

## Supplementary Online Content

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This supplementary material has been provided by the authors to give readers additional information about their work.

## eMethods

### Data Set and Ethical Approval:

We analysed buccal cells from 790 women enrolled in the MRC National Survey of Health and Development (NSHD) study, a birth cohort study of men and women all born in Britain in March 1946 [1]. These 790 women were selected from those who provided a buccal and blood sample at the age of 53 in 1999, who had not previously developed any cancer, and who had complete information on epidemiological variables of interest and follow up. For 152 of these women we also analysed a matched blood sample. The study was approved by the Central Manchester Ethics Committee (07/H1008/168).

### Experimental Protocol for DNA methylation data and data availability:

DNA from 790 buccal and 152 blood samples was extracted at Gen-Probe ([www.gen-probe.com](http://www.gen-probe.com)). Methylation analysis was performed using the Illumina Infinium Human Methylation450 BeadChip array [2]. The NSHD data are made available to researchers who submit data requests to [mrcfha.swiftinfo@ucl.ac.uk](mailto:mrcfha.swiftinfo@ucl.ac.uk); see full policy documents at <http://www.nshd.mrc.ac.uk/data.aspx>. Managed access is in place for this 69 year old study to ensure that use of the data are within the bounds of consent given previously by participants, and to safeguard any potential threat to anonymity since the participants are all born in the same week.

### Quality Control and Normalization Analysis:

Quality control and intra-sample normalization was performed on each of the 790 buccal and then separately on the 152 matched whole blood samples. In each case, raw .idat data files were processed using the minfi package [3], using the Illumina definition of beta-values and extracting P-values of detection for each sample. The Illumina methylation beta-value of a specific CpG site is calculated from the intensity of the methylated (M) and unmethylated (U) alleles, as the ratio of fluorescent signals  $\beta = \text{Max}(M,0)/[\text{Max}(M,0)+\text{Max}(U,0)+100]$ . On this scale,  $0 < \beta < 1$ , with  $\beta$  values close to 1 (0) indicating 100% methylation (no methylation). Probes with more than 5% values not passing the detection P-value threshold were removed from further analysis, and the rest of NA's were imputed using the k-nearest neighbors imputation procedure [4]. In the case of the 790 sample set, this resulted in 479,491 probes. To correct for the well-known bias of type-2 probes, we used the SWAN package [5]. To check robustness of this correction procedure, we verified that results were largely unchanged using BMIQ [6]. This completed the intra-sample normalization.

Next, the 790 unmatched buccal samples were divided into two sets, one set defining a discovery set of 400 samples, with the remaining 390 defining a replication set. Sample selection was performed randomly (large sample size ensured that proportions of epidemiological factors, e.g. never-smokers, ex-smokers and current smokers, was similar between the two sets -see Table-1). To assess inter-sample variability within the discovery set, we first centered the intra-sample normalized beta-valued data matrix so that each probe had a mean zero across all samples. We then used Singular Value Decomposition (SVD) on this centered matrix to identify the components of maximal variation [7]. Random Matrix Theory was used to predict the number of significant components of variation [8]. In order to assess the relative contributions of biological and technical variables to data variability, significant components of variation were correlated to phenotypic and technical factors and results rendered in a P-value heatmap, a procedure previously implemented by us [7,9]. The SVD analysis revealed that the top component of variation correlated with Smoking Pack Years (SPY), an epidemiological indicator of an individual's smoking history. Technical factors, notably, beadchip effects and variations in bisulfite conversion (BSC) efficiency were associated with the 2<sup>nd</sup> largest component of variation. Similar results were obtained in the replication cohort of 390 buccal samples.

### Supervised Analysis:

Using the discovery set of 400 buccal samples, we next performed linear regressions between smoking pack years (SPY) and the beta methylation profiles. In detail, for each CpG, we ran a

multivariate linear regression using the estimated bisulfite conversion (BSC) efficiency (BSC) as a covariate to ensure that results would not be confounded by variations in BSC efficiency. Because there were only a maximum of 12 samples per beadchip, robustness against beadchip effects was tested at the very end of our analyses, by repeating all analyses with a different choice of discovery and replication sets. Specifically, instead of randomly picking samples, we randomly picked beadchips, thus ensuring that all samples from the discovery set were done on one set of beadchips, and all samples from the replication set done on a mutually exclusive set of chips.

CpGs from the supervised regressions in the discovery set were ranked according to P-value, histograms of P-values was generated and the False Discovery Rate (FDR) estimated using the q-value procedure [10]. Given the observed strong association, we used a very stringent Bonferroni threshold ( $1.04e-7=0.05/479,491$ ) to define smoking associated differentially methylated CpGs (DMCs). A total of 1501 CpGs passed this threshold, defining our buccal DNA methylation signature. Linear regression with adjustment for BSC efficiency were also used in the replication set, i.e. the 390 buccal set, to derive t-statistics of association between probe's DNA methylation profiles and smoking pack years.

In the case of the matched 152 whole blood set, we observed that the histogram of P-values exhibited a shape indicating the presence of a confounding factor [11]. SVD analysis over the 152 whole blood set revealed that the top component of variation did not correlate with any known biological, epidemiological or technical factor. Hence, for this data set, we applied Independent Surrogate Variable Analysis (ISVA) [8], to derive statistics of association and P-values, resulting in an improved FDR (q-values were used as FDR estimates). After application of ISVA, the resulting histogram of P-values exhibited a shape that was consistent with statistical theory. The fact that the top ranked CpGs derived from ISVA mapped to genes previously reported to undergo significant DNAm changes in independent blood EWAS (e.g. genes like *AHRR*, *CYP1A1*, *PTK2*, *GFI1*) attests to the quality of our normalized blood DNAm data.

### **Correction for cellular heterogeneity:**

Although confounding variation by cell-type has been known to inflate signals in blood tissue [12], buccal tissue is more homogeneous and no deconvolution method has yet been properly validated on this type of tissue [13]. Nevertheless, we applied a reference-free deconvolution algorithm [13], which resulted in 897 of the 1501 CpGs retaining significance at a false discovery rate (FDR) threshold of 0.05 ( $FDR < 0.05$ ). This supports the view that putative changes in sample composition only has a moderate effect in buccal cells. Because the algorithm has been not been extensively tested on a tissue like buccal, results in this manuscript are based on the full set of 1501 CpGs. Results, however, do not change appreciably had we used the 897 CpGs instead.

### **Gene Set Enrichment Analysis:**

Gene Set Enrichment Analysis (GSEA) was performed using a one-tailed Fisher-exact test against biological terms derived from the Molecular Signatures Database [14] ([www.broadinstitute.org/gsea/msigdb](http://www.broadinstitute.org/gsea/msigdb)), as well as publicly available transcription factor binding sites (TFBS) from the ENCODE consortium ([www.genome.ucsc.edu/encode](http://www.genome.ucsc.edu/encode)) [15]. Briefly, the significant probes were mapped to unique Entrez gene IDs (MSigDB-analysis), or to binding sites of transcription factors as assessed using ChIP-Seq in the H1-hESC line. A total of 57 transcription factors were considered. The method followed to map probes to binding sites is described in [16].

### **Construction of the Smoking Index:**

In order to assess whether the 1501 smoking-associated DMCs, derived from buccal cells, exhibit similar DNA methylation changes in other tissues and in relation to other risk factors (e.g. HPV infection) or other phenotypes (e.g. cancer), we devised a novel algorithm to construct a smoking index score. This smoking index measures the deviation in DNA methylation at these CpG sites from a normal reference, taking the directionality of the expected and observed DNA methylation change into account. The use of a normal reference is important to avoid tissue-specific effects which otherwise may confound the analysis. In the discovery cohort, the normal reference consists of buccal cells from never-smokers. In the TCGA cancer DNA methylation data sets, we used corresponding normal tissue samples from non-smokers, if smoking information was available,

otherwise all normal tissue samples were used. Briefly, given a set of normal reference DNAm profiles, we computed, for each of the 1501 CpGs, labeled here by  $c$ , (or the subset of 1501 CpGs present in the study), the mean beta-value,  $\mu_c$ , and standard deviation,  $\sigma_c$ , across the reference samples. For any given sample,  $s$ , we then computed a smoking index score,  $SI(s)$ , as

$$SI(s) = \frac{1}{n} \sum_{c \in \{SDMC\}} w_c \frac{\beta_{cs} - \mu_c}{\sigma_c}$$

where  $w_c$  is +1 (-1) if the smoking-DMC is hypermethylated (hypomethylated) in smokers, and where  $\beta_{cs}$  is the beta-methylation value of CpG  $c$  in sample  $s$ . In the above,  $n$  is the number of 1501 CpGs which are present in the study and the summation is over all of these smoking-associated CpGs (sDMCs). Thus, the smoking index is a measure of the average deviation in DNA methylation from a normal reference, but weighted in a manner to ensure that the directionality of the changes reflects deviations as seen for the smoking-associated CpGs in buccal tissue. We stress again that the reference profiles were always taken to be normal tissue samples of the same tissue type as the corresponding “cases”. By normalizing the index values to this normal reference we ensure that results are not confounded by tissue specific effects [17].

This smoking index was first validated in the independent replication buccal cell cohort, before assessing its variation in normal/cancer DNA methylation data sets.

#### **Normal/Cancer DNA methylation data sets:**

We collected a number of normal/cancer DNA methylation data sets. We used datasets from The Cancer Genome Atlas (TCGA), which had profiled sufficient numbers of normal tissue specimens (ideally not less than 15, to allow reasonable estimates of the mean and standard deviation for the normal reference DNA methylation profiles) on Illumina 450k DNA methylation arrays. This included lung squamous cell cancer (LSCC, nN=41, nC=275), lung adenocarcinoma (LUAD, nN=32, nC=403), head and neck squamous cell carcinoma (HNSC, nN=45, nC=405), esophageal carcinoma (ESCA, nN=15, nC=126), endometrial cancer (EC, nN=46, nC=403), breast invasive carcinoma (BRCA, nN=81, nC=652), bladder urothelial carcinoma (BLCA, nN=19, nC=204), colon adenocarcinoma (COAD, nN=38, nC=278), kidney renal cell carcinoma (KIRC, nN=160, nC=301), kidney renal papilloma carcinoma (KIRP, nN=45, nC=196), liver hepatocellular carcinoma (LIHC, nN=47, nC=176), pancreatic adenoma carcinoma (PAAD, nN=10, nC=146), prostate adenoma carcinoma (PRAD, nN=48, nC=278), thyroid cancer (THCA, nN=53, nC=489) and rectum adenocarcinoma (READ, nN=7, nC=95). In all cases, the level-3 data was retrieved from the TCGA data portal (<http://tcga-data.nci.nih.gov/>). Quality of the level-3 data was assessed using Singular Value Decomposition, by checking that normal/cancer status is associated with the top component of variation.

In order to check robustness of the smoking index values to the DNA methylation technology used, we also computed the values in an independent lung adenocarcinoma data set, generated using Illumina Infinium 27k DNA methylation beadchips, and consisting of 59 matched tumour - normal lung tissue pairs. Smoking information was available for this set and as reference we used the normal lung tissue samples from non-smokers. The data was retrieved from Gene Expression Omnibus (GSE32861) [18], and provided a validation of the smoking index values obtained in the TCGA LUAD dataset.

Discriminative analysis: to assess how well the smoking index can discriminate normal/cancer status, we used the AUC from a ROC analysis.

#### **Pre-neoplastic and cancer progression DNA methylation data sets:**

In order to assess the smoking index in stages prior to cancer we focused on cervical and endometrial carcinogenesis, since for these cancers we were able to obtain pre-neoplastic tissues. This also allowed us to assess the relation of the smoking index to other risk factors (e.g human papillomavirus –HPV infection). We computed the smoking index in the 152 cervical smear samples from the ARTISTIC cohort, previously analyzed in [19] using the older Illumina Infinium 27k technology. These samples are all of normal cytology, with approximately half of the women (75)

developing a cervical intraepithelial neoplasia of grade 2 or higher (CIN2+), 3 years after sample collection. These samples are denoted as precursor CIN2+. The other 77 samples were from women who remained normal 3 years after sample collection and served as controls. Approximately half of the 75 precursor CIN2+ samples were HPV- with the rest HPV+. Similarly, the controls were also matched for HPV status (see [19]). In this study, we considered all HPV- samples which did not progress to CIN2+ within 3 years as samples at “no-risk”, with all HPV+ samples and samples which did progress to CIN2+ within 3 years as samples “at-risk”.

In addition, we also performed Illumina 450k DNAm profiling of 8 endometrial hyperplasias and 33 primary endometrial cancers. This data was generated and analysed following the same experimental and bioinformatic protocol as for the NSHD samples. The endometrial data has been submitted to GEO and will be available under accession number GSE67116. When computing the smoking index in these samples, we used the normal endometrial samples from the TCGA study [20] as the reference. The endometrial cancers from the same TCGA study were used to validate the index values of our own 33 endometrial cancers. This procedure thus allowed us to compare the index values across three different disease stages in endometrial carcinogenesis: normal, hyperplasia and cancer.

#### **Pre-invasive lung lesion set:**

Illumina 450k data was normalized with ChAMP [21] and BMIQ [6]. Inter-sample variation was further assessed using Singular Value Decomposition. From an initial total of 95 samples, including multiple lung biopsies from the same patient, we first performed hierarchical clustering to check whether samples cluster according to individual. Since, the multiple biopsies from the same patients were generally always more similar than the samples from different patients, we averaged multiple biopsies of the same patient, whenever these had the same outcome (regression or progression). This resulted in 21 normal samples, 13 samples which did not progress and 22 samples which did. In order to not confound the analysis by potential differences in the SPY between regressors and progressors, we selected a subset which were matched for SPY (focusing on those with SPY>40). This resulted in 5 regressive and 19 progressive samples. The normal samples were used as a common reference to estimate the smoking index in all 24 samples.

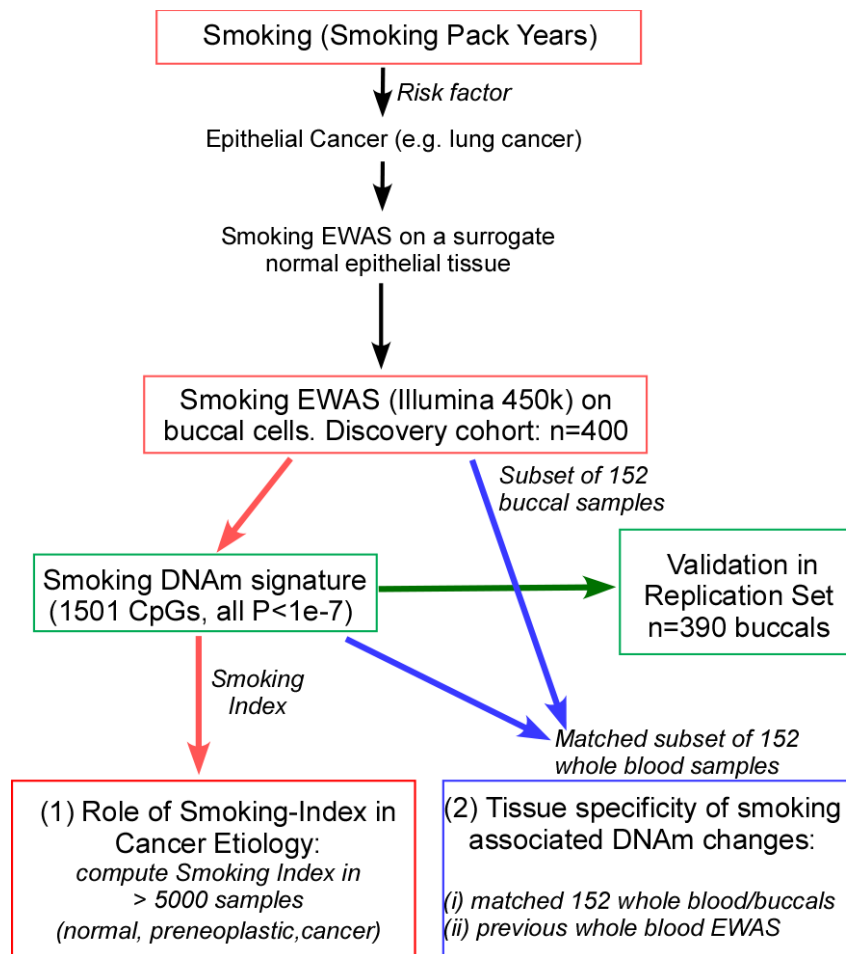
#### **Prediction of smoking status based on the DNA methylation profile in buccal cells:**

The smoking index provides a tissue-independent framework in which to assess the buccal DNA methylation signature in other tissue types. A disadvantage of the smoking index however is that it does not provide the most powerful classification framework, since it was derived from 1501 CpGs which were selected in a univariate fashion from the discovery cohort. Hence, in order to assess how well DNA methylation changes in buccal cells can predict smoking history, we instead used the elastic net based classifier [22], a state-of-the-art multivariate classification algorithm, which has previously been applied very successfully in a variety of different contexts [23]. Briefly, the Elastic Net is a generalized penalized regression method for high-dimensional variable selection. Here we used the elastic net regression model using smoking history as a binary phenotype. Specifically, we performed two separate analysis: in one case samples were dichotomized into never-smokers and current smokers (i.e. smokers at sample collection i.e. at age 53), and in another case samples were dichotomized according to less or more than 10 smoking pack years. The choice of 10 as threshold was motivated from the SVD analysis, where we observed that the top principal component showed a marked difference at 10 smoking pack years.

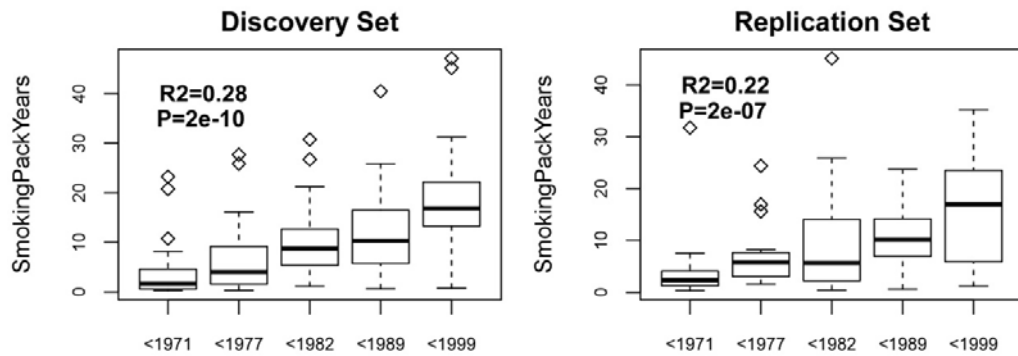
All samples from the discovery cohort, dichotomized according to one of the two procedures above, were randomly divided into ten groups, ensuring equal relative proportions of the two phenotypes in each group. In each training/testing round, one group was used as the test set with the remaining nine groups combined into a training set. The elastic net classifier was then run on this training set, using a 10-fold internal cross-validation to select the optimal penalty parameter, as implemented in the *glmnet R-package* [22]. Thus, for each round, estimated regression parameters were obtained at this optimal penalty. A predicted smoking status was then obtained in the test set samples. Because each round leads to a slightly different classifier, an overall classifier was constructed by averaging the estimated regression coefficients over all 10 rounds. Smoking status in the two independent replication cohorts was then predicted based on this overall classifier and performance assessed

using ROC/AUC analysis.

In the replication set, the elastic net classifier yielded a very high AUC ( $AUC > 0.95$ ), comparable to the AUC value obtained in the internal cross-validation of the training set (**eFigure 16**). We checked that this high classification accuracy was not driven by beadchip effects (**eFigure 17**).

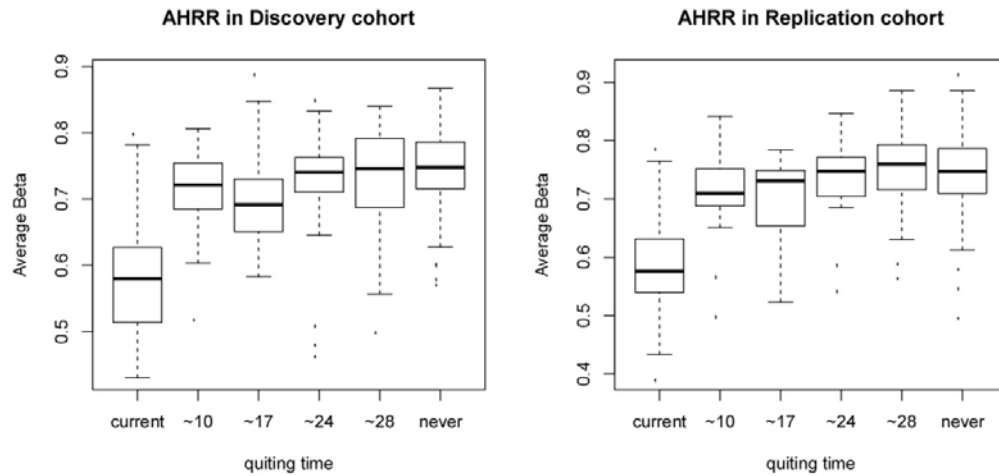


**eFigure 1. Flowchart Figure.** Figure summarizing the overall analysis strategy. Given that smoking is a major risk factor for many diseases, including epithelial cancers such as lung cancer, we decided to conduct an EWAS on an easily accessible epithelial cell which may serve as a surrogate. We thus used Illumina 450k beadarrays on a discovery set of 400 buccal samples, all collected from women (all at the age of 53) within the MRC NSHD 1946 birth cohort. The resulting smoking DNA methylation signature was then validated in a replication set. By estimating a smoking index constructed from the buccal smoking DNA methylation signature in over 5000 samples, encompassing normal, preneoplastic and cancer tissue across 14 different tissue types, this allowed us to assess the relevance of such a signature in cancer etiology. For a subset of 152 women we had matched buccal and whole blood samples (also profiled with Illumina 450k), allowing us to assess the tissue specificity of smoking-associated DNA methylation changes.

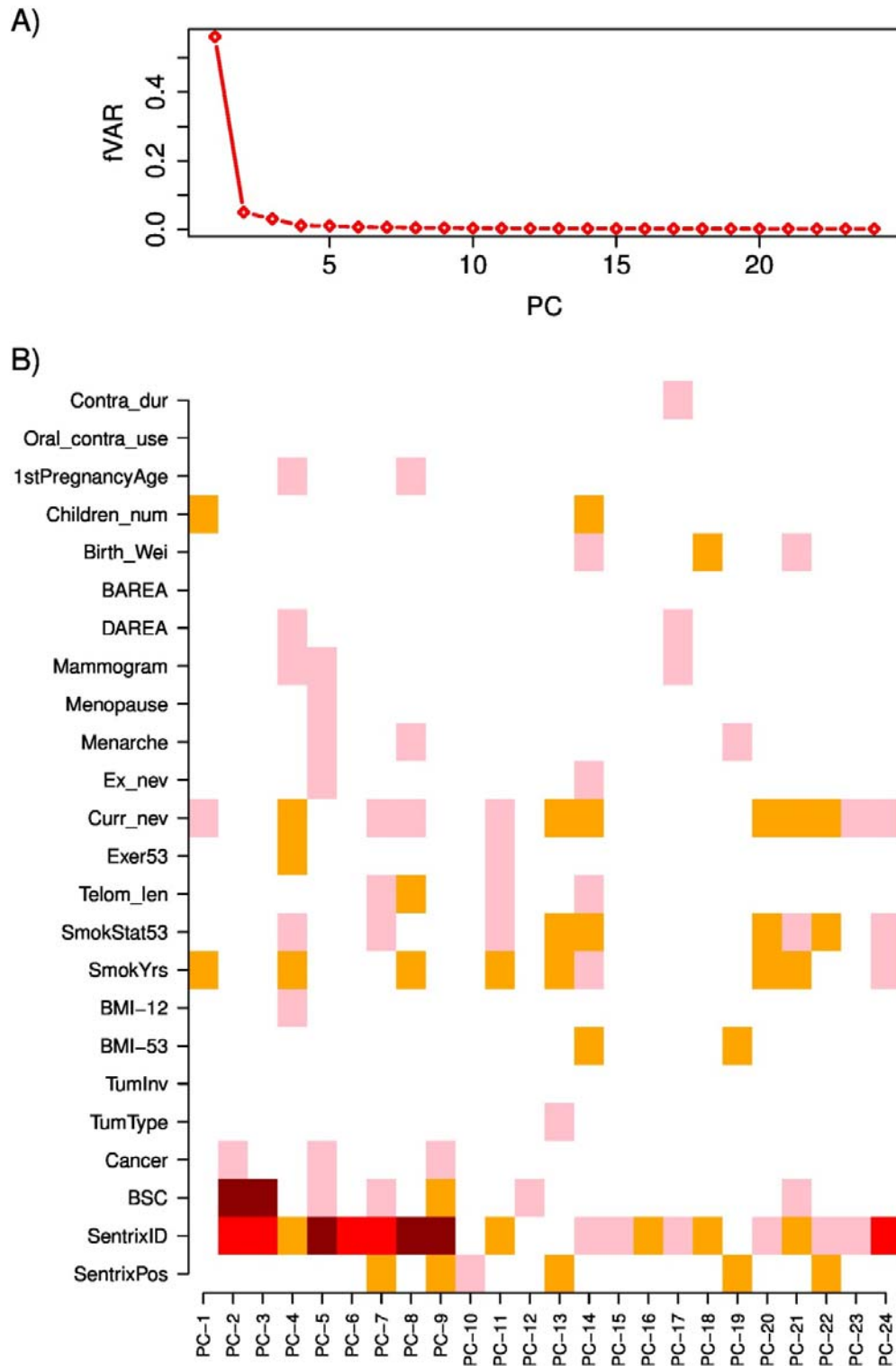


**eFigure 2. Correlation between smoking pack years and the time of last quit before sample collection.** For the discovery and replication sets, we plot Smoking Pack Years (y-axis) against the estimate of the quitting time (x-axis) of ex-smokers at age-53 (1999). For instance, “<1982” means woman was an ex-smoker at age-53 and quitting smoking in the interval between 1977 and 1982. We provide the  $R^2$  and p-value of a linear regression.



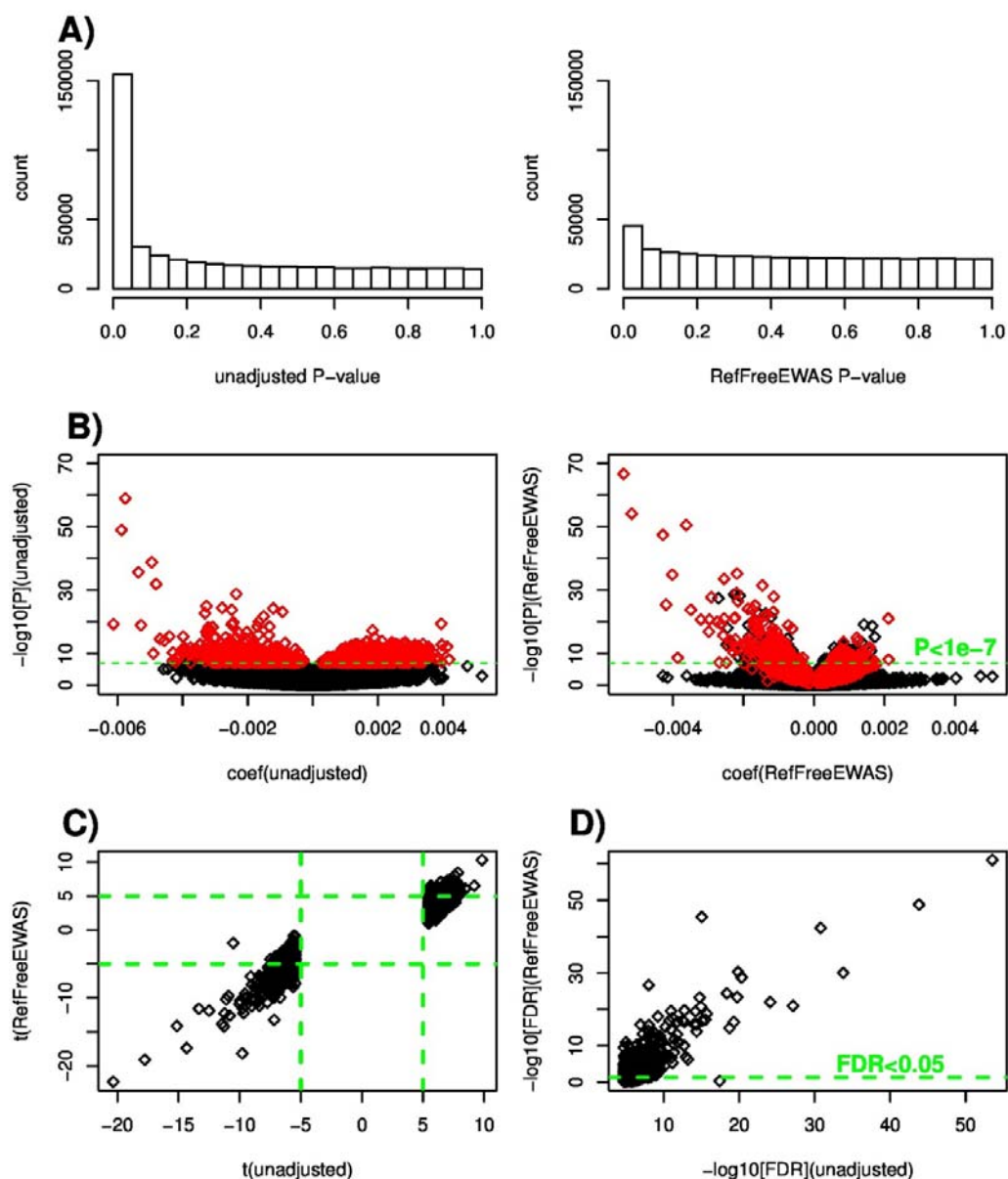


**eFigure 3. DNA methylation reversal for AHRR.** For the discovery and replication sets, we plot the average beta-value of significantly associated AHRR probes (y-axis) against smoking status and quitting time (x-axis) of ex-smokers at age-53 (1999). Observe how a >10 year quitting time leads to a reversal in DNA methylation, resulting in levels similar to those observed in never-smokers.

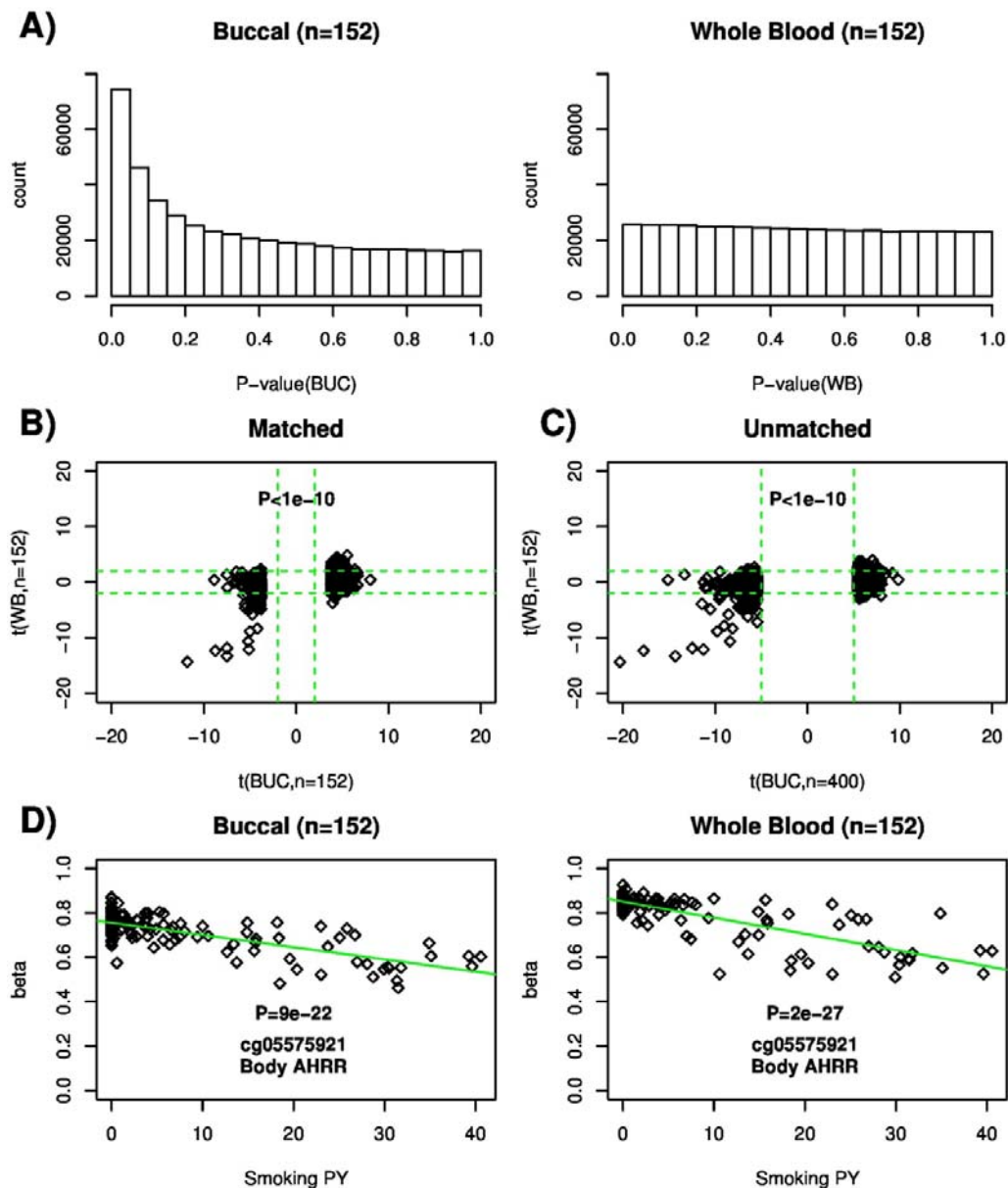


**eFigure 4. Singular Value Decomposition analysis of the discovery set DNA methylation data matrix of 400 buccal samples and 479,491 CpGs. A)** Fraction of data variation explained by the top significant components, where the number of significant components was estimated using RMT (see text). Approx. 55% of the data variation is explained by the top component. **B)** P-value association heatmap between biological and technical factors with the top components of variation. Color depth represents different significance levels (darkred:  $P < 1e-10$ , red:  $P < 1e-5$ , orange:  $P < 1e-3$ , pink:  $P < 0.05$ , white:  $P > 0.05$ ). Kruskal-Wallis test

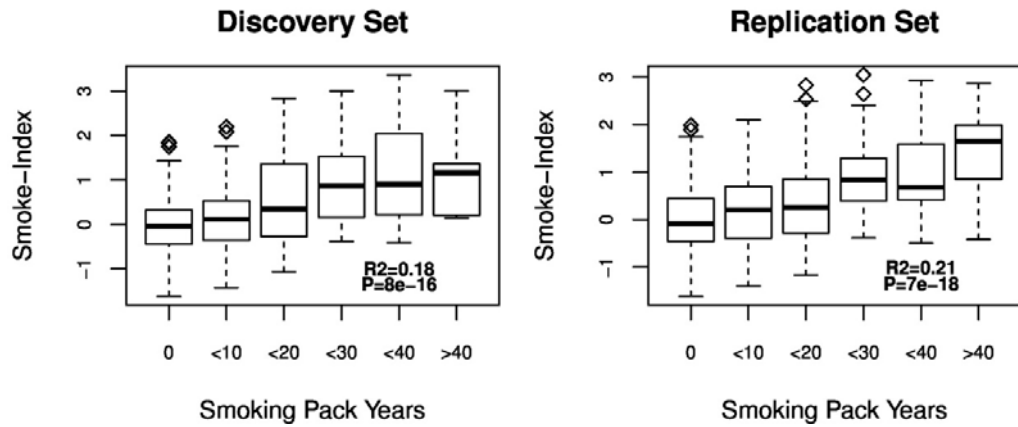
(binary/categorical variable) or linear regression (numerical variable) was used depending on the nature of the factor. Technical factors include the sentrix position (SentrixPos), sentrix ID and bi-sulphite conversion (BSC) efficiency. Biological/Epidemiological factors included prospective cancer status (Cancer), type of tumor developed after sample collection (TumType), if tumour developed was invasive (TumInv), body mass index at age 53 (BMI-53), body mass index at age 12 (BMI-12), smoking pack years (SPY), smoking status at age 53 (SmokStats53: current, ex- or never smoker), telomere length (Telom\_len), exercise levels at age 53 (Exer53: never, 1-4 or 5+ times per week), current versus never smokers at age-53 (Curr\_nev), ex-smokers versus never-smokers at age-53 (Ex\_nev), age at menarche (Menarche), age of menopause (Menopause), mammographic density (Mammogram), area of dense tissue (DAREA), area of delimited projected breast (BAREA), weight at birth (Birth\_wei), total number of children (Children\_num), age of 1<sup>st</sup> pregnancy (1stPregnancyAge), oral contraceptive use (oral\_contra\_use), duration of oral contraceptive use (Contra\_dur). Observe how the top component correlates with SPY and parity (number of children). Detailed P-values were SPY ( $P=3e-5$ ) and parity ( $P=0.003$ ) with SPY the stronger predictor of PC1 in a multivariate model that included parity.



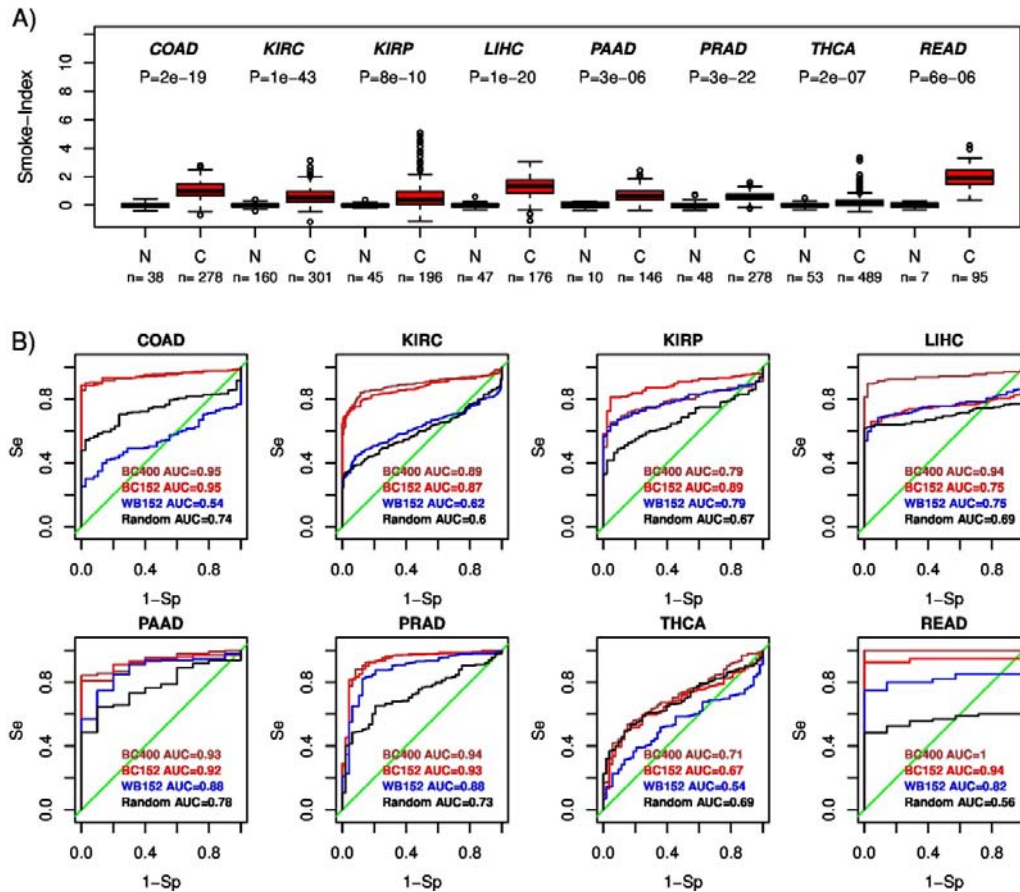
**eFigure 5. Correction for cellular heterogeneity using RefFreeEWAS in the discovery buccal sample set (n=400).** **A)** Histograms of unadjusted (i.e. no correction for tissue heterogeneity) and adjusted P-values (as estimated using the RefFreeEWAS R-package [13]). **B)** Volcano plots of the unadjusted and adjusted (RefFreeEWAS) analysis. Green dashed line denotes the line of Bonferroni significance ( $P = 0.05/479491 \sim 1e-7$ ). **C) Left panel:** Scatterplot of adjusted (RefFreeEWAS) versus unadjusted t-statistics for the 1501 smoking-associated CpGs which passed the Bonferroni threshold  $P < 1e-7$  in the unadjusted analysis. Unadjusted t-statistics derive from linear regressions of CpG methylation profiles against smoking pack years adjusted only for bisulfite conversion efficiency variations. Adjusted t-statistics derive from the RefFreeEWAS model, which corrects for possible changes in cell-type composition. **Right panel:** Scatterplot of adjusted versus unadjusted  $-\log_{10}(Q\text{-values})$  (i.e.  $-\log_{10}(\text{FDR})$ ) for the 1501 smoking-associated CpGs. The green dashed lines indicates the line  $Q = \text{FDR} = 0.05$ .



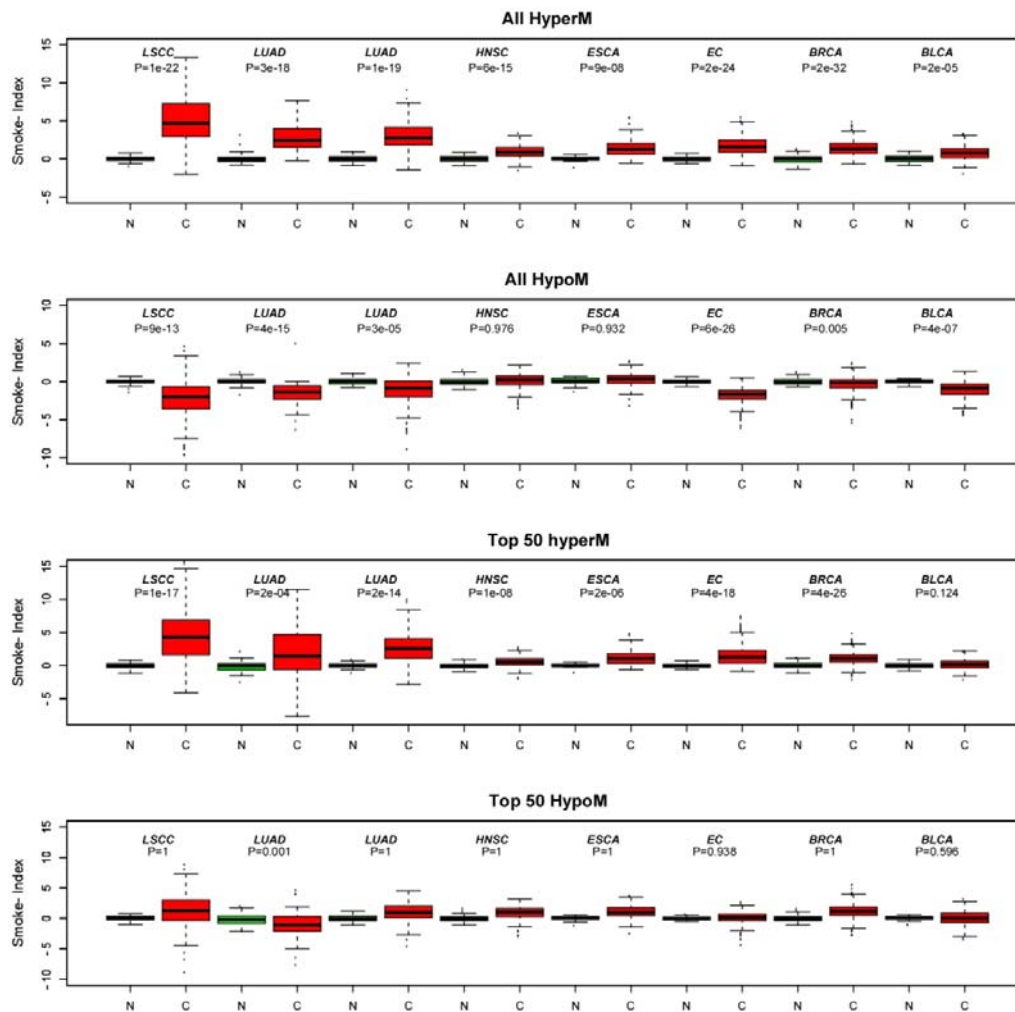
**eFigure 6. Comparison of Buccal and Whole Blood smoking DNA methylation signatures:** **A)** Histograms of smoking associated P-values derived from the matched n=152 buccal and whole blood sets. **B)** Scatterplot of the linear regression DNA methylation t-statistics of smoking-associated CpGs derived from the n=152 buccal subset (x-axis), against those derived from the matched whole blood samples. P-value of agreement is from a Fisher's exact test. **C)** Scatterplot of the linear regression DNA methylation t-statistics of the 1501 smoking-associated CpGs in the discovery set (x-axis), against the corresponding t-statistics derived from the 152 whole blood sample set (y-axis). P-value of agreement is from a Fisher's exact test. **D)** The methylation profile of the top ranked CpG, mapping to the gene body of AHRR, common to both the buccal and whole blood set, as a function of smoking pack years. P-value from a linear regression is given.



**eFigure 7. Linear correlation between smoking index and smoking pack years.** From left to right, panels represent the results in the discovery (n=400 buccals) and (n=390 buccals) replication cohorts. The R-square and P-values derived from a linear regression are indicated. For visualization purposes, smoking pack years (SPY) has been categorized into 6 groups as indicated (i.e. samples with SPY < 10 means women with 0<SPY≤10).

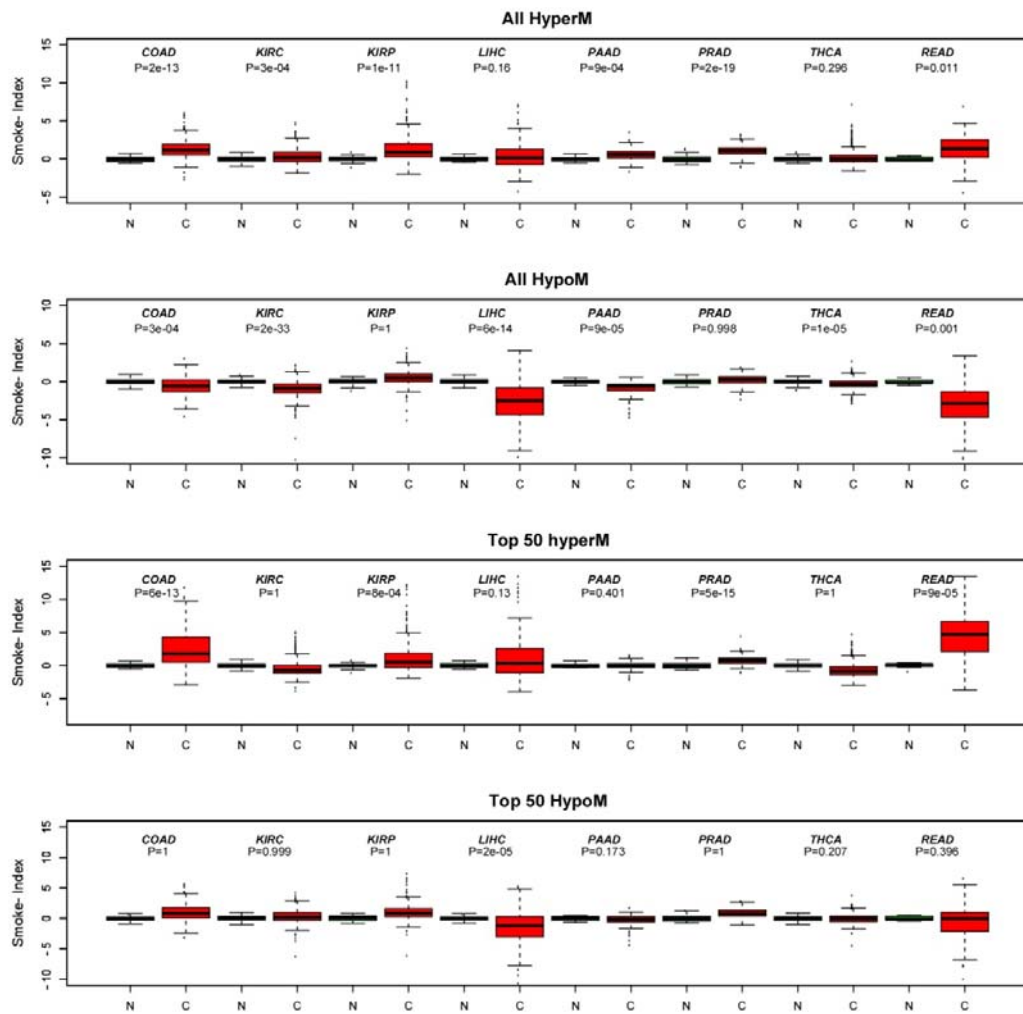


**eFigure 8. The smoking index is aggravated in cancer: A)** Boxplots comparing the smoking index of cancers (C, red) to their respective normal tissue (N, green) for 8 independent TCGA data sets encompassing the following cancers: COAD (colon adenocarcinoma), KIRC (kidney renal carcinoma), KIRP (kidney renal papilloma carcinoma), LIHC (liver hepatocarcinoma), PAAD (pancreatic adenocarcinoma), PRAD (prostate adenocarcinoma), THCA (thyroid cancer), READ (rectum adenocarcinoma). The number of samples in each category is given above lower x-axis. P-values are from a Wilcoxon rank sum test. The smoking index for each sample was computed using the 1501 smoking-associated CpGs derived from the discovery set of 400 buccal samples. **B)** Corresponding ROC and AUC analysis for each of the 8 datasets and for three different smoking indices: brown-smoking index derived from the original 400 buccal samples; orange-smoking index derived from the 152 matched buccal samples; blue-smoking index derived from the 152 matched blood samples; black-smoking index derived from a random 1501 CpG signature.

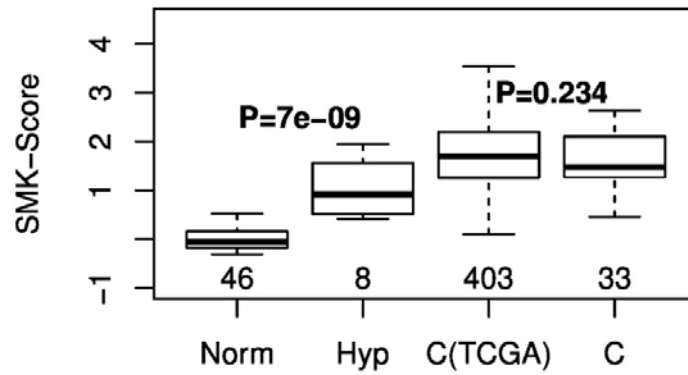


**eFigure 9. The smoking index across normal/cancer sets (part-1), as evaluated by restricting to four different CpG subsets from the full 1501 smoking-associated DNAm signature.** From top to bottom, we show the results restricting to the hypermethylated subset, the hypomethylated subset, and the top-50 ranked hyper- and hypo-methylated sites. One-tailed Wilcoxon-rank sum test P-values are given.

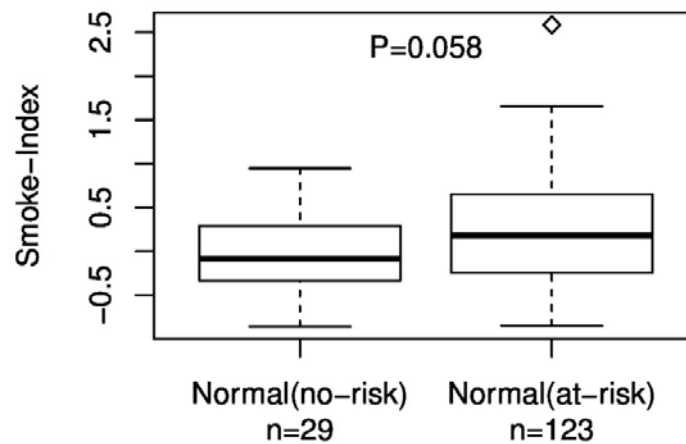




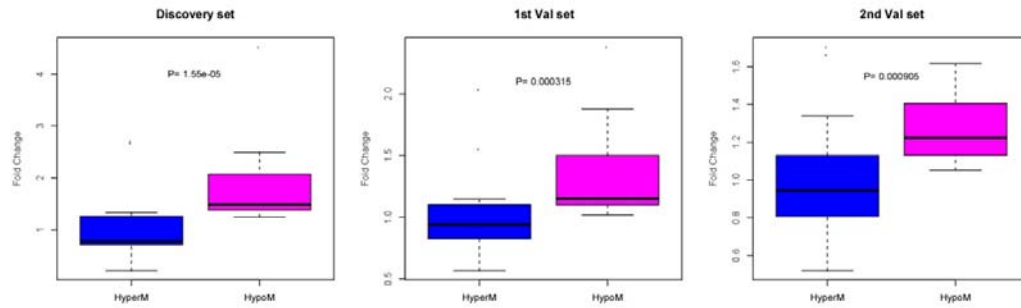
**eFigure 10. The smoking index across normal/cancer sets (part-2), as evaluated by restricting to four different CpG subsets from the full 1501 smoking-associated DNAm signature.** From top to bottom, we show the results restricting to the hypermethylated subset, the hypomethylated subset, and the top-50 ranked hyper- and hypo-methylated sites. One-tailed Wilcoxon-rank sum test P-values are given.



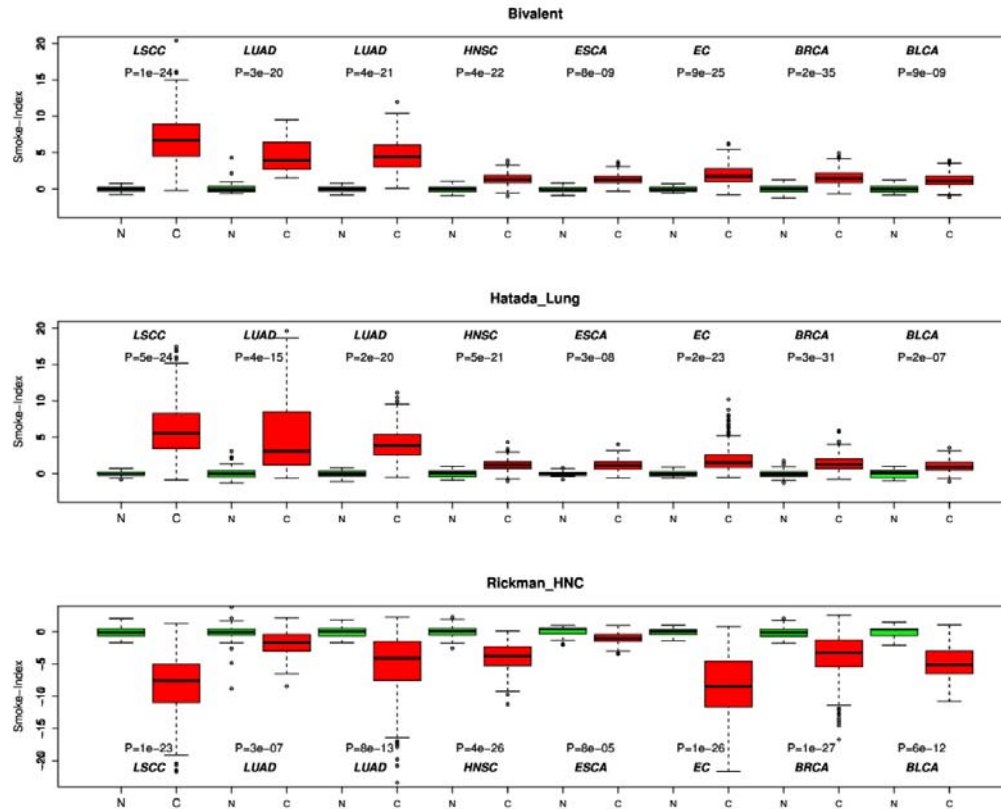
**eFigure 11. The smoking index as evaluated in endometrial carcinogenesis.** Illumina 450k data was available for two different studies: the TCGA study (46 normals + 403 endometrial cancers) and our own study (8 hyperplasias + 33 endometrial cancers). The smoking index was evaluated in each of these samples using the normal samples from the TCGA as reference. We quote two P-values from a Wilcoxon rank sum test, comparing the normal to the hyperplasias and another comparing the cancers from the two different studies. Attesting to the robustness of the procedure, the latter P-value is not significant, whereas hyperplasias show a significant increase compared to normals. This increase is unlikely to be due to a batch effect since the cancers from each study show comparable smoking index values. Number of samples in each group is given above x-axis.



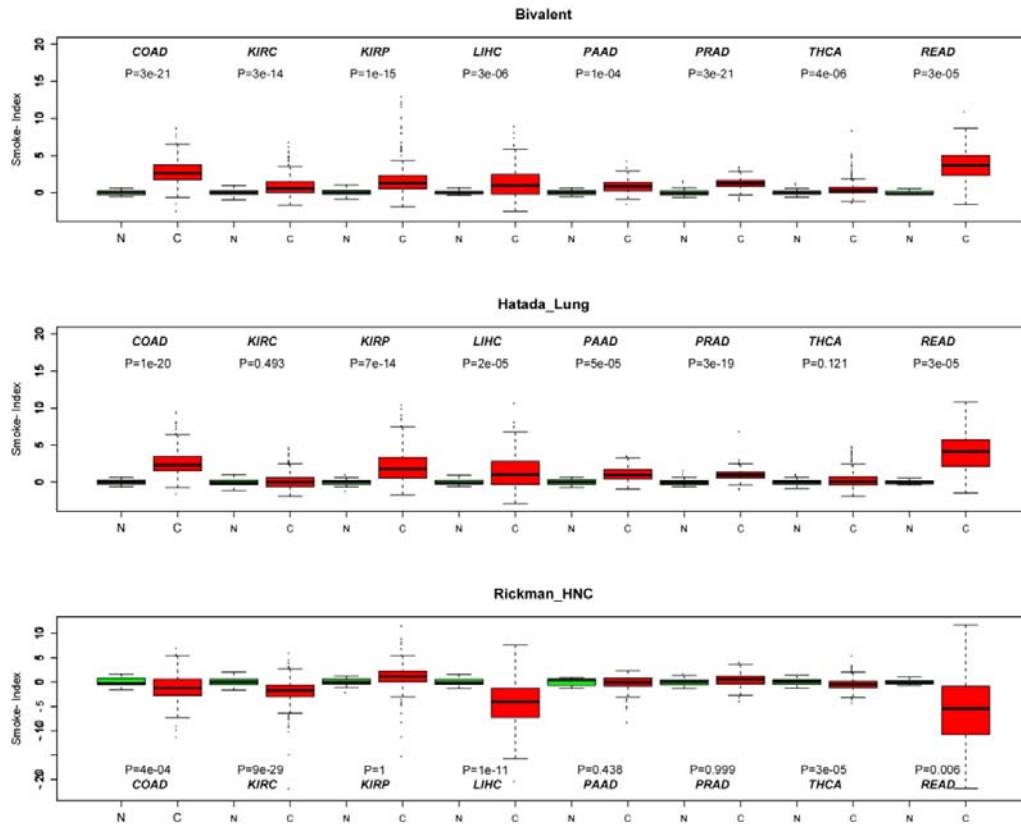
**eFigure 12. The smoking index evaluated in a series of 152 cytologically normal cervical smear samples.** The cervical smear samples were all cytologically normal, with 29 samples being HPV- and free of neoplastic progression for 3 years after sample collection (no-risk). The rest of samples (at-risk) were either HPV+ or progressed to a cervical intraepithelial neoplasia of grade 2 or higher within 3 years after sample collection. P-value is from a one-tailed Wilcoxon rank sum test (alternative hypothesis is that the index is higher in the at-risk group). All samples were generated with Illumina Infinium 27k beadarrays.



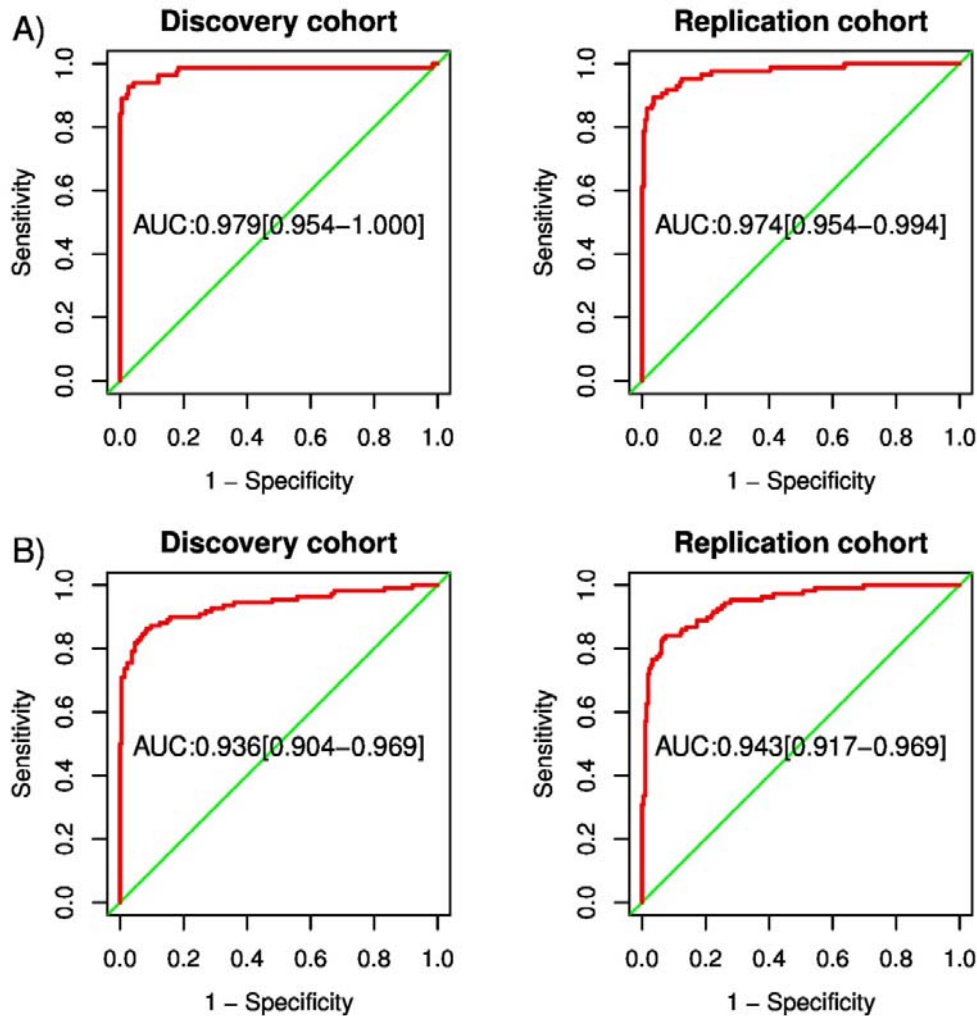
**eFigure 13. Functional significance of smoking DNAm signature.** Comparison of smoking-associated fold-changes, as published by Bosse et al [24], of genes with smoking-associated hyper or hypomethylation CpGs (within 200bp of TSS of gene) in buccal cells as determined here. See eTable 6 for details. Results are shown for the 3 independent data sets (n=344, n=285, n=244) considered in Bosse et al. P-value is from a Wilcoxon-rank sum test. Observe how the mean fold-change is less than 1 for hypermethylated TSS200 sites, whilst it is higher than 1 for hypomethylated TSS200 sites.



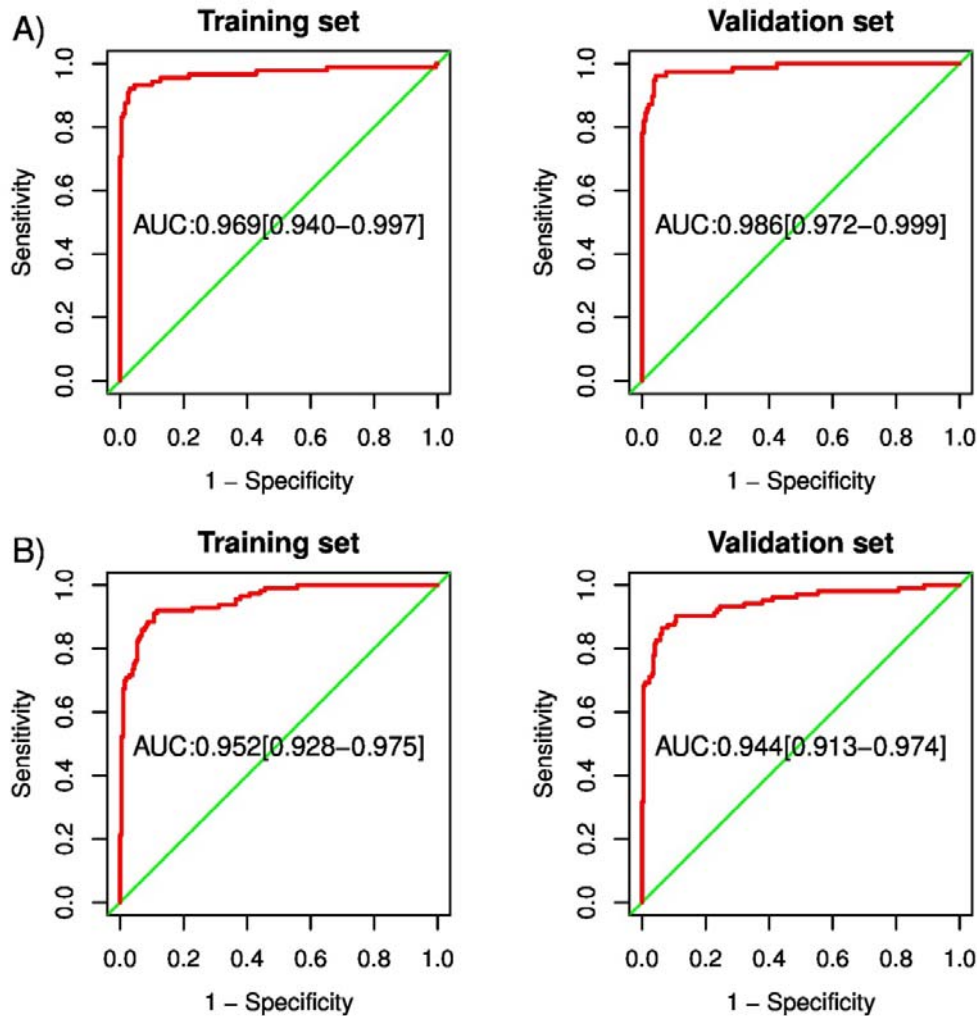
**eFigure 14. The smoking index from three GSEA-enriched DNAm subsignatures in the normal cancer data sets (part-1).** The three GSEA enriched categories were (i) bivalent genes in hESCs (“Bivalent”), (ii) genes hypermethylated in lung cancer as reported in Hatada et al (“Hatada\_Lung”) and (iii) genes hypomethylated and overexpressed in a Head&Neck Cancer subset (“Rickman\_HNC”). Red boxplots are cancers and green boxplots are the respective normal tissues across the following cancer types: LSCC (lung squamous cell carcinoma), LUAD (lung adenocarcinoma), HNSC (head&neck squamous carcinoma), ESCA (esophageal carcinoma), EC (endometrial cancer), BRCA (breast cancer), BLCA (bladder cancer). The smoking index for each sample was computed using the overlap between the 1501 smoking-associated CpGs derived from the buccal discovery cohort and the CpGs from these three different DNAm signatures. P-values are from a Wilcoxon rank sum test.



