Rat Leukocyte Population Dynamics Predicts a Window for Intervention in Aging

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Abstract

Age-associated changes in human hematopoiesis have been mostly recapitulated in mouse models; but not much has been explored in rats, a physiologically closer model to humans. To establish whether rat hematopoiesis closely mirrors humans', we examined the peripheral blood of rats throughout their lifespan. Significant age-associated changes showed distinctive population shifts predictive of age. A divergence between predicted versus chronological age changes was indicative of fragility; thus, these data may be a valuable tool to identify underlying diseases or as a surrogate predictor for intervention efficacy. Notably, several blood parameters and DNA methylation alterations defined specific leverage points during aging, supporting non-linear aging effects and highlighting a roadmap for interventions at these junctures. Overall, we present a simple set of rat blood metrics that can provide a window into their health and inform the implementation of interventions in a model system physiologically relevant for humans.

Key words

Aging, Rat, hematopoiesis, flow cytometry, DNA methylation, intervention timepoint, blood

Introduction

Among all mammalian tissues, blood is perhaps most easily collected in fairly large quantities for various advanced analyses, with modest discomfort to the donor. This has made blood the prevailing tissue for a wide variety of applications such as clinical diagnosis, immune surveillance, and molecular investigations, including DNA methylation, that require a sizable amount mass of genetic material ^{1,2}.

To date, peripheral blood aging has been largely characterized in humans ³⁻⁵ and mice ⁶. Studies in the mouse model have provided important insights as this model system allows investigation of the impact of a variety of genetic interventions and hematopoietic stem cell (HSC) transplant assays. Many murine aging phenotypes accurately reflect reports from human studies including a decline in immunogenic response of lymphoid cells ⁶, decreased CD4/CD8 T-cell ratio ⁷, and an increase in myeloid cells at the expense of lymphoid cells ⁸. These phenotypes have been shown to be influenced, at least in part, by intrinsic HSC aging ⁹.

However, the mouse as a model of human hematopoiesis has drawbacks including the fact that the common laboratory strains do not reliably develop spontaneous blood cancers, which is a common aging phenotype in humans ¹⁰. The differences between the two species are further exemplified by the fact that mouse blood is dominated by lymphocytes whereas human blood is rich in neutrophils ¹¹; which in the murine model may dampen the impact of the age-associated decrease in lymphoid potential.

An attractive alternative system is the rat model. Rat physiology is more analogous to humans ^{12,13}, yet still have relatively short lifespans ¹⁴ in which to study aging phenotypes. Further, the rat and human genomes share genes involved in immunity and hematopoiesis absent in mice ¹³. Importantly, rats, especially the Fischer 344 CDF (F344) strain, display age-related incidence of leukemia ¹⁵. All the above suggest the rat may be better suited to study the aging of the blood and immune systems. Despite these advantages, use of the rat model has been in decline as mice are smaller, generally cost less to maintain, and transgenic tools to manipulate the murine genomes have been

robustly developed. As a result, the impact of aging on the blood compartment in rats is not well characterized.

We sought to describe changes in the composition of the peripheral blood during aging in the F344 male rat using flow cytometry. In addition, we found that CD25⁺ T cell frequency is a novel marker for predicting aging and rats have defined age-associated inflection points linked to altered methylation profiles and cell composition. These results indicate that age-associated blood phenotypes in rats provide relevant insight into human blood aging and point to a critical time period of hematopoiesis which may best be targeted for anti-aging interventions

Results

Aging patterns in rat peripheral blood leukocyte populations

We analyzed the peripheral blood composition of 146 male F344 rats ranging in age from 3 to 27 months, using a panel of seven monoclonal antibodies to evaluate major leukocyte populations. As cell-specific gating strategies for rat blood populations are less defined than in humans or mice, we initially evaluated the flow cytometry results in an unbiased manner using t-distributed stochastic neighbor embedding (t-SNE) and Self-Organizing Maps analyses. Cells generally clustered in a manner that allowed for identification of defined populations (Fig. 1a and Supplementary Fig. 1) and clustering analysis helped inform decisions for gating strategies we devised for cell-type classification (Supplementary Fig. 2). Age-related changes were also profiled from single-cell analyses and revealed an accumulation of cells in clusters corresponding to myeloid lineage cells and a reduction of cells in clusters expressing markers associated with B and CD8⁺ T cells (Fig. 1b). Globally CD4⁺ T cells decreased with age, but we identified 2 distinct CD4⁺ populations with different trajectories during aging. The CD4⁺ T cell cluster expressing high levels of CD25 did not show an age-associated decline in cell number and instead increased in frequency over time. t-SNE defined clusters 5 and 9 (brown and cyan, Fig. 1a) also show age-associated increases in frequency (same top left location as Fig 1a,

but blue in Fig. 1b); however, these clusters could not be fully identified from this combination of antibodies (Supplementary Fig. 2). Cluster 5, due to a high expression of CD11b/c, is most likely a type of myeloid cell, whereas cluster 9 most likely consists of debris (Supplementary Fig. 1) as it stained equally positive for all antibodies. Most identified cell populations that were categorized encompassed 2 or more clusters, indicating potential subpopulations we were unable to define with the panel of antibodies in this study.

Figure 1. Unsupervised clustering of all F344 rat peripheral blood cells. Clustering of rat peripheral blood using a self-organizing map algorithm. For detailed clustering also see Supplementary Fig. 1. **(a)** Overall clustering of all leukocytes from 146 rats overlaid on a t-SNE map; each cluster is denoted as a different color (see legend). **(b)** Specific blood cell types illustrated on the same t-SNE map for three age groups (n=10,000 cells from each age group; total 30,000 cells). For visualization purposes, rats were divided into age groups: Young (3-4 mo), Middle-aged (15-23 mo) and Old (24+ mo).

We next sought to determine if age-specific blood parameter characteristics could be defined using frequencies of the distinct cell populations identified (Supplementary Fig. 2). Using unsupervised clustering of all rats based on leukocyte population frequencies, animals clustered into three discrete groups (Fig. 2), indicating the overall “fingerprint” of

blood composition is age dependent. The cluster classified as “young” is characterized by a high proportion of lymphocytes in general, and T cells in particular, but with a low frequency of CD25⁺ CD4⁺ T cells.

Figure 2. Distinct age clustering of rats based on white blood cell frequencies. Hierarchical agglomerative clustering with distance matrix by Ward’s method. The top lines represent the distance matrix for the individual rats and the three major branches are annotated by green, dark gray, and orange. The heatmap represents the normalized frequency of each population as indicated by the legend. The lines on the left indicate the distance matrix of the frequencies. The bottom histogram represents the age distribution for each of the major clusters in the same colors as above.

In contrast, the “old” cluster, on the far right, is characterized by a low overall lymphocyte frequency, and elevated proportions of both myeloid and CD25⁺ CD4⁺ T cells (Fig. 2). This increase in CD25⁺ CD4⁺ T cells is similar to what is seen in human peripheral blood aging¹⁶, while in the murine model CD25⁺ CD4⁺ T cells only accumulate in secondary

lymphoid organs (spleen and lymph nodes) but not in the peripheral blood¹⁷. This analysis also defines a specific “mid-age” profile that is distinct from both young and old phenotypes, but clusters more closely to the young rat profile than the old.

Peripheral blood parameters predict age and pathology in rats

To assess the blood cell types most predictive of aging, we fit all leukocyte frequencies in a standard least square model to predict aging in animals with no detected pathology and then eliminated the least significant parameters in a backstep fashion (Fig. 3a). The health status of all rats was recorded throughout the study, and necropsy was performed on all animals, less than a month post blood collection (for full health/pathology report see Supplementary Data 1). This enabled testing of how the health status of each rat fit into the model. One caveat was animals with overt sickness were excluded and euthanized per vet recommendation, so the health analysis captures mostly underlying illnesses only discernable during necropsy. The resulting blood parameter model predicted age with an approximate 2-month margin of error (as indicated by the root mean square error value). The single most predictive parameter of rat age was the proportion of CD25 expression in CD4⁺ T cells (Fig. 3a, right panel). Animals with histological indication of disease, including indications of large granular lymphocytic leukemia (LGLL) in spleen or liver, described in Finesso et al.¹⁸, are generally predicted by our model as more variable than their actual age (i.e., have stronger residual age values) (Fig. 3b). When constructing an age prediction model only for ill animals, we found the myeloid/lymphoid ratio was the strongest contributor to age prediction (Fig. 3d). Additionally, we constructed a nominal logistic regression model to predict illness and found that myeloid/lymphoid ratio is the strongest contributor, even more so than age (Supplementary Fig. 3). While the myeloid/lymphoid ratio increases with aging, this phenomenon is more pronounced in sick animals. However, this ratio alone is not sufficient to predict illness (Fig. 3d, left), and must be combined with the other blood parameters that are characteristic of age and how variable the predicted age is from the chronologic age (Fig. 3b, c). We also observed that myeloid/lymphoid ratio increases concurrently with severity of LGLL¹⁸ (Fig. 3d, right).

Figure 3. Age and illness prediction by blood leukocyte composition. All blood cell population frequencies were used to create a standard least square model of age prediction. Variables that did not contribute to the model were removed in a backstep fashion. **(a)** Predicted age vs. actual age, the red line indicating the mean and fit. Animals excluded due to illness are depicted in light gray. The effect summary for the variables used is depicted in the right panel (Effect Summary) with the LogWorth cutoff depicted by a blue line. **(b)** Residual age (i.e., the difference between actual age and predicted age) plotted as absolute mean values against assessment of health as determined by necropsy. Yes = no health issues; Mild = mild health problems (e.g., minor foot lesions); No = Clear health issues found during necropsy (Supplementary Data 1). **(c)** The correlation between myeloid/lymphoid ratio and age in healthy (blue) and ill (red) animals. **(d)** Myeloid/lymphoid ratio in the peripheral blood plotted against health status (left panel) and large granular lymphocytic leukemia (LGLL) pathology score as detected in the liver and spleen. Each dot represents a single rat. Dot color denotes age.

As blood samples from the 159 rats were analyzed post-fixation (see Methods), we were interested to determine whether the model generated is also applicable for freshly isolated

blood. We thus generated data for both fresh and fixed rat blood, taken from the same donors. We found only small differences (<10%) in population frequencies associated with fixation, with changes in the T and B cell population frequencies post fixation showing the biggest variation (Supplementary Fig. 4a). Despite these differences, applying the age-prediction model, generated from fixed blood samples, on the blood profiles generated on un-fixed samples of varying ages (Supplementary Fig. 4b) demonstrated that the existing model (from fixed blood) could be used in a similar fashion to predict age with only minor mathematical adjustments.

Figure 4. Dynamics of leukocyte frequencies during aging. (a) Aging trends of variables with inflection points depicted by a cubic spline regression ($\lambda=0.521$). Shaded colored areas indicate the fit. Inflection/breakpoints are depicted as dotted vertical lines with SE in shaded grey. (b) Variance (S^2) and coefficient of variation (CV) for each parameter as a function of age (in a sliding window of 3 months). (c) Summary of leukocyte critical aging points (color coded) in relation to reproductive capacity (orange) and survival curve points (grey) ¹⁴.

Regression analysis reveals potential aging intervention points

This study involved a minimum of 5 rats from each month of age starting from 3 months to 27 months (Supplementary Data 2) which enabled us to cross-sectionally examine the dynamics of blood changes during aging. Overall, the changes of leukocyte frequencies with age-matched rats, reflected described changes in aging human blood, including a reduction in B and T cells, and an increase in monocytes, neutrophils, and CD25⁺ CD4⁺ T cells (Supplementary Fig. 5). To better understand the dynamics of these blood composition shifts, we performed a multiple regression analysis for each cell population and identified time points in which there was a major trajectory shift (Fig. 4a and Supplementary Fig. 5b). Most of these shifts appear to converge at approximately 15 months of age. A strong age-associated increase in the overall variance of the different parameters was also observed, which was especially pronounced at close to 24 months of age (Fig. 4b). Interestingly, the first hematopoietic inflections appeared prior to the decline in survival of the classic Gompertz curve for this rat strain ¹⁴.

Peripheral rat blood DNA methylation changes with age

DNA methylation data was generated from the peripheral blood of these rats and was previously analyzed for defining a rat aging “methylation clock” ². We analyzed the epigenic landscapes for hematopoietic-specific changes in methylation associated with aging using the Bismark pipeline. Global, age-dependent hypomethylation (Fig. 5a) occurred, located mostly in intergenic and intronic regions. Promoter regions had a more balanced ratio of sites that either gained or lost methylation (Fig. 5b). Interestingly, overall decreases in methylation were more pronounced in the transition between middle and old age compared to the global methylation changes seen in the shift from young to middle age (Fig. 5a). To gain insight into the difference between the early- and late-aging changes, we performed differentially methylated region (DMR) analysis on locations near transcription start sites (TSS). Most regions with significant DNA methylation changes were progressively altered during aging, which is slightly incongruous with the phase shifts seen in blood composition. However, we also found non-linear changes in methylation using a differential methylation analysis of 3 major age groups (Fig. 5). We

identified 140 DMRs unique to the young vs. middle-age comparison and 94 DMRs unique to the middle-aged vs old (Fig. 5c). 456 DMRs appeared as significantly differential only between the young and old animals, which we attribute to a slow progressive change that only passed the cutoff of significance and fold change in the young vs old comparison (Fig 5c). Enrichment analysis of differentially methylated regions showed age-associated hyper-methylation for several processes and included some overlaps between the early (Y-M) and late (M-O) aging phenotypes, such as regulation of T cells and differentiation (Fig. 5d). However, some enrichments were unique to the middle age transition (regulation of apoptosis) and the late age (Notch signaling pathway), again indicating a difference between the early and late aging phenotypes. Of note, while hypomethylated DMRs between young and middle age were identified for several processes (Fig. 5d, right panel), hypomethylated DMRs in the transition from middle-aged to old were not enriched for any specific process (Supplementary Data 3); perhaps suggesting that these changes are more reflective of drift or random alterations and not necessarily concerted DNA methylation changes.

To eliminate a potential bias of pre-determining age groups, we also analyzed DNA methylation at all transcription start sites to determine if changes occurred as a function of age using the Response Screening platform (see Experimental Procedures) (Supplementary Fig. 6). The most significantly changed sites were all located near the TSS of RUNX family transcription factor 1 (*Runx1*) and these sites all show strong hypermethylation with age (Fig. 5e, left panel). The hypermethylation of *Runx1* can be mapped immediately distal to the TSS (Fig. 5e, middle panel). The second most significantly changed DMR was located near the TSS of *Dnmt3a* (Fig. 5e, right panel). A principal component analysis (PCA) based only on the 2,311 DMRs that significantly changed as a function of age (Supplementary Fig. 6) demonstrates a marked increase in variation around the 2-year mark, analogous to the increased variation observed for population frequencies (Fig. 4b).

Figure 5. Differentially methylated regions with rat aging. (a) Global differential methylation

histograms per age group comparison. A cut-off of 5% methylation difference was used. **(b)** Proportion of hyper- and hypo- methylated regions (DMR) compared to distance from the closest transcription start site (TSS). **(c)** Venn diagram for the number of differentially methylated regions within 20k bp distance of the nearest TSS based on age group comparisons. A cut-off of FDR<0.05, >5% CpG mean change, and at least 3 CpG differential DMR site per block was used. Hyper- and hypo-methylated changes are indicated by the noted colors. **(d)** Summary of gene set enrichment analysis for DMRs in proximity of TSSs (<20k bp). Analysis was performed for 3 age groups: Young (3-8 mo), Middle-aged (13-17 mo), and Old (22-27 mo). Combined score was calculated as $-\log_{10}(\text{FDR}) \times \text{fold enrichment}$. YM - Young vs. Middle aged; MO - Middle aged vs. Old; YO - Young vs. Old. The list of hypomethylated DMRs for the MO comparison had statistically significant enrichments. For a full enrichment analysis see Table S4. **(e)** Individual methylation levels of regions near the Runx1 and Dnmt3a genes. Left panel - Runx1; Middle panel - Methylation map in the Runx1 TSS; Right panel - Dnmt3a.

Early and late life DNA methylation switches

As the blood population frequencies indicated a mid-life inflection, we explored whether DNA methylation patterns exhibited similar signature transitions. First, we performed both linear and logistic regressions on significant age-associated DMRs near TSSs (Supplementary Fig. 6 and Supplementary Fig. 7). We next selected the regression with the best fit (based on Akaike Information Criterion Shavlakadze, et al. ¹⁹). 62.9% of the sites changed linearly with age while 37.1% showed a better fit to a logistic regression (Fig. S7). The break point was calculated for sites that did not change linearly with age (Fig. 6, left) and a module enrichment analysis was performed for genes with switches before and after 15 months of age (Fig. 6, right). The methylation switch points defined converged at around 22 months of age and mildly at close to 12 months of age. Genes that had a breakpoint earlier than 15 months of age were enriched for cytokine production, regulation of differentiation and hematopoiesis, and include Apolipoprotein E (*ApoE*) and *Runx1*. Genes identified to have a switch later in life were enriched for myeloid differentiation, leukocyte activation, ion transport, and epithelial development. Similar to the changes in blood parameter composition, these DNA methylation results highlight differences come in waves, notably at around 15 months, rather than occurring in a linear fashion and suggest a key remodeling time-point of the hematopoietic system.

Figure 6. Early and late life methylation breakpoints. (a) Distribution of breakpoints by age. Each dot represents the breakpoint of a single gene TSS; color scales by age from young (blue) to old (red). Contour violin plot of the distribution is displayed in gray. (b) Functional module networks of the genes with breakpoints before (bottom - blue) and after (top - red) 15 months of age. Each dot represents a single gene with size corresponding to its' connectivity in the network. The lines indicate interactions (edges). The networks were built for blood tissue, with human orthologs as input. The interaction network is built using the closest gene neighbors and then clustered based on enrichment in GO categories. Networks were generated using HumanBase (<https://hb.flatironinstitute.org>).

Discussion

Although the rat peripheral blood compartment has been analyzed in regard to aging²⁰, newer panels of monoclonal antibodies offer improved insight into changes of the hematopoietic system. Here, a relatively simple blood profiling technique using 8 antibodies led us to construct a model that predicts both age and, potentially, pathology. The model can be used to predict the risk of illness as a function of the deviation from predicted age to actual age, and we propose such a model could also be used to determine if intervention experiments mitigate aging phenotypes. While our dataset and

analyses were for a specific set of flow cytometric parameters generated on fixed cells, we found we were able to adapt these analyses to also predict the age of freshly isolated blood (using similar flow cytometry markers). Thus, with inclusion of proper controls to account for experimental design variation, this resource of aging rat blood parameters could be adapted for studies of rat aging or pathology without requiring euthanasia of the animals. We believe this would be especially useful for longitudinal or intervention studies given the ease of blood collection at multiple time points.

A strong predictor of age was the accumulation of CD25 on CD4⁺ T cells in the F344 rat model. These results support previous findings that report an age dependent accumulation of regulatory T cells (Tregs)^{17,21,22}. This stable increase in the F344 rat is more similar to that observed in humans¹⁶ than in mice¹⁷ and highlights the relevance of the rat model to study hematopoietic aging. Garg et al.²³ have previously suggested that this accumulation is driven by hypomethylation of forkhead box P3 (Foxp3) in CD25⁺CD4⁺ T cells, however in our dataset analyzing total blood cell methylation, we do not see differential methylation of Foxp3. This is likely because CD25⁺CD4⁺ T cells are a rare subpopulation of the total blood and DNA methylation changes in this population would not significantly affect the global blood methylation profiles.

We observed an age-dependent myeloid bias with rat aging, similar to mice⁹ and humans⁸. The observed myeloid bias was a strong predictor of pathology in general, and of LGLL in particular. Importantly, strong myeloid bias was correlated with illness that was otherwise only noticeable during autopsy and undetectable during routine veterinary observation. A caveat to this observation is that myeloid-bias increases with age, even in healthy animals, meaning that the myeloid/lymphoid ratio can only be useful as a diagnostic parameter when plotted against the expected “normal” age-dependent increase. In this reference dataset, we found a significant association between severity of LGLL and increased myeloid cell numbers. The myeloid bias we report in rats has previously been documented in mice, however most mouse models do not develop age-associated blood diseases seen in humans. Thus, we find the correlation between increased myeloid cells and LGLL severity in rats to be of particular relevance for potential modeling of human blood aging phenotypes.

Our analysis of the age-related changes in leukocyte profiles indicates inflection points in the trajectories occurring at early middle-age (~15 months) and at ~24 months of age. The first inflection point is characterized by several shifts in leukocyte frequencies, including a stabilization of T cell decline, peak in CD8⁺ T cells, rapid drop of B cells, deceleration in the accumulation of CD25⁺ CD4⁺ T cells, and an acceleration in the increase of stimulated monocytes. The second shift point we observed is defined by a marked increase in variance between individual rats which alludes to a pan-hematopoietic loss of homeostasis. We hypothesize that interventions aiming at mitigating aging phenotypes would be significantly more effective if performed prior to these defined shift points. The inflection points in the blood are similar to the transition patterns (linear, early logistic, and mid-logistic) of gene expression on tissues isolated from aging Sprague-Dawley rats¹⁹. Further supporting a claim for interventions predating the observed switch point are studies of caloric restriction (CR). It is quite clear that early onset CR has more benefits than late onset, but it is yet unclear what the ideal age of onset should be²⁴. In fact, late onset CR has even been shown to be potentially detrimental to cognitive function when applied too late²⁵. However, Chen et al²⁶ reported a beneficial effect of late onset CR to muscle mass and metabolism in Sprague-Dawley rats, indicating that the ideal points of intervention could vary greatly between different systems. In fact, interventions that aim to prevent or delay aging could be fundamentally different than those that aim to reverse it, even to the extent where harm could be caused when one strategy is applied instead of the other²⁷. It is therefore critical to understand which systems display aging switch points, and when, in order to design the appropriate intervention regimen. This is especially true when translating experimental paradigms to human interventions due to the great heterogeneity between the aging rates of both individuals and different systems within the individual²⁸.

The combined results of changes in population frequencies and the DNA methylome indicate that hematopoietic aging of rats occurs in phases as opposed to a continuous process. However, with the current data, we cannot ascertain the drivers underlying the shift between these aging phases, whether they are triggered by a specific event, or simply manifest when a critical mass of small changes reaches a threshold. Whichever

the case, investigating these relatively early time points in which blood profiles begin to irreversibly shift, indicating critical trajectory alterations, is of great interest.

The age-related DNA methylation changes in all leukocytes highlights the potential involvement of epigenetic changes that have occurred in hematopoietic stem cells and/or early progenitors, and are transmitted to all the differentiated progeny, as indicated by the hypermethylation of *Runx1* and the gene enrichment analysis. In addition, the lack of enrichment for hypomethylated transcription start sites in the transition from middle age to old indicates that age-related gains of methylation may be a directed process, whereas loss of methylation later in life is more non-specific and perhaps attributed to drift. If so, mitigating the seemingly random loss of methylation would be an interesting potential aging intervention.

In summary, we present this work as a resource for investigators studying aging in the rat model, which appears to be a robust system for modeling the aging human hematopoietic system. Our research emphasizes the importance of studying changes in homeostasis during aging as we present key trajectory shifts in blood populations that occur at relatively early age (15 months). Finally, our research model describes aging “junction points.” Given these specific breakpoints in composition of the hematopoietic system, we posit that strategic aging interventions would likely be more robust and beneficial if performed earlier in life to mitigate or stall the major changes that occur under homeostatic conditions. It would be exciting to further explore if an illness prediction model based off of these defined blood parameters could be extrapolated for a broad range of diseases, and ultimately if similar age-associated shifts occur in other organs /tissue systems, animal models, and specifically in humans.

Methods

Animals

All experimental procedures were conducted in accordance with the *Guide for the Care and Use of Laboratory Animals* and approved by the NIA Animal Care and Use Committee. Male Fischer 344 CDF (F344) rats were obtained from the NIA Aged Rodent

Colony housed at the Charles River Laboratories (Frederick, MD). Animals were housed with Nylabone supplementation and ad libitum access to food (Envigo 2018SX) and water. Rats younger than 3 months were housed in groups of three; all other rats were single housed. All rats were maintained on a 12/12 lighting schedule, with all procedures carried out during the light cycle. Rats were habituated to the facility for at least 3 days before sample collection. The same rats were analyzed in previous studies ^{2,18}.

