Supplementary Appendix

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

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Supplementary Appendix

A. Supplementary Methods

Whole Genome Sequencing and mutation validation.

Whole genome sequencing (with paired end reads) and analysis was performed exactly as described.[1] Validation of putative somatic SNVs and indels with Sanger sequencing was performed as described.[1]

Measuring expression levels of identified somatic mutations using RT-PCR followed by 454 readcounts.

Deep readcounts of variant alleles in cDNA obtained from primary AML bone marrow samples was performed exactly as described.[1]

RNA expression arrays and analysis.

Specimen RNA was extracted, assayed for quality, and subjected to Affymetrix Human Genome U133 Plus 2.0 Array GeneChip microarrays (Affymetrix) as described.[2] Profiling data for all specimens have been deposited on the Gene Expression Omnibus (GEO;http://www.ncbi.nlm.nih.gov/geo/; accession no. GSE12662). Cel files were processed using the MAS5 algorithm (Affymetrix) and only probesets called "present" in at least 75% of specimens in either *DNMT3A* mutated or wild type groups were retained. These filtered probesets were z-scored and Ward's unsupervised hierarchical clustering was performed (Spotfire DecisionSite 8.2 software, TIBCO).

Measuring 5-methylcytosine content by mass spectrometry.

Reagents and calibration solutions. Deoxyribonucleoside compounds were purchased from USB Corporation (Cleveland, OH) (5-methyl-2'-deoxycytidine monophosphate disodium salt (mdCMP), 2'-deoxyguanosine-5'-monophosphate disodium salt (dGMP), 2'-deoxyadenosine-5'-monophosphate free acid (dAMP)) or from Sigma Aldrich (2'-deoxycytidine monophosphate sodium salt (dCMP), thymidine (T), 2'-deoxyadenosine monohydrate (dA), 2'-deoxycyidine (dC), thymidine 5'-monophosphate disodium salt hydrate (TMP)). Water (LC-MS Chromasolv) and formic acid (1.00 mL ampoules, Puriss) were purchased from Fluka. Methanol (HPLC grade) was purchased from Fisher Scientific. The reference nucleosides and nucleoside monophosphates were weighed on an analytical balance and then dissolved in 1.00 mL of 5% methanol/0.1% formic acid. The concentrations of stock solutions accounted for the organic purity and water content as supplied by the manufacturer. The resulting stock solutions were used to prepare a 50 pmol/μL working stock solution, from which was prepared analytical solutions of 0.0050, 0.010, 0.050, 0.10, 0.50, 1.0, and 5.0 fmol/uL.

LC-ESI-MS/MS. Liquid chromatography-tandem mass spectrometry (LC-MS/MS) analyses were performed using a Shimadzu SCL-10A VP HPLC system (Columbia, MD) which was interfaced with a 4000 Q-Trap (MS/MS) mass

spectrometer (Applied Biosystems, Foster City, CA). Instrument operation and data acquisition were controlled with the Analyst software package (Version 1.4.2, Applied Biosystems). The HPLC system consisted of an autosampler, a binary pump, and a degasser. Chromatography and optimization of mass spectrometer source and MRM parameters was performed as previously described.[3] Samples were analyzed at a flow rate of 0.22 ml/min on an Atlantis dC18 column (2.1 x 150 mm, 5µ, Waters Corporation). Mobile phases were 0.1% formic acid (A) and 0.1% formic acid/100% methanol (B). Compounds of interest were eluted using the following gradient: linear gradient from 0% B to 12.5% B (0 to 15 min), linear gradient from 12.5% B to 80% B (15 to 17 min), 80% B (17 to 18 min), linear gradient from 100% B to 0% B (18 to 18.5 min), and 0% B (16 min. and after). Total run time was 25 min. Injection volume was 20 µl. All MS/MS analyses were performed in positive ion mode by electrospray ionization (ESI) using a Turbo IonSpray source. Curtain, nebulizer, turbo, and collisionally-activated dissociation gases were 30 psig, 25 psig, 30 psig, 4 psig, respectively. Turbo heater temperature was 500 ºC, and ion spray voltage was 5500 V. Dwell time for each MRM transition was 100 msec; total duty cycle time was 0.945 sec.

Preparation of DNA samples. Total genomic DNA was hydrolyzed exactly as described.[4] From a test sample with a DNA concentration of ~ 35 ng/µL, tenfold dilutions gave signal responses within the working quantification range (0.1-100 fmols on column). After DNA hydrolysis, each of the test samples had a theoretical concentration of approximately 10 ng/µL DNA. Based on these initial estimates, the samples were analyzed after a three-fold dilution of the DNA hydrolysates. Several of the samples required repeat analysis with a five-fold dilution of the hydrolysate. Standard curves were prepared for each set of analyses on the same day. An injection volume of 20 µL was used, resulting in on-column amounts of 0.10, 0.20, 1.0, 2.0, 10.0, 20.0, and 100.0 fmols for each nucleoside or nucleoside monophosphate compound. Peak areas and the corresponding molar amount of analyte were determined using Analyst software, and the resulting values were exported to an Excel spreadsheet for calculation of methylation ratios using two methods. The percentage methylation was calculated by dividing the measured level of mdCMP by the measured level of dGMP [3] or by using the sum of mdCMP and dCMP.[5]

MeDIP-chip assays and analysis.
Genomic DNA from the bone marrow of five AML samples without the R882H mutation and five AML samples with the mutation were prepared for methylated DNA immunoprecipitation (MeDIP) exactly as described (http://app.roche-biochem.jp/pdf/products/microarray/trust_srv/DNA_Methylation_Sample_Prep_v4p1.pdf).

Comparative hybridization was performed on NimbleGen Human DNA Methylation 2.1M Deluxe Pro Arrays, which contain targets for all annotated CpG islands and most gene and miRNA promoters, using established protocols (http://www.nimblegen.com/products/lit/methylation_userguide_v7p1.pdf). The

log ratios of the probe intensities were scaled around zero by subtracting the biweight mean of all values from each log-ratio. The resulting 2.1M log ratios for ten samples were made available in GFF file format for data analysis.

The top 2,000 differentially methylated probes among the 10 samples based on mean absolute deviation were selected, and both Pearson-Ward clustering and k-means clustering were performed (k=2). The samples that did not cluster in the appropriate groups were the M5 AML subtype UPN# 737451 with the R882H mutation, and the M4 AML subtype UPN# 418499 without the mutation.

The following method was developed to identify regions with significant difference in methylation between AML samples with or without the R882H mutation in *DNMT3A*.

1. The following criteria were applied to select probes among the 2.1M for the statistical test.
   - The mean $\log_2$-ratio (signal intensity of immunoprecipitated sample/signal intensity of non-immunoprecipitated sample) for 5 DNMT3A mutant samples vs. the mean $\log_2$-ratio of 5 DNMT3A wild type samples were different by a value of 1 or more
   - At least 4 out of 5 *DNMT3A* mutant $\log_2$-ratios >= 1, or at least 4 out of 5 *DNMT3A* wild type $\log_2$-ratios >= 1. This allows for the two outliers detected during unsupervised clustering.
2. For all probes selected, we calculated the mean of $\log_2$-ratios for both groups using 5 consecutive probes, which include the current probe and two on either side.
3. We performed a paired t-test between the 5 *DNMT3A* mutant means and 5 *DNMT3A* wild type means, calculated above. If the resulting p-value is <= 0.05, we considered this probe as differentially methylated.
4. We clustered the differentially methylated probes identified above if they were 220bp or closer to each other. This resulted in 1,214 clusters. Among them, 423 clusters contained 2 or more differentially methylated probes and 182 clusters contained 3 or more differentially methylated probes.

Statistical analysis of survival by risk group.
Mean differences between patients with and without the *DNMT3A* mutation were compared with two-sided independent-sample t-tests. Differences in distribution of the highly skewed WBC measurements were compared with a Wilcoxon rank-sum tests. Differences in the distribution of nominal variables between those with or without the *DNMT3A* mutation were compared with Fisher's Exact tests or Pearson chi-squared tests. Figures were generated with SAS PROC LIFETEST, which also calculated the log-rank and Wilcoxon test statistics comparing survival between the two *DNMT3A*-mutation groups. Multivariate Cox proportional-hazards analyses[6] were performed with SAS PROC PHREG. Variables evaluated as potential confounders in the proportional hazards model were *FLT3* mutation, IDH1 mutation, NPMc mutation, male sex, white race, age, FAB

category of M3, normal cytogenetics, and cytogenetic risk group. The analyses were generated using SAS/STAT software (Version 9.2 of the SAS System for Windows, SAS Institute Inc., Cary, NC).

B. Supplementary Results and Discussion

Clinical AML treatment protocols. Among the 188 patients treated at Washington University, 72 were treated with a standard seven day induction regimen of infusional cytarabine plus three days of an anthracycline ("7+3"), and 61 received a similar regimen that also included 3 days of etoposide ("7+3+3"). Twenty-four patients with acute promyelocytic leukemia (AML M3), were treated with 7+3 plus concurrent ATRA. Thirteen patients were treated with either azacytidine or decitabine. Nine patients were treated with lenalidomide. Two patients received an induction regimen of cladribine, mitoxantrone, and high-dose cytarabine ("CLAM"). Six patients received no chemotherapy (except hydroxyurea), and one patient was treated with infusional cytarabine alone. Seventy-nine patients subsequently underwent stem cell transplantation. Of these, 24 underwent autologous stem transplantation, of which 10 also underwent allogeneic transplant after relapsing. Fifty-five patients underwent allogeneic transplant (without prior autologous transplant). One of the allogeneic transplant only patients failed *DNMT3A* genotyping.

Among the 94 CALGB patients, fifty-eight patients were treated according to CALGB 9621, in which they were randomized to receive PSC833 vs placebo with concurrent infusional cytarabine, daunorubicin, and etoposide, followed by risk-adapted consolidation. Thirteen patients were treated with according to CALGB 9222, in which they received infusional cytarabine plus daunorubicin induction, followed by randomization to consolidation with high dose cytarabine, with or without cyclophosphamide and etoposide, or diaziquone and mitoxantrone. Thirteen patients with AML M3 were enrolled in CALGB 9191 and were randomized to induction therapy with ATRA vs cytarabine and daunorubicin. Fourteen AML M3 patients were enrolled in CALGB 9710 and were randomized to receive cytarabine, daunorubicin, and ATRA induction, with or without arsenic trioxide during consolidation. No patients in the CALGB group underwent stem cell transplantation.

Variant allele frequency of the *DNMT3A* mutation in sample 933124
Using PCR, we amplified DNA containing the position of the frameshift mutation at L723, and performed "deep readcounts" to determine the variant allele frequency of this mutation in the de novo and relapse specimens. The variant allele frequency of this mutation was 38.86% (1819/4706 reads) in the de novo AML genome, and 29.75% (1600/5405 reads) at relapse. These data suggest that this mutation was present in most cells of the dominant clone at presentation (100% bone marrow blasts) and at relapse (78% blasts).[7]

5-Methylcytosine measurements in genomic DNA from AML samples
The LC-ESI-MS/MS conditions were optimized by infusing a 10 ng/μL solution of each standard compound in 5% methanol/0.1% formic acid.[3] The reported transition pairs 288.2/112.2, 308.0/112.0, 322.0/126.1, 332.1/136.2, 252.1/135.9, 348.8/152.1, 323.0/81.0, and 243.3/127.2 were used for dC, dCMP, mdCMP, dAMP, dA, dGMP, TMP, and T, respectively.[4] The source parameters were optimized by infusing a solution of mdCMP (10 ng/μL in 5% methanol/0.1% formic acid) at 0.22 mL/min in order to minimize in-source fragmentation. Quantification was performed by injecting standard solutions of the standard mixture as described above in the Supplementary Methods. Under these conditions, all standard analytes gave linear curves with correlation coefficients greater than 0.99 in the range of 0.1 to 100 fmols injected. For five replicate standard curves, the coefficients of variation were 15-24% for mdCMP, 18-29% for dCMP, and 15-25% for dGMP.

The LC-MS-MS analysis for patient samples was performed using 3.5-5 ng/μL of DNA hydrolysis products. The percentage of methylation was determined by either dividing the measured amount of mdCMP (in fmols) by the amount of dGMP in each sample or by dividing the sum of mdCMP and dCMP detected in each sample. The quantity of dGMP was used based on the assumption that dGMP = dCMP + mdCMP.[3] For a control sample containing approximately 5% mdCMP, the average percentage of mdCMP was determined to be 4.2 +/- 0.1%, with a coefficient of variation of 3.5%, for four replicate measurements. The percentages of mdCMP in the control and patient samples are summarized in **Supplementary Table 5**. Both calculation methods gave approximately the same values of 5-methyl deoxycytidine monophosphate in the patient samples.

Regions of differential methylation in genomes with R882H mutations detected by meDIP-chip
182 genomic regions had statistically different methylation levels (at specific genomic locations) that were related to *DNMT3A* mutation status (**Supplementary Figure 8B** and **Supplementary Table 6**).The methylation status of only two loci correlated precisely with the R882 mutation. An example of one such region near the *ESRP2* gene on chromosome 16 is shown in **Supplementary Figure 9**. In one region (shaded in gray), all non-mutated genomes (top 5 samples) have a methylation peak, and all *DNMT3A* mutant genomes (bottom 5 colored samples) have no detectable peak at the same location. Of note, there was no change in the level of expression of the nearest neighbor genes in the samples with the mutation.

Predicted consequences of *DNMT3A* mutations
The most common mutation in *DNMT3A* was found at amino acid position R882. Strong selection for mutations at this position suggest that the R882 mutations have a gain-of-function activity, similar in principle to that recently demonstrated for *IDH1* and 2.[8, 9] In our study, 37/62 (60%) of patients with *DNMT3A* mutations

had mutations at this site (R to H most common, followed by R to C, and R to P or R to S; **Supplementary Table 2**). Yamashita, *et al*, recently reported R882H or R882C mutations in 3/74 AML samples tested; the low frequency could be related to technical issues, or the selection of patients used in their study.[10] The pattern of mutations is remarkably similar to the pattern seen in the *IDH1* gene, where recurring missense mutations (predominantly R to H or R to C) are found only at amino acid R132. Our data show that heterozygous R882H mutations are associated with reduced methylation at a small subset of genomic positions, suggesting that the mutation may in fact have a dominant negative effect on the methylase activity of this enzyme. Yamashita, *et al*, found that *DNMT3A* with an R882H mutation had reduced activity in a *de novo* methylation assay, and did not confer global changes in CpG methylation when transfected into Ba/F3 cells.[10] In a domain-mapping experiment, Gowher, *et al*, also showed that a mutation at position R882 reduced the enzymatic activity of the methylase domain, and reduced DNA binding activity.[11] Importantly, an inherited, homologous mutation (R823G) in the *DNMT3B* gene has been identified in patients with the ICF syndrome (immunodeficiency, centromeric instability, and facial abnormalities), which is characterized in part by chromosomal rearrangements in lymphocytes.[12, 13] Since *DNMT3A* has been shown to interact with many proteins, including *DNMT3L*, SUMO-1, transcriptional repressors, histone modifying proteins, and TP53,[14] it is also possible that the R882 mutations alter one or more of these interactions, or create alternative activities that are currently unknown. In addition to the *de novo* methylation activity of *DNMT3A,* there is evidence that *DNMT3A* may also play a role in maintenance of methylation through its recruitment to nucleosomes and specific chromatin regions that contain methylated DNA.[15]

The diversity of mutations in the *DNMT3A* gene is reminiscent of the large number of mutations that inactivate classical tumor suppressor genes like *TP53* or *BRCA1*.[16, 17] The nonsense and frameshift mutations of *DNMT3A* are all predicted to result in truncated proteins that eliminate (8 of 11) or shorten (3 of 11) the methylase domain;[18] several are associated with nonsense-mediated decay, clearly demonstrating loss of function (**Supplementary Figure 4**). The distribution of frameshift, nonsense, and missense mutions in *DNMT3A* are remarkably similar to the pattern of mutations seen in the *DNMT3B* gene in the ICF syndrome.[19, 20] Missense mutations are generally found within the methylase domain (37 of 38), near the homodimer interface (R882C, R882H, R882P), along the length of the *DNMT3L* interacting helix (R729Q, R729W, R736H, A741V), or near the DNA binding groove (P718L, R792H, R803S, K829R, R882C, R882H, R882P, F909C; see **Supplementary Figure 16**).[18, 21] Mutations commonly occur at charged positions (10 of 12) and may alter or abolish homo/heterodimeric complexes and DNA binding properties. The SIFT/Polyphen algorithms suggest that many of the missense mutations are deleterious for protein function, but some are not (**Supplementary Table 2**). Of note, *DNMT3A* haploinsufficiency is not deleterious to mice,[22] and complete loss of *DNMT3A* in the bone marrow cells of mice does not overtly alter hematopoiesis in the short term.[23] Although

many *DNMT3A* mutations clearly cause loss-of-function (nonsense mediated decay, truncation, deletion, some missense mutations), many more studies will be required to understand how these mutations contribute to AML pathogenesis.

Overall survival of patients with *DNMT3A* mutations and other common AML mutations

Several large studies have documented that adult AML patients harboring poor risk genotypes (*FLT3* mutations, *FLT3* mutations with *NPM* wild-type, and *IDH* mutants) have an inferior overall survival. We, therefore, examined the impact of *DNMT3A* mutations in patients with poor risk genotypes. *DNMT3A* mutations conferred a significantly worse overall survival for patients with *FLT3* mutations (p=0.0006), for patients with WT *NPM1* (p=0.01), and for patients with *FLT3* mutations who are *NPM1* wild-type (p=0.04) (**Supplementary Figure 13**). There was a trend towards worse overall survival for patients with *DNMT3A* mutations and *IDH1* mutations (p=0.06), but not for the few patients with *IDH2* mutations, or *IDH1* and 2 mutations combined. *DNMT3A* mutations were also associated with a worse overall survival for patients with favorable risk genotypes (*FLT3* wild-type, *NPMc*, *IDH1* or *IDH2* wild-type (p≤0.02), but not for patients who were both *FLT3* wild-type and *NPMc* mutant (**Supplementary Figure 14**). The presence of a *FLT3* ITD mutation did confer a worse overall survival for patients with *DNMT3A* mutations, although the number of cases with both mutations is small (n=16) (**Supplementary Figure 15**, p=0.02).

Multivariate Analysis of Event Free and Overall Survival

The relationship between *DNMT3A* status and both overall and event-free survival was examined by multivariate Cox Proportional Hazards models. The variables that were independently associated with overall survival were *DNMT3A* mutations, age>60, and *FLT3* mutations. FAB=M3 was used as a stratifying variable because it did not satisfy the proportionality assumption. After adjusting for age, FAB=M3, and *FLT3* mutations, the hazard ratio for *DNMT3A* mutations was 1.90 (95% confidence interval: 1.34-2.71.) The variables that were independently associated with event-free survival included age>60, *FLT3* mutations, favorable cytogenetics, and *DNMT3A* mutations. As with overall survival, FAB=M3 was used as a stratifying variable. After adjusting for age>60, FAB=M3, *FLT3* mutation, and favorable cytogenetics, the hazard ratio for *DNMT3A* mutation was 1.46 (95% confidence interval: 1.02 – 2.08)

Inherited SNPs in the *DNMT3A* gene

Six inherited single nucleotide polymorphisms (SNPs) were identified in the coding region of *DNMT3A* in normal DNA from AML cases (**Supplementary Table 7**). All six SNPs were synonymous, four were novel alleles, and two were previously known (rs2276598, rs41284843). The minor allele frequencies (MAFs) of the four novel alleles were all <0.01 and were not considered further. For rs2276598 and rs41284843, there was no difference in allele or genotype frequencies between AML cases with or without *DNMT3A* mutations, or between

AML cases (Caucasian only) and CEU controls from pilot 1 of the 1,000 Genomes project.

C. Supplementary Literature Cited.

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D. Supplementary Figure Legends.

Supplementary Figure 1. Summary of *DNMT3A* SNVs found in CALGB AML samples. The locations of validated SNVs (single nucleotide variants) in the *DNMT3A* gene are shown for 94 AML samples obtained from CALGB are shown. These cases are described in **Supplementary Table 1** and Mardis, et al[1]. Since no matched normal tissue was available for these tumor samples, these mutations are not proven to be somatic. However, none has been described in dbSNP, and none were inherited SNPs in our analysis of 188 additional AML cases. The locations of the PWWP (proline-tryptophan-tryptophan-proline), ZNF (zinc finger), and MTase (methyltransferase) domains are shown. Each patient with a *DNMT3A* mutation is designated with a circle.

Supplementary Figure 2. Map of a 1.5 Mb deletion encompassing *DNMT3A*. A 1.5 Mb deletion was detected in UPN 113971 with whole genome sequencing, by defining low coverage of this region of chromosome 2 in the tumor sample only. The results were confirmed on Affymetrix 6.0 SNP arrays. The deleted region includes all or part of 9 genes, including *DNMT3A*.

Supplementary Figure 3. Expression data for *DNMT* genes in AML cases. Expression arrays were performed for 180 AML cases, and data for the probesets measuring *DNMT3A* (upper left), *DNMT3L* (upper right), *DNMT3B* (lower left) and *DNMT1* (lower right) are shown. Each dot represents one sample. Expression levels for R882 mutations, any other *DNMT3A* mutation, or no *DNMT3A* mutation, are shown; expression levels are not significantly altered by *DNMT3A* mutations. All of the expression calls for the *DNMT3L* gene were called "absent" on the expression arrays. Expression levels for these genes are also shown for normal adult bone marrow derived CD34 cells, flow-purified promyelocytes (pros), and flow-purified polymorphonuclear leukocytes (PMNs).[2]

Supplementary Figure 4. **cDNA readcounts for *DNMT3A* mutations.** Variant allele frequencies from cDNAs obtained from the bone marrow RNA of 21 different AML patients are shown. Regions containing the mutations were amplified by RT-PCR, and then sequenced using the 454-FLX platform to obtain deep readcounts for variant alleles. The data used to generate this figure are presented in **Supplementary Table 3**. Below each bar, the UPN for the patient sample is shown, followed by the mutation annotation.

Supplementary Figure 5. Total numbers of putative somatic single nucleotide variants (SNVs) in sequenced AML genomes with and without *DNMT3A* mutations. The data for this figure were extracted from whole genome sequencing data from 38 AML samples with normal cytogenetics, and a variety of FAB subtypes (M0,1,2,4, and 5). 11 of these samples had validated somatic mutations in *DNMT3A*, and 27 did not. The number of high confidence somatic SNVs for each "Tier" of each genome (described in Mardis, et al[1]) are plotted as a function of *DNMT3A* mutation status. Each genome is represented by a single point. The mean number of SNVs called is shown as a bar. The mean number of Tier 1 (genic) SNVs is significantly reduced in samples with *DNMT3A* mutations ($p=0.0216$), but it is not different for any other Tier, nor for total mutations per genome ("All Calls").

Supplementary Figure 6. Summary of somatic SNV types and frequencies in AML genomes. From the 38 sequenced AML genomes described in **Supplementary Figure 5**, we classified SNVs based on the nature of the base change identified, and the *DNMT3A* mutation status of that genome. All mutation types occur at nearly identical frequencies in genomes with *DNMT3A* mutations (n=11) and without (n=27). None of the differences is statistically different.

Supplementary Figure 7. Summary of 5-methylcytosine content data from 51 AML genomes. The percentage of 5-methylcytosine as a fraction of total cytosine is plotted from data presented in **Supplementary Table 5**. The 5-methylcytosine content of samples with and without *DNMT3A* mutations was not significantly different for all samples, nor for samples with R882 mutations.

Supplementary Figure 8. **Heatmaps of methylated genomic regions defined by Methyl-Chip analysis. (A)** Global heatmap of MeDIP-chip analysis using the NimbleGen 2.1M deluxe promoter array (containing all annotated CpG islands and promoters) using DNA samples from 5 AML samples without *DNMT3A* mutations (WT) or patients with R882H mutations. Each mutant sample was matched with a WT sample for FAB type and bone marrow blast %. Regions with reduced methylation are shown in blue, and with increased methylation, in green. The average log2 ratios from 56,392 clusters with at least 20 probes in the cluster region were displayed by chromosomal position. The global pattern of methylation for CpG islands was unchanged in genomes with the R882H mutation. **(B)** Locations of 182 loci that were significantly hypomethylated (for at least three consecutive probes) in the five samples with *DNMT3A* mutations. Locations of each region and the methylation values are available in **Supplementary Table 6.** The data for the region near ESRP2, detailed in **Supplementary Figure 9**, is indicated**.**

Supplementary Figure 9. Differential methylation of the *ESRP2* locus in samples with *DNMT3A* mutations. Log2-normalized data are shown for a genomic region on chromosome 16 near the *ESRP2* gene. The data for five samples with wild-type *DNMT3A* genes (WT) are shown in black and gray at the top. The data for the five samples with R882H mutations are shown at the bottom. The shaded region is methylated in the WT samples, and unmethylated in the R882H samples. The center of this region is located 430 bp upstream from the 5' end of the *ESRP2* gene. The locations of known CpG islands are shown at the bottom.

Supplementary Figure 10. Lack of a gene expression signature correlated with *DNMT3A* mutations. Heatmap depicting unsupervised clustering of expression array data (Affymetrix U133+2) from 180 *de novo* AML cases. Relatively increased expression is indicated by red; relatively decreased expression by green; intermediate expression by black. The color legend below the heatmap indicates clinicopathological data; each row corresponds to the position of the row above the heatmap. The top row indicates the common AML karyotypes and cytogenetic risk groups: green = t(15;17), yellow = inv(16) or t(8;21), dark blue = normal karyotype, light blue = intermediate risk, gray = adverse risk including complex (>3 changes), white = not done. The middle row indicates the FAB subtype: orange = M0/M1, yellow = M2, dark green = M3, teal = M4, purple = M5, dark pink = M6, light pink = M7. The bottom row shows *DNMT3A* mutation status: white is wild type for *DNMT3A*, red indicates any of the R882 mutations, and yellow indicates non-R882 *DNMT3A* mutations.

Supplementary Figure 11. Heatmap of unsupervised clustering analysis of 76 AML cases with normal karyotypes. Heatmap depicting unsupervised clustering of expression array data (Affymetrix U133+2) from 76 de novo AML cases (Spotfire software). Relatively increased expression is indicated by red color; relatively decreased expression by green color; intermediate expression by

black color. The color legend below the heatmap indicates clinicopathological data. The top row shows *DNMT3A* mutation status: white is wild type for *DNMT3A*, red indicates one of the R882 mutations, and yellow indicates one of the non-R882 *DNMT3A* mutations. The bottom row indicates the FAB subtype: orange = M0/M1, yellow = M2, dark green = M3, teal = M4, purple = M5, dark pink = M6, light pink = M7.

Supplementary Figure 12. Overall survival of AML patients with *DNMT3A* and intermediate risk cytogenetics. Overall survival of AML patients without a *DNMT3A* mutation (dashed red line) compared to those with any *DNMT3A* mutation (blue line), with an R882 mutation (dashed green line), or with a non-R882 mutation (dashed brown line).

Supplementary Figure 13. Overall survival of AML patients with *DNMT3A* mutations and poor risk genotypes. (A) Overall survival of AML patients with (blue line) or without (dashed red line) *DNMT3A* mutations and a concurrent *FLT3* mutation (either ITD or any other mutation). Note that this dataset represents all *FLT3* mutations (ITD or any other mutation) in contrast to **Figure 3C**, where only *FLT3* ITD mutations are considered. (B) *NPM1* wild type patients, (C) patients with *FLT3* mutations (either ITD or any other mutation) and *NPM1* wild type, (D) patients with *IDH1* mutations, (E) patients with *IDH2* mutations, (F) patients with *IDH1* or *IDH2* mutations.

Supplementary Figure 14. Overall survival of AML patients with *DNMT3A* mutations and favorable risk genotypes. (A) Overall survival of AML patients with (blue line) or without (dashed red line) *DNMT3A* mutations that are *FLT3* wild type, (B) patients with *NPMc* mutations, (C) patients with wild type *FLT3* and *NPMc* mutations, (D) patients with wild type *IDH1*, (E) patients with wild type *IDH2*, or (F) patients with wild type *IDH1* and *IDH2*.

Supplementary Figure 15. Overall survival of AML patients with *DNMT3A* and *FLT3* ITD mutations. Overall survival of AML patients with *DNMT3A* mutations with (blue line) and without (dashed red line) *FLT3* ITD mutations.

Supplementary Figure 16. Locations of AML mutations within the three dimensional structure of *DNMT3A*. Side view of tetrameric *DNMT3A* (murine AA 623 – 908 (teal and dark blue) which corresponds to conserved human AA 627 - 912) and DNMT3L (light blue), interacting with S-adenosyl-L-methionine (AdoMet - white spacefill).[21, 24] Jia et al suggested that DNA binds this tetrameric complex along a structural groove (indicated by arrow).[21] Amino acids mutated along the proposed DNA binding groove are highlighted in red; amino acids mutated along the DNMT3L interacting helix are highlighted in green. R882 mutations occur near the homodimerization plane, but this residue has not been implicated in homodimerization (Jia et al calculated R885 to be a critical residue)[21]. The R882 side-chain protrudes into the DNA binding groove, and mutations at this position decrease both DNA binding and catalytic activity.[11]

Amino acids P718, R729, K829, R803, and F909 all occur along the DNA binding groove, and their side-chains are positioned into the solute; mutations at these positions may therefore alter DNA affinity or specificity. R729 and R736 occur along the DNMT3L interacting helix, and mutations at these positions may alter heterodimerization. A741V does not obviously alter the DNMT3L interacting helix, but this mutation occurs in conjunction with E477* and may not be functionally relevant, since this mRNA is subject to nonsense mediated decay.

Supplementary Figure 17. Overall survival of AML patients based on the number of mutations detected in the commonly mutated genes in AML (*FLT3, DNMT3A, IDH1/2,* and *NPM1*). Patients with favorable cytogenetic risk profiles had either no mutations in these genes, or in *FLT3* only. The presence of a *FLT3* mutation did not alter OS in this group (data not shown). For all other cases, the impact of the numbers of mutations in the common AML genes on overall survival is shown. *IDH1* and *IDH2* mutations were pooled (these mutations are mutually exclusive). Only 4 cases had 4 mutations, so they were pooled with cases with 3 mutations (n=23) for clarity.

Supplementary Figure 18. Overall survival of 187 AML patients collected at Washington University stratified by *DNMT3A* mutation status and allogeneic transplantation status. (A) 48 patients without *DNMT3A* mutations were treated with an allogeneic transplantation at any time during their treatment course. 41 patients had an allogeneic transplant only and 7 had an allogeneic transplant following an autologous transplant. 94 patients without *DNMT3A* mutations were treated with an autologous transplant (n=7) or no transplant (n=87) during their treatment course. **(B)** Patients with *DNMT3A* mutations were treated with (n=16) or without (n=29) an allogeneic transplant during their treatment course, as defined in Panel A. 13 patients had an allogeneic transplant only and 3 had an allogeneic transplant following an autologous transplant. 29 patients with DNMT3A mutations were treated with an autologous transplant (n=7) or no transplant (n=22) during their treatment course. **(C)** 64 patients were treated with an allogeneic transplantation at any time during their treatment course. 16 patients had a *DNMT3A* mutation and 48 patients did not have a *DNMT3A* mutation. Overall survival of patients treated with an allogeneic transplant was independent of *DNMT3A* mutation status (p=0.30).

Supplementary Table 1. Patient Characteristics.

Supplementary Table 2. Summary of *DNMT3A* Mutations.

Supplementary Table 3. *DNMT3A* cDNA variant allele readcounts.

Supplementary Table 4. Mutation types in *DNMT3A* mutant vs. wild type genomes.

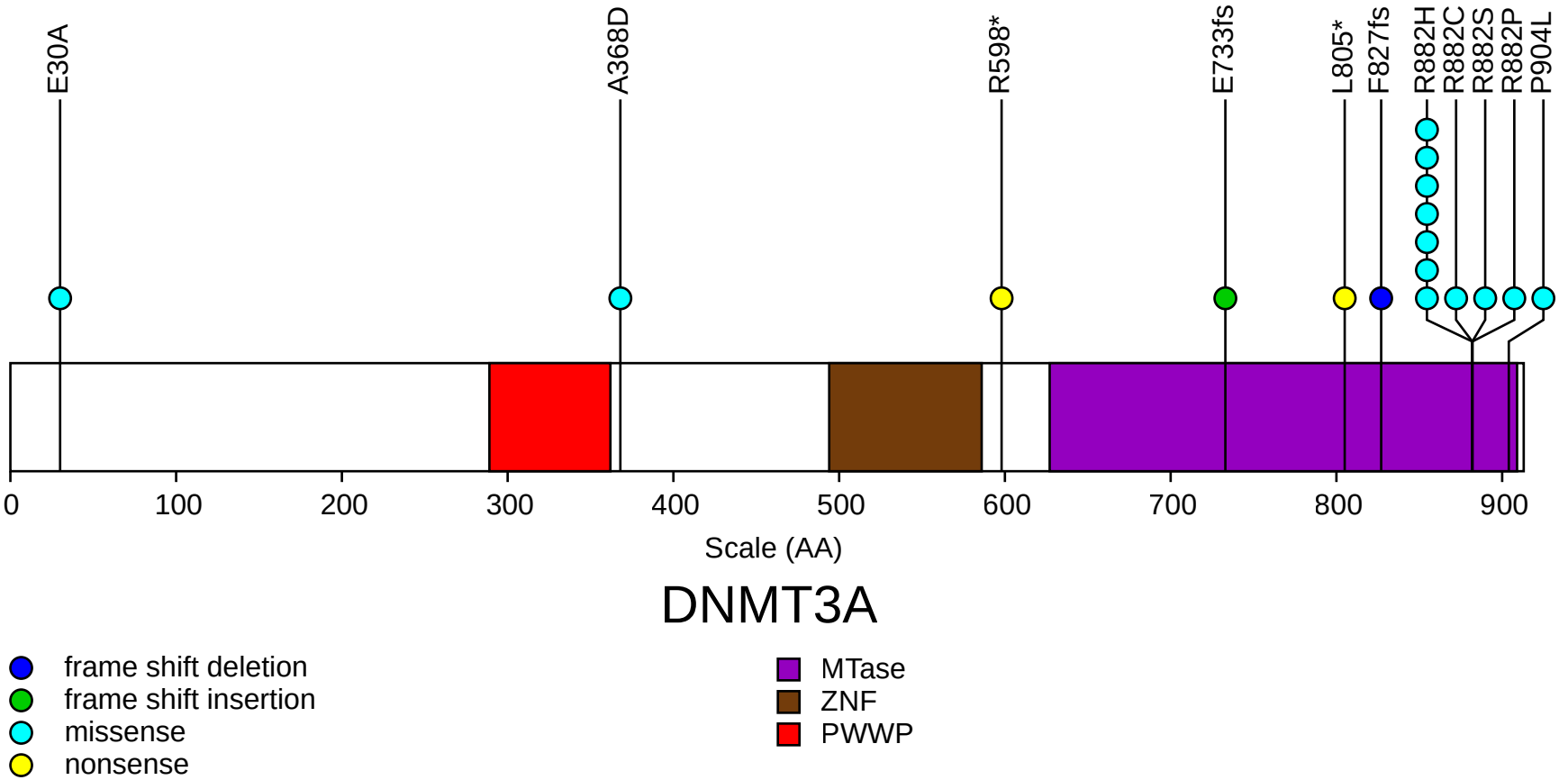
Supplementary Table 5. 5-methylcytosine content in *DNMT3A* mutant vs. wild type genomes.

Supplementary Table 6. Differentially methylated loci in *DNMT3A* genomes defined by meDIP-chip analysis.