**eFigure 15. The smoking index from three GSEA-enriched DNAm subsignatures in the normal cancer data sets (part-2).** The three GSEA enriched categories were (i) bivalent genes in hESCs (“Bivalent”), (ii) genes hypermethylated in lung cancer as reported in Hatada et al (“Hatada\_Lung”) and (iii) genes hypomethylated and overexpressed in a Head&Neck Cancer subset (“Rickman\_HNC”). COAD (colon adenocarcinoma), KIRC (kidney renal carcinoma), KIRP (kidney renal papilloma carcinoma), LIHC (liver hepatocarcinoma), PAAD (pancreatic adenoma carcinoma), PRAD (prostate adenoma carcinoma), THCA (thyroid cancer), READ (rectum adenocarcinoma). Red boxplots are cancers and green boxplots are the respective normal tissues across the following cancer types: The smoking index for each sample was computed using the overlap between the 1501 smoking-associated CpGs derived from the buccal discovery cohort and the CpGs from these three different DNAm signatures. P-values are from a Wilcoxon rank sum test.



**eFigure 16. Prediction of smoking status using DNA methylation profiles based on an elastic net classifier.** Receiver operating characteristic (ROC) curves are shown for the elastic net classifier trained on a binary smoking phenotype. **A)** binary phenotype is current versus never smokers, and **B)** binary phenotype is smoking pack years larger or less than 10 (this threshold is motivated from the SVD analysis). From left to right, the panels represent the results in the discovery cohort, and the replication set. The prediction accuracy is indicated by the area under the curve (AUC) plus the 95% confidence intervals.



**eFigure 17. Prediction of smoking status from buccal DNA methylation profiles using an elastic net classifier, and using a different training/test set partition of the 790 buccal samples.** Receiver operating characteristic (ROC) curves are shown for the elastic net classifier trained on a binary smoking phenotype and using a different discovery/replication partition of the 790 buccal samples. Here, the training/discovery set was generated by randomly sampling beadchips so as to yield 400 samples, with the samples done on other beadchips constituting the validation/replication set. Thus, in this analysis, the samples from the training and validation sets were done on entirely different beadchips. **A)** binary phenotype is current versus never smokers, and **B)** binary phenotype is smoking pack years larger or less than 10 (motivated from the SVD analysis). From left to right, the panels represent the results in the training and validation sets, respectively. The prediction accuracy is indicated by the area under the curve (AUC) plus the 95% confidence intervals.



**eTable 1. Statistics of association of the 1501 smoking-associated CpGs.** Table lists the CpG ID from the Illumina 450k Beadchip, the corresponding UCSC RefGene Name, relative location of the CpG to the host gene (UCSC RefGene group), whether related to enhancer, regulatory feature, DNase I hypersensitive site (DHS), t-statistic, P-value and the corrected Q value for the discovery set (DISC) are provided. In addition, the t-statistic and P-value obtained in the replication set (REP) is also provided.

IlmnID	UCSC_RefGene_Name	UCSC_RefGene_Group	Enhancer	Regulatory_Feature_Group	DHS	t (DISC-n=400)	P (DISC-n=400)	Q (DISC-n=400)	t(REP-n=390)	P(REP-n=390)
cg05575921	AHRR	Body	TRUE		NA	-20.34	1.04E-59	2.99E-54	-17.09	6.17E-47
cg05951221			NA		NA	-17.77	1.06E-49	1.53E-44	-16.39	3.08E-44
cg02162897	CYP1B1	Body	NA	NonGene_Associated_Cell_type_specific	NA	-15.14	1.74E-39	1.68E-34	-15.28	6.05E-40
cg21566642			NA		NA	-14.33	2.27E-36	1.64E-31	-13.29	2.14E-32
cg20408276	CYP1B1	Body	NA	NonGene_Associated_Cell_type_specific	NA	-13.34	1.33E-32	7.65E-28	-15.03	5.73E-39
cg03636183	F2RL3	Body	NA		TRUE	-12.5	1.64E-29	7.91E-25	-11.37	2.16E-25
cg14753356			TRUE		TRUE	-11.44	1.16E-25	4.78E-21	-9.22	4.05E-18
cg01940273			NA		NA	-11.29	3.89E-25	1.40E-20	-9.43	8.99E-19
cg16323911			TRUE		NA	-11.24	5.82E-25	1.87E-20	-11.22	7.31E-25
cg10880599	GPX2	Body	NA		NA	-11.1	1.80E-24	5.20E-20	-11.82	5.71E-27
cg23167235			NA		NA	-10.93	7.32E-24	1.92E-19	-11.61	3.09E-26
cg26516004	CYP1A1	TSS1500	NA		NA	-10.82	1.80E-23	4.33E-19	-9.32	1.94E-18
cg06644428			NA	Unclassified_Cell_type_specific	NA	-10.53	1.76E-22	3.91E-18	-9.65	1.71E-19
cg13378563	KCNIP3	Body	NA		NA	-10.02	9.59E-21	1.98E-16	-8.83	7.30E-17
cg12802310	CYP1B1	TSS1500	TRUE		NA	-9.95	1.62E-20	3.12E-16	-11.52	6.36E-26

cg14663177	C2orf58	Body	TRUE		TRUE	9.82	4.52E-20	8.16E-16	10.93	8.11E-24
cg06126421			TRUE		TRUE	-9.79	5.44E-20	9.24E-16	-8.9	4.34E-17
cg23160522	CYP1A1	5UTR	NA		NA	-9.76	7.18E-20	1.15E-15	-9.21	4.47E-18
cg19753864			TRUE		NA	-9.69	1.16E-19	1.76E-15	-10.28	1.36E-21
cg17248487	AHRR	Body	TRUE	Unclassified_Cell_type_specific	TRUE	-9.56	3.09E-19	4.47E-15	-9.29	2.45E-18
cg11554391	AHRR	Body	NA		NA	-9.56	3.28E-19	4.51E-15	-9.43	8.74E-19
cg00565882	CYP1B1	Body	NA		NA	-9.5	4.81E-19	6.32E-15	-10.94	7.41E-24
cg12101586	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	NA	-9.45	7.19E-19	9.03E-15	-7.86	5.90E-14
cg06035270			TRUE	Unclassified	NA	9.18	5.28E-18	6.36E-14	10.31	1.08E-21
cg11879188	ABO	Body	NA		NA	-9.1	9.91E-18	1.14E-13	-8.56	4.85E-16
cg18092474	CYP1A1	TSS1500	NA		NA	-9.03	1.66E-17	1.81E-13	-8.01	2.14E-14
cg03329539			NA		NA	-9.02	1.69E-17	1.81E-13	-6.32	8.99E-10
cg20004659	ABCC3;ABCC3	Body;Body	TRUE		TRUE	-9	1.95E-17	2.01E-13	-7.88	5.37E-14
cg11924019	CYP1A1	TSS1500	NA		NA	-8.94	3.19E-17	3.17E-13	-7.42	1.07E-12
cg26672604			TRUE		NA	-8.77	1.09E-16	1.05E-12	-9.56	3.25E-19
cg00370022	CYP1A1	Body	NA		NA	-8.69	1.83E-16	1.68E-12	-8.05	1.61E-14
cg27492584			TRUE	Unclassified_Cell_type_specific	TRUE	-8.69	1.86E-16	1.68E-12	-7.76	1.14E-13
cg25189904	GNG12	TSS1500	NA		TRUE	-8.57	4.31E-16	3.77E-12	-8.72	1.60E-16
cg21715189	CYP1B1	TSS1500	TRUE		NA	-8.56	4.66E-16	3.96E-12	-9.22	4.18E-18
cg05062676	CYP1B1	TSS1500	TRUE		NA	-8.54	5.46E-16	4.50E-12	-8.99	2.21E-17
cg16340268	ITPKB	5UTR	NA		NA	8.47	8.62E-16	6.89E-12	9.37	1.40E-18
cg04802238	SLC7A5	Body	NA	Unclassified_Cell_type_specific	NA	-8.47	8.83E-16	6.89E-12	-8.98	2.43E-17
cg12557254	NDST1	Body	NA		NA	-8.42	1.25E-15	9.51E-12	-6.01	5.12E-09

cg04144218	AUTS2;AUTS2;AUTS2	Body;Body;Body	TRUE		NA	-8.4	1.47E-15	1.06E-11	-9.71	1.07E-19
cg21161138	AHRR	Body	NA		NA	-8.4	1.47E-15	1.06E-11	-8.61	3.35E-16
cg26144569	CYP1B1	TSS1500	TRUE		NA	-8.32	2.59E-15	1.83E-11	-8.9	4.33E-17
cg14454127	AHRR	Body	TRUE	Unclassified_Cell_type_specific	TRUE	-8.31	2.67E-15	1.83E-11	-8.01	2.20E-14
cg06492111	SLC7A5	Body	NA		NA	-8.19	6.26E-15	4.20E-11	-8.34	2.31E-15
cg09935388	GFI1;GFI1;GFI1	Body;Body;Body	TRUE		NA	-8.13	9.41E-15	6.17E-11	-8.2	5.76E-15
cg03742137	AGAP1;AGAP1	Body;Body	NA	Unclassified	TRUE	8.1	1.19E-14	7.61E-11	7.86	6.11E-14
cg15269394	ATP6V0A1;ATP6V0A1;ATP6V0A1	Body;Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	8.02	2.04E-14	1.28E-10	7.42	1.08E-12
cg05033295			TRUE		NA	-8.01	2.10E-14	1.29E-10	-8.38	1.71E-15
cg11233000	CASZ1;CASZ1	5UTR;5UTR	TRUE	Unclassified_Cell_type_specific	NA	7.94	3.47E-14	2.09E-10	8.52	6.59E-16
cg19723805			TRUE		NA	7.93	3.73E-14	2.20E-10	5.53	6.65E-08
cg00069417	SLC7A5	Body	NA		NA	-7.91	4.06E-14	2.35E-10	-7.89	5.02E-14
cg12920004			TRUE	Unclassified	TRUE	-7.9	4.49E-14	2.54E-10	-8.38	1.65E-15
cg10468961	NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.89	4.91E-14	2.72E-10	10.57	1.43E-22
cg11439308			TRUE		NA	-7.88	4.99E-14	2.72E-10	-8.04	1.79E-14
cg16824126	CHADL;L3MBTL2	Body;3UTR	NA		NA	-7.86	6.01E-14	3.22E-10	-7.56	4.45E-13
cg01998750	FRMD4B	Body	NA		NA	7.84	6.46E-14	3.39E-10	9.14	7.49E-18
cg04482794	ITPKB	5UTR	NA		TRUE	7.83	7.20E-14	3.71E-10	10.28	1.30E-21
cg13570656	CYP1A1	TSS1500	NA	Unclassified_Cell_type	NA	-7.81	8.06E-14	4.08E-10	-6.67	1.15E-10

				_specific						
cg08003353			TRUE		TRUE	7.81	8.33E-14	4.14E-10	11.72	1.26E-26
cg02426623	TSPAN9;TSPAN9	5UTR;5UTR	TRUE		NA	-7.78	9.69E-14	4.74E-10	-8.72	1.60E-16
cg01278596	NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.77	1.08E-13	5.19E-10	10.34	8.16E-22
cg20082547	TGM6;TGM6	5UTR;1stExon	NA		NA	-7.76	1.12E-13	5.31E-10	-5.89	9.64E-09
cg27064337			TRUE		TRUE	7.76	1.17E-13	5.45E-10	9.02	1.74E-17
cg14389122	EDC3;EDC3;EDC3	Body;Body;Body	TRUE		NA	-7.75	1.24E-13	5.69E-10	-7.84	7.00E-14
cg00073090			NA	Promoter_Associated	NA	-7.74	1.30E-13	5.85E-10	-7.45	8.55E-13
cg14711690	ITPKB	Body	NA	Promoter_Associated	TRUE	7.73	1.38E-13	6.11E-10	9.18	5.68E-18
cg15992535	NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.7	1.69E-13	7.41E-10	9.84	4.01E-20
cg10801607	SLC3A1	Body	TRUE	Unclassified_Cell_type_specific	TRUE	7.69	1.76E-13	7.58E-10	6.55	2.27E-10
cg05652757	NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.69	1.86E-13	7.88E-10	10.08	6.13E-21
cg27560132			TRUE		NA	-7.68	1.89E-13	7.92E-10	-6.48	3.45E-10
cg23678985			TRUE		NA	-7.68	1.95E-13	8.05E-10	-10.22	2.21E-21
cg10513161	ABCC5;ABCC5	Body;Body	TRUE		NA	-7.66	2.17E-13	8.82E-10	-6.43	4.53E-10
cg24884265	NDST1	Body	NA		NA	-7.65	2.35E-13	9.43E-10	-5.58	5.11E-08
cg04972459			TRUE	Unclassified_Cell_type_specific	TRUE	7.65	2.40E-13	9.49E-10	7.99	2.45E-14
cg00227225	SEMA6D;SEMA6D;SEMA6D;	5UTR;5UTR;5UTR;5UTR;5UTR;5	NA	Unclassified_Cell_type_specific	TRUE	7.64	2.43E-13	9.49E-10	9.28	2.57E-18

	SEMA6D; SEMA6D; SEMA6D	UTR								
cg04764812			NA	Unclassified_Cell_type_specific	NA	7.63	2.68E-13	1.03E-09	7.5	6.46E-13
cg00781658	HNRNPUL1;HNRNPUL1	Body;Body	NA	Gene_Associated_Cell_type_specific	TRUE	7.63	2.71E-13	1.03E-09	7.78	1.04E-13
cg21489622	HIVEP2	5UTR	NA	Promoter_Associated	TRUE	7.62	2.82E-13	1.05E-09	9.39	1.16E-18
cg04264781	SLC7A5	Body	NA		NA	-7.62	2.85E-13	1.05E-09	-8.16	7.88E-15
cg24129626	CD300LG; CD300LG; CD300LG; CD300LG	TSS200;TSS200;TSS200;TSS200	TRUE	Unclassified	NA	7.61	3.11E-13	1.12E-09	8.84	6.56E-17
cg05157702	PIR;PIR	5UTR;5UTR	NA		NA	-7.61	3.11E-13	1.12E-09	-8.48	8.32E-16
cg22060611	NRG2;NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.6	3.18E-13	1.13E-09	9.6	2.40E-19
cg10791966	ALDH3A1; ALDH3A1; ALDH3A1	Body;Body;Body	NA		NA	-7.59	3.57E-13	1.26E-09	-5.35	1.71E-07
cg18033092	C11orf49; C11orf49; C11orf49; C11orf49	Body;Body;Body;Body	TRUE		NA	7.58	3.76E-13	1.31E-09	8.26	3.86E-15
cg05711474			TRUE		TRUE	7.58	3.83E-13	1.31E-09	7.81	8.42E-14
cg02905900	ACOT11;ACOT11	TSS1500;TSS1500	NA		TRUE	7.56	4.27E-13	1.45E-09	9.24	3.53E-18
cg05964212	SLC25A20	TSS1500	NA	Promoter_Associated	NA	7.52	5.57E-13	1.86E-09	7.19	4.77E-12
cg24805089	GRK6;GRK6;GRK6	Body;Body;Body	NA		NA	-7.52	5.60E-13	1.86E-09	-7.58	3.75E-13
cg26432350	NBEAL2	Body	NA	Gene_Asso	NA	7.51	6.03E-13	1.98E-09	9.89	2.71E-20

				ciated						
cg22936884	TPPP	3UTR	NA		NA	-7.49	6.52E-13	2.12E-09	-6.17	2.07E-09
cg07251887	LOC100130933;RECQL5	TSS1500;Body	NA		TRUE	-7.49	6.71E-13	2.15E-09	-8.07	1.41E-14
cg15999165	PAM;PAM;PAM;PAM	TSS200;TSS200;TSS200;TSS200	NA		NA	7.48	7.07E-13	2.24E-09	9.43	9.08E-19
cg14898623	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	7.47	7.82E-13	2.45E-09	7.43	1.00E-12
cg13167372			NA	Unclassified	NA	7.46	7.90E-13	2.45E-09	6.13	2.60E-09
cg04916091	JAK3	5UTR	NA	Unclassified	NA	7.46	8.25E-13	2.54E-09	8.48	8.28E-16
cg08697797	UGT1A10;UGT1A6;UGT1A8;UGT1A4;UGT1A3;UGT1A6;UGT1A9;UGT1A7;UGT1A1;UGT1A5	Body;Body;Body;Body;Body;Body;TSS200;Body	NA		NA	-7.45	8.67E-13	2.64E-09	-6.96	1.89E-11
cg17934130			NA		NA	-7.44	9.12E-13	2.72E-09	-4.93	1.31E-06
cg07945335	CD300LG;CD300LG;CD300LG;CD300LG	TSS200;TSS200;TSS200;TSS200	TRUE	Unclassified	NA	7.44	9.13E-13	2.72E-09	9.2	4.77E-18
cg14399183	GSN;GSN;GSN;GSN;GSN;GSN	5UTR;5UTR;5UTR;5UTR;5UTR;5UTR	NA		NA	7.42	1.02E-12	3.00E-09	5.31	2.02E-07
cg27200446	MDFI	5UTR	NA		TRUE	7.41	1.10E-12	3.21E-09	10.09	5.71E-21
cg21160290	ABO	Body	NA		NA	-7.4	1.22E-12	3.53E-09	-6.99	1.63E-11
cg23874600	UGT1A10;UGT1A6;	Body;1stExon;5UTR;B	NA		NA	-7.39	1.27E-12	3.63E-09	-7.22	3.75E-12

	UGT1A6; UGT1A9; UGT1A7; UGT1A8	ody;Body;B ody								
cg19479935			NA		NA	-7.39	1.31E-12	3.72E-09	-8.17	7.34E-15
cg00107629	DGKZ;DG KZ;DGKZ; DGKZ	Body;Body; Body;Body	TRUE	Gene_Associated	NA	7.38	1.34E-12	3.74E-09	9.57	3.14E-19
cg16374343	ABR;ABR	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	7.37	1.44E-12	4.01E-09	9.74	8.73E-20
cg08094280	SLC7A5	3UTR	NA		NA	-7.37	1.47E-12	4.04E-09	-7.95	3.16E-14
cg19353431			TRUE	Unclassified_Cell_type_specific	NA	-7.37	1.48E-12	4.04E-09	-5.59	4.81E-08
cg17228232	BAIAP2;B AIAP2;BAI AP2;BAIA P2	Body;Body; Body;Body	NA		NA	-7.35	1.61E-12	4.35E-09	-6.86	3.59E-11
cg15048832	TSC22D2	Body	NA		NA	7.35	1.63E-12	4.35E-09	5.93	7.72E-09
cg08139206			TRUE		TRUE	-7.34	1.75E-12	4.61E-09	-5.24	2.96E-07
cg24489015	LPO;LPO; LPO	5UTR;Body ;5UTR	NA		NA	7.34	1.76E-12	4.61E-09	8.17	7.24E-15
cg13912573	LOC10012 9066	Body	TRUE		TRUE	-7.34	1.78E-12	4.62E-09	-5.59	4.96E-08
cg10044101	VNN2	5UTR	NA		NA	7.34	1.81E-12	4.67E-09	8.85	6.05E-17
cg07554046			TRUE		NA	7.33	1.90E-12	4.82E-09	8.81	8.43E-17
cg07720851	KIAA0182; KIAA0182	5UTR;Body	NA	Promoter_Associated	NA	7.33	1.90E-12	4.82E-09	8.63	2.94E-16
cg07541559	ABTB2	Body	TRUE	Unclassified_Cell_type_specific	TRUE	7.31	2.11E-12	5.30E-09	7.37	1.45E-12
cg17619755	VARS	Body	NA		NA	7.3	2.22E-12	5.50E-09	8.2	6.02E-15
cg10357657	JAK3	5UTR	NA	Unclassified	TRUE	7.3	2.23E-12	5.50E-09	8.79	9.32E-17

cg04656424	FAM38A	Body	TRUE		TRUE	7.3	2.28E-12	5.58E-09	7.72	1.54E-13
cg03486383	SLC7A5	3UTR	NA		NA	-7.28	2.55E-12	6.19E-09	-7.76	1.13E-13
cg25467634	ARHGAP22	Body	TRUE		NA	7.28	2.62E-12	6.30E-09	6.87	3.40E-11
cg20390237			TRUE		NA	-7.25	3.12E-12	7.45E-09	-5.44	1.06E-07
cg17804100	HIVEP3;HIVEP3	5UTR;5UTR	TRUE	Unclassified	TRUE	7.23	3.44E-12	8.15E-09	7.32	2.07E-12
cg22549041	CYP1A1	TSS1500	NA		NA	-7.23	3.48E-12	8.17E-09	-4.23	3.09E-05
cg05590619			NA		TRUE	7.22	3.69E-12	8.59E-09	8.42	1.25E-15
cg10172887			TRUE		NA	-7.22	3.75E-12	8.59E-09	-4.89	1.57E-06
cg08490791			TRUE	Unclassified	NA	7.22	3.75E-12	8.59E-09	10.14	3.97E-21
cg17430979	JAKMIP1	Body	NA		NA	-7.22	3.80E-12	8.59E-09	-6.05	4.02E-09
cg19005335	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	7.22	3.81E-12	8.59E-09	7.92	4.02E-14
cg00278392			TRUE		NA	7.22	3.85E-12	8.61E-09	8.3	2.90E-15
cg10925364	GOT1L1	TSS200	NA		NA	-7.2	4.23E-12	9.34E-09	-6.19	1.87E-09
cg05486035			NA	Unclassified_Cell_type_specific	NA	7.2	4.24E-12	9.34E-09	7.82	7.55E-14
cg05345286	MDF1	Body	NA		TRUE	7.2	4.33E-12	9.40E-09	8.81	7.99E-17
cg08836861	NQO1;NQO1	Body;Body;Body	NA		NA	-7.2	4.35E-12	9.40E-09	-8.53	6.10E-16
cg19502457	GPX2	1stExon	NA		NA	-7.2	4.39E-12	9.40E-09	-8.06	1.52E-14
cg23079012			NA		NA	-7.2	4.39E-12	9.40E-09	-4.72	3.56E-06
cg24090911	AHRR	Body	TRUE	Gene_Associated_Cell_type_specific	TRUE	-7.19	4.44E-12	9.43E-09	-9.26	3.08E-18
cg26883837			TRUE		TRUE	-7.19	4.53E-12	9.51E-09	-6.97	1.79E-11
cg05971148	ACTB	Body	NA	Promoter_Associated	NA	7.19	4.54E-12	9.51E-09	5.94	7.65E-09
cg16450654	KCNIP3	Body	NA		NA	-7.19	4.63E-12	9.62E-09	-6.99	1.61E-11



cg05357229	UGT1A6; UGT1A10; UGT1A9; UGT1A6; UGT1A7; UGT1A8	Body;Body; Body;Body; Body;Body	TRUE		NA	-7.18	4.71E-12	9.67E-09	-6.91	2.66E-11
cg05441854	KIAA0182; KIAA0182	5UTR;Body	NA	Promoter_A ssociated	NA	7.18	4.72E-12	9.67E-09	8.98	2.48E-17
cg25103337	H6PD	TSS1500	NA		NA	7.17	5.19E-12	1.05E-08	7.86	6.01E-14
cg04328729	DIP2C	Body	NA		NA	-7.17	5.23E-12	1.05E-08	-6.42	4.95E-10
cg06071246	SLC7A5	3UTR	NA		NA	-7.16	5.43E-12	1.09E-08	-7.53	5.15E-13
cg20629021	CPT1A;C PT1A	Body;Body	NA		NA	-7.15	5.71E-12	1.14E-08	-7.8	9.06E-14
cg26849830	SSH1	3UTR	TRUE		NA	-7.15	6.00E-12	1.18E-08	-7.05	1.12E-11
cg04939302			TRUE		NA	-7.15	6.02E-12	1.18E-08	-5.42	1.17E-07
cg26723054	KIAA0182; KIAA0182	5UTR;Body	NA	Promoter_A ssociated	NA	7.14	6.30E-12	1.23E-08	9.72	9.67E-20
cg19421526	CRTAC1	Body	TRUE		NA	7.12	7.03E-12	1.36E-08	7.96	2.95E-14
cg23409608	PVT1	Body	TRUE		NA	-7.12	7.26E-12	1.40E-08	-7.46	8.52E-13
cg16786136			TRUE		NA	-7.11	7.69E-12	1.47E-08	-6.67	1.12E-10
cg27135163	SLC7A5	3UTR	NA		NA	-7.1	7.96E-12	1.51E-08	-7.99	2.47E-14
cg02898994	TGM6	TSS200	NA		NA	-7.09	8.44E-12	1.59E-08	-6.83	4.31E-11
cg09561663	TGM3	TSS200	NA		NA	-7.09	8.69E-12	1.63E-08	-6.39	5.82E-10
cg25247520	MIR1204; PVT1	TSS200;Bo dy	NA		NA	-7.08	8.92E-12	1.66E-08	-7.98	2.69E-14
cg05631486	TPPP	3UTR	NA		NA	-7.06	1.05E-11	1.93E-08	-5.82	1.40E-08
cg16021428	ADCY2	TSS1500	NA		NA	7.06	1.05E-11	1.93E-08	9	2.07E-17
cg04964062			NA	Unclassifie d	TRUE	7.06	1.06E-11	1.93E-08	5.66	3.33E-08
cg23209976			TRUE		NA	7.04	1.18E-11	2.14E-08	7.35	1.65E-12
cg20911180	GUCY2E	Body	TRUE		TRUE	7.04	1.19E-11	2.14E-08	8.04	1.72E-14
cg03789645	CUL1	TSS1500	NA		NA	7.03	1.20E-11	2.14E-08	9.23	3.99E-18
cg05315206	JAK3	5UTR	NA	Unclassifie	TRUE	7.03	1.21E-11	2.14E-08	8.5	7.65E-16

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cg04583842	BANP;BANP	Body;Body	NA	Unclassified	NA	7.03	1.22E-11	2.14E-08	6.45	4.23E-10
cg17924476	AHRR	Body	NA		NA	7.03	1.22E-11	2.14E-08	10.31	1.07E-21
cg23363971	IKZF4;IKZF4	1stExon;5UTR	TRUE	Promoter_Associated	NA	7.03	1.24E-11	2.17E-08	8.72	1.58E-16
cg04605590			TRUE		NA	7.02	1.28E-11	2.23E-08	6.77	6.16E-11
cg24313303	PIGV	TSS1500	NA	Promoter_Associated	NA	7.02	1.35E-11	2.34E-08	6.8	5.11E-11
cg20951255			TRUE	Unclassified_Cell_type_specific	NA	7.01	1.42E-11	2.43E-08	7.56	4.33E-13
cg25774643	SCT	TSS200	NA	Unclassified_Cell_type_specific	NA	6.99	1.61E-11	2.74E-08	6.65	1.26E-10
cg02583484	HNRNPA1;HNRNPA1L-2;HNRNPA1	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-6.98	1.69E-11	2.86E-08	-6.88	3.15E-11
cg24862483	CD300LG;CD300LG;CD300LG;CD300LG	TSS200;TSS200;TSS200;TSS200	TRUE	Unclassified	NA	6.96	1.88E-11	3.17E-08	8.34	2.33E-15
cg24398933	CGN	Body	TRUE		NA	-6.95	2.04E-11	3.43E-08	-7.54	4.93E-13
cg19589396			TRUE	Unclassified_Cell_type_specific	TRUE	-6.95	2.07E-11	3.45E-08	-6.26	1.23E-09
cg00159243	SELPLG	5UTR	TRUE	Promoter_Associated	TRUE	6.94	2.10E-11	3.49E-08	7.26	2.95E-12
cg26337070	ATOX1	Body	TRUE		NA	-6.94	2.23E-11	3.68E-08	-6.27	1.20E-09
cg03993839	CES1;CES1;CES1	Body;Body;Body	NA		NA	-6.93	2.31E-11	3.80E-08	-7.91	4.39E-14
cg25720755	CD300LG;CD300LG;CD300LG;CD300LG	5UTR;5UTR;1stExon;1stExon;5UTR;5UTR;1	TRUE	Unclassified	NA	6.93	2.35E-11	3.84E-08	8.9	4.18E-17

	CD300LG; CD300LG; CD300LG; CD300LG	stExon;1stE xon								
cg10691866	TPST1	Body	TRUE		NA	-6.92	2.48E-11	4.01E-08	-6.13	2.56E-09
cg26381210	BMPR1A	5UTR	TRUE		NA	6.92	2.49E-11	4.01E-08	6.01	5.07E-09
cg19930417	SECTM1	3UTR	TRUE	Unclassified	NA	6.92	2.52E-11	4.04E-08	8.42	1.33E-15
cg15722293			TRUE	Unclassified	TRUE	6.91	2.59E-11	4.11E-08	8.23	4.83E-15
cg08521677	PER1	5UTR	NA	Promoter_Associated	NA	6.91	2.59E-11	4.11E-08	9.68	1.36E-19
cg05598363	C5orf32	TSS1500	NA	Promoter_Associated	NA	6.91	2.64E-11	4.16E-08	9.51	4.67E-19
cg04554564	CYTSB;C YTSB	TSS200;TS S200	NA		NA	-6.89	2.88E-11	4.53E-08	-6.54	2.47E-10
cg13110239	CSNK1E; CSNK1E	5UTR;5UT R	TRUE		NA	6.89	2.91E-11	4.55E-08	9.19	5.30E-18
cg13698261	C9orf3	Body	TRUE		NA	-6.88	3.07E-11	4.76E-08	-6.21	1.67E-09
cg02009088	NRG2;NR G2;NRG2; NRG2	Body;Body; Body;Body	NA		TRUE	6.88	3.18E-11	4.91E-08	9.28	2.72E-18
cg02839029	BAIAP2;B AIAP2;BAI AP2;BAIA P2	Body;Body; Body;Body	NA		NA	-6.87	3.33E-11	5.11E-08	-6.84	3.98E-11
cg05486924	C3orf21	Body	TRUE		NA	6.86	3.45E-11	5.26E-08	8.44	1.13E-15
cg14248553			NA		NA	6.86	3.54E-11	5.38E-08	8.45	1.02E-15
cg15935965			TRUE		NA	6.86	3.57E-11	5.40E-08	7.68	1.97E-13
cg03855388	CPT1A;C PT1A	Body;Body	NA		NA	-6.86	3.59E-11	5.40E-08	-8.05	1.67E-14
cg03228288	ZNF83;ZN F83;ZNF8 3;ZNF83;Z NF83;ZNF 83;ZNF83;	Body;TSS2 00;TSS200; TSS200;TS S200;TSS2 00;TSS200;	NA	Promoter_Associated	NA	6.85	3.66E-11	5.47E-08	5.07	6.83E-07

	ZNF83	TSS200								
cg00230120	LOC100292680	TSS1500	TRUE		TRUE	-6.85	3.79E-11	5.65E-08	-4.18	3.75E-05
cg20489946	NEK3;NEK3;NEK3;NEK3	5UTR;5UTR;5UTR;Body	NA		NA	6.84	3.92E-11	5.80E-08	6	5.36E-09
cg20537629	MAGI2	TSS1500	NA		NA	6.84	3.98E-11	5.85E-08	8.49	7.73E-16
cg07185131			TRUE		NA	6.84	4.01E-11	5.85E-08	6.6	1.69E-10
cg03310939	CUX1;CUX1;CUX1	Body;Body;Body	TRUE		TRUE	6.84	4.01E-11	5.85E-08	7.83	7.06E-14
cg02917867			NA	Promoter_Associated	TRUE	-6.84	4.04E-11	5.86E-08	-6	5.43E-09
cg10266490	ACOT11;ACOT11	TSS200;TSS200	NA	Unclassified	NA	6.84	4.10E-11	5.92E-08	7.43	9.88E-13
cg09643186	GPX2;GPX2	1stExon;5UTR	NA		NA	-6.83	4.13E-11	5.93E-08	-7	1.52E-11
cg08337959	TNNT3;TNNT3;TNNT3;TNNT3	Body;Body;Body;Body	NA		NA	-6.83	4.24E-11	6.06E-08	-5.68	2.97E-08
cg22409100	SLC8A1;SLC8A1;SLC8A1;SLC8A1	TSS1500;5UTR;TSS1500;TSS1500	TRUE		NA	6.83	4.26E-11	6.06E-08	5.19	3.70E-07
cg20360704	ANK2	TSS200	TRUE	Unclassified_Cell_type_specific	TRUE	6.82	4.38E-11	6.19E-08	7.36	1.61E-12
cg20758882			TRUE		TRUE	6.82	4.48E-11	6.31E-08	8.8	8.63E-17
cg01350077	MDFI;MDFI	5UTR;1stExon	NA	Unclassified_Cell_type_specific	TRUE	6.82	4.52E-11	6.31E-08	9.79	5.85E-20
cg26756193			TRUE		NA	-6.82	4.53E-11	6.31E-08	-6.08	3.47E-09
cg20780998			NA		NA	6.82	4.59E-11	6.38E-08	7.25	3.27E-12
cg20431135	MFAP4	TSS1500	TRUE		TRUE	6.81	4.80E-11	6.63E-08	7.95	3.19E-14
cg01127300			TRUE	Unclassified_Cell_type_specific	TRUE	-6.81	4.83E-11	6.64E-08	-5.81	1.55E-08

cg11751707	CYP1B1	5UTR	NA		NA	-6.81	4.90E-11	6.70E-08	-7.57	3.97E-13
cg14593418	TPPP	3UTR	NA		NA	-6.81	4.94E-11	6.72E-08	-5.51	7.32E-08
cg00279406	ITPKB	Body	NA		NA	6.8	5.13E-11	6.96E-08	7.86	6.00E-14
cg06665333	SLC7A5	Body	NA		NA	-6.8	5.24E-11	7.07E-08	-7.31	2.21E-12
cg19598567			NA		NA	6.79	5.56E-11	7.46E-08	7	1.54E-11
cg17833419			NA	Unclassified_Cell_type_specific	NA	-6.78	5.63E-11	7.50E-08	-4.93	1.35E-06
cg14701072	MCHR1;MCHR1	5UTR;1stExon	TRUE		NA	6.78	5.66E-11	7.50E-08	6.15	2.36E-09
cg00788739	TCN2	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	6.78	5.66E-11	7.50E-08	8.34	2.29E-15
cg11869499	POLG;POLG	Body;Body	NA	Promoter_Associated_Cell_type_specific	NA	6.78	5.70E-11	7.52E-08	6.48	3.49E-10
cg27099880			NA	Unclassified_Cell_type_specific	NA	-6.78	5.88E-11	7.72E-08	-7.3	2.35E-12
cg26330518	NEFM	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	6.78	5.93E-11	7.74E-08	7.31	2.16E-12
cg24118547	ZHX2	5UTR	TRUE		NA	-6.77	6.00E-11	7.80E-08	-6.32	8.87E-10
cg21766191	CIT	3UTR	NA		NA	-6.77	6.07E-11	7.86E-08	-5.35	1.69E-07
cg24471922	CTBP1;CTBP1	Body;Body	NA		NA	-6.76	6.42E-11	8.28E-08	-5.49	8.06E-08
cg14165909	LOXHD1	Body	NA	Unclassified_Cell_type_specific	NA	6.76	6.54E-11	8.39E-08	7.21	4.07E-12
cg00232453	EHMT2;EHMT2	Body;Body	NA		NA	6.76	6.59E-11	8.39E-08	6.43	4.67E-10
cg14817906	CNNM4	Body	TRUE	Promoter_Associated	NA	6.76	6.61E-11	8.39E-08	7.45	9.06E-13
cg23795217	ITGA5	Body	NA		NA	6.76	6.63E-11	8.39E-08	7.6	3.28E-13

cg22624391			NA	Unclassified_Cell_type_specific	NA	-6.75	6.74E-11	8.50E-08	-8.33	2.36E-15
cg23546512			TRUE		TRUE	6.75	6.87E-11	8.62E-08	8.3	2.89E-15
cg23576855	AHRR	Body	TRUE		NA	-6.75	6.96E-11	8.69E-08	-7.56	4.38E-13
cg26898087	GUCY1A2	Body	NA	Unclassified_Cell_type_specific	TRUE	6.75	7.00E-11	8.69E-08	5.73	2.34E-08
cg01380884	EDC3;EDC3;EDC3	3UTR;3UTR;3UTR	NA	Gene_Associated	NA	-6.75	7.02E-11	8.69E-08	-7.22	3.91E-12
cg17033086			NA	Unclassified_Cell_type_specific	NA	-6.74	7.53E-11	9.29E-08	-9.85	3.76E-20
cg16784943	ITPK1;ITPK1;ITPK1	Body;Body;Body	NA		NA	-6.73	7.66E-11	9.41E-08	-5.85	1.23E-08
cg27310710	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	6.73	7.77E-11	9.50E-08	7.3	2.35E-12
cg09524946			NA	Unclassified	NA	6.73	7.87E-11	9.59E-08	8.15	8.19E-15
cg16374080	SLC12A7	Body	NA	Unclassified_Cell_type_specific	NA	-6.73	7.96E-11	9.65E-08	-6.18	1.98E-09
cg15963095			TRUE		NA	-6.72	8.19E-11	9.89E-08	-6.38	6.37E-10
cg26824126	FXD5;FXD5;FXD5	Body;Body;Body;Body	NA		NA	6.72	8.32E-11	1.00E-07	4.62	5.48E-06
cg21791662	GLI2	Body	NA		TRUE	6.72	8.50E-11	1.02E-07	7.36	1.60E-12
cg01271455	PTPRN2;PTPRN2;PTPRN2	Body;Body;Body	NA	Unclassified_Cell_type_specific	TRUE	6.71	8.77E-11	1.05E-07	7.26	2.90E-12
cg02417427	SERINC5	Body	TRUE		NA	-6.71	8.87E-11	1.05E-07	-6.01	5.00E-09
cg15193228	SEC14L3	3UTR	NA		NA	-6.7	9.15E-11	1.08E-07	-4.82	2.21E-06
cg22459204	ANKRD33B	Body	NA		NA	6.69	1.01E-10	1.18E-07	6.13	2.63E-09
cg20828084	KIAA1199	TSS1500	NA	Unclassified_Cell_type	NA	-6.69	1.01E-10	1.18E-07	-6.23	1.43E-09

				_specific						
cg24126592	DGKZ;DGKZ;DGKZ;DGKZ	Body;Body;Body;Body	TRUE	Gene_Associated	TRUE	6.68	1.02E-10	1.19E-07	8.4	1.49E-15
cg08267072	CTAGE5;CTAGE5;CTAGE5;CTAGE5	Body;Body;Body;5UTR	NA		NA	-6.68	1.02E-10	1.19E-07	-6.16	2.14E-09
cg26843110	EDC3;EDC3;EDC3	Body;Body;Body	TRUE		NA	-6.68	1.04E-10	1.21E-07	-7.14	6.35E-12
cg13399816	GNG12	TSS1500	NA		TRUE	-6.68	1.05E-10	1.22E-07	-7.13	6.85E-12
cg19144497	ARID3B	5UTR	NA	Unclassified	NA	6.67	1.15E-10	1.32E-07	7.2	4.32E-12
cg25796129	NTN1	Body	TRUE		NA	-6.66	1.16E-10	1.33E-07	-4.91	1.49E-06
cg11040777	RPH3AL	Body	NA	Unclassified_Cell_type_specific	NA	-6.66	1.17E-10	1.33E-07	-3.63	0.00032801
cg14588642	LOC100130987;CLCF1;CLCF1	Body;Body;5UTR	TRUE		NA	6.66	1.18E-10	1.34E-07	8.2	5.85E-15
cg04876978	TMEM168	TSS1500	NA		NA	-6.65	1.23E-10	1.39E-07	-6.34	7.76E-10
cg04128884	PCGF3	5UTR	TRUE		TRUE	-6.64	1.31E-10	1.47E-07	-5.47	9.17E-08
cg20782117	SLC25A13;SLC25A13;SLC25A13	Body;Body;Body	TRUE		NA	6.64	1.34E-10	1.50E-07	8.2	5.85E-15
cg09678615	TOX3;TOX3	5UTR;Body	NA		NA	6.64	1.34E-10	1.50E-07	6.61	1.60E-10
cg16520038	MIR130A	TSS200	NA		TRUE	6.64	1.37E-10	1.52E-07	8.05	1.65E-14
cg05047401	SEMA4A	Body	TRUE	Gene_Associated_Cell_type_specific	TRUE	6.63	1.42E-10	1.58E-07	7.1	8.33E-12
cg05302489	VAR5	Body	NA		NA	6.62	1.48E-10	1.64E-07	5.81	1.52E-08
cg00850193	TLX1NB	Body	NA		NA	-6.62	1.48E-10	1.64E-07	-4.6	6.07E-06

cg03897436	UNKL	5UTR	NA		NA	-6.62	1.52E-10	1.66E-07	-5.05	7.44E-07
cg23420286	BMP7	Body	NA		NA	-6.62	1.52E-10	1.66E-07	-6.3	1.01E-09
cg22782986	ODZ4	TSS1500	NA		NA	6.62	1.54E-10	1.67E-07	8.23	4.85E-15
cg27035251	JAK3;JAK3	5UTR;1stExon	TRUE	Unclassified	TRUE	6.62	1.54E-10	1.67E-07	8.56	4.98E-16
cg08778851			NA	Unclassified_Cell_type_specific	NA	6.62	1.55E-10	1.67E-07	5.01	9.05E-07
cg16374411	SLC16A11	TSS1500	NA		NA	-6.61	1.56E-10	1.68E-07	-4.56	7.27E-06
cg03936449			NA	Unclassified_Cell_type_specific	NA	6.61	1.58E-10	1.69E-07	9.48	5.86E-19
cg05603985	SKI	1stExon	NA	Promoter_Associated	NA	-6.61	1.59E-10	1.70E-07	-5.48	8.47E-08
cg07021906	SLC7A5	Body	NA		NA	-6.6	1.71E-10	1.82E-07	-7.83	7.19E-14
cg06727242	RAD51L1; RAD51L1; RAD51L1	Body;Body; Body	TRUE		NA	6.6	1.72E-10	1.82E-07	8.01	2.15E-14
cg23278885	TGM6	TSS200	NA		NA	-6.6	1.73E-10	1.82E-07	-5.73	2.39E-08
cg16246573	CAPN10; CAPN10; CAPN10; CAPN10	Body;Body; Body;Body	NA		NA	-6.59	1.75E-10	1.84E-07	-5.77	1.85E-08
cg00211174	MCM2	Body	TRUE		NA	6.59	1.77E-10	1.86E-07	7.66	2.25E-13
cg12211856	SDCCAG8	Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.59	1.84E-10	1.92E-07	7.82	7.96E-14
cg26740494	MMP23A; MMP23B	TSS1500;TSS1500	NA		NA	-6.59	1.85E-10	1.92E-07	-6.29	1.05E-09
cg23369529	GADD45A	TSS1500	NA	Unclassified_Cell_type_specific	NA	6.58	1.89E-10	1.97E-07	5.32	1.92E-07
cg10176463			TRUE	Unclassified_Cell_type_specific	TRUE	6.58	1.92E-10	1.99E-07	6.8	5.03E-11



cg04018738	VARs	Body	NA		NA	6.58	1.95E-10	2.01E-07	7.92	4.05E-14
cg19998150	FRMD4A	Body	NA	Unclassified	NA	6.57	1.98E-10	2.03E-07	7.47	7.61E-13
cg22395765	PTPRN2; PTPRN2; PTPRN2	Body;Body; Body	NA	Unclassified_Cell_type_specific	TRUE	6.57	2.07E-10	2.12E-07	7.65	2.43E-13
cg17580935	MAGI1;MAGI1; MAGI1	Body;Body; Body	NA		NA	6.56	2.16E-10	2.20E-07	7.46	8.18E-13
cg20009354			TRUE	Unclassified_Cell_type_specific	TRUE	6.56	2.17E-10	2.21E-07	8.07	1.46E-14
cg19957162	FZD5	3UTR	NA		NA	6.55	2.24E-10	2.27E-07	7.57	4.17E-13
cg05911153	POU2F3	Body	TRUE		NA	6.55	2.33E-10	2.35E-07	6.15	2.37E-09
cg06373360			NA		NA	-6.54	2.37E-10	2.39E-07	-6.16	2.24E-09
cg01917657	PANX2;PANX2; PANX2	Body;Body; Body	NA	Unclassified_Cell_type_specific	NA	6.54	2.43E-10	2.43E-07	5.92	8.24E-09
cg07992044	LRP5	Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.53	2.50E-10	2.50E-07	9.35	1.56E-18
cg01832218	SURF6	Body	NA	Promoter_Associated_Cell_type_specific	NA	-6.53	2.51E-10	2.50E-07	-6.03	4.59E-09
cg01923999	FAM84B	3UTR	NA	Promoter_Associated_Cell_type_specific	NA	6.53	2.54E-10	2.51E-07	9.55	3.49E-19
cg15046507	LOC221122	Body	TRUE	Promoter_Associated	NA	6.53	2.54E-10	2.51E-07	8.2	5.95E-15
cg07830557	SH3GL1	Body	NA		NA	6.53	2.62E-10	2.58E-07	7.54	4.93E-13
cg05635754	JAK3	5UTR	TRUE	Unclassified	TRUE	6.52	2.64E-10	2.60E-07	7.87	5.48E-14
cg04433051	ABCC3	Body	TRUE		TRUE	6.52	2.66E-10	2.60E-07	7.83	7.23E-14
cg26039954	SPEN	Body	TRUE		NA	-6.52	2.69E-10	2.62E-07	-8.14	9.01E-15

cg09416908	ME3;ME3; ME3	TSS1500;T SS1500;TS S1500	NA		NA	6.52	2.70E-10	2.63E-07	7.04	1.18E-11
cg16198315	DACH1;D ACH1;DA CH1	Body;Body; Body	NA		NA	6.52	2.75E-10	2.66E-07	5.65	3.52E-08
cg05049329	ITPKB	Body	NA	Promoter_A ssociated	NA	6.51	2.81E-10	2.71E-07	6.87	3.29E-11
cg24804144			TRUE	Unclassifie d	TRUE	6.51	2.84E-10	2.73E-07	9	2.03E-17
cg12075928	PTK2;PTK 2	Body;Body	TRUE	Unclassifie d_Cell_type _specific	TRUE	-6.51	2.92E-10	2.80E-07	-4.6	6.01E-06
cg06023345	FAM84B	3UTR	NA	Promoter_A ssociated_ Cell_type_s pecific	NA	6.5	3.09E-10	2.95E-07	9.65	1.66E-19
cg11267879	CYP2F1	TSS1500	NA		NA	-6.5	3.10E-10	2.95E-07	-4.66	4.60E-06
cg08279008	POLR1A	Body	NA	Promoter_A ssociated	TRUE	6.49	3.15E-10	2.99E-07	6.28	1.08E-09
cg05673882	POLK	Body	TRUE		NA	-6.49	3.17E-10	3.00E-07	-6.25	1.34E-09
cg00780520	PVT1	Body	NA		NA	-6.49	3.21E-10	3.03E-07	-6.91	2.69E-11
cg22911054	CPT1A;C PT1A	5UTR;5UT R	NA		NA	-6.49	3.23E-10	3.04E-07	-5.58	5.04E-08
cg27241845			NA		TRUE	-6.49	3.26E-10	3.05E-07	-4.39	1.57E-05
cg01999938			TRUE		NA	6.49	3.27E-10	3.05E-07	8.02	2.05E-14
cg13475665	MAGI1;M AGI1;MAG I1	Body;Body; Body	NA		NA	6.49	3.27E-10	3.05E-07	6.6	1.70E-10
cg26764244	GNG12	TSS1500	NA		NA	-6.48	3.37E-10	3.13E-07	-6.95	2.05E-11
cg22542751	TCN2	TSS1500	NA	Unclassifie d_Cell_type _specific	TRUE	6.47	3.73E-10	3.45E-07	8.19	6.54E-15
cg09963123	FLJ13197; KLF3	Body;TSS1 500	NA		NA	6.46	3.79E-10	3.49E-07	6.88	3.15E-11
cg12768969	MYOM3	TSS1500	TRUE	Unclassifie	TRUE	6.46	3.82E-10	3.50E-07	7.91	4.41E-14

cg20149780	EFHD2	Body	NA	d Unclassified_Cell_type_specific	NA	-6.46	3.83E-10	3.50E-07	-3.61	0.00034974
cg00538298	MUC2	Body	NA		NA	-6.46	3.83E-10	3.50E-07	-5.62	4.13E-08
cg07045054	TMEM111	Body	NA		NA	-6.46	3.90E-10	3.55E-07	-6.68	1.08E-10
cg09853702			TRUE		NA	6.46	3.96E-10	3.59E-07	8.14	9.06E-15
cg10503298	CTBP1;CTBP1	Body;Body	NA		NA	-6.46	3.97E-10	3.59E-07	-5.54	6.38E-08
cg25498731	THSD7B	Body	TRUE		NA	-6.45	4.01E-10	3.61E-07	-4.41	1.42E-05
cg01892547	NBEAL2	Body	NA	Gene_Associated	NA	6.45	4.01E-10	3.61E-07	7.43	1.01E-12
cg24724084	SEMA6D; SEMA6D; SEMA6D; SEMA6D; SEMA6D; SEMA6D	5UTR;5UTR; 5UTR;5UTR; 5UTR	NA	Unclassified_Cell_type_specific	TRUE	6.45	4.08E-10	3.65E-07	8.42	1.25E-15
cg16663155	INCENP;INCENP	Body;Body	NA	Gene_Associated_Cell_type_specific	NA	-6.45	4.08E-10	3.65E-07	-6.22	1.56E-09
cg02101203	FRMD4A	Body	NA		NA	6.45	4.10E-10	3.65E-07	7.08	9.21E-12
cg06149302	GLB1L3	Body	NA		NA	6.44	4.31E-10	3.82E-07	8.34	2.23E-15
cg25234117	PLCH1	TSS1500	NA		NA	6.44	4.35E-10	3.86E-07	7.04	1.18E-11
cg10956333			TRUE		NA	-6.44	4.44E-10	3.92E-07	-5.18	3.95E-07
cg26113809			NA	Unclassified	TRUE	6.43	4.54E-10	3.99E-07	7.11	7.59E-12
cg02044895	LPXN;LPXN; LPXN	Body;1stExon; 5UTR	NA	Promoter_Associated_Cell_type_specific	NA	6.43	4.54E-10	3.99E-07	6.68	1.05E-10
cg02532700	NCF4;NCF4	Body;Body	NA	Promoter_Associated	NA	-6.43	4.58E-10	4.00E-07	-5.42	1.17E-07
cg02268620	MIR24-1;C	TSS1500;3	NA		NA	-6.43	4.61E-10	4.02E-07	-5.63	4.03E-08

	9orf3	UTR								
cg23562406	KHK;KHK	Body;Body	TRUE	Unclassified	TRUE	6.43	4.65E-10	4.04E-07	5.26	2.66E-07
cg05209518			NA	Unclassified_Cell_type_specific	NA	6.42	4.75E-10	4.12E-07	5.2	3.49E-07
cg22588983			TRUE		TRUE	-6.42	4.77E-10	4.13E-07	-5.22	3.25E-07
cg00030296	SEPT9;SEPT9;SEPT9	5UTR;Body;Body	TRUE		NA	6.42	4.97E-10	4.28E-07	8.44	1.15E-15
cg10189362	STEAP3;STEAP3;STEAP3	Body;Body;Body	NA		NA	-6.42	4.99E-10	4.29E-07	-5.47	9.01E-08
cg08871244	FAM38A	Body	TRUE	Promoter_Associated	NA	6.41	5.12E-10	4.38E-07	5.6	4.60E-08
cg15393221	PRX;PRX	TSS1500;TSS1500	TRUE		NA	6.41	5.14E-10	4.38E-07	8.17	7.35E-15
cg01715680	BTBD7	Body	TRUE		NA	-6.41	5.15E-10	4.38E-07	-6.99	1.58E-11
cg21327194	GPRC5C;GPRC5C	Body;Body	NA		NA	6.41	5.16E-10	4.38E-07	8.02	1.98E-14
cg03126561	PARVA	Body	TRUE		TRUE	6.41	5.17E-10	4.38E-07	8.16	7.93E-15
cg02203067	SLC7A5	Body	NA		NA	-6.41	5.19E-10	4.38E-07	-7.78	1.01E-13
cg24713122	DGKZ;DGKZ;DGKZ	Body;Body;Body;Body	TRUE	Gene_Associated	TRUE	6.4	5.38E-10	4.52E-07	8.36	1.95E-15
cg02223351	CDH5	5UTR	TRUE		NA	6.4	5.38E-10	4.52E-07	7.45	9.08E-13
cg01284869	TCN2	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	6.4	5.45E-10	4.56E-07	8.13	9.48E-15
cg03616377			TRUE	Unclassified_Cell_type_specific	NA	6.4	5.46E-10	4.56E-07	6.06	3.80E-09
cg17887364	EIF4EBP1	Body	NA		NA	-6.4	5.56E-10	4.62E-07	-5.49	8.31E-08
cg17817532	TET1	5UTR	NA	Unclassified_Cell_type_specific	NA	6.4	5.57E-10	4.62E-07	6.92	2.45E-11

cg24524702	MEF2A;MEF2A;MEF2A	5UTR;5UTR;5UTR	NA	Unclassified_Cell_type_specific	NA	-6.39	5.65E-10	4.66E-07	-6.55	2.31E-10
cg22836769			NA		NA	-6.39	5.65E-10	4.66E-07	-7.69	1.89E-13
cg03970350	TCN2	TSS200	NA	Unclassified_Cell_type_specific	TRUE	6.39	5.69E-10	4.68E-07	9.05	1.45E-17
cg16671160			NA		TRUE	6.39	5.79E-10	4.75E-07	7.87	5.40E-14
cg18844145			NA		NA	-6.39	5.85E-10	4.78E-07	-5.84	1.28E-08
cg00858840	SP5	Body	NA		NA	6.39	5.89E-10	4.81E-07	8.1	1.15E-14
cg11553755	TJAP1;TJAP1;TJAP1;TJAP1;TJAP1;TJAP1	5UTR;5UTR;5UTR;5UTR;5UTR;5UTR	TRUE		NA	-6.38	6.00E-10	4.88E-07	-7.31	2.20E-12
cg27628839			NA	Promoter_Associated_Cell_type_specific	NA	-6.38	6.06E-10	4.89E-07	-6.43	4.75E-10
cg01883425	MDF1	Body	NA		TRUE	6.38	6.06E-10	4.89E-07	7.79	9.20E-14
cg13453589	UBE2R2	Body	TRUE		NA	-6.38	6.08E-10	4.89E-07	-4.78	2.68E-06
cg18410110	PDZD2	Body	TRUE	Unclassified_Cell_type_specific	NA	-6.38	6.08E-10	4.89E-07	-4.87	1.75E-06
cg20313963	SLC2A3	TSS1500	NA	Promoter_Associated	TRUE	6.38	6.12E-10	4.90E-07	5.07	6.78E-07
cg26855208	AVEN;CHRM5	TSS1500;5UTR	NA		NA	6.38	6.17E-10	4.93E-07	6.48	3.49E-10
cg22863744	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	6.37	6.36E-10	5.07E-07	6.96	1.95E-11
cg07706375	MIR23A;MIR24-2;MIR27A	TSS200;TSS1500;TSS1500	NA	Unclassified	TRUE	6.37	6.44E-10	5.12E-07	6.62	1.54E-10
cg17580614	ADORA2B	Body	NA	Unclassified_Cell_type_specific	NA	-6.37	6.48E-10	5.14E-07	-6.32	8.76E-10

cg03291396	SLC11A1	Body	TRUE		NA	6.37	6.51E-10	5.15E-07	7.52	5.58E-13
cg06470626	CDR2	Body	TRUE		NA	6.37	6.57E-10	5.18E-07	6.62	1.53E-10
cg16476048	C10orf122	TSS1500	NA		NA	-6.37	6.61E-10	5.20E-07	-4.53	8.42E-06
cg11172693	PPP1R16B	TSS200	NA	Promoter_Associated	TRUE	6.36	6.83E-10	5.36E-07	7.76	1.15E-13
cg10257521	LSP1;LSP1;LSP1;LSP1	Body;Body;Body;Body	TRUE	Unclassified_Cell_type_specific	NA	6.36	7.04E-10	5.51E-07	7.86	5.85E-14
cg12985929	SEPT9;SEPT9;SEPT9;SEPT9	5UTR;Body;Body;Body	NA	Promoter_Associated	NA	6.36	7.10E-10	5.54E-07	7.96	3.04E-14
cg13972491	C9orf3	3UTR	NA		NA	-6.36	7.11E-10	5.54E-07	-5.68	2.97E-08
cg14947787	GPX2	3UTR	NA		NA	-6.35	7.21E-10	5.57E-07	-8.06	1.52E-14
cg11551560			TRUE		NA	6.35	7.22E-10	5.57E-07	7.42	1.06E-12
cg15987211	MYOM3	TSS1500	NA	Unclassified	TRUE	6.35	7.23E-10	5.57E-07	6.75	7.17E-11
cg12513616			NA		TRUE	-6.35	7.25E-10	5.57E-07	-6.34	7.81E-10
cg00956964	SLMO1;SLMO1	Body;Body	NA	Unclassified	NA	6.35	7.25E-10	5.57E-07	7.87	5.43E-14
cg04920032	FAIM2	3UTR	TRUE		TRUE	6.35	7.29E-10	5.59E-07	5.61	4.48E-08
cg17822706			TRUE	Promoter_Associated	NA	6.35	7.37E-10	5.61E-07	6.38	6.22E-10
cg12431188			NA	Unclassified_Cell_type_specific	NA	-6.35	7.37E-10	5.61E-07	-7.5	6.54E-13
cg16443812	KLHDC7B	1stExon	NA	Promoter_Associated	NA	6.35	7.40E-10	5.63E-07	7.48	7.24E-13
cg19406511	RAB25	Body	NA	Unclassified	TRUE	6.35	7.50E-10	5.69E-07	6.44	4.50E-10
cg27093944			TRUE	Unclassified	TRUE	6.35	7.52E-10	5.69E-07	7.81	8.14E-14
cg20054248	IKZF4	TSS200	NA		NA	6.34	7.77E-10	5.85E-07	7.53	5.13E-13
cg27501612	HERPUD1;HERPUD1;HERPUD1	3UTR;3UTR;3UTR	NA		NA	-6.34	7.78E-10	5.85E-07	-5.54	6.37E-08

	D1									
cg05894719			TRUE		NA	-6.34	7.81E-10	5.86E-07	-5.59	4.83E-08
cg00737979	LOC340074	TSS1500	NA		NA	-6.34	7.87E-10	5.89E-07	-5.93	7.75E-09
cg08105590	FAM38A	Body	NA	Promoter_Associated	NA	6.34	7.90E-10	5.90E-07	7.72	1.52E-13
cg08772789	SEPT9;SEPT9;SEPT9	5UTR;Body;Body	TRUE		NA	6.34	7.94E-10	5.90E-07	8.28	3.48E-15
cg18612461			NA		NA	6.34	7.95E-10	5.90E-07	7.44	9.34E-13
cg01775514	BMP7	Body	NA		NA	-6.33	8.05E-10	5.96E-07	-7.08	9.07E-12
cg14678430	FLNC;FLNC	Body;Body	NA		NA	-6.33	8.12E-10	5.99E-07	-4.2	3.47E-05
cg16293835			TRUE		NA	-6.33	8.18E-10	6.03E-07	-4.97	1.08E-06
cg05910443	CUX1;CUX1;CUX1	Body;Body;Body	TRUE		TRUE	6.33	8.24E-10	6.05E-07	7.52	5.47E-13
cg26443127			TRUE		TRUE	6.32	8.52E-10	6.24E-07	8.44	1.11E-15
cg08283206	ARHGEF10	Body	NA		NA	-6.32	8.56E-10	6.26E-07	-5.12	5.27E-07
cg20550458	SNORA52;RPLP2	Body;Body	NA		NA	6.32	8.61E-10	6.28E-07	5.83	1.37E-08
cg16622061			TRUE		NA	-6.32	8.66E-10	6.30E-07	-5.73	2.29E-08
cg03960874	STEAP3;STEAP3;STEAP3	Body;Body;Body	NA		NA	-6.32	8.70E-10	6.31E-07	-5.49	8.21E-08
cg20866810	ZDHHC4;ZDHHC4;ZDHHC4;ZDHHC4	Body;Body;Body;Body	NA		NA	-6.32	8.79E-10	6.36E-07	-6.23	1.44E-09
cg03324175	CYBASC3;CYBASC3;CYBASC3	TSS200;5UTR;Body	NA		NA	-6.32	8.84E-10	6.38E-07	-7.48	7.42E-13
cg15407505			TRUE	Unclassified_Cell_type_specific	TRUE	6.31	9.24E-10	6.65E-07	6.97	1.78E-11

cg17693957	TCN2	TSS1500	NA	Unclassified_Cell_type_specific	NA	6.31	9.26E-10	6.65E-07	6.4	5.47E-10
cg12709970	P2RX1	Body	TRUE	Promoter_Associated	NA	6.31	9.44E-10	6.76E-07	3.96	9.21E-05
cg05125838	UCN2;COL7A1	TSS1500;3UTR	NA		TRUE	6.3	9.69E-10	6.92E-07	5.8	1.56E-08
cg26831416	ACTN4	Body	NA		TRUE	6.3	9.75E-10	6.95E-07	5.44	1.07E-07
cg00061860			NA		NA	-6.3	9.93E-10	7.06E-07	-7.12	6.98E-12
cg01519094	PKNOX2	TSS1500	NA	Unclassified	NA	6.29	1.01E-09	7.16E-07	7.73	1.37E-13
cg15708990			TRUE		NA	6.29	1.01E-09	7.17E-07	7.14	6.40E-12
cg25449466	BMP7	Body	TRUE		NA	-6.29	1.02E-09	7.19E-07	-4.44	1.23E-05
cg25305879			TRUE		TRUE	6.29	1.02E-09	7.21E-07	6.98	1.70E-11
cg25075684			NA	Unclassified_Cell_type_specific	NA	6.29	1.06E-09	7.43E-07	7.41	1.12E-12
cg22276612	FBRSL1	Body	NA	Unclassified_Cell_type_specific	NA	-6.28	1.10E-09	7.67E-07	-6.21	1.67E-09
cg01544903			NA	Unclassified_Cell_type_specific	NA	6.28	1.10E-09	7.67E-07	8.42	1.33E-15
cg13382769	MAGI2	TSS1500	NA		NA	6.28	1.12E-09	7.81E-07	7.55	4.60E-13
cg03345059	NDST1	Body	NA		NA	-6.28	1.12E-09	7.81E-07	-5.86	1.13E-08
cg26720452			NA	Unclassified_Cell_type_specific	NA	6.27	1.13E-09	7.87E-07	8.56	4.81E-16
cg04346283	FAM46A	Body	NA		NA	6.27	1.16E-09	8.01E-07	7.43	1.01E-12
cg23681440			TRUE		NA	-6.27	1.18E-09	8.15E-07	-5.53	6.76E-08
cg22762813			NA		TRUE	6.27	1.19E-09	8.19E-07	7.02	1.31E-11
cg15448210	SYNGAP1	Body	NA		TRUE	6.26	1.22E-09	8.37E-07	6.78	5.72E-11
cg11109845	CUL1	TSS1500	NA		NA	6.26	1.25E-09	8.54E-07	8.3	2.96E-15
cg17331199	IKZF4;IKZF1	1stExon;5UTR	TRUE	Promoter_Associated	NA	6.25	1.26E-09	8.65E-07	7.87	5.74E-14



