.22E-03	3.06E-04	1.09E-04	5.08E-04	2.21E-04	2.18E-02
cg06528160	4	137634 559				4.00E-04	1.00E-04	2.80E-05	6.70E-04	2.69E-04	1.37E-02	3.29E-04	9.22E-05	3.81E-04
cg01634340	9	946013 87	ROR2	Body		2.00E-04	1.00E-04	2.81E-05	2.68E-04	1.60E-04	9.64E-02	2.24E-04	5.81E-05	1.30E-04
cg07922513	1	608945 4	KCNAB2;KCNAB2 ;KCNAB2	5URT;5URT; 5URT		6.00E-04	1.00E-04	2.82E-05	8.09E-04	1.91E-04	3.96E-05	3.38E-04	2.38E-04	1.56E-01
cg25029035	1	207669 003	CR1;CR1	TSS1500;TSS 1500		5.00E-04	1.00E-04	2.82E-05	4.98E-04	1.90E-04	9.53E-03	4.73E-04	1.45E-04	1.17E-03
cg05183753	1	239553 133				-6.00E-04	1.00E-04	2.83E-05	-6.39E-04	1.89E-04	9.12E-04	-5.37E-04	2.15E-04	1.29E-02
cg13492133	1	183516 266	SMG7;SMG7;SMG 7;SMG7	Body;Body;B ody;Body		4.00E-04	1.00E-04	2.84E-05	5.74E-04	2.16E-04	8.61E-03	3.29E-04	9.69E-05	7.32E-04
cg07711192	12	144269 94				7.00E-04	2.00E-04	2.84E-05	7.44E-04	2.55E-04	4.15E-03	6.30E-04	2.08E-04	2.56E-03
cg07728579	15	834750 13	FSD2;FSD2;FSD2	TSS200;TSS2 00;TSS200		5.00E-04	1.00E-04	2.84E-05	9.07E-04	2.06E-04	1.93E-05	3.00E-04	1.61E-04	6.31E-02
cg23232188	3	121556 543	EAF2	Body		6.00E-04	2.00E-04	2.85E-05	8.36E-04	2.51E-04	1.11E-03	5.33E-04	1.97E-04	6.85E-03

cg04565088	18	191849 21				9.00E-04	2.00E-04	2.87E-05	7.63E-04	2.56E-04	3.32E-03	1.09E-03	3.59E-04	2.59E-03
cg19500225	8	840264 0				6.00E-04	1.00E-04	2.88E-05	5.71E-04	2.05E-04	5.95E-03	5.68E-04	1.82E-04	1.91E-03
cg18871648	14	742274 31	ELMSAN1;ELMSA N1	TSS1500;5UR T		-6.00E-04	2.00E-04	2.92E-05	-8.12E-04	2.95E-04	6.66E-03	-5.86E-04	1.82E-04	1.38E-03
cg07719512	2	219246 576	SLC11A1	TSS200		5.00E-04	1.00E-04	2.93E-05	5.49E-04	2.01E-04	7.20E-03	4.56E-04	1.43E-04	1.49E-03
cg26022608	1	109915 765	SORT1;SORT1	Body;5URT		7.00E-04	2.00E-04	2.94E-05	-1.35E-04	3.20E-04	6.74E-01	9.06E-04	1.80E-04	6.25E-07
cg27352622	5	156646 570	ITK	Body N Shore		5.00E-04	1.00E-04	2.95E-05	2.87E-04	2.02E-04	1.57E-01	6.82E-04	1.62E-04	2.89E-05
cg18112787	19	181686 39				-7.00E-04	2.00E-04	2.97E-05	-6.87E-04	3.01E-04	2.37E-02	-6.65E-04	1.90E-04	5.04E-04
cg14279167	8	124151 837	TBC1D31;TBC1D3 1	Body;Body N Shelf		-6.00E-04	1.00E-04	3.01E-05	-9.28E-04	2.71E-04	8.03E-04	-4.63E-04	1.65E-04	5.21E-03
cg00630090	1	950615 57				-7.00E-04	2.00E-04	3.03E-05	-8.34E-04	2.71E-04	2.48E-03	-5.69E-04	1.94E-04	3.55E-03
cg21529871	3	425496 37	VIPR1;VIPR1;VIPR 1;VIPR1;VIPR1	5URT;5URT; Body;Body;B ody		7.00E-04	2.00E-04	3.03E-05	7.47E-04	2.22E-04	9.49E-04	6.39E-04	2.58E-04	1.35E-02
cg20822254	16	900480 20	AFG3L1P;AFG3L1 P;AFG3L1P	Body;Body;B ody		7.00E-04	2.00E-04	3.04E-05	5.74E-04	2.26E-04	1.19E-02	9.18E-04	2.66E-04	6.02E-04
cg09060241	2	255988 65				3.00E-04	1.00E-04	3.08E-05	3.11E-04	1.80E-04	8.69E-02	3.49E-04	9.18E-05	1.60E-04
cg16958695	1	202131 884	PTPN7;PTPN7;PTP N7;PTPN7	TSS1500;TSS 1500;TSS1500 ;TSS1500		5.00E-04	1.00E-04	3.11E-05	6.88E-04	1.70E-04	8.23E-05	3.40E-04	2.08E-04	1.03E-01
cg01624068	13	113137 799				5.00E-04	1.00E-04	3.12E-05	5.38E-04	1.86E-04	4.46E-03	4.43E-04	1.46E-04	2.57E-03
cg18866825	5	150477 744				4.00E-04	1.00E-04	3.13E-05	4.15E-04	1.26E-04	1.28E-03	3.99E-04	1.55E-04	1.06E-02
cg11586890	6	334202 27	SYNGAP1	3UTR		3.00E-04	1.00E-04	3.14E-05	4.47E-04	1.19E-04	2.40E-04	2.08E-04	8.63E-05	1.61E-02
cg26572459	3	486669 5	ITPR1;ITPR1;ITPR 1	Body;Body;B ody		-1.00E-03	2.00E-04	3.14E-05	-1.19E-03	3.31E-04	4.14E-04	-7.33E-04	3.18E-04	2.15E-02
cg02569820	19	516940 13				2.00E-04	1.00E-04	3.15E-05	1.86E-04	1.23E-04	1.32E-01	2.25E-04	5.80E-05	1.12E-04
cg26647135	7	999544 00	PILRB;STAG3L5P- PVRIG2P- PILRB;STAG3L5P- PVRIG2P-PILRB	TSS1500;Bod y;Body		6.00E-04	1.00E-04	3.16E-05	5.99E-04	1.89E-04	1.90E-03	5.26E-04	1.93E-04	6.68E-03

cg01104053	14	773911 73			S Shelf	5.00E-04	1.00E-04	3.16E-05	-4.41E-05	2.10E-04	8.34E-01	8.20E-04	1.54E-04	1.44E-07
cg21436756	17	401905 01	ZNF385C	TSS1500		5.00E-04	1.00E-04	3.17E-05	4.94E-04	2.15E-04	2.28E-02	5.72E-04	1.64E-04	5.38E-04
cg08824454	2	285965 77				5.00E-04	1.00E-04	3.18E-05	5.17E-04	1.59E-04	1.37E-03	5.91E-04	2.27E-04	9.61E-03
cg03164552	10	134243 533				4.00E-04	1.00E-04	3.18E-05	2.63E-04	1.60E-04	1.03E-01	5.08E-04	1.27E-04	6.84E-05
cg05180756	1	444303 18	IPO13	Body		1.30E-03	3.00E-04	3.19E-05	1.25E-03	5.23E-04	1.82E-02	1.26E-03	3.69E-04	6.97E-04
cg04849878	5	176516 112	FGFR4;FGFR4;FGFR4;FGFR4	5URT;5URT; 5URT;TSS1500		3.00E-04	1.00E-04	3.21E-05	2.63E-04	1.86E-04	1.61E-01	2.58E-04	6.59E-05	1.01E-04
cg26714968	2	234267 824	DGKD	Body		6.00E-04	1.00E-04	3.24E-05	5.84E-04	1.88E-04	2.30E-03	5.77E-04	2.08E-04	5.80E-03
cg19882414	19	182484 76	MAST3	Body		3.00E-04	1.00E-04	3.24E-05	2.10E-04	1.60E-04	1.92E-01	3.73E-04	9.22E-05	5.96E-05
cg01577029	12	133000 830			Island	5.00E-04	1.00E-04	3.25E-05	1.43E-04	3.84E-04	7.09E-01	5.99E-04	1.40E-04	2.09E-05
cg08353615	5	137151 533				3.00E-04	1.00E-04	3.25E-05	5.48E-04	1.98E-04	6.44E-03	2.93E-04	8.84E-05	9.60E-04
cg26145152	1	681636 09				3.00E-04	1.00E-04	3.26E-05	3.69E-04	1.64E-04	2.58E-02	2.45E-04	6.87E-05	3.98E-04
cg21446345	15	703909 85	TLE3;TLE3;TLE3;TLE3;TLE3	TSS1500;TSS1500;TSS1500;TSS1500;TSS1500		-2.00E-04	0.00E+00	3.28E-05	-2.21E-04	9.03E-05	1.57E-02	-1.61E-04	4.71E-05	6.91E-04
cg18908419	10	758000 04	VCL;VCL	Body;Body		7.00E-04	2.00E-04	3.30E-05	7.82E-04	2.53E-04	2.40E-03	6.02E-04	2.13E-04	4.79E-03
cg25777459	2	232829 998	DIS3L2;DIS3L2;DIS3L2;DIS3L2;DIS3L2	5URT;5URT;5URT;Body;Body		9.00E-04	2.00E-04	3.31E-05	1.21E-03	3.03E-04	1.04E-04	5.74E-04	3.05E-04	6.07E-02
cg12589340	19	600405 8	LOC100128568;RFX2;RFX2	Body;Body;Body		3.00E-04	1.00E-04	3.32E-05	4.07E-04	1.46E-04	5.99E-03	3.20E-04	1.03E-04	1.93E-03

cg22533969	2	144160 209	ARHGAP15	Body		1.00E-03	3.00E-04	3.82E-05	1.50E-03	3.48E-04	2.73E-05	5.22E-04	3.70E-04	1.59E-01
cg08297686	14	689434 86	RAD51B;RAD51B; RAD51B	Body;Body;B ody		9.00E-04	2.00E-04	3.82E-05	8.16E-04	4.45E-04	6.88E-02	9.30E-04	2.52E-04	2.38E-04
cg00960204	6	140802 228			N Shelf	7.00E-04	2.00E-04	3.85E-05	9.80E-05	3.52E-04	7.81E-01	8.78E-04	1.93E-04	6.61E-06
cg27366815	19	578706 34	ZNF304;ZNF304; NF304	3UTR;3UTR; 3UTR		-2.00E-04	0.00E+00	3.85E-05	-3.08E-04	1.05E-04	3.84E-03	-1.48E-04	4.61E-05	1.42E-03
cg15530946	14	754691 36	EIF2B2	TSS1500		-5.00E-04	1.00E-04	3.86E-05	-6.27E-04	1.96E-04	1.64E-03	-3.72E-04	1.33E-04	5.32E-03
cg14099685	11	475460 68	CELF1;CELF1	5URT;TSS15 00		-4.00E-04	1.00E-04	3.86E-05	-4.92E-04	1.53E-04	1.58E-03	-3.60E-04	1.36E-04	8.32E-03
cg04359978	1	897590 435761	KLHL17	Body		3.00E-04	1.00E-04	3.89E-05	2.97E-04	1.42E-04	3.89E-02	3.62E-04	1.02E-04	3.88E-04
cg26595364	10	80	RET;RET	Body;Body		3.00E-04	1.00E-04	3.89E-05	3.83E-04	1.28E-04	3.16E-03	3.01E-04	1.05E-04	4.39E-03
cg22103219	7	101934 892	MIR4285;SH2B2	TSS1500;Bod y		-9.00E-04	2.00E-04	3.90E-05	-1.02E-03	3.20E-04	1.78E-03	-7.95E-04	2.99E-04	8.06E-03
cg22014955	15	924013 73	SLCO3A1;SLCO3A 1	Body;Body		5.00E-04	1.00E-04	3.91E-05	6.69E-04	2.97E-04	2.58E-02	5.05E-04	1.45E-04	5.41E-04
cg04867468	8	144956 083				5.00E-04	1.00E-04	3.92E-05	6.26E-04	1.98E-04	1.87E-03	4.77E-04	1.78E-04	7.46E-03
cg01368219	3	549997 91	LRTM1;CACNA2 D3	5URT;Body		7.00E-04	2.00E-04	3.94E-05	3.67E-04	2.75E-04	1.84E-01	8.40E-04	2.04E-04	4.14E-05
cg10184740	7	198131 49	TMEM196	TSS1500	S Shore	8.00E-04	2.00E-04	3.95E-05	6.96E-04	3.14E-04	2.79E-02	7.83E-04	2.26E-04	5.60E-04
cg03995830	10	147829 91	FAM107B;FAM107 B	Body;5URT		6.00E-04	1.00E-04	4.06E-05	3.94E-04	2.29E-04	8.78E-02	6.99E-04	1.81E-04	1.19E-04
cg01833890	12	256406 3	CACNA1C;CAC A1C;CACNA1C;C ACNA1C;CACNA 1C;CACNA1C;CA CNA1C;CACNA1 C;CACNA1C;CAC NA1C;CACNA1C; CACNA1C;CACN A1C;CACNA1C;C ACNA1C;CACNA 1C;CACNA1C;CA CNA1C;CACNA1 C;CACNA1C;CAC NA1C;CACNA1C; CACNA1C	Body;Body;B ody;Body;Bo dy;Body;Bod y;Body;Body ;Body;Body; Body;Body;B ody;Body;Bo dy;Body;Bod y;Body;Body ;Body;Body; Body	N Shore	6.00E-04	1.00E-04	4.06E-05	6.52E-04	2.10E-04	2.22E-03	4.99E-04	1.83E-04	6.45E-03

cg24190664	17	712586	24	CPSF4L	TSS1500			5.00E-04	1.00E-04	4.10E-05	6.51E-04	2.61E-04	1.36E-02	4.82E-04	1.46E-04	1.01E-03
cg02034473	12	838493	3	FAM86FP	Body			7.00E-04	2.00E-04	4.12E-05	5.99E-04	2.40E-04	1.34E-02	7.84E-04	2.38E-04	1.04E-03
cg13329867	2	181120	163					-6.00E-04	1.00E-04	4.17E-05	-5.59E-04	1.91E-04	3.85E-03	-7.03E-04	2.43E-04	3.89E-03
cg07281747	17	571051	12	TRIM37;TRIM37	Body;Body	N Shore		6.00E-04	2.00E-04	4.19E-05	8.54E-04	2.12E-04	8.89E-05	3.90E-04	2.38E-04	1.01E-01
cg03785532	19	364091	64					5.00E-04	1.00E-04	4.23E-05	6.89E-04	1.73E-04	1.04E-04	3.18E-04	1.80E-04	7.85E-02
cg11202345	17	769760	57	LGALS3BP;LGALS3BP	5URT;1stExo	Island		9.00E-04	2.00E-04	4.25E-05	6.81E-04	3.16E-04	3.26E-02	9.90E-04	2.78E-04	4.04E-04
cg21691116	1	161171	819	NDUFS2;NDUFS2	T			-7.00E-04	2.00E-04	4.26E-05	-6.79E-04	2.49E-04	7.08E-03	-8.19E-04	2.66E-04	2.20E-03
cg16451527	3	568897	95	ARHGEF3;ARHGEF3	Body;Body			1.20E-03	3.00E-04	4.27E-05	6.19E-04	4.29E-04	1.51E-01	1.58E-03	3.77E-04	3.37E-05
cg10840851	11	607126	77	SLC15A3;SLC15A3	Body;Body			6.00E-04	2.00E-04	4.27E-05	5.63E-04	2.87E-04	5.15E-02	6.64E-04	1.84E-04	3.38E-04
cg21883904	7	259671	3	BRAT1	TSS1500			7.00E-04	2.00E-04	4.27E-05	8.15E-04	2.75E-04	3.57E-03	6.43E-04	2.24E-04	4.27E-03
cg05826823	9	130968	072	CIZ1;CIZ1;DNM1;DNM1;DNM1;DNM1	TSS1500;TSS1500;Body;Body;Body;Body			4.00E-04	1.00E-04	4.28E-05	5.61E-04	1.41E-04	1.00E-04	2.42E-04	1.27E-04	5.70E-02
cg25753411	6	138727	287	HEBP2;HEBP2	Body;Exon	S Shore		8.00E-04	2.00E-04	4.28E-05	8.00E-04	3.23E-04	1.43E-02	8.37E-04	2.57E-04	1.18E-03
cg09834258	19	426871	4	CCDC94	3UTR			1.00E-04	0.00E+00	4.30E-05	2.37E-04	8.53E-05	6.11E-03	1.10E-04	3.33E-05	1.00E-03
cg15964066	4	173771	911	GALNTL6	Body	N Shelf		-4.00E-04	1.00E-04	4.30E-05	-1.10E-03	2.56E-04	3.22E-05	-2.99E-04	1.19E-04	1.19E-02
cg18307303	5	158757	456	IL12B;LOC285626;IL12B	5URT;TSS1500;1stExon			4.00E-04	1.00E-04	4.31E-05	5.87E-04	1.82E-04	1.51E-03	3.64E-04	1.35E-04	7.20E-03
cg14476101	1	120255	992	PHGDH	Body			-1.10E-03	3.00E-04	4.35E-05	-1.33E-03	4.13E-04	1.54E-03	-9.50E-04	3.64E-04	9.35E-03
cg09577455	6	295933	82	GABBR1;GABBR1;GABBR1	Body;Body;Body			-8.00E-04	2.00E-04	4.36E-05	-1.08E-03	3.24E-04	1.02E-03	-5.93E-04	2.23E-04	8.08E-03
cg20272496	11	466853	96	ATG13;ATG13;ATG13;ATG13	Body;Body;Body;Body			6.00E-04	1.00E-04	4.38E-05	6.42E-04	2.20E-04	4.03E-03	5.01E-04	1.73E-04	3.82E-03

Table S4. Epigenome-wide associations of 628 significant (FDR 0.05 threshold) CpG sites with BMI from the meta-analysis of InterGEN and GENOA. Female only.

CpG	CHR	POS	UCSC Ref Gene Name	UCSC_R efGene_ Group	Relation_ to_UCSC_ CpG_ Island	META			InterGEN			GENOA		
						BETA	SE	P	BETA	SE	P	BETA	SE	P
cg03067296	17	76274577	LOC10099 6291	TSS200		-1.90E-03	2.00E-04	1.74E-22	-2.66E-03	3.59E-04	7.99E-12	-1.54E-03	2.24E-04	1.15E-11
cg18181703	17	76354621	SOCS3	Body	N Shore	-2.10E-03	2.00E-04	5.08E-20	-2.78E-03	3.58E-04	1.02E-12	-1.60E-03	2.91E-04	5.13E-08
cg11047325	17	76354934	SOCS3	Body	Island	-3.20E-03	4.00E-04	4.63E-17	-4.96E-03	6.49E-04	2.03E-12	-2.28E-03	4.75E-04	1.82E-06
cg19748455	17	76274856	LOC10099 6291	TSS1500		-1.70E-03	2.00E-04	1.31E-16	-2.33E-03	3.73E-04	4.11E-09	-1.44E-03	2.49E-04	9.89E-09
cg09349128	22	50327986			N Shore	-1.30E-03	2.00E-04	3.92E-16	-2.22E-03	3.70E-04	1.28E-08	-1.07E-03	1.73E-04	9.87E-10
cg13343932	17	76355061	SOCS3;LO C10192867 4;LOC1019 28674	Body;TS S1500;TS S1500	Island	-2.70E-03	3.00E-04	2.75E-15	-4.14E-03	5.90E-04	6.69E-11	-1.95E-03	4.12E-04	2.51E-06
cg19758958	11	62319222				-1.10E-03	2.00E-04	3.95E-13	-1.29E-03	2.37E-04	1.88E-07	-1.03E-03	2.12E-04	1.42E-06
cg00840791	19	16453259				-3.60E-03	5.00E-04	7.80E-13	-3.76E-03	7.14E-04	4.70E-07	-3.47E-03	7.12E-04	1.31E-06
cg03770138	9	136009651	RALGDS	Body		-1.20E-03	2.00E-04	1.23E-12	-1.28E-03	2.25E-04	6.72E-08	-1.05E-03	2.42E-04	1.66E-05
cg02370334	19	17955786	JAK3	5URT	S Shelf	-1.50E-03	2.00E-04	4.29E-12	-1.53E-03	3.38E-04	1.10E-05	-1.48E-03	2.83E-04	2.10E-07
cg12170787	19	1130965	SBNO2;SB NO2	Body;Bo dy		-9.00E-04	1.00E-04	1.96E-11	-1.56E-03	3.31E-04	5.86E-06	-7.44E-04	1.40E-04	1.48E-07
cg18608055	19	1130866	SBNO2;SB NO2	Body;Bo dy		-1.20E-03	2.00E-04	5.54E-11	-1.78E-03	3.64E-04	2.40E-06	-9.90E-04	2.08E-04	2.39E-06
cg24382141	16	67944348	PSKH1	Body	S Shore	-9.00E-04	1.00E-04	9.15E-11	-1.29E-03	2.33E-04	1.16E-07	-6.91E-04	1.77E-04	9.69E-05
cg09536368	6	149461319				-5.00E-04	1.00E-04	1.17E-10	-4.88E-04	1.61E-04	2.85E-03	-4.70E-04	8.26E-05	1.74E-08
cg15781610	6	36992554	FGD2	Body		-1.20E-03	2.00E-04	1.86E-10	-1.70E-03	3.22E-04	4.09E-07	-9.34E-04	2.31E-04	5.65E-05
cg00574958	11	68607622	CPT1A;CP T1A	5URT;5U RT	S Shore	-5.00E-04	1.00E-04	2.11E-10	-2.70E-04	1.32E-04	4.27E-02	-5.25E-04	8.43E-05	6.95E-10
cg00160670	21	35320599	LINC00649 LINC0064 9	TSS1500; Body		-1.60E-03	2.00E-04	2.50E-10	-1.55E-03	3.31E-04	6.43E-06	-1.59E-03	3.73E-04	2.20E-05
cg09063556	16	66653795	CMTM4;C MTM4	3UTR;Bo dy		6.00E-04	1.00E-04	3.52E-10	6.38E-04	1.78E-04	4.62E-04	6.34E-04	1.23E-04	3.14E-07
cg09832683	17	15013038				1.30E-03	2.00E-04	4.65E-10	1.71E-03	3.48E-04	2.25E-06	1.05E-03	2.53E-04	3.97E-05
cg24993990	2	166428802	CSRNP3;C SRNP3	TSS200;5 URT		1.30E-03	2.00E-04	7.93E-10	1.50E-03	3.36E-04	1.49E-05	1.12E-03	2.60E-04	1.82E-05
cg17936938	6	7866213	BMP6	Body		1.20E-03	2.00E-04	8.13E-10	1.78E-03	3.39E-04	4.96E-07	9.37E-04	2.49E-04	1.74E-04
cg08548559	22	31686097	PIK3IP1;PI K3IP1	Body;Bo dy	N Shore	-1.50E-03	2.00E-04	9.59E-10	-1.85E-03	4.34E-04	3.56E-05	-1.33E-03	2.95E-04	7.65E-06
cg10508317	17	76355146	SOCS3;LO C10192867	Body;TS S1500;TS S1500	Island	-5.00E-04	1.00E-04	9.79E-10	-8.21E-04	1.57E-04	5.66E-07	-4.16E-04	1.09E-04	1.42E-04