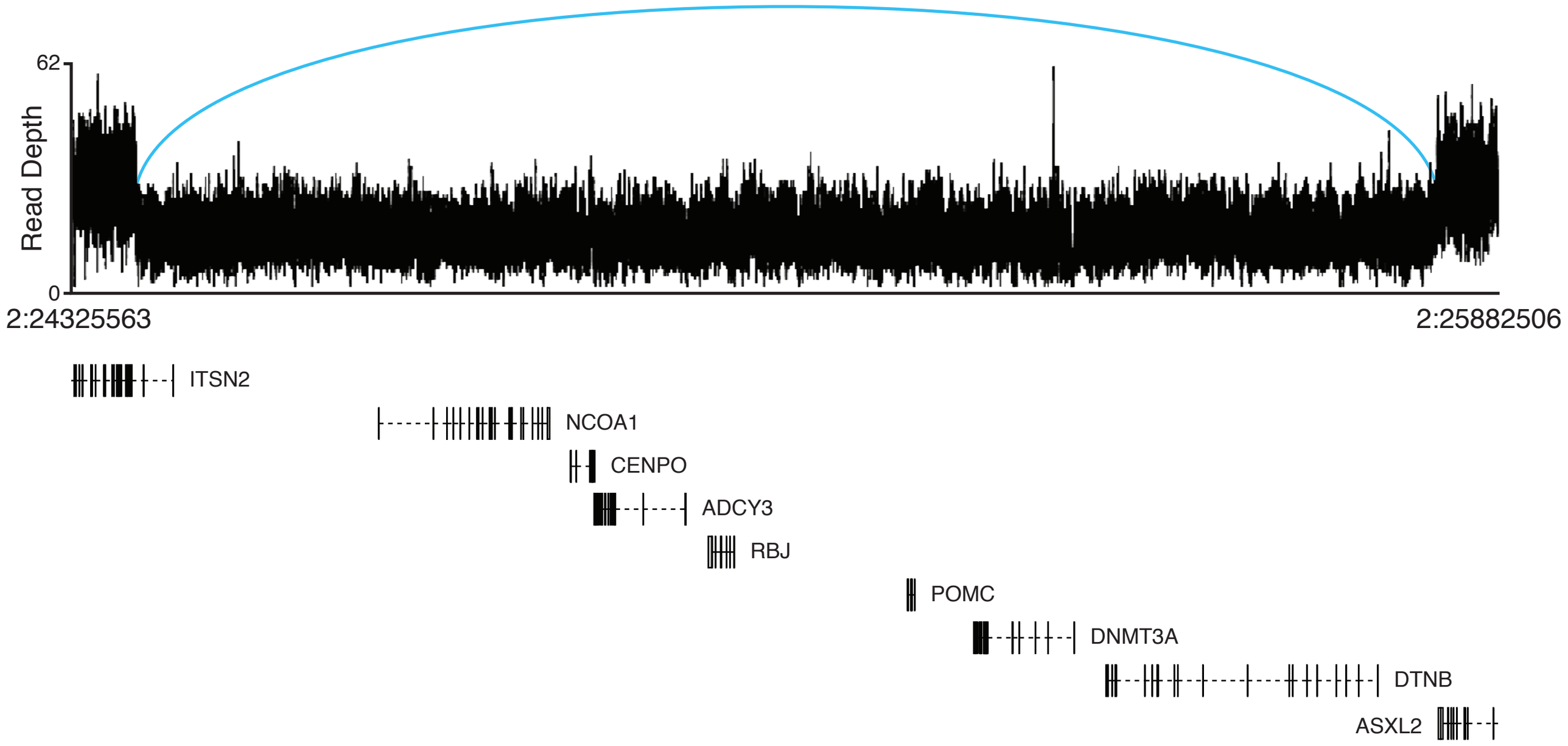
Supplementary Table 7. *DNMT3A* SNP frequencies.

Supplementary Table 8. *DNMT3A* primers used to sequence all coding exons.

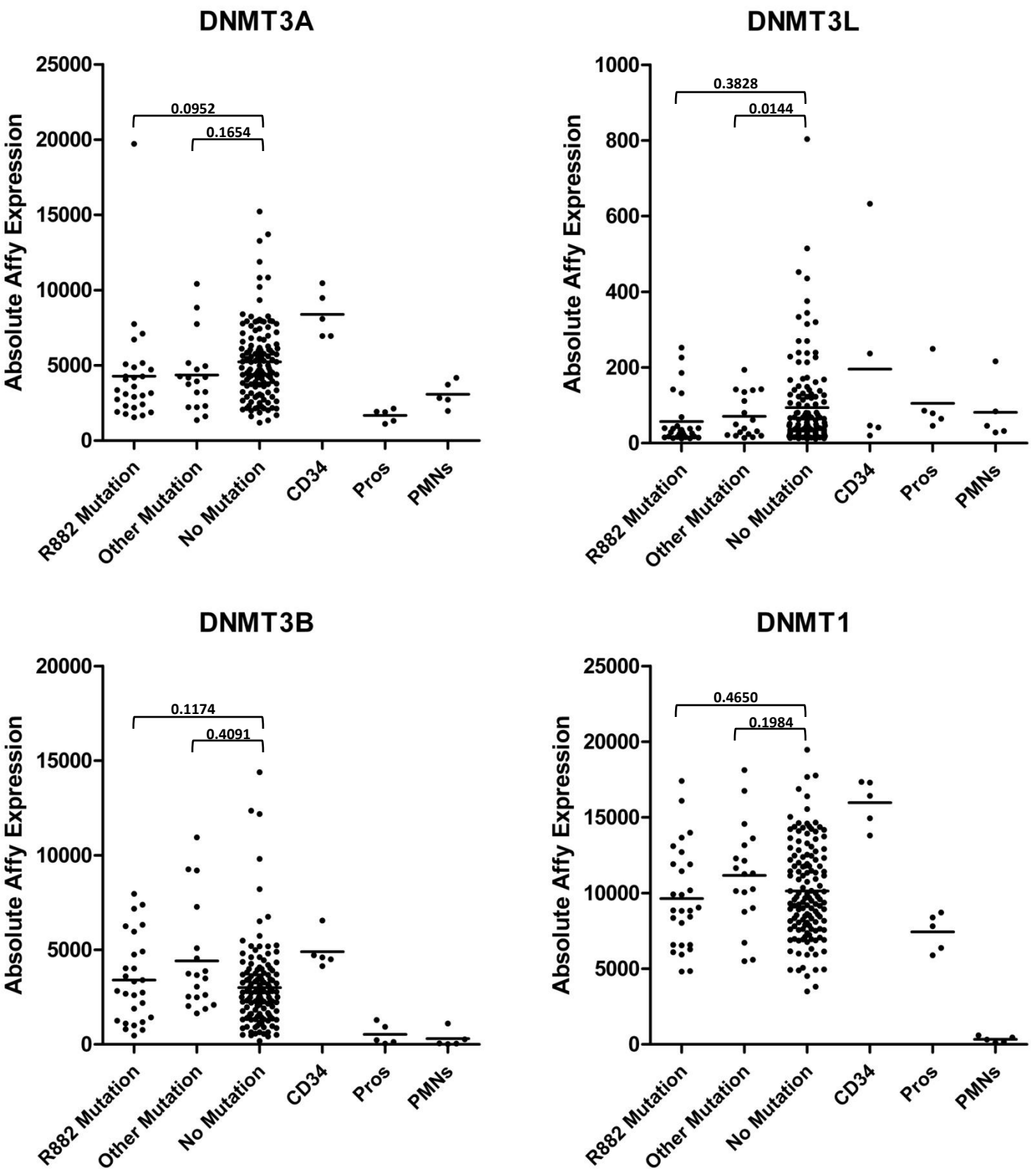
Supplementary Table 9. *DNMT3L* primers used to sequence all coding exons.



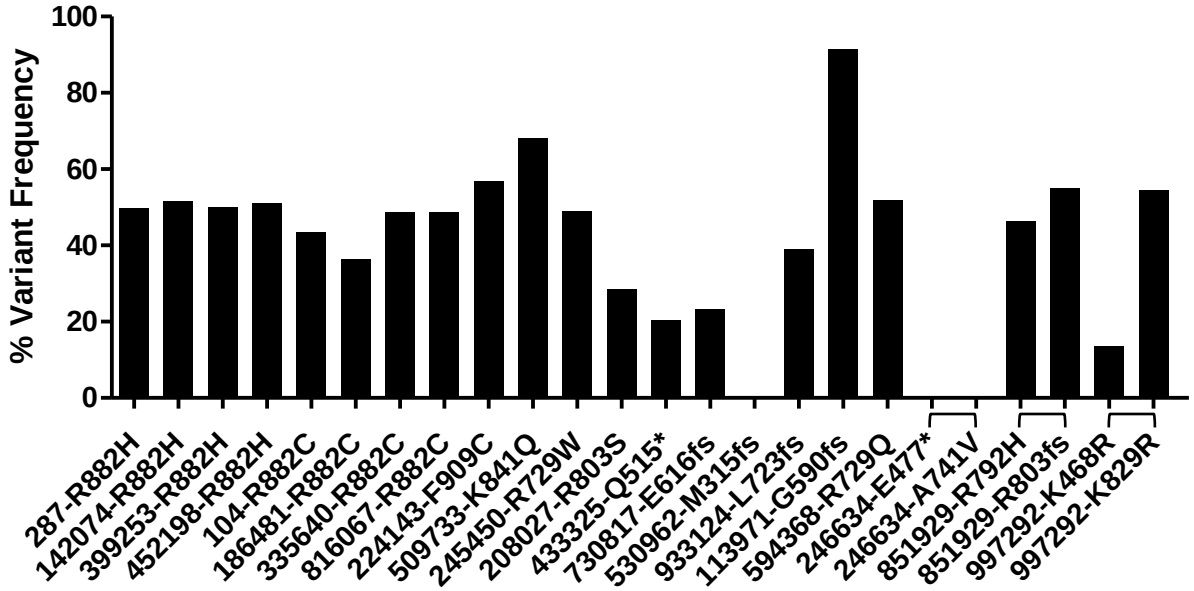
Supplementary Figure 1.



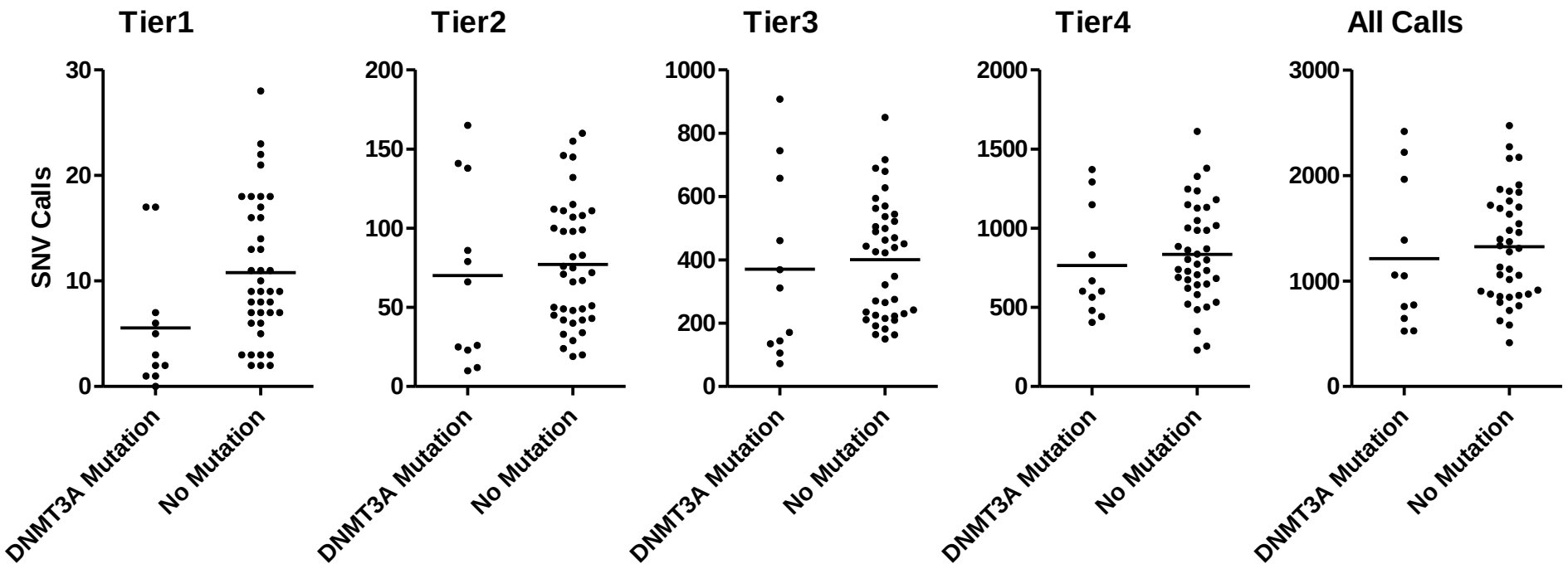
Supplementary Figure 2.



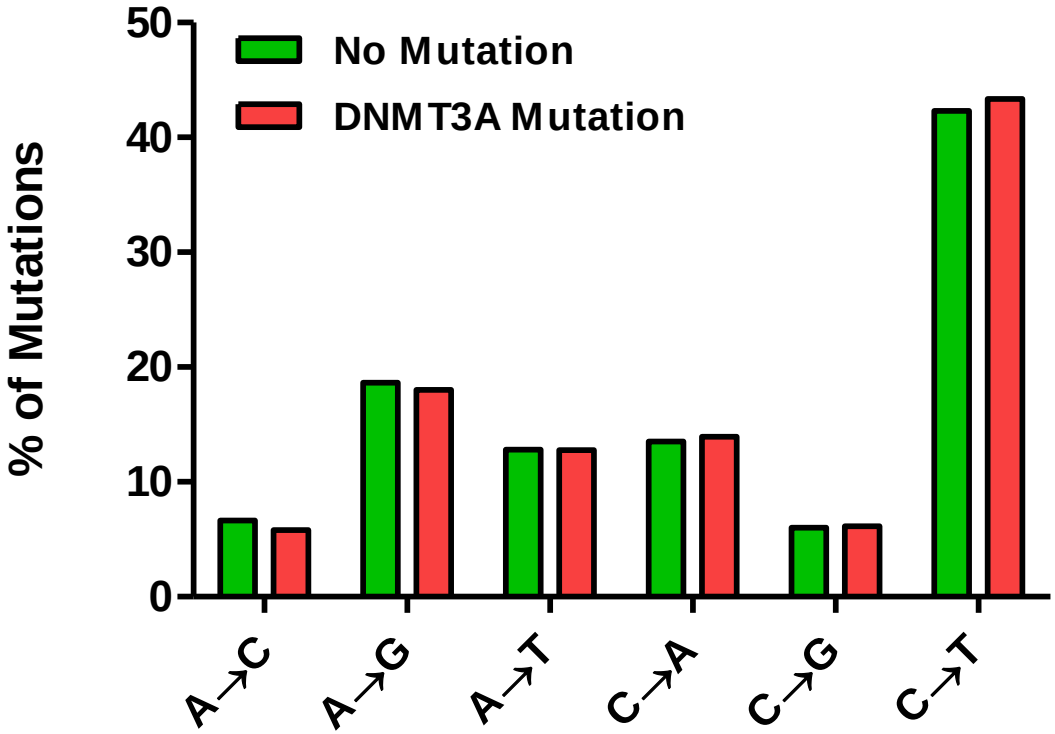
Supplementary Figure 3.



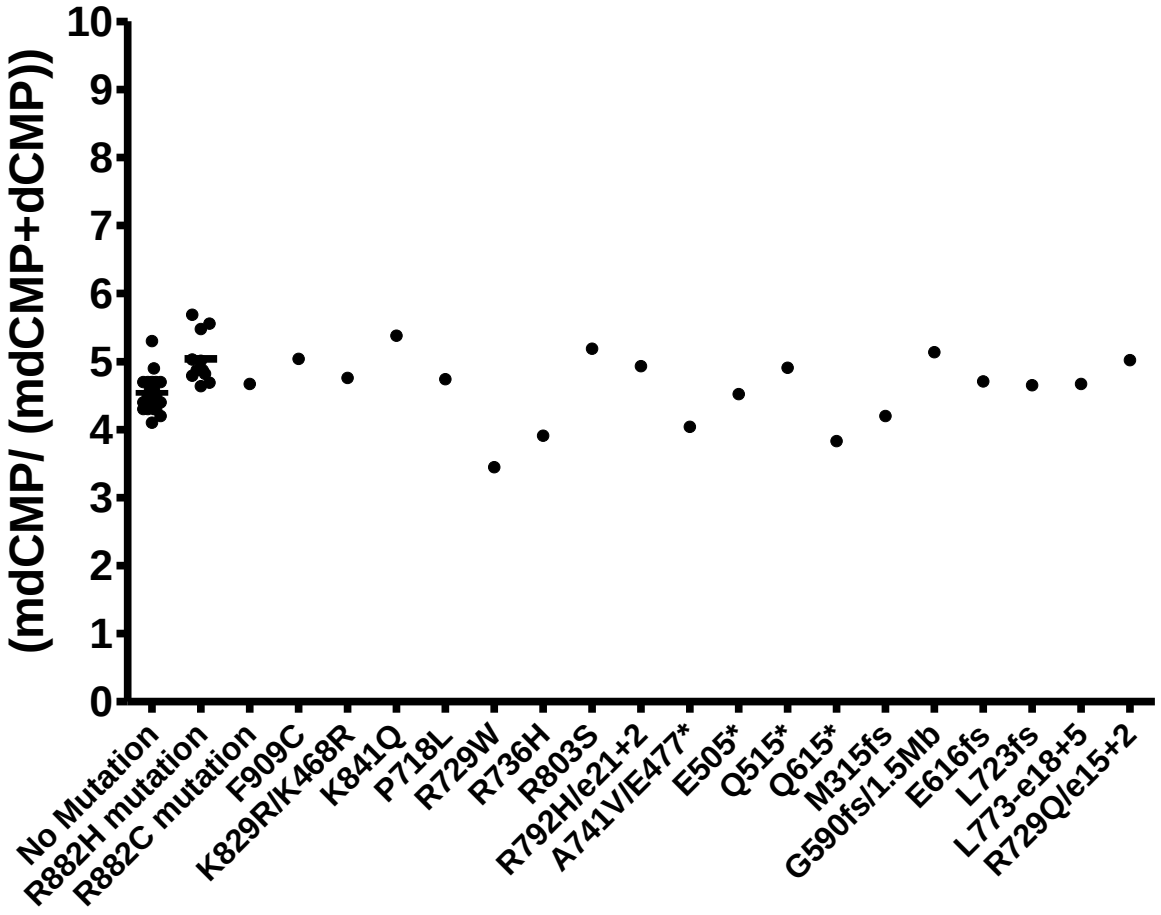
Supplementary Figure 4.



Supplementary Figure 5.



Supplementary Figure 6.



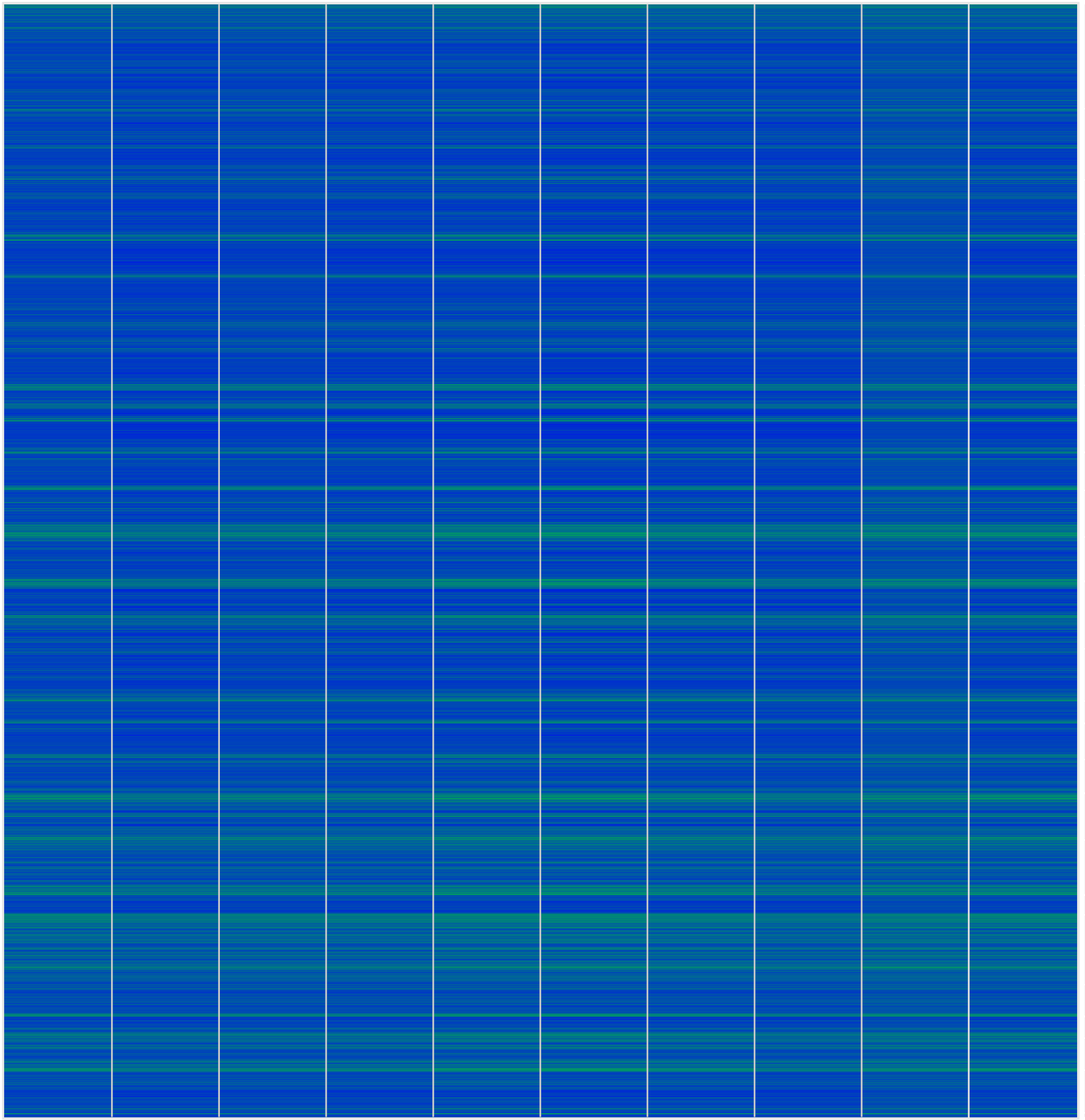
Supplementary Figure 7.

low methylation

high methylation

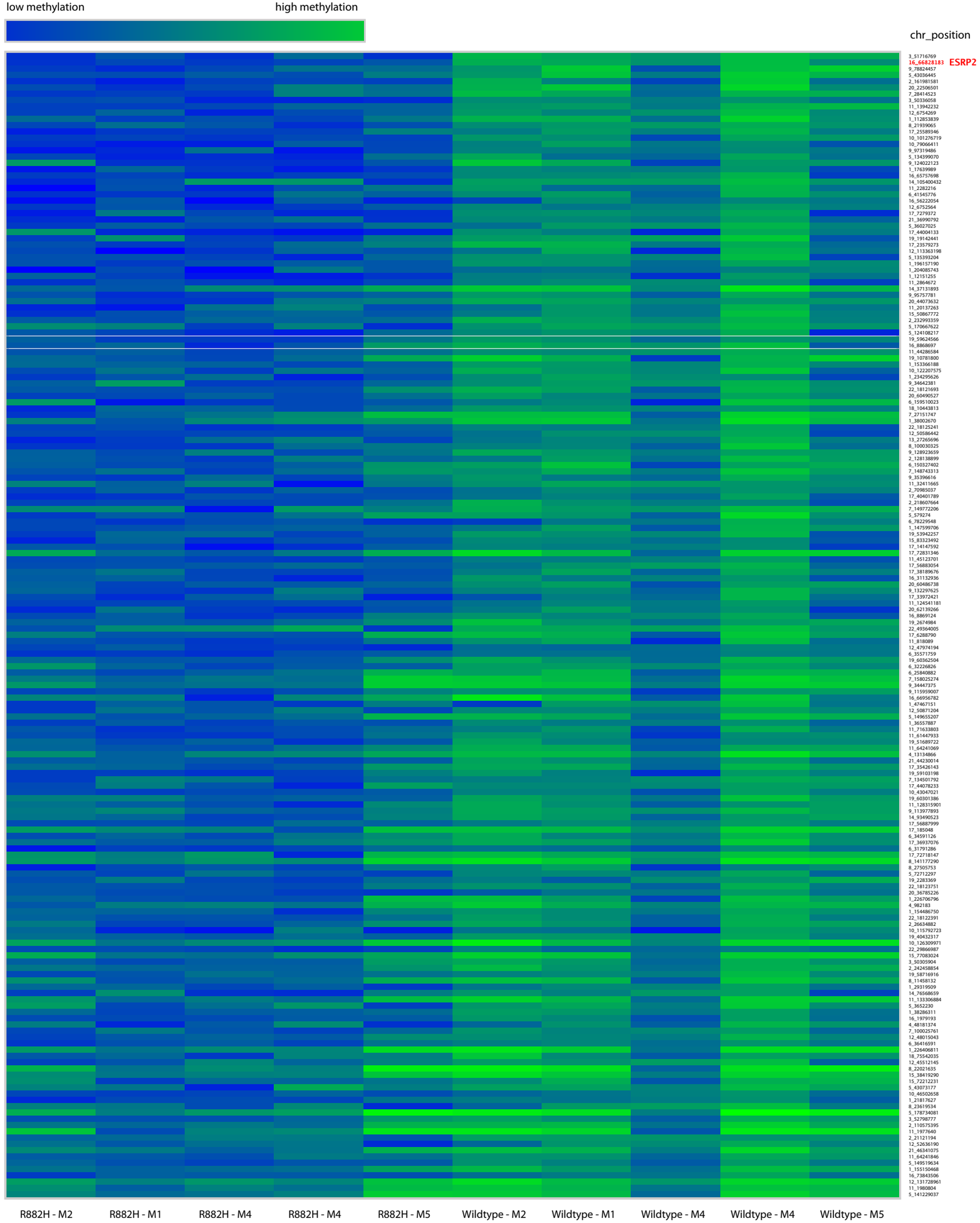
Supplementary Figure 8A

chromosome

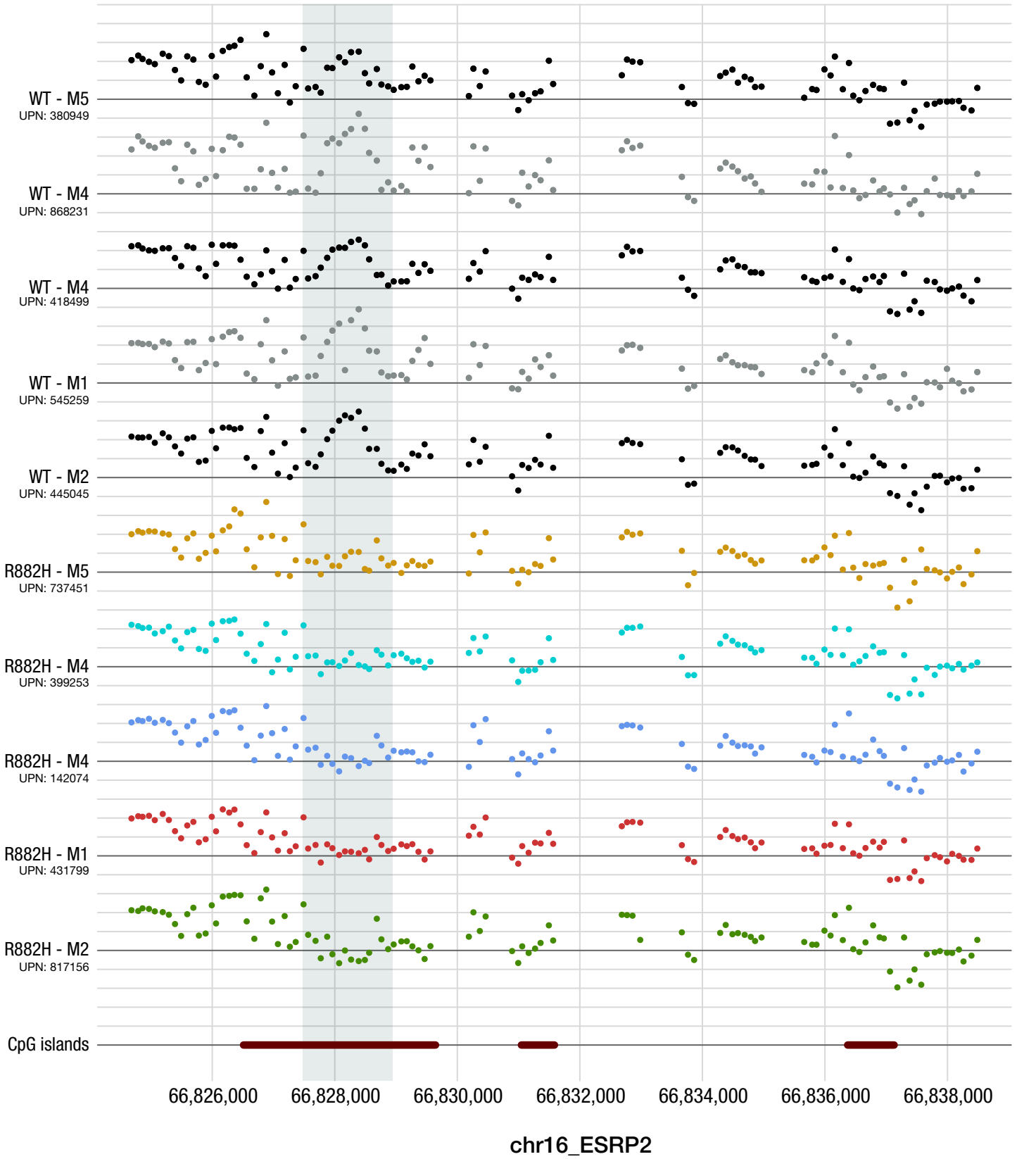


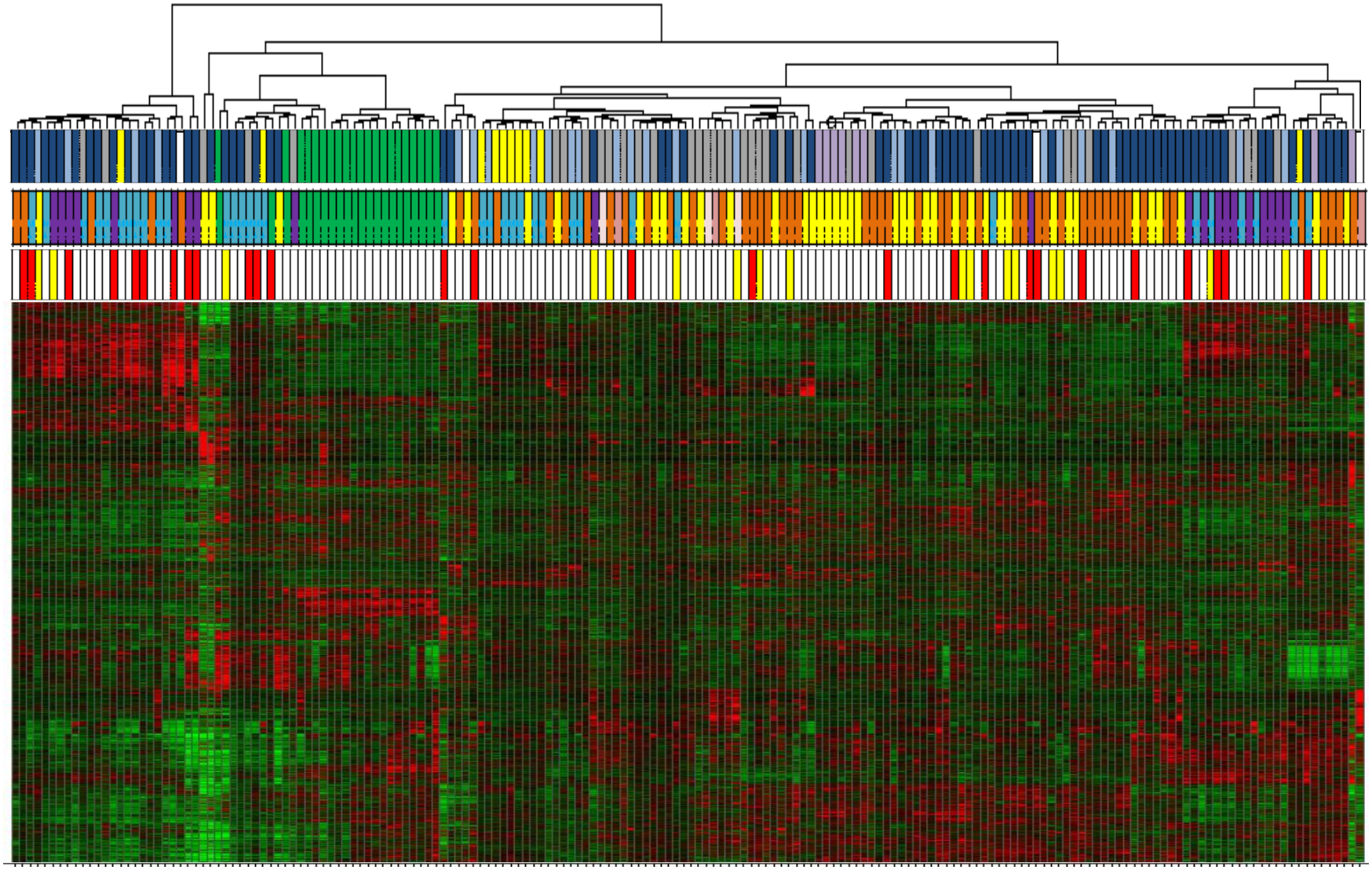
R882H - M2	R882H - M1	R882H - M4	R882H - M4	R882H - M5	Wildtype - M2	Wildtype - M1	Wildtype - M4	Wildtype - M4	Wildtype - M5
UPN: 817156	UPN: 431799	UPN: 142074	UPN: 399253	UPN: 737451	UPN: 445045	UPN: 545259	UPN: 418499	UPN: 868231	UPN: 380949