	F4	TR		ssociated						
cg01367627	TRRAP	5UTR	NA	Promoter_A ssociated	NA	6.25	1.29E-09	8.78E-07	4.52	8.75E-06
cg14979620	TP73;TP7 3;TP73;TP 73	Body;Body; Body;Body	NA		NA	6.25	1.29E-09	8.78E-07	6.35	7.44E-10
cg04745805	STAT5B	5UTR	NA		NA	6.25	1.29E-09	8.78E-07	5.01	8.90E-07
cg17032372			NA		NA	-6.25	1.31E-09	8.85E-07	-5.83	1.36E-08
cg04846710	LIX1L	Body	NA	Promoter_A ssociated	NA	6.25	1.31E-09	8.85E-07	6.22	1.55E-09
cg01718447	CRHR2	TSS200	NA	Unclassifie d	NA	6.25	1.31E-09	8.86E-07	6.33	8.52E-10
cg24208886	STEAP3;S TEAP3;ST EAP3	Body;Body; Body	NA		NA	-6.25	1.32E-09	8.86E-07	-5.11	5.56E-07
cg23110422	ETS2	Body	NA		NA	-6.25	1.32E-09	8.88E-07	-5.05	7.50E-07
cg01363714			NA		NA	6.25	1.33E-09	8.88E-07	7.48	7.09E-13
cg03115379			NA		TRUE	6.24	1.34E-09	8.95E-07	6.75	7.18E-11
cg07121644	DGKZ;DG KZ;DGKZ; DGKZ	Body;TSS2 00;Body;Bo dy	NA	Promoter_A ssociated	TRUE	6.24	1.35E-09	9.00E-07	7.3	2.35E-12
cg04884798	ADCY4	Body	NA		NA	-6.24	1.36E-09	9.07E-07	-5.88	1.01E-08
cg14345497	HOXB4	1stExon	NA	Unclassifie d	TRUE	6.24	1.39E-09	9.24E-07	7.51	5.81E-13
cg05184938	SEPT9;SE PT9;SEPT 9;SEPT9	5UTR;Body ;Body;Body	NA		NA	6.23	1.42E-09	9.37E-07	7.43	9.78E-13
cg05503062			NA	Unclassifie d_Cell_type _specific	NA	-6.23	1.42E-09	9.37E-07	-6.32	8.79E-10
cg22540600	NDST1	Body	NA		NA	-6.23	1.42E-09	9.37E-07	-5.77	1.89E-08
cg11027140	GPR144	TSS1500	NA		NA	6.23	1.45E-09	9.56E-07	6.79	5.40E-11
cg14655700	PC;PC;PC	Body;Body; Body	NA	Unclassifie d_Cell_type _specific	NA	-6.23	1.46E-09	9.57E-07	-6.09	3.25E-09

cg02320862	SEPT9;SEPT9;SEPT9	5UTR;Body;Body;Body	NA		NA	6.23	1.46E-09	9.57E-07	7.26	3.03E-12
cg16145216	HIVEP3;HIVEP3	TSS1500;TSS1500	NA	Promoter_Associated	NA	6.23	1.48E-09	9.67E-07	6.66	1.17E-10
cg02610723	FAM38A	Body	NA	Promoter_Associated	NA	6.23	1.49E-09	9.67E-07	4.55	7.55E-06
cg26708220	MEIS2;MEIS2;MEIS2;MEIS2;MEIS2	Body;Body;Body;Body;Body	NA		NA	6.23	1.49E-09	9.67E-07	9.86	3.47E-20
cg07875146			NA		NA	6.22	1.54E-09	9.99E-07	6.35	7.48E-10
cg08063051	UNKL	5UTR	TRUE	Promoter_Associated_Cell_type_specific	NA	-6.22	1.57E-09	1.02E-06	-6.45	4.26E-10
cg24049468	AK3L1;AK3L1;AK3L1	Body;Body;Body	NA		NA	6.22	1.57E-09	1.02E-06	5.48	8.47E-08
cg08486160	PC;PC;PC	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-6.22	1.58E-09	1.02E-06	-5.5	7.95E-08
cg27295118			NA		NA	6.22	1.58E-09	1.02E-06	6.56	2.15E-10
cg07434244	G0S2	TSS1500	NA		NA	6.21	1.59E-09	1.02E-06	7.35	1.65E-12
cg01983492			NA		NA	-6.21	1.61E-09	1.03E-06	-5.15	4.63E-07
cg23856536			NA	Unclassified	NA	6.21	1.62E-09	1.03E-06	2.58	0.010376905
cg26588825	FAM198B;FAM198B;FAM198B	TSS200;5UTR;5UTR	NA		NA	6.21	1.64E-09	1.04E-06	6.17	2.02E-09
cg14234406	PLEC1;PLEC1;PLEC1	Body;Body;TSS200	NA		NA	6.21	1.64E-09	1.05E-06	7.66	2.22E-13
cg05316864			TRUE	Unclassified	NA	-6.21	1.67E-09	1.06E-06	-7.33	1.85E-12

cg14950751	SLC16A11	TSS1500	NA		NA	-6.21	1.68E-09	1.06E-06	-5.98	6.08E-09
cg24914185			TRUE		NA	6.2	1.71E-09	1.08E-06	7.44	9.43E-13
cg08414108	SYNJ2	Body	NA		NA	-6.2	1.75E-09	1.10E-06	-5.61	4.49E-08
cg20059928			TRUE		TRUE	-6.19	1.79E-09	1.12E-06	-6.35	7.61E-10
cg10238080			NA		TRUE	6.19	1.80E-09	1.13E-06	7.9	4.44E-14
cg02519681	FRMD4B	1stExon	TRUE		TRUE	6.19	1.84E-09	1.15E-06	6.37	6.69E-10
cg12686441			NA	Unclassified	TRUE	6.18	1.89E-09	1.18E-06	6.31	9.51E-10
cg05032059			TRUE		NA	6.18	1.92E-09	1.20E-06	6.76	6.65E-11
cg02272667	MAD1L1; MAD1L1; MAD1L1	Body;Body; Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.18	1.93E-09	1.20E-06	7.14	6.16E-12
cg04509266	LOC148696	TSS200	NA		NA	-6.18	1.97E-09	1.22E-06	-3.14	0.001831345
cg16850254	ARHGEF4 ;ARHGEF4	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	6.18	1.98E-09	1.23E-06	7.5	6.52E-13
cg21371809	FRMD4A	Body	TRUE	Unclassified	NA	6.18	1.99E-09	1.23E-06	7.71	1.59E-13
cg03662014	RRN3P2	Body	NA		NA	6.18	1.99E-09	1.23E-06	6.57	2.10E-10
cg05455036			NA		NA	6.18	1.99E-09	1.23E-06	5.37	1.49E-07
cg18287591	TCHH	Body	NA	Unclassified_Cell_type_specific	NA	6.17	2.00E-09	1.23E-06	6.61	1.57E-10
cg23485307	TGFBR2;TGFBR2	Body;Body	TRUE		NA	6.17	2.01E-09	1.23E-06	7.62	2.84E-13
cg06630241	SOCS2	Body	NA		NA	6.17	2.02E-09	1.24E-06	6.98	1.68E-11
cg11668844	MCF2L;MCF2L	Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.17	2.04E-09	1.24E-06	7.65	2.33E-13
cg11411865	TTYH3	3UTR	NA		NA	-6.17	2.04E-09	1.25E-06	-5	9.30E-07
cg01780990	ECE1;ECE1;ECE1;ECE1	TSS1500;Body;Body;Body	NA		NA	-6.17	2.05E-09	1.25E-06	-5.88	1.01E-08

cg04418091	ATP5G2;ATP5G2	TSS1500;TSS1500	NA	Promoter_Associated	NA	6.17	2.08E-09	1.26E-06	6.92	2.45E-11
cg25685983	CDKN2D;KRI1;CDKN2D	3UTR;TSS1500;3UTR	TRUE	Promoter_Associated	NA	6.17	2.10E-09	1.27E-06	6.76	6.46E-11
cg20019546	SFRP4	1stExon	NA		NA	6.17	2.10E-09	1.27E-06	6.14	2.42E-09
cg17296220			NA		NA	-6.16	2.14E-09	1.29E-06	-6.4	5.53E-10
cg21996227	SEMA4A	Body	TRUE	Gene_Associated_Cell_type_specific	TRUE	6.16	2.15E-09	1.29E-06	6.72	8.45E-11
cg23518532			NA		NA	-6.16	2.19E-09	1.31E-06	-5.66	3.40E-08
cg19501536	MADD;MADD;MADD;MADD;MADD;MADD;MADD;MADD;MADD;MADD	Body;Body;Body;Body;Body;Body;Body;Body	NA		NA	-6.16	2.21E-09	1.32E-06	-4.2	3.45E-05
cg04742345	SLC29A1;SLC29A1	TSS1500;TSS1500	NA		TRUE	6.16	2.22E-09	1.32E-06	7	1.49E-11
cg22325958	SFRS8	Body	NA		NA	-6.16	2.22E-09	1.32E-06	-5.46	9.35E-08
cg04466886			TRUE		TRUE	6.15	2.25E-09	1.34E-06	5.35	1.68E-07
cg07984614	FAM53B	Body	NA		NA	-6.15	2.28E-09	1.36E-06	-2.7	0.00728273
cg25216196	MFAP4	TSS200	TRUE	Unclassified_Cell_type_specific	TRUE	6.15	2.29E-09	1.36E-06	7.84	6.77E-14
cg04566512			TRUE		TRUE	-6.15	2.29E-09	1.36E-06	-6.65	1.24E-10
cg10346364	LOC100130987;CLCF1;CLCF1	Body;TSS1500;TSS1500	NA		NA	6.15	2.30E-09	1.36E-06	7.2	4.43E-12
cg08527603	PMM1	Body	NA		NA	-6.15	2.31E-09	1.36E-06	-3.4	0.000771651
cg19240637	RNF144A	Body	NA		NA	-6.15	2.34E-09	1.37E-06	-4.25	2.81E-05
cg18156204			NA	Unclassified_Cell_type	TRUE	6.15	2.35E-09	1.37E-06	8.87	5.34E-17

				_specific						
cg14615768	NTN1	TSS1500	NA	Unclassified	NA	6.15	2.35E-09	1.37E-06	4.92	1.39E-06
cg04368724	VARS	Body	NA		NA	6.15	2.35E-09	1.37E-06	5.51	7.34E-08
cg22620221	DPP6	TSS200	NA		NA	6.15	2.36E-09	1.37E-06	6.03	4.64E-09
cg00731785	BST1;BST1	1stExon;5UTR	NA	Unclassified_Cell_type_specific	TRUE	6.14	2.37E-09	1.38E-06	7.16	5.48E-12
cg08865625	HLF	Body	NA		NA	-6.14	2.40E-09	1.39E-06	-5.3	2.13E-07
cg03379552	CRTAC1	Body	TRUE		NA	6.14	2.40E-09	1.39E-06	6.76	6.42E-11
cg02990289	MIR27A;MIR24-2	Body;TSS200	NA	Unclassified	NA	6.14	2.41E-09	1.40E-06	7.3	2.29E-12
cg09143713	PLCB4;PLCB4	5UTR;5UTR	TRUE		NA	6.14	2.44E-09	1.41E-06	7.14	6.45E-12
cg05384198	TBC1D2	Body	NA		NA	-6.14	2.44E-09	1.41E-06	-6.13	2.54E-09
cg13376199			NA		NA	-6.14	2.47E-09	1.42E-06	-3.02	0.002725829
cg11925381	RAC1;RAC1	Body;Body	NA		NA	-6.14	2.48E-09	1.42E-06	-2.42	0.016071467
cg02596779	RNF130	Body	TRUE		NA	6.13	2.51E-09	1.44E-06	6.46	3.86E-10
cg09941112	RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4; RASGRP4;	1stExon;1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR; 1stExon;5UTR;	TRUE	Unclassified	NA	6.13	2.52E-09	1.44E-06	6.91	2.61E-11

cg01565774	IKZF4	TSS200	NA		NA	6.13	2.53E-09	1.44E-06	6.89	2.92E-11
cg13030582	MFAP4	TSS1500	TRUE		NA	6.13	2.55E-09	1.45E-06	7.08	9.02E-12
cg14278260			NA	Promoter_A ssociated	NA	6.13	2.57E-09	1.46E-06	8.21	5.64E-15
cg16544989			NA		NA	6.13	2.59E-09	1.47E-06	7.67	2.09E-13
cg24135293			TRUE		NA	-6.12	2.65E-09	1.50E-06	-4.48	1.05E-05
cg06324373	CRTAC1	Body	TRUE		NA	6.12	2.66E-09	1.50E-06	8.41	1.44E-15
cg07558761	SLC7A5	Body	NA		NA	-6.12	2.66E-09	1.50E-06	-6.54	2.42E-10
cg20541456	CYFIP2;C YFIP2;CY FIP2;CYFI P2	1stExon;5U TR;5UTR;5 UTR	NA		NA	6.12	2.67E-09	1.50E-06	5.93	7.86E-09
cg20022223			NA		NA	6.12	2.69E-09	1.51E-06	6.31	9.38E-10
cg14872828	GABRP;G ABRP	1stExon;5U TR	NA		NA	-6.12	2.71E-09	1.52E-06	-3.19	0.00155028 6
cg03277515	PGLYRP4	TSS200	NA		NA	-6.12	2.72E-09	1.52E-06	-6.24	1.35E-09
cg23067299	AHRR	Body	NA		NA	6.12	2.74E-09	1.53E-06	5.47	9.10E-08
cg00476054			NA	Unclassifie d_Cell_type _specific	TRUE	6.12	2.75E-09	1.53E-06	7.97	2.86E-14
cg23769143	SYN2;TIM P4;SYN2	Body;TSS2 00;Body	NA		NA	-6.12	2.76E-09	1.53E-06	-5.05	7.62E-07
cg24975642	NCOR2;N COR2	Body;Body	TRUE	Unclassifie d_Cell_type _specific	TRUE	6.12	2.77E-09	1.54E-06	5.71	2.52E-08
cg25336874			NA		NA	6.11	2.84E-09	1.57E-06	7.5	6.55E-13
cg25318579			TRUE		NA	-6.11	2.84E-09	1.57E-06	-5.64	3.76E-08
cg07874646			TRUE		NA	-6.11	2.89E-09	1.59E-06	-2.19	0.02916560 9
cg14718363			NA	Promoter_A ssociated	NA	6.11	2.89E-09	1.59E-06	6.3	9.72E-10
cg13489049	TMPRSS2 ;TMPRSS 2	Body;5UTR	NA		NA	6.11	2.92E-09	1.60E-06	6.31	9.25E-10

cg22434226	C5orf32	TSS200	NA	Promoter_A ssociated	NA	6.11	2.92E-09	1.60E-06	7.71	1.57E-13
cg06452769	PLEC1;PLEC EC1;PLEC 1	Body;Body; TSS200	NA		NA	6.11	2.94E-09	1.61E-06	6.33	8.21E-10
cg27302539			TRUE		NA	6.1	3.00E-09	1.64E-06	8.57	4.39E-16
cg18610261	CDC42EP 3	TSS1500	NA		NA	6.1	3.01E-09	1.64E-06	7.94	3.58E-14
cg03541338	RGS10	Body	NA	Promoter_A ssociated	NA	6.1	3.02E-09	1.65E-06	4.4	1.47E-05
cg26015087			NA		NA	6.1	3.09E-09	1.68E-06	6.1	3.11E-09
cg22013564			TRUE		NA	6.1	3.09E-09	1.68E-06	3.04	0.00253236 5
cg01611017	CLMN	Body	TRUE		TRUE	6.1	3.10E-09	1.68E-06	7.89	4.97E-14
cg21067652	ELF1;ELF 1	Body;Body	TRUE	Promoter_A ssociated_ Cell_type_s pecific	NA	6.1	3.11E-09	1.68E-06	6.41	5.12E-10
cg01721754	NHLRC4	TSS200	TRUE	Promoter_A ssociated	NA	6.09	3.13E-09	1.69E-06	6.08	3.53E-09
cg20011326			NA	Promoter_A ssociated	TRUE	6.09	3.15E-09	1.70E-06	8.08	1.33E-14
cg19268652	HIVEP1	Body	TRUE	Unclassifie d_Cell_type specific	NA	-6.09	3.16E-09	1.70E-06	-5.93	7.98E-09
cg01369114	TCN2	TSS200	NA	Unclassifie d_Cell_type specific	TRUE	6.09	3.17E-09	1.70E-06	7.92	4.05E-14
cg00834536	ADCY9	3UTR	TRUE	Unclassifie d_Cell_type specific	NA	6.09	3.20E-09	1.71E-06	6.35	7.52E-10
cg10692693	CUX1;CU X1;CUX1	Body;Body; Body	TRUE		TRUE	6.09	3.21E-09	1.71E-06	6.79	5.62E-11
cg23500931	C5orf32	TSS200	NA	Promoter_A ssociated	NA	6.09	3.24E-09	1.73E-06	3.21	0.00146068 8
cg24115040	DLX5	Body	NA	Unclassifie d_Cell_type	NA	6.09	3.25E-09	1.73E-06	7.38	1.41E-12

				_specific						
cg21043424			TRUE		TRUE	6.09	3.28E-09	1.74E-06	5.9	9.05E-09
cg04907257	ADCY2	TSS1500	NA		NA	6.09	3.29E-09	1.75E-06	8.16	7.70E-15
cg07806552			TRUE	Unclassified	NA	6.09	3.30E-09	1.75E-06	6.21	1.70E-09
cg10639435	ZNF250;ZNF250	3UTR;3UTR	NA	Unclassified	NA	6.08	3.37E-09	1.78E-06	6.31	9.17E-10
cg05655534			TRUE		NA	6.08	3.37E-09	1.78E-06	6.59	1.85E-10
cg16887422	HDAC4	Body	TRUE		NA	6.08	3.45E-09	1.82E-06	5.61	4.44E-08
cg19848140	STK39	Body	TRUE		NA	-6.08	3.49E-09	1.83E-06	-5.74	2.20E-08
cg26271591	NFE2L2;NFE2L2;NFE2L2	Body;5UTR;5UTR	NA		NA	-6.07	3.52E-09	1.85E-06	-3.91	0.000112584
cg23011788	FRMD4A	Body	NA		NA	6.07	3.53E-09	1.85E-06	5.66	3.42E-08
cg17275432			NA		NA	-6.07	3.54E-09	1.85E-06	-4.18	3.84E-05
cg26133217	DIS3L2	Body	TRUE	Promoter_Associated	NA	6.07	3.57E-09	1.87E-06	6.85	3.80E-11
cg26782108	SLC13A5;SLC13A5	TSS1500;TSS1500	NA	Unclassified	TRUE	6.07	3.58E-09	1.87E-06	6.99	1.58E-11
cg21042248	MGC2752	Body	TRUE	Gene_Associated	TRUE	6.07	3.61E-09	1.88E-06	6.81	4.72E-11
cg19601144	ZNF710	Body	NA	Gene_Associated	TRUE	6.07	3.64E-09	1.89E-06	6.99	1.64E-11
cg21746071	ETFA;ETFA	Body;Body	TRUE	Unclassified	NA	-6.07	3.68E-09	1.91E-06	-4.26	2.67E-05
cg18953784			NA	Promoter_Associated	TRUE	6.07	3.68E-09	1.91E-06	5.99	5.67E-09
cg20244340	SLC24A3	Body	NA		TRUE	-6.06	3.72E-09	1.92E-06	-5.24	2.88E-07
cg06541783	CAPZA2	TSS1500	NA		NA	-6.06	3.74E-09	1.93E-06	-5.02	8.41E-07
cg04481596	SLC7A5	3UTR	NA		NA	-6.06	3.77E-09	1.93E-06	-6.44	4.29E-10
cg17391087			NA	Promoter_Associated	NA	6.06	3.78E-09	1.93E-06	5.87	1.09E-08
cg16490191	UNKL	5UTR	TRUE	Promoter_Associated	NA	-6.06	3.78E-09	1.93E-06	-5.73	2.29E-08



				Cell_type_s pecific						
cg23212751	ARTN;ARTN; ARTN;ARTN; ARTN;ARTN	TSS1500;Body;Body;Body	NA		NA	-6.06	3.78E-09	1.93E-06	-5.93	7.75E-09
cg26048630	PRRX1;PRRX1	Body;Body	NA	Unclassified_Cell_type_specific	NA	6.06	3.78E-09	1.93E-06	6.57	1.99E-10
cg13293295			TRUE		NA	6.06	3.80E-09	1.94E-06	7.92	3.91E-14
cg17568996	NFAM1	Body	TRUE		NA	6.06	3.81E-09	1.94E-06	7.01	1.47E-11
cg10537807			TRUE	Promoter_Associated	TRUE	6.06	3.83E-09	1.94E-06	7.06	1.03E-11
cg03186333			NA		NA	6.06	3.83E-09	1.94E-06	5.58	5.24E-08
cg27303981	APBB1IP	TSS200	TRUE	Promoter_Associated	NA	6.06	3.90E-09	1.98E-06	5	9.60E-07
cg11342789	C1orf226;C1orf226	Body;Body	NA		NA	-6.05	3.93E-09	1.99E-06	-3.52	0.000496641
cg25328184	TSLP	TSS1500	NA		NA	6.05	3.94E-09	1.99E-06	6.85	3.75E-11
cg20274430	MCHR1	Body	TRUE		NA	6.05	3.96E-09	2.00E-06	6.17	2.07E-09
cg21005412	WDR43;SNORD53	Body;TSS200	NA		NA	6.05	3.98E-09	2.00E-06	7.46	8.20E-13
cg04655481	GPR21;RABGAP1	TSS200;Body	NA		NA	6.05	4.02E-09	2.02E-06	7.81	8.44E-14
cg20646782			NA		NA	-6.05	4.06E-09	2.04E-06	-6.38	6.33E-10
cg00751021	PARD3B;PARD3B;PARD3B	Body;Body;Body	TRUE		NA	6.05	4.09E-09	2.05E-06	6.75	7.00E-11
cg19741167	POLR1A	Body	NA	Promoter_Associated	TRUE	6.05	4.10E-09	2.05E-06	6.35	7.33E-10
cg18263572	ZBTB48	3UTR	NA		NA	6.05	4.10E-09	2.05E-06	3.87	0.000130877
cg10364968	CASR	Body	NA	Unclassified	TRUE	6.04	4.16E-09	2.07E-06	6.26	1.21E-09
cg25193782			TRUE		TRUE	-6.04	4.19E-09	2.08E-06	-6.65	1.26E-10

cg24791666	CSRNP1	5UTR	TRUE		NA	6.04	4.25E-09	2.11E-06	5.62	4.11E-08
cg23619769	PHOX2A	Body	NA		NA	6.04	4.29E-09	2.12E-06	8.45	1.02E-15
cg05549655	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	-6.04	4.29E-09	2.12E-06	-5.49	8.38E-08
cg07063912	LRRFIP1	Body	NA		NA	6.04	4.31E-09	2.13E-06	6.17	2.13E-09
cg23670188	LSP1;LSP1;LSP1;LSP1	Body;Body;Body;Body	NA		NA	-6.04	4.32E-09	2.13E-06	-7.81	8.60E-14
cg27128761	SPARC	Body	TRUE		NA	6.04	4.33E-09	2.13E-06	7.47	7.95E-13
cg23918047	ARHGDI1A	5UTR	NA		NA	6.04	4.34E-09	2.13E-06	5.59	4.76E-08
cg07477282	SPG11;SPG11	TSS1500;TSS1500	NA	Promoter_Associated	NA	6.03	4.41E-09	2.15E-06	3.74	0.000217424
cg17852385	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	NA	-6.03	4.41E-09	2.15E-06	-6.16	2.15E-09
cg02863489	PRSS27	Body	NA	Unclassified_Cell_type_specific	TRUE	6.03	4.41E-09	2.15E-06	8.06	1.50E-14
cg00249511	SCT;SCT	5UTR;1stExon	NA	Unclassified_Cell_type_specific	NA	6.03	4.42E-09	2.15E-06	5.44	1.06E-07
cg23205276	KIAA1026;KIAA1026;KIAA1026;KIAA1026	Body;5UTR;Body;Body	TRUE		NA	-6.03	4.42E-09	2.15E-06	-5.77	1.92E-08
cg06555661	SFRS8	Body	NA		NA	-6.03	4.48E-09	2.18E-06	-4.99	9.82E-07
cg09997244	KIRREL3;KIRREL3	Body;Body	TRUE		NA	-6.03	4.52E-09	2.19E-06	-5.24	2.92E-07
cg17550009			NA		NA	-6.03	4.52E-09	2.19E-06	-7.3	2.32E-12
cg13417862	NXN	Body	NA		TRUE	6.03	4.54E-09	2.20E-06	7.45	8.78E-13
cg22208536	SNX25	Body	TRUE		TRUE	6.03	4.56E-09	2.20E-06	5.18	3.86E-07
cg04256466	PALLD;PALLD;PALLD;PALLD	Body;Body;Body;TSS1500	NA		NA	6.02	4.65E-09	2.24E-06	8.21	5.55E-15

cg22635402	GABRP	TSS200	NA		NA	-6.02	4.70E-09	2.26E-06	-4.31	2.15E-05
cg02926160	EPB41L3	5UTR	NA		NA	6.02	4.70E-09	2.26E-06	7.83	7.32E-14
cg20556402	MDFI	Body	NA		NA	6.02	4.74E-09	2.27E-06	7.11	7.54E-12
cg17518949			NA	Unclassified_Cell_type_specific	NA	-6.02	4.76E-09	2.28E-06	-4.84	2.03E-06
cg00765705	NCOR2;NCOR2	Body;Body	NA	Unclassified	TRUE	6.02	4.77E-09	2.28E-06	7.94	3.50E-14
cg24366968			NA	Unclassified_Cell_type_specific	NA	-6.02	4.78E-09	2.28E-06	-5.45	1.01E-07
cg10556036			NA		NA	-6.02	4.82E-09	2.30E-06	-6.34	7.71E-10
cg15205547			NA	Unclassified	NA	6.02	4.85E-09	2.30E-06	5.66	3.42E-08
cg05334190			TRUE		NA	-6.02	4.86E-09	2.31E-06	-3.91	0.000112643
cg12516954	H2AFY;H2AFY;H2AFY;H2AFY	Body;Body;Body;Body	TRUE		NA	6.01	4.89E-09	2.32E-06	7.19	4.66E-12
cg01911077			TRUE	Gene_Associated	NA	6.01	4.92E-09	2.33E-06	5.81	1.47E-08
cg05593411	PDE4D;PDE4D;PDE4D	Body;TSS1500;Body	TRUE		NA	6.01	4.92E-09	2.33E-06	7.86	5.88E-14
cg11539351			TRUE		NA	-6.01	4.95E-09	2.33E-06	-6.48	3.58E-10
cg18398056			NA		NA	6.01	4.95E-09	2.33E-06	6.1	3.15E-09
cg12584520			NA		NA	-6.01	4.98E-09	2.34E-06	-5.66	3.30E-08
cg06933370	MEIS2;MEIS2;MEIS2;MEIS2;MEIS2;MEIS2	Body;Body;Body;Body;Body;Body	NA		NA	6.01	5.00E-09	2.34E-06	8.64	2.70E-16
cg17929169	FYN	TSS1500	NA		NA	6.01	5.00E-09	2.34E-06	5.13	4.94E-07
cg12670347	TBX5;TBX5	TSS1500;TSS1500	NA		NA	6.01	5.01E-09	2.34E-06	6.54	2.49E-10

cg17351376	CD248;CD248	1stExon;3UTR	NA		NA	6.01	5.03E-09	2.35E-06	4.04	6.60E-05
cg04131792			NA		NA	-6.01	5.09E-09	2.37E-06	-6.27	1.20E-09
cg05857283			NA		NA	-6.01	5.12E-09	2.38E-06	-7.25	3.07E-12
cg06877366	MAD1L1;MAD1L1;MAD1L1	Body;Body;Body	NA		NA	-6	5.20E-09	2.42E-06	-5.67	3.21E-08
cg11762018			TRUE	Promoter_Associated	NA	6	5.30E-09	2.46E-06	6.68	1.09E-10
cg22541038			NA	Promoter_Associated	TRUE	6	5.31E-09	2.46E-06	7.57	4.04E-13
cg08696931	CDK2AP1	Body	TRUE		NA	6	5.39E-09	2.49E-06	7.79	9.48E-14
cg26263675	RAB37;RAB37;RAB37	3UTR;3UTR;3UTR	NA	Unclassified_Cell_type_specific	NA	5.99	5.51E-09	2.55E-06	2.62	0.009151849
cg02305757	PHF1;PHF1;PHF1	Body;Body;Body	NA	Gene_Associated	NA	5.99	5.52E-09	2.55E-06	8.37	1.82E-15
cg15767955			NA	Unclassified	NA	5.99	5.63E-09	2.59E-06	5.11	5.48E-07
cg00288463	SGPP2	Body	TRUE		NA	-5.99	5.74E-09	2.63E-06	-5.5	7.64E-08
cg23524184			NA	Unclassified_Cell_type_specific	NA	-5.99	5.74E-09	2.63E-06	-4.61	5.72E-06
cg03706951			NA	Promoter_Associated_Cell_type_specific	NA	5.99	5.75E-09	2.63E-06	7.11	7.43E-12
cg05469695	CDC42EP3	TSS1500	NA		NA	5.99	5.76E-09	2.63E-06	7.22	3.82E-12
cg05674602			TRUE		NA	5.98	5.78E-09	2.64E-06	6.31	9.19E-10
cg26401796	NTF3	Body	TRUE		NA	-5.98	5.80E-09	2.65E-06	-5.9	9.24E-09
cg20030796	BTBD17	Body	NA		NA	-5.98	5.82E-09	2.65E-06	-6.16	2.16E-09
cg03071808			NA	Unclassified	TRUE	5.98	5.82E-09	2.65E-06	8.86	5.64E-17
cg21581873	PLEKHA6	TSS1500	NA		TRUE	5.98	5.88E-09	2.67E-06	5.89	1.00E-08

cg13914004	ST6GALN AC6	Body	NA	Unclassified	NA	5.98	5.91E-09	2.68E-06	8.3	3.04E-15
cg06232130			TRUE	Unclassified_Cell_type_specific	TRUE	5.98	5.93E-09	2.68E-06	7.33	1.96E-12
cg20670085	ZNF491	TSS1500	TRUE	Unclassified	NA	5.98	5.96E-09	2.69E-06	5.1	5.90E-07
cg06907033			TRUE		NA	-5.98	5.99E-09	2.70E-06	-5.1	5.75E-07
cg11696576	SLC22A3	Body	TRUE		NA	-5.98	6.00E-09	2.70E-06	-3.92	0.000106468
cg16336586	LAPTM4B	Body	TRUE		NA	-5.98	6.01E-09	2.70E-06	-4.74	3.16E-06
cg23058194	LOC390594	TSS200	NA		NA	5.98	6.04E-09	2.71E-06	3.52	0.000492186
cg03365311	MIR129-2	Body	NA		NA	5.98	6.06E-09	2.72E-06	5.39	1.39E-07
cg04449108	UGT1A10; UGT1A6; UGT1A9; UGT1A6; UGT1A7; UGT1A8	Body;5UTR; Body;TSS1500;Body;Body	NA		NA	-5.97	6.13E-09	2.74E-06	-5.97	6.39E-09
cg05028773	MIR24-2	Body	NA	Unclassified	NA	5.97	6.14E-09	2.74E-06	6.62	1.51E-10
cg07241090	NCOR2;NCOR2	Body;Body	TRUE	Unclassified	TRUE	5.97	6.17E-09	2.75E-06	7.03	1.23E-11
cg06723829	LGR6;LGR6; LGR6	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.97	6.27E-09	2.80E-06	-4.47	1.08E-05
cg10374258			NA	Unclassified_Cell_type_specific	TRUE	5.97	6.30E-09	2.80E-06	6.76	6.41E-11
cg19653212	GUCA1A	Body	NA		NA	5.97	6.44E-09	2.86E-06	6.77	6.16E-11
cg18986335			TRUE	Unclassified_Cell_type_specific	NA	-5.96	6.54E-09	2.90E-06	-5.27	2.50E-07
cg26298409	MKX	Body	NA	Unclassified	NA	5.96	6.55E-09	2.90E-06	5.79	1.72E-08

cg15542713	HIVEP3;HIVEP3	TSS1500;TSS1500	NA	Promoter_A associated	NA	5.96	6.61E-09	2.92E-06	5.59	4.96E-08
cg00393487	RTP1	Body	NA		NA	-5.96	6.66E-09	2.94E-06	-2.85	0.004703974
cg07168526	ST7;ST7	Body;Body	TRUE		NA	5.96	6.74E-09	2.97E-06	7.36	1.57E-12
cg05887082	C19orf38	TSS200	NA	Unclassified_Cell_type_specific	NA	5.95	6.83E-09	3.01E-06	6.62	1.56E-10
cg16120833	GPRC5C;GPRC5C	Body;Body	NA		NA	5.95	6.86E-09	3.01E-06	7.15	5.79E-12
cg19240569	HRASLS2	TSS1500	NA	Unclassified_Cell_type_specific	NA	-5.95	6.89E-09	3.02E-06	-4.11	5.06E-05
cg01110759	MT1A	TSS200	NA	Unclassified_Cell_type_specific	TRUE	5.95	6.97E-09	3.05E-06	8.36	2.00E-15
cg25919362			TRUE		NA	5.95	7.02E-09	3.07E-06	6.33	8.51E-10
cg09513276	BMP7	Body	NA		NA	-5.95	7.12E-09	3.11E-06	-5.64	3.72E-08
cg17198772			NA		NA	-5.95	7.17E-09	3.12E-06	-6.86	3.67E-11
cg02659920	EPS8L2	Body	NA	Unclassified	NA	5.95	7.18E-09	3.12E-06	8.33	2.46E-15
cg15032615	C9orf86;C9orf86	Body;Body	TRUE	Unclassified_Cell_type_specific	NA	5.95	7.19E-09	3.12E-06	6.64	1.38E-10
cg20051949	KIRREL3;KIRREL3	Body;Body	NA		NA	-5.94	7.20E-09	3.13E-06	-5.56	5.65E-08
cg14280181	SGPP2	Body	NA	Unclassified_Cell_type_specific	NA	-5.94	7.24E-09	3.14E-06	-5.9	9.14E-09
cg06794253			TRUE		TRUE	5.94	7.27E-09	3.15E-06	7.35	1.66E-12
cg15122358			NA		NA	-5.94	7.32E-09	3.16E-06	-5.96	6.81E-09
cg13298389			NA		NA	-5.94	7.35E-09	3.17E-06	-4.38	1.58E-05
cg18087256			TRUE		NA	-5.94	7.36E-09	3.17E-06	-3.11	0.002069825
cg07796002	ARHGEF1;ARHGEF	Body;Body;Body	TRUE	Promoter_A associated	TRUE	5.94	7.36E-09	3.17E-06	6.61	1.58E-10

	1;ARHGE F1									
cg23844527	EPB41L5	Body	NA	Unclassified_Cell_type _specific	NA	5.94	7.39E-09	3.17E-06	2.71	0.00719066 6
cg00430895			NA		TRUE	5.94	7.42E-09	3.18E-06	5.37	1.53E-07
cg02381279			NA		NA	5.94	7.43E-09	3.18E-06	7.01	1.42E-11
cg02357046	FAM53A	TSS1500	NA		NA	-5.94	7.46E-09	3.19E-06	-5.04	7.79E-07
cg14857764			NA	Unclassified	NA	5.94	7.47E-09	3.19E-06	7.71	1.58E-13
cg12183594	ZNF425	Body	NA		NA	-5.94	7.49E-09	3.19E-06	-4.09	5.57E-05
cg10194295	LOC73075 5	TSS200	NA		TRUE	5.94	7.56E-09	3.22E-06	5.58	5.11E-08
cg00470972	UGT1A10; UGT1A7; UGT1A9; UGT1A8	Body;1stEx on;Body;Bo dy	NA		NA	-5.93	7.65E-09	3.25E-06	-3.67	0.00028306 5
cg06636541	BAHCC1	Body	NA		NA	-5.93	7.68E-09	3.26E-06	-3.87	0.00013281 2
cg07563400	ADORA2B	Body	TRUE	Unclassified_Cell_type _specific	NA	-5.93	7.77E-09	3.30E-06	-5.1	5.92E-07
cg04438525	CBLN1	3UTR	NA		NA	5.93	7.80E-09	3.30E-06	5.25	2.76E-07
cg05926314	PTPRN2; PTPRN2; PTPRN2	Body;Body; Body	NA		NA	-5.93	7.81E-09	3.30E-06	-6.79	5.55E-11
cg21241410			TRUE	Unclassified_Cell_type _specific	NA	5.93	7.85E-09	3.31E-06	7.56	4.38E-13
cg17687442	LOC10013 0691	Body	TRUE		NA	-5.93	7.87E-09	3.32E-06	-6.35	7.45E-10
cg14052728	PROM2;P ROM2;PR OM2	Body;Body; Body	NA		NA	-5.93	7.88E-09	3.32E-06	-6.02	4.84E-09
cg23109968			TRUE	Unclassified	TRUE	5.93	7.92E-09	3.33E-06	7.9	4.49E-14

cg06268632	WNT9A	Body	NA		NA	-5.93	7.96E-09	3.34E-06	-3.46	0.00062408
cg06998507	KCNG4	TSS1500	TRUE	Unclassified_Cell_type_specific	NA	5.92	8.13E-09	3.41E-06	5.12	5.24E-07
cg01382864	PTPRN	TSS200	NA		NA	5.92	8.18E-09	3.42E-06	6.43	4.75E-10
cg20538228	ASPSCR1	Body	NA	Unclassified_Cell_type_specific	NA	-5.92	8.19E-09	3.42E-06	-5.53	6.77E-08
cg27585939			TRUE		NA	5.92	8.22E-09	3.43E-06	7.94	3.44E-14
cg17329859			NA		NA	-5.92	8.25E-09	3.44E-06	-5.11	5.48E-07
cg05604874			NA		NA	5.92	8.32E-09	3.46E-06	7.13	6.77E-12
cg00336149	CACNA1D ;CACNA1D; CACNA1D	Body;Body; Body	NA		NA	5.92	8.35E-09	3.47E-06	5.98	5.90E-09
cg13475583			NA	Promoter_Associated	NA	5.92	8.43E-09	3.50E-06	7.45	9.06E-13
cg18920088	MTHFD1L	Body	NA		NA	-5.92	8.45E-09	3.50E-06	-3.57	0.000410923
cg00031896	KDM2B	TSS1500	NA	Promoter_Associated	NA	5.92	8.47E-09	3.50E-06	5.26	2.62E-07
cg07512993	TK2	Body	NA	Promoter_Associated	NA	5.91	8.52E-09	3.52E-06	5.4	1.27E-07
cg14950169			NA	Unclassified	NA	5.91	8.56E-09	3.52E-06	6.37	6.76E-10
cg04176246	MSI2;MSI2	Body;Body	TRUE	Unclassified_Cell_type_specific	NA	5.91	8.56E-09	3.52E-06	5.34	1.73E-07
cg11112615	SERPINB6	5UTR	NA		NA	5.91	8.57E-09	3.52E-06	5.94	7.49E-09
cg27290624			NA	Promoter_Associated	NA	5.91	8.64E-09	3.55E-06	7.05	1.14E-11
cg16572957			NA	Unclassified_Cell_type_specific	NA	-5.91	8.69E-09	3.55E-06	-4.24	2.89E-05
cg03785076	SNED1	TSS1500	TRUE		NA	-5.91	8.69E-09	3.55E-06	-5.46	9.71E-08



cg07258627	PRNT;PRNT;PRNT	TSS1500;TSS1500;TSS1500	NA	Unclassified	NA	5.91	8.69E-09	3.55E-06	4.97	1.08E-06
cg04228935	RUNX1	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.91	8.78E-09	3.59E-06	7.71	1.61E-13
cg01146808	PRDM1;PRDM1	Body;Body	NA	Unclassified	NA	-5.91	8.80E-09	3.59E-06	-5.47	9.02E-08
cg26470501	BCL3	Body	NA	Promoter_Associated	NA	-5.91	8.81E-09	3.59E-06	-6.46	3.83E-10
cg21730993	NT5E	TSS200	NA	Unclassified	NA	5.91	8.86E-09	3.60E-06	7.7	1.72E-13
cg19185414			NA		NA	-5.9	9.02E-09	3.66E-06	-4.86	1.86E-06
cg26850624	AHRR	Body	NA	Gene_Associated_Cell_type_specific	NA	5.9	9.03E-09	3.66E-06	5.9	9.51E-09
cg15524283	LEMD1	3UTR	NA		NA	-5.9	9.03E-09	3.66E-06	-3.82	0.000160685
cg03531247	NRXN1;NRXN1;NRXN1	Body;Body;Body	NA		NA	5.9	9.09E-09	3.67E-06	6.86	3.58E-11
cg26559829			NA		NA	5.9	9.10E-09	3.67E-06	5.32	1.96E-07
cg20040765	ADHFE1	Body	TRUE		NA	5.9	9.19E-09	3.70E-06	6.77	6.22E-11
cg06327150	OSBPL9;OSBPL9;OSBPL9;OSBPL9;OSBPL9;OSBPL9;OSBPL9;OSBPL9	5UTR;Body;Body;5UTR;Body;Body;1stExon;1stExon;5UTR	NA	Promoter_Associated	NA	5.9	9.19E-09	3.70E-06	8.2	6.13E-15
cg01294327	LINGO3	Body	NA		NA	-5.9	9.23E-09	3.71E-06	-5.69	2.85E-08
cg04718883	MTHFD1L	Body	NA		NA	-5.9	9.24E-09	3.71E-06	-2.81	0.005257036

cg19827780	RAPGEFL1	Body	TRUE	Unclassified	NA	5.9	9.31E-09	3.73E-06	6.18	2.00E-09
cg00699392	CCDC140	3UTR	NA	Unclassified_Cell_type_specific	NA	5.9	9.34E-09	3.74E-06	6.1	3.07E-09
cg06770731	SLC7A5	3UTR	TRUE		NA	-5.9	9.37E-09	3.74E-06	-6.64	1.32E-10
cg04409030	SOCS2	TSS1500	NA		NA	-5.9	9.37E-09	3.74E-06	-5.37	1.52E-07
cg03078672			NA		NA	-5.9	9.39E-09	3.74E-06	-3.33	0.000955059
cg12547807			TRUE	Unclassified	TRUE	-5.9	9.42E-09	3.75E-06	-6.37	6.58E-10
cg26105278	TP73;TP73;TP73	Body;Body;Body;Body	NA		TRUE	-5.89	9.51E-09	3.78E-06	-4.99	9.73E-07
cg16378215	SV2A	Body	NA		NA	-5.89	9.51E-09	3.78E-06	-3.43	0.000673771
cg27192708	PPBP	TSS1500	NA		NA	-5.89	9.56E-09	3.79E-06	-5.99	5.61E-09
cg23956760	SLC25A42	5UTR	NA		NA	5.89	9.75E-09	3.86E-06	6.62	1.51E-10
cg04025127	PTPRF;PTPRF	Body;Body	TRUE		NA	-5.89	9.76E-09	3.86E-06	-5.49	8.20E-08
cg11966524			NA		NA	-5.89	9.78E-09	3.86E-06	-5.61	4.41E-08
cg04650271	ANGPT4	TSS200	TRUE		NA	5.89	9.80E-09	3.86E-06	7.82	7.58E-14
cg04724387			TRUE		NA	-5.89	9.81E-09	3.86E-06	-4.62	5.68E-06
cg21493127	FAM134B	TSS1500	NA	Promoter_Associated	TRUE	5.89	9.92E-09	3.90E-06	7.06	1.03E-11
cg06212289			TRUE		NA	5.88	1.00E-08	3.94E-06	8.18	7.01E-15
cg12543219	KNDC1	Body	NA		NA	-5.88	1.00E-08	3.94E-06	-4.54	8.07E-06
cg21523564			NA	Unclassified	NA	5.88	1.00E-08	3.94E-06	7.79	9.46E-14
cg14392725			TRUE		NA	-5.88	1.01E-08	3.94E-06	-3.99	8.36E-05
cg09907758	C11orf95	TSS1500	NA		NA	5.88	1.02E-08	3.98E-06	7.29	2.45E-12
cg27434149			TRUE		NA	5.88	1.03E-08	4.00E-06	7.01	1.40E-11
cg12411994	ACTR3C	5UTR	NA		NA	-5.88	1.04E-08	4.04E-06	-4.55	7.68E-06

cg03517919	KIF1B	Body	NA	Unclassified	TRUE	5.88	1.04E-08	4.04E-06	5.91	8.89E-09
cg13899718	LASS2;LASS2	TSS1500;TSS1500	NA		NA	5.88	1.04E-08	4.04E-06	7.93	3.70E-14
cg26494929	KREMEN2;KREMEN2	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	5.88	1.05E-08	4.06E-06	6.07	3.62E-09
cg13827179			TRUE		NA	5.88	1.05E-08	4.07E-06	8.19	6.54E-15
cg17668731	CCNJL	Body	TRUE		TRUE	5.87	1.06E-08	4.11E-06	6.55	2.35E-10
cg05254946	RYR1;RYR1	Body;Body	NA		NA	-5.87	1.06E-08	4.11E-06	-5.47	8.90E-08
cg00545196	RXRA	Body	NA	Unclassified	NA	-5.87	1.07E-08	4.11E-06	-6.7	9.33E-11
cg25700513	KIF13A;KIF13A;KIF13A;KIF13A	Body;Body;Body;Body	TRUE		NA	-5.87	1.07E-08	4.11E-06	-5.61	4.29E-08
cg01979157	SKI	1stExon	NA	Promoter_Associated	NA	-5.87	1.07E-08	4.11E-06	-5.3	2.22E-07
cg15015340	DAGLA	5UTR	TRUE		TRUE	5.87	1.07E-08	4.11E-06	6.48	3.40E-10
cg08718490	SPATA18	Body	NA		NA	5.87	1.07E-08	4.11E-06	7.77	1.05E-13
cg20074340	MCF2L;MCF2L	Body;Body	NA		NA	-5.87	1.07E-08	4.11E-06	-5.85	1.21E-08
cg22453818	LHFPL2	5UTR	TRUE		NA	-5.87	1.07E-08	4.11E-06	-4.43	1.28E-05
cg13215862			NA	Promoter_Associated_Cell_type_specific	TRUE	5.87	1.08E-08	4.13E-06	6.49	3.27E-10
cg19372602			TRUE	Unclassified	NA	-5.87	1.08E-08	4.13E-06	-5.55	6.16E-08
cg04205769	DPH5;DPH5;DPH5	Body;Body;Body	NA		NA	5.87	1.09E-08	4.15E-06	5.49	8.41E-08
cg04257969	LOC552889;LOC552889	1stExon;3UTR	NA	NonGene_Associated	NA	5.87	1.10E-08	4.17E-06	6.11	2.87E-09
cg14005246			TRUE		NA	5.87	1.10E-08	4.19E-06	7.81	8.57E-14
cg00355315	SSU72	Body	NA		NA	-5.87	1.10E-08	4.19E-06	-5.77	1.87E-08

cg26132298	C14orf39	TSS200	NA		NA	5.87	1.11E-08	4.22E-06	5.01	8.87E-07
cg10553415			NA		NA	5.86	1.12E-08	4.25E-06	4.52	8.91E-06
cg12807924	SRC;SRC	Body;Body	NA	Promoter_A associated	TRUE	5.86	1.12E-08	4.25E-06	7.36	1.59E-12
cg06882058	SDCCAG8	Body	TRUE	Unclassified_Cell_type specific	TRUE	5.86	1.13E-08	4.27E-06	7.26	3.05E-12
cg19246761	MIB2;MIB2; MIB2;MIB2; MIB2	TSS1500;TSS1500; TSS1500;TSS1500; TSS1500	NA		TRUE	5.86	1.13E-08	4.28E-06	4.74	3.30E-06
cg00020474			TRUE	Unclassified_Cell_type specific	NA	5.86	1.14E-08	4.30E-06	7.32	2.02E-12
cg13338137			TRUE	Unclassified	TRUE	5.86	1.14E-08	4.30E-06	5.9	9.31E-09
cg21940042	ZNF69	TSS200	NA	Unclassified	TRUE	5.86	1.14E-08	4.30E-06	4.75	3.08E-06
cg00264129	HBEGF	Body	TRUE	Promoter_A associated	NA	-5.86	1.15E-08	4.32E-06	-4.17	3.91E-05
cg05600740	B4GALNT1	5UTR	TRUE		NA	5.86	1.16E-08	4.34E-06	8.64	2.73E-16
cg06061092	DIP2C	Body	NA		NA	-5.86	1.16E-08	4.34E-06	-5.25	2.83E-07
cg14506175	ASS1;ASS1	Body;Body	NA	Unclassified	NA	5.86	1.16E-08	4.35E-06	7.84	6.97E-14
cg20654468	LPXN;LPXN	Body;Body	NA		NA	5.86	1.18E-08	4.39E-06	5.13	4.92E-07
cg14891022	RAC2	Body	TRUE	Promoter_A associated	TRUE	5.85	1.18E-08	4.41E-06	7.68	2.01E-13
cg13467672			NA	Promoter_A associated	TRUE	5.85	1.18E-08	4.41E-06	7.19	4.74E-12
cg16353615			TRUE		NA	5.85	1.19E-08	4.44E-06	6.95	2.08E-11
cg03623878	MCF2L;MCF2L	Body;Body	TRUE	Unclassified_Cell_type specific	TRUE	5.85	1.20E-08	4.45E-06	8.47	9.40E-16

cg17901584	DHCR24	TSS1500	NA	Promoter_Associated_Cell_type_specific	NA	-5.85	1.20E-08	4.45E-06	-5.17	4.06E-07
cg15746696	ZNF814	TSS200	NA	NonGene_Associated	TRUE	5.85	1.20E-08	4.46E-06	5.97	6.19E-09
cg19974448	LOC100169752	TSS200	NA		NA	-5.85	1.21E-08	4.47E-06	-5.1	5.78E-07
cg01362541	BMP7	Body	NA		NA	-5.85	1.21E-08	4.47E-06	-5.71	2.57E-08
cg05284742	ITPK1;ITPK1;ITPK1	Body;Body;Body	TRUE		NA	-5.85	1.21E-08	4.47E-06	-6.32	8.68E-10
cg04126866	C10orf99	TSS1500	NA		NA	-5.85	1.22E-08	4.48E-06	-5.51	7.34E-08
cg26461695	SNTG1	TSS1500	NA		NA	5.85	1.23E-08	4.52E-06	4.23	3.04E-05
cg23522475	RHOBTB3	Body	NA		NA	5.85	1.23E-08	4.52E-06	7.27	2.73E-12
cg04694437	MEF2C	5UTR	NA		NA	5.85	1.23E-08	4.52E-06	7.86	5.94E-14
cg18642234	GPX1;GPX1;GPX1	3UTR;3UTR;1stExon	NA		NA	-5.85	1.23E-08	4.52E-06	-4.67	4.36E-06
cg00228735			TRUE	Unclassified_Cell_type_specific	NA	5.85	1.24E-08	4.53E-06	5.07	6.84E-07
cg08780398	LOC100192378	Body	TRUE		NA	5.85	1.24E-08	4.54E-06	5.73	2.37E-08
cg24540678			NA		NA	-5.85	1.24E-08	4.54E-06	-6.46	3.84E-10
cg01928820	PTCRA	TSS200	NA		NA	5.84	1.25E-08	4.55E-06	5.47	9.10E-08
cg21441211			TRUE		NA	-5.84	1.25E-08	4.55E-06	-5.64	3.82E-08
cg13184736	GNG12	TSS1500	NA		TRUE	-5.84	1.25E-08	4.55E-06	-6.01	5.07E-09
cg25587868	RNF212;RNF212	Body;3UTR	NA	Unclassified	TRUE	5.84	1.25E-08	4.55E-06	4.95	1.18E-06
cg21972431			TRUE		NA	-5.84	1.26E-08	4.59E-06	-5.71	2.60E-08
cg07727884	MFAP4	TSS200	TRUE	Unclassified_Cell_type_specific	TRUE	5.84	1.28E-08	4.64E-06	7.41	1.12E-12
cg14115756	GPR21;RABGAP1	TSS1500;Body	NA		NA	5.84	1.28E-08	4.65E-06	6.95	2.00E-11

cg15815827	DIDO1;DIDO1;DIDO1	5UTR;5UTR;5UTR;5UTR	NA	Promoter_Associated_Cell_type_specific	TRUE	5.84	1.28E-08	4.65E-06	6.84	3.95E-11
cg14700707	NOTCH4;NOTCH4	1stExon;5UTR	TRUE		NA	5.84	1.29E-08	4.65E-06	5.91	8.95E-09
cg17616283	EFEMP2	Body	NA		TRUE	5.84	1.30E-08	4.68E-06	6.67	1.15E-10
cg23431989	FOXJ1	TSS1500	NA		NA	5.84	1.30E-08	4.69E-06	6.04	4.21E-09
cg06207052	PPP1R16B	TSS200	NA	Promoter_Associated	TRUE	5.83	1.33E-08	4.77E-06	6.9	2.74E-11
cg19572487	RARA;RARA;RARA	5UTR;5UTR;5UTR	NA	Promoter_Associated	NA	-5.83	1.33E-08	4.77E-06	-5.31	2.07E-07
cg02836864			TRUE	Unclassified	NA	5.83	1.33E-08	4.77E-06	8.08	1.39E-14
cg14893857	HSP90AA1;HSP90AA1	TSS1500;Body	NA		NA	5.83	1.33E-08	4.78E-06	4.86	1.86E-06
cg27191312			NA	Unclassified	TRUE	5.83	1.34E-08	4.79E-06	6.61	1.61E-10
cg17214455	HLA-DOA	Body	NA		NA	5.83	1.35E-08	4.84E-06	5.97	6.35E-09
cg04329347	ALDOA	TSS1500	NA		NA	5.83	1.36E-08	4.86E-06	5.62	4.19E-08
cg10395685	CCDC81;CCDC81	TSS200;TSS200	TRUE		NA	5.83	1.36E-08	4.86E-06	6.56	2.14E-10
cg10217713	KNDC1	Body	NA		NA	-5.83	1.36E-08	4.86E-06	-5.52	7.08E-08
cg18641697	SEPT6;SEPT6;SEPT6	TSS200;TSS200;TSS200	NA	Promoter_Associated	NA	5.83	1.37E-08	4.86E-06	2.94	0.003486799
cg14184886			TRUE	Unclassified	NA	-5.83	1.37E-08	4.86E-06	-5.98	6.05E-09
cg09509365	PRDM16;PRDM16	Body;Body	NA		NA	-5.83	1.37E-08	4.87E-06	-5	9.55E-07
cg04269907	BICD2;BICD2	Body;3UTR	NA		NA	-5.83	1.38E-08	4.89E-06	-5.45	1.02E-07
cg09792204	OCA2	5UTR	NA	Unclassified	NA	5.83	1.38E-08	4.89E-06	8.18	6.67E-15
cg07241925	MAEA;MA	Body;Body	TRUE		TRUE	5.82	1.39E-08	4.90E-06	6.25	1.31E-09

	EA									
cg13582028	ERICH1	Body	TRUE		TRUE	5.82	1.39E-08	4.90E-06	4.91	1.45E-06
cg03131092	KIAA1543; KIAA1543	3UTR;3UT R	NA		TRUE	-5.82	1.39E-08	4.90E-06	-6.11	2.91E-09
cg14958635	NEUROG 1	1stExon	TRUE		NA	5.82	1.39E-08	4.90E-06	7.6	3.32E-13
cg25684105	TXNRD1	Body	NA	Unclassified_Cell_type specific	TRUE	-5.82	1.40E-08	4.92E-06	-4.55	7.61E-06
cg06890522	RNASEK; C17orf49; C17orf49; C17orf49	Body;TSS1 500;TSS15 00;TSS150 0	NA	Promoter_Associated	NA	-5.82	1.40E-08	4.92E-06	-4.89	1.60E-06
cg23652859	MGC2752	Body	TRUE	Gene_Associated	TRUE	5.82	1.40E-08	4.93E-06	6.66	1.19E-10
cg27043548			TRUE		NA	-5.82	1.40E-08	4.93E-06	-6.7	9.40E-11
cg11811840	UGT1A10; UGT1A1; UGT1A6; UGT1A8; UGT1A4; UGT1A3; UGT1A6; UGT1A9; UGT1A7; UGT1A5	Body;1stExon; Body;Body; Body;Body; Body;Body; Body	NA		NA	-5.82	1.41E-08	4.93E-06	-5.43	1.12E-07
cg00183107	INPP4B;IN PP4B	5UTR;5UT R	NA	Unclassified_Cell_type specific	NA	5.82	1.42E-08	4.97E-06	2.6	0.009715633
cg23707540	CTBP2;CT BP2	5UTR;5UT R	TRUE		TRUE	5.82	1.42E-08	4.98E-06	7.27	2.80E-12
cg27259271	SDCCAG8	Body	TRUE	Unclassified_Cell_type specific	NA	5.82	1.43E-08	5.00E-06	8.56	4.84E-16
cg20912205	NAT6;HY AL3	TSS1500;T SS1500	NA	Promoter_Associated	NA	-5.82	1.44E-08	5.03E-06	-5.35	1.64E-07
cg00866399	EMX1	Body	NA		NA	5.82	1.44E-08	5.03E-06	7.53	5.38E-13

cg21038291			TRUE		NA	5.82	1.45E-08	5.06E-06	7.17	5.24E-12
cg01350686	MYOM3	TSS1500	NA	Unclassified	NA	5.82	1.46E-08	5.07E-06	6.62	1.50E-10
cg26663490	GPRC5C; GPRC5C	Body;Body	NA		NA	5.81	1.48E-08	5.13E-06	6.97	1.85E-11
cg15973171	TCHH	Body	NA	Unclassified_Cell_type_specific	NA	5.81	1.48E-08	5.13E-06	5.58	5.22E-08
cg16239278			TRUE		NA	-5.81	1.48E-08	5.14E-06	-5.27	2.56E-07
cg20449048	C7orf50;C7orf50;C7orf50	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.81	1.49E-08	5.14E-06	-7.04	1.19E-11
cg00196407	ABR;ABR;ABR	Body;Body;Body	TRUE	Unclassified	NA	5.81	1.49E-08	5.14E-06	7.1	8.40E-12
cg17518931	MPPED2	TSS1500	NA		TRUE	5.81	1.49E-08	5.15E-06	6.96	1.92E-11
cg00090261	RGS22	TSS1500	TRUE		NA	5.81	1.51E-08	5.19E-06	6.51	2.97E-10
cg11137160			NA		NA	5.81	1.51E-08	5.19E-06	7.07	9.58E-12
cg24137511	MAST3	Body	NA		NA	-5.81	1.51E-08	5.19E-06	-5.81	1.54E-08
cg10533624	TEAD4;TEAD4;TEAD4	Body;Body;Body	TRUE	Unclassified	NA	5.81	1.52E-08	5.21E-06	7.54	4.94E-13
cg26695123			NA	Unclassified	TRUE	5.81	1.53E-08	5.23E-06	6.24	1.42E-09
cg26274662			TRUE	Unclassified_Cell_type_specific	NA	5.81	1.53E-08	5.23E-06	6.94	2.19E-11
cg14883070	SPIRE1;SPIRE1;SPIRE1	5UTR;Body;Body	TRUE		NA	-5.8	1.54E-08	5.27E-06	-4.75	3.13E-06
cg02010481	JAZF1	Body	NA		NA	5.8	1.54E-08	5.27E-06	6.43	4.70E-10
cg26581714	SPATA18	Body	NA		NA	5.8	1.55E-08	5.28E-06	7.46	8.35E-13
cg24003955	CTNNBIP1;CTNNBIP1	Body;Body	TRUE		TRUE	5.8	1.55E-08	5.30E-06	6.75	6.88E-11
cg24395452	SPATA18	Body	NA		NA	5.8	1.56E-08	5.30E-06	7.69	1.85E-13



cg18664369			NA	Unclassified	NA	5.8	1.57E-08	5.33E-06	6.73	8.06E-11
cg19368145	CROCC	TSS200	NA	Unclassified_Cell_type_specific	TRUE	5.8	1.57E-08	5.33E-06	7.69	1.80E-13
cg25298189	ARID3A	Body	NA		TRUE	5.8	1.58E-08	5.37E-06	7.9	4.41E-14
cg10125703	RASIP1	Body	NA	Unclassified_Cell_type_specific	TRUE	5.8	1.59E-08	5.38E-06	7.33	1.93E-12
cg13395868	EHMT1	Body	NA	Gene_Associated_Cell_type_specific	NA	-5.8	1.59E-08	5.39E-06	-4.97	1.10E-06
cg13793810	ATL3	Body	NA		NA	-5.8	1.60E-08	5.40E-06	-6.37	6.49E-10
cg15802396	DLG4;DLG4	Body;Body	NA	Promoter_Associated	NA	5.8	1.62E-08	5.45E-06	7.38	1.35E-12
cg06488957	RAI1	5UTR	NA	Unclassified	NA	5.8	1.62E-08	5.46E-06	7.78	1.01E-13
cg06245338	UBE2O	Body	TRUE		NA	5.8	1.63E-08	5.48E-06	6.25	1.29E-09
cg08234168			NA	Unclassified_Cell_type_specific	TRUE	5.79	1.63E-08	5.49E-06	6.24	1.36E-09
cg22183049			TRUE		NA	5.79	1.64E-08	5.50E-06	6.95	2.11E-11
cg01550716	SDCCAG8	Body	TRUE	Unclassified_Cell_type_specific	TRUE	5.79	1.64E-08	5.51E-06	7.46	8.09E-13
cg00026033	IKZF4	TSS200	NA		NA	5.79	1.65E-08	5.54E-06	6.68	1.05E-10
cg02844899	TTC7A	Body	TRUE		TRUE	5.79	1.66E-08	5.55E-06	3.57	0.000412518
cg22383924	TP73	5UTR	NA	Unclassified_Cell_type_specific	NA	-5.79	1.67E-08	5.58E-06	-5.08	6.36E-07
cg13729891	DLG4;DLG4	Body;Body	NA	Promoter_Associated	NA	5.79	1.67E-08	5.58E-06	6.06	3.86E-09
cg13713922	GLI2	Body	TRUE		TRUE	5.79	1.67E-08	5.58E-06	6.83	4.22E-11
cg15247247	FOXK1	3UTR	NA		NA	-5.79	1.67E-08	5.58E-06	-6.29	1.04E-09

cg17130474	PINX1	3UTR	NA		NA	-5.79	1.68E-08	5.58E-06	-7.04	1.22E-11
cg22784023	FLJ23834	Body	TRUE	Unclassified	NA	5.79	1.69E-08	5.61E-06	6.11	2.96E-09
cg03395898	TGFB3;TGFB3	1stExon;5UTR	NA	Promoter_Associated	NA	-5.79	1.70E-08	5.63E-06	-5.19	3.68E-07
cg05194114	CCNDBP1;CCNDBP1;CCNDBP1;CCNDBP1	TSS200;TSS200;TSS1500;TSS200	NA	Promoter_Associated	NA	5.79	1.70E-08	5.64E-06	5.08	6.37E-07
cg14785681	HOXA11AS;HOXA11	TSS1500;Body	NA		NA	5.79	1.70E-08	5.65E-06	3.8	0.000173751
cg09633604			NA	Unclassified_Cell_type_specific	TRUE	5.79	1.71E-08	5.66E-06	6.52	2.80E-10
cg07891271	CHSY1	Body	TRUE	Promoter_Associated	NA	5.79	1.72E-08	5.68E-06	5.25	2.84E-07
cg26164488			TRUE	Unclassified_Cell_type_specific	NA	5.78	1.72E-08	5.68E-06	5.45	1.03E-07
cg07049086	LSP1;LSP1;LSP1;LSP1	5UTR;5UTR;Body;5UTR	NA		NA	-5.78	1.73E-08	5.70E-06	-8.33	2.46E-15
cg19583819	NRG2;NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	-5.78	1.73E-08	5.70E-06	-5.35	1.65E-07
cg04171052	SLC7A5	Body	NA		NA	-5.78	1.75E-08	5.75E-06	-5.76	1.96E-08
cg15426660			TRUE	Unclassified_Cell_type_specific	TRUE	5.78	1.75E-08	5.75E-06	5.91	8.57E-09
cg18241962	SEPT9;SEPT9;SEPT9;SEPT9	5UTR;5UTR;Body;Body;Body	NA	Promoter_Associated	TRUE	5.78	1.76E-08	5.78E-06	6.41	5.28E-10
cg01719718	MIR548F5;DCLK1	Body;Body	TRUE		NA	-5.78	1.77E-08	5.81E-06	-6.13	2.67E-09

cg04611395	FKBP4	TSS1500	NA		NA	5.78	1.77E-08	5.81E-06	6.68	1.04E-10
cg14880257	MYT1L	Body	NA		NA	-5.78	1.78E-08	5.84E-06	-6.08	3.53E-09
cg23935642	MUC2	Body	NA		NA	-5.78	1.80E-08	5.88E-06	-6.11	2.92E-09
cg27366395	CHADL;L3 MBTL2	3UTR;Body	NA		NA	-5.78	1.80E-08	5.88E-06	-5.58	5.13E-08
cg25386426	PANK4	TSS1500	NA	Unclassified	NA	-5.78	1.81E-08	5.90E-06	-6.21	1.63E-09
cg06499262	NFAT5;NFAT5;NFAT5;NFAT5	TSS1500;TSS1500;TSS1500;TSS1500	NA	Promoter_Associated	NA	5.77	1.81E-08	5.91E-06	7.68	1.91E-13
cg12068346			TRUE		TRUE	5.77	1.82E-08	5.91E-06	7.16	5.75E-12
cg26689848	PTPRN2;PTPRN2;PTPRN2	Body;Body;Body	NA		NA	-5.77	1.83E-08	5.95E-06	-5.25	2.73E-07
cg18018581			NA		NA	-5.77	1.84E-08	5.98E-06	-4.99	9.95E-07
cg18898125	NEFM	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	5.77	1.86E-08	6.04E-06	6.88	3.21E-11
cg01653727	FBXL18	Body	TRUE	Promoter_Associated	NA	5.77	1.87E-08	6.04E-06	6.18	2.00E-09
cg18425651	CAPN3;CAPN3;CAPN3;CAPN3;CAPN3;CAPN3;CAPN3	Body;Body;Body;5UTR;Body;5UTR;Body;Body	NA		NA	-5.77	1.89E-08	6.12E-06	-4.02	7.37E-05
cg21872037	SLC13A5;SLC13A5	TSS1500;TSS1500	NA	Unclassified_Cell_type_specific	TRUE	5.77	1.90E-08	6.14E-06	8.07	1.45E-14
cg08324801			TRUE	Promoter_Associated	NA	5.77	1.90E-08	6.14E-06	6.44	4.48E-10
cg07362969	TTPA	1stExon	NA		TRUE	5.77	1.91E-08	6.14E-06	3.89	0.000124156

cg06475223	LAMA3;LAMA3;LAMA3	Body;Body;Body;Body	NA	Unclassified	TRUE	5.77	1.91E-08	6.14E-06	7.29	2.49E-12
cg12776171	GPRC5C;GPRC5C	Body;Body	NA		NA	5.77	1.91E-08	6.14E-06	6.89	3.07E-11
cg03143457	GNG12	5UTR	TRUE	Unclassified_Cell_type_specific	NA	-5.76	1.93E-08	6.21E-06	-5.78	1.74E-08
cg04661888			NA		NA	5.76	1.94E-08	6.22E-06	6.67	1.13E-10
cg05116424	TRNP1	3UTR	TRUE		NA	-5.76	1.96E-08	6.27E-06	-6.52	2.78E-10
cg01495363	LOC100287216;SH3RF3	TSS1500;Body	NA		NA	-5.76	1.96E-08	6.29E-06	-6.34	7.83E-10
cg25252561	CAMK2G;CAMK2G;CAMK2G;CAMK2G;CAMK2G	Body;Body;Body;Body;Body	TRUE		TRUE	5.76	1.98E-08	6.33E-06	6.64	1.39E-10
cg03827689			TRUE	Unclassified	NA	5.76	1.98E-08	6.33E-06	7.13	6.62E-12
cg08734600	NKX1-2	Body	NA		NA	5.76	2.00E-08	6.37E-06	7.6	3.29E-13
cg09313740	INPPL1	Body	NA		NA	-5.76	2.00E-08	6.37E-06	-5.42	1.17E-07
cg15042811	FREM3	TSS200	NA		NA	5.76	2.01E-08	6.40E-06	5.15	4.51E-07
cg13683827	FAM113B	5UTR	TRUE		NA	5.75	2.02E-08	6.43E-06	6.85	3.78E-11
cg03246954	MKNK2;MKNK2	Body;Body	NA		NA	-5.75	2.02E-08	6.43E-06	-5.8	1.56E-08
cg07709148			TRUE	Unclassified	TRUE	5.75	2.03E-08	6.44E-06	4.83	2.16E-06
cg19825898			NA	Unclassified_Cell_type_specific	NA	-5.75	2.04E-08	6.46E-06	-4.12	4.75E-05
cg10277523			NA		NA	-5.75	2.04E-08	6.46E-06	-4.71	3.77E-06
cg24470133	SSU72	Body	NA		NA	-5.75	2.04E-08	6.46E-06	-5.44	1.08E-07
cg02709068	GLI3	Body	TRUE	Unclassified_Cell_type	NA	5.75	2.04E-08	6.46E-06	7.56	4.24E-13