			4;LOC1019 28674											
cg20803896	12	99006941				9.00E-04	1.00E-04	1.50E-09	1.09E-03	2.15E-04	1.20E-06	6.98E-04	1.95E-04	3.72E-04
cg20710777	5	110411740	TSLP;TSLP ;TSLP	Body;Bo dy;Body	S Shelf	-6.00E-04	1.00E-04	1.54E-09	-1.70E-03	3.31E-04	8.70E-07	-5.19E-04	1.12E-04	3.96E-06
cg19157500	13	31271994				1.10E-03	2.00E-04	1.77E-09	1.27E-03	3.35E-04	2.16E-04	1.02E-03	2.16E-04	2.74E-06
cg26402346	12	101864876				1.50E-03	3.00E-04	3.10E-09	1.45E-03	4.51E-04	1.62E-03	1.54E-03	3.09E-04	7.39E-07
cg06898549	12	41083590			N Shelf	1.20E-03	2.00E-04	4.17E-09	1.06E-03	3.74E-04	5.24E-03	1.21E-03	2.35E-04	3.00E-07
cg08309687	21	35320596	LINC00649 ;LINC0064 9	TSS1500; Body		-1.40E-03	2.00E-04	4.81E-09	-1.27E-03	3.35E-04	2.21E-04	-1.56E-03	3.46E-04	7.42E-06
cg20090157	17	76274606	LOC10099 6291	TSS200		-1.00E-03	2.00E-04	4.84E-09	-1.34E-03	3.38E-04	1.11E-04	-9.27E-04	2.09E-04	1.08E-05
cg01198738	8	121597619	SNTB1	Body		-1.50E-03	3.00E-04	5.21E-09	-1.29E-03	4.46E-04	4.46E-03	-1.65E-03	3.22E-04	3.73E-07
cg00014380	16	4424290	VASN;CO RO7- PAM16;C ORO7;CO RO7;COR O7	5URT;Bo dy;Body; Body;Bo dy	S Shelf	6.00E-04	1.00E-04	5.70E-09	8.92E-04	2.40E-04	2.77E-04	5.42E-04	1.16E-04	3.46E-06
cg03260624	1	91970722	CDC7;CD C7;CDC7	Body;Bo dy;Body	S Shelf	8.00E-04	1.00E-04	6.20E-09	6.39E-04	2.06E-04	2.26E-03	8.60E-04	1.73E-04	7.58E-07
cg21650866	8	142297256			S Shore	1.30E-03	2.00E-04	6.25E-09	1.16E-03	2.89E-04	9.27E-05	1.50E-03	3.52E-04	2.20E-05
cg14369893	21	46501109	ADARB1; ADARB1; ADARB1; ADARB1; ADARB1; ADARB1; ADARB1; ADARB1	5URT;5U RT;5URT ;5URT;B ody;Bod y;Body;B ody		-1.50E-03	3.00E-04	6.34E-09	-1.67E-03	3.79E-04	2.00E-05	-1.42E-03	3.71E-04	1.43E-04
cg16740586	21	43655919	ABCG1;AB CG1;ABC G1;ABCG1 ;ABCG1;A BCG1	Body;Bo dy;Body; Body;Bo dy;Body	S Shore	8.00E-04	1.00E-04	8.10E-09	4.44E-04	2.54E-04	8.31E-02	8.79E-04	1.55E-04	1.73E-08
cg06192883	15	52554171	MYO5C	Body		1.00E-03	2.00E-04	8.25E-09	1.26E-03	3.51E-04	4.32E-04	9.52E-04	2.08E-04	5.62E-06
cg08373547	14	52794541	PTGER2	3UTR		1.20E-03	2.00E-04	1.07E-08	9.31E-04	3.20E-04	4.13E-03	1.37E-03	2.72E-04	5.86E-07
cg00926657	17	79880822	MAFG;MA FG	Body;Bo dy	Island	8.00E-04	1.00E-04	1.07E-08	5.46E-04	2.44E-04	2.66E-02	9.65E-04	1.77E-04	6.83E-08
cg18840187	4	169608898	PALLD;PA LLD;PALL D	Body;Bo dy;Body		6.00E-04	1.00E-04	1.07E-08	5.64E-04	1.73E-04	1.42E-03	5.56E-04	1.18E-04	2.93E-06

cg22652934	21	36180035	RUNX1;R UNX1	Body;Bo dy		-1.20E-03	2.00E-04	1.19E-08	-2.04E-03	4.93E-04	5.64E-05	-9.98E-04	2.29E-04	1.43E-05
cg03295554	11	128395450	LOC10192 9517;ETS1	TSS1500; Body	S Shelf	-1.70E-03	3.00E-04	1.25E-08	-1.26E-03	4.32E-04	3.91E-03	-1.99E-03	3.95E-04	5.80E-07
cg01671681	3	155421735	PLCH1	5URT		-1.00E-03	2.00E-04	1.32E-08	-1.40E-03	2.69E-04	5.69E-07	-6.78E-04	2.21E-04	2.27E-03
cg10288525	13	33455187	LINC00423	Body		8.00E-04	1.00E-04	1.51E-08	4.82E-04	2.20E-04	2.97E-02	1.03E-03	1.85E-04	3.61E-08
cg16291589	20	6023178	LRRN4	Body	S Shore	1.00E-03	2.00E-04	1.53E-08	1.26E-03	3.19E-04	1.14E-04	9.17E-04	2.22E-04	3.82E-05
cg09613192	2	181388538				1.20E-03	2.00E-04	1.55E-08	1.17E-03	3.56E-04	1.20E-03	1.18E-03	2.56E-04	4.96E-06
cg19957386	17	47836122	FAM117A	Body		-9.00E-04	2.00E-04	1.78E-08	-1.09E-03	2.51E-04	2.37E-05	-7.71E-04	2.08E-04	2.29E-04
cg02398240	2	128256334	IWS1	Body		-1.10E-03	2.00E-04	1.91E-08	-1.62E-03	2.94E-04	1.41E-07	-6.65E-04	2.45E-04	6.71E-03
cg02734358	4	90227074	GPRIN3	5URT	N Shore	-1.10E-03	2.00E-04	2.30E-08	-1.58E-03	3.55E-04	1.66E-05	-9.08E-04	2.44E-04	2.06E-04
cg20493906	4	106113303	TET2;TET2 ;TET2-AS1	5URT;5U RT;Body		8.00E-04	1.00E-04	2.50E-08	6.56E-04	2.23E-04	3.85E-03	8.15E-04	1.71E-04	2.13E-06
cg21313072	18	43640508	PSTPIP2	Body		5.00E-04	1.00E-04	2.91E-08	3.81E-04	1.53E-04	1.40E-02	5.71E-04	1.13E-04	5.14E-07
cg14377972	15	99356110	IGF1R;IGF 1R	Body;Bo dy		-6.00E-04	1.00E-04	2.95E-08	-4.41E-04	2.46E-04	7.52E-02	-6.28E-04	1.19E-04	1.51E-07
cg15721584	3	181326755	SOX2- OT;SOX2- OT;SOX2- OT;SOX2- OT;SOX2- OT;SOX2- OT	TSS1500; TSS1500; TSS1500; Body;Bo dy;Body		1.90E-03	4.00E-04	3.51E-08	1.63E-03	5.35E-04	2.70E-03	2.18E-03	4.67E-04	3.66E-06
cg01364674	1	24348512				4.00E-04	1.00E-04	3.85E-08	3.75E-04	1.11E-04	8.93E-04	3.95E-04	9.11E-05	1.64E-05
cg17901584	1	55353706	DHCR24	TSS1500	S Shore	-1.50E-03	3.00E-04	4.00E-08	-2.46E-03	5.34E-04	8.32E-06	-1.15E-03	3.14E-04	2.69E-04
cg17457241	16	8814411	ABAT;AB AT;ABAT	TSS200;5 URT;5U RT		7.00E-04	1.00E-04	4.17E-08	3.96E-04	2.09E-04	6.05E-02	8.22E-04	1.52E-04	8.31E-08
cg15183129	1	160759781				7.00E-04	1.00E-04	4.29E-08	8.74E-04	1.93E-04	1.21E-05	5.48E-04	1.63E-04	8.40E-04
cg09152259	2	128156114			N Shelf	-1.00E-03	2.00E-04	4.56E-08	-1.66E-03	3.82E-04	2.41E-05	-7.82E-04	2.01E-04	1.10E-04
cg25705792	21	35320017	LINC00649 ;LINC0064 9	TSS1500; Body		-9.00E-04	2.00E-04	5.18E-08	-1.07E-03	2.62E-04	7.09E-05	-8.29E-04	2.26E-04	2.59E-04
cg09310636	14	90760903	NRDE2	Body		7.00E-04	1.00E-04	5.62E-08	7.82E-04	2.14E-04	3.45E-04	6.67E-04	1.65E-04	5.96E-05
cg02233071	21	36181046	RUNX1;R UNX1	Body;Bo dy		-1.50E-03	3.00E-04	5.87E-08	-1.33E-03	4.78E-04	5.95E-03	-1.52E-03	3.26E-04	3.60E-06
cg14728380	17	80280330	SECTM1	Body	S Shelf	1.20E-03	2.00E-04	5.87E-08	1.09E-03	3.61E-04	2.90E-03	1.20E-03	2.66E-04	7.45E-06
cg22413912	7	2255758	MAD1L1; MAD1L1; MAD1L1; MAD1L1; MAD1L1	Body;Bo dy;Body; Body;Bo dy		-7.00E-04	1.00E-04	5.96E-08	-6.03E-04	2.42E-04	1.37E-02	-8.11E-04	1.67E-04	1.35E-06
cg01101459	1	234871477				8.00E-04	2.00E-04	6.31E-08	1.55E-03	4.32E-04	4.49E-04	7.35E-04	1.66E-04	1.13E-05

cg08350157	3	131219430	MRPL3	Body	N Shelf	-6.00E-04	1.00E-04	6.37E-08	-4.00E-04	1.99E-04	4.59E-02	-6.83E-04	1.32E-04	3.06E-07
cg10192877	21	43641690	BCG1	dy;Body	S Shore	3.00E-04	1.00E-04	6.82E-08	2.39E-04	1.04E-04	2.33E-02	3.67E-04	7.37E-05	7.44E-07
cg01355089	1	93495018				1.00E-03	2.00E-04	6.90E-08	1.17E-03	2.93E-04	9.79E-05	8.83E-04	2.39E-04	2.30E-04
cg10969521	21	36355537	RUNX1	Body		-1.60E-03	3.00E-04	6.94E-08	-1.52E-03	4.60E-04	1.19E-03	-1.58E-03	3.70E-04	2.22E-05
cg15218293	16	77771284	T7	Body		1.60E-03	3.00E-04	7.34E-08	2.38E-03	6.83E-04	6.58E-04	1.38E-03	3.21E-04	1.77E-05
cg16531578	6	42370098	RERF1	RT		-1.60E-03	3.00E-04	7.62E-08	-2.61E-03	5.92E-04	2.02E-05	-1.26E-03	3.45E-04	2.69E-04
cg08108165	15	57410418	CF12	Body		-9.00E-04	2.00E-04	9.48E-08	-1.03E-03	2.73E-04	2.28E-04	-8.57E-04	2.25E-04	1.52E-04
cg12712122	6	88435312				9.00E-04	2.00E-04	1.06E-07	7.04E-04	2.75E-04	1.13E-02	1.13E-03	2.35E-04	1.86E-06
cg18522582	2	223915743	KCNE4	TSS1500	N Shore	1.70E-03	3.00E-04	1.06E-07	1.15E-03	5.70E-04	4.53E-02	2.00E-03	3.94E-04	4.89E-07
cg12808636	1	11987986			S Shore	6.00E-04	1.00E-04	1.08E-07	6.16E-04	1.87E-04	1.22E-03	6.30E-04	1.51E-04	3.39E-05
cg15730234	1	101759418				-1.00E-03	2.00E-04	1.11E-07	-9.84E-04	2.45E-04	9.31E-05	-9.97E-04	2.87E-04	5.36E-04
cg08857797	17	40927699	VPS25	Body		1.10E-03	2.00E-04	1.24E-07	1.43E-03	3.31E-04	2.90E-05	8.64E-04	2.58E-04	8.63E-04
cg19432644	1	156165820	SLC25A44	dy;Body	S Shore	6.00E-04	1.00E-04	1.31E-07	7.00E-04	1.66E-04	4.15E-05	4.84E-04	1.46E-04	9.46E-04
cg26002437	10	45473231	ASSF4	dy	S Shelf	-1.00E-04	0.00E+00	1.37E-07	-2.49E-04	9.07E-05	6.76E-03	-1.05E-04	2.20E-05	2.32E-06
cg07458272	19	34744396	KIAA0355	TSS1500	N Shore	9.00E-04	2.00E-04	1.40E-07	1.30E-03	2.94E-04	1.86E-05	6.59E-04	1.94E-04	7.35E-04
cg14624311	16	85942538	IRF8	Body		6.00E-04	1.00E-04	1.43E-07	9.53E-04	1.94E-04	2.17E-06	4.11E-04	1.40E-04	3.44E-03
cg09831562	3	181327125	OT	dy;Body		6.00E-04	1.00E-04	1.50E-07	7.84E-04	2.60E-04	2.98E-03	5.93E-04	1.36E-04	1.52E-05
cg03413355	15	56537579			S Shore	1.10E-03	2.00E-04	1.56E-07	8.84E-04	3.30E-04	8.08E-03	1.33E-03	2.87E-04	4.39E-06
cg17739917	17	38477572	RARA	RT;5URT	S Shelf	1.50E-03	3.00E-04	1.65E-07	5.82E-04	4.25E-04	1.73E-01	2.25E-03	3.86E-04	7.77E-09
cg19572574	10	63592731				-1.10E-03	2.00E-04	1.67E-07	-1.49E-03	3.71E-04	9.66E-05	-9.57E-04	2.69E-04	3.88E-04

cg19089201	7	45002287	MYO1G	3UTR	Island	-1.00E-03	2.00E-04	3.40E-07	-8.13E-04	3.67E-04	2.83E-02	-1.04E-03	2.24E-04	4.31E-06
cg14017705	20	24754564				-1.40E-03	3.00E-04	3.55E-07	-8.97E-04	3.97E-04	2.54E-02	-1.81E-03	3.72E-04	1.37E-06
cg02535555	3	121990376	CASR;CAS R	Body;Bo dy		-5.00E-04	1.00E-04	3.55E-07	-4.28E-04	1.58E-04	7.58E-03	-6.05E-04	1.38E-04	1.23E-05
cg11121826	17	75105957	SEC14L1;S EC14L1	5URT;5U RT		5.00E-04	1.00E-04	3.56E-07	3.13E-04	1.77E-04	8.01E-02	5.20E-04	1.07E-04	1.26E-06
cg24531955	8	23154691	LOXL2	3UTR		-7.00E-04	1.00E-04	3.64E-07	-7.31E-04	2.56E-04	4.88E-03	-7.38E-04	1.75E-04	2.81E-05
cg02108045	12	93962028	SOCS2- AS1	Body	N Shore	6.00E-04	1.00E-04	3.65E-07	3.89E-04	1.80E-04	3.19E-02	8.39E-04	1.70E-04	8.89E-07
cg02786370	4	2747928	TNIP2;TNI P2;TNIP2	Body;Bo dy;Body		-1.20E-03	2.00E-04	3.72E-07	-1.48E-03	3.98E-04	2.80E-04	-1.02E-03	2.84E-04	3.46E-04
cg05284742	14	93552128	ITPK1;ITP K1;ITPK1	Body;Bo dy;Body		4.00E-04	1.00E-04	3.77E-07	3.30E-04	1.63E-04	4.52E-02	4.81E-04	1.02E-04	2.63E-06
cg15533397	1	76695186	ST6GAL- NAC3;ST6 GALNAC3	Body;Bo dy		5.00E-04	1.00E-04	3.96E-07	5.89E-04	1.88E-04	2.08E-03	5.24E-04	1.31E-04	6.89E-05
cg00437879	10	92619295			S Shore	-8.00E-04	2.00E-04	3.99E-07	-1.11E-03	3.42E-04	1.41E-03	-7.10E-04	1.76E-04	6.11E-05
cg02119938	15	78505051	ACSBG1;A CSBG1	Body;Bo dy		-7.00E-04	1.00E-04	4.05E-07	-6.46E-04	2.88E-04	2.64E-02	-6.52E-04	1.43E-04	6.28E-06
cg26470501	19	45252955	BCL3	Body	S Shore	-8.00E-04	2.00E-04	4.09E-07	-1.14E-03	2.58E-04	1.73E-05	-6.22E-04	2.15E-04	3.89E-03
cg26236214	13	111867078	ARHGEF7; ARHGEF7; ARHGEF7; ARHGEF7; ARHGEF7	5URT;5U RT;Body; Body;Bo dy		9.00E-04	2.00E-04	4.44E-07	1.30E-03	3.33E-04	1.42E-04	7.28E-04	2.07E-04	4.54E-04
cg03276602	7	150451580				-5.00E-04	1.00E-04	4.55E-07	-7.52E-04	1.83E-04	6.29E-05	-3.65E-04	1.06E-04	6.00E-04
cg27345524	15	67393714	SMAD3	Body		7.00E-04	1.00E-04	4.60E-07	8.27E-04	2.76E-04	3.21E-03	6.78E-04	1.66E-04	4.81E-05
cg20651995	2	69525471				-7.00E-04	1.00E-04	4.84E-07	-1.11E-03	2.65E-04	4.79E-05	-5.60E-04	1.70E-04	1.02E-03
cg25817701	7	2140143	MAD1L1; MAD1L1; MAD1L1; MAD1L1; MAD1L1	Body;Bo dy;Body; Body;Bo dy		6.00E-04	1.00E-04	4.93E-07	4.44E-04	2.53E-04	8.14E-02	6.98E-04	1.46E-04	1.92E-06
cg16809457	6	90399677	MDN1	Body		9.00E-04	2.00E-04	5.12E-07	9.59E-04	3.47E-04	6.36E-03	9.29E-04	2.22E-04	3.03E-05
cg00307819	17	47817938	FAM117A	Body		-8.00E-04	1.00E-04	5.24E-07	-6.21E-04	2.16E-04	4.57E-03	-8.73E-04	2.08E-04	3.01E-05
cg26326160	20	41921081				1.30E-03	3.00E-04	5.25E-07	1.74E-03	4.12E-04	4.26E-05	9.78E-04	3.16E-04	2.06E-03
cg27579586	20	45196529	SLC13A3;S LC13A3;SL C13A3;SL C13A3;SL C13A3	Body;Bo dy;Body; Body;Bo dy		9.00E-04	2.00E-04	5.30E-07	3.97E-04	2.77E-04	1.54E-01	1.15E-03	2.18E-04	1.83E-07
cg20959703	19	17959783	JAK3	TSS1500	S Shore	-8.00E-04	2.00E-04	5.30E-07	-1.29E-03	2.80E-04	8.32E-06	-5.80E-04	2.04E-04	4.54E-03
cg04927537	17	76976091	LGALS3BP	TSS200		1.40E-03	3.00E-04	5.64E-07	1.19E-03	4.23E-04	5.65E-03	1.67E-03	3.96E-04	2.62E-05

cg05304729	1	158800024	MNDA	TSS1500		9.00E-04	2.00E-04	5.64E-07	1.49E-03	3.91E-04	1.96E-04	7.77E-04	2.15E-04	3.20E-04
cg19695507	10	13526193	BEND7;BE	Body;Bo										
cg13053471	1	235147039	ND7	dy		6.00E-04	1.00E-04	5.77E-07	1.29E-03	2.66E-04	3.00E-06	4.24E-04	1.35E-04	1.70E-03
cg03866862	6	33401542	SYNGAP1	Body		8.00E-04	2.00E-04	6.21E-07	6.69E-04	2.93E-04	2.36E-02	8.58E-04	1.92E-04	9.12E-06
cg26315985	1	65363870	JAK1	5URT		-7.00E-04	2.00E-04	6.25E-07	-8.45E-04	3.45E-04	1.55E-02	-7.27E-04	1.67E-04	1.51E-05
cg19541622	4	56180	ZNF718;ZNF595;ZNF595;ZNF595;ZNF718;ZNF718	TSS1500;5URT;5UR;Body;dy;Body	S Shelf	1.10E-03	2.00E-04	6.28E-07	1.14E-03	3.55E-04	1.65E-03	1.08E-03	2.83E-04	1.44E-04
cg12769615	4	95653156				7.00E-04	1.00E-04	6.33E-07	5.60E-04	2.55E-04	3.00E-02	8.31E-04	1.82E-04	5.91E-06
cg13195276	5	127203128				7.00E-04	1.00E-04	6.33E-07	7.39E-04	3.11E-04	1.86E-02	7.11E-04	1.62E-04	1.34E-05
cg15001240	12	27615408				-8.00E-04	2.00E-04	6.37E-07	-1.16E-03	2.63E-04	1.84E-05	-5.94E-04	2.08E-04	4.47E-03
cg04816311	7	1066650	C7orf50;C7orf50;C7orf50	Body;Bo	N Shore	1.10E-03	2.00E-04	6.57E-07	8.74E-04	4.22E-04	3.99E-02	1.13E-03	2.48E-04	6.06E-06
cg17075888	7	95225339	PDK4	Body	N Shore	-1.30E-03	3.00E-04	6.61E-07	-6.83E-04	3.42E-04	4.77E-02	-1.97E-03	3.78E-04	2.40E-07
cg10581989	16	11964386	GSPT1;GSPT1	3UTR;3UTR		9.00E-04	2.00E-04	6.91E-07	1.42E-03	3.45E-04	6.11E-05	7.40E-04	2.30E-04	1.34E-03
cg16954329	5	10323987				1.00E-03	2.00E-04	7.27E-07	1.17E-03	3.98E-04	3.71E-03	9.73E-04	2.43E-04	6.70E-05
cg23545556	6	6928585				9.00E-04	2.00E-04	7.38E-07	8.63E-04	2.38E-04	3.88E-04	9.78E-04	2.89E-04	7.48E-04
cg14115749	19	19596444	GA-TAD2A;GATAD2A	Body;Bo		7.00E-04	1.00E-04	7.40E-07	7.85E-04	2.55E-04	2.43E-03	7.16E-04	1.85E-04	1.12E-04
cg03484180	3	49967517	MON1A;MON1A	TSS200;TSS200	S Shore	-9.00E-04	2.00E-04	7.62E-07	-7.64E-04	2.70E-04	5.36E-03	-1.00E-03	2.44E-04	4.30E-05
cg16696202	3	93945049				6.00E-04	1.00E-04	7.86E-07	7.32E-04	2.24E-04	1.32E-03	6.05E-04	1.62E-04	2.06E-04
cg02485044	13	50234343				6.00E-04	1.00E-04	7.93E-07	3.09E-04	2.26E-04	1.73E-01	7.23E-04	1.45E-04	7.27E-07
cg10780778	6	26351915				-9.00E-04	2.00E-04	8.60E-07	-1.61E-03	4.62E-04	6.49E-04	-7.71E-04	2.00E-04	1.24E-04
cg25124889	13	24327015	MIPEP	Body		8.00E-04	2.00E-04	8.76E-07	7.90E-04	2.28E-04	6.71E-04	7.35E-04	2.11E-04	5.11E-04
cg04610187	17	76360794	LOC101928674;LOC101928674;LOC101928674	Body;Bo	S Shelf	-1.00E-03	2.00E-04	8.87E-07	-1.43E-03	2.77E-04	7.43E-07	-4.97E-04	3.03E-04	1.02E-01
cg22246215	1	203118486	ADORA1;ADORA1	Body;Bo		6.00E-04	1.00E-04	9.12E-07	5.40E-04	1.89E-04	4.87E-03	6.28E-04	1.57E-04	6.60E-05
cg07190151	5	58338574	PDE4D;PDE4D;PDE4D	Body;Bo	S Shelf	-6.00E-04	1.00E-04	9.28E-07	-8.36E-04	1.89E-04	1.82E-05	-4.42E-04	1.68E-04	8.68E-03