Supplemental Figure 8B

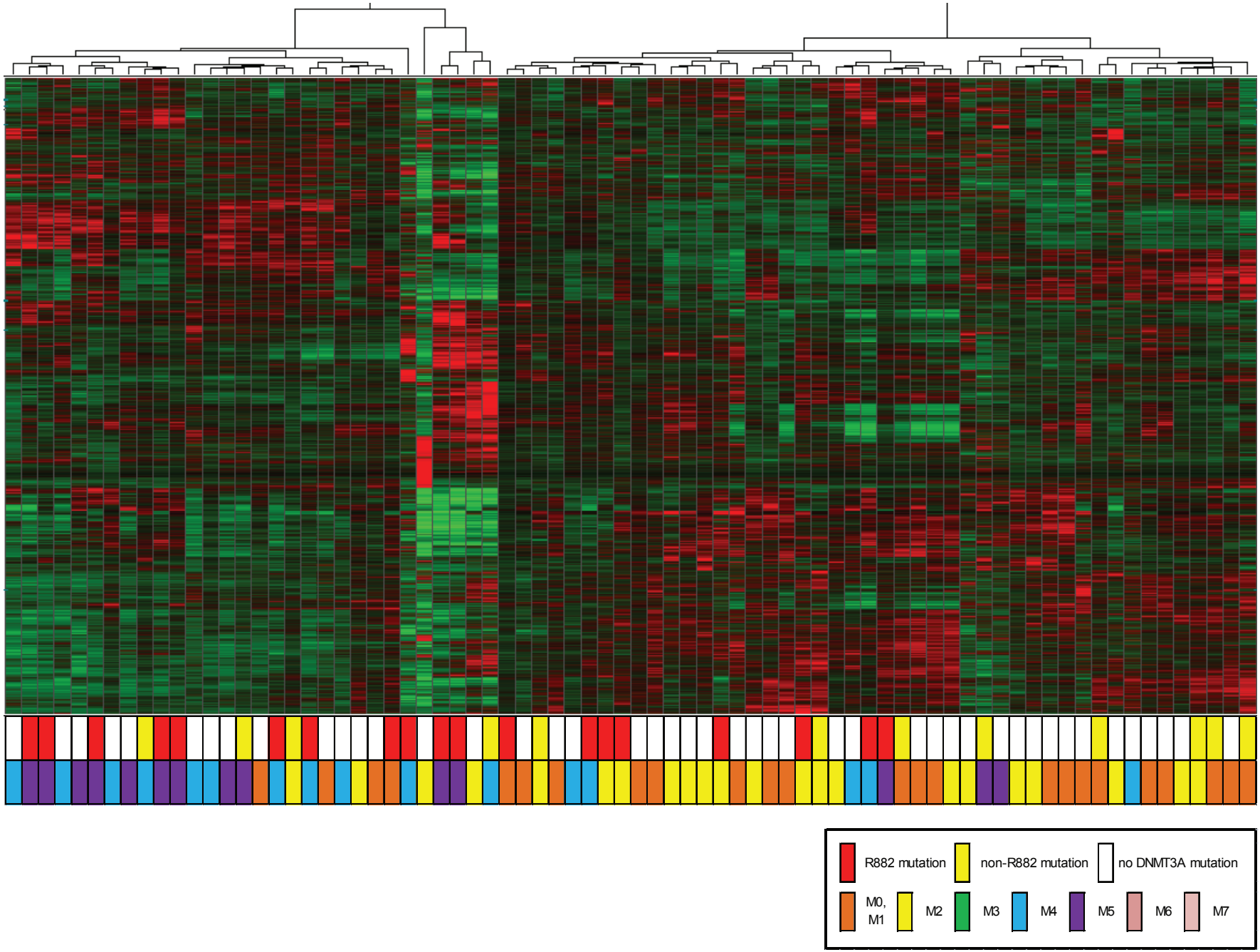


Supplementary Figure 9

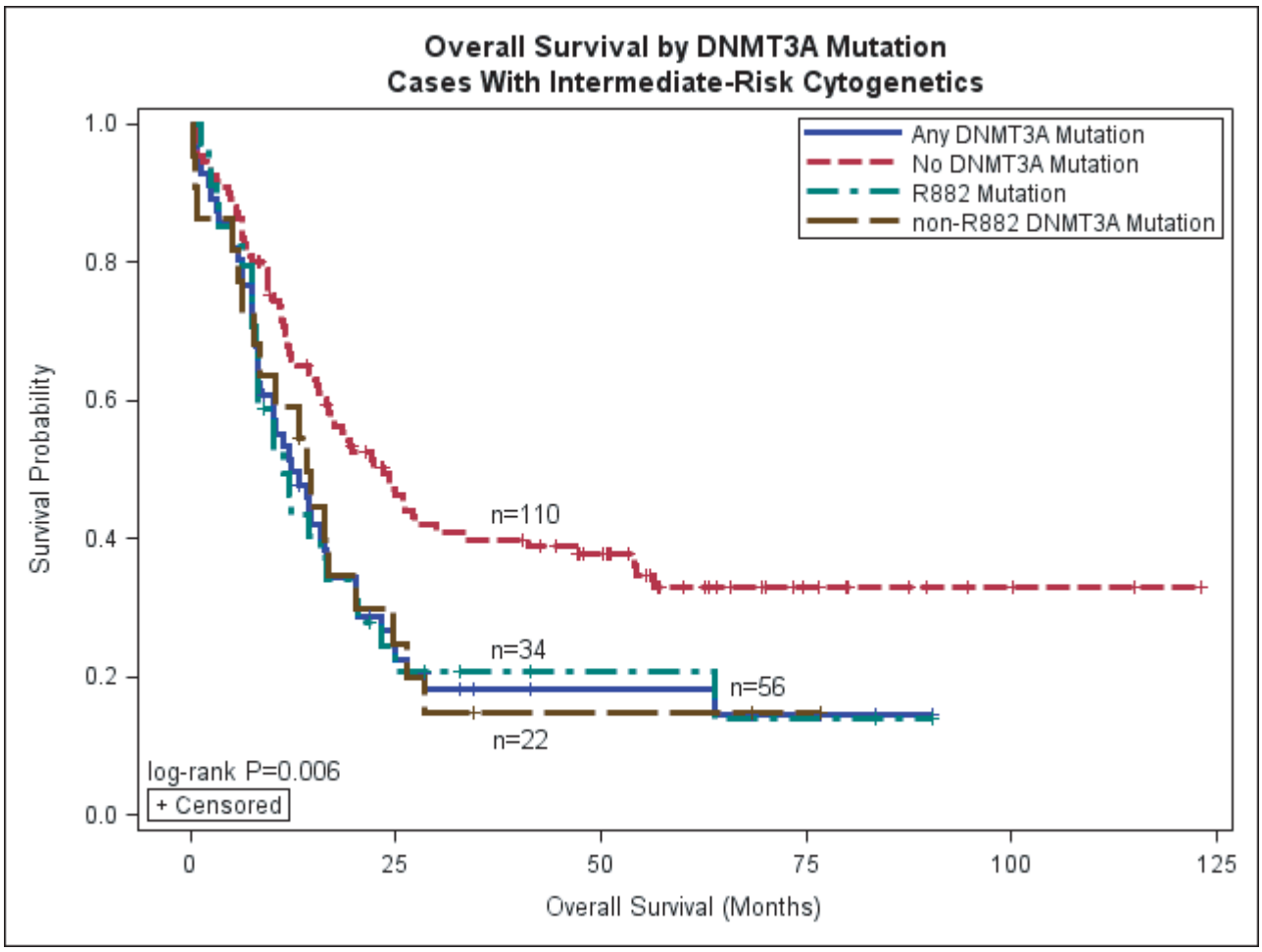




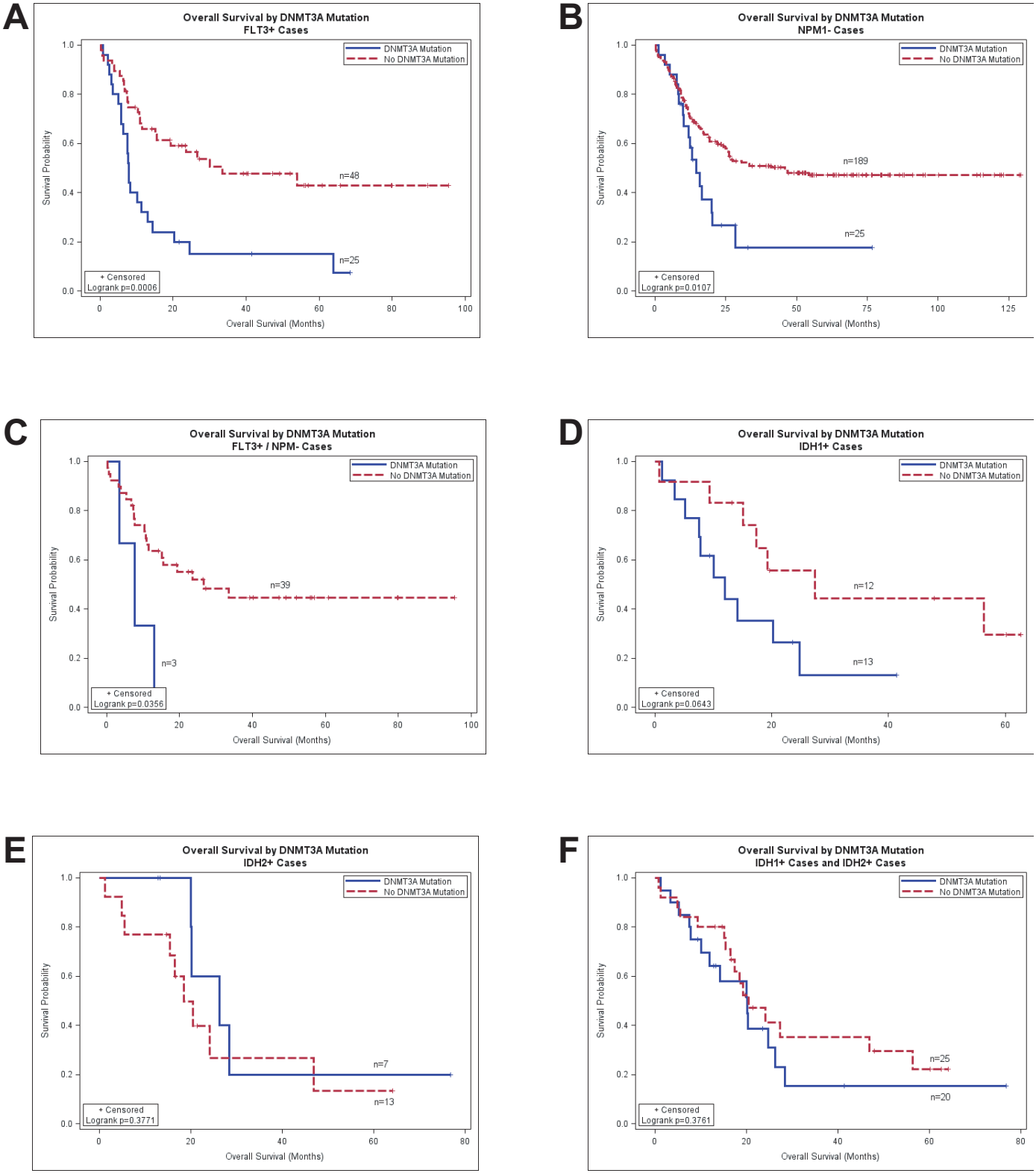
Supplementary Figure 10.



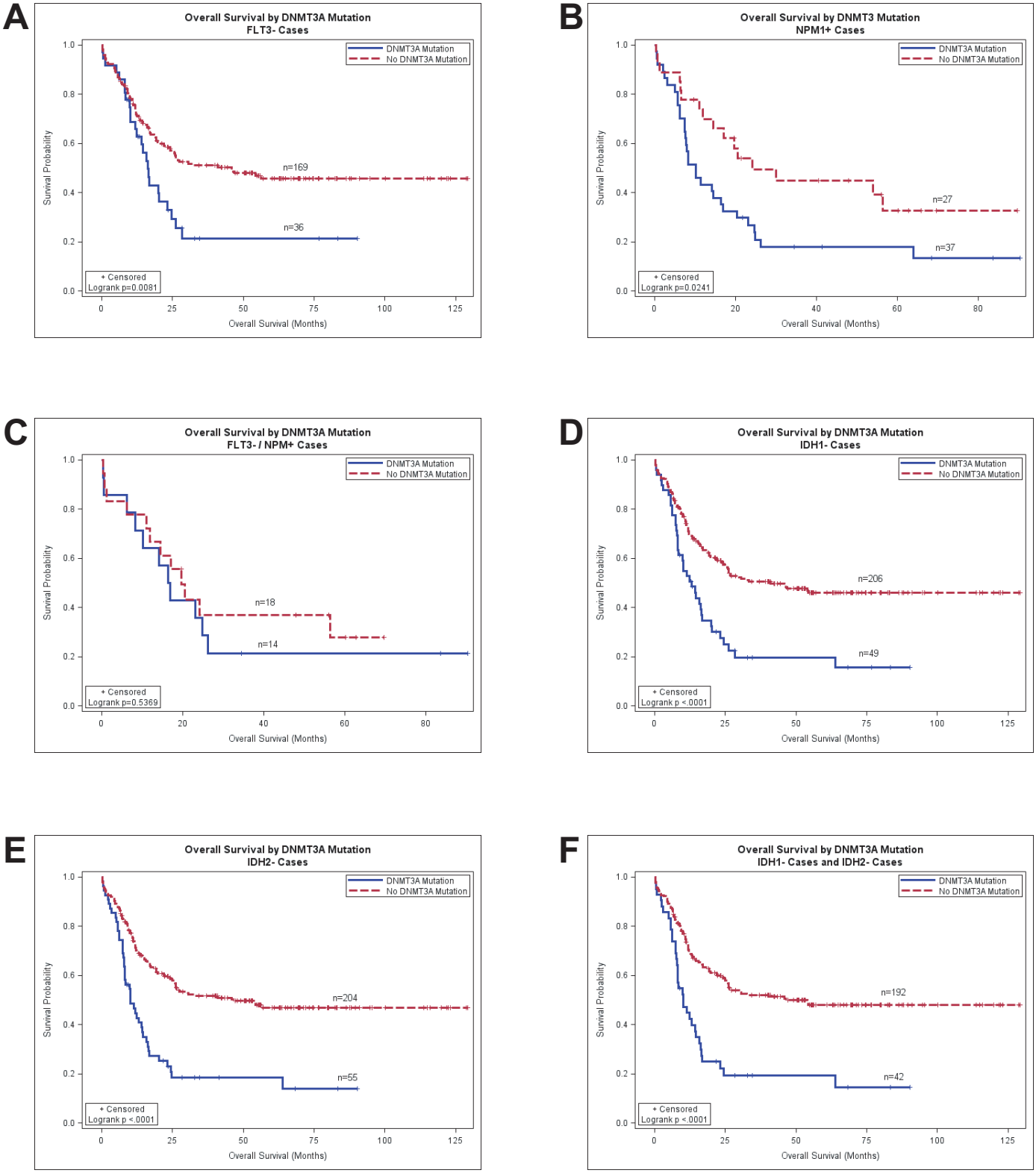
Supplementary Figure 11.



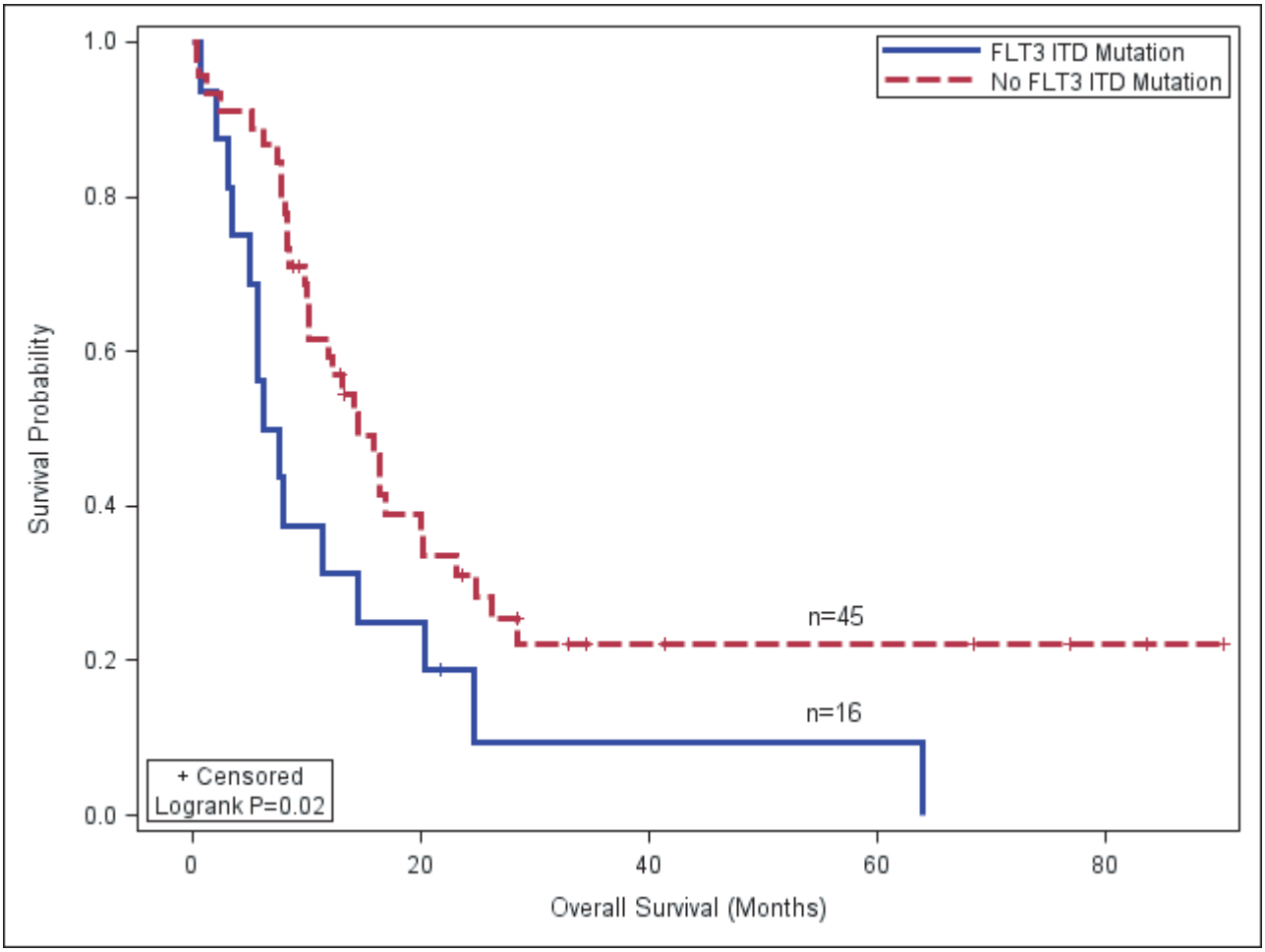
Supplementary Figure 12.



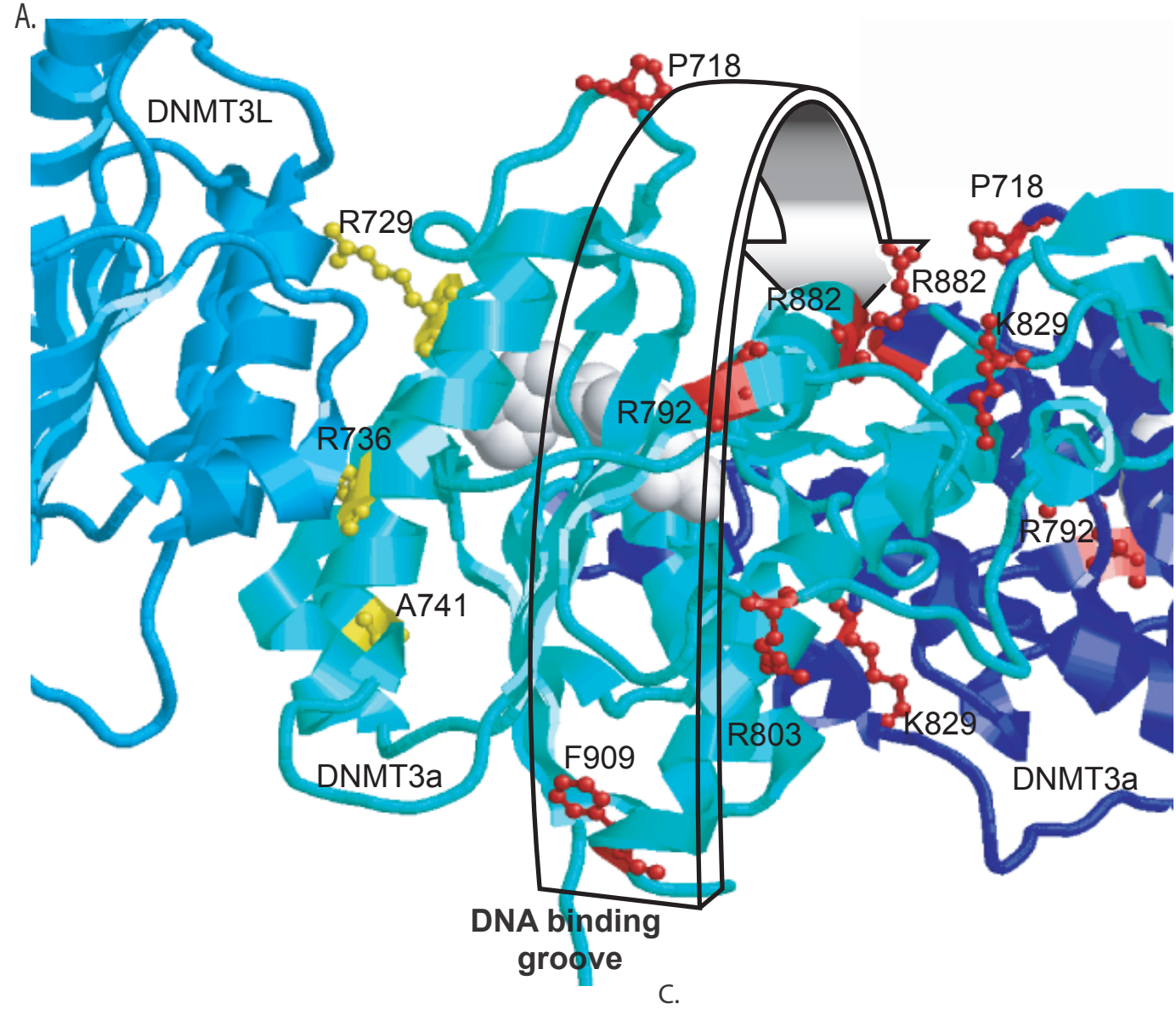
Supplementary Figure 13.



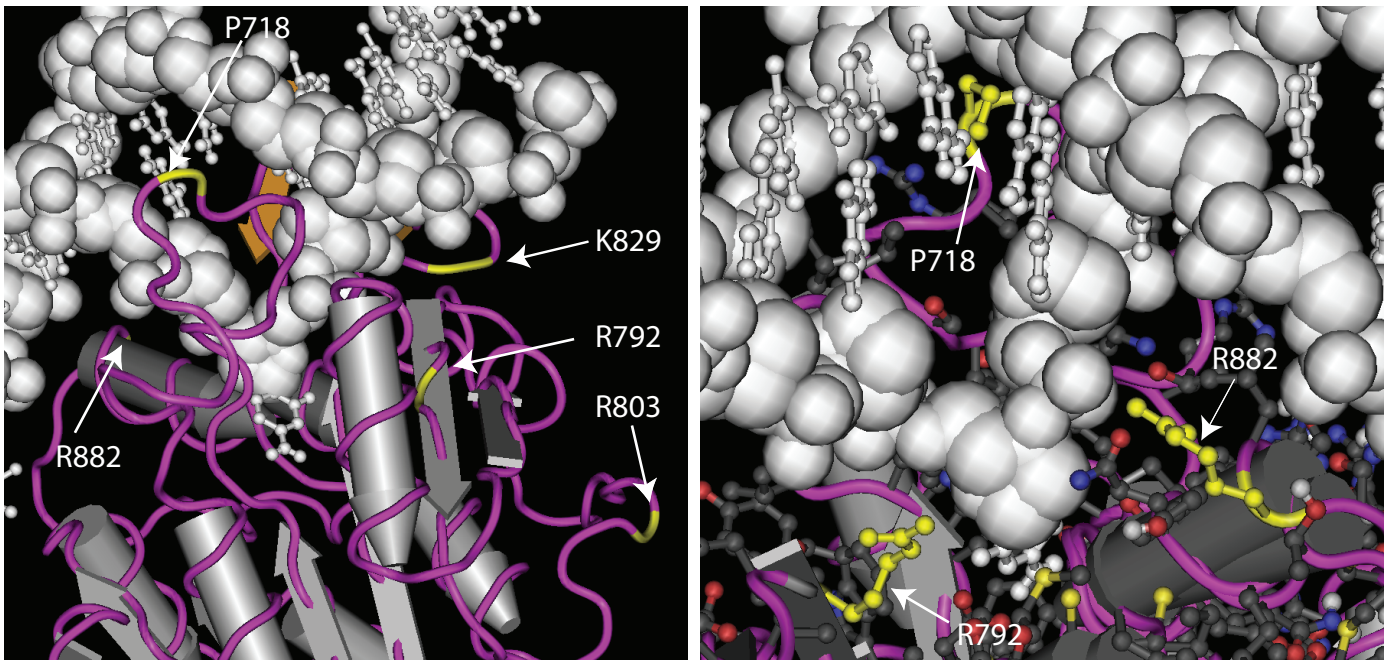
Supplementary Figure 14.



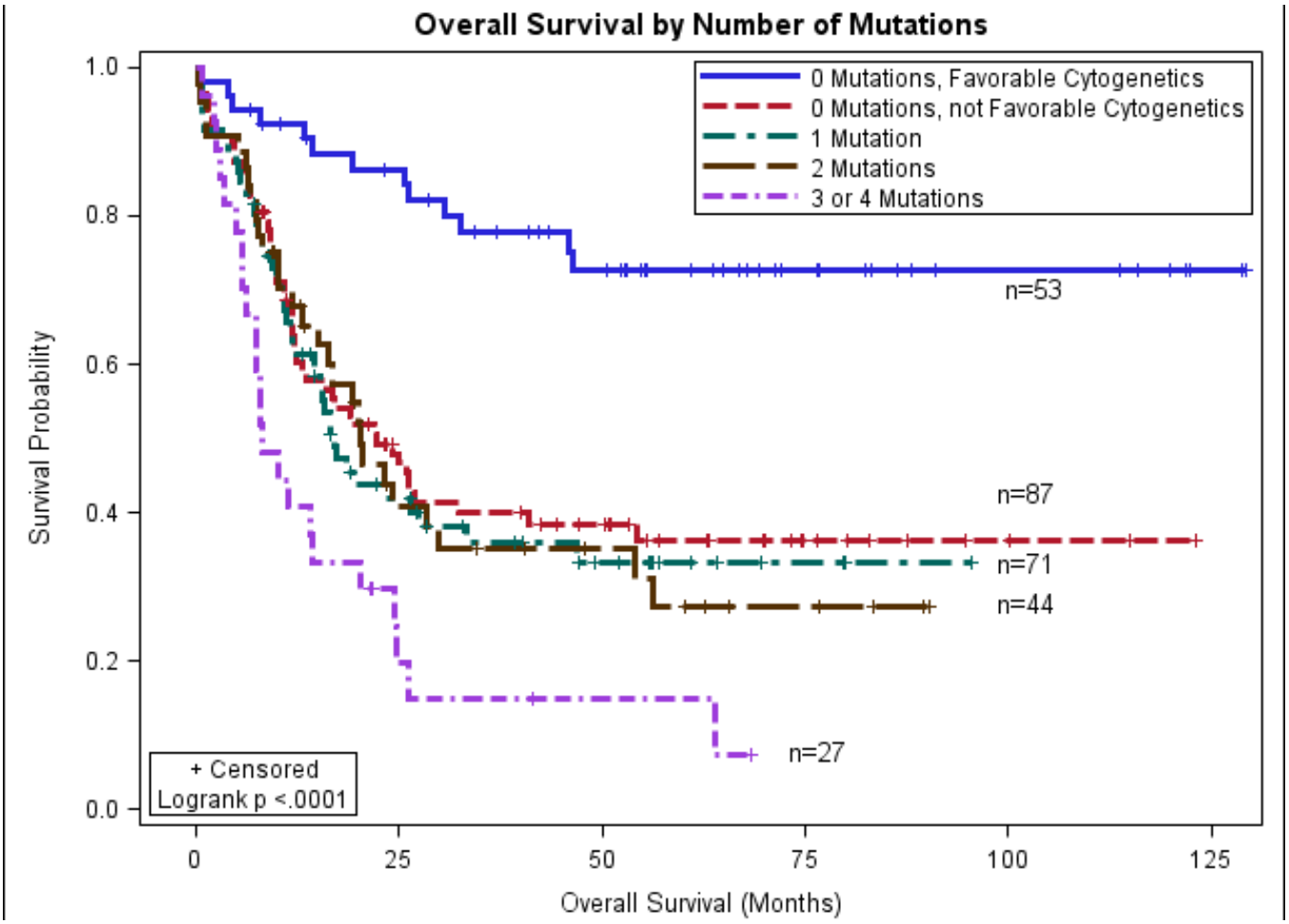
Supplementary Figure 15.



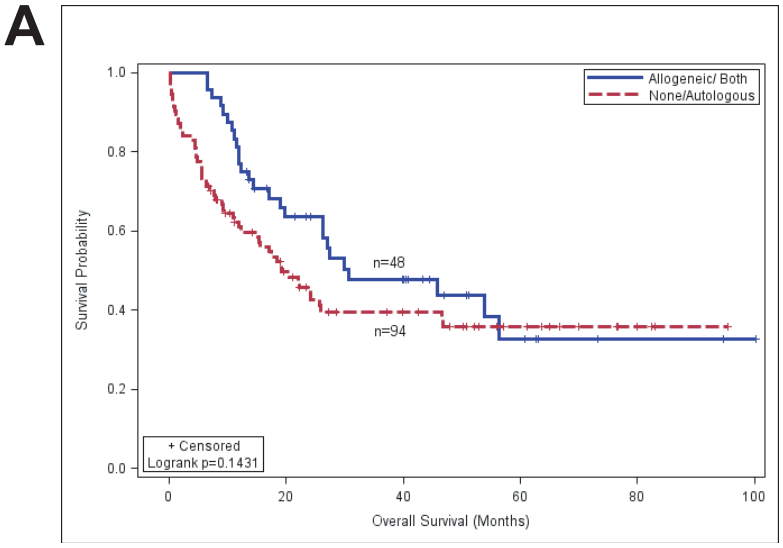
B.

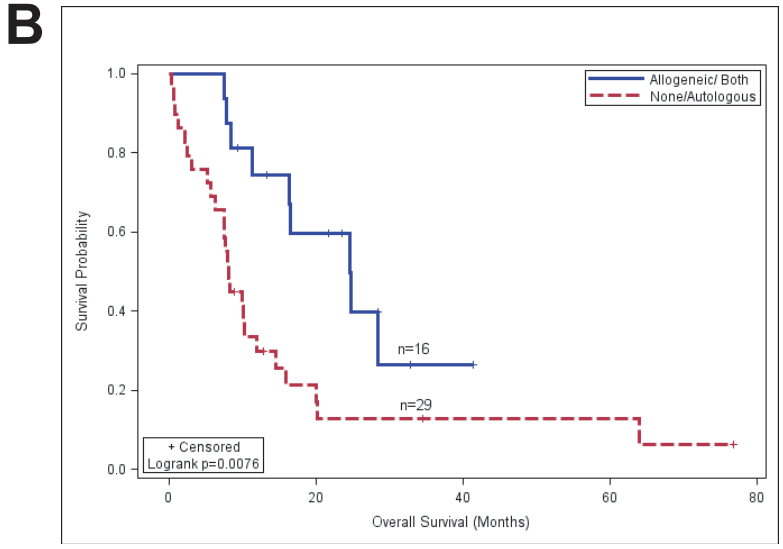


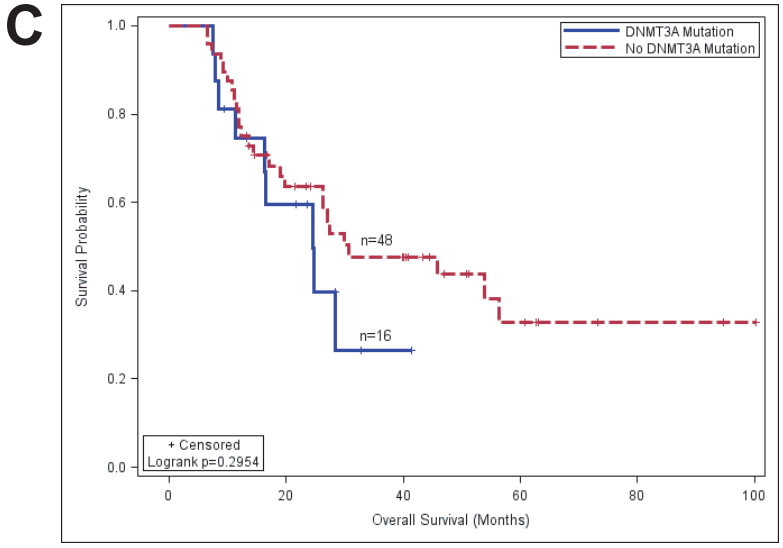
Supplementary Figure 16.



Supplementary Figure 17.







Supplementary Figure 18.

Supplementary Table 1. Patient Characteristics.