				_specific						
cg15621656	TNFAIP8	Body	NA		NA	5.75	2.04E-08	6.46E-06	8.15	8.65E-15
cg06048436	ENOX1;ENOX1	Body;Body	TRUE		NA	5.75	2.06E-08	6.49E-06	6.03	4.63E-09
cg22699026	SDCCAG8	Body	TRUE	Unclassified_Cell_type_specific	TRUE	5.75	2.06E-08	6.51E-06	8.77	1.08E-16
cg23221603			NA		NA	5.75	2.07E-08	6.52E-06	5.92	8.44E-09
cg12117658	BZRAP1;BZRAP1	TSS200;TS S200	NA	Promoter_Associated	TRUE	5.75	2.08E-08	6.52E-06	7.14	6.21E-12
cg21448423	ACOT11;ACOT11;ACOT11;ACOT11	1stExon;5UTR;1stExon;5UTR	NA	Unclassified	TRUE	5.75	2.08E-08	6.52E-06	6.33	8.26E-10
cg00035074	TTYH3	3UTR	NA	Unclassified_Cell_type_specific	NA	-5.75	2.09E-08	6.55E-06	-4.23	3.00E-05
cg08165796			TRUE	Unclassified_Cell_type_specific	NA	5.75	2.09E-08	6.56E-06	6.81	4.90E-11
cg10397527	HLA-DOA	Body	NA		TRUE	5.75	2.09E-08	6.56E-06	7.07	9.54E-12
cg18433784	S100B	TSS200	NA		NA	5.75	2.10E-08	6.58E-06	6.79	5.47E-11
cg01415909	RTN4RL1	Body	TRUE	Unclassified_Cell_type_specific	NA	5.75	2.11E-08	6.59E-06	8.12	1.01E-14
cg08856420			NA	Unclassified	TRUE	5.74	2.14E-08	6.69E-06	4.97	1.09E-06
cg07264124	ZNF69;ZNF69	5UTR;1stExon	NA	Unclassified	NA	5.74	2.14E-08	6.69E-06	3.49	0.000553058
cg23845168			TRUE		TRUE	-5.74	2.16E-08	6.72E-06	-4.85	1.94E-06
cg25000600	DNAH2	TSS1500	NA	Unclassified_Cell_type_specific	NA	5.74	2.16E-08	6.72E-06	7.11	7.56E-12
cg16798537	CDH16	Body	NA	Unclassified_Cell_type_specific	TRUE	5.74	2.17E-08	6.74E-06	6.41	5.15E-10

cg25809905	ITGA2B	TSS1500	NA		NA	5.74	2.17E-08	6.74E-06	5.18	3.98E-07
cg20625588	MUC6	Body	NA		NA	-5.74	2.17E-08	6.74E-06	-4.8	2.40E-06
cg11986861	ZNRF3	5UTR	NA		NA	-5.74	2.18E-08	6.74E-06	-5.8	1.57E-08
cg01220680	ANGPT4	Body	TRUE		TRUE	5.74	2.20E-08	6.80E-06	7.83	7.40E-14
cg20552263			NA		NA	-5.74	2.22E-08	6.86E-06	-6.71	9.07E-11
cg24293614	MPPED1	TSS1500	NA		NA	5.74	2.23E-08	6.90E-06	5.51	7.27E-08
cg04506190	PLXND1	Body	NA		NA	-5.74	2.24E-08	6.90E-06	-5.32	1.97E-07
cg22538557			NA	Unclassified_Cell_type_specific	NA	5.74	2.24E-08	6.90E-06	6.81	4.91E-11
cg27446185	VTCN1	TSS1500	NA		NA	-5.74	2.24E-08	6.91E-06	-5.58	5.19E-08
cg02226939	BLMH	TSS1500	NA	Promoter_Associated	NA	5.73	2.26E-08	6.95E-06	5.94	7.63E-09
cg23510527	UGT1A6; UGT1A10; UGT1A6; UGT1A9; UGT1A7; UGT1A8	TSS200;Body; 5UTR;Body; Body;Body; Body	NA		NA	-5.73	2.26E-08	6.95E-06	-6.06	3.75E-09
cg02099474	CYP2W1	Body	NA		NA	5.73	2.27E-08	6.95E-06	5.16	4.44E-07
cg26062204	CLRN1;CLRN1;CLRN1	5UTR;1stExon;Body	NA		NA	-5.73	2.27E-08	6.95E-06	-5.99	5.75E-09
cg03562360	GLI2	Body	NA		TRUE	-5.73	2.29E-08	7.00E-06	-5.62	4.23E-08
cg02224369	CD59;CD59;CD59;CD59	TSS1500;TSS1500;TSS1500;TSS1500	NA	Promoter_Associated	NA	5.73	2.29E-08	7.00E-06	5.13	5.16E-07
cg15572396	PXK	Body	NA	Promoter_Associated	TRUE	5.73	2.29E-08	7.00E-06	6.36	7.16E-10
cg10058920	PDYN	TSS200	NA		NA	5.73	2.30E-08	7.03E-06	7.02	1.31E-11
cg14478589	GSN;GSN;GSN;GSN;GSN;GSN	Body;Body;Body;Body;Body;Body	NA		NA	5.73	2.32E-08	7.08E-06	5.47	9.29E-08

	GSN									
cg21770622	DGKZ;DGKZ;DGKZ	Body;TSS200;Body;Body	NA	Promoter_Associated	TRUE	5.73	2.33E-08	7.09E-06	7.15	6.04E-12
cg01275661			TRUE		NA	5.73	2.33E-08	7.09E-06	7.13	6.59E-12
cg25561140	MSI1	Body	TRUE	Unclassified_Cell_type_specific	TRUE	5.73	2.33E-08	7.09E-06	9.09	1.08E-17
cg23754392	BMI1	5UTR	NA		NA	5.73	2.35E-08	7.14E-06	8.28	3.37E-15
cg03287111	GLI2	Body	TRUE		TRUE	5.73	2.37E-08	7.18E-06	7.26	2.89E-12
cg24833464	KRTAP3-1	TSS200	TRUE		NA	-5.72	2.40E-08	7.26E-06	-4.4	1.48E-05
cg08985078	ARHGEF10	Body	NA		NA	-5.72	2.40E-08	7.27E-06	-3.68	0.000274677
cg04162383	GLIS1	Body	TRUE		NA	-5.72	2.45E-08	7.41E-06	-6.04	4.29E-09
cg21292033	SEPT9;SEPT9;SEPT9;SEPT9;SEPT9	Body;5UTR;Body;Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	5.72	2.48E-08	7.49E-06	7.07	9.95E-12
cg25890391			NA		NA	-5.72	2.49E-08	7.50E-06	-4.2	3.47E-05
cg26222132	ZNF69	TSS200	NA	Unclassified	TRUE	5.71	2.50E-08	7.55E-06	4.74	3.18E-06
cg12488187	MSRB3;MSRB3	TSS1500;TSS1500	NA		NA	5.71	2.51E-08	7.56E-06	6.2	1.79E-09
cg16606320	LOC644145	TSS1500	TRUE		NA	5.71	2.52E-08	7.56E-06	6.88	3.10E-11
cg09688579	ADRBK1	Body	TRUE	Promoter_Associated	NA	5.71	2.54E-08	7.63E-06	6.31	9.25E-10
cg17639394	HCG9	Body	TRUE	Unclassified_Cell_type_specific	NA	5.71	2.54E-08	7.63E-06	6.39	5.73E-10
cg20030711	SEPT9;SEPT9;SEPT9;SEPT9;SEPT9	Body;TSS200;5UTR;Body;Body;Body	NA	Promoter_Associated_Cell_type_specific	NA	5.71	2.54E-08	7.63E-06	6.08	3.41E-09

	9									
cg05135521	RBMS1;RBMS1	Body;Body	TRUE		NA	-5.71	2.55E-08	7.65E-06	-5.17	4.16E-07
cg23261327	BAIAP2;BAIAP2;BAIAP2;BAIAP2	Body;Body;Body;Body	NA	Unclassified	NA	5.71	2.56E-08	7.66E-06	6.77	6.21E-11
cg04367216	KCNJ1;KCNJ1;KCNJ1;KCNJ1;KCNJ1;KCNJ1	5UTR;5UTR;5UTR;1stExon;1stExon;1stExon;5UTR	NA	Unclassified_Cell_type_specific	NA	-5.71	2.57E-08	7.68E-06	-3.35	0.000920446
cg10756887	C22orf15	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.71	2.58E-08	7.69E-06	6.6	1.72E-10
cg02737619	SKI	Body	TRUE	Promoter_Associated_Cell_type_specific	TRUE	5.71	2.58E-08	7.69E-06	7.4	1.21E-12
cg20795569	TCHH	Body	NA	Unclassified_Cell_type_specific	NA	5.71	2.58E-08	7.69E-06	7.46	8.07E-13
cg16985778	MTMR9L	TSS1500	NA		NA	5.71	2.60E-08	7.74E-06	5.33	1.88E-07
cg05194346			TRUE		TRUE	5.71	2.61E-08	7.75E-06	5.63	4.01E-08
cg19102771	CCDC140	5UTR	NA		NA	5.71	2.62E-08	7.79E-06	3.29	0.001122666
cg23866916	SBNO2	5UTR	TRUE		NA	-5.71	2.63E-08	7.80E-06	-4.96	1.17E-06
cg22373687			TRUE		NA	5.71	2.63E-08	7.80E-06	6.09	3.24E-09
cg10068417			NA	Unclassified	NA	5.71	2.63E-08	7.80E-06	7.03	1.25E-11
cg08890503			NA		NA	-5.71	2.64E-08	7.80E-06	-4.87	1.77E-06
cg09618385	SLC7A5	3UTR	NA		NA	-5.7	2.66E-08	7.85E-06	-6.49	3.32E-10
cg04636402	NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	-5.7	2.66E-08	7.85E-06	-6.29	1.05E-09



	NRG2									
cg07607922	CASR	5UTR	NA		NA	5.7	2.67E-08	7.88E-06	5.85	1.22E-08
cg12930176			TRUE	Unclassified_Cell_type_specific	NA	5.7	2.68E-08	7.90E-06	6.53	2.54E-10
cg09761230			NA	Unclassified_Cell_type_specific	NA	5.7	2.69E-08	7.91E-06	5.86	1.13E-08
cg01628067	SKI	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.7	2.72E-08	7.99E-06	7.84	6.98E-14
cg26558111	DTX2;DTX2;DTX2;DTX2	5UTR;5UTR;5UTR;TS S1500	NA		NA	-5.7	2.74E-08	8.04E-06	-5.1	5.86E-07
cg23922804			NA		NA	5.7	2.74E-08	8.04E-06	6.19	1.81E-09
cg13793145	SLC29A1; SLC29A1	TSS200;TS S200	NA	Unclassified	TRUE	5.7	2.75E-08	8.04E-06	7.32	2.03E-12
cg12586150	SERPINB1	Body	TRUE		NA	5.7	2.75E-08	8.04E-06	5.58	5.17E-08
cg08556107	AHRR	Body	NA	Gene_Associated_Cell_type_specific	NA	-5.7	2.75E-08	8.04E-06	-6.23	1.44E-09
cg07870237	ACSL6;ACSL6	TSS1500;TSS1500	NA	Unclassified	TRUE	5.7	2.75E-08	8.04E-06	6.46	3.83E-10
cg13713728	LOC100169752	TSS200	NA		NA	-5.7	2.76E-08	8.07E-06	-5.06	7.16E-07
cg18390495	DEFB132	Body	NA		NA	5.7	2.77E-08	8.08E-06	6.56	2.22E-10
cg04643145			NA		NA	5.7	2.77E-08	8.08E-06	6.27	1.17E-09
cg27303421			TRUE		NA	-5.7	2.78E-08	8.09E-06	-5.38	1.41E-07
cg04764012	CSDAP1	TSS200	NA		NA	5.69	2.78E-08	8.09E-06	3.99	8.27E-05
cg16293484	SEPT9;SEPT9;SEPT9;SEPT9;SEPT9;SE	Body;5UTR;1stExon;5UTR;Body;Body;Body;	NA		NA	5.69	2.82E-08	8.18E-06	5.35	1.65E-07

	PT9;SEPT9;SEPT9	Body								
cg12150784			TRUE	Unclassified_Cell_type_specific	TRUE	5.69	2.82E-08	8.18E-06	6.42	4.98E-10
cg00183186	HTR1B	TSS1500	NA		NA	5.69	2.83E-08	8.20E-06	5.8	1.58E-08
cg16465939	KCNQ1;KCNQ1	Body;Body	TRUE		NA	5.69	2.83E-08	8.21E-06	7.41	1.13E-12
cg09491709	C3orf20	TSS200	NA		NA	-5.69	2.84E-08	8.22E-06	-5.05	7.63E-07
cg11177833	GLTPD2	1stExon	NA		NA	-5.69	2.85E-08	8.22E-06	-5.33	1.87E-07
cg24807547			TRUE		NA	5.69	2.86E-08	8.25E-06	6.66	1.17E-10
cg18188739	PRKCZ;PRKCZ;PRKCZ	5UTR;Body;5UTR	NA	Unclassified_Cell_type_specific	NA	5.69	2.86E-08	8.25E-06	5.26	2.71E-07
cg08334310	SCAND3	TSS1500	TRUE	Promoter_Associated	TRUE	5.69	2.87E-08	8.27E-06	4.22	3.17E-05
cg16341836	STAMBPL1	5UTR	NA		NA	5.69	2.87E-08	8.27E-06	7.31	2.22E-12
cg09890775	EBF3	Body	NA		TRUE	5.69	2.88E-08	8.27E-06	6.49	3.30E-10
cg02753187	CALCO2	Body	NA	Unclassified	NA	5.69	2.91E-08	8.35E-06	7.43	9.93E-13
cg00908631	CDKN2C	TSS1500	NA	Promoter_Associated	NA	-5.68	2.93E-08	8.42E-06	-5.92	8.21E-09
cg21045608	STK33;STK33	1stExon;5UTR	NA	Unclassified	TRUE	5.68	2.95E-08	8.45E-06	6.01	5.12E-09
cg24723731			TRUE		NA	5.68	2.95E-08	8.46E-06	7.45	9.10E-13
cg23516002			NA	Gene_Associated	TRUE	5.68	2.96E-08	8.46E-06	6.57	2.10E-10
cg01606023	NXPH4	Body	NA	Unclassified_Cell_type_specific	NA	5.68	2.96E-08	8.47E-06	6.77	6.13E-11
cg19192878	CECR1	TSS1500	NA		NA	-5.68	2.97E-08	8.49E-06	-5.28	2.34E-07
cg22679626			NA	Promoter_Associated	NA	5.68	2.98E-08	8.51E-06	4.27	2.63E-05
cg23677243	MEIS2;MEIS2;MEIS2	Body;Body;Body;Body;	NA		NA	5.68	2.99E-08	8.51E-06	8.39	1.64E-15

	;MEIS2;MEIS2;MEIS2	Body;Body;Body								
cg17232357	SMAD6;SMAD6;SMAD6	Body;Body;Body	TRUE		TRUE	-5.68	2.99E-08	8.51E-06	-5.6	4.52E-08
cg16937168	SNED1	TSS1500	TRUE		NA	-5.68	3.03E-08	8.61E-06	-3.84	0.000146671
cg13945576	ROR2	Body	TRUE	Unclassified_Cell_type_specific	NA	-5.68	3.03E-08	8.61E-06	-7.38	1.38E-12
cg20317521	BAIAP2;BAIAP2;BAIAP2;BAIAP2	Body;Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.68	3.06E-08	8.68E-06	-4.89	1.61E-06
cg14909464			NA		TRUE	5.68	3.06E-08	8.68E-06	5.97	6.17E-09
cg14219256	MYST4	Body	TRUE	Unclassified_Cell_type_specific	NA	5.68	3.07E-08	8.71E-06	4.84	1.99E-06
cg08684879			TRUE		NA	5.68	3.09E-08	8.74E-06	5.29	2.29E-07
cg08461949			NA		NA	5.67	3.10E-08	8.78E-06	7.45	8.59E-13
cg10931190	TSLP	TSS1500	NA		NA	5.67	3.11E-08	8.79E-06	5.93	8.04E-09
cg15359163	PRDM6	Body	TRUE		NA	5.67	3.12E-08	8.79E-06	5.14	4.81E-07
cg06201717			NA	Unclassified_Cell_type_specific	NA	-5.67	3.14E-08	8.85E-06	-4.46	1.16E-05
cg23489390	CRIM1	Body	TRUE		NA	-5.67	3.14E-08	8.85E-06	-5.02	8.47E-07
cg05418915			TRUE	Unclassified_Cell_type_specific	TRUE	5.67	3.15E-08	8.85E-06	6.03	4.62E-09
cg24631065	MUC2	Body	NA		NA	-5.67	3.15E-08	8.85E-06	-6.24	1.39E-09
cg07739604	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	5.67	3.15E-08	8.85E-06	6.04	4.39E-09
cg19792544	KIFC2;FOXH1	3UTR;3UTR	NA	Unclassified	NA	5.67	3.15E-08	8.85E-06	6.97	1.82E-11

cg15795984	PRND	5UTR	NA		NA	-5.67	3.17E-08	8.88E-06	-4.9	1.53E-06
cg01619562	ITPK1;ITPK1	Body;Body;Body	TRUE		NA	-5.67	3.17E-08	8.88E-06	-6.06	3.81E-09
cg17300047	RCBTB2	TSS1500	NA		NA	5.67	3.18E-08	8.90E-06	6.43	4.58E-10
cg11505417	C1QA	3UTR	NA	Unclassified_Cell_type_specific	NA	5.67	3.19E-08	8.90E-06	5.27	2.47E-07
cg20456243	SPEG	Body	NA	Unclassified_Cell_type_specific	NA	-5.67	3.19E-08	8.90E-06	-3.71	0.000246875
cg18742814			NA		NA	5.67	3.19E-08	8.90E-06	6.73	7.90E-11
cg08351203	ZNF83;ZNF83;ZNF83;ZNF83;ZNF83;ZNF83	Body;TSS200;TSS200;TSS200;TSS200;TSS200	NA	Promoter_Associated	NA	5.67	3.19E-08	8.90E-06	5	9.53E-07
cg04242132	FERMT1	Body	NA	Unclassified	NA	5.67	3.20E-08	8.91E-06	6.22	1.58E-09
cg09555544			NA	Promoter_Associated	TRUE	5.67	3.22E-08	8.95E-06	6.72	8.46E-11
cg24698211	FGF18	Body	NA		TRUE	-5.67	3.23E-08	8.98E-06	-5.55	5.89E-08
cg18114313			TRUE		NA	-5.67	3.23E-08	8.98E-06	-4.94	1.23E-06
cg07636194	HIST1H2BK;HIST1H4I	3UTR;1stExon	NA	Promoter_Associated	NA	5.67	3.24E-08	9.00E-06	5.82	1.40E-08
cg05922610	NR2E1	Body	NA		TRUE	5.67	3.25E-08	9.02E-06	7.3	2.24E-12
cg13320436			TRUE		NA	-5.67	3.26E-08	9.02E-06	-4.79	2.60E-06
cg09386458	QPCT	TSS1500	TRUE		NA	-5.66	3.26E-08	9.03E-06	-3.75	0.000207018
cg10645640	CEACAM7	Body	NA		NA	-5.66	3.29E-08	9.10E-06	-4.65	4.92E-06
cg12397274	TINAG	TSS1500	NA		NA	-5.66	3.31E-08	9.12E-06	-3.42	0.000715464
cg11834730	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	5.66	3.31E-08	9.12E-06	6.55	2.35E-10

cg22755679			NA		NA	-5.66	3.34E-08	9.20E-06	-6.51	2.97E-10
cg18337963	DGKZ;DGKZ;DGKZ;DGKZ	1stExon;Body;5UTR;Body;Body	NA	Promoter_Associated	TRUE	5.66	3.35E-08	9.20E-06	6.67	1.10E-10
cg07515196	DOCK6	Body	TRUE	Unclassified	NA	5.66	3.35E-08	9.20E-06	7.08	9.51E-12
cg11539857			NA		NA	-5.66	3.35E-08	9.20E-06	-5.15	4.51E-07
cg14979593	PGAP2;PGAP2;PGAP2;PGAP2;PGAP2;PGAP2;PGAP2;PGAP2	Body;Body;5UTR;Body;Body;Body;Body;Body	NA	Promoter_Associated	TRUE	-5.66	3.35E-08	9.20E-06	-6.18	1.99E-09
cg25251204			NA	Promoter_Associated	NA	5.66	3.36E-08	9.20E-06	3.59	0.000383059
cg26088753	EXOC3	Body	NA		NA	-5.66	3.36E-08	9.21E-06	-2.25	0.024989007
cg01383955	NFAM1	TSS200	NA		NA	5.66	3.37E-08	9.21E-06	6.81	4.82E-11
cg09314495	CDK14	Body	TRUE		NA	-5.66	3.37E-08	9.21E-06	-3.9	0.000115312
cg17951713			TRUE		NA	5.66	3.38E-08	9.22E-06	6.67	1.15E-10
cg08572767	CD52;UBXN11	TSS200;5UTR	TRUE	Unclassified	NA	5.66	3.38E-08	9.22E-06	5.65	3.49E-08
cg24809529	CLDN15	TSS200	TRUE		TRUE	5.66	3.38E-08	9.23E-06	6.03	4.43E-09
cg09817985			NA		NA	-5.66	3.39E-08	9.23E-06	-5.37	1.53E-07
cg21199093	ZMYM4	Body	TRUE		TRUE	5.66	3.39E-08	9.23E-06	6.38	6.19E-10
cg24428325			NA		NA	5.66	3.40E-08	9.24E-06	6.57	2.09E-10
cg00369811			TRUE	Unclassified	TRUE	5.66	3.40E-08	9.24E-06	7.58	3.67E-13
cg17936572	ARPP-21	5UTR	NA		NA	5.66	3.43E-08	9.29E-06	6.14	2.50E-09
cg18450254	PRICKLE2	5UTR	TRUE		TRUE	5.66	3.43E-08	9.29E-06	4.25	2.77E-05
cg05523911	TCHH	Body	NA	Unclassified_Cell_type	NA	5.66	3.43E-08	9.30E-06	5.64	3.82E-08

				_specific						
cg23720898			NA	Unclassified_Cell_type_specific	TRUE	-5.66	3.44E-08	9.30E-06	-4.88	1.66E-06
cg12829141	PRRT4	5UTR	TRUE	Promoter_Associated_Cell_type_specific	NA	5.65	3.44E-08	9.31E-06	6.07	3.70E-09
cg23253752	ELL3	Body	TRUE	Promoter_Associated	NA	-5.65	3.45E-08	9.31E-06	-4.9	1.50E-06
cg15246238	FSCN1	Body	NA	Unclassified	NA	-5.65	3.46E-08	9.32E-06	-5.95	7.14E-09
cg11650479	RHOBTB1;RHOBTB1;RHOBTB1;RHOBTB1	TSS1500;Body;TSS1500;Body	NA		TRUE	5.65	3.46E-08	9.32E-06	4.47	1.10E-05
cg06637517	DNAH1	Body	NA	Unclassified	TRUE	5.65	3.46E-08	9.32E-06	6.96	1.96E-11
cg26519184	PRDM15;PRDM15	Body;Body	TRUE	Unclassified	NA	5.65	3.47E-08	9.33E-06	7.22	3.91E-12
cg06680852			NA		TRUE	5.65	3.48E-08	9.37E-06	6.07	3.58E-09
cg20335735	NUP43	TSS1500	NA	Promoter_Associated	NA	-5.65	3.49E-08	9.38E-06	-6.18	2.01E-09
cg21527621	ACOT11;ACOT11	TSS1500;TSS1500	NA		TRUE	5.65	3.50E-08	9.38E-06	8.24	4.67E-15
cg08966624			NA	Unclassified	NA	5.65	3.50E-08	9.38E-06	7.07	9.96E-12
cg01408486	CXXC5	TSS1500	NA		NA	5.65	3.50E-08	9.38E-06	6.4	5.51E-10
cg03192598			NA	Unclassified_Cell_type_specific	NA	5.65	3.51E-08	9.40E-06	5.85	1.22E-08
cg14928932	SYNGAP1	Body	NA		TRUE	5.65	3.52E-08	9.41E-06	6.55	2.30E-10
cg23213230	TRIM13;TRIM13;TRIM13;TRIM13;DLEU2	TSS1500;TSS1500;TSS1500;TSS1500;Body	NA		NA	5.65	3.53E-08	9.41E-06	6.59	1.87E-10

cg15634980	PNPLA1;PNPLA1;PNPLA1	5UTR;Body;5UTR	NA		NA	5.65	3.53E-08	9.41E-06	7.58	3.88E-13
cg22916586	DUSP16	5UTR	TRUE		NA	5.65	3.53E-08	9.41E-06	6.09	3.28E-09
cg04259904	ARTN;ARTN;ARTN;ARTN;ARTN	1stExon;1stExon;5UTR;1stExon;5UTR;5UTR	TRUE	Unclassified_Cell_type_specific	NA	-5.65	3.54E-08	9.42E-06	-5.35	1.71E-07
cg00931925	C14orf153	Body	NA		NA	-5.65	3.55E-08	9.43E-06	-3.36	0.000882006
cg04307508	C19orf38	TSS200	NA	Unclassified_Cell_type_specific	NA	5.65	3.56E-08	9.47E-06	5.75	2.07E-08
cg07258167	QDPR	TSS1500	NA	Promoter_Associated	NA	5.65	3.56E-08	9.47E-06	5.79	1.72E-08
cg04930469	SOST	Body	TRUE		TRUE	5.65	3.58E-08	9.50E-06	7.73	1.38E-13
cg05394456	MPG;MPG;MPG	5UTR;Body;5UTR	NA	Promoter_Associated	NA	5.65	3.58E-08	9.50E-06	5.48	8.78E-08
cg14024937			TRUE		NA	-5.65	3.59E-08	9.50E-06	-4.91	1.48E-06
cg15119221	MFAP4	TSS1500	TRUE		TRUE	5.65	3.59E-08	9.51E-06	6.77	6.05E-11
cg05475934	APBB1IP;APBB1IP	1stExon;5UTR	TRUE	Promoter_Associated	NA	5.65	3.61E-08	9.55E-06	5.53	6.75E-08
cg07408456	PGLYRP2	TSS1500	NA		NA	5.65	3.62E-08	9.56E-06	3.7	0.000255274
cg19831957			TRUE	Unclassified	NA	-5.64	3.66E-08	9.67E-06	-6.15	2.31E-09
cg15457390	ADD1;ADD1;ADD1;ADD1	TSS1500;TSS1500;TSS1500;TSS1500	NA		NA	5.64	3.67E-08	9.69E-06	4.22	3.21E-05
cg06894469	NRD1;NRD1	Body;Body	TRUE		NA	-5.64	3.68E-08	9.70E-06	-4.76	3.00E-06
cg20039048			TRUE		TRUE	5.64	3.69E-08	9.72E-06	9.23	3.81E-18
cg10813544			NA		NA	5.64	3.70E-08	9.73E-06	7.42	1.08E-12
cg19854744	FOXR1	Body	TRUE		NA	5.64	3.71E-08	9.75E-06	5.44	1.08E-07

cg14331899	CYBASC3 ;CYBASC3; CYBASC3	TSS1500;5 UTR;5UTR	NA		NA	-5.64	3.72E-08	9.77E-06	-7.12	7.24E-12
cg12447744			TRUE		NA	-5.64	3.74E-08	9.80E-06	-6.77	6.22E-11
cg13834112			NA		NA	5.64	3.75E-08	9.81E-06	4.95	1.22E-06
cg18941614	UBTF;UB TF;UBTF	Body;Body; Body	TRUE	Gene_Associated	TRUE	5.64	3.75E-08	9.81E-06	9.08	1.13E-17
cg26810214	HDAC7;H DAC7	Body;Body	TRUE	Promoter_Associated	NA	5.64	3.76E-08	9.82E-06	6.98	1.70E-11
cg17932096			NA		NA	5.64	3.77E-08	9.84E-06	4.57	6.89E-06
cg12084388			NA		TRUE	5.64	3.77E-08	9.84E-06	6.21	1.63E-09
cg19419291	ELL2	Body	NA	Promoter_Associated	NA	-5.64	3.78E-08	9.86E-06	-5.08	6.53E-07
cg21353232	SEZ6L	TSS1500	NA		NA	5.64	3.79E-08	9.86E-06	6.88	3.21E-11
cg14122633	EXOC3	Body	NA		NA	-5.64	3.79E-08	9.86E-06	-4.25	2.81E-05
cg11740099	SECTM1	3UTR	TRUE	Unclassified	TRUE	5.64	3.80E-08	9.88E-06	5.95	7.22E-09
cg15917625	CREB3L1	Body	NA	Unclassified	TRUE	5.64	3.81E-08	9.88E-06	5.61	4.39E-08
cg13429270	FAM38B	Body	NA		NA	-5.64	3.81E-08	9.88E-06	-6.11	2.82E-09
cg02760031	TCF15	TSS1500	NA	Unclassified	TRUE	5.64	3.82E-08	9.90E-06	6.9	2.73E-11
cg03029146			TRUE	Unclassified	NA	5.64	3.82E-08	9.90E-06	6.07	3.69E-09
cg26643377	FBXO2	Body	NA	Unclassified	NA	5.64	3.82E-08	9.90E-06	6.34	7.87E-10
cg23213887	FBN2	Body	NA	Unclassified_Cell_type_specific	NA	5.63	3.83E-08	9.90E-06	5.44	1.04E-07
cg02319392	HSBP1	TSS1500	NA	Promoter_Associated	NA	-5.63	3.84E-08	9.92E-06	-4.32	2.09E-05
cg23547017	HOXD3	5UTR	NA		NA	5.63	3.87E-08	9.99E-06	6.53	2.55E-10
cg12026563			TRUE	Promoter_Associated	NA	5.63	3.88E-08	9.99E-06	5.82	1.46E-08



cg18653195	SMOC1;S MOC1	Body;Body	TRUE		NA	-5.63	3.88E-08	9.99E-06	-5.87	1.10E-08
cg18424393	FSTL5;FS TL5;FSTL 5	TSS200;TS S200;TSS2 00	NA		NA	5.63	3.89E-08	1.00E-05	3.98	8.59E-05
cg05070626	SYT17	Body	NA	Unclassifie d	TRUE	5.63	3.91E-08	1.01E-05	6.7	9.70E-11
cg26551865	TRABD	5UTR	NA	Promoter_A ssociated	TRUE	5.63	3.92E-08	1.01E-05	5.39	1.37E-07
cg16961816	DLX6AS	Body	NA	Unclassifie d_Cell_type _specific	NA	5.63	3.94E-08	1.01E-05	4.88	1.69E-06
cg03703839	BANP;BA NP	5UTR;5UT R	TRUE	Promoter_A ssociated	NA	5.63	3.94E-08	1.01E-05	6.48	3.42E-10
cg24867468	TMC6;TM C6	3UTR;3UT R	NA	Gene_Asso ciated	NA	5.63	3.96E-08	1.01E-05	4.27	2.59E-05
cg20222695	ANKLE2	Body	TRUE		NA	-5.63	3.96E-08	1.01E-05	-4.91	1.45E-06
cg12552820	SKI	Body	TRUE	Promoter_A ssociated	TRUE	5.63	3.96E-08	1.01E-05	6.27	1.20E-09
cg13066983	FAM19A1	Body	NA	Unclassifie d_Cell_type _specific	NA	5.63	3.97E-08	1.02E-05	5.02	8.79E-07
cg08257009			NA		NA	-5.63	3.98E-08	1.02E-05	-6.09	3.17E-09
cg16187635			TRUE		NA	-5.63	3.98E-08	1.02E-05	-6.1	3.15E-09
cg01866606			TRUE		TRUE	5.62	4.05E-08	1.03E-05	6.35	7.58E-10
cg19417526	NTM;NTM ;NTM;NT M	Body;Body; Body;Body	TRUE		NA	-5.62	4.06E-08	1.03E-05	-3.68	0.00027220 6
cg23690893	TECR	Body	NA		NA	5.62	4.06E-08	1.03E-05	5.9	9.14E-09
cg10201685	CAMK2B; CAMK2B; CAMK2B; CAMK2B; CAMK2B; CAMK2B; CAMK2B;	Body;Body; Body;Body; Body;Body; Body;Body	TRUE		NA	5.62	4.06E-08	1.03E-05	7.3	2.26E-12

	CAMK2B									
cg05524458	ANKRD33B	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.62	4.06E-08	1.03E-05	6.97	1.83E-11
cg13882345			NA		NA	-5.62	4.08E-08	1.04E-05	-5.19	3.72E-07
cg10986946	DKK3;DKK3;DKK3	Body;Body;Body	TRUE		NA	-5.62	4.08E-08	1.04E-05	-4.7	3.94E-06
cg11373356	RGS12;RGS12	Body;Body	NA		TRUE	-5.62	4.08E-08	1.04E-05	-5.39	1.39E-07
cg02778678			NA		NA	-5.62	4.09E-08	1.04E-05	-2.74	0.006504862
cg17747199			TRUE		NA	-5.62	4.09E-08	1.04E-05	-3.93	0.000105243
cg09650495			NA		NA	-5.62	4.10E-08	1.04E-05	-4.15	4.24E-05
cg09875444			TRUE	Unclassified	TRUE	5.62	4.10E-08	1.04E-05	5.7	2.79E-08
cg11973877	OSBPL9;OSBPL9;OSBPL9;OSBPL9;OSBPL9;OSBPL9	TSS200;Body;5UTR;Body;Body;TSS200;TSS200	NA	Promoter_Associated	TRUE	5.62	4.11E-08	1.04E-05	5.6	4.55E-08
cg12580783	WNT10B	Body	NA	Unclassified_Cell_type_specific	NA	-5.62	4.16E-08	1.05E-05	-4.95	1.22E-06
cg00418663	C10orf105;CDH23	5UTR;Body	NA		NA	-5.62	4.17E-08	1.05E-05	-4.45	1.20E-05
cg04636269			NA		NA	5.62	4.18E-08	1.05E-05	6.22	1.57E-09
cg10426658			NA		NA	-5.62	4.21E-08	1.06E-05	-4.21	3.37E-05
cg05281645			TRUE	Promoter_Associated_Cell_type_specific	TRUE	5.61	4.26E-08	1.07E-05	7.35	1.73E-12
cg17545418	MT1IP	Body	NA	Unclassified	NA	5.61	4.28E-08	1.07E-05	7	1.49E-11

				d_Cell_type _specific						
cg13428567	C1orf175; C1orf175	TSS1500;T SS1500	NA		NA	-5.61	4.28E-08	1.07E-05	-4.05	6.41E-05
cg21752469			TRUE		TRUE	5.61	4.28E-08	1.07E-05	4.93	1.32E-06
cg05323725	LHX1;LHX 1	1stExon;5U TR	TRUE		NA	5.61	4.29E-08	1.07E-05	5.81	1.55E-08
cg09278980			NA	Promoter_A ssociated	TRUE	5.61	4.32E-08	1.08E-05	6.19	1.90E-09
cg23395310	SNHG7;S NHG7;SN HG7	TSS1500;T SS1500;TS S1500	NA		NA	-5.61	4.32E-08	1.08E-05	-4.41	1.42E-05
cg02159731			TRUE	Unclassifie d_Cell_type _specific	TRUE	5.61	4.32E-08	1.08E-05	6.46	3.82E-10
cg26745764	GLB1L3	Body	NA		NA	5.61	4.33E-08	1.08E-05	6.26	1.24E-09
cg01450736	C1orf110	TSS200	NA		NA	-5.61	4.35E-08	1.08E-05	-2.76	0.00608924 8
cg26589753			TRUE		NA	-5.61	4.36E-08	1.09E-05	-5.1	5.89E-07
cg26189283	RAG1AP1 ;RAG1AP 1;RAG1A P1	Body;Body; Body	NA	Promoter_A ssociated_ Cell_type_s pecific	NA	-5.61	4.38E-08	1.09E-05	-5.56	5.81E-08
cg25195968			TRUE		NA	-5.61	4.38E-08	1.09E-05	-3.87	0.00012952
cg14224203	C9orf86;C 9orf86	Body;Body	TRUE	Unclassifie d_Cell_type _specific	TRUE	5.61	4.40E-08	1.09E-05	6.17	2.10E-09
cg10028884	PER1	5UTR	NA	Promoter_A ssociated	NA	5.61	4.43E-08	1.10E-05	8.22	5.33E-15
cg26652266			TRUE		NA	-5.61	4.43E-08	1.10E-05	-7.24	3.44E-12
cg05549970			NA		NA	-5.61	4.43E-08	1.10E-05	-6.81	4.84E-11
cg09717585	ZCCHC14	Body	NA		NA	-5.61	4.44E-08	1.10E-05	-5.12	5.40E-07
cg21732625	ADAMTSL 5	Body	NA	Unclassifie d_Cell_type _specific	NA	-5.61	4.44E-08	1.10E-05	-4.97	1.08E-06

cg25015613	MMP1;MM P1	Body;Body	NA	Unclassified	NA	-5.61	4.45E-08	1.10E-05	-3.04	0.002530054
cg03998104	TLX2	3UTR	NA		NA	5.61	4.45E-08	1.10E-05	5.69	2.84E-08
cg11824827	ZNF668	Body	NA	Gene_Associated_Cell_type_specific	NA	5.61	4.45E-08	1.10E-05	4.01	7.48E-05
cg21815667	HOXD8	TSS1500	TRUE	Unclassified_Cell_type_specific	NA	5.61	4.47E-08	1.10E-05	4.74	3.26E-06
cg00728848	C6orf114; GFOD1	5UTR;Body	NA		NA	-5.61	4.47E-08	1.10E-05	-5.7	2.79E-08
cg16164923	CCDC150	TSS1500	NA	Promoter_Associated	NA	-5.6	4.48E-08	1.10E-05	-6.04	4.24E-09
cg15975217	MAML3	Body	NA	Unclassified_Cell_type_specific	TRUE	5.6	4.53E-08	1.11E-05	6.58	1.97E-10
cg05192898	TXNRD1; TXNRD1; TXNRD1; TXNRD1; TXNRD1	TSS1500;TSS1500;Body;TSS1500;TSS1500	NA		NA	-5.6	4.54E-08	1.11E-05	-5.17	4.09E-07
cg25365260	LOC404266;LOC404266;LOC404266;LOC404266;HOXB5	Body;Body;Body;Body;Body	NA		NA	5.6	4.56E-08	1.12E-05	5.25	2.74E-07
cg03311232			NA		NA	5.6	4.56E-08	1.12E-05	7.83	7.42E-14
cg08070646	LOC283404	Body	TRUE	Unclassified	NA	5.6	4.60E-08	1.13E-05	6.04	4.35E-09
cg11721554	MIR377	TSS1500	TRUE		NA	-5.6	4.60E-08	1.13E-05	-5.84	1.31E-08
cg23715749	GRIK3	Body	TRUE		NA	-5.6	4.62E-08	1.13E-05	-5.96	6.73E-09
cg26895571	C1orf212; C1orf212; C1orf212	Body;Body;Body	NA		NA	-5.6	4.64E-08	1.13E-05	-5.25	2.73E-07
cg16497340			NA		TRUE	5.6	4.66E-08	1.14E-05	4.61	5.72E-06

cg12563372			TRUE		NA	5.6	4.68E-08	1.14E-05	4.09	5.50E-05
cg15131146	MAN1C1	Body	NA	Unclassified_Cell_type_specific	NA	5.6	4.69E-08	1.14E-05	5.78	1.76E-08
cg15657888	IL1F9;IL1F9	5UTR;1stExon	NA		NA	-5.6	4.70E-08	1.14E-05	-4.84	2.00E-06
cg27648946	RHOBTB1;RHOBTB1	Body;TSS200	NA		TRUE	5.59	4.72E-08	1.15E-05	7.26	2.96E-12
cg11607742	PSMD8	Body	NA		NA	-5.59	4.73E-08	1.15E-05	-4.39	1.54E-05
cg11429111			NA		NA	5.59	4.74E-08	1.15E-05	5.16	4.33E-07
cg03454711			NA		TRUE	5.59	4.74E-08	1.15E-05	6.39	5.92E-10
cg05164634	WNT10B	TSS1500	NA		NA	5.59	4.75E-08	1.15E-05	6.51	2.89E-10
cg04323925			TRUE	Promoter_Associated	NA	-5.59	4.78E-08	1.16E-05	-5.86	1.13E-08
cg05636891			NA		NA	-5.59	4.79E-08	1.16E-05	-5.32	2.00E-07
cg22974982			NA		NA	5.59	4.80E-08	1.16E-05	6.43	4.72E-10
cg05492306	ERCC1;ERCC1;ERCC1	TSS1500;TSS1500;TSS1500	NA	Promoter_Associated	NA	-5.59	4.81E-08	1.16E-05	-5.58	5.06E-08
cg22907103	CYBASC3;CYBASC3;CYBASC3;CYBASC3	5UTR;1stExon;5UTR;Body	NA		NA	-5.59	4.82E-08	1.17E-05	-6.19	1.87E-09
cg19619387	RTN4RL1	Body	TRUE		NA	5.59	4.83E-08	1.17E-05	8	2.34E-14
cg12958813	ATP6V1G3;ATP6V1G3	Body;Body	NA		NA	-5.59	4.85E-08	1.17E-05	-5.6	4.51E-08
cg01969115	TPPP	3UTR	NA		NA	-5.59	4.87E-08	1.17E-05	-3.06	0.002395723
cg26061357	SMARCD3;SMARCD3	Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	5.59	4.87E-08	1.17E-05	7.79	9.30E-14
cg08968329	FAM38A	Body	TRUE	Unclassified	NA	5.59	4.88E-08	1.17E-05	6.2	1.73E-09

				d_Cell_type _specific						
cg22840216			TRUE		NA	5.59	4.90E-08	1.18E-05	6.37	6.56E-10
cg26407309	TBXAS1;H IPK2;HIPK 2;TBXAS1	5UTR;TSS 1500;TSS1 500;5UTR	NA	Unclassifie d_Cell_type _specific	NA	-5.59	4.91E-08	1.18E-05	-6.08	3.35E-09
cg18335991	SEMA7A; SEMA7A; SEMA7A	Body;Body; 5UTR	NA	Unclassifie d_Cell_type _specific	NA	-5.59	4.91E-08	1.18E-05	-2.4	0.01693400 7
cg22539182			TRUE	Unclassifie d	NA	5.59	4.92E-08	1.18E-05	6.04	4.37E-09
cg17108958			TRUE		NA	-5.59	4.93E-08	1.18E-05	-3.79	0.00017927 7
cg05991902	ASAP2;AS AP2	Body;Body	TRUE		NA	-5.59	4.93E-08	1.18E-05	-5.63	4.01E-08
cg10191210			TRUE	Promoter_A ssociated	NA	5.59	4.95E-08	1.18E-05	6.64	1.39E-10
cg17024919	ZNF385D	Body	TRUE		NA	-5.59	4.96E-08	1.19E-05	-5.57	5.37E-08
cg17515753			NA		TRUE	5.58	5.00E-08	1.19E-05	4.24	2.98E-05
cg12972233	C9orf47;C 9orf47;C9 orf47;S1P R3;C9orf4 7	1stExon;1st Exon;5UTR ;TSS1500;5 UTR	NA		NA	5.58	5.06E-08	1.20E-05	5.72	2.41E-08
cg20305578			NA		NA	5.58	5.06E-08	1.20E-05	6.04	4.25E-09
cg16439198	CYP1B1	5UTR	NA	Unclassifie d_Cell_type _specific	NA	-5.58	5.06E-08	1.20E-05	-4.54	7.98E-06
cg06213327	SORBS2; SORBS2; SORBS2; SORBS2; SORBS2; SORBS2; SORBS2; SORBS2	Body;Body; Body;Body; Body;Body; Body;Body	NA		NA	5.58	5.08E-08	1.21E-05	8.32	2.66E-15
cg24227984	HDGF2;H	Body;Body	NA		TRUE	5.58	5.09E-08	1.21E-05	7.77	1.09E-13

	DGF2									
cg10132208	ZSCAN1	5UTR	NA		TRUE	5.58	5.09E-08	1.21E-05	5.98	6.11E-09
cg21707187			TRUE	Unclassified_Cell_type_specific	NA	5.58	5.11E-08	1.21E-05	5.87	1.07E-08
cg18020955			NA	Promoter_Associated	NA	5.58	5.12E-08	1.22E-05	5.71	2.54E-08
cg02433564			TRUE	Unclassified	TRUE	5.58	5.14E-08	1.22E-05	6.91	2.70E-11
cg04462662	ZDHHC7; ZDHHC7	Body;Body	TRUE		NA	-5.58	5.16E-08	1.22E-05	-2.64	0.008775197
cg13518625			TRUE	Unclassified	TRUE	-5.58	5.17E-08	1.22E-05	-5.06	6.99E-07
cg05957567	BCL7A;BCL7A	Body;Body	TRUE		NA	5.58	5.19E-08	1.23E-05	5.53	6.63E-08
cg04330449	NEUROG1	1stExon	TRUE		NA	5.58	5.21E-08	1.23E-05	7.75	1.24E-13
cg18150339	06-Mar	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	-5.58	5.24E-08	1.24E-05	-7.4	1.22E-12
cg01554316	GALNT2	Body	TRUE	Unclassified_Cell_type_specific	NA	-5.58	5.24E-08	1.24E-05	-3.99	8.04E-05
cg09479818	PEPD;PEPD;PEPD	Body;Body;Body	NA		NA	-5.57	5.24E-08	1.24E-05	-4.18	3.77E-05
cg17288560			TRUE		NA	5.57	5.26E-08	1.24E-05	6.92	2.52E-11
cg09956037	LSP1;LSP1;LSP1;LSP1	5UTR;5UTR;Body;5UTR	NA	Unclassified_Cell_type_specific	NA	-5.57	5.29E-08	1.24E-05	-6.78	5.84E-11
cg14912644			TRUE	Unclassified_Cell_type_specific	TRUE	5.57	5.29E-08	1.24E-05	5.54	6.29E-08
cg24845763	TRIM26	5UTR	NA		NA	-5.57	5.31E-08	1.25E-05	-4.05	6.42E-05
cg08032924	CMTM2	TSS1500	NA	Unclassified_Cell_type_specific	NA	5.57	5.31E-08	1.25E-05	7.85	6.22E-14

cg03372205			NA		NA	-5.57	5.32E-08	1.25E-05	-3.06	0.002413377
cg20359445	IKZF4	Body	TRUE	Promoter_Associated	NA	5.57	5.33E-08	1.25E-05	6.68	1.04E-10
cg12244275			NA	Unclassified_Cell_type_specific	NA	5.57	5.35E-08	1.25E-05	5.72	2.41E-08
cg21056723	LOC644145	TSS200	TRUE		NA	5.57	5.37E-08	1.25E-05	6.69	1.03E-10
cg18252616			NA		NA	5.57	5.37E-08	1.25E-05	4.83	2.08E-06
cg16199747			TRUE		TRUE	5.57	5.37E-08	1.25E-05	6.63	1.45E-10
cg14941291			NA	Unclassified	TRUE	5.57	5.38E-08	1.26E-05	5.53	6.81E-08
cg06096184	LRIG1	Body	NA		NA	5.57	5.40E-08	1.26E-05	7.45	8.68E-13
cg02408538	CHST15	Body	NA		NA	-5.57	5.40E-08	1.26E-05	-3.78	0.000183856
cg10030504	ODZ4	Body	NA		NA	-5.57	5.41E-08	1.26E-05	-4.66	4.67E-06
cg01915791	HSPB6	Body	NA		NA	5.57	5.44E-08	1.26E-05	6.63	1.40E-10
cg08703971	SGPP1	1stExon	NA		NA	5.57	5.44E-08	1.27E-05	3.67	0.000288382
cg00938658			NA		TRUE	5.57	5.47E-08	1.27E-05	5.02	8.69E-07
cg21491587	TGM6	TSS200	NA		NA	-5.57	5.48E-08	1.27E-05	-3.52	0.000503275
cg11209338			TRUE	Unclassified_Cell_type_specific	NA	5.57	5.49E-08	1.27E-05	7.54	5.04E-13
cg02758964			NA		NA	-5.57	5.51E-08	1.28E-05	-6.66	1.18E-10
cg07211212			NA		NA	5.56	5.53E-08	1.28E-05	4.95	1.18E-06
cg15775779	EDAR	5UTR	NA		NA	-5.56	5.54E-08	1.28E-05	-3.19	0.00155608
cg03969763			TRUE		NA	-5.56	5.54E-08	1.28E-05	-5.29	2.23E-07
cg12893373	MINA;MINA;MINA	Body;Body;Body	TRUE		NA	-5.56	5.55E-08	1.28E-05	-5.66	3.29E-08
cg08427067			TRUE		NA	5.56	5.56E-08	1.28E-05	3.49	0.000553135



cg22491548	PRRT4	5UTR	TRUE	Promoter_Associated_Cell_type_specific	TRUE	5.56	5.59E-08	1.29E-05	4.67	4.48E-06
cg01347682	MAML3	Body	NA	Unclassified_Cell_type_specific	TRUE	5.56	5.63E-08	1.30E-05	7.15	5.78E-12
cg05562851	UNC119B	Body	NA	Gene_Associated	TRUE	5.56	5.64E-08	1.30E-05	5.76	2.01E-08
cg08832414	ECE2;ECE2;ECE2	Body;TSS1500;TSS1500;TSS1500	TRUE		NA	5.56	5.65E-08	1.30E-05	7.2	4.30E-12
cg11693364	ZNF69	TSS1500	NA	Unclassified	TRUE	5.56	5.66E-08	1.30E-05	6.51	2.87E-10
cg05826596	GPATCH8	Body	TRUE	Unclassified_Cell_type_specific	NA	5.56	5.66E-08	1.30E-05	4.71	3.78E-06
cg16289618	LOC285830;LOC285830	Body;Body	NA	Unclassified	TRUE	5.56	5.73E-08	1.31E-05	6.53	2.57E-10
cg23470914	MBP;MBP	Body;Body	NA		NA	-5.56	5.75E-08	1.32E-05	-4.52	8.60E-06
cg12910851	IL1R2;IL1R2;IL1R2	1stExon;5UTR;5UTR	NA		NA	-5.56	5.82E-08	1.33E-05	-4.17	3.93E-05
cg03811629	PSD2	5UTR	TRUE	Unclassified_Cell_type_specific	NA	5.55	5.85E-08	1.34E-05	6.75	7.03E-11
cg22331349	ZNF577;ZNF577;ZNF577	TSS200;TSS200;TSS200	NA		TRUE	-5.55	5.91E-08	1.35E-05	-4.92	1.40E-06
cg21960680	OTP	Body	NA		NA	5.55	5.92E-08	1.35E-05	3.79	0.000177671
cg02433882	SLC29A1;SLC29A1	TSS1500;TSS1500	NA		TRUE	5.55	5.94E-08	1.36E-05	6.65	1.28E-10
cg17281810	BCOR;BCOR	5UTR;5UTR	NA	Unclassified_Cell_type_specific	NA	5.55	5.94E-08	1.36E-05	5.92	8.46E-09

cg05597001	C6orf103	TSS200	TRUE		TRUE	5.55	5.95E-08	1.36E-05	4.28	2.48E-05
cg22626659			TRUE		TRUE	5.55	5.96E-08	1.36E-05	7.21	4.18E-12
cg08195512			NA	Unclassified_Cell_type_specific	TRUE	5.55	5.97E-08	1.36E-05	7.75	1.22E-13
cg17751153	EXOC3	Body	NA	Promoter_Associated	NA	-5.55	5.98E-08	1.36E-05	-5.81	1.51E-08
cg08435157	NPTN;NPTN;NPTN	Body;Body;Body;Body	TRUE		NA	-5.55	6.03E-08	1.37E-05	-4.63	5.34E-06
cg12345672	SND1	Body	NA		NA	5.55	6.04E-08	1.37E-05	6.73	7.82E-11
cg23612492	WDR25;WDR25	Body;Body	TRUE		NA	-5.55	6.04E-08	1.37E-05	-3.46	0.000618815
cg11498607	RUNX1	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.55	6.06E-08	1.37E-05	7.07	9.54E-12
cg06792538			NA		NA	-5.55	6.07E-08	1.37E-05	-5.11	5.55E-07
cg22158992	NKD2	Body	NA		NA	5.55	6.07E-08	1.37E-05	7.39	1.33E-12
cg09805403	GSPT1;GSPT1;GSPT1	TSS1500;TSS1500;TSS200	NA		NA	-5.55	6.10E-08	1.38E-05	-4.25	2.76E-05
cg25841987	FAM198B;FAM198B;FAM198B	TSS200;5UTR	NA		NA	5.55	6.10E-08	1.38E-05	3.52	0.000498173
cg07390647	ST3GAL6	5UTR	NA		NA	5.55	6.11E-08	1.38E-05	7.85	6.36E-14
cg24867665	BEND7;BEND7	TSS1500;TSS1500	TRUE		TRUE	5.54	6.14E-08	1.39E-05	5.8	1.62E-08
cg12194336	FLNB;FLNB;FLNB;FLNB	Body;Body;Body;Body	TRUE	Unclassified_Cell_type_specific	NA	5.54	6.17E-08	1.39E-05	6.36	6.96E-10
cg12916580			TRUE		TRUE	-5.54	6.18E-08	1.39E-05	-6.41	5.34E-10
cg17291521			NA		NA	5.54	6.19E-08	1.39E-05	2.14	0.033287241
cg05692123			NA		NA	5.54	6.20E-08	1.40E-05	5.97	6.44E-09

cg11130441	C2orf58	TSS200	NA		NA	5.54	6.23E-08	1.40E-05	6.59	1.87E-10
cg03731896	GYS1;GYS1;GYS1	Body;Body;Body	NA	Gene_Associated	TRUE	5.54	6.25E-08	1.40E-05	6.65	1.27E-10
cg15825970	IFI30	TSS1500	TRUE	Promoter_Associated	NA	5.54	6.25E-08	1.40E-05	5.7	2.77E-08
cg14956201	TRIO	Body	NA		NA	5.54	6.25E-08	1.40E-05	6.13	2.54E-09
cg16165575			TRUE		NA	5.54	6.27E-08	1.41E-05	6.91	2.72E-11
cg25734726	SERTAD3;SERTAD3;SERTAD3	1stExon;5UTR	NA		NA	5.54	6.29E-08	1.41E-05	7.48	7.20E-13
cg11584690			NA	Unclassified_Cell_type_specific	NA	5.54	6.31E-08	1.41E-05	7.99	2.44E-14
cg13320898	FOXK1	Body	NA		NA	-5.54	6.33E-08	1.41E-05	-6.58	1.95E-10
cg20383948	COL18A1;COL18A1;COL18A1	Body;Body;Body	NA	Unclassified	TRUE	5.54	6.33E-08	1.41E-05	7.58	3.77E-13
cg10919344	OR5A1	TSS200	NA		NA	-5.54	6.35E-08	1.42E-05	-4.35	1.87E-05
cg00526387			TRUE		NA	-5.54	6.36E-08	1.42E-05	-2.63	0.009001878
cg27664085			NA	Unclassified	TRUE	-5.54	6.36E-08	1.42E-05	-3.2	0.001536587
cg00875805	MAML3	Body	NA	Unclassified_Cell_type_specific	TRUE	5.54	6.37E-08	1.42E-05	7.26	3.04E-12
cg07001963	CXCL12;CXCL12;CXCL12	Body;Body;Body	NA		NA	5.54	6.38E-08	1.42E-05	7.01	1.44E-11
cg05384139	PITPNM2	5UTR	TRUE	Unclassified	NA	5.54	6.39E-08	1.42E-05	3.1	0.002084579
cg03565659	TPH2	TSS200	NA	Unclassified	NA	5.53	6.46E-08	1.44E-05	5.46	9.70E-08
cg07955474	IRF8	5UTR	NA		NA	-5.53	6.54E-08	1.45E-05	-5.56	5.70E-08
cg00841725	MCF2L;MCF2L	Body;Body	TRUE	Unclassified_Cell_type	TRUE	5.53	6.55E-08	1.45E-05	5.76	2.03E-08

				_specific						
cg00077426	EXOC3	Body	NA	Gene_Associated_Cell_type_specific	NA	-5.53	6.55E-08	1.45E-05	-4.33	2.00E-05
cg26467753	C12orf59	Body	NA		NA	5.53	6.58E-08	1.46E-05	3.99	8.32E-05
cg12196853			TRUE		TRUE	5.53	6.63E-08	1.47E-05	5.44	1.05E-07
cg12428727			TRUE	Unclassified_Cell_type_specific	NA	5.53	6.65E-08	1.47E-05	6.45	4.23E-10
cg22627981	LMX1A	Body	NA		NA	5.53	6.68E-08	1.48E-05	6.06	3.78E-09
cg23657179	C10orf41; C10orf41	Body;Body	NA		NA	-5.53	6.69E-08	1.48E-05	-5.61	4.39E-08
cg24704940			NA		NA	-5.53	6.69E-08	1.48E-05	-4.07	5.84E-05
cg25375860	SGPP2	Body	TRUE		NA	-5.53	6.75E-08	1.49E-05	-7.2	4.36E-12
cg07355757			TRUE	Unclassified	NA	5.53	6.76E-08	1.49E-05	7.09	8.63E-12
cg00257296	MSI1	Body	TRUE		TRUE	5.53	6.76E-08	1.49E-05	8.28	3.50E-15
cg15560495			NA	Unclassified_Cell_type_specific	TRUE	5.53	6.77E-08	1.49E-05	7.27	2.78E-12
cg03599078			NA		NA	5.53	6.77E-08	1.49E-05	7.04	1.20E-11
cg10461878	IQCJ;IQCJ	Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.53	6.77E-08	1.49E-05	-4.41	1.41E-05
cg23893406			TRUE		NA	-5.53	6.78E-08	1.49E-05	-4.59	6.31E-06
cg08549396	PAX7;PAX7; PAX7	Body;Body; Body	NA	Unclassified_Cell_type_specific	NA	5.53	6.78E-08	1.49E-05	5.59	4.98E-08
cg01282195	TP53INP1; TP53INP1	Body;Body	NA		NA	-5.52	6.82E-08	1.49E-05	-4.21	3.28E-05
cg02970836			NA	Unclassified_Cell_type_specific	NA	5.52	6.88E-08	1.51E-05	7.11	7.58E-12

cg12956688			TRUE	Promoter_Associated	NA	5.52	6.91E-08	1.51E-05	6.82	4.53E-11
cg17509612	C9orf78;USP20;USP20	TSS1500;5UTR;5UTR	NA	Promoter_Associated	NA	5.52	6.92E-08	1.51E-05	3.94	0.000101789
cg10084993	SLC9A3R2;SLC9A3R2	Body;Body	NA	Unclassified	NA	-5.52	6.96E-08	1.52E-05	-6.83	4.23E-11
cg11699517	BAHCC1	Body	NA		NA	5.52	6.96E-08	1.52E-05	3.82	0.000163098
cg10462778	ERGIC1	Body	TRUE		NA	5.52	6.96E-08	1.52E-05	6.04	4.35E-09
cg12129117	CAPN2;CAPN2	Body;Body	NA		NA	5.52	6.98E-08	1.52E-05	5.14	4.83E-07
cg09768821	UQCRHL	TSS1500	NA		NA	-5.52	6.99E-08	1.52E-05	-4.72	3.61E-06
cg27634695	ANK2	TSS200	TRUE	Unclassified_Cell_type_specific	TRUE	5.52	6.99E-08	1.52E-05	3.18	0.001614222
cg24771152	VAR5	Body	NA		NA	5.52	6.99E-08	1.52E-05	5.91	8.88E-09
cg16202734	ARL5C	Body	NA	Unclassified	NA	5.52	7.00E-08	1.52E-05	6.3	9.83E-10
cg06573856	GPT2;GPT2	Body;Body	NA	Gene_Associated	NA	-5.52	7.02E-08	1.53E-05	-4.1	5.25E-05
cg04692023			NA		NA	5.52	7.05E-08	1.53E-05	6.33	8.53E-10
cg25536676	DHCR24	TSS1500	NA		NA	-5.52	7.08E-08	1.53E-05	-4.04	6.63E-05
cg12029281	TEAD3	5UTR	NA	Unclassified_Cell_type_specific	NA	5.52	7.08E-08	1.53E-05	7.25	3.18E-12
cg25033360	OSCP1	Body	TRUE	Unclassified	TRUE	5.52	7.10E-08	1.54E-05	6.95	2.04E-11
cg19221545	KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2	TSS200;TSS200;TSS200;TSS200;TSS200	NA	Unclassified	NA	5.52	7.16E-08	1.55E-05	6.82	4.71E-11
cg02544002	PLXND1	Body	NA		NA	-5.51	7.20E-08	1.56E-05	-5.02	8.41E-07
cg20201177			TRUE		NA	-5.51	7.23E-08	1.56E-05	-5.74	2.15E-08

cg12543949	FAM198B; FAM198B; FAM198B; FAM198B; FAM198B	TSS1500;5 UTR;1stEx on;5UTR;1s tExon	NA		NA	5.51	7.24E-08	1.56E-05	7.3	2.35E-12
cg00548098			TRUE		TRUE	-5.51	7.27E-08	1.57E-05	-6.02	4.71E-09
cg00839579	MEOX2	TSS1500	TRUE		NA	5.51	7.27E-08	1.57E-05	5	9.40E-07
cg07349805	PCGF3	5UTR	TRUE		TRUE	-5.51	7.28E-08	1.57E-05	-4.77	2.83E-06
cg14881470	CLYBL	Body	NA	Unclassified	NA	5.51	7.30E-08	1.57E-05	7.26	3.04E-12
cg21917740			NA		NA	5.51	7.32E-08	1.57E-05	5.83	1.35E-08
cg03138928	EPHX1	5UTR	TRUE		NA	-5.51	7.33E-08	1.57E-05	-6.43	4.53E-10
cg16770774	DTX4	Body	NA		NA	-5.51	7.33E-08	1.57E-05	-5.41	1.22E-07
cg02575712			TRUE	Unclassified	TRUE	5.51	7.34E-08	1.57E-05	6.3	9.83E-10
cg15948030	VAR5	Body	NA		NA	5.51	7.37E-08	1.58E-05	6.97	1.84E-11
cg20471736	SERPINB 13	3UTR	NA	Unclassified_Cell_type specific	NA	-5.51	7.37E-08	1.58E-05	-5.72	2.51E-08
cg02456087			TRUE	Unclassified_Cell_type specific	NA	5.51	7.38E-08	1.58E-05	3.68	0.00027558 6
cg10520740	CACNA2D 4	Body	TRUE		NA	-5.51	7.39E-08	1.58E-05	-5.8	1.58E-08
cg02509086			NA		NA	5.51	7.41E-08	1.58E-05	5.67	3.21E-08
cg05758467	HDAC4	Body	TRUE		TRUE	5.51	7.42E-08	1.59E-05	5.41	1.25E-07
cg07160746	KCNS1	Body	NA	Promoter_Associated_Cell_type specific	TRUE	5.51	7.43E-08	1.59E-05	5.14	4.73E-07
cg15369821			TRUE		NA	5.51	7.45E-08	1.59E-05	4.91	1.48E-06
cg11933779	C17orf46; LOC10013 3991;LOC 10013399	Body;Body; TSS1500	NA	Promoter_Associated	TRUE	5.51	7.47E-08	1.59E-05	5.78	1.81E-08

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cg07711099	DNAH2	TSS1500	NA	Unclassified_Cell_type_specific	NA	5.51	7.47E-08	1.59E-05	6.46	3.82E-10
cg01015663	TCEA3	Body	TRUE		NA	-5.51	7.48E-08	1.59E-05	-5.51	7.22E-08
cg14924469	LOC286467	TSS200	NA	Promoter_Associated	NA	5.51	7.48E-08	1.59E-05	6.38	6.24E-10
cg13088465	CABC1	Body	NA		NA	-5.5	7.56E-08	1.61E-05	-3.49	0.000555225
cg18456459	RAB31	TSS1500	NA		TRUE	5.5	7.58E-08	1.61E-05	6.12	2.74E-09
cg17174023	KLHDC7B	1stExon	NA	Promoter_Associated	NA	5.5	7.63E-08	1.62E-05	6.91	2.67E-11
cg05513983	SOX2OT	Body	NA		NA	5.5	7.65E-08	1.62E-05	4.57	7.04E-06
cg21757127			NA	Unclassified_Cell_type_specific	NA	5.5	7.67E-08	1.62E-05	5.59	4.84E-08
cg02039485	ITPK1;ITPK1;ITPK1	Body;Body;Body	TRUE		NA	-5.5	7.69E-08	1.63E-05	-6.85	3.74E-11
cg07152755			NA		NA	5.5	7.73E-08	1.64E-05	6.27	1.18E-09
cg27563968			TRUE		NA	-5.5	7.73E-08	1.64E-05	-3.74	0.00021974
cg02932364			TRUE		TRUE	-5.5	7.75E-08	1.64E-05	-5.32	1.96E-07
cg13480549	PRKCZ;PRKCZ;PRKCZ	5UTR;Body;5UTR	NA	Unclassified_Cell_type_specific	NA	5.5	7.76E-08	1.64E-05	5.09	6.15E-07
cg13558754	HSPB6;C19orf55	1stExon;TS S1500	NA		NA	5.5	7.79E-08	1.64E-05	6.47	3.75E-10
cg08129129	BCL11B;BCL11B	Body;Body	TRUE	Unclassified_Cell_type_specific	NA	-5.5	7.82E-08	1.65E-05	-5.67	3.14E-08
cg18340983	P2RY2;P2RY2;P2RY2	5UTR;5UTR;5UTR	NA		NA	-5.5	7.82E-08	1.65E-05	-5.15	4.57E-07
cg04265797	SSTR1	3UTR	NA	Unclassified_Cell_type_specific	TRUE	5.5	7.83E-08	1.65E-05	3.79	0.000177115

cg25061843			NA		NA	5.5	7.84E-08	1.65E-05	5.08	6.53E-07
cg01435643	MCF2L;MCF2L	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	5.5	7.89E-08	1.66E-05	3.58	0.000403983
cg09941381	RTKN2	Body	NA	Promoter_Associated_Cell_type_specific	NA	5.5	7.92E-08	1.66E-05	6.32	8.91E-10
cg04175292	SLC29A1;SLC29A1	TSS200;TSS200	NA	Unclassified	TRUE	5.5	7.93E-08	1.67E-05	7.72	1.48E-13
cg24567424	FAM155A	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	5.49	7.96E-08	1.67E-05	5.86	1.13E-08
cg20299703	DNAJC6	Body	TRUE	Unclassified	NA	5.49	8.01E-08	1.68E-05	8.28	3.43E-15
cg04703476	AATF	Body	TRUE		NA	-5.49	8.03E-08	1.68E-05	-5.68	2.97E-08
cg23833543			NA		NA	-5.49	8.06E-08	1.69E-05	-4.86	1.85E-06
cg03450842	ZMIZ1	5UTR	TRUE		NA	-5.49	8.11E-08	1.70E-05	-4.94	1.26E-06
cg10004897	TADA2B	Body	NA		NA	5.49	8.16E-08	1.71E-05	5.36	1.63E-07
cg24783499	ZC3H3	Body	TRUE	Unclassified	NA	5.49	8.18E-08	1.71E-05	6.28	1.09E-09
cg09145546			NA	Unclassified_Cell_type_specific	NA	5.49	8.18E-08	1.71E-05	7.7	1.72E-13
cg22098115	ARHGEF4;ARHGEF4	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	5.49	8.19E-08	1.71E-05	7.85	6.45E-14
cg24738611	WDR43;SNORD53	Body;TSS200	NA		NA	5.49	8.21E-08	1.71E-05	7.32	2.05E-12
cg22952459	C10orf99	TSS1500	NA		NA	-5.49	8.21E-08	1.71E-05	-5.37	1.54E-07
cg06917763			TRUE	Unclassified_Cell_type_specific	NA	5.49	8.24E-08	1.72E-05	5.71	2.65E-08
cg00397849	ALS2CL	5UTR	NA		NA	-5.49	8.27E-08	1.72E-05	-6.23	1.46E-09
cg13430755			TRUE		TRUE	5.49	8.31E-08	1.73E-05	7.13	6.81E-12



cg25851152	MIR146B	TSS1500	TRUE	Unclassified	NA	5.49	8.31E-08	1.73E-05	5.18	4.01E-07
cg02839351	HDGF2;HDGF2	Body;Body	NA		TRUE	5.49	8.35E-08	1.73E-05	7.28	2.70E-12
cg06153634	KRT7	Body	NA	Unclassified_Cell_type_specific	NA	5.49	8.35E-08	1.73E-05	5.46	9.45E-08
cg00323916	PDXP	Body	TRUE	Promoter_Associated	TRUE	5.48	8.39E-08	1.74E-05	4.25	2.81E-05
cg05845217			NA		NA	-5.48	8.40E-08	1.74E-05	-4.78	2.71E-06
cg17180633			TRUE		TRUE	5.48	8.41E-08	1.74E-05	5.77	1.92E-08
cg19808205	TCTEX1D1	TSS200	TRUE		NA	5.48	8.41E-08	1.74E-05	5.66	3.35E-08
cg11558474	TMEM2;TMEM2	5UTR;5UTR	NA		NA	5.48	8.42E-08	1.74E-05	3.96	9.07E-05
cg04881103			TRUE	Unclassified	TRUE	5.48	8.43E-08	1.74E-05	6.11	2.93E-09
cg20564892	KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2;KCNIP2	1stExon;5UTR;1stExon;1stExon;1stExon;5UTR;5UTR;5UTR;5UTR;1stExon;5UTR;1stExon	NA	Unclassified	NA	5.48	8.44E-08	1.74E-05	8.41	1.41E-15
cg16465643			NA		NA	-5.48	8.45E-08	1.74E-05	-4.89	1.59E-06
cg15191887	TPPP	3UTR	NA		NA	-5.48	8.45E-08	1.74E-05	-4.84	2.01E-06
cg07441794	USH1G	Body	NA		NA	-5.48	8.48E-08	1.75E-05	-5.78	1.81E-08
cg00069261	CDR2	TSS1500	NA	Promoter_Associated	NA	5.48	8.61E-08	1.77E-05	5.42	1.18E-07
cg11267683	DNAH17	Body	NA		NA	-5.48	8.63E-08	1.78E-05	-5.39	1.38E-07
cg20284629			TRUE	Unclassified_Cell_type_specific	NA	5.48	8.71E-08	1.79E-05	5.93	7.68E-09

cg26472326			TRUE		NA	5.48	8.73E-08	1.79E-05	3.95	9.73E-05
cg07051721	C2orf76	Body	NA	Unclassified	NA	5.48	8.77E-08	1.80E-05	5.2	3.51E-07
cg26312888			NA		NA	-5.48	8.77E-08	1.80E-05	-5.94	7.33E-09
cg16942327			TRUE		NA	5.48	8.77E-08	1.80E-05	3.13	0.001889507
cg08533783	C11orf88; C11orf88	TSS200;TS S200	NA	Unclassified_Cell_type_specific	NA	5.48	8.79E-08	1.80E-05	6.86	3.55E-11
cg26624026			TRUE	Promoter_Associated	NA	5.48	8.80E-08	1.80E-05	6.23	1.46E-09
cg04197371			TRUE		NA	-5.48	8.80E-08	1.80E-05	-5.36	1.59E-07
cg16274376	LATS2	5UTR	NA	Promoter_Associated	NA	-5.48	8.80E-08	1.80E-05	-4.78	2.73E-06
cg17025741	CAMK2D; CAMK2D; CAMK2D; CAMK2D; CAMK2D; CAMK2D	Body;Body; Body;Body; Body;Body	TRUE	Unclassified	TRUE	5.48	8.81E-08	1.80E-05	5.66	3.38E-08
cg09762533	LSP1;LSP 1;LSP1;LS P1	5UTR;5UT R;Body;5U TR	NA	Unclassified	NA	-5.47	8.82E-08	1.80E-05	-7.19	4.62E-12
cg00429107			NA		NA	5.47	8.87E-08	1.81E-05	6.8	5.29E-11
cg27534072			TRUE		NA	-5.47	8.88E-08	1.81E-05	-3.23	0.001382206
cg22851200	TRIP6	Body	NA		NA	-5.47	8.94E-08	1.82E-05	-4.97	1.07E-06
cg22029284	PRDM16; PRDM16	Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.47	8.97E-08	1.82E-05	-4.81	2.35E-06
cg20469744	ENOX1;E NOX1	Body;Body	TRUE		NA	5.47	8.99E-08	1.83E-05	4.1	5.22E-05
cg22999025			TRUE		NA	5.47	9.00E-08	1.83E-05	6.23	1.49E-09
cg21488279	PRDM6	Body	NA		NA	5.47	9.02E-08	1.83E-05	6.8	5.19E-11
cg00835857	SPATC1;S PATC1;SP	1stExon;5U TR;1stExon	NA		NA	5.47	9.02E-08	1.83E-05	5.06	6.95E-07

