Supplementary Material and Methods

Patients, controls and tissue handling

Fresh frozen lymphoma biopsies were obtained from100 newly diagnosed cases of DLBCL. The diagnoses were based on standard histology and immunphenotyping according to the 2008 WHO lymphoma classification.[1] The fraction of tumor cells was scored, and samples with more than 50% and 80% tumor cells were selected for DNA and RNA extraction, respectively. Peripheral blood B-lymphocytes (PBL-B) were obtained from random, anonymous donors and isolated using CD19+ selection kit on a RoboSep Device (Stemcell). Genomic DNA was isolated after proteinase K digestion using the Purescript DNA Isolation Kit (Gentra Systems). Paraffin-embedded tissue from the same patient with no morphological signs of DLBCL (“normal control tissue”) was used as control material. The allelic frequencies of the lymphoma associated sequence variants were analysed in 500 other alleles from the Danish population. Clinical data were obtained from the patient files and from the Danish lymphoma registry LYFO. All patients were treated with antracyclin containing regimens, however only 21 patients received immunotherapy with Rituximab. Approval of this study was obtained from the regional ethical committee.

Cell lines

Diffuse large B-cell derived lymphoma cell lines: Farage, DB1, HT, RL, and Toledo were purchased from the American Type Culture Collection (ATCC). The cells were cultured in RPMI 1640 medium with Glutamax supplemented with 10% fetal calf serum.

Mutation detection

Detection of TET2 mutations

The melting characteristics of each exonic region were calculated and appropriate GC- and AT-clamps were included in the PCR primers to modulate the melting properties into a two-domain profile.[2] For *TET2* sequences, PCR was performed in 15-µL reactions containing 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 1.5 mM $MgCl_2$, 0.2 mM cresol red, 12% sucrose, 10 pmol of each primer, 100 µM each dNTP, 10 ng of genomic DNA, and 0.8 units of hot-star Taq polymerase. PCR conditions were 38 cycles at 95°C for 20 seconds, 55-62°C for 20 seconds, and 72°C for 30 seconds. PCR products were analyzed in a 10% denaturant/6% polyacrylamide-70% denaturant/12% polyacrylamide double-gradient gel. The gels were run at 170 V for 4-5 hours in 1× TAE buffer kept at a constant temperature of 55-58°C, stained with ethidium bromide, and photographed under UV transillumination. Automated Sanger sequence analysis of aberrant DGGE bands was performed with non-clamped primers (Eurofins, MWG).

Detection of mutations in potential DNA methylation regulators *IDH1*, *IDH2* and *DNMT3A*

The genomic region that encodes the DNA methylation regulators *IDH1*, *IDH2* and *DNMT3A*, which have frequently been shown to be mutated in myeloid cancers (*IDH1* R132 and *IDH2* R140 and R172 and *DNMT3A* exons 20-22), were scanned for mutations using DGGE and direct sequencing (for details see Supplementary Table 1b).

DNA methylation analysis

Data filtering and normalization of DNA methylation

Infinium probes that failed in any of the samples were excluded from the analysis. Probes corresponding to X and Y chromosomes and those containing a single nucleotide polymorphism

(SNP) or containing a repetitive element within five base pairs of targeted CpG sites were excluded. Since the primary aim of the current study was to identify signature genes which can differentiate *TET2*mut from *TET2*wt, we excluded probes in *TET2*wt samples which were constitutively methylated (β-value ≥ 0.2) while most variable probes with Sd >0.3 were retained for further analysis.

Bioinformatic analysis of DNA methylation data

Hierarchial clustering was used to classify samples into various groups as described previously.[3] All data visualization as well as statistical analysis was performed in R software environment except as noted. For differential methylation analysis various criterias have been described in the litterature and no consensus methods have been reported. Therefore, we used a stringent method of detecting differential methylation in our study, based on (1) a mean β-value difference ≥ 0.2 between *TET2*mut and *TET2*wt samples,[4-6] (2) a false discovery rate <0.05 calculated by using a two way t-test and correcting raw p values for multiple hypothesis using a linear step up method of Benjamini and Hochberg (BH).[7] Thereby, a set of 597 probes were identified which had β-value difference ≥ 0.2. Of these, 578 probes showed a BH adjusted $p<0.05$ (Supplementary Table 2) and were selected for further analysis.

A similar separation of strongly hypermethylated *TET2*mut and *TET2*wt samples was confirmed by RPMM and K means consensus clustering using the 578 differentially methylated probes (data not shown).

To overlap the differentially methylated probes from the array with distinct histone lysine methyltransferase targets, ChIP-seq data corresponding to trimethylation of histone H3 lysine 4 (H3K4me3) and histone H3 lysine 27 (H3K27me3) in human embryonic stem cells (hESCs) was downloaded from ENCODE (GSM 33748 and GSM33657), and coordinates of ChIP-seq peaks with adjusted $p<0.01$ were mapped to the 450K probe locations. A value computed by Fisher's exact test was used to test the statistical significance of enrichment of loci in our experiment to either histon mark compared to the total number of loci mapping to these marks on the 450K plateform.

Pathway and meta-analysis

Functional interpretation of significantly differentially expressed genes was analyzed in the context of gene ontology and molecular networks by using Ingenuity pathway software (IPA; www.ingenuity.com). Differentially methylated genes were uploaded to IPA, which categorizes genes into various closely related functional groups (threshold $p<0.05$) as well as mapped to genetic networks. This functional analysis of dataset suggests the most important disease or biological function associated with the dataset. Fisher's exact test was used to calculate the p-values determining the probability of that each biological function and /or disease is due to a chance. In addition, differentially methylated genes were also mapped to genetic networks based upon the published genes associated with various networks. The significance of the association between genes from our datset and various networks was measured by two ways as detailed in IPA documentation. Briefly, (A) a ratio was calculated of the number of genes from the dataset in a given pathway divided by the total number of molecules that make up that particular network; (B) Pathways of highly interconnected genes were identified by a statistical likelihood method as described[8]. We considered the networks with a stringent score greater than 15 (p value< 0.01) statistically significant.

Verification of differentially methylated regions (DMR) by Methylation-Specific Melting Curve Analysis (MsMCA)

The methylation status of selected DMRs was examined by MsMCA.[9] DNA treated *in vitro* with *SssI* methyltransferase (New England Biolabs) was used as a positive control for methylated alleles, and purified CD19+ B-cell was used as normal controls (primers in Supplementary Table 1c).

Gene expression profiling

RNA from 4 *TET2*mut (G7, G11, G12, G15) and 5 *TET2*wt samples (G2, G18, G26, G28, G33) with > 80% tumor cells were isolated using standard RNAeasy kit protocol (Qiagen). RNA was then processed and hybridized to Affymetrix Gene 1.0 ST arrays (Affymetrix) providing whole transcript coverage of 28.869 genes.

The probe cell intensity data from Affymetrix Gene Chip was extracted as CEL files. The signal intensities from CEL files were extracted using PLIER 16 (Probe logarithmic intensity Error) algorithm and data was quantile normalized. Wilcoxon Rank sum test was used to calculate the differential expression between *TET2*wt and *TET2*mut samples.

Keeping in view the complex gene expression profiles associated with DLBCL and challenges in separation of tumor cells in patient samples[10,11] it has been reported that a fold change of as low as 1.1 [12]or 1.2 fold[13] is optimal. However, in order to have optimal gene expression overview of the microarray data[11] we have used two stringent criteria to call differentially expressed genes: At least a subtle fold change of 1.2 and a differential FDR corrected $p<0.01$.

Data accessibility

The data has been submitted to NCBI GEO with GSE37362 (DNA methylation) GSE37363 (Gene expression).

Integrated analysis of gene expression and DNA methylation

The gene expression and DNA methylation data were linked by Entrez gene Ids. Genes with multiple expression probe sets were identified, and a mean normalized fluorescence of all probes corresponding to one gene was used for further analysis. For genes with multiple probes for DNA methylation a median β-value was used to calculate differential methylation per gene between *TET2*mut and *TET2*wt samples. We used a mean β-value difference ($|\Delta\beta|$) of 0.2 as a threshold for differential DNA methylation between *TET2*mut and *TET2*wt samples as detailed above. Similarly, genes showing a subtle fold change > 1.2 and $p < 0.05$ were considered as differentially expressed.

Statistics of clinical data

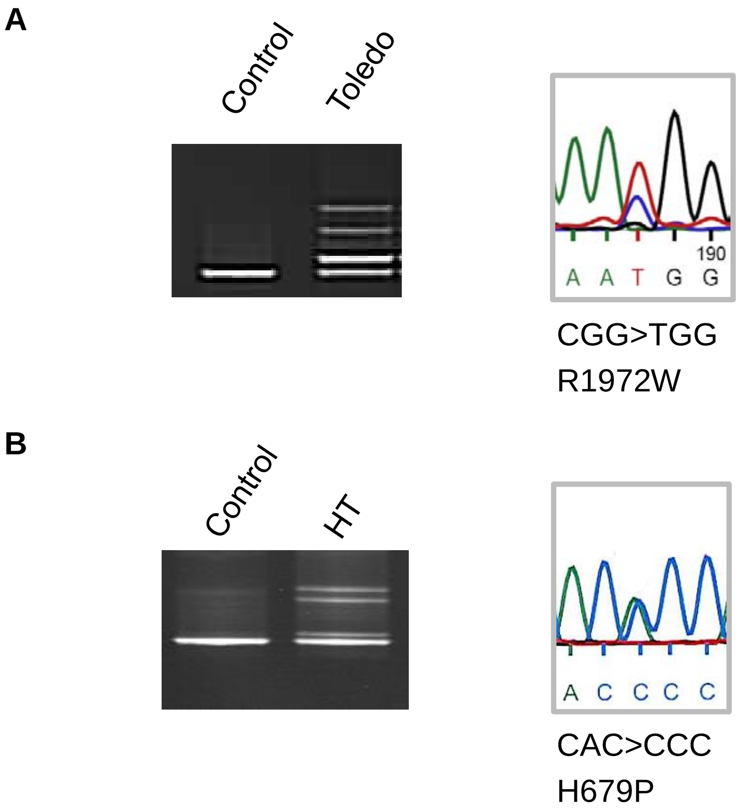
Differences in clinical characteristics of patients with or without mutation of *TET2* were assessed using the Pearson chi-square, Fisher's exact test or One-Way Anova. Overall survival was estimated using the Kaplan-Meier method. Statistical analyses were performed in SPSS 19.0 for Windows (SPSS Inc.) Any differences were considered to be statistically significant when the P value was < 0.05.