			PDE4D;PD E4D											
cg07913959	6	46672552	PLA2G7;P LA2G7	Body;Bo dy		3.00E-04	1.00E-04	9.36E-07	3.31E-04	1.66E-04	4.76E-02	2.67E-04	5.94E-05	7.87E-06
cg17822325	1	31896462	SERINC2;S ERINC2;S ERINC2;S ERINC2;S ERINC2	5URT;Bo dy;Body; Body;Bo dy		9.00E-04	2.00E-04	9.38E-07	7.69E-04	2.28E-04	9.39E-04	1.04E-03	2.87E-04	2.91E-04
cg05713943	13	97912352	MBNL2;M BNL2;MB NL2	5URT;5U RT;5URT		-7.00E-04	1.00E-04	9.38E-07	-9.41E-04	2.56E-04	3.22E-04	-5.58E-04	1.60E-04	5.23E-04
cg02650017	17	47301614	PHOS- PHO1;PH OSPHO1	Body;Bo dy	Island	-2.00E-04	0.00E+00	9.46E-07	-4.20E-04	1.47E-04	4.75E-03	-1.89E-04	4.45E-05	2.33E-05
cg10785394	1	178993006			N Shore	7.00E-04	1.00E-04	9.57E-07	7.91E-04	1.98E-04	9.97E-05	5.91E-04	2.02E-04	3.56E-03
cg10381071	15	70391035	TLE3;TLE3 ;TLE3;TLE 3;TLE3	TSS1500; TSS1500; TSS1500; TSS1500; TSS1500	Island	-5.00E-04	1.00E-04	9.61E-07	-5.55E-04	1.73E-04	1.63E-03	-5.23E-04	1.41E-04	2.23E-04
cg05241923	9	136010810	RALGDS	Body		-1.00E-03	2.00E-04	9.73E-07	-1.36E-03	3.02E-04	1.43E-05	-6.95E-04	2.72E-04	1.08E-02
cg17680767	5	73623208	LINC01333	Body		-8.00E-04	2.00E-04	9.85E-07	-6.92E-04	2.62E-04	9.03E-03	-8.49E-04	2.05E-04	3.70E-05
cg23204398	8	126365081	NSMCE2	Body		1.40E-03	3.00E-04	9.91E-07	7.82E-04	4.34E-04	7.34E-02	1.83E-03	3.72E-04	1.12E-06
cg11928146	2	19546630			N Shore	6.00E-04	1.00E-04	1.00E-06	4.73E-04	1.75E-04	7.80E-03	6.32E-04	1.53E-04	3.80E-05
cg22530144	2	46300869	PRKCE	Body		-9.00E-04	2.00E-04	1.03E-06	-7.86E-04	2.62E-04	3.13E-03	-9.04E-04	2.33E-04	1.16E-04
cg05973262	6	32191895	NOTCH4	TSS200		9.00E-04	2.00E-04	1.06E-06	8.15E-04	3.32E-04	1.52E-02	9.84E-04	2.32E-04	2.48E-05
cg03351508	21	16591598				-1.30E-03	3.00E-04	1.07E-06	-2.03E-03	5.77E-04	5.67E-04	-1.14E-03	3.13E-04	2.87E-04
cg23006541	11	68075647				1.00E-03	2.00E-04	1.07E-06	4.36E-04	3.15E-04	1.67E-01	1.28E-03	2.49E-04	3.65E-07
cg02688432	1	91970745	CDC7;CD C7;CDC7	Body;Bo dy;Body	S Shelf	8.00E-04	2.00E-04	1.12E-06	6.06E-04	2.78E-04	3.08E-02	9.94E-04	2.22E-04	8.05E-06
cg27086356	3	170627562	EIF5A2	TSS1500	S Shore	-1.20E-03	2.00E-04	1.13E-06	-1.34E-03	4.02E-04	1.09E-03	-1.05E-03	2.93E-04	3.40E-04
cg19640090	12	11975155	ETV6;RNU 6-19P	Body;Bo dy		-6.00E-04	1.00E-04	1.16E-06	-6.38E-04	2.43E-04	9.65E-03	-5.63E-04	1.37E-04	4.42E-05
cg08640498	12	57828515	IN- HBC;IN- HBC	5URT;1st Exon		5.00E-04	1.00E-04	1.22E-06	5.80E-04	1.63E-04	5.07E-04	4.38E-04	1.30E-04	7.71E-04
cg17871993	7	65673056	TPST1	5URT	S Shelf	5.00E-04	1.00E-04	1.24E-06	4.65E-04	1.70E-04	6.96E-03	5.31E-04	1.32E-04	6.41E-05
cg05613192	2	223912416				9.00E-04	2.00E-04	1.24E-06	1.21E-03	3.56E-04	8.50E-04	8.20E-04	2.29E-04	3.66E-04
cg14279167	8	124151837	TBC1D31; TBC1D31	Body;Bo dy		-7.00E-04	1.00E-04	1.24E-06	-9.28E-04	2.71E-04	8.03E-04	-5.62E-04	1.55E-04	2.97E-04

cg11202345	17	76976057	LGALS3BP ;LGALS3B	5URT;1st Exon		1.00E-03	2.00E-04	1.24E-06	6.81E-04	3.16E-04	3.26E-02	1.20E-03	2.66E-04	6.93E-06
cg09897881	15	86195808	AKAP13;A KAP13;AK	Body;Bo dy;Body		-6.00E-04	1.00E-04	1.25E-06	-9.55E-04	2.32E-04	6.45E-05	-4.45E-04	1.39E-04	1.48E-03
cg21414092	15	81248254	MESDC2; MESDC2	Body;Bo dy		-8.00E-04	2.00E-04	1.26E-06	-1.23E-03	2.89E-04	3.73E-05	-5.74E-04	1.91E-04	2.77E-03
cg26248007	13	48730782				7.00E-04	1.00E-04	1.27E-06	8.57E-04	3.05E-04	5.68E-03	6.57E-04	1.65E-04	7.09E-05
cg19377661	3	142605811	PCOLCE2	Body	N Shore	-2.00E-03	4.00E-04	1.32E-06	-1.20E-03	6.47E-04	6.56E-02	-2.51E-03	5.31E-04	2.54E-06
cg03358113	7	2253070	MAD1L1; MAD1L1; MAD1L1; MAD1L1; MAD1L1	Body;Bo dy;Body; Body;Bo dy	S Shelf	-3.00E-04	1.00E-04	1.39E-06	-4.12E-04	1.22E-04	8.90E-04	-2.30E-04	6.24E-05	2.43E-04
cg26663590	16	28959310			N Shelf	1.00E-03	2.00E-04	1.40E-06	1.12E-03	3.55E-04	1.87E-03	9.40E-04	2.56E-04	2.61E-04
cg01104053	14	77391173				6.00E-04	1.00E-04	1.51E-06	-4.41E-05	2.10E-04	8.34E-01	8.34E-04	1.41E-04	4.28E-09
cg21586215	12	22777913	ETNK1;ET NK1	TSS200;T SS200	N Shore	-1.00E-04	0.00E+00	1.51E-06	-1.46E-04	6.89E-05	3.54E-02	-1.06E-04	2.44E-05	1.51E-05
cg06710464	17	79047695	BAIAP2;B AIAP2;BAI AP2;BAIA P2	Body;Bo dy;Body; Body	S Shore	6.00E-04	1.00E-04	1.54E-06	6.15E-04	2.61E-04	1.97E-02	6.39E-04	1.52E-04	3.07E-05
cg03318904	22	39801522	TAB1;TAB 1	Body;Bo dy		5.00E-04	1.00E-04	1.55E-06	2.18E-04	1.77E-04	2.20E-01	5.87E-04	1.18E-04	8.51E-07
cg16305292	8	142219965	SLC45A4;S LC45A4	3UTR;3U TR	S Shore	8.00E-04	2.00E-04	1.58E-06	1.21E-03	2.88E-04	4.62E-05	5.94E-04	2.04E-04	3.67E-03
cg13708645	12	121974305	KDM2B;K DM2B	Body;Bo dy	N Shore	1.10E-03	2.00E-04	1.62E-06	1.32E-03	4.65E-04	5.02E-03	1.08E-03	2.78E-04	1.09E-04
cg26955383	10	105218660	CALHM1	TSS200	S Shelf	7.00E-04	1.00E-04	1.66E-06	6.36E-04	2.34E-04	7.21E-03	6.59E-04	1.67E-04	8.69E-05
cg22690339	6	38249061	BTBD9;BT BD9;BTBD 9;BTBD9	Body;Bo dy;Body; Body		8.00E-04	2.00E-04	1.68E-06	9.04E-04	2.78E-04	1.41E-03	7.77E-04	2.20E-04	4.31E-04
cg00607627	16	28995994	TSS1500; TSS1500; LAT;LAT; LAT;LAT	TSS1500; TSS1500; TSS200		-5.00E-04	1.00E-04	1.69E-06	-3.96E-04	1.82E-04	3.11E-02	-5.73E-04	1.32E-04	1.62E-05
cg05183753	1	239553133			S Shore	-7.00E-04	1.00E-04	1.72E-06	-6.39E-04	1.89E-04	9.12E-04	-6.73E-04	1.99E-04	7.38E-04
cg22770295	20	3779418	CDC25B;C DC25B;CD C25B;CDC 25B;CDC2 5B;CDC25	TSS1500; Body;Bo dy;Body; Body;Bo dy;Body;	S Shelf	-2.00E-04	0.00E+00	1.78E-06	-1.06E-04	7.47E-05	1.58E-01	-2.62E-04	5.39E-05	1.34E-06

			B;CDC25B; CDC25B;C DC25B;CD C25B	Body;Bo dy;Body										
cg24392515	14	24578415				7.00E-04	1.00E-04	1.79E-06	7.60E-04	2.03E-04	2.57E-04	6.21E-04	2.07E-04	2.72E-03
cg01641754	5	98355983				-1.10E-03	2.00E-04	1.79E-06	-1.67E-03	3.59E-04	7.06E-06	-7.11E-04	3.10E-04	2.19E-02
cg07814318	15	31624584	KLF13;KLF 13	Body;Bo dy	S Shelf	1.00E-03	2.00E-04	1.80E-06	7.61E-04	3.18E-04	1.78E-02	1.08E-03	2.58E-04	2.86E-05
cg02040103	4	22475152	ADGRA3	Body		-1.10E-03	2.00E-04	1.82E-06	-1.79E-03	4.38E-04	6.77E-05	-8.32E-04	2.70E-04	2.12E-03
cg15357118	2	128927972	UGGT1;U GGT1;UG GT1;UGG T1	Ex- onBnd;E xonBnd; Body;Bo dy		7.00E-04	1.00E-04	1.82E-06	7.81E-04	2.17E-04	4.21E-04	6.36E-04	2.01E-04	1.60E-03
cg20630633	15	91100491	CRTC3;CR TC3	Body;Bo dy		5.00E-04	1.00E-04	1.84E-06	4.25E-04	1.74E-04	1.57E-02	5.02E-04	1.22E-04	4.26E-05
cg12962778	12	54778312	ZNF385A; ZNF385A; ZNF385A; ZNF385A; ZNF385A; ZNF385A; ZNF385A; ZNF385A; LOC10272 4050;LOC1 02724050	1stExon; 1stExon; 5URT;5U RT;5URT ;5URT;B ody;Bod y;Body;B ody		8.00E-04	2.00E-04	1.85E-06	6.93E-04	2.92E-04	1.89E-02	8.62E-04	2.07E-04	3.43E-05
cg16097041	1	154965544	LE- NEP;FLAD 1;FLAD1;F LAD1	TSS1500; 3UTR;3U TR;3UTR		6.00E-04	1.00E-04	1.88E-06	4.97E-04	2.11E-04	1.97E-02	7.13E-04	1.69E-04	2.71E-05
cg17256791	15	85547764	PDE8A;PD E8A;PDE8 A	5URT;Bo dy;Body		1.30E-03	3.00E-04	1.89E-06	1.01E-03	4.90E-04	4.17E-02	1.39E-03	3.19E-04	1.52E-05
cg19542445	12	2596220	CACNA1C ;CACNA1 C;CACNA 1C;CACN A1C;CAC NA1C;CA CNA1C;C ACNA1C; CACNA1C	Body;Bo dy;Body; Body;Bo dy;Body; Body;Bo dy;Body; Body;Bo dy;Body; Body;Bo		7.00E-04	1.00E-04	1.92E-06	5.06E-04	2.08E-04	1.63E-02	8.06E-04	1.91E-04	2.57E-05

			;CACNA1 C,CACNA 1C,CACN A1C,CAC NA1C,CA CNA1C,C ACNA1C; CACNA1C ;CACNA1 C,CACNA 1C,CACN A1C,CAC NA1C,CA CNA1C,C ACNA1C; CACNA1C ;CACNA1 C	dy;Body; Body;Bo dy;Body; Body;Bo dy;Body; Body;Bo dy										
cg05708512	5	31731391				-8.00E-04	2.00E-04	1.94E-06	-7.00E-04	2.18E-04	1.59E-03	-8.22E-04	2.33E-04	4.35E-04
cg20902443	10	13387198	SEPHS1;SE PHS1;SEP HS1	5URT;5U RT;5URT		7.00E-04	2.00E-04	1.95E-06	5.20E-04	2.13E-04	1.56E-02	9.31E-04	2.17E-04	1.89E-05
cg25922935	3	156747491	LEKR1	Body		9.00E-04	2.00E-04	2.00E-06	7.96E-04	2.90E-04	6.76E-03	1.06E-03	2.69E-04	8.84E-05
cg10922280	16	68034227	DPEP2	TSS1500		6.00E-04	1.00E-04	2.02E-06	4.78E-04	1.92E-04	1.39E-02	7.67E-04	1.83E-04	3.05E-05
cg14017402	2	86225602				6.00E-04	1.00E-04	2.06E-06	4.16E-04	1.85E-04	2.58E-02	8.38E-04	1.87E-04	8.47E-06
cg11303839	7	75405967	CCL26	5URT		-1.50E-03	3.00E-04	2.10E-06	-1.54E-03	4.60E-04	1.05E-03	-1.43E-03	4.25E-04	7.79E-04
cg26038971	3	14185774				-7.00E-04	1.00E-04	2.11E-06	-4.25E-04	2.38E-04	7.58E-02	-7.90E-04	1.73E-04	5.66E-06
cg12269535	6	43142014	SRF;SRF	Body;Bo dy	Island	-9.00E-04	2.00E-04	2.12E-06	-1.14E-03	2.76E-04	6.31E-05	-7.18E-04	2.77E-04	9.79E-03
cg26440042	22	37590110				1.30E-03	3.00E-04	2.12E-06	9.91E-04	4.04E-04	1.53E-02	1.56E-03	3.72E-04	3.09E-05
cg12378285	2	136808729				9.00E-04	2.00E-04	2.18E-06	1.09E-03	3.16E-04	7.59E-04	8.07E-04	2.42E-04	8.91E-04
cg22893494	3	140952551	PXYLP1;P XYLP1;PX YLP1	5URT;5U RT;5URT	S Shore	-2.00E-04	0.00E+00	2.25E-06	-3.35E-04	1.38E-04	1.67E-02	-2.01E-04	4.82E-05	3.40E-05
cg20941062	5	132299811	AFF4	TSS1500	S Shore	-9.00E-04	2.00E-04	2.28E-06	-9.70E-04	2.61E-04	2.77E-04	-8.30E-04	2.83E-04	3.39E-03
cg13518625	8	29522838				-5.00E-04	1.00E-04	2.41E-06	-5.34E-04	2.84E-04	6.22E-02	-5.08E-04	1.17E-04	1.68E-05
cg04169527	11	9759805	SWAP70;S WAP70	Body;Bo dy		8.00E-04	2.00E-04	2.43E-06	4.16E-04	2.67E-04	1.22E-01	9.69E-04	2.04E-04	2.41E-06
cg22513955	17	1665123	SERPINF1	TSS200		5.00E-04	1.00E-04	2.44E-06	6.76E-04	1.58E-04	3.17E-05	3.43E-04	1.36E-04	1.17E-02
cg13264822	7	137565290	CREB3L2	Body		4.00E-04	1.00E-04	2.45E-06	9.38E-04	3.18E-04	3.71E-03	3.74E-04	9.24E-05	5.54E-05
cg12042252	2	73596096				8.00E-04	2.00E-04	2.47E-06	5.45E-04	2.54E-04	3.34E-02	9.34E-04	2.15E-04	1.48E-05
cg04725636	8	67004538	DNAJC5B	Body		-1.20E-03	3.00E-04	2.48E-06	-1.84E-03	4.81E-04	1.90E-04	-9.65E-04	3.07E-04	1.70E-03

cg09880117	8	56685930	MEM68;T MEM68;T GS1;TGS1; TMEM68;T MEM68;T MEM68;T MEM68	5URT;5U RT;5URT ;1stExon; 1stExon; 1stExon; 1stExon; 5URT	Island	0.00E+00	0.00E+00	2.48E-06	1.18E-05	4.45E-05	7.91E-01	3.67E-05	7.75E-06	2.59E-06
cg23998749	1	154968781			N Shelf	5.00E-04	1.00E-04	2.49E-06	3.94E-04	1.67E-04	1.93E-02	5.83E-04	1.40E-04	3.43E-05
cg00379740	17	38507518	RARA;RA RA;RARA; RARA	Body;Bo dy;Body; Body		5.00E-04	1.00E-04	2.51E-06	6.71E-04	1.74E-04	1.67E-04	4.34E-04	1.50E-04	4.01E-03
cg09577455	6	29593382	GABBR1;G ABBR1;GA BBR1	Body;Bo dy;Body	N Shore	-8.00E-04	2.00E-04	2.56E-06	-1.08E-03	3.24E-04	1.02E-03	-7.06E-04	2.05E-04	5.90E-04
cg07728579	15	83475013	FSD2;FSD2 ;FSD2	TSS200;T SS200;TS S200	N Shelf	6.00E-04	1.00E-04	2.59E-06	9.07E-04	2.06E-04	1.93E-05	3.88E-04	1.48E-04	9.01E-03
cg15938090	1	10570921	PEX14	Body		-8.00E-04	2.00E-04	2.61E-06	-9.84E-04	2.50E-04	1.25E-04	-6.16E-04	2.21E-04	5.31E-03
cg22028323	10	98486758				8.00E-04	2.00E-04	2.68E-06	6.97E-04	3.15E-04	2.85E-02	9.19E-04	2.20E-04	3.18E-05
cg11155434	11	128358527	ETS1;ETS1; ETS1	Body;Bo dy;Body		-6.00E-04	1.00E-04	2.73E-06	-1.10E-03	2.84E-04	1.59E-04	-5.04E-04	1.57E-04	1.32E-03
cg01995927	1	24257839				9.00E-04	2.00E-04	2.77E-06	8.86E-04	3.01E-04	3.69E-03	8.61E-04	2.36E-04	2.83E-04
cg24575378	1	24583120				1.00E-03	2.00E-04	2.79E-06	1.49E-03	3.92E-04	2.20E-04	7.59E-04	2.38E-04	1.51E-03
cg09702859	1	198901839	MIR181A1 HG	Body		1.50E-03	3.00E-04	2.81E-06	1.43E-03	5.17E-04	6.42E-03	1.49E-03	3.94E-04	1.65E-04
cg11902329	2	228253636				-8.00E-04	2.00E-04	2.86E-06	-1.27E-03	5.51E-04	2.26E-02	-7.47E-04	1.79E-04	3.29E-05
cg21134922	5	60586909				6.00E-04	1.00E-04	2.88E-06	3.59E-04	2.13E-04	9.38E-02	7.39E-04	1.61E-04	5.03E-06
cg25651593	16	8814501	ABAT;AB AT;ABAT	TSS200;5 URT;5U RT		5.00E-04	1.00E-04	2.90E-06	4.05E-04	2.43E-04	9.76E-02	5.91E-04	1.34E-04	1.09E-05
cg24830274	7	41826734				8.00E-04	2.00E-04	2.91E-06	7.53E-04	3.13E-04	1.74E-02	7.93E-04	1.98E-04	6.48E-05
cg24974982	22	46403316	LOC73066 8	Body		5.00E-04	1.00E-04	2.91E-06	7.21E-04	2.54E-04	5.22E-03	4.84E-04	1.27E-04	1.46E-04
cg13300580	1	27440539	SLC9A1;SL C9A1	Body;Bo dy		5.00E-04	1.00E-04	2.96E-06	2.59E-04	1.84E-04	1.61E-01	5.93E-04	1.26E-04	2.98E-06
cg03068437	1	170037915	KIFAP3;KI FAP3;KIF AP3;KIFA P3;KIFAP3	1stExon; 5URT;5U RT;Body; Body		-9.00E-04	2.00E-04	2.97E-06	-1.07E-03	2.95E-04	3.77E-04	-8.30E-04	2.77E-04	2.82E-03
cg13072940	3	49967521	MON1A;M ON1A	TSS200;T SS200	S Shore	-6.00E-04	1.00E-04	3.05E-06	-7.89E-04	1.72E-04	9.64E-06	-3.42E-04	1.64E-04	3.73E-02
cg12407462	5	76112776			N Shore	9.00E-04	2.00E-04	3.09E-06	9.58E-04	3.02E-04	1.82E-03	9.40E-04	2.75E-04	6.56E-04

cg20646219	17	38490228	RARA;RA RA;RARA	Body;Bo dy;Body		6.00E-04	1.00E-04	3.11E-06	7.79E-04	1.99E-04	1.32E-04	4.53E-04	1.60E-04	4.78E-03
cg12256648	3	143752097				1.40E-03	3.00E-04	3.22E-06	1.56E-03	3.84E-04	7.79E-05	1.13E-03	4.72E-04	1.71E-02
cg19741548	8	74963339				6.00E-04	1.00E-04	3.23E-06	4.31E-04	1.89E-04	2.44E-02	8.61E-04	1.98E-04	1.48E-05
cg09057405	14	24820950				8.00E-04	2.00E-04	3.32E-06	5.94E-04	2.51E-04	1.91E-02	8.87E-04	2.16E-04	4.53E-05
cg09035925	20	19915769	RIN2;RIN2	Body;Bo dy		8.00E-04	2.00E-04	3.33E-06	8.69E-04	2.38E-04	3.55E-04	6.93E-04	2.37E-04	3.55E-03
cg17077319	3	149886667				1.20E-03	3.00E-04	3.39E-06	7.42E-04	4.17E-04	7.73E-02	1.55E-03	3.41E-04	6.19E-06
cg21786446	2	160462426	BAZ2B;BA Z2B	5URT;5U RT		9.00E-04	2.00E-04	3.50E-06	8.32E-04	2.36E-04	5.49E-04	1.14E-03	3.68E-04	2.06E-03
cg08505450	17	47836075	FAM117A	Body		-2.00E-04	0.00E+00	3.50E-06	-2.27E-04	1.84E-04	2.19E-01	-2.27E-04	5.08E-05	8.76E-06
cg13507563	11	17952483	SERGEF;S ERGEF;SE RGEF	Body;Bo dy;Body		5.00E-04	1.00E-04	3.54E-06	1.15E-03	2.75E-04	4.83E-05	3.98E-04	1.24E-04	1.43E-03
cg17850049	1	15670516	FHAD1	Body		7.00E-04	1.00E-04	3.54E-06	4.17E-04	2.00E-04	3.87E-02	9.93E-04	2.17E-04	5.33E-06
cg14980020	1	154992262	DCST2	Body	S Shelf	3.00E-04	1.00E-04	3.58E-06	2.69E-04	1.35E-04	4.76E-02	2.64E-04	6.32E-05	3.17E-05
cg04869770	1	164561550	PBX1;PBX1 ;PBX1	Body;Bo dy;Body		5.00E-04	1.00E-04	3.59E-06	5.42E-05	1.92E-04	7.78E-01	8.11E-04	1.45E-04	2.93E-08
cg08726900	16	89550474	ANKRD11; ANKRD11; ANKRD11; ANKRD11	Body;5U RT;5URT ;5URT		-1.00E-03	2.00E-04	3.79E-06	-7.23E-04	3.84E-04	6.16E-02	-1.22E-03	2.81E-04	1.50E-05
cg00565561	3	41730513	ULK4	Body		-4.00E-04	1.00E-04	4.02E-06	-2.76E-04	1.78E-04	1.23E-01	-3.86E-04	8.82E-05	1.34E-05
cg08782002	17	61847885	CCDC47	5URT	N Shelf	-6.00E-04	1.00E-04	4.02E-06	-6.14E-04	2.18E-04	5.53E-03	-5.91E-04	1.62E-04	2.74E-04
cg04842352	16	49907368			N Shelf	4.00E-04	1.00E-04	4.13E-06	2.70E-04	2.07E-04	1.94E-01	4.82E-04	1.07E-04	7.43E-06
cg03808896	5	132160489	SHROOM 1;SHROO M1	Body;Bo dy	S Shore	8.00E-04	2.00E-04	4.13E-06	8.56E-04	2.84E-04	3.00E-03	7.20E-04	2.06E-04	4.87E-04
cg14390798	6	56536532	RNU6- 71P;DST;D ST;DST	Body;Bo dy;Body; Body		8.00E-04	2.00E-04	4.21E-06	7.81E-04	3.24E-04	1.70E-02	8.57E-04	2.19E-04	9.41E-05
cg11918171	3	111314495	ZBED2;CD 96;CD96	TSS1500; Body;Bo dy		1.10E-03	2.00E-04	4.23E-06	1.35E-03	3.54E-04	2.06E-04	8.82E-04	3.19E-04	5.77E-03
cg03741348	1	32712237	FAM167B	TSS1500	N Shore	6.00E-04	1.00E-04	4.23E-06	7.88E-04	2.03E-04	1.56E-04	5.16E-04	1.94E-04	8.01E-03
cg18112787	19	18168639				-7.00E-04	2.00E-04	4.26E-06	-6.87E-04	3.01E-04	2.37E-02	-6.92E-04	1.73E-04	7.11E-05
cg05013695	10	99079798	FRAT1	1stExon	Island	1.00E-04	0.00E+00	4.29E-06	5.53E-05	8.91E-05	5.36E-01	6.97E-05	1.53E-05	5.86E-06
cg16936953	17	57915665	VMP1;VM P1	Ex- onBnd;B ody		-1.60E-03	4.00E-04	4.38E-06	-2.63E-03	6.13E-04	3.11E-05	-1.12E-03	4.35E-04	9.91E-03
cg04211591	2	230159830				1.70E-03	4.00E-04	4.39E-06	2.34E-03	6.23E-04	2.38E-04	1.34E-03	4.58E-04	3.45E-03
cg19818308	14	75946745				8.00E-04	2.00E-04	4.41E-06	1.06E-03	2.74E-04	1.54E-04	6.70E-04	2.51E-04	7.70E-03

cg12989718	16	4739352	MGRN1;MGRN1;MG RN1;MGRN1;MGRN1;MGRN1;MGRN1;MG	3UTR;3UTR;3UTR;3UTR;3UTR;B ody	N Shelf	3.00E-04	1.00E-04	4.45E-06	3.96E-04	1.23E-04	1.55E-03	2.99E-04	8.99E-05	9.08E-04
cg00218090	14	100485810				5.00E-04	1.00E-04	4.45E-06	4.24E-04	2.59E-04	1.03E-01	5.12E-04	1.19E-04	1.91E-05
cg23830794	14	94476186	LINC00521	Body		1.80E-03	4.00E-04	4.53E-06	1.16E-03	5.80E-04	4.75E-02	2.31E-03	5.27E-04	1.32E-05
cg15043602	17	17079454	MPRIP;MP RIP	Body;Bo dy		6.00E-04	1.00E-04	4.58E-06	7.81E-04	2.09E-04	2.68E-04	4.67E-04	1.60E-04	3.61E-03
cg14970975	12	6444675	TNFRSF1A	Body		-4.00E-04	1.00E-04	4.71E-06	-6.29E-04	1.43E-04	1.94E-05	-2.61E-04	1.09E-04	1.72E-02
cg16029189	1	201504437			N Shelf	-6.00E-04	1.00E-04	4.84E-06	-5.87E-04	2.43E-04	1.69E-02	-6.57E-04	1.69E-04	1.08E-04
cg05778424	17	55169508	AKAP1;A KAP1;AK AP1	5URT;5U RT;5URT		8.00E-04	2.00E-04	4.88E-06	9.47E-04	3.26E-04	4.21E-03	7.94E-04	2.24E-04	4.07E-04
cg20301125	5	130975565				9.00E-04	2.00E-04	4.96E-06	1.24E-03	2.89E-04	3.06E-05	5.85E-04	2.54E-04	2.14E-02
cg20426042	8	97778709	CPQ	5URT		1.30E-03	3.00E-04	4.98E-06	1.34E-03	4.00E-04	1.04E-03	1.23E-03	3.96E-04	1.89E-03
cg18219562	17	41773643				5.00E-04	1.00E-04	5.02E-06	2.91E-04	1.58E-04	6.73E-02	6.13E-04	1.38E-04	9.74E-06
cg19500225	8	8402640				6.00E-04	1.00E-04	5.06E-06	5.71E-04	2.05E-04	5.95E-03	6.15E-04	1.70E-04	3.18E-04
cg12776836	9	1232682				9.00E-04	2.00E-04	5.09E-06	9.34E-04	3.63E-04	1.10E-02	9.43E-04	2.50E-04	1.77E-04
cg07821355	6	116706621	DSE;DSE	5URT;5U RT		-6.00E-04	1.00E-04	5.10E-06	-6.04E-04	2.02E-04	3.25E-03	-5.92E-04	1.72E-04	5.98E-04
cg10380546	11	942218	AP2A2;AP 2A2	Body;Bo dy	N Shore	9.00E-04	2.00E-04	5.10E-06	1.62E-04	3.17E-04	6.10E-01	1.33E-03	2.47E-04	9.31E-08
cg13274938	17	38493822	RARA;RA RA;RARA	Body;Bo dy;Body	N Shelf	4.00E-04	1.00E-04	5.17E-06	3.43E-04	1.50E-04	2.31E-02	4.09E-04	1.03E-04	8.31E-05
cg18871648	14	74227431	ELMSAN1 ;ELMSAN	TSS1500; 5URT	S Shore	-7.00E-04	1.00E-04	5.17E-06	-8.12E-04	2.95E-04	6.66E-03	-6.15E-04	1.67E-04	2.47E-04
cg19822755	16	30108259	YPEL3;YP EL3	TSS1500; TSS1500	S Shore	6.00E-04	1.00E-04	5.20E-06	5.94E-04	2.88E-04	4.10E-02	6.14E-04	1.51E-04	5.24E-05
cg14578060	7	76434789				-1.00E-03	2.00E-04	5.31E-06	-1.19E-03	2.92E-04	7.38E-05	-7.04E-04	3.01E-04	1.95E-02
cg03523676	14	24540235	CPNE6;CP NE6	TSS1500; 1stExon		7.00E-04	2.00E-04	5.43E-06	9.21E-04	2.82E-04	1.32E-03	6.22E-04	1.90E-04	1.08E-03
cg04557677	19	17959082	JAK3	TSS1500	S Shore	-2.00E-04	0.00E+00	5.49E-06	-5.81E-04	1.58E-04	3.30E-04	-1.73E-04	4.76E-05	2.87E-04
cg06096336	2	231989800	HTR2B;HT R2B;PSMD 1;PSMD1;P SMD1	5URT;1st Exon;Bo dy;Body; Body		1.10E-03	2.00E-04	5.50E-06	1.47E-03	3.46E-04	3.64E-05	7.31E-04	3.27E-04	2.59E-02
cg07960624	8	119208486	SAMD12;S AMD12	3UTR;Bo dy		-1.30E-03	3.00E-04	5.50E-06	-1.65E-03	4.53E-04	3.69E-04	-1.02E-03	3.49E-04	3.46E-03
cg09627709	7	97755719	LMTK2	Body		8.00E-04	2.00E-04	5.54E-06	8.25E-04	3.45E-04	1.81E-02	8.08E-04	2.09E-04	1.19E-04
cg05948408	5	88178572	MEF2C;M EF2C;MEF	5URT;5U RT;5URT	N Shore	1.00E-04	0.00E+00	5.55E-06	1.26E-04	8.30E-05	1.30E-01	1.11E-04	2.58E-05	2.02E-05