	ATC1;SPATC1	;5UTR								
cg24125648	SERINC4;C15orf63	TSS1500;TSS200	NA	Promoter_Associated	NA	5.47	9.04E-08	1.83E-05	5.89	9.76E-09
cg05059607	PITPNC1;PITPNC1	Body;Body	TRUE		NA	5.47	9.05E-08	1.83E-05	6.51	2.99E-10
cg09157272	GRAMD2	Body	TRUE		NA	5.47	9.06E-08	1.83E-05	6.98	1.77E-11
cg15892280	ETS2	5UTR	NA	Promoter_Associated	NA	-5.47	9.06E-08	1.83E-05	-5.68	3.03E-08
cg08602008			NA	Unclassified_Cell_type_specific	TRUE	5.47	9.07E-08	1.83E-05	7.22	3.90E-12
cg09194159	HOXB4	1stExon	NA	Unclassified	NA	5.47	9.09E-08	1.84E-05	5.95	7.01E-09
cg21952686	ARHGEF5	Body	NA		NA	-5.47	9.10E-08	1.84E-05	-4.53	8.29E-06
cg03431846	REC8;REC8	TSS200;TSS200	NA	Promoter_Associated	NA	5.47	9.12E-08	1.84E-05	6.43	4.78E-10
cg13528854	BST1	1stExon	NA	Unclassified_Cell_type_specific	TRUE	5.47	9.14E-08	1.84E-05	6.43	4.69E-10
cg00242020	GOT1L1;GOT1L1	5UTR;1stExon	NA		NA	-5.47	9.15E-08	1.84E-05	-4.39	1.54E-05
cg02807859			TRUE		NA	5.47	9.15E-08	1.84E-05	5.28	2.35E-07
cg21398186	PPBP	TSS1500	NA		NA	-5.47	9.16E-08	1.84E-05	-5.78	1.73E-08
cg11452354	SLC29A1;SLC29A1	TSS200;TSS200	NA	Unclassified	TRUE	5.47	9.18E-08	1.85E-05	7.35	1.63E-12
cg26403416	TFF2	TSS200	NA		NA	-5.47	9.19E-08	1.85E-05	-5.21	3.40E-07
cg23169111	AVP	TSS1500	NA		NA	5.47	9.28E-08	1.86E-05	5.69	2.82E-08
cg00029282	PROM2;PROM2;PROM2	Body;Body;Body	NA		NA	-5.47	9.28E-08	1.86E-05	-5.72	2.39E-08
cg26797723	WNT5A	Body	NA		NA	-5.46	9.29E-08	1.86E-05	-2.11	0.035838914
cg08423533	MKX	Body	NA	Unclassified	NA	5.46	9.30E-08	1.86E-05	6.03	4.53E-09
cg20788020			TRUE		NA	-5.46	9.32E-08	1.86E-05	-8.12	1.02E-14

cg24049493	HIVEP3;HIVEP3	TSS1500;TSS1500	NA	Promoter_Associated	NA	5.46	9.32E-08	1.86E-05	5.38	1.47E-07
cg22122174	SLC29A1;SLC29A1	TSS200;TSS200	NA	Unclassified	TRUE	5.46	9.32E-08	1.86E-05	7.26	2.96E-12
cg16667251	SPTBN1	5UTR	TRUE	Unclassified_Cell_type_specific	NA	5.46	9.35E-08	1.87E-05	6.25	1.35E-09
cg14517133	PRPH2	3UTR	TRUE		NA	5.46	9.37E-08	1.87E-05	5.78	1.78E-08
cg11213707			NA	Unclassified_Cell_type_specific	NA	-5.46	9.38E-08	1.87E-05	-5.11	5.44E-07
cg09499849	ACVR1;ACVR1	5UTR;5UTR	TRUE		NA	5.46	9.45E-08	1.88E-05	5.56	5.76E-08
cg17253407			TRUE		TRUE	-5.46	9.46E-08	1.88E-05	-4.78	2.69E-06
cg26081841			NA		NA	5.46	9.48E-08	1.89E-05	7.02	1.37E-11
cg10539670			NA		NA	-5.46	9.50E-08	1.89E-05	-4.87	1.76E-06
cg06450952	C8orf56	Body	TRUE		NA	-5.46	9.51E-08	1.89E-05	-2.66	0.008210547
cg02412399			TRUE		NA	-5.46	9.52E-08	1.89E-05	-3.66	0.000293394
cg09120877			NA	Unclassified_Cell_type_specific	NA	5.46	9.53E-08	1.89E-05	3.86	0.000135975
cg17109725			NA		NA	-5.46	9.54E-08	1.89E-05	-5.4	1.33E-07
cg18114235	ZNF69	TSS200	NA	Unclassified	TRUE	5.46	9.54E-08	1.89E-05	5.09	6.12E-07
cg27110177			NA		NA	-5.46	9.56E-08	1.89E-05	-6.41	5.19E-10
cg16519300	FBLIM1	TSS1500	NA		TRUE	5.46	9.57E-08	1.90E-05	6.86	3.59E-11
cg22165480			NA		NA	-5.46	9.62E-08	1.90E-05	-5.74	2.16E-08
cg21922731	HSD17B6;HSD17B6	5UTR;1stExon	NA	Unclassified_Cell_type_specific	NA	5.46	9.63E-08	1.90E-05	5.99	5.61E-09
cg10773972	FAM108C1	Body	TRUE		NA	-5.46	9.64E-08	1.90E-05	-3.22	0.001397027
cg20529344			NA		NA	5.46	9.64E-08	1.90E-05	5.99	5.58E-09

cg27125591			TRUE		NA	5.46	9.65E-08	1.90E-05	4.63	5.35E-06
cg25262528	NT5E	TSS1500	NA	Unclassified	NA	5.46	9.71E-08	1.91E-05	6.08	3.43E-09
cg25882597	LPIN3	TSS200	TRUE	Unclassified	NA	-5.46	9.71E-08	1.91E-05	-4.7	3.89E-06
cg20403938	HOXC10	TSS1500	NA	Unclassified_Cell_type_specific	NA	5.46	9.71E-08	1.91E-05	5.88	1.02E-08
cg19496155	FAAH	Body	NA		NA	-5.46	9.73E-08	1.91E-05	-4.78	2.74E-06
cg02927448	UHRF1BP1L;UHRF1BP1L	Body;Body	NA	Unclassified_Cell_type_specific	NA	5.45	9.79E-08	1.93E-05	5.37	1.55E-07
cg00794174			NA		NA	-5.45	9.81E-08	1.93E-05	-5.88	1.02E-08
cg23173517	IL16	Body	TRUE	Unclassified	TRUE	5.45	9.82E-08	1.93E-05	4.72	3.59E-06
cg23755074	EXPH5;EXPH5	Body;TSS1500	NA		NA	-5.45	9.83E-08	1.93E-05	-5.88	1.03E-08
cg05651143			NA		NA	5.45	9.84E-08	1.93E-05	6.16	2.13E-09
cg09190188			NA		NA	5.45	9.84E-08	1.93E-05	5.44	1.08E-07
cg15342087			TRUE		TRUE	-5.45	9.88E-08	1.93E-05	-5.55	6.10E-08
cg17490844	HS6ST1	Body	TRUE		NA	-5.45	9.88E-08	1.93E-05	-3.2	0.001518789
cg09539908	REEP4	Body	NA	Gene_Associated	NA	5.45	9.90E-08	1.94E-05	6.52	2.69E-10
cg23762633	ODC1	TSS1500	NA	Promoter_Associated	NA	5.45	9.91E-08	1.94E-05	6.73	8.02E-11
cg25203031	SGIP1	TSS200	NA	Unclassified_Cell_type_specific	TRUE	5.45	9.93E-08	1.94E-05	5.4	1.32E-07
cg23963024			NA		NA	5.45	9.94E-08	1.94E-05	7.08	9.39E-12
cg08021797	C16orf74	TSS1500	NA	Unclassified	NA	-5.45	9.94E-08	1.94E-05	-4.74	3.19E-06
cg01606085	TLL1	TSS200	NA		TRUE	5.45	9.95E-08	1.94E-05	6.05	3.96E-09
cg18252039			NA		NA	5.45	9.97E-08	1.94E-05	3.36	0.000864513

cg13897222			TRUE		NA	-5.45	1.00E-07	1.95E-05	-3.99	8.29E-05
cg22865700			NA		NA	-5.45	1.00E-07	1.95E-05	-6.84	4.05E-11
cg03699074	FAM38A	Body	NA	Promoter_Associated	NA	5.45	1.00E-07	1.95E-05	8.82	7.60E-17
cg03430633	PVRL1;PVRL1;PVRL1	Body;Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	5.45	1.00E-07	1.95E-05	6.24	1.42E-09
cg05709770			TRUE	Unclassified_Cell_type_specific	NA	5.45	1.01E-07	1.95E-05	6.55	2.24E-10
cg22822656			NA		TRUE	5.45	1.01E-07	1.96E-05	5.72	2.40E-08
cg21995484			NA		TRUE	5.45	1.01E-07	1.96E-05	5.31	2.09E-07
cg24960947	GAL3ST3	5UTR	NA	Unclassified_Cell_type_specific	NA	5.45	1.01E-07	1.96E-05	6.86	3.57E-11
cg08827700	SLC22A18;SLC22A18;SLC22A18AS	Body;Body;TSS1500	NA		NA	-5.45	1.01E-07	1.96E-05	-4.4	1.48E-05
cg18617808	RNF216;RNF216	Body;Body	TRUE	Unclassified	TRUE	5.45	1.01E-07	1.96E-05	7.23	3.58E-12
cg00653312	SLC7A5	3UTR	TRUE		NA	-5.45	1.01E-07	1.96E-05	-5.86	1.13E-08
cg00028013	LOXL1	TSS200	NA		NA	-5.45	1.01E-07	1.96E-05	-5.12	5.20E-07
cg15538767			TRUE		NA	5.45	1.02E-07	1.97E-05	5.73	2.33E-08
cg24259244	ZIC5	TSS200	NA		NA	5.45	1.03E-07	1.98E-05	5.64	3.72E-08
cg05000748	RUNX1	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.45	1.03E-07	1.98E-05	6.36	7.17E-10
cg00414384	MTL5;MTL5	Body;Body	NA	Unclassified	NA	5.44	1.03E-07	1.98E-05	8.27	3.60E-15
cg27073068	REST	TSS1500	NA		NA	-5.44	1.03E-07	1.99E-05	-3.06	0.002409806
cg24673765	HSPB6;C19orf55	1stExon;TSS1500	NA		NA	5.44	1.04E-07	1.99E-05	6.26	1.24E-09

[illegible]

**eTable 2. RefFreeEWAS selected CpGs.** Table listing the 897 CpGs, passing the Bonferroni threshold of  $\sim 1e-7$  in the unadjusted analysis, and with a FDR<0.05 in the adjusted RefFreeEWAS analysis. Table lists the CpG ID from the Illumina 450k Beadchip, the t-statistic, P-value and Q value from the unadjusted analysis, plus the corresponding values from the adjusted RefFreeEWAS analysis.

IlmnID	UCSC_RefGene_Name	UCSC_RefGene_Group	Enhancer	Regulatory_Feature_Group	DHS	t	P	Q	t(RefFreeEWAS)	P(RefFreeEWAS)	Q(RefFreeEWAS)	t(REF,n=390)	P(REF,n=390)
cg05575921	AHRR	Body	TRUE		NA	-20.34	1.04E-59	2.99E-54	-22.32	2.04E-67	8.69E-62	-17.09	6.17E-47
cg05951221			NA		NA	-17.77	1.06E-49	1.53E-44	-19.07	7.82E-55	1.66E-49	-16.39	3.08E-44
cg02162897	CYP1B1	Body	NA	NonGen e_Associated_Cell_type_specific	NA	-15.14	1.74E-39	1.68E-34	-14.12	1.35E-35	9.54E-31	-15.28	6.05E-40
cg21566642			NA		NA	-14.33	2.27E-36	1.64E-31	-17.36	3.93E-48	4.18E-43	-13.29	2.14E-32
cg20408276	CYP1B1	Body	NA	NonGen e_Associated_Cell_type_specific	NA	-13.34	1.33E-32	7.65E-28	-11.57	3.76E-26	1.00E-21	-15.03	5.73E-39
cg03636183	F2RL3	Body	NA		TRUE	-12.5	1.64E-29	7.91E-25	-11.85	3.73E-27	1.06E-22	-11.37	2.16E-25
cg14753356			TRUE		TRUE	-11.44	1.16E-25	4.78E-21	-13.77	2.81E-34	1.71E-29	-9.22	4.05E-18
cg01940273			NA		NA	-11.29	3.89E-25	1.40E-20	-14.21	6.37E-36	5.42E-31	-9.43	8.99E-19
cg16323911			TRUE		NA	-11.24	5.82E-25	1.87E-20	-12.26	1.24E-28	4.41E-24	-11.22	7.31E-25
cg10880599	GPX2	Body	NA		NA	-11.1	1.80E-24	5.20E-20	-10.2	2.26E-21	2.91E-17	-11.82	5.71E-27
cg23167235			NA		NA	-10.93	7.32E-24	1.92E-19	-9.69	1.19E-19	1.27E-15	-11.61	3.09E-26
cg26516004	CYP1A1	TSS1500	NA		NA	-10.82	1.80E-23	4.33E-19	-12.58	8.34E-30	3.94E-25	-9.32	1.94E-18



cg13378563	KCNIP3	Body	NA		NA	-10.02	9.59E-21	1.98E-16	-10.92	7.61E-24	1.54E-19	-8.83	7.30E-17
cg12802310	CYP1B1	TSS1500	TRUE		NA	-9.95	1.62E-20	3.12E-16	-10.42	4.06E-22	6.40E-18	-11.52	6.36E-26
cg14663177	C2orf58	Body	TRUE		TRUE	9.82	4.52E-20	8.16E-16	10.31	9.64E-22	1.37E-17	10.93	8.11E-24
cg06126421			TRUE		TRUE	-9.79	5.44E-20	9.24E-16	-18.16	2.89E-51	4.09E-46	-8.9	4.34E-17
cg23160522	CYP1A1	5UTR	NA		NA	-9.76	7.18E-20	1.15E-15	-11.5	6.94E-26	1.74E-21	-9.21	4.47E-18
cg19753864			TRUE		NA	-9.69	1.16E-19	1.76E-15	-12.21	1.82E-28	5.96E-24	-10.28	1.36E-21
cg17248487	AHRR	Body	TRUE	Unclassified_Cell_type_specific	TRUE	-9.56	3.09E-19	4.47E-15	-10	1.13E-20	1.37E-16	-9.29	2.45E-18
cg11554391	AHRR	Body	NA		NA	-9.56	3.28E-19	4.51E-15	-9.37	1.30E-18	1.21E-14	-9.43	8.74E-19
cg00565882	CYP1B1	Body	NA		NA	-9.5	4.81E-19	6.32E-15	-11.11	1.66E-24	3.52E-20	-10.94	7.41E-24
cg12101586	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	NA	-9.45	7.19E-19	9.03E-15	-10.02	9.51E-21	1.19E-16	-7.86	5.90E-14
cg06035270			TRUE	Unclassified	NA	9.18	5.28E-18	6.36E-14	6.53	2.60E-10	5.39E-07	10.31	1.08E-21
cg11879188	ABO	Body	NA		NA	-9.1	9.91E-18	1.14E-13	-6.81	4.81E-11	1.22E-07	-8.56	4.85E-16
cg18092474	CYP1A1	TSS1500	NA		NA	-9.03	1.66E-17	1.81E-13	-10.21	2.12E-21	2.82E-17	-8.01	2.14E-14
cg03329539			NA		NA	-9.02	1.69E-17	1.81E-13	-11.2	8.05E-25	1.90E-20	-6.32	8.99E-10
cg20004659	ABCC3;ABCC3	Body;Body	TRUE		TRUE	-9	1.95E-17	2.01E-13	-8.04	1.75E-14	9.91E-11	-7.88	5.37E-14
cg11924019	CYP1A1	TSS1500	NA		NA	-8.94	3.19E-17	3.17E-13	-10.33	8.48E-22	1.29E-17	-7.42	1.07E-12
cg2667260			TRUE		NA	-8.77	1.09E-1	1.05E-1	-8.36	1.86E-1	1.22E-1	-9.56	3.25E-1

4							6	2		5	1		9
cg00370022	CYP1A1	Body	NA		NA	-8.69	1.83E-16	1.68E-12	-9.11	8.65E-18	7.36E-14	-8.05	1.61E-14
cg27492584			TRUE	Unclassified_Cell_type_specific	TRUE	-8.69	1.86E-16	1.68E-12	-10.23	1.90E-21	2.60E-17	-7.76	1.14E-13
cg25189904	GNG12	TSS1500	NA		TRUE	-8.57	4.31E-16	3.77E-12	-8.66	2.24E-16	1.70E-12	-8.72	1.60E-16
cg21715189	CYP1B1	TSS1500	TRUE		NA	-8.56	4.66E-16	3.96E-12	-8.14	8.63E-15	5.03E-11	-9.22	4.18E-18
cg05062676	CYP1B1	TSS1500	TRUE		NA	-8.54	5.46E-16	4.50E-12	-7.34	1.77E-12	6.84E-09	-8.99	2.21E-17
cg16340268	ITPKB	5UTR	NA		NA	8.47	8.62E-16	6.89E-12	6.09	3.12E-09	4.68E-06	9.37	1.40E-18
cg04802238	SLC7A5	Body	NA	Unclassified_Cell_type_specific	NA	-8.47	8.83E-16	6.89E-12	-10.55	1.44E-22	2.44E-18	-8.98	2.43E-17
cg12557254	NDST1	Body	NA		NA	-8.42	1.25E-15	9.51E-12	-6.7	9.09E-11	2.10E-07	-6.01	5.12E-09
cg04144218	AUTS2;AUTS2;AUTS2	Body;Body;Body	TRUE		NA	-8.4	1.47E-15	1.06E-11	-9.55	3.34E-19	3.30E-15	-9.71	1.07E-19
cg21161138	AHRR	Body	NA		NA	-8.4	1.47E-15	1.06E-11	-11.14	1.27E-24	2.83E-20	-8.61	3.35E-16
cg26144569	CYP1B1	TSS1500	TRUE		NA	-8.32	2.59E-15	1.83E-11	-10.32	9.16E-22	1.34E-17	-8.9	4.33E-17
cg14454127	AHRR	Body	TRUE	Unclassified_Cell_type_specific	TRUE	-8.31	2.67E-15	1.83E-11	-6.93	2.30E-11	6.44E-08	-8.01	2.20E-14
cg06492111	SLC7A5	Body	NA		NA	-8.19	6.26E-15	4.20E-11	-6.97	1.81E-11	5.33E-08	-8.34	2.31E-15
cg09935388	GFI1;GFI1;GFI1	Body;Body;Body	TRUE		NA	-8.13	9.41E-15	6.17E-11	-9.79	5.47E-20	6.12E-16	-8.2	5.76E-15

cg03742137	AGAP1;AGAP1	Body;Body	NA	Unclassified	TRUE	8.1	1.19E-14	7.61E-11	5.69	2.90E-08	3.01E-05	7.86	6.11E-14
cg15269394	ATP6V0A1;ATP6V0A1;ATP6V0A1	Body;Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	8.02	2.04E-14	1.28E-10	6.4	5.57E-10	1.06E-06	7.42	1.08E-12
cg05033295			TRUE		NA	-8.01	2.10E-14	1.29E-10	-8.39	1.48E-15	1.02E-11	-8.38	1.71E-15
cg11233000	CASZ1;CASZ1	5UTR;5UTR	TRUE	Unclassified_Cell_type_specific	NA	7.94	3.47E-14	2.09E-10	5.1	5.71E-07	0.000344984	8.52	6.59E-16
cg19723805			TRUE		NA	7.93	3.73E-14	2.20E-10	6.62	1.54E-10	3.41E-07	5.53	6.65E-08
cg00069417	SLC7A5	Body	NA		NA	-7.91	4.06E-14	2.35E-10	-7.59	3.41E-13	1.51E-09	-7.89	5.02E-14
cg12920004			TRUE	Unclassified	TRUE	-7.9	4.49E-14	2.54E-10	-8.69	1.91E-16	1.47E-12	-8.38	1.65E-15
cg10468961	NRG2;NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.89	4.91E-14	2.72E-10	6.12	2.71E-09	4.11E-06	10.57	1.43E-22
cg11439308			TRUE		NA	-7.88	4.99E-14	2.72E-10	-6.61	1.62E-10	3.53E-07	-8.04	1.79E-14
cg16824126	CHADL;L3MBTL2	Body;3UTR	NA		NA	-7.86	6.01E-14	3.22E-10	-8.97	2.48E-17	2.00E-13	-7.56	4.45E-13
cg01998750	FRMD4B	Body	NA		NA	7.84	6.46E-14	3.39E-10	8.44	1.05E-15	7.33E-12	9.14	7.49E-18
cg04482794	ITPKB	5UTR	NA		TRUE	7.83	7.20E-14	3.71E-10	5.26	2.65E-07	0.000182998	10.28	1.30E-21
cg13570656	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	NA	-7.81	8.06E-14	4.08E-10	-7.59	3.36E-13	1.51E-09	-6.67	1.15E-10

cg08003353			TRUE		TRUE	7.81	8.33E-14	4.14E-10	6.93	2.35E-11	6.53E-08	11.72	1.26E-26
cg02426623	TSPAN9;TS PAN9	5UTR;5 UTR	TRUE		NA	-7.78	9.69E-14	4.74E-10	-8.26	3.82E-15	2.35E-11	-8.72	1.60E-16
cg01278596	NRG2; NRG2; NRG2; NRG2	Body;Body;Body;Body	NA		TRUE	7.77	1.08E-13	5.19E-10	5.35	1.71E-07	0.000129039	10.34	8.16E-22
cg20082547	TGM6; TGM6	5UTR;1 stExon	NA		NA	-7.76	1.12E-13	5.31E-10	-7.59	3.41E-13	1.51E-09	-5.89	9.64E-09
cg27064337			TRUE		TRUE	7.76	1.17E-13	5.45E-10	7.09	8.61E-12	2.80E-08	9.02	1.74E-17
cg14389122	EDC3; EDC3; EDC3	Body;Body;Body	TRUE		NA	-7.75	1.24E-13	5.69E-10	-7.59	3.52E-13	1.51E-09	-7.84	7.00E-14
cg00073090			NA	Promoter_Associated	NA	-7.74	1.30E-13	5.85E-10	-10.69	4.93E-23	8.73E-19	-7.45	8.55E-13
cg14711690	ITPKB	Body	NA	Promoter_Associated	TRUE	7.73	1.38E-13	6.11E-10	5.33	1.85E-07	0.00013738	9.18	5.68E-18
cg15992535	NRG2; NRG2; NRG2; NRG2	Body;Body;Body;Body	NA		TRUE	7.7	1.69E-13	7.41E-10	5.91	8.81E-09	1.12E-05	9.84	4.01E-20
cg10801607	SLC3A1	Body	TRUE	Unclassified_Cell_type_specific	TRUE	7.69	1.76E-13	7.58E-10	5.97	6.35E-09	8.45E-06	6.55	2.27E-10
cg05652757	NRG2; NRG2; NRG2; NRG2	Body;Body;Body;Body	NA		TRUE	7.69	1.86E-13	7.88E-10	5.48	8.75E-08	7.50E-05	10.08	6.13E-21
cg27560132			TRUE		NA	-7.68	1.89E-13	7.92E-10	-5.46	9.67E-08	8.10E-05	-6.48	3.45E-10
cg23678985			TRUE		NA	-7.68	1.95E-13	8.05E-10	-6.69	9.87E-11	2.27E-07	-10.22	2.21E-21

cg10513161	ABCC5;ABCC5	Body;Body	TRUE		NA	-7.66	2.17E-13	8.82E-10	-6.83	4.17E-11	1.07E-07	-6.43	4.53E-10
cg24884265	NDST1	Body	NA		NA	-7.65	2.35E-13	9.43E-10	-6.47	3.68E-10	7.42E-07	-5.58	5.11E-08
cg04972459			TRUE	Unclassified_Cell_type_specific	TRUE	7.65	2.40E-13	9.49E-10	4.37	1.68E-05	0.00475267	7.99	2.45E-14
cg00227225	SEMA6D;SEMA6D;SEMA6D;SEMA6D;SEMA6D;SEMA6D	5UTR;5UTR;5UTR;5UTR;5UTR	NA	Unclassified_Cell_type_specific	TRUE	7.64	2.43E-13	9.49E-10	5.29	2.25E-07	0.000161417	9.28	2.57E-18
cg04764812			NA	Unclassified_Cell_type_specific	NA	7.63	2.68E-13	1.03E-09	4.03	6.93E-05	0.013509991	7.5	6.46E-13
cg00781658	HNRNPUL1;HNRNPUL1	Body;Body	NA	Gene_Associated_Cell_type_specific	TRUE	7.63	2.71E-13	1.03E-09	4.92	1.39E-06	0.000690335	7.78	1.04E-13
cg21489622	HIVEP2	5UTR	NA	Promoter_Associated	TRUE	7.62	2.82E-13	1.05E-09	5.21	3.34E-07	0.000221093	9.39	1.16E-18
cg04264781	SLC7A5	Body	NA		NA	-7.62	2.85E-13	1.05E-09	-5.45	1.01E-07	8.28E-05	-8.16	7.88E-15
cg24129626	CD300LG;CD300LG;CD300LG;CD300L	TSS200;TSS200;TSS200;TSS200	TRUE	Unclassified	NA	7.61	3.11E-13	1.12E-09	7.99	2.33E-14	1.25E-10	8.84	6.56E-17

	G												
cg05157702	PIR;PIR	5UTR;5UTR	NA		NA	-7.61	3.11E-13	1.12E-09	-7.22	3.63E-12	1.32E-08	-8.48	8.32E-16
cg22060611	NRG2;NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	7.6	3.18E-13	1.13E-09	5.68	3.00E-08	3.09E-05	9.6	2.40E-19
cg10791966	ALDH3A1;ALDH3A1	Body;Body	NA		NA	-7.59	3.57E-13	1.26E-09	-6.23	1.48E-09	2.42E-06	-5.35	1.71E-07
cg18033092	C11orf49;C11orf49;C11orf49	Body;Body;Body	TRUE		NA	7.58	3.76E-13	1.31E-09	3.98	8.55E-05	0.015644272	8.26	3.86E-15
cg05711474			TRUE		TRUE	7.58	3.83E-13	1.31E-09	8.06	1.50E-14	8.62E-11	7.81	8.42E-14
cg02905900	ACOT11;ACOT11	TSS1500;TSS1500	NA		TRUE	7.56	4.27E-13	1.45E-09	6.54	2.36E-10	5.00E-07	9.24	3.53E-18
cg05964212	SLC25A20	TSS1500	NA	Promoter_Associated	NA	7.52	5.57E-13	1.86E-09	5.91	8.68E-09	1.10E-05	7.19	4.77E-12
cg24805089	GRK6;GRK6;GRK6	Body;Body;Body	NA		NA	-7.52	5.60E-13	1.86E-09	-9.26	2.94E-18	2.61E-14	-7.58	3.75E-13
cg26432350	NBEAL2	Body	NA	Gene_Associated	NA	7.51	6.03E-13	1.98E-09	6.5	2.96E-10	6.06E-07	9.89	2.71E-20
cg22936884	TPPP	3UTR	NA		NA	-7.49	6.52E-13	2.12E-09	-4.29	2.36E-05	0.006085304	-6.17	2.07E-09
cg07251887	LOC10130933;RE	TSS1500;Body	NA		TRUE	-7.49	6.71E-13	2.15E-09	-8.89	4.36E-17	3.43E-13	-8.07	1.41E-14

	CQL5												
cg15999165	PAM;PAM;PAM;PAM	TSS200;TSS200;TSS200;TSS200	NA		NA	7.48	7.07E-13	2.24E-09	5.16	4.28E-07	0.000273862	9.43	9.08E-19
cg14898623	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	7.47	7.82E-13	2.45E-09	4.82	2.20E-06	0.000972481	7.43	1.00E-12
cg13167372			NA	Unclassified	NA	7.46	7.90E-13	2.45E-09	7.2	4.13E-12	1.45E-08	6.13	2.60E-09
cg04916091	JAK3	5UTR	NA	Unclassified	NA	7.46	8.25E-13	2.54E-09	6.56	2.14E-10	4.56E-07	8.48	8.28E-16
cg08697797	UGT1A10;UGT1A6;UGT1A8;UGT1A4;UGT1A3;UGT1A6;UGT1A9;UGT1A7;UGT1A1;UGT1A5	Body;Body;Body;Body;Body;Body;TSS200;Body	NA		NA	-7.45	8.67E-13	2.64E-09	-6.38	6.15E-10	1.14E-06	-6.96	1.89E-11
cg17934130			NA		NA	-7.44	9.12E-13	2.72E-09	-7.08	9.23E-12	2.95E-08	-4.93	1.31E-06
cg07945335	CD300LG;CD300LG;CD300LG;CD300LG	TSS200;TSS200;TSS200;TSS200	TRUE	Unclassified	NA	7.44	9.13E-13	2.72E-09	7.13	6.68E-12	2.22E-08	9.2	4.77E-18
cg1439918	GSN;	5UTR;5	NA		NA	7.42	1.02E-1	3.00E-0	4.95	1.22E-0	0.00062	5.31	2.02E-0

3	GSN; GSN; GSN; GSN; GSN; GSN	UTR;5UTR; 5UTR; 5UTR					2	9		6	4156		7
cg27200446	MDFI	5UTR	NA		TRUE	7.41	1.10E-12	3.21E-09	5.06	6.95E-07	0.000397632	10.09	5.71E-21
cg21160290	ABO	Body	NA		NA	-7.4	1.22E-12	3.53E-09	-5.51	7.19E-08	6.41E-05	-6.99	1.63E-11
cg23874600	UGT1A10;UGT1A6;UGT1A9;UGT1A7;UGT1A8	Body;1stExon;5UTR;Body;Body;Body	NA		NA	-7.39	1.27E-12	3.63E-09	-7.59	3.49E-13	1.51E-09	-7.22	3.75E-12
cg19479935			NA		NA	-7.39	1.31E-12	3.72E-09	-5.22	3.16E-07	0.000212246	-8.17	7.34E-15
cg00107629	DGKZ; DGKZ; DGKZ; DGKZ	Body;Body;Body;Body	TRUE	Gene_Associated	NA	7.38	1.34E-12	3.74E-09	6.2	1.76E-09	2.82E-06	9.57	3.14E-19
cg16374343	ABR;ABR	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	7.37	1.44E-12	4.01E-09	6.73	7.59E-11	1.81E-07	9.74	8.73E-20
cg08094280	SLC7A5	3UTR	NA		NA	-7.37	1.47E-12	4.04E-09	-6.92	2.46E-11	6.78E-08	-7.95	3.16E-14
cg19353431			TRUE	Unclassified_Cell_type_specific	NA	-7.37	1.48E-12	4.04E-09	-7.59	3.50E-13	1.51E-09	-5.59	4.81E-08
cg17228232	BAIAP2;BAIAP2;BAI	Body;Body;Body;Body	NA		NA	-7.35	1.61E-12	4.35E-09	-7.55	4.44E-13	1.89E-09	-6.86	3.59E-11



	AP2;B AIAP2												
cg15048832	TSC22 D2	Body	NA		NA	7.35	1.63E-12	4.35E-09	4.89	1.56E-06	0.000752773	5.93	7.72E-09
cg08139206			TRUE		TRUE	-7.34	1.75E-12	4.61E-09	-7.77	1.08E-13	5.32E-10	-5.24	2.96E-07
cg24489015	LPO;L PO;LP O	5UTR;B ody;5U TR	NA		NA	7.34	1.76E-12	4.61E-09	4.61	5.76E-06	0.002105154	8.17	7.24E-15
cg13912573	LOC10 01290 66	Body	TRUE		TRUE	-7.34	1.78E-12	4.62E-09	-5.34	1.76E-07	0.000132016	-5.59	4.96E-08
cg10044101	VNN2	5UTR	NA		NA	7.34	1.81E-12	4.67E-09	4.69	4.02E-06	0.001584117	8.85	6.05E-17
cg07554046			TRUE		NA	7.33	1.90E-12	4.82E-09	5.13	4.96E-07	0.000307642	8.81	8.43E-17
cg07720851	KIAA0 182;KI AA018 2	5UTR;B ody	NA	Promote r_Associ ated	NA	7.33	1.90E-12	4.82E-09	3.6	0.000366533	0.042800328	8.63	2.94E-16
cg07541559	ABTB2	Body	TRUE	Unclassi fied_Cell _type_s pecific	TRUE	7.31	2.11E-12	5.30E-09	4.25	2.77E-05	0.006820955	7.37	1.45E-12
cg17619755	VAR5	Body	NA		NA	7.3	2.22E-12	5.50E-09	6.83	4.12E-11	1.07E-07	8.2	6.02E-15
cg10357657	JAK3	5UTR	NA	Unclassi fied	TRUE	7.3	2.23E-12	5.50E-09	5.7	2.67E-08	2.78E-05	8.79	9.32E-17
cg04656424	FAM3 8A	Body	TRUE		TRUE	7.3	2.28E-12	5.58E-09	6.27	1.17E-09	1.98E-06	7.72	1.54E-13
cg03486383	SLC7A 5	3UTR	NA		NA	-7.28	2.55E-12	6.19E-09	-7.5	6.21E-13	2.59E-09	-7.76	1.13E-13
cg25467634	ARHG AP22	Body	TRUE		NA	7.28	2.62E-12	6.30E-09	6.05	3.93E-09	5.65E-06	6.87	3.40E-11
cg20390237			TRUE		NA	-7.25	3.12E-12	7.45E-09	-5.75	2.09E-08	2.26E-05	-5.44	1.06E-07
cg17804100	HIVEP 3;HIVE	5UTR;5 UTR	TRUE	Unclassi fied	TRUE	7.23	3.44E-12	8.15E-09	5.78	1.72E-08	1.94E-05	7.32	2.07E-12

	P3												
cg22549041	CYP1A1	TSS1500	NA		NA	-7.23	3.48E-12	8.17E-09	-9.06	1.26E-17	1.05E-13	-4.23	3.09E-05
cg05590619			NA		TRUE	7.22	3.69E-12	8.59E-09	4.35	1.86E-05	0.005098268	8.42	1.25E-15
cg10172887			TRUE		NA	-7.22	3.75E-12	8.59E-09	-8.01	2.16E-14	1.18E-10	-4.89	1.57E-06
cg08490791			TRUE	Unclassified	NA	7.22	3.75E-12	8.59E-09	5.17	4.11E-07	0.000264732	10.14	3.97E-21
cg17430979	JAKMIP1	Body	NA		NA	-7.22	3.80E-12	8.59E-09	-7.18	4.96E-12	1.69E-08	-6.05	4.02E-09
cg19005335	NCOR2;NCO R2	Body;Body	NA	Promoter_Associated	TRUE	7.22	3.81E-12	8.59E-09	4.76	2.90E-06	0.001227489	7.92	4.02E-14
cg00278392			TRUE		NA	7.22	3.85E-12	8.61E-09	5.4	1.27E-07	9.93E-05	8.3	2.90E-15
cg10925364	GOT1L1	TSS200	NA		NA	-7.2	4.23E-12	9.34E-09	-4.38	1.59E-05	0.004531529	-6.19	1.87E-09
cg05486035			NA	Unclassified_Cell_type_specific	NA	7.2	4.24E-12	9.34E-09	4.6	6.20E-06	0.002206927	7.82	7.55E-14
cg05345286	MDFI	Body	NA		TRUE	7.2	4.33E-12	9.40E-09	7.36	1.54E-12	5.99E-09	8.81	7.99E-17
cg08836861	NQO1;NQO1;NQO1	Body;Body;Body	NA		NA	-7.2	4.35E-12	9.40E-09	-8.01	2.16E-14	1.18E-10	-8.53	6.10E-16
cg19502457	GPX2	1stExon	NA		NA	-7.2	4.39E-12	9.40E-09	-9.93	1.87E-20	2.15E-16	-8.06	1.52E-14
cg23079012			NA		NA	-7.2	4.39E-12	9.40E-09	-9.36	1.38E-18	1.25E-14	-4.72	3.56E-06
cg24090911	AHRR	Body	TRUE	Gene_Associated_Cell_type_specific	TRUE	-7.19	4.44E-12	9.43E-09	-8.97	2.49E-17	2.00E-13	-9.26	3.08E-18
cg26883837			TRUE		TRUE	-7.19	4.53E-12	9.51E-09	-7.2	4.28E-12	1.49E-08	-6.97	1.79E-11

cg05971148	ACTB	Body	NA	Promoter_Associated	NA	7.19	4.54E-12	9.51E-09	6.55	2.32E-10	4.93E-07	5.94	7.65E-09
cg16450654	KCNIP3	Body	NA		NA	-7.19	4.63E-12	9.62E-09	-13.21	3.71E-32	1.97E-27	-6.99	1.61E-11
cg05357229	UGT1A6;UGT1A10;UGT1A9;UGT1A6;UGT1A7;UGT1A8	Body;Body;Body;Body	TRUE		NA	-7.18	4.71E-12	9.67E-09	-5.09	6.05E-07	0.000357725	-6.91	2.66E-11
cg05441854	KIAA0182;KIAA0182	5UTR;Body	NA	Promoter_Associated	NA	7.18	4.72E-12	9.67E-09	4.19	3.55E-05	0.008269698	8.98	2.48E-17
cg25103337	H6PD	TSS1500	NA		NA	7.17	5.19E-12	1.05E-08	7.4	1.22E-12	4.85E-09	7.86	6.01E-14
cg04328729	DIP2C	Body	NA		NA	-7.17	5.23E-12	1.05E-08	-7.01	1.40E-11	4.31E-08	-6.42	4.95E-10
cg06071246	SLC7A5	3UTR	NA		NA	-7.16	5.43E-12	1.09E-08	-9.45	7.06E-19	6.83E-15	-7.53	5.15E-13
cg20629021	CPT1A;CPT1A	Body;Body	NA		NA	-7.15	5.71E-12	1.14E-08	-6.15	2.27E-09	3.53E-06	-7.8	9.06E-14
cg26849830	SSH1	3UTR	TRUE		NA	-7.15	6.00E-12	1.18E-08	-7.52	5.35E-13	2.25E-09	-7.05	1.12E-11
cg04939302			TRUE		NA	-7.15	6.02E-12	1.18E-08	-5.97	6.20E-09	8.37E-06	-5.42	1.17E-07
cg19421526	CRTA1	Body	TRUE		NA	7.12	7.03E-12	1.36E-08	6.33	8.38E-10	1.48E-06	7.96	2.95E-14
cg23409608	PVT1	Body	TRUE		NA	-7.12	7.26E-12	1.40E-08	-7.27	2.73E-12	1.04E-08	-7.46	8.52E-13
cg16786136			TRUE		NA	-7.11	7.69E-12	1.47E-08	-6.97	1.83E-11	5.38E-08	-6.67	1.12E-10
cg2713516	SLC7A	3UTR	NA		NA	-7.1	7.96E-1	1.51E-0	-6.75	6.97E-1	1.69E-0	-7.99	2.47E-1

3	5						2	8		1	7		4
cg02898994	TGM6	TSS200	NA		NA	-7.09	8.44E-12	1.59E-08	-7.22	3.85E-12	1.37E-08	-6.83	4.31E-11
cg09561663	TGM3	TSS200	NA		NA	-7.09	8.69E-12	1.63E-08	-5.43	1.10E-07	8.89E-05	-6.39	5.82E-10
cg25247520	MIR1204;PV T1	TSS200;Body	NA		NA	-7.08	8.92E-12	1.66E-08	-4.49	1.00E-05	0.003142049	-7.98	2.69E-14
cg05631486	TPPP	3UTR	NA		NA	-7.06	1.05E-11	1.93E-08	-3.84	0.000147923	0.023134137	-5.82	1.40E-08
cg16021428	ADCY2	TSS1500	NA		NA	7.06	1.05E-11	1.93E-08	4.55	7.68E-06	0.002611318	9	2.07E-17
cg04964062			NA	Unclassified	TRUE	7.06	1.06E-11	1.93E-08	4.15	4.29E-05	0.009580756	5.66	3.33E-08
cg23209976			TRUE		NA	7.04	1.18E-11	2.14E-08	6.38	6.04E-10	1.13E-06	7.35	1.65E-12
cg20911180	GUCY2E	Body	TRUE		TRUE	7.04	1.19E-11	2.14E-08	5.1	5.93E-07	0.000353181	8.04	1.72E-14
cg03789645	CUL1	TSS1500	NA		NA	7.03	1.20E-11	2.14E-08	4.33	2.00E-05	0.005387071	9.23	3.99E-18
cg05315206	JAK3	5UTR	NA	Unclassified	TRUE	7.03	1.21E-11	2.14E-08	4.87	1.75E-06	0.000823488	8.5	7.65E-16
cg04583842	BANP;BANP	Body;Body	NA	Unclassified	NA	7.03	1.22E-11	2.14E-08	5.68	3.01E-08	3.09E-05	6.45	4.23E-10
cg17924476	AHRR	Body	NA		NA	7.03	1.22E-11	2.14E-08	5.54	6.15E-08	5.67E-05	10.31	1.07E-21
cg23363971	IKZF4;IKZF4	1stExon;5UTR	TRUE	Promoter_Associated	NA	7.03	1.24E-11	2.17E-08	4.75	3.09E-06	0.001285415	8.72	1.58E-16
cg04605590			TRUE		NA	7.02	1.28E-11	2.23E-08	6.24	1.41E-09	2.33E-06	6.77	6.16E-11
cg24313303	PIGV	TSS1500	NA	Promoter_Associated	NA	7.02	1.35E-11	2.34E-08	5.66	3.32E-08	3.36E-05	6.8	5.11E-11
cg20951255			TRUE	Unclassified_Cell_type_specific	NA	7.01	1.42E-11	2.43E-08	4.78	2.73E-06	0.001162338	7.56	4.33E-13

cg25774643	SCT	TSS200	NA	Unclassified_Cell_type_specific	NA	6.99	1.61E-11	2.74E-08	4.24	2.90E-05	0.007086645	6.65	1.26E-10
cg02583484	HNRNPA1;HNRPA1L-2;HNRNPA1	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-6.98	1.69E-11	2.86E-08	-8.39	1.55E-15	1.05E-11	-6.88	3.15E-11
cg24862483	CD300LG;CD300LG;CD300LG;CD300LG	TSS200;TSS200;TSS200;TSS200	TRUE	Unclassified	NA	6.96	1.88E-11	3.17E-08	7.3	2.32E-12	8.89E-09	8.34	2.33E-15
cg24398933	CGN	Body	TRUE		NA	-6.95	2.04E-11	3.43E-08	-6.72	8.17E-11	1.90E-07	-7.54	4.93E-13
cg19589396			TRUE	Unclassified_Cell_type_specific	TRUE	-6.95	2.07E-11	3.45E-08	-4.88	1.64E-06	0.000785754	-6.26	1.23E-09
cg00159243	SELPLG	5UTR	TRUE	Promoter_Associated	TRUE	6.94	2.10E-11	3.49E-08	5.33	1.81E-07	0.000135196	7.26	2.95E-12
cg26337070	ATOH8	Body	TRUE		NA	-6.94	2.23E-11	3.68E-08	-6.33	8.18E-10	1.46E-06	-6.27	1.20E-09
cg03993839	CES1;CES1;CES1	Body;Body;Body	NA		NA	-6.93	2.31E-11	3.80E-08	-6.25	1.31E-09	2.19E-06	-7.91	4.39E-14
cg25720755	CD300LG;CD300LG;CD300LG;CD300LG	5UTR;5UTR;1stExon;1stExon;5UTR;5UTR;1stExon;1stExon	TRUE	Unclassified	NA	6.93	2.35E-11	3.84E-08	6.78	5.61E-11	1.39E-07	8.9	4.18E-17

	00LG; CD300 LG;CD 300LG ;CD30 0LG	stExon											
cg10691866	TPST1	Body	TRUE		NA	-6.92	2.48E-11	4.01E-08	-6.78	5.78E-11	1.42E-07	-6.13	2.56E-09
cg26381210	BMPR1A	5UTR	TRUE		NA	6.92	2.49E-11	4.01E-08	4.17	3.89E-05	0.008901339	6.01	5.07E-09
cg19930417	SECTM1	3UTR	TRUE	Unclassified	NA	6.92	2.52E-11	4.04E-08	5.59	4.76E-08	4.54E-05	8.42	1.33E-15
cg15722293			TRUE	Unclassified	TRUE	6.91	2.59E-11	4.11E-08	4.86	1.80E-06	0.000839531	8.23	4.83E-15
cg05598363	C5orf32	TSS1500	NA	Promoter_Associated	NA	6.91	2.64E-11	4.16E-08	5.06	7.06E-07	0.000401352	9.51	4.67E-19
cg04554564	CYT5B;CYTSB	TSS200;TSS200	NA		NA	-6.89	2.88E-11	4.53E-08	-6.88	3.18E-11	8.45E-08	-6.54	2.47E-10
cg13110239	CSNK1E;CSNK1E	5UTR;5UTR	TRUE		NA	6.89	2.91E-11	4.55E-08	4.76	2.99E-06	0.001260342	9.19	5.30E-18
cg13698261	C9orf3	Body	TRUE		NA	-6.88	3.07E-11	4.76E-08	-4.38	1.61E-05	0.004566774	-6.21	1.67E-09
cg02009088	NRG2;NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	6.88	3.18E-11	4.91E-08	4.94	1.25E-06	0.000631368	9.28	2.72E-18
cg02839029	BAIAP2;BAIAP2;BAIAP2;BAIAP2	Body;Body;Body;Body	NA		NA	-6.87	3.33E-11	5.11E-08	-7.46	7.83E-13	3.17E-09	-6.84	3.98E-11
cg05486924	C3orf21	Body	TRUE		NA	6.86	3.45E-11	5.26E-08	4.23	3.06E-05	0.007383712	8.44	1.13E-15
cg14248553			NA		NA	6.86	3.54E-11	5.38E-08	4.03	7.02E-05	0.013632247	8.45	1.02E-15

cg15935965			TRUE		NA	6.86	3.57E-11	5.40E-08	6.28	1.09E-09	1.87E-06	7.68	1.97E-13
cg03855388	CPT1A;CPT1A	Body;Body	NA		NA	-6.86	3.59E-11	5.40E-08	-5.1	5.75E-07	0.000346759	-8.05	1.67E-14
cg03228288	ZNF83;ZNF83;ZNF83;ZNF83;ZNF83;ZNF83;ZNF83;ZNF83	Body;TSS200;TSS200;TSS200;TSS200;TSS200;TSS200;TSS200	NA	Promoter_Associated	NA	6.85	3.66E-11	5.47E-08	3.99	8.21E-05	0.015155476	5.07	6.83E-07
cg00230120	LOC10292680	TSS1500	TRUE		TRUE	-6.85	3.79E-11	5.65E-08	-6.07	3.62E-09	5.28E-06	-4.18	3.75E-05
cg20489946	NEK3;NEK3;NEK3;NEK3	5UTR;5UTR;Body	NA		NA	6.84	3.92E-11	5.80E-08	4.37	1.70E-05	0.004775948	6	5.36E-09
cg07185131			TRUE		NA	6.84	4.01E-11	5.85E-08	4.75	3.08E-06	0.001285415	6.6	1.69E-10
cg03310939	CUX1;CUX1;CUX1	Body;Body;Body	TRUE		TRUE	6.84	4.01E-11	5.85E-08	4.32	2.11E-05	0.005584479	7.83	7.06E-14
cg02917867			NA	Promoter_Associated	TRUE	-6.84	4.04E-11	5.86E-08	-5.59	4.94E-08	4.70E-05	-6	5.43E-09
cg10266490	ACOT11;ACOT11	TSS200;TSS200	NA	Unclassified	NA	6.84	4.10E-11	5.92E-08	5.46	9.74E-08	8.14E-05	7.43	9.88E-13
cg09643186	GPX2;GPX2	1stExon;5UTR	NA		NA	-6.83	4.13E-11	5.93E-08	-9.14	7.28E-18	6.31E-14	-7	1.52E-11
cg08337959	TNNT3;TNNT3	Body;Body;Body	NA		NA	-6.83	4.24E-11	6.06E-08	-6.84	3.92E-11	1.02E-07	-5.68	2.97E-08

	NT3;T NNT3												
cg22409100	SLC8A1;SLC8A1;SLC8A1	TSS1500;5UTR;TSS1500;TSS1500	TRUE		NA	6.83	4.26E-11	6.06E-08	3.61	0.000357186	0.042067003	5.19	3.70E-07
cg20360704	ANK2	TSS200	TRUE	Unclassified_Cell_type_specific	TRUE	6.82	4.38E-11	6.19E-08	4.9	1.50E-06	0.000730055	7.36	1.61E-12
cg20758882			TRUE		TRUE	6.82	4.48E-11	6.31E-08	4.47	1.07E-05	0.003316336	8.8	8.63E-17
cg01350077	MDFI;MDFI	5UTR;1stExon	NA	Unclassified_Cell_type_specific	TRUE	6.82	4.52E-11	6.31E-08	4.41	1.41E-05	0.004119172	9.79	5.85E-20
cg26756193			TRUE		NA	-6.82	4.53E-11	6.31E-08	-5.53	6.66E-08	5.98E-05	-6.08	3.47E-09
cg20780998			NA		NA	6.82	4.59E-11	6.38E-08	5.62	4.19E-08	4.14E-05	7.25	3.27E-12
cg20431135	MFAP4	TSS1500	TRUE		TRUE	6.81	4.80E-11	6.63E-08	6.39	5.92E-10	1.11E-06	7.95	3.19E-14
cg01127300			TRUE	Unclassified_Cell_type_specific	TRUE	-6.81	4.83E-11	6.64E-08	-7.49	6.60E-13	2.73E-09	-5.81	1.55E-08
cg11751707	CYP1B1	5UTR	NA		NA	-6.81	4.90E-11	6.70E-08	-6.22	1.53E-09	2.49E-06	-7.57	3.97E-13
cg14593418	TPPP	3UTR	NA		NA	-6.81	4.94E-11	6.72E-08	-3.75	0.000207505	0.029221095	-5.51	7.32E-08
cg00279406	ITPKB	Body	NA		NA	6.8	5.13E-11	6.96E-08	5.21	3.29E-07	0.000218711	7.86	6.00E-14
cg06665333	SLC7A5	Body	NA		NA	-6.8	5.24E-11	7.07E-08	-6.29	1.03E-09	1.78E-06	-7.31	2.21E-12
cg17833419			NA	Unclassified_Cell	NA	-6.78	5.63E-11	7.50E-08	-6.82	4.61E-11	1.18E-07	-4.93	1.35E-06



				_type_s pecific									
cg14701072	MCHR1;MCHR1	5UTR;1stExon	TRUE		NA	6.78	5.66E-11	7.50E-08	3.65	0.000300728	0.037571509	6.15	2.36E-09
cg00788739	TCN2	TSS1500	NA	Unclassified_Cell_type_s pecific	TRUE	6.78	5.66E-11	7.50E-08	4.35	1.81E-05	0.004998769	8.34	2.29E-15
cg11869499	POLG;POLG	Body;Body	NA	Promoter_Associated_Cell_type_s pecific	NA	6.78	5.70E-11	7.52E-08	4.36	1.75E-05	0.004890449	6.48	3.49E-10
cg27099880			NA	Unclassified_Cell_type_s pecific	NA	-6.78	5.88E-11	7.72E-08	-5.64	3.80E-08	3.78E-05	-7.3	2.35E-12
cg26330518	NEFM	TSS1500	NA	Unclassified_Cell_type_s pecific	TRUE	6.78	5.93E-11	7.74E-08	4.3	2.23E-05	0.005842652	7.31	2.16E-12
cg24118547	ZHX2	5UTR	TRUE		NA	-6.77	6.00E-11	7.80E-08	-6.45	4.00E-10	7.98E-07	-6.32	8.87E-10
cg21766191	CIT	3UTR	NA		NA	-6.77	6.07E-11	7.86E-08	-3.92	0.000110052	0.018872127	-5.35	1.69E-07
cg24471922	CTBP1;CTBP1	Body;Body	NA		NA	-6.76	6.42E-11	8.28E-08	-5.99	5.65E-09	7.71E-06	-5.49	8.06E-08
cg14165909	LOXHD1	Body	NA	Unclassified_Cell_type_s pecific	NA	6.76	6.54E-11	8.39E-08	6.81	4.77E-11	1.21E-07	7.21	4.07E-12
cg00232453	EHMT2;EHMT2	Body;Body	NA		NA	6.76	6.59E-11	8.39E-08	3.94	9.85E-05	0.017371339	6.43	4.67E-10
cg14817906	CNNM4	Body	TRUE	Promoter_Associ	NA	6.76	6.61E-11	8.39E-08	4.35	1.86E-05	0.00510982	7.45	9.06E-13

				ated									
cg22624391			NA	Unclassified_Cell_type_specific	NA	-6.75	6.74E-11	8.50E-08	-5.56	5.66E-08	5.29E-05	-8.33	2.36E-15
cg23546512			TRUE		TRUE	6.75	6.87E-11	8.62E-08	3.77	0.000192053	0.027866323	8.3	2.89E-15
cg23576855	AHRR	Body	TRUE		NA	-6.75	6.96E-11	8.69E-08	-6.14	2.43E-09	3.73E-06	-7.56	4.38E-13
cg26898087	GUCY1A2	Body	NA	Unclassified_Cell_type_specific	TRUE	6.75	7.00E-11	8.69E-08	4.29	2.37E-05	0.006101015	5.73	2.34E-08
cg01380884	EDC3; EDC3; EDC3	3UTR;3UTR;3UTR	NA	Gene_Associated	NA	-6.75	7.02E-11	8.69E-08	-8.34	2.16E-15	1.37E-11	-7.22	3.91E-12
cg17033086			NA	Unclassified_Cell_type_specific	NA	-6.74	7.53E-11	9.29E-08	-5.43	1.11E-07	8.92E-05	-9.85	3.76E-20
cg16784943	ITPK1; ITPK1; ITPK1	Body;Body;Body	NA		NA	-6.73	7.66E-11	9.41E-08	-3.95	9.46E-05	0.016846957	-5.85	1.23E-08
cg27310710	NCOR2;NCO R2	Body;Body	NA	Promoter_Associated	TRUE	6.73	7.77E-11	9.50E-08	5.43	1.10E-07	8.87E-05	7.3	2.35E-12
cg09524946			NA	Unclassified	NA	6.73	7.87E-11	9.59E-08	3.91	0.000114318	0.019330839	8.15	8.19E-15
cg16374080	SLC12A7	Body	NA	Unclassified_Cell_type_specific	NA	-6.73	7.96E-11	9.65E-08	-4.51	9.23E-06	0.00297471	-6.18	1.98E-09
cg15963095			TRUE		NA	-6.72	8.19E-11	9.89E-08	-5.74	2.20E-08	2.34E-05	-6.38	6.37E-10
cg26824126	FXD5;FXD5;FXD5;F	Body;Body;Body;Body	NA		NA	6.72	8.32E-11	1.00E-07	3.75	0.000207217	0.029219168	4.62	5.48E-06

	XYD5												
cg21791662	GLI2	Body	NA		TRUE	6.72	8.50E-11	1.02E-07	4.06	6.07E-05	0.012302233	7.36	1.60E-12
cg01271455	PTPRN2;PTPRN2;PTPRN2	Body;Body;Body	NA	Unclassified_Cell_type_specific	TRUE	6.71	8.77E-11	1.05E-07	3.88	0.000128017	0.020892948	7.26	2.90E-12
cg02417427	SERINC5	Body	TRUE		NA	-6.71	8.87E-11	1.05E-07	-7.24	3.32E-12	1.22E-08	-6.01	5.00E-09
cg15193228	SEC14L3	3UTR	NA		NA	-6.7	9.15E-11	1.08E-07	-4.07	6.03E-05	0.012227883	-4.82	2.21E-06
cg22459204	ANKRD33B	Body	NA		NA	6.69	1.01E-10	1.18E-07	5.08	6.51E-07	0.000377951	6.13	2.63E-09
cg20828084	KIAA1199	TSS1500	NA	Unclassified_Cell_type_specific	NA	-6.69	1.01E-10	1.18E-07	-4.01	7.41E-05	0.014143878	-6.23	1.43E-09
cg24126592	DGKZ;DGKZ;DGKZ;DGKZ	Body;Body;Body;Body	TRUE	Gene_Associated	TRUE	6.68	1.02E-10	1.19E-07	4.38	1.60E-05	0.004556758	8.4	1.49E-15
cg08267072	CTAGE5;CTAGE5;CTAGE5;CTAGE5	Body;Body;Body;5UTR	NA		NA	-6.68	1.02E-10	1.19E-07	-4.02	7.37E-05	0.014104188	-6.16	2.14E-09
cg26843110	EDC3;EDC3;EDC3	Body;Body;Body	TRUE		NA	-6.68	1.04E-10	1.21E-07	-9.96	1.47E-20	1.73E-16	-7.14	6.35E-12
cg13399816	GNG12	TSS1500	NA		TRUE	-6.68	1.05E-10	1.22E-07	-5.13	4.94E-07	0.000307392	-7.13	6.85E-12
cg19144497	ARID3B	5UTR	NA	Unclassified	NA	6.67	1.15E-10	1.32E-07	5.24	2.93E-07	0.000198274	7.2	4.32E-12
cg25796129	NTN1	Body	TRUE		NA	-6.66	1.16E-10	1.33E-07	-5.2	3.55E-07	0.000233275	-4.91	1.49E-06

cg11040777	RPH3AL	Body	NA	Unclassified_Cell_type_specific	NA	-6.66	1.17E-10	1.33E-07	-6.42	4.91E-10	9.50E-07	-3.63	0.00032801
cg04876978	TMEM168	TSS1500	NA		NA	-6.65	1.23E-10	1.39E-07	-4.86	1.82E-06	0.000845394	-6.34	7.76E-10
cg04128884	PCGF3	5UTR	TRUE		TRUE	-6.64	1.31E-10	1.47E-07	-7.01	1.42E-11	4.36E-08	-5.47	9.17E-08
cg20782117	SLC25A13;SLC25A13	Body;Body;Body	TRUE		NA	6.64	1.34E-10	1.50E-07	4.51	9.01E-06	0.002920866	8.2	5.85E-15
cg09678615	TOX3;TOX3	5UTR;Body	NA		NA	6.64	1.34E-10	1.50E-07	3.6	0.000366699	0.04280801	6.61	1.60E-10
cg16520038	MIR130A	TSS200	NA		TRUE	6.64	1.37E-10	1.52E-07	4.52	8.64E-06	0.002841274	8.05	1.65E-14
cg05047401	SEMA4A	Body	TRUE	Gene_Associated_Cell_type_specific	TRUE	6.63	1.42E-10	1.58E-07	5.3	2.12E-07	0.000153814	7.1	8.33E-12
cg05302489	VAR5	Body	NA		NA	6.62	1.48E-10	1.64E-07	5.17	4.15E-07	0.000266986	5.81	1.52E-08
cg00850193	TLX1NB	Body	NA		NA	-6.62	1.48E-10	1.64E-07	-4.36	1.78E-05	0.004937636	-4.6	6.07E-06
cg03897436	UNKL	5UTR	NA		NA	-6.62	1.52E-10	1.66E-07	-4.28	2.48E-05	0.006323522	-5.05	7.44E-07
cg23420286	BMP7	Body	NA		NA	-6.62	1.52E-10	1.66E-07	-6.04	4.20E-09	5.96E-06	-6.3	1.01E-09
cg22782986	ODZ4	TSS1500	NA		NA	6.62	1.54E-10	1.67E-07	4.9	1.49E-06	0.000726574	8.23	4.85E-15
cg27035251	JAK3;JAK3	5UTR;1stExon	TRUE	Unclassified	TRUE	6.62	1.54E-10	1.67E-07	6.08	3.45E-09	5.07E-06	8.56	4.98E-16
cg08778851			NA	Unclassified_Cell_type_s	NA	6.62	1.55E-10	1.67E-07	4.2	3.46E-05	0.008109412	5.01	9.05E-07

				pecific									
cg16374411	SLC16A11	TSS1500	NA		NA	-6.61	1.56E-10	1.68E-07	-7.75	1.24E-13	6.06E-10	-4.56	7.27E-06
cg03936449			NA	Unclassified_Cell_type_specific	NA	6.61	1.58E-10	1.69E-07	4.48	1.02E-05	0.003179663	9.48	5.86E-19
cg05603985	SKI	1stExon	NA	Promoter_Associated	NA	-6.61	1.59E-10	1.70E-07	-6.79	5.50E-11	1.37E-07	-5.48	8.47E-08
cg07021906	SLC7A5	Body	NA		NA	-6.6	1.71E-10	1.82E-07	-5.27	2.45E-07	0.000172603	-7.83	7.19E-14
cg06727242	RAD51L1;RAD51L1;RAD51L1	Body;Body;Body	TRUE		NA	6.6	1.72E-10	1.82E-07	5.02	8.70E-07	0.000475026	8.01	2.15E-14
cg23278885	TGM6	TSS200	NA		NA	-6.6	1.73E-10	1.82E-07	-7.03	1.25E-11	3.89E-08	-5.73	2.39E-08
cg16246573	CAPN10;CAPN10;CAPN10;CAPN10	Body;Body;Body;Body	NA		NA	-6.59	1.75E-10	1.84E-07	-4.75	3.10E-06	0.001285415	-5.77	1.85E-08
cg12211856	SDCCAG8	Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.59	1.84E-10	1.92E-07	4.06	6.14E-05	0.012410516	7.82	7.96E-14
cg26740494	MMP23A;MMP23B	TSS1500;TSS1500	NA		NA	-6.59	1.85E-10	1.92E-07	-5.11	5.66E-07	0.000343178	-6.29	1.05E-09
cg10176463			TRUE	Unclassified_Cell_type_specific	TRUE	6.58	1.92E-10	1.99E-07	5.55	6.09E-08	5.64E-05	6.8	5.03E-11
cg04018738	VARS	Body	NA		NA	6.58	1.95E-10	2.01E-07	5.9	9.12E-09	1.14E-05	7.92	4.05E-14

cg19998150	FRMD4A	Body	NA	Unclassified	NA	6.57	1.98E-10	2.03E-07	5.24	2.90E-07	0.000196676	7.47	7.61E-13
cg22395765	PTPRN2;PTPRN2;PTPRN2	Body;Body;Body	NA	Unclassified_Cell_type_specific	TRUE	6.57	2.07E-10	2.12E-07	3.81	0.000165102	0.024934083	7.65	2.43E-13
cg20009354			TRUE	Unclassified_Cell_type_specific	TRUE	6.56	2.17E-10	2.21E-07	5.53	6.51E-08	5.88E-05	8.07	1.46E-14
cg19957162	FZD5	3UTR	NA		NA	6.55	2.24E-10	2.27E-07	4.37	1.69E-05	0.004753377	7.57	4.17E-13
cg05911153	POU2F3	Body	TRUE		NA	6.55	2.33E-10	2.35E-07	4.68	4.18E-06	0.001633146	6.15	2.37E-09
cg06373360			NA		NA	-6.54	2.37E-10	2.39E-07	-5.57	5.42E-08	5.12E-05	-6.16	2.24E-09
cg01917657	PANX2;PANX2;PANX2	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	6.54	2.43E-10	2.43E-07	5.32	1.93E-07	0.000142683	5.92	8.24E-09
cg01832218	SURF6	Body	NA	Promoter_Associated_Cell_type_specific	NA	-6.53	2.51E-10	2.50E-07	-5.46	9.41E-08	7.93E-05	-6.03	4.59E-09
cg01923999	FAM84B	3UTR	NA	Promoter_Associated_Cell_type_specific	NA	6.53	2.54E-10	2.51E-07	6.34	7.74E-10	1.39E-06	9.55	3.49E-19
cg15046507	LOC221122	Body	TRUE	Promoter_Associated	NA	6.53	2.54E-10	2.51E-07	5.13	5.06E-07	0.000312669	8.2	5.95E-15
cg07830557	SH3GL1	Body	NA		NA	6.53	2.62E-10	2.58E-07	3.6	0.000366296	0.042784415	7.54	4.93E-13
cg05635754	JAK3	5UTR	TRUE	Unclassified	TRUE	6.52	2.64E-10	2.60E-07	5.01	9.02E-07	0.000485072	7.87	5.48E-14

cg04433051	ABCC3	Body	TRUE		TRUE	6.52	2.66E-10	2.60E-07	5.45	9.81E-08	8.17E-05	7.83	7.23E-14
cg26039954	SPEN	Body	TRUE		NA	-6.52	2.69E-10	2.62E-07	-6.67	1.12E-10	2.55E-07	-8.14	9.01E-15
cg09416908	ME3;ME3	TSS1500;TSS1500;TS S1500	NA		NA	6.52	2.70E-10	2.63E-07	4.01	7.69E-05	0.01449331	7.04	1.18E-11
cg05049329	ITPKB	Body	NA	Promoter_Associated	NA	6.51	2.81E-10	2.71E-07	4.6	6.19E-06	0.002206807	6.87	3.29E-11
cg24804144			TRUE	Unclassified	TRUE	6.51	2.84E-10	2.73E-07	5.49	8.19E-08	7.13E-05	9	2.03E-17
cg12075928	PTK2;PTK2	Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	-6.51	2.92E-10	2.80E-07	-6.15	2.23E-09	3.48E-06	-4.6	6.01E-06
cg06023345	FAM84B	3UTR	NA	Promoter_Associated_Cell_type_specific	NA	6.5	3.09E-10	2.95E-07	6.09	3.14E-09	4.70E-06	9.65	1.66E-19
cg11267879	CYP2F1	TSS1500	NA		NA	-6.5	3.10E-10	2.95E-07	-5.13	4.97E-07	0.000307949	-4.66	4.60E-06
cg08279008	POLR1A	Body	NA	Promoter_Associated	TRUE	6.49	3.15E-10	2.99E-07	3.98	8.49E-05	0.015569887	6.28	1.08E-09
cg05673882	POLK	Body	TRUE		NA	-6.49	3.17E-10	3.00E-07	-5.1	5.88E-07	0.000352012	-6.25	1.34E-09
cg22911054	CPT1A;CPT1A	5UTR;5UTR	NA		NA	-6.49	3.23E-10	3.04E-07	-5.3	2.14E-07	0.000154642	-5.58	5.04E-08
cg27241845			NA		TRUE	-6.49	3.26E-10	3.05E-07	-8.16	7.38E-15	4.42E-11	-4.39	1.57E-05
cg01999938			TRUE		NA	6.49	3.27E-10	3.05E-07	4.52	8.66E-06	0.002844862	8.02	2.05E-14
cg26764244	GNG12	TSS1500	NA		NA	-6.48	3.37E-10	3.13E-07	-5.81	1.54E-08	1.76E-05	-6.95	2.05E-11

cg22542751	TCN2	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	6.47	3.73E-10	3.45E-07	3.93	0.000102127	0.017835817	8.19	6.54E-15
cg09963123	FLJ13197;KLF3	Body;TSS1500	NA		NA	6.46	3.79E-10	3.49E-07	4.5	9.36E-06	0.003009492	6.88	3.15E-11
cg20149780	EFHD2	Body	NA	Unclassified_Cell_type_specific	NA	-6.46	3.83E-10	3.50E-07	-6.22	1.52E-09	2.47E-06	-3.61	0.00034974
cg00538298	MUC2	Body	NA		NA	-6.46	3.83E-10	3.50E-07	-5.46	9.32E-08	7.88E-05	-5.62	4.13E-08
cg07045054	TMEM111	Body	NA		NA	-6.46	3.90E-10	3.55E-07	-5.87	1.10E-08	1.34E-05	-6.68	1.08E-10
cg09853702			TRUE		NA	6.46	3.96E-10	3.59E-07	4.54	8.01E-06	0.002689753	8.14	9.06E-15
cg10503298	CTBP1;CTBP1	Body;Body	NA		NA	-6.46	3.97E-10	3.59E-07	-8.16	7.73E-15	4.57E-11	-5.54	6.38E-08
cg25498731	THSD7B	Body	TRUE		NA	-6.45	4.01E-10	3.61E-07	-3.73	0.000224675	0.03098245	-4.41	1.42E-05
cg01892547	NBEAL2	Body	NA	Gene_Associated	NA	6.45	4.01E-10	3.61E-07	7.08	9.03E-12	2.91E-08	7.43	1.01E-12
cg16663155	INCENP;INCENP	Body;Body	NA	Gene_Associated_Cell_type_specific	NA	-6.45	4.08E-10	3.65E-07	-5.06	7.03E-07	0.000400908	-6.22	1.56E-09
cg02101203	FRMD4A	Body	NA		NA	6.45	4.10E-10	3.65E-07	3.83	0.000151519	0.023560466	7.08	9.21E-12
cg10956333			TRUE		NA	-6.44	4.44E-10	3.92E-07	-6.16	2.13E-09	3.34E-06	-5.18	3.95E-07
cg26113809			NA	Unclassified	TRUE	6.43	4.54E-10	3.99E-07	3.82	0.000160561	0.024509489	7.11	7.59E-12
cg02532700	NCF4;NCF4	Body;Body	NA	Promoter_Associated	NA	-6.43	4.58E-10	4.00E-07	-5.71	2.55E-08	2.67E-05	-5.42	1.17E-07



				ated									
cg22588983			TRUE		TRUE	-6.42	4.77E-10	4.13E-07	-3.66	0.00028932	0.036630445	-5.22	3.25E-07
cg10189362	STEAP3;STEAP3;STEAP3	Body;Body;Body	NA		NA	-6.42	4.99E-10	4.29E-07	-4.29	2.32E-05	0.005995717	-5.47	9.01E-08
cg15393221	PRX;PRX	TSS1500;TSS1500	TRUE		NA	6.41	5.14E-10	4.38E-07	4.66	4.59E-06	0.001754886	8.17	7.35E-15
cg01715680	BTBD7	Body	TRUE		NA	-6.41	5.15E-10	4.38E-07	-5.3	2.13E-07	0.000154308	-6.99	1.58E-11
cg21327194	GPRC5C;GPRC5C	Body;Body	NA		NA	6.41	5.16E-10	4.38E-07	4.13	4.58E-05	0.010027097	8.02	1.98E-14
cg03126561	PARVA	Body	TRUE		TRUE	6.41	5.17E-10	4.38E-07	4.72	3.47E-06	0.001410185	8.16	7.93E-15
cg02203067	SLC7A5	Body	NA		NA	-6.41	5.19E-10	4.38E-07	-5	9.44E-07	0.000504382	-7.78	1.01E-13
cg24713122	DGKZ;DGKZ;DGKZ;DGKZ	Body;Body;Body;Body	TRUE	Gene_Associated	TRUE	6.4	5.38E-10	4.52E-07	5.15	4.51E-07	0.000283913	8.36	1.95E-15
cg02223351	CDH5	5UTR	TRUE		NA	6.4	5.38E-10	4.52E-07	5.37	1.53E-07	0.000117328	7.45	9.08E-13
cg01284869	TCN2	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	6.4	5.45E-10	4.56E-07	4.2	3.39E-05	0.007973501	8.13	9.48E-15
cg03616377			TRUE	Unclassified_Cell_type_specific	NA	6.4	5.46E-10	4.56E-07	3.91	0.000112863	0.019163378	6.06	3.80E-09
cg17887364	EIF4EBP1	Body	NA		NA	-6.4	5.56E-10	4.62E-07	-4.8	2.38E-06	0.001040804	-5.49	8.31E-08
cg17817532	TET1	5UTR	NA	Unclassified_Cell	NA	6.4	5.57E-10	4.62E-07	4.84	2.02E-06	0.000913074	6.92	2.45E-11