Reference List

1. Swerdlow SH. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues. Lyon: IARC press; 2008.
2. Lerman LS, Silverstein K. Computational simulation of DNA melting and its application to denaturing gradient gel electrophoresis. Methods Enzymol. 1987;155:482-501:482-501.
3. Houseman EA, Christensen BC, Yeh RF, Marsit CJ, Karagas MR, Wrensch M et al. Model-based clustering of DNA methylation array data: a recursive-partitioning algorithm for high-dimensional data arising as a mixture of beta distributions. BMC Bioinformatics. 2008;9:365.
4. Bibikova M, Lin Z, Zhou L, Chudin E, Garcia EW, Wu B et al. High-throughput DNA methylation profiling using universal bead arrays. Genome Res. 2006;16(3):383-93.
5. Hinoue T, Weisenberger DJ, Lange CP, Shen H, Byun HM, Van Den Berg D et al. Genome-scale analysis of aberrant DNA methylation in colorectal cancer. Genome Res. 2012;22(2):271-82.
6. Etcheverry A, Aubry M, de TM, Vauleon E, Boniface R, Guenot F et al. DNA methylation in glioblastoma: impact on gene expression and clinical outcome. BMC Genomics. 2010;11:701.
7. Perez C, Martinez-Calle N, Martin-Subero JI, Segura V, Delabesse E, Fernandez-Mercado M et al. TET2 mutations are associated with specific 5-methylcytosine and 5-

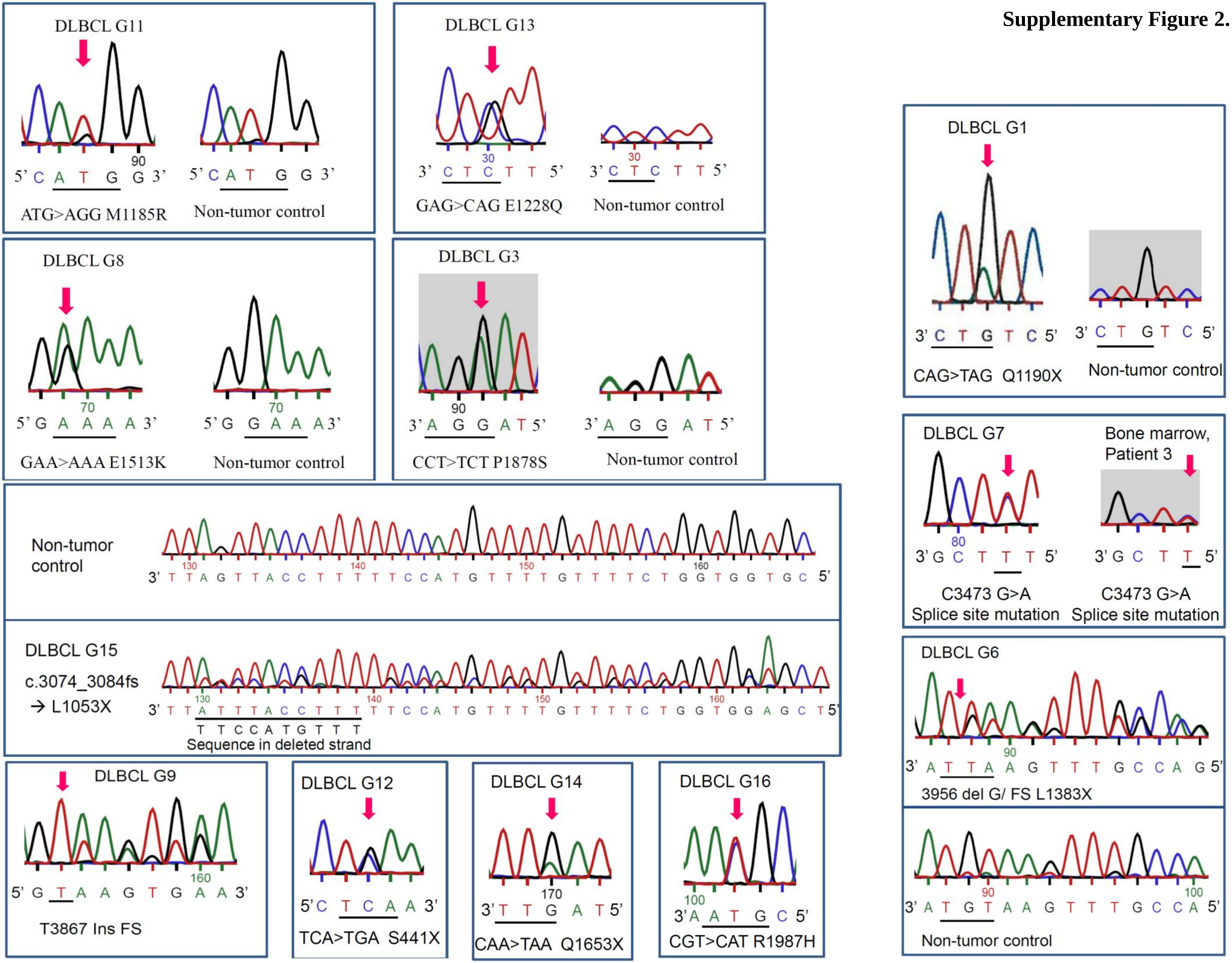
hydroxymethylcytosine profiles in patients with chronic myelomonocytic leukemia. PLoS One. 2012;7(2):e31605.

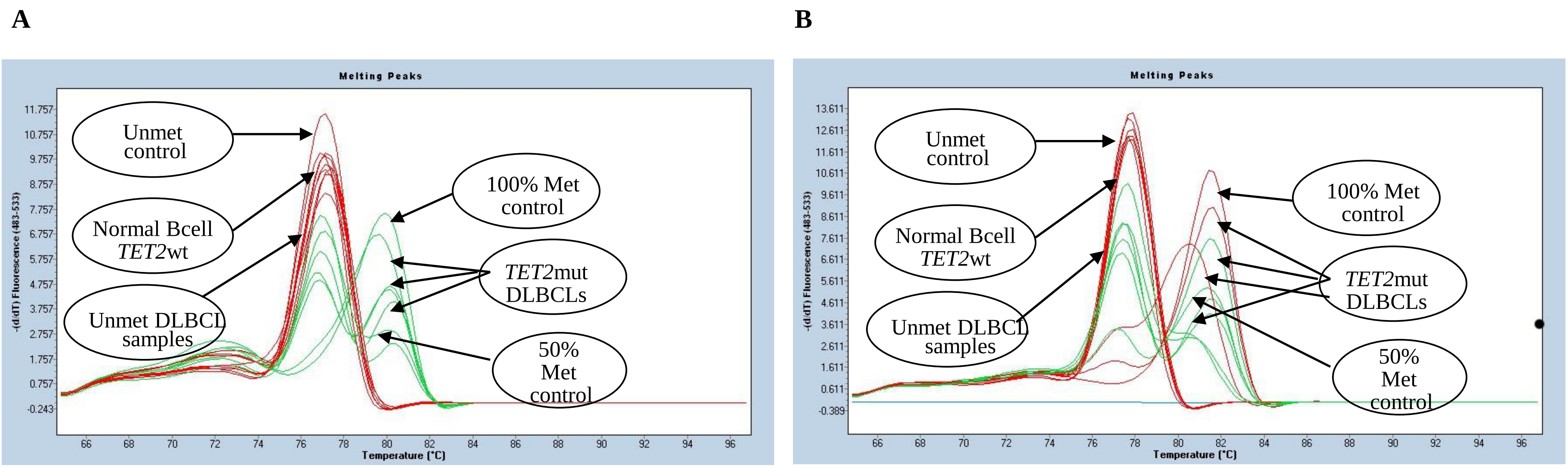
8. Nakou M, Bertsias G, Stagakis I, Centola M, Tassiulas I, Hatziapostolou M et al. Gene network analysis of bone marrow mononuclear cells reveals activation of multiple kinase pathways in human systemic lupus erythematosus. PLoS One. 2010;5(10):e13351.
9. Guldberg P, Worm J, Grønbæk K. Profiling DNA methylation by melting analysis. Methods. 2002;27(2):121-7.
10. Alizadeh AA, Eisen MB, Davis RE, Ma C, Lossos IS, Rosenwald A et al. Distinct types of diffuse large B-cell lymphoma identified by gene expression profiling. Nature. 2000;403(6769):503-11.
11. Miller LD, Long PM, Wong L, Mukherjee S, McShane LM, Liu ET. Optimal gene expression analysis by microarrays. Cancer Cell. 2002;2(5):353-61.
12. Booman M, Douwes J, Glas AM, Riemersma SA, Jordanova ES, Kok K et al. Mechanisms and effects of loss of human leukocyte antigen class II expression in immune-privileged site-associated B-cell lymphoma. Clin Cancer Res. 2006;12(9):2698-705.
13. Gustavsson E, Sernbo S, Andersson E, Brennan DJ, Dictor M, Jerkeman M et al. SOX11 expression correlates to promoter methylation and regulates tumor growth in hematopoietic malignancies. Mol Cancer. 2010;9:187.



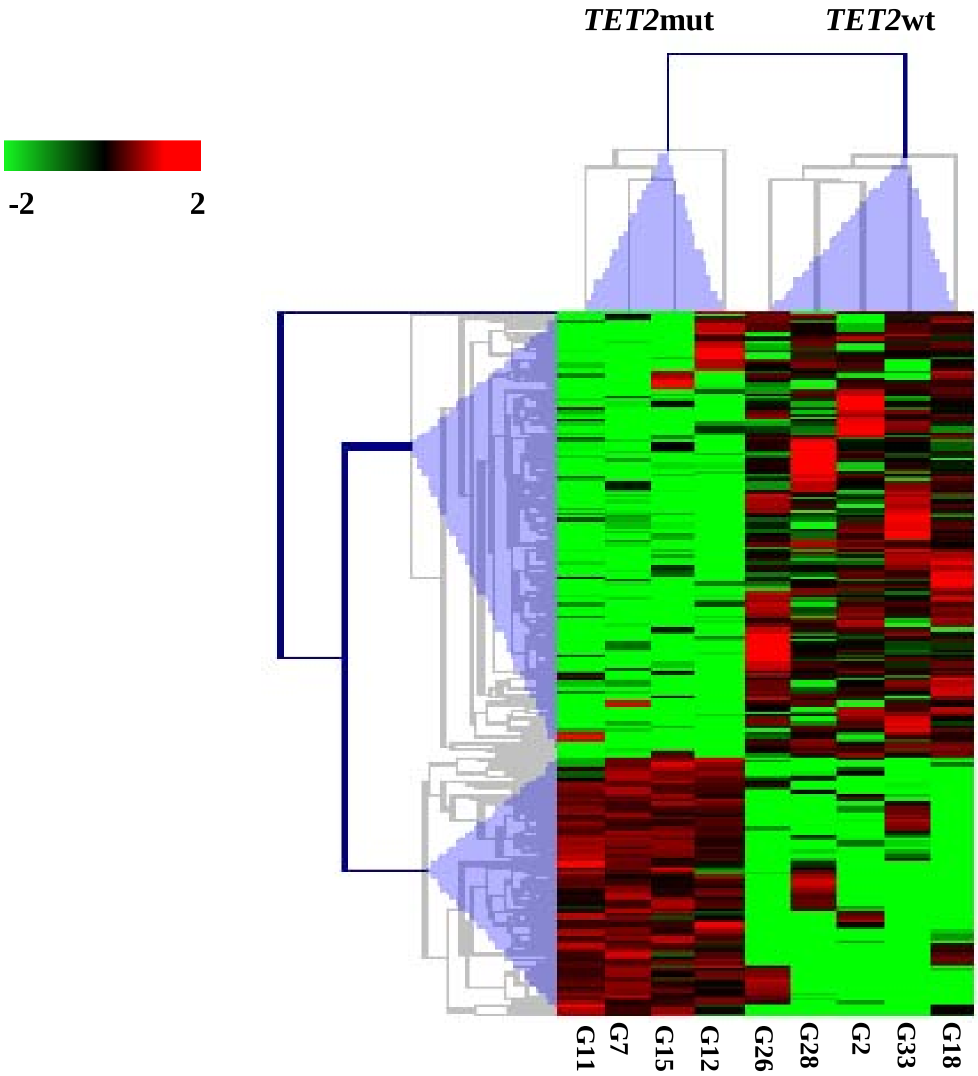
Supplementary Figure 1. *TET2* point mutations in DLBCL cell lines
Two of 5 DLBCL cell lines carried *TET2* missense mutations.
(A) DGGE and sequencing in the Toledo cell line caused by the R1972W substitution. **(B)** DGGE and sequencing in HT cell line caused by the H679P substitution.