UPN	Age	Sex	Race	FAB	Cytogenetics	MLL Status	%BM Blasts	PB WBC@ presentation	%PB Blast	Vital Status	EFS months (3.31.10)	OS months (3.31.10)	DNMT3A	DNMT3A predicted mutation consequences	FLT3 ITD	FLT3 other	IDH1	IDH2	NPM1
104	50	M	W	M4	normal		88	16.9	52	Dead	8.7	12	R882C	missense			R132H		
110	61	F	W	M3	t(15;17)		44	1	N/A	Dead	24.1	25.7							
201	30	M	W	M3	normal		82	5.7	N/A	Alive	57.2	100.2							
203	77	M	W	M0	normal		67	92	56	Dead	11.6	18.5						R140Q	
237	46	M	W	M1	t(8;7;21)		90	47.7	81	Dead	16.1	30.6							
245	68	F	W	M1	+21 only		91	3.1	55	Dead	4.9	4.9						R140Q	
262	16	F	W	M3	t(15;17)		100	77.2	93	Alive	95.4	95.4			ITD				
269	23	M	W	M2	+y		59	32.4	N/A	Alive	10	94.7							
287	64	F	W	M3	normal		60	116.5	N/A	Dead	1.7	2.2	R882H	missense	ITD				W288fs
295	76	F	B	M2	not done		48	61.6	88	Dead	1.3	1.3						R140Q	W288fs
296	81	M	W	M4	normal		98	90.6	37	Dead	8.2	8.2	R882H	missense		D835Y			W288fs
103342	61	F	W	M2	normal		43	9.8	32	Alive	23.4	23.4							
104851	25	F	B	M2	normal		53	140.1	87	Dead	7.3	11.5			ITD				
108135	48	F	W	M2	-7, +21		81	39.5	15	Alive	82.9	82.9							
113971	57	F	W	M2	normal		43	3.5	35	Dead	8.6	28.4	G590fs/ 1.5Mb deletion	adds 60 aa before stop/del, chr2:24,460,563-25,807,506				R140Q	
123172	56	M	W	M1	normal		90	30.5	45	Dead	53.9	53.9				D835Y			W288fs
128392	65	M	W	M0	complex [no favorable]		83	0.9	0	Dead	17.1	17.1							
141273	64	F	B	M2	normal		80	2.6	46	Alive	8.1	8.1			0		0	0	
142074	60	M	W	M4	normal		89	79.9	56	Dead	9.9	11.3	R882H	missense	ITD				W288fs
146218	76	M	W	M1	inv(16)		73	98.2	55	Dead	4.5	4.5							
147796	78	M	W	M4	complex [no favorable]		40	9.9	6	Dead	1.3	1.3							
150288	51	M	B	M1	normal		62	1.5	10	Alive	8.4	8.4							0
150951	39	F	W	M0	del(5) only		75	2.3	4	Dead	22.2	26.3				0			
156704	49	M	W	M4	inv(16)		81	105.6	48	Dead	14.2	26.3							
179016	42	M	B	M3	complex [incl: t(15;17)]		88	2.1	2	Alive	21.2	21.2							
179223	82	F	W	M2	normal		53	1.4	25	Dead	1.5	1.5							W288fs
180168	51	F	W	M5	normal		57	80.9	0	Alive	8.8	8.8	R882H	missense					0
186481	57	F	W	M4	normal		90	110.2	84	Dead	5.1	7.5	R882C	missense		D835Y	R132H		W288fs
195182	63	M	W	M2	-7,t(9;22)		57	77.3	70	Dead	9.3	9.3							
202127	68	F	W	M3	t(15;17)		85	44	32	Dead	1	1			ITD				
208027	62	F	Asian	M2	1 cell +7		46	75.2	53	Dead	6.9	10.2	R803S	missense		D835Y			W288fs
224143	67	F	W	M1	normal		76	45.6	49	Dead	0.8	0.8	F909C	missense	ITD				W288fs
225373	71	F	W	M2	normal		70	35.9	67	Dead	0.8	0.8					R132C		
237983	59	M	W	M2	-7 only		70	11.5	48	Alive	14.7	14.7						R140Q	
242129	51	F	B	M4	complex [no favorable]	t(11;19)(q23;p13.1): FISH+	39	61.4	39	Alive	3.7	40							
245450	63	M	W	M4	+8,-17		62	33.3	9	Dead	8.4	8.4	R729W	missense					
246634	79	M	W	M4	normal		58	18.5	0	Dead	14.6	14.6	A741V/E477*	missense/nonsense					
254137	31	F	W	M2	normal		63	12.6	45	Dead	6.6	6.6			ITD				W288fs
255108	61	M	W	M0	+8		95	61.6	86	Alive	6.6	40.5			ITD				W288fs
258135	22	F	W	M2	inv(16), t(3;3)		55	51.8	70	Alive	28.6	28.6							
263578	52	F	W	M2	t(8;21)		67	4.1	18	Alive	82.4	82.4							
269542	76	M	B	M0	complex [no favorable]		74	14.5	82	Dead	0.3	0.3							
273919	25	M	W	M2	normal		56	126.1	71	Alive	47	47							
274429	64	M	W	M1	+8		60	1.2	5	Dead	27.4	27.4					R132C		
275382	65	M	W	M0	+8		99	2.9	34	Dead	32.3	32.3	No data obtained						
275786	43	M	W	M2	t(8;21)		40	4.3	39	Alive	7.1	7.1			ITD				
290344	49	F	W	M4	+11		51	12.4	5	Alive	28.4	28.4	R882C	missense					
291696	61	F	W	M3	t(15;17),+mar		73	86.4	68	Dead	0.2	0.2			ITD				
294154	44	M	W	M5	normal		74	8.8	5	Dead	0.3	0.3	R736H	missense					W288fs
296361	31	F	W	M5	normal		83	221.2	6	Dead	6.4	7.5	R882H	missense	ITD				W288fs
301733	76	M	W	M2	failed		68	3.9	3	Dead	13.8	19.3							
303818	41	F	W	M0	complex [no favorable]		42	47.6	74	Alive	39	39.9							
311636	64	F	W	M4	normal		72	131.5	90	Dead	12.1	24.1						R140Q	W288fs
312340	33	M	W	M2	de(9),del(20)		33	2.8	0	Dead	5.7	8.8							
318433	55	M	W	M4	t(2;4),inv(16)		35	22.2	67	Alive	76.7	76.7							
319955	45	F	W	M2	1~50dmin,der(6)		56	29.4	37	Alive	44.5	44.5							
321258	31	F	W	M3	t(15;17)		40	1.6	0	Alive	52.9	52.9							
322110	60	F	W	M1	9qh+		86	11.5	43	Alive	21.4	21.4			ITD			R140Q	W288fs
325028	44	M	W	M2	complex [no favorable]		39	34.8	83	Dead	5.2	11.8							
326772	47	F	W	M2	complex [no favorable]		37	12	0	Dead	12.2	12.2							
327733	32	F	W	M1	normal		94	5.1	70	Dead	11.9	56.3					R132C		W288fs
327929	50	M	B	M6	failed		70	5.5	0	Dead	3.7	8.9							
329614	68	F	W	M1	normal		90	202.2	91	Alive	4.3	9.6			ITD				W288fs
332131	24	M	W	M1	normal		77	223.8	76	Alive	9.8	14.1			ITD				
335640	67	F	W	M5	normal		85	93.3	3	Dead	2.5	2.5	R882C	missense		D835Y			W288fs
344551	48	M	H	M3	t(15;17)		65	0.6	28 Promy	Alive	61.1	61.1							
345701	48	F	W	M1	inv(16)		75	33.2	41	Alive	8.8	13.7							
346190	64	F	W	M4	+i(11)(q10)		85	2.9	22	Dead	8.1	8.1	R882P	missense					
369065	59	M	W	M0	normal		61	1.4	12	Dead	17.2	20.2	L773fs (L773-e18+5)	adds 48 aa before stop				R140Q	
375182	57	M	W	M5	normal		52	99.2	4	Dead	7.8	7.9	R882H	missense	ITD				W288fs
380949	59	F	W	M5	normal		95	12.1	0	Dead	11.4	11.8							
387919	57	F	W	M1	+8		91	19.8	91	Dead	13.3	15.1				D835Y	R132C		
399253	77	M	W	M4	normal		80	40.4	2	Dead	9.3	15.8	R882H	missense					
400220	34	F	W	M4	normal		71	19.6	58	Dead	8.3	10.7			ITD				
400830	73	F	W	M2	-7		37	1.7	16	Dead	11	11							
407992	33	M	W	M4	t(11;19),inv(12)	t(11;19)(q23;p13): FISH+	71	25.9	14	Dead	7.7	7.7				D835E			
410324	60	M	W	M5	complex [no favorable]	del(11)(q23); FISH+	94	6.7	30	Alive	24.2	24.2							
412761	48	M	W	M5	normal on PB		83	116.2	3	Alive	56	56							W288fs
415172	71	F	W	M0	complex [no favorable]		55	5.6	50	Dead	4.6	4.6							
418499	35	M	W	M4	normal		90	52.9	18	Dead	17	17							W288fs
426980	68	M	W	M2	normal		64	5.5	48	Dead	26.2	46.8						R140L	
427366	66	F	W	M5	normal		90	82.9	7	Dead	0.7	0.7							W288fs
431799	44	F	W	M1	normal		86	57	17	Dead	13.8	24.8	R882H	missense			R132H		W288fs
432398	67	M	W	M2	complex [no favorable]	add(11q23)	50	2.1	17	Dead	10.3	12.4							
433325	51	F	W	M2	normal		64	34.5	79	Dead	10.2	16.3	Q515*	nonsense					W288fs
434640	71	M	W	M0	complex [no favorable]		97	5.4	54	Dead	7	7							
440422	69	M	W	M0	normal		82	1.6	0	Alive	16.6	16.6						R140Q	0
445045	75	M	W	M2	normal		63	2.5	2	Alive	50.2	50.2							
447649	74	M	W	M3	t(15;17)		51	50.8	71 Promy	Dead	0.7	0.7			ITD				
452198	55	M	W	M5	normal		97	72.6	8	Alive	16.6	41.4	R882H	missense		D835H	R132H		W288fs
455499	29	F	H	M3	t(15;17)		85	1.2	1	Alive	37.1	37.1							
456892	58	M	W	M4	normal		58	19.9	10	Alive	34.5	34.5	E505*	nonsense					W288fs
463352	25	M	W	M2	-Y,t(8;21),del(9)		72	12.6	50	Alive	6.7	6.7							
465080	39	F	W	M3	del(7)(q34),t(15;17)		90	0.6	6	Alive	39.9	39.9							
470690	58	M	W	M4	i(17),+13		79	101.3	64	Dead	4.6	4.6							
478908	50	M	W	M3	t(15;17)		74	0.5	10	Alive	23.4	23.4			ITD				
494454	56	F	W	M5	-X		68	20.8	35	Dead	63.9	63.9	R882C	missense	ITD				W288fs
498463	60	F	W	M1	del(7)(q11.2) only		87	46.5	65	Alive	4.9	9.4	P718L	missense			R132C		
499294	57	M	W	M4	inv(16)		40	4.9	0	Alive	11.1	11.1							
501944	40	F	W	M3	t(15;17),+8		90	0.4	0	Alive	66.8	66.8							
507696	55	F	W	M4	inv(16)		52	30.9	59	Alive	10.3	10.3							
509733	38	M	W	M1	normal		86	42.4	94	Alive	76.7	76.7	K841Q	missense				R140Q	
509754	21	F	W	M1	normal		91	8.2	83	Alive	62.7	62.7					R132S		W288fs
514066	35	F	W	M1	t(8;21)		81	56.6	86	Dead	4.6	8							
529205	59	M	W	M3	t(15;17)		79	0.7	15	Alive	19.1	19.1			ITD				
530962	76	M	W	M7	-Y		33	3.6	6	Dead	7.2	9.9	M315fs	creates in frame stop at 315					
537782	51	F	W	M3	t(15;17)		93	3.6	40	Dead	5.4	46.5							
545259	30	F	W	M1	normal		86	22.9	88	Alive	23.3	23.3							
548327	51	M	W	M1	normal		85	63.7	85	Alive	19.6	19.6					R132G		W288fs
553863	69	M	W	M0	complex [no favorable]		60	6.1	22	Dead	0.5	0.5							
558395	64	M	W	M4	del(11) only		95	2.3	0	Dead	0.3	0.3							
569053	77	M	W	M6	del(20)		75	2.6	8	Dead	3.7	6.3							
570755	63	M	W	M2	t(11;19)	t(11;19)(q23;p13.1): FISH+	80	17	71	Dead	3.9	3.9			ITD				
573988	67	F	W	M4	normal		75	15.2	10	Dead	12	20.5						R140Q	W288fs
575512	60	F	B	M3	complex [incl: t(15;17)]		70	16.2	77	Alive	69.9	69.9							
585686	26	M	W	M1	t(12;22)		90	76.2	25	Dead	24.2	24.2							
593890	35	M	W	M2	+21		34	38	40	Alive	14.6	50.7							
594368	42	M	B	M1	complex [no favorable]		68	10.7	51	Alive	12.9	12.9	R729Q/D618fs(e15+2)	missense/adds RVLGLGRGLELPWLSLGCGA before stop				R140Q	
595704	67	F	W	M4	inv(16)		69	37	61	Alive	22.3	22.3			ITD				
606061	37	F	W	M2	normal		52	18.7	33	Dead	8.5	9.3							
619751	57	F	W	M4	inv(16)		61	13.6	17	Dead	10.8	45.8							
631879	76	M	W	M2	normal		40	1.4	0	Dead	14.9	17.4					R132C		
633734	53	M	W	M1	del(7)(q21q36)		72	2.7	41	Alive	19.3	63.1							
645137	40	F	W	M2	t(8;21), del(9)		44	2.9	8	Alive	76.5	76.5							
670224	62	M	W	M4	normal		65	104.1	65	Dead	13.4	14.5							W288fs
671473	42	F	W	M4	inv(16)		40	37.9	16	Alive	9.8	40.9							
673778	53	M	W	M3	t(15;17)		42	1	29	Alive	65	65							
690397	45	M	W	M5	t(6;11)	t(6;11)(q27;q23); FISH+	95	5.1	6	Dead	6.6	6.6							
692900	39	M	W	M0	+del(5)q, t(10;11)		83	5	53	Alive	73.3	73.3							
700717	45	M	W	M0	normal		75	2.3	0	Dead	3.8	11.2							
702808	75	F	W	M5	normal		41	66.1	0	Dead	5.3	6.3	R882H	missense					W288fs
708512	65	F	W	M4	complex [no favorable]		90	48.5	76	Dead	1.9	7.8	R882H	missense		D835E	R132H		W288fs
709968	25	M	W	M3	t(15;17)		91	8.2	63	Alive	24.2	60.9			ITD				
717456	50	F	W	M5	-7,i(9;11)	t(9;11)(p22;q23); FISH+	81	6.7	10	Dead	5.6	5.6							

721214	41	F	W	M1	failed		92	151.8	90	Dead	5.7	5.7	R882H	missense	ITD				W288fs
724606	72	F	W	M2	normal		45	3	0	Dead	1.9	1.9							
730817	66	F	W	M5	normal		32	78.5	11	Dead	5.9	7.7	E616fs	adds 34 aa before stop		D835Y			
731274	18	M	B	M3	t(15;17)		90	84.9	95	Alive	80	80			ITD				
737451	21	F	W	M5	normal		90	103.7	72	Dead	7.5	7.5	R882H	missense	0				W288fs
740266	58	M	Amer	M0	complex [no favorable]		59	56.5	72	Alive	23.6	23.6	R882H	missense			R132H		
750152	34	F	W	M2	t(8;21)		57	14.3	59	Alive	23.3	23.3							
753374	29	M	W	M2	normal		45	2.2	9	Dead	8.9	11.9							W288fs
757199	50	F	W	M3	t(15;17),t(16;19)		90	3.4	0	Alive	8.2	8.2							
758168	25	F	W	M3	t(15;17)		93	16.3	40	Alive	31.6	43.4							
767545	72	M	W	M2	+11 only		30	1.6	0	Dead	13.8	22.1							
775109	45	M	W	M5	normal		81	1.6	0	Alive	76.5	76.5							
804168	53	M	W	M1	normal		86	99.8	52	Dead	7.7	30			ITD				W288fs
807615	51	M	W	M1	normal		85	103.6	85	Dead	3.1	3.1	R882H	missense	ITD				W288fs
807970	38	M	W	M1	normal		86	39.8	97	Alive	47.9	47.9					R132C		W288fs
808642	61	M	W	M1	normal		49	2.9	14	Dead	12	15.5			ITD				
809653	60	F	W	M1	complex [no favorable]		62	16	29	Dead	1.9	1.9							
816067	35	F	W	M5	normal		87	156.1	8	Alive	21.7	21.7	R882C	missense	ITD				W288fs
817156	54	M	B	M2	normal		67	45	83	Alive	8.5	32.9	R882H	missense					
818119	40	F	W	M4	normal		50	3.3	4	Dead	10.5	19.7							W288fs
826984	51	F	W	M4	t(5;21)		73	2.9	2	Dead	8	11.1							
831711	57	F	W	M1	normal		64	2.5	61	Alive	42.5	42.5							
849660	22	M	W	M1	normal		71	167.5	90	Dead	7.7	27							
851929	69	F	W	M1	+8		42	10.1	32	Alive	13.3	13.3	R792H/R803fs(e21+2)	missense/fusion of e20:e22, fs adds SSAK before stop				R172K	
852559	18	M	W	M1	complex [no favorable]		86	35	90	Dead	6.7	7.2							
862507	55	F	Unk	M4	del(16),+22		54	114.5	24	Alive	50.9	50.9							
863018	62	M	W	M3	t(15;17)		82	0.9	11	Alive	63.6	63.6							
868231	63	M	W	M4	normal		82	76.7	39	Dead	5.3	5.3			ITD				
869586	23	M	W	M4	normal		51	27.1	63	Dead	7.7	19							
869922	56	F	W	M2	normal		60	202.7	96	Dead	9.6	16.4	R882H	missense					
884262	54	M	W	M6	complex [no favorable]		30	2.3	0	Dead	6.5	10							
905179	75	F	W	M2	t(8;21), del(9)		48	8.3	54	Dead	18.2	19.2							
906708	76	F	W	M4	normal		91	5	16	Dead	17	25.8							
907786	81	F	W	M5	normal		53	16.8	7	Dead	9.2	9.2							
923966	61	M	W	M5	t(9;11)	t(9;11)(p22;q23)	89	286	0	Dead	3.2	5.7							
933124	57	F	W	M1	normal		100	97.1	91	Dead	11.1	24.6	L723fs	adds 55 aa before stop	ITD				W288fs
936028	40	M	B	M2	normal		47	8.3	23	Dead	8	10.2	R882H	missense					W288fs
938150	60	F	W	M7	complex [no favorable]		58	0.8	0	Dead	12	13.6							
943309	35	M	W	M3	del(7),+8,t(15;17)		90	1.5	7	Alive	52.1	52.1			ITD				
944281	31	M	W	M4	inv(16)		82	336.8	53	Alive	27.2	27.2				D835Y			
957664	76	M	W	M5	+8		78	4	0	Dead	0.6	0.6	Q615*	nonsense					W288fs
962561	76	F	W	M4	+13,-21		37	2.7	0	Dead	17.3	22.3							
964886	33	F	B	M3	normal		100	0.9	0	Alive	57.1	57.1			ITD				
972783	71	M	W	M0	+13		90	1	13	Dead	13.4	15.4						R140Q	
974749	63	M	W	M1	+8, +8		81	46.4	97	Dead	1.2	1.2	R882H	missense			R132C		
975684	53	F	W	M1	+8 only		82	1.2	42	Dead	20.1	20.1	R882H	missense				R172K	
982009	70	M	B	M1	normal		84	282.4	49	Dead	4.9	6.3				D835Y			W288fs
984036	75	M	W	M1	+21,+3		40	6.4	48	Dead	2.3	2.3							
986000	77	M	W	M7	complex [no favorable]		47	1.9	0	Dead	4.5	4.5							
987523	27	M	B	M1	complex [no favorable]		77	262	88	Alive	13.2	13.2					R132C		
989176	76	F	W	M1	normal		99	352.3	98	Dead	0.4	0.4							W288fs
991612	63	M	W	M2	normal		35	0.6	0	Alive	51.1	51.1							
992966	67	M	W	M1	normal		89	30.8	61	Dead	4.5	5.5						R140Q	
997292	66	F	W	M2	normal		70	3.4	6	Dead	5.2	5.2	K829R/K468R	missense/missense			R132C		
93-C-100	24	M	W	M3	t(15;17)		93	NA	NA	Alive	10.1	122.3							
93-C-184	45	M	W	M4	inv(16)		69	NA	NA	Alive	128.8	128.8							
93-C-206	29	F	W	M3	t(15;17)		90	NA	NA	Alive	113.7	113.7							
93-C-230	41	F	B	M3	t(15;17)		81	NA	NA	Alive	83.1	83.1							
93-C-234	50	M	B	M3	t(15;17)		89	NA	NA	Dead	5.8	10.3			ITD				
93-C-270	40	M	W	M3	t(15;17)		90	NA	NA	Dead	2	6.8			ITD				
93-C-275	38	M	W	M3	t(15;17)		87	NA	NA	Alive	26.3	26.3			ITD				
93-C-287	46	M	W	M4	inv(16)		63	NA	NA	Alive	129.3	129.3							
93-C-290	37	F	H	M2	t(8;21)		31	NA	NA	Alive	121.9	121.9							
93-C-44	51	F	W	M2	t(8;21)		74	NA	NA	Dead	9.5	10.9				D835Y			
93-C-57	50	M	H	M3	t(15;17)		99	NA	NA	Alive	115.9	115.9							
94-C-022	28	F	Asian	M2	t(8;21)		83	NA	NA	Dead	1.3	4							
94-C-024	54	M	W	M4	inv(16)		65	NA	NA	Dead	14.1	32.5							
94-C-046	41	M	W	M4	del(9)		73	NA	NA	Dead	13.8	23.1	R882H	missense					W288fs
94-C-149	47	M	W	M3	t(15;17)		80	NA	NA	Alive	15.2	119.8							
94-C-163	32	M	W	M1	del(9)		89	NA	NA	Alive	123.2	123.2							
94-C-207	45	M	Other	M4	normal		96	NA	NA	Dead	12.9	20.3	R882H	missense	ITD		R132H		W288fs
94-C-240	38	F	Asian	M1	add(9)		88	NA	NA	Dead	28	33.5			ITD	D342N		0	
94-C-271	25	M	W	M3	t(15;17)		70	NA	NA	Alive	91	91							
C-00-102	48	M	W	M4	normal		50	NA	NA	Dead	8.8	12.3	R882C	missense					
C-00-111	52	M	W	M2	normal		64	NA	NA	Dead	1.3	8.2	R882S	missense					W288fs
C-00-1297	42	M	H	M3	t(15;17)		87	NA	NA	Alive	37.2	55.6							
C-00-1539	51	M	W	M3	t(15;17)		78	NA	NA	Alive	54.7	54.7							
C-00-155	59	M	W	M2	normal		47	NA	NA	Dead	0.9	9.4					R132H		
C-00-1819	33	F	H	M3	t(15;17)		92	NA	NA	Alive	49.1	49.1			ITD				
C-00-1895	33	M	W	M3	t(15;17)		80	NA	NA	Alive	55.3	55.3							
C-00-2017	34	M	W	M3	t(15;17)		77	NA	NA	Alive	55.9	55.9			ITD				
C-00-205	49	M	W	M3	t(15;17)		53	NA	NA	Alive	53	53							
C-00-266	32	M	H	M2	normal		53	NA	NA	Dead	29.7	41.1							
C-00-391	37	F	W	M1	normal		76	NA	NA	Dead	7.4	11							W288fs
C-00-407	70	M	W	M3	t(15;17)		90	NA	NA	Alive	56.2	56.2				D324N			
C-00-574	22	F	W	M3	t(15;17)		96	NA	NA	Alive	52.3	52.3							
C-00-784	59	M	Asian	M1	normal		90	NA	NA	Dead	6.3	6.3							W288fs
C-00-969	37	F	W	M3	t(15;17)		81	NA	NA	Alive	50.7	50.7							
C-01-1143	60	F	B	M3	t(15;17)		78	NA	NA	Alive	40.2	40.2			ITD				
C-01-1211	28	M	Asian	M3	t(15;17)			NA	NA	Alive	42.3	42.3							
C-01-1658	40	M	H	M3	t(15;17)		83	NA	NA	Dead	0.2	0.2							
C-01-1729	26	F	W	M3	t(15;17)		81	NA	NA	Alive	39.2	39.2			ITD				
C-01-1931	53	M	W	M3	t(15;17)			NA	NA	Alive	34.4	34.4							
C-95-058	54	F	Other	M4	+21		84	NA	NA	Dead	2	26.2	F827fs^	adds LAK before stop				R140Q	W288fs
C-95-135	43	M	W	M2	normal		72	NA	NA	Alive	10.4	115							
C-95-318	49	F	W	M2	normal		44	NA	NA	Dead	1.1	11.8							
C-97-286	23	F	H	M4	normal		86	NA	NA	Alive	64.1	64.1						R140Q	
C-97-398	34	F	H	M4	inv(16)		51	NA	NA	Alive	88.1	88.1							
C-97-408	33	M	W	M4	normal		51	NA	NA	Alive	90.3	90.3	R882H	missense					W288fs
C-97-464	49	F	H	M4	t(11;19)	t(11;19)(q23;p13.1)	44	NA	NA	Dead	6.6	23.5				V571I			
C-97-509	37	M	B	M1	normal		81	NA	NA	Dead	7.5	14.2	L805*^	nonsense			R132H		W288fs
C-97-529	33	M	W	M1	normal		71	NA	NA	Alive	87.5	87.5							
C-97-553	54	F	W	M1	normal		72	NA	NA	Dead	1.5	3.4	R882H	missense	ITD		R132H		
C-97-581	54	F	W	M1	normal		86	NA	NA	Alive	25.3	89.6			ITD				W288fs
C-97-592	30	F	H	M4	inv(16)		76	NA	NA	Alive	86.2	86.2							
C-97-651	26	M	W	M1	normal		86	NA	NA	Dead	11.5	19.3			ITD		R132H		
C-97-779	58	M	W	M0	normal		65	NA	NA	Dead	2	16.5						R140Q	
C-97-856	49	F	W	M2	normal		54	NA	NA	Alive	83.5	83.5	R882H	missense					W288fs
C-98-1077	44	F	W	M1	-13		68	NA	NA	Dead	2	10.1	R882H	missense			R132C		
C-98-110	43	F	W	M4	normal		45	NA	NA	Dead	5.7	16.9	E733fs^	creates in frame stop					W288fs
C-98-1202	57	M	W	M4	normal		79	NA	NA	Dead	3.5	5.1	R882P	missense	ITD				W288fs
C-98-1243	51	F	W	M2	normal		50	NA	NA	Alive	74.6	74.6							
C-98-1252	36	M	W	M2	-9, add(9), +mar		68	NA	NA	Dead	3.4	9.3							
C-98-1301	22	M	W	M1	del(7)		73	NA	NA	Alive	74.8	74.8							
C-98-154	20	F	W	M2	normal		67	NA	NA	Alive	79.8	79.8			ITD				
C-98-183	41	M	W	M2	normal		80	NA	NA	Dead	1.8	3.2			ITD				
C-98-319	43	M	W	M0	t(3;3)		96	NA	NA	Dead	1.4	16.7							
C-98-354	31	M	W	M2	+10		46	NA	NA	Alive	11	70.1							
C-98-358	22	F	W	M2	t(8;21)		53	NA	NA	Dead	10.3	26.5			ITD	D835Y			
C-98-383	32	M	W	M4	t(9;11)	t(9;11)(p22;q23)	81	NA	NA	Dead	10.1	12.1							
C-98-395	55	M	W	M4	inv(16)		58	NA	NA	Dead	8.3	14.4							
C-98-412	38	M	W	M0	t(11;19)	t(11;19)(q23;p13.3)	60	NA	NA	Alive	80.1	80.1							
C-98-430	27	F	W	M1	normal		88	NA	NA	Dead	23.9	26.1							
C-98-520	39	F	W	M4	+21		71	NA	NA	Dead	9.4	16							
C-98-650	35	M	W	M4	inv(16)		63	NA	NA	Alive	68	68							
C-98-840	37	F	W	M4	normal		80	NA	NA	Dead	5	6.2	R598*^	nonsense	ITD				W288fs
C-98-925	40	M	W	M4	inv(16)		52	NA	NA	Alive	72	72							
C-98-974	23	M	W	M0	normal		80	NA	NA	Dead	9.9	13							
C-99-1142	51	F	Other	M1	normal		77	NA	NA	Alive	60.1	60.1					R132C		W288fs
C-99-1148	30	F	W	M4	normal		63	NA	NA	Dead	9.1	14.4	R882H	missense	ITD				W288fs
C-99-1255	22	M	W	M1	normal		70	NA	NA	Alive	55.4	55.4							
C-99-1632	50	F	W	M1	normal		62	NA	NA	Dead	1.4	5.7	P904L^	missense	ITD				W288fs
C-99-1646	42	M	W	M2	normal		46	NA	NA	Alive	53.4	53.4							
C-99-1652	56	M	W	M0	normal		65	NA	NA	Dead	2	25							
C-99-27	22	M	B	M4	t(6;9)		56	NA	NA	Dead	1.4	7.4			ITD				
C-99-313	33	F	W	M2	normal		32	NA	NA	Dead	6.6	10							
C-99-325	48	F	W	M2	normal		32	NA	NA	Alive	63	63							
C-99-430	35	F	W	M2	normal		48	NA	NA	Alive	69.6	69.6							W288fs

C-99-474	25	M	W	M2	normal		48	NA	NA	Dead	9.7	13.1	E30A^	missense		D324N			
C-99-483	28	F	W	M2	normal		53	NA	NA	Alive	68.4	68.4	A368D^	missense		D324N			W288fs
C-99-508	55	M	H	M2	t(8;10;21)		60	NA	NA	Alive	69.5	69.5							
C-99-550	38	M	W	M4	inv(16)		45	NA	NA	Alive	71.2	71.2							
C-99-627	38	M	W	M2	t(8;21)		60	NA	NA	Dead	5.1	13.5							
C-99-67	35	F	W	M1	normal		76	NA	NA	Dead	47.7	54.3							
C-99-709	59	F	W	M1	normal		75	NA	NA	Alive	56.9	56.9							
C-99-860	54	M	W	M4	normal		45	NA	NA	Dead	2	7.3			ITD				
C-99-901	38	F	B	M4	t(16;16)		42	NA	NA	Alive	47.2	47.2				D835Y, V571I			
C-99-934	37	F	W	M1	normal		80	NA	NA	Alive	65.7	65.7				D835Y			W288fs

^novel mutation, not confirmed somatic

0=no data obtained

Supplementary Table 2. Summary of *DNMT3A* Mutations.

Mutation	Predicted Consequence	Evidence	n	PolyPhen[#]	SIFT[&]
R882H	missense	Prediction based on NM_022552.2	27	benign	deleterious
R882C	missense	Prediction based on NM_022552.2	7	probably damaging	deleterious
R882P	missense	Prediction based on NM_022552.2	2	probably damaging	deleterious
R882S	missense	Prediction based on NM_022552.2	1	probably damaging	deleterious
R803S	missense	Prediction based on NM_022552.2	1	probably damaging	no prediction
R792H	missense	Prediction based on NM_022552.2	1	benign	tolerated
R736H	missense	Prediction based on NM_022552.2	1	benign	no prediction
R729W	missense	Prediction based on NM_022552.2	1	probably damaging	tolerated
R729Q	missense	Prediction based on NM_022552.2	1	possibly damaging	tolerated
P904L^	missense	Prediction based on NM_022552.2	1	possibly damaging	deleterious
P718L	missense	Prediction based on NM_022552.2	1	probably damaging	deleterious
K841Q	missense	Prediction based on NM_022552.2	1	benign	no prediction
K829R	missense	Prediction based on NM_022552.2	1	possibly damaging	deleterious
K468R	missense	Prediction based on NM_022552.2	1	benign	tolerated
F909C	missense	Prediction based on NM_022552.2	1	probably damaging	deleterious
E30A^	missense	Prediction based on NM_022552.2	1	benign	deleterious
A741V	missense	Prediction based on NM_022552.2	1	benign	deleterious
A368D^	missense	Prediction based on NM_022552.2	1	probably damaging	deleterious
M315fs*	p.M315fs*	Prediction based on NM_022552.2	1	no prediction	no prediction
E616fs	p.E616fsNLTLQRFTHLSQLRRGSPSGCCLSLMESLQGSWC*	Prediction based on NM_022552.2	1	no prediction	no prediction
F827fs^	p.F827fsLAK*	Prediction based on NM_022552.2	1	no prediction	no prediction
L723fs	p.L723fsPTRALAGSSLSSTASCMMRGPRREMIAPSSGSLRMWWPWALVTRGTSRDFSSPTL*	Prediction based on NM_022552.2	1	no prediction	no prediction
E733fs^	p.E733fs*	Prediction based on NM_022552.2	1	no prediction	no prediction
G590fs	p.G590fsVPTGCCGGERTGPPGSRCSSLITTTRNLTLQRFTHLSQLRRGSPSGCCLSLMESLQGSWC*	Prediction based on NM_022552.2	1	no prediction	no prediction
E477*	nonsense	Prediction based on NM_022552.2	1	no prediction	no prediction
R598*^	nonsense	Prediction based on NM_022552.2	1	no prediction	no prediction
Q615*	nonsense	Prediction based on NM_022552.2	1	no prediction	no prediction
Q515*	nonsense	Prediction based on NM_022552.2	1	no prediction	no prediction
E505*	nonsense	Prediction based on NM_022552.2	1	no prediction	no prediction
L805*^	nonsense	Prediction based on NM_022552.2	1	no prediction	no prediction
e21+2	mutation at donor splice site at 3' end of exon 21; causes p.R803fsSSAK*	RT-PCR indicates skipping of exon21 (fusion of exon 20 to 22)	1	no prediction	no prediction
e15+2	mutation at donor splice site at 3' end of exon 15; causes p.D618fsRVLGLGRGLELPWLSLGCGA*	RT-PCR confirms intron 15 retention	1	no prediction	no prediction
L773-e18+5	deletion at L773 also deletes splice donor site; causes p.L773fsRQQPWFGQLTNGFYLGLLLHPVSSALWSWGLVTSALQGACLGSPRLPG*	Predicted based on intron retention	1	no prediction	no prediction
Deletion	del chr2:24,460,563-25,807,506, removes all or part of 9 genes	Prediction based on NM_022552.2	1	no prediction	no prediction

^=CALGB sample, not verified as somatic

[&]deleterious, SIFT score <= 0.05; tolerated, SIFT score > 0.05 (http://sift.jcvi.org/www/SIFT_help.html#SIFT_OUTPUT)

[#]version 1.13

Supplementary Table 3. DNMT3A cDNA variant allele readcounts.

UPN	DNMT3A Mutation	WT Reads	Variant Reads	Total Reads	% Variant Reads
287	R882H	5668	5582	11250	49.62%
142074	R882H	1833	1951	3784	51.56%
399253	R882H	756	759	1515	50.10%
452198	R882H	827	861	1688	51.01%
104	R882C	1368	1048	2416	43.38%
186481	R882C	1040	597	1637	36.47%
335640	R882C	1247	1179	2426	48.60%
816067	R882C	762	725	1487	48.76%
224143	F909C	95	125	220	56.82%
509733	K841Q	977	2071	3048	67.95%
245450	R729W	2227	2141	4368	49.02%
208027	R803S	2231	885	3116	28.40%
433325	Q515*	140	36	176	20.45%
730817	E616fs	66	20	86	23.26%
530962	M315fs	106	0	106	0.00%
933124	L723fs	2862	1819	4681	38.86%
113971	G590fs^	603	6421	7024	91.42%
246634	E477*	8282	0	8282	0.00%
246634	A741V	86940	69	87009	0.08%
594368	D618fs/e15+2^^	445	12182	12627	96.48%
594368	R729Q	13610	14665	28275	51.87%
851929	R792H	32291	27959	60250	46.40%
851929	R803fs/e21+2^^^	30030	36605	66635	54.93%
997292	K468R	4585	714	5299	13.47%
997292	K829R	14458	17368	31826	54.57%

UPN, unique patient number; WT, wildtype

^Mutant allele frequency is 91% because one copy of *DNMT3A* was deleted in this sample

^^Primer pairs designed to detect aberrantly spliced transcript only (retained intron 15)

^^^54.93% of transcripts reveal skipping of exon 21 (i.e. fusion of exon 20 to 22)

Supplementary Table 4. DNMT3A Mutation Types.

Reference Base	Variant Base	Total in 11 DNMT3A Mutant* genomes (%)	Total in 27 DNMT3A WT genomes (%)
A	C	773 (5.8)	1661 (6.9)
A	G	2403 (18.0)	4580 (19.1)
A	T	1703 (12.8)	3004 (12.5)
C	A	1856 (13.9)	3195 (13.3)
C	G	820 (6.2)	1488 (6.2)
C	T	5778 (43.3)	10074 (42.0)
	Total:	13,333	24,002

Mutations in each genome included: A741V/E477, E505*, F909C, L723fs, G590fs/1.5Mb deletion, R882H (n=4), and R882C (n=2).