			2C;MEF2C; MEF2C- AS1	;5URT;T SS1500										
cg09018739	16	57180107	CPNE2	Body		7.00E-04	2.00E-04	5.56E-06	1.06E-03	2.92E-04	3.77E-04	5.69E-04	1.85E-04	2.17E-03
cg08673945	9	20490677	MLLT3;M LLT3	Body;Bo dy		-1.00E-03	2.00E-04	5.60E-06	-1.44E-03	3.50E-04	6.25E-05	-6.82E-04	2.64E-04	9.94E-03
cg14237301	16	28506477	APOBR	Body	S Shelf	7.00E-04	2.00E-04	5.60E-06	8.93E-04	2.79E-04	1.69E-03	6.23E-04	1.87E-04	9.22E-04
cg11793449	17	76313872			S Shelf	-5.00E-04	1.00E-04	5.61E-06	-7.14E-04	1.73E-04	6.08E-05	-3.81E-04	1.61E-04	1.84E-02
cg08709029	10	1102713	WDR37	TSS200	Island	2.00E-04	0.00E+00	5.68E-06	1.29E-04	8.80E-05	1.46E-01	1.68E-04	3.89E-05	1.76E-05
cg16296829	1	154832535	KCNN3;K CNN3;K NN3	TSS200;B ody;Bod y		1.30E-03	3.00E-04	5.82E-06	9.28E-04	5.12E-04	7.16E-02	1.51E-03	3.55E-04	2.27E-05
cg22688566	17	27459835	MYO18A; MYO18A	Body;Bo dy		7.00E-04	2.00E-04	5.88E-06	5.14E-04	2.35E-04	3.01E-02	8.73E-04	2.12E-04	4.03E-05
cg15254759	1	38763833				-1.00E-03	2.00E-04	5.94E-06	-7.00E-04	3.29E-04	3.48E-02	-1.28E-03	3.05E-04	2.92E-05
cg14114804	14	77606990	ZDHHC22	5URT	Island	5.00E-04	1.00E-04	5.94E-06	4.63E-04	1.68E-04	6.46E-03	4.67E-04	1.30E-04	3.51E-04
cg22351187	12	52586089	KRT80;KR T80	TSS1500; TSS1500		-1.00E-03	2.00E-04	5.95E-06	-1.09E-03	4.38E-04	1.36E-02	-1.03E-03	2.73E-04	1.67E-04
cg13123009	6	31681882	LY6G6D;L Y6G6E;LY 6G6E	TSS1500; TSS200;T SS200		6.00E-04	1.00E-04	5.96E-06	1.93E-04	2.13E-04	3.66E-01	8.52E-04	1.68E-04	5.14E-07
cg19488267	14	85763019				1.50E-03	3.00E-04	5.97E-06	1.96E-03	5.41E-04	4.09E-04	1.28E-03	4.42E-04	3.88E-03
cg09837467	1	183523933				8.00E-04	2.00E-04	5.98E-06	9.68E-04	2.86E-04	9.03E-04	7.47E-04	2.44E-04	2.26E-03
cg07078732	2	30501565				4.00E-04	1.00E-04	6.00E-06	5.88E-04	1.55E-04	2.12E-04	3.49E-04	1.28E-04	6.27E-03
cg25753411	6	138727287	HEBP2;HE BP2	Body;Ex- onBnd	S Shore	9.00E-04	2.00E-04	6.17E-06	8.00E-04	3.23E-04	1.43E-02	9.34E-04	2.46E-04	1.57E-04
cg09530861	6	107776494	PDSS2	Body	N Shelf	4.00E-04	1.00E-04	6.18E-06	5.92E-04	2.21E-04	8.34E-03	3.44E-04	9.07E-05	1.60E-04
cg14634473	10	23105437				-8.00E-04	2.00E-04	6.22E-06	-8.89E-04	2.66E-04	1.06E-03	-7.54E-04	2.46E-04	2.22E-03
cg02112168	14	45579561	SNORD12 7;PRPF39	TSS1500; Body		9.00E-04	2.00E-04	6.28E-06	1.13E-03	3.23E-04	6.03E-04	7.84E-04	2.64E-04	3.04E-03
cg02032970	17	9885713	GAS7;GAS 7;GAS7	Body;Bo dy;Body		6.00E-04	1.00E-04	6.31E-06	8.73E-04	2.28E-04	1.93E-04	4.93E-04	1.80E-04	6.32E-03
cg10457997	17	64796507	PRKCA	Body		8.00E-04	2.00E-04	6.53E-06	7.37E-04	2.80E-04	9.48E-03	8.13E-04	2.21E-04	2.56E-04
cg11586890	6	33420227	SYNGAP1	3UTR	N Shore	3.00E-04	1.00E-04	6.75E-06	4.47E-04	1.19E-04	2.40E-04	2.29E-04	7.89E-05	3.75E-03
cg04430748	16	67550573				7.00E-04	2.00E-04	6.83E-06	2.21E-04	2.72E-04	4.18E-01	9.09E-04	1.86E-04	1.18E-06
cg07834321	7	159531			N Shore	2.00E-04	1.00E-04	6.85E-06	1.36E-04	2.45E-04	5.80E-01	2.50E-04	5.58E-05	8.23E-06
cg13093111	17	66308577	ARSG;ARS G	Body;Bo dy		1.40E-03	3.00E-04	6.94E-06	1.87E-03	5.10E-04	3.44E-04	1.09E-03	3.80E-04	4.08E-03
cg17868815	16	81476731			N Shore	8.00E-04	2.00E-04	6.99E-06	7.66E-04	2.80E-04	7.06E-03	7.84E-04	2.20E-04	3.76E-04
cg01334549	20	50137002	NFATC2; NFATC2; NFATC2; NFATC2;	Body;Bo dy;Body; Body;Bo dy;Body;	N Shelf	-4.00E-04	1.00E-04	7.08E-06	-5.95E-04	1.33E-04	1.58E-05	-2.29E-04	1.02E-04	2.49E-02

			NFATC2; NFATC2; NFATC2; NFATC2	Body;Bo dy											
cg01867298	11	117689143					-4.00E-04	1.00E-04	7.09E-06	-4.06E-04	1.95E-04	3.87E-02	-4.44E-04	1.12E-04	7.41E-05
cg22714777	2	119605229	EN1;EN1	5URT	Island		4.00E-04	1.00E-04	7.27E-06	2.41E-04	1.58E-04	1.31E-01	4.62E-04	1.06E-04	1.34E-05
cg00045592	1	160714299	SLAMF7;S LAMF7;SL AMF7;SLA MF7;SLA MF7;SLA MF7;SLA MF7;SLA MF7;SLA MF7;SLA	5URT;Bo dy;Body; Body;Bo dy;Body; Body;Bo dy;Body;			1.00E-03	2.00E-04	7.48E-06	7.48E-04	3.20E-04	2.07E-02	1.17E-03	2.96E-04	8.76E-05
cg12445970	3	104323736					1.00E-03	2.00E-04	7.50E-06	7.38E-04	3.07E-04	1.73E-02	1.24E-03	3.13E-04	8.59E-05
cg19543782	10	35775490	CCNY;CC NY;CCNY; CCNY;CC NY	Body;Bo dy;5URT ;Body;Bo dy			5.00E-04	1.00E-04	7.55E-06	8.74E-04	2.15E-04	7.63E-05	3.64E-04	1.32E-04	5.89E-03
cg21691116	1	161171819	NDUFS2; NDUFS2	TSS200;5 URT	Island		-8.00E-04	2.00E-04	7.64E-06	-6.79E-04	2.49E-04	7.08E-03	-8.96E-04	2.49E-04	3.36E-04
cg21506763	3	38060329	PLCD1;PL CD1;PLCD 1	Body;Bo dy;Body			6.00E-04	1.00E-04	7.68E-06	9.83E-04	2.83E-04	6.74E-04	5.07E-04	1.59E-04	1.52E-03
cg17980786	3	32933637	TRIM71	3UTR			6.00E-04	1.00E-04	7.71E-06	7.11E-04	2.00E-04	5.15E-04	4.86E-04	1.70E-04	4.39E-03
cg06629453	2	98852910	VWA3B	Body			4.00E-04	1.00E-04	7.72E-06	2.93E-04	1.35E-04	3.10E-02	5.03E-04	1.23E-04	5.07E-05
cg25536676	1	55353327	DHCR24	TSS1500	Island		-4.00E-04	1.00E-04	7.72E-06	-6.35E-04	1.75E-04	3.76E-04	-3.48E-04	1.18E-04	3.37E-03
cg23576855	5	373299	AHRR;AH RR	Body;Bo dy	S Shelf		1.80E-03	4.00E-04	7.83E-06	8.68E-04	8.16E-04	2.89E-01	2.05E-03	4.54E-04	6.87E-06
cg00630090	1	95061557					-7.00E-04	2.00E-04	7.90E-06	-8.34E-04	2.71E-04	2.48E-03	-6.02E-04	1.82E-04	9.48E-04
cg16956116	6	82456876	FAM46A	3UTR			1.00E-03	2.00E-04	7.93E-06	1.31E-03	3.55E-04	3.15E-04	7.67E-04	2.74E-04	5.25E-03
cg00094538	7	142505684					-7.00E-04	2.00E-04	8.09E-06	-6.53E-04	2.51E-04	1.02E-02	-7.97E-04	2.18E-04	2.76E-04
cg16341248	15	85904673					7.00E-04	2.00E-04	8.14E-06	5.74E-04	2.21E-04	1.03E-02	7.78E-04	2.11E-04	2.40E-04
cg07084617	16	17553768	XYLT1	Body			7.00E-04	2.00E-04	8.20E-06	6.57E-04	2.97E-04	2.85E-02	7.82E-04	2.01E-04	1.08E-04
cg23508887	18	13502053	LDLRAD4; LDLRAD4	Body;Bo dy	S Shelf		8.00E-04	2.00E-04	8.32E-06	1.18E-03	3.32E-04	5.02E-04	6.64E-04	2.23E-04	2.94E-03
cg01414567	12	82204306					1.60E-03	4.00E-04	8.35E-06	3.59E-04	5.81E-04	5.37E-01	2.28E-03	4.44E-04	3.42E-07
cg01883759	7	28220576	JAZF1;JAZ F1-AS1	TSS200;B ody	S Shore		-4.00E-04	1.00E-04	8.40E-06	-1.58E-04	1.80E-04	3.81E-01	-4.23E-04	9.28E-05	5.79E-06

cg02066340	9	97715233	C9orf3;C9orf3	Body;Body		4.00E-04	1.00E-04	8.44E-06	2.92E-04	1.30E-04	2.64E-02	4.73E-04	1.19E-04	7.39E-05
cg05575921	5	373378	AHRR;AHRR	Body;Body	S Shelf	1.10E-03	3.00E-04	8.52E-06	8.41E-04	7.47E-04	2.62E-01	1.16E-03	2.69E-04	1.70E-05
cg07580762	1	161171810	NDUFS2;NDUFS2	TSS200;5URT	Island	-9.00E-04	2.00E-04	8.54E-06	-8.03E-04	2.70E-04	3.45E-03	-9.77E-04	2.92E-04	8.59E-04
cg22460123	12	52638294	KRT7	Body	N Shore	-5.00E-04	1.00E-04	8.58E-06	-7.78E-04	1.60E-04	2.87E-06	-2.32E-04	1.32E-04	7.83E-02
cg19338722	10	92900861				-5.00E-04	1.00E-04	8.68E-06	-7.14E-04	2.03E-04	5.68E-04	-4.18E-04	1.41E-04	3.05E-03
cg01155138	2	86306243	POLR1A	Body		6.00E-04	1.00E-04	8.68E-06	5.71E-04	1.76E-04	1.44E-03	5.52E-04	1.81E-04	2.42E-03
cg04817410	7	129992661	CPA5;CPA5	Body;Body		-1.00E-03	2.00E-04	8.74E-06	-7.98E-04	4.46E-04	7.56E-02	-1.14E-03	2.77E-04	4.07E-05
cg04253214	1	78942099				1.40E-03	3.00E-04	9.06E-06	1.03E-03	6.70E-04	1.28E-01	1.53E-03	3.63E-04	2.70E-05
cg08036259	1	169081528	ATP1B1	Body		-6.00E-04	1.00E-04	9.16E-06	-4.33E-04	2.00E-04	3.18E-02	-6.37E-04	1.61E-04	8.38E-05
cg11804293	4	90056255				7.00E-04	1.00E-04	9.24E-06	6.56E-04	2.59E-04	1.23E-02	6.53E-04	1.79E-04	2.90E-04
cg22648996	10	63946213				5.00E-04	1.00E-04	9.26E-06	4.28E-04	1.53E-04	5.87E-03	5.67E-04	1.62E-04	4.90E-04
cg15871086	18	56526595			N Shelf	5.00E-04	1.00E-04	9.30E-06	3.78E-04	1.83E-04	3.98E-02	5.23E-04	1.32E-04	7.71E-05
cg05396897	1	247611448	NLRP3;NLRP3;NLRP3;NLRP3;NLRP3	Body;Body;dy;Body;Body;Body	N Shelf	2.00E-03	5.00E-04	9.33E-06	2.51E-03	7.05E-04	4.95E-04	1.66E-03	5.94E-04	5.26E-03
cg13373351	14	24539601	CPNE6;CPNE6	TSS1500;TSS1500		7.00E-04	2.00E-04	9.34E-06	7.93E-04	2.68E-04	3.60E-03	6.57E-04	1.97E-04	9.13E-04
cg09092525	20	58570133	CDH26;CDH26	TSS1500;Body		-9.00E-04	2.00E-04	9.51E-06	-1.33E-03	2.96E-04	1.48E-05	-5.16E-04	2.69E-04	5.58E-02
cg07328569	1	61524438				-6.00E-04	1.00E-04	9.52E-06	-1.19E-03	3.07E-04	1.59E-04	-4.71E-04	1.58E-04	2.88E-03
cg06373268	2	79041585				5.00E-04	1.00E-04	9.53E-06	7.82E-04	2.91E-04	8.08E-03	4.35E-04	1.18E-04	2.37E-04
cg09664445	17	2612406	CLUH	5URT	N Shore	5.00E-04	1.00E-04	9.59E-06	4.96E-04	1.88E-04	9.38E-03	5.60E-04	1.57E-04	3.77E-04
cg13520904	18	33039043				-5.00E-04	1.00E-04	9.68E-06	-6.59E-04	1.67E-04	1.18E-04	-3.41E-04	1.38E-04	1.36E-02
cg07281747	17	57105112	TRIM37;TRIM37	Body;Body		7.00E-04	2.00E-04	9.69E-06	8.54E-04	2.12E-04	8.89E-05	4.88E-04	2.24E-04	2.92E-02
cg14694639	1	147039678	BCL9	5URT		7.00E-04	2.00E-04	9.76E-06	6.44E-04	2.27E-04	5.20E-03	8.02E-04	2.34E-04	6.34E-04
cg15195477	1	159851933	CFAP45	Body		-7.00E-04	2.00E-04	9.77E-06	-7.44E-04	3.51E-04	3.57E-02	-7.28E-04	1.87E-04	1.11E-04
cg26242726	18	59999053	TNFRSF11A;TNFRSF11A;TNFRSF11A;TNFRSF11A	Body;Body;dy;Body;Body;Body		7.00E-04	2.00E-04	9.77E-06	5.53E-04	2.47E-04	2.67E-02	7.61E-04	1.97E-04	1.16E-04
cg04595884	17	58870064	BCAS3;BCAS3	Body;Body		8.00E-04	2.00E-04	9.95E-06	5.18E-04	3.24E-04	1.12E-01	9.59E-04	2.25E-04	2.18E-05
cg07549924	4	54036	ZNF595;ZNF595	5URT;5URT;Body;	S Shore	-1.00E-03	2.00E-04	9.95E-06	-1.19E-03	3.51E-04	8.83E-04	-8.96E-04	3.09E-04	3.82E-03

			F595;ZNF595;ZNF718;ZNF718	Body;Body										
cg04585778	17	54395292	ANKFN1	Body		6.00E-04	1.00E-04	1.00E-05	6.20E-04	2.16E-04	4.74E-03	5.52E-04	1.64E-04	7.84E-04
cg16626764	14	91077172	TTC7B;TTC7B	Ex-onBnd;Body		8.00E-04	2.00E-04	1.01E-05	9.16E-04	3.04E-04	3.01E-03	7.03E-04	2.15E-04	1.09E-03
cg26120813	12	133000792			S Shelf	9.00E-04	2.00E-04	1.01E-05	3.29E-04	4.40E-04	4.55E-01	1.12E-03	2.41E-04	4.26E-06
cg27243685	21	43642366	ABCG1;ABCG1;ABCG1;ABCG1;A	5URT;Body;Body;Body	S Shelf	4.00E-04	1.00E-04	1.02E-05	6.51E-04	1.55E-04	4.44E-05	2.52E-04	9.84E-05	1.07E-02
cg04312927	12	57873880	ARHGAP9;ARHGAP9	TSS1500;TSS1500	S Shelf	-3.00E-04	1.00E-04	1.04E-05	-3.81E-04	1.66E-04	2.34E-02	-2.49E-04	6.48E-05	1.32E-04
cg04537738	22	51143999	SHANK3	Body	S Shelf	4.00E-04	1.00E-04	1.05E-05	3.67E-04	2.12E-04	8.57E-02	4.18E-04	1.03E-04	5.37E-05
cg10183965	17	3824497			N Shelf	6.00E-04	1.00E-04	1.05E-05	8.93E-04	2.71E-04	1.24E-03	4.87E-04	1.52E-04	1.39E-03
cg14711465	8	120710593				7.00E-04	2.00E-04	1.05E-05	2.81E-04	2.45E-04	2.53E-01	1.11E-03	2.25E-04	9.70E-07
cg09138892	17	79005662	BAIAP2-AS1	Body	N Shelf	8.00E-04	2.00E-04	1.07E-05	1.41E-03	3.90E-04	3.82E-04	6.09E-04	1.97E-04	2.00E-03
cg08353615	5	137151533				4.00E-04	1.00E-04	1.08E-05	5.48E-04	1.98E-04	6.44E-03	3.13E-04	8.73E-05	3.47E-04
cg08018468	1	43768048	TIE1;TIE1	Body;Body	N Shelf	5.00E-04	1.00E-04	1.09E-05	4.79E-04	1.53E-04	2.04E-03	4.71E-04	1.53E-04	2.11E-03
cg00701951	10	124228478	HTRA1	Body		-7.00E-04	2.00E-04	1.09E-05	-2.44E-03	5.59E-04	2.42E-05	-5.46E-04	1.66E-04	1.01E-03
cg20378147	1	32050627	TINAGL1;TINAGL1;TINAGL1;TINAGL1;TINAGL1;TINAGL1	Ex-onBnd;ExonBnd;Ex-onBnd;Body	N Shore	1.00E-04	0.00E+00	1.12E-05	3.76E-04	1.06E-04	4.80E-04	1.17E-04	3.39E-05	5.49E-04
cg23226831	1	115700937				-2.00E-04	0.00E+00	1.12E-05	-1.72E-04	2.09E-04	4.11E-01	-1.80E-04	4.17E-05	1.80E-05
cg07747616	6	7729794	BMP6	Body	S Shelf	-8.00E-04	2.00E-04	1.13E-05	-1.09E-03	2.79E-04	1.39E-04	-6.06E-04	2.55E-04	1.77E-02
cg01507087	6	123038784	PKIB;PKIB;PKIB;PKIB;PKIB	Body;Body;5URT;5URT;5URT;5URT		9.00E-04	2.00E-04	1.13E-05	2.91E-04	3.19E-04	3.63E-01	1.35E-03	2.71E-04	7.43E-07
cg23883807	6	16595692	ATXN1;ATXN1	5URT;5URT		4.00E-04	1.00E-04	1.14E-05	5.45E-04	1.64E-04	1.12E-03	3.28E-04	1.07E-04	2.15E-03
cg01864395	17	76274140	LOC100996291	Body		-4.00E-04	1.00E-04	1.14E-05	-5.87E-04	1.41E-04	4.99E-05	-2.67E-04	1.22E-04	2.86E-02