				_type_s pecific									
cg24524702	MEF2A;MEF2A;MEF2A	5UTR;5UTR;5UTR	NA	Unclassified_Cell_type_s pecific	NA	-6.39	5.65E-10	4.66E-07	-6.66	1.15E-10	2.61E-07	-6.55	2.31E-10
cg22836769			NA		NA	-6.39	5.65E-10	4.66E-07	-5.25	2.78E-07	0.000191056	-7.69	1.89E-13
cg03970350	TCN2	TSS200	NA	Unclassified_Cell_type_s pecific	TRUE	6.39	5.69E-10	4.68E-07	5.12	5.26E-07	0.000322956	9.05	1.45E-17
cg16671160			NA		TRUE	6.39	5.79E-10	4.75E-07	4.61	5.84E-06	0.002121259	7.87	5.40E-14
cg18844145			NA		NA	-6.39	5.85E-10	4.78E-07	-4.04	6.55E-05	0.013012668	-5.84	1.28E-08
cg00858840	SP5	Body	NA		NA	6.39	5.89E-10	4.81E-07	3.95	9.44E-05	0.016824713	8.1	1.15E-14
cg11553755	TJAP1;TJAP1;TJAP1;TJAP1;TJAP1;TJAP1	5UTR;5UTR;5UTR;Body;5UTR;5UTR	TRUE		NA	-6.38	6.00E-10	4.88E-07	-6.99	1.55E-11	4.65E-08	-7.31	2.20E-12
cg27628839			NA	Promoter_Associated_Cell_type_s pecific	NA	-6.38	6.06E-10	4.89E-07	-4.93	1.32E-06	0.000660221	-6.43	4.75E-10
cg01883425	MDF1	Body	NA		TRUE	6.38	6.06E-10	4.89E-07	5.6	4.60E-08	4.43E-05	7.79	9.20E-14
cg13453589	UBE2R2	Body	TRUE		NA	-6.38	6.08E-10	4.89E-07	-6.87	3.24E-11	8.57E-08	-4.78	2.68E-06
cg18410110	PDZD2	Body	TRUE	Unclassified_Cell	NA	-6.38	6.08E-10	4.89E-07	-5.44	1.03E-07	8.39E-05	-4.87	1.75E-06

				_type_s pecific									
cg20313963	SLC2A3	TSS1500	NA	Promote r_Associ ated	TRUE	6.38	6.12E-10	4.90E-07	4.13	4.54E-05	0.009949585	5.07	6.78E-07
cg22863744	NCOR2;NCO R2	Body;B ody	NA	Promote r_Associ ated	TRUE	6.37	6.36E-10	5.07E-07	3.68	0.00027048	0.035067528	6.96	1.95E-11
cg07706375	MIR23A;MIR 24-2;MIR27A	TSS200;TSS1500;TSS1500	NA	Unclassi fied	TRUE	6.37	6.44E-10	5.12E-07	4.86	1.83E-06	0.000847096	6.62	1.54E-10
cg17580614	ADORA2B	Body	NA	Unclassi fied_Cell _type_s pecific	NA	-6.37	6.48E-10	5.14E-07	-7.07	9.35E-12	2.97E-08	-6.32	8.76E-10
cg03291396	SLC11A1	Body	TRUE		NA	6.37	6.51E-10	5.15E-07	5.82	1.40E-08	1.63E-05	7.52	5.58E-13
cg06470626	CDR2	Body	TRUE		NA	6.37	6.57E-10	5.18E-07	4.16	4.02E-05	0.009117175	6.62	1.53E-10
cg16476048	C10orf122	TSS1500	NA		NA	-6.37	6.61E-10	5.20E-07	-4.21	3.34E-05	0.00788625	-4.53	8.42E-06
cg10257521	LSP1; LSP1; LSP1; LSP1	Body;B ody;Bo dy;Body	TRUE	Unclassi fied_Cell _type_s pecific	NA	6.36	7.04E-10	5.51E-07	5.53	6.65E-08	5.98E-05	7.86	5.85E-14
cg13972491	C9orf3	3UTR	NA		NA	-6.36	7.11E-10	5.54E-07	-4.59	6.41E-06	0.00226285	-5.68	2.97E-08
cg14947787	GPX2	3UTR	NA		NA	-6.35	7.21E-10	5.57E-07	-5.5	7.86E-08	6.90E-05	-8.06	1.52E-14
cg11551560			TRUE		NA	6.35	7.22E-10	5.57E-07	3.57	0.000410723	0.045677874	7.42	1.06E-12
cg12513616			NA		TRUE	-6.35	7.25E-10	5.57E-07	-6.46	3.77E-10	7.57E-07	-6.34	7.81E-10
cg04920032	FAIM2	3UTR	TRUE		TRUE	6.35	7.29E-10	5.59E-07	4.47	1.08E-05	0.003357582	5.61	4.48E-08
cg17822706			TRUE	Promote r_Associ	NA	6.35	7.37E-10	5.61E-07	4.26	2.66E-05	0.006611829	6.38	6.22E-10

				ated									
cg12431188			NA	Unclassified_Cell_type_specific	NA	-6.35	7.37E-10	5.61E-07	-4.8	2.41E-06	0.001052531	-7.5	6.54E-13
cg19406511	RAB25	Body	NA	Unclassified	TRUE	6.35	7.50E-10	5.69E-07	5.66	3.37E-08	3.40E-05	6.44	4.50E-10
cg27093944			TRUE	Unclassified	TRUE	6.35	7.52E-10	5.69E-07	4.88	1.66E-06	0.00078755	7.81	8.14E-14
cg20054248	IKZF4	TSS200	NA		NA	6.34	7.77E-10	5.85E-07	5.01	8.77E-07	0.000475766	7.53	5.13E-13
cg27501612	HERPUD1;HERPUD1;HERPUD1	3UTR;3UTR	NA		NA	-6.34	7.78E-10	5.85E-07	-5.55	6.09E-08	5.64E-05	-5.54	6.37E-08
cg05894719			TRUE		NA	-6.34	7.81E-10	5.86E-07	-5.97	6.34E-09	8.45E-06	-5.59	4.83E-08
cg00737979	LOC340074	TSS1500	NA		NA	-6.34	7.87E-10	5.89E-07	-5.81	1.51E-08	1.73E-05	-5.93	7.75E-09
cg08105590	FAM38A	Body	NA	Promoter_Associated	NA	6.34	7.90E-10	5.90E-07	5.99	5.46E-09	7.46E-06	7.72	1.52E-13
cg01775514	BMP7	Body	NA		NA	-6.33	8.05E-10	5.96E-07	-5.15	4.50E-07	0.000283902	-7.08	9.07E-12
cg14678430	FLNC;FLNC	Body;Body	NA		NA	-6.33	8.12E-10	5.99E-07	-4.01	7.43E-05	0.01416035	-4.2	3.47E-05
cg16293835			TRUE		NA	-6.33	8.18E-10	6.03E-07	-3.97	8.79E-05	0.015953938	-4.97	1.08E-06
cg05910443	CUX1;CUX1;CUX1	Body;Body;Body	TRUE		TRUE	6.33	8.24E-10	6.05E-07	4.01	7.51E-05	0.01425463	7.52	5.47E-13
cg20550458	SNORA52;RPLP2	Body;Body	NA		NA	6.32	8.61E-10	6.28E-07	4.82	2.17E-06	0.000962648	5.83	1.37E-08
cg03960874	STEAP3;ST	Body;Body;Bo	NA		NA	-6.32	8.70E-10	6.31E-07	-4.82	2.24E-06	0.000991765	-5.49	8.21E-08

	EAP3; STEAP3	dy											
cg20866810	ZDHC4;ZDHC4;ZDHC4;ZDHC4	Body;Body;Body;Body	NA		NA	-6.32	8.79E-10	6.36E-07	-7.21	4.08E-12	1.45E-08	-6.23	1.44E-09
cg03324175	CYBASC3;CYBASC3	TSS200;5UTR;Body	NA		NA	-6.32	8.84E-10	6.38E-07	-6.32	8.86E-10	1.55E-06	-7.48	7.42E-13
cg17693957	TCN2	TSS1500	NA	Unclassified_Cell_type_specific	NA	6.31	9.26E-10	6.65E-07	3.65	0.000305488	0.037943248	6.4	5.47E-10
cg12709970	P2RX1	Body	TRUE	Promoter_Associated	NA	6.31	9.44E-10	6.76E-07	4.44	1.25E-05	0.003768629	3.96	9.21E-05
cg05125838	UCN2;COL7A1	TSS1500;3UTR	NA		TRUE	6.3	9.69E-10	6.92E-07	4.8	2.46E-06	0.001069486	5.8	1.56E-08
cg26831416	ACTN4	Body	NA		TRUE	6.3	9.75E-10	6.95E-07	3.72	0.000238145	0.032336639	5.44	1.07E-07
cg00061860			NA		NA	-6.3	9.93E-10	7.06E-07	-4.71	3.76E-06	0.001498871	-7.12	6.98E-12
cg01519094	PKNOX2	TSS1500	NA	Unclassified	NA	6.29	1.01E-09	7.16E-07	4.81	2.36E-06	0.001036116	7.73	1.37E-13
cg25449466	BMP7	Body	TRUE		NA	-6.29	1.02E-09	7.19E-07	-5.8	1.59E-08	1.81E-05	-4.44	1.23E-05
cg25305879			TRUE		TRUE	6.29	1.02E-09	7.21E-07	5.88	1.01E-08	1.24E-05	6.98	1.70E-11
cg25075684			NA	Unclassified_Cell_type_s	NA	6.29	1.06E-09	7.43E-07	5.51	7.27E-08	6.46E-05	7.41	1.12E-12

				pecific									
cg22276612	FBRSL1	Body	NA	Unclassified_Cell_type_specific	NA	-6.28	1.10E-09	7.67E-07	-5.38	1.45E-07	0.00011158	-6.21	1.67E-09
cg03345059	NDST1	Body	NA		NA	-6.28	1.12E-09	7.81E-07	-5.5	7.69E-08	6.77E-05	-5.86	1.13E-08
cg26720452			NA	Unclassified_Cell_type_specific	NA	6.27	1.13E-09	7.87E-07	5.28	2.39E-07	0.000169272	8.56	4.81E-16
cg04346283	FAM46A	Body	NA		NA	6.27	1.16E-09	8.01E-07	4.01	7.52E-05	0.01425644	7.43	1.01E-12
cg23681440			TRUE		NA	-6.27	1.18E-09	8.15E-07	-5.06	7.12E-07	0.000403693	-5.53	6.76E-08
cg22762813			NA		TRUE	6.27	1.19E-09	8.19E-07	3.63	0.000334882	0.04040241	7.02	1.31E-11
cg11109845	CUL1	TSS1500	NA		NA	6.26	1.25E-09	8.54E-07	3.94	0.000100948	0.017667184	8.3	2.96E-15
cg17331199	IKZF4; IKZF4	1stExon;5UTR	TRUE	Promoter_Associated	NA	6.25	1.26E-09	8.65E-07	3.67	0.000286475	0.036389505	7.87	5.74E-14
cg01367627	TRRAP	5UTR	NA	Promoter_Associated	NA	6.25	1.29E-09	8.78E-07	3.82	0.000159731	0.024426607	4.52	8.75E-06
cg14979620	TP73; TP73; TP73; TP73	Body;Body;Body;Body	NA		NA	6.25	1.29E-09	8.78E-07	5.82	1.45E-08	1.67E-05	6.35	7.44E-10
cg04745805	STAT5B	5UTR	NA		NA	6.25	1.29E-09	8.78E-07	3.55	0.000437434	0.047331534	5.01	8.90E-07
cg17032372			NA		NA	-6.25	1.31E-09	8.85E-07	-4.36	1.75E-05	0.004891038	-5.83	1.36E-08
cg04846710	LIX1L	Body	NA	Promoter_Associated	NA	6.25	1.31E-09	8.85E-07	4.88	1.66E-06	0.00078831	6.22	1.55E-09
cg23110422	ETS2	Body	NA		NA	-6.25	1.32E-09	8.88E-07	-3.89	0.00012345	0.020396564	-5.05	7.50E-07

cg07121644	DGKZ; DGKZ; DGKZ; DGKZ	Body;TSS200; Body;Body	NA	Promoter_Associated	TRUE	6.24	1.35E-09	9.00E-07	4.84	2.03E-06	0.000914008	7.3	2.35E-12
cg04884798	ADCY4	Body	NA		NA	-6.24	1.36E-09	9.07E-07	-5.75	2.12E-08	2.27E-05	-5.88	1.01E-08
cg22540600	NDST1	Body	NA		NA	-6.23	1.42E-09	9.37E-07	-6.4	5.46E-10	1.05E-06	-5.77	1.89E-08
cg11027140	GPR144	TSS1500	NA		NA	6.23	1.45E-09	9.56E-07	3.97	8.95E-05	0.016158066	6.79	5.40E-11
cg14655700	PC;PC; PC	Body;Body; Body	NA	Unclassified_Cell_type_specific	NA	-6.23	1.46E-09	9.57E-07	-5.81	1.49E-08	1.72E-05	-6.09	3.25E-09
cg16145216	HIVEP3;HIVEP3	TSS1500;TSS1500	NA	Promoter_Associated	NA	6.23	1.48E-09	9.67E-07	4.11	4.92E-05	0.010571559	6.66	1.17E-10
cg02610723	FAM38A	Body	NA	Promoter_Associated	NA	6.23	1.49E-09	9.67E-07	4.54	8.04E-06	0.002693436	4.55	7.55E-06
cg08063051	UNKL	5UTR	TRUE	Promoter_Associated_Cell_type_specific	NA	-6.22	1.57E-09	1.02E-06	-5.45	1.01E-07	8.29E-05	-6.45	4.26E-10
cg24049468	AK3L1;AK3L1; AK3L1	Body;Body; Body	NA		NA	6.22	1.57E-09	1.02E-06	4.79	2.58E-06	0.001115373	5.48	8.47E-08
cg08486160	PC;PC; PC	Body;Body; Body	NA	Unclassified_Cell_type_specific	NA	-6.22	1.58E-09	1.02E-06	-4.69	3.99E-06	0.001576491	-5.5	7.95E-08
cg27295118			NA		NA	6.22	1.58E-09	1.02E-06	5.09	5.95E-07	0.000353873	6.56	2.15E-10
cg07434244	G0S2	TSS1500	NA		NA	6.21	1.59E-09	1.02E-06	4.05	6.40E-05	0.012831827	7.35	1.65E-12
cg0198349			NA		NA	-6.21	1.61E-0	1.03E-0	-5.67	3.19E-0	3.24E-0	-5.15	4.63E-0

2							9	6		8	5		7
cg23856536			NA	Unclassified	NA	6.21	1.62E-09	1.03E-06	4.01	7.45E-05	0.014174045	2.58	0.010376905
cg26588825	FAM198B;FAM198B;FAM198B	TSS200;5UTR;5UTR	NA		NA	6.21	1.64E-09	1.04E-06	4.56	7.34E-06	0.002522126	6.17	2.02E-09
cg14234406	PLEC1;PLEC1;PLEC1	Body;Body;TS200	NA		NA	6.21	1.64E-09	1.05E-06	4.9	1.54E-06	0.000746268	7.66	2.22E-13
cg05316864			TRUE	Unclassified	NA	-6.21	1.67E-09	1.06E-06	-3.88	0.000128631	0.02095944	-7.33	1.85E-12
cg14950751	SLC16A11	TSS1500	NA		NA	-6.21	1.68E-09	1.06E-06	-7.46	8.14E-13	3.26E-09	-5.98	6.08E-09
cg08414108	SYNJ2	Body	NA		NA	-6.2	1.75E-09	1.10E-06	-4.47	1.09E-05	0.003357582	-5.61	4.49E-08
cg20059928			TRUE		TRUE	-6.19	1.79E-09	1.12E-06	-5.63	4.00E-08	3.95E-05	-6.35	7.61E-10
cg02519681	FRMD4B	1stExon	TRUE		TRUE	6.19	1.84E-09	1.15E-06	3.57	0.00041414	0.045840865	6.37	6.69E-10
cg12686441			NA	Unclassified	TRUE	6.18	1.89E-09	1.18E-06	4.53	8.28E-06	0.002759023	6.31	9.51E-10
cg05032059			TRUE		NA	6.18	1.92E-09	1.20E-06	4.5	9.40E-06	0.003020095	6.76	6.65E-11
cg02272667	MAD1L1;MAD1L1;MAD1L1	Body;Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.18	1.93E-09	1.20E-06	4.99	1.00E-06	0.000528105	7.14	6.16E-12
cg04509266	LOC148696	TSS200	NA		NA	-6.18	1.97E-09	1.22E-06	-5.15	4.61E-07	0.000289884	-3.14	0.001831345
cg21371809	FRMD4A	Body	TRUE	Unclassified	NA	6.18	1.99E-09	1.23E-06	4.69	3.99E-06	0.001575943	7.71	1.59E-13
cg03662014	RRN3P2	Body	NA		NA	6.18	1.99E-09	1.23E-06	4.02	7.19E-05	0.01387589	6.57	2.10E-10



cg06630241	SOCS2	Body	NA		NA	6.17	2.02E-09	1.24E-06	3.74	0.000216769	0.030195674	6.98	1.68E-11
cg11668844	MCF2L;MCF2L	Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.17	2.04E-09	1.24E-06	5.09	6.06E-07	0.000357739	7.65	2.33E-13
cg11411865	TTYH3	3UTR	NA		NA	-6.17	2.04E-09	1.25E-06	-4.71	3.62E-06	0.001454714	-5	9.30E-07
cg01780990	ECE1;ECE1;ECE1;ECE1	TSS1500;Body;Body;Body	NA		NA	-6.17	2.05E-09	1.25E-06	-4.93	1.31E-06	0.000657953	-5.88	1.01E-08
cg25685983	CDKN2D;KR1;CDKN2D	3UTR;TSS1500;3UTR	TRUE	Promoter_Associated	NA	6.17	2.10E-09	1.27E-06	4.26	2.64E-05	0.006601161	6.76	6.46E-11
cg20019546	SFRP4	1stExon	NA		NA	6.17	2.10E-09	1.27E-06	4.67	4.51E-06	0.001730377	6.14	2.42E-09
cg17296220			NA		NA	-6.16	2.14E-09	1.29E-06	-4.93	1.35E-06	0.000672504	-6.4	5.53E-10
cg23518532			NA		NA	-6.16	2.19E-09	1.31E-06	-3.74	0.000220962	0.030609359	-5.66	3.40E-08
cg19501536	MADD;MADD;MADD;MADD;MADD;MADD;MADD;MADD;MADD;MADD	Body;Body;Body;Body;Body;Body;Body;Body;Body;Body	NA		NA	-6.16	2.21E-09	1.32E-06	-3.89	0.000119826	0.019960666	-4.2	3.45E-05
cg22325958	SFRS8	Body	NA		NA	-6.16	2.22E-09	1.32E-06	-4.09	5.55E-05	0.01150659	-5.46	9.35E-08
cg0798461	FAM5	Body	NA		NA	-6.15	2.28E-0	1.36E-0	-3.56	0.00042	0.04653	-2.7	0.00728

4	3B						9	6		5017	7333		273
cg04566512			TRUE		TRUE	-6.15	2.29E-09	1.36E-06	-5.15	4.48E-07	0.000282917	-6.65	1.24E-10
cg10346364	LOC10130987;CLCF1;CLCF1	Body;TSS1500;TSS1500	NA		NA	6.15	2.30E-09	1.36E-06	4.76	2.95E-06	0.001243639	7.2	4.43E-12
cg08527603	PMM1	Body	NA		NA	-6.15	2.31E-09	1.36E-06	-4.18	3.75E-05	0.008647665	-3.4	0.000771651
cg19240637	RNF144A	Body	NA		NA	-6.15	2.34E-09	1.37E-06	-4.66	4.68E-06	0.001782737	-4.25	2.81E-05
cg14615768	NTN1	TSS1500	NA	Unclassified	NA	6.15	2.35E-09	1.37E-06	4.62	5.54E-06	0.00204768	4.92	1.39E-06
cg04368724	VAR5	Body	NA		NA	6.15	2.35E-09	1.37E-06	6.42	4.92E-10	9.50E-07	5.51	7.34E-08
cg08865625	HLF	Body	NA		NA	-6.14	2.40E-09	1.39E-06	-3.59	0.000385904	0.044153102	-5.3	2.13E-07
cg03379552	CRTAC1	Body	TRUE		NA	6.14	2.40E-09	1.39E-06	4.7	3.86E-06	0.001534881	6.76	6.42E-11
cg02990289	MIR27A;MIR24-2	Body;TSS200	NA	Unclassified	NA	6.14	2.41E-09	1.40E-06	4.09	5.41E-05	0.011344603	7.3	2.29E-12
cg05384198	TBC1D2	Body	NA		NA	-6.14	2.44E-09	1.41E-06	-6.39	5.95E-10	1.11E-06	-6.13	2.54E-09
cg13376199			NA		NA	-6.14	2.47E-09	1.42E-06	-4.91	1.42E-06	0.000700419	-3.02	0.002725829
cg11925381	RAC1;RAC1	Body;Body	NA		NA	-6.14	2.48E-09	1.42E-06	-4.26	2.64E-05	0.006601161	-2.42	0.016071467
cg02596779	RNF130	Body	TRUE		NA	6.13	2.51E-09	1.44E-06	3.62	0.00034304	0.040924122	6.46	3.86E-10
cg01565774	IKZF4	TSS200	NA		NA	6.13	2.53E-09	1.44E-06	4.49	9.90E-06	0.00312935	6.89	2.92E-11
cg13030582	MFAP4	TSS1500	TRUE		NA	6.13	2.55E-09	1.45E-06	4.27	2.52E-05	0.006377344	7.08	9.02E-12
cg14278260			NA	Promoter_Associated	NA	6.13	2.57E-09	1.46E-06	3.99	8.20E-05	0.015150954	8.21	5.64E-15

cg16544989			NA		NA	6.13	2.59E-09	1.47E-06	3.64	0.00031883	0.039104963	7.67	2.09E-13
cg24135293			TRUE		NA	-6.12	2.65E-09	1.50E-06	-4.81	2.37E-06	0.00103679	-4.48	1.05E-05
cg07558761	SLC7A5	Body	NA		NA	-6.12	2.66E-09	1.50E-06	-4.56	7.33E-06	0.002522126	-6.54	2.42E-10
cg20022223			NA		NA	6.12	2.69E-09	1.51E-06	5.04	7.88E-07	0.00044043	6.31	9.38E-10
cg03277515	PGLYRP4	TSS200	NA		NA	-6.12	2.72E-09	1.52E-06	-5.78	1.77E-08	1.97E-05	-6.24	1.35E-09
cg23067299	AHRR	Body	NA		NA	6.12	2.74E-09	1.53E-06	5.35	1.65E-07	0.000125841	5.47	9.10E-08
cg23769143	SYN2;TIMP4;SYN2	Body;TSS200;Body	NA		NA	-6.12	2.76E-09	1.53E-06	-7.14	6.22E-12	2.10E-08	-5.05	7.62E-07
cg24975642	NCOR2;NCOR2	Body;Body	TRUE	Unclassified_Cell_type_specific	TRUE	6.12	2.77E-09	1.54E-06	4.02	7.24E-05	0.013936275	5.71	2.52E-08
cg25318579			TRUE		NA	-6.11	2.84E-09	1.57E-06	-4.02	7.35E-05	0.014092412	-5.64	3.76E-08
cg07874646			TRUE		NA	-6.11	2.89E-09	1.59E-06	-4	7.74E-05	0.014541237	-2.19	0.029165609
cg14718363			NA	Promoter_Associated	NA	6.11	2.89E-09	1.59E-06	4.17	3.94E-05	0.008995979	6.3	9.72E-10
cg13489049	TMPRSS2;TMPRSS2	Body;5UTR	NA		NA	6.11	2.92E-09	1.60E-06	4.43	1.32E-05	0.003905364	6.31	9.25E-10
cg06452769	PLEC1;PLEC1;PLEC1	Body;Body;TS S200	NA		NA	6.11	2.94E-09	1.61E-06	4.45	1.17E-05	0.003570082	6.33	8.21E-10
cg27302539			TRUE		NA	6.1	3.00E-09	1.64E-06	3.73	0.000224555	0.030982406	8.57	4.39E-16
cg26015087			NA		NA	6.1	3.09E-09	1.68E-06	3.99	8.07E-05	0.014987837	6.1	3.11E-09

cg22013564			TRUE		NA	6.1	3.09E-09	1.68E-06	3.81	0.000163393	0.024753788	3.04	0.002532365
cg01611017	CLMN	Body	TRUE		TRUE	6.1	3.10E-09	1.68E-06	3.59	0.000383418	0.04397211	7.89	4.97E-14
cg21067652	ELF1; ELF1	Body;Body	TRUE	Promoter_Associated_Cell_type_specific	NA	6.1	3.11E-09	1.68E-06	4.43	1.30E-05	0.003876914	6.41	5.12E-10
cg01369114	TCN2	TSS200	NA	Unclassified_Cell_type_specific	TRUE	6.09	3.17E-09	1.70E-06	4.25	2.82E-05	0.006920973	7.92	4.05E-14
cg10692693	CUX1; CUX1; CUX1	Body;Body;Body	TRUE		TRUE	6.09	3.21E-09	1.71E-06	4.14	4.53E-05	0.009943896	6.79	5.62E-11
cg04907257	ADCY2	TSS1500	NA		NA	6.09	3.29E-09	1.75E-06	3.78	0.00018738	0.027382651	8.16	7.70E-15
cg07806552			TRUE	Unclassified	NA	6.09	3.30E-09	1.75E-06	4.31	2.16E-05	0.005693698	6.21	1.70E-09
cg19848140	STK39	Body	TRUE		NA	-6.08	3.49E-09	1.83E-06	-5.03	8.18E-07	0.000451437	-5.74	2.20E-08
cg26271591	NFE2L2;NFE2L2;NFE2L2	Body;5UTR;5UTR	NA		NA	-6.07	3.52E-09	1.85E-06	-5.92	8.17E-09	1.06E-05	-3.91	0.000112584
cg23011788	FRMD4A	Body	NA		NA	6.07	3.53E-09	1.85E-06	3.58	0.000396334	0.044786476	5.66	3.42E-08
cg17275432			NA		NA	-6.07	3.54E-09	1.85E-06	-4.87	1.75E-06	0.000823488	-4.18	3.84E-05
cg26133217	DIS3L2	Body	TRUE	Promoter_Associated	NA	6.07	3.57E-09	1.87E-06	5.6	4.50E-08	4.37E-05	6.85	3.80E-11
cg26782108	SLC13A5;SLC13A5	TSS1500;TSS1500	NA	Unclassified	TRUE	6.07	3.58E-09	1.87E-06	3.6	0.000370285	0.043072984	6.99	1.58E-11
cg19601144	ZNF710	Body	NA	Gene_Associate	TRUE	6.07	3.64E-09	1.89E-06	4.03	7.01E-05	0.013629672	6.99	1.64E-11

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cg21746071	ETFA; ETFA	Body;Body	TRUE	Unclassified	NA	-6.07	3.68E-09	1.91E-06	-4.08	5.57E-05	0.011528255	-4.26	2.67E-05
cg18953784			NA	Promoter_Associated	TRUE	6.07	3.68E-09	1.91E-06	4.14	4.45E-05	0.009843718	5.99	5.67E-09
cg20244340	SLC24A3	Body	NA		TRUE	-6.06	3.72E-09	1.92E-06	-4.42	1.32E-05	0.003920635	-5.24	2.88E-07
cg06541783	CAPZ A2	TSS1500	NA		NA	-6.06	3.74E-09	1.93E-06	-4.41	1.44E-05	0.004200821	-5.02	8.41E-07
cg04481596	SLC7A5	3UTR	NA		NA	-6.06	3.77E-09	1.93E-06	-6.6	1.65E-10	3.59E-07	-6.44	4.29E-10
cg16490191	UNKL	5UTR	TRUE	Promoter_Associated_Cell_type_specific	NA	-6.06	3.78E-09	1.93E-06	-5.5	7.87E-08	6.90E-05	-5.73	2.29E-08
cg23212751	ARTN; ARTN; ARTN; ARTN; ARTN	TSS1500;Body;Body;Body;Body	NA		NA	-6.06	3.78E-09	1.93E-06	-4.73	3.39E-06	0.001383399	-5.93	7.75E-09
cg17568996	NFAM1	Body	TRUE		NA	6.06	3.81E-09	1.94E-06	3.75	0.000212717	0.02975117	7.01	1.47E-11
cg11342789	C1orf226;C1orf226	Body;Body	NA		NA	-6.05	3.93E-09	1.99E-06	-4.16	4.03E-05	0.009139743	-3.52	0.000496641
cg21005412	WDR43;SNORD53	Body;TSS200	NA		NA	6.05	3.98E-09	2.00E-06	4.4	1.48E-05	0.004294724	7.46	8.20E-13
cg20646782			NA		NA	-6.05	4.06E-09	2.04E-06	-6.54	2.42E-10	5.10E-07	-6.38	6.33E-10
cg00751021	PARD3B;PARD3B;PARD3B	Body;Body;Body	TRUE		NA	6.05	4.09E-09	2.05E-06	3.8	0.000174981	0.026001363	6.75	7.00E-11

cg19741167	POLR1A	Body	NA	Promoter_Associated	TRUE	6.05	4.10E-09	2.05E-06	3.99	8.03E-05	0.014929705	6.35	7.33E-10
cg25193782			TRUE		TRUE	-6.04	4.19E-09	2.08E-06	-6.13	2.53E-09	3.87E-06	-6.65	1.26E-10
cg05549655	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	TRUE	-6.04	4.29E-09	2.12E-06	-5.53	6.47E-08	5.85E-05	-5.49	8.38E-08
cg07063912	LRRFP1	Body	NA		NA	6.04	4.31E-09	2.13E-06	4.15	4.18E-05	0.009401797	6.17	2.13E-09
cg23670188	LSP1;LSP1;LSP1;LSP1	Body;Body;Body;Body	NA		NA	-6.04	4.32E-09	2.13E-06	-6.37	6.59E-10	1.20E-06	-7.81	8.60E-14
cg27128761	SPARC	Body	TRUE		NA	6.04	4.33E-09	2.13E-06	3.95	9.52E-05	0.016906849	7.47	7.95E-13
cg23918047	ARHGDI A	5UTR	NA		NA	6.04	4.34E-09	2.13E-06	4.58	6.64E-06	0.002327738	5.59	4.76E-08
cg07477282	SPG11;SPG11	TSS1500;TSS1500	NA	Promoter_Associated	NA	6.03	4.41E-09	2.15E-06	5.28	2.37E-07	0.000167769	3.74	0.000217424
cg17852385	CYP1A1	TSS1500	NA	Unclassified_Cell_type_specific	NA	-6.03	4.41E-09	2.15E-06	-6.73	7.76E-11	1.83E-07	-6.16	2.15E-09
cg02863489	PRSS27	Body	NA	Unclassified_Cell_type_specific	TRUE	6.03	4.41E-09	2.15E-06	3.55	0.000436584	0.04729252	8.06	1.50E-14
cg23205276	KIAA1026;KIAA1026;KIAA1026;KIAA1026	Body;5UTR;Body;Body	TRUE		NA	-6.03	4.42E-09	2.15E-06	-4.44	1.26E-05	0.003789921	-5.77	1.92E-08
cg0655566	SFRS	Body	NA		NA	-6.03	4.48E-0	2.18E-0	-3.95	9.46E-0	0.01684	-4.99	9.82E-0

1	8						9	6		5	0641		7
cg09997244	KIRREL3;KIRREL3	Body;Body	TRUE		NA	-6.03	4.52E-09	2.19E-06	-4.04	6.74E-05	0.013269021	-5.24	2.92E-07
cg13417862	NXN	Body	NA		TRUE	6.03	4.54E-09	2.20E-06	5.07	6.87E-07	0.000394087	7.45	8.78E-13
cg22208536	SNX25	Body	TRUE		TRUE	6.03	4.56E-09	2.20E-06	4.37	1.68E-05	0.00475267	5.18	3.86E-07
cg02926160	EPB41L3	5UTR	NA		NA	6.02	4.70E-09	2.26E-06	4.35	1.80E-05	0.004970108	7.83	7.32E-14
cg20556402	MDFI	Body	NA		NA	6.02	4.74E-09	2.27E-06	4.15	4.28E-05	0.00955855	7.11	7.54E-12
cg17518949			NA	Unclassified_Cell_type_specific	NA	-6.02	4.76E-09	2.28E-06	-4.14	4.53E-05	0.009943896	-4.84	2.03E-06
cg00765705	NCOR2;NCOR2	Body;Body	NA	Unclassified	TRUE	6.02	4.77E-09	2.28E-06	4.05	6.47E-05	0.012916338	7.94	3.50E-14
cg24366968			NA	Unclassified_Cell_type_specific	NA	-6.02	4.78E-09	2.28E-06	-4	7.89E-05	0.014756589	-5.45	1.01E-07
cg10556036			NA		NA	-6.02	4.82E-09	2.30E-06	-6.39	5.67E-10	1.08E-06	-6.34	7.71E-10
cg12516954	H2AFY;H2AFY;H2AFY;H2AFY	Body;Body;Body;Body	TRUE		NA	6.01	4.89E-09	2.32E-06	4.3	2.29E-05	0.005947355	7.19	4.66E-12
cg01911077			TRUE	Gene_Associated	NA	6.01	4.92E-09	2.33E-06	3.89	0.000123335	0.02039347	5.81	1.47E-08
cg05593411	PDE4D;PDE4D;PDE4D	Body;TSS1500;Body	TRUE		NA	6.01	4.92E-09	2.33E-06	3.83	0.000153109	0.023729601	7.86	5.88E-14

cg11539351			TRUE		NA	-6.01	4.95E-09	2.33E-06	-5.78	1.77E-08	1.98E-05	-6.48	3.58E-10
cg17929169	FYN	TSS1500	NA		NA	6.01	5.00E-09	2.34E-06	4.05	6.34E-05	0.012735892	5.13	4.94E-07
cg17351376	CD248;CD248	1stExon;3UTR	NA		NA	6.01	5.03E-09	2.35E-06	5.54	6.23E-08	5.71E-05	4.04	6.60E-05
cg04131792			NA		NA	-6.01	5.09E-09	2.37E-06	-3.8	0.000169707	0.025443498	-6.27	1.20E-09
cg05857283			NA		NA	-6.01	5.12E-09	2.38E-06	-5.27	2.49E-07	0.000174712	-7.25	3.07E-12
cg06877366	MAD1L1;MAD1L1;MAD1L1	Body;Body;Body	NA		NA	-6	5.20E-09	2.42E-06	-5.54	6.17E-08	5.68E-05	-5.67	3.21E-08
cg22541038			NA	Promoter_Associated	TRUE	6	5.31E-09	2.46E-06	3.59	0.000387453	0.044247	7.57	4.04E-13
cg08696931	CDK2AP1	Body	TRUE		NA	6	5.39E-09	2.49E-06	3.75	0.000210906	0.029572733	7.79	9.48E-14
cg02305757	PHF1;PHF1;PHF1	Body;Body;Body	NA	Gene_Associated	NA	5.99	5.52E-09	2.55E-06	4.83	2.07E-06	0.000930429	8.37	1.82E-15
cg00288463	SGPP2	Body	TRUE		NA	-5.99	5.74E-09	2.63E-06	-5.82	1.40E-08	1.63E-05	-5.5	7.64E-08
cg26401796	NTF3	Body	TRUE		NA	-5.98	5.80E-09	2.65E-06	-7.18	4.76E-12	1.65E-08	-5.9	9.24E-09
cg20030796	BTBD17	Body	NA		NA	-5.98	5.82E-09	2.65E-06	-3.81	0.000167964	0.025258665	-6.16	2.16E-09
cg03071808			NA	Unclassified	TRUE	5.98	5.82E-09	2.65E-06	3.96	9.12E-05	0.016340306	8.86	5.64E-17
cg21581873	PLEKHA6	TSS1500	NA		TRUE	5.98	5.88E-09	2.67E-06	4.15	4.19E-05	0.009426105	5.89	1.00E-08
cg13914004	ST6GALNAC6	Body	NA	Unclassified	NA	5.98	5.91E-09	2.68E-06	4.51	8.91E-06	0.002902418	8.3	3.04E-15
cg0690703			TRUE		NA	-5.98	5.99E-09	2.70E-06	-4.31	2.18E-06	0.00573	-5.1	5.75E-0



3							9	6		5	8584		7
cg11696576	SLC22A3	Body	TRUE		NA	-5.98	6.00E-09	2.70E-06	-6.23	1.48E-09	2.42E-06	-3.92	0.000106468
cg16336586	LAPT M4B	Body	TRUE		NA	-5.98	6.01E-09	2.70E-06	-5.44	1.04E-07	8.46E-05	-4.74	3.16E-06
cg23058194	LOC390594	TSS200	NA		NA	5.98	6.04E-09	2.71E-06	5.15	4.47E-07	0.000282917	3.52	0.000492186
cg04449108	UGT1A10;UGT1A6;UGT1A9;UGT1A6;UGT1A7;UGT1A8	Body;5 UTR;Body;TSS1500;Body;Body	NA		NA	-5.97	6.13E-09	2.74E-06	-5.52	6.97E-08	6.24E-05	-5.97	6.39E-09
cg05028773	MIR24-2	Body	NA	Unclassified	NA	5.97	6.14E-09	2.74E-06	5.65	3.47E-08	3.48E-05	6.62	1.51E-10
cg06723829	LGR6;LGR6;LGR6	Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.97	6.27E-09	2.80E-06	-5.28	2.40E-07	0.000169317	-4.47	1.08E-05
cg18986335			TRUE	Unclassified_Cell_type_specific	NA	-5.96	6.54E-09	2.90E-06	-4.52	8.53E-06	0.002815557	-5.27	2.50E-07
cg26298409	MKX	Body	NA	Unclassified	NA	5.96	6.55E-09	2.90E-06	3.91	0.000110911	0.018965908	5.79	1.72E-08
cg15542713	HIVEP3;HIVEP3	TSS1500;TSS1500	NA	Promoter_Associated	NA	5.96	6.61E-09	2.92E-06	4.17	3.97E-05	0.009033943	5.59	4.96E-08
cg16120833	GPRC5C;GPRC5C	Body;Body	NA		NA	5.95	6.86E-09	3.01E-06	3.73	0.000228483	0.031344819	7.15	5.79E-12
cg19240569	HRASLS2	TSS1500	NA	Unclassified_Cell_type_specific	NA	-5.95	6.89E-09	3.02E-06	-4.82	2.18E-06	0.000967349	-4.11	5.06E-05

cg09513276	BMP7	Body	NA		NA	-5.95	7.12E-09	3.11E-06	-7.89	4.60E-14	2.33E-10	-5.64	3.72E-08
cg17198772			NA		NA	-5.95	7.17E-09	3.12E-06	-5	9.60E-07	0.00051101	-6.86	3.67E-11
cg14280181	SGPP2	Body	NA	Unclassified_Cell_type_specific	NA	-5.94	7.24E-09	3.14E-06	-5.49	8.35E-08	7.23E-05	-5.9	9.14E-09
cg06794253			TRUE		TRUE	5.94	7.27E-09	3.15E-06	4.27	2.59E-05	0.006489203	7.35	1.66E-12
cg13298389			NA		NA	-5.94	7.35E-09	3.17E-06	-4.36	1.76E-05	0.004903506	-4.38	1.58E-05
cg18087256			TRUE		NA	-5.94	7.36E-09	3.17E-06	-4.43	1.30E-05	0.003875797	-3.11	0.002069825
cg07796002	ARHG EF1;ARHG EF1;ARHGEF1	Body;Body;Body	TRUE	Promoter_Associated	TRUE	5.94	7.36E-09	3.17E-06	3.59	0.000383757	0.04397211	6.61	1.58E-10
cg23844527	EPB41L5	Body	NA	Unclassified_Cell_type_specific	NA	5.94	7.39E-09	3.17E-06	5.1	5.83E-07	0.00034948	2.71	0.007190666
cg02381279			NA		NA	5.94	7.43E-09	3.18E-06	3.65	0.000303789	0.037820585	7.01	1.42E-11
cg02357046	FAM53A	TSS1500	NA		NA	-5.94	7.46E-09	3.19E-06	-5.65	3.58E-08	3.59E-05	-5.04	7.79E-07
cg00470972	UGT1A10;UGT1A7;UGT1A9;UGT1A8	Body;1stExon;Body;Body	NA		NA	-5.93	7.65E-09	3.25E-06	-5.75	2.08E-08	2.26E-05	-3.67	0.000283065
cg06636541	BAHC1	Body	NA		NA	-5.93	7.68E-09	3.26E-06	-4.55	7.71E-06	0.002614255	-3.87	0.000132812
cg07563400	ADORA2B	Body	TRUE	Unclassified_Cell	NA	-5.93	7.77E-09	3.30E-06	-5.7	2.75E-08	2.86E-05	-5.1	5.92E-07

				_type_s pecific									
cg14052728	PROM2;PROM2;PROM2	Body;Body;Body	NA		NA	-5.93	7.88E-09	3.32E-06	-3.59	0.000381244	0.043820287	-6.02	4.84E-09
cg20538228	ASPS CR1	Body	NA	Unclassified_Cell _type_s pecific	NA	-5.92	8.19E-09	3.42E-06	-4.12	4.88E-05	0.010492921	-5.53	6.77E-08
cg17329859			NA		NA	-5.92	8.25E-09	3.44E-06	-5.02	8.38E-07	0.000460335	-5.11	5.48E-07
cg00336149	CACNA1D;CACNA1D;CACNA1D	Body;Body;Body	NA		NA	5.92	8.35E-09	3.47E-06	4.63	5.24E-06	0.001952999	5.98	5.90E-09
cg13475583			NA	Promoter_Associated	NA	5.92	8.43E-09	3.50E-06	4.61	5.94E-06	0.002148077	7.45	9.06E-13
cg00031896	KDM2B	TSS1500	NA	Promoter_Associated	NA	5.92	8.47E-09	3.50E-06	3.87	0.000129715	0.021080807	5.26	2.62E-07
cg07512993	TK2	Body	NA	Promoter_Associated	NA	5.91	8.52E-09	3.52E-06	3.68	0.000273168	0.03528944	5.4	1.27E-07
cg11112615	SERPINB6	5UTR	NA		NA	5.91	8.57E-09	3.52E-06	4.59	6.38E-06	0.002260124	5.94	7.49E-09
cg03785076	SNED1	TSS1500	TRUE		NA	-5.91	8.69E-09	3.55E-06	-4.84	2.04E-06	0.000917422	-5.46	9.71E-08
cg26470501	BCL3	Body	NA	Promoter_Associated	NA	-5.91	8.81E-09	3.59E-06	-4.2	3.44E-05	0.008068988	-6.46	3.83E-10
cg19185414			NA		NA	-5.9	9.02E-09	3.66E-06	-4.33	2.01E-05	0.005416985	-4.86	1.86E-06
cg26850624	AHRR	Body	NA	Gene_Associate	NA	5.9	9.03E-09	3.66E-06	5.47	9.15E-08	7.75E-05	5.9	9.51E-09

				d_Cell_t ype_spe cific									
cg20040765	ADHF E1	Body	TRUE		NA	5.9	9.19E-09	3.70E-06	4.54	7.81E-06	0.002643915	6.77	6.22E-11
cg01294327	LINGO3	Body	NA		NA	-5.9	9.23E-09	3.71E-06	-5.16	4.29E-07	0.000274002	-5.69	2.85E-08
cg06770731	SLC7A5	3UTR	TRUE		NA	-5.9	9.37E-09	3.74E-06	-5.79	1.69E-08	1.92E-05	-6.64	1.32E-10
cg03078672			NA		NA	-5.9	9.39E-09	3.74E-06	-4.1	5.15E-05	0.010927625	-3.33	0.000955059
cg12547807			TRUE	Unclassi fied	TRUE	-5.9	9.42E-09	3.75E-06	-5.02	8.42E-07	0.000461612	-6.37	6.58E-10
cg26105278	TP73; TP73; TP73; TP73	Body;B ody;Bo dy;Body	NA		TRUE	-5.89	9.51E-09	3.78E-06	-3.93	0.000105516	0.018330801	-4.99	9.73E-07
cg27192708	PPBP	TSS1500	NA		NA	-5.89	9.56E-09	3.79E-06	-4.55	7.71E-06	0.002614255	-5.99	5.61E-09
cg04025127	PTPRF;PTP RF	Body;B ody	TRUE		NA	-5.89	9.76E-09	3.86E-06	-6.27	1.16E-09	1.97E-06	-5.49	8.20E-08
cg11966524			NA		NA	-5.89	9.78E-09	3.86E-06	-5.73	2.29E-08	2.42E-05	-5.61	4.41E-08
cg04724387			TRUE		NA	-5.89	9.81E-09	3.86E-06	-4.5	9.45E-06	0.003030061	-4.62	5.68E-06
cg12543219	KNDC1	Body	NA		NA	-5.88	1.00E-08	3.94E-06	-3.53	0.000471851	0.049695022	-4.54	8.07E-06
cg14392725			TRUE		NA	-5.88	1.01E-08	3.94E-06	-6.03	4.47E-09	6.19E-06	-3.99	8.36E-05
cg12411994	ACTR3C	5UTR	NA		NA	-5.88	1.04E-08	4.04E-06	-4.98	1.06E-06	0.000553413	-4.55	7.68E-06
cg03517919	KIF1B	Body	NA	Unclassi fied	TRUE	5.88	1.04E-08	4.04E-06	4.64	5.05E-06	0.001892714	5.91	8.89E-09
cg13827179			TRUE		NA	5.88	1.05E-08	4.07E-06	4.13	4.67E-05	0.01014545	8.19	6.54E-15
cg17668731	CCNJL	Body	TRUE		TRUE	5.87	1.06E-08	4.11E-06	5.29	2.24E-07	0.000160811	6.55	2.35E-10

cg05254946	RYR1; RYR1	Body;Body	NA		NA	-5.87	1.06E-08	4.11E-06	-4.74	3.25E-06	0.001335907	-5.47	8.90E-08
cg00545196	RXRA	Body	NA	Unclassified	NA	-5.87	1.07E-08	4.11E-06	-6.1	2.95E-09	4.45E-06	-6.7	9.33E-11
cg25700513	KIF13A;KIF13A;KIF13A;KIF13A	Body;Body;Body;Body	TRUE		NA	-5.87	1.07E-08	4.11E-06	-3.71	0.000239531	0.032441904	-5.61	4.29E-08
cg01979157	SKI	1stExon	NA	Promoter_Associated	NA	-5.87	1.07E-08	4.11E-06	-5.13	5.08E-07	0.000313322	-5.3	2.22E-07
cg20074340	MCF2L;MCF2L	Body;Body	NA		NA	-5.87	1.07E-08	4.11E-06	-4.33	2.03E-05	0.005442309	-5.85	1.21E-08
cg22453818	LHFPL2	5UTR	TRUE		NA	-5.87	1.07E-08	4.11E-06	-4.78	2.73E-06	0.001162338	-4.43	1.28E-05
cg13215862			NA	Promoter_Associated_Cell_type_specific	TRUE	5.87	1.08E-08	4.13E-06	3.77	0.000195403	0.028137717	6.49	3.27E-10
cg19372602			TRUE	Unclassified	NA	-5.87	1.08E-08	4.13E-06	-4.88	1.65E-06	0.00078755	-5.55	6.16E-08
cg14005246			TRUE		NA	5.87	1.10E-08	4.19E-06	4	7.91E-05	0.014762948	7.81	8.57E-14
cg00355315	SSU72	Body	NA		NA	-5.87	1.10E-08	4.19E-06	-3.93	0.00010508	0.018275385	-5.77	1.87E-08
cg10553415			NA		NA	5.86	1.12E-08	4.25E-06	3.7	0.000248653	0.033292388	4.52	8.91E-06
cg12807924	SRC;SRC	Body;Body	NA	Promoter_Associated	TRUE	5.86	1.12E-08	4.25E-06	3.83	0.000151908	0.023595026	7.36	1.59E-12
cg00020474			TRUE	Unclassified_Cell_type_specific	NA	5.86	1.14E-08	4.30E-06	3.6	0.000362599	0.042469283	7.32	2.02E-12
cg0026412	HBEG	Body	TRUE	Promoter	NA	-5.86	1.15E-08	4.32E-06	-4.12	4.81E-06	0.01034	-4.17	3.91E-0

9	F			r_Associated			8	6		5	8057		5
cg06061092	DIP2C	Body	NA		NA	-5.86	1.16E-08	4.34E-06	-6.61	1.62E-10	3.53E-07	-5.25	2.83E-07
cg14506175	ASS1; ASS1	Body;Body	NA	Unclassified	NA	5.86	1.16E-08	4.35E-06	4.15	4.20E-05	0.009449954	7.84	6.97E-14
cg20654468	LPXN; LPXN	Body;Body	NA		NA	5.86	1.18E-08	4.39E-06	3.75	0.000207082	0.029216825	5.13	4.92E-07
cg14891022	RAC2	Body	TRUE	Promoter_Associated	TRUE	5.85	1.18E-08	4.41E-06	5.85	1.21E-08	1.46E-05	7.68	2.01E-13
cg17901584	DHCR24	TSS1500	NA	Promoter_Associated_Cell_type_specific	NA	-5.85	1.20E-08	4.45E-06	-4.67	4.42E-06	0.001711097	-5.17	4.06E-07
cg19974448	LOC10169752	TSS200	NA		NA	-5.85	1.21E-08	4.47E-06	-4.55	7.69E-06	0.002611318	-5.1	5.78E-07
cg01362541	BMP7	Body	NA		NA	-5.85	1.21E-08	4.47E-06	-4.39	1.56E-05	0.004468547	-5.71	2.57E-08
cg05284742	ITPK1; ITPK1; ITPK1	Body;Body;Body	TRUE		NA	-5.85	1.21E-08	4.47E-06	-7.94	3.32E-14	1.77E-10	-6.32	8.68E-10
cg04126866	C10orf99	TSS1500	NA		NA	-5.85	1.22E-08	4.48E-06	-5.32	1.98E-07	0.000145686	-5.51	7.34E-08
cg18642234	GPX1; GPX1; GPX1	3UTR;3UTR;1stExon	NA		NA	-5.85	1.23E-08	4.52E-06	-4.2	3.40E-05	0.008008413	-4.67	4.36E-06
cg24540678			NA		NA	-5.85	1.24E-08	4.54E-06	-5.07	6.62E-07	0.000382879	-6.46	3.84E-10
cg01928820	PTCRA	TSS200	NA		NA	5.84	1.25E-08	4.55E-06	4.5	9.62E-06	0.003062663	5.47	9.10E-08
cg21441211			TRUE		NA	-5.84	1.25E-08	4.55E-06	-5.4	1.30E-07	0.000101687	-5.64	3.82E-08
cg13184736	GNG12	TSS1500	NA		TRUE	-5.84	1.25E-08	4.55E-06	-4.69	4.12E-06	0.001612185	-6.01	5.07E-09
cg2558786	RNF21	Body;3	NA	Unclassified	TRUE	5.84	1.25E-08	4.55E-06	3.56	0.00042	0.04694	4.95	1.18E-0

8	2:RNF212	UTR		fied			8	6		9943	3737		6
cg21972431			TRUE		NA	-5.84	1.26E-08	4.59E-06	-5.97	6.39E-09	8.47E-06	-5.71	2.60E-08
cg14700707	NOTCH4;NOTCH4	1stExon;5UTR	TRUE		NA	5.84	1.29E-08	4.65E-06	4.84	1.99E-06	0.000903652	5.91	8.95E-09
cg17616283	EFEMP2	Body	NA		TRUE	5.84	1.30E-08	4.68E-06	4.11	5.11E-05	0.010857289	6.67	1.15E-10
cg19572487	RARA;RARA;RARA	5UTR;5UTR	NA	Promoter_Associated	NA	-5.83	1.33E-08	4.77E-06	-5.32	1.95E-07	0.000143995	-5.31	2.07E-07
cg02836864			TRUE	Unclassified	NA	5.83	1.33E-08	4.77E-06	5.03	8.14E-07	0.00045059	8.08	1.39E-14
cg17214455	HLA-D OA	Body	NA		NA	5.83	1.35E-08	4.84E-06	4.2	3.50E-05	0.008159234	5.97	6.35E-09
cg04329347	ALDOA	TSS1500	NA		NA	5.83	1.36E-08	4.86E-06	4.35	1.83E-05	0.005045554	5.62	4.19E-08
cg10217713	KNDC1	Body	NA		NA	-5.83	1.36E-08	4.86E-06	-3.88	0.000125794	0.020647511	-5.52	7.08E-08
cg18641697	SEPT6;SEPT6;SEPT6;SEPT6	TSS200;TSS200;TSS200;TSS200	NA	Promoter_Associated	NA	5.83	1.37E-08	4.86E-06	3.78	0.000188414	0.027469461	2.94	0.003486799
cg14184886			TRUE	Unclassified	NA	-5.83	1.37E-08	4.86E-06	-5.2	3.55E-07	0.000233275	-5.98	6.05E-09
cg04269907	BICD2;BICD2	Body;3UTR	NA		NA	-5.83	1.38E-08	4.89E-06	-4.4	1.45E-05	0.004220156	-5.45	1.02E-07
cg07241925	MAEA;MAEA	Body;Body	TRUE		TRUE	5.82	1.39E-08	4.90E-06	4.55	7.61E-06	0.002594558	6.25	1.31E-09
cg13582028	ERICH1	Body	TRUE		TRUE	5.82	1.39E-08	4.90E-06	3.71	0.000241379	0.032598803	4.91	1.45E-06
cg03131092	KIAA1543;KIAA1543	3UTR;3UTR	NA		TRUE	-5.82	1.39E-08	4.90E-06	-5.42	1.17E-07	9.33E-05	-6.11	2.91E-09

cg25684105	TXNRD1	Body	NA	Unclassified_Cell_type_specific	TRUE	-5.82	1.40E-08	4.92E-06	-5.6	4.49E-08	4.37E-05	-4.55	7.61E-06
cg27043548			TRUE		NA	-5.82	1.40E-08	4.93E-06	-5.56	5.55E-08	5.21E-05	-6.7	9.40E-11
cg11811840	UGT1A10;UGT1A1;UGT1A6;UGT1A8;UGT1A4;UGT1A3;UGT1A6;UGT1A9;UGT1A7;UGT1A5	Body;1stExon;Body;Body;Body;Body;Body	NA		NA	-5.82	1.41E-08	4.93E-06	-4.93	1.29E-06	0.000650969	-5.43	1.12E-07
cg00183107	INPP4B;INPP4B	5UTR;5UTR	NA	Unclassified_Cell_type_specific	NA	5.82	1.42E-08	4.97E-06	3.61	0.000350023	0.041533914	2.6	0.009715633
cg20912205	NAT6;HYAL3	TSS1500;TSS1500	NA	Promoter_Associated	NA	-5.82	1.44E-08	5.03E-06	-5.44	1.03E-07	8.43E-05	-5.35	1.64E-07
cg00866399	EMX1	Body	NA		NA	5.82	1.44E-08	5.03E-06	4.66	4.63E-06	0.001765634	7.53	5.38E-13
cg21038291			TRUE		NA	5.82	1.45E-08	5.06E-06	3.77	0.000196818	0.028277917	7.17	5.24E-12
cg01350686	MYOM3	TSS1500	NA	Unclassified	NA	5.82	1.46E-08	5.07E-06	4.15	4.30E-05	0.009585926	6.62	1.50E-10
cg26663490	GPRC5C;GPRC5C	Body;Body	NA		NA	5.81	1.48E-08	5.13E-06	3.58	0.000401697	0.045098608	6.97	1.85E-11
cg2044904	C7orf5	Body;B	NA	Unclassified	NA	-5.81	1.49E-08	5.14E-06	-5.27	2.49E-08	0.00017	-7.04	1.19E-1