Supplementary Table 5. LC-MS quantification of deoxyribonucleoside phosphates.[1]

Sample Name	DNMT3A Mutation	Peak Area (counts)			Calculated amount of analyte (fmol)			Percentage of mdCMP	
		mdCMP	dCMP	dGMP	mdCMP	dCMP	dGMP	(mdCMP/ mGMP)	(mdCMP/ (mdCMP+ dCMP))
246634	A741V/E477*	4.92E+05	8.48E+06	1.04E+07	0.922	21.9	22.8	4.00%	4.04%
456892	E505*	2.13E+05	3.78E+06	4.65E+06	0.463	9.78	10.2	4.50%	4.52%
730817	E616fs	6.26E+05	1.00E+07	1.26E+07	1.28	25.9	27.4	4.70%	4.71%
224143	F909C	1.00E+06	1.47E+07	1.87E+07	2.01	37.9	40.7	4.90%	5.04%
113971	G590fs/deletion	5.37E+05	7.86E+06	1.02E+07	1.1	20.3	22.2	5.00%	5.14%
997292	K829R/K468R	6.71E+05	1.06E+07	1.29E+07	1.37	27.4	28.1	4.90%	4.76%
509733	K841Q	6.46E+05	8.98E+06	1.17E+07	1.32	23.2	25.5	5.20%	5.38%
933124	L723fs	3.42E+05	5.69E+06	7.23E+06	0.717	14.7	15.8	4.50%	4.65%
369065	L773-e18+5	6.92E+05	1.11E+07	1.43E+07	1.41	28.8	31.1	4.50%	4.67%
530962	M315fs	5.16E+05	9.36E+06	1.16E+07	1.06	24.2	25.4	4.20%	4.20%
498463	P718L	4.22E+05	6.81E+06	8.58E+06	0.875	17.6	18.8	4.70%	4.74%
433325	Q515*	6.81E+05	1.04E+07	1.33E+07	1.39	26.9	29	4.80%	4.91%
957664	Q615*	3.76E+05	7.63E+06	9.32E+06	0.784	19.7	20.4	3.80%	3.83%
594368	R729Q/e15+2	4.45E+05	6.74E+06	8.49E+06	0.92	17.4	18.6	4.90%	5.02%
245450	R729W	4.46E+05	7.16E+06	9.12E+06	0.662	18.5	19.9	3.30%	3.45%
294154	R736H	2.34E+05	4.32E+06	5.18E+06	0.81	19.9	18.8	4.30%	3.91%
851929	R792H/e21+2	1.30E+06	1.94E+07	2.57E+07	2.6	50.1	55.9	4.70%	4.93%
208027	R803S	2.14E+06	3.02E+07	3.97E+07	4.26	77.9	86.2	4.90%	5.19%
186481	R882C	5.68E+05	9.15E+06	1.15E+07	1.16	23.7	25.2	4.60%	4.67%
142074	R882H	1.70E+06	2.72E+07	2.59E+07	3.95	74.9	81.3	4.90%	5.01%
375182	R882H	5.01E+06	7.16E+07	8.81E+07	11.6	197	277	4.20%	5.56%
431799	R882H	9.37E+05	1.57E+07	1.58E+07	2.19	43.2	49.8	4.40%	4.82%
452198	R882H	1.00E+06	1.73E+07	1.72E+07	2.34	47.6	54	4.30%	4.69%
721214	R882H	1.12E+06	1.88E+07	1.67E+07	2.61	51.9	52.5	5.00%	4.79%
737451	R882H	1.33E+06	2.12E+07	2.15E+07	3.09	58.4	67.5	4.60%	5.03%
740266	R882H	4.66E+06	6.51E+07	7.38E+07	10.8	179	232	4.70%	5.69%
817156	R882H	4.04E+06	5.83E+07	6.94E+07	9.34	161	218	4.30%	5.48%
869922	R882H	3.50E+05	5.98E+06	5.55E+06	0.839	16.4	17.5	4.80%	4.87%
399253	R882H	5.30E+05	8.22E+06	1.06E+07	1.09	21.3	23.2	4.70%	4.87%
807615	R882H	6.40E+05	1.03E+07	1.35E+07	1.3	26.7	29.4	4.40%	4.64%
103342	Wild Type	1.67E+06	2.63E+07	2.81E+07	3.89	72.5	88.3	4.40%	5.09%
179223	Wild Type	3.11E+06	4.46E+07	5.38E+07	7.21	123	169	4.30%	5.54%
329614	Wild Type	7.34E+05	1.20E+07	1.03E+07	1.72	33	32.4	5.30%	4.95%
804168	Wild Type	7.13E+06	8.93E+07	1.08E+08	16.5	246	339	4.90%	6.29%
804168	Wild Type	1.76E+06	2.69E+07	2.78E+07	4.1	74	87.3	4.70%	5.25%
906708	Wild Type	6.93E+06	8.66E+07	1.07E+08	16	238	337	4.70%	6.30%
907786	Wild Type	6.84E+05	1.18E+07	1.14E+07	1.61	32.6	35.9	4.50%	4.71%
982009	Wild Type	3.00E+06	4.61E+07	5.22E+07	6.95	127	164	4.20%	5.19%
380949	Wild Type	5.61E+05	9.60E+06	1.24E+07	1.15	24.8	27	4.30%	4.43%
418499	Wild Type	6.44E+05	1.00E+07	1.36E+07	1.31	25.9	29.7	4.40%	4.81%

445045	Wild Type	4.00E+05	6.53E+06	8.33E+06	0.832	16.9	18.2	4.60%	4.69%
545259	Wild Type	1.05E+06	1.68E+07	2.24E+07	2.12	43.4	48.7	4.40%	4.66%
868231	Wild Type	6.50E+05	9.71E+06	1.29E+07	1.32	25.1	28.1	4.70%	5.00%
311636	Wild Type	1.16E+06	1.99E+07	2.49E+07	3.92	91.5	90.2	4.30%	4.11%
103342	Wild Type	7.03E+05	1.13E+07	1.42E+07	1.43	29.2	31	4.60%	4.67%
179223	Wild Type	8.90E+05	1.48E+07	1.91E+07	1.8	38.2	41.5	4.30%	4.50%
329614	Wild Type	6.40E+05	9.64E+06	1.28E+07	1.3	24.9	27.8	4.70%	4.96%
573988	Wild Type	9.81E+05	1.54E+07	1.99E+07	1.97	39.8	43.3	4.50%	4.72%
804168	Wild Type	6.17E+05	1.02E+07	1.25E+07	1.26	26.3	27.3	4.60%	4.57%
804168	Wild Type	7.97E+05	1.28E+07	1.60E+07	1.61	33.1	34.9	4.60%	4.64%
906708	Wild Type	7.64E+05	1.19E+07	1.52E+07	1.55	30.8	33	4.70%	4.79%
907786	Wild Type	1.02E+06	1.83E+07	2.32E+07	3.46	84.2	84	4.10%	3.95%
982009	Wild Type	5.45E+05	9.11E+06	1.10E+07	1.12	23.5	24.1	4.60%	4.55%
CONTROL 1[2]	Control	1.08E+06	1.79E+07	2.45E+07	2.17	46.1	53.3	4.10%	4.50%
CONTROL 2[2]	Control	1.16E+06	1.92E+07	2.44E+07	2.33	49.7	53.1	4.40%	4.48%
CONTROL 3[2]	Control	1.54E+06	2.47E+07	3.46E+07	3.07	63.9	75.2	4.10%	4.58%
CONTROL 4[2]	Control	8.30E+05	1.47E+07	1.84E+07	2.82	67.6	66.7	4.20%	4.00%

[1] Determined from 3.5-5 ug DNA with 23% of total hydrolysate analyzed.

[2] The control samples were derived from a single pool of genomic DNA derived from the spleens of 6 young C57Bl/6 male mice. The same control sample was run in the assay 4 independent times.

Supplementary Table 6. meDIP chip analysis.

chr	start	stop	mut_817156_m2	mut_431799_m1	mut_142074_m4	mut_399253_m4	mut_737451_m5	non_445045_m2	non_545259_m1	non_418499_m4	non_868231_m4	non_380949_m5	P-value	False Discovery Rate
Nearby Gene: ANGPTL2														
chr9	128923152	128923201	0.78	0.32	1.49	0.22	0.69	2.04	1.78	1.69	1.85	1.99	0.0031784640	0.0614230982
chr9	128923242	128923300	0.91	0.54	1.37	0.47	1	2.18	1.89	1.94	2.54	2.22	0.0033313840	0.0623207242
chr9	128923442	128923491	0.76	0.22	1.46	0.27	1.11	2.27	1.78	1.47	2.53	1.98	0.0000515484	0.0233324165
chr9	128923557	128923606	0.81	0.32	1.62	0.41	1.31	2.41	2.1	1.48	2.26	1.46	0.0003709806	0.0338757494
chr9	128923672	128923728	1.04	0.38	1.62	0.49	1.51	2.79	2.41	1.55	2.25	2.3	0.0014562606	0.0485066711
chr9	128923752	128923801	1.44	0.36	1.78	0.69	2.47	3.42	2.97	1.72	3.65	3.03	0.0015659923	0.0495476086
chr9	128923962	128924011	0.96	0.29	1.57	0.3	1.08	2.98	2.37	1.34	1.96	2.55	0.0013442122	0.0474965834
chr9	128924042	128924091	1.01	0.64	2.09	0.58	2.07	3.41	3.07	1.62	2.97	2.96	0.0014466856	0.0484193458
chr9	128924167	128924216	0.51	0.32	1.93	0.04	1.37	2.87	2.4	1.54	2.57	2.64	0.0095395876	0.0915859846
Nearby Gene: WT1														
chr11	32411263	32411312	2.11	1.41	2.22	-1.03	1.49	2.06	2.78	2.84	2.34	2.26	0.0077567049	0.0841684302
chr11	32411363	32411414	1.74	0.87	1.69	-1.33	0.96	1.85	2.28	2.22	1.13	1.69	0.0001490052	0.0289451001
chr11	32411438	32411487	1.68	0.83	1.71	-1.34	1.15	1.98	2.34	2.44	2.05	1.97	0.0000918609	0.0264076198
chr11	32411568	32411617	1.71	0.85	1.75	-0.9	0.96	1.8	2.33	2.12	2.12	1.87	0.0002524900	0.0318920172
chr11	32411643	32411692	1.66	0.92	1.68	-1.28	1.54	2.4	2.75	2.3	2.51	2.12	0.0000688635	0.0251473615
chr11	32411738	32411794	1.8	0.79	1.54	-1.36	1.87	2.47	2.93	2.25	3	2.26	0.0000701104	0.0251733309
chr11	32411863	32411912	1.67	1	1.68	-0.69	1.92	2.4	2.73	2.32	2.56	2.23	0.0000310175	0.0218810115
chr11	32411938	32411987	1.78	0.79	1.59	-1.14	1.71	2.35	2.87	2.22	2.29	1.71	0.0088280859	0.0887956248
chr11	32412068	32412117	1.77	0.82	1.58	-0.71	1.42	2.05	2.62	2.42	2.17	2.08	0.0148536877	0.1094289229
Nearby Gene: GRM2														
chr3	51716434	51716483	-0.08	0.49	-0.07	0.94	0.07	3.56	2.98	1.99	3.57	3.32	0.0170145726	0.1159673552
chr3	51716524	51716573	-0.67	0.22	-0.68	0.83	-0.4	3.74	2.88	2.24	4.06	3.47	0.0005946030	0.0384487121
chr3	51716604	51716653	-0.54	0.21	-0.77	0.65	-0.35	3.28	2.47	2.25	3.29	2.54	0.0000463163	0.0228099481
chr3	51716704	51716753	-0.8	0.06	-0.63	0.82	-0.68	2.8	2.18	2.07	2.88	2.49	0.0001139211	0.0278463335
chr3	51716814	51716863	-0.22	0.54	-0.61	1.12	-0.52	2.65	2.41	2.28	2.94	2.52	0.0009538393	0.0431956680
chr3	51716934	51716983	-0.45	0.65	-0.2	1.24	-0.43	2.75	2.64	1.59	2.93	2.7	0.0007603753	0.0409798364
chr3	51717034	51717083	1.25	1.65	1.37	1.93	1.14	2.75	2.7	2.78	2.97	2.92	0.0007384828	0.0407658514
chr3	51717104	51717153	-0.5	0.9	-0.2	1.65	-0.5	2.71	2.92	2.93	3.34	2.89	0.0271051840	0.1424147668
Nearby Gene: HYAL2														
chr3	50335673	50335722	0.31	0.27	-0.59	-1.17	-0.68	1.9	1.82	1.34	1.91	1.09	0.0288322901	0.1465178668
chr3	50335768	50335817	0.55	0.68	-1.01	-0.9	-0.59	2.26	2.33	1.75	2.59	1.58	0.0063009861	0.0779617846
chr3	50335848	50335897	0.34	0.64	-0.71	-0.61	-0.32	2.09	2.22	1.55	1.82	1.23	0.0000198295	0.0213337524
chr3	50335948	50335997	0.45	0.52	-0.63	-0.21	-0.69	2.07	2	1.73	2.47	1.53	0.0088021961	0.0886965969
chr3	50336053	50336102	-0.2	0.03	-1.1	-0.88	-0.89	2.01	1.69	1.57	2.19	1.2	0.0094542288	0.0912465374
chr3	50336248	50336297	0.22	0.38	-0.26	-0.1	0.18	1.75	1.52	1.51	2.08	1.41	0.0101237717	0.0936244351
chr3	50336348	50336397	0.72	0.67	0	-0.03	0.4	1.99	1.9	1.79	2.06	1.65	0.0110963449	0.0972947658
chr3	50336443	50336492	0.58	0.64	-0.25	-0.64	-0.29	2.07	1.92	1.79	2.33	1.4	0.0155441156	0.1115443341
Nearby Gene: unknown														
chr20	60490131	60490180	-0.2	0.6	1.08	0.17	1.88	3.06	2.37	1.72	3.5	2.11	0.0100773803	0.0934438715
chr20	60490223	60490272	0.13	0.58	1.01	0.05	0.68	2.5	1.45	1.25	2.21	1.09	0.0099584549	0.0929898063
chr20	60490439	60490488	0.22	0.37	1.14	0.56	1.49	2.39	1.66	1.33	2.77	1.79	0.0012151214	0.0462151098
chr20	60490523	60490572	0.27	0.28	0.85	0.44	1.16	1.88	1.3	1.05	2.53	1.45	0.0012016594	0.0460422146
chr20	60490625	60490674	-0.02	0.23	0.91	0.22	1.53	2.49	2.33	1.59	3.33	2.1	0.0005913553	0.0384487121
chr20	60490735	60490784	0.17	0.41	0.94	0.35	1.02	2.14	1.82	1.62	1.94	1.49	0.0004906777	0.0362975313
chr20	60490847	60490896	0.19	0.12	0.58	0.3	1.19	2.73	2.04	1.24	2.1	2.41	0.0054361730	0.0738611110
chr20	60490923	60490972	0.36	0.19	0.77	0.45	1.26	2.27	1.66	1.19	2.39	2.25	0.0462391055	0.1826720289
Nearby Gene: LOC729808														
chr2	218607261	218607310	0.52	0.58	0.26	0.26	1.17	2.96	2.42	2.07	1.92	0.21	0.0021776431	0.0546367222
chr2	218607386	218607435	0.42	0.66	0.57	0.58	1.26	2.67	2.04	1.91	1.8	0.4	0.0017921094	0.0515516386
chr2	218607486	218607535	0.04	0.03	-0.01	-0.13	0.94	2.85	2.2	1.26	1.49	0.01	0.0000264796	0.0214648509
chr2	218607587	218607636	0.22	0.31	0.24	0.59	1.36	2.98	1.81	1.49	1.47	1.17	0.0001620330	0.0293939442
chr2	218607667	218607716	-0.03	0.02	0.04	0.36	1.54	3.25	2.07	1.36	1.37	0.6	0.0000963846	0.0265549911
chr2	218607787	218607836	0.16	0.34	-0.02	0.39	1.89	3.32	2.53	1.69	2.89	0.63	0.0000999965	0.0269138319
chr2	218607857	218607906	0.28	0.48	0.33	0.39	1.46	2.34	1.94	1.56	2.27	0.58	0.0003308658	0.0333745941
chr2	218608067	218608116	-0.09	0.21	0.13	0.08	1.32	2.77	2.03	1.74	1.63	0.06	0.0161733457	0.1134320840
Nearby Gene: LAG3														
chr12	6753934	6753983	0.26	1.23	-0.48	0.39	0.99	2.25	1.55	2.04	3.14	1.87	0.0134815624	0.1051737044
chr12	6754034	6754083	0.06	1.45	-0.56	0.69	1.5	2.9	2.24	2.45	3.82	2.38	0.0004585057	0.0358414892
chr12	6754109	6754158	0.07	1.08	-0.41	0.48	1.13	2.53	1.84	2.18	2.6	2	0.0000964161	0.0265549911
chr12	6754234	6754283	0.05	1.21	-0.89	0.46	1.32	2.71	2.33	2.53	4.01	2.49	0.0000812512	0.0261180431
chr12	6754314	6754363	0.07	0.81	-0.73	0.44	1.03	2.32	1.74	2.11	3.28	1.86	0.0000752172	0.0256048306
chr12	6754404	6754453	0.35	0.7	-0.24	0.45	0.58	2.11	1.67	2.04	3.07	1.63	0.0001300984	0.0285641142
chr12	6754534	6754583	0.11	0.75	-0.96	0.3	0.61	2	1.87	2.24	3.16	1.86	0.0128752478	0.1032024559
chr12	6754604	6754653	0.19	0.56	-0.36	0.02	0.72	1.79	1.48	1.78	2.57	1.59	0.0307807826	0.1508401512
Nearby Gene: LHX6														
chr9	124021786	124021835	2.61	-0.62	-0.45	-0.83	0.46	3.3	2.61	-0.13	2.26	1.87	0.0316634620	0.1528562983
chr9	124021891	124021940	2.46	-0.93	-0.41	-0.25	0.16	3.34	2.15	-0.71	1.9	2.29	0.0100597812	0.0933859688
chr9	124022091	124022140	2.59	-0.48	0.05	0.03	1.05	4.04	3.26	-0.38	3	3.11	0.0031769077	0.0614085586
chr9	124022181	124022230	2.01	0.27	0.37	0.56	0.83	3.13	2.36	0.43	1.88	2.25	0.0039922128	0.0661961609
chr9	124022281	124022330	2.46	-0.35	-0.69	-0.62	0.14	3.72	3.07	0.24	2.44	2.03	0.0009631472	0.0433152575
chr9	124022391	124022440	2.42	-0.16	-0.52	-0.38	0.83	3.59	3.11	0.75	3.29	2.49	0.0016245554	0.0500881946
chr9	124022461	124022510	2.02	0.43	0.22	-0.49	0.74	2.99	2.35	1.13	1.58	1.71	0.0145634325	0.1085282671
Nearby Gene: UGT3A1														
chr5	36026680	36026729	-0.55	0.53	0.3	0.18	0.77	0.65	1.49	1.57	1.99	1.37	0.0143917572	0.1080286775

chr5	36026890	36026939	0.12	0.84	0.32	0.35	1.42	1.38	2.53	2.31	3.5	1.92	0.0076183529	0.0836329180
chr5	36026970	36027019	-0.32	0.69	0.18	0.24	1.65	1.64	2.83	2.67	3.73	2.19	0.0055192991	0.0742835658
chr5	36027065	36027114	0.09	0.87	0.55	0.39	1.75	1.58	2.69	2.51	3.56	2.02	0.0000330194	0.0221998959
chr5	36027190	36027239	0.15	0.95	0.29	0.19	1.57	1.62	2.54	2.35	3.13	1.94	0.0004658075	0.0359459511
chr5	36027285	36027334	-0.16	0.84	0.34	0.18	0.86	1.14	2.27	2.33	2.81	1.74	0.0023497371	0.0558329515
chr5	36027370	36027420	0.16	1.04	0.59	0.18	0.8	0.82	2.04	2.03	2.44	1.09	0.0103467479	0.0945608710
Nearby Gene: ZNF512B														
chr20	62138971	62139020	-0.27	1.21	0.24	-0.03	1.05	1.66	2.39	1.19	2.22	0.57	0.0070753092	0.0812782865
chr20	62139066	62139115	-0.67	1.33	-0.19	-0.57	0.19	1.38	2.41	1.43	2.07	-0.19	0.0000087084	0.0198162491
chr20	62139161	62139210	-0.23	1.45	0.02	-0.28	0.26	1.5	2.44	1.73	1.91	-0.15	0.0000129924	0.0213173427
chr20	62139246	62139295	-0.66	1.58	-0.02	-0.29	0.39	1.74	2.69	1.81	2.22	-0.53	0.0000056877	0.0197834138
chr20	62139336	62139385	-0.24	1.27	0.21	-0.29	1.02	1.34	2.21	1.49	2.95	-0.06	0.0000023726	0.0197834138
chr20	62139466	62139515	-0.42	1.58	-0.04	-0.74	0.42	1.77	2.7	1.43	1.72	-0.4	0.0000695689	0.0251473615
chr20	62139561	62139610	-0.54	1.43	-0.17	-0.83	0.5	1.26	2.37	1.5	2.16	-0.57	0.0092396017	0.0904317756
Nearby Gene: MMP9														
chr20	44073287	44073336	1.4	-0.55	0.19	0.51	1.65	2.29	1.76	2.64	1.65	2.6	0.0340739352	0.1580820784
chr20	44073487	44073538	0.92	-0.31	0.04	1.34	0.53	1.92	1.72	1.32	1.88	1.73	0.0195370452	0.1230327693
chr20	44073567	44073616	1.24	0.09	-0.27	1.85	1.52	2.52	2.7	1.67	2.66	2.21	0.0228570423	0.1319847867
chr20	44073687	44073736	1.42	0.25	-0.08	1.59	2.38	2.82	2.89	1.85	3.18	2.46	0.0002403320	0.0316653673
chr20	44073762	44073811	1.28	-0.2	-0.34	1.49	2.11	3.53	3.37	1.65	3.09	2.62	0.0001503903	0.0289910777
chr20	44073882	44073931	1.5	0.05	-0.22	1.96	2.38	3.34	3.14	1.87	2.64	2.67	0.0012348291	0.0464085402
chr20	44073977	44074026	0.85	-0.29	-0.59	1.64	1.46	2.98	2.5	1.72	0.76	1.65	0.0257509135	0.1391386609
Nearby Gene: ESRP2														
chr16	66827876	66827925	0.73	0.61	0.29	0.23	0.81	2.03	2.17	1.62	2.68	1.67	0.0350138272	0.1600813561
chr16	66827961	66828010	-0.2	0.41	-0.13	0.24	0.34	2.48	2.77	2.05	2.92	1.65	0.0017678798	0.0514084984
chr16	66828071	66828120	-0.67	0.05	-0.53	0.04	0.33	3.01	3.14	2.16	2.68	2.22	0.0007111607	0.0403855332
chr16	66828166	66828215	0	0.24	0.25	0.33	0.84	3.29	0.68	2.15	3.17	1.96	0.0003583913	0.0337350386
chr16	66828266	66828315	-0.48	0.22	0.17	0.73	1.08	3.16	3.32	2.46	3.43	2.49	0.0002629108	0.0319720681
chr16	66828391	66828440	-0.56	0.14	-0.25	0.09	1.07	3.49	3.9	2.58	4.23	2.52	0.0010588520	0.0444770225
chr16	66828491	66828540	-0.5	0.32	0.03	0.02	0.17	2.59	2.89	2.28	3.44	1.38	0.0195618854	0.1230984089
Nearby Gene: DBX1														
chr11	20136976	20137025	-0.45	-1.24	1.2	1.53	0.05	1.14	2.25	1.29	3.03	1.49	0.0339331424	0.1577876402
chr11	20137046	20137095	-0.01	-0.42	1.21	1.54	0.88	1.46	2.22	1.52	2.73	1.69	0.0131870497	0.1041762264
chr11	20137151	20137200	-1.07	-1.55	1.09	1.62	0.49	1.73	2.7	1.47	3.72	1.82	0.0012458566	0.0465188835
chr11	20137266	20137315	-0.26	-0.43	1.23	1.28	0.63	1.2	1.56	1.26	2.37	1.3	0.0015185110	0.0490782260
chr11	20137346	20137395	-0.97	-1.02	1.28	2.01	0.48	1.47	2.58	1.48	3.38	1.6	0.0016991455	0.0508186890
chr11	20137461	20137523	-0.67	-0.88	1.6	2.14	0.09	1.03	2.36	1.57	2.78	1.36	0.0018581454	0.0521825212
chr11	20137551	20137603	-0.44	-0.73	1.58	2.1	0.26	0.89	2.29	1.62	2.75	1.32	0.0188365311	0.1211159533
Nearby Gene: unknown														
chr10	101276404	101276453	-0.12	0.09	-0.2	0.18	-0.14	2.34	2.02	0.41	2.89	2.26	0.0174957437	0.1173072070
chr10	101276524	101276573	-0.04	0.31	-0.06	0.37	0.02	1.97	1.56	0.53	2.46	2.1	0.0175752746	0.1175071525
chr10	101276629	101276678	-0.1	0.21	-0.04	0.59	0.48	2.29	2.05	0.46	2.19	2.38	0.0000296402	0.0218810115
chr10	101276709	101276758	-0.15	0.25	-0.35	0.48	0.38	2.38	2.33	0.4	2.66	2.54	0.0000186963	0.0213233265
chr10	101276799	101276848	0.02	0.38	-0.19	0.39	0.09	2.36	2.42	0.3	2.85	2.56	0.0000085570	0.0198162491
chr10	101276929	101276978	0.13	0.28	-0.17	0.32	0.11	2.11	2.08	0	2.71	2.32	0.0016096064	0.0499049309
chr10	101277034	101277083	0.02	-0.15	0.09	-0.05	0.19	2.29	1.96	0.05	2.56	2.07	0.0020362910	0.0536035569
Nearby Gene: TNFRSF1B														
chr1	12150853	12150902	0.54	-0.09	-1	-0.78	-0.29	1.3	1.27	-0.23	2.25	1.07	0.0248466131	0.1369805052
chr1	12150948	12150997	0.87	-0.17	-1.3	-1.3	-0.61	1.69	1.62	-0.65	2.02	1.33	0.0348527841	0.1597854195
chr1	12151078	12151127	0.93	0.21	-0.45	-0.41	-0.19	1.5	1.37	-0.05	1.97	1.27	0.0010345264	0.0441841382
chr1	12151278	12151327	1.24	0.45	-0.68	-0.49	0.47	1.71	1.85	0.01	2.56	1.73	0.0052398312	0.0728289574
chr1	12151458	12151507	0.76	0.1	-1.51	-0.93	-0.03	1.85	2	-0.32	2.63	1.66	0.0022298194	0.0551290561
chr1	12151568	12151617	1.1	0.22	-1.21	-0.71	-0.05	1.84	2.05	-0.26	2.53	1.62	0.0036504981	0.0642552466
chr1	12151658	12151707	1.14	0.35	-0.62	-1.06	-0.56	1.49	1.64	-0.53	2.3	1.29	0.0308779066	0.1510617101
Nearby Gene: FBXO24														
chr7	100025469	100025518	0.68	1.59	1	0.57	1.44	2.27	1.92	2.01	2.71	1.47	0.0000541179	0.0234834523
chr7	100025655	100025704	0.26	1.44	0.7	0.26	0.96	2.04	1.67	1.85	2.11	1.06	0.0003390622	0.0334846984
chr7	100025767	100025816	0.17	1.45	0.51	0.24	1.1	2.14	1.57	1.95	2.48	1.07	0.0003797594	0.0340687310
chr7	100025865	100025914	0.09	1.67	0.49	0.2	1.11	2.34	1.95	2.15	2.57	1.21	0.0000371266	0.0224051377
chr7	100025963	100026012	0.15	1.49	0.45	-0.2	0.96	2.21	1.79	1.83	2.25	1.05	0.0000478786	0.0228099481
chr7	100026053	100026102	0.33	1.49	0.59	-0.08	0.82	2.11	1.78	1.7	1.99	0.87	0.0177034144	0.1178982572
Nearby Gene: LOC728145														
chr5	170667327	170667385	1.94	1.69	-0.33	1.34	-0.93	1.19	2.67	2.59	2.06	1.7	0.0148040078	0.1092735112
chr5	170667527	170667584	2.31	2.03	0.39	2.29	-0.49	2.21	2.7	2.64	3.48	2.46	0.0001674946	0.0297367609
chr5	170667597	170667646	1.77	1.56	0.18	1.35	-0.16	1.73	2.22	2.1	2.91	2.01	0.0001908228	0.0303512552
chr5	170667692	170667749	1.86	1.59	-0.21	1.55	-0.61	2.17	2.28	2.18	3.34	2.1	0.0000903819	0.0264076198
chr5	170667792	170667841	2.02	1.69	0.33	1.59	0.13	2.43	2.65	2.35	3.42	2.28	0.0006756651	0.0397928737
chr5	170667917	170667966	2.24	1.86	0.18	2.1	0.12	3.02	3.24	2.65	3.77	2.89	0.0226473442	0.1314019889
Nearby Gene: TBX1														
chr22	18124941	18124990	0.15	0.41	-0.46	0.18	0.34	1.54	1.32	1.33	2.23	0.27	0.0460815450	0.1823671150
chr22	18125026	18125075	0.45	0.63	0.26	0.24	1.04	1.61	1.57	1.48	2.82	0.84	0.0175299658	0.1174033553
chr22	18125126	18125175	-0.18	0.44	-0.16	0.03	1.28	1.91	2.13	1.8	3.23	0.55	0.0001820850	0.0301524282
chr22	18125226	18125275	-0.05	0.17	-0.24	-0.33	0.68	1.46	1.23	1.63	2.46	0.48	0.0001522694	0.0290369421
chr22	18125426	18125475	0.15	0.58	-0.39	0.13	0.74	1.83	1.64	1.79	2.33	0.26	0.0047222891	0.0700352926
chr22	18125541	18125590	0.32	0.48	-0.13	-0.18	1.04	2.05	1.62	1.69	2.79	0.51	0.0058978497	0.0759218880
Nearby Gene: TBX4														
chr17	56887707	56887756	0.02	0.43	0.3	0.66	0.71	1.07	1.77	1.61	2.28	1.14	0.0129595926	0.1034438143

chr17	56887822	56887871	0.31	0.61	0.55	1.01	0.69	1.39	1.68	1.54	2.78	1.54	0.0126040720	0.1024045825
chr17	56887912	56887961	0.5	0.77	0.46	1.48	1.39	1.86	2.39	1.75	3.11	1.88	0.0000420146	0.0227261622
chr17	56888017	56888066	0.65	0.72	0.35	1.7	1.51	2.23	2.62	1.74	2.84	1.97	0.0000446488	0.0228099481
chr17	56888192	56888241	0.29	0.09	-0.26	0.07	0.37	1.33	1.56	0.91	1.05	1.32	0.0000726947	0.0255112991
chr17	56888292	56888341	0.49	0.2	0.2	2.35	1.11	1.52	2.01	2.38	2.4	1.86	0.0179266315	0.1185527614
Nearby Gene: SYNGR3														
chr16	1978886	1978935	0.41	0.49	0.55	0.96	0.51	1.82	1.71	1.09	2.63	1.05	0.0013410725	0.0474718099
chr16	1979006	1979055	0.47	0.55	0.53	0.98	0.55	1.97	1.85	0.81	2.78	1.29	0.0003316451	0.0333745941
chr16	1979076	1979125	0.28	0.39	0.18	0.83	0.56	2.08	1.8	0.59	2.35	1.07	0.0000228027	0.0213691480
chr16	1979176	1979225	0.29	0.26	0.32	0.82	0.97	2.34	2.04	0.8	2.72	1.3	0.0000442926	0.0228099481
chr16	1979286	1979335	0.74	0.48	0.68	1.06	1.28	2.99	2.1	0.29	2.24	1.65	0.0000507692	0.0231810550
chr16	1979501	1979550	0.33	0.05	0.12	0.11	0.93	2.47	1.93	-0.15	2.06	1.23	0.0141858407	0.1073665488
Nearby Gene: ONECUT1														
chr15	50867530	50867579	0.08	0.86	1.15	1.57	0.52	0.96	1.97	1.86	3.1	1.4	0.0101666599	0.0937996179
chr15	50867635	50867684	-0.47	0.61	0.97	1.56	0.34	1.24	2.22	1.84	3.74	1.44	0.0028022430	0.0588918662
chr15	50867715	50867764	-1.14	0.35	0.77	1.02	0.24	1.62	2.43	1.7	3.54	1.7	0.0007680381	0.0410373091
chr15	50867835	50867884	0.93	0.86	1.21	1.4	0.93	2.21	2.74	1.48	3.05	2.02	0.0002569150	0.0319695200
chr15	50867905	50867954	-0.3	0.24	0.62	0.71	1.5	1.59	2.1	1	3.48	1.8	0.0031767041	0.0614085086
chr15	50868015	50868064	-0.76	-0.2	0.45	0.4	0.44	1.65	2.22	0.82	2.91	1.78	0.0038601363	0.0654917804
Nearby Gene: ENSG00000211900														
chr14	105400177	105400226	-0.29	0.54	2.6	2.72	-0.66	2.44	2.39	2.46	2.96	1.82	0.0210122559	0.1269909401
chr14	105400277	105400326	-0.26	0.48	2.38	2.12	-0.42	2.27	2.25	2.37	2.97	2.04	0.0131719323	0.1041375757
chr14	105400381	105400430	-0.13	0.53	2.16	1.91	-0.12	2.09	1.92	2.16	2.97	1.96	0.0003470796	0.0335796391
chr14	105400501	105400552	-1.02	0.3	2.55	2.41	-0.14	2.6	2.88	2.66	3.6	2.58	0.0002288997	0.0313773513
chr14	105400585	105400634	-0.63	0.51	2.41	2.4	-0.26	2.73	2.88	2.55	3.7	2.61	0.0095673433	0.0916673953
chr14	105400687	105400736	-0.86	0.36	2.08	2.17	-0.18	2.69	2.58	2.34	3.23	2.36	0.0275699738	0.1435090900
Nearby Gene: NRXN2														
chr11	64240714	64240763	1.12	0.52	0.19	1.22	2.08	3.61	3.43	0.37	2.46	3.06	0.0004995036	0.0364249020
chr11	64240789	64240838	1.03	0.49	0.3	0.96	1.7	2.85	2.58	0.46	2.6	2.56	0.0005813978	0.0383281325
chr11	64240889	64240938	1	0.6	0.43	1.08	2.62	2.82	2.57	0.51	2.69	2.65	0.0003898560	0.0343082261
chr11	64241089	64241138	1.14	0.84	0.6	1.71	2.05	2.77	2.81	0.74	3.03	2.67	0.0007625134	0.0409885433
chr11	64241224	64241273	1.06	0.81	0.82	1.65	1.68	2.35	2.54	1.05	3.04	2.61	0.0007031068	0.0402526648
chr11	64241424	64241473	1.06	0.74	0.77	1.39	1.46	2.51	2.4	1.14	2.37	2.13	0.0005484674	0.0375321216
Nearby Gene: ALX4														
chr11	44286334	44286385	0.94	1.06	0.43	1.1	1.37	1.83	1.97	2.08	2.66	2.06	0.0013172674	0.0473453882
chr11	44286434	44286483	0.93	1.19	0.55	1.15	1.4	1.77	2.03	2.19	2.76	2.02	0.0031063365	0.0608786085
chr11	44286509	44286558	0.69	0.92	0.56	0.96	1.41	1.82	1.9	2.04	2.88	2.03	0.0011010674	0.0449124252
chr11	44286614	44286663	0.36	0.68	-0.11	0.79	1.4	2.18	1.85	2.22	2.85	2.17	0.0006342917	0.0390695800
chr11	44286714	44286763	0.22	0.62	-0.14	0.64	1.38	2.38	1.95	2.39	3.39	2.51	0.0070940755	0.0813495841
chr11	44286834	44286883	0.47	0.84	0.08	0.82	1.05	2.39	2.11	2.27	2.35	2.21	0.0287034140	0.1462710818
Nearby Gene: C9orf25														
chr9	34447180	34447229	2.02	1.32	1.3	1.97	3.03	3.04	3.08	2.13	3.68	2.82	0.0014287437	0.0482330100
chr9	34447300	34447349	1.87	1.04	1.29	1.63	2.58	3.15	2.84	1.57	3.19	3.2	0.0008824702	0.0426192168
chr9	34447400	34447449	2.24	0.93	1.06	0.77	3.22	3.48	3.13	1.29	3.03	3.31	0.0001326319	0.0285644804
chr9	34447485	34447534	2.58	1.19	1.37	1.23	4.47	4.26	4.01	1.46	4.34	4.36	0.0065820551	0.0790976308
chr9	34447570	34447619	2.75	1.37	1.6	1.43	4.79	3.99	4.06	1.62	4.42	4.2	0.0063947973	0.0783198444
Nearby Gene: TRAPPC9														
chr8	141177050	141177099	2.29	1.66	2.22	1.84	3.54	4.3	3.48	2.04	3.43	3.77	0.0011726973	0.0457145473
chr8	141177120	141177169	2.22	1.78	2.05	1.8	3.35	3.86	3.43	2.11	4.03	3.8	0.0009651889	0.0433369114
chr8	141177225	141177274	2.56	1.89	2.36	2.17	4.48	4.47	4.07	2.23	5	4.3	0.0000850862	0.0263635838
chr8	141177320	141177369	2.09	1.53	2.06	1.71	3.67	3.94	3.19	1.98	4.11	3.61	0.0000787848	0.0259474655
chr8	141177530	141177579	2.38	1.68	2.43	2.14	4	4.06	3.7	2.06	4.45	4.08	0.0001739107	0.0299218284
Nearby Gene: BLK														
chr8	11457945	11457994	2.44	0.38	0.87	1.19	3.03	3.8	3.21	0.03	3.48	3.19	0.0191490928	0.1219398563
chr8	11458045	11458094	2.31	0.39	0.71	0.91	3.2	3.76	3.49	0.35	3.58	3.21	0.0117063216	0.0993692549
chr8	11458120	11458169	1.96	0.58	0.92	1.16	2.71	2.9	2.6	0.9	3.44	2.56	0.0000627033	0.0244446441
chr8	11458245	11458295	2.06	0.71	1.07	1.42	2.86	3.08	3.29	1.16	3.62	2.83	0.0007608157	0.0409798364
chr8	11458320	11458369	1.65	0.6	1	1.27	2.13	2.75	2.57	1.23	3.16	2.04	0.0169258255	0.1156952454
Nearby Gene: CREB5														
chr7	28414278	28414327	0.38	0.66	0.25	1.35	0.25	2.18	1.45	1.3	2.14	2.27	0.0091870300	0.0902047037
chr7	28414468	28414517	-0.28	0.13	-0.1	2	1.03	3.38	2.77	1.01	2.23	2.76	0.0018831818	0.0524999583
chr7	28414568	28414617	0.46	0.48	0.41	1.98	2.15	3.5	3.25	1.25	4.21	3.37	0.0008733871	0.0424527805
chr7	28414703	28414752	-0.37	-0.24	-0.46	1.66	1.83	3.64	3.13	0.98	3.9	3.3	0.0063309801	0.0780973385
chr7	28414768	28414817	-0.62	-0.53	-0.43	1.68	1.23	3.16	2.86	0.99	2.56	2.71	0.0063193967	0.0780435448
Nearby Gene: unknown														
chr7	149772004	149772053	2.15	2.07	-1.17	2.5	1.46	2.59	2.25	2.24	3.03	2.76	0.0309940854	0.1513780082
chr7	149772094	149772143	1.99	1.95	-0.68	2.49	1.61	2.84	2.36	2.29	3.32	2.88	0.0022544548	0.0552790154
chr7	149772199	149772248	1.93	2.08	-0.91	2.55	1.65	2.97	2.37	2.37	3.33	2.78	0.0000094967	0.0202255545
chr7	149772294	149772343	2.05	2.02	-0.64	2.36	1.95	3.11	2.48	2.26	3.67	2.92	0.0046261395	0.0694976252
chr7	149772409	149772458	1.67	1.62	-1.89	2.01	1.69	2.65	2.28	1.98	2.83	2.64	0.0339968854	0.1579353874
Nearby Gene: unknown														
chr7	148743113	148743162	0.62	1.29	0.08	1.26	2.06	1.67	2.41	1.38	3.07	2.05	0.0288227502	0.1465055432
chr7	148743243	148743292	0.47	1.21	-0.07	0.98	2.34	2.04	2.5	1.43	3.43	2.38	0.0001225261	0.0284267443
chr7	148743338	148743387	0.52	1.24	0.09	1.05	2.79	2.52	3.05	1.65	3.85	2.61	0.0001709608	0.0297954242
chr7	148743425	148743474	0.45	1.22	0.01	1.1	2.21	2.19	2.73	1.6	3.35	2.53	0.0000554957	0.0236788893
chr7	148743513	148743562	0.88	1.55	0.29	1.49	2.17	1.93	2.94	1.73	3.16	2.53	0.0232855724	0.1330588718