Supplementary Figure 2.

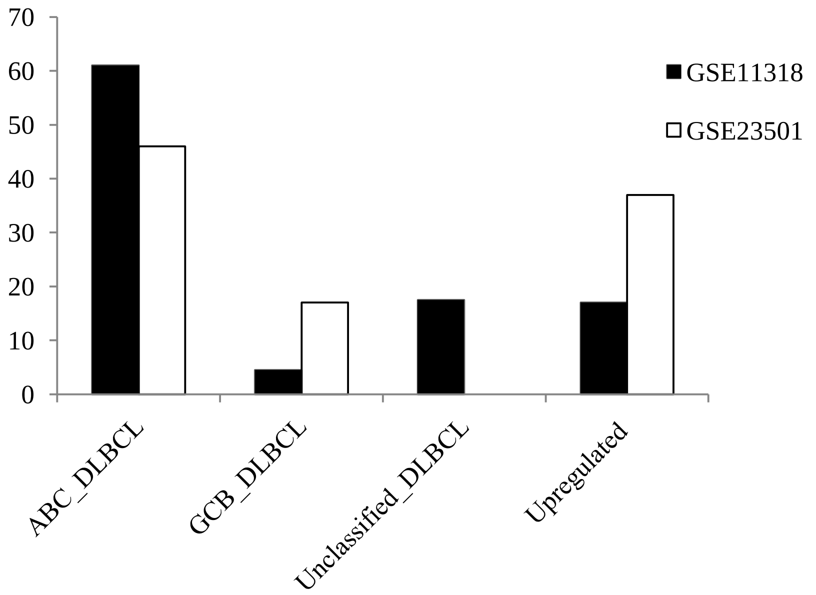




Supplementary Figure 3. Validation of methylation array data by MSMCA
Methylation status of *TET2* signature genes was examined by MSMCA and two examples, (A) F*oxc1* and (B) *Ephb1*, are shown here. *Sss* I was used as a positive control for methylated genes and purified CD19+ B-cells as normal controls.

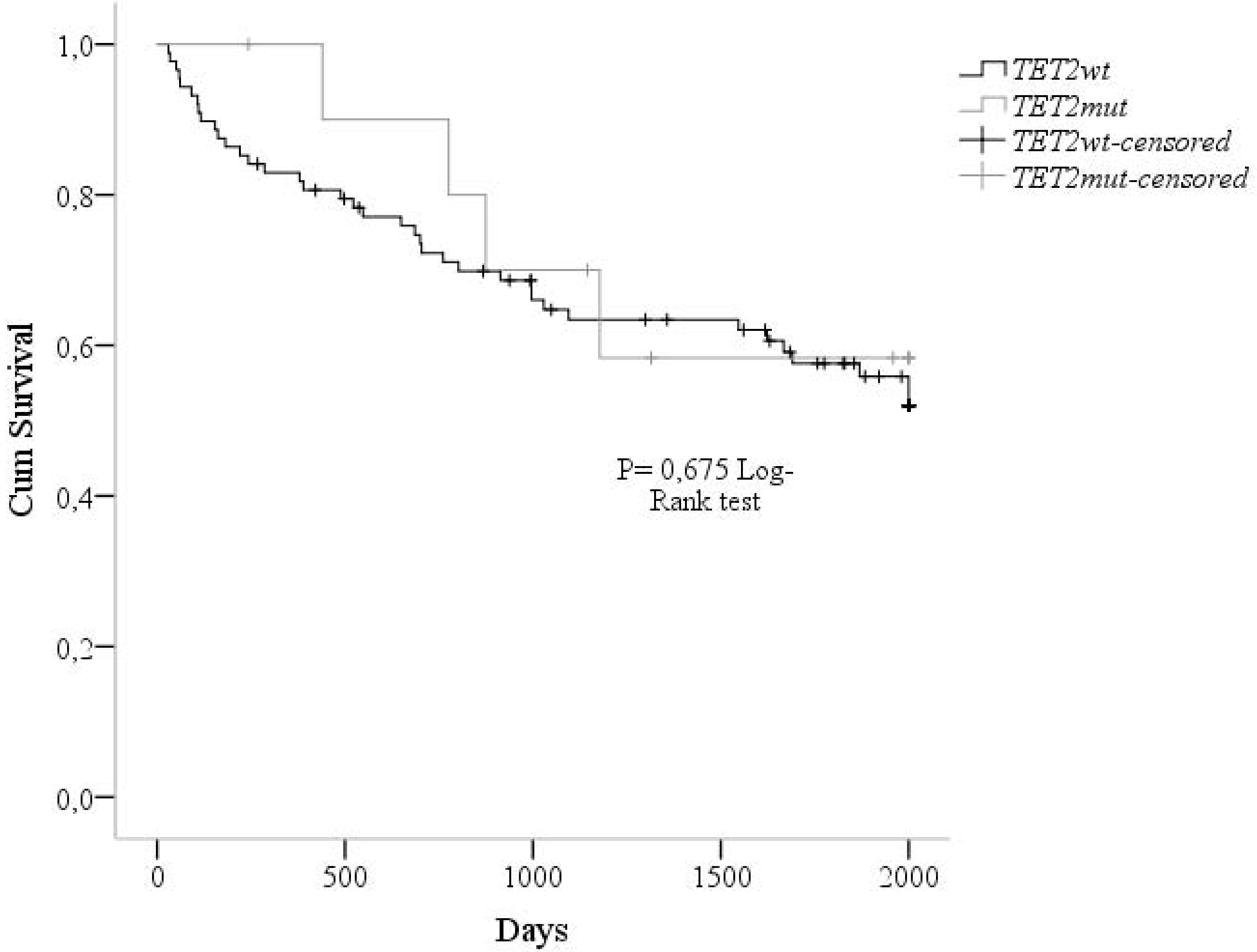


Supplementary Figure 4. Hiearchical clustering of differentially expressed genes among *TET2*mut (G7, G11, G12, G15) versus *TET2*wt samples (G2, G26, G28, G33, G18) (fold change >1.2 and p<0.01).



Supplementary Figure 5. GSEA of the 35 hypermethylated and downregulated genes in *TET2*mut samples with comparison to previous published gene expression array data from GEO GSE11318 and GSE23501.

31 of the genes were found to be present in each data set. A total of 23 (GSE11318) and 24 (GSE23501) genes that showed a subtle expression fold change >1.2 were merged with the genes from Supplementary Table 4 based on Entrez gene ids. Enrichment of genes identified in our study was observed in the ABC subgroup of DLBCL samples



Supplementary Figure 6. Overall survival data for *TET2*mut and *TET2*wt DLBCL patients. Cumulative survival analysis showed no statistical difference in overall survival between patients with *TET2*mut (N= 11, clinical data is missing for 1 patient) and *TET2*wt (N= 88) DLBCLs (P= 0,675, Log-Rank test).

Supplementary Table 1: List of primers

Supplementary Table 1a: DGGE primers for mutation analysis

Exon	Forward primer sequence (5’→3’)	Reverse primer sequence (5’→3’)	Product length (bp)
3_1	CCTTGTGGATGGCCCCGA	40[CG]CGACTATTCTGGCTTCCCTTCATACA	286
3_2	[10CG]CAAAAGTTATTATGGAATACCC	[40CG][10AT]TCTTTCTTGGCTTACCCC	283
3_3	[7CG]TGAAACAAGACCAAAAGGCTAATG	[40CG]TTTTCAGGCCCACTGCAGTTA	240
3_4	[40CG]AGTGATAAGAAAGAATCTGTGAGTT	GACAGTGTTTTTTCCAGGAGT	300
3_5	[40CG]TCCGTGGAACACACACATGGT	CAGCTGGCTTTGGAGGCAG	260
3_6	TCCGCACAGACCTCTAACTC	[40CG]GTTGTTGTAGTTGTTCTGGTTTCT	188
3_7	[40CG]GCAATGCTAAATACCTGTTCC	TTTTGTTTTAAATACCGTTCAGA	237
3_8	[40CG]TGCAAGCTCCTGGTGGCAG	TCTGAAGGAAGCTGAGGAACCTG	224
3_9	[40CG][13AT]CTCCCCCTCCTCCTCTTCC	[7CG]GCCTTTCAGAAAGCATCGGA	278
3_10	[40CG]CTACACATGTATGCAGCCCTT	AAGATCTCGTGTTTGCTCCTT	300
3_11	AAGGAGCAAACACGAGA	[40CG]GTAAGCTTGCCTTGGGAGC	265
3_12	CTGGAAATTCCAACATGCCT	[40CG]TGCTCTTTGTTGAAAATGAAATCT	285
3_13	[40CG]ATGTGCAGTCACTGTGTGGC	TTCTTTATTTGTAATTTTTGCTGCT	281
3_14	[40CG]TCTCCCTCAAAACCAGCAA	TTATATTCTGTACTTCCTCCAGTCC	267
3_15	[40CG][14AT]TTCGAGACTCATAATGTCCAAA	CACATTATTTGGAAAATATTGCA	282
3_16	[40CG]AAGACCCAAAACTTGCATCAC	AGTGTGACTTCCTCCCTGGTC	282
3_17	TGCAAATGTTTTTCCTGTGC	[40CG]GTTACCTTTTTCCATGTTTTGTT	289
3_18	[40CG]GCACACAGCACCACCAGA	[11CG]CTGACATTTCAACTTTTACTT	253
3_19	[7CG]ACCATAAGGCTCTTACTCTCAAA	[40CG]GAGTATCTAGTAATTTGGAAGGTGA	266
3_20	CAGCTGCTTCTGTTCTCAATAA	[40CG]TGTGTCTCAGTACATTTCTGGC	191
4	[40CG]ATTGAGGTCTAAGATAATAATCTTCTA	CTGTGCCTTTGCGTTAAT	191
5	[40CG][11AT]GTGTGTTTCTGTGGGTTTCT	AAAGGCTTTATCAAGTCACAC	197
6_1	[40CG]GTGTTTGGGATGGAATGGTGA	CAATCACTGCAGCCTCACAGG	155
6_2	TACTGTGTTTGGTGCGGGAGC	[40CG][9AT]GAGAGGCCCTGGGCTTCACTT	249
7	AATGAATTTGGTCTTTTGATT	[40CG]AAAAATAAAGCGATTATACATCA	255
8	[12CG]ATTTAATATGTAGAATTATTCACTTTA	[40CG]GCTGCCAATGATTATTTAAA	199