			IL5RA;IL5 RA;IL5RA; IL5RA;IL5 RA;IL5RA; IL5RA;IL5 RA;IL5RA; IL5RA;IL5 RA;IL5RA; IL5RA;IL5 RA;IL5RA; IL5RA;IL5	5URT;5U RT;5URT ;5URT;5 URT;5U RT;5URT ;1stExon; 1stExon; 1stExon; 1stExon; 1stExon; 1stExon; 1stExon;										
cg23032421	3	3152038	RA	1stExon		-7.00E-04	2.00E-04	1.15E-05	-6.55E-04	2.37E-04	6.32E-03	-6.96E-04	2.04E-04	6.92E-04
cg03957124	6	37016869			S Shelf	-5.00E-04	1.00E-04	1.16E-05	-4.91E-04	1.61E-04	2.78E-03	-5.75E-04	1.81E-04	1.53E-03
cg07922513	1	6089454	KCNAB2; KCNAB2; KCNAB2	5URT;5U RT;5URT	S Shelf	6.00E-04	1.00E-04	1.17E-05	8.09E-04	1.91E-04	3.96E-05	4.05E-04	2.29E-04	7.71E-02
cg10128003	21	43642166	ABCG1;AB CG1;ABC G1;ABCG1 ;ABCG1;A BCG1	5URT;Bo dy;Body; Body;Bo dy;Body	S Shelf	5.00E-04	1.00E-04	1.18E-05	6.85E-04	2.98E-04	2.26E-02	4.68E-04	1.24E-04	1.62E-04
cg21091503	1	161171785	NDUFS2; NDUFS2	TSS200;5 URT	N Shore	-8.00E-04	2.00E-04	1.18E-05	-5.94E-04	2.59E-04	2.32E-02	-1.01E-03	2.58E-04	1.03E-04
cg14565721	19	38916488	RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4	Body;Bo dy;Body; Body;Bo dy;Body; Body		6.00E-04	1.00E-04	1.20E-05	4.97E-04	1.98E-04	1.30E-02	6.27E-04	1.73E-04	3.15E-04
cg10964502	21	44752105	LINC00322	TSS200		8.00E-04	2.00E-04	1.20E-05	6.83E-04	3.39E-04	4.55E-02	7.90E-04	2.03E-04	1.06E-04
cg17750024	1	175538621	TNR	5URT		-1.20E-03	3.00E-04	1.21E-05	-1.01E-03	4.50E-04	2.57E-02	-1.39E-03	3.66E-04	1.49E-04
cg04695090	22	38609508	MAFF;MA FF;MAFF; MAFF	5URT;5U RT;5URT ;5URT	N Shore	5.00E-04	1.00E-04	1.21E-05	4.56E-04	1.90E-04	1.74E-02	5.98E-04	1.62E-04	2.27E-04
cg05776323	1	161165053	ADAMTS4	Body		6.00E-04	1.00E-04	1.22E-05	6.53E-04	2.24E-04	4.15E-03	5.40E-04	1.64E-04	1.04E-03
cg10919522	14	74227441	ELMSAN1 ;ELMSAN 1	TSS1500; 5URT	S Shore	-8.00E-04	2.00E-04	1.24E-05	-6.98E-04	3.32E-04	3.73E-02	-8.77E-04	2.27E-04	1.22E-04
cg05245822	18	37550141				1.00E-03	2.00E-04	1.24E-05	2.63E-04	4.44E-04	5.54E-01	1.37E-03	2.85E-04	1.75E-06
cg11378135	12	76547651				9.00E-04	2.00E-04	1.25E-05	1.29E-03	3.66E-04	5.57E-04	7.56E-04	2.67E-04	4.66E-03
cg11406521	2	86226603				3.00E-04	1.00E-04	1.26E-05	3.39E-04	2.85E-04	2.37E-01	2.86E-04	6.81E-05	2.84E-05
cg02191659	17	10154629				6.00E-04	1.00E-04	1.26E-05	7.94E-04	2.24E-04	5.31E-04	4.43E-04	1.55E-04	4.27E-03

cg19494100	6	18387313	RNF144B	TSS1500	N Shore	-5.00E-04	1.00E-04	1.27E-05	-7.71E-04	1.45E-04	3.88E-07	-1.23E-04	1.48E-04	4.05E-01
cg06566477	20	61078502				5.00E-04	1.00E-04	1.28E-05	7.88E-04	2.03E-04	1.59E-04	3.68E-04	1.40E-04	8.63E-03
cg13677199	22	38138706	TRIOBP	Body	N Shelf	-6.00E-04	1.00E-04	1.28E-05	-8.69E-04	2.27E-04	1.89E-04	-4.54E-04	1.79E-04	1.12E-02
cg04401764	12	54777396	ZNF385A; ZNF385A; ZNF385A; ZNF385A; ZNF385A; ZNF385A; LOC10272 4050;LOC1 02724050	Body;Bo dy;Body; Body;Bo dy;Body; Body;Bo dy		7.00E-04	2.00E-04	1.28E-05	7.54E-04	2.86E-04	9.26E-03	6.83E-04	1.96E-04	5.17E-04
cg08836972	6	26532914				1.00E-03	2.00E-04	1.29E-05	9.90E-04	2.87E-04	7.23E-04	9.60E-04	3.60E-04	7.76E-03
cg00994936	19	1423902	DAZAP1; DAZAP1	Body;Bo dy	Island	4.00E-04	1.00E-04	1.30E-05	7.25E-04	2.05E-04	5.25E-04	3.24E-04	1.05E-04	2.12E-03
cg03164552	10	134243533				4.00E-04	1.00E-04	1.30E-05	2.63E-04	1.60E-04	1.03E-01	5.10E-04	1.21E-04	2.64E-05
cg18216572	22	36278607	RBFOX2;R BFOX2	Body;Bo dy		4.00E-04	1.00E-04	1.31E-05	4.67E-04	1.84E-04	1.23E-02	3.31E-04	9.18E-05	3.25E-04
cg25205489	13	24125993				1.20E-03	3.00E-04	1.31E-05	1.55E-03	4.33E-04	4.55E-04	9.71E-04	3.62E-04	7.37E-03
cg26468779	14	59958011	JKAMP;JK AMP;JKA MP;JKAM P;JKAMP;J KAMP	Body;Bo dy;Body; Body;Bo dy;Body		-2.00E-04	1.00E-04	1.32E-05	-2.79E-04	1.50E-04	6.59E-02	-2.39E-04	6.06E-05	8.36E-05
cg04444771	10	45473712	C10orf10;R ASSF4	5URT;Bo dy	S Shelf	-4.00E-04	1.00E-04	1.34E-05	-3.00E-04	1.61E-04	6.44E-02	-4.27E-04	1.07E-04	7.17E-05
cg12489028	2	32568146				-8.00E-04	2.00E-04	1.36E-05	-1.04E-03	2.29E-04	1.02E-05	-3.63E-04	2.71E-04	1.81E-01
cg18942579	17	57915773	VMP1;VM PI	Ex- onBnd;B ody		-1.30E-03	3.00E-04	1.36E-05	-1.99E-03	4.81E-04	5.58E-05	-8.61E-04	3.79E-04	2.33E-02
cg12429551	7	30635762	GARS	Body	S Shore	-1.50E-03	3.00E-04	1.36E-05	-1.80E-03	4.99E-04	4.06E-04	-1.22E-03	4.77E-04	1.06E-02
cg10937494	17	80195101	SLC16A3;S LC16A3;SL C16A3;SL C16A3;SL C16A3;SL C16A3	Body;Bo dy;Body; Body;Bo dy;Body	Island	5.00E-04	1.00E-04	1.37E-05	7.99E-04	2.17E-04	3.28E-04	4.09E-04	1.49E-04	5.97E-03
cg12902625	11	64527603	PYGM;PY GM;PYGM ;PYGM	1stExon; 1stExon; 5URT;5U RT		4.00E-04	1.00E-04	1.38E-05	2.56E-04	1.50E-04	8.92E-02	4.56E-04	1.10E-04	3.80E-05
cg21946195	2	86012225	MIR6071;A TOH8	TSS1500; Body		-7.00E-04	2.00E-04	1.39E-05	-8.50E-04	2.25E-04	2.31E-04	-5.54E-04	2.36E-04	1.94E-02

cg25583591	15	90590483	ZNF710	5URT		7.00E-04	2.00E-04	1.39E-05	5.84E-04	2.74E-04	3.47E-02	7.19E-04	1.89E-04	1.49E-04
cg08949269	20	31443298				7.00E-04	2.00E-04	1.40E-05	8.01E-04	2.74E-04	4.04E-03	7.05E-04	2.18E-04	1.29E-03
cg06646796	14	24104741	DHRS2;D HRS2	TSS1500; TSS1500		7.00E-04	2.00E-04	1.41E-05	4.64E-04	2.26E-04	4.19E-02	8.18E-04	2.04E-04	6.85E-05
cg26943120	4	5472116	STK32B;ST K32B	Body;Bo dy		1.10E-03	2.00E-04	1.42E-05	1.35E-03	4.30E-04	2.06E-03	9.50E-04	3.07E-04	2.01E-03
cg15242769	22	43670935	SCUBE1	Body		6.00E-04	1.00E-04	1.42E-05	5.67E-04	2.33E-04	1.61E-02	6.88E-04	1.90E-04	3.13E-04
cg02790691	18	32289550	DTNA;DT NA;DTNA ;DTNA;DT NA;DTNA ;DTNA;DT NA;DTNA ;DTNA	TSS1500; TSS1500; 5URT;5U RT;5URT ;5URT;5 URT;5U RT;5URT ;5URT		-9.00E-04	2.00E-04	1.43E-05	-1.20E-03	4.02E-04	3.38E-03	-7.47E-04	2.26E-04	9.91E-04
cg02868338	8	145133133	EXOSC4	TSS1500	N Shore	2.00E-04	0.00E+00	1.45E-05	1.58E-04	6.85E-05	2.23E-02	1.54E-04	4.19E-05	2.55E-04
cg07203167	1	183551326	NCF2;NCF 2;NCF2;N CF2	Body;Bo dy;Body; Body		4.00E-04	1.00E-04	1.46E-05	4.21E-04	1.41E-04	3.34E-03	4.38E-04	1.39E-04	1.70E-03
cg04598105	19	9812938	ZNF812	TSS1500		-5.00E-04	1.00E-04	1.49E-05	-4.71E-04	1.81E-04	1.02E-02	-4.75E-04	1.37E-04	5.62E-04
cg04258833	2	102697002	IL1R1	5URT		-8.00E-04	2.00E-04	1.49E-05	-6.26E-04	2.60E-04	1.71E-02	-9.82E-04	2.64E-04	2.09E-04
cg08862479	5	177889945	COL23A1	Body		9.00E-04	2.00E-04	1.50E-05	1.55E-03	3.79E-04	7.16E-05	6.41E-04	2.63E-04	1.50E-02
cg24597457	7	129028641	AHCYL2; AHCYL2; AHCYL2; AHCYL2	Body;Bo dy;Body; Body		7.00E-04	2.00E-04	1.52E-05	1.17E-03	3.62E-04	1.56E-03	6.25E-04	1.97E-04	1.56E-03
cg17367948	17	71863334				5.00E-04	1.00E-04	1.54E-05	6.14E-04	1.88E-04	1.35E-03	4.21E-04	1.43E-04	3.25E-03
cg27352622	5	156646570	ITK	Body		5.00E-04	1.00E-04	1.55E-05	2.87E-04	2.02E-04	1.57E-01	6.45E-04	1.49E-04	1.71E-05
cg22256420	10	4060366				5.00E-04	1.00E-04	1.56E-05	4.52E-04	1.70E-04	8.78E-03	6.44E-04	1.84E-04	5.02E-04
cg03500056	16	8814507	ABAT;AB AT;ABAT	TSS200;5 URT;5U RT		7.00E-04	2.00E-04	1.58E-05	4.20E-04	3.38E-04	2.16E-01	8.55E-04	2.00E-04	2.06E-05
cg15626919	16	69647419	NFAT5;NF AT5;NFAT 5;NFAT5; NFAT5;NF AT5	5URT;5U RT;5URT ;Body;Bo dy;Body		5.00E-04	1.00E-04	1.58E-05	6.25E-04	1.61E-04	1.57E-04	3.57E-04	1.59E-04	2.53E-02
cg17808676	2	182332122	ITGA4	Body		1.00E-03	2.00E-04	1.59E-05	1.11E-03	3.61E-04	2.50E-03	8.71E-04	2.83E-04	2.17E-03
cg04382851	9	96159985				-3.00E-04	1.00E-04	1.59E-05	-8.22E-04	2.59E-04	1.80E-03	-2.70E-04	7.56E-05	3.78E-04
cg12259187	9	82238785	TLE4;TLE4 ;TLE4;TLE 4;TLE4;TL E4	5URT;Bo dy;Body; Body;Bo dy;Body		6.00E-04	1.00E-04	1.61E-05	5.02E-04	1.77E-04	5.06E-03	6.05E-04	1.85E-04	1.12E-03

cg02560388	2	11969958				-6.00E-04	1.00E-04	1.62E-05	-4.64E-04	2.20E-04	3.70E-02	-6.25E-04	1.64E-04	1.49E-04
cg01751802	19	11309639	KANK2	TSS1500	N Shelf	9.00E-04	2.00E-04	1.62E-05	6.58E-05	3.86E-04	8.65E-01	1.35E-03	2.65E-04	3.91E-07
cg13218558	1	11631121				7.00E-04	2.00E-04	1.63E-05	6.49E-04	2.30E-04	5.43E-03	6.83E-04	2.10E-04	1.15E-03
cg23640231	1	2844871			N Shelf	-2.00E-04	1.00E-04	1.65E-05	3.03E-04	3.19E-04	3.44E-01	-2.49E-04	5.49E-05	6.52E-06
cg08972190	7	2138995	MAD1L1; MAD1L1; MAD1L1; MAD1L1; MAD1L1	Body;Bo dy;Body; Body;Bo dy		4.00E-04	1.00E-04	1.68E-05	3.21E-04	1.24E-04	1.05E-02	4.26E-04	1.22E-04	5.09E-04
cg16625765	16	29838413	MVP;MVP	RT		8.00E-04	2.00E-04	1.69E-05	1.01E-03	2.95E-04	7.45E-04	6.29E-04	2.26E-04	5.50E-03
cg12032603	12	111872336	SH2B3;SH 2B3	TSS1500; Body		6.00E-04	1.00E-04	1.69E-05	5.36E-04	1.95E-04	6.69E-03	6.59E-04	1.97E-04	8.75E-04
cg09823288	1	239552128			S Shore	-1.40E-03	3.00E-04	1.69E-05	-1.34E-03	4.93E-04	7.53E-03	-1.50E-03	4.49E-04	8.34E-04
cg00010572	2	8345013	LINC00299	Body		4.00E-04	1.00E-04	1.71E-05	5.35E-04	3.12E-04	8.86E-02	4.22E-04	1.07E-04	8.21E-05
cg21025810	9	4301370	GLIS3	TSS1500	S Shore	-6.00E-04	1.00E-04	1.72E-05	-1.08E-03	2.94E-04	3.56E-04	-4.56E-04	1.56E-04	3.46E-03
cg11363234	8	102500879			N Shelf	8.00E-04	2.00E-04	1.72E-05	4.40E-04	3.45E-04	2.04E-01	9.56E-04	2.23E-04	1.95E-05
cg07120889	1	150535935	ADAMTSL 4-AS1	Body	S Shore	-6.00E-04	1.00E-04	1.73E-05	-8.60E-04	2.07E-04	5.31E-05	-3.60E-04	1.65E-04	2.94E-02
cg25763292	10	115442231	CASP7;CA SP7;CASP7 ;CASP7;C ASP7;CAS P7	5URT;5U RT;5URT ;5URT;5 URT;Bod y	S Shelf	5.00E-04	1.00E-04	1.73E-05	5.10E-04	1.80E-04	5.13E-03	4.87E-04	1.51E-04	1.29E-03
cg23722790	1	67467602	SLC35D1	3UTR		5.00E-04	1.00E-04	1.74E-05	4.83E-04	2.14E-04	2.53E-02	5.38E-04	1.47E-04	2.65E-04
cg20779663	10	13569995			N Shore	-7.00E-04	2.00E-04	1.74E-05	-1.26E-03	2.71E-04	6.69E-06	-3.84E-04	2.24E-04	8.72E-02
cg06540722	13	34111966	STARD13	5URT		9.00E-04	2.00E-04	1.78E-05	7.25E-04	3.40E-04	3.44E-02	1.06E-03	2.79E-04	1.55E-04
cg20360704	4	113739170	ANK2	TSS200		4.00E-04	1.00E-04	1.80E-05	5.10E-04	1.79E-04	5.05E-03	3.38E-04	1.02E-04	9.48E-04
cg01928516	17	2208377	SMG6;SRR ;SRR	TSS1500; 5URT;5U RT	S Shore	8.00E-04	2.00E-04	1.80E-05	6.03E-04	2.82E-04	3.39E-02	8.82E-04	2.32E-04	1.58E-04
cg26935416	12	48202318	HDAC7;H DAC7;HD AC7	Body;Bo dy;Body		-3.00E-04	1.00E-04	1.80E-05	-3.06E-04	1.39E-04	2.91E-02	-3.33E-04	9.05E-05	2.44E-04
cg11847601	16	57180054	CPNE2	Body		4.00E-04	1.00E-04	1.80E-05	5.86E-04	1.59E-04	3.20E-04	2.86E-04	1.06E-04	7.04E-03
cg00547480	10	103875961	LDB1;LDB 1	TSS1500; Body	N Shelf	5.00E-04	1.00E-04	1.81E-05	5.41E-04	1.82E-04	3.42E-03	5.01E-04	1.62E-04	2.05E-03
cg16406078	20	825634	FAM110A; FAM110A; FAM110A; FAM110A; FAM110A; FAM110A	1stExon; Body;Bo dy;Body; Body;Bo dy	Island	-9.00E-04	2.00E-04	1.82E-05	-1.02E-03	3.08E-04	1.09E-03	-7.95E-04	2.89E-04	6.02E-03

cg21481630	2	72770278	EXOC6B	Body		3.00E-04	1.00E-04	1.84E-05	4.42E-04	1.71E-04	1.07E-02	2.44E-04	6.80E-05	3.60E-04
cg18473335	14	24540174	CPNE6;CPNE6;CPNE6	TSS1500;5URT;1st Exon		1.10E-03	3.00E-04	1.85E-05	1.02E-03	4.16E-04	1.50E-02	1.24E-03	3.50E-04	4.42E-04
cg20428112	5	31023350				-3.00E-04	1.00E-04	1.85E-05	-1.96E-04	1.61E-04	2.24E-01	-2.78E-04	6.72E-05	3.93E-05
cg23187532	1	15499085	TMEM51;TMEM51;TMEM51;MEM51;C1orf195;C1orf195	5URT;5URT;5URT;5URT;SS1500;SS1500		1.00E-04	0.00E+00	1.86E-05	2.78E-04	1.06E-04	9.20E-03	9.78E-05	2.60E-05	1.82E-04
cg00705600	4	185820660	LINC01093;LINC01093;LINC01010	TSS200;TSS200;TS200		-4.00E-04	1.00E-04	1.87E-05	-4.34E-04	2.50E-04	8.42E-02	-4.34E-04	1.11E-04	9.84E-05
cg12352605	2	143624904				4.00E-04	1.00E-04	1.88E-05	3.27E-04	1.54E-04	3.54E-02	3.81E-04	1.02E-04	2.06E-04
cg26212639	11	95670486				-4.00E-04	1.00E-04	1.89E-05	-2.76E-04	1.59E-04	8.44E-02	-4.27E-04	1.07E-04	7.18E-05
cg10261371	1	59782515	FGGY;FGGY;FGGY	5URT;5URT;5URT;Body		8.00E-04	2.00E-04	1.89E-05	5.42E-04	2.68E-04	4.51E-02	9.35E-04	2.38E-04	9.27E-05
cg14052997	10	89575546	ATAD1	5URT	N Shore	3.00E-04	1.00E-04	1.89E-05	3.69E-04	1.04E-04	5.28E-04	2.28E-04	8.70E-05	9.06E-03
cg18217136	20	36157651	BLCAP;BLCAP	TSS1500;TSS1500	S Shore	4.00E-04	1.00E-04	1.90E-05	6.30E-05	2.70E-04	8.16E-01	5.05E-04	1.11E-04	6.69E-06
cg26429850	16	4464427	CORO7;PAM16;CORO7;CORO7;CORO7	Body;Body;Body;Body	N Shore	4.00E-04	1.00E-04	1.91E-05	4.41E-04	1.42E-04	2.31E-03	3.79E-04	1.28E-04	3.12E-03
cg27190410	8	101348639	RNF19A	TSS200		1.00E-03	2.00E-04	1.93E-05	7.14E-04	4.64E-04	1.26E-01	1.14E-03	2.81E-04	5.22E-05
cg27397830	11	60679809			N Shore	5.00E-04	1.00E-04	1.93E-05	6.99E-04	1.87E-04	2.65E-04	3.91E-04	1.61E-04	1.56E-02
cg07930159	8	80964882	TPD52;TPD52;TPD52;TPD52;TPD52;TPD52;TPD52;TPD52	Body;Body;Body;Body;Body;Body;Body;Body		8.00E-04	2.00E-04	1.94E-05	2.29E-04	2.92E-04	4.34E-01	1.27E-03	2.55E-04	7.40E-07
cg01320200	10	112248821				1.00E-03	2.00E-04	1.95E-05	1.09E-03	3.69E-04	3.57E-03	8.90E-04	2.86E-04	1.93E-03
cg23025447	10	70883043	VPS26A;VPS26A	TSS1500;TSS1500	N Shore	9.00E-04	2.00E-04	1.95E-05	9.30E-04	3.05E-04	2.68E-03	8.13E-04	2.71E-04	2.76E-03
cg13139542	2	8242815	LINC00299	Body		3.00E-04	1.00E-04	1.95E-05	7.91E-04	2.44E-04	1.44E-03	2.91E-04	8.60E-05	7.48E-04
cg04224661	11	123375288				7.00E-04	2.00E-04	2.00E-05	5.88E-04	2.46E-04	1.79E-02	7.04E-04	1.98E-04	4.05E-04

cg00328137	11	111852793	DIXDC1;D IXDC1	Body;Bo dy		1.00E-04	0.00E+00	2.00E-05	1.23E-04	1.41E-04	3.84E-01	7.44E-05	1.78E-05	3.10E-05
cg27216853	2	10205672	CYS1	Body		7.00E-04	2.00E-04	2.01E-05	1.25E-03	3.02E-04	5.86E-05	4.82E-04	2.06E-04	1.95E-02
cg09964698	3	71235448	FOXPI;FO XP1;FOXP 1;FOXPI;F OXPI;FOX PI	Body;Bo dy;Body; Body;Bo dy;Body		-1.10E-03	3.00E-04	2.03E-05	-9.37E-04	4.00E-04	2.04E-02	-1.24E-03	3.44E-04	3.28E-04
cg22045206	21	44752369	LINC00322	TSS1500		3.00E-04	1.00E-04	2.03E-05	6.92E-04	1.57E-04	2.00E-05	1.92E-04	7.15E-05	7.50E-03
cg21219966	9	101142609	GABBR2	Body		7.00E-04	2.00E-04	2.04E-05	1.07E-03	2.57E-04	5.11E-05	4.32E-04	2.01E-04	3.19E-02
cg21081097	19	45458610	CLPTM1;C LPTM1;CL PTM1;CLP TM1	5URT;1st Exon;5U RT;Body	Island	2.00E-04	0.00E+00	2.04E-05	2.16E-04	6.93E-05	2.14E-03	1.44E-04	4.77E-05	2.58E-03
cg05785686	2	20101506	TTC32	1stExon	Island	0.00E+00	0.00E+00	2.05E-05	4.95E-05	2.62E-05	6.05E-02	2.09E-05	5.27E-06	7.95E-05
cg01088579	2	85660497	SH2D6	TSS1500		6.00E-04	1.00E-04	2.05E-05	4.74E-04	2.07E-04	2.30E-02	6.31E-04	1.74E-04	2.95E-04
ch.14.96436 874F	14	97367121				-1.00E-04	0.00E+00	2.06E-05	-1.33E-04	1.00E-04	1.87E-01	-8.32E-05	2.04E-05	4.97E-05
cg19750024	8	22068189	BMP1;BM PI	Body;Bo dy		-7.00E-04	2.00E-04	2.06E-05	-1.24E-03	2.97E-04	5.27E-05	-4.70E-04	2.03E-04	2.07E-02
cg23248055	4	56185	ZNF718;Z NF595;ZN F595;ZNF5 95;ZNF595 ;ZNF718;Z NF718	TSS1500; 5URT;5U RT;Body; Body;Bo dy;Body	S Shelf	9.00E-04	2.00E-04	2.08E-05	1.08E-03	3.57E-04	2.81E-03	7.98E-04	2.62E-04	2.35E-03
cg14946327	9	96918529				4.00E-04	1.00E-04	2.09E-05	4.31E-04	1.40E-04	2.54E-03	3.76E-04	1.27E-04	3.15E-03
cg21579726	6	26600049	ABT1	3UTR	S Shelf	6.00E-04	1.00E-04	2.10E-05	6.39E-04	1.72E-04	2.78E-04	4.39E-04	2.00E-04	2.83E-02
cg27275941	3	15751015	ANKRD28; ANKRD28; ANKRD28	Body;Bo dy;Body		-8.00E-04	2.00E-04	2.10E-05	-1.05E-03	3.14E-04	1.03E-03	-7.03E-04	2.54E-04	5.85E-03
cg10705487	5	179108352	CBY3	TSS1500	S Shore	5.00E-04	1.00E-04	2.11E-05	5.24E-04	1.86E-04	5.38E-03	4.48E-04	1.40E-04	1.44E-03
cg27637521	17	76355202	LOC10192 8674;LOC1 01928674;S OCS3	TSS1500; TSS1500; 5URT	Island	-3.00E-04	1.00E-04	2.15E-05	-5.69E-04	1.38E-04	6.43E-05	-1.88E-04	7.03E-05	7.53E-03
cg20003499	7	97755792	LMTK2	Body		7.00E-04	2.00E-04	2.17E-05	1.42E-03	4.04E-04	5.91E-04	5.66E-04	1.84E-04	2.23E-03
cg18931885	10	112100739				6.00E-04	1.00E-04	2.18E-05	7.27E-04	2.50E-04	4.13E-03	5.81E-04	1.86E-04	1.83E-03
cg07235958	1	155974953				-6.00E-04	1.00E-04	2.18E-05	-4.47E-04	2.01E-04	2.77E-02	-8.25E-04	2.15E-04	1.32E-04
cg25763898	2	102092013	RFX8	TSS1500	S Shore	-7.00E-04	2.00E-04	2.21E-05	-7.33E-04	2.47E-04	3.49E-03	-7.07E-04	2.33E-04	2.48E-03
cg09176736	20	3779584	CDC25B;C DC25B;CD C25B;CDC	TSS1500; Body;Bo dy;Body;	S Shelf	-2.00E-04	0.00E+00	2.23E-05	-1.04E-04	6.01E-05	8.54E-02	-2.49E-04	5.87E-05	2.50E-05