Flow cytometry and sample collection

500 µl of whole blood was collected via retro-orbital bleedings for DNA and FACS analysis. Blood for DNA was collected in heparinized tubes, spun, and the plasma removed; buffy coat and red blood cells were frozen at -80°C until DNA extraction. Blood for FACS analysis was collected in EDTA-treated tubes, chilled on ice, and 100 µL was stained and then processed using a Beckman Coulter TQ-prep (fixation step) and the Beckman Coulter immunoprep reagent system. For the fresh sample analysis, blood was drawn as above, ACK treated and immediately stained on ice. Antibodies used for fluorescence analysis are as follows: FITC-conjugated anti-rat CD3 (clone 1F4, Cat#201403), PE-conjugated anti-rat CD25 (clone OX-39, Cat#202105), PerCP-conjugated anti-rat CD8a (clone OX-8, Cat#201712), PE-Cy7 conjugated anti-rat CD11b/c (clone OX-42, Cat#201818), APC-Cy7 conjugated anti-rat CD4 (clone W3/25, Cat#201518) from Biolegend (San Diego, USA), and AF647-conjugated anti-rat RT1B (clone OX-6, Cat#562223), BV421-conjugated anti-rat CD45RA (clone OX-33, Cat#740043), and BV605-conjugated anti-rat CD45 (clone OX-1, Cat#740515) from BD Biosciences (Franklin Lakes, USA). Immunophenotyping data was acquired on a BD FACSCanto II and analyzed using FlowJo (<https://www.flowjo.com/>).

DNA methylation analysis

Samples were treated and sequenced for DNA methylation as described in Levine et al.². The raw sequencing datasets are available from GEO (GSE161141). To identify differentially methylated loci: we trimmed reads of adapter dimers using Trim Galore (0.4.3) and quality trimmed with a minimum quality score above >25 (--rrbs -q 25). The attached adapter dimers were trimmed using cutadapter. Firstly, bisulfite-converted index

(GA and CT conversion) was generated using F344 rat genome with Bismark build option and trimmed reads were aligned with bismark ²⁹. Once we created aligned reads and corresponding locations, we used the bismark_methylation_extractor tool to summarize the level of methylation in CpG sites (bismark_methylation_extractor -p -comprehensive -no_overlap -bedGraph -counts -buffer_size 16G (\$Aligned read bam file). Approximately a total 1-2 million sites per sample were predicted with DNA methylated sites (or unmethylated). Differentially methylated regions (DMR) and blocks of differentially methylated sites were identified with a minimum of 3 CpG sites per block and at least >5% Methylation difference (FDR <0.05) using MethyKit [PMID: 23034086 ³⁰] and DMRseq ³¹. Functional annotation was performed using ClusterProfiler ³². To generate RRBS DNA methylation block: RRBS datasets were processed in a uniform way and DNA methylation levels for each sample were extracted. Then, we generated 200 base-pair binned DNA methylation levels across the genome. Each DNA methylation block contains 1-20 CpG sites. We first calculated the average DNAm level per DNAm block for each rat age then used this average DNAm level for mean CpG imputation. We calculated the DNAm level using all methylated and unmethylated sites from the binned CpG sites when the minimum coverage was more than 5. The F344 build of the rat reference genome was used for bisulfite sequencing alignment, and the rn6 genome feature was used to extract genomic annotation information using the Homer package ³³. Genes, exons, introns, and UTRs were taken from Homer annotation tools (annotatePeaks.pl DMR rn6). TSS-promoter sites were considered the identified DMRs close to TSS (less than 1kb). TSS-proximal sites were considered the identified DMRs close to TSS (less than 20kb) and TSS-distal sites were considered the DNAm block whose distance to TSS is above 20kb. For downstream analysis to find inflection points, we used the TSS-promoter DNAm block for searching inflection point analysis (e.g. Runx1, Dnmt3a).

Statistical analysis and software used

Population frequencies were determined with FlowJo™ v10.8 Software (BD Life Sciences) ViSNE and Self-Organizing Maps (SOM) analyses were performed using Cytobank ³⁴. All statistical analyses except those specifically detailed otherwise were

performed using JMP (JMP®, Version 16. SAS Institute Inc., Cary, NC, 1989–2021). The predictive model of age based on leukocyte frequencies was constructed using the least square method with backstep elimination of insignificant variables. Analysis of pathology prediction was performed using the JMP Decision Tree Platform. Determination of regression formulas and breakpoints were performed in JMP according to the formulas indicated in Fig. S7.

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Competing Interests

The authors declare that they have no conflict of interest.

Author contributions

C.D., T.M., and M.L. conducted experiments; B.P. and C.C. participated in the bioinformatics analysis; R.M. was involved in study design and data analysis; R.W., and K.P. participated in study design; I.B. supervised the study and edited the manuscript. H.Y. conducted experiments, analyzed the data, and wrote the manuscript with input from all authors

Data availability statement

The data that support the findings of this study are available in the supplementary material and Supplementary Tables of this article. The DNA methylation raw data is available via GEO Accession (GSE161141). Further information and requests for

resources and reagents should be directed to and will be replied to by the
corresponding authors.

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Supplementary information

Figure S1-S7

Supplementary Data 1-4

Supplementary Figure 1

Supplementary Figure 1. Self organizing map clustering of F344 rat leukocytes.
1.3 million random cells from all samples were chosen to perform a self organizing map analysis on the cytobank platform using default settings. **(a)** Heatmap of Ab fluorophore intensities per cluster. **(b)** Fluorophore intensities (blue = low intensity to red = high intensity) overlaid on a tSNE plot generated on the same platform using default settings. **(c)** Divergence tree of clustering.

Supplementary Figure 2

Supplementary Figure 2. Gating strategy.

The staining panel was uniform for all samples and consisted of the following anti-rat Abs: CD45-BV605, CD3-FITC, CD8a-PerCP, CD4-APC.Cy7, CD25-PE, RT1B-AF647, CD45RA-BV421, and CD11b/c-PE.Cy7.

Supplementary Figure 3

Supplementary Figure 3. Prediction of pathology. Several methods were used to identify myeloid/lymphoid ratio as a strong predictor of pathology. **(a)** Prediction of age only among animals with any kind of pathology by least square method. Statistics are depicted and the variable contribution is depicted in the lower panel. **(b)** Visualization of a nominal regression model to predict pathology, the X axis is divided into animals that were predicted to be healthy/ailing and the proportions of actual health status are denoted in blue (healthy) and red (ill). The lower panels denote the nominal regression model statistics and parameter contributions and odd ratios. **(c)** Probability of being ill is plotted as a function of myeloid/lymphoid ratio (line denotes a spline regression with the colored area denoting the fit).

Supplementary Figure 4

Supplementary Figure 4. Fresh Vs fixed samples.

(a) Blood from the same rats (10 months old) was divided and stained after fixation and on fresh live cells. The cells were analyzed by flow cytometry and the delta for each parameter was calculated as Fresh value – Fixed value. Each dot represents the delta for the given parameter in the same rat and the box indicates the mean and quantiles. $n = 14$. **(b)** Blood from 5 young (5 mo), 5 middle-aged (15 mo), and 11 old (24 mo) rats was collected and analyzed, and the results were fitted (red) to the model generated from fixed samples (blue).

Supplementary Figure 5

(a)

(b)

Supplementary Figure 5. Major leukocyte population frequencies as a function of age

(a) Each dot represents a reading from a single rat and the cell type is indicated for each plot. The line represents a spline regression, and the colored area represents the fit. (b) Bivariate correlation matrix. The diagonal indicates the univariate distribution for the given variable

Supplementary Figure 6

Supplementary Figure 6. Response Screening to determine transcription start sites that change their methylation as a function of age.

The Response Screening function (JMP - <https://www.jmp.com>) performs multiple correlation analyses and corrects for False Discovery Rate (FDR). The analysis was performed on 200 bp bins that are within 500 bp of TSS.

(a) Correlation P values are depicted in red and the FDR in blue where each TSS is a single dot. The horizontal blue line indicates the cut-off (FDR p value < 0.05, measured in >50 rats, n = 2,311). Only sites that were successfully sequenced in >50 animals were included (n = 58,000). **(b)** PCA for all rats based on the genes that passed the cut-off; each dot represents a rat and the color represents age as indicated.

Supplementary Figure 7

Supplementary Figure 7. Determination of methylation changes “switch” points.

A logistic 4P and linear regression were both tested for each bin near a TSS and the results were compared using the Bayesian Information Criterion (BIC) and Corrected Akaike Information Criterion (AICc). **(a)** Example of a linear (top) and a logistic (bottom) regression. **(b)** Comparison of weighted AICc delta (linear-logistic). Each dot represents a site. Values over 0 (red) indicate a linear regression fits better than a logistic one and vice versa for values under 0 (blue). **(c)** Breakpoint analysis formula used to determine the optimal switch point.

Suppl Table 1. Animal Pathology

Animal ID	Study ID	DOB	BW (g) Terminal	Date of Death	LGL Pathology Score	Clinical/Necropsy (date; finding)
643620	3m-1	17/10/2016	400	18/07/2017		
643621	3m-2	17/10/2016	421	20/07/2017		6/14/17 HL plantar lesions, mild; housed on soft bedding
643622	3m-3	17/10/2016	243	18/07/2017		6/21/17 reported for low BCS, decreased feces, porphyrin staining; 7/18/17 2/5 BCS, alopecia of both FLs, gas-filled colon; gastric masses (L side - aggregates of whitish round masses, 5-7 mm in diameter; stomach saved in formalin); pale liver
653183	3m-4	04/01/2017	409	03/10/2017		
653184	3m-5	04/01/2017	413	03/10/2017		
653185	3m-6	04/01/2017	332	22/06/2017		Mild autolysis; Tissues tacky; Brain tissue gelatinous - right hemisphere obliterated by 0.5 cm round lesion that expressed blood when removed from skull
643623	4m-1	17/09/2016	376	18/07/2017		
643624	4m-2	17/09/2016	418	20/07/2017		
643625	4m-3	17/09/2016	388	20/07/2017		
646221	4m-4	07/10/2016	380	15/08/2017		

646222	4m-5	07/10/2016	434	18/08/2017	8/19/17 HL plantar lesions, mild; housed on soft bedding R corneal edema; mild head tilt
646223	4m-6	07/10/2016	413	18/08/2017	
643628	5m-1	17/08/2016	359	14/02/2017	
643629	5m-2	17/08/2016	321	24/02/2017	
643630	5m-3	17/08/2016	362	06/03/2017	
650645	5m-4	14/10/2016	340	06/04/2017	
650644	5m-5	14/10/2016	357	13/04/2017	0
650643	5m-6	14/10/2016	291	13/04/2017	
643631	6m-1	17/07/2016	397	14/02/2017	
643632	6m-2	17/07/2016	364	24/02/2017	
643633	6m-3	17/07/2016	381	10/03/2017	
646226	6m-4	07/08/2016	385	07/03/2017	
646227	6m-5	07/08/2016	374	10/03/2017	0
646228	6m-6	07/08/2016	310	17/03/2017	
643638	7m-1	17/06/2016	372	14/02/2017	
643639	7m-2	17/06/2016	385	17/02/2017	
643640	7m-3	17/06/2016	371	06/03/2017	
653186	7m-4	04/09/2016	372	28/04/2017	
653187	7m-5	04/09/2016	355	04/05/2017	0
653188	7m-6	04/09/2016	375	04/05/2017	
643641	8m-1	17/05/2016	403	14/02/2017	
643642	8m-2	17/05/2016	407	28/02/2017	
643643	8m-3	17/05/2016	410	06/03/2017	

646232	8m-4	07/06/2016	362	07/03/2017	
646233	8m-5	07/06/2016	348	10/03/2017	
646234	8m-6	07/06/2016	361	17/03/2017	
643644	9m-1	17/04/2016	392	17/02/2017	
643645	9m-2	17/04/2016	409	24/02/2017	
643646	9m-3	17/04/2016	379	06/03/2017	
650646	9m-4	14/06/2016	404	06/04/2017	
650647	9m-5	14/06/2016	392	13/04/2017	
650648	9m-6	14/06/2016	398	13/04/2017	
643652	10m-1	17/03/2016	398	17/02/2017	
643653	10m-2	17/03/2016	408	24/02/2017	
643654	10m-3	17/03/2016	400	28/02/2017	
646243	10m-4	07/04/2016	394	17/03/2017	
646244	10m-5	07/04/2016	370	10/03/2017	
646245	10m-6	07/04/2016	415	17/03/2017	
643655	11m-1	17/02/2016	419	06/03/2017	
643656	11m-2	17/02/2016	431	28/02/2017	
643657	11m-3	17/02/2016	399	07/03/2017	
653189	11m-4	04/05/2016	411	28/04/2017	
653190	11m-5	04/05/2016	393	28/04/2017	
653191	11m-6	04/05/2016	414	04/05/2017	
643658	12m-1	17/01/2016	426	17/02/2017	0
643659	12m-2	17/01/2016	422	24/02/2017	0
643660	12m-3	17/01/2016	417	06/03/2017	0

646246	12m-4	07/02/2016	416	07/03/2017	0	
646247	12m-5	07/02/2016	435	10/03/2017	0	
646248	12m-6	07/02/2016	384	17/03/2017	0	
643668	13m-1	17/12/2015	405	18/07/2017	0	6/21/17 HL plantar lesions, mild; housed on soft bedding
643669	13m-2	17/12/2015	449	20/07/2017	0	
643670	13m-3	17/12/2015	399	20/07/2017	0	
650649	13m-4	14/02/2016	448	12/09/2017	0	
650650	13m-5	14/02/2016	457	12/09/2017	0	7/19/17 HL plantar lesions, mild; housed on soft bedding
650651	13m-6	14/02/2016	427	12/09/2017	0	
643671	14m-1	17/11/2015	422	20/07/2017	0	
643672	14m-2	17/11/2015	473	18/07/2017	0	3/29/17 mild plantar lesions; housed on soft bedding; 7/18/17 hemoabdomen on necropsy (5-10 cc serosanguinous fluid, many clots) precluded any blood collection
643673	14m-3	17/11/2015	402	06/03/2017	0	
646253	14m-4	07/12/2015	465	15/08/2017	3	5/17/17 HL plantar lesions, mild; housed on soft bedding; 8/15/17 splenomegaly 8-10x
646254	14m-5	07/12/2015	415	18/08/2017	0	6/14/17 HL plantar lesions, mild; housed on soft bedding

646255	14m-6	07/12/2015	443	15/08/2017	0	5/9/17 PUPD, resolved over several weeks; 7/19/17 HL plantar lesions, mild; housed on soft bedding
643674	15m-1	17/10/2015	419	18/07/2017	0	6/14/17 HL plantar lesions, mild; housed on soft bedding
643675	15m-2	17/10/2015	427	18/07/2017	0	4/3/17 eye bleed complication; 4/26/17 HL plantar lesions, mild; housed on soft bedding; 7/18/17 mod-severe porphyrin staining noted at necropsy
643676	15m-3	17/10/2015	447	18/05/2017	2	Enlarged black pituitary on necropsy, 2x; minimal blood collected
653192	15m-4	04/01/2016	430	03/10/2017	1	10/3/17 moderate porphyrin staining right eye
653193	15m-5	04/01/2016	411	03/10/2017	3	7/5/17 HL plantar lesions, mild; housed on soft bedding; 10/3/17 splenomegaly 5x (9g), hepatomegaly, moderate petechiation of lungs, mild porphyrin staining left eye
653194	15m-6	04/01/2016	418	03/10/2017	2	mild HL plantar lesions; 6/20/17 porphyrin staining right eye

643677	16m-1	17/09/2015	446	18/07/2017	0	
643678	16m-2	17/09/2015	261	16/02/2017	0	
643679	16m-3	17/09/2015	365	03/07/2017	0	
646262	16m-4	07/10/2015	430	15/08/2017	0	7/12/17 HL plantar lesions, mild; housed on soft bedding
646263	16m-5	07/10/2015	407	15/08/2017	0	6/14/17 HL plantar lesions, mild; housed on soft bedding; 8/15/17 SC L abdominal round fatty mass approx 2.5 cm
646264	16m-6	07/10/2015	287	09/03/2017	3	
643680	17m-1	17/08/2015	432	17/02/2017	0	
643681	17m-2	17/08/2015	402	23/02/2017	0	
643682	17m-3	17/08/2015	463	28/02/2017	0	
650652	17m-4	14/10/2015	423	06/04/2017	0	
650653	17m-5	14/10/2015	428	06/04/2017	0	
650654	17m-6	14/10/2015	425	13/04/2017	0	
643683	18m-1	17/07/2015	414	09/02/2017	0	
643684	18m-2	17/07/2015	432	28/02/2017	0	
646265	18m-4	07/08/2015	411	07/03/2017	0	
646266	18m-5	07/08/2015	415	10/03/2017	0	
646267	18m-6	07/08/2015	406	17/03/2017	0	
643686	19m-1	17/06/2015	371	09/02/2017	0	

643687	19m-2	17/06/2015	401	17/02/2017	3	1/20/17 intraorbital facial mass, diagnosed as abscess; treated and resolved; 2/17/17 splenomegaly 3-4x
643688	19m-3	17/06/2015	447	28/02/2017	0	
653195	19m-4	04/09/2015	434	28/04/2017	0	
653196	19m-5	04/09/2015	391	04/05/2017	0	no bone marrow collected
653197	19m-6	04/09/2015	393	04/05/2017	1	no bone marrow collected
643689	20m-1	17/05/2015	428	09/02/2017	0	Enlarged L testicle, 2-3x
643690	20m-2	17/05/2015	342	23/02/2017	1	
643691	20m-3	17/05/2015	415	28/02/2017	0	
646268	20m-4	07/06/2015	420	07/03/2017	0	
646269	20m-5	07/06/2015	490	10/03/2017	0	
646270	20m-6	07/06/2015	457	17/03/2017	0	
643712	21m-1	17/04/2015	389	09/02/2017	1	
643713	21m-2	17/04/2015	385	23/02/2017	0	
643714	21m-3	17/04/2015	386	28/02/2017	0	
650655	21m-4	14/06/2015	388	06/04/2017	0	
650656	21m-5	14/06/2015	408	13/04/2017	0	
650657	21m-6	14/06/2015	407	13/04/2017	1	
643715	22m-1	17/03/2015	377	16/02/2017	0	
643716	22m-2	17/03/2015	398	28/02/2017	3	Splenomegaly, 5x
643717	22m-3	17/03/2015	384	28/02/2017	1	
646271	22m-4	07/04/2015	405	07/03/2017	1	

646272	22m-5	07/04/2015	386	10/03/2017	0	
646273	22m-6	07/04/2015	426	17/03/2017	2	Splenomegaly, 3x
643718	23m-1	17/02/2015	436	16/02/2017	1	2/15/17 approx 20-25 mm round left mandible mass; meets study criteria for euthanasia/already scheduled for sac; at necropsy, suspect lipoma
643719	23m-2	17/02/2015	394	23/02/2017	2	
643720	23m-3	17/02/2015	371	28/02/2017	0	
653198	23m-4	04/05/2015	400	28/04/2017	3	
653199	23m-5	04/05/2015	395	28/04/2017	0	Splenomegaly, 2x
643721	24m-1	17/01/2015	371	09/02/2017	3	Splenomegaly noted at necropsy (7x)
643722	24m-2	17/01/2015		04/02/2017	0	Dehydration reported on 2/2/17
643723	24m-3	17/01/2015	405	28/02/2017	2	Splenomegaly, 3x
646274	24m-4	27/02/2015	401	07/03/2017	0	
646275	24m-5	27/02/2015	421	10/03/2017	2	Splenomegaly, 3x
646276	24m-6	27/02/2015	437	17/03/2017	1	
646277	25m-1	07/01/2015	445	07/03/2017	0	
646278	25m-2	07/01/2015	389	10/03/2017	0	
646279	25m-3	07/01/2015	390	17/03/2017	0	
650663	25m-4	14/02/2015	379	06/04/2017	2	3/23/17 approx 20 mm round left axillary mass; gait/locomotion unaffected

650664	25m-5	14/02/2015	310	06/04/2017	3	2/5 BCS, pale (r/o anemia), 3x splenomegaly, pale mottled liver (r/o cirrhosis)
650665	25m-6	14/02/2015	386	13/04/2017	0	Pituitary enlargement, 2x
650671	26m-1	14/01/2015	385	06/04/2017	3	3/24/17 mild-mod plantar lesions; housed on soft bedding; 4/6/17 4x splenomegaly
650672	26m-2	14/01/2015	383	06/04/2017	3	3/29/17 mild plantar lesions; housed on soft bedding; 4/6/17 globular, abnormally shaped spleen 3x, pale liver, pale lungs with petechiation
650673	26m-3	14/01/2015	382	13/04/2017	3	Muscle wasting, 2x splenomegaly, pale mottled liver with rounded edges and 2x enlargement, 2x left testicle enlargement, 10 cc abdominal effusion, 2-3x black pituitary
653201	26m-4	04/02/2015	334	28/04/2017	3	Small spleen with round pale lesion at distal end; liver mottled with rough surface
653202	26m-5	04/02/2015	398	04/05/2017	1	4/26/17 mild plantar lesions noted on both hind feet; 5/4/17 Enlarged black pituitary gland, 2x

653203	26m-6	04/02/2015		26/04/2017	0	4/20/17 serum yellow with low cell count r/o bilirubinemia, anemia; reported poor recovery from anesthesia for blood/tissue collection with chest compressions performed
646280	27m-1	07/11/2014	401	07/03/2017	1	SC mass R axilla 2cmx2cm r/o fibroadenoma
646281	27m-2	07/11/2014	400	10/03/2017	0	SC diffuse lobulated L inguinal mass 3cmx1.5cm; 2mm splenic plaque
646282	27m-3	07/11/2014	416	17/03/2017	3	Severe urine staining, 1 cm round SC inguinal mass, 6-7 cm round L intrabdominal mass adherent to cranial pole of L kidney (r/o pheochromocytoma), pale mottled liver, enlarged L kidney, 3-4x splenomegaly, pituitary tumor, r/o Cushing's
653205	27m-5	02/02/2015	373	18/05/2017	1	
653206	27m-6	02/02/2015	368	18/05/2017	2	Enlarged black pituitary, 2x