8	0:C7orf50;C7orf50	ody;Body		fied_Cell_type_specific			8	6		7	469		1
cg00196407	ABR;ABR;ABR	Body;Body;Body	TRUE	Unclassified	NA	5.81	1.49E-08	5.14E-06	3.58	0.000395929	0.044782044	7.1	8.40E-12
cg24137511	MAST3	Body	NA		NA	-5.81	1.51E-08	5.19E-06	-4.31	2.14E-05	0.005652494	-5.81	1.54E-08
cg10533624	TEAD4;TEAD4;TEAD4	Body;Body;Body	TRUE	Unclassified	NA	5.81	1.52E-08	5.21E-06	4.65	4.74E-06	0.001795091	7.54	4.94E-13
cg26274662			TRUE	Unclassified_Cell_type_specific	NA	5.81	1.53E-08	5.23E-06	4.41	1.44E-05	0.004200821	6.94	2.19E-11
cg14883070	SPIRE1;SPIRE1;SPIRE1	5UTR;Body;Body	TRUE		NA	-5.8	1.54E-08	5.27E-06	-5.76	1.96E-08	2.16E-05	-4.75	3.13E-06
cg02010481	JAZF1	Body	NA		NA	5.8	1.54E-08	5.27E-06	4.66	4.54E-06	0.001739712	6.43	4.70E-10
cg24003955	CTNNBIP1;CTNNBIP1	Body;Body	TRUE		TRUE	5.8	1.55E-08	5.30E-06	3.89	0.000121723	0.020229148	6.75	6.88E-11
cg25298189	ARID3A	Body	NA		TRUE	5.8	1.58E-08	5.37E-06	3.62	0.000340918	0.04078347	7.9	4.41E-14
cg10125703	RASIP1	Body	NA	Unclassified_Cell_type_specific	TRUE	5.8	1.59E-08	5.38E-06	3.91	0.000112782	0.019163378	7.33	1.93E-12
cg06488957	RAI1	5UTR	NA	Unclassified	NA	5.8	1.62E-08	5.46E-06	3.63	0.000331839	0.040172077	7.78	1.01E-13
cg00026033	IKZF4	TSS200	NA		NA	5.79	1.65E-08	5.54E-06	3.93	0.000105954	0.018363718	6.68	1.05E-10
cg02844899	TTC7A	Body	TRUE		TRUE	5.79	1.66E-08	5.55E-06	4.2	3.42E-05	0.00803283	3.57	0.000412518

cg15247247	FOXK1	3UTR	NA		NA	-5.79	1.67E-08	5.58E-06	-4.15	4.29E-05	0.009576336	-6.29	1.04E-09
cg17130474	PINX1	3UTR	NA		NA	-5.79	1.68E-08	5.58E-06	-3.69	0.000261636	0.03440579	-7.04	1.22E-11
cg03395898	TGFB3;TGF B3	1stExon;5UTR	NA	Promoter_Associated	NA	-5.79	1.70E-08	5.63E-06	-5	9.63E-07	0.000511124	-5.19	3.68E-07
cg05194114	CCND BP1;CCNDB P1;CCNDBP1;CCNDBP1	TSS200;TSS200;TSS1500;TSS200	NA	Promoter_Associated	NA	5.79	1.70E-08	5.64E-06	3.54	0.000454006	0.048488063	5.08	6.37E-07
cg07049086	LSP1;LSP1;LSP1;LSP1	5UTR;5UTR;Body;5UTR	NA		NA	-5.78	1.73E-08	5.70E-06	-4.69	4.02E-06	0.001584117	-8.33	2.46E-15
cg19583819	NRG2;NRG2;NRG2;NRG2	Body;Body;Body;Body	NA		TRUE	-5.78	1.73E-08	5.70E-06	-6.5	3.04E-10	6.19E-07	-5.35	1.65E-07
cg04171052	SLC7A5	Body	NA		NA	-5.78	1.75E-08	5.75E-06	-8.03	1.78E-14	9.95E-11	-5.76	1.96E-08
cg14880257	MYT1L	Body	NA		NA	-5.78	1.78E-08	5.84E-06	-6.72	7.99E-11	1.87E-07	-6.08	3.53E-09
cg23935642	MUC2	Body	NA		NA	-5.78	1.80E-08	5.88E-06	-3.78	0.000189136	0.027563773	-6.11	2.92E-09
cg27366395	CHADL;L3MBTL2	3UTR;Body	NA		NA	-5.78	1.80E-08	5.88E-06	-4.87	1.78E-06	0.000829647	-5.58	5.13E-08
cg25386426	PANK4	TSS1500	NA	Unclassified	NA	-5.78	1.81E-08	5.90E-06	-4.45	1.18E-05	0.003591834	-6.21	1.63E-09
cg18018581			NA		NA	-5.77	1.84E-08	5.98E-06	-3.99	8.02E-05	0.014929705	-4.99	9.95E-07
cg08324801			TRUE	Promoter_Associated	NA	5.77	1.90E-08	6.14E-06	3.76	0.000200357	0.028564472	6.44	4.48E-10

cg07362969	TPPA	1stExon	NA		TRUE	5.77	1.91E-08	6.14E-06	4.36	1.77E-05	0.004934332	3.89	0.000124156
cg06475223	LAMA3;LAMA3;LAMA3;LAMA3	Body;Body;Body	NA	Unclassified	TRUE	5.77	1.91E-08	6.14E-06	3.6	0.000372811	0.043224865	7.29	2.49E-12
cg03143457	GNG12	5UTR	TRUE	Unclassified_Cell_type_specific	NA	-5.76	1.93E-08	6.21E-06	-4.56	7.43E-06	0.00254658	-5.78	1.74E-08
cg01495363	LOC100287216;SH3RF3	TSS1500;Body	NA		NA	-5.76	1.96E-08	6.29E-06	-5.11	5.48E-07	0.000334455	-6.34	7.83E-10
cg25252561	CAMK2G;CAMK2G;CAMK2G;CAMK2G;CAMK2G	Body;Body;Body;Body	TRUE		TRUE	5.76	1.98E-08	6.33E-06	4.04	6.65E-05	0.013154239	6.64	1.39E-10
cg09313740	INPPL1	Body	NA		NA	-5.76	2.00E-08	6.37E-06	-4.72	3.45E-06	0.001404503	-5.42	1.17E-07
cg13683827	FAM113B	5UTR	TRUE		NA	5.75	2.02E-08	6.43E-06	3.89	0.000121842	0.02024102	6.85	3.78E-11
cg03246954	MKNK2;MKNK2	Body;Body	NA		NA	-5.75	2.02E-08	6.43E-06	-3.73	0.00022963	0.031481866	-5.8	1.56E-08
cg10277523			NA		NA	-5.75	2.04E-08	6.46E-06	-4.78	2.64E-06	0.001133294	-4.71	3.77E-06
cg24470133	SSU72	Body	NA		NA	-5.75	2.04E-08	6.46E-06	-3.95	9.71E-05	0.017195246	-5.44	1.08E-07
cg02709068	GLI3	Body	TRUE	Unclassified_Cell_type_specific	NA	5.75	2.04E-08	6.46E-06	4.46	1.16E-05	0.003531461	7.56	4.24E-13

cg15621656	TNFAIP8	Body	NA		NA	5.75	2.04E-08	6.46E-06	3.59	0.000379546	0.043684208	8.15	8.65E-15
cg00035074	TTYH3	3UTR	NA	Unclassified_Cell_type_specific	NA	-5.75	2.09E-08	6.55E-06	-5.42	1.20E-07	9.50E-05	-4.23	3.00E-05
cg08165796			TRUE	Unclassified_Cell_type_specific	NA	5.75	2.09E-08	6.56E-06	5.36	1.58E-07	0.000120781	6.81	4.90E-11
cg18433784	S100B	TSS200	NA		NA	5.75	2.10E-08	6.58E-06	3.56	0.000429634	0.046922076	6.79	5.47E-11
cg25809905	ITGA2B	TSS1500	NA		NA	5.74	2.17E-08	6.74E-06	3.81	0.000164079	0.024841406	5.18	3.98E-07
cg11986861	ZNRF3	5UTR	NA		NA	-5.74	2.18E-08	6.74E-06	-5.31	2.06E-07	0.000150157	-5.8	1.57E-08
cg20552263			NA		NA	-5.74	2.22E-08	6.86E-06	-3.63	0.000331187	0.040104541	-6.71	9.07E-11
cg04506190	PLXND1	Body	NA		NA	-5.74	2.24E-08	6.90E-06	-4.93	1.30E-06	0.00065385	-5.32	1.97E-07
cg27446185	VTCN1	TSS1500	NA		NA	-5.74	2.24E-08	6.91E-06	-4.09	5.35E-05	0.011257306	-5.58	5.19E-08
cg23510527	UGT1A6;UGT1A10;UGT1A6;UGT1A9;UGT1A7;UGT1A8	TSS200;Body;5UTR;Body;Body;Body	NA		NA	-5.73	2.26E-08	6.95E-06	-6.18	1.89E-09	3.01E-06	-6.06	3.75E-09
cg02099474	CYP2W1	Body	NA		NA	5.73	2.27E-08	6.95E-06	5.05	7.25E-07	0.000409914	5.16	4.44E-07
cg10058920	PDYN	TSS200	NA		NA	5.73	2.30E-08	7.03E-06	3.75	0.000207485	0.029221095	7.02	1.31E-11
cg14478589	GSN;GSN;GSN;	Body;Body;Body;Body	NA		NA	5.73	2.32E-08	7.08E-06	3.69	0.000267547	0.034870437	5.47	9.29E-08

	GSN; GSN; GSN; GSN;	;Body;B ody;Bo dy;Body											
cg2177062 2	DGKZ; DGKZ; DGKZ; DGKZ	Body;T SS200; Body;B ody	NA	Promote r_Associ ated	TRUE	5.73	2.33E-0 8	7.09E-0 6	4.61	5.71E-0 6	0.00209 2389	7.15	6.04E-1 2
cg0127566 1			TRUE		NA	5.73	2.33E-0 8	7.09E-0 6	3.55	0.00044 8318	0.04808 5861	7.13	6.59E-1 2
cg2556114 0	MSI1	Body	TRUE	Unclassi fied_Cell _type_s pecific	TRUE	5.73	2.33E-0 8	7.09E-0 6	3.55	0.00044 5623	0.04790 5529	9.09	1.08E-1 7
cg2375439 2	BMI1	5UTR	NA		NA	5.73	2.35E-0 8	7.14E-0 6	3.66	0.00029 4928	0.03703 188	8.28	3.37E-1 5
cg2483346 4	KRTA P3-1	TSS200	TRUE		NA	-5.72	2.40E-0 8	7.26E-0 6	-3.68	0.00027 5421	0.03547 2672	-4.4	1.48E-0 5
cg0416238 3	GLIS1	Body	TRUE		NA	-5.72	2.45E-0 8	7.41E-0 6	-6.33	8.24E-1 0	1.47E-0 6	-6.04	4.29E-0 9
cg1248818 7	MSRB 3;MSR B3	TSS150 0;TSS1 500	NA		NA	5.71	2.51E-0 8	7.56E-0 6	3.62	0.00034 1691	0.04084 1566	6.2	1.79E-0 9
cg0968857 9	ADRB K1	Body	TRUE	Promote r_Associ ated	NA	5.71	2.54E-0 8	7.63E-0 6	4.03	7.00E-0 5	0.01361 747	6.31	9.25E-1 0
cg0513552 1	RBMS 1;RBM S1	Body;B ody	TRUE		NA	-5.71	2.55E-0 8	7.65E-0 6	-4.81	2.31E-0 6	0.00101 5938	-5.17	4.16E-0 7
cg2326132 7	BAIAP 2;BAIA P2;BAI AP2;B AIAP2	Body;B ody;Bo dy;Body	NA	Unclassi fied	NA	5.71	2.56E-0 8	7.66E-0 6	6.17	2.04E-0 9	3.22E-0 6	6.77	6.21E-1 1
cg0519434 6			TRUE		TRUE	5.71	2.61E-0 8	7.75E-0 6	5.87	1.09E-0 8	1.34E-0 5	5.63	4.01E-0 8
cg2386691	SBNO	5UTR	TRUE		NA	-5.71	2.63E-0	7.80E-0	-4.18	3.70E-0	0.00855	-4.96	1.17E-0

6	2						8	6		5	3447		6
cg09618385	SLC7A5	3UTR	NA		NA	-5.7	2.66E-08	7.85E-06	-5.86	1.12E-08	1.36E-05	-6.49	3.32E-10
cg04636402	NRG2; NRG2; NRG2; NRG2	Body;Body; Body;Body; Body;Body	NA		TRUE	-5.7	2.66E-08	7.85E-06	-5.15	4.45E-07	0.00028267	-6.29	1.05E-09
cg09761230			NA	Unclassified_Cell_type_specific	NA	5.7	2.69E-08	7.91E-06	4.53	8.43E-06	0.002789283	5.86	1.13E-08
cg23922804			NA		NA	5.7	2.74E-08	8.04E-06	3.67	0.000284059	0.036158231	6.19	1.81E-09
cg12586150	SERPINB1	Body	TRUE		NA	5.7	2.75E-08	8.04E-06	4.16	4.10E-05	0.009271082	5.58	5.17E-08
cg08556107	AHRR	Body	NA	Gene_Associated_Cell_type_specific	NA	-5.7	2.75E-08	8.04E-06	-6.94	2.15E-11	6.09E-08	-6.23	1.44E-09
cg13713728	LOC100169752	TSS200	NA		NA	-5.7	2.76E-08	8.07E-06	-4.62	5.64E-06	0.002070815	-5.06	7.16E-07
cg18390495	DEFB132	Body	NA		NA	5.7	2.77E-08	8.08E-06	3.99	8.20E-05	0.015150954	6.56	2.22E-10
cg27303421			TRUE		NA	-5.7	2.78E-08	8.09E-06	-3.81	0.000163415	0.024753788	-5.38	1.41E-07
cg09491709	C3orf20	TSS200	NA		NA	-5.69	2.84E-08	8.22E-06	-3.76	0.00020516	0.029054378	-5.05	7.63E-07
cg11177833	GLTPD2	1stExon	NA		NA	-5.69	2.85E-08	8.22E-06	-5.14	4.68E-07	0.000293215	-5.33	1.87E-07
cg02753187	CALCO2	Body	NA	Unclassified	NA	5.69	2.91E-08	8.35E-06	4.57	7.04E-06	0.002446377	7.43	9.93E-13
cg00908631	CDKN2C	TSS1500	NA	Promoter_Associated	NA	-5.68	2.93E-08	8.42E-06	-3.74	0.00022113	0.030622668	-5.92	8.21E-09
cg24723731			TRUE		NA	5.68	2.95E-08	8.46E-06	3.57	0.000412035	0.045768252	7.45	9.10E-13

cg19192878	CECR1	TSS1500	NA		NA	-5.68	2.97E-08	8.49E-06	-4.28	2.48E-05	0.006310642	-5.28	2.34E-07
cg22679626			NA	Promoter_Associated	NA	5.68	2.98E-08	8.51E-06	4.27	2.55E-05	0.006422668	4.27	2.63E-05
cg17232357	SMAD6;SMAD6;SMAD6	Body;Body;Body	TRUE		TRUE	-5.68	2.99E-08	8.51E-06	-4.43	1.30E-05	0.003877204	-5.6	4.52E-08
cg16937168	SNED1	TSS1500	TRUE		NA	-5.68	3.03E-08	8.61E-06	-5.79	1.65E-08	1.88E-05	-3.84	0.000146671
cg13945576	ROR2	Body	TRUE	Unclassified_Cell_type_specific	NA	-5.68	3.03E-08	8.61E-06	-4.56	7.24E-06	0.002500688	-7.38	1.38E-12
cg20317521	BAIAP2;BAIAP2;BAIAP2;BAIAP2	Body;Body;Body;Body	NA	Unclassified_Cell_type_specific	NA	-5.68	3.06E-08	8.68E-06	-6.22	1.56E-09	2.53E-06	-4.89	1.61E-06
cg14219256	MYST4	Body	TRUE	Unclassified_Cell_type_specific	NA	5.68	3.07E-08	8.71E-06	3.86	0.00013926	0.022223002	4.84	1.99E-06
cg08684879			TRUE		NA	5.68	3.09E-08	8.74E-06	3.95	9.79E-05	0.017306888	5.29	2.29E-07
cg23489390	CRIM1	Body	TRUE		NA	-5.67	3.14E-08	8.85E-06	-4.66	4.57E-06	0.001746695	-5.02	8.47E-07
cg24631065	MUC2	Body	NA		NA	-5.67	3.15E-08	8.85E-06	-3.6	0.000372297	0.043200665	-6.24	1.39E-09
cg07739604	NCOR2;NCOR2	Body;Body	NA	Promoter_Associated	TRUE	5.67	3.15E-08	8.85E-06	3.77	0.000193976	0.02803322	6.04	4.39E-09
cg19792544	KIFC2;FOXH1	3UTR;3UTR	NA	Unclassified	NA	5.67	3.15E-08	8.85E-06	3.61	0.00035584	0.041978191	6.97	1.82E-11
cg15795984	PRND	5UTR	NA		NA	-5.67	3.17E-08	8.88E-06	-4.36	1.72E-05	0.004825254	-4.9	1.53E-06

cg01619562	ITPK1; ITPK1; ITPK1	Body;B ody;Bo dy	TRUE		NA	-5.67	3.17E-08	8.88E-06	-4.11	5.10E-05	0.010851043	-6.06	3.81E-09
cg17300047	RCBT B2	TSS1500	NA		NA	5.67	3.18E-08	8.90E-06	4	7.87E-05	0.014728733	6.43	4.58E-10
cg11505417	C1QA	3UTR	NA	Unclassified_Cell_type_specific	NA	5.67	3.19E-08	8.90E-06	4.03	6.87E-05	0.013435319	5.27	2.47E-07
cg20456243	SPEG	Body	NA	Unclassified_Cell_type_specific	NA	-5.67	3.19E-08	8.90E-06	-4.65	4.86E-06	0.001828574	-3.71	0.000246875
cg04242132	FERMT1	Body	NA	Unclassified	NA	5.67	3.20E-08	8.91E-06	3.67	0.000280294	0.035861369	6.22	1.58E-09
cg24698211	FGF18	Body	NA		TRUE	-5.67	3.23E-08	8.98E-06	-5.01	9.01E-07	0.000484821	-5.55	5.89E-08
cg18114313			TRUE		NA	-5.67	3.23E-08	8.98E-06	-3.84	0.000145928	0.022928251	-4.94	1.23E-06
cg09386458	QPCT	TSS1500	TRUE		NA	-5.66	3.26E-08	9.03E-06	-4.35	1.82E-05	0.005021558	-3.75	0.000207018
cg12397274	TINAG	TSS1500	NA		NA	-5.66	3.31E-08	9.12E-06	-4.4	1.48E-05	0.004297201	-3.42	0.000715464
cg18337963	DGKZ; DGKZ; DGKZ; DGKZ; DGKZ	1stExon; Body;5 UTR;Bo dy;Body	NA	Promoter_Associated	TRUE	5.66	3.35E-08	9.20E-06	4.08	5.58E-05	0.011536406	6.67	1.10E-10
cg14979593	PGAP2;PGA P2;PGA P2;P GAP2; PGAP2;PGA P2;PGA P2;P GAP2	Body;B ody;5U TR;Bod y;Body; Body;B ody;Bo dy	NA	Promoter_Associated	TRUE	-5.66	3.35E-08	9.20E-06	-3.69	0.000261206	0.034370514	-6.18	1.99E-09



cg01383955	NFAM1	TSS200	NA		NA	5.66	3.37E-08	9.21E-06	3.96	9.23E-05	0.016498297	6.81	4.82E-11
cg17951713			TRUE		NA	5.66	3.38E-08	9.22E-06	3.59	0.000384567	0.044047551	6.67	1.15E-10
cg24809529	CLDN15	TSS200	TRUE		TRUE	5.66	3.38E-08	9.23E-06	4.23	3.07E-05	0.007399889	6.03	4.43E-09
cg21199093	ZMYM4	Body	TRUE		TRUE	5.66	3.39E-08	9.23E-06	5.03	8.05E-07	0.00044715	6.38	6.19E-10
cg18450254	PRICKLE2	5UTR	TRUE		TRUE	5.66	3.43E-08	9.29E-06	4.32	2.07E-05	0.005528667	4.25	2.77E-05
cg23720898			NA	Unclassified_Cell_type_specific	TRUE	-5.66	3.44E-08	9.30E-06	-4.02	7.15E-05	0.013808401	-4.88	1.66E-06
cg23253752	ELL3	Body	TRUE	Promoter_Associated	NA	-5.65	3.45E-08	9.31E-06	-3.65	0.00030205	0.037667785	-4.9	1.50E-06
cg06680852			NA		TRUE	5.65	3.48E-08	9.37E-06	4.81	2.30E-06	0.00101113	6.07	3.58E-09
cg20335735	NUP43	TSS1500	NA	Promoter_Associated	NA	-5.65	3.49E-08	9.38E-06	-3.63	0.000328456	0.039898814	-6.18	2.01E-09
cg01408486	CXXC5	TSS1500	NA		NA	5.65	3.50E-08	9.38E-06	3.57	0.000408281	0.045573148	6.4	5.51E-10
cg15634980	PNPLA1;PNPLA1;PNPLA1	5UTR;Body;5UTR	NA		NA	5.65	3.53E-08	9.41E-06	3.56	0.000423196	0.046454214	7.58	3.88E-13
cg22916586	DUSP16	5UTR	TRUE		NA	5.65	3.53E-08	9.41E-06	5.07	6.75E-07	0.000388646	6.09	3.28E-09
cg04259904	ARTN;ARTN;ARTN;ARTN;ARTN	1stExon;1stExon;5UTR;1stExon;5UTR;5UTR	TRUE	Unclassified_Cell_type_specific	NA	-5.65	3.54E-08	9.42E-06	-4.79	2.59E-06	0.001118834	-5.35	1.71E-07
cg0093192	C14orf	Body	NA		NA	-5.65	3.55E-08	9.43E-06	-4.46	1.12E-06	0.00343	-3.36	0.00088

5	153						8	6		5	5274		2006
cg04307508	C19orf38	TSS200	NA	Unclassified_Cell_type_specific	NA	5.65	3.56E-08	9.47E-06	3.7	0.000249087	0.03331811	5.75	2.07E-08
cg04930469	SOST	Body	TRUE		TRUE	5.65	3.58E-08	9.50E-06	3.59	0.000376973	0.043517599	7.73	1.38E-13
cg05394456	MPG; MPG; MPG	5UTR;Body;5UTR	NA	Promoter_Associated	NA	5.65	3.58E-08	9.50E-06	6.54	2.44E-10	5.10E-07	5.48	8.78E-08
cg14024937			TRUE		NA	-5.65	3.59E-08	9.50E-06	-4.88	1.67E-06	0.000793192	-4.91	1.48E-06
cg15119221	MFAP4	TSS1500	TRUE		TRUE	5.65	3.59E-08	9.51E-06	4.69	4.04E-06	0.001588365	6.77	6.05E-11
cg07408456	PGLYRP2	TSS1500	NA		NA	5.65	3.62E-08	9.56E-06	4.01	7.52E-05	0.01425644	3.7	0.000255274
cg19831957			TRUE	Unclassified	NA	-5.64	3.66E-08	9.67E-06	-4.78	2.66E-06	0.001141037	-6.15	2.31E-09
cg06894469	NRD1; NRD1	Body;Body	TRUE		NA	-5.64	3.68E-08	9.70E-06	-5.31	2.05E-07	0.000149267	-4.76	3.00E-06
cg14331899	CYBAS3;CYBAS3;CYBAS3	TSS1500;5UTR;5UTR	NA		NA	-5.64	3.72E-08	9.77E-06	-5.78	1.78E-08	1.98E-05	-7.12	7.24E-12
cg12447744			TRUE		NA	-5.64	3.74E-08	9.80E-06	-5.33	1.82E-07	0.000135588	-6.77	6.22E-11
cg13834112			NA		NA	5.64	3.75E-08	9.81E-06	4.99	9.79E-07	0.000518618	4.95	1.22E-06
cg18941614	UBTF; UBTF; UBTF	Body;Body;Body	TRUE	Gene_Associated	TRUE	5.64	3.75E-08	9.81E-06	3.74	0.000220382	0.03056361	9.08	1.13E-17
cg26810214	HDAC7;HDAC7	Body;Body	TRUE	Promoter_Associated	NA	5.64	3.76E-08	9.82E-06	5.46	9.41E-08	7.93E-05	6.98	1.70E-11
cg19419291	ELL2	Body	NA	Promoter_Associated	NA	-5.64	3.78E-08	9.86E-06	-4.55	7.50E-06	0.002564904	-5.08	6.53E-07

				ated									
cg11740099	SECT M1	3UTR	TRUE	Unclassified	TRUE	5.64	3.80E-08	9.88E-06	3.58	0.000399489	0.044981317	5.95	7.22E-09
cg13429270	FAM38B	Body	NA		NA	-5.64	3.81E-08	9.88E-06	-4.44	1.26E-05	0.003775872	-6.11	2.82E-09
cg03029146			TRUE	Unclassified	NA	5.64	3.82E-08	9.90E-06	4.6	6.04E-06	0.002169237	6.07	3.69E-09
cg26643377	FBXO2	Body	NA	Unclassified	NA	5.64	3.82E-08	9.90E-06	4.16	4.17E-05	0.009397046	6.34	7.87E-10
cg02319392	HSBP1	TSS1500	NA	Promoter_Associated	NA	-5.63	3.84E-08	9.92E-06	-3.71	0.000242117	0.032677751	-4.32	2.09E-05
cg26551865	TRABD	5UTR	NA	Promoter_Associated	TRUE	5.63	3.92E-08	1.01E-05	3.62	0.000335923	0.04049359	5.39	1.37E-07
cg24867468	TMC6; TMC6	3UTR;3UTR	NA	Gene_Associated	NA	5.63	3.96E-08	1.01E-05	4.1	5.16E-05	0.010934217	4.27	2.59E-05
cg20222695	ANKLE2	Body	TRUE		NA	-5.63	3.96E-08	1.01E-05	-5.89	9.66E-09	1.21E-05	-4.91	1.45E-06
cg08257009			NA		NA	-5.63	3.98E-08	1.02E-05	-3.97	8.74E-05	0.015908413	-6.09	3.17E-09
cg16187635			TRUE		NA	-5.63	3.98E-08	1.02E-05	-5.1	5.71E-07	0.000344984	-6.1	3.15E-09
cg05524458	ANKRD33B	Body	TRUE	Promoter_Associated_Cell_type_specific	NA	5.62	4.06E-08	1.03E-05	4.07	5.81E-05	0.011866991	6.97	1.83E-11
cg13882345			NA		NA	-5.62	4.08E-08	1.04E-05	-4.54	8.05E-06	0.002694074	-5.19	3.72E-07
cg10986946	DKK3; DKK3; DKK3	Body;Body;Body	TRUE		NA	-5.62	4.08E-08	1.04E-05	-8.37	1.80E-15	1.20E-11	-4.7	3.94E-06
cg11373356	RGS12;RGS12	Body;Body	NA		TRUE	-5.62	4.08E-08	1.04E-05	-4.55	7.55E-06	0.002577572	-5.39	1.39E-07

cg09650495			NA		NA	-5.62	4.10E-08	1.04E-05	-4.16	4.09E-05	0.009271082	-4.15	4.24E-05
cg13428567	C1orf175;C1orf175	TSS1500;TSS1500	NA		NA	-5.61	4.28E-08	1.07E-05	-3.97	8.87E-05	0.016064852	-4.05	6.41E-05
cg23395310	SNHG7;SNHG7;SNHG7	TSS1500;TSS1500;TS1500	NA		NA	-5.61	4.32E-08	1.08E-05	-4.29	2.39E-05	0.006141069	-4.41	1.42E-05
cg26189283	RAG1AP1;RAG1AP1;RAG1AP1	Body;Body;Body	NA	Promoter_Associated_Cell_type_specific	NA	-5.61	4.38E-08	1.09E-05	-4.31	2.14E-05	0.005653824	-5.56	5.81E-08
cg25195968			TRUE		NA	-5.61	4.38E-08	1.09E-05	-4.99	9.85E-07	0.00052051	-3.87	0.00012952
cg26652266			TRUE		NA	-5.61	4.43E-08	1.10E-05	-3.84	0.000146844	0.023018658	-7.24	3.44E-12
cg05549970			NA		NA	-5.61	4.43E-08	1.10E-05	-5.33	1.82E-07	0.000135588	-6.81	4.84E-11
cg09717585	ZCCHC14	Body	NA		NA	-5.61	4.44E-08	1.10E-05	-4.75	3.06E-06	0.00128166	-5.12	5.40E-07
cg25015613	MMP1;MMP1	Body;Body	NA	Unclassified	NA	-5.61	4.45E-08	1.10E-05	-4.77	2.77E-06	0.001178443	-3.04	0.002530054
cg11824827	ZNF668	Body	NA	Gene_Associated_Cell_type_specific	NA	5.61	4.45E-08	1.10E-05	3.96	9.21E-05	0.016476227	4.01	7.48E-05
cg00728848	C6orf114;GFOD1	5UTR;Body	NA		NA	-5.61	4.47E-08	1.10E-05	-4.59	6.36E-06	0.002257587	-5.7	2.79E-08
cg05192898	TXNRD1;TXNRD1;TXNRD1;TXNRD1;TXNRD1;TXNRD1	TSS1500;TSS1500;Body;TSS1500;TSS1500;TSS1500	NA		NA	-5.6	4.54E-08	1.11E-05	-3.74	0.000217949	0.03030048	-5.17	4.09E-07

	NRD1; TXNR D1	SS1500											
cg1256337 2			TRUE		NA	5.6	4.68E-0 8	1.14E-0 5	3.87	0.00013 3032	0.02146 0352	4.09	5.50E-0 5
cg1513114 6	MAN1 C1	Body	NA	Unclassi fied_Cell _type_s pecific	NA	5.6	4.69E-0 8	1.14E-0 5	4.67	4.49E-0 6	0.00172 7404	5.78	1.76E-0 8
cg1160774 2	PSMD 8	Body	NA		NA	-5.59	4.73E-0 8	1.15E-0 5	-3.77	0.00019 1885	0.02785 1517	-4.39	1.54E-0 5
cg1142911 1			NA		NA	5.59	4.74E-0 8	1.15E-0 5	4.8	2.43E-0 6	0.00105 8756	5.16	4.33E-0 7
cg0516463 4	WNT1 0B	TSS150 0	NA		NA	5.59	4.75E-0 8	1.15E-0 5	4.74	3.20E-0 6	0.00132 0565	6.51	2.89E-1 0
cg0432392 5			TRUE	Promote r_Associ ated	NA	-5.59	4.78E-0 8	1.16E-0 5	-4.1	5.33E-0 5	0.01123 9191	-5.86	1.13E-0 8
cg0549230 6	ERCC 1;ERC C1;ER CC1	TSS150 0;TSS1 500;TS S1500	NA	Promote r_Associ ated	NA	-5.59	4.81E-0 8	1.16E-0 5	-5.01	9.12E-0 7	0.00048 925	-5.58	5.06E-0 8
cg2290710 3	CYBA SC3;C YBAS C3;CY BASC 3;CYB ASC3	5UTR;1 stExon; 5UTR;B ody	NA		NA	-5.59	4.82E-0 8	1.17E-0 5	-3.73	0.00022 8239	0.03132 1465	-6.19	1.87E-0 9
cg2606135 7	SMAR CD3;S MARC D3	Body;B ody	TRUE	Unclassi fied_Cell _type_s pecific	TRUE	5.59	4.87E-0 8	1.17E-0 5	4.68	4.17E-0 6	0.00162 9544	7.79	9.30E-1 4
cg0896832 9	FAM3 8A	Body	TRUE	Unclassi fied_Cell _type_s pecific	NA	5.59	4.88E-0 8	1.17E-0 5	4.95	1.20E-0 6	0.00061 3985	6.2	1.73E-0 9
cg2640730	TBXA	5UTR;T	NA	Unclassi	NA	-5.59	4.91E-0	1.18E-0	-3.94	0.00010	0.01781	-6.08	3.35E-0

9	S1;HIP K2;HIP K2;TB XAS1	SS1500 ;TSS15 00;5UT R		fied_Cell _type_s pecific			8	5		1887	6101		9
cg1833599 1	SEMA 7A;SE MA7A; SEMA 7A	Body;B ody;5U TR	NA	Unclassi fied_Cell _type_s pecific	NA	-5.59	4.91E-0 8	1.18E-0 5	-5.75	2.12E-0 8	2.27E-0 5	-2.4	0.01693 4007
cg2253918 2			TRUE	Unclassi fied	NA	5.59	4.92E-0 8	1.18E-0 5	4.02	7.14E-0 5	0.01380 4693	6.04	4.37E-0 9
cg0599190 2	ASAP 2;ASA P2	Body;B ody	TRUE		NA	-5.59	4.93E-0 8	1.18E-0 5	-4.67	4.47E-0 6	0.00172 5086	-5.63	4.01E-0 8
cg1702491 9	ZNF38 5D	Body	TRUE		NA	-5.59	4.96E-0 8	1.19E-0 5	-4.33	1.95E-0 5	0.00530 3745	-5.57	5.37E-0 8
cg1297223 3	C9orf4 7;C9or f47;C9 orf47; S1PR3 ;C9orf 47	1stExon ;1stExo n;5UTR ;TSS15 00;5UT R	NA		NA	5.58	5.06E-0 8	1.20E-0 5	3.87	0.00013 2681	0.02142 6689	5.72	2.41E-0 8
cg1643919 8	CYP1 B1	5UTR	NA	Unclassi fied_Cell _type_s pecific	NA	-5.58	5.06E-0 8	1.20E-0 5	-4.34	1.92E-0 5	0.00523 106	-4.54	7.98E-0 6
cg1351862 5			TRUE	Unclassi fied	TRUE	-5.58	5.17E-0 8	1.22E-0 5	-4.53	8.42E-0 6	0.00278 9283	-5.06	6.99E-0 7
cg0595756 7	BCL7A ;BCL7 A	Body;B ody	TRUE		NA	5.58	5.19E-0 8	1.23E-0 5	4.92	1.41E-0 6	0.00069 5166	5.53	6.63E-0 8
cg1815033 9	Mar-06	Body	TRUE	Promote r_Associ ated_Ce ll_type_s pecific	NA	-5.58	5.24E-0 8	1.24E-0 5	-3.8	0.00017 4703	0.02598 7321	-7.4	1.22E-1 2
cg0947981	PEPD;	Body;B	NA		NA	-5.57	5.24E-0	1.24E-0	-5.07	6.69E-0	0.00038	-4.18	3.77E-0

8	PEPD; PEPD	ody;Bo dy					8	5		7	5764		5
cg09956037	LSP1; LSP1; LSP1; LSP1	5UTR;5 UTR;Bo dy;5UT R	NA	Unclassi fied_Cell _type_s pecific	NA	-5.57	5.29E-0 8	1.24E-0 5	-5.24	2.95E-0 7	0.00019 8923	-6.78	5.84E-1 1
cg03372205			NA		NA	-5.57	5.32E-0 8	1.25E-0 5	-3.68	0.00027 2567	0.03525 4567	-3.06	0.00241 3377
cg12244275			NA	Unclassi fied_Cell _type_s pecific	NA	5.57	5.35E-0 8	1.25E-0 5	5.83	1.31E-0 8	1.55E-0 5	5.72	2.41E-0 8
cg10030504	ODZ4	Body	NA		NA	-5.57	5.41E-0 8	1.26E-0 5	-4.09	5.42E-0 5	0.01135 0545	-4.66	4.67E-0 6
cg21491587	TGM6	TSS200	NA		NA	-5.57	5.48E-0 8	1.27E-0 5	-4.66	4.73E-0 6	0.00179 1781	-3.52	0.00050 3275
cg02758964			NA		NA	-5.57	5.51E-0 8	1.28E-0 5	-4.22	3.16E-0 5	0.00756 6929	-6.66	1.18E-1 0
cg15775779	EDAR	5UTR	NA		NA	-5.56	5.54E-0 8	1.28E-0 5	-6.9	2.70E-1 1	7.36E-0 8	-3.19	0.00155 608
cg03969763			TRUE		NA	-5.56	5.54E-0 8	1.28E-0 5	-4.2	3.44E-0 5	0.00807 4299	-5.29	2.23E-0 7
cg12893373	MINA; MINA; MINA	Body;B ody;Bo dy	TRUE		NA	-5.56	5.55E-0 8	1.28E-0 5	-3.58	0.00038 921	0.04438 8014	-5.66	3.29E-0 8
cg16289618	LOC28 5830;L OC285 830	Body;B ody	NA	Unclassi fied	TRUE	5.56	5.73E-0 8	1.31E-0 5	4.59	6.42E-0 6	0.00226 3511	6.53	2.57E-1 0
cg23470914	MBP; MBP	Body;B ody	NA		NA	-5.56	5.75E-0 8	1.32E-0 5	-4.8	2.42E-0 6	0.00105 6332	-4.52	8.60E-0 6
cg12910851	IL1R2; IL1R2; IL1R2	1stExon ;5UTR; 5UTR	NA		NA	-5.56	5.82E-0 8	1.33E-0 5	-3.83	0.00015 3399	0.02375 7244	-4.17	3.93E-0 5
cg22331349	ZNF57 7;ZNF 577;Z NF577	TSS200 ;TSS20 0;TSS2 00	NA		TRUE	-5.55	5.91E-0 8	1.35E-0 5	-4.23	3.04E-0 5	0.00736 1095	-4.92	1.40E-0 6

cg22626659			TRUE		TRUE	5.55	5.96E-08	1.36E-05	4.17	4.00E-05	0.009096502	7.21	4.18E-12
cg08435157	NPTN; NPTN; NPTN; NPTN	Body;Body; Body;Body	TRUE		NA	-5.55	6.03E-08	1.37E-05	-3.56	0.000422151	0.046369667	-4.63	5.34E-06
cg23612492	WDR25; WDR25	Body;Body	TRUE		NA	-5.55	6.04E-08	1.37E-05	-4.09	5.56E-05	0.011514356	-3.46	0.000618815
cg25841987	FAM198B; FAM198B; FAM198B	TSS200; 5UTR; 5UTR	NA		NA	5.55	6.10E-08	1.38E-05	4.07	5.96E-05	0.01211847	3.52	0.000498173
cg24867665	BEND7; BEND7	TSS1500; TSS1500	TRUE		TRUE	5.54	6.14E-08	1.39E-05	3.97	8.82E-05	0.015993946	5.8	1.62E-08
cg12194336	FLNB; FLNB; FLNB; FLNB	Body;Body; Body;Body	TRUE	Unclassified_Cell_type_specific	NA	5.54	6.17E-08	1.39E-05	3.71	0.000243374	0.032826559	6.36	6.96E-10
cg12916580			TRUE		TRUE	-5.54	6.18E-08	1.39E-05	-3.62	0.00034272	0.040918548	-6.41	5.34E-10
cg14956201	TRIO	Body	NA		NA	5.54	6.25E-08	1.40E-05	3.65	0.000308622	0.038187539	6.13	2.54E-09
cg27664085			NA	Unclassified	TRUE	-5.54	6.36E-08	1.42E-05	-4.82	2.19E-06	0.000968485	-3.2	0.001536587
cg05384139	PITPNM2	5UTR	TRUE	Unclassified	NA	5.54	6.39E-08	1.42E-05	4.07	5.86E-05	0.011967563	3.1	0.002084579
cg00077426	EXOC3	Body	NA	Gene_Associated_Cell_type_specific	NA	-5.53	6.55E-08	1.45E-05	-4.06	6.19E-05	0.012499891	-4.33	2.00E-05
cg23657179	C10orf41; C10orf41	Body;Body	NA		NA	-5.53	6.69E-08	1.48E-05	-4.48	1.02E-05	0.003193139	-5.61	4.39E-08
cg2470494			NA		NA	-5.53	6.69E-08	1.48E-05	-3.56	0.00042	0.04661	-4.07	5.84E-0



0							8	5		5858	7381		5
cg25375860	SGPP2	Body	TRUE		NA	-5.53	6.75E-08	1.49E-05	-5.71	2.56E-08	2.67E-05	-7.2	4.36E-12
cg07355757			TRUE	Unclassified	NA	5.53	6.76E-08	1.49E-05	3.54	0.000463379	0.049171274	7.09	8.63E-12
cg01282195	TP53INP1;TP53INP1	Body;Body	NA		NA	-5.52	6.82E-08	1.49E-05	-3.92	0.000106336	0.018411068	-4.21	3.28E-05
cg17509612	C9orf78;USP20;USP20;USP20	TSS1500;5UTR;5UTR;5UTR	NA	Promoter_Associated	NA	5.52	6.92E-08	1.51E-05	3.64	0.000312335	0.038534892	3.94	0.000101789
cg10084993	SLC9A3R2;SLC9A3R2	Body;Body	NA	Unclassified	NA	-5.52	6.96E-08	1.52E-05	-4.75	3.07E-06	0.001284267	-6.83	4.23E-11
cg11699517	BAHC1	Body	NA		NA	5.52	6.96E-08	1.52E-05	3.79	0.000180283	0.026594126	3.82	0.000163098
cg12129117	CAPN2;CAPN2	Body;Body	NA		NA	5.52	6.98E-08	1.52E-05	3.88	0.000126883	0.020758424	5.14	4.83E-07
cg09768821	UQCRHL	TSS1500	NA		NA	-5.52	6.99E-08	1.52E-05	-5.24	2.86E-07	0.000194888	-4.72	3.61E-06
cg27634695	ANK2	TSS200	TRUE	Unclassified_Cell_type_specific	TRUE	5.52	6.99E-08	1.52E-05	3.78	0.000183799	0.026991004	3.18	0.001614222
cg24771152	VAR5	Body	NA		NA	5.52	6.99E-08	1.52E-05	6.09	3.23E-09	4.80E-06	5.91	8.88E-09
cg06573856	GPT2;GPT2	Body;Body	NA	Gene_Associated	NA	-5.52	7.02E-08	1.53E-05	-4.52	8.82E-06	0.002883922	-4.1	5.25E-05
cg04692023			NA		NA	5.52	7.05E-08	1.53E-05	3.84	0.000149147	0.023268201	6.33	8.53E-10
cg25536676	DHCR24	TSS1500	NA		NA	-5.52	7.08E-08	1.53E-05	-4.44	1.26E-05	0.003775872	-4.04	6.63E-05

cg12029281	TEAD3	5UTR	NA	Unclassified_Cell_type_specific	NA	5.52	7.08E-08	1.53E-05	4.29	2.41E-05	0.006185735	7.25	3.18E-12
cg02544002	PLXND1	Body	NA		NA	-5.51	7.20E-08	1.56E-05	-5.35	1.71E-07	0.000129039	-5.02	8.41E-07
cg20201177			TRUE		NA	-5.51	7.23E-08	1.56E-05	-3.53	0.00046983	0.049543494	-5.74	2.15E-08
cg12543949	FAM198B;FAM198B;FAM198B;FAM198B	TSS1500;5UTR;1stExon;5UTR;1stExon	NA		NA	5.51	7.24E-08	1.56E-05	3.57	0.00040741	0.045487798	7.3	2.35E-12
cg00548098			TRUE		TRUE	-5.51	7.27E-08	1.57E-05	-4.61	5.80E-06	0.002115737	-6.02	4.71E-09
cg07349805	PCGF3	5UTR	TRUE		TRUE	-5.51	7.28E-08	1.57E-05	-5.14	4.86E-07	0.000303783	-4.77	2.83E-06
cg03138928	EPHX1	5UTR	TRUE		NA	-5.51	7.33E-08	1.57E-05	-3.88	0.000125921	0.020660384	-6.43	4.53E-10
cg16770774	DTX4	Body	NA		NA	-5.51	7.33E-08	1.57E-05	-4.68	4.29E-06	0.001666176	-5.41	1.22E-07
cg15948030	VAR5	Body	NA		NA	5.51	7.37E-08	1.58E-05	4.09	5.51E-05	0.011458842	6.97	1.84E-11
cg20471736	SERPINB13	3UTR	NA	Unclassified_Cell_type_specific	NA	-5.51	7.37E-08	1.58E-05	-4.62	5.57E-06	0.002051475	-5.72	2.51E-08
cg10520740	CACNA2D4	Body	TRUE		NA	-5.51	7.39E-08	1.58E-05	-3.82	0.000157834	0.024214913	-5.8	1.58E-08
cg07711099	DNAH2	TSS1500	NA	Unclassified_Cell_type_specific	NA	5.51	7.47E-08	1.59E-05	3.62	0.000337739	0.040609686	6.46	3.82E-10
cg0101566	TCEA	Body	TRUE		NA	-5.51	7.48E-08	1.59E-05	-4.39	1.56E-05	0.00446	-5.51	7.22E-0

3	3						8	5		5	2863		8
cg13088465	CABC1	Body	NA		NA	-5.5	7.56E-08	1.61E-05	-4.49	1.01E-05	0.003152734	-3.49	0.000555225
cg05513983	SOX2OT	Body	NA		NA	5.5	7.65E-08	1.62E-05	3.65	0.00030411	0.037828361	4.57	7.04E-06
cg02039485	ITPK1; ITPK1; ITPK1	Body;Body;Body	TRUE		NA	-5.5	7.69E-08	1.63E-05	-4.62	5.52E-06	0.002042396	-6.85	3.74E-11
cg02932364			TRUE		TRUE	-5.5	7.75E-08	1.64E-05	-5.19	3.71E-07	0.000242659	-5.32	1.96E-07
cg08129129	BCL11B;BCL11B	Body;Body	TRUE	Unclassified_Cell_type_specific	NA	-5.5	7.82E-08	1.65E-05	-4.93	1.31E-06	0.000654981	-5.67	3.14E-08
cg18340983	P2RY2;P2RY2;P2RY2	5UTR;5UTR;5UTR	NA		NA	-5.5	7.82E-08	1.65E-05	-6.63	1.39E-10	3.14E-07	-5.15	4.57E-07
cg01435643	MCF2L;MCF2L	Body;Body	NA	Unclassified_Cell_type_specific	TRUE	5.5	7.89E-08	1.66E-05	4.52	8.50E-06	0.002810804	3.58	0.000403983
cg04703476	AATF	Body	TRUE		NA	-5.49	8.03E-08	1.68E-05	-3.54	0.000463668	0.049171274	-5.68	2.97E-08
cg23833543			NA		NA	-5.49	8.06E-08	1.69E-05	-3.86	0.000134347	0.021642098	-4.86	1.85E-06
cg03450842	ZMIZ1	5UTR	TRUE		NA	-5.49	8.11E-08	1.70E-05	-6.96	1.85E-11	5.39E-08	-4.94	1.26E-06
cg24783499	ZC3H3	Body	TRUE	Unclassified	NA	5.49	8.18E-08	1.71E-05	3.54	0.000459479	0.048863972	6.28	1.09E-09
cg22952459	C10orf99	TSS1500	NA		NA	-5.49	8.21E-08	1.71E-05	-5.1	5.90E-07	0.000352458	-5.37	1.54E-07
cg00397849	ALS2CL	5UTR	NA		NA	-5.49	8.27E-08	1.72E-05	-4.61	5.73E-06	0.002096621	-6.23	1.46E-09
cg00323916	PDXP	Body	TRUE	Promoter_Associated	TRUE	5.48	8.39E-08	1.74E-05	5.51	7.26E-08	6.46E-05	4.25	2.81E-05

cg11558474	TMEM2;TME M2	5UTR;5 UTR	NA		NA	5.48	8.42E-08	1.74E-05	4.15	4.32E-05	0.009616636	3.96	9.07E-05
cg07441794	USH1G	Body	NA		NA	-5.48	8.48E-08	1.75E-05	-5.67	3.12E-08	3.19E-05	-5.78	1.81E-08
cg16942327			TRUE		NA	5.48	8.77E-08	1.80E-05	4.27	2.54E-05	0.006398587	3.13	0.001889507
cg09762533	LSP1; LSP1; LSP1; LSP1	5UTR;5 UTR;Body;5UTR	NA	Unclassified	NA	-5.47	8.82E-08	1.80E-05	-4.1	5.20E-05	0.011021847	-7.19	4.62E-12
cg27534072			TRUE		NA	-5.47	8.88E-08	1.81E-05	-4.51	9.03E-06	0.002923458	-3.23	0.001382206
cg22851200	TRIP6	Body	NA		NA	-5.47	8.94E-08	1.82E-05	-4.08	5.57E-05	0.011528255	-4.97	1.07E-06
cg20469744	ENOX1;ENOX1	Body;Body	TRUE		NA	5.47	8.99E-08	1.83E-05	4.61	5.88E-06	0.002133546	4.1	5.22E-05
cg15892280	ETS2	5UTR	NA	Promoter_Associated	NA	-5.47	9.06E-08	1.83E-05	-4.98	1.03E-06	0.000539877	-5.68	3.03E-08
cg21952686	ARHG EF5	Body	NA		NA	-5.47	9.10E-08	1.84E-05	-3.87	0.000132708	0.021426689	-4.53	8.29E-06
cg21398186	PPBP	TSS1500	NA		NA	-5.47	9.16E-08	1.84E-05	-3.65	0.000308352	0.038181129	-5.78	1.73E-08
cg20788020			TRUE		NA	-5.46	9.32E-08	1.86E-05	-3.94	9.83E-05	0.017369035	-8.12	1.02E-14
cg24049493	HIVEP3;HIVEP3	TSS1500;TSS1500	NA	Promoter_Associated	NA	5.46	9.32E-08	1.86E-05	3.8	0.000174229	0.025935532	5.38	1.47E-07
cg14517133	PRPH2	3UTR	TRUE		NA	5.46	9.37E-08	1.87E-05	4.12	4.73E-05	0.010243451	5.78	1.78E-08
cg11213707			NA	Unclassified_Cell_type_specific	NA	-5.46	9.38E-08	1.87E-05	-4.33	2.01E-05	0.005416985	-5.11	5.44E-07
cg10539670			NA		NA	-5.46	9.50E-08	1.89E-05	-3.56	0.000424497	0.046516279	-4.87	1.76E-06

[illegible]

**eTable 3. Gene Set Enrichment Analysis summary table of the hypermethylated smoking-associated CpGs.** Enriched gene set name, number of the genes in the set, number of genes present on the beadchip and used in supervised analysis (nRep), fraction of genes present on the beadchip (fRep), number of overlapping genes (nOVLAP), odds ratio (OR), P-value, Benjamini-Hochberg adjusted P-value (adjPval ) and gene symbols of enriched genes.

Gene List	nList	nRep	fRep	nOVLAP	OR	P-value	adjPval	Genes
Biv	3447	3266	0.947491	160	2.7493	1.42E-21	1.19E-17	MCF2L NRG2 ECE2 MAGI2 ACSL6 SEZ6L ARHGEF4 TMEM2 HIVEP3 PARD3B FERMT1 ZNF250 CAMK2D PDE4D NRXN1 ABCC3 SEPT9 TLL1 MAN1C1 FAM46A SEMA6D PANX2 PXK SEPT6 GPRC5C APBB1IP TMC6 FZD5 IFI30 DNAH1 B4GALNT1 NBEAL2 NR2E1 SLC13A5 EBF3 RGS22 KCNIP2 BCOR LAMA3 SOST CXCL12 ARID3A CMTM2 BAIAP2 C9orf86 HOXD3 CXXC5 EPB41L3 OCA2 NKD2 FBXO2 ITPKB NT5E KIAA0182 NFAM1 HOXD8 TSLP PKNOX2 REEP4 CD248 FAM134B NXPH4 CNNM4 CUX1 ARHGEF1 PTPRN TEAD3 SSTR1 SLC8A1 C22orf15 KHK CAMK2B RUNX1 FAM155A CACNA1D GSN TBX5 KCNQ1 TTPA CASR PLEC1 HTR1B SMARCD3 SP5 RGS10 AK3L1 ABR ADCY9 FOXJ1 CAPN2 CRHR2 FBN2 MEF2C MEIS2 MSI1 ODC1 PAX7 PTPRN2 SECTM1 SFRP4 WNT10B SOCS2 EMX1 CBLN1 DACH1 NTN1 H2AFY REC8 PHOX2A BMI1 DLX5 NEFM TP73 KRT7 LHX1 MDFI TMPRSS2 HCG9 MEOX2 MT1A ST3GAL6 DAGLA NEUROG1 PRRX1 FAIM2 POU2F3 RHOBTB1 RHOBTB3 CENTG2 PLEKHA6 PPP1R16B G0S2 TLX2 EFEMP2 HOXC10 CRTAC1 RNF130 MAML3 ARHGAP22 SCT HOXB4 KREMEN2 CLMN RAI1 OTP PSD2 ASS1 COL18A1 KLHDC7B HSPB6 ABTB2 CCDC140 LIX1L MKX LMX1A SLC25A42 RTN4RL1 RNF212 DGKZ BCL7A
HATADA_MET HYLATED_IN_ LUNG_CANCE R_UP	390	371	0.951282	30	3.83145	4.81E-09	1.93E-05	CXCL12 NFAM1 ANK2 REC8 BANP ADRBK1 ACTB IL16 FAM134B LHX1 ITPKB FBLIM1 CMTM2 LSP1 HSPB6 CYP2W1 ME3 ARHGEF1 HOXB4 PAM NEFM RAPGEFL1 ARHGAP22 CCDC140 LRIG1 BCOR EBF3 SECTM1 HOXD3 HDAC7
V\$AML_Q6	266	251	0.943609	24	4.56757	6.90E-09	1.93E-05	H2AFY FAM113B ADD1 OTP DLX5 KIAA0182 EPB41L3 SEMA4A PER1 TLX2 TBX5 SOST MEOX2

								ATP6V0A1 SLC2A3 PITPNC1 RUNX1 HOXB4 SGIP1 NRXN1 PIGV FAIM2 MSI2 CNNM4
Single	1591	1518	0.954117	71	2.2238 6	1.88E-08	3.93E-0 5	ABCC3 ABTB2 PARD3B APBB1P ARL5C BAIAP2 MKX CACNA1D CAMK2B CASZ1 CBLN1 CMTM2 CRTAC1 CSNK1E CXCL12 DACH1 DLX5 DPP6 EBF3 EMX1 FBN2 CCDC140 FOXJ1 B4GALNT1 GSN GUCY1A2 HCG9 HOXD3 HOXD8 HTR1B ITPKB KCNIP2 KCNQ1 LAMA3 MAGI2 MAN1C1 MEOX2 MT1A NEFM NEUROG1 NR2E1 NRG2 NRXN1 NTN1 NXPH4 OCA2 OTP PAX7 BMI1 PHOX2A PIGV PKNOX2 PLEC1 PSD2 PTPRN2 RAB31 RGS10 SECTM1 SEMA6D SFRP4 SPATA18 SSTR1 ST3GAL6 TBX5 TCF15 TLL1 TLX2 TP73 TSLP TTPA WNT10B
BENPORATH_ ES_WITH_H3K 27ME3	1118	1078	0.964222	55	2.3960 7	5.64E-08	9.10E-0 5	OTP CACNA1D HOXD8 PARD3B ABCC3 NEUROG1 NXPH4 PLEC1 WNT10B TLL1 SFRP4 SECTM1 DACH1 CRTAC1 TLX2 ABTB2 NTN1 NEFM HCG9 CBLN1 CAMK2B KCNIP2 PHOX2A OCA2 PAX7 GSN KCNQ1 CASZ1 PTPRN2 TBX5 CMTM2 MT1A NR2E1 FOXJ1 DPP6 ARL5C MEOX2 CCDC140 EBF3 B4GALNT1 RGS10 NRG2 HOXD3 TSLP TP73 PSD2 SSTR1 MAN1C1 MKX FBN2 DLX5 TTPA SEMA6D NRXN1 PKNOX2
CAGGTG_V\$E 12_Q6	2485	2414	0.971429	97	1.9336	6.85E-08	9.10E-0 5	MEF2C ASS1 CCDC140 LRP5 NR2E1 MAGI1 CXXC5 PARD3B NXPH4 PAX7 NRG2 SNX25 EMX1 ALDOA COL18A1 ABR FBXO2 UBTF FYN GAL3ST3 PIGV CAMK2G ARPP-21 POU2F3 CAMK2B PVRL1 CDC42EP3 ODC1 FLNB PER1 LSP1 MFAP4 LRIG1 DIS3L2 FRMD4A DACH1 PDYN CASZ1 ADRBK1 PALLD KIAA0182 CTNNBIP1 H6PD ABTB2 HOXD3 RUNX1 FAM19A1 ERGIC1 PLEC1 SSTR1 RAC2 EPB41L5 LMX1A CDH16 CXCL12 ME3 MEIS2 TEAD4 RAB25 C1QA FBLIM1 TCF15 KCNIP2 GLI2 KREMEN2 CBLN1 RHOBTB1 PHF1 PRKCZ MPPED2 HDAC7 PHOX2A WNT10B RTKN2 SOST DGKZ CCNJL ANK2 HIVEP3 CACNA1D H2AFY AXUD1 OSBPL9 JAZF1 ZNF710 SORBS2 ACOT11 CLDN15 DAGLA TLX2 MYOM3 FZD5 PPP1R16B LASS2 SGIP1 KCNQ1 NRXN1

MARTENS_BO UND_BY_PML_ RARA_FUSION	456	443	0.971491	31	3.2719 8	7.60E-08	9.10E-0 5	SKI ZNF710 GPATCH8 MPG TK2 RAC2 BANP H6PD FLNB RUNX1 HIVEP2 HDAC4 CXXC5 CUX1 SERPINB1 MIRN24-2 UBE2O SPTBN1 PVRL1 CAMK2G RAB37 ARID3B NCOR2 APBB1IP BZRAP1 PITPNM2 RAB31 ADRBK1 HIVEP3 LOC651746 KIAA0182
BENPORATH_ EED_TARGET S	1062	1014	0.954802	52	2.3993 4	1.15E-07	0.00012	TP73 NEUROG1 KCNQ1 BMI1 HOXD3 CCDC140 DLX5 PKNOX2 MKX CXCL12 CRTAC1 B4GALNT1 NTN1 SSTR1 CASZ1 NEFM DACH1 CACNA1D MT1A HTR1B ABTB2 CSNK1E SEMA6D PAX7 HOXD8 HCG9 PLEC1 TLL1 OTP FBN2 BAIAP2 NXPH4 TTPA OCA2 PHOX2A NRG2 NR2E1 APBB1IP CBLN1 CMTM2 MAGI2 WNT10B MEOX2 TBX5 SFRP4 PSD2 CAMK2B TCF15 RGS10 FOXJ1 TSLP TLX2
KEGG_WNT_SI GNALING_PAT HWAY	151	149	0.986755	16	5.1285 8	4.83E-07	0.00044 9	LRP5 CTBP2 CTNNBIP1 WNT10B NFAT5 CSNK1E CAMK2B CAMK2D CAMK2G PLCB4 PRICKLE2 RAC2 CUL1 FZD5 NKD2 SFRP4
CHYLA_CBFA2 T3_TARGETS_ UP	387	374	0.966408	26	3.2222	9.83E-07	0.00082 3	GYS1 CLDN15 MTL5 AXUD1 SELPLG H6PD CD300LG CXXC5 SERPINB1 TCN2 SEPT6 TNFAIP8 KRT7 RHOBTB1 PAM SOCS2 TMEM2 ASS1 TSLP RAB31 ITPKB SPTBN1 PARD3B TTPA MAN1C1 HIVEP3
SENESE_HDA C1_TARGETS_ DN	260	242	0.930769	20	3.8579 3	1.30E-06	0.00099 1	ABCC3 GSN CXXC5 EPS8L2 CDC42EP3 SYT17 LSP1 PTPRN GLI2 TOX3 TK2 EFEMP2 RHOBTB3 ASS1 ERGIC1 BAIAP2 KRT7 NXN LRRFIP1 EPB41L5
TGACCTY_V\$E RR1_Q2	1043	998	0.956855	48	2.2221 5	2.25E-06	0.00138 3	MEF2C PLEC1 TSC22D2 CDH16 LRP5 SNTG1 FAM38A ME3 CXXC5 MEIS2 NXPH4 PAX7 HOXC10 EPS8L2 ALDOA LHX1 ABR KCNIP2 SLC25A13 SPATC1 NEFM CAMK2G MPPED2 HTR1B CRTAC1 CDC42EP3 KCNG4 G0S2 PKNOX2 ATP5G2 AXUD1 SCT KIAA0182 ABTB2 TLX2 TBX5 MYOM3 MAEA SOCS2 HOXD3 SYT17 PPP1R16B FAM19A1 SGIP1 ERGIC1 NRXN1 MSI2 C4orf18
ONKEN_UVEA L_MELANOMA _UP	783	765	0.977011	40	2.4097 3	2.28E-06	0.00138 3	CAPN2 CDC42EP3 TRRAP PAM AK3L1 BCOR C1QA SOCS2 SPARC FXD5 ANK2 ACTB FAM134B CDK2AP1 QDPR PITPNC1 FRMD4B



								ACTN4 CENTG2 NXN HDAC4 MAD1L1 CUX1 INPP4B TRIO SLC25A13 TNFAIP8 NT5E ABTB2 NEK3 ASS1 RAB31 ABR COL18A1 MAN1C1 FZD5 LASS2 BAIAP2 MEIS2 ADCY9
BENPORATH_SUZ12_TARGETS	1038	999	0.962428	48	2.2197	2.31E-06	0.001383	ARL5C CASZ1 PHOX2A NEFM CRTAC1 TLL1 RGS10 EBF3 EMX1 CBLN1 FOXJ1 NRG2 MT1A PLEC1 SPATA18 DPP6 PIGV PAX7 CCDC140 TLX2 DACH1 NTN1 NEUROG1 PKNOX2 OCA2 LAMA3 ST3GAL6 MKX SSTR1 ITPKB SEMA6D GUCY1A2 ABTB2 TP73 WNT10B TBX5 TSLP APBB1IP FBN2 SECTM1 RAB31 CACNA1D B4GALNT1 BMI1 HOXD8 HOXD3 OTP CMTM2
MODULE_55	834	801	0.960432	41	2.35733	2.87E-06	0.001603	TGFBR2 SLC2A3 PER1 RAB31 G0S2 CXCL12 PLEC1 MAGI1 EPB41L3 ATP6V0A1 QDPR KRT7 RAC2 MCM2 ITGA5 CREB3L1 PTPRN2 KCNQ1 MEF2C NRG2 TBX5 PTPRN SORBS2 ACSL6 CDH16 FBN2 ITGA2B ECE2 SEZ6L SLMO1 WNT10B PAX7 RGS10 P2RX1 ABCC3 COL18A1 HSD17B6 JAK3 AK3L1 MPPED1 TCN2
REACTOME_CELL_CELL_COMMUNICATION	120	115	0.958333	13	5.40497	3.21E-06	0.00168	CDH5 CLDN15 FYN LAMA3 PLEC1 FBLIM1 PARVA PVRL1 SPTBN1 SRC ACTN4 NTN1 MAGI2
CUI_TCF21_TARGETS_2_DN	830	814	0.980723	41	2.3162	4.26E-06	0.002098	NT5E SGIP1 TMEM2 LOC651746 HSP90AA1 PPP1R16B PALLD MSRB3 DACH1 PARVA ITPKB MGC21874 FAM134B ELF1 GSN PRX PITPNC1 ST3GAL6 PARD3B FAM46A KRT7 FYN MAGI2 CDH5 CDC42EP3 MEF2C HIVEP2 NOTCH4 KIF1B LRRFIP1 SLC2A3 BMI1 H6PD GADD45A SYT17 BMPR1A CAMK2D PDE4D RTN4RL1 TGFBR2 SGPP1
V\$RP58_01	207	198	0.956522	17	4.00318	4.86E-06	0.002216	ABR TGFBR2 SEMA6D DLX5 TLL1 BLMH UBTF LRP5 RNF216 ANK2 SND1 TNFAIP8 RUNX1 NTN1 NXPH4 ARHGAP22 ACVR1
AACTTT_UNKNOWN	1890	1828	0.967196	73	1.8615	5.05E-06	0.002216	MEF2C VNN2 RCBTB2 IL16 NR2E1 MAGI1 SNTG1 CXXC5 HDAC4 NXPH4 PAX7 HOXC10 CUX1 OTP MAML3 MDFI FBXO2 SEMA6D CTBP2 REEP4 NEFM ARPP-21 NFAT5 CAMK2D PVRL1 MCHR1 ARID3B NEUROG1 LOXHD1 ZIC5 CDH5 DACH1

								ADCY2 PDYN CASZ1 ADRBK1 SOCS2 HOXD3 SRC RUNX1 HOXB4 FAM19A1 BMI1 PRRX1 ACTB SPARC CUL1 UBE2O LMX1A MEIS2 NTN1 FKBP4 LHX1 BCOR HNRNPUL1 RHOTB1 SEZ6L CRTAC1 ZMYM4 CCNJL PITPNC1 PDE4D CACNA1D CDK2AP1 AXUD1 OSBPL9 JAZF1 ZNF710 TBX5 FZD5 NRXN1 MSI2 C4orf18
CHICAS_RB1_TARGETS_CO_NFLUENT	567	541	0.954145	31	2.62929	5.40E-06	0.002216	CREB3L1 MSRB3 H2AFY PALLD CXXC5 RGS10 HIVEP3 ASS1 CDC42EP3 SPTBN1 CAMK2D CXCL12 JAZF1 SPARC EFEMP2 ACTN4 ACTB TSLP PXXK TGFB2 NXN HSPB6 C4orf18 FBN2 MAN1C1 LOC730755 ODZ4 MFAP4 GSN ADD1 ITGA5
Triple	654	624	0.954128	34	2.49945	5.63E-06	0.002216	ABTB2 MKX CACNA1D CASZ1 CBLN1 CMTM2 CRTAC1 DACH1 FBN2 CCDC140 FOXJ1 B4GALNT1 HOXD3 HOXD8 MT1A NEFM NEUROG1 NRG2 NTN1 OCA2 OTP PAX7 PHOX2A PKNOX2 PLEC1 RGS10 SEMA6D SSTR1 TBX5 TLL1 TLX2 TP73 TSLP WNT10B
BENPORATH_PRC2_TARGETS	652	625	0.958589	34	2.49509	5.82E-06	0.002216	TP73 FBN2 NRG2 CCDC140 TBX5 OTP HOXD3 SEMA6D TLX2 PHOX2A MT1A WNT10B FOXJ1 CRTAC1 NEFM PLEC1 MKX CACNA1D DACH1 B4GALNT1 HOXD8 NTN1 TSLP CASZ1 CMTM2 SSTR1 NEUROG1 RGS10 CBLN1 ABTB2 TLL1 OCA2 PAX7 PKNOX2
GGGAGGRR_V\$MAZ_Q6	2274	2217	0.974934	84	1.77463	6.75E-06	0.002459	TSC22D2 ASS1 CSNK1E IL16 NR2E1 PLEKHA6 CXXC5 HDAC4 NXPH4 HOXC10 ALDOA MDFI COL18A1 SDCCAG8 UBTF FYN PIGV CAMK2G POU2F3 FAM46A CD248 CDC42EP3 RAPGEFL1 PER1 RNF216 EFEMP2 NEUROG1 DOCK6 PSD2 ATP5G2 DACH1 CASZ1 CTNNBIP1 IKZF4 SOCS2 HOXD3 SRC HOXB4 ST7 GSN ACTB SPARC PLEC1 LMX1A MEIS2 TEAD3 RAI1 KIF1B FKBP4 C1QA LHX1 BCOR TCF15 KCNIP2 RAB31 KREMEN2 HNRNPUL1 ITGA5 GPRC5C FSTL5 SERTAD3 DGKZ CCDC81 EHMT2 CCNJL SMARCD3 PITPNC1 CD300LG ACVR1 ZNF668 AXUD1 JAZF1 ZNF710 RASIP1 ACOT11 B4GALNT1

								CLDN15 DAGLA FZD5 TRRAP KCNS1 PPP1R16B MSI1 MSI2
RYTTCCTG_V\$ ETS2_B	1085	1043	0.96129	48	2.1164 5	7.41E-06	0.00258 5	MEF2C PLEC1 TSC22D2 LRP5 LIX1L SLC13A5 SND1 MEIS2 TEAD4 TEAD3 CNNM4 STAT5B EPS8L2 OTP LHX1 ABR FBLIM1 DLX5 TCF15 SDCCAG8 UBTX FXD5 RHOTB1 NFAT5 PTPRN CD248 TGFB2 TLL1 ARHGEF4 FLNB PER1 LSP1 DGKZ CCNJL PITPNC1 PDE4D HIVP2 CDH5 ZNF668 JAK3 AXUD1 NOTCH4 SORBS2 B4GALNT1 PPP1R16B PRICKLE2 ACTB SPARC
MEISSNER_BR AIN_HCP_WIT H_H3K4ME3_A ND_H3K27ME3	1069	1056	0.987839	48	2.0876 8	1.03E-05	0.00344	TMC6 FRMD4B NKX1-2 TEAD4 HTR1B LRP5 TCF15 CXCL12 TLL1 CBLN1 CD248 TGFB2 NKD2 NR2E1 ASS1 FZD5 CRTAC1 NXN MKX KREMEN2 RUNX1 CASZ1 RGS10 GLI3 CREB3L1 ODZ4 GLI2 COL18A1 SP5 SEZ6L LOC651746 PRKCZ SSTR1 SLC13A5 NXPH4 ITPKB DPP6 EBF3 ABTB2 DLX5 NTN1 TNFAIP8 FOXJ1 ITGA5 GPRC5C SLC25A13 EMX1 ZIC5
PID_HDAC_CL ASSII_PATHW AY	34	34	1	7	10.892 1	1.20E-05	0.00374	NCOR2 BCOR HDAC7 MEF2C HSP90AA1 ADRBK1 HDAC4
DODD_NASOP HARYNGEAL_ CARCINOMA_ UP	1821	1675	0.919824	67	1.8516 5	1.25E-05	0.00374	GPRC5C SORBS2 MIB2 ADHFE1 TCTEX1D1 CXXC5 PHF1 TMRSS2 FLJ23834 STK33 PARVA CASZ1 MEIS2 LRRFIP1 CCDC81 SERPINB1 C22orf15 BAIAP2 ST6GALNAC6 RAB37 FRMD4B KCNQ1 C5orf32 EFEMP2 DNAH1 UBTX TOX3 RUNX1 DNAH2 ERGIC1 MSI2 TSLP PER1 PRSS27 PTPRN2 CLMN REC8 MSI1 CD59 GSN PLEKHA6 MCF2L ASS1 SPATA18 C1orf102 ADCY2 MGC21874 MKX LOC283404 KRT7 MAGI1 CROCC PRKCZ C11orf88 RGS22 TTC7A PXX DDO1 SERPINB6 MGC2752 CAMK2G FOXJ1 TK2 C6orf103 MEF2C ME3 EPS8L2
TGANTCA_V\$A P1_C	1121	1095	0.976806	49	2.0543 9	1.25E-05	0.00374	MEF2C PLEC1 ASS1 AVP IL16 HOXC10 STAT5B ALDOA OTP SLC11A1 MDFI FBXO2 GLI2 MCF2L BLMH ATP6V0A1 REEP4 C11orf49 NEFM ARPP-21 FAM46A PTPRN TGFB2 TLL1 G0S2 PKNOX2 SOST PITPNC1 ACTN4 PDE4D HSPB6 ARID3B