9	[40CG]CGCATTCACACACACTTTTATTT	GCCTTCCTTCAGACCCAGA	119
10_1	[40CG][6AT]AGGCTGTAATGTCTTACTTCCCT	GCTTTCTTGGCTTCTAGTTTCC	313
10_2	GAGCCAGTCAAGACTTGCC	[40CG]TTATCTACAAATGCTTTACATTAAATT	233
11_1	[40CG]TTCTGTTCTCTCTTACCCTGTC	[16CG]AGCAGAATAAGAGTTGACAGACT	232
11_2	AGCCACATCACCCTCAGAC	[40CG]CATTGCATTGATATGATGGATAT	301
11_3	[40CG]CTGGGCTTTTGAATCAGAA	[11CG]CTAAATACTTAGGTTATGGAA	288
11_4	[40CG]GGAAATAGCCAGAGTTTTACA	[8CG]TTCACCATTTTTATAGTCCATG	264
11_5	[40CG]CCCAATCTGAGCAATCCAA	CATGTCATTCTCCTTGTTTTGG	184
11_6	[40CG] TCTCTTCATGCCCTGCATC	TGACCAGACCTCATCGTTGT	259
11_7	GTGTGGCTTCTGGTGCAGAG	[40CG]TCCTGGTGGGGTGATTCCTA	225
11_8	[40CG]CCACAACCCCTTTAAAGAATC	GATGAAACGCAGGTAAGTGG	300
11_9	GAGCCACATGAAACTTCAGAG	[40CG]ACCAACAAAAGGGGGTGAT	207

[7CG]= CCCGCCC
[8CG]= CCCGCCCG
[10CG]= CCCGCCCGCC
[11CG]= CCCGCCCGCCG
[12CG]= CCCGCCCGCCCG
[40CG]= CGCCCGCCGCGCCCCGCGCCCGTCCCGCCGCCCCCGCCCG
[40GC]= GCGGGCGGCGCGGGGCGCGGGCAGGGCGGCGGGGGCGGGC

[6AT]= AAATAA
[10AT]= AAATAAATAA
[13AT]= AAATAAATAAAAT
[14AT]= TAAATAAATAAATT

Supplementary Table 1b:
DGGE Primers for mutation analysis of *IDH1* R132, *IDH2* R140,R172, *DNMT3A* exons 20-22

	Forward primer sequence (5’→3’)	Reverse primer sequence (5’→3’)	Product length (bp)
IDH1	AAATATTCTGGGTGGCACGGT	[40CG][4AT]AAAAAAACATGCAAAATCACATTATTG	200
IDH2	[40CG]GAAGAAGATGTGGAAAAGTCCC	GATCCCCTCTCCACCCTG	215
DNMT3A_20	[40CG][6AT]CTCCTTGGCTCATCTTCAAAC	AGGCCCAGGAGCTTTCAC	192
DNMT3A_21	[40CG]CTGTTATCCAGGTTTCTGTTGTTAC	CCCAGCAGAGGTTCTAGACG	187
DNMT3A_22	[40CG]CTTATTCCTCTTTTCTCCTCTTCA	CAGATGCCAGCACAACCC	210

Supplementary Table 1c: Primers for MsMCA

	Forward primer sequence (5’→3’)	Reverse primer sequence (5’→3’)	Product length (bp)
FOXC1	GGGTAGAGTTTTTTGGAAGG	ACAAACCCCCTTACAAAAACT	125
EPHB1	ATGGTTTTGGATTATTTATTATTGT	CAAAACAACCAAAAAAACCC	152

Supplementary Table 2: List of differentially methylated probes in *TET2*wt and *TET2*mut samples along with their histone mark status.

Probe Id	CpG Island*	CpG Island location	Neighboring Gene**	p-value	BH-adjusted p-value	hESC-H3k27me3$^{\$}$	hESC-H3k4me3$^{\$}$
cg18749015	TRUE	chr6:45630986-45631814	No	1.77E-05	0.00363	1	1
cg13384781	TRUE	chr10:102414425-102416315	No	2.51E-05	0.00363	1	1
cg12918895	TRUE	chr4:3464799-3465440	YES	7.76E-06	0.00363	1	1
cg08508041	TRUE	chr2:172959267-172962054	No	2.46E-05	0.00363	1	1
cg03551456	TRUE	chr11:35965642-35966454	YES	3.53E-05	0.00363	1	1
cg03425110	TRUE	chr10:71331926-71333392	YES	4.26E-05	0.00363	1	1
cg00654814	TRUE	chr17:74864170-74866657	YES	4.11E-05	0.00363	0	1
cg16410656	TRUE	chr11:35965642-35966454	YES	4.91E-05	0.00367	1	1
cg25237365	TRUE	chr4:3464799-3465440	YES	0.000124	0.00825	1	1
cg16195091	TRUE	chr17:76228110-76228380	YES	0.000307	0.01763	1	1
cg11987534	TRUE	chr2:172959267-172962054	No	0.000352	0.01763	1	1
cg05886671	TRUE	chr10:71331926-71333392	YES	0.000354	0.01763	0	1
cg22959667	TRUE	chr2:109744585-109746833	No	0.000524	0.01795	0	1
cg20472551	TRUE	chr4:150999250-151000706	YES	0.000511	0.01795	0	1
cg18466859	TRUE	chr14:91282227-91282757	YES	0.00059	0.01795	1	1
cg17960516	TRUE	chr4:3464799-3465440	YES	0.000632	0.01795	0	0
cg11685394	TRUE	chr19:49631105-49631494	YES	0.000589	0.01795	1	1
cg06905823	TRUE	chr22:39638219-39640966	YES	0.000623	0.01795	1	1
cg03840647	TRUE	chr14:36974548-36975425	YES	0.000574	0.01795	1	1
cg03108139	TRUE	chr7:155164557-155167854	No	0.000432	0.01795	0	1
cg02771661	TRUE	chr12:49371690-49375550	YES	0.000604	0.01795	1	0
cg26942121	FALSE		YES	0.001098	0.01843	0	1
cg24768078	FALSE		YES	0.001036	0.01843	1	1
cg23834013	FALSE		YES	0.001066	0.01843	0	1
cg23042796	TRUE	chr2:89064493-89065513	YES	0.000889	0.01843	1	1
cg20132273	TRUE	chr13:49549822-49551042	YES	0.000936	0.01843	0	1
cg17328659	TRUE	chr16:729438-735815	YES	0.001003	0.01843	1	1

cg13726682	TRUE	chr17:29718230-29719291	YES	0.00107	0.01843	0	1
cg12349858	TRUE	chr3:160822494-160823260	YES	0.000803	0.01843	0	1
cg10962535	TRUE	chr19:3933473-3933816	YES	0.001103	0.01843	0	1
cg06073351	TRUE	chr10:22623350-22625875	No	0.000989	0.01843	0	1
cg04184836	TRUE	chr15:83315116-83317541	YES	0.000693	0.01843	1	1
cg03772064	FALSE		No	0.001099	0.01843	0	1
cg03543495	TRUE	chr11:94276894-94278913	YES	0.000829	0.01843	1	1
cg02400449	TRUE	chr22:38857573-38857860	No	0.001111	0.01843	1	1
cg01645753	TRUE	chr15:83315116-83317541	YES	0.000873	0.01843	0	1
cg04569837	TRUE	chr5:60921534-60922472	No	0.001146	0.0185	0	1
cg12107018	FALSE		No	0.001321	0.02075	1	1
cg21158501	TRUE	chr8:7537626-7538267	No	0.001444	0.02172	1	1
cg03623155	TRUE	chr15:90319583-90320476	YES	0.001481	0.02172	1	1
cg00447682	TRUE	chr1:20810462-20813511	YES	0.001492	0.02172	0	1
cg23757738	TRUE	chr4:3464799-3465440	YES	0.001723	0.02182	1	1
cg20252022	TRUE	chr12:77272632-77273216	YES	0.001597	0.02182	1	1
cg19935945	TRUE	chr11:44337697-44338783	No	0.001791	0.02182	1	1
cg16574134	TRUE	chr10:102590122-102590402	YES	0.001705	0.02182	1	1
cg11502597	FALSE		YES	0.001651	0.02182	1	1
cg08946731	TRUE	chr7:32981938-32982865	YES	0.001786	0.02182	1	1
cg04770088	FALSE		No	0.001651	0.02182	0	1
cg03467580	TRUE	chr3:42695528-42696575	YES	0.001736	0.02182	1	1
cg26361329	TRUE	chr1:246887264-246888028	YES	0.002001	0.02199	0	1
cg18022777	TRUE	chr2:30142831-30144624	YES	0.001961	0.02199	1	0
cg16043144	TRUE	chr15:83315116-83317541	YES	0.00191	0.02199	1	0
cg13497475	TRUE	chr15:73976559-73977323	YES	0.002043	0.02199	1	1
cg09060908	TRUE	chr1:223741965-223744525	YES	0.001862	0.02199	0	1
cg08552042	TRUE	chr16:58058712-58058928	YES	0.00192	0.02199	1	1
cg05226061	TRUE	chr17:37307498-37307775	YES	0.002063	0.02199	1	1
cg14124788	TRUE	chr12:100378243-100378582	YES	0.002134	0.02235	1	1
cg23837867	TRUE	chr2:219848919-219850541	YES	0.002406	0.02304	1	1

cg21755725	TRUE	chr19:50708601-50708855	YES	0.002446	0.02304	1	0
cg21565130	TRUE	chr11:125365137-125366319	YES	0.0023	0.02304	0	1
cg13861122	FALSE		No	0.002509	0.02304	0	1
cg12322132	TRUE	chr11:2165135-2165672	No	0.002314	0.02304	1	1
cg04480386	FALSE		YES	0.00239	0.02304	1	1
cg03061435	TRUE	chr1:205537751-205538443	YES	0.002489	0.02304	1	1
cg00643111	TRUE	chr16:31483276-31483646	YES	0.00248	0.02304	0	1
cg09983897	TRUE	chr16:31483276-31483646	YES	0.002608	0.02357	0	1
cg01915994	TRUE	chr3:134514085-134515980	YES	0.002645	0.02357	1	1
cg18084798	TRUE	chr19:33555246-33556431	YES	0.00271	0.02359	0	1
cg15313459	TRUE	chr2:68546339-68547111	YES	0.002766	0.02359	1	1
cg06945523	TRUE	chr14:36974548-36975425	YES	0.002754	0.02359	0	0
cg27583307	TRUE	chr2:200320502-200329681	YES	0.003291	0.0237	1	1
cg22973789	TRUE	chr2:200320502-200329681	YES	0.003092	0.0237	0	1
cg22802813	TRUE	chr12:95941906-95942979	YES	0.003295	0.0237	0	1
cg22020558	TRUE	chr14:103589353-103590246	No	0.002999	0.0237	0	1
cg21485895	TRUE	chr2:200320502-200329681	YES	0.003202	0.0237	1	1
cg08074820	TRUE	chr20:2732746-2733630	YES	0.003247	0.0237	0	1
cg07988060	FALSE		No	0.003035	0.0237	1	1
cg05671070	TRUE	chr10:8091374-8098329	No	0.002971	0.0237	1	1
cg02433671	TRUE	chr19:11529722-11529966	YES	0.003262	0.0237	1	1
cg02384857	TRUE	chr7:27198182-27198514	YES	0.003272	0.0237	0	1
cg01297357	TRUE	chr12:50451197-50451943	YES	0.003059	0.0237	0	1
cg00925096	TRUE	chr7:16460778-16461265	YES	0.002828	0.0237	1	1
cg00029353	TRUE	chr12:52240772-52242547	No	0.003199	0.0237	1	1
cg25849196	TRUE	chr2:175199463-175202639	No	0.003464	0.02384	1	1
cg23773252	FALSE		YES	0.003475	0.02384	1	1
cg06407634	TRUE	chr20:33460430-33460866	YES	0.003362	0.02384	1	1
cg03585778	TRUE	chr1:205537751-205538443	YES	0.003471	0.02384	0	1
cg26062223	TRUE	chr6:168771137-168771640	No	0.003732	0.02425	1	0
cg24060037	TRUE	chr1:210405952-210407250	No	0.003667	0.02425	0	1