ID	Age (g)	FoL	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells	FoL of CD4+ T cells
3m-1	3.20	270	58.10	3.01	26.80	4.07	4.07	0.60	34.95	65.05	4.89	1.74	33.80	19.30	0.09	0.03	
3m-2	3.50	303	63.20	0.98	26.40	3.71	3.11	0.40	37.01	62.99	6.40	2.44	35.70	22.70	0.05	0.04	
3m-3	3.60	310	67.80	2.34	15.90	5.43	4.09	0.43	34.76	65.24	5.52	2.33	39.80	22.60	0.08	0.04	
3m-4	3.20	294	61.30	2.39	28.70	2.51	2.23	0.39	35.20	64.80	5.94	2.21	35.00	20.40	0.05	0.04	
3m-5	3.20	283	55.30	2.81	26.70	4.51	4.41	0.63	35.75	64.25	5.87	1.94	31.00	18.50	0.09	0.04	
3m-6	3.50	311	59.60	2.21	28.30	2.83	2.97	0.42	36.84	63.16	7.21	2.58	33.20	21.10	0.06	0.05	
4m-1	4.50	313	62.60	1.31	23.90	6.12	2.78	0.36	38.14	61.86	6.38	2.37	34.80	23.20	0.05	0.04	
4m-2	4.50	314	63.50	2.45	23.20	4.48	2.73	0.80	39.00	61.00	7.52	2.81	34.50	24.20	0.07	0.05	
4m-3	4.50	317	62.40	3.82	19.00	4.08	5.43	0.64	37.11	62.89	6.36	2.39	35.20	22.50	0.12	0.04	
4m-4	4.10	269	59.40	2.68	29.60	2.17	2.32	0.81	37.79	62.21	6.49	2.25	32.40	21.30	0.06	0.04	
4m-5	4.20	401	63.80	3.03	25.50	3.00	1.90	0.34	35.77	64.23	5.85	2.28	36.60	21.90	0.06	0.04	
4m-6	4.50	288	70.40	1.85	19.30	2.63	2.83	0.27	34.62	65.38	5.76	2.37	38.80	22.10	0.05	0.04	
5m-1	5.20	350	58.10	2.45	24.10	5.20	4.43	0.67	38.85	61.15	9.37	3.14	30.40	21.70	0.09	0.06	
5m-2	5.50	340	65.20	2.19	21.70	3.42	3.64	0.76	38.75	61.25	8.74	3.36	35.00	24.70	0.07	0.05	
5m-3	5.70	356	58.50	2.52	26.30	5.12	3.30	0.75	39.48	60.52	8.19	2.74	30.80	22.20	0.07	0.05	
5m-4	5.30	337	62.80	4.50	14.70	5.49	6.04	0.71	35.68	64.32	7.76	2.85	33.90	20.70	0.14	0.05	
5m-5	5.50	369	58.70	3.12	24.00	3.86	4.71	0.56	37.01	62.99	7.56	2.61	31.80	20.50	0.10	0.05	
5m-6	5.50	334	57.90	5.04	20.60	5.82	5.30	0.74	34.93	65.07	5.38	1.89	33.20	19.10	0.13	0.04	
6m-1	6.30	385	58.00	3.06	24.40	4.91	4.82	0.62	37.59	62.41	7.97	2.76	31.80	21.20	0.10	0.05	
6m-2	6.50	360	59.20	2.79	27.60	3.73	3.00	0.87	37.55	62.45	8.80	3.13	32.50	21.80	0.07	0.05	
6m-3	6.70	376	59.00	3.32	24.00	3.98	4.72	0.59	36.72	63.28	9.16	3.24	32.10	20.90	0.10	0.06	
6m-4	6.20	370	63.30	3.76	23.80	4.25	1.55	0.39	35.96	64.04	7.14	2.69	34.90	21.40	0.06	0.05	
6m-5	6.30	373	60.50	3.42	22.60	5.33	3.46	0.40	34.24	65.76	7.26	2.72	34.80	19.80	0.08	0.05	
6m-6	6.50	312	60.90	4.46	15.20	6.22	6.76	0.85	33.59	66.41	5.53	2.01	34.40	18.70	0.15	0.04	
7m-1	7.20	363	54.10	2.85	26.80	4.71	6.14	0.87	37.10	62.90	8.30	2.68	29.60	19.40	0.12	0.05	
7m-2	7.50	385	62.30	1.31	25.90	4.28	3.17	0.49	37.25	62.75	10.59	3.92	33.00	22.30	0.05	0.07	
7m-3	7.70	351	55.70	2.88	25.20	6.70	5.03	0.58	37.19	62.81	9.84	3.28	30.10	20.00	0.10	0.06	
7m-4	7.20	365	63.20	2.13	22.90	4.47	2.82	0.44	35.20	64.80	10.37	4.04	34.90	21.50	0.06	0.07	
7m-5	7.50	365	60.60	4.69	18.70	4.94	5.48	0.63	37.13	62.87	9.70	3.47	32.30	21.50	0.13	0.06	
7m-6	7.50	390	57.40	1.60	29.70	3.63	3.33	0.28	39.44	60.56	9.92	3.25	29.50	21.70	0.06	0.06	
8m-1	8.30	408	48.10	2.94	27.50	6.41	8.11	1.37	37.93	62.07	9.69	2.71	25.30	17.50	0.15	0.06	
8m-2	8.60	419	57.00	3.38	29.20	2.66	3.51	0.69	41.64	58.36	11.52	3.67	28.20	23.20	0.09	0.07	
8m-3	8.70	426	57.50	4.35	23.10	4.79	4.46	0.65	36.48	63.52	9.44	3.19	30.60	19.80	0.11	0.06	
8m-4	8.20	352	56.50	5.88	26.40	2.56	3.84	0.84	39.16	60.84	9.54	2.99	28.40	20.60	0.12	0.06	
8m-5	8.30	348	52.70	5.23	18.20	9.90	6.36	1.15	35.84	64.16	7.74	2.39	28.50	17.50	0.16	0.05	
8m-6	8.50	360	61.70	5.77	7.36	9.07	8.27	0.72	35.11	64.89	5.59	1.86	31.40	18.30	0.19	0.04	
9m-1	9.50	411	65.00	0.38	25.80	5.49	1.37	0.08	38.33	61.67	10.15	3.86	34.20	24.10	0.02	0.06	
9m-2	9.50	400	55.30	4.13	27.80	4.17	3.65	0.97	39.77	60.23	11.52	3.65	28.10	21.40	0.10	0.07	
9m-3	9.70	378	48.90	4.84	24.60	6.74	7.28	0.91	36.88	63.13	14.23	4.13	24.80	17.30	0.16	0.09	
9m-4	9.30	415	54.10	5.47	21.90	6.61	4.14	0.73	37.19	62.81	16.12	4.70	24.50	17.70	0.13	0.10	
9m-5	9.50	413	53.10	3.14	23.40	8.79	5.58	0.52	32.59	67.41	14.04	4.15	25.50	14.70	0.11	0.09	
9m-6	9.50	409	46.80	4.91	26.40	5.62	7.35	0.65	35.15	64.85	16.24	4.40	22.70	15.10	0.16	0.11	
10m-1	10.50	404	57.00	4.15	21.90	6.23	5.56	0.74	37.13	62.87	12.05	4.09	29.80	20.40	0.12	0.08	
10m-2	10.60	413	55.20	3.51	24.50	4.74	7.18	0.82	39.50	60.50	12.65	4.00	27.60	21.10	0.14	0.08	
10m-3	10.60	407	65.90	2.96	13.80	8.12	4.54	0.36	30.83	69.17	10.16	3.89	34.40	17.30	0.09	0.07	
10m-4	10.20	382	52.50	2.63	26.30	6.89	6.32	0.57	35.63	64.37	12.90	3.94	26.70	17.30	0.11	0.08	
10m-5	10.30	374	53.50	4.97	21.80	5.88	5.76	0.93	36.31	63.69	9.80	3.04	28.00	18.00	0.14	0.06	
10m-6	10.50	423	55.30	2.69	26.40	5.67	4.97	0.60	35.66	64.34	10.73	3.49	29.00	18.40	0.09	0.07	
11m-1	11.70	431	54.60	5.65	24.90	3.22	5.68	0.54	38.39	61.61	15.30	4.80	26.50	20.00	0.14	0.09	

11m-3	11.70	409	56.20	6.56	16.50	8.82	5.42	1.18	33.23	66.77	10.50	3.69	31.50	17.90	0.16	0.07
11m-4	11.20	410	53.50	3.68	25.90	4.39	4.78	0.47	38.61	61.39	15.34	4.45	24.60	18.70	0.11	0.09
11m-5	11.20	412	49.50	3.27	27.60	6.21	5.51	0.53	38.40	61.60	11.81	3.40	25.40	18.30	0.11	0.07
11m-6	11.50	430	58.80	3.46	27.40	5.47	1.85	0.36	35.67	64.33	12.77	4.59	31.30	20.30	0.06	0.08
12m-1	12.50	430	59.30	2.49	27.00	2.68	4.65	0.57	36.52	63.48	14.87	5.29	30.40	21.00	0.09	0.09
12m-2	12.50	407	44.80	6.01	30.30	5.04	6.74	1.13	39.57	60.43	16.84	4.31	21.20	17.10	0.17	0.10
12m-3	12.70	429	48.60	3.65	28.10	8.14	5.30	0.84	36.07	63.93	12.42	3.65	25.70	16.90	0.12	0.08
12m-4	12.10	422	59.50	3.54	23.90	4.29	4.93	0.56	31.97	68.03	12.68	4.81	33.00	18.10	0.10	0.09
12m-5	12.20	443	57.70	3.26	24.10	4.31	5.23	0.56	39.16	60.84	12.97	4.26	28.60	21.60	0.11	0.08
12m-6	12.50	390	51.00	4.11	26.70	4.42	7.68	0.64	36.01	63.99	12.99	3.93	26.30	17.40	0.15	0.08
13m-1	13.30	373	49.60	4.35	22.40	7.95	7.72	1.07	36.52	63.48	15.21	4.28	23.90	16.70	0.16	0.10
13m-2	13.60	414	53.50	4.36	29.20	2.30	5.77	0.87	36.47	63.53	16.03	5.08	26.60	18.70	0.13	0.10
13m-3	13.70	415	53.00	3.32	23.90	7.34	6.64	0.90	38.09	61.91	13.79	4.10	25.60	18.80	0.13	0.09
13m-4	13.30	413	55.20	5.75	18.30	7.00	6.14	0.76	39.49	60.51	12.26	3.64	26.10	19.80	0.16	0.07
13m-5	13.30	417	58.90	3.60	25.00	3.32	4.73	0.41	35.83	64.17	10.12	3.31	29.40	18.60	0.10	0.06
13m-6	13.50	406	52.00	4.35	27.70	4.94	5.23	0.52	35.36	64.64	8.63	2.72	28.80	17.50	0.12	0.06
14m-1	14.50	389	51.70	2.78	26.00	6.38	6.59	1.25	36.81	63.19	15.49	4.67	25.50	18.00	0.13	0.10
14m-2	14.50	436	46.40	2.86	33.90	3.61	7.71	0.63	39.47	60.53	19.92	5.12	20.60	17.40	0.13	0.12
14m-3	14.70	420	46.70	7.35	12.90	14.60	8.82	1.94	33.26	66.74	13.55	3.82	24.40	14.50	0.24	0.09
14m-4	14.20	456	42.70	6.06	29.10	4.69	8.15	1.49	34.57	65.43	13.09	3.25	21.60	13.50	0.21	0.09
14m-5	14.30	426	43.00	5.73	22.50	8.12	9.78	0.98	36.62	63.38	16.99	4.09	20.00	14.30	0.22	0.11
14m-6	14.50	450	38.30	8.59	12.80	15.70	14.10	1.36	38.09	61.91	16.77	3.51	17.50	13.30	0.36	0.10
15m-1	15.30	401	45.80	4.45	29.90	4.69	8.57	1.06	35.61	64.39	18.14	4.95	22.30	15.50	0.18	0.12
15m-2	15.60	430	47.90	3.01	31.70	4.58	7.56	0.70	35.13	64.87	17.75	5.16	23.90	16.30	0.13	0.12
15m-3	15.70	438	48.00	3.79	31.40	3.92	5.91	1.12	40.10	59.90	16.70	4.49	22.50	18.50	0.13	0.10
15m-4	15.20	436	53.90	3.93	21.10	5.24	7.29	0.85	38.12	61.88	16.02	4.80	25.30	19.00	0.15	0.10
15m-5	15.50	418	46.50	7.83	18.30	7.58	10.10	0.73	35.37	64.63	18.14	4.93	22.30	15.40	0.26	0.12
15m-6	15.50	421	46.30	6.34	22.90	7.52	8.21	0.97	39.67	60.33	20.74	5.40	20.70	17.70	0.20	0.13
16m-1	16.30	436	43.90	3.93	33.40	4.78	7.43	1.02	34.71	65.29	20.37	5.34	20.80	14.40	0.15	0.13
16m-2	16.50	388	51.20	4.73	19.30	5.89	5.97	4.20	35.51	64.49	15.72	4.88	26.20	17.60	0.20	0.10
16m-3	16.70	448	49.80	3.44	27.30	5.30	7.35	0.81	36.19	63.81	17.57	5.21	24.40	17.20	0.14	0.11
16m-4	16.20	434	55.00	4.01	22.10	3.67	7.86	1.10	34.24	65.76	16.15	5.23	27.20	17.40	0.16	0.11
16m-5	16.30	431	54.70	4.10	20.10	5.19	7.86	1.12	32.98	67.02	18.00	6.00	27.30	16.90	0.16	0.12
17m-1	17.50	452	52.30	4.98	21.90	5.89	6.18	1.70	37.31	62.69	19.65	5.86	23.90	18.30	0.16	0.12
17m-2	17.60	414	47.50	6.37	19.60	6.96	8.97	2.44	34.67	65.33	17.75	5.06	23.50	15.60	0.24	0.12
17m-3	17.60	453	52.00	5.79	11.00	10.90	10.90	1.26	32.46	67.54	14.49	4.75	27.90	16.10	0.24	0.10
17m-4	17.30	441	56.40	7.17	15.10	4.90	7.45	0.86	35.10	64.90	19.50	6.00	24.80	17.20	0.20	0.13
17m-5	17.30	452	49.20	6.89	17.20	6.56	8.92	1.88	38.03	61.97	20.37	5.41	21.20	16.90	0.24	0.13
17m-6	17.50	447	47.80	4.82	15.50	13.60	9.57	0.82	35.75	64.25	19.67	5.32	21.70	15.60	0.20	0.13
18m-1	18.30	399	38.30	8.37	21.20	8.70	15.00	0.96	29.06	70.94	18.03	4.47	20.30	10.50	0.36	0.13
18m-2	18.60	474	51.80	6.09	18.40	6.07	8.53	1.76	36.86	63.14	19.44	5.86	24.30	18.30	0.21	0.12
18m-4	18.20	418	46.80	6.00	23.80	6.07	8.46	0.65	40.04	59.96	16.26	4.13	21.20	17.40	0.20	0.10
18m-5	18.30	418	48.80	6.64	26.10	4.61	6.35	0.83	36.67	63.33	18.16	4.67	21.00	15.40	0.17	0.12
18m-6	18.60	413	52.00	3.41	31.00	4.76	4.49	0.61	35.67	64.33	16.77	5.13	25.50	17.50	0.10	0.11
19m-1	19.30	367	52.80	7.12	18.40	4.17	7.48	1.59	34.79	65.21	19.40	6.00	25.00	17.20	0.21	0.13
19m-2	19.50	409	43.30	5.04	12.90	18.00	11.80	1.57	41.46	58.54	16.60	3.65	18.30	16.20	0.25	0.10
19m-3	19.60	456	51.50	4.29	5.56	13.70	13.50	0.80	28.50	71.50	17.05	5.73	27.90	13.80	0.26	0.12
19m-4	19.20	440	50.50	4.23	18.40	8.47	8.46	1.08	34.87	65.13	21.38	6.18	22.70	16.00	0.18	0.14
19m-5	19.50	409	49.90	7.73	8.09	12.20	10.60	1.26	32.92	67.08	18.53	5.33	23.50	14.70	0.28	0.12
19m-6	19.50	413	44.60	7.08	21.00	4.90	11.50	1.49	31.93	68.07	18.58	5.20	22.70	13.50	0.28	0.13
20m-1	20.30	431	45.70	9.72	11.60	4.38	14.10	3.26	36.25	63.75	14.93	3.92	22.30	15.40	0.44	0.10
20m-2	20.60	375	49.20	4.87	9.66	13.50	13.50	2.47	30.04	69.96	18.61	5.90	25.80	14.10	0.29	0.13

20m-4	20.20	424	57.50	3.92	18.00	3.74	6.93	2.11	30.56	69.44	12.11	4.48	32.50	16.70	0.16	0.08
20m-5	20.30	491	61.60	7.35	8.49	4.91	7.78	1.51	33.21	66.79	15.21	5.12	28.60	17.20	0.22	0.10
20m-6	20.60	472	44.20	7.80	10.50	9.92	13.10	1.85	35.52	64.48	15.05	3.73	21.10	14.10	0.35	0.10
21m-1	21.30	398	55.00	7.46	9.25	4.44	9.99	2.08	34.95	65.05	18.90	5.93	25.50	17.50	0.28	0.12
21m-2	21.60	407	59.30	3.69	17.00	3.65	7.94	1.43	36.50	63.50	21.45	7.32	26.80	20.30	0.16	0.14
21m-3	21.60	405	71.50	4.90	11.30	3.73	3.28	1.32	29.63	70.37	16.49	7.53	38.10	19.80	0.11	0.12
21m-4	21.30	411	55.50	7.32	7.76	7.30	11.00	1.45	31.38	68.62	22.10	6.66	23.40	14.30	0.28	0.15
21m-5	21.50	418	52.20	7.68	12.40	7.93	10.00	1.28	28.25	71.75	22.30	7.21	25.00	13.10	0.26	0.16
21m-6	21.50	427	55.10	7.91	5.15	8.08	12.80	2.04	28.71	71.29	13.46	4.31	27.70	13.20	0.33	0.10
22m-1	22.60	374	53.40	7.40	9.08	6.70	9.82	3.13	31.73	68.27	19.50	6.57	27.10	16.20	0.29	0.13
22m-2	22.60	414	39.20	6.28	9.75	20.80	14.50	1.78	34.99	65.01	21.44	4.83	17.70	12.70	0.32	0.14
22m-3	22.60	410	48.90	5.94	12.40	5.58	14.00	2.65	31.07	68.93	15.50	4.83	26.40	14.50	0.34	0.11
22m-4	22.20	406	49.90	9.41	8.84	7.33	11.40	1.81	33.48	66.52	18.67	5.35	23.20	14.90	0.34	0.12
22m-5	22.30	392	48.70	4.24	16.70	11.80	9.15	1.25	31.73	68.27	18.84	5.52	23.80	14.10	0.19	0.13
22m-6	22.60	451	37.50	8.37	9.82	14.30	22.30	1.28	39.77	60.23	15.42	2.85	15.70	12.80	0.52	0.09
23m-1	23.50	458	49.60	6.53	7.53	12.40	12.00	2.08	27.19	72.81	16.41	5.37	27.30	12.60	0.30	0.12
23m-2	23.50	397	66.10	5.71	8.36	3.74	6.75	2.36	24.39	75.61	13.23	6.10	39.90	15.20	0.19	0.10
23m-3	23.60	388	54.70	4.39	9.70	7.22	14.10	1.94	27.98	72.02	17.62	6.29	29.50	14.40	0.29	0.13
23m-4	23.30	413	42.10	5.87	11.90	11.60	14.40	1.09	33.68	66.32	24.10	5.58	17.60	12.20	0.33	0.16
23m-5	23.30	407	57.20	4.94	12.80	4.72	10.20	1.20	33.80	66.20	18.01	6.06	27.60	17.80	0.22	0.12
24m-1	24.20	402	29.40	8.76	2.82	2.04	21.40	7.36	41.80	58.20	14.65	2.14	12.50	11.10	1.10	0.09
24m-2	24.50	326	27.40	0.35	38.80	27.60	7.02	0.22	33.48	66.52	11.02	1.82	14.80	8.60	0.08	0.07
24m-3	24.60	420	54.10	10.20	10.40	1.71	13.20	1.52	31.72	68.28	17.01	5.75	28.00	16.30	0.38	0.12
24m-4	23.50	409	53.50	7.82	5.47	9.46	12.50	1.22	26.83	73.17	17.15	5.92	28.70	13.10	0.31	0.13
24m-5	23.60	424	45.20	8.15	6.14	3.43	22.20	1.32	30.14	69.86	16.95	4.32	21.20	11.50	0.58	0.12
24m-6	23.80	390	52.40	7.32	11.30	7.49	12.00	0.73	31.57	68.43	15.76	4.97	26.60	15.00	0.28	0.11
25m-1	25.20	460	46.70	7.55	7.75	8.70	14.70	1.17	25.32	74.68	18.67	5.93	25.80	11.20	0.37	0.14
25m-2	25.30	428	55.60	3.49	8.82	8.20	12.60	2.63	30.99	69.01	17.36	5.56	26.50	15.00	0.26	0.12
25m-3	25.50	404	51.40	12.10	2.77	14.30	10.50	1.44	17.22	82.78	18.21	7.07	31.70	8.49	0.35	0.15
25m-4	25.30	402	46.20	9.00	7.11	8.81	14.60	2.99	24.11	75.89	30.20	9.73	22.50	10.60	0.43	0.23
25m-5	25.30	356	4.64	11.50	0.05	62.70	5.45	2.67	38.12	61.88	27.91	0.35	0.91	0.83	0.29	0.17
25m-6	25.50	402	47.40	5.46	10.20	8.39	17.00	2.63	25.81	74.19	22.18	7.19	25.30	11.70	0.38	0.16
26m-1	26.30	420	43.50	8.07	3.33	19.50	16.50	1.20	52.64	47.36	14.48	2.39	14.10	19.10	0.39	0.07
26m-2	26.30	405	18.30	11.40	3.05	7.99	36.80	2.61	35.85	64.15	27.06	2.24	6.04	4.95	1.73	0.17
26m-3	26.50	399	37.40	9.82	13.70	8.01	14.00	3.95	32.00	68.00	21.52	4.66	17.00	10.80	0.47	0.15
26m-4	26.20	378	38.20	10.00	10.00	9.71	18.40	2.78	32.63	67.37	21.45	5.00	18.30	11.90	0.54	0.14
26m-5	26.50	424	44.00	7.75	10.30	14.30	10.30	2.05	26.50	73.50	19.83	5.88	23.70	11.10	0.29	0.15
26m-6	26.50	336	8.04	5.97	0.80	77.50	4.46	0.33	31.89	68.11	18.61	0.80	3.48	2.07	0.12	0.13
27m-1	27.20	427	43.90	8.88	19.10	2.61	12.10	2.80	26.23	73.77	14.18	4.03	24.30	10.50	0.36	0.10
27m-2	27.30	437	48.20	7.01	8.73	4.57	16.00	3.18	30.78	69.22	11.51	3.10	23.70	12.40	0.43	0.08
27m-3	27.50	434	37.90	13.30	0.47	19.50	25.20	0.69	9.85	90.15	66.05	19.70	10.10	3.54	0.68	0.60
27m-5	27.00	393	53.90	7.62	8.70	3.81	9.91	1.33	24.20	75.80	10.99	3.95	32.00	11.80	0.28	0.08
27m-6	27.00	372	37.40	11.90	8.44	4.93	20.40	2.17	31.58	68.42	20.27	4.61	18.20	11.00	0.68	0.14