Nearby Gene: C7orf49														
chr7	134501475	134501524	0.19	2.18	1.77	0.48	1.57	1.54	2.1	2.42	3.29	2.73	0.0001288583	0.0285641142
chr7	134501580	134501629	0	1.87	1.52	0.35	1.44	1.72	1.94	2.17	2.58	2.37	0.0001021636	0.0270030146
chr7	134501675	134501724	-0.06	1.72	1.39	0.22	1.23	1.76	1.85	1.99	2.6	2.38	0.0002911032	0.0328035370
chr7	134501890	134501939	-0.22	1.29	0.97	-0.38	1.11	1.75	1.41	1.67	2.68	2.57	0.0011030693	0.0449142069
chr7	134502110	134502159	0.2	1.7	1.72	-0.18	1.66	1.64	1.49	1.93	2.71	2.5	0.0011336762	0.0452735547
Nearby Gene: SLC10A4														
chr4	48181119	48181168	1.38	-0.33	0.31	0.77	0.61	1.58	1.82	0.19	2.05	2.63	0.0012661514	0.0467352153
chr4	48181324	48181373	1.81	-0.66	0.8	2.31	-0.39	1.2	2.32	0.69	3.18	1.73	0.0013199949	0.0473770559
chr4	48181439	48181488	1.76	-0.63	0.89	2.39	-0.46	1.06	2.21	1.09	3.48	2.43	0.0013243443	0.0473770559
chr4	48181514	48181563	1.69	-0.42	0.89	2.45	-0.42	0.92	2.29	1.14	3.28	2.38	0.0000931064	0.0264867944
chr4	48181629	48181686	1.46	-0.49	0.8	2.07	-0.61	0.52	2.03	1.14	3.15	1.98	0.0002078934	0.0308633745
Nearby Gene: SIM2														
chr21	36990592	36990641	-0.82	-1.55	0.64	1.67	-0.58	2.68	2.78	2.01	3.79	1.79	0.0298814332	0.1489474030
chr21	36990682	36990731	-0.54	-0.8	0.54	1.19	-0.54	2.08	1.86	1.32	2.16	0.8	0.0316484592	0.1528403681
chr21	36990792	36990841	-0.25	-0.29	0.43	1.06	0.22	1.54	1.62	1.07	1.9	0.71	0.0054865232	0.0740867392
chr21	36990867	36990916	-0.1	-0.41	0.68	1.32	-0.17	1.76	1.69	1.62	2.47	0.89	0.0007668428	0.0410373091
chr21	36990992	36991041	-0.05	-0.39	0.85	1.31	-0.07	1.46	1.51	1.62	2.07	0.66	0.0002853065	0.0327336328
Nearby Gene: VAX2														
chr2	70984842	70984894	-0.12	1.02	-0.9	1.08	0.41	1.28	1.92	1.77	1.32	0.81	0.0227658265	0.1317367086
chr2	70984942	70984991	-0.21	1.22	-0.79	1.34	0.28	1.03	1.97	1.99	2.6	1.62	0.0028381904	0.0591588838
chr2	70985032	70985081	0.47	1.21	0.03	1.17	0.38	1.22	1.86	1.69	2.19	1.58	0.0001702865	0.0297687845
chr2	70985112	70985161	-0.39	0.9	0.5	0.73	0.58	1.52	2.26	1.47	2.46	2.31	0.0015807719	0.0496107387
chr2	70985232	70985281	0.28	0.49	0.64	0.44	0.39	1.62	1.7	1.19	2.45	2.33	0.0291724687	0.1473623858
Nearby Gene: PNMAL2														
chr19	51689537	51689586	0.83	0.43	1.19	-0.01	0.75	2.09	1.72	1	1.84	1.62	0.0107645097	0.0960872358
chr19	51689607	51689656	1.21	0.37	1.07	-0.43	0.63	2.74	2.11	1.45	2.14	2.06	0.0052988388	0.0731565854
chr19	51689707	51689756	1.24	0.36	1.25	-0.28	0.46	2.62	1.83	1.12	1.42	1.78	0.0001943209	0.0304108099
chr19	51689832	51689881	0.85	0.37	0.63	0.1	0.7	2.44	1.42	0.51	1.99	1.64	0.0080193082	0.0851049876
chr19	51689907	51689956	1.43	0.1	0.57	-0.26	0.93	3.04	1.83	0.13	1.93	2.3	0.0233653193	0.1332870006
Nearby Gene: LSR														
chr19	40432069	40432118	0.91	0.54	0.18	0.8	0.33	1.86	1.72	1.23	2	1.34	0.0243063988	0.1356247249
chr19	40432159	40432208	1.37	0.91	0.76	1.25	1.14	2.48	2.4	2.07	2.83	1.74	0.0002300376	0.0313904582
chr19	40432260	40432309	1.23	0.82	0.67	1.14	1.05	2.37	2.29	2.03	2.96	1.7	0.0022690685	0.0553444770
chr19	40432365	40432414	1.13	0.96	0.62	1.3	0.85	2.44	2.31	1.96	2.54	1.65	0.0023369062	0.0557453126
chr19	40432565	40432614	1.73	1.31	1.09	1.95	1.16	2.63	2.62	2.15	2.97	2.03	0.0097413505	0.0922273535
Nearby Gene: unknown														
chr17	56882789	56882838	0.28	0.5	0.62	0.92	0.91	1.04	2.13	2.39	3.15	0.92	0.0069108395	0.0806555927
chr17	56882999	56883048	0.29	0.34	0.62	1.01	0.65	1.23	2.15	2.29	3.1	1.03	0.0002627067	0.0319720681
chr17	56883119	56883169	0.58	0.8	0.92	1.23	0.93	1.33	2.5	2.57	3.34	1.32	0.0002876764	0.0327336328
chr17	56883214	56883263	0.5	0.56	0.7	1.17	0.99	1.45	2.21	2.62	2.98	1.3	0.0000894079	0.0263635838
chr17	56883319	56883368	0.52	0.47	0.8	1.28	0.26	1.72	2.06	2.36	2.18	0.73	0.0001372927	0.0286870313
Nearby Gene: PDE8A														
chr15	83323307	83323358	-0.28	0.6	0.1	0.32	0.55	1.73	1.34	1.12	1.65	0.79	0.0117098362	0.0993749997
chr15	83323407	83323456	-0.57	0.98	-0.2	0.48	0.52	1.94	1.91	1.37	1.95	0.84	0.0002549850	0.0319695200
chr15	83323507	83323556	-0.75	1.17	-0.15	0.48	0.39	2.05	1.95	1.42	2.32	0.71	0.0000425062	0.0227592432
chr15	83323607	83323656	-0.67	1.12	-0.26	0.63	0.33	1.9	1.99	1.17	1.99	0.35	0.0000215424	0.0213691480
chr15	83323677	83323726	-0.65	1.25	-0.56	0.73	0.44	1.93	2.03	1.3	2.05	0.75	0.0000244792	0.0213691480
Nearby Gene: HOXC12														
chr12	52635984	52636033	1.3	0.62	1.16	1.33	-0.57	1.06	2.15	1.87	2.56	1.33	0.0065627840	0.0790140785
chr12	52636115	52636164	1.6	0.78	1.43	1.5	-0.16	1.12	2.31	2.08	2.75	1.94	0.0014998956	0.0489768993
chr12	52636206	52636255	1.45	0.77	1.35	1.54	-0.6	1.06	2.38	2.06	2.6	1.94	0.0000246278	0.0213691480
chr12	52636306	52636355	1.31	0.95	1.41	1.48	-0.01	1.14	2.11	2.03	2.98	1.91	0.0000692282	0.0251473615
chr12	52636396	52636445	1.07	0.46	1.13	1.37	-0.79	1.01	2.1	1.91	2.83	1.71	0.0096528044	0.0919167772
Nearby Gene: PRDM11														
chr11	45123501	45123550	0.33	0.33	-0.06	-0.09	0.38	1.76	1.68	1.67	2.36	0.46	0.0125643041	0.1022737749
chr11	45123571	45123620	0.3	0.38	0.22	-0.11	0.78	1.51	1.21	1.48	2.07	0.9	0.0001229369	0.0284267443
chr11	45123691	45123740	0.75	0.74	0.45	0.2	0.7	1.59	1.67	1.72	2.43	0.61	0.0001298499	0.0285641142
chr11	45123786	45123835	0.11	0.47	-0.04	-0.13	0.48	1.59	1.71	1.97	2.66	0.36	0.0018313227	0.0519489467
chr11	45123901	45123950	0.22	0.56	0.14	-0.13	0.47	1.63	1.77	1.96	2.64	0.3	0.0043268244	0.0679814481
Nearby Gene: PKNOX2														
chr11	124540945	124540994	0.09	0.15	0.06	0.28	0.5	1.67	1.77	1.23	2.67	1.07	0.0087362696	0.0884406188
chr11	124541025	124541074	0.13	0.16	-0.16	0.61	0.5	1.18	1.34	1.23	1.9	0.6	0.0008942403	0.0427900988
chr11	124541228	124541277	0.23	0.42	0.48	0.44	0.89	1.28	1.97	1.73	2.37	1.16	0.0003064085	0.0331269751
chr11	124541318	124541367	0.3	0.48	0.24	0.41	0.5	1.22	2.11	1.76	2.25	0.91	0.0004415663	0.0353926496
chr11	124541418	124541467	0.08	-0.1	0.46	0.07	0.88	1.45	1.83	1.86	2.5	1.04	0.0139451994	0.1066044189
Nearby Gene: EFNA1														
chr1	153366003	153366052	1.37	0.88	0.66	0.42	1.35	2.54	2.56	1.58	2.81	2.06	0.0109471172	0.0967479882
chr1	153366098	153366147	0.88	0.74	0.49	0.2	0.38	2.2	2.02	1.71	2.62	1.7	0.0002868828	0.0327336328
chr1	153366178	153366227	0.94	0.97	1	0.09	0.6	2.27	2.15	2	2.95	1.71	0.0000073280	0.0197834138
chr1	153366293	153366342	1.26	1.11	1.22	0.46	0.73	2.26	2.28	1.99	2.89	1.8	0.0048298573	0.0706751827
chr1	153366373	153366422	1.31	1.19	1.28	0.39	0.94	2.61	2.58	2.03	3.3	2.3	0.0188922590	0.1212586604
Nearby Gene: PTCH1														
chr9	97319351	97319400	-0.48	-0.33	1.37	-0.36	0.3	1.83	1.58	1.12	1.95	1.53	0.0347924034	0.1596379460

chr9	97319421	97319470	-0.21	-0.18	0.92	-0.19	0.4	1.35	1.18	1.01	1.46	1.04	0.0041273881	0.0669212667
chr9	97319536	97319585	-1.29	-0.5	1.34	-1.27	0.41	2	1.83	1.69	2.1	1.69	0.0018200812	0.0518522048
chr9	97319621	97319670	-1.67	-0.87	1.46	-1.97	0.08	1.84	2.04	1.5	2.36	1.65	0.0147133330	0.1090152438
Nearby Gene: BARX1														
chr9	95757631	95757680	0.97	0.13	0.55	0.67	0.92	1.94	1.82	1.11	2.28	1.23	0.0488090047	0.1875013959
chr9	95757756	95757805	0.82	0.2	0.44	0.88	1.45	2.31	2.16	1.1	2.86	1.5	0.0266403692	0.1412712961
chr9	95757841	95757890	0.52	-0.67	-0.15	0.65	0.81	2.56	2.21	0.5	2.92	1.41	0.0057560996	0.0752969181
chr9	95757931	95757980	0.04	-1.12	-0.57	0.37	0.7	2.58	2.62	0.61	2.98	1.35	0.0086760473	0.0881463789
Nearby Gene: FOXB2														
chr9	78824325	78824374	0.45	-0.64	0.61	1.29	1.64	2.83	3.79	0.08	3.58	3.89	0.0354815614	0.1610442364
chr9	78824405	78824454	-0.02	-0.39	-0.14	1.98	1.55	2.33	3.68	1.53	3.93	3.84	0.0068540748	0.0803580119
chr9	78824505	78824554	-0.32	-0.3	0.57	1.6	1.02	2.04	3.66	0.76	3.59	3.59	0.0070456501	0.0812079795
chr9	78824590	78824639	-0.13	-0.4	0.15	0.51	0.64	1.73	3.03	-0.31	1.92	3.62	0.0251985101	0.1378673103
Nearby Gene: ENSG00000175223														
chr9	132297475	132297524	0.99	-0.05	-0.13	1.55	1.01	1.85	2.1	0.68	2.92	2.19	0.0007261527	0.0405763694
chr9	132297575	132297624	1.22	0.14	-0.12	1.76	0.22	1.84	2.06	0.68	3.07	1.79	0.0002305414	0.0313904582
chr9	132297680	132297729	0.93	0.11	-0.4	1.58	0.58	1.86	1.83	1.23	3.24	2.11	0.0002879063	0.0327336328
chr9	132297775	132297824	1.01	0.28	-0.03	1.55	0.32	1.4	1.61	1.21	2.86	1.66	0.0076302276	0.0836980152
Nearby Gene: COL27A1														
chr9	115958762	115958811	0.25	0.34	-0.23	0.55	2.18	2.09	2.49	-0.37	2.71	2.78	0.0069430523	0.0808144037
chr9	115958962	115959011	0.46	0.88	0.1	0.85	2.37	2.76	2.73	0.11	2.72	3.12	0.0002320387	0.0314543152
chr9	115959072	115959121	0.22	0.67	-0.03	0.43	1.91	2.33	2.36	-0.02	2.18	2.44	0.0093213118	0.0907364385
chr9	115959252	115959301	0.22	0.43	-0.18	-0.17	0.58	1.17	1.23	0.35	1.62	1.51	0.0103665029	0.0946516482
Nearby Gene: CLU														
chr8	27505603	27505652	-1.78	0.5	0.72	-0.14	0.73	1.51	2.23	0.03	1.44	1.07	0.0092978575	0.0906392039
chr8	27505708	27505757	-0.56	0.68	0.89	0.42	1.44	1.69	2.42	0.4	1.77	1.72	0.0001896509	0.0302738033
chr8	27505788	27505837	-0.12	0.31	0.84	0.45	2.34	2.7	2.92	-0.35	2.07	3.07	0.0001311825	0.0285641142
chr8	27505903	27505952	-0.36	-0.02	0.35	0.01	1.46	1.65	2.37	-0.59	1.36	2.35	0.0010230263	0.0440599858
Nearby Gene: NPM2														
chr8	21938903	21938952	1.43	1.33	1.26	0.82	1.9	2.28	2.52	2.24	2.96	2.53	0.0165312248	0.1145042582
chr8	21939003	21939052	-0.17	1.19	0.36	-0.72	0.12	2.22	2.49	2.44	2.8	2.16	0.0028748506	0.0594420235
chr8	21939103	21939152	-0.04	1.2	0.61	-0.52	0.12	1.81	2.01	2.32	2.47	2.14	0.0006874577	0.0400356225
chr8	21939228	21939277	-0.18	1.2	0.39	-0.91	-0.2	1.67	2.19	2.4	2.96	2	0.0146423963	0.1088185727
Nearby Gene: C6orf222														
chr6	36416441	36416490	-0.41	0.37	0.83	0.03	1	1.21	1.31	1.62	2.02	1.18	0.0002198648	0.0310517649
chr6	36416545	36416594	-0.29	0.47	0.73	0.18	0.87	1.26	1.55	1.38	1.7	1.25	0.0004619193	0.0358791634
chr6	36416661	36416710	0.19	0.83	0.92	0.47	1.72	1.91	2.22	1.09	2.48	1.56	0.0015982898	0.0497516614
chr6	36416741	36416790	-0.05	0.35	0.77	0.07	1.9	2.23	2.28	0.98	2.64	1.74	0.0133617698	0.1047714610
Nearby Gene: PRRT1														
chr6	32226671	32226720	2.52	1.2	0.15	0.82	0.94	2.48	2.62	2.16	2.76	2.11	0.0153488841	0.1109523687
chr6	32226756	32226812	2.3	1.01	0.34	0.71	0.93	2.27	2.23	1.69	2.33	1.78	0.0008955186	0.0427932984
chr6	32226856	32226908	2.41	1.03	0.22	0.74	0.75	2.55	2.65	2	2.91	1.88	0.0060186179	0.0765892137
chr6	32226981	32227030	1.93	0.79	0.26	0.78	0.76	2.41	2.24	1.94	2.39	1.76	0.0097027496	0.0920988185
Nearby Gene: ULBP1														
chr6	150327160	150327209	0.71	0.11	-0.06	0.69	2.75	2.82	3.92	0.07	3.24	3.15	0.0169697114	0.1158321272
chr6	150327345	150327394	1.09	0.46	0.94	1.2	2.21	2.72	3.66	0.38	2.71	2.99	0.0131370777	0.1040056892
chr6	150327435	150327484	0.86	0.4	0.05	0.77	1.55	1.99	2.79	0.26	1.83	2.14	0.0061364697	0.0771779637
chr6	150327645	150327694	0.75	0.59	0.4	0.92	2.38	2.32	3.05	0.26	2.47	2.82	0.0093164447	0.0907219866
Nearby Gene: ENSG00000215068														
chr5	43072970	43073028	1.74	1.49	-0.71	2.68	1.53	2.43	2.32	1.63	3.16	2.5	0.0001453535	0.0289383717
chr5	43073055	43073104	1.89	1.66	-0.44	2.8	1.82	2.6	2.63	1.98	3.36	2.84	0.0001881523	0.0302702364
chr5	43073175	43073224	1.95	1.57	-0.97	3	1.81	2.77	2.69	1.84	3.37	2.98	0.0000698447	0.0251473615
chr5	43073385	43073434	1.46	0.96	-0.41	2.49	1.4	2.2	2.41	1.55	2.7	2.21	0.0164673544	0.1143523030
Nearby Gene: IRX1														
chr5	3652073	3652122	2.5	0.43	1.35	2.58	-0.44	2.12	2.72	1.9	3.53	1.78	0.0009198570	0.0429657111
chr5	3652193	3652242	2.39	0.28	1.2	2.35	-0.05	2.14	2.63	1.76	3.66	1.93	0.0010446470	0.0442975712
chr5	3652283	3652332	2.32	0.26	1.21	2.01	-0.16	2.03	2.39	1.4	3.13	1.97	0.0016338293	0.0502068534
chr5	3652388	3652437	2.53	0.29	1.41	2.09	1.11	2.77	2.85	1.38	3.86	2.64	0.0035686366	0.0638318407
Nearby Gene: unknown														
chr4	13134714	13134763	2.3	0.51	1.38	1.29	2.54	3.15	3.18	1.12	3.44	3.16	0.0103349606	0.0945084158
chr4	13134844	13134900	2.15	0.88	1.97	1.97	3.11	3.39	3.25	1.74	4.37	3.48	0.0031711303	0.0613862038
chr4	13134939	13134988	1.95	1.08	2.04	2.23	2.68	3.12	3.23	2.36	4.44	3.37	0.0137894832	0.1060908963
chr4	13135019	13135068	1.9	1.26	1.96	2.23	2.42	2.84	2.91	2.23	4.11	3.09	0.0489419242	0.1877382054
Nearby Gene: TBX1														
chr22	18122226	18122275	0.86	0.61	0.64	0.29	1.77	2.38	1.84	0.81	2.72	1.67	0.0016573240	0.0504374125
chr22	18122336	18122385	0.46	0.07	0.1	0.07	1.12	2.09	1.79	0.77	2.84	1.67	0.0013914109	0.0479135850
chr22	18122431	18122480	1.72	1.14	1.28	1.13	1.2	3.1	2.47	1.13	2.94	1.87	0.0072717317	0.0821676269
chr22	18122556	18122605	0.86	0.39	0.29	0.33	1.15	2.08	1.81	0.86	2.78	1.33	0.0415461744	0.1735436994
Nearby Gene: TBX1														
chr22	18121556	18121605	0.74	0.71	0.74	0.69	2.22	2.64	2.61	1.03	3.25	2.24	0.0125748356	0.1022995251
chr22	18121636	18121685	0.66	0.59	0.67	0.49	1.71	2.53	2.04	0.75	2.36	2.17	0.0045601567	0.0691515060
chr22	18121751	18121800	0.99	0.41	0.6	0.63	2.36	3	2.61	0.83	3.4	2.18	0.0058966690	0.0759118498
chr22	18121831	18121880	0.54	0.13	0.01	-0.02	2.09	3.34	2.74	0.65	3.17	1.79	0.0081222377	0.0855965578

Nearby Gene: AGPAT3														
chr21	44229802	44229851	1.11	1.14	0.81	0.26	0.39	2.32	1.94	1.35	2.18	1.09	0.0078505392	0.0845440976
chr21	44230002	44230052	0.78	1.03	0.8	0.28	0.93	2.46	2.12	1.03	2.44	1.11	0.0048764703	0.0708818708
chr21	44230122	44230171	0.53	0.77	0.58	0.1	1.13	2.81	2.23	1.09	2.88	1.48	0.0411079320	0.1726627068
chr21	44230227	44230276	0.76	0.77	0.44	0.18	0.91	2.7	2.08	0.95	2.26	1.31	0.0417609084	0.1739718994
Nearby Gene: FOXA2														
chr20	22506351	22506400	0.46	-0.11	0.49	1.48	1.01	2.54	2.52	1.05	3.39	1.76	0.0496546474	0.1890740458
chr20	22506421	22506470	0.43	-0.39	0.21	2.03	1.63	3.97	4.51	1.15	4.47	2.46	0.0064444837	0.0785051822
chr20	22506521	22506570	0.29	-0.27	0.17	1.35	1.55	2.92	3.64	1.16	4.31	2	0.0074075338	0.0827305740
chr20	22506651	22506700	0.46	-0.16	0.45	1.95	0.65	2.26	3.19	1.47	3.3	1.67	0.0214196199	0.1280650507
Nearby Gene: APOB														
chr2	21121039	21121088	1.22	1.07	1.6	1.58	0.39	2.46	2.37	2.26	2.19	2.24	0.0023485435	0.0558305073
chr2	21121139	21121188	1.1	1.11	1.73	1.69	0.69	2.52	2.52	2.34	1.8	2.29	0.0016491671	0.0503851217
chr2	21121239	21121290	0.98	1.21	1.68	1.6	0.82	2.43	2.4	2.33	2.41	2.3	0.0000202059	0.0213691480
chr2	21121349	21121398	0.7	1.11	1.53	1.39	0.69	2.33	2.1	2.04	2.11	2.12	0.0006470305	0.0393153427
Nearby Gene: uc002tfr.2														
chr2	110575230	110575279	1.43	1.21	1.51	1.44	3.12	3.16	3.02	1.44	4.07	2.59	0.0016984282	0.0508071797
chr2	110575445	110575494	1.13	0.9	1.29	0.87	2.48	2.48	2.58	1.23	3.16	2.35	0.0000359828	0.0223182185
chr2	110575545	110575594	1.39	1.06	1.51	1.09	2.92	3.03	3.32	1.31	3.59	2.74	0.0205589723	0.1258414033
chr2	110575560	110575609	1.93	1.2	1.69	1.2	3.3	3.04	3.44	1.33	3.89	3.07	0.0192139048	0.1221146182
Nearby Gene: TTYH1														
chr19	59624416	59624465	0.95	0.42	0.18	-0.08	1.25	2.07	1.9	1.45	2.11	1.57	0.0161084508	0.1132655338
chr19	59624491	59624540	0.83	0.05	-0.18	-0.31	1.34	2.34	2.13	1.33	2.28	1.79	0.0000225594	0.0213691480
chr19	59624616	59624665	0.88	0.07	0.12	0.02	1.71	2.35	2.14	0.88	2.48	1.93	0.0000286186	0.0218810115
chr19	59624716	59624765	0.96	-0.19	0.08	0.33	1.41	2.62	2.39	1.17	1.99	1.97	0.0066465526	0.0793787427
Nearby Gene: IZUMO1														
chr19	53942052	53942101	0.15	1.57	1.37	0.64	1.1	2.27	2.16	1.95	3.41	0.72	0.0238015122	0.1343905321
chr19	53942257	53942306	0.05	0.95	1	-0.11	1.17	2.6	2.16	1.77	3.17	0.85	0.0203351607	0.1252461043
chr19	53942357	53942406	-0.2	1.04	1.2	-0.06	0.7	2.5	2.25	1.95	3.22	0.39	0.0230340558	0.1324510226
chr19	53942462	53942511	-0.04	0.89	1.02	0.42	0.7	1.91	1.64	1.91	2.52	0.27	0.0201711421	0.1247883421
Nearby Gene: DNM2														
chr19	10781615	10781664	0.74	1.07	0.37	1.41	1.56	2.82	1.94	0.46	2.34	2.6	0.0104436918	0.0949905208
chr19	10781800	10781849	1.06	0.8	0.3	1.39	2.68	3.76	2.75	0.07	3.1	3.61	0.0019794536	0.0532309594
chr19	10781895	10781944	1.43	0.47	0.51	1.07	3.61	3.96	3.39	-0.21	3.35	4.33	0.0107182237	0.0959046745
chr19	10781985	10782034	1.24	0.3	-0.03	0.87	3.31	4.29	3.37	-0.39	3.12	4.45	0.0125845738	0.1023343702
Nearby Gene: APCDD1														
chr18	10443676	10443725	-0.49	1.18	1.03	0.53	1.17	2.26	2.07	1.75	2.23	1.55	0.0129594345	0.1034438143
chr18	10443776	10443825	-0.61	0.9	0.83	0.13	1.04	2.1	1.98	1.42	1.89	1.25	0.0002289464	0.0313773513
chr18	10443861	10443910	-0.72	1.21	1.02	0.18	1.21	2.58	2.59	2.05	2.83	1.83	0.0005123770	0.0368017065
chr18	10443951	10444000	-0.04	1.19	1.04	0.49	1.21	2.36	1.93	1.72	1.85	1.98	0.0355867829	0.1612072347
Nearby Gene: CSF3														
chr17	35425946	35425995	1.55	1.34	0.58	0.83	2.16	2.54	2.6	1.25	2.91	2.28	0.0036333354	0.0641991607
chr17	35426021	35426070	1.17	0.65	0.17	0.48	2.32	2.37	2.41	0.6	2.87	2.23	0.0019360167	0.0528742405
chr17	35426241	35426290	1.23	1.01	0.27	0.67	2.29	2.95	2.82	1.1	3.38	2.29	0.0042027945	0.0673307722
chr17	35426341	35426390	1.06	1.12	0.44	0.95	2.37	2.86	2.85	1.16	3.01	2.29	0.0042983631	0.0678167435
Nearby Gene: SNIP														
chr17	33972266	33972315	0.12	-0.34	0.52	0.89	-0.74	0.33	1.08	1.13	2.4	1.05	0.0098608453	0.0926198011
chr17	33972376	33972425	0.62	-0.65	0.72	1.46	-1.35	0.27	1.78	1.2	3.15	1.31	0.0065953501	0.0791331738
chr17	33972476	33972525	0.58	-0.79	0.74	1.42	-0.81	0.67	1.86	1.15	3.39	1.4	0.0023023725	0.0555334433
chr17	33972576	33972625	0.37	0.27	0.99	1.12	0.19	1.07	1.8	1.18	3.2	1.52	0.0161858576	0.1134521271
Nearby Gene: RPH3AL														
chr17	184858	184907	2.09	1.63	1.38	0.72	2.44	2.66	2.44	2.01	3.24	3.34	0.0033572573	0.0624871971
chr17	184968	185017	2.29	1.78	1.56	0.37	2.88	3.19	2.94	2	2.92	3.52	0.0004248241	0.0351808856
chr17	185038	185087	2.6	1.95	1.92	0.22	4.27	3.9	3.71	1.89	4.45	3.82	0.0000596216	0.0242630579
chr17	185238	185287	2.65	2.26	2.07	0.4	3.53	3.36	3.33	2.34	4.27	3.49	0.0021703026	0.0546120913
Nearby Gene: ISLR2														
chr15	72212031	72212080	1.56	0.49	1.63	1.62	1.2	1.69	2.7	1.65	3.35	2.37	0.0160013025	0.1129409771
chr15	72212231	72212280	2	-0.25	0.99	0.94	1.11	1.75	2.66	0.46	2.44	2.71	0.0000344585	0.0223182185
chr15	72212301	72212350	2.64	0.09	1.24	1.03	1.98	2.79	3.4	0.4	3.07	3.74	0.0011862384	0.0458404132
chr15	72212431	72212480	2.15	-0.04	0.58	0.5	1.3	1.62	2.55	0.09	2.57	3.26	0.0038239668	0.0652622530
Nearby Gene: C15orf52														
chr15	38419153	38419202	2.07	1.84	2.01	1.92	2.84	3.92	3.67	1.98	4.36	2.99	0.0007470101	0.0409163596
chr15	38419228	38419277	2.08	1.5	1.76	1.93	4.41	4.24	3.7	1.65	4.38	3.26	0.0001816413	0.0301242599
chr15	38419358	38419407	1.88	1.2	1.41	1.32	2.82	4.01	3.03	1.31	2.36	3.11	0.0011862183	0.0458404132
chr15	38419428	38419477	1.97	1.34	1.65	1.85	3.46	3.82	3.39	1.39	3.79	3.43	0.0063010096	0.0779617846
Nearby Gene: GSX1														
chr13	27265514	27265563	-0.44	0.35	1.64	2.1	0.24	1.49	1.85	1.84	3.26	1.63	0.0056164428	0.0747482530
chr13	27265604	27265653	-0.74	0.38	1.75	2.44	0.06	1.7	2.23	2.26	3.49	1.68	0.0085014636	0.0873281076
chr13	27265704	27265753	-0.37	0	1.47	1.81	0.16	1.42	1.8	1.82	3.32	1.33	0.0079207230	0.0847681045
chr13	27265879	27265928	-0.87	-0.63	-0.1	0.35	0.45	1.1	1.32	0	1.82	1.71	0.0499376107	0.1895656272
Nearby Gene: unknown														
chr12	45511933	45511982	0.26	0.26	1.76	0.97	1.93	2.35	1.97	2.33	3.24	0.6	0.0204239806	0.1254735041