cg26404075	17	19206602	EPN2;EPN2; EPN2;EPN2;AS1	5URT;Body; dy;Body; Body		6.00E-04	1.00E-04	2.39E-05	3.85E-04	2.02E-04	5.88E-02	8.07E-04	1.99E-04	5.45E-05
cg10452282	4	166136676	KLHL2;KLHL2; HL2;KLHL2	5URT;Body; dy;Body		-4.00E-04	1.00E-04	2.39E-05	-7.21E-04	1.99E-04	4.00E-04	-3.16E-04	1.12E-04	5.09E-03
cg21446345	15	70390985	TLE3;TLE3 ;TLE3;TLE3	TSS1500; TSS1500; TSS1500; TSS1500; TSS1500	Island	-2.00E-04	0.00E+00	2.39E-05	-2.21E-04	9.03E-05	1.57E-02	-1.50E-04	4.27E-05	4.56E-04
cg05660634	15	38965109				1.00E-03	2.00E-04	2.39E-05	1.27E-03	3.64E-04	6.49E-04	8.22E-04	3.20E-04	1.05E-02
cg09323079	10	115476444	CASP7;CASP7; CASP7;CASP7; CASP7;CASP7	Body;Body; dy;Body; Body;Body; dy;Body; Body		7.00E-04	2.00E-04	2.40E-05	4.57E-04	2.46E-04	6.52E-02	8.21E-04	2.07E-04	8.11E-05
cg05826823	9	130968072	CIZ1;CIZ1; DNM1;DNM1; M1;DNM1; DNM1;DNM1	TSS1500; TSS1500; Body;Body; dy;Body; Body;Body; dy	S Shore	4.00E-04	1.00E-04	2.41E-05	5.61E-04	1.41E-04	1.00E-04	2.57E-04	1.20E-04	3.26E-02
cg23825586	20	37507788	PPP1R16B; PPP1R16B	Body;Body; dy		4.00E-04	1.00E-04	2.41E-05	5.79E-04	1.98E-04	4.07E-03	3.92E-04	1.24E-04	1.65E-03
cg09409865	20	33169887	PIGU	Body		-7.00E-04	2.00E-04	2.41E-05	-1.06E-03	2.37E-04	1.49E-05	-3.51E-04	2.07E-04	8.97E-02
cg08824454	2	28596577				5.00E-04	1.00E-04	2.42E-05	5.17E-04	1.59E-04	1.37E-03	5.51E-04	2.05E-04	7.36E-03
cg04809899	2	223824915				6.00E-04	2.00E-04	2.42E-05	6.77E-04	2.38E-04	5.06E-03	6.13E-04	1.96E-04	1.82E-03
cg05095590	7	2139259	MAD1L1; MAD1L1; MAD1L1; MAD1L1	Body;Body; dy;Body; Body;Body; dy		1.30E-03	3.00E-04	2.43E-05	7.79E-04	4.80E-04	1.07E-01	1.69E-03	4.06E-04	3.53E-05
cg21534299	1	44821474	ERI3;ERI3; ERI3;ERI3	TSS1500; TSS1500; TSS1500; TSS1500; TSS1500	S Shore	1.40E-03	3.00E-04	2.44E-05	2.20E-03	6.67E-04	1.23E-03	1.16E-03	3.91E-04	3.13E-03
cg12054453	17	57915717	VMP1	Body		-1.40E-03	3.00E-04	2.45E-05	-2.76E-03	6.36E-04	2.59E-05	-9.03E-04	4.01E-04	2.44E-02
cg20978247	6	32905085	HLA-DMB	Body		1.50E-03	4.00E-04	2.46E-05	2.07E-03	6.02E-04	7.48E-04	1.19E-03	4.39E-04	6.80E-03
cg11080651	5	10445523	ROPN1L;R OPN1L	Body;Body; dy	S Shelf	-4.00E-04	1.00E-04	2.46E-05	-1.89E-04	1.22E-04	1.23E-01	-5.02E-04	1.16E-04	1.55E-05

cg16105303	10	14791342	FAM107B; FAM107B	Body;5U RT		5.00E-04	1.00E-04	2.46E-05	7.30E-04	2.82E-04	1.06E-02	4.91E-04	1.44E-04	6.62E-04
cg24295963	6	35681420	FKBP5	5URT		4.00E-04	1.00E-04	2.46E-05	3.14E-04	1.40E-04	2.64E-02	4.01E-04	1.11E-04	3.27E-04
cg24795795	1	171449338				1.00E-03	2.00E-04	2.49E-05	9.52E-04	3.83E-04	1.40E-02	1.05E-03	3.06E-04	6.78E-04
cg02020366	1	101471573	DPH5;DP H5;DPH5	Body;Bo dy;Body		-3.00E-04	1.00E-04	2.54E-05	-3.12E-04	1.86E-04	9.56E-02	-3.56E-04	9.21E-05	1.18E-04
cg08848814	15	99201259	IGF1R;IGF 1R	Body;Bo dy		-5.00E-04	1.00E-04	2.54E-05	-5.08E-04	1.57E-04	1.43E-03	-4.20E-04	1.55E-04	6.82E-03
cg20958086	1	160759689				7.00E-04	2.00E-04	2.56E-05	1.06E-03	2.66E-04	9.70E-05	4.46E-04	1.95E-04	2.26E-02
cg19560798	3	182458668				1.10E-03	2.00E-04	2.57E-05	1.16E-03	4.07E-04	4.86E-03	9.82E-04	3.16E-04	1.93E-03
cg02735037	9	130081227	GARNL3; GARNL3; GARNL3	Body;Bo dy;Body		6.00E-04	1.00E-04	2.58E-05	4.33E-04	2.16E-04	4.67E-02	7.89E-04	2.03E-04	1.08E-04
cg00758961	4	9929384	SLC2A9;SL C2A9	Body;Bo dy		9.00E-04	2.00E-04	2.60E-05	1.08E-03	3.44E-04	1.96E-03	7.87E-04	2.74E-04	4.23E-03
cg16766623	2	218812908				3.00E-04	1.00E-04	2.62E-05	4.98E-04	1.45E-04	7.83E-04	2.26E-04	7.68E-05	3.33E-03
cg07021906	16	87866833	SLC7A5	Body		6.00E-04	1.00E-04	2.65E-05	1.03E-03	3.75E-04	6.55E-03	5.52E-04	1.63E-04	7.48E-04
cg17803993	3	71276214	FOXP1;FO XP1;FOXP 1;FOXP1;F OXP1;FOX P1;FOXP1	5URT;5U RT;5URT ;5URT;5 URT;5U RT;5URT		-8.00E-04	2.00E-04	2.65E-05	-9.82E-04	2.88E-04	8.28E-04	-7.21E-04	2.84E-04	1.13E-02
cg18545915	14	24867261	NYNRIN	TSS1500	N Shore	6.00E-04	1.00E-04	2.66E-05	6.64E-04	2.29E-04	4.25E-03	5.78E-04	1.90E-04	2.35E-03
cg07989312	3	136506546				5.00E-04	1.00E-04	2.67E-05	8.96E-04	2.86E-04	2.11E-03	4.38E-04	1.39E-04	1.68E-03
cg01676795	7	75586348	POR	Body		1.00E-03	2.00E-04	2.68E-05	1.34E-03	4.71E-04	5.09E-03	8.39E-04	2.60E-04	1.29E-03
cg10992736	6	158036370	ZDHHC14 ;ZDHHC1	Body;Bo dy		-6.00E-04	1.00E-04	2.71E-05	-1.07E-03	2.56E-04	5.03E-05	-3.91E-04	1.75E-04	2.59E-02
cg16315329	3	50648706	CISH;MAP KAPK3;CI SH	Body;TS S1500;5U RT	N Shore	-3.00E-04	1.00E-04	2.73E-05	-2.15E-04	1.78E-04	2.30E-01	-3.25E-04	8.01E-05	5.37E-05
cg03169557	16	89598950	SPG7;SPG7	Body;Bo dy		7.00E-04	2.00E-04	2.74E-05	1.27E-03	3.38E-04	2.48E-04	4.92E-04	1.78E-04	5.78E-03
cg05155595	2	70008161	ANXA4	5URT		6.00E-04	2.00E-04	2.75E-05	5.76E-04	2.37E-04	1.65E-02	6.79E-04	1.98E-04	6.13E-04
cg19998073	14	89078443	ZC3H14;Z C3H14;ZC 3H14;ZC3 H14;ZC3H 14;ZC3H14	3UTR;3U TR;3UTR ;3UTR;3 UTR;3U TR		5.00E-04	1.00E-04	2.81E-05	4.00E-04	1.64E-04	1.62E-02	4.91E-04	1.43E-04	6.16E-04
cg11540855	3	11643500	VGLL4;VG LL4;VGLL 4;VGLL4;V GLL4;VGL	5URT;Ex onBnd;E xonBnd;		4.00E-04	1.00E-04	2.82E-05	5.14E-04	1.52E-04	9.00E-04	3.65E-04	1.42E-04	1.04E-02

			L4;VGLL4; VGLL4	Ex- onBnd;E xonBnd; Body;Bo dy;Body										
cg02188675	15	95909577				5.00E-04	1.00E-04	2.84E-05	3.30E-04	2.13E-04	1.23E-01	6.47E-04	1.59E-04	5.18E-05
cg08592212	3	125367223				-4.00E-04	1.00E-04	2.87E-05	-5.98E-04	2.33E-04	1.11E-02	-3.99E-04	1.18E-04	7.35E-04
cg00960204	6	140802228				7.00E-04	2.00E-04	2.89E-05	9.80E-05	3.52E-04	7.81E-01	7.96E-04	1.75E-04	6.54E-06
cg26145152	1	68163609				2.00E-04	1.00E-04	2.89E-05	3.69E-04	1.64E-04	2.58E-02	2.27E-04	6.27E-05	3.16E-04
cg12765376	8	6502531	MCPH1- AS1	Body		-6.00E-04	1.00E-04	2.90E-05	-7.45E-04	2.25E-04	1.13E-03	-5.16E-04	1.94E-04	7.97E-03
cg26453543	16	18943348				8.00E-04	2.00E-04	2.92E-05	8.57E-04	2.25E-04	1.97E-04	5.75E-04	3.09E-04	6.31E-02
cg01820374	12	6882083	LAG3	Body	N Shore	-7.00E-04	2.00E-04	2.93E-05	-9.81E-04	2.38E-04	5.99E-05	-4.03E-04	2.07E-04	5.20E-02
cg22533969	2	144160209	ARHGAPI 5	Body		1.00E-03	2.00E-04	2.95E-05	1.50E-03	3.48E-04	2.73E-05	5.50E-04	3.49E-04	1.15E-01
cg06102340	6	8859229				-6.00E-04	1.00E-04	2.99E-05	-4.62E-04	2.31E-04	4.72E-02	-6.71E-04	1.80E-04	2.02E-04
cg25080300	11	65261429			N Shelf	3.00E-04	1.00E-04	3.00E-05	2.95E-04	1.32E-04	2.64E-02	2.88E-04	8.17E-05	4.52E-04
cg01855290	21	45132261				4.00E-04	1.00E-04	3.00E-05	1.32E-04	2.04E-04	5.19E-01	4.22E-04	9.78E-05	1.73E-05
cg13078565	17	3754116				4.00E-04	1.00E-04	3.01E-05	4.08E-04	1.43E-04	5.00E-03	3.98E-04	1.31E-04	2.36E-03
cg07711192	12	14426994				6.00E-04	2.00E-04	3.02E-05	7.44E-04	2.55E-04	4.15E-03	5.74E-04	1.89E-04	2.46E-03
cg17876683	5	141053017	ARAP3;AR AP3	Ex- onBnd;B ody		6.00E-04	1.00E-04	3.03E-05	5.49E-04	2.76E-04	4.82E-02	5.55E-04	1.51E-04	2.61E-04
cg15404917	11	69687810				-6.00E-04	1.00E-04	3.04E-05	-6.12E-04	2.32E-04	9.26E-03	-5.25E-04	1.62E-04	1.21E-03
cg24533408	7	128704939				5.00E-04	1.00E-04	3.04E-05	6.80E-04	2.13E-04	1.70E-03	4.53E-04	1.61E-04	5.02E-03
cg06469895	16	69418206	TERF2	Body	N Shore	6.00E-04	1.00E-04	3.04E-05	1.16E-03	2.68E-04	2.71E-05	3.78E-04	1.76E-04	3.17E-02
cg26867370	13	100262973	CLYBL;CL YBL	Body;Bo dy	S Shelf	3.00E-04	1.00E-04	3.06E-05	3.84E-04	1.79E-04	3.34E-02	2.61E-04	7.19E-05	2.99E-04
cg04565088	18	19184921			S Shelf	8.00E-04	2.00E-04	3.08E-05	7.63E-04	2.56E-04	3.32E-03	9.81E-04	3.32E-04	3.19E-03
cg10474597	13	51917676	SERPINE3	Body		9.00E-04	2.00E-04	3.10E-05	4.57E-04	3.02E-04	1.31E-01	1.29E-03	2.97E-04	1.50E-05
cg22400959	1	3458577	MEGF6	Body	N Shore	8.00E-04	2.00E-04	3.11E-05	1.01E-03	3.42E-04	3.70E-03	7.60E-04	2.53E-04	2.77E-03
cg03080569	12	57828396	INHBC	TSS200		4.00E-04	1.00E-04	3.12E-05	5.28E-04	1.66E-04	1.80E-03	3.60E-04	1.28E-04	5.05E-03
cg09153462	8	62602643	ASPH;ASP H;ASPH,A SPH;ASPH ;ASPH;AS PH;ASPH; ASPH;ASP H;ASPH,A SPH	Body;Bo dy;Body; Body;TS S1500;TS S1500;TS S1500;TS S1500;TS S1500;TS S1500;TS S1500;Bo dy		6.00E-04	1.00E-04	3.12E-05	2.24E-04	3.00E-04	4.58E-01	6.68E-04	1.55E-04	1.87E-05

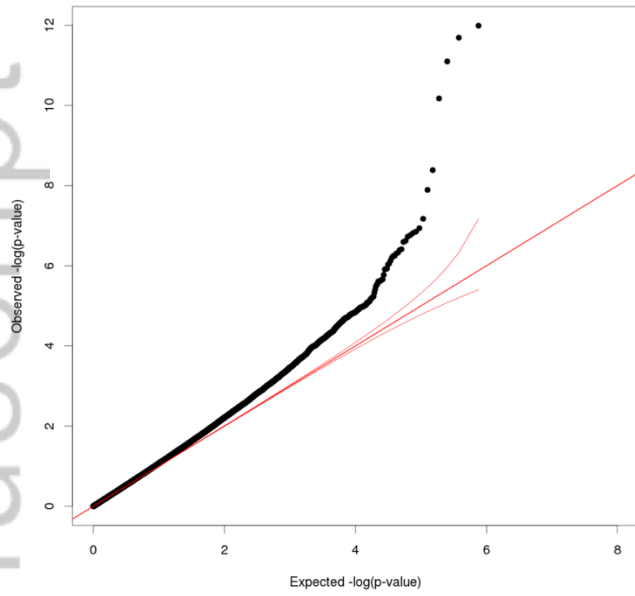
cg02042600	15	42800833	SNAP23;S NAP23	5URT;5U RT		6.00E-04	1.00E-04	3.47E-05	8.56E-04	2.52E-04	8.57E-04	4.47E-04	1.64E-04	6.53E-03
cg00850551	9	129968071	RALGPS1; RALGPS1; RALGPS1	Body;Bo dy;Body		1.00E-04	0.00E+00	3.49E-05	1.87E-04	8.67E-05	3.21E-02	7.83E-05	2.10E-05	2.00E-04
cg13696490	3	151488006	AADACP1 ;MIR548H2 ;AADACL 2- AS1;AAD ACL2-AS1	TSS1500; Body;Bo dy;Body		-1.00E-03	2.00E-04	3.49E-05	-1.34E-03	3.85E-04	6.56E-04	-7.69E-04	3.05E-04	1.18E-02
cg14153069	9	131683257	PHYHD1; PHYHD1; PHYHD1; PHYHD1; PHYHD1	TSS1500; 1stExon; 1stExon; 5URT;5U RT		3.00E-04	1.00E-04	3.50E-05	4.67E-04	1.67E-04	6.02E-03	2.24E-04	6.68E-05	8.61E-04
cg12324048	3	193823125				6.00E-04	2.00E-04	3.52E-05	3.76E-04	2.72E-04	1.68E-01	7.41E-04	1.83E-04	5.44E-05
cg18333255	2	203686636	ICA1L;ICA 1L;ICA1L;I CA1L	Body;Bo dy;Body; Body		6.00E-04	1.00E-04	3.55E-05	3.15E-04	2.13E-04	1.40E-01	7.21E-04	1.75E-04	3.92E-05
cg25345365	11	114050114	ZBTB16;ZB TB16	Body;Bo dy		9.00E-04	2.00E-04	3.56E-05	5.94E-04	3.47E-04	8.84E-02	1.08E-03	2.76E-04	9.53E-05
cg12432980	20	5987794	MCM8- AS1;CRLS 1;CRLS1	TSS1500; TSS200;B ody	S Shore	8.00E-04	2.00E-04	3.57E-05	6.48E-04	2.61E-04	1.39E-02	8.92E-04	2.65E-04	7.96E-04
cg06373648	6	33401536	SYNGAP1	Body		8.00E-04	2.00E-04	3.59E-05	7.09E-04	3.35E-04	3.60E-02	8.03E-04	2.26E-04	3.93E-04
cg04048370	5	61032938	LOC10050 6526	TSS1500		4.00E-04	1.00E-04	3.59E-05	4.88E-04	1.92E-04	1.21E-02	4.19E-04	1.28E-04	1.10E-03
cg09495478	3	44938102	TGM4	Body		3.00E-04	1.00E-04	3.61E-05	4.58E-04	1.27E-04	4.18E-04	2.52E-04	1.06E-04	1.81E-02
cg13770461	11	46016312	PHF21A;P HF21A	Body;Bo dy		-5.00E-04	1.00E-04	3.62E-05	-5.67E-04	2.28E-04	1.39E-02	-5.32E-04	1.61E-04	1.01E-03
cg18866825	5	150477744				4.00E-04	1.00E-04	3.63E-05	4.15E-04	1.26E-04	1.28E-03	3.56E-04	1.41E-04	1.16E-02
cg26931608	1	170036455	KIFAP3;KI FAP3;KIF AP3;KIFA P3	5URT;5U RT;Body; Body		-1.40E-03	3.00E-04	3.66E-05	-2.26E-03	5.31E-04	3.63E-05	-8.09E-04	4.41E-04	6.71E-02
cg08817540	3	108020727	HHLA2;H HLA2;HH LA2;HHL A2	TSS1500; 5URT;5U RT;5URT		1.80E-03	4.00E-04	3.67E-05	2.24E-03	8.38E-04	8.42E-03	1.67E-03	5.24E-04	1.43E-03
cg03046907	2	27227401	MAPRE3	5URT		-1.00E-04	0.00E+00	3.69E-05	-1.42E-04	1.00E-04	1.57E-01	-1.31E-04	3.39E-05	1.14E-04
cg03918655	17	54996166				-2.00E-04	0.00E+00	3.73E-05	-2.27E-04	1.49E-04	1.31E-01	-1.83E-04	4.76E-05	1.29E-04
cg12875749	6	6556546	LY86-AS1	Body		-8.00E-04	2.00E-04	3.75E-05	-1.17E-03	3.28E-04	4.73E-04	-5.68E-04	2.22E-04	1.06E-02

cg08936253	18	44334486	ST8SIA5;S T8SIA5;ST	Body;Bo dy;Body	N Shore	7.00E-04	2.00E-04	3.78E-05	5.52E-04	2.51E-04	2.91E-02	9.01E-04	2.49E-04	3.10E-04
cg22356061	1	227954102	SNAP47	Body		-6.00E-04	2.00E-04	3.80E-05	-6.45E-04	2.52E-04	1.14E-02	-6.10E-04	1.89E-04	1.29E-03
cg02385309	22	38609371	MAFF;MA FF;MAFF; MAFF	5URT;5U RT;5URT ;5URT	N Shore	7.00E-04	2.00E-04	3.86E-05	6.96E-04	2.60E-04	8.20E-03	7.67E-04	2.45E-04	1.80E-03
cg25858982	3	153091368				-4.00E-04	1.00E-04	3.87E-05	-9.91E-04	2.20E-04	1.31E-05	-2.55E-04	1.06E-04	1.69E-02
cg17540192	7	97875259	TECPRI	Body		4.00E-04	1.00E-04	3.87E-05	4.24E-04	1.69E-04	1.29E-02	3.88E-04	1.19E-04	1.15E-03
cg05576256	1	6069135	KCNAB2	5URT		-1.00E-04	0.00E+00	3.88E-05	-1.54E-04	1.00E-04	1.26E-01	-1.03E-04	2.67E-05	1.28E-04
cg23459817	17	56806313	RAD51C;R AD51C	Body;Bo dy		6.00E-04	2.00E-04	3.89E-05	8.66E-04	2.17E-04	1.00E-04	4.03E-04	2.28E-04	7.68E-02
cg27260821	18	30020777	GAREM;G AREM	Body;Bo dy		-1.00E-04	0.00E+00	3.90E-05	-9.43E-05	1.03E-04	3.64E-01	-1.19E-04	2.96E-05	6.38E-05
cg21406003	9	127052763	NEK6;NE K6;NEK6; NEK6;NE K6;NEK6	TSS1500; TSS1500; Body;5U RT;5URT ;5URT		5.00E-04	1.00E-04	3.90E-05	5.07E-04	1.70E-04	3.43E-03	4.64E-04	1.63E-04	4.48E-03
cg24033280	14	45712290	MIS18BP1	Body		3.00E-04	1.00E-04	3.90E-05	1.22E-04	2.40E-04	6.13E-01	3.43E-04	8.23E-05	3.30E-05
cg24567196	3	18782489				-7.00E-04	2.00E-04	3.91E-05	-6.82E-04	2.47E-04	6.35E-03	-7.40E-04	2.43E-04	2.38E-03
cg04422501	12	56508302			N Shelf	-1.00E-04	0.00E+00	3.92E-05	-8.39E-05	1.76E-04	6.34E-01	-1.11E-04	2.72E-05	4.80E-05
cg08867908	1	2284179	LOC10012 9534;MOR N1	TSS200;B ody		-1.00E-04	0.00E+00	3.92E-05	-8.09E-05	1.69E-04	6.32E-01	-6.76E-05	1.66E-05	4.85E-05
cg10513161	3	183705727	ABCC5;AB CC5	Body;Bo dy		3.00E-04	1.00E-04	3.94E-05	7.54E-05	2.07E-04	7.16E-01	3.07E-04	7.27E-05	2.58E-05
cg15298831	11	60754076	CD6;CD6; CD6;CD6	Body;Bo dy;Body; Body		7.00E-04	2.00E-04	3.95E-05	7.08E-04	2.55E-04	6.20E-03	6.18E-04	2.03E-04	2.40E-03
cg03995830	10	14782991	FAM107B; FAM107B	Body;5U RT		6.00E-04	1.00E-04	3.95E-05	3.94E-04	2.29E-04	8.78E-02	6.43E-04	1.68E-04	1.34E-04
cg06403535	2	177116896				-7.00E-04	2.00E-04	3.98E-05	-9.49E-04	2.47E-04	1.81E-04	-4.70E-04	2.31E-04	4.19E-02
cg19693031	1	145441552	TXNIP;NB PF20;NBPF 10;NBPF10	3UTR;Bo dy;Body; Body		-8.00E-04	2.00E-04	4.02E-05	-5.73E-04	2.90E-04	4.99E-02	-9.40E-04	2.52E-04	2.07E-04
cg13296238	3	127323965	MCM2;MC M2	Body;Bo dy	Island	4.00E-04	1.00E-04	4.03E-05	5.34E-04	1.57E-04	8.41E-04	3.28E-04	1.31E-04	1.25E-02
cg24450239	8	101348501	RNF19A	TSS200		1.00E-03	2.00E-04	4.05E-05	6.60E-04	4.00E-04	1.01E-01	1.23E-03	3.14E-04	9.37E-05
cg15530946	14	75469136	EIF2B2	TSS1500	N Shore	-4.00E-04	1.00E-04	4.06E-05	-6.27E-04	1.96E-04	1.64E-03	-3.48E-04	1.23E-04	4.71E-03
cg21969887	20	43180861	PKIG;PKI G;PKIG;PK IG	5URT;5U RT;5URT ;5URT		2.00E-04	1.00E-04	4.06E-05	2.71E-04	1.52E-04	7.59E-02	2.22E-04	6.00E-05	2.23E-04

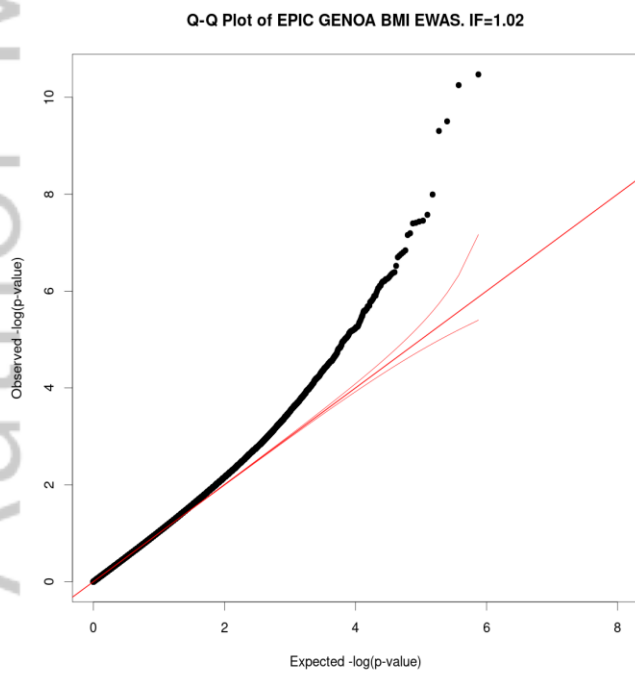
cg17758563	6	16323116	ATXN1;AT XN1	Body;Bo dy	N Shelf	1.00E-03	2.00E-04	4.07E-05	1.19E-03	4.36E-04	6.96E-03	9.25E-04	2.98E-04	1.99E-03
cg13415859	6	3414680	SLC22A23; SLC22A23; SLC22A23; SLC22A23; SLC22A23	5URT;5U RT;Body; Body;Bo dy		8.00E-04	2.00E-04	4.08E-05	8.58E-04	2.88E-04	3.31E-03	7.18E-04	2.53E-04	4.61E-03
cg24418947	1	46836023				1.40E-03	3.00E-04	4.11E-05	2.28E-03	7.12E-04	1.62E-03	1.13E-03	3.86E-04	3.53E-03
cg03181246	20	41872397				6.00E-04	2.00E-04	4.12E-05	1.01E-03	2.88E-04	6.27E-04	4.86E-04	1.84E-04	8.55E-03
cg26298192	10	134066014	STK32C	Body		4.00E-04	1.00E-04	4.16E-05	5.88E-04	1.80E-04	1.34E-03	3.03E-04	1.07E-04	4.87E-03
cg11614245	4	146539248	MMAA	TSS1500	N Shore	8.00E-04	2.00E-04	4.17E-05	8.38E-04	3.01E-04	6.11E-03	8.18E-04	2.72E-04	2.68E-03

Figure 1. Q-Q Plot of InterGEN and GENOA. Inflation factor of InterGEN, GENOA and GENOA female only EWAS are 1.09, 1.01 and 1.02, respectively.