								DLG4 CDH5 AXUD1 LAMA3 NOTCH4 JAZF1 KIAA0182 GADD45A CLDN15 TLX2 RUNX1 HOXB4 PRX NRXN1 MSI1 SPARC C4orf18
MULTICELLULAR_ORGANISMAL_DEVELOPMENT	1049	1006	0.959009	46	2.09598	1.37E-05	0.003948	MEF2C SH3GL1 NR2E1 BST1 BAIAP2 TEAD4 HDAC4 S100B SECTM1 LHX1 MAML3 COL18A1 MDFI DLX5 TCF15 KCNIP2 GLI2 MKX NFAM1 MEOX2 CASR CBLN1 CUX1 POU2F3 HDAC7 TLL1 RAPGEFL1 MPPED2 ECE2 NEUROG1 DLG4 ACVR1 LAMA3 NOTCH4 SFRP4 CTNNBIP1 TBX5 MAEA RUNX1 ZMYM4 BMI1 NRXN1 RTN4RL1 RASGRP4 MSI1 SPARC
CAGCTG_V\$AP4_Q5	1524	1453	0.953412	60	1.90379	1.48E-05	0.004118	MEF2C ASS1 LRP5 NR2E1 PLEKHA6 BAIAP2 MAGI1 HDAC4 NXPH4 NRG2 SELPLG STAT5B CREB3L1 ABR SEMA6D SEMA4A UBTf SPTBN1 CAMK2G ARPP-21 CDC42EP3 TGFBR2 LSP1 RNF216 PAM DOCK6 PSD2 MAN1C1 ADRBK1 SCT ABTB2 HOXD3 SRC RAD51L1 RUNX1 ACTB PLEC1 UBE2O MEIS2 RAI1 KIF1B KCNIP2 PHF1 MPPED2 WNT10B ANGPT4 ZMYM4 SOST ANK2 HSPB6 HIVEP3 ACVR1 ZNF668 BCL7A ZNF710 CLDN15 SYT17 PPP1R16B PRICKLE2 SGIP1
MODULE_88	838	805	0.960621	39	2.21346	1.79E-05	0.004835	SLC2A3 PER1 RAB31 G0S2 SMARCD3 PLEC1 MAGI1 EPB41L3 ATP6V0A1 QDPR KRT7 RAC2 ITGA5 CREB3L1 PTPRN2 KCNQ1 MEF2C NRG2 TBX5 PTPRN SORBS2 ACSL6 CDH16 FBN2 ITGA2B ECE2 SEZ6L SLMO1 WNT10B PAX7 LSP1 RGS10 ABCC3 COL18A1 HSD17B6 JAK3 AK3L1 MPPED1 TCN2
CTTTGT_V\$LEF1_Q2	1972	1904	0.965517	73	1.7764	2.05E-05	0.005308	MEF2C TMEM2 CSNK1E LRP5 NR2E1 MAGI1 SNTG1 CXXC5 HOXC10 STAT5B OTP SEMA6D MCF2L SDCCAG8 UBTf FYN ATP6V0A1 PIGV NEFM ARPP-21 CDC42EP3 ODC1 ARHGEF4 TMPRSS2 NEUROG1 ZIC5 CDH5 DACH1 PDYN KIAA0182 CTNNBIP1 GADD45A IKZF4 HOXD3 HOXB4 ST7 BMI1 PRRX1 GSN C9orf86 ACTB PLEC1 FLJ23834 CUL1 RAC2 UBE2O LIX1L MEIS2 NTN1 KIF1B TCF15 CBLN1 RHOTB1 RHOTB3 CYFIP2 GPRC5C MPPED2 FSTL5 RTKN2 DGKZ

								CCNJL ANK2 PITPNC1 PDE4D ZNF668 H2AFY SORBS2 PPP1R16B NXN PRICKLE2 SGIP1 MSI2 C4orf18
V\$T3R_Q6	251	244	0.972112	18	3.3943	2.09E-05	0.005308	DUSP16 ABR FBXL10 SCT KCNG4 KIAA0182 CCDC140 TBX5 MYOM3 LRP5 MAEA SND1 GAL3ST3 ME3 FXVD5 NXPH4 GUCA1A PRSS27
TTGTTT_V\$FOX04_01	2061	1985	0.963125	75	1.75062	2.55E-05	0.006284	MEF2C LRP5 MAGI1 CXXC5 HOXC10 SELPLG STAT5B C11orf88 OTP MAML3 SEMA6D SPATA18 MEOX2 ATP6V0A1 NEFM PTCRA GLB1L3 GUCY1A2 PER1 TMPRSS2 PKNOX2 RNF216 PAM NEUROG1 ZIC5 FRMD4A CDH5 GUCA1A PPK PALLD KIAA0182 IKZF4 HOXD3 RUNX1 BMI1 PRX PRRX1 C9orf86 CUL1 ELF1 UBE2O LIX1L CXCL12 MEIS2 TEAD4 NTN1 LHX1 BCOR TCF15 KCNIP2 HNRNPUL1 CBLN1 MSRB3 FAIM2 GPRC5C HTR1B FSTL5 SERTAD3 SOST CCDC81 STK33 EHMT2 PITPNC1 PDE4D ACVR1 FBN2 H2AFY BCL7A SORBS2 TPH2 TBX5 NXN SGIP1 MSI1 MSI2
AATGTGA,MIR-23A,MIR-23B	419	407	0.97136	24	2.68484	3.97E-05	0.009072	MEF2C MAGI1 TGFB2 TMEM2 MPPED2 LRP5 CXCL12 DNAJC6 LRIG1 MEIS2 EBF3 FBN2 DACH1 STAT5B ADRBK1 MDFI SEMA6D CTNNBIP1 HOXB4 PLCB4 NRXN1 PALLD UBE2O MSI1
TAATTA_V\$CHX10_01	810	775	0.95679	37	2.17242	4.03E-05	0.009072	MEF2C EPB41L3 LMX1A LRP5 PLEKHA6 SNTG1 HOXC10 STAT5B C1QA OTP BLMH FYN MYST4 MSRB3 REEP4 CYFIP2 SGPP1 SEZ6L GPRC5C ARPP-21 MPPED2 PITPNM2 CDC42EP3 TLL1 RAPGEFL1 PITPNC1 ARID3B NEUROG1 LOXHD1 ATP5G2 DACH1 SORBS2 KIAA0182 HOXB4 FAM19A1 PRRX1 RTN4RL1
MODULE_430	55	55	1	8	7.15781	4.12E-05	0.009072	RAC2 ADRBK1 LSP1 ARHGEF1 CYFIP2 HDAC7 NBEAL2 TTC7A
V\$COREBINDINGFACTOR_Q6	273	257	0.941392	18	3.20744	4.16E-05	0.009072	CRTAC1 ADD1 C11orf88 OTP EPB41L3 TBX5 SOST LRP5 SLC2A3 PITPNC1 MEIS2 RUNX1 LPO HOXB4 SGIP1 NRXN1 PIGV MSI2
PHONG_TNF_RESPONSE_NOT_VIA_P38	337	331	0.982196	21	2.89388	4.23E-05	0.009072	TNFAIP8 TRIO G0S2 MDFI RAC2 LPXN GADD45A INPP4B ABTB2 MEIS2 FKBP4 PLCB4 MEF2C CDC42EP3 ABR FZD5 NXN RHOTB3 LRIG1 HIVEP2 GPRC5C

MODULE_484	42	42	1	7	8.3979 6	5.09E-05	0.01056 8	RAC2 ADRBK1 LSP1 ARHGEF1 CYFIP2 HDAC7 NBEAL2
MODULE_11	540	523	0.968519	28	2.4315 7	5.17E-05	0.01056 8	SLC2A3 PER1 RAB31 SMARCD3 EPB41L3 ATP6V0A1 QDPR NEFM S100B PTPRN2 NRXN1 MEF2C NRG2 CBLN1 ARHGEF4 MEIS2 PTPRN SORBS2 DPP6 MAGI2 PRKCZ DLG4 MYST4 ACSL6 ODZ4 KIF1B CDH16 BZRAP1
ZWANG_EGF_PERSISTENTLY_DN	61	58	0.95082	8	6.7282 2	6.10E-05	0.01216 7	PIGV ACOT11 ODZ4 PVRL1 CCNDBP1 ABCC3 TTC7A NBEAL2
TGGAAA_V\$N_FAT_Q4_01	1896	1804	0.951477	68	1.7323 4	6.94E-05	0.01322 3	MEF2C CCDC140 LRP5 IL16 HDAC4 SNX25 ENOX1 EMX1 MAML3 ABR SEMA6D MEOX2 GAL3ST3 SLC25A13 SPTBN1 CAMK2G POU2F3 NFAT5 FAM46A PVRL1 CDC42EP3 TMPRSS2 DIS3L2 ZIC5 CDH5 MAN1C1 ADCY2 GADD45A SOCS2 HOXD8 HOXD3 SRC RUNX1 HOXB4 FAM19A1 BMI1 PRRX1 GSN C9orf86 PLEC1 UBE2O CDH16 LIX1L SND1 GPSN2 LHX1 BCOR KCNIP2 BLMH DIDO1 CYFIP2 TCTEX1D1 FSTL5 CRTAC1 TLL1 ZMYM4 DGKZ EHMT2 PITPNC1 PDE4D TNFAIP8 CDK2AP1 SFRP4 ZNF710 CLDN15 TBX5 SGIP1 RASGRP4
FAELT_B_CLL_WITH_VH3_21_UP	44	44	1	7	7.9437 9	6.95E-05	0.01322 3	ZBTB48 SLC25A42 RGS10 ARHGEF1 UBTF SRC ACTN4
V\$IPF1_Q4	260	244	0.938462	17	3.1841 6	7.22E-05	0.01342 9	MEF2C RNF212 C14orf39 OTP MAML3 CDC42EP3 SEMA6D NR2E1 BAIAP2 SNTG1 MEIS2 RHOBTB1 ARID3B BMI1 SGIP1 ARPP-21 CUX1
COULOUARN_TEMPORAL_TGFB1_SIGNALTURE_DN	138	134	0.971014	12	4.1580 6	7.98E-05	0.01452 2	GADD45A TSC22D2 EPS8L2 SORBS2 COL18A1 ABCC3 CXXC5 ACVR1 SLC25A13 KIAA0182 ARID3A CXCL12
ST_WNT_CA2_CYCLIC_GMP_PATHWAY	20	20	1	5	13.942 2	8.23E-05	0.01465 7	CAMK2D CAMK2G CAMK2B NFAT5 ITPKB
V\$SP1_Q6	256	248	0.96875	17	3.1283 5	8.82E-05	0.01520 3	PHOX2A OSBPL9 ARHGEF1 PER1 TLX2 UBE2O CBLN1 ME3 EFEMP2 CACNA1D NXPH4 NRG2 PIGV NEFM CAMK2G NFAT5 CNM4

TRANSC_FAC T	1385	1347	0.972563	54	1.8286	8.97E-05	0.01520 3	HIVEP3 MEIS2 ARID3B BMI1 POU2F3 DLX5 BANP ZBTB48 EMX1 TOX3 NCOR2 NFAT5 HIVEP2 TSC22D2 MYST4 ELF1 TEAD3 ZNF83 PKNX2 DIDO1 MEOX2 STAT5B NEUROG1 LHX1 ARID3A CDR2 NR2E1 TBX5 DACH1 PRRX1 KCNIP2 TP73 MEF2C CASZ1 HOXD3 PHOX2A UBTF CUX1 IKZF4 GLI3 PAX7 SND1 TCF15 RUNX1 HDAC4 TLX2 PER1 ZMYM4 FOXJ1 ZNF668 HOXC10 CREB3L1 TEAD4 GLI2
PEREZ_TP53_ TARGETS	1174	1120	0.954003	47	1.9086 9	9.16E-05	0.01520 3	TP73 MAN1C1 MCHR1 BCOR ABTB2 KIF1B CAMK2B MCF2L KIAA0182 NTN1 ITPKB BLMH BAIAP2 MAD1L1 ZNF83 EPS8L2 LRP5 SEPT9 DNAJC6 FBLIM1 MIB2 SORBS2 COL18A1 DGKZ ACVR1 FAM134B C4orf18 SPATA18 GRAMD2 ARHGEF4 GPRC5C CNM4 FBXL10 ABR DIDO1 CAMK2G NRG2 CYFIP2 CXXC5 C10orf30 DIS3L2 EPB41L3 CROCC CENTG2 ZBTB48 FYN KCNQ1
V\$NRF2_Q4	255	249	0.976471	17	3.1147	9.26E-05	0.01520 3	PLEC1 ALDOA SLC11A1 MDFI LAMA3 ASS1 NOTCH4 TLL1 KIAA0182 BLMH CLDN15 SOST ATP6V0A1 PITPNC1 PDE4D PRX FRMD4A
V\$POU6F1_01	240	229	0.954167	16	3.1889 5	0.00011316	0.01822 1	C14orf39 CASZ1 TLL1 FYN CBLN1 CXXC5 MEIS2 RHOTB1 NEUROG1 HOXB4 PRICKLE2 CYFIP2 RTN4RL1 MPPED2 CAMK2D CUX1
MODULE_242	214	207	0.96729	15	3.3128 2	0.00012298 8	0.01917 8	MAGI1 NRXN1 PVRL1 NRG2 PTPRN ACSL6 CDH16 ECE2 SEZ6L SLMO1 UNC119B PAX7 H6PD P2RX1 MSI1
V\$AP2_Q6	258	255	0.988372	17	3.0352 2	0.00012368 7	0.01917 8	CREB3L1 LHX1 ASS1 GUCY1A2 KIAA0182 RASIP1 RAPGEFL1 DAGLA LMX1A FZD5 UBTF MEIS2 EFEMP2 BANP ATP5G2 ACTB CNM4
UDAYAKUMAR _MED1_TARG ETS_DN	240	232	0.966667	16	3.1441 5	0.00013161 9	0.02003 7	FRMD4B POLG GADD45A PALLD RHOTB1 ST7 GSN RCBTB2 ADCY9 CENTG2 GPRC5C TRIO ABTB2 MGC3032 SLC2A3 FBXL18
MODULE_45	583	554	0.950257	28	2.2843 4	0.00013801 7	0.02054 4	TGFBR2 SLC2A3 RAB31 MAGI1 RAC2 ITGA5 SECTM1 SERPINB1 LPXN KCNQ1 NRG2 ARID3A TNFAIP8 FBN2 ITGA2B ECE2 SLMO1 WNT10B CRHR2 LSP1 RGS10 P2RX1 JAK3 SLC11A1 MPPED1 SELPLG RCBTB2 ARHGEF1
CAGGTA_V\$A	792	763	0.963384	35	2.0745	0.00014250	0.02054	LMX1A CDH16 LIX1L TET1 TEAD3 HDAC4 RGS22

REB6_01					1	5	4	HOXC10 ENOX1 C11orf88 MAML3 MDFI CBLN1 MSRB3 PRKCZ GPRC5C CHSY1 RAPGEFL1 TMPRSS2 SOST PDE4D NEUROG1 HIVEP2 CACNA1D CDK2AP1 LAMA3 MAEA ITPKB SOCS2 HOXD8 HOXB4 FAM19A1 BMI1 C9orf86 MSI1
GCANCTGNY_V\$MYOD_Q6	924	887	0.959957	39	1.9903 3	0.00014435 9	0.02054 4	UBE2O LRP5 NR2E1 PLEKHA6 MAGI1 PARD3B KIF1B SELPLG ENOX1 EMX1 OTP LHX1 ABR FBLIM1 FYN CYFIP2 MPPED2 CDC42EP3 ODC1 PER1 ZMYM4 SOST ANK2 HSPB6 PAM MCHR1 HIVEP3 FRMD4A ACVR1 BCL7A ZNF710 CLDN15 MYOM3 HOXD3 SYT17 PPP1R16B RUNX1 KCNQ1 ACTB
SYSTEM_DEV ELOPMENT	861	825	0.958188	37	2.0290 4	0.00014476 1	0.02054 4	MEF2C SH3GL1 NR2E1 BAIAP2 TEAD4 HDAC4 S100B SECTM1 LHX1 MAML3 COL18A1 DLX5 TCF15 GLI2 KCNIP2 MKX NFAM1 CASR CBLN1 POU2F3 HDAC7 TLL1 RAPGEFL1 MPPED2 ECE2 NEUROG1 DLG4 ACVR1 LAMA3 NOTCH4 TBX5 RUNX1 NRXN1 RTN4RL1 RASGRP4 MSI1 SPARC
NERVOUS_SY STEM_DEVEL OPMENT	385	365	0.948052	21	2.6031 3	0.00016801 8	0.02325 3	MEF2C HDAC7 SH3GL1 RAPGEFL1 MPPED2 NR2E1 BAIAP2 ECE2 NEUROG1 HDAC4 S100B DLG4 LHX1 MAML3 DLX5 KCNIP2 GLI2 CBLN1 NRXN1 RTN4RL1 MSI1
YCATTAA_UN KNOWN	556	532	0.956835	27	2.2916 6	0.00016940 4	0.02325 3	SSTR1 ZMYM4 NR2E1 PDE4D INPP4B ACVR1 ENOX1 STAT5B CREB3L1 H2AFY PDYN BCOR JAZF1 KCNIP2 KIAA0182 SEMA4A MEOX2 HOXD8 HOXD3 PPP1R16B RHOBTB1 RUNX1 SGIP1 ARHGAP22 RTN4RL1 MPPED2 MSI2
TGASTMAGC_V\$NFE2_01	195	190	0.974359	14	3.3682 8	0.00017249	0.02329 4	PLEC1 PTPRN ALDOA MDFI FBXO2 LAMA3 ASS1 TLL1 KIAA0182 BLMH GADD45A CLDN15 TLX2 PDE4D
IL-2	675	651	0.964444	31	2.1498 1	0.00017842 2	0.02371 3	CDR2 VNN2 ITPKB PTPRN2 IL16 TGFB2 RGS10 SMARCD3 SEPT9 ITGA2B ELF1 SOCS2 FLNB LSP1 STAT5B GPSN2 ARHGDIA FYN SRC ACTB FRMD4B SLC2A3 GUCA1A CHSY1 ODC1 PPP1R16B HDAC4 ANK2 TBX5 RAB31 SLC25A20
REACTOME_D CC_MEDIATED ATTRACTIVE	13	13	1	4	18.558 4	0.00018380 7	0.02391 1	FYN SRC TRIO NTN1



_SIGNALING								
GGATTA_V\$PI TX2_Q2	587	564	0.960818	28	2.2407	0.00018562 2	0.02391 1	EPB41L5 ZMYM4 LMX1A NR2E1 PLEKHA6 HSPB6 CXXC5 MCHR1 PAX7 DLG4 ACVR1 ENOX1 STAT5B MAML3 GLI2 CTBP2 MEOX2 UBTF SOCS2 HOXD3 PPP1R16B HOXB4 PRICKLE2 PRX PRRX1 RTN4RL1 MPPED2 C4orf18
V\$AP1_C	275	268	0.974545	17	2.8760 3	0.00022391 2	0.02840 6	STAT5B PLEC1 MDFI FBXO2 LAMA3 NOTCH4 TLL1 KIAA0182 BLMH GADD45A CLDN15 TLX2 PITPNC1 HSPB6 REEP4 PRX MSI1
DANG_REGUL ATED_BY_MY C_DN	253	244	0.964427	16	2.9767 8	0.00023431 2	0.02928 2	VARS MAGI2 HIVEP2 TGFB2 SERPINB1 TCHH MT1A CYFIP2 SPARC DGKZ NXN GADD45A SLC11A1 PTPRN PAM TCN2
TTANTCA_UN KNOWN	952	910	0.955882	39	1.9353 1	0.00024274 5	0.02989	SSTR1 SLC8A1 LMX1A NR2E1 BAIAP2 MEIS2 KIF1B CUX1 OTP KCNIP2 GAL3ST3 SLC25A13 CYFIP2 NEFM ARPP-21 NFAT5 CAMK2D MAGI1 CRTAC1 RTKN2 PITPNC1 PDE4D NEUROG1 ZIC5 HIVEP3 CDK2AP1 ACVR1 FBN2 POLG CASZ1 SFRP4 JAZF1 CTNNBIP1 HOXD3 RUNX1 FAM19A1 BMI1 PRRX1 FERMT1
MODULE_379	204	197	0.965686	14	3.2382 3	0.00025109 8	0.03047	MAGI1 NRXN1 PVRL1 NRG2 PTPRN ACSL6 ECE2 SEZ6L SLMO1 UNC119B PAX7 H6PD P2RX1 MSI1
COLLER_MYC TARGETS_UP	25	25	1	5	10.456 8	0.00025582 2	0.0306	FKBP4 ODC1 G0S2 ASS1 AK3L1
TGTATGA,MIR- 485-3P	153	152	0.993464	12	3.6197 4	0.00026334 1	0.03071 3	MAGI2 PDE4D MEIS2 MAML3 ZMYM4 HDAC4 PHF1 BMI1 NRXN1 FBN2 DAGLA MKX
DOUGLAS_BMI 1_TARGETS_U P	566	547	0.966431	27	2.2238 8	0.00026410 3	0.03071 3	CDK2AP1 C9orf86 NXPH4 ADCY9 ADRBK1 FRMD4A FAM84B REEP4 GSN NCOR2 GLI3 INPP4B DOCK6 POLR1A HNRNPUL1 DLG4 SLC29A1 HDAC7 MFAP4 FXD5 UBTF LOXHD1 DLX5 DDO1 TBX5 FZD5 BCOR
MIKKELSEN_M EF_HCP_WITH _H3K27ME3	590	577	0.977966	28	2.1860 4	0.00026913 9	0.03087	KCNQ1 POU2F3 PHOX2A LMX1A TMPRSS2 AVP DNAJC6 CRTAC1 RAB37 OTP NR2E1 KCNS1 NEUROG1 MPPED1 C14orf39 EMX1 ACSL6 PTPRN2 MCF2L CAMK2B PPP1R16B SEZ6L SCT PSD2 TCF15 PAX7 PRKCZ NKX1-2
CTTTGA_V\$LE F1_Q2	1232	1176	0.954545	47	1.8082 3	0.00028156 7	0.03185 9	MEF2C PLEC1 ASS1 SLC13A5 NR2E1 C12orf59 SNTG1 CXXC5 MEIS2 DPH5 OTP LHX1 MAML3 COL18A1 ABR SEMA6D DLX5 GLI2 MEOX2

								ARPP-21 MPPED2 WNT10B CDC42EP3 PER1 CMTM2 PAM NEUROG1 DACH1 PDYN CASZ1 ADRBK1 PXX LAMA3 ZNF710 GADD45A CLDN15 SOCS2 HOXD3 RUNX1 HOXB4 FAM19A1 SGIP1 BMI1 PRRX1 C9orf86 NRXN1 MSI2
KEGG_ADHERENS_JUNCTION	75	73	0.973333	8	5.1717	0.000314663	0.034613	ACTN4 RAC2 TGFB2 ACTB SRC BAIAP2 FYN PVRL1
POOLA_INVASIVE_BREAST_CANCER_DN	134	133	0.992537	11	3.80321	0.000315714	0.034613	INPP4B SORBS2 CD59 CACNA1D FLNB FRMD4A SYT17 MPPED2 DACH1 FBXO2 CLMN
V\$MYOGENIN_Q6	255	251	0.984314	16	2.88704	0.000321783	0.034613	WNT10B EMX1 C1QA FBLIM1 KCNIP2 EPB41L5 SOST UBTF DGKZ LRP5 SYT17 TEAD4 PARD3B SGIP1 CDH5 SELPLG
RIZ_ERYTHROID_DIFFERENTIATION_6HR	40	40	1	6	7.39229	0.000322443	0.034613	ELF1 RAB25 MEF2C CUX1 HOXB4 NEUROG1
RNGTGGGC_UNKNOWN	766	737	0.962141	33	2.01575	0.000339972	0.036033	SSTR1 EPB41L3 NR2E1 MAGI1 MEIS2 LRRFIP1 NRG2 HOXC10 SNX25 EMX1 ALDOA MAML3 BCOR SEMA4A FYN GPRC5C CENTG2 PVRL1 TLL1 FBXL18 EFEMP2 NEUROG1 CDH5 KIAA0182 TBX5 FZD5 ITPKB PPP1R16B FAM19A1 PRX BMI1 PRRX1 C9orf86
CYTOSKELETAL_PROTEIN_BINDING	159	157	0.987421	12	3.4943	0.000354605	0.037114	CROCC ACTN4 BAIAP2 ADD1 FXYD5 CDC42EP3 S100B SPTBN1 PALLD KIF1B SORBS2 LSP1
V\$E12_Q6	262	255	0.973282	16	2.83812	0.000383445	0.039153	PLEC1 ODC1 FBLIM1 ZNF710 MYOM3 SOST FYN LRP5 CCNJL ANK2 ME3 TEAD4 RUNX1 CDH5 MPPED2 POU2F3
V\$OSF2_Q6	264	255	0.965909	16	2.83812	0.000383445	0.039153	H2AFY OTP CHSY1 LPXN SLC8A1 TBX5 ATP6V0A1 IL16 PLEKHA6 HNRNPUL1 RUNX1 HOXB4 PRRX1 PIGV GPRC5C MSI2
SCHUETZ_BREAST_CANCER_DUCTAL_INVASIVE_UP	351	334	0.951567	19	2.56426	0.000390491	0.039393	LPXN SPARC FYN ST3GAL6 EFEMP2 SLC2A3 PARVA FXYD5 PAM IFI30 FBN2 C1QA MEIS2 MEF2C PALLD HSD17B6 TGFB2 PRRX1 RCBTB2
MULLIGHAN_NPM1_SIGNATU	162	159	0.981481	12	3.44639	0.000397952	0.039667	ITGA5 FXYD5 KCNQ1 ARID3B RNF130 TMPRSS2 PPP1R16B FAM134B LASS2 PLCB4 TGFB2

RE_3_DN								PDE4D
LEIN_ASTROCYTE_MARKERS	42	42	1	6	6.98216	0.000423516	0.041719	C1QA SELPLG MAGI1 MT1A SPARC GSN
DELACROIX_RAR_BOUND_ES	462	448	0.969697	23	2.30824	0.000432318	0.042091	RAI1 TLX2 HOXB4 ACTN4 HIVEP3 C4orf18 ST6GALNAC6 ZC3H3 C1QA KIAA0182 ITGA5 SRC POU2F3 UBE2O POLR1A ZNF710 G0S2 ZIC5 NOTCH4 MSI2 VARS C22orf15 C5orf32
PETROVA_ENDOTHELIAL_LYMPHATIC_VSBLOOD_DN	162	161	0.993827	12	3.39977	0.000445694	0.042481	CYFIP2 MT1A CDC42EP3 RAC2 LPXN RGS10 ARHGAP22 CD59 GADD45A TCN2 ITGA5 KRT7
MODULE_202	28	28	1	5	9.09296	0.000446475	0.042481	GSN SORBS2 LSP1 FLNB ACTN4
ANATOMICAL_STRUCTURE_DEVELOPMENT	1013	972	0.959526	40	1.85326	0.000457103	0.043004	MEF2C SH3GL1 NR2E1 BAIAP2 TEAD4 HDAC4 S100B PAX7 SECTM1 LHX1 MAML3 COL18A1 DLX5 TCF15 GLI2 KCNIP2 MKX NFAM1 CASR CBLN1 POU2F3 HDAC7 TLL1 RAPGEFL1 MPPED2 ECE2 NEUROG1 DLG4 ACVR1 FBN2 LAMA3 NOTCH4 TBX5 FZD5 RUNX1 NRXN1 RTN4RL1 RASGRP4 MSI1 SPARC
YATTNATC_UNKNOWN	377	366	0.970822	20	2.45881	0.000463398	0.043111	PLEC1 SSTR1 RTKN2 ANK2 PITPNC1 NXPH4 HOXC10 KIF1B DACH1 STAT5B RNF212 AXUD1 KCNIP2 CTBP2 MEOX2 HOXD3 HOXB4 FAM19A1 ST7 CAMK2D
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	435	423	0.972414	22	2.33765	0.000481334	0.044012	CAMK2B NEUROG1 SSTR1 TBX5 CBLN1 WNT10B KRT7 HOXC10 PSD2 JAZF1 LMX1A HOXD8 TP73 POU2F3 NKD2 PANX2 FAM155A SEZ6L CACNA1D EMX1 KCNQ1 EPB41L3
CAGCTTT,MIR-320	256	235	0.917969	15	2.8869	0.000483592	0.044012	SEMA6D TMEM2 HSPB6 PPP1R16B RHOBTB1 RUNX1 HOXB4 HDAC4 PHF1 HIVEP2 BANP PALLD MSI2 CUX1 BMPR1A
TGACCTTG_V\$SF1_Q6	249	238	0.955823	15	2.84761	0.000551985	0.048589	MEF2C EPS8L2 ALDOA KCNG4 ABTB2 MYOM3 CDH16 MAEA SNTG1 SYT17 PPP1R16B NXPH4 HOXC10 CAMK2G MSI2
POSITIVE_REGULATION_OF_TRANSCRIPTI	144	142	0.986111	11	3.54002	0.000552354	0.048589	SMARCD3 MYST4 MAML3 RUNX1 NOTCH4 HIVEP3 ELF1 GLI2 ACVR1 TBX5 TP73

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HOX_GENES	65	61	0.938462	7	5.43748	0.000560882	0.048589	MEOX2 HOXC10 PRRX1 PKNOX2 TLX2 HOXD3 PHOX2A
TTGCCAA,MIR-182	327	317	0.969419	18	2.55565	0.000563121	0.048589	MEF2C ADCY2 MAGI1 JAZF1 FBXL10 PLCH1 CSNK1E ABCC3 ANK2 SEPT9 MEIS2 RHOBTB1 ARHGDIA EBF3 PRRX1 PALLD ACVR1 FAM134B
WIKMAN_ASB ESTOS_LUNG _CANCER_UP	17	17	1	4	12.846	0.000567704	0.048589	SORBS2 ADD1 CTBP2 MAEA
MODULE_33	384	372	0.96875	20	2.41618	0.000568698	0.048589	CXCL12 KRT7 ITGA5 SECTM1 RAC2 LSP1 JAK3 PRPH2 SPARC ITPKB TCN2 ME3 ASS1 TEAD4 RUNX1 ARHGAP22 PRRX1 GLI2 TK2 ZBTB48
HUANG_GATA 2_TARGETS_U P	149	143	0.959732	11	3.51308	0.00058599	0.049065	IL16 H2AFY LPXN RAB31 SELPLG TGFB2 TNFAIP8 GSN RNF130 PLEC1 ARID3A
GACAATC,MIR-219	143	143	1	11	3.51308	0.00058599	0.049065	DNAJC6 PDE4D ERGIC1 CXXC5 TGFB2 ARID3B SYNGAP1 KIAA0182 KIF1B CAMK2G TSC22D2

**eTable 4. Gene Set Enrichment Analysis summary table of the hypomethylated smoking-associated CpGs.** Enriched gene set name, number of the genes in the set, number of genes present on the beadchip and used in supervised analysis (nRep), fraction of genes present on the beadchip (fRep), number of overlapping genes (nOVLAP), odds ratio (OR), P-value, Benjamini-Hochberg adjusted P-value (adjPval ) and gene symbols of enriched genes.

Gene List	nList	nRep	fRep	nOVLAP	OR	P-value	adjPval	Genes
RICKMAN_HEAD_AND_N ECK_CANCER_E	89	87	0.97753	10	8.97638	5.97E-07	0.005	C10orf99 TGM3 SOCS2 CEACAM7 C1orf110 VTCN1 ALDH3A1 HLF SERPINB13 CES1
PEREZ_TP53_TARGETS	1174	1120	0.954	38	2.56112	1.33E-06	0.00556	TP73 DIP2C KIAA1545 FAM108C1 MCF2L RP1-21O18.1 EDAR GPT2 NTN1 TP53INP1 BAIAP2 GRIK3 MAD1L1 ECE1 LOXL1 TRIM26 MEF2A KNDC1 AUTS2 UNKL CES1 ZCCHC14 FLNC BMP7 NRG2 KIAA1199 CABG1 HS6ST1 FGF18 CAPN3 ASPSCR1 FAM53B HBEGF SMAD6 ABCC5 KCNIP3 GALNAC4S-6ST MUC2
TTTGCAC,MIR-19A,MIR-1 9B	516	496	0.96124	21	3.11758	1.56E-05	0.03525	RXRA BTBD7 SPIRE1 HLF ZDHHC7 FLNC NPTN TTYH3 JAKMIP1 SMOC1 DDEF2 CGN GRK6 SLC24A3 SPEN BCL3 TP53INP1 RBMS1 ELL2 SV2A TGM3
EGFR_UP.V1_UP	193	190	0.98446	12	4.67048	2.58E-05	0.03525	CYP1B1 KIAA1199 MMP1 ETS2 ELL2 HBEGF WNT5A ABCC3 SOCS2 BCL3 BMP7 LHFPL2
OZEN_MIR125B1_TARGE TS	25	25	1	5	17.0174	2.77E-05	0.03525	MKNK2 RNF144A EIF4EBP1 TP53INP1 CGN
MEK_UP.V1_UP	196	194	0.9898	12	4.56656	3.17E-05	0.03525	CYP1A1 KIAA1199 CYP1B1 ALDH3A1 LOXL1 ABCC3 EPHX1 BCL3 BMP7 GPX2 ELL2 EFHD2
MARTENS_BOUND_BY_P ML_RARA_FUSION	456	443	0.97149	19	3.14471	3.34E-05	0.03525	SKI TNRP EFHD2 RARA SLC24A3 P2RY2 SLC7A5 PLXND1 BCL3 IRF8 GALNAC4S-6ST GRK6 MBP LATS2 WNT9A FAM53B ECE1 UBE2R2 ZMIZ1
V\$GCM_Q2	242	228	0.94215	13	4.19572	3.51E-05	0.03525	WNT10B ZHX2 PRDM1 KCNJ1 SMAD6 ETS2 TGFB3 CDKN2C RBMS1 ELL2 WNT5A NRG2 SPEG
MILI_PSEUDOPODIA_HA PTOTAXIS_DN	668	652	0.97605	24	2.70359	3.79E-05	0.03525	STEAP3 ANKLE2 ZNRF3 NPTN BICD2 RAG1AP1 ECE1 HBEGF SLC7A5 LAPTM4B PTPRF ADORA2B SBNO2

								PANK4 BAIAP2 UNKL ABCC5 SSH1 TSPAN9 NDST1 ZCCHC14 SFRS8 INCENP FLNC
V\$IK1_01	278	267	0.96043	14	3.8464	4.43E-05	0.03708	PRDM1 MKNK2 BCL3 ABCC5 TJAP1 CDKN2C RBMS1 SOCS2 SPEN ADAMTSL5 TINAG HIVEP1 SMOC1 TGM3
Biv	3447	3266	0.94749	74	1.7476	5.98E-05	0.03827	MCF2L NRG2 HS6ST1 KIRREL3 ALS2CL ABCC3 FLNC ABO STEAP3 SLC24A3 GRIK3 MINA SPEG ADCY4 TXNRD1 SYNJ2 CPT1A BAIAP2 ITPK1 BMP7 SMOC1 AUTS2 SLC9A3R2 TGFB3 KIAA1199 C8orf56 FAM53B ROR2 KIAA1543 JAKMIP1 QPCT RBMS1 WNT5A MBP MYT1L RARA CYP1B1 ADORA2B CTBP1 FAM53A LGR6 CDKN2C FAAH HBEGF HLF PTPRN2 FSCN1 WNT10B WNT9A SEMA7A FGF18 SOCS2 NTN1 GFI1 TP73 PCGF3 TPPP ELL2 AATF ZHX2 DIP2C PLXND1 DKK3 CRIM1 PANK4 GNG12 SLC22A3 ATOH8 SGPP2 SLC16A11 USH1G PDZD2 C16orf74 ADAMTSL5
LIU_PROSTATE_CANCE R_DN	481	464	0.96466	19	2.99296	6.22E-05	0.03827	SPEG TPST1 GLIS1 TRIP6 LAPTM4B SMOC1 ZCCHC14 SLC24A3 ADCY4 C9orf3 DKK3 ABCC3 CRIM1 HLF TGFB3 FLNC ETS2 GPX2 RBMS1
chr7p22	104	68	0.65385	7	7.85331	6.23E-05	0.03827	C7orf50 TTYH3 RAC1 FSCN1 MAD1L1 FOXK1 ZDHHC4
ACTGTGA,MIR-27A,MIR-2 7B	474	465	0.98101	19	2.98609	6.40E-05	0.03827	RXRA MKNK2 GNG12 CAPN3 HBEGF RNF144A STK39 NFE2L2 ADORA2B UNKL EDAR RARA BCL3 CIT ELL2 PLXND1 SV2A KIAA1199 GSPT1
GOBERT_OLIGODENDR OCYTE_DIFFERENTIATI ON_DN	1080	1047	0.96944	32	2.25289	7.47E-05	0.04058	TGFB3 LHFPL2 QPCT MBP SV2A ERCC1 CPT1A INPPL1 SLC9A3R2 FAM53B SERINC5 LATS2 RP1-21O18.1 RBMS1 TPPP KIF13A TP53INP1 KCNIP3 SPECC1 RNF144A SPEG LOC388419 SNED1 KIRREL3 TJAP1 SEC14L3 CABCC1 C9orf3

								ABCC5 ETS2 C14orf153 HLF
SMIRNOV_CIRCULATING_ENDOTHELIOCYTES_IN_CANCER_UP	158	150	0.94937	10	4.92157	7.75E-05	0.04058	SERPINB13 P2RY2 RARA WNT5A CYP1B1 SLC7A5 DKK3 PPBP HBEGF CYP1A1
JAEGER_METASTASIS_DN	258	251	0.97287	13	3.78583	9.37E-05	0.04263	ABCC3 ETS2 EXPH5 GPX2 BCL11B SERPINB13 BICD2 IL1R2 WNT5A C9orf3 QPCT HLF BMP7
MODULE_6	416	399	0.95913	17	3.10665	9.40E-05	0.04263	CRIM1 EPHX1 ETS2 CYP1B1 DTX4 NQO1 CES1 CYP2F1 GPX2 ALDH3A1 PTPRN2 GABRP CYP1A1 STK39 TGFB3 ELL2 HLF
FARMER_BREAST_CANCER_APOCRINE_VS_LUMINAL	326	324	0.99387	15	3.37672	9.76E-05	0.04263	ZDHC4 ANKLE2 DHCR24 STK39 MCF2L MINA ETFA MKNK2 ABCC5 EIF4EBP1 GALNAC4S-6ST DIP2C CES1 PDZD2 STEAP3
CTCAGGG,MIR-125B,MIR-125A	329	326	0.99088	15	3.35465	0.0001	0.04263	PTPRF CGN PRDM1 KCNIP3 MKNK2 ABCC5 TP53INP1 EIF4EBP1 ATOH8 MADD LOXL1 TXNRD1 TMEM168 UBE2R2 SPEG
IL-6	104	99	0.95192	8	6.02877	0.00011	0.04263	TXNRD1 PRDM1 SBNO2 ABCC3 ABCC5 BCL3 SOCS2 HBEGF
ONDER_CDH1_TARGETS_2_DN	464	455	0.9806	18	2.87774	0.00015	0.05316	SERPINB13 ARTN PTPRF EXPH5 HBEGF IL1R2 CYP1A1 SLC7A5 IL1F9 P2RY2 QPCT ZHX2 RP1-21O18.1 ALS2CL ARHGEF5 SERINC5 MBP MMP1
MODULE_433	61	55	0.90164	6	8.35456	0.00015	0.05316	TGFB3 NRG2 PPBP HBEGF NTF3 BMP7
ENK_UV_RESPONSE_EPIDERMIS_DN	508	497	0.97835	19	2.78142	0.00015	0.05316	LSP1 SLC7A5 PTPRF DKK3 ELL2 BCL11B IRF8 GALNT2 FSCN1 TXNRD1 MARCH6 HLF BCL3 IL1R2 ALDH3A1 GSPT1 DHCR24 ABCC3 IL1F9
MODULE_204	86	80	0.93023	7	6.55822	0.00018	0.05889	CRIM1 AUTS2 STK39 SV2A ABCC5 FRAG1 SOCS2
MEISSNER_BRAIN_HCP_WITH_H3K4ME3_AND_H3K27ME3	1069	1056	0.98784	31	2.15138	0.0002	0.06427	THSD7B PRDM1 TNRP WNT5A SMOC1 SNED1 SLC12A7 EIF4EBP1 ADORA2B PRDM16 ALS2CL IRF8 WNT9A LHFPL2 ATOH8 ODZ4 NFE2L2 ADAMTSL5 GRIK3 GLI2 BMP7 NTF3 SLC22A3 KIAA1199 SMAD6 GLIS1 CPT1A NTN1 LEMD1 P2RY2 ROR2

TATTATA,MIR-374	284	282	0.99296	13	3.34398	0.00029	0.09139	PRDM1 NTF3 SMAD6 HLF ZCCHC14 CAPZA2 BICD2 WNT5A PCGF3 EDAR HNT KIAA1199 CRIM1
ODONNELL_METASTASI S_DN	24	23	0.95833	4	14.2858	0.00033	0.09735	SMAD6 HLF GRK6 TGM3
PID_LYSOPHOSPHOLIPID_PATHWAY	66	65	0.98485	6	6.93463	0.00038	0.1107	PTK2 ADCY4 RAC1 HBEGF TRIP6 SLC9A3R2
DODD_NASOPHARYNGEAL_CARCINOMA_UP	1821	1675	0.91982	42	1.84805	0.00045	0.12269	CGN C1orf110 EFHD2 MBP SEC14L3 BAIAP2 TPPP DTX4 TCEA3 NQO1 PDZD2 EDAR MTHFD1L CYBASC3 EXPH5 HLF ALS2CL CES1 HSBP1 GRK6 RP1-21O18.1 PTPRN2 KNDC1 TNRP CYP2F1 MCF2L WDR25 SERPINB13 GABRP VTCN1 DHCR24 GPT2 CEACAM7 P2RY2 SNED1 ITPK1 WNT9A NFE2L2 BTBD7 HRASLS2 ALDH3A1 TMEM111
P53_DN.V1_UP	194	187	0.96392	10	3.88543	0.00047	0.12269	LOXL1 AUTS2 ADORA2B CRIM1 EXPH5 SMAD6 KIAA1199 SYNJ2 LHFPL2 MMP1
BANDRES_RESPONSE_TO_CARMUSTIN_MGMT_4 8HR_DN	161	154	0.95652	9	4.2602	0.00047	0.12269	LOXL1 BMP7 BAIAP2 MAD1L1 EPHX1 MUC2 SPEG ARTN INPPL1
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	26	26	1	4	12.3348	0.00053	0.12993	AHRR TPPP EXOC3 SLC12A7
G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	27	26	0.96296	4	12.3348	0.00053	0.12993	LATS2 CDKN2C GF11 GSPT1
LEF1_UP.V1_UP	195	191	0.97949	10	3.79883	0.00055	0.12993	EDAR LOXL1 PDZD2 AUTS2 RYR1 FLNC PTPRN2 WNT5A ROR2 BMP7
NUYTEN_NIPP1_TARGETS_DN	848	828	0.97642	25	2.18991	0.00056	0.12993	STK39 MARCH6 TTYH3 CYP1B1 DHCR24 KIAA1199 ABCC3 TCEA3 TFF2 MKNK2 CPT1A CDKN2C SKI GRK6 EXPH5 FSCN1 CAPZA2 PCGF3 PLXND1 ZCCHC14 STEAP3 PIR ADORA2B GALNT2 EPHX1
BLALOCK_ALZHEIMERS_DISEASE_UP	1691	1642	0.97102	41	1.83593	0.00057	0.12993	HSBP1 EXPH5 MBP ECE1 CTBP1 CABP1 GRK6 TRIM26 MKNK2 FLNC DKK3 FGF18 MARCH6 SPEN REST NDST1 GNG12 ITPK1 CDKN2C PC INPPL1 TBC1D2 SLC7A5 SFERS8 ZMIZ1 CAPN3 SSH1 HBEGF RBMS1 GLI2 RAC1 RGS12 PTPRF



								NQO1 TJP1 ARHGEF10 SNED1 NUP43 C9orf3 EDAR SLC12A7
CAFFAREL_RESPONSE_ TO_THC_24HR_3_DN	13	12	0.92308	3	22.5342	0.00063	0.13836	RYR1 CPT1A PSMD8
GENTILE_UV_HIGH_DOS E_DN	312	309	0.99038	13	3.0346	0.0007	0.14011	NFE2L2 AUTS2 HBEGF PTK2 LHFPL2 RBMS1 PCGF3 SPEN SSH1 TPST1 NTF3 HERPUD1 ZMIZ1
DACOSTA_UV_RESPON SE_VIA_ERCC3_DN	855	844	0.98713	25	2.14534	0.00074	0.14011	ADORA2B WNT5A CRIM1 PTK2 RBMS1 HIVEP1 MEF2A LHFPL2 ARHGEF10 ELL2 TXNRD1 KIAA1199 TPST1 RP1-21O18.1 ANKLE2 SMAD6 DDEF2 SYNJ2 MAD1L1 CTAGE5 ZMIZ1 SPEN MARCH6 STK39 ZHX2
MODULE_118	410	392	0.9561	15	2.75767	0.00074	0.14011	GNG12 CRIM1 GALNAC4S-6ST CYP1B1 PIR NQO1 MMP1 SLC7A5 EIF4EBP1 NRG2 PEPD SV2A CDKN2C LSP1 QPCT
CAGCTG_V\$AP4_Q5	1524	1453	0.95341	37	1.86245	0.00076	0.14011	KCNIP3 GRIK3 TGFB3 CDKN2C BAIAP2 PTK2 NRG2 SEMA7A LHFPL2 BCL11B ZMIZ1 ATOH8 GF11 NCF4 PEPD ARHGEF5 FLNC CYP2F1 LSP1 ADCY4 SPECC1 INPPL1 WDR25 RYR1 NTF3 WNT9A MBP GPX1 SLC24A3 WNT10B LOXL1 SPEG RARA ELL3 TNNT3 SV2A RGS12
HELLER_HDAC_TARGET S_SILENCED_BY_METHY LATION_DN	281	273	0.97153	12	3.17103	0.00076	0.14011	IRF8 GALNAC4S-6ST BCL3 QPCT AUTS2 HERPUD1 ZMIZ1 MARCH6 ZHX2 PFTK1 CDKN2C SLC7A5
KOINUMA_TARGETS_OF _SMAD2_OR_SMAD3	824	799	0.96966	24	2.17326	0.00078	0.14011	NDST1 TXNRD1 GSPT1 PTK2 EDAR ELL2 BTBD7 SMAD6 ETS2 CGN HBEGF SLC7A5 GNG12 UBE2R2 DKK3 PTPRF NPTN WNT9A SPECC1 RGS12 ARHGEF5 PC TBC1D2 MEF2A
POOLA_INVASIVE_BREA ST_CANCER_DN	134	133	0.99254	8	4.38144	0.0008	0.14011	WNT5A ARHGEF5 VTCN1 NQO1 CAPN3 DKK3 CYP1A1 ECE1
REACTOME_DCC_MEDIA TED_ATTRACTIVE_SIGN ALING	13	13	1	3	20.2816	0.00081	0.14011	PTK2 RAC1 NTN1
GRAHAM_CML_DIVIDING	13	13	1	3	20.2816	0.00081	0.14011	FAM38B PPBP CYP1B1

_VS_NORMAL_DIVIDING_UP								
V\$HOXA3_01	13	13	1	3	20.2816	0.00081	0.14011	GRK6 TXNRD1 RBMS1
CHIANG_LIVER_CANCER_SUBCLASS_INTERFERON_DN	52	50	0.96154	5	7.55641	0.00082	0.14011	SLC16A11 HLF ZNRF3 ASPSCR1 EXPH5
BHAT_ESR1_TARGETS_VIA_AKT1_UP	281	276	0.98221	12	3.13449	0.00084	0.14021	RNF144A TFF2 CYP1B1 SBNO2 BCL11B AATF EFHD2 RARA ADAMTSL5 RP1-21O18.1 C16orf74 SLC7A5
GROSS_HYPOXIA_VIA_ELK3_UP	209	206	0.98565	10	3.50514	0.00098	0.15995	SLC9A3R2 CPT1A TP53INP1 CDKN2C MKNK2 RGS12 GPX1 RXRA SSH1 SKI
CHIANG_LIVER_CANCER_SUBCLASS_CTNNB1_UP	176	171	0.97159	9	3.80987	0.00099	0.15995	SLC16A11 CYP1A1 DDEF2 ASPSCR1 EXPH5 ZNRF3 ALDH3A1 HLF HRASLS2
CAGGTG_V\$E12_Q6	2485	2414	0.97143	54	1.65765	0.00103	0.16325	CYP1A1 CYP1B1 GRIK3 TGFB3 EIF4EBP1 CDKN2C AUTS2 NRG2 EDAR CTBP1 BCL11B RBMS1 KIRREL3 RTP1 CRIM1 PFTK1 ZHX2 FLNC LSP1 PRDM16 LEMD1 FAM53B BMP7 PDZD2 SLC16A11 ITPK1 MADD RYR1 NTF3 WNT9A RP1-21O18.1 PC JAKMIP1 SMOC1 PRDM1 EXPH5 ETS2 GLI2 GPX2 GPX1 SLC24A3 ARTN HBEGF WNT10B HIVEP1 GALNT2 SPEG KIF13A POLK ELL3 TNNT3 SV2A DTX2 DNAH17
ABE_VEGFA_TARGETS_2HR	34	32	0.94118	4	9.68513	0.00119	0.18139	HERPUD1 HBEGF ZCCHC14 CYP1A1
KIM_ALL_DISORDERS_CALB1_CORR_DN	37	32	0.86486	4	9.68513	0.00119	0.18139	GFI1 ROR2 ALDH3A1 SBNO2
SINGH_NFE2L2_TARGETS	15	15	1	3	16.9036	0.00126	0.18463	GRK6 TXNRD1 NQO1
LIU_TOPBP1_TARGETS	16	15	0.9375	3	16.9036	0.00126	0.18463	CABC1 TP53INP1 TP73
TGANNYRGCA_V\$TCF11_MAFG_01	301	290	0.96346	12	2.97444	0.00128	0.18488	DDEF2 RYR1 PRDM1 ASPSCR1 RAG1AP1 FLNC CTAGE5 TINAG PSMD8 UNKL DTX2 SPEG
ZWANG_CLASS_3_TRANSIENTLY_INDUCED_BY_EGF	222	215	0.96847	10	3.34978	0.00136	0.18988	ELL2 TXNRD1 LATS2 MBP BCL3 SBNO2 DDEF2 RBMS1 ETS2 HBEGF

KEGG_HEDGEHOG_SIG NALING_PATHWAY	56	56	1	5	6.66482	0.00138	0.18988	WNT9A WNT10B WNT5A GLI2 BMP7
V\$TEF1_Q6	226	216	0.95575	10	3.33334	0.0014	0.18988	TSPAN9 PTPRF FAM53B CGN CPT1A CDKN2C ZMIZ1 MADD KIRREL3 PRDM16
NGUYEN_NOTCH1_TAR GETS_DN	86	83	0.96512	6	5.30946	0.00141	0.18988	HERPUD1 TGM3 ELL2 ETS2 MEF2A RBMS1
NIKOLSKY_BREAST_CA NCER_7P22_AMPLICON	38	34	0.89474	4	9.04005	0.0015	0.19344	TTYH3 FOXK1 C7orf50 MAD1L1
MURAKAMI_UV_RESPON SE_6HR_UP	37	34	0.91892	4	9.04005	0.0015	0.19344	RAC1 TRIP6 PTPRF ERCC1
PLASARI_TGFB1_TARGE TS_1HR_UP	34	34	1	4	9.04005	0.0015	0.19344	FGF18 HBEGF ZMIZ1 WNT9A
VETTER_TARGETS_OF_ PRKCA_AND_ETS1_DN	16	16	1	3	15.6051	0.00153	0.19413	NQO1 PTPRN2 MMP1
ONDER_CDH1_TARGETS _3_DN	59	58	0.98305	5	6.41268	0.00161	0.19856	HBEGF IL1R2 IL1F9 P2RY2 SERPINB13
CREIGHTON_ENDOCRIN E_THERAPY_RESISTAN CE_3	720	698	0.96944	21	2.16359	0.00161	0.19856	PTPRN2 TCEA3 CRIM1 MINA RNF144A HSBP1 CYP1B1 CGN SGPP2 ERCC1 TNRP TBC1D2 STK39 DTX4 ELL2 TPST1 FAM108C1 DHCR24 SYNJ2 AUTS2 ABCC3
LINDGREN_BLADDER_C ANCER_CLUSTER_3_DN	229	221	0.96507	10	3.25349	0.00166	0.20126	RGS12 ABCC5 SMAD6 GPX2 ETFA PTPRN2 TNRP MADD BMP7 TRIP6
MARTINEZ_RB1_TARGE TS_UP	673	653	0.97028	20	2.20081	0.00168	0.20126	GABRP INPPL1 RBMS1 PC ODZ4 CRIM1 NTN1 ABCC5 PTPRF WNT5A INCENP AATF EPHX1 IL1R2 MEF2A RYR1 IL1F9 FSCN1 EIF4EBP1 RXRA
KEGG_METABOLISM_OF _XENOBIOTICS_BY_CYT OCHROME_P450	70	59	0.84286	5	6.29365	0.00174	0.2025	CYP2F1 EPHX1 ALDH3A1 CYP1A1 CYP1B1
ERB2_UP.V1_UP	191	186	0.97382	9	3.48415	0.00178	0.2025	CYP1A1 CYP1B1 KIAA1199 VTCN1 BCL3 EPHX1 ABCC3 LOXL1 SLC9A3R2
DELYS_THYROID_CANC ER_UP	443	429	0.9684	15	2.50637	0.00181	0.2025	ABCC3 CYP1B1 PRDM1 PLXND1 HNT ECE1 PTPRF MMP1 SLC7A5 GPX1 PC RYR1 SV2A DTX4 QPCT
WONG_ADULT_TISSUE_ STEM_MODULE	721	705	0.97781	21	2.14068	0.00182	0.2025	LSP1 HLF LATS2 CRIM1 F2RL3 TPST1 WNT5A ARHGEF10 ARHGEF5 REST SOCS2 GSPT1 MEF2A DKK3 CYP1B1

								DIP2C ETS2 SKI HBEGF AHRR ELL2
GRATIAS_RETINOBLAST OMA_16Q24	17	17	1	3	14.4924	0.00184	0.2025	ZCCHC14 SLC7A5 ZDHHC7
MATTHEWS_AP1_TARGETS	17	17	1	3	14.4924	0.00184	0.2025	BCL3 FLNC HBEGF
HOUSTIS_ROS	36	36	1	4	8.47521	0.00186	0.20269	CYP1B1 TXNRD1 GPX1 GPX2
MODULE_88	838	805	0.96062	23	2.05545	0.00191	0.20516	GNG12 CRIM1 EPHX1 ETS2 DTX4 NQO1 EIF4EBP1 CES1 CYP2F1 GPX2 PTPRN2 STK39 NRG2 PEPD SV2A WNT10B LSP1 SBNO2 QPCT ABCC3 PPBP HBEGF TNNT3
WGTTNNNNNAAA_UNKN OWN	547	523	0.95612	17	2.32985	0.002	0.21212	PFTK1 PTPRF ZHX2 NTF3 GALNAC4S-6ST CLRN1 SLC7A5 CDKN2C HIVEP1 C3orf20 PRDM16 KIF13A PRDM1 ETS2 GPX1 ATOH8 SOCS2
SULFUR_METABOLIC_P ROCESS	37	37	1	4	8.21811	0.00207	0.2128	TPST1 NDST1 GPX1 HS6ST1
MARTINEZ_RB1_AND_TP 53_TARGETS_DN	591	571	0.96616	18	2.2601	0.00208	0.2128	PTPRF ECE1 KRTAP3-1 EPHX1 NTN1 ALDH3A1 EIF4EBP1 MBP CPT1A RYR1 SLC9A3R2 AATF CRIM1 INCENP ODZ4 GABRP WNT5A SLC7A5
MYLLYKANGAS_AMPLIFI CATION_HOT_SPOT_5	7	5	0.71429	2	44.9033	0.00209	0.2128	HLF ASPSCR1
V\$CEBP_C	200	191	0.955	9	3.38758	0.00213	0.2128	SEMA7A WNT10B GPX1 SEC14L3 BCL11B ITPK1 NPTN TGM3 CRIM1
RAF_UP.V1_UP	196	191	0.97449	9	3.38758	0.00213	0.2128	HBEGF CYP1B1 VTCN1 QPCT RNF144A ABCC3 TBC1D2 CRIM1 SOCS2
AGCGCTT,MIR-518F,MIR- 518E,MIR-518A	18	18	1	3	13.523	0.00218	0.21492	CAPN3 MCF2L AUTS2
SHIPP_DLBCL_CURED_V S_FATAL_UP	39	38	0.97436	4	7.97621	0.00228	0.21969	NTF3 FAAH MMP1 CES1
VALK_AML_WITH_FLT3_I TD	40	38	0.95	4	7.97621	0.00228	0.21969	LAPTM4B SOCS2 BAHCC1 FAM38B
YCATTAA_UNKNOWN	556	532	0.95683	17	2.28795	0.00239	0.22728	PFTK1 ZHX2 GALNAC4S-6ST CLRN1 GRIK3 PTK2 SMOC1 MARCH6 LEMD1 SFRS8 PRDM1 EXPH5 RBMS1 TINAG SV2A HNT TGM6

CAMP_UP.V1_DN	200	196	0.98	9	3.29613	0.00254	0.2379	ETS2 GALNAC4S-6ST DDEF2 TTYH3 ZCCHC14 HNT GNG12 ZMIZ1 PRDM1
PID_EPHA2_FWDPATHWAY	19	19	1	3	12.6782	0.00256	0.2379	INPPL1 RAC1 PTK2
KIM_WT1_TARGETS_8HR_UP	164	160	0.97561	8	3.59775	0.00259	0.2379	ZMIZ1 SYNJ2 BAIAP2 MKNK2 HBEGF TBC1D2 PLXND1 SPEN
TTGCCAA,MIR-182	327	317	0.96942	12	2.70716	0.00269	0.24437	PRDM1 RAC1 ETS2 ZCCHC14 ABCC3 TP53INP1 TSPAN9 ATOH8 ELL2 PC PCGF3 UBE2R2
TTCYNRGAA_V\$STAT5B_01	335	319	0.95224	12	2.68924	0.00283	0.25441	RARA POLK PPBP PRDM1 LAPTM4B EXPH5 RAG1AP1 CTAGE5 ABCC5 SOCS2 IRF8 DTX2
GENTILE_UV_LOW_DOSE_DN	67	66	0.98507	5	5.57023	0.00286	0.25462	TPST1 RBMS1 KIAA1199 PFTK1 STK39
KEGG_PATHWAYS_IN_CANCER	328	320	0.97561	12	2.68038	0.0029	0.25545	CTBP1 PTK2 WNT9A WNT10B TGFB3 RARA WNT5A FGF18 MMP1 RXRA RAC1 GLI2
V\$TCF11MAFG_01	207	201	0.97101	9	3.20944	0.00301	0.25779	ASPSCR1 GRK6 GPX2 FLNC ITPK1 TINAG KIRREL3 UNKL TXNRD1
GENTILE_UV_RESPONSE_CLUSTER_D2	41	41	1	4	7.3296	0.00303	0.25779	NTF3 NFE2L2 PCGF3 AUTS2
CCTGAGT,MIR-510	45	41	0.91111	4	7.3296	0.00303	0.25779	HLF CAPZA2 CRIM1 ZHX2
MODULE_220	333	322	0.96697	12	2.66281	0.00305	0.25779	ROR2 CYP1B1 HLF SEMA7A CAPN3 NRG2 ARTN WNT10B HBEGF TNNT3 WNT5A SPEG
V\$FOX_Q2	213	202	0.94836	9	3.19265	0.00311	0.25786	ZHX2 PRDM1 NTF3 BCL11B GRIK3 TGFB3 ATOH8 NTN1 CRIM1

**eTable 5. Enrichment Analysis Table of Transcription Factor (TF) Binding Sites:** Odds Ratios (OR) and P-values (P) of Transcription Factor (TF) Binding Sites among the 912 hypermethylated and 589 hypomethylated smoking-associated CpGs.

TF	HyperM OR	HyperM P	HypoM OR	HypoM P
ATF2_SC.81188_None__HudsonAlpha	0.49	0.999	0.32	1
ATF3_None__HudsonAlpha	0.56	0.977	0.19	1
Bach1_sc.14700_None__Stanford	0.68	0.972	0.42	0.999
BCL11A_None__HudsonAlpha	1.17	0.575	<0.01	1
BRCA1_A300.000A_None__Stanford	0.37	0.994	0.14	0.999
CEBPB_None__Stanford	1.77	0.013	0.67	0.861
CHD1_A301.218A_None__Broad	1.16	0.224	0.26	1
CHD1_A301.218A_None__Stanford	0.39	0.991	<0.01	1
CHD2_AB68301_None__Stanford	0.87	0.798	0.08	1
c.Jun_None__Stanford	0.5	0.909	0.39	0.925
c.Myc_None__Stanford	1.1	0.361	0.16	1
c.Myc_None__UT.A	0	1	2.42	0.202
CtBP2_None__USC	1.81	3.00E-05	0.54	0.992
CTCF_None__Broad	2.23	4.00E-10	0.31	1
CTCF_None__UT.A	2.68	1.00E-11	0.29	1
CTCF_SC.5916_None__HudsonAlpha	2.46	2.00E-10	0.26	1
Egr.1_None__HudsonAlpha	0.9	0.729	0.15	1
EZH2_39875_None__Broad	2.19	6.00E-09	0.39	1
FOSL1_SC.183_None__HudsonAlpha	0.65	0.81	0.51	0.862
GABP_None__HudsonAlpha	1.13	0.296	0.25	1
GTF2F1_AB28179_None__Stanford	0.29	1	<0.01	1
HDAC2_SC.6296_None__HudsonAlpha	0.69	0.89	0.4	0.98
JARID1A_ab26049_None__Broad	0.09	1	<0.01	1
JunD_None__HudsonAlpha	1.04	0.462	0.38	0.997
JunD_None__Stanford	1.18	0.239	0.22	1

MafK_ab50322_None__Stanford	2.74	6.00E-04	1.12	0.483
Max_None__USC	1.47	0.01	0.24	1
Mxi1_AF4185_None__Stanford	0.74	0.941	0.1	1
NANOG_SC.33759_None__HudsonAlpha	0.97	0.584	0.9	0.645
Nrf1_None__Stanford	0.63	0.97	<0.01	1
NRSF_None__HudsonAlpha	1.25	0.236	0.69	0.849
p300_None__HudsonAlpha	0.61	0.983	0.31	1
Pol2.4H8_None__HudsonAlpha	0.84	0.913	0.14	1
Pol2_None__HudsonAlpha	0.56	1	0.11	1
Pol2_None__UT.A	0.6	1	0.1	1
POU5F1_SC.9081_None__HudsonAlpha	1.87	0.171	<0.01	1
Rad21_None__HudsonAlpha	2.58	5.00E-15	0.34	1
Rad21_None__Stanford	2.63	2.00E-12	0.31	1
RBBP5_A300.109A_None__Broad	1.06	0.285	0.14	1
RFX5_200.401.194_None__Stanford	1.7	0.09	<0.01	1
RXRA_None__HudsonAlpha	0.49	0.871	0.76	0.734
Sin3Ak.20_None__HudsonAlpha	0.99	0.541	0.31	1
SIN3A_NB600.1263_None__Stanford	1.09	0.205	0.15	1
SIX5_None__HudsonAlpha	0.15	1	0.58	0.929
SP1_None__HudsonAlpha	1.08	0.308	0.32	1
SP2_SC.643_None__HudsonAlpha	0.17	1	0.09	1
SP4_V.20_None__HudsonAlpha	0.58	0.999	0.09	1
SRF_None__HudsonAlpha	0.46	0.983	0.14	0.999
SUZ12_None__USC	1.78	0.031	0.39	0.964
TAF1_None__HudsonAlpha	0.73	0.998	0.12	1
TAF7_SC.101167_None__HudsonAlpha	0.47	1	0.09	1
TBP_None__Stanford	0.95	0.674	0.16	1
TCF12_None__HudsonAlpha	1.15	0.345	0.68	0.855
TEAD4_SC.101184_None__HudsonAlpha	1.18	0.24	0.68	0.911

USF.1_None__HudsonAlpha	1.28	0.088	0.21	1
USF2_None__Stanford	0.71	0.911	<0.01	1
YY1_SC.281_None__HudsonAlpha	1.01	0.487	0.13	1
Znf143_16618.1.AP_None__Stanford	1.4	0.007	0.25	1



**eTable 6. Smoking associated fold-expression changes in non-tumour lung tissue of smoking associated CpGs:** Table lists the smoking fold-expression changes in each of the three non-tumour lung tissue data sets of Bosse et al, for all genes with corresponding smoking-associated CpGs (from 1501 CpG signature) in their TSS200 region. Table lists if corresponding CpGs are hypermethylation or hypomethylated in the buccal tissue.

Gene	t(Average)	FC1	FC2	FC3	DNAm
CD300LG	7.235	0.54296	0.65468	0.6649889	HyperM
ACOT11	6.45	1.27994	1.01594	0.9526869	HyperM
ADCY2	6.575	0.72045	0.72249	0.5181805	HyperM
SLC8A1	6.83	1.24944	1.12373	1.0882274	HyperM
MFAP4	6.116	0.77741	0.97253	0.8650012	HyperM
PRX	6.41	0.64207	0.68323	0.9930995	HyperM
PPP1R16B	6.095	0.71146	0.80795	1.144703	HyperM
HOXB4	5.855	0.78212	0.83412	0.7447377	HyperM
DPP6	6.15	0.21275	0.56494	0.7395076	HyperM
CDC42EP3	6.045	1.23757	1.146	0.9867531	HyperM
PALLD	6.02	0.78314	0.94567	0.8846493	HyperM
FYN	6.01	0.71933	0.90385	1.0841664	HyperM
TBX5	6.01	0.78237	0.88465	0.892102	HyperM
NOTCH4	5.84	0.71502	0.82174	0.904622	HyperM
ALDOA	5.83	1.21267	1.07284	1.1842654	HyperM
MPPED2	5.81	0.62257	0.95904	0.5532704	HyperM
BZRAP1	5.75	0.78275	0.86239	0.7962838	HyperM
S100B	5.75	2.71374	1.55807	1.1158178	HyperM
MSRB3	5.71	0.73853	0.93417	0.817781	HyperM
CD52	5.66	1.29431	1.14576	1.6653132	HyperM
ECE2	5.56	1.33725	1.07516	1.191553	HyperM
BEND7	5.54	0.79936	0.91345	0.9343346	HyperM
C2orf58	5.54	2.67963	2.03752	1.7077012	HyperM
IFI30	5.54	1.29991	1.1333	1.3381606	HyperM

CYP1A1	-8.16875	2.33569	1.87795	1.2149942	HypoM
CYP1B1	-8.8425	4.52613	2.38476	1.6172552	HypoM
GPX2	-7.015	2.49063	1.63024	1.2233348	HypoM
KIAA1199	-6.69	1.80503	1.37226	1.0514647	HypoM
GPX1	-5.85	1.4104	1.05456	1.3825008	HypoM
DTX2	-5.7	1.3563	1.02016	1.0600163	HypoM
CECR1	-5.68	1.36161	1.15071	1.2354955	HypoM
TXNRD1	-5.6	1.4871	1.15779	1.4290348	HypoM
TBXAS1	-5.59	1.50616	1.13902	1.4702083	HypoM
GSPT1	-5.55	1.25025	1.09047	1.149074	HypoM
SLC22A18	-5.45	1.44517	1.1066	1.1143282	HypoM

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