cg17780624	TRUE	chr2:172949242-172950126	YES	0.003818	0.02425	0	1
cg15075170	TRUE	chr9:103235171-103236627	YES	0.00365	0.02425	1	1
cg13279566	TRUE	chr3:160822494-160823260	YES	0.00368	0.02425	1	1
cg08181610	TRUE	chr8:144510850-144513957	YES	0.003789	0.02425	0	1
cg00229245	TRUE	chr4:150999250-151000706	YES	0.003812	0.02425	0	1
cg18247307	TRUE	chr7:16460778-16461265	YES	0.003864	0.02428	0	1
cg26870725	TRUE	chr19:12978359-12978785	YES	0.004216	0.02454	1	1
cg24199599	TRUE	chr20:62681074-62681332	YES	0.004249	0.02454	1	0
cg21486470	TRUE	chr14:103010784-103011625	No	0.003991	0.02454	1	0
cg20045888	TRUE	chr4:150999250-151000706	YES	0.00423	0.02454	1	0
cg19846700	TRUE	chr12:56472792-56474393	YES	0.004231	0.02454	1	1
cg18039789	FALSE		YES	0.004275	0.02454	1	1
cg16805994	TRUE	chr7:14029378-14029593	YES	0.004124	0.02454	0	0
cg16534499	FALSE		YES	0.004114	0.02454	1	1
cg07282889	TRUE	chr15:89910521-89912177	No	0.004006	0.02454	1	1
cg27031435	TRUE	chr15:37403042-37403267	No	0.00569	0.02469	1	1
cg27004639	TRUE	chr14:91282227-91282757	YES	0.005592	0.02469	0	1
cg26880187	TRUE	chr12:56472792-56474393	YES	0.006874	0.02469	1	1
cg26650731	TRUE	chr11:46354091-46355190	YES	0.00563	0.02469	1	1
cg25876656	TRUE	chr1:210407401-210407637	No	0.008203	0.02469	1	1
cg25601136	TRUE	chr1:21766272-21767224	YES	0.005456	0.02469	1	1
cg25489169	TRUE	chr17:46690390-46691055	YES	0.006249	0.02469	0	1
cg25296343	TRUE	chr19:49865341-49865690	YES	0.008436	0.02469	1	1
cg24361162	TRUE	chr1:156358050-156358252	No	0.006105	0.02469	1	1
cg23708337	FALSE		No	0.007159	0.02469	1	1
cg23531640	FALSE		YES	0.005906	0.02469	1	1
cg23214755	TRUE	chr2:11605743-11606385	YES	0.00685	0.02469	1	1
cg23177772	TRUE	chr2:223170486-223171140	No	0.00536	0.02469	1	1
cg23140554	TRUE	chr4:150999250-151000706	YES	0.004667	0.02469	0	1
cg23061718	TRUE	chr2:73143055-73148260	YES	0.00793	0.02469	1	1
cg22775000	TRUE	chr9:103235171-103236627	YES	0.008176	0.02469	0	0

cg22669260	TRUE	chr4:150999250-151000706	YES	0.005611	0.02469	1	1
cg22498143	TRUE	chr19:40995880-40996119	YES	0.00541	0.02469	1	0
cg21733154	TRUE	chr4:3464799-3465440	YES	0.006371	0.02469	1	1
cg21640187	TRUE	chr6:4282004-4282310	No	0.00667	0.02469	0	1
cg21634933	TRUE	chr11:10952350-10953072	No	0.006426	0.02469	0	1
cg21595039	TRUE	chr6:166720239-166722275	YES	0.007725	0.02469	1	1
cg21489303	FALSE		YES	0.007224	0.02469	0	0
cg20295671	TRUE	chr22:22089624-22090909	YES	0.005293	0.02469	1	1
cg20270863	TRUE	chr1:210407401-210407637	No	0.005247	0.02469	1	1
cg19949441	TRUE	chr17:59473060-59483266	YES	0.005568	0.02469	1	1
cg19778698	TRUE	chr7:1570406-1571136	YES	0.005188	0.02469	1	1
cg19256292	TRUE	chr2:25563309-25563661	YES	0.006507	0.02469	0	1
cg19099281	TRUE	chr15:83620950-83621727	YES	0.007365	0.02469	1	1
cg18991611	TRUE	chr8:49468683-49468959	No	0.005	0.02469	1	0
cg18924298	TRUE	chr6:6006689-6007043	YES	0.005061	0.02469	0	1
cg18704110	TRUE	chr2:73143055-73148260	YES	0.006324	0.02469	0	0
cg18251612	TRUE	chr20:39316550-39319987	YES	0.007882	0.02469	1	1
cg18041884	TRUE	chr12:109162408-109162722	No	0.008133	0.02469	1	1
cg18022012	TRUE	chr2:10442308-10444509	YES	0.006563	0.02469	1	1
cg17772028	TRUE	chr20:61806254-61810867	No	0.00803	0.02469	0	1
cg17468773	TRUE	chr8:143591567-143592674	YES	0.007153	0.02469	1	0
cg16991765	TRUE	chr5:178593903-178594656	YES	0.008434	0.02469	1	1
cg16558432	TRUE	chr17:5403131-5404602	YES	0.008284	0.02469	1	1
cg16448058	TRUE	chr10:102882977-102883551	YES	0.006924	0.02469	0	0
cg16019142	TRUE	chr6:30418844-30419630	No	0.004807	0.02469	0	1
cg15927682	FALSE		YES	0.007381	0.02469	1	1
cg15789607	FALSE		No	0.005665	0.02469	1	1
cg14948279	TRUE	chr4:150999250-151000706	YES	0.005275	0.02469	1	1
cg14848284	TRUE	chr2:73143055-73148260	YES	0.006876	0.02469	0	1
cg14579819	TRUE	chr11:133825337-133827457	YES	0.007533	0.02469	1	1
cg14251622	TRUE	chr14:36002598-36005013	YES	0.008212	0.02469	1	1

cg14126020	TRUE	chr20:61150437-61150646	No	0.006108	0.02469	1	0
cg13957558	FALSE		No	0.008384	0.02469	0	1
cg13876462	TRUE	chr9:103235171-103236627	YES	0.006533	0.02469	0	1
cg13376404	FALSE		YES	0.00729	0.02469	1	1
cg13072057	TRUE	chr3:160822494-160823260	YES	0.004786	0.02469	1	0
cg12910175	TRUE	chr12:105478089-105478517	YES	0.004832	0.02469	1	1
cg12716838	TRUE	chr3:160822494-160823260	YES	0.006882	0.02469	1	0
cg12573705	TRUE	chr13:36052553-36053119	No	0.006301	0.02469	1	1
cg12122034	TRUE	chr2:223170486-223171140	No	0.004474	0.02469	0	1
cg12060499	TRUE	chr14:102172003-102172705	No	0.005012	0.02469	1	1
cg11784305	TRUE	chr20:1757779-1758134	No	0.0055	0.02469	0	1
cg10954251	TRUE	chr2:162273294-162273725	YES	0.007793	0.02469	1	1
cg10147797	TRUE	chr16:82044886-82045306	YES	0.006902	0.02469	0	1
cg09476611	TRUE	chr15:76638472-76639823	No	0.006174	0.02469	0	1
cg09324514	TRUE	chr16:58497033-58498595	YES	0.007875	0.02469	1	1
cg09221932	TRUE	chr1:87597543-87598515	YES	0.004935	0.02469	0	1
cg09195389	TRUE	chr13:20766208-20767779	YES	0.00472	0.02469	1	1
cg09093388	TRUE	chr15:65066916-65068352	YES	0.008469	0.02469	1	0
cg08690379	TRUE	chr2:233251361-233253414	YES	0.004943	0.02469	0	1
cg08317738	TRUE	chr16:89034060-89034293	YES	0.007721	0.02469	0	1
cg07856714	TRUE	chr19:18899037-18902284	YES	0.007789	0.02469	1	0
cg07850604	TRUE	chr14:36002598-36005013	YES	0.006864	0.02469	0	1
cg07642566	FALSE		No	0.008007	0.02469	1	1
cg07475468	TRUE	chr22:38857573-38857860	No	0.005708	0.02469	1	0
cg07098902	TRUE	chr2:17720155-17720417	YES	0.007259	0.02469	0	1
cg06911113	TRUE	chr1:20512360-20512797	YES	0.005355	0.02469	1	0
cg06817490	FALSE		No	0.004772	0.02469	0	1
cg06650115	TRUE	chr16:58497033-58498595	YES	0.007242	0.02469	1	1
cg06481158	TRUE	chr13:49549822-49551042	YES	0.005863	0.02469	1	1
cg06372015	TRUE	chr11:43602545-43603215	YES	0.007133	0.02469	1	1
cg06091881	TRUE	chr21:48087200-48088106	No	0.005171	0.02469	1	0