Suppl. Table 3. List of differentially methylated regions (DMRs) that are located <20kb from a transcription start site (TSS)							
Young to middle aged							
Hyper methylated				Hypo methylated			
Chromosome	Start	End	Gene symbol	Chromosome	Start	End	Gene symbol
chr17	76529000	76529200	CAMK1D	chr4	169107000	169107200	PBP2
chr3	23018200	23018400	NR5A1	chr19	52751200	52751400	ZDHHC7
chr3	47689000	47689200	TBR1	chr3	175824000	175824200	SLCO4A1
chr12	38843800	38844000	HPD	chr15	48465400	48465600	EXTL3
chr1	100360800	100361000	RGD1309036	chr3	3944200	3944400	NOTCH1
chr1	264895800	264896000	TLX1	chr8	128734800	128735000	CX3CR1
chr7	130041600	130041800	PANX2	chrX	155845200	155845400	DKC1
chr3	121660600	121660800	CHCHD5	chr4	120665600	120665800	MGLL
chr15	41691600	41691800	EBPL	chr6	99411200	99411400	ZBTB1
chr6	94834200	94834400	L3HYPDH	chr7	123160000	123160200	POLR3H
chr13	52978200	52978400	KIF21B	chr1	82579400	82579600	AXL
chr16	19223000	19223200	KLF2	chr13	82487200	82487400	F5
chr3	141405800	141406000	NKX2-2	chr19	55387600	55387800	APRT
chr8	33820200	33820400	ETS1	chr1	59784200	59784400	FPR1
chr15	28404600	28404800	ZFP219	chr15	4568400	4568600	KCNK5
chr20	13971200	13971400	SUSD2	chr7	131334400	131334600	ALG10
chr8	23061800	23062000	ELAVL3	chr7	3320200	3320400	GDF11
chr10	61697800	61698000	MNT	chr8	13242600	13242800	PIWIL4
chr1	198214000	198214200	TBX6	chr12	18527600	18527800	ASMT
chr1	170410400	170410600	APBB1	chr10	4951600	4951800	PRM3
chr10	56412000	56412200	FGF11	chr10	18955200	18955400	KCNIP1
chr3	15772000	15772200	OLR397	chr11	64952600	64952800	POPDC2
chr19	58519800	58520000	MAP10	chr5	151792600	151792800	GPN2
chr5	147776200	147776400	LCK	chr15	34452200	34452400	LTB4R

chr17	13823000	13823200	S1PR3	chr5	61385200	61385400	ALDH1B1
chr5	159436000	159436200	PADI2	chr16	36094000	36094200	HMGB2
chr1	143277600	143277800	CPEB1	chr20	31987200	31987400	HK1
chr1	216683000	216683200	SLC22A18	chr8	22758000	22758200	LDLR
chr6	75074400	75074600	EGLN3	chr12	41517200	41517400	TPCN1
chrX	156226200	156226400	OLR1768	chr3	15574400	15574600	PTGS1
chr6	53404600	53404800	TWIST1	chr12	14260600	14260800	FOXK1
chr12	21832200	21832400	CLDN3	chr10	109089800	109090000	CHMP6
chr3	160854200	160854400	MATN4	chr10	88620800	88621000	HSPB9
chr7	141053000	141053200	TMBIM6	chr8	57971600	57971800	POGLUT3
chr10	87081200	87081400	CCR7	chr10	59567600	59567800	P2RX1
chr1	277352200	277352400	DCLRE1A	chr6	137668400	137668600	GPR132
chr7	144629800	144630000	MIR615	chr12	25166800	25167000	ERVFRD-1
chr3	15429800	15430000	LHX6	chr20	5087400	5087600	ABHD16A
chr1	216648000	216648200	CDKN1C	chr16	69025400	69025600	GOT1L1
chr4	157406400	157406600	CD4	chr5	57410800	57411000	AQP3
chr7	121798000	121798200	GRAP2	chr2	200205600	200205800	NOTCH2
chr8	14373400	14373600	MTNR1B	chr20	27164400	27164600	HNRNPH3
chr18	79336800	79337000	MBP	chr3	11114600	11114800	PLPP7
chr11	32858400	32858600	RUNX1	chr10	82296200	82296400	CHAD
chr20	7672200	7672400	TCP11	chr1	252456200	252456400	ANKRD22
chr6	69972600	69972800	FOXG1	chr12	21840000	21840200	CLDN3
chr14	91797800	91798000	IKZF1	chr9	98182600	98182800	LRRFIP1
chr8	120433200	120433400	ARPP21	chr1	141672000	141672200	ARPIN
chr8	63090800	63091000	LOXL1	chr4	168131400	168131600	BCL2L14
chr13	83919200	83919400	RCSD1	chr12	39014600	39014800	KDM2B
chr1	23238800	23239000	EYA4	chr6	137375200	137375400	CLBA1
chr3	61597600	61597800	HOXD12	chr13	89830600	89830800	F11R

chr14	45349600	45349800	MIR328B	chr1	163458600	163458800	LRRC32
chr10	64543000	64543200	NXN	chr16	69248400	69248600	ZFP703
chr4	115440600	115440800	TEX261	chr10	64969400	64969600	PIPOX
chr13	47614400	47614600	IL24	chr6	129600200	129600400	PAPOLA
chr7	128500000	128500200	TAF5A	chr19	52485600	52485800	COTL1
chr10	56576000	56576200	CLDN7	chr15	33356800	33357000	CEBPE
chr18	30896400	30896600	PCDHGA10	chr9	81451400	81451600	CXCR1
chr16	79708000	79708200	KBTBD11	chr2	189880000	189880200	SNAPIN
chr10	107265200	107265400	CYTH1	chr10	56429800	56430000	SPEM1
chr16	21294800	21295000	CILP2	chr7	13042000	13042200	MIER2
chr16	67047800	67048000	UNC5D	chr6	10532000	10532200	RHOQ
chr5	133712400	133712600	FOXE3	chr5	135994800	135995000	PLK3
chr20	4394000	4394200	PRRT1	chr9	16667800	16668000	PTK7
chr12	41663200	41663400	LHX5	chr19	58825200	58825400	KCNK1
chr10	18443800	18444000	RANBP17	chr2	200205400	200205600	NOTCH2
chr5	133712600	133712800	FOXE3	chr20	4610600	4610800	NEU1
chr1	166601600	166601800	MIR139	chr19	43616600	43616800	FA2H
chr19	10099800	10100000	MMP15	chr8	55270400	55270600	PPP2R1B
chr3	145032000	145032200	SYNDIG1	chr10	84153400	84153600	HOXB5
chr15	47292600	47292800	SOX7	chr10	103735600	103735800	NAT9
chr17	78771800	78772000	SUV39H2	chr2	196293600	196293800	TMOD4
chr6	69972000	69972200	FOXG1	chr1	263796000	263796200	CYP2C23
chr19	10310000	10310200	KIFC3	chr10	103480200	103480400	CD300LB
chr12	13362400	13362600	ZFP316	chr18	76749200	76749400	HSBP1L1
chr13	52978000	52978200	KIF21B	chr6	9769600	9769800	RGD1562146
chr13	90949600	90949800	VSIG8	chr5	167117400	167117600	GPR157
chr20	37587800	37588000	MSL3L2	chr3	6227400	6227600	RXRA
chr19	25899200	25899400	NF1X	chr9	10770800	10771000	ARRDC5

chr20	7882000	7882200	FANCE	chr2	207441600	207441800	WNT2B
chr10	39655600	39655800	ACSL6	chr19	48183600	48183800	MAF
chr8	95388800	95389000	TBX18	chr6	51270800	51271000	HBP1
chr1	53051800	53052000	MPC1	chr13	110090800	110091000	PPP2R5A
chr19	44124600	44124800	CHST5	chr17	16403400	16403600	MIRLET7A1
chr6	89292800	89293000	MDGA2	chr3	11114800	11115000	PLPP7
chrX	156226400	156226600	OLR1768	chr13	50175800	50176000	LAX1
chr2	40655200	40655400	PDE4D	chr10	5295200	5295400	TVP23A
chr5	147776400	147776600	LCK	chr1	164648800	164649000	SLCO2B1
chr3	141406000	141406200	NKX2-2	chr5	143109000	143109200	ZC3H12A
chr9	12734400	12734600	RFTN1	chr4	120125600	120125800	GATA2
chr18	61639200	61639400	RAX	chr5	161878200	161878400	PRDM2
chr3	2802400	2802600	PHPT1	chr3	160948600	160948800	PIGT
chr19	19403800	19404000	SNX20	chr9	18652000	18652200	RUNX2
chr3	43116000	43116200	NR4A2	chr20	31333600	31333800	AIFM2
chr5	58163400	58163600	CCL27	chr10	61994000	61994200	HIC1
chr1	261670200	261670400	CRTAC1	chr14	23496800	23497000	UBA6
chr1	164426200	164426400	RPS3	chr7	41301800	41302000	GALNT4
chr2	189855200	189855400	NPR1	chr3	164041600	164041800	B4GALT5
chr4	83970000	83970200	TRIL	chr3	29990400	29990600	ZEB2OS
chr7	61797000	61797200	DYRK2	chr12	6876800	6877000	ALOX5AP
chr14	83754600	83754800	SELENOM	chr13	110091800	110092000	PPP2R5A
chr1	78053600	78053800	MEIS3	chr18	28668800	28669000	CXXC5
chr10	86687000	86687200	NR1D1	chr16	6958400	6958600	MUSTN1
chr17	88216000	88216200	GPR158	chr13	109978800	109979000	NENF
chr14	84246000	84246200	GAL3ST1	chr19	14351800	14352000	HMGXB4
chr10	82419400	82419600	XYLT2	chr3	164238000	164238200	SPATA2
chr4	169096200	169096400	PBP2	chr1	89269600	89269800	FFAR2

chr8	108108600	108108800	SOX14	chr14	36688600	36688800	USP46
chr10	85555800	85556000	EPOP	chr15	33357200	33357400	CEBPE
chr6	132950400	132950600	BEGAIN	chr20	7204600	7204800	NUDT3
chr7	31876800	31877000	TMPO	chr10	45521000	45521200	IBA57
chr3	159322400	159322600	SRSF6	chr9	17798600	17798800	SLC29A1
chr1	216661800	216662000	CDKN1C	chr4	15519400	15519600	HGF
chr1	65532000	65532200	UBE2M	chr5	76183200	76183400	GNG10
chr1	78592400	78592600	ARHGAP35	chr8	22204000	22204200	PDE4A
chr16	21295200	21295400	CILP2	chr5	117879000	117879200	ATG4C
chr3	145032200	145032400	SYNDIG1	chr7	139273800	139274000	SLC48A1
chr2	145173200	145173400	MAB21L1	chr1	89365800	89366000	HAMP
chr14	78312400	78312600	CRMP1	chr7	12581800	12582000	WDR18
chr1	209636400	209636600	EBF3	chr8	54927800	54928000	PLET1
chr18	30820400	30820600	PCDHGA3	chr8	36299600	36299800	ST3GAL4
chr8	71166800	71167000	RBPM52	chr7	34325400	34325600	HAL
chr7	11302800	11303000	TJP3	chr19	37290400	37290600	TMEM208
chr20	10273600	10273800	NDUFV3	chr3	9805000	9805200	TOR1A
chr12	13363000	13363200	ZFP316	chr1	221300800	221301000	CDC42EP2
chr20	8395600	8395800	CCDC167	chr12	40500000	40500200	MAPKAPK5
chr10	91175000	91175200	PLCD3	chr20	18498600	18498800	CISD1
chr6	104072000	104072200	GALNT16	chr4	85196000	85196200	GGCT
chr6	146786800	146787000	SP8	chr1	12827000	12827200	CITED2
chr5	57899200	57899400	MYORG	chr15	4488600	4488800	KCNK16
chr1	196866000	196866200	NSMCE1	chr12	16116800	16117000	LFNG
chr4	142453000	142453200	GRM7	chr20	5529200	5529400	PHF1
chr2	186875000	186875200	ETV3	chr10	93519200	93519400	MRC2
chr20	4389600	4389800	PPT2	chr6	9769800	9770000	RGD1562146
chr7	144626400	144626600	HOXC5	chr12	9858600	9858800	GTF3A

chr11	32858200	32858400	RUNX1	chr17	15761600	15761800	FGD3
chr20	14185800	14186000	UPB1	chr10	103201200	103201400	RPL38
chr19	25134600	25134800	MISP3	chr20	10037200	10037400	SLC37A1
chr7	117354200	117354400	SMPD5	chr19	52356800	52357000	ATP2C2
chr3	124144200	124144400	ADRA1D	chr5	159388000	159388200	PADI1
chr5	169189400	169189600	KLHL21	chr9	98460200	98460400	ESPNL
chr18	28444400	28444600	MZB1	chr15	51212000	51212200	ENTPD4
chr3	43115800	43116000	NR4A2	chr10	106966800	106967000	SOCS3
chr1	78053400	78053600	MEIS3	chr3	164655200	164655400	PTPN1
chr7	57662600	57662800	TRHDE	chr5	48306800	48307000	GABRR2
chr5	155398000	155398200	ZBTB40	chr16	54319000	54319200	MTUS1
chr3	165040400	165040600	KCNG1	chr16	36093800	36094000	HMGB2
chr10	103891800	103892000	OTOP3	chr6	110999600	110999800	ZDHHC22
chr19	6031800	6032000	CDH8	chr7	130052800	130053000	TRABD
chr13	88995400	88995600	OLFML2B	chr7	12561400	12561600	WDR18
chr12	13362800	13363000	ZFP316	chr13	90977400	90977600	SLAMF8
chr8	62919600	62919800	STRA6	chr3	4022400	4022600	EGFL7
chr20	6927000	6927200	PI16	chr11	71216800	71217000	MUC20
chr3	14482200	14482400	GSN	chr7	11078800	11079000	S1PR4
chr19	58550800	58551000	NTPCR	chr11	82732400	82732600	TMEM41A
chr7	10991400	10991600	TLE2	chr7	130297200	130297400	ADM2
chr1	150797000	150797200	NOX4	chr8	23469200	23469400	RP9
chr4	58250000	58250200	KLF14	chr20	4563800	4564000	C2
chr5	169305200	169305400	TNFRSF25	chr7	25911000	25911200	RIC8B
chr5	63785600	63785800	NR4A3	chr8	128631800	128632000	GORASP1
chr3	121660400	121660600	CHCHD5	chr11	79722000	79722200	LPP
chr7	31876600	31876800	TMPO	chr10	67518400	67518600	RNF135
chr6	124902800	124903000	GPR68	chr5	57411000	57411200	AQP3

chr10	105775000	105775200	JMJD6	chr6	43888600	43888800	RRM2
chr5	149056600	149056800	LAPTM5	chr1	252456400	252456600	ANKRD22
chr7	121800600	121800800	GRAP2	chr19	52034400	52034600	MLYCD
chr10	86305400	86305600	PPP1R1B	chr15	34531000	34531200	CBLN3
chr5	153502600	153502800	RUNX3	chr1	266410000	266410200	CYP17A1
chr3	160558600	160558800	KCNS1	chr7	120982200	120982400	DNAL4
chr10	13077000	13077200	PAQR4	chr16	20396600	20396800	MAST3
chr20	3989200	3989400	PSMB8	chr10	103739200	103739400	TMEM104
chr12	14092600	14092800	RADIL	chr13	52107000	52107200	RNPEP
chr10	12879400	12879600	ZFP213	chr1	86987600	86987800	HNRNPL
chr8	71167000	71167200	RBPM52	chr15	51500600	51500800	RHOBTB2
chr1	112946800	112947000	GABRA5	chr6	111113400	111113600	NGB
chr10	85955800	85956000	ARL5C	chr3	147964600	147964800	DEFB22
chr4	113752000	113752200	SEMA4F	chr7	60759800	60760000	MDM2
chr5	119903200	119903400	RAVER2	chr7	121095800	121096000	APOBEC3
chr19	49171800	49172000	CDYL2	chr5	152349000	152349200	SH3BGRL3
chr11	64935800	64936000	POPDC2	chr3	80843200	80843400	MDK
chr3	82544200	82544400	ALX4	chr17	68560400	68560600	PFKP
chr17	44766800	44767000	HIST1H1B	chr1	47163000	47163200	TMEM181
chr12	49348600	49348800	SGSM1	chr2	140707200	140707400	MGST2
chr18	30896600	30896800	PCDHGA10	chr12	46809400	46809600	RPLP0
chr1	80664800	80665000	NECTIN2	chr5	76187800	76188000	GNG10
chr9	15495000	15495200	TAF8	chr3	175823800	175824000	SLCO4A1
chr1	23907200	23907400	TCF21	chr15	33357000	33357200	CEBPE
chr10	56576200	56576400	CLDN7	chr19	19404000	19404200	SNX20
chr10	86490600	86490800	IKZF3	chr10	106296800	106297000	Sept9
chr1	216661600	216661800	CDKN1C	chr1	91283800	91284000	CEBPG
chr3	14482400	14482600	GSN	chr7	141503600	141503800	LIMA1

chr1	80253000	80253200	ERCC1	chr12	38124200	38124400	DENR
chr16	79698600	79698800	KBTBD11	chr2	196293400	196293600	TMOD4
chr3	95150400	95150600	WT1	chr14	17275000	17275200	NAAA
chr12	51249400	51249600	MN1	chr6	132620800	132621000	DEGS2
chr5	164942200	164942400	MAD2L2	chr3	9806400	9806600	TOR1A
chr4	114859000	114859200	LOC500227	chr9	113590800	113591000	RALBP1
chr12	22189200	22189400	TFR2	chr11	31237800	31238000	RGD1562726
chr19	55520800	55521000	CBFA2T3	chr5	138155800	138156000	SLC2A1
chr10	86490800	86491000	IKZF3	chr15	61687400	61687600	KBTBD7
chr9	100135200	100135400	GPR35	chr5	169526000	169526200	CHD5
chr20	4852600	4852800	LTA	chr5	148257600	148257800	COL16A1
chr1	87256800	87257000	DPF1	chr2	188523800	188524000	MTX1
chr10	12879600	12879800	ZFP213	chr3	22838200	22838400	NEK6
chr13	102774000	102774200	RGD1310587	chr1	185149600	185149800	NUCB2
chr10	82419200	82419400	XYLT2	chr13	50994000	50994200	CHIT1
chr2	210365000	210365200	ALX3	chr20	7771800	7772000	ZFP523
chr10	90154200	90154400	HDAC5	chr10	106298000	106298200	9-Sep
chr19	25899400	25899600	NF1X	chr17	78911600	78911800	ACBD7
chr4	182745400	182745600	RPS4Y2	chr10	92652400	92652600	ITGB3
chr3	159322200	159322400	SRSF6	chr8	122594600	122594800	TRIM71
chr1	81365200	81365400	CADM4	chr1	226245400	226245600	FEN1
chr3	164275200	164275400	SNAI1	chr3	111547400	111547600	ITPKA
chr8	120446200	120446400	ARPP21	chr2	220536400	220536600	PALMD
chr5	62164800	62165000	TRIM14	chr7	36647800	36648000	NUDT4
chr7	130050200	130050400	PANX2	chr9	113509600	113509800	RAB31
chr5	58394000	58394200	DNAJB5	chr14	105997400	105997600	PELI1
chr1	221684400	221684600	CDC42BPG	chr3	165742800	165743000	ZFP64
chr1	169409800	169410000	TRIM6	chr3	79909000	79909200	SPI1

chr4	127809000	127809200	SUCLG2	chr15	35109600	35109800	CTSG
chr9	98085000	98085200	MLPH	chr12	48384800	48385000	DAO
chr1	15299600	15299800	SLC35D3	chr1	225186000	225186200	AHNAK
chr2	140445600	140445800	MGARP	chr7	107710400	107710600	CCN4
chr7	140308400	140308600	CACNB3	chr20	3549400	3549600	DDR1
chr12	49339400	49339600	SGSM1	chr20	11396200	11396400	PFKL
chr3	160853200	160853400	MATN4	chr1	239072800	239073000	GDA
chr10	106974800	106975000	SOCS3	chr3	159580600	159580800	TOX2
chr7	11181000	11181200	DOHH	chr8	127709600	127709800	MIR26A
chr10	106975600	106975800	SOCS3	chr7	2901000	2901200	MYL6L
chr10	91431400	91431600	ARHGAP27	chr7	117262200	117262400	PLEC
chr5	140889400	140889600	NT5C1A	chr14	85397800	85398000	EMID1
chr8	119566400	119566600	TRANK1	chr2	196310200	196310400	LYSMD1
chr8	116058400	116058600	CISH	chr13	35538000	35538200	RALB
chrX	156228200	156228400	OLR1768	chr1	79912400	79912600	IRF2BP1
chr10	86283800	86284000	NEUROD2	chr19	10642600	10642800	CX3CL1
chr8	117250200	117250400	CCDC71	chr3	11679600	11679800	ENG
chr16	19914400	19914600	PLVAP	chr4	100259400	100259600	VAMP8
chr4	113752200	113752400	SEMA4F	chr12	24457200	24457400	FZD9
chr1	216648200	216648400	CDKN1C	chr2	27355800	27356000	POLK
chr16	21295000	21295200	CILP2	chr10	29073400	29073600	C1QTNF2
chr10	88497800	88498000	CNP	chr17	16223000	16223200	PHF2
chr1	247476800	247477000	INSL6	chr17	9836200	9836400	RAB24
chr1	32639400	32639600	IRX4	chr10	85761000	85761200	LASP1
chr5	164970600	164970800	FBXO44	chr5	74942400	74942600	AKAP2
chr14	107607600	107607800	B3GNT2	chr8	130019600	130019800	TRAK1
chr12	28381000	28381200	GALNT17	chr11	33836000	33836200	CBR1
chr18	30896000	30896200	PCDHGA10	chr7	137157000	137157200	ANO6

chr19	6032000	6032200	CDH8	chr6	124436800	124437000	TTC7B
chr11	32857200	32857400	RUNX1	chr6	124801400	124801600	DGLUCY
chr3	165021400	165021600	KCNG1	chr9	46192800	46193000	TBC1D8
chr1	177495600	177495800	TEAD1	chr10	67863400	67863600	CDK5R1
chr10	90551000	90551200	FZD2	chr13	50440000	50440200	SOX13
chr9	43337400	43337600	ZAP70	chr14	5102600	5102800	LRRC8D
chr5	166514200	166514400	CLSTN1	chr19	55110000	55110200	ZFPM1
chr1	203971400	203971600	GPR26	chr3	162866000	162866200	SULF2
chr20	14283200	14283400	ADORA2A	chr13	26173600	26173800	PHLPP1
chr14	104209200	104209400	SPRED2	chr1	91373600	91373800	CEBPA
chr1	80378400	80378600	MARK4	chr2	187228200	187228400	SH2D2A
chr1	80253200	80253400	ERCC1	chr20	10019200	10019400	RSPH1
chr16	21294400	21294600	CILP2	chr17	13509200	13509400	SEMA4D
chr6	132239800	132240000	CYP46A1	chr12	15909600	15909800	GNA12
chr10	106221400	106221600	Sept9	chr1	8897200	8897400	GJE1
chr12	13362000	13362200	ZFP316	chr5	141008000	141008200	OXCT2A
chr6	25620800	25621000	FOSL2	chr8	45358200	45358400	UBASH3B
chr1	247476600	247476800	INSL6	chr4	80357600	80357800	LOC500124
chr3	9630600	9630800	RGD1311084	chr19	58825400	58825600	KCNK1
chr18	30881600	30881800	PCDHGA9	chr7	11441000	11441200	ZBTB7A
chr19	52105800	52106000	NECAB2	chr11	68201000	68201200	SLC49A4
chr4	99205800	99206000	CD8B	chr4	153390600	153390800	BCL2L13
chr7	117146600	117146800	NRBP2	chr1	261975400	261975600	PYROXD2
chr6	78540000	78540200	FOXA1	chr20	5153400	5153600	PRRC2A
chr5	57899400	57899600	MYORG	chr3	15542200	15542400	PTGS1
chr7	12609800	12610000	KISS1R	chr5	157206600	157206800	PLA2G2F
chr6	69971800	69972000	FOXG1	chr7	121095600	121095800	APOBEC3
chr1	222191000	222191200	KCNK4	chr7	143347600	143347800	KRT71

chr7	11302600	11302800	TJP3	chr13	51004600	51004800	CHI3L1
chr17	33957000	33957200	FOXC1	chr12	50380400	50380600	TPST2
chr1	84139600	84139800	LTBP4	chr20	5114800	5115000	GPANK1
chr18	30914000	30914200	PCDHGA12	chr19	25311600	25311800	MIR23A
chr6	43021600	43021800	HPCAL1	chr17	9167000	9167200	NEUROG1
chr14	25590000	25590200	EPHA5	chr3	164422000	164422200	CEBPB
chr4	99178400	99178600	CD8B	chr3	94042000	94042200	RGD1563222
chr2	22018800	22019000	ANKRD34B	chr19	10643400	10643600	CX3CL1
chr2	211222400	211222600	SARS	chr1	1942400	1942600	ZC3H12D
chr13	91071000	91071200	CRP	chr15	108977400	108977600	PCCA
chr5	61382600	61382800	ALDH1B1	chr11	74309000	74309200	HES1
chr16	21343000	21343200	PBX4	chr13	48909000	48909200	CDK18
chr8	119566200	119566400	TRANK1	chr15	33356200	33356400	CEBPE
chr10	88497600	88497800	CNP	chr12	38002200	38002400	VPS37B
chr13	102630000	102630200	HLX	chr16	7316400	7316600	SEMA3G
chr1	124989400	124989600	TRPM1	chr10	106297800	106298000	9-Sep
chr20	54522600	54522800	GRIK2	chr10	56965400	56965600	ALOX15
chr1	87046600	87046800	LGALS7	chr11	35766800	35767000	ERG
chr1	73249400	73249600	FCAR	chr7	2902400	2902600	MYL6L
chr4	160334600	160334800	PRMT8	chr13	26163000	26163200	PHLPP1
chr11	32857400	32857600	RUNX1	chr18	55907400	55907600	SYNPO
chr3	15771800	15772000	OLR397	chr20	3549600	3549800	DDR1
chr20	3891200	3891400	RT1-DOA	chr10	83642200	83642400	PHOSPHO1
chr12	13362200	13362400	ZFP316	chr12	38003000	38003200	VPS37B
chr1	140867000	140867200	MFGE8	chr7	12281000	12281200	RPS15
chr20	3102200	3102400	RT1-T18	chr16	10699000	10699200	FAM25A
chr1	81292400	81292600	IRGC	chr16	20294600	20294800	RPL18A
chr20	7241800	7242000	PACSIN1	chr15	2346400	2346600	LRMDA