A. InterGEN



B. GENOA



C. GENOA Female Only

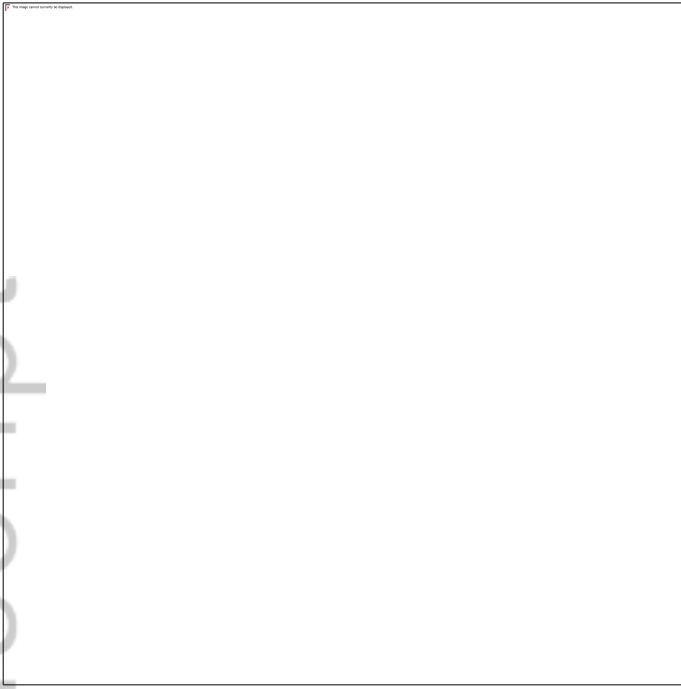
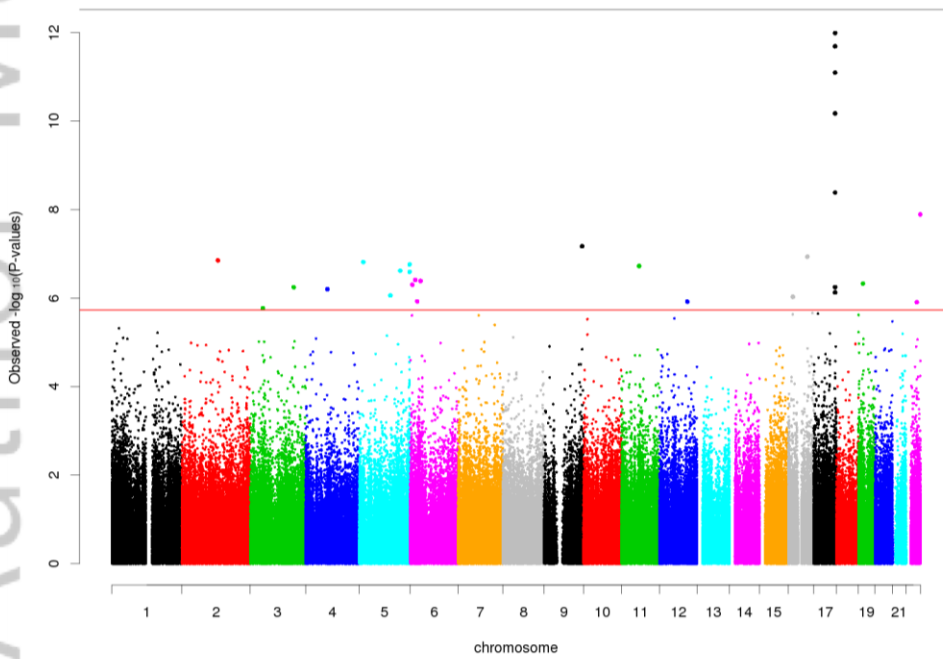
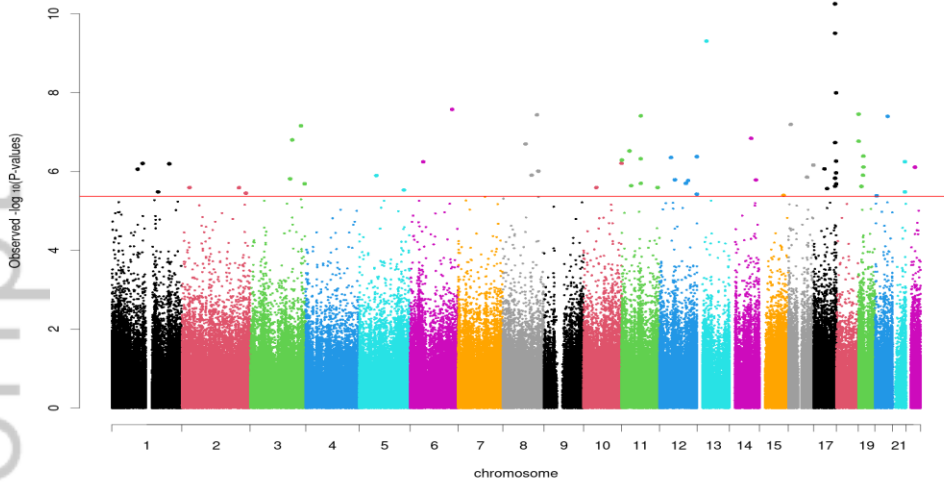


Figure 2. Manhattan plot of InterGEN and GENOA BMI EWAS

A. InterGEN



B. GENOA



C. GENOA Female Only

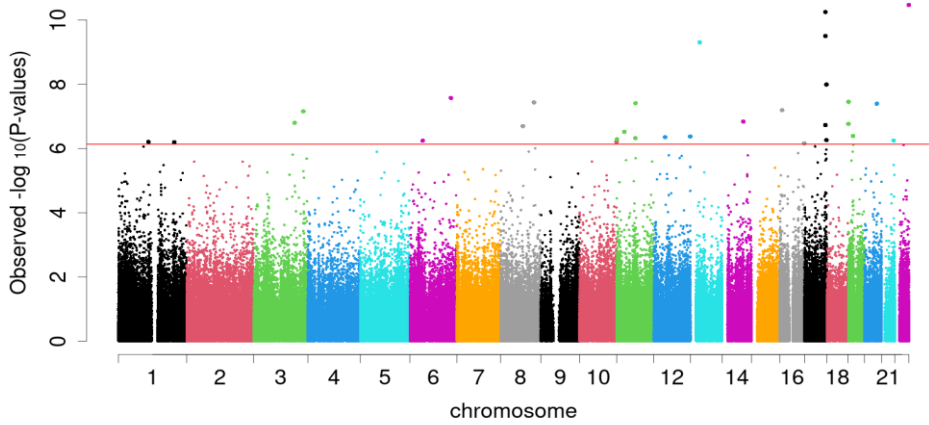


Figure 3. Meta-analysis of epigenome-wide associations with BMI from InterGEN and GENOA.

A. Manhattan plot of the meta-analysis of BMI EWAS. Horizontal line indicates genome-wide significance of Bonferroni corrected p-value of 0.05.

B. Quantile-quantile (QQ) plot of the meta-analysis of BMI EWAS. Inflation factor of 1.06.

C. Scatter plot comparing the beta coefficients of the top BMI associations between the InterGEN and GENOA samples. Correlation coefficient: 0.93 (p value: $< 2.2E-16$); Beta coefficient: 0.70 (SE: 0.035, p-value: $< 2E-16$).

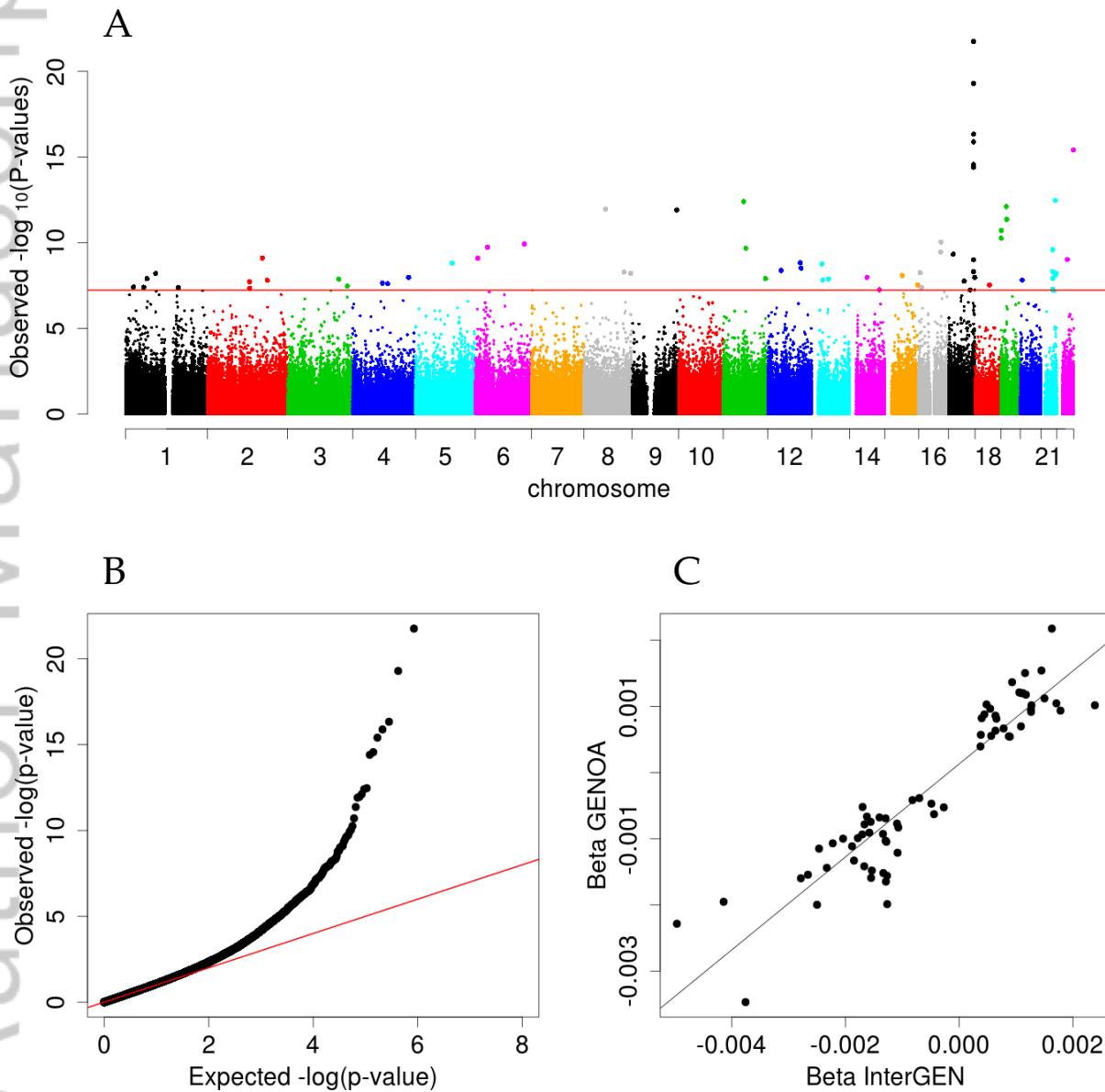
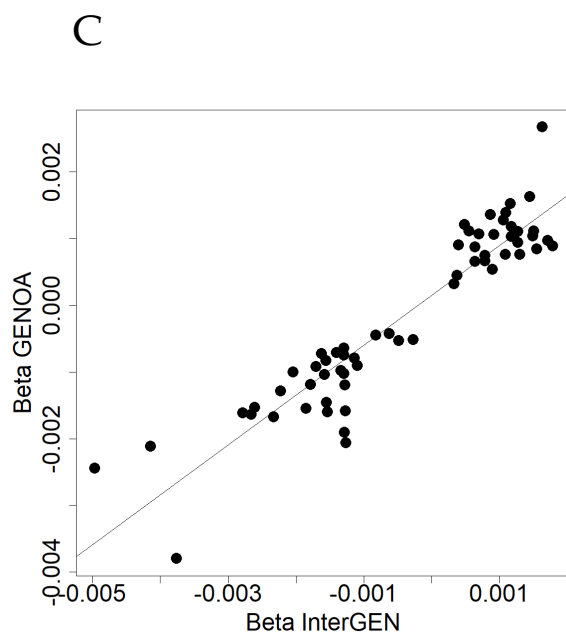
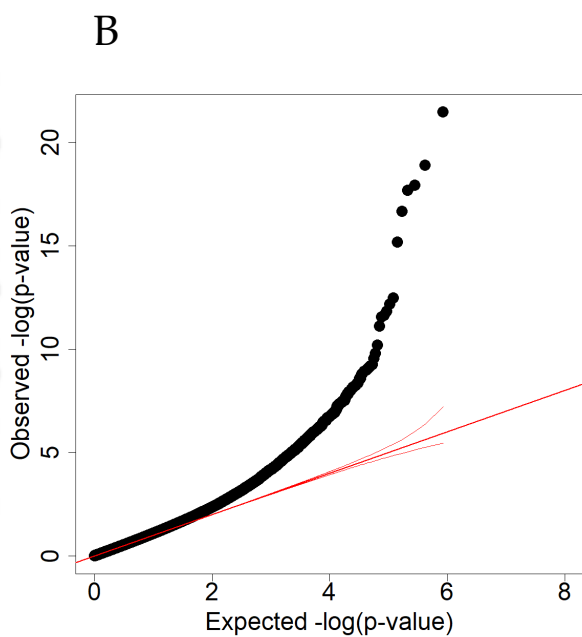
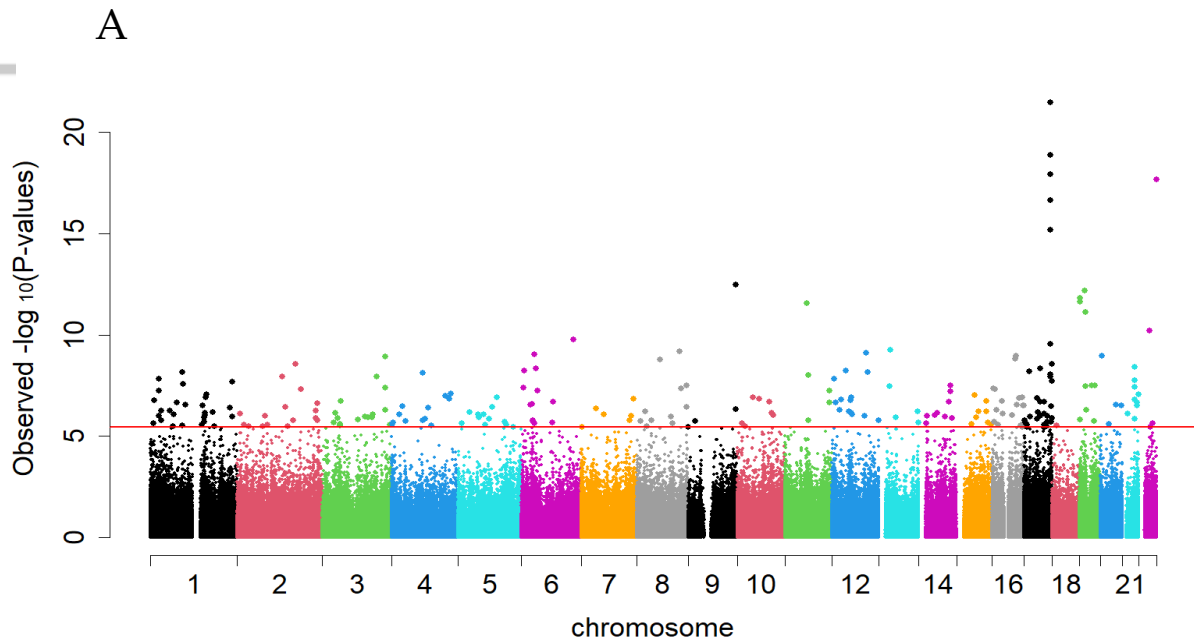


Figure 4. Meta-analysis of epigenome-wide associations with BMI from InterGEN and GENOA female only.

A: Manhattan plot of the femal-only meta-analysis. Horizontal line indicates genome-wide significance of Bonferroni corrected p-value of 0.05.

B: Quantile-quantile plot: Inflation factor of 1.07

C: Scatter plot of beta coefficients among 65 genome-wide significant DNAm sites in the female-only meta-analysis. Correlation coefficient of 0.93 (p value: $< 2.2E-16$); Beta coefficient of 0.75 (SE 0.039, p-value: $< 2E-16$).



Appendix

Table S5. Summary of literature review on EWAS of BMI with discovery set cohort characteristics and study design if available. All studies consist of mixed gender. None of the studies include participants with HIV. All samples came from peripheral blood except noted otherwise.

First author (Year)	(Discovery) Cohort Characteristics					Study Design				
	Size	Population	Age, Gender	BMI, Mean (SD)	Underlying conditions	Array, Sample	Study design	Validation	Statistical Analysis	Co-variables
Sharp, (2021)[58]	4894	Northern European	47.7% Female	26.98 (3.2)	NA	450K	Meta-analysis	Yes	Linear regression	Age, sex
Karlsson (2020)[32]	535	Swedish	68.2yrs; 58.5% female	26.4 (4.2)	Smoking, T2D	450K, EPIC	Cross-sectional, longitudinal Cis-expression quantitative trait methylation	Yes	Linear mixed effects regression	GLU, CHOL, triglycerides, smoking, T2D, age, sex, methylation array
Sharma, (2020)[59]	230	African Americans	46% Female	NA	NA	450K		No	Linear regression	Age, sex, insulin sensitivity
Crocker, (2020)[60]	2325	American Indians	NA	29.6 (na)	NA	Illumina's EPIC	Population-based prospective cohort study	Yes	Linear regression	Age
He (2019)[61]	263	Penn State	16.7yrs. 44.1%female.	65.4 (28.5)	Tobacco, alcohol,	Illumina HiSeq 2500	Cross sectional	Yes	Linear regression	Age, race, sex, batch of assay
Sun (2019)[62]	1485	The Bogalusa Heart Study	44yrs; 59% female	28.7-33.3	Smoker identified	450K	Cross-sectional, longitudinal	Yes	GLM	Age, sex, smoking status, estimated WBC
Li (2019)[23]	60	CN monozygotic twins	53.53yrs; 50% female	25.1 (4.33)	NA	Illumina HiSeq X Ten	Cross-sectional, longitudinal	Yes	Linear mixed effects regression	Cell type composition, GLU, CHOL, TG, HDLC, LDLC
Campanella (2018)[63]	1941	European	NA	NA	Breast cancer, colorectal cancer, MI, b-cell malignancy, smoking	450K	Meta-analysis	Yes	Meta-analysis	Microarray and position, sex, age at blood draw, case control status
Dhana (2018)[15]	1450	Dutch	63.7yrs; 55.9%female	27.7 (4.4)	Smoking, T2D	450K	Cross-sectional	Yes	Linear mixed effects regression	Sex, age, smoking, leukocyte proportions, array number, position on array
Geurts (2018)[17]	5361	Melbourne cohort	60yrs, 32% female	NA	Prostate, colorectal, lung or kidney cancer, urothelial carcinoma or mature B neoplasms, smoking	450K	Cross-sectional, longitudinal	No	Linear mixed effects regression of case & control	Age, sex, smoking status, country of birth, sample type, white blood cell composition
Wang, (2018)[64]	700	African Americans	64% Females	NA	T2D, CVD	Sequenom's MassARRAY	Meta-analysis	Yes	Cross-sectional	Age, sex

Kvaløy, (2018)[25]	120	Norwegian	27.2yrs, 100% Female	37.04 (na)	NA	450K	Cross-sectional	Yes	Linear regression	Age
Wahl (2017)[1]	5387	European, Asian Indian	>50yrs. >50% female	>26.8	Alcohol, hypertension, coronary heart disease, T2D, smoking	450K	Cross-sectional, longitudinal	Yes	Inverse variance meta-analysis	Age, sex, smoking, physical activity, alcohol, probe, estimated WBC proportions
Sayols-Baixeras (2017)[4]	641	REGICOR, FOS	63.2yrs, 50.7% female	27.0 (4.0)	Hypertension, diabetes, smoking,	450K	Cross-sectional	Yes	Fixed effects meta-analysis of two cohorts	Age, sex, smoking, surrogate var
Mendelson (2017)[65]	3743	FHS & LBC	67yrs, 55% female	28.3 (5.4)	Diabetes, coronary artery disease.	450K	Cross-sectional	Yes	Meta-analysis of two cohorts	Age, sex
Meeks (2017)[8]	547	African	50.5yrs, 57.8% female	26.7 (0.5)	Without T2D	450K	Cross-sectional	Yes	Linear regression	Age, sex, recruitment site, estimated cell distributions, technical effects, first principal component from genotyping data
Crujeiras (2017)[66]	55	European Caucasian	27.4yrs; 23% female;	NA	Diabetes	450K; adipose tissue, leukocytes	Case control	No	Wilcoxon rank test	Age
Ali (2016)[67]	192	Northern European ancestry	36.2yrs, 55% females	NA	Insulin resistance, hypertriglyceridemia	450K	bisulfite validation seq	Yes	SOLAR, rank-normal transformation	Sex, age, interactions
Al Muf-tah, (2016)[68]	123	Middle Eastern	39yrs, 58% female	28.3 (6.2)	T2D	450K	Meta-analysis	Yes	Linear mixed model	T2D, BMI, age, sex
Demerath (2015)[16]	2097	African	56.2yrs, 64% female	30.1 (6.1)	Smoking, alcohol	450K	Cross-sectional	Yes	Linear mixed effects regression	Leukocyte proportions, sex, age, study center, WBC, education, household income, smoking, alcohol, physical activity, array
Aslibekyan (2015)[6]	991	GOLDN	49yrs; 52% female	28 (6)	Smoking	450K	Cross sectional; bisulfite sequencing	Yes	Linear mixed effects regression	Age, sex, smoking status, T cell purity, study site, family structure
Wang, (2015)[69]	220	Chinese Han	NA	28.4 (3.8)	NA	Se-quenom's MassARRAY	Case-control study	Yes	Liner regression	Age
Dick (2014)[10]	479	European	43.8yrs, 78% female	24.2 (na)	MI, smoking, diabetes,	450K; skin, adipose tissue	Cross-sectional	Yes	Linear mixed effects regression	age, sex, smoking, methylation array batch, MI

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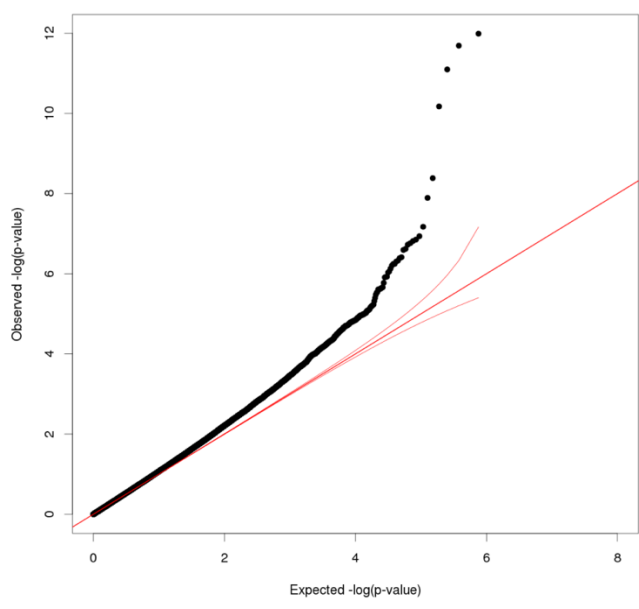
Online Supporting Information

1. Centers for Disease Control and Prevention (CDC). (2020). About Adult BMI. https://www.cdc.gov/healthy-weight/assessing/bmi/adult_bmi/index.html
2. Centers for Disease Control and Prevention (CDC). (2020). Adult Obesity Causes & Consequences. <https://www.cdc.gov/obesity/adult/causes.html>

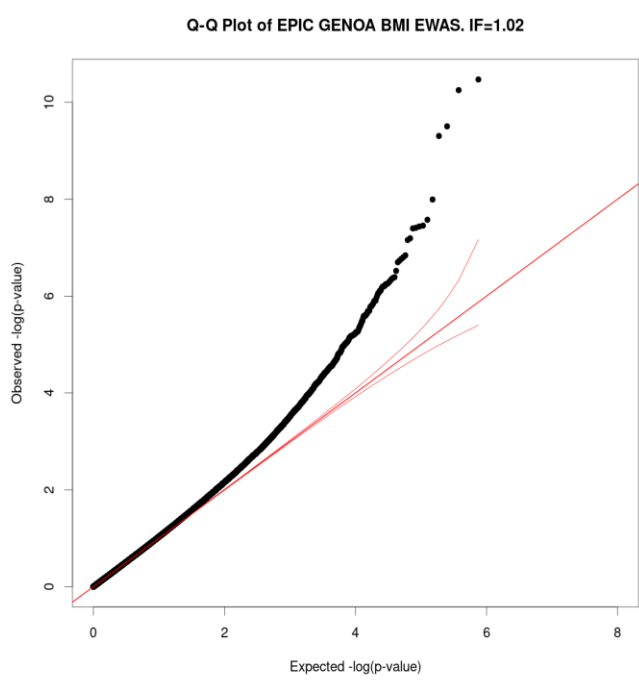
Figure 1. Q-Q Plot of InterGEN and GENOA.