chr12	45512149	45512206	0.29	0.97	1.95	1.09	1.94	2.55	2.51	2.73	3.57	0.93	0.0001840632	0.0302236820
chr12	45512233	45512282	0.19	0.74	1.88	1.11	1.53	2.39	2.21	2.6	3.21	1.17	0.0003592147	0.0337350386
chr12	45512357	45512406	-0.11	0.46	1.81	0.93	1.41	1.99	1.83	2.07	2.86	0.84	0.0003592147	0.0337350386
Nearby Gene: RAB3IL1														
chr11	61447736	61447785	0.13	-0.14	-0.25	0	0.77	1.84	1.38	0.05	1.35	1.3	0.0054270494	0.0738061329
chr11	61447828	61447877	0.31	-0.24	-0.5	0.35	0.92	2.38	2.03	-0.36	1.49	1.99	0.0018267940	0.0519273837
chr11	61447922	61447971	0.78	0.01	0.13	0.87	2.19	2.78	2.51	-0.13	2.6	2.72	0.0004484491	0.0355964912
chr11	61448130	61448179	0.74	0.13	0.27	0.33	1.46	1.98	2.04	-0.12	2.46	2.22	0.0026066791	0.0576765267
Nearby Gene: CDKN1C														
chr11	2864527	2864576	-0.41	0.56	-0.22	-0.96	0.37	1.89	2.26	2.24	2.03	-0.02	0.0010718344	0.0446212236
chr11	2864612	2864661	-0.24	0.57	0.09	-0.29	0.35	1.7	1.9	1.83	2.22	0.23	0.0008168346	0.0418055105
chr11	2864717	2864766	-0.11	0.72	0.14	-0.61	0.32	1.88	2.35	2.07	2.3	0.07	0.0019641206	0.0530901436
chr11	2864817	2864866	-0.04	0.43	0.16	-0.15	0.26	1.29	1.48	1.77	1.65	0.32	0.0289016171	0.1466761197
Nearby Gene: unknown														
chr11	1980702	1980751	2.2	1.02	1.8	1.52	3.67	3.76	3.24	1.36	3.57	3.41	0.0135164140	0.1052450904
chr11	1980907	1980956	1.89	0.68	1.67	1.08	2.64	3.02	2.74	1.58	3.09	2.73	0.0117909515	0.0996401692
Nearby Gene: C1orf113														
chr1	36557645	36557694	0.23	1.08	0.43	0.78	0.73	1.96	1.59	1.69	1.94	1.28	0.0009331223	0.0431064954
chr1	36557820	36557869	0.26	1.16	0.54	1.06	0.91	2.27	1.89	1.99	2.88	1.34	0.0002783015	0.0323288240
chr1	36558040	36558089	-0.21	0.71	-0.19	0.49	0.35	1.79	1.44	1.33	1.61	0.96	0.0005530036	0.0376721293
chr1	36558130	36558179	-0.04	0.24	-0.37	0.3	0.06	1.77	1.39	1.33	1.96	0.46	0.0004591273	0.0358414892
Nearby Gene: RAP1GAP														
chr1	21817425	21817474	-0.34	0.49	0.34	0.49	1.69	1.63	1.37	1.8	2.38	0.96	0.0015155013	0.0490639934
chr1	21817535	21817584	-0.58	0.3	0.29	0.21	1.4	1.47	1.42	1.55	2.23	0.7	0.0012820538	0.0469018022
chr1	21817735	21817784	-0.41	0.11	0.63	0	1.12	1.67	1.21	1.36	1.77	0.83	0.0122134114	0.1010570737
chr1	21817830	21817879	-0.52	0.48	0.41	0.33	1.38	1.6	1.45	1.7	2.12	0.9	0.0453009527	0.1808836209
Nearby Gene: LHX9														
chr1	196157055	196157104	0.91	0.21	0.93	1.19	0.68	2.25	2.2	1.65	2.92	2.03	0.0283775914	0.1455081071
chr1	196157155	196157204	1.24	0.56	0.67	1.26	1.01	2.45	2.5	1.41	2.84	2.3	0.0051064138	0.0720895480
chr1	196157235	196157284	-0.1	-0.54	-0.08	0.43	0.5	2.52	2.24	1	2.93	2.09	0.0014702246	0.0487155119
chr1	196157325	196157374	0.1	-0.28	0.37	0.28	0.41	1.73	1.53	0.71	1.72	1.43	0.0388129283	0.1680078896
Nearby Gene: RCC2														
chr1	17639834	17639883	-1	1.4	-0.01	-0.86	-0.04	2.33	2.22	2.02	2.85	0.62	0.0149912370	0.1098284566
chr1	17639944	17639993	-1.63	1.05	-0.48	-1.49	-0.59	1.82	1.71	1.51	2.03	-0.1	0.0032896266	0.0620475189
chr1	17640019	17640069	-0.97	1.02	-0.23	-0.87	0	1.76	1.72	1.4	1.9	0.11	0.0013214695	0.0473770559
chr1	17640144	17640198	-0.1	0.75	0.61	-0.05	0.13	1.78	1.29	1.46	2.22	0.58	0.0270899786	0.1423908556
Nearby Gene: LOC158381														
chr9	35396469	35396518	1.48	-0.3	1.64	0.87	2.5	2.45	2.12	1.67	2.95	2.54	0.0008004581	0.0415805050
chr9	35396679	35396728	-0.01	0.11	0.83	0.53	1.41	2.56	1.49	0.7	2.42	1.97	0.0005313485	0.0372725758
chr9	35396764	35396813	-0.94	-0.03	0.9	-0.74	0.86	1.85	1.07	1	3.03	1.25	0.0001125886	0.0277211424
Nearby Gene: IL11RA														
chr9	34642284	34642333	1.05	2.46	0.01	0.04	1.16	2.17	2.41	2.17	2.82	2.2	0.0101963380	0.0939598534
chr9	34642379	34642428	0.83	2.45	-0.01	0.22	1.14	2.03	2.45	2.51	3.29	2.12	0.0019414002	0.0529047986
chr9	34642479	34642529	0.76	2.37	0.09	0.27	0.95	1.96	2.32	2.18	2.76	1.74	0.0037113827	0.0645833346
Nearby Gene: SUSD1														
chr9	113977798	113977847	1.57	2.06	1.1	0.85	2.06	2.95	2.56	2.27	3.29	2.71	0.0230009886	0.1323412379
chr9	113977908	113977957	1.49	1.92	0.96	0.82	1.61	2.8	2.37	2.14	3.31	2.52	0.0165343749	0.1145106088
chr9	113977988	113978037	1.56	1.64	0.99	0.55	1.35	2.45	2.26	1.93	2.72	2.17	0.0002392108	0.0316404449
Nearby Gene: NKX2-6														
chr8	23619422	23619471	1.73	1.42	0.45	1.94	-0.23	0.87	2.44	2.43	3.3	1.75	0.0311838744	0.1517498368
chr8	23619537	23619586	1.72	1.59	0.68	1.96	-0.62	1.02	2.45	2.57	3.13	1.34	0.0067098516	0.0796965187
chr8	23619647	23619696	1.66	1.38	0.01	1.84	-0.56	0.97	2.14	2.36	3.33	1.59	0.0145115266	0.1083477606
Nearby Gene: NUDT18														
chr8	22021543	22021592	2.61	1.39	1.89	1.47	3.69	3.96	3.61	1.24	3.65	3.96	0.0070365264	0.0811911862
chr8	22021633	22021682	3.15	1.47	2.13	2	4.78	4.71	4.1	1.17	4.32	4.79	0.0091183478	0.0899397910
chr8	22021728	22021777	3.12	1.24	2.01	1.64	4.99	4.79	4.57	0.65	4.28	4.7	0.0349435800	0.1599472855
Nearby Gene: OSR2														
chr8	100030175	100030224	-0.32	-0.01	-0.17	1.27	1.33	1.16	1.67	1.13	3.44	0.96	0.0128732449	0.1031992544
chr8	100030375	100030424	0.4	0.46	0.25	1.47	1.68	1.94	1.95	1.07	3.39	1.62	0.0221295929	0.1299800908
chr8	100030475	100030524	-0.47	-0.59	-0.36	0.93	1.45	2.04	1.9	0.54	3.59	1.18	0.0383995346	0.1672012613
Nearby Gene: HOXA6														
chr7	27151647	27151696	-0.7	-0.08	0.35	0.99	1.19	1.57	1.56	0.34	2.55	1.57	0.0021491629	0.0544972362
chr7	27151757	27151806	0.2	1.49	2.02	2.5	4.29	4.09	3.99	1.12	4.63	4.25	0.0018085355	0.0517605966
chr7	27151847	27151896	0.1	1.44	1.89	2.45	4.22	4.03	4.19	1.08	3.99	3.94	0.0009420859	0.0431064954
Nearby Gene: PTPRN2														
chr7	158025177	158025226	1.63	0.99	1.52	1.28	3.71	3.61	3.26	1.29	3.92	3.34	0.0233664941	0.1332870006
chr7	158025287	158025336	1.46	0.83	1.37	1.04	3.55	3.17	2.97	1.21	3.74	3.17	0.0106254202	0.0955348044
chr7	158025372	158025421	1.7	1.01	1.43	1.36	3.61	3.63	3.17	1.28	3.83	3.3	0.0115462827	0.0987725691
Nearby Gene: HTR1B														
chr6	78229441	78229490	-0.1	-0.21	0.34	0.75	-0.57	-0.29	1.38	1.72	2.67	1.56	0.0004792121	0.0361580891
chr6	78229541	78229590	0.15	-0.07	0.36	0.51	-0.4	-0.03	1.1	1.42	2.55	1.34	0.0000893211	0.0263635838

chr6	78229656	78229705	0.83	-0.15	0.64	0.74	0.35	0.42	1.96	1.26	3.49	2.18	0.0017128147	0.0509978822
Nearby Gene: unknown														
chr6	41545616	41545665	-0.76	-0.37	-0.26	1.25	0.18	1.6	2.3	0.65	2.8	1.46	0.0395272151	0.1693919346
chr6	41545736	41545785	-0.13	-0.09	-0.01	1.6	1.28	2.37	2.51	1.03	3.04	2.52	0.0173791405	0.1169942031
chr6	41545936	41545985	0.05	0.11	0.04	1.25	1.3	2.05	2.31	1.06	3.03	2.23	0.0394968053	0.1693304506
Nearby Gene: TEAD3														
chr6	35571609	35571658	-0.2	-0.25	-0.38	0.37	0.3	0.99	1.24	1.11	1.32	1.2	0.0051934881	0.0725532456
chr6	35571714	35571763	-0.37	-0.2	-0.56	0.46	0.4	1.24	1.38	1.11	1.74	1.5	0.0047448225	0.0701493998
chr6	35571909	35571958	0	0.5	0.07	0.63	1.55	1.63	1.32	1.23	2.14	1.65	0.0397875704	0.1699284802
Nearby Gene: PACSIN1														
chr6	34590976	34591025	0.2	1.16	0.18	1.45	2.03	2.6	1.75	1.23	2.92	2.09	0.0307554934	0.1508081343
chr6	34591056	34591105	0.49	1.06	0.49	1.49	1.89	2.84	2.18	1.64	3.22	2.26	0.0012155584	0.0462151098
chr6	34591276	34591325	0.59	0.88	0.42	1.3	2.06	2.75	1.59	1.55	3.03	1.85	0.0232450953	0.1329638944
Nearby Gene: LY6G6D														
chr6	31791201	31791250	-0.96	0.15	0.05	0.06	1.16	1.31	1.18	0.39	1.85	1.28	0.0058432291	0.0756531434
chr6	31791296	31791345	-1.13	0.01	-0.09	0.36	1.12	1.4	1.09	0.44	1.98	1.29	0.0049058597	0.0710372013
chr6	31791371	31791420	-0.71	0.26	-0.22	0.42	1.3	1.46	1.46	0.7	2.3	1.43	0.0130090607	0.1035870021
Nearby Gene: ENSG00000178762														
chr6	25840780	25840829	1.34	0.37	0.99	1.5	3.06	3.15	3.36	0.84	3.37	2.88	0.0274764802	0.1432860624
chr6	25840885	25840934	0.26	-0.09	0.53	0.73	2.8	2.01	2.6	0.49	3.17	2.92	0.0256062292	0.1387917490
chr6	25840985	25841034	0.88	0.63	1.04	1.83	2.84	2.3	3.26	1.13	2.63	3.02	0.0454611268	0.1812131089
Nearby Gene: FNDC1														
chr6	159509928	159509977	2.27	-1.12	-0.36	0.07	0.73	1.8	1.9	-0.91	3.55	3.29	0.0008140642	0.0417476362
chr6	159510018	159510067	2.25	-0.8	0.08	0.49	0.76	1.55	2.05	-0.49	3.21	3.04	0.0100560298	0.0933738394
chr6	159510118	159510167	2.48	-0.68	0.19	0.35	0.5	1.34	1.88	-0.39	3.37	2.95	0.0440965619	0.1786075603
Nearby Gene: unknown														
chr5	72712210	72712259	0.48	-0.17	1.13	0.39	-0.31	1.82	1.84	1.06	2.3	0.93	0.0144519344	0.1082094738
chr5	72712300	72712349	0.84	0.68	1.46	0.63	0.47	1.77	1.83	1.7	3.09	1.16	0.0270335684	0.1422417348
chr5	72712385	72712434	0.8	0.11	1.57	0.77	0.22	1.88	2.1	1.83	2.49	1.02	0.0027941267	0.0588464629
Nearby Gene: SLC9A3														
chr5	579169	579218	0.05	0.43	0.22	0.66	2.45	2.34	2.25	0.71	4.01	2.06	0.0025344599	0.0571715778
chr5	579274	579323	0.06	0.9	0.64	1.58	2.92	2.72	2.38	0.93	4	2.22	0.0082783018	0.0863359880
chr5	579379	579428	-0.21	1.02	0.67	1.82	2.31	2.43	2.08	1.16	3.67	2.13	0.0076050059	0.0835669966
Nearby Gene: unknown														
chr5	43036303	43036352	0.13	0.17	0.81	0.47	1.92	2.92	3.54	1.44	3.8	3.21	0.0014531945	0.0484720005
chr5	43036503	43036552	-0.53	-0.75	-0.76	-0.34	0.34	1.15	3.25	1	3.12	2.88	0.0228377924	0.1319251660
chr5	43036588	43036637	1.69	1.75	2.29	1.19	2.55	2.81	3.41	2.25	3.96	2.97	0.0435878344	0.1776684438
Nearby Gene: unknown														
chr5	178733946	178733995	2.9	1.68	2.26	2.51	4.81	4.54	4.14	1.66	5.14	4.71	0.0363104511	0.1627630934
chr5	178734141	178734190	2.84	1.64	2.26	2.52	4.49	4.27	3.93	1.6	4.83	4.36	0.0027122089	0.0582893132
chr5	178734216	178734265	2.79	1.61	2.34	2.41	4.61	4.42	4.22	1.61	4.68	4.28	0.0018523034	0.0521280691
Nearby Gene: ARSI														
chr5	149655054	149655103	1.46	0.85	1.05	1.19	2.99	3.07	2.67	1.16	3.65	3.12	0.0066863691	0.0796065948
chr5	149655160	149655209	1.34	-0.27	0.96	1.15	3.04	2.97	2.67	1.21	3.24	2.8	0.0002147756	0.0310517649
chr5	149655360	149655409	1.15	1.14	0.97	1.36	2.83	2.89	2.59	1.28	3.48	2.68	0.0078665489	0.0846002189
Nearby Gene: PDGFRB														
chr5	149519516	149519565	1.07	0.81	0.27	0.88	0.66	1.94	1.83	1.01	2.49	1.51	0.0135168686	0.1052450904
chr5	149519583	149519632	1.01	0.7	0.21	0.86	0.7	2.08	1.72	0.9	2.53	1.46	0.0022242308	0.0550675320
chr5	149519753	149519802	0.99	0.12	0.01	0.19	0.86	2.36	1.66	0.37	1.94	1.54	0.0001387833	0.0287413292
Nearby Gene: PCDH1														
chr5	141228882	141228931	1.62	1.17	1.26	1.74	3.59	3.59	3.03	1.06	3.62	3.22	0.0022448490	0.0552521466
chr5	141229082	141229131	1.74	0.99	1.24	1.42	3.46	3.28	2.96	1.08	3.42	3.13	0.0000020706	0.0197834138
chr5	141229192	141229241	2.03	1.34	1.49	1.91	3.76	3.68	3.4	1.26	4.12	3.19	0.0000015565	0.0188335181
Nearby Gene: TGFBI														
chr5	135393099	135393148	0.62	0.73	0.32	-0.3	0.89	2.25	2.18	1.84	3.1	0.18	0.0046879058	0.0698533158
chr5	135393194	135393243	0.5	0.6	0.3	-0.55	1.52	2.29	2.23	1.89	3.76	0.54	0.0258969730	0.1395261010
chr5	135393309	135393358	0.38	0.21	-0.05	-0.79	0.78	1.83	1.97	1.56	2.75	-0.12	0.0199482946	0.1241537842
Nearby Gene: LOC389328														
chr5	134398970	134399019	0.36	-0.56	-0.18	-0.58	1.25	2.6	1.04	1.14	2.25	1.01	0.0155665155	0.1116057432
chr5	134399100	134399149	0.29	-0.61	-0.4	-0.47	1.55	2.95	1.52	0.95	3.06	1.72	0.0018804356	0.0524823446
chr5	134399170	134399219	0.18	-0.63	-0.44	-0.6	0.95	2.45	1.24	1.06	2.56	1.28	0.0056867392	0.0750237063
Nearby Gene: ZNF608														
chr5	124108117	124108166	0.8	0.41	-0.5	-0.63	1.47	2.28	2.6	2.19	3.06	-0.74	0.0024714003	0.0567775397
chr5	124108237	124108293	0.79	0.07	-0.62	-1.13	1.1	1.99	2.21	2.02	3.05	-0.83	0.0034244872	0.0629125047
chr5	124108317	124108366	0.55	0.32	0	-0.46	0.92	1.5	1.82	1.76	2.27	-0.19	0.0020613995	0.0538331824
Nearby Gene: IDUA														
chr4	982083	982132	0.51	1.49	1.68	1.34	2.81	3.67	2.7	1.67	3.17	3.1	0.0353282746	0.1607473057
chr4	982201	982250	0.78	1.64	1.81	1.41	3.48	3.9	3.16	1.82	3.34	3.02	0.0017910925	0.0515516386
chr4	982283	982332	0.77	1.67	1.71	1.3	2.46	3.1	2.54	1.8	2.68	2.82	0.0005418971	0.0374006068

Nearby Gene: ITIH1														
chr3	52798685	52798734	0.55	0.63	0.46	1.16	2.25	2.36	2.07	0.95	2.72	2.26	0.0003223193	0.0332828630
chr3	52798775	52798824	0.57	0.65	0.49	1.24	2.69	2.75	2.28	0.95	3.04	2.53	0.0082528399	0.0862243782
chr3	52798870	52798919	0.44	0.33	0.66	0.78	1.93	2.4	1.77	0.66	2.7	2.1	0.0146116669	0.1087061132
Nearby Gene: HYAL3														
chr3	50305754	50305803	0.85	0.3	0.7	0.46	2.02	2.48	2.25	1.05	2.68	2.45	0.0087311272	0.0884128597
chr3	50305959	50306009	1	0.41	0.93	0.93	2.9	3.04	2.63	1.03	3.15	1.7	0.0014909477	0.0489126461
chr3	50306054	50306103	0.79	0.38	0.85	1.06	2.28	2.48	2.01	1.17	2.73	2.37	0.0062509516	0.0777338333
Nearby Gene: CPT1B														
chr22	49363855	49363904	0.7	1.88	1.94	2.34	0.24	2.66	2.5	2.21	2.7	2.15	0.0333885548	0.1566403481
chr22	49363950	49364000	0.69	2.14	2.42	3.12	-0.29	2.92	3.03	2.82	3.59	2.58	0.0065048535	0.0787943437
chr22	49364155	49364204	0.19	1.91	1.72	2.71	-0.23	2.57	2.52	2.61	3.5	2.12	0.0007094593	0.0403855332
Nearby Gene: PLA2G3														
chr22	29866872	29866921	0.31	0.32	0.35	-0.19	0.22	1.88	1.34	1.05	1.04	0.77	0.0051746871	0.0724740827
chr22	29867002	29867051	0.36	0.6	0.43	-0.38	0.55	1.8	1.31	1.28	2.43	1.84	0.0079106367	0.0847313881
chr22	29867102	29867151	0.49	0.42	0.09	-0.25	-0.14	1.6	0.52	1.02	1.44	1.26	0.0021177147	0.0542712343
Nearby Gene: TBX1														
chr22	18123646	18123695	0.74	0.62	0.45	0.74	1.92	2.32	2.1	0.98	2.66	1.82	0.0036383957	0.0642251758
chr22	18123736	18123785	0.31	0.35	0.36	-0.09	1.1	1.86	2.07	0.88	2.69	1.14	0.0021378563	0.0543795435
chr22	18123856	18123905	1.15	0.71	0.57	0.33	1.73	2.32	1.97	0.95	3.18	1.75	0.0010126458	0.0439409085
Nearby Gene: COL6A2														
chr21	46340978	46341027	1.93	1.46	1.05	1.32	3.1	3.34	3	1.53	3.88	2.56	0.0328879189	0.1555362110
chr21	46341078	46341127	1.89	1.43	0.77	1.21	2.71	3.09	2.8	1.55	3.78	2.25	0.0000311118	0.0218810115
chr21	46341173	46341222	1.97	1.7	0.91	1.66	2.91	3.19	2.99	1.78	3.84	2.63	0.0038199940	0.0652272403
Nearby Gene: GATA5														
chr20	60486551	60486600	1.41	0.2	0.84	1	1.76	3.38	3.62	0.13	2.61	3.46	0.0338096834	0.1575396261
chr20	60486751	60486800	0.62	0.04	0.39	0.42	0.6	1.4	1.5	0.59	1.99	1.84	0.0006111533	0.0386440867
chr20	60486926	60486975	0.75	0.31	1.03	0.75	0.56	1.41	2.28	0.88	2.8	2.05	0.0004504395	0.0356644438
Nearby Gene: SLC32A1														
chr20	36785134	36785183	0.59	0.2	0.21	0.04	-0.49	0.51	1.37	1.58	2.6	1.07	0.0000075687	0.0197834138
chr20	36785229	36785278	0.73	0.45	0.57	0.08	0.17	0.89	1.49	1.39	2.3	1.53	0.0000104249	0.0206310965
chr20	36785319	36785368	0.78	0.53	0.69	-0.04	0.01	0.96	1.42	1.35	2.3	1.44	0.0175973313	0.1175708403
Nearby Gene: OTOF														
chr2	26634682	26634731	1.47	0.24	0.37	1.57	1.96	2.72	2.29	1.39	3.1	2.46	0.0054914460	0.0741072287
chr2	26634902	26634951	1.56	0.13	0.37	0.44	1.86	2.6	2.17	0.45	2.55	2.44	0.0044761757	0.0687923722
chr2	26635082	26635131	1.64	0.28	0.49	0.99	2.5	2.65	2.06	0.86	2.99	2.66	0.0160967769	0.1132251390
Nearby Gene: C2orf85														
chr2	242458712	242458761	1.64	1.34	1.09	0.94	2.52	3.35	2.62	1.41	3.15	3	0.0031747931	0.0613909221
chr2	242458922	242458971	1.43	0.95	0.87	0.94	2.13	3.19	1.96	1.24	2.83	2.79	0.0014461593	0.0484129826
chr2	242458997	242459046	1.33	0.91	0.84	0.9	1.88	2.92	1.98	1.16	2.68	2.72	0.0066788950	0.0795686166
Nearby Gene: LOC100131546														
chr2	232993272	232993321	1.21	0.51	1.29	1.1	1.46	3	2.71	2.07	3.08	1.91	0.0302120808	0.1497100228
chr2	232993342	232993391	0.61	0.28	1.06	1.06	1.04	3.17	2.67	2.11	3.3	1.88	0.0054677982	0.0739914487
chr2	232993447	232993496	0.53	0.47	0.98	0.77	1.13	2.49	1.94	1.57	2.45	1.41	0.0400728598	0.1705209211
Nearby Gene: TBR1														
chr2	161981466	161981515	-1.32	-1.92	-0.82	-0.07	-1.03	3.35	1.98	0.04	4.15	1.14	0.0029451663	0.0598683574
chr2	161981591	161981640	0.16	-0.1	0.37	0.52	0.6	2.61	1.42	-0.09	3.42	1.56	0.0030794340	0.0607191391
chr2	161981696	161981745	0.35	-0.18	0.79	0.39	0.86	2.71	1.91	0.66	3.1	1.15	0.0245992105	0.1363053173
Nearby Gene: LIMS2														
chr2	128138794	128138843	0.97	0.48	-0.12	1.6	1.1	1.74	2.48	1.22	3.14	2.42	0.0121290695	0.1007165019
chr2	128138919	128138968	0.97	0.58	-0.01	1.74	1.23	1.61	2.59	1.51	3.55	2.58	0.0024936337	0.0569060378
chr2	128139004	128139053	0.89	0.5	0.13	1.48	0.82	1.19	2.2	1.19	2.87	2.24	0.0009301906	0.0431008335
Nearby Gene: C19orf51														
chr19	60362392	60362441	1.12	0.54	0.57	0.5	1.86	2.73	1.86	0.99	2.68	2.12	0.0162484972	0.1136487236
chr19	60362487	60362536	1.2	0.73	0.67	0.76	2.28	2.99	2.38	1.39	3.36	2.64	0.0024951804	0.0569060378
chr19	60362617	60362666	1.21	0.74	0.88	0.7	1.96	2.63	2.05	1.18	3.03	2.15	0.0105567498	0.0953291022
Nearby Gene: PPP1R12C														
chr19	60301295	60301344	1.82	1.82	0.94	1	0.83	2.81	2.29	1.52	3.41	2.49	0.0027504171	0.0585707722
chr19	60301399	60301448	1.56	1.64	0.61	0.93	0.91	2.52	2.06	1.29	3.16	2.21	0.0027504171	0.0585707722
chr19	60301477	60301526	1.65	1.65	0.59	0.87	0.94	2.46	2.16	1.49	3.45	2.37	0.0109922910	0.0969149072
Nearby Gene: CACNG7														
chr19	59103103	59103152	0.2	0.29	-0.17	0.22	1.65	2.39	1.66	-0.26	2.48	1.61	0.0009706078	0.0434293326
chr19	59103193	59103242	0.1	0.13	-0.3	0.25	1.94	2.5	1.81	-0.44	2.55	1.92	0.0004190321	0.0350917639
chr19	59103293	59103342	-0.23	-0.17	-0.21	0.01	1.44	2.15	1.63	-0.35	2.04	1.54	0.0008180832	0.0418395788
Nearby Gene: LOC100129088														
chr19	58716816	58716865	0.17	0.84	1.44	1	1.46	1.93	2.03	1.85	3.37	1.95	0.0000740376	0.0256044041
chr19	58716891	58716940	0.58	0.49	1.13	1	1.65	1.91	2.07	1.14	3.03	2.22	0.0005907333	0.0384487121
chr19	58717016	58717065	0.23	0.59	1.34	0.94	1.06	1.35	1.72	1.8	3.02	1.8	0.0133771334	0.1048241393
Nearby Gene: DIRAS1														
chr19	2674879	2674928	0.72	0.88	0.46	1.32	1.9	3.27	2.32	1.51	2.62	2.7	0.0061540309	0.0772430351

chr19	2674964	2675013	0.91	0.85	0.53	1.27	2.05	3.39	2.2	1.39	2.16	2.7	0.0125331265	0.1021777837
chr19	2675089	2675138	1.25	0.83	0.76	0.99	2.04	3.35	2.03	1.16	2.41	2.59	0.0146408304	0.1088182618
Nearby Gene: uc010dsz.1														
chr19	2283219	2283268	0.64	1.3	0.37	0.26	1.22	1.59	0.95	1.78	2.19	2.7	0.0009001752	0.0428303139
chr19	2283299	2283348	0.35	1.69	0.16	-0.01	1.32	1.66	0.57	2.22	2.15	2.81	0.0003755118	0.0340057473
chr19	2283519	2283568	0.45	1.79	0.42	-0.14	1.06	1.64	0.91	2.11	2.35	2.97	0.0128919096	0.1032492927
Nearby Gene: MEF2B														
chr19	19142349	19142398	0.29	2.12	0.22	-0.15	1.81	2.3	2.53	2.44	3.44	0.47	0.0143049771	0.1077719674
chr19	19142448	19142497	0.06	2.23	-0.04	-0.38	1.65	2.53	2.81	2.7	3.99	0.58	0.0254015586	0.1382852101
chr19	19142533	19142582	-0.01	1.99	0.08	0.1	1.01	2.31	2.31	2.56	3.16	0.7	0.0358760778	0.1618232425
Nearby Gene: CTDP1														
chr18	75541938	75541987	0.8	1.06	0.11	1.9	1.48	3.07	1.67	0.88	2.67	2.27	0.0055405418	0.0744029893
chr18	75542068	75542117	0.61	1.07	-0.14	1.78	1.79	3.65	2.12	0.72	2.76	2.29	0.0026305038	0.0577959917
chr18	75542133	75542182	0.75	1.18	-0.11	1.74	1.67	3.63	2.11	0.66	2.08	2.07	0.0040443116	0.0664470157
Nearby Gene: SEPT9														
chr17	72831246	72831295	2.95	1.26	0.74	1.58	3.36	4.51	3.61	1.14	4.16	4.01	0.0139211251	0.1064923201
chr17	72831376	72831425	2.79	1.19	0.75	1.48	2.63	3.99	3	1.09	3.26	3.63	0.0110137644	0.0969736202
chr17	72831446	72831495	2.53	1.18	0.54	1.49	2.6	3.38	2.76	0.98	3.65	3.32	0.0125444953	0.1022095307
Nearby Gene: TMEM102														
chr17	7279267	7279316	-0.65	1.53	0.37	-0.47	-0.16	2.07	2.27	1.85	2.6	-0.49	0.0010796979	0.0447245146
chr17	7279387	7279436	-0.94	1.66	0.24	-0.37	-0.29	2.34	2.38	2.11	3.14	-0.42	0.0033388253	0.0623554214
chr17	7279477	7279526	-0.79	1.31	0.32	-0.61	-0.38	1.78	1.81	1.59	2.48	-0.27	0.0149201702	0.1096121297
Nearby Gene: SEC14L1														
chr17	72718037	72718086	2.12	1.52	2.22	-1.02	2.7	2.93	2.61	2.31	2.97	2.81	0.0024812280	0.0568431063
chr17	72718132	72718181	2.24	1.71	2.41	-0.39	3.18	3.47	2.78	2.43	3.6	3.29	0.0005833492	0.0383436457
chr17	72718257	72718306	2.3	1.68	2.34	-0.18	3.23	3.19	2.77	2.17	3.47	3.03	0.0015022165	0.0489960182
Nearby Gene: FAM64A														
chr17	6288690	6288739	1.84	0.55	0.67	0.35	3.72	4.11	3.63	0.52	3.67	3.15	0.0144331890	0.1081485715
chr17	6288785	6288834	1.7	0.72	0.85	0.77	2.73	2.95	2.75	0.78	3.68	2.38	0.0020123547	0.0534615452
chr17	6288890	6288939	1.45	0.63	0.58	0.44	2.05	2.44	2.22	0.81	3.09	1.87	0.0009223928	0.0429977236
Nearby Gene: unknown														
chr17	44078086	44078143	0.28	1.69	0.57	-0.63	2.29	1.74	1.86	1.92	2.38	1.99	0.0072102607	0.0819215596
chr17	44078251	44078300	0.27	1.9	0.62	-0.99	2.73	2.05	2.12	2.21	2.56	2.64	0.0036491264	0.0642552466
chr17	44078381	44078430	0.48	1.28	0.72	-0.04	2.45	1.93	1.72	1.63	2.44	2.42	0.0131705012	0.1041345887
Nearby Gene: HOXB3														
chr17	44004023	44004072	2.33	-1.01	-1.16	-1.6	-0.98	2.34	1.83	-0.87	3.02	1.68	0.0003261712	0.0333344587
chr17	44004143	44004192	2.47	-0.05	-0.43	-0.76	-0.52	2.17	1.98	-0.48	2.77	1.68	0.0093709667	0.0909341208
chr17	44004243	44004298	2.01	-0.29	-0.2	-0.72	-0.34	1.79	1.22	-0.2	2.4	1.39	0.0190575883	0.1216913639
Nearby Gene: C1QL1														
chr17	40401684	40401733	-0.63	-0.12	0.46	0.38	0.8	1.33	1.85	1.33	2.55	0.68	0.0233839815	0.1333290150
chr17	40401779	40401828	-0.88	-0.33	0.6	0.29	0.13	1.29	1.79	1.17	2.79	0.4	0.0010060479	0.0438567402
chr17	40401894	40401943	0.44	0.06	0.69	0.45	0.59	1.54	1.57	1.08	2.25	1.07	0.0043275354	0.0679819294
Nearby Gene: WNK4														
chr17	38189579	38189628	1.05	1.34	0.27	0.41	0.59	1.84	2.91	0.85	2.97	1.89	0.0008979063	0.0428292979
chr17	38189669	38189718	0.8	1.48	0.21	0.29	0.43	1.6	2.64	1.17	2.49	1.7	0.0079226961	0.0847773432
chr17	38189774	38189823	0.78	1.49	0.26	-0.04	0.33	1.45	2.26	1.09	2.64	1.47	0.0041326450	0.0669405364
Nearby Gene: KRT19														
chr17	36936966	36937015	1.28	0.87	0.95	1.85	1.88	2.62	2.36	2	3.36	1.84	0.0013936973	0.0479310057
chr17	36937096	36937145	1.4	0.78	0.77	1.7	2.37	2.87	2.62	1.65	3.85	2.07	0.0029486294	0.0598713157
chr17	36937186	36937235	1.19	0.64	0.74	1.33	2.32	2.73	2.49	1.48	3.58	2.36	0.0264327831	0.1407859447
Nearby Gene: SLC6A4														
chr17	25589239	25589288	-0.51	0.14	0.4	0.38	1.57	1.49	2.34	2.06	3.15	2.15	0.0462673643	0.1827160223
chr17	25589339	25589388	0.12	0.23	0.78	0.38	2.75	2	2.88	1.79	3.86	1.9	0.0039284657	0.0658651551
chr17	25589454	25589503	-1.72	-0.65	-0.74	-0.33	0.79	1.3	2.02	1.22	2	0.75	0.0204978958	0.1256821470
Nearby Gene: PYY2														
chr17	23579181	23579237	0.76	-0.19	0.11	1.07	1.65	2.8	3.06	1.22	2.63	1.14	0.0017361186	0.0511632530
chr17	23579296	23579345	0.42	-0.01	0.3	1.29	1.95	3.22	2.97	1.7	3.06	1.35	0.0012381665	0.0464531368
chr17	23579366	23579415	0.32	0.07	0.22	1.21	1.52	3.16	2.84	1.7	2.64	0.93	0.0005936707	0.0384487121
Nearby Gene: HS3ST3B1														
chr17	14147477	14147526	0.54	0.47	-1.15	-0.38	0.58	1.47	1.51	1.5	1.67	-0.32	0.0128897408	0.1032482408
chr17	14147587	14147636	0.6	0.44	-0.97	-0.32	0.71	1.91	1.43	1.64	2.24	0.29	0.0149104487	0.1095888855
chr17	14147707	14147756	0.93	0.66	-1.2	-0.1	1.17	2.07	1.95	1.8	2.09	0.17	0.0064448948	0.0785051822
Nearby Gene: CARHSP1														
chr16	8869029	8869078	0.25	0.79	-0.25	0.24	1.91	2.12	1.79	1.81	2.73	0.51	0.0023295488	0.0556933071
chr16	8869124	8869173	0.23	0.59	0.01	0.22	1.27	2.02	1.44	1.84	2.47	0.78	0.0015575423	0.0494185162
chr16	8869219	8869268	0.57	1.1	-0.23	0.41	1.81	2.51	2.24	2.23	2.82	0.67	0.0105030552	0.0951880612
Nearby Gene: CARHSP1														
chr16	8868597	8868646	0.73	1	-0.3	0.4	2.47	3.11	2.52	1.89	3.19	0.66	0.0388285002	0.1680259043
chr16	8868712	8868761	0.43	0.7	-0.48	0.48	1.69	2.28	1.95	2	2.78	0.46	0.0126734522	0.1025859283
chr16	8868797	8868846	0.94	1.57	-0.61	0.92	2.87	3.06	3.05	2.73	3.77	1.11	0.0023579382	0.0559184939