chr16	19223200	19223400	KLF2	chr20	45419600	45419800	AMD1
chr4	181477000	181477200	KLHL42	chr14	2894800	2895000	EVI5
chrX	156226600	156226800	OLR1768	chr1	99611200	99611400	CTU1
chr16	69240000	69240200	ZFP703	chr18	28669000	28669200	CXXC5
chr1	100343200	100343400	RGD1309036	chr10	103739000	103739200	TMEM104
chr13	84012200	84012400	CD247	chr7	144939800	144940000	GPR84
chr4	168685200	168685400	CDKN1B	chr3	155151200	155151400	PPP1R16B
chr1	91673400	91673600	CEP89	chr1	141672200	141672400	ARPIN
chr1	84080400	84080600	NUMBL	chr17	78546600	78546800	FAM107B
chr20	10273400	10273600	NDUFV3	chr8	61594800	61595000	SNX33
chr4	157745400	157745600	TAPBPL	chr2	23754400	23754600	LHFPL2
chr3	61578400	61578600	HOXD13	chr8	119156600	119156800	TMIE
chr5	171647800	171648000	ARHGEF16	chr1	188151000	188151200	ITPRIPL2
chr4	51843200	51843400	GPR37	chr7	141503800	141504000	LIMA1
chr20	7724600	7724800	SCUBE3	chr9	14721200	14721400	TREM3
chr4	157836800	157837000	SCNN1A	chr11	36545800	36546000	LCA5L
chr2	258935800	258936000	ADGRL2	chr1	227117800	227118000	LOC100910973
chr1	221108800	221109000	LTBP3	chr10	93519400	93519600	MRC2
chr20	5445600	5445800	B3GALT4	chr1	102895200	102895400	LDHA
chr11	32858600	32858800	RUNX1	chr10	5295000	5295200	TVP23A
chrX	156227600	156227800	OLR1768	chr5	76188000	76188200	GNG10
chr1	260267800	260268000	BLNK	chr10	103738400	103738600	TMEM104
chr4	177177800	177178000	ST8SIA1	chr7	11772400	11772600	JSRP1
chr10	84112000	84112200	MIR196C	chr3	2645600	2645800	FUT7
chr18	402000	402200	FUNDC2	chr1	91374400	91374600	CEBPA
chr20	37588200	37588400	MSL3L2	chr2	116168800	116169000	GPR160
chr7	2848200	2848400	RNF41	chr5	151907400	151907600	PIGV
chr19	26026600	26026800	DNASE2	chr5	157206400	157206600	PLA2G2F

chr1	102416000	102416200	KCNC1	chr7	3320000	3320200	GDF11
chr5	61382400	61382600	ALDH1B1	chr3	171294600	171294800	PMEPA1
chr19	38671600	38671800	CDH3	chr15	33356600	33356800	CEBPE
chr16	69239600	69239800	ZFP703	chr12	40499800	40500000	MAPKAPK5
chr19	53045000	53045200	FOXC2	chr17	23922000	23922200	GFOD1
chr7	10991800	10992000	TLE2	chr5	48303400	48303600	GABRR2
chr2	156793200	156793400	LOC302022	chr3	10684200	10684400	GPR107
				chr5	152758800	152759000	MTFR1L
				chr3	2881400	2881600	LCN5
				chr2	140303200	140303400	NOCT
				chr11	31709600	31709800	IFNGR2
				chr5	64912000	64912200	RNF20
Middle aged to old							
Hyper methylated				Hypo methylated			
Chromosome	Start	End	Gene symbol	Chromosome	Start	End	Gene symbol
chr8	71167000	71167200	RBPMS2	chr7	11752600	11752800	OAZ1
chr10	71159000	71159200	HNF1B	chr1	200679200	200679400	FGFR2
chr7	125796200	125796400	ARHGAP8	chr5	48303400	48303600	GABRR2
chr1	112946800	112947000	GABRA5	chr5	153973200	153973400	LOC500567
chr10	13081400	13081600	KREMEN2	chr7	144979600	144979800	ZFP385A
chr3	123715000	123715200	SPEF1	chr1	82579400	82579600	AXL
chr15	56958000	56958200	LRCH1	chr5	158083000	158083200	ALDH4A1
chr4	153816000	153816200	USP18	chr1	59784200	59784400	FPR1
chr20	5742800	5743000	UQCC2	chr6	137371400	137371600	CLBA1
chr5	147776200	147776400	LCK	chr15	4568400	4568600	KCNK5
chr1	80203800	80204000	RTN2	chr10	110379600	110379800	UTS2R
chr1	85492400	85492600	SELENOV	chr5	173391000	173391200	C10TNF12

chr11	64935800	64936000	POPDC2	chr20	14601400	14601600	GNAZ
chr9	97063800	97064000	GBX2	chr12	18527600	18527800	ASMT
chr12	13363400	13363600	ZFP316	chr16	10417200	10417400	ANXA8
chr6	94834200	94834400	L3HYPDH	chr7	34325400	34325600	HAL
chr13	52978200	52978400	KIF21B	chr5	151792600	151792800	GPN2
chr16	19223000	19223200	KLF2	chr5	59044600	59044800	CREB3
chr5	3431200	3431400	KCNB2	chr8	22758000	22758200	LDLR
chr14	106859200	106859400	OTX1	chr10	45528400	45528600	GJC2
chr13	79816200	79816400	SUCO	chr1	56679400	56679600	THBS2
chr7	57662200	57662400	TRHDE	chr7	28928400	28928600	DRAM1
chr1	270472800	270473000	SORCS1	chr8	127709600	127709800	MIR26A
chr3	152912600	152912800	TGIF2	chr10	105669000	105669200	ST6GALNAC2
chr10	56412000	56412200	FGF11	chr3	11625600	11625800	ST6GALNAC6
chr18	30896600	30896800	PCDHGA10	chr19	58825400	58825600	KCNK1
chr1	33910600	33910800	IRX1	chr5	57410800	57411000	AQP3
chr5	88630400	88630600	TLE1	chr14	35140800	35141000	KIT
chr9	15495000	15495200	TAF8	chr10	106815400	106815600	SYNGR2
chr4	122224800	122225000	LOC685964	chr3	13961000	13961200	PHF19
chr10	27366200	27366400	GABRA1	chr1	252456200	252456400	ANKRD22
chr17	13823000	13823200	S1PR3	chr19	10400400	10400600	DRC7
chr4	58250000	58250200	KLF14	chr20	22468400	22468600	EGR2
chr13	50898200	50898400	BTG2	chr7	12281000	12281200	RPS15
chr20	37587800	37588000	MSL3L2	chr12	39014600	39014800	KDM2B
chr5	159436000	159436200	PADI2	chr10	40497800	40498000	SLC36A3
chr18	69729800	69730000	ELAC1	chr13	47887600	47887800	MAPKAPK2
chr2	229718800	229719000	UGT8	chr19	52668400	52668600	CRISPLD2
chr1	81500200	81500400	LYPD3	chr8	63521200	63521400	REC114
chr2	247046400	247046600	UNC5C	chr13	90977400	90977600	SLAMF8

chr6	104072000	104072200	GALNT16	chr9	84418200	84418400	MOGAT1
chr5	155398000	155398200	ZBTB40	chr6	129600200	129600400	PAPOLA
chr12	21832200	21832400	CLDN3	chr1	213818800	213819000	IFITM3
chr10	85062800	85063000	TBX21	chr9	81451400	81451600	CXCR1
chr3	124144200	124144400	ADRA1D	chr10	82100800	82101000	ABCC3
chr18	59749600	59749800	ST8SIA3	chr2	189880000	189880200	SNAPIN
chr3	1924400	1924600	CACNA1B	chr19	55387600	55387800	APRT
chr12	22189200	22189400	TFR2	chr5	135994800	135995000	PLK3
chr9	17224800	17225000	RSPH9	chr13	88349200	88349400	DDR2
chr17	44595000	44595200	POM121L2	chr2	200205400	200205600	NOTCH2
chr7	144629800	144630000	MIR615	chr5	141008000	141008200	OXCT2A
chr17	44550400	44550600	PRSS16	chr10	85761000	85761200	LASP1
chr16	20032200	20032400	NIBAN3	chr10	10640000	10640200	PPL
chr1	216648000	216648200	CDKN1C	chr12	47578800	47579000	ANKRD13A
chr3	61578400	61578600	HOXD13	chr10	89257400	89257600	AOC3
chr5	57899400	57899600	MYORG	chr19	10329400	10329600	KIFC3
chr1	277815000	277815200	AFAP1L2	chr6	132752800	132753000	MIR345
chr6	132239800	132240000	CYP46A1	chr10	93519200	93519400	MRC2
chr13	51137200	51137400	MYOG	chr7	129610800	129611000	ZDHHC25
chr14	35582800	35583000	PDGFRA	chr9	10770800	10771000	ARRDC5
chr11	32858400	32858600	RUNX1	chr14	21602800	21603000	VCSA2
chr20	7672200	7672400	TCP11	chr10	12938000	12938200	ZSCAN10
chr6	69972600	69972800	FOXG1	chr6	51270800	51271000	HBP1
chr19	25899400	25899600	NF1X	chr10	28972600	28972800	MIR146A
chr6	119520000	119520200	FLRT2	chr5	155208600	155208800	EPHB2
chr17	21381800	21382000	ELOVL2	chr10	5295200	5295400	TVP23A
chr20	9596200	9596400	GLP1R	chr3	164664400	164664600	PTPN1
chr11	86519000	86519200	GP1BB	chr2	187228200	187228400	SH2D2A

chr3	5957800	5958000	VAV2	chr9	67702800	67703000	CTLA4
chr12	13363600	13363800	ZFP316	chr9	18652000	18652200	RUNX2
chr8	63090800	63091000	LOXL1	chr10	61994000	61994200	HIC1
chr1	56168200	56168400	DACT2	chr7	116926000	116926200	NAPRT
chr10	91046000	91046200	C1QL1	chr19	52662200	52662400	CRISPLD2
chr6	77509800	77510000	NKX2-8	chr6	133736800	133737000	MIR370
chr5	153773800	153774000	RCAN3	chr16	81851000	81851200	F7
chr16	8821800	8822000	DRGX	chr3	9035200	9035400	IER5L
chr12	42489600	42489800	TBX3	chr20	4542400	4542600	CFB
chr7	144578400	144578600	HOXC10	chr10	103739000	103739200	TMEM104
chr10	35749800	35750000	LTC4S	chr8	82366600	82366800	LEO1
chr1	33911000	33911200	IRX1	chr15	108471000	108471200	TIMM8A2
chrX	1800800	1801000	NDUFB11	chr10	14934000	14934200	SOX8
chr10	56576000	56576200	CLDN7	chr7	143347600	143347800	KRT71
chr3	170039600	170039800	CBLN4	chr1	89269600	89269800	FFAR2
chr5	62164800	62165000	TRIM14	chr10	66243400	66243600	LGALS5
chr7	14190000	14190200	NOTCH3	chr6	136324400	136324600	KLC1
chr1	33273200	33273400	IRX2	chr16	7668400	7668600	COLQ
chr3	22641400	22641600	LHX2	chr7	70460200	70460400	SLC26A10
chr16	21294800	21295000	CILP2	chr1	214208400	214208600	MIR3574
chr15	90194200	90194400	SPRY2	chr15	33357200	33357400	CEBPE
chr12	14092600	14092800	RADIL	chr5	59152000	59152200	HINT2
chr1	221108800	221109000	LTBP3	chr3	122195600	122195800	PDYN
chr16	77152800	77153000	CSMD1	chr5	117879000	117879200	ATG4C
chr3	160853200	160853400	MATN4	chr2	196293600	196293800	TMOD4
chr5	58978400	58978600	SIT1	chr3	94034800	94035000	RGD1563222
chr10	23663600	23663800	EBF1	chr13	102706800	102707000	1-Mar
chr10	18443800	18444000	RANBP17	chr10	91292400	91292600	SPATA32

chr10	55928200	55928400	KCNAB3	chr1	214328200	214328400	EPS8L2
chr1	166601600	166601800	MIR139	chr1	89043400	89043600	MIR3569
chr10	106975600	106975800	SOCS3	chr19	57063600	57063800	GALNT2
chr8	119566400	119566600	TRANK1	chr5	172642000	172642200	FAAP20
chr12	13362400	13362600	ZFP316	chr10	109193000	109193200	MIR3065
chr16	20032000	20032200	NIBAN3	chr8	36309800	36310000	ST3GAL4
chr13	52978000	52978200	KIF21B	chr9	65968400	65968600	MPP4
chr5	144761800	144762000	TFAP2E	chr7	70617200	70617400	ARHGAP9
chr8	95388800	95389000	TBX18	chr4	148805000	148805200	RASSF4
chr14	106859000	106859200	OTX1	chr16	10279600	10279800	RBP3
chr6	134626800	134627000	DIO3	chr1	12827000	12827200	CITED2
chr10	88497800	88498000	CNP	chr15	4488600	4488800	KCNK16
chr17	72426600	72426800	GATA3	chr19	43616600	43616800	FA2H
chr13	47614400	47614600	IL24	chr19	9792000	9792200	NDRG4
chr12	23548600	23548800	ORAI2	chr14	46142600	46142800	LOC498368
chr20	7882000	7882200	FANCE	chr1	80496000	80496200	GEMIN7
chr16	21058800	21059000	NCAN	chr15	18457000	18457200	ACOX2
chr14	107607600	107607800	B3GNT2	chr12	9858600	9858800	GTF3A
chr1	53051800	53052000	MPC1	chr12	22710000	22710200	MIR702
chr2	185851400	185851600	MAB21L2	chr16	54319000	54319200	MTUS1
chr10	56576600	56576800	CLDN7	chr18	60719600	60719800	LOC502176
chr10	108145400	108145600	CBX8	chr11	24275200	24275400	ATP5PF
chr18	56180200	56180400	ARSI	chr17	9992600	9992800	FGFR4
chr6	3807800	3808000	THUMP2	chr17	9166800	9167000	NEUROG1
chr5	153756200	153756400	NCMAP	chr7	122998000	122998200	ZC3H7B
chr12	47674200	47674400	GLTP	chr1	82496800	82497000	CCDC97
chr8	93491200	93491400	TPBG	chr9	98205000	98205200	LRRFIP1
chr5	60184600	60184800	PAX5	chr20	4563800	4564000	C2

chr6	75074400	75074600	EGLN3	chr5	57411000	57411200	AQP3
chr10	87081200	87081400	CCR7	chr2	250824000	250824200	CLCA4L
chr1	221758800	221759000	PYGM	chr9	113590800	113591000	RALBP1
chr3	141406000	141406200	NKX2-2	chr1	267323800	267324000	STN1
chr12	47665200	47665400	GLTP	chr7	11676600	11676800	TIMM13
chr9	15294600	15294800	FRS3	chr17	21368200	21368400	ELOVL2
chr15	52244800	52245000	HR	chr6	132950600	132950800	BEGAIN
chr18	61639200	61639400	RAX	chrX	159170200	159170400	FHL1
chr3	2802400	2802600	PHPT1	chr10	103739200	103739400	TMEM104
chr1	80253200	80253400	ERCC1	chr12	45714000	45714200	SRRM4
chr11	86521200	86521400	GP1BB	chr5	126166200	126166400	DHCR24
chr9	98085000	98085200	MLPH	chr17	68560400	68560600	PFKP
chr4	109042400	109042600	CTNNA2	chr3	9805000	9805200	TOR1A
chr3	43116000	43116200	NR4A2	chr3	5720400	5720600	DBH
chr5	147146000	147146200	AZIN2	chr5	76187800	76188000	GNG10
chr1	261670200	261670400	CRTAC1	chr15	33357000	33357200	CEBPE
chr3	1924600	1924800	CACNA1B	chr11	31237800	31238000	RGD1562726
chr1	164426200	164426400	RPS3	chr19	15068000	15068200	CESL1
chr1	226435400	226435600	SYT7	chr7	12764400	12764600	GRIN3B
chr2	189855200	189855400	NPR1	chr2	196293400	196293600	TMOD4
chr12	13362000	13362200	ZFP316	chr19	17285000	17285200	AKTIP
chr20	8319200	8319400	CMTR1	chr7	123160000	123160200	POLR3H
chr7	144641000	144641200	HOXC4	chr19	52034400	52034600	MLYCD
chr18	30901600	30901800	PCDHGB7	chr4	176934600	176934800	ABCC9
chr5	133712400	133712600	FOXE3	chr3	159938400	159938600	HNF4A
chr1	131452000	131452200	NR2F2	chr7	3320200	3320400	GDF11
chr3	160558600	160558800	KCNS1	chr20	5529200	5529400	PHF1
chr11	32858200	32858400	RUNX1	chr2	188523800	188524000	MTX1

chr1	163443000	163443200	LRR32	chr6	136536600	136536800	RD3L
chrX	156227600	156227800	OLR1768	chr7	142779000	142779200	ACVRL1
chr14	83754600	83754800	SELENOM	chr13	50994000	50994200	CHIT1
chr1	143277600	143277800	CPEB1	chr5	143109000	143109200	ZC3H12A
chr4	121595000	121595200	TXNRD3	chr10	106298000	106298200	Sept9
chr10	85555800	85556000	EPOP	chr19	19403800	19404000	SNX20
chr10	86687000	86687200	NR1D1	chr19	26100600	26100800	JUNB
chr1	33915000	33915200	IRX1	chr10	92652400	92652600	ITGB3
chr8	98737600	98737800	ZIC1	chr3	162866000	162866200	SULF2
chr1	256384000	256384200	CYP26A1	chr2	141268200	141268400	MAML3
chr13	90938000	90938200	VSIG8	chr5	148398600	148398800	TINAGL1
chr10	89916200	89916400	DUSP3	chr3	14018000	14018200	TRAF1
chr5	169494400	169494600	RPL22	chr1	226245400	226245600	FEN1
chr5	147776400	147776600	LCK	chr13	26173800	26174000	PHLPP1
chr12	28381400	28381600	GALNT17	chr12	48384800	48385000	DAO
chr1	33917000	33917200	IRX1	chr2	240685000	240685200	MANBA
chr20	7135000	7135200	HMGA1	chr7	2901000	2901200	MYL6L
chr1	47630000	47630200	FNDC1	chr8	49748400	49748600	DSCAML1
chr18	14016600	14016800	NOL4	chr11	86356000	86356200	CLDN5
chr18	30808400	30808600	PCDHGA1	chr1	79912400	79912600	IRF2BP1
chr18	83470800	83471000	NETO1	chr4	168903800	168904000	GPRC5D
chr7	31876800	31877000	TMPO	chr5	152758800	152759000	MTFR1L
chr20	14185800	14186000	UPB1	chr9	16539200	16539400	CNPY3
chr1	216661800	216662000	CDKN1C	chr2	188196800	188197000	MSTO1
chr15	45376200	45376400	DLEU7	chr7	117265400	117265600	PLEC
chr2	145173200	145173400	MAB21L1	chr8	70712200	70712400	PARP16
chr7	31876600	31876800	TMPO	chr13	26173600	26173800	PHLPP1
chr16	21295200	21295400	CILP2	chr1	91373600	91373800	CEBPA

chr3	124144400	124144600	ADRA1D	chr20	10019200	10019400	RSPH1
chr3	145032200	145032400	SYNDIG1	chr7	11646000	11646200	GADD45B
chr4	56337400	56337600	LEP	chr5	160420400	160420600	EFHD2
chr1	169418600	169418800	TRIM6	chr1	221300800	221301000	CDC42EP2
chr7	57662400	57662600	TRHDE	chr4	80357600	80357800	LOC500124
chr14	78312400	78312600	CRMP1	chr17	10195000	10195200	UNC5A
chr17	44558600	44558800	PRSS16	chr8	55270400	55270600	PPP2R1B
chr3	172417400	172417600	GNAS	chr20	5013400	5013600	VWA7
chr12	14092400	14092600	RADIL	chr3	7184800	7185000	GFI1B
chr5	169464200	169464400	HES3	chr2	240684800	240685000	MANBA
chr18	30820400	30820600	PCDHGA3	chr13	71168200	71168400	RGS16
chr5	63784800	63785000	NR4A3	chr6	133584800	133585000	DLK1
chr20	10273600	10273800	NDUFV3	chr10	98720200	98720400	MAP2K6
chr7	34714000	34714200	USP44	chr16	81950200	81950400	MCF2L
chr6	8960000	8960200	SIX2	chr20	5114800	5115000	GPANK1
chr10	109786200	109786400	NPB	chr20	7880200	7880400	FANCE
chr8	98737400	98737600	ZIC1	chr17	15043600	15043800	LOC689316
chr6	89292800	89293000	MDGA2	chr2	23754400	23754600	LHFPL2
chr19	58519800	58520000	MAP10	chr5	64912000	64912200	RNF20
chr4	181477200	181477400	KLHL42	chr15	28731800	28732000	METTL3
chr10	91175000	91175200	PLCD3	chr5	79213400	79213600	AKNA
chr1	136061200	136061400	SLCO3A1	chr4	78374600	78374800	GIMAP1
chr5	60515200	60515400	GRHPR	chr14	85748200	85748400	XBP1
chr10	73337800	73338000	TBX4	chr6	11000600	11000800	MIR3558
chr4	50312200	50312400	FEZF1	chr2	225650400	225650600	ABCA4
chr12	13364000	13364200	ZFP316	chr1	198286800	198287000	DOC2A
chr7	57661600	57661800	TRHDE	chr13	51004600	51004800	CHI3L1
chr1	87046600	87046800	LGALS7	chr18	55907400	55907600	SYNPO

chr8	98735600	98735800	ZIC1	chr6	109047200	109047400	EIF2B2
chr4	94068200	94068400	GRID2	chr5	151202600	151202800	AHDC1
chr6	46631400	46631600	SOX11	chr1	170154000	170154200	OLR200
chr1	196866000	196866200	NSMCE1	chr3	164422000	164422200	CEBPB
chr16	67047800	67048000	UNC5D	chr11	33836000	33836200	CBR1
chr6	39363200	39363400	LRATD1	chr16	10699000	10699200	FAM25A
chr7	61797000	61797200	DYRK2	chr9	15622000	15622200	GUCA1B
chr20	4330000	4330200	NOTCH4	chr4	157170400	157170600	LPCAT3
chr18	30880400	30880600	PCDHGA9	chr20	4539000	4539200	CFB
chr2	78825600	78825800	March11	chr5	61385000	61385200	ALDH1B1
chr1	80378400	80378600	MARK4	chr18	76749200	76749400	HSBP1L1
chr5	140889400	140889600	NT5C1A	chr10	45927000	45927200	OLR1462
chr7	120273000	120273200	GALR3	chr5	153522000	153522200	RUNX3
chr16	21274400	21274600	TSSK6	chr8	119156600	119156800	TMIE
chr2	56892200	56892400	GDNF	chr5	139615800	139616000	CITED4
chr12	9469200	9469400	CDX2	chr20	5477000	5477200	TAPBP
chr10	46568600	46568800	SREBF1	chr11	36545800	36546000	LCA5L
chr6	42632600	42632800	ATP6V1C2	chr10	107369400	107369600	CEP295NL
chr12	13362200	13362400	ZFP316	chr7	117262200	117262400	PLEC
chr11	31391600	31391800	OLIG2	chr16	69248400	69248600	ZFP703
chr3	15430000	15430200	LHX6	chr5	76188000	76188200	GNG10
chr8	30479600	30479800	NTM	chr10	106191800	106192000	Sept9
chr16	19223200	19223400	KLF2	chr13	51969400	51969600	ARL8A
chr3	43115800	43116000	NR4A2	chr3	140090600	140090800	NAA20
chr13	84012200	84012400	CD247	chr1	7219600	7219800	PLAGL1
chr6	28235000	28235200	DNMT3A	chr14	7108200	7108400	HSD17B13
chr18	30901400	30901600	PCDHGB7	chr1	91374400	91374600	CEBPA
chr13	88995400	88995600	OLFML2B	chr19	25821600	25821800	LYL1

chr1	91673400	91673600	CEP89	chr10	19669200	19669400	SPDL1
chr12	46974600	46974800	TRIAP1	chr2	116168800	116169000	GPR160
chr10	91045800	91046000	C1QL1	chr11	31225200	31225400	RGD1562726
chr7	57662600	57662800	TRHDE	chr5	151907400	151907600	PIGV
chr2	5592800	5593000	NR2F1	chr5	169526000	169526200	CHD5
chr3	145031800	145032000	SYNDIG1	chr3	162866200	162866400	SULF2
chr9	97064000	97064200	GBX2	chr2	140303200	140303400	NOCT
chr5	169465000	169465200	HES3	chr1	78938400	78938600	CCDC8
chr1	84080400	84080600	NUMBL				
chr1	33914400	33914600	IRX1				
chr10	27366000	27366200	GABRA1				
chr3	56768400	56768600	SP5				
chr8	127186600	127186800	GOLGA4				
chr6	95817200	95817400	SIX6				
chr5	61382600	61382800	ALDH1B1				
chr19	6032600	6032800	CDH8				
chr15	62198200	62198400	PCDH8				
chr16	21295000	21295200	CILP2				
chr20	7724600	7724800	SCUBE3				
chr5	107825000	107825200	CDKN2A				
chr5	63785600	63785800	NR4A3				
chr5	169270800	169271000	TNFRSF25				
chr1	101526200	101526400	PLEKHA4				
chr19	25143200	25143400	MISP3				
chr19	31031200	31031400	FREM3				
chr1	85492600	85492800	SELENOV				
chr1	72546600	72546800	SHISA7				
chr1	216648200	216648400	CDKN1C				

chr2	181874000	181874200	RBM46
chr11	86521800	86522000	GP1BB
chr20	13971200	13971400	SUSD2
chr16	20683600	20683800	CRLF1
chr12	47807800	47808000	FAM222A
chr20	9928600	9928800	TMPRSS3
chr17	52568800	52569000	GLI3
chr1	226435200	226435400	SYT7
chr7	141053000	141053200	TMBIM6
chr5	98468800	98469000	LURAP1L
chr2	116526600	116526800	EGFEM1
chr7	57663000	57663200	TRHDE
chr13	51136800	51137000	MYOG
chr10	43071200	43071400	GALNT10
chr19	55520800	55521000	CBFA2T3
chr3	61669000	61669200	HOXD3
chr19	26026600	26026800	DNASE2
chr7	11559200	11559400	DIRAS1
chr1	102416000	102416200	KCNC1
chr3	145032000	145032200	SYNDIG1
chr7	144274200	144274400	ATP5MC2
chr14	4350200	4350400	BARHL2
chr7	2848200	2848400	RNF41
chr8	48085000	48085200	NECTIN1
chr5	107825200	107825400	CDKN2A
chr15	52326000	52326200	DMTN
chr7	57661800	57662000	TRHDE
chr19	53045000	53045200	FOXC2

chr18	61641800	61642000	RAX
chr17	11684000	11684200	MSX2
chr15	110075600	110075800	NALCN
chr9	94280400	94280600	CHRND
chr1	64334400	64334600	MIR935