cg06082920	TRUE	chr1:51796097-51796589	YES	0.007616	0.02469	1	1
cg05210798	FALSE		YES	0.008091	0.02469	0	0
cg04780909	TRUE	chr6:1604606-1615866	YES	0.006828	0.02469	1	1
cg04499152	TRUE	chr10:13570128-13570864	No	0.00808	0.02469	1	1
cg04112019	TRUE	chr11:2165135-2165672	No	0.008512	0.02469	1	1
cg03848381	TRUE	chr15:40573628-40576118	No	0.004654	0.02469	1	0
cg03591594	TRUE	chr9:2621308-2623685	No	0.00797	0.02469	1	1
cg03527422	TRUE	chr6:99279317-99283842	YES	0.007803	0.02469	1	1
cg03070095	TRUE	chr17:80655335-80657183	YES	0.006705	0.02469	1	1
cg02900213	TRUE	chr11:20385161-20385673	YES	0.007578	0.02469	0	0
cg02767202	TRUE	chr2:220306855-220307096	YES	0.006127	0.02469	1	0
cg02732804	TRUE	chr16:28073817-28075296	YES	0.005992	0.02469	0	0
cg02598441	TRUE	chr17:62774366-62777797	YES	0.007571	0.02469	1	0
cg02380595	TRUE	chr16:85157830-85158048	No	0.008289	0.02469	1	1
cg02202923	TRUE	chr10:135038085-135038506	No	0.005106	0.02469	1	0
cg01941219	TRUE	chr13:98794398-98796241	YES	0.007453	0.02469	1	1
cg01339704	TRUE	chr17:4487398-4488482	YES	0.00782	0.02469	0	1
cg01038484	TRUE	chr8:145909676-145912846	No	0.008518	0.02469	0	1
cg00770155	FALSE		YES	0.005844	0.02469	1	0
cg00770085	TRUE	chr1:51810327-51810687	YES	0.006938	0.02469	1	0
cg00697129	FALSE		YES	0.004724	0.02469	0	0
cg00444847	TRUE	chr6:34433411-34434371	YES	0.007255	0.02469	0	0
cg00119117	TRUE	chr20:20344400-20350605	YES	0.007151	0.02469	0	1
cg00039801	TRUE	chr17:77783809-77789842	No	0.004765	0.02469	1	1
cg27231188	TRUE	chr1:233463526-233464414	YES	0.008792	0.02474	1	1
cg26522543	TRUE	chr16:28303973-28304770	YES	0.009394	0.02474	1	1
cg24831305	TRUE	chr19:53426078-53426389	No	0.009481	0.02474	1	1
cg23522427	TRUE	chr7:150675206-150675866	YES	0.009355	0.02474	1	1
cg22904737	TRUE	chr17:36734659-36735246	YES	0.009279	0.02474	0	1
cg22536554	TRUE	chr10:94833272-94835256	YES	0.009452	0.02474	1	1
cg21348997	TRUE	chr15:80696076-80697393	YES	0.00963	0.02474	0	1

cg20730198	TRUE	chr2:160654229-160654631	YES	0.009169	0.02474	0	1
cg20211816	TRUE	chr6:17987415-17988405	YES	0.008924	0.02474	1	1
cg19696583	TRUE	chr6:17987415-17988405	YES	0.009413	0.02474	1	1
cg19665362	TRUE	chr15:83315116-83317541	YES	0.009556	0.02474	1	1
cg18265162	TRUE	chr1:210407401-210407637	No	0.00964	0.02474	0	1
cg17949402	TRUE	chr10:135039937-135040196	No	0.008903	0.02474	1	1
cg15971010	TRUE	chr17:19436788-19437692	YES	0.008966	0.02474	0	1
cg15843262	TRUE	chr2:25474757-25475598	YES	0.009781	0.02474	1	1
cg14677048	TRUE	chr6:4282004-4282310	No	0.00974	0.02474	1	1
cg14239329	TRUE	chr2:202897386-202901046	YES	0.00927	0.02474	0	1
cg13899678	TRUE	chr2:105478600-105479188	No	0.009047	0.02474	0	1
cg13735819	TRUE	chr19:2250560-2253959	YES	0.009225	0.02474	1	1
cg13634242	TRUE	chr5:60921534-60922472	No	0.00972	0.02474	1	1
cg10392164	TRUE	chr11:65547499-65549261	YES	0.00871	0.02474	0	1
cg09028204	TRUE	chr20:43729515-43729791	YES	0.008775	0.02474	0	0
cg08900371	TRUE	chr1:210407401-210407637	No	0.008974	0.02474	1	1
cg08592305	TRUE	chr19:12978359-12978785	YES	0.009277	0.02474	1	1
cg05762694	TRUE	chr10:103990213-103991829	YES	0.009557	0.02474	1	1
cg05536984	TRUE	chr1:32083149-32084069	YES	0.009353	0.02474	0	1
cg04803994	TRUE	chr11:1592498-1592810	No	0.009115	0.02474	1	1
cg01406482	TRUE	chr11:15136058-15136545	YES	0.008976	0.02474	1	0
cg00281467	TRUE	chr22:23522550-23524465	YES	0.009755	0.02474	1	1
cg00107982	TRUE	chr22:37815803-37816477	YES	0.009366	0.02474	1	1
cg27196808	TRUE	chr12:49371690-49375550	YES	0.010223	0.02503	0	1
cg26539524	TRUE	chr19:51221447-51222704	YES	0.010683	0.02503	1	1
cg24498031	TRUE	chr15:40544352-40545512	No	0.01119	0.02503	1	1
cg24319381	TRUE	chr15:83315116-83317541	YES	0.010363	0.02503	1	1
cg24127874	TRUE	chr2:239147592-239149900	YES	0.010666	0.02503	1	1
cg23946695	TRUE	chr6:1604606-1615866	YES	0.010505	0.02503	1	0
cg22407458	TRUE	chr6:35108801-35109499	YES	0.011445	0.02503	0	0
cg22046408	TRUE	chr19:41106058-41106415	YES	0.010164	0.02503	1	1

cg21881034	TRUE	chr19:18722358-18724001	YES	0.010019	0.02503	1	0
cg21578090	TRUE	chr17:4487398-4488482	YES	0.011244	0.02503	1	1
cg20641465	TRUE	chr10:103990213-103991829	YES	0.011273	0.02503	1	1
cg20003368	FALSE		No	0.010485	0.02503	0	1
cg18448949	TRUE	chr2:176992950-176993186	YES	0.011268	0.02503	1	1
cg17186066	FALSE		No	0.010218	0.02503	1	0
cg17147728	TRUE	chr15:55879792-55881228	YES	0.01049	0.02503	0	0
cg16145703	TRUE	chr8:10916662-10917097	YES	0.010115	0.02503	1	1
cg16063587	TRUE	chr6:31691425-31691718	YES	0.011419	0.02503	1	1
cg15962187	TRUE	chr10:103051128-103052162	No	0.010486	0.02503	0	1
cg15803756	TRUE	chr10:13933482-13934184	YES	0.010604	0.02503	1	1
cg15355146	TRUE	chr1:40366595-40368213	YES	0.010694	0.02503	1	1
cg15020726	TRUE	chr15:31195673-31196392	YES	0.011287	0.02503	1	1
cg14451276	FALSE		YES	0.011311	0.02503	1	1
cg13605398	TRUE	chr17:7826127-7826414	YES	0.01105	0.02503	0	1
cg12126857	FALSE		No	0.010836	0.02503	1	1
cg11544522	FALSE		No	0.011441	0.02503	1	0
cg09342567	TRUE	chr3:178978948-178979364	YES	0.010598	0.02503	1	0
cg08186362	TRUE	chr20:60794179-60796121	YES	0.011406	0.02503	1	1
cg08021273	TRUE	chr7:5458503-5469256	No	0.010751	0.02503	1	1
cg07786760	TRUE	chr4:155410623-155413393	YES	0.010693	0.02503	0	1
cg07157571	FALSE		No	0.010211	0.02503	0	0
cg06494592	TRUE	chr3:125709066-125709452	No	0.010828	0.02503	1	1
cg05295671	TRUE	chr13:79232822-79233417	YES	0.011032	0.02503	1	1
cg04840494	TRUE	chr5:79551369-79552294	YES	0.01113	0.02503	0	1
cg04178858	TRUE	chr17:38333605-38334795	YES	0.010585	0.02503	1	1
cg00827989	TRUE	chr2:175199463-175202639	YES	0.010338	0.02503	1	1
cg00347757	TRUE	chr13:20766208-20767779	YES	0.011101	0.02503	1	1
cg00038711	TRUE	chr8:22014152-22014559	YES	0.011034	0.02503	1	1
cg25580018	TRUE	chr9:136399367-136400274	YES	0.011501	0.02506	0	1
cg13635455	TRUE	chr14:91730743-91731041	No	0.011648	0.02529	1	0

cg02479575	FALSE		No	0.011718	0.02535	1	0
cg05233674	TRUE	chr6:34433411-34434371	YES	0.011763	0.02535	1	1
cg06412434	TRUE	chr4:84457115-84457860	YES	0.011896	0.02536	1	1
cg03356490	FALSE		YES	0.011891	0.02536	0	1
cg03003689	TRUE	chr1:156674858-156676654	YES	0.011836	0.02536	0	1
cg25387636	TRUE	chr17:19436788-19437692	YES	0.012007	0.02536	1	1
cg16458671	TRUE	chr18:30050115-30051345	YES	0.012097	0.02536	1	1
cg15723350	TRUE	chr1:46954793-46957121	No	0.011997	0.02536	0	1
cg13643585	TRUE	chr17:46702280-46704166	YES	0.012035	0.02536	1	1
cg06482019	TRUE	chr16:51147490-51147944	No	0.012109	0.02536	1	1
cg21321248	TRUE	chr7:150674737-150675026	YES	0.012201	0.02547	1	1
cg00578638	TRUE	chr17:38333605-38334795	YES	0.012335	0.02566	1	1
cg23452969	TRUE	chr11:62690974-62691488	No	0.012607	0.02583	1	1
cg21912556	FALSE		YES	0.012714	0.02583	1	1
cg18402987	FALSE		No	0.012715	0.02583	0	0
cg16629158	TRUE	chr2:122042066-122043093	YES	0.012793	0.02583	1	1
cg14603620	TRUE	chr17:38333605-38334795	YES	0.012789	0.02583	1	1
cg12406391	TRUE	chr1:6520584-6521955	YES	0.012808	0.02583	0	0
cg11582100	TRUE	chr2:171672310-171675447	YES	0.012587	0.02583	1	1
cg07367232	TRUE	chr17:7826127-7826414	YES	0.012717	0.02583	1	1
cg03568064	TRUE	chr11:45907006-45907809	YES	0.012733	0.02583	1	1
cg07594636	TRUE	chr2:68546339-68547111	YES	0.013	0.02596	0	0
cg05298922	TRUE	chr2:175190866-175192123	No	0.012976	0.02596	1	1
cg00927554	TRUE	chr12:95941906-95942979	YES	0.012982	0.02596	0	1
cg27625456	FALSE		YES	0.013209	0.02598	1	1
cg14210607	TRUE	chr15:68126920-68128400	No	0.013272	0.02598	0	1
cg11594498	TRUE	chr19:34286184-34289135	No	0.013183	0.02598	0	0
cg09790502	TRUE	chr13:20766208-20767779	YES	0.013189	0.02598	1	0
cg07139330	TRUE	chr8:143591567-143592674	YES	0.013254	0.02598	0	1
cg00173141	TRUE	chr1:210465709-210466212	No	0.013236	0.02598	1	1
cg16018211	FALSE		YES	0.013341	0.02603	0	0