Inflation factor of InterGEN, GENOA and GENOA female only EWAS are 1.09, 1.01 and 1.02, respectively.

A. InterGEN



B. GENOA



C. GENOA Female Only

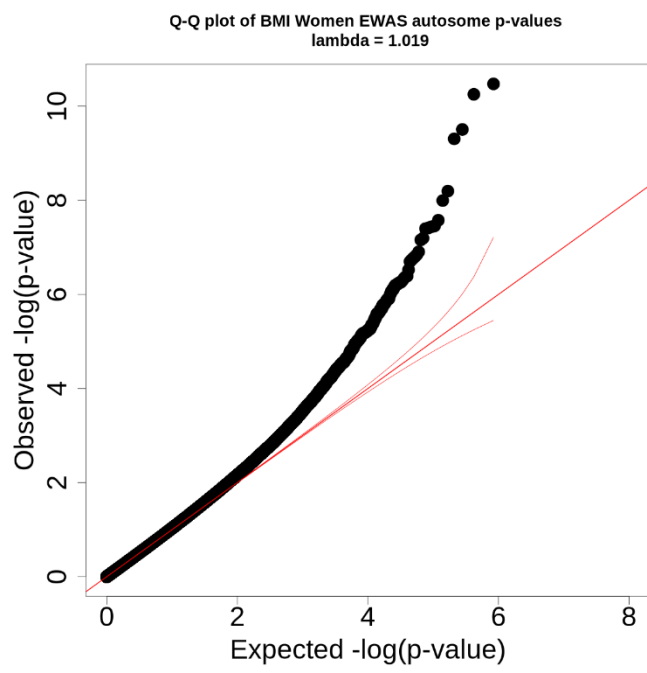
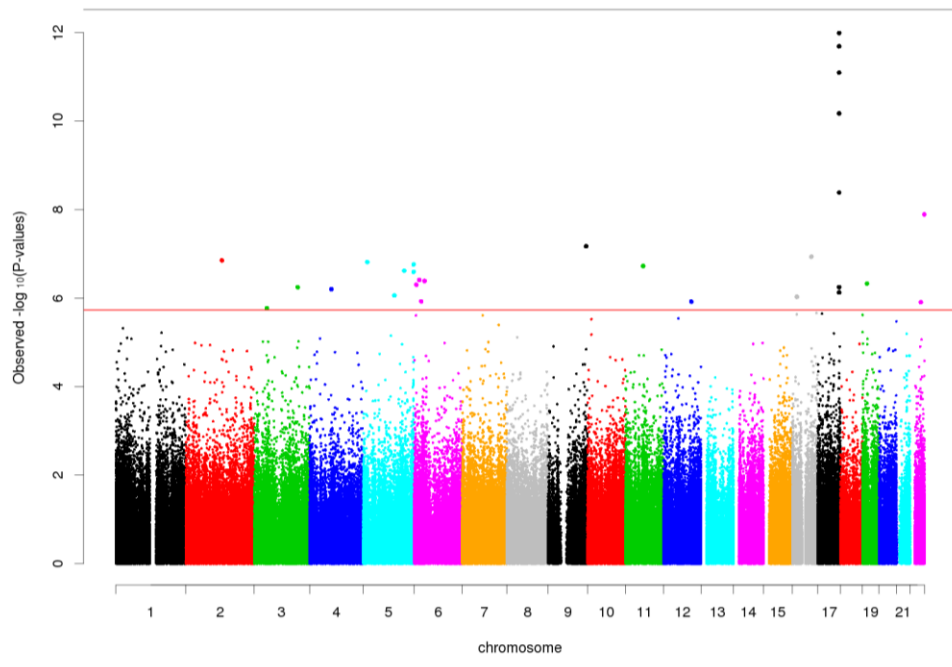
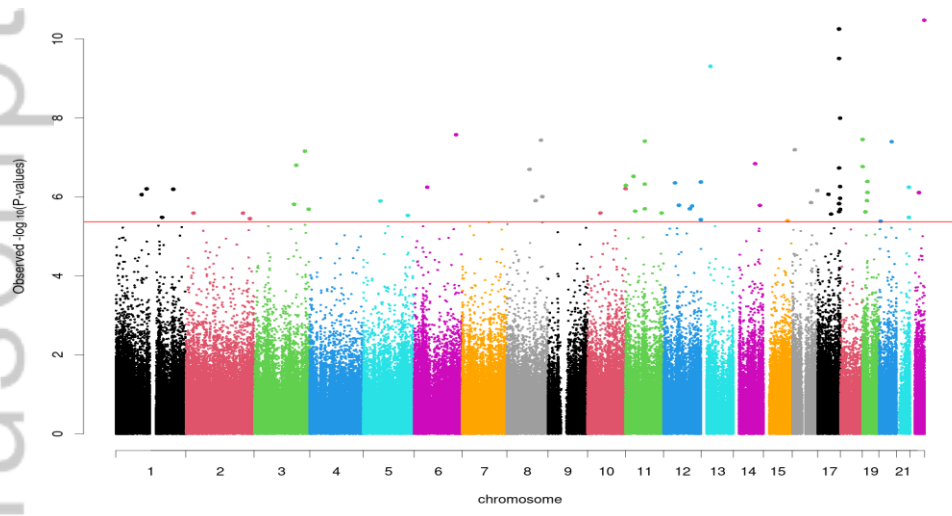


Figure 2. Manhattan plot of InterGEN and GENOA BMI EWAS

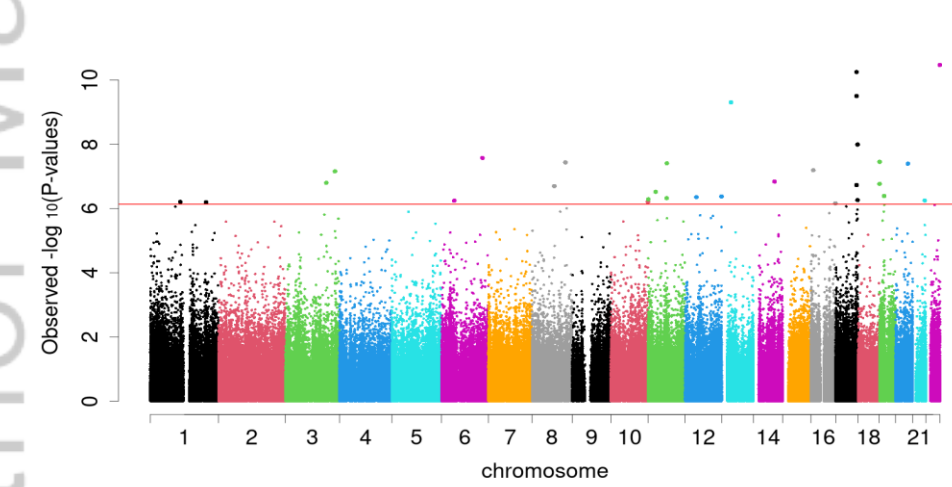
A. InterGEN



B. GENOA



C. GENOA Female Only



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Figure 3. Meta-analysis of epigenome-wide associations with BMI from InterGEN and GENOA

A. Manhattan plot of the meta-analysis of BMI EWAS. Horizontal line indicates genome-wide significance of Bonferroni corrected p-value of 0.05.

B. Quantile-quantile (QQ) plot of the meta-analysis of BMI EWAS. Inflation factor of 1.06.

C. Scatter plot comparing the beta coefficients of the top BMI associations between the InterGEN and GENOA samples.

Correlation coefficient: 0.93 (p value: < 2.2E-16); Beta coefficient: 0.70 (SE: 0.035, p-value: < 2E-16).

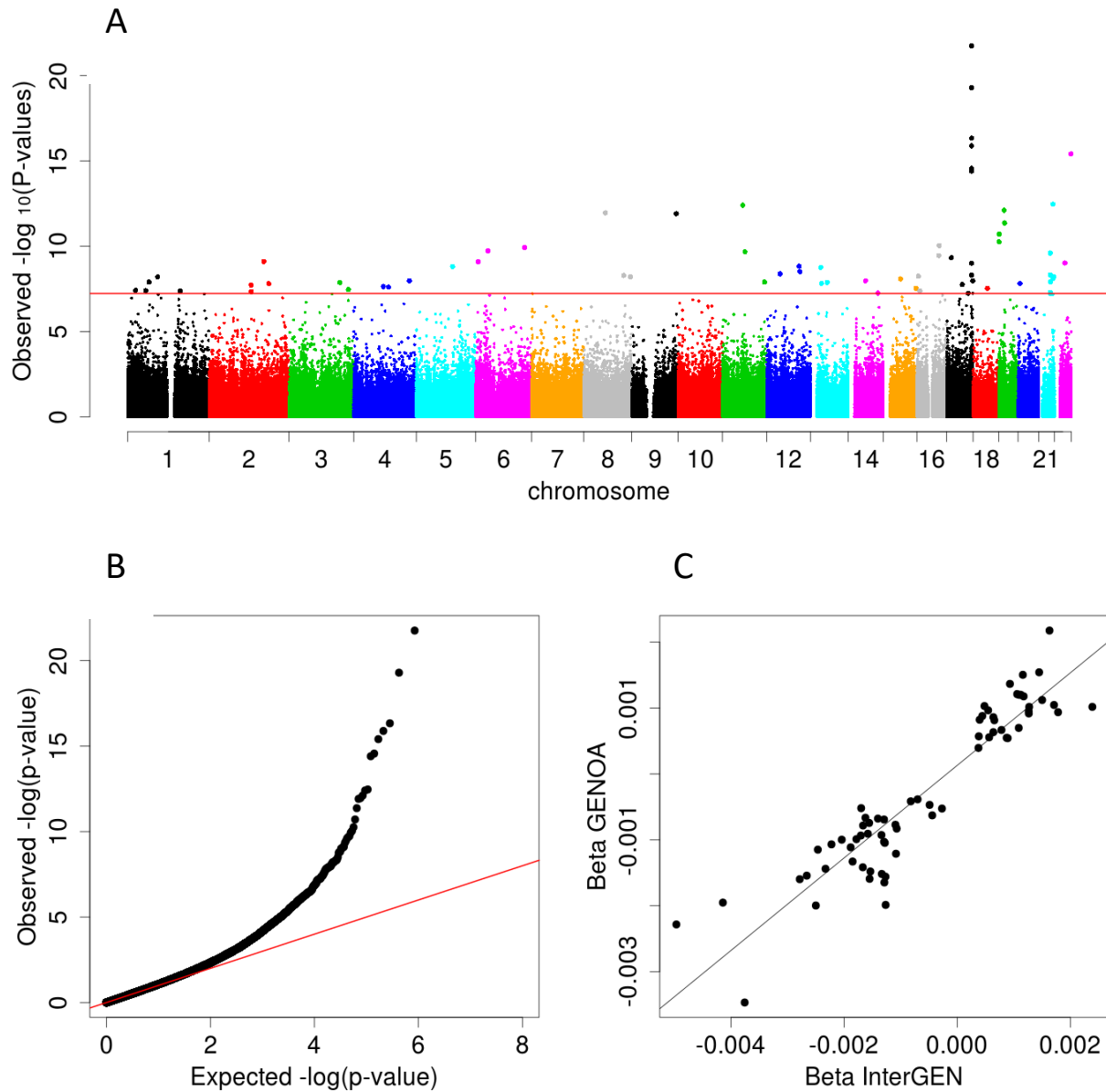


Figure 4. Meta-analysis of epigenome-wide associations with BMI from InterGEN and GENOA female only.

A: Manhattan plot of the femal-only meta-analysis. Horizontal line indicates genome-wide significance of Bonferroni corrected p-value of 0.05.

B: Quantile-quantile plot: Inflation factor of 1.07

C: Scatter plot of beta coefficients among 65 genome-wide significant DNAm sites in the female-only meta-analysis. Correlation coefficient of 0.93 (p value: < 2.2E-16); Beta coefficient of 0.75 (SE 0.039, p-value: < 2E-16).

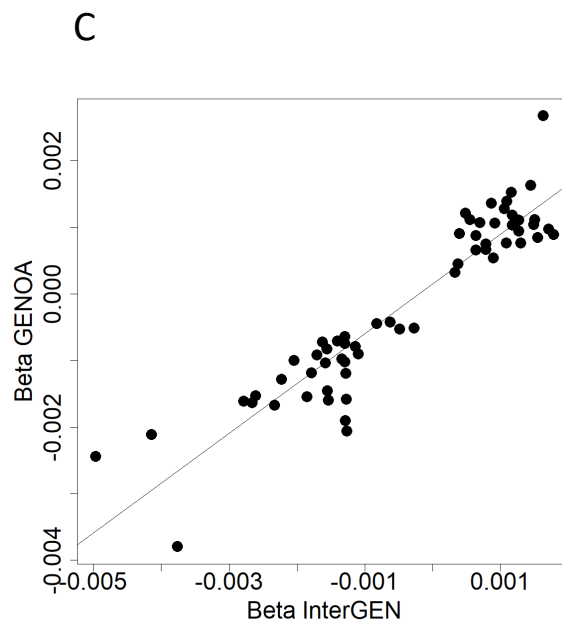
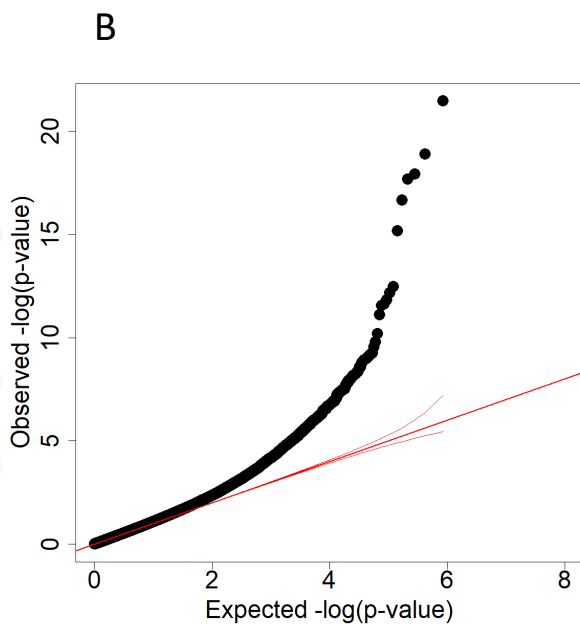
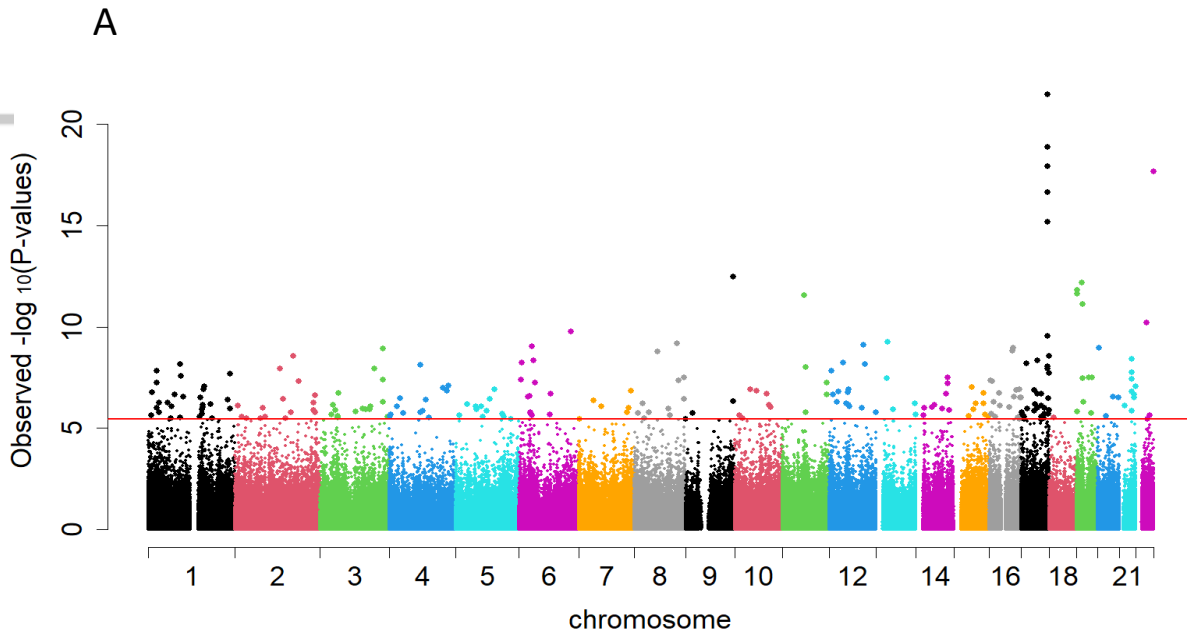


Table 1. Participant characteristics, InterGEN study (n=239) and GENOA study (N=961).

	InterGEN	GENOA	
	Women (N=239)	Total Sample (N=961)	Women (N=685)
Mean Age in years (SD)**	31.3 (5.8)	57.5 (10.3)	57.1 (10.4)
Education, N (%) **			
High school or less	100 (41.8)	587 (61.1)	421 (65.5)
Some college or Associates degree	105 (44)	157 (16.3)	111 (16.2)
Bachelor's degree or higher	34 (14.2)	217 (22.6)	153 (22.3)
BMI Category, N (%) **			
Underweight (<18.5 kg/m ²)	13 (5.4)	4 (0.4)	3 (0.4)
Normal (18.5-24.9 kg/m ²)	58 (24.3)	140 (14.6)	79 (11.5)
Overweight (25-29.9 kg/m ²)	59 (24.7)	319 (33.2)	197 (28.8)
Obese (≥30 kg/m ²)	109 (45.6)	498 (51.8)	406 (59.3)
Mean BMI kg/m² (SD)*	29.7 (8.3)	31.3 (6.5)	32.3 (6.8)
Current Smoker, N (%) *			
Yes	52 (21.8)	161 (16.8)	92 (13.4)
No	187 (78.2)	800 (83.2)	593 (86.6)

Note. Participants were given the option not to respond to any of the questions, so all number may not add up to total N; *: p-value<0.01; **: p-value<0.001 from either t-test for continuous variables or chi-squared test for categorical variables.

Table 2. Discovery of 28 Epigenome-wide Significant Associations in InterGEN (FDR-q < 0.05), with Replication in GENOA Full Sample and Females Only.

CpG	CHR	BP	Gene	Genomic Region	Relation to UCSC CpG Island	InterGEN (Discovery, n = 239)			GENOA (Replication, n = 961)			GENOA (Replication, Female Only, n = 685)		
						Beta	SE	P	Beta	SE	P	Beta	SE	P
cg18181703	17	76354621	<i>SOCS3</i>	Body	N Shore	-0.28	3.58E-02	1.02E-12	-1.60E-03	2.91E-04	5.13E-08	-0.0016	3.07E-04	1.85E-07
cg11047325	17	76354934	<i>SOCS3</i>	Body	Island	-0.50	6.49E-02	2.03E-12	-2.28E-03	4.75E-04	1.82E-06	-0.0024	5.13E-04	2.37E-06
cg03067296	17	76274577	<i>LOC100996291</i>	TSS200		-0.27	3.59E-02	7.99E-12	-1.54E-03	2.24E-04	1.15E-11	-0.0016	2.46E-04	5.60E-11
cg13343932	17	76355061	<i>SOCS3</i>	Body	Island	-0.41	5.90E-02	6.69E-11	-1.95E-03	4.12E-04	2.51E-06	-0.0021	4.35E-04	1.48E-06
cg19748455	17	76274856	<i>LOC100996291</i>	TSS1500		-0.23	3.73E-02	4.11E-09	-1.44E-03	2.49E-04	9.89E-09	-0.0017	2.62E-04	3.13E-10
cg09349128	22	50327986	Intergenic		N Shore	-0.22	3.70E-02	1.28E-08	-1.07E-03	1.73E-04	9.87E-10	-0.0013	1.90E-04	3.37E-11
cg03770138	9	136009651	<i>RALGDS</i>	Body		-0.13	2.25E-02	6.72E-08	-1.05E-03	2.42E-04	1.66E-05	-0.0012	2.62E-04	6.06E-06
cg24382141	16	67944348	<i>PSKHI</i>	Body	S Shore	-0.13	2.33E-02	1.16E-07	-6.91E-04	1.77E-04	9.69E-05	-0.0006	1.97E-04	1.06E-03
cg02398240	2	128256334	<i>IWS1</i>	Body		-0.16	2.94E-02	1.41E-07	-6.65E-04	2.45E-04	6.71E-03	-0.0007	2.70E-04	7.60E-03
cg11917181	5	14108303	Intergenic			-0.11	2.05E-02	1.53E-07	-1.66E-05	1.21E-04	8.91E-01	0.0001	1.31E-04	4.35E-01
cg16843099	5	178956830	Intergenic		N Shore	-0.24	4.41E-02	1.73E-07	-6.94E-05	2.36E-04	7.69E-01	-0.0002	2.71E-04	4.26E-01
cg19758958	11	62319222	Intergenic			-0.13	2.37E-02	1.88E-07	-1.03E-03	2.12E-04	1.42E-06	-0.0010	2.30E-04	1.05E-05
cg19679801	5	145422431	<i>SH3RF2</i>	Body		-0.19	3.43E-02	2.40E-07	4.95E-05	1.28E-04	6.98E-01	3.38E-06	1.38E-04	9.80E-01
cg12367539	5	178956838	Intergenic		N Shore	-0.25	4.70E-02	2.55E-07	1.14E-04	2.21E-04	6.05E-01	-4.57E-05	2.51E-04	8.56E-01
cg19494100	6	18387313	<i>RNF144B</i>	TSS1500	N Shore	-0.08	1.45E-02	3.88E-07	-1.23E-04	1.48E-04	4.05E-01	-0.0001	1.58E-04	4.01E-01
cg15781610	6	36992554	<i>FGD2</i>	Body		-0.17	3.22E-02	4.09E-07	-9.34E-04	2.31E-04	5.65E-05	-0.0009	2.55E-04	3.22E-04
cg00840791	19	16453259	Intergenic			-0.38	7.14E-02	4.70E-07	-3.47E-03	7.12E-04	1.31E-06	-0.0038	7.76E-04	1.24E-06
cg17936938	6	7866213	<i>BMP6</i>	Body		0.18	3.39E-02	4.96E-07	9.37E-04	2.49E-04	1.74E-04	0.0009	2.75E-04	1.23E-03
cg10508317	17	76355146	<i>SOCS3</i>	Body	Island	-0.08	1.57E-02	5.66E-07	-4.16E-04	1.09E-04	1.42E-04	-0.0004	1.11E-04	6.24E-05
cg01671681	3	155421735	<i>PLCH1</i>	5UTR		-0.14	2.69E-02	5.69E-07	-6.78E-04	2.21E-04	2.27E-03	-0.0007	2.35E-04	2.59E-03
cg03578005	4	77170672	<i>FAM47E</i>	Body	N Shore	-0.06	1.07E-02	6.25E-07	-2.76E-05	3.29E-05	4.03E-01	-2.34E-05	3.65E-05	5.22E-01
cg04610187	17	76360794	<i>LOC101928674</i>	Body	S Shelf	-0.14	2.77E-02	7.43E-07	-4.97E-04	3.03E-04	1.02E-01	-0.0003	3.20E-04	3.14E-01
cg20710777	5	110411740	<i>TSLP</i>	Body	S Shelf	-0.17	3.31E-02	8.70E-07	-5.19E-04	1.12E-04	3.96E-06	-0.0005	1.25E-04	2.19E-04
cg04730825	16	16116191	<i>ABCC1</i>	Body		-0.07	1.29E-02	9.31E-07	8.72E-05	1.55E-04	5.74E-01	7.56E-05	1.72E-04	6.60E-01
cg13258453	6	25180502	Intergenic			-0.19	3.73E-02	1.18E-06	-3.76E-04	2.45E-04	1.26E-01	-0.0003	2.73E-04	2.12E-01
cg20803896	12	99006941	Intergenic			0.11	2.15E-02	1.20E-06	6.98E-04	1.95E-04	3.72E-04	0.0008	2.08E-04	2.58E-04
cg15227014	22	38037179	<i>SH3BP1</i>	Body	S Shore	0.12	2.43E-02	1.23E-06	2.50E-04	2.19E-04	2.55E-01	0.0003	2.37E-04	2.72E-01
cg20647087	3	45709608	<i>LIMD1</i>	Body		-0.11	2.19E-02	1.69E-06	-1.16E-04	1.67E-04	4.86E-01	-5.19E-05	1.73E-04	7.64E-01

Note: The CpG sites were mapped to Genome Research Consortium human build 37 (GRCh37). The genes mapped to each CpG site were identified according to Illumina's annotation file of the EPIC BeadChip. Body: gene body; TSS: transcription start site; 5UTR: 5'-untranslated region; 3UTR: 3'-untranslated region.