Young to old							
Hyper methylated				Hypo methylated			
Chromosome	Start	End	Gene symbol	Chromosome	Start	End	Gene symbol
chr17	76529000	76529200	CAMK1D	chr4	169107000	169107200	PBP2
chr11	32857200	32857400	RUNX1	chr19	52751200	52751400	ZDHHC7
chr10	71159000	71159200	HNF1B	chr3	175824000	175824200	SLCO4A1
chr1	176982000	176982200	DKK3	chr8	116369600	116369800	SEMA3B
chr4	83970000	83970200	TRIL	chr6	99411200	99411400	ZBTB1
chr4	98769400	98769600	FOXI3	chr7	123160000	123160200	POLR3H
chr2	111792600	111792800	NLGN1	chr1	82579400	82579600	AXL
chr1	14777800	14778000	OLIG3	chr13	82487200	82487400	F5
chr10	97229800	97230000	AXIN2	chr19	55387600	55387800	APRT
chr12	14092800	14093000	RADIL	chr1	59784200	59784400	FPR1
chr15	43902400	43902600	EBF2	chr13	71176400	71176600	RGS16
chr9	12734400	12734600	RFTN1	chr6	137371400	137371600	CLBA1
chr1	85492400	85492600	SELEN OV	chr19	55368000	55368200	PIEZO1
chr12	13363400	13363600	ZFP316	chr4	126291600	126291800	MAGI1
chr6	94834200	94834400	L3HYPDH	chr5	173391000	173391200	C1QTNF12
chr13	52978200	52978400	KIF21B	chr13	51565400	51565600	SYT2
chr10	97216600	97216800	AXIN2	chr10	40498000	40498200	SLC36A3
chr15	51758800	51759000	EGR3	chr4	153932200	153932400	SLC6A12
chr3	141405800	141406000	NKX2-2	chr7	3320200	3320400	GDF11

chr13	79816200	79816400	SUCO	chr20	7204600	7204800	NUDT3
chr8	23061800	23062000	ELAVL3	chr16	10417200	10417400	ANXA8
chr10	61697800	61698000	MNT	chr11	64952600	64952800	POPDC2
chr1	33277000	33277200	IRX2	chr1	89551600	89551800	HPN
chr1	270472800	270473000	SORCS1	chr15	33357200	33357400	CEBPE
chr5	3431200	3431400	KCNB2	chr9	10953400	10953600	LRG1
chr1	170410400	170410600	APBB1	chr5	59044600	59044800	CREB3
chr10	56412000	56412200	FGF11	chr5	153842800	153843000	MIR6333
chr12	9605600	9605800	GSX1	chr8	22758000	22758200	LDLR
chr10	63499200	63499400	TRARG1	chr12	41517200	41517400	TPCN1
chr7	11302800	11303000	TJP3	chr1	102843800	102844000	HPS5
chr5	147776200	147776400	LCK	chr12	14260600	14260800	FOXK1
chr10	27366200	27366400	GABRA1	chr3	170255800	170256000	MC3R
chr17	13823000	13823200	S1PR3	chr4	181087200	181087400	ARNTL2
chr13	50898200	50898400	BTG2	chr10	88620800	88621000	HSPB9
chr5	159436000	159436200	PADI2	chr7	130145000	130145200	MIR349
chr10	73337800	73338000	TBX4	chr10	59567600	59567800	P2RX1
chr1	216683000	216683200	SLC22A18	chr5	74942400	74942600	AKAP2
chr1	53840600	53840800	AFDN	chr12	25166800	25167000	ERVFRD-1
chr18	14016400	14016600	NOL4	chr3	11625600	11625800	ST6GALNAC6
chr7	117146600	117146800	NRBP2	chr7	72933000	72933200	LAPTM4B
chr1	198396400	198396600	CDIPT	chr3	11114600	11114800	PLPP7
chr8	127186600	127186800	GOLGA4	chr10	82296200	82296400	CHAD
chr1	81500200	81500400	LYPD3	chr1	273752400	273752600	XPNPEP1
chr2	247046400	247046600	UNC5C	chr19	55913200	55913400	RPL13
chr7	116357000	116357200	LY6E	chr7	117262200	117262400	PLEC
chr12	21832200	21832400	CLDN3	chr9	98182600	98182800	LRRFIP1
chr7	70839000	70839200	NXPH4	chr1	266916200	266916400	CALHM2

chr13	76055600	76055800	ASTN1	chr20	5064600	5064800	LY6G6D
chr7	141053000	141053200	TMBIM6	chr12	39014600	39014800	KDM2B
chr10	87081200	87081400	CCR7	chr20	6567000	6567200	MLN
chr1	165181400	165181600	KCNE3	chr4	120665600	120665800	MGLL
chr1	277352200	277352400	DCLRE1A	chr10	95237000	95237200	RGD1565033
chr16	57136600	57136800	SGCZ	chr4	145610800	145611000	IRAK2
chr5	43603600	43603800	EPHA7	chr1	211272000	211272200	BNIP3
chr7	141374800	141375000	GPD1	chr9	14722200	14722400	TREM3
chr3	159823800	159824000	GDAP1L1	chr7	144979600	144979800	ZFP385A
chr18	30826200	30826400	PCDHGA3	chr13	90977400	90977600	SLAMF8
chr17	44550400	44550600	PRSS16	chr10	4951600	4951800	PRM3
chr10	106856400	106856600	BIRC5	chr17	16403400	16403600	MIRLET7A1
chr7	140316200	140316400	CACNB3	chr1	213818800	213819000	IFITM3
chr7	57663000	57663200	TRHDE	chr17	42054800	42055000	MRS2
chr18	29961200	29961400	PCDHA2	chr7	117265400	117265600	PLEC
chr7	121798000	121798200	GRAP2	chr15	33356800	33357000	CEBPE
chr1	277815000	277815200	AFAP1L2	chr2	189880000	189880200	SNAPIN
chr2	210365000	210365200	ALX3	chr5	138156000	138156200	SLC2A1
chr4	49941000	49941200	PTPRZ1	chr19	58825200	58825400	KCNK1
chr11	32858400	32858600	RUNX1	chr15	27933600	27933800	RNASE10
chr5	143500000	143500200	GRIK3	chr10	11215800	11216000	TFAP4
chr20	7672200	7672400	TCP11	chr10	84153400	84153600	HOXB5
chr17	88216200	88216400	GPR158	chr19	10329400	10329600	KIFC3
chr3	61580800	61581000	HOXD13	chr9	84420400	84420600	MOGAT1
chr8	120433200	120433400	ARPP21	chr20	7957200	7957400	TULP1
chr11	34314000	34314200	SIM2	chr10	103480200	103480400	CD300LB
chr10	96020000	96020200	CACNG4	chr10	93519200	93519400	MRC2
chr8	63090800	63091000	LOXL1	chr4	68831600	68831800	TAS2R138

chr3	56768400	56768600	SP5	chr1	86988800	86989000	HNRNPL
chr1	170398600	170398800	APBB1	chr13	101364400	101364600	TLR5
chr1	23238800	23239000	EYA4	chr9	10770800	10771000	ARRDC5
chr5	57899200	57899400	MYORG	chr7	70460200	70460400	SLC26A10
chr16	8821800	8822000	DRGX	chr10	5295200	5295400	TVP23A
chr3	61597600	61597800	HOXD12	chr10	101297000	101297200	SOX9
chr3	171055800	171056000	RBM38	chr9	67702800	67703000	CTLA4
chr14	45349600	45349800	MIR328B	chr9	100165200	100165400	AQP12A
chr6	78540000	78540200	FOXA1	chr10	55049000	55049200	PIK3R5
chr17	44549400	44549600	PRSS16	chr1	217348600	217348800	SHANK2
chr10	35749800	35750000	LTC4S	chr8	54927800	54928000	PLET1
chr7	57662000	57662200	TRHDE	chr9	116242400	116242600	ARHGAP28
chr12	31759600	31759800	FZD10	chr7	141072200	141072400	TMBIM6
chr2	179704800	179705000	GRIA2	chr2	187863000	187863200	LMNA
chr4	115440600	115440800	TEX261	chr1	219136600	219136800	TCIRG1
chr7	128500000	128500200	TAFAS	chr9	113590800	113591000	RALBP1
chr13	91071000	91071200	CRP	chr7	34325400	34325600	HAL
chr3	170039600	170039800	CBLN4	chr9	40975000	40975200	PTPN18
chr3	95133600	95133800	WT1	chr19	11295200	11295400	MT1
chr5	61382600	61382800	ALDH1B1	chr16	81851000	81851200	F7
chr3	61598000	61598200	HOXD12	chr10	103739000	103739200	TMEM104
chr18	30896400	30896600	PCDHGA10	chr1	82497000	82497200	CCDC97
chr10	31144800	31145000	ADAM19	chr17	11698000	11698200	MSX2
chr8	29452800	29453000	OPCML	chr20	5875600	5875800	SRPK1
chr5	107825000	107825200	CDKN2A	chr13	110091800	110092000	PPP2R5A
chr11	87058200	87058400	PRODH1	chr16	6958400	6958600	MUSTN1
chr2	186905400	186905600	ETV3L	chr7	143347600	143347800	KRT71
chr8	108109200	108109400	SOX14	chr12	41591000	41591200	SLC8B1

chr6	128719600	128719800	SYNE3	chr3	164238000	164238200	SPATA2
chr3	156339600	156339800	MAFB	chr14	7167400	7167600	KLHL8
chr3	15429800	15430000	LHX6	chr15	17671800	17672000	LOC361016
chr10	84028200	84028400	HOXB13	chr6	136324400	136324600	KLC1
chr12	41663200	41663400	LHX5	chr14	36688600	36688800	USP46
chr10	23663600	23663800	EBF1	chr16	7668400	7668600	COLQ
chr6	95922600	95922800	SIX1	chr12	40500000	40500200	MAPKAPK5
chr10	18443800	18444000	RANBP17	chr3	44734000	44734200	GAPDH-PS1
chr10	55928200	55928400	KCNAB3	chr20	27000000	27000200	MYPN
chr5	133712600	133712800	FOXE3	chr4	15519400	15519600	HGF
chr1	166601600	166601800	MIR139	chr5	76183200	76183400	GNG10
chr19	10099800	10100000	MMP15	chr5	117879000	117879200	ATG4C
chr8	48085000	48085200	NECTIN1	chr3	58444400	58444600	ITGA6
chr1	212526400	212526600	MSX3	chr10	91292400	91292600	SPATA32
chr15	47292600	47292800	SOX7	chr1	214328200	214328400	EPS8L2
chr17	78771800	78772000	SUV39H2	chr20	31333600	31333800	AIFM2
chr7	134723800	134724000	PRICKLE1	chr5	172642000	172642200	FAAP20
chr12	13362400	13362600	ZFP316	chr1	101397200	101397400	KCNA7
chr3	129357000	129357200	PAK7	chr1	81118200	81118400	ZFP61
chr13	52978000	52978200	KIF21B	chr7	137157000	137157200	ANO6
chr16	79698800	79699000	KBTD11	chr7	70617200	70617400	ARHGAP9
chr10	73280000	73280200	TBX2	chr4	85196000	85196200	GGCT
chr20	37587800	37588000	MSL3L2	chr15	4488600	4488800	KCNK16
chr19	25899200	25899400	NF1X	chr19	43616600	43616800	FA2H
chr17	31440200	31440400	TUBB2B	chr5	152700000	152700200	PAQR7
chr12	41676000	41676200	LHX5	chr12	16116800	16117000	LFNG
chr13	89528800	89529000	MPZ	chr14	46142600	46142800	LOC498368
chr7	31876600	31876800	TMPO	chr15	28396800	28397000	ZFP219

chr1	218003000	218003200	FGF3	chr17	15761600	15761800	FGD3
chr1	11907200	11907400	RN5-8S	chr8	128528000	128528200	SCN11A
chr7	12235200	12235400	ADAMTSL5	chr1	94610200	94610400	PLEKHF1
chr12	13363200	13363400	ZFP316	chr5	48306800	48307000	GABRR2
chr13	47614400	47614600	IL24	chr13	83850600	83850800	MPZL1
chr16	77153000	77153200	CSMD1	chr18	60719600	60719800	LOC502176
chr12	22189400	22189600	TFR2	chr7	12561400	12561600	WDR18
chr20	7882000	7882200	FANCE	chr11	71218400	71218600	MUC20
chr12	47790400	47790600	FAM222A	chr7	12198000	12198200	MBD3
chr14	9561000	9561200	NKX6-1	chr1	198740400	198740600	ITGAL
chr8	95388800	95389000	TBX18	chr18	77303000	77303200	NFATC1
chr18	67628400	67628600	DCC	chr7	130297200	130297400	ADM2
chr1	53051800	53052000	MPC1	chr1	82496800	82497000	CCDC97
chr19	44124600	44124800	CHST5	chr20	4563800	4564000	C2
chr5	61382400	61382600	ALDH1B1	chr8	13242600	13242800	PIWIL4
chr10	91293600	91293800	SPATA32	chr15	27851600	27851800	APEX1
chr1	100669400	100669600	MYH14	chr2	250824000	250824200	CLCA4L
chr14	4350400	4350600	BARHL2	chr10	85076600	85076800	TBKBP1
chr6	89292800	89293000	MDGA2	chr8	47521000	47521200	OAF
chr1	280637600	280637800	EMX2	chr17	21368200	21368400	ELOVL2
chr17	8886600	8886800	PITX1	chr6	129600200	129600400	PAPOLA
chr3	160853400	160853600	MATN4	chr1	266410000	266410200	CYP17A1
chr5	147776400	147776600	LCK	chr2	219590400	219590600	LRRC39
chr8	93491200	93491400	TPBG	chr10	103739200	103739400	TMEM104
chr7	117060000	117060200	MAPK15	chr6	132964000	132964200	BEGAIN
chr3	141406000	141406200	NKX2-2	chr9	84211600	84211800	SGPP2
chr4	115014400	115014600	MTHFD2	chr9	9944400	9944600	TUBB4A
chr4	48308600	48308800	KCND2	chr5	145394000	145394200	GJB3

chr1	100340200	100340400	RGD1309036	chr3	147964600	147964800	DEFB22
chr20	29510000	29510200	DDIT4	chr3	80843200	80843400	MDK
chr12	47665200	47665400	GLTP	chr17	68560400	68560600	PFKP
chr10	72272400	72272600	CA4	chr3	160948600	160948800	PIGT
chr4	94069800	94070000	GRID2	chr5	76187800	76188000	GNG10
chr4	117964600	117964800	TGFA	chr13	89349800	89350000	FCGR2B
chr7	11559200	11559400	DIRAS1	chr5	157215800	157216000	PLA2G2D
chr10	91048000	91048200	C1QL1	chr3	175823800	175824000	SLCO4A1
chr3	2802400	2802600	PHPT1	chr15	33357000	33357200	CEBPE
chr6	99843000	99843200	GPX2	chr19	25934600	25934800	GADD45GIP1
chr1	100590000	100590200	KCNC3	chr14	80960200	80960400	DOK7
chr19	19403800	19404000	SNX20	chr5	158083200	158083400	ALDH4A1
chr7	143227800	143228000	KRT75	chr10	57267200	57267400	SLC25A11
chr3	95150400	95150600	WT1	chrX	159170200	159170400	FHL1
chr4	109042400	109042600	CTNNA2	chr7	123578200	123578400	PHETA2
chr3	43116000	43116200	NR4A2	chr20	10037200	10037400	SLC37A1
chr5	58163400	58163600	CCL27	chr2	196293400	196293600	TMOD4
chr5	147146000	147146200	AZIN2	chr8	52955000	52955200	NNMT
chr1	261670200	261670400	CRTAC1	chr19	52034400	52034600	MLYCD
chr1	164426200	164426400	RPS3	chr15	18456600	18456800	ACOX2
chr1	226435400	226435600	SYT7	chr5	61379000	61379200	ALDH1B1
chr10	87081000	87081200	CCR7	chr5	169526000	169526200	CHD5
chr12	52376800	52377000	LRCOL1	chr5	167117400	167117600	GPR157
chr2	189855200	189855400	NPR1	chr4	176934600	176934800	ABCC9
chr11	32857400	32857600	RUNX1	chr15	61687400	61687600	KBTBD7
chr18	30901600	30901800	PCDHGB7	chr4	7069600	7069800	SMARCD3
chr10	76361400	76361600	TRIM25	chr3	22838200	22838400	NEK6
chr5	145304600	145304800	SMIM12	chr1	185149600	185149800	NUCB2

chr2	113066400	113066600	GHSR	chr10	92652400	92652600	ITGB3
chr10	91063800	91064000	C1QL1	chr8	130224000	130224200	LYZL4
chr7	61797000	61797200	DYRK2	chr1	225140000	225140200	MTA2
chr10	73338000	73338200	TBX4	chr5	148398600	148398800	TINAGL1
chr14	83754600	83754800	SELENOM	chr17	15761800	15762000	FGD3
chr1	78053600	78053800	MEIS3	chr5	135994800	135995000	PLK3
chr1	143277600	143277800	CPEB1	chr13	26173800	26174000	PHLPP1
chr14	35596200	35596400	PDGFRA	chr3	111547400	111547600	ITPKA
chr1	165890200	165890400	RELT	chr14	105997400	105997600	PELI1
chr10	89185600	89185800	WNK4	chr1	212262000	212262200	UTF1
chr18	30896000	30896200	PCDHGA10	chr5	79213400	79213600	AKNA
chr10	103799600	103799800	GRIN2C	chr4	153390600	153390800	BCL2L13
chr10	86687000	86687200	NR1D1	chr8	55270400	55270600	PPP2R1B
chr8	98737600	98737800	ZIC1	chr6	111113400	111113600	NGB
chr17	88216000	88216200	GPR158	chr20	11396200	11396400	PFKL
chr10	48569000	48569200	ADORA2B	chr1	168911000	168911200	OLR127
chr12	28381400	28381600	GALNT17	chr3	159580600	159580800	TOX2
chr10	82419400	82419600	XYLT2	chr8	127709600	127709800	MIR26A
chr1	33917000	33917200	IRX1	chr14	85397800	85398000	EMID1
chr2	210378800	210379000	ALX3	chr8	128631800	128632000	GORASP1
chr6	46631000	46631200	SOX11	chr13	35538000	35538200	RALB
chr1	270473000	270473200	SORCS1	chr1	79912400	79912600	IRF2BP1
chr13	102631000	102631200	HLX	chr12	24457200	24457400	FZD9
chr19	52086800	52087000	NECAB2	chr4	169992600	169992800	GRIN2B
chr20	1980800	1981000	GABBR1	chr10	85761000	85761200	LASP1
chr5	144161400	144161600	EVA1B	chr6	137668400	137668600	GPR132
chr18	83470800	83471000	NETO1	chr20	5153200	5153400	PRRC2A
chr7	31876800	31877000	TMPO	chr9	16539200	16539400	CNPY3

chr20	14185800	14186000	UPB1	chr6	124801400	124801600	DGLUCY
chr9	17844800	17845000	TMEM151B	chr10	73902400	73902600	MIR21
chr8	15012800	15013000	FAT3	chr1	91373600	91373800	CEBPA
chr1	174411200	174411400	NRIP3	chr10	103803200	103803400	GRIN2C
chr1	216682800	216683000	SLC22A18	chr17	13509200	13509400	SEMA4D
chr1	52908200	52908400	TBXT	chr7	11646000	11646200	GADD45B
chr5	60184600	60184800	PAX5	chr8	129222400	129222600	RPL14
chr16	21295200	21295400	CILP2	chr10	82400400	82400600	XYLT2
chr14	80731200	80731400	ADRA2C	chr3	4022400	4022600	EGFL7
chr7	54248800	54249000	PHLDA1	chr3	64528200	64528400	ZFP385B
chr3	145032200	145032400	SYNDIG1	chr19	25311400	25311600	MIR23A
chr3	152912600	152912800	TGIF2	chr20	10238800	10239000	WDR4
chr2	145173200	145173400	MAB21L1	chr11	71216800	71217000	MUC20
chr1	169418600	169418800	TRIM6	chr20	7785400	7785600	DEF6
chr14	78312400	78312600	CRMP1	chr20	5013400	5013600	VWA7
chr1	221758800	221759000	PYGM	chr10	106296800	106297000	9-Sep
chr12	51249400	51249600	MN1	chr1	100511000	100511200	EMC10
chr1	209636400	209636600	EBF3	chr16	14347000	14347200	CDHR1
chr7	120401600	120401800	SOX10	chr3	165742800	165743000	ZFP64
chr12	14092400	14092600	RADIL	chr7	121095600	121095800	APOBEC3
chr18	30820400	30820600	PCDHGA3	chr4	56714400	56714600	FLNC
chr20	10273600	10273800	NDUFV3	chr12	45712800	45713000	SRRM4
chrX	156228200	156228400	OLR1768	chr7	11078800	11079000	S1PR4
chr6	8960000	8960200	SIX2	chr12	47408400	47408600	HNF1A
chr6	135874200	135874400	EXOC3L4	chr12	40879600	40879800	RPL6
chr10	109786200	109786400	NPB	chr3	164664400	164664600	PTPN1
chr20	8395600	8395800	CCDC167	chr6	11000600	11000800	MIR3558
chr9	43337400	43337600	ZAP70	chr1	100576000	100576200	NAPSA