cg09035284	TRUE	chr2:219848919-219850541	YES	0.01345	0.02612	1	0
cg07566833	TRUE	chr15:41851723-41851970	YES	0.013476	0.02612	1	0
cg17169566	TRUE	chr4:150999250-151000706	YES	0.01354	0.02616	1	1
cg19744587	TRUE	chr3:53879638-53880831	No	0.013634	0.02617	1	1
cg16509658	TRUE	chr5:160974692-160975384	YES	0.013618	0.02617	0	1
cg13036855	TRUE	chr3:53879638-53880831	No	0.013698	0.02621	0	1
cg22473620	TRUE	chr19:46379883-46380207	No	0.013839	0.02622	1	1
cg10254000	TRUE	chr22:19748650-19749189	YES	0.01388	0.02622	1	1
cg05989669	TRUE	chr12:133562710-133563453	YES	0.013858	0.02622	0	0
cg03734784	TRUE	chr19:58111229-58111770	YES	0.013876	0.02622	1	0
cg19736608	TRUE	chr4:47838604-47839946	YES	0.013946	0.02626	0	1
cg25765619	TRUE	chr20:39316550-39319987	YES	0.014115	0.0264	0	1
cg21749794	TRUE	chr13:114876499-114877101	YES	0.014064	0.0264	1	1
cg15205204	TRUE	chr1:6545143-6545559	YES	0.014195	0.0264	1	1
cg00238897	TRUE	chr2:10442308-10444509	YES	0.014152	0.0264	0	1
cg09972864	TRUE	chr13:22247803-22249755	YES	0.014429	0.02675	1	1
cg26495865	TRUE	chr20:62102541-62103995	YES	0.014603	0.02675	1	1
cg13500576	TRUE	chr1:51796097-51796589	YES	0.014538	0.02675	1	0
cg09473745	TRUE	chr10:31422709-31423316	No	0.014504	0.02675	1	1
cg04387347	TRUE	chr16:88536936-88537375	YES	0.014608	0.02675	1	1
cg17368254	TRUE	chr12:95941906-95942979	YES	0.014862	0.02705	1	1
cg03207574	TRUE	chr10:25241110-25241900	YES	0.014836	0.02705	1	1
cg26027796	TRUE	chr19:55962482-55964247	No	0.014982	0.02719	1	1
cg20176349	TRUE	chr4:168155005-168155765	YES	0.01532	0.02731	1	1
cg17064250	TRUE	chr6:45389420-45391646	YES	0.015394	0.02731	1	1
cg14445507	FALSE		No	0.015227	0.02731	1	1
cg07815287	TRUE	chr2:9346383-9347944	YES	0.015341	0.02731	0	1
cg07565540	TRUE	chr1:6639427-6640361	No	0.01533	0.02731	1	1
cg07382923	FALSE		No	0.01528	0.02731	1	0
cg01738022	TRUE	chr16:4015001-4015232	YES	0.015201	0.02731	0	1
cg01514415	TRUE	chr1:6301695-6302856	No	0.015417	0.02731	0	1

cg15167646	TRUE	chr17:47653211-47654369	YES	0.015541	0.02745	1	1
cg24796651	TRUE	chr4:76911843-76912252	YES	0.015669	0.02751	0	0
cg22882523	TRUE	chr8:145103285-145108027	YES	0.015798	0.02751	1	1
cg08498787	TRUE	chr11:57249946-57250848	No	0.015791	0.02751	1	1
cg04305879	TRUE	chr15:40544352-40545512	No	0.015804	0.02751	1	0
cg00299943	FALSE		YES	0.015628	0.02751	0	1
cg20020464	TRUE	chr6:1604606-1615866	YES	0.015926	0.02764	0	1
cg25132878	TRUE	chr11:27493640-27494357	YES	0.015978	0.02765	1	1
cg11956953	TRUE	chr17:27346853-27347222	No	0.01605	0.02768	1	1
cg05920454	TRUE	chr12:6309152-6310392	YES	0.016089	0.02768	1	0
cg09541256	TRUE	chr6:45389420-45391646	YES	0.016196	0.0277	0	1
cg05916707	FALSE		No	0.016157	0.0277	1	1
cg14615784	TRUE	chr5:94955630-94957244	YES	0.016526	0.02803	1	0
cg05219131	TRUE	chr10:25241110-25241900	YES	0.016511	0.02803	1	1
cg01151135	TRUE	chr19:34310744-34311517	No	0.016497	0.02803	1	0
cg26005082	FALSE		No	0.016726	0.02828	0	1
cg14855657	TRUE	chr8:10587304-10591109	YES	0.016768	0.02828	1	1
cg26530701	FALSE		YES	0.017767	0.02835	0	1
cg25813864	TRUE	chr17:38333605-38334795	YES	0.017761	0.02835	0	1
cg25649038	TRUE	chr6:6546370-6547230	YES	0.017526	0.02835	0	0
cg23572376	TRUE	chr6:1604606-1615866	YES	0.017522	0.02835	0	1
cg21019315	TRUE	chr8:133687573-133687998	YES	0.017474	0.02835	0	1
cg20387815	TRUE	chr2:25391072-25391875	YES	0.017743	0.02835	0	1
cg19781133	TRUE	chr7:150674737-150675026	YES	0.017555	0.02835	1	0
cg18328965	TRUE	chr10:102106182-102107722	YES	0.017391	0.02835	1	1
cg17771031	TRUE	chr20:44875253-44875454	YES	0.017748	0.02835	0	1
cg16276290	TRUE	chr19:34286184-34289135	YES	0.017581	0.02835	1	1
cg15714846	TRUE	chr2:208631558-208634934	YES	0.017022	0.02835	1	1
cg15693066	TRUE	chr11:66824118-66824621	YES	0.017618	0.02835	1	1
cg12630336	TRUE	chr20:62679424-62680883	YES	0.017126	0.02835	1	1
cg10658573	TRUE	chr6:33181010-33181256	No	0.016872	0.02835	0	1

cg09055236	TRUE	chr7:2671156-2671937	YES	0.017389	0.02835	1	0
cg06476192	TRUE	chr16:31453943-31454561	YES	0.017511	0.02835	0	1
cg05914242	FALSE		YES	0.01744	0.02835	0	1
cg04287982	TRUE	chr1:21766272-21767224	YES	0.01737	0.02835	0	0
cg04246880	TRUE	chr10:135148196-135150565	YES	0.017806	0.02835	0	1
cg03892045	TRUE	chr17:6945389-6947521	YES	0.017055	0.02835	1	1
cg01097881	TRUE	chr12:108522950-108523852	YES	0.017548	0.02835	0	0
cg26157756	FALSE		No	0.01794	0.02839	0	1
cg03945700	TRUE	chr6:166720239-166722275	YES	0.017947	0.02839	0	1
cg00912926	TRUE	chr10:134774213-134774485	No	0.017977	0.02839	0	1
cg27409650	TRUE	chr22:37914768-37915883	YES	0.018311	0.0285	1	1
cg26351104	TRUE	chr1:51796097-51796589	YES	0.018226	0.0285	1	1
cg24472375	TRUE	chr6:108485671-108490539	No	0.018286	0.0285	0	1
cg08848958	TRUE	chr16:1382916-1384735	YES	0.018185	0.0285	0	1
cg08611491	TRUE	chr20:10652573-10655611	YES	0.018323	0.0285	1	1
cg05603881	TRUE	chr4:42399152-42400802	YES	0.018334	0.0285	0	1
cg18011045	TRUE	chr17:15163930-15164810	YES	0.018598	0.02854	1	1
cg14732998	TRUE	chr19:37997790-37998125	YES	0.018574	0.02854	1	1
cg13407975	TRUE	chr19:18705929-18706147	YES	0.018544	0.02854	1	1
cg03906033	TRUE	chr2:220306855-220307096	YES	0.018563	0.02854	1	0
cg01283834	TRUE	chr4:141489962-141490378	YES	0.018417	0.02854	1	0
cg15826437	TRUE	chr17:38333605-38334795	YES	0.018699	0.02855	1	1
cg08853419	TRUE	chr19:18722358-18724001	YES	0.018672	0.02855	1	1
cg27369401	TRUE	chr6:166720239-166722275	YES	0.018771	0.02859	1	0
cg15245625	TRUE	chr18:55862653-55862873	YES	0.01914	0.02865	1	1
cg11548411	TRUE	chr10:103051128-103052162	No	0.018884	0.02865	0	1
cg07256473	TRUE	chr22:29709281-29712013	YES	0.019067	0.02865	1	0
cg06970510	TRUE	chr12:52400467-52401696	YES	0.019145	0.02865	0	1
cg06627617	FALSE		YES	0.019122	0.02865	1	1
cg04141796	TRUE	chr5:42951076-42952410	No	0.018993	0.02865	0	1
cg03869498	TRUE	chr6:1604606-1615866	YES	0.01906	0.02865	0	1

cg25591867	TRUE	chr12:106640880-106642374	YES	0.019313	0.02868	1	1
cg22957381	TRUE	chr1:112531559-112533773	YES	0.01925	0.02868	1	1
cg05270634	TRUE	chr17:41177336-41177593	YES	0.019292	0.02868	1	1
cg24144419	TRUE	chr10:104178528-104179548	No	0.019488	0.02887	1	0
cg17718457	TRUE	chr19:4535069-4535339	YES	0.019697	0.02896	1	1
cg10641615	TRUE	chr12:54359658-54359906	YES	0.01969	0.02896	1	1
cg10021043	TRUE	chr2:68546339-68547111	YES	0.019617	0.02896	0	1
cg22700691	TRUE	chr10:21814786-21815716	YES	0.020108	0.02914	1	1
cg10684547	TRUE	chr7:155579868-155580392	No	0.02002	0.02914	0	0
cg08382542	TRUE	chr17:77770672-77778468	YES	0.020022	0.02914	1	1
cg08180070	TRUE	chr2:109647955-109648230	No	0.019866	0.02914	0	1
cg04034767	TRUE	chr12:52400467-52401696	YES	0.019967	0.02914	1	1
cg01629620	TRUE	chr9:139024316-139025832	No	0.020071	0.02914	1	1
cg12736438	TRUE	chr13:111213589-111214477	YES	0.02026	0.02915	1	1
cg10188732	TRUE	chr10:98945062-98946239	YES	0.0202	0.02915	0	1
cg07026599	TRUE	chr16:79632619-79635537	YES	0.020229	0.02915	0	1
cg10646395	TRUE	chr11:45168618-45169101	YES	0.020362	0.02922	1	0
cg12086936	TRUE	chr11:31831620-31839038	YES	0.020599	0.02935	1	0
cg07544748	TRUE	chr14:60336951-60337461	YES	0.020594	0.02935	1	1
cg06440960	TRUE	chr1:155829109-155829431	YES	0.020622	0.02935	0	1
cg01952313	TRUE	chr13:36052553-36053119	No	0.020648	0.02935	1	1
cg09307742	TRUE	chr12:123634826-123636176	No	0.020713	0.02937	0	1
cg10932068	TRUE	chr22:19748650-19749189	YES	0.020791	0.02941	0	0
cg05432017	TRUE	chr15:42119817-42120128	No	0.021051	0.02971	1	1
cg26961808	TRUE	chr7:128470443-128471161	YES	0.021173	0.02972	1	1
cg24032190	FALSE		YES	0.021146	0.02972	0	1
cg20172627	TRUE	chr2:25438725-25439276	No	0.021213	0.02972	1	1
cg17316564	FALSE		YES	0.0213	0.02972	1	1
cg06829538	TRUE	chr8:21905461-21905757	No	0.021309	0.02972	1	1
cg27610821	TRUE	chr22:39096373-39097754	YES	0.021426	0.02973	1	1
cg24950182	TRUE	chr3:183947040-183948801	YES	0.021665	0.02973	1	1