Nearby Gene: BCAR1														
chr16	73843421	73843470	-0.06	0.95	0.88	0.64	0.45	1.23	1.69	1.38	2.67	1.42	0.0189416109	0.1213725891
chr16	73843501	73843550	0.06	0.83	0.68	0.74	0.48	1.3	1.5	1.37	2.64	1.19	0.0015639934	0.0495098213
chr16	73843591	73843640	-0.07	0.95	0.74	0.84	0.53	1.24	1.54	1.47	2.53	1.22	0.0144157607	0.1080999856
Nearby Gene: SMPD3														
chr16	66956690	66956739	1.74	1.59	-0.88	1.72	2.28	4.13	3.21	0.85	2.92	1.47	0.0203356619	0.1252461043
chr16	66956800	66956849	1.86	1.71	-0.51	1.89	3.05	4.35	3.32	0.73	4.04	1.82	0.0009164503	0.0429142990
chr16	66956875	66956924	1.84	1.65	-0.66	1.8	2.65	4.27	3.37	0.72	3.49	1.4	0.0005037631	0.0365696839
Nearby Gene: HSF4														
chr16	65757596	65757645	-0.25	0.08	-0.45	0.1	0.33	2.16	2.33	2.24	3.21	-0.11	0.0287781244	0.1464130686
chr16	65757716	65757765	-0.22	0.11	-0.46	0.1	0.42	1.74	1.92	2	2.53	0.02	0.0024382127	0.0565307013
chr16	65757801	65757850	0.41	0.43	-0.11	0.15	0.27	1.8	1.62	1.99	3.22	0.12	0.0121038745	0.1006599689
Nearby Gene: GPR56														
chr16	56221957	56222006	-0.58	0.62	-0.97	0.69	-0.54	0.22	1.9	1.03	1.97	1.54	0.0011065151	0.0449407203
chr16	56222077	56222126	-1.39	0.63	-1.38	0.84	-0.7	0.25	1.98	1.01	1.66	1.27	0.0047974962	0.0704733742
chr16	56222152	56222201	-1.49	0.89	-1.62	0.99	-0.69	0.14	2.32	1.41	1.93	1.71	0.0076203236	0.0836348547
Nearby Gene: TRIM72														
chr16	31132829	31132878	0.77	1.08	0.05	-0.73	0.47	2.44	1.52	1.81	2.26	0.4	0.0007919946	0.0413519441
chr16	31132914	31132963	0.59	0.84	0.22	-0.48	0.49	2.29	1.53	1.92	2.11	0.38	0.0173056394	0.1167763752
chr16	31133044	31133093	1.07	0.97	0.55	-0.51	0.63	2.21	1.64	1.57	2.33	0.88	0.0159858300	0.1128945266
Nearby Gene: RASGRF1														
chr15	77082859	77082908	2.44	1.47	1.02	2.09	2.1	3.15	2.89	1.63	3.52	3.3	0.0190828392	0.1217575322
chr15	77082989	77083038	2.87	1.52	1.29	2.27	2.94	3.92	3.49	1.44	3.79	3.99	0.0196381630	0.1232967565
chr15	77083189	77083238	3	1.07	1.37	1.8	2.81	4.04	3.77	0.85	3.65	4	0.0217593380	0.1290024421
Nearby Gene: ASB2														
chr14	93490386	93490435	1.67	1.22	0.54	0.71	2.43	3.17	2.68	1.16	2.78	2.85	0.0013428615	0.0474947536
chr14	93490581	93490630	1.17	0.84	0.02	0.27	1.43	2.3	1.92	0.96	2.18	2.42	0.0009160570	0.0429142990
chr14	93490661	93490710	1.54	1.22	0.02	0.33	1.42	2.55	2.37	0.93	2.03	2.45	0.0170278208	0.1160084835
Nearby Gene: C14orf4														
chr14	76568588	76568637	0.01	2.16	-0.38	-0.42	1.47	2.15	1.73	2.39	1.97	-0.03	0.0016146548	0.0499441255
chr14	76568707	76568756	0.14	1.86	-0.18	-0.35	1.61	2.05	1.61	2.08	2.5	0.13	0.0007447835	0.0408987033
chr14	76568731	76568780	0.17	2.23	-0.21	-0.38	1.77	2.46	1.8	2.52	2.96	0.38	0.0099622110	0.0930057991
Nearby Gene: FOXA1														
chr14	37131803	37131852	0.85	0.47	1.72	1.51	2.41	2.69	2.4	1.63	3.73	2.55	0.0020266355	0.0535065496
chr14	37131878	37131934	1.22	0.65	2.07	2.45	3.25	4.32	4.12	2.04	4.6	3.54	0.0093428244	0.0908192080
chr14	37131983	37132032	1.27	0.77	2.04	2.04	2.62	3.55	3.64	1.95	4.39	3.03	0.0245762155	0.1362617986
Nearby Gene: LAG3														
chr12	6752404	6752453	-0.32	0.76	-0.85	-0.28	0.83	1.66	1.71	2.07	3.21	1.98	0.0329141565	0.1555992926
chr12	6752604	6752653	-0.09	0.38	-0.36	0.14	0.55	1.89	1.36	1.38	1.56	1.42	0.0077136204	0.0840022255
chr12	6752724	6752773	0.15	0.8	-0.17	0.19	0.72	2	1.33	1.66	2.4	1.63	0.0101452359	0.0937019966
Nearby Gene: KRT80														
chr12	50871102	50871151	-0.24	1.26	0.58	1.62	-0.06	1.9	1.81	1.57	2.66	1.86	0.0004059248	0.0346443169
chr12	50871207	50871256	0.16	1.53	0.77	1.77	0.86	2.09	2.12	1.76	2.8	2.04	0.0012151430	0.0462151098
chr12	50871307	50871356	-0.12	1.29	0.47	1.51	0.09	1.68	1.82	1.54	2.36	1.78	0.0010188388	0.0440145013
Nearby Gene: ACVRL1														
chr12	50586352	50586401	0.18	0.27	0.3	0.29	0.66	1.32	2.28	2.1	3.02	0.47	0.0068524406	0.0803568557
chr12	50586447	50586496	0.19	0.23	0.24	0.06	0.83	1.34	2.17	2	2.63	0.13	0.0355669153	0.1611703576
chr12	50586532	50586581	0.43	0.1	0.27	0.27	0.65	1.39	1.82	2.04	2.44	0.17	0.0352061575	0.1604880151
Nearby Gene: C1QL4														
chr12	48014936	48014985	0.63	1.06	1.17	1.18	2.03	2.42	2.07	1.77	3.29	3.03	0.0001920414	0.0303749074
chr12	48015036	48015085	0.23	0.75	1	0.57	2.52	2.04	1.98	1.56	3.36	1.51	0.0000614479	0.0244289612
chr12	48015151	48015200	-0.36	0.38	0.76	0.44	1.46	1.62	1.44	1.53	2.23	0.98	0.0001585798	0.0292340585
Nearby Gene: PRPH														
chr12	47974082	47974131	0.47	1.1	0.19	0.24	-0.26	1.37	1.23	1.39	1.88	1.67	0.0123435576	0.1014880781
chr12	47974207	47974256	0.19	0.66	-0.1	-0.14	-0.61	1.07	0.95	1.12	1.89	1.42	0.0115984589	0.0989742842
chr12	47974307	47974356	0.11	0.7	-0.26	-0.05	-0.4	1.22	0.97	1.1	1.78	1.38	0.0289338681	0.1467660083
Nearby Gene: POLE														
chr12	131728756	131728805	2.29	1.73	2.3	1.86	3.12	3.73	3.19	2.46	3.76	3.42	0.0240214811	0.1348748472
chr12	131728972	131729021	2.54	1.73	2.13	1.94	3.39	4.01	3.33	2.32	3.61	3.77	0.0020762366	0.0539008016
chr12	131729166	131729215	2.48	1.69	2.33	1.71	3.48	4.16	2.95	2.06	4.1	3.59	0.0016266774	0.0501383555
Nearby Gene: unknown														
chr12	113363056	113363105	0.38	-1.06	-0.29	1.01	0.58	1.29	2.56	-0.44	2.67	1.36	0.0002984927	0.0329549981
chr12	113363156	113363205	0.33	-1.84	-0.14	0.8	0.5	1.62	3.06	-0.65	3.25	1.6	0.0002473300	0.0317897892
chr12	113363341	113363390	0.22	-1.58	-0.13	1.33	0.57	1.26	2.69	-0.43	3.11	1.04	0.0022405120	0.0552343881
Nearby Gene: EFCAB4A														
chr11	817937	817986	0.82	0.22	-0.15	0.16	1.55	2.58	2.58	-0.75	2.82	1.36	0.0200889641	0.1245424565
chr11	818127	818176	0.49	0.36	-0.01	0.33	1.54	1.95	2.56	-0.16	3.38	1.4	0.0024980597	0.0569060378
chr11	818242	818291	0.4	0.44	-0.19	0.34	1.2	1.91	2.76	-0.37	3.33	1.09	0.0083235670	0.0865451557
Nearby Gene: PHOX2A														

chr11	71633653	71633702	0.57	0.14	0.61	0.37	1.22	1.46	2.24	0.66	2.62	1.12	0.0226771833	0.1314922098
chr11	71633778	71633827	0.56	-0.49	0.27	0.89	1.31	1.7	2.63	-0.33	3.46	2.02	0.0217108430	0.1288771222
chr11	71633953	71634002	0.83	-0.3	0.02	-0.02	1	1.8	1.92	0.09	2.41	1.43	0.0070776516	0.0812891022
Nearby Gene: NRXN2														
chr11	64241704	64241753	0.96	0.72	0.47	1.56	1.47	2.12	2.37	1.05	2.82	2.29	0.0009861325	0.0436215808
chr11	64241809	64241858	0.74	0.63	0.5	1.46	1.25	2.08	2.16	1.02	2.52	2.36	0.0009511072	0.0431511989
chr11	64241989	64242038	0.7	0.88	0.47	1.64	1.27	2.18	1.96	1.08	2.69	2.2	0.0011660927	0.0456368265
Nearby Gene: TSPAN32														
chr11	2282124	2282173	-1.89	0.68	-0.74	0.57	1.52	2.56	1.25	1.11	3.14	1.42	0.0047487892	0.0701592796
chr11	2282194	2282243	-1.69	0.45	-0.81	0.52	1.53	2.49	1.27	1.05	3.2	1.33	0.0086478760	0.0880769511
chr11	2282309	2282358	-0.67	0.48	-0.11	0.48	1.25	2.12	1.04	1.34	2.65	1.24	0.0287873861	0.1464366692
Nearby Gene: H19														
chr11	1977616	1977665	3.39	0.41	1.75	1.94	4.26	4.28	3.86	0.66	4.34	4.14	0.0028838980	0.0594963170
Nearby Gene: SPON1														
chr11	13942147	13942196	0.06	-0.05	0.54	1.1	1.08	2.35	2.48	1.62	3.12	3.42	0.0261531802	0.1401021606
chr11	13942242	13942291	0.96	0.58	0.49	1.56	1.29	2.67	2.83	1.7	3.31	3.62	0.0149461225	0.1097051926
chr11	13942317	13942366	-0.68	-0.28	-0.18	0.33	0.51	1.58	1.78	1.28	2.36	2.35	0.0033889790	0.0626919052
Nearby Gene: IGSF9B														
chr11	133306794	133306843	2.31	1.08	1.69	1.33	3.44	4.09	3.04	1.23	3.85	3.75	0.0038285388	0.0652855818
chr11	133306880	133306929	2.11	1	1.34	0.86	2.85	3.39	3.01	0.96	3.16	3.32	0.0019740802	0.0531912663
chr11	133306974	133307023	2.27	1.34	1.71	1.38	3.29	3.67	3.03	1.43	3.79	3.48	0.0199562203	0.1241631706
Nearby Gene: TP53AIP1														
chr11	128315801	128315850	1.31	0.93	0.6	-0.67	1.81	2.41	1.74	0.92	2.33	2.32	0.0080591031	0.0852989680
chr11	128315911	128315960	1.32	0.85	0.44	-0.11	2.19	2.82	2.16	0.94	2.12	2.56	0.0017845146	0.0514959912
chr11	128316001	128316050	1.5	0.9	0.44	-0.51	1.83	2.95	2.35	0.67	1.94	2.52	0.0004841118	0.0361927873
Nearby Gene: KCNMA1														
chr10	79066324	79066373	-0.38	-0.91	-0.73	0.88	0.33	1.9	2.68	1.55	2.36	0.75	0.0009475184	0.0431230530
chr10	79066429	79066478	-0.03	-0.5	-0.55	0.9	0.28	1.57	2.16	1.39	2.03	0.74	0.0085110403	0.0873643261
chr10	79066499	79066550	-0.32	-1.04	-0.86	0.67	0.2	1.68	2.59	1.45	1.73	0.22	0.0479023150	0.1857265632
Nearby Gene: PPYR1														
chr10	46502543	46502593	0.23	0.12	0.34	1.04	0.31	1.02	1.46	1.71	2.29	1.15	0.0109079906	0.0965937595
chr10	46502653	46502702	0.04	0.04	0.22	1.05	0.45	1.11	1.44	1.84	2.28	1.29	0.0094215844	0.0910852626
chr10	46502773	46502822	0.49	0.11	0.14	0.86	0.52	1.11	1.32	1.54	2.03	1.17	0.0003646392	0.0337940199
Nearby Gene: RASGEF1A														
chr10	43046926	43046975	0.32	0.25	0.36	0.71	0.86	1.49	1.85	0.65	2.25	1.72	0.0028215525	0.0590728005
chr10	43047011	43047060	0.6	0.16	0.55	0.62	1.2	2.16	2.43	0.64	3.31	2.12	0.0122732012	0.1012730986
chr10	43047116	43047165	0.24	-0.13	0.21	0.07	0.19	1.53	1	0.22	1.73	1.1	0.0199620191	0.1241724224
Nearby Gene: FAM53B														
chr10	126309880	126309929	2.43	1.51	1.95	2.08	3.18	3.99	3.2	1.92	3.59	3.59	0.0319063625	0.1533625563
chr10	126309986	126310035	2.6	1.46	1.91	2.21	3.98	4.59	2.35	2.03	4.55	4.62	0.0333080097	0.1564727345
chr10	126310062	126310111	2.64	1.33	1.83	1.86	3.29	4.72	3.72	1.57	3.34	3.92	0.0003933046	0.0344040191
Nearby Gene: PPAPDC1A														
chr10	122207490	122207539	0.38	1.28	0.09	1.42	1.08	2.91	2.32	1.77	3.15	0.95	0.0058691212	0.0757775093
chr10	122207585	122207634	0.46	1.34	0.17	1.36	1.09	2.75	2.21	1.91	3.59	1.09	0.0028639710	0.0593291180
chr10	122207660	122207709	0.32	1.55	-0.1	1.45	0.66	2.81	2.32	1.95	3.57	0.68	0.0379516855	0.1661400336
Nearby Gene: LOC100132839														
chr10	115792628	115792687	1.48	-0.53	-0.95	1.83	-0.53	1.6	1.35	-0.97	2.78	2.03	0.0336738651	0.1572232304
chr10	115792698	115792747	1.3	-0.68	-1.3	1.82	-0.92	1.45	1.48	-0.94	2.71	2.19	0.0171503636	0.1163711014
chr10	115792818	115792867	0.54	-0.48	-0.71	1.29	-0.63	1.09	1.18	-0.67	2.21	1.55	0.0115786363	0.0988906083
Nearby Gene: TAL1														
chr1	47467048	47467097	0.95	0.98	0.85	0.15	1.73	1.14	2.42	1.96	2.83	1.72	0.0018096876	0.0517605966
chr1	47467159	47467208	-0.7	0.93	0.4	-0.1	1.45	-0.78	2.34	2.25	3.34	1.31	0.0011192217	0.0450979647
chr1	47467254	47467303	-0.45	0.92	0.55	-0.12	1.65	-0.38	2.4	2.08	3.64	1.24	0.0003666117	0.0338757494
Nearby Gene: POU3F1														
chr1	38286214	38286263	1.09	0.05	0.7	0.75	1.32	2.61	2.3	1.22	2.85	1.4	0.0107158082	0.0958998033
chr1	38286294	38286343	1.19	0.23	0.93	0.89	1.27	2.45	2.37	1.48	2.51	1.37	0.0001408040	0.0287990422
chr1	38286409	38286458	1.1	0.46	0.91	0.96	0.96	2.22	2.26	1.64	2.09	1.2	0.0004015897	0.0345766746
Nearby Gene: EPHA10														
chr1	38002568	38002617	1.58	0.54	1.73	2.15	1.72	3.02	3.33	1.35	3.39	2.75	0.0219268406	0.1294156564
chr1	38002673	38002722	1.64	0.68	1.81	1.91	2.41	3.25	3.45	1.4	4.15	3.1	0.0079304797	0.0848024173
chr1	38002773	38002822	1.89	0.53	2.09	2.3	2.85	4.01	3.77	1.38	4.52	3.46	0.0124453661	0.1018549345
Nearby Gene: TMEM200B														
chr1	29319407	29319456	1.18	1.03	0.19	0.84	-0.13	1.28	1.79	1.62	2.33	1.21	0.0041907560	0.0672747667
chr1	29319512	29319561	1.22	1.28	0.38	1.02	0.14	1.74	2.25	2.12	3.04	1.7	0.0022447090	0.0552521466
chr1	29319612	29319661	1.01	0.96	0.3	0.71	-0.19	1.25	1.73	1.66	2.17	1.27	0.0003358679	0.0334846984
Nearby Gene: NID1														
chr1	234295539	234295588	-0.15	0.67	1.24	-0.37	0.29	2.17	2.67	1.86	1.64	0.04	0.0245542929	0.1362020384
chr1	234295649	234295698	-0.04	0.56	1.09	-0.66	0.51	2	2.46	2.1	1.82	0.38	0.0095934602	0.0917252233
chr1	234295714	234295763	0.07	0.68	1.4	-0.85	0.6	1.86	2.55	2.1	2.42	0.33	0.0111801946	0.0976011821

Nearby Gene: ENSG00000216862													
chr1	226706706	226706755	0.99	0.69	0.36	0.52	3	3.32	2.4	0.27	3.39	2.51	0.0014966832	0.0489592741
chr1	226706776	226706825	1.04	0.54	0.4	0.45	3.06	3.17	2.38	0.38	3.29	2.5	0.0001404431	0.0287990422
chr1	226706886	226706935	1.2	0.38	0.42	0.45	3.57	3.38	2.51	-0.07	3.06	2.26	0.0024254359	0.0564372399
Nearby Gene: GJC2														
chr1	226406704	226406753	2.25	1.34	1.92	1.89	4.11	4.51	3.67	1.51	4.4	4.11	0.0059194867	0.0760236858
chr1	226406829	226406878	2.12	1.25	1.72	1.41	3.36	3.57	3.06	1.32	3.58	3.61	0.0066112750	0.0791939228
chr1	226406919	226406968	2.65	1.55	2.21	2.17	4.44	4.59	3.96	1.28	4.08	4.13	0.0114571396	0.0984634730
Nearby Gene: PM20D1														
chr1	204085603	204085652	-0.88	0.38	-0.7	1.52	0.88	1.32	1.35	1.19	1.37	1.94	0.0308053580	0.1508980136
chr1	204085683	204085732	-2.06	0.28	-2.12	1.38	0.41	1.31	1.37	1.04	1.87	1.78	0.0052841880	0.0730874803
chr1	204085883	204085932	-1.49	0.49	-1.48	1.49	0.71	1.03	1.38	1.09	1.79	1.95	0.0332018060	0.1562079455
Nearby Gene: PEAR1														
chr1	155150366	155150415	1.27	1.07	1.07	1.47	2.23	3.07	2.28	1.4	3.21	2.77	0.0062223244	0.0775930908
chr1	155150471	155150520	1.56	0.88	1.2	1.27	2.85	3.28	2.35	1.22	3.38	2.72	0.0000903933	0.0264076198
chr1	155150571	155150620	1.28	0.86	1.12	1.05	2.51	2.92	2.23	1.12	3.1	2.45	0.0038358647	0.0653266507
Nearby Gene: SMG5														
chr1	154486638	154486687	1.25	1.18	1.13	-0.28	1.44	2.01	1.87	1.48	2.59	1.94	0.0117956978	0.0996572570
chr1	154486763	154486812	1.31	1.18	1.21	-0.12	2.26	2.31	2.24	1.62	3.01	2.31	0.0035746149	0.0638631274
chr1	154486863	154486912	0.72	0.7	0.7	-0.55	1.79	2.38	1.86	1.34	2.45	2.14	0.0005105192	0.0367458364
Nearby Gene: LOC100131974														
chr1	147599626	147599675	0.3	1.06	1.3	1.48	0.84	1.34	2.48	1.41	2.83	2.33	0.0078575878	0.0845543707
chr1	147599691	147599740	0.12	0.63	0.92	1.2	0.99	1.69	2.52	0.99	3.56	2.73	0.0013409318	0.0474718099
chr1	147599786	147599835	0.44	-0.17	0.14	0.09	0.85	1.33	2.33	-0.23	2.57	1.87	0.0023009935	0.0555334433
Nearby Gene: WNT2B														
chr1	112853677	112853726	1.42	0.03	0.62	0.12	2.36	3.8	3.65	1.09	4.08	2.41	0.0376206105	0.1655391443
chr1	112853782	112853831	1.28	0.07	0.61	0.28	1.38	2.83	2.7	1.35	4.04	2.06	0.0059510566	0.0761878250
chr1	112854002	112854051	0.85	0.13	0.32	0.25	0.72	2.26	2.24	1.49	3.15	1.69	0.0287674793	0.1464027898

Supplementary Table 7. Inherited *DNMT3A* coding variants in AML cases vs. controls.

				AML patients*				CEU[#]				P-value^	
Genome coordinate	rsID	Variant	Codon	n	AA	AB	BB	n	AA	AB	BB	Allele	Genotype
chr2:25,323,006	rs2276598	C>T	L422	166	120	40	6	60	43	15	2	0.884	0.987
chr2:25,390,331	rs41284843	G>A	P9	168	122	43	3	60	46	12	2	0.879	0.561
chr2:25,324,464	novel	G>A	S267	167	165	2	0	--	--	--	--	NA	NA
chr2:25,324,473	novel	G>A	P264	168	166	2	0	--	--	--	--	NA	NA
chr2:25,324,506[@]	novel	G>A	P253	168	168	0	0	--	--	--	--	NA	NA
chr2:25,390,336	novel	C>T	G8S	168	167	1	0	--	--	--	--	NA	NA

*Caucasian only, [#]from 1,000 Genomes (build 130), [@]polymorphic in African American cases only, ^by Fisher's exact test (allele) or chi-square test (genotype).

Supplementary Table 8. Primers used for DNMT3A sequencing.

Amplicon Name	L Primer Coord	R Primer Coord	L Amp Coord	R Amp Coord	Primer 1 Sequence	Primer 2 Sequence	Target Name +	Target Start	Target Stop	Build	Gene	Ensembl_TranscriptID	NCBI_TranscriptID	Exon#	ExonID	Exon_Start	Exon_Stop
0001788_10W	25310553	25310780	25310578	25310757	TGTAAAACGACGGCCAGTTCCCAGTCCACTATACTGACGTCTC	CAGGAAACAGCTATGACCTCTCTCCATCCTCATGTTCTTGG	1788-0	25310652	25310793	36	DNMT3A	ENST00000264709	NM_022552.2	23	ENSE00001166323	25309350(includes UTR)	25310793
0001788_12K	25310643	25310868	25310663	25310847	TGTAAAACGACGGCCAGTGTGTGGTTAGACGGCTTCCG	CAGGAAACAGCTATGACCCCCATGTCCCTTACACACACG	1788-0	25310652	25310793	36	DNMT3A	ENST00000264709	NM_022552.2	23	ENSE00001166323	25309350(includes UTR)	25310793
0001788_11i	25311941	25312278	25311965	25312254	TGTAAAACGACGGCCAGTTGGCATATTTGGTAGACGCATGAC	CAGGAAACAGCTATGACCTGGGAAATGCTTGATAAAACCCAC	1788-1	25312080	25312198	36	DNMT3A	ENST00000264709	NM_022552.2	22	ENSE00001071017	25312080	25312198
0001788_129	25312053	25312263	25312075	25312245	TGTAAAACGACGGCCAGTGTAGACGCATGACCAGTGTTGG	CAGGAAACAGCTATGACCAGATGCCAGCACAACCCG	1788-1	25312080	25312198	36	DNMT3A	ENST00000264709	NM_022552.2	22	ENSE00001071017	25312080	25312198
0001788_14p	25313252	25313432	25313272	25313412	TGTAAAACGACGGCCAGTCCTTCCCGCTGTTATCCAGG	CAGGAAACAGCTATGACCCATCCTGCCCTTCCTTCTCC	1788-2	25313309	25313378	36	DNMT3A	ENST00000264709	NM_022552.2	21	ENSE00001071025	25313309	25313378
0001788_13r	25315442	25315651	25315460	25315628	TGTAAAACGACGGCCAGTGCCGGCGCTGTTTCATGC	CAGGAAACAGCTATGACCCCACTATGGGTCATCCCACCTGC	1788-3	25315503	25315588	36	DNMT3A	ENST00000264709	NM_022552.2	20	ENSE00001071036	25315503	25315588
0001788_14b	25316597	25316933	25316618	25316911	TGTAAAACGACGGCCAGTGACAGCTATTCCCGATGACCC	CAGGAAACAGCTATGACCTGCAGATGAGACAGGATGAAGC	1788-4	25316675	25316823	36	DNMT3A	ENST00000264709	NM_022552.2	19	ENSE00001071032	25316675	25316823
H_02_00jns	25316866	25317164	25316887	25317142	TGTAAAACGACGGCCAGTATAGGACAGTGGTGTGGCTCG	CAGGAAACAGCTATGACCTTCTTCCTGTCTGCCTCTGTCC	1788-5	25317013	25317103	36	DNMT3A	ENST00000264709	NM_022552.2	18	ENSE00001071021	25317013	25317103
0001788_11j	25317851	25318193	25317872	25318173	TGTAAAACGACGGCCAGTGACTTGGGCCTACAGCTGACC	CAGGAAACAGCTATGACCAAATGAAGGAGGCAAGGGC	1788-6	25317935	25318080	36	DNMT3A	ENST00000264709	NM_022552.2	17	ENSE00001071020	25317935	25318080
0001788_126	25320170	25320457	25320191	25320433	TGTAAAACGACGGCCAGTAGGGTGTGTGGGTCTAGGAGC	CAGGAAACAGCTATGACCGCTGTGAAGCTAACCATCATTTCG	1788-7	25320271	25320355	36	DNMT3A	ENST00000264709	NM_022552.2	16	ENSE00001281558	25320271	25320355
0001788_14l	25320431	25320788	25320453	25320767	TGTAAAACGACGGCCAGTTTTCCATTCCAGGTAGCACACC	CAGGAAACAGCTATGACCAGGCTCCTAGACCCACACACC	1788-8	25320528	25320711	36	DNMT3A	ENST00000264709	NM_022552.2	15	ENSE00001281418	25320528	25320711
0001788_055	25320772	25321136	25320794	25321114	TGTAAAACGACGGCCAGTGGTCATGTCTTCAGGGCTTAGG	CAGGAAACAGCTATGACCTGCTACCTGGAATGGAAAGACC	1788-9	25320913	25321025	36	DNMT3A	ENST00000264709	NM_022552.2	14	ENSE00001071031	25320913	25321025
0001788_139	25321560	25321758	25321580	25321737	TGTAAAACGACGGCCAGTAGGGAGAGGCCCTTCGGTGG	CAGGAAACAGCTATGACCACACAGTCAGCCAGAAGGCCG	1788-10	25321626	25321705	36	DNMT3A	ENST00000264709	NM_022552.2	13	ENSE00001071029	25321626	25321705
0001788_13i	25322304	25322553	25322326	25322531	TGTAAAACGACGGCCAGTTTATTGATGAGCGCACAAGAGG	CAGGAAACAGCTATGACCTCCATGTCATTCAAACCTTCC	1788-11	25322393	25322437	36	DNMT3A	ENST00000264709	NM_022552.2	12	ENSE00001281442	25322393	25322437
0001788_14h	25322483	25322724	25322506	25322706	TGTAAAACGACGGCCAGTTTCCTGTCAGCCTGTAACTGACC	CAGGAAACAGCTATGACCATGCAGGCCTCCTGGTGC	1788-12	25322533	25322682	36	DNMT3A	ENST00000264709	NM_022552.2	11	ENSE00001071035	25322533	25322682
0001788_12g	25322831	25323218	25322851	25323196	TGTAAAACGACGGCCAGTCTTGAGCCTGACCCATCTGC	CAGGAAACAGCTATGACCGCAGGTCATTCAAGTCCTGACC	1788-13	25322993	25323149	36	DNMT3A	ENST00000264709	NM_022552.2	10	ENSE00001281455	25322993	25323149
0001788_13B	25322981	25323230	25323003	25323208	TGTAAAACGACGGCCAGTACTCAGAGTCTGGCCTTGAGCC	CAGGAAACAGCTATGACCGCCCTCATTTACCTTCTGGTGG	1788-13	25322993	25323149	36	DNMT3A	ENST00000264709	NM_022552.2	10	ENSE00001281455	25322993	25323149
0001788_12s	25323352	25323579	25323374	25323559	TGTAAAACGACGGCCAGTGTGCTTGCAAGTGTAAGCCTCG	CAGGAAACAGCTATGACCCCTGCACTCCAACTTCCAGG	1788-14	25323424	25323531	36	DNMT3A	ENST00000264709	NM_022552.2	9	ENSE00001071033	25323424	25323531
0001788_13n	25323908	25324257	25323930	25324236	TGTAAAACGACGGCCAGTTCTTGCCTCATTCAGATGGAGC	CAGGAAACAGCTATGACCCCTGGGATCAAGAACCTTCCC	1788-15	25323964	25324122	36	DNMT3A	ENST00000264709	NM_022552.2	8	ENSE00001281470	25323964	25324122
0001788_10s	25324321	25324672	25324345	25324649	TGTAAAACGACGGCCAGTCTAATTCCTGGAGAGGTCAAGGTG	CAGGAAACAGCTATGACCAGATGGAGAGAGGAGAGCAGGAC	1788-16	25324410	25324625	36	DNMT3A	ENST00000264709	NM_022552.2	7	ENSE00001071019	25324410	25324625
0001788_13N	25325824	25326217	25325847	25326194	TGTAAAACGACGGCCAGTAAATCTGGTATGGTGGAAATGGG	CAGGAAACAGCTATGACCTGGAGTTCTTATGGATCACACCC	1788-17	25326030	25326097	36	DNMT3A	ENST00000380746	NM_153759.2	2	ENSE00001486123	25326030	25326097
0001788_083	25328395	25328743	25328419	25328719	TGTAAAACGACGGCCAGTACAAAGAAAATGTTCCCTCCCTCC	CAGGAAACAGCTATGACCCCAGCACTAAGTCAGCATCTCCAG	1788-18	25328567	25328687	36	DNMT3A	ENST00000380746	NM_153759.2	1	ENSE00001486094	25328567	25328688
0001788_11Z	25351242	25351541	25351264	25351520	TGTAAAACGACGGCCAGTACATTGTGTTTGAGGCGAGTGC	CAGGAAACAGCTATGACCACTGAGGCCCATCACTTCTGG	1788-19	25351314	25351460	36	DNMT3A	ENST00000264709	NM_022552.2	6	ENSE00000808931	25351314	25351460
H_02_0038m	25351760	25352045	25351783	25352024	TGTAAAACGACGGCCAGTGGATGTGTAAAGAAGGAGGAGGG	CAGGAAACAGCTATGACCGAACAGCTAAACGGCCAGAGG	1788-20	25351873	25351916	36	DNMT3A	ENST00000264709	NM_022552.2	5	ENSE00001486208	25351873	25351916
0001788_11q	25358694	25358988	25358715	25358966	TGTAAAACGACGGCCAGTACTTGGAGAAGCGGAGTGAGC	CAGGAAACAGCTATGACCAAGCAGACCTTTAGCCACGACC	1788-21	25358761	25359084	36	DNMT3A	ENST00000264709	NM_022552.2	4	ENSE00001326003	25358814	25359084
0001788_11W	25358752	25359137	25358775	25359115	TGTAAAACGACGGCCAGTAGGCTAAGCCCACTGATCTAACC	CAGGAAACAGCTATGACCCCTGACTCTCAGGGTATGCTGG	1788-21	25358761	25359084	36	DNMT3A	ENST00000264709	NM_022552.2	4	ENSE00001326003	25358814	25359084
0001788_10P	25376434	25376677	25376455	25376655	TGTAAAACGACGGCCAGTCTGGAATGCTACACTGCTGGG	CAGGAAACAGCTATGACCATACATCACTGCCATCGACAGG	1788-22	25376512	25376616	36	DNMT3A	ENST00000264709	NM_022552.2	3	ENSE00000808934	25376512	25376616
0001788_11m	25390235	25390433	25390259	25390415	TGTAAAACGACGGCCAGTTCCAAAGACCACGATAATTCCTTC	CAGGAAACAGCTATGACCTCCCTCTCCCAGGCCAGA	1788-23	25390286	25390357	36	DNMT3A	ENST00000264709	NM_022552.2	2	ENSE00001408175	25390286	25390534(includes UTR)

The exons highlighted in yellow are from an alternate transcript (ENST00000380746). They are exons 1 and 2 in that transcript (ENST00000380746), but the genomic positions do fall between exons 6 and 7 of the main transcript (ENST00000264709).

Supplementary Table 9. Primers used for DNMT3L sequencing.

Amplicon Name	L Primer Coord	R Primer Coord	L Amp Coord	R Amp Coord	Primer 1 Sequence	Primer 2 Sequence	Target Name +	Target Start	Target Stop	Build	Hugo Name	TranscriptID	Exon#	ExonID	Exon_Start	Exon_Stop	Entrez ID	Chrom
0029947_04B	44505296	44505643	44505316	44505621	TGTAAAACGACGGCCAGTGCATCAGGGATCTGAGCAGG	CAGGAAACAGCTATGACCTGGTGTGTTAAACGCCCATACC	29947-10	44505465	44505570	36	DNMT3L	ENST00000270172	2	ENSE00000952757	44505465	44505577	29947	21
0029947_04D	44505034	44505298	44505056	44505276	TGTAAAACGACGGCCAGTCACCAAGATAAGGTGTGAGGGC	CAGGAAACAGCTATGACCGCTGGGATTATAGGTGTGAGCC	29947-9	44505106	44505150	36	DNMT3L	ENST00000270172	3	ENSE00000952758	44505106	44505150	29947	21
0029947_04F	44505074	44505376	44505096	44505355	TGTAAAACGACGGCCAGTTTCATGCATTATTCAGGCACCC	CAGGAAACAGCTATGACCGTCTGGTGTGGGCCAGTATGC	29947-9	44505106	44505150	36	DNMT3L	ENST00000270172	3	ENSE00000952758	44505106	44505150	29947	21
0029947_04C	44505074	44505296	44505096	44505276	TGTAAAACGACGGCCAGTCACCAAGATAAGGTGTGAGGGC	CAGGAAACAGCTATGACCTCTGGTGTGGGCCAGTATGC	29947-9	44505106	44505150	36	DNMT3L	ENST00000270172	3	ENSE00000952758	44505106	44505150	29947	21
0029947_059	44503802	44504095	44503829	44504073	TGTAAAACGACGGCCAGTTGGCTAAATTTATTCCTAATCGTCTGC	CAGGAAACAGCTATGACCGTAGGATTGGTACCCGTCATCG	29947-8	44503943	44504022	36	DNMT3L	ENST00000270172	4	ENSE00000952759	44503943	44504022	29947	21
0029947_057	44503740	44503947	44503762	44503928	TGTAAAACGACGGCCAGTCATGTAAGGTAGGCAGGGAGGC	CAGGAAACAGCTATGACCCTCACCGGGTGCAATCAGG	29947-7	44503748	44503860	36	DNMT3L	ENST00000270172	5	ENSE00000952760	44503748	44503860	29947	21
0029947_059	44503802	44504095	44503829	44504073	TGTAAAACGACGGCCAGTTGGCTAAATTTATTCCTAATCGTCTGC	CAGGAAACAGCTATGACCGTAGGATTGGTACCCGTCATCG	29947-7	44503748	44503860	36	DNMT3L	ENST00000270172	5	ENSE00000952760	44503748	44503860	29947	21
0029947_038	44503637	44503884	44503657	44503863	TGTAAAACGACGGCCAGTAGCCTTGCTTTGCTCCTTCC	CAGGAAACAGCTATGACCCAGGGAAATCATCCATTTGGG	29947-7	44503748	44503860	36	DNMT3L	ENST00000270172	5	ENSE00000952760	44503748	44503860	29947	21
0029947_04Q	44502773	44503134	44502793	44503114	TGTAAAACGACGGCCAGTCTGGTCTTCCCAAAGGGAGC	CAGGAAACAGCTATGACCAGGGAAGGCCGTAAGTCAGG	29947-6	44502834	44503005	36	DNMT3L	ENST00000270172	6	ENSE00001286863	44502834	44503005	29947	21
0029947_03o	44502771	44503011	44502793	44502991	TGTAAAACGACGGCCAGTGGCCTTAGATGCTACTGCTTCG	CAGGAAACAGCTATGACCAGGGAAGGCCGTAAGTCAGG	29947-6	44502834	44503005	36	DNMT3L	ENST00000270172	6	ENSE00001286863	44502834	44503005	29947	21
0029947_04M	44500254	44500524	44500277	44500505	TGTAAAACGACGGCCAGTAACTCAAGGGCTCTGTAGCCAAG	CAGGAAACAGCTATGACCGGACATCAGCAGTTGGCCG	29947-5	44500378	44500465	36	DNMT3L	ENST00000270172	7	ENSE00001297260	44500378	44500465	29947	21
0029947_04S	44498752	44499116	44498774	44499094	TGTAAAACGACGGCCAGTTGGTAGGAGGGTCCTCTGATCG	CAGGAAACAGCTATGACCGCTGACTCCTGTCAGACCCAGG	29947-4	44498928	44499016	36	DNMT3L	ENST00000270172	8	ENSE00001311957	44498928	44499016	29947	21
0029947_05d	44495835	44496152	44495857	44496130	TGTAAAACGACGGCCAGTCTAGTGGGCTCCACTCCTCAGC	CAGGAAACAGCTATGACCTGACAATTTGCAGTTTCTGCCC	29947-3	44495934	44496009	36	DNMT3L	ENST00000270172	9	ENSE00001291091	44495934	44496009	29947	21
H_21_00elz	44494985	44495378	44495007	44495357	TGTAAAACGACGGCCAGTGCCCTGTACACACCTGGAAACC	CAGGAAACAGCTATGACCCTCAGCCCTTCTCTCAAGCCC	29947-2	44495121	44495260	36	DNMT3L	ENST00000270172	10	ENSE00000952765	44495121	44495260	29947	21
0029947_03P	44493280	44493474	44493298	44493455	TGTAAAACGACGGCCAGTGGCGCTTACCGTCCAGGT	CAGGAAACAGCTATGACCCCGCTTCTGGGTCCATGTT	29947-1	44493337	44493422	36	DNMT3L	ENST00000270172	11	ENSE00000952766	44493337	44493422	29947	21
0029947_03T	44490629	44490993	44490650	44490971	TGTAAAACGACGGCCAGTAACTGAGAGGCAGGCTGTTCC	CAGGAAACAGCTATGACCTCCGAAGAGGAAAGAGACAACG	29947-0	44490708	44490876	36	DNMT3L	ENST00000270172	12	ENSE00000952767	44490651(includes UTR)	44490876	29947	21

Annotation based on Ensembl release 54_36p.