chr8	49738400	49738600	DSCAML1	chr17	15043600	15043800	LOC689316
chr5	166514200	166514400	CLSTN1	chr10	13870000	13870200	CASKIN1
chr19	58519800	58520000	MAP10	chr20	5529200	5529400	PHF1
chr17	8607400	8607600	RGD1562024	chr2	23754400	23754600	LHFPL2
chr5	14894200	14894400	SOX17	chr7	129610800	129611000	ZDHHC25
chr10	91175000	91175200	PLCD3	chr11	74309000	74309200	HES1
chr6	146786800	146787000	SP8	chr1	261975600	261975800	PYROXD2
chr6	71349000	71349200	PRKD1	chr20	14627800	14628000	GNAZ
chr14	4372200	4372400	BARHL2	chr13	51004600	51004800	CHI3L1
chr10	101289000	101289200	SOX9	chr1	80028000	80028200	FBXO46
chr1	203971400	203971600	GPR26	chr17	9228400	9228600	TIFAB
chr3	142391800	142392000	FOXA2	chr20	4610600	4610800	NEU1
chr8	98735600	98735800	ZIC1	chr3	43243400	43243600	GPD2
chr20	13971200	13971400	SUSD2	chr7	120652800	120653000	TMEM184B
chr4	94068200	94068400	GRID2	chr10	85992000	85992200	STAC2
chr1	56168200	56168400	DACT2	chr16	10699000	10699200	FAM25A
chr1	196866000	196866200	NSMCE1	chr8	114941200	114941400	ALAS1
chr20	55604000	55604200	SIM1	chr8	45358200	45358400	UBASH3B
chr18	61639200	61639400	RAX	chr5	158083000	158083200	ALDH4A1
chr16	67047800	67048000	UNC5D	chr16	20525600	20525800	PGPEP1
chr2	186875000	186875200	ETV3	chr3	9035200	9035400	IER5L
chr9	99999400	99999600	GPC1	chr16	19233000	19233200	KLF2
chr20	4389600	4389800	PPT2	chr14	87457000	87457200	IGFBP1
chr5	48562200	48562400	RNGTT	chr20	22468400	22468600	EGR2
chr11	32858200	32858400	RUNX1	chr10	109104800	109105000	BAIAP2
chr7	120273000	120273200	GALR3	chr4	148805000	148805200	RASSF4
chr2	121165600	121165800	SOX2	chr5	153522000	153522200	RUNX3
chr3	110500400	110500600	PLCB2	chr8	119156600	119156800	TMIE

chr17	86199400	86199600	PTF1A	chr7	141503800	141504000	LIMA1
chr5	58169000	58169200	CCL27	chr10	105635600	105635800	CYGB
chr11	31391600	31391800	OLIG2	chr3	176475200	176475400	ARFGAP1
chr8	30479600	30479800	NTM	chr5	166852600	166852800	LOC100125366
chr3	124144200	124144400	ADRA1D	chr11	68201000	68201200	SLC49A4
chr15	345200	345400	KCNMA1	chr1	163386000	163386200	GUCY2D
chr1	243477800	243478000	DMRT1	chr3	140090600	140090800	NAA20
chr10	58833600	58833800	SLC13A5	chr14	7108200	7108400	HSD17B13
chr8	22993600	22993800	RGL3	chr10	57179400	57179600	MINK1
chr18	28444400	28444600	MZB1	chr12	38002200	38002400	VPS37B
chr2	189855000	189855200	NPR1	chr12	17310800	17311000	GPER1
chr12	42507000	42507200	TBX3	chr1	78938400	78938600	CCDC8
chr3	43115800	43116000	NR4A2	chr7	11752600	11752800	OAZ1
chr1	78053400	78053600	MEIS3	chr20	31987200	31987400	HK1
chr10	84292200	84292400	SKAP1	chr10	91507400	91507600	PLEKHM1
chr18	30901400	30901600	PCDHGB7	chr15	48465400	48465600	EXTL3
chr13	88995400	88995600	OLFML2B	chr3	3944200	3944400	NOTCH1
chr8	59607000	59607200	CHRNA3	chrX	155845200	155845400	DKC1
chr12	24732600	24732800	ABHD11	chr19	52668400	52668600	CRISPLD2
chr7	11589600	11589800	GNG7	chr12	22278800	22279000	EPO
chr12	46974600	46974800	TRIAP1	chr9	113585800	113586000	RALBP1
chr10	91045800	91046000	C1QL1	chr15	4568400	4568600	KCNK5
chr7	130050400	130050600	PANX2	chr5	160002400	160002600	ZBTB17
chr5	172350600	172350800	HES5	chr7	144066200	144066400	PRR13
chr20	7931800	7932000	TEAD3	chr10	13542400	13542600	ATP6VOC
chr1	216661800	216662000	CDKN1C	chr8	49748400	49748600	DSCAML1
chr10	106307400	106307600	Sept9	chr1	282145800	282146000	MIR3084A-2
chr3	145031800	145032000	SYNDIG1	chr12	18527600	18527800	ASMT

chr3	170547400	170547600	TFAP2C	chr10	18955200	18955400	KCNIP1
chr6	99434400	99434600	HSPA2	chr6	43888600	43888800	RRM2
chr6	104070800	104071000	GALNT16	chr11	67296400	67296600	STFA3
chr5	155398000	155398200	ZBTB40	chr15	34452200	34452400	LTB4R
chr1	86938000	86938200	NFKBIB	chr2	32811600	32811800	CD180
chr9	82618000	82618200	GMPPA	chr7	2902400	2902600	MYL6L
chr10	27366000	27366200	GABRA1	chr16	9075200	9075400	VSTM4
chr3	14482200	14482400	GSN	chr1	56679400	56679600	THBS2
chr4	50312000	50312200	FEZF1	chr1	198286800	198287000	DOC2A
chr7	10991400	10991600	TLE2	chr1	87064400	87064600	CAPN12
chr7	57662600	57662800	TRHDE	chr1	199609000	199609200	ITGAD
chr15	62198200	62198400	PCDH8	chr9	84418200	84418400	MOGAT1
chr18	14015000	14015200	NOL4	chr9	16668000	16668200	PTK7
chr4	58250000	58250200	KLF14	chr18	55907400	55907600	SYNPO
chr9	82618400	82618600	GMPPA	chr3	11921000	11921200	NIBAN2
chr10	86283800	86284000	NEUROD2	chr5	157330800	157331000	PLA2G2E
chr16	21295000	21295200	CILP2	chr20	5087400	5087600	ABHD16A
chr5	63785600	63785800	NR4A3	chr1	83409000	83409200	CYP2B21
chr13	73929400	73929600	NPHS2	chr19	58825400	58825600	KCNK1
chr7	117059800	117060000	MAPK15	chr16	69025400	69025600	GOT1L1
chr4	56981800	56982000	TSPAN33	chr5	57410800	57411000	AQP3
chr19	15840200	15840400	IRX3	chr9	81451400	81451600	CXCR1
chr13	74268800	74269000	TOR3A	chr13	50440000	50440200	SOX13
chr5	49308200	49308400	CNR1	chr14	35140800	35141000	KIT
chr12	9501400	9501600	PDX1	chr1	86987600	86987800	HNRNPL
chr17	8883800	8884000	PITX1	chr10	106815400	106815600	SYNGR2
chr11	86521800	86522000	GP1BB	chr3	13961000	13961200	PHF19
chr3	95133800	95134000	WT1	chr1	252456200	252456400	ANKRD22

chr13	93535600	93535800	RGS7	chr1	221530600	221530800	ARL2
chr17	85382200	85382400	SPAG6L	chr1	82185600	82185800	MEGF8
chr12	21831400	21831600	CLDN3	chr15	51500600	51500800	RHOBTB2
chr6	124902800	124903000	GPR68	chr19	10400400	10400600	DRC7
chr6	75074400	75074600	EGLN3	chr4	168131400	168131600	BCL2L14
chr3	100787800	100788000	BDNF	chr10	40497800	40498000	SLC36A3
chr6	8959800	8960000	SIX2	chr10	93519400	93519600	MRC2
chr2	185851200	185851400	MAB21L2	chr13	82224200	82224400	SCYL3
chr7	34714000	34714200	USP44	chr13	89830600	89830800	F11R
chr3	176281800	176282000	BHLHE23	chr7	13042000	13042200	MIER2
chr10	85555600	85555800	EPOP	chr16	69248400	69248600	ZFP703
chr13	51136800	51137000	MYOG	chr3	79909000	79909200	SPI1
chr3	100771400	100771600	BDNF	chr20	6113400	6113600	PNPLA1
chr10	43071200	43071400	GALNT10	chr18	28426000	28426200	SLC23A1
chr1	243601200	243601400	DMRT3	chr10	82100800	82101000	ABCC3
chr19	55520800	55521000	CBFA2T3	chr9	98205000	98205200	LRRFIP1
chr10	105775000	105775200	JMJD6	chr5	146427200	146427400	HMGB4
chr14	4350200	4350400	BARHL2	chr13	88349200	88349400	DDR2
chr5	171311600	171311800	SMIM1	chr9	16667800	16668000	PTK7
chr6	95927200	95927400	SIX1	chr18	76865800	76866000	KCNG2
chr15	52326000	52326200	DMTN	chr2	200205400	200205600	NOTCH2
chr5	149056600	149056800	LAPTM5	chr15	46629600	46629800	FAM167A
chr10	86305400	86305600	PPP1R1B	chr7	141110400	141110600	NCKAP5L
chr18	61641800	61642000	RAX	chr10	94574200	94574400	ICAM2
chr5	153502600	153502800	RUNX3	chr10	69727200	69727400	TMEM132E
chr13	31081800	31082000	CDH7	chr1	267203800	267204000	SH3PXD2A
chr3	58170800	58171000	DLX1	chr13	50933600	50933800	CHIT1
chr1	64334400	64334600	MIR935	chr1	81842600	81842800	RABAC1

chr1	131464200	131464400	NR2F2	chr7	11074400	11074600	S1PR4
chr8	71167000	71167200	RBPMS2	chr12	47195400	47195600	CABP1
chr7	125796200	125796400	ARHGAP8	chr10	103210800	103211000	RPL38
chr1	112946800	112947000	GABRA5	chr14	21602800	21603000	VCSA2
chr3	59990800	59991000	SP9	chr2	207441600	207441800	WNT2B
chr4	157745400	157745600	TAPBPL	chr10	12938000	12938200	ZSCAN10
chr10	85955800	85956000	ARL5C	chr10	89081600	89081800	PLEKHH3
chr12	5822600	5822800	FRY	chr13	110090800	110091000	PPP2R5A
chr18	54108600	54108800	MINAR2	chr5	155208600	155208800	EPHB2
chr20	5742800	5743000	UQCC2	chr1	31619600	31619800	AHRR
chr4	34968000	34968200	NXPH1	chr1	47163000	47163200	TMEM181
chr4	113752000	113752200	SEMA4F	chr10	35319000	35319200	MAPK9
chr5	153773800	153774000	RCAN3	chr5	161878200	161878400	PRDM2
chr19	49171800	49172000	CDYL2	chr2	140707200	140707400	MGST2
chr11	38273600	38273800	RIPK4	chr9	18652000	18652200	RUNX2
chr11	64935800	64936000	POPDC2	chr10	61994000	61994200	HIC1
chr2	247045800	247046000	UNC5C	chr14	23496800	23497000	UBA6
chr4	175432000	175432200	PDE3A	chr10	10640000	10640200	PPL
chr9	15495000	15495200	TAF8	chr3	13960800	13961000	PHF19
chr7	117582400	117582600	SCRT1	chr15	2346400	2346600	LRMDA
chr15	52244800	52245000	HR	chr7	140655400	140655600	TUBA1A
chr8	119135200	119135400	PRSS46	chr10	107369400	107369600	CEP295NL
chr7	143959200	143959400	AAAS	chr12	5841800	5842000	FRY
chr1	235167200	235167400	GNA14	chr8	71931000	71931200	DAPK2
chr6	42632600	42632800	ATP6V1C2	chr12	48303200	48303400	SVOP
chr5	14411800	14412000	RG520	chr1	89269600	89269800	FFAR2
chr14	106859200	106859400	OTX1	chr1	215853600	215853800	INS2
chr1	216648000	216648200	CDKN1C	chr10	56425000	56425200	SPEM2

chr11	31391400	31391600	OLIG2	chr10	16968200	16968400	DUSP1
chr12	49348600	49348800	SGSM1	chr1	48441400	48441600	SLC22A3
chr6	132950400	132950600	BEGAIN	chr2	198136600	198136800	PLEKHO1
chr18	30896600	30896800	PCDHGA10	chr7	144926600	144926800	GPR84
chr1	33910600	33910800	IRX1	chr14	104469200	104469400	RAB1A
chr1	80664800	80665000	NECTIN2	chr9	92526200	92526400	SLC16A14
chr13	49313800	49314000	CNTN2	chr5	169515200	169515400	CHD5
chr7	57662400	57662600	TRHDE	chr8	22204000	22204200	PDE4A
chr1	23907200	23907400	TCF21	chr10	94464600	94464800	SMARCD2
chr1	264496000	264496200	PAX2	chr5	126166200	126166400	DHCR24
chr10	56576200	56576400	CLDN7	chr20	31980600	31980800	HK1
chr4	157406400	157406600	CD4	chr3	94034800	94035000	RGD1563222
chr1	216661600	216661800	CDKN1C	chr1	89365800	89366000	HAMP
chr1	25173000	25173200	CLVS2	chr8	65701200	65701400	UACA
chr2	229718800	229719000	UGT8	chr3	6227400	6227600	RXRA
chr5	48223000	48223200	RRAGD	chr4	157170400	157170600	LPCAT3
chr3	14482400	14482600	GSN	chr8	36299600	36299800	ST3GAL4
chr1	80253000	80253200	ERCC1	chr11	71218600	71218800	MUC20
chr6	137383400	137383600	CLBA1	chr10	109193000	109193200	MIR3065
chr10	85062800	85063000	TBX21	chr1	100578400	100578600	NAPSA
chr15	33216800	33217000	AJUBA	chr3	9805000	9805200	TOR1A
chr20	9928600	9928800	TMPRSS3	chr2	23287400	23287600	BHMT2
chr3	1924400	1924600	CACNA1B	chr20	18498600	18498800	CISD1
chr12	22189200	22189400	TFR2	chr1	12827000	12827200	CITED2
chr17	44595000	44595200	POM121L2	chr2	112877200	112877400	NCEH1
chr3	100770000	100770200	BDNF	chr14	7167600	7167800	KLHL8
chr20	3890200	3890400	RT1-DOA	chr8	115071000	115071200	DUSP7
chr17	9731600	9731800	F12	chr15	18457000	18457200	ACOX2

chr14	80731800	80732000	ADRA2C	chr12	9858600	9858800	GTF3A
chr13	102774000	102774200	RGD1310587	chr9	98460200	98460400	ESPNL
chr6	95817200	95817400	SIX6	chr16	54319000	54319200	MTUS1
chr5	57899400	57899600	MYORG	chr7	41301800	41302000	GALNT4
chr14	77710600	77710800	MSX1	chr19	25952200	25952400	RAD23A
chr10	13081200	13081400	KREMEN2	chr7	123576400	123576600	PHETA2
chr3	170951000	170951200	BMP7	chr17	9166800	9167000	NEUROG1
chr15	62199200	62199400	PCDH8	chr12	45012400	45012600	VSIG10
chr13	51137200	51137400	MYOG	chr7	1176000	1176200	ARL13B
chr14	35582800	35583000	PDGFRA	chr15	28731600	28731800	METTL3
chr7	130826000	130826200	SYT10	chr7	122998000	122998200	ZC3H7B
chr10	90154200	90154400	HDAC5	chr13	89349600	89349800	FCGR2B
chr10	105498600	105498800	SPHK1	chr10	45521000	45521200	IBA57
chr4	115412000	115412200	ATP6V1B1	chr11	79722000	79722200	LPP
chr9	98085000	98085200	MLPH	chr12	31614800	31615000	PIWIL1
chr18	14015200	14015400	NOL4	chr5	57411000	57411200	AQP3
chr19	25899400	25899600	NF1X	chr11	44201600	44201800	ST3GAL6
chr6	119520000	119520200	FLRT2	chr1	252456400	252456600	ANKRD22
chr4	182745400	182745600	RPS4Y2	chr6	132620800	132621000	DEGS2
chr4	133951000	133951200	PDZRN3	chr13	52107000	52107200	RNPEP
chr3	159322200	159322400	SRSF6	chr18	27191400	27191600	PKD2L2
chr20	9596200	9596400	GLP1R	chr12	45714000	45714200	SRRM4
chr1	81365200	81365400	CADM4	chr6	51270800	51271000	HBP1
chr12	13363600	13363800	ZFP316	chr7	60759800	60760000	MDM2
chr1	56242400	56242600	SMOC2	chr3	7119200	7119400	RALGDS
chr12	13225600	13225800	KDEL2	chr5	152349000	152349200	SH3BGRL3
chr10	91046000	91046200	C1QL1	chr12	51248000	51248200	MN1
chr14	25590000	25590200	EPHA5	chr1	105352800	105353000	NELL1

chr18	30173000	30173200	PCDHAC2	chr1	85316600	85316800	GMFG
chr4	171250000	171250200	PTPRO	chr11	31237800	31238000	RGD1562726
chr1	33911000	33911200	IRX1	chr13	90101400	90101600	CD48
chr11	65845400	65845600	FSTL1	chr19	19404000	19404200	SNX20
chr3	98293200	98293400	KCNA4	chr1	91283800	91284000	CEBPG
chr3	22641400	22641600	LHX2	chr3	11114800	11115000	PLPP7
chr4	127809000	127809200	SUCLG2	chr3	160838000	160838200	RBPJL
chr3	58170600	58170800	DLX1	chr19	17285000	17285200	AKTIP
chr6	69972600	69972800	FOXG1	chr8	128428400	128428600	SCN10A
chr5	169494400	169494600	RPL22	chr1	221754000	221754200	PYGM
chr1	163443000	163443200	LRRC32	chr2	188523800	188524000	MTX1
chr16	71323600	71323800	FGFR1	chr6	136536600	136536800	RD3L
chr1	256383800	256384000	CYP26A1	chr13	50994000	50994200	CHIT1
chr14	45175000	45175200	KLF3	chr20	7771800	7772000	ZFP523
chr20	4330000	4330200	NOTCH4	chr5	143109000	143109200	ZC3H12A
chr2	220101000	220101200	PLPPR5	chr17	78911600	78911800	ACBD7
chr16	77152800	77153000	CSMD1	chr4	10326400	10326600	FGL2
chr3	160853200	160853400	MATN4	chr4	83970000	83970200	TRIL
chr5	82167800	82168000	ASTN2	chr2	141268200	141268400	MAML3
chr10	106974800	106975000	SOCS3	chr1	21853400	21853600	CCN2
chr2	115678400	115678600	SLC7A14	chr5	148257600	148257800	COL16A1
chr20	19318200	19318400	PHYHIPL	chr1	226245400	226245600	FEN1
chr10	106975600	106975800	SOCS3	chr2	220536400	220536600	PALMD
chr5	140889400	140889600	NT5C1A	chr4	157818600	157818800	LTBR
chr8	119566400	119566600	TRANK1	chr6	137375200	137375400	CLBA1
chr6	99434800	99435000	HSPA2	chr12	48384800	48385000	DAO
chr1	100360800	100361000	RGD1309036	chr20	3549400	3549600	DDR1
chr16	20032000	20032200	NIBAN3	chr5	151792600	151792800	GPN2

chr9	94280400	94280600	CHRNA4	chr7	2901000	2901200	MYL6L
chr8	117250200	117250400	CCDC71	chr4	153873000	153873200	SLC6A13
chr5	144761800	144762000	TFAP2E	chr4	168903800	168904000	GPRC5D
chr16	19914400	19914600	PLVAP	chr19	26100600	26100800	JUNB
chr1	216648200	216648400	CDKN1C	chr5	152758800	152759000	MTFR1L
chr3	123176800	123177000	LZTS3	chr2	196310200	196310400	LYSMD1
chr7	140308400	140308600	CACNB3	chr2	27355800	27356000	POLK
chr2	233600000	233600200	PITX2	chr10	106298000	106298200	9-Sep
chr5	133712200	133712400	FOXE3	chr19	52485600	52485800	COTL1
chr1	247476800	247477000	INSL6	chr7	121227800	121228000	PDGFB
chr12	42489600	42489800	TBX3	chr17	16223000	16223200	PHF2
chr17	72426600	72426800	GATA3	chr17	9836200	9836400	RAB24
chr15	12826200	12826400	FEZF2	chr8	32013400	32013600	ADAMTS15
chr12	23548600	23548800	ORAI2	chr5	152233000	152233200	DHDDS
chr11	28212800	28213000	GRIK1	chr19	32198800	32199000	SMAD1
chr1	32639400	32639600	IRX4	chr4	157236200	157236400	MIR141
chr12	46915200	46915400	MSI1	chr2	57193800	57194000	WDR70
chr3	61597200	61597400	HOXD12	chr16	81677200	81677400	GRTP1
chr16	21058800	21059000	NCAN	chr11	33836000	33836200	CBR1
chr14	107607600	107607800	B3GNT2	chr9	41069800	41070000	PRSS40
chr11	86553800	86554000	TBX1	chr20	12361000	12361200	SLC19A1
chr16	75968200	75968400	ANGPT2	chr10	67863400	67863600	CDK5R1
chr19	38670600	38670800	CDH3	chr10	5295000	5295200	TVP23A
chr5	43604400	43604600	EPHA7	chr15	51212000	51212200	ENTPD4
chr18	30880600	30880800	PCDHGA9	chr4	148848600	148848800	TMEM72
chr18	56180200	56180400	ARSI	chr3	162866000	162866200	SULF2
chr14	80544000	80544200	HMX1	chr8	128734800	128735000	CX3CR1
chr3	176548600	176548800	CHRNA4	chr13	26173600	26173800	PHLPP1

chr17	18339800	18340000	NUP153	chr2	187228200	187228400	SH2D2A
chr10	103937800	103938000	HID1	chr20	10019200	10019400	RSPH1
chr8	61532400	61532600	CSPG4	chr20	4803600	4803800	RT1-CE12
chr5	82168000	82168200	ASTN2	chr10	106816200	106816400	SYNGR2
chr1	85492600	85492800	SELENOV	chr12	15909600	15909800	GNA12
chr5	164977000	164977200	FBXO2	chr6	132223600	132223800	CYP46A1
chr16	19223000	19223200	KLF2	chr1	199163000	199163200	CTF1
chr3	3696200	3696400	QSOX2	chr3	2688600	2688800	PTGDS
chr12	47674200	47674400	GLTP	chr16	20675600	20675800	REX1BD
chr11	32656200	32656400	CLIC6	chr5	141008000	141008200	OXCT2A
chr10	90551000	90551200	FZD2	chr1	221300800	221301000	CDC42EP2
chr17	75992600	75992800	ECHDC3	chr4	80357600	80357800	LOC500124
chr2	228544400	228544600	TRAM1L1	chr7	11441000	11441200	ZBTB7A
chr7	144602400	144602600	HOXC8	chr19	53737600	53737800	RGD1304884
chr10	71158800	71159000	HNF1B	chr1	1942400	1942600	ZC3H12D
chr11	86556200	86556400	TBX1	chr1	101095200	101095400	FCGRT
chr7	117074200	117074400	FAM83H	chr20	5153400	5153600	PRRC2A
chr20	14283200	14283400	ADORA2A	chr6	129596600	129596800	PAPOLA
chr1	80378400	80378600	MARK4	chr2	240684800	240685000	MANBA
chr13	74268600	74268800	TOR3A	chr3	15542200	15542400	PTGS1
chr1	80253200	80253400	ERCC1	chr6	132228400	132228600	CYP46A1
chr11	86521200	86521400	GP1BB	chr8	122596600	122596800	TRIM71
chr6	109469400	109469600	JDP2	chr12	38978600	38978800	ORA1
chr6	132239800	132240000	CYP46A1	chr16	2683400	2683600	IL17RD
chr3	1924600	1924800	CACNA1B	chr12	50380400	50380600	TPST2
chr15	62200000	62200200	PCDH8	chr20	5114800	5115000	GPANK1
chr15	52325800	52326000	DMTN	chr20	50191600	50191800	PREP
chr3	141577800	141578000	PAX1	chr3	9035000	9035200	IER5L

chr20	29523800	29524000	DDIT4	chr19	25311600	25311800	MIR23A
chr12	13362000	13362200	ZFP316	chr17	9167000	9167200	NEUROG1
chr6	25620800	25621000	FOSL2	chr3	164422000	164422200	CEBPB
chr6	48452200	48452400	MYT1L	chr3	94042000	94042200	RGD1563222
chr20	8319200	8319400	CMTR1	chr19	10643400	10643600	CX3CL1
chr3	10351400	10351600	ASS1	chr5	126347400	126347600	FAM151A
chr12	47807800	47808000	FAM222A	chr1	222363600	222363800	FLRT1
chr1	131452000	131452200	NR2F2	chr3	162866200	162866400	SULF2
chr5	147306000	147306200	HPCA	chr3	102980200	102980400	OLR774
chr17	13670600	13670800	SHC3	chr10	75096000	75096200	MPO
chr1	90684200	90684400	CHST8	chr11	35766800	35767000	ERG
chr3	160558600	160558800	KCNS1	chr7	142355000	142355200	GALNT6
chr7	57662200	57662400	TRHDE	chr20	3549600	3549800	DDR1
chr15	71778800	71779000	PCDH20	chr7	12281000	12281200	RPS15
chr1	220847000	220847200	CTSW	chr12	24655400	24655600	VPS37D
chr6	71349200	71349400	PRKD1	chr5	59507400	59507600	CLTA
chr16	21290400	21290600	CILP2	chr10	19669200	19669400	SPDL1
chr10	85555800	85556000	EPOP	chr20	3889800	3890000	RT1-DOA
chr5	159333400	159333600	PADI3	chr2	188671400	188671600	ADAM15
chr14	3872200	3872400	HFM1	chr13	24846800	24847000	CDH20
chr7	140453000	140453200	WNT10B	chr7	11581600	11581800	GNG7
chr1	33915000	33915200	IRX1	chr5	154392800	154393000	RPL11
chr7	12609800	12610000	KISS1R	chr9	15622000	15622200	GUCA1B
chr9	82062600	82062800	WNT10A	chr16	20294600	20294800	RPL18A
chr20	9596000	9596200	GLP1R	chr7	10935800	10936000	ANKRD24
chr7	11302600	11302800	TJP3	chr1	166433400	166433600	STARD10
chr3	123107000	123107200	OXT	chr3	164041600	164041800	B4GALT5
chr4	117294000	117294200	EGR4	chr1	99611200	99611400	CTU1

chr1	84139600	84139800	LTBP4	chr18	76749200	76749400	HSBP1L1
chr5	153756200	153756400	NCMAP	chr9	43120000	43120200	ANKRD23
chr1	280635200	280635400	EMX2	chr10	45927000	45927200	OLR1462
chr18	30914000	30914200	PCDHGA12	chr3	155151200	155151400	PPP1R16B
chr18	59748600	59748800	ST8SIA3	chr1	168470600	168470800	OLR94
chr1	47630000	47630200	FNDC1	chr16	62484400	62484600	PURG
chr11	31422200	31422400	OLIG1	chr2	189854600	189854800	NPR1
chr13	51954600	51954800	PTPRV	chr10	105635800	105636000	CYGB
chr1	88896600	88896800	APLP1	chr19	57665400	57665600	SPRTN
chr8	108104200	108104400	SOX14	chr1	212607400	212607600	SPRN
chr4	83971200	83971400	TRIL	chr20	12364000	12364200	SLC19A1
chr4	177177800	177178000	ST8SIA1	chr1	239072800	239073000	GDA
chr1	101776000	101776200	SULT2B1	chr8	21813600	21813800	COL5A3
chr1	78592400	78592600	ARHGAP35	chr9	14721200	14721400	TREM3
chr1	226435200	226435400	SYT7	chr4	57932400	57932600	CPA5
chr4	124856800	124857000	ADAMTS9	chr5	48303400	48303600	GABRR2
chr8	15011000	15011200	FAT3	chr11	36545800	36546000	LCA5L
chr2	211222400	211222600	SARS	chr19	10635200	10635400	CCL17
chr6	134626800	134627000	DIO3	chr20	4406800	4407000	FKBPL
chr3	43116400	43116600	NR4A2	chr5	76188000	76188200	GNG10
chr9	82584600	82584800	SPEG	chr8	130019600	130019800	TRAK1
chr4	430200	430400	EN2	chr1	91374400	91374600	CEBPA
chr7	119352400	119352600	CACNG2	chr1	217357400	217357600	SHANK2
chr10	56576000	56576200	CLDN7	chr2	116168800	116169000	GPR160
chr17	85372200	85372400	BMI1	chr11	31225200	31225400	RGD1562726
chr9	15502000	15502200	TAF8	chr5	151907400	151907600	PIGV
chr10	56861000	56861200	ALOX12	chr5	157206400	157206600	PLA2G2F
chr10	84112000	84112200	MIR196C	chr3	171294600	171294800	PMEPA1

chr5	62164800	62165000	TRIM14	chr17	23922000	23922200	GFOD1
chr12	12385600	12385800	TECPR1	chr3	10684200	10684400	GPR107
chr11	31391200	31391400	OLIG2	chr3	2881400	2881600	LCN5
chr20	9233200	9233400	BTBD9	chr2	140303200	140303400	NOCT
chr1	80665000	80665200	NECTIN2	chr7	139212000	139212200	ENDOU
chr10	73279400	73279600	TBX2	chr5	64912000	64912200	RNF20
chr11	31833000	31833200	DONSON				
chr19	23386800	23387000	SALL1				
chr6	8947800	8948000	SIX2				
chr20	37588200	37588400	MSL3L2				
chr19	15840400	15840600	IRX3				
chr10	56576400	56576600	CLDN7				
chr1	87046600	87046800	LGALS7				
chr15	56958000	56958200	LRCH1				
chr8	98737400	98737600	ZIC1				
chr20	47307800	47308000	NR2E1				
chr6	46631200	46631400	SOX11				
chr4	181477200	181477400	KLHL42				
chr7	134603200	134603400	PPHLN1				
chr3	82553800	82554000	ALX4				
chr4	50312200	50312400	FEZF1				
chr3	160854200	160854400	MATN4				
chr11	34317800	34318000	SIM2				
chr11	28213000	28213200	GRIK1				
chr5	133708400	133708600	FOXE3				
chr7	24850200	24850400	POLR3B				
chr6	46631400	46631600	SOX11				
chr18	30896200	30896400	PCDHGA10				

chr7	2848200	2848400	RNF41
chr6	49324600	49324800	SNTG2
chr12	47665000	47665200	GLTP
chr4	160334600	160334800	PRMT8
chr17	53230000	53230200	HECW1
chr16	79708000	79708200	KBTBD11
chr6	39363200	39363400	LRATD1
chr1	15299600	15299800	SLC35D3
chr9	17224800	17225000	RSPH9
chr16	20305200	20305400	SLC5A5
chr5	148033200	148033400	PTP4A2
chr2	229719000	229719200	UGT8
chr2	28471000	28471200	FOXD1
chr1	90685800	90686000	CHST8
chr16	21294800	21295000	CILP2
chr19	11043400	11043600	HERPUD1
chr16	21274400	21274600	TSSK6
chr2	56892200	56892400	GDNF
chr6	104340200	104340400	PLEKHD1
chr9	97060600	97060800	GBX2
chr7	144274200	144274400	ATP5MC2
chr12	13362200	13362400	ZFP316
chr17	44594800	44595000	POM121L2
chr4	56337400	56337600	LEP
chr17	14825200	14825400	BARX1
chr4	153816000	153816200	USP18
chr5	144762000	144762200	TFAP2E
chr15	62199400	62199600	PCDH8

chr16	19223200	19223400	KLF2
chr4	181477000	181477200	KLHL42
chr3	56768800	56769000	SP5
chr2	5576200	5576400	NR2F1
chr14	60764200	60764400	LGI2
chr5	109625600	109625800	ELAVL2
chr13	84012200	84012400	CD247
chr7	25040000	25040200	NUAK1
chr10	23663400	23663600	EBF1
chr9	97057400	97057600	GBX2
chr5	107825200	107825400	CDKN2A
chr6	28235000	28235200	DNMT3A
chr1	91673400	91673600	CEP89
chr3	100771600	100771800	BDNF
chr5	133712400	133712600	FOXE3
chr18	14016600	14016800	NOL4
chr12	14092600	14092800	RADIL
chr4	115701400	115701600	DYSF
chr13	89765800	89766000	ARHGAP30
chr4	7185800	7186000	GBX1
chr1	11907400	11907600	RN5-8S
chr2	5592800	5593000	NR2F1
chr12	17193200	17193400	UNCX
chr3	145032000	145032200	SYNDIG1
chr2	36246200	36246400	HTR1A
chr1	84080400	84080600	NUMBL
chr5	158304600	158304800	PAX7
chr10	13081400	13081600	KREMEN2

chr6	109110800	109111000	ZC2HC1C
chr1	33914400	33914600	IRX1
chr4	114859000	114859200	LOC500227
chr7	11180800	11181000	DOHH
chr7	44770400	44770600	ALX1
chr5	169464200	169464400	HES3
chr1	25173200	25173400	CLVS2
chr3	61578400	61578600	HOXD13
chr4	51843200	51843400	GPR37
chr14	39963800	39964000	GABRG1
chr20	7724600	7724800	SCUBE3
chr1	144833800	144834000	MEX3B
chr1	173682200	173682400	RIC3
chr1	221108800	221109000	LTBP3
chr17	43903400	43903600	BTN1A1
chr20	5445600	5445800	B3GALT4
chrX	156227600	156227800	OLR1768
chr3	100770200	100770400	BDNF
chr3	15430000	15430200	LHX6
chr10	73336800	73337000	TBX4
chr5	63784800	63785000	NR4A3
chr19	31031200	31031400	FREM3
chr1	33273200	33273400	IRX2
chr1	52896600	52896800	TBXT
chr1	197001200	197001400	IL21R
chr1	260267800	260268000	BLNK
chr1	247476600	247476800	INSL6
chr20	9567800	9568000	GLP1R

chr9	82419800	82420000	TUBA4A
chr17	52568800	52569000	GLI3
chr4	137785200	137785400	CNTN4
chr6	99434600	99434800	HSPA2
chr12	12025000	12025200	NPTX2
chr14	106859000	106859200	OTX1
chr9	66703600	66703800	FAM117B
chr5	98468800	98469000	LURAP1L
chr18	402000	402200	FUNDC2
chr2	116526600	116526800	EGFEM1
chr3	61669000	61669200	HOXD3
chr19	26026600	26026800	DNASE2
chr1	81946400	81946600	GRIK5
chr1	102416000	102416200	KCNC1
chr3	22626600	22626800	LHX2
chr7	117354000	117354200	SMPD5
chr14	4372400	4372600	BARHL2
chr13	98843800	98844000	PARP1
chr15	46428600	46428800	GATA4
chr15	62199800	62200000	PCDH8
chr16	69239600	69239800	ZFP703
chr1	100314200	100314400	SHANK1
chr19	53045000	53045200	FOXC2
chr10	56576600	56576800	CLDN7
chr2	45104600	45104800	ESM1
chr17	11684000	11684200	MSX2
chr7	10991800	10992000	TLE2
chr18	30905000	30905200	PCDHGA11

chr18	8359200	8359400	CDH2
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Suppl. Table 4. Go enrichment. Analysis was performed using Gene Ontology (<http://geneontology.org/docs/go-enrichment-analysis/>)

GO biological process complete		# of genes in the Rattus norvegicus - REFLIST (out of 21586)	# of genes in gene list	Expected	Fold enrich ment	P-value	FDR	Combined score. (- log10(FDR)*FC)
YM hyper								
Differentiation	regulation of cell population proliferation (GO:0042127)	1730	57	21.64	2.63	2.21E-11	4.41E-08	19.35
	negative regulation of developmental process (GO:0051093)	975	37	12.2	3.03	3.51E-09	2.00E-06	17.27
	multicellular organism development (GO:0007275)	4851	112	60.68	1.85	4.47E-12	2.38E-08	14.10
	cellular developmental process (GO:0048869)	3515	87	43.97	1.98	1.52E-10	1.10E-07	13.78
	system development (GO:0048731)	4522	105	56.56	1.86	2.98E-11	4.31E-08	13.70
	cell differentiation (GO:0030154)	3467	86	43.37	1.98	2.02E-10	1.40E-07	13.57
	developmental process (GO:0032502)	5734	123	71.72	1.71	3.95E-11	4.84E-08	12.51
	anatomical structure development (GO:0048856)	5256	115	65.74	1.75	7.67E-11	7.19E-08	12.50
	negative regulation of cell differentiation (GO:0045596)	700	26	8.76	2.97	1.30E-06	3.10E-04	10.42
	animal organ development (GO:0048513)	3576	83	44.73	1.86	1.42E-08	6.86E-06	9.60
	regulation of cell differentiation (GO:0045595)	1619	46	20.25	2.27	3.29E-07	1.01E-04	9.07
	cell fate commitment (GO:0045165)	261	12	3.26	3.68	1.60E-04	2.01E-02	6.24
	negative regulation of cell population proliferation (GO:0008285)	721	23	9.02	2.55	5.55E-05	7.90E-03	5.36
	tissue development (GO:0009888)	1744	43	21.81	1.97	2.57E-05	4.10E-03	4.70
	positive regulation of developmental process (GO:0051094)	1446	35	18.09	1.94	2.12E-04	2.54E-02	3.09
Apoptosis regulation	negative regulation of apoptotic process involved in development (GO:1904746)	8	3	0.1	29.98	2.86E-04	3.28E-02	44.49
	regulation of programmed cell death (GO:0043067)	1537	42	19.22	2.18	2.36E-06	4.95E-04	7.21
	regulation of apoptotic process (GO:0042981)	1504	41	18.81	2.18	3.40E-06	6.69E-04	6.92
	regulation of cell death (GO:0010941)	1706	43	21.34	2.02	1.31E-05	2.41E-03	5.29

T cell activation	negative regulation of programmed cell death (GO:0043069)	975	26	12.2	2.13	3.44E-04	3.83E-02	3.02
	regulation of T cell receptor signaling pathway (GO:0050856)	44	6	0.55	10.9	3.39E-05	5.14E-03	24.95
	negative regulation of alpha-beta T cell activation (GO:0046636)	43	5	0.54	9.3	3.08E-04	3.50E-02	13.54
	regulation of antigen receptor-mediated signaling pathway (GO:0050854)	62	6	0.78	7.74	1.94E-04	2.36E-02	12.59
	regulation of antigen receptor-mediated signaling pathway (GO:0050854)	94	7	1.18	5.95	2.60E-04	3.03E-02	9.04
	regulation of immune system process (GO:0002682)	1481	42	18.52	2.27	8.58E-07	2.24E-04	8.28
	positive regulation of T cell activation (GO:0050870)	209	10	2.61	3.83	4.16E-04	4.45E-02	5.18
	regulation of leukocyte activation (GO:0002694)	657	21	8.22	2.56	1.14E-04	1.47E-02	4.69
	regulation of T cell activation (GO:0050863)	331	13	4.14	3.14	3.77E-04	4.14E-02	4.34
	cell surface receptor signaling pathway (GO:0007166)	1832	44	22.91	1.92	3.94E-05	5.93E-03	4.28
Resonse to hypoxia	response to decreased oxygen levels (GO:0036293)	437	18	5.47	3.29	1.60E-05	2.80E-03	8.40
	response to hypoxia (GO:0001666)	416	17	5.2	3.27	3.04E-05	4.70E-03	7.61
	response to oxygen levels (GO:0070482)	478	18	5.98	3.01	4.96E-05	7.25E-03	6.44
	response to oxygen-containing compound (GO:1901700)	2043	49	25.55	1.92	1.44E-05	2.61E-03	4.96
Response to immune response	multicellular organismal response to stress (GO:0033555)	102	7	1.28	5.49	4.14E-04	4.46E-02	7.42
	response to lipid (GO:0033993)	1204	33	15.06	2.19	2.90E-05	4.54E-03	5.13
	cellular response to cytokine stimulus (GO:0071345)	797	23	9.97	2.31	2.63E-04	3.04E-02	3.50
	response to cytokine (GO:0034097)	935	26	11.7	2.22	2.28E-04	2.69E-02	3.49
	regulation of immune response (GO:0050776)	919	25	11.49	2.17	3.79E-04	4.11E-02	3.01
MO hyper								
regulation of proliferation	positive regulation of cell population proliferation (GO:0008284)	1020	25	11.58	2.16	3.90E-04	2.85E-02	3.34
	negative regulation of cell population proliferation (GO:0008285)	721	25	8.18	3.05	1.19E-06	1.72E-04	11.48

Differentiation	regulation of cell population proliferation (GO:0042127)	1730	51	19.64	2.6	3.88E-10	1.55E-07	17.71
	cell fate specification (GO:0001708)	85	10	0.96	10.37	1.16E-07	2.00E-05	48.73
	cell fate commitment (GO:0045165)	261	20	2.96	6.75	6.68E-11	3.44E-08	50.38
	stem cell differentiation (GO:0048863)	175	9	1.99	4.53	2.43E-04	1.99E-02	7.71
	cell morphogenesis involved in differentiation (GO:0000904)	582	26	6.61	3.94	5.96E-09	1.53E-06	22.91
	developmental growth (GO:0048589)	474	20	5.38	3.72	8.67E-07	1.28E-04	14.48
	growth (GO:0040007)	478	20	5.43	3.69	9.82E-07	1.44E-04	14.18
	cellular component morphogenesis (GO:0032989)	626	25	7.11	3.52	9.58E-08	1.73E-05	16.76
	cell morphogenesis (GO:0000902)	755	30	8.57	3.5	5.04E-09	1.34E-06	20.56
	taxis (GO:0042330)	482	19	5.47	3.47	4.25E-06	5.55E-04	11.30
	negative regulation of cell differentiation (GO:0045596)	700	25	7.94	3.15	7.12E-07	1.07E-04	12.51
	negative regulation of developmental process (GO:0051093)	975	30	11.07	2.71	1.08E-06	1.57E-04	10.31
	cell development (GO:0048468)	1814	55	20.59	2.67	2.34E-11	1.49E-08	20.90
	tissue development (GO:0009888)	1744	50	19.79	2.53	2.17E-09	6.29E-07	15.69
	regulation of cell development (GO:0060284)	596	17	6.76	2.51	5.96E-04	4.01E-02	3.51
	regulation of cell differentiation (GO:0045595)	1619	46	18.38	2.5	1.35E-08	3.21E-06	13.73
	positive regulation of cell differentiation (GO:0045597)	946	25	10.74	2.33	1.16E-04	1.02E-02	4.64
	positive regulation of developmental process (GO:0051094)	1446	37	16.41	2.25	4.54E-06	5.88E-04	7.27
	cell differentiation (GO:0030154)	3467	87	39.35	2.21	1.77E-13	3.13E-10	21.00
T cell receptor signaling pathway	cellular developmental process (GO:0048869)	3515	88	39.9	2.21	1.30E-13	2.58E-10	21.19
	regulation of developmental process (GO:0050793)	2541	61	28.84	2.12	1.46E-08	3.41E-06	11.59
	developmental process (GO:0032502)	5734	127	65.08	1.95	1.15E-16	4.60E-13	24.06
Notch signaling pathway	regulation of T cell receptor signaling pathway (GO:0050856)	44	5	0.5	10.01	2.18E-04	1.82E-02	17.42
	regulation of T cell activation (GO:0050863)	331	13	3.76	3.46	1.48E-04	1.28E-02	6.55
Notch signaling pathway	Notch signaling pathway (GO:0007219)	113	7	1.28	5.46	4.18E-04	3.00E-02	8.31

regulation of leukocyte activation and adhesion	cell-cell adhesion via plasma-membrane adhesion molecules (GO:0098742)	216	13	2.45	5.3	2.07E-06	2.82E-04	18.81
	homophilic cell adhesion via plasma membrane adhesion molecules (GO:0007156)	136	8	1.54	5.18	2.28E-04	1.88E-02	8.94
	negative regulation of cell activation (GO:0050866)	222	10	2.52	3.97	3.07E-04	2.40E-02	6.43
	negative regulation of leukocyte activation (GO:0002695)	201	9	2.28	3.95	6.37E-04	4.21E-02	5.43
	regulation of cell-cell adhesion (GO:0022407)	446	18	5.06	3.56	5.61E-06	7.15E-04	11.20
	regulation of leukocyte cell-cell adhesion (GO:1903037)	324	13	3.68	3.54	1.21E-04	1.06E-02	6.99
	chemotaxis (GO:0006935)	477	19	5.41	3.51	3.68E-06	4.88E-04	11.62
	cell-cell adhesion (GO:0098609)	447	17	5.07	3.35	2.14E-05	2.30E-03	8.84
	negative regulation of cell adhesion (GO:0007162)	297	11	3.37	3.26	7.60E-04	4.81E-02	4.30
	negative regulation of immune system process (GO:0002683)	446	14	5.06	2.77	7.44E-04	4.74E-02	3.67
	cell adhesion (GO:0007155)	788	24	8.94	2.68	1.63E-05	1.85E-03	7.32
	biological adhesion (GO:0022610)	797	24	9.05	2.65	1.95E-05	2.13E-03	7.08
	regulation of cell activation (GO:0050865)	701	20	7.96	2.51	1.97E-04	1.67E-02	4.46
	locomotion (GO:0040011)	1232	34	13.98	2.43	2.51E-06	3.40E-04	8.43
	regulation of cell adhesion (GO:0030155)	762	21	8.65	2.43	3.39E-04	2.59E-02	3.86
	regulation of leukocyte activation (GO:0002694)	657	18	7.46	2.41	6.52E-04	4.29E-02	3.30
	cell migration (GO:0016477)	883	23	10.02	2.29	2.68E-04	2.12E-02	3.83
	localization of cell (GO:0051674)	1033	25	11.72	2.13	4.43E-04	3.16E-02	3.20
	cell motility (GO:0048870)	1033	25	11.72	2.13	4.43E-04	3.15E-02	3.20
	cell surface receptor signaling pathway (GO:0007166)	1832	38	20.79	1.83	3.22E-04	2.49E-02	2.93
	regulation of cell communication (GO:0010646)	3311	63	37.58	1.68	3.60E-05	3.66E-03	4.09
	regulation of signaling (GO:0023051)	3323	63	37.72	1.67	3.71E-05	3.74E-03	4.05
	regulation of localization (GO:0032879)	2954	56	33.53	1.67	1.15E-04	1.02E-02	3.33
	regulation of response to stimulus (GO:0048583)	3847	66	43.66	1.51	4.10E-04	2.97E-02	2.31

YM hypo

B cell differentiation	B cell differentiation (GO:0030183)	115	8	1.58	5.07	2.74E-04	3.70E-02	7.26
Glycolysis	canonical glycolysis (GO:0061621)	7	3	0.1	31.25	2.74E-04	3.61E-02	45.08
	glucose catabolic process (GO:0006007)	12	4	0.16	24.31	5.25E-05	1.03E-02	48.31
	NAD metabolic process (GO:0019674)	18	4	0.25	16.21	1.98E-04	2.87E-02	25.00
	monosaccharide catabolic process (GO:0046365)	21	4	0.29	13.89	3.32E-04	3.95E-02	19.49
	glucose catabolic process to pyruvate (GO:0061718)	7	3	0.1	31.25	2.74E-04	3.64E-02	44.97
Granulocyte differentiation	granulocyte differentiation (GO:0030851)	25	6	0.34	17.5	3.23E-06	1.47E-03	49.57
Regulation of differentiation	leukocyte differentiation (GO:0002521)	381	18	5.22	3.45	9.36E-06	3.32E-03	8.55
	positive regulation of cell differentiation (GO:0045597)	946	30	12.97	2.31	2.72E-05	6.89E-03	4.99
	regulation of cell differentiation (GO:0045595)	1619	44	22.2	1.98	1.95E-05	5.87E-03	4.42
	cell differentiation (GO:0030154)	3467	78	47.54	1.64	7.35E-06	2.86E-03	4.17
Negative regulation of adhesion	negative regulation of cell-cell adhesion (GO:0022408)	198	12	2.72	4.42	3.10E-05	7.50E-03	9.39
	negative regulation of cell adhesion (GO:0007162)	297	14	4.07	3.44	9.45E-05	1.57E-02	6.21
	regulation of cell adhesion (GO:0030155)	762	26	10.45	2.49	4.64E-05	9.60E-03	5.02
	regulation of cell-cell adhesion (GO:0022407)	446	21	6.12	3.43	1.76E-06	1.04E-03	10.23
Positive regulation of inflammatory response	positive regulation of inflammatory response (GO:0050729)	139	9	1.91	4.72	1.91E-04	2.84E-02	7.30
Regulation of phagocytosis	regulation of phagocytosis, engulfment (GO:0060099)	20	4	0.27	14.59	2.82E-04	3.68E-02	20.92
Leukocyte chemotaxis	leukocyte chemotaxis involved in inflammatory response (GO:0002232)	8	3	0.11	27.35	3.73E-04	4.19E-02	37.68
	leukocyte migration involved in inflammatory response (GO:0002523)	32	5	0.44	11.39	1.34E-04	2.11E-02	19.09

MO hypo

No enrichment