cg24078451	TRUE	chr6:166720239-166722275	YES	0.021567	0.02973	1	1
cg19653212	TRUE	chr6:42145847-42146053	YES	0.021425	0.02973	0	0
cg14614314	TRUE	chr10:135148196-135150565	YES	0.021635	0.02973	0	1
cg02971581	TRUE	chr1:10895895-10896117	No	0.021567	0.02973	1	1
cg02077100	TRUE	chr2:177502240-177502910	No	0.021526	0.02973	1	1
cg23483765	TRUE	chr5:156886969-156887440	YES	0.021839	0.0299	1	1
cg23867624	TRUE	chr6:1604606-1615866	YES	0.022026	0.03002	1	1
cg23268653	TRUE	chr1:213224611-213224867	YES	0.022006	0.03002	0	1
cg01433610	TRUE	chr17:5403131-5404602	YES	0.022102	0.03006	0	1
cg00207926	TRUE	chr22:37914768-37915883	YES	0.022154	0.03006	1	1
cg26202340	TRUE	chr11:126152722-126153400	YES	0.022374	0.03029	1	1
cg20748955	TRUE	chr11:118016237-118016984	YES	0.022445	0.03032	0	1
cg24562066	TRUE	chr2:219848919-219850541	YES	0.022688	0.0305	0	1
cg20631654	TRUE	chr20:56283891-56285395	YES	0.022803	0.0305	1	1
cg11331678	TRUE	chr20:44540445-44540957	YES	0.022759	0.0305	1	1
cg07831351	TRUE	chr20:3229238-3229693	No	0.02284	0.0305	0	1
cg00740822	TRUE	chr19:49939610-49940045	YES	0.02278	0.0305	0	0
cg15139588	TRUE	chr19:37997790-37998125	YES	0.023153	0.03085	0	0
cg19256731	TRUE	chr20:1874933-1875718	YES	0.023265	0.03093	0	1
cg13975523	TRUE	chr13:43148277-43149282	YES	0.023334	0.03096	1	1
cg17171801	TRUE	chr17:15163930-15164810	YES	0.023465	0.03106	0	1
cg25693302	TRUE	chr18:55862653-55862873	YES	0.023982	0.03128	0	1
cg25090510	TRUE	chr5:156886969-156887440	YES	0.023886	0.03128	1	1
cg24128130	TRUE	chr14:60336951-60337461	YES	0.023832	0.03128	1	1
cg13019878	TRUE	chr14:105877371-105878152	No	0.024029	0.03128	1	1
cg10662643	FALSE		No	0.023873	0.03128	1	1
cg07935500	TRUE	chr15:80696076-80697393	YES	0.024047	0.03128	1	1
cg06832898	TRUE	chr16:89033529-89033786	YES	0.023851	0.03128	1	1
cg00225902	FALSE		YES	0.023992	0.03128	0	1
cg03405114	TRUE	chr18:43651796-43652455	YES	0.024167	0.03136	0	0
cg18859089	TRUE	chr2:232276742-232277135	No	0.024315	0.03142	0	0

cg16343533	TRUE	chr20:46413742-46415507	YES	0.024298	0.03142	1	1
cg21716444	TRUE	chr22:37914768-37915883	YES	0.024427	0.0315	0	0
cg00823783	FALSE		YES	0.024518	0.03155	1	1
cg19640166	FALSE		YES	0.024646	0.03163	0	1
cg00020052	TRUE	chr2:68546339-68547111	YES	0.024689	0.03163	0	0
cg05052633	TRUE	chr17:29248847-29249926	YES	0.024925	0.03166	1	1
cg04407853	TRUE	chr18:33876727-33878487	YES	0.024824	0.03166	1	1
cg02687055	TRUE	chr2:24232680-24233260	YES	0.024883	0.03166	1	0
cg01545587	TRUE	chr14:105992499-105996414	YES	0.02482	0.03166	1	1
cg22538054	TRUE	chr12:95941906-95942979	YES	0.025168	0.03183	1	0
cg02182440	TRUE	chr4:141294666-141295274	YES	0.025166	0.03183	1	1
cg10349758	TRUE	chr11:63683743-63684628	YES	0.025272	0.0319	1	1
cg24474130	TRUE	chr6:99279317-99283842	YES	0.025419	0.03191	0	0
cg16881064	FALSE		No	0.025432	0.03191	1	1
cg13373360	TRUE	chr4:149363212-149367056	YES	0.025505	0.03191	1	1
cg03949284	TRUE	chr6:33160945-33161337	YES	0.025548	0.03191	1	0
cg02711801	TRUE	chr19:37997790-37998125	YES	0.025458	0.03191	0	0
cg04117372	TRUE	chr20:21083501-21083847	No	0.025609	0.03192	1	0
cg00151810	TRUE	chr16:75298976-75300186	YES	0.025702	0.03197	1	1
cg23513567	TRUE	chr17:881733-883381	YES	0.026075	0.03223	1	1
cg08583507	TRUE	chr20:56283891-56285395	YES	0.026078	0.03223	0	1
cg06033738	TRUE	chr20:20344400-20350605	YES	0.026051	0.03223	1	0
cg26705720	TRUE	chr20:10652573-10655611	YES	0.026153	0.03226	0	0
cg02003183	FALSE		YES	0.026381	0.03247	1	0
cg23515460	TRUE	chr14:73358789-73360934	YES	0.026605	0.03268	0	1
cg19175649	TRUE	chr17:15163930-15164810	YES	0.026673	0.0327	0	0
cg13577493	TRUE	chr3:50540220-50541123	YES	0.026988	0.03302	0	1
cg17876497	TRUE	chr10:88730554-88731632	YES	0.027254	0.03321	1	1
cg01893669	TRUE	chr2:39663897-39664667	YES	0.027223	0.03321	1	1
cg25185518	TRUE	chr4:146402870-146403983	YES	0.027387	0.0333	1	1
cg19716433	TRUE	chr14:103589353-103590246	No	0.027526	0.0334	1	1

cg12931523	TRUE	chr15:90792559-90792929	YES	0.027604	0.03343	1	1
cg00557354	FALSE		YES	0.027819	0.03362	0	1
cg17332326	TRUE	chr19:37997790-37998125	YES	0.027974	0.03363	1	1
cg07563569	TRUE	chr17:47653211-47654369	YES	0.027899	0.03363	1	1
cg04184208	TRUE	chr14:96505311-96506402	YES	0.027996	0.03363	0	0
cg12312988	TRUE	chr2:5832041-5834208	YES	0.028446	0.0341	1	1
cg22036160	TRUE	chr7:95064073-95064409	YES	0.028676	0.03431	0	0
cg00431837	TRUE	chr6:107810066-107812733	YES	0.028755	0.03433	1	1
cg14128890	TRUE	chr1:36786500-36789402	YES	0.029797	0.03537	0	1
cg09062550	TRUE	chr20:20344400-20350605	YES	0.029797	0.03537	0	1
cg00633736	TRUE	chr17:15163930-15164810	YES	0.029783	0.03537	1	1
cg14208112	TRUE	chr1:111148983-111150186	YES	0.030066	0.03561	0	1
cg16427096	TRUE	chr16:1202414-1204624	YES	0.030335	0.03586	1	0
cg16998835	TRUE	chr7:32767535-32768848	YES	0.030487	0.03597	1	1
cg10433812	TRUE	chr11:10952350-10953072	No	0.030621	0.03606	1	1
cg05322217	TRUE	chr17:36575499-36575782	No	0.030789	0.03618	1	1
cg25875316	TRUE	chr2:239067512-239068028	No	0.031148	0.03653	0	1
cg04420309	TRUE	chr11:66824118-66824621	YES	0.031226	0.03655	1	1
cg15496956	TRUE	chr1:47696504-47698197	No	0.031303	0.03657	0	1
cg24197091	TRUE	chr14:74706188-74708192	YES	0.031527	0.03676	0	0
cg16523372	TRUE	chr19:30364035-30364803	No	0.031795	0.03686	0	1
cg06768188	TRUE	chr20:44540445-44540957	YES	0.031784	0.03686	1	1
cg02120463	TRUE	chr22:39638219-39640966	YES	0.031776	0.03686	1	1
cg04048250	TRUE	chr4:788825-789738	YES	0.031915	0.03692	1	1
cg12389545	TRUE	chr11:72353222-72354358	YES	0.03216	0.03714	1	1
cg23282051	TRUE	chr2:239067512-239068028	No	0.032538	0.0375	0	1
cg16640865	TRUE	chr11:72301302-72301746	YES	0.032885	0.03768	1	1
cg06974961	TRUE	chr1:23543377-23544237	No	0.032761	0.03768	1	1
cg06206801	TRUE	chr18:24126780-24131138	YES	0.032823	0.03768	1	1
cg12162377	TRUE	chr2:232260100-232261134	YES	0.033043	0.03779	1	0
cg13484581	TRUE	chr9:133813631-133815781	YES	0.033404	0.03812	1	1

cg03719509	TRUE	chr5:77943868-77945220	YES	0.033456	0.03812	0	1
cg06310422	TRUE	chr2:234762496-234763579	YES	0.033656	0.03827	1	1
cg10322504	TRUE	chr20:3229238-3229693	No	0.034295	0.03892	1	1
cg01853367	FALSE		YES	0.034431	0.039	0	0
cg10253929	TRUE	chr19:41106058-41106415	YES	0.034792	0.03934	1	0
cg05501285	TRUE	chr5:131563094-131563954	YES	0.035166	0.03969	0	0
cg06714180	TRUE	chr12:54408426-54408713	No	0.035518	0.03993	1	1
cg05727225	TRUE	chr11:10327013-10329831	YES	0.035486	0.03993	0	1
cg06734962	TRUE	chr8:48649766-48651653	YES	0.035664	0.04002	0	1
cg23296010	TRUE	chr19:37997790-37998125	YES	0.035882	0.04008	1	0
cg22604316	TRUE	chr1:46954793-46957121	No	0.035916	0.04008	1	1
cg03636488	FALSE		YES	0.035852	0.04008	1	1
cg22219136	TRUE	chr17:15163930-15164810	YES	0.0361	0.04013	1	0
cg07980518	TRUE	chr18:59560494-59562016	YES	0.036055	0.04013	1	1
cg02917596	TRUE	chr11:61447599-61448273	YES	0.036209	0.04018	1	1
cg05756848	TRUE	chr4:84457115-84457860	YES	0.036367	0.04028	1	1
cg12071544	TRUE	chr16:4421642-4422240	No	0.036453	0.0403	1	1
cg16791186	TRUE	chr15:67134823-67135145	No	0.036824	0.04064	1	1
cg06976395	TRUE	chr20:44935932-44937310	No	0.037531	0.04134	1	1
cg13558971	TRUE	chr1:203598471-203598853	YES	0.037778	0.04146	0	1
cg00204645	TRUE	chr16:58059380-58061477	YES	0.037771	0.04146	1	1
cg18974926	TRUE	chr1:109940074-109940894	YES	0.037953	0.04157	0	1
cg24760848	FALSE		No	0.03838	0.04196	0	1
cg00928596	FALSE		YES	0.038537	0.04206	1	1
cg26246807	TRUE	chr19:58094739-58095764	YES	0.038923	0.04225	1	1
cg02407342	TRUE	chr17:42988741-42989148	YES	0.038885	0.04225	0	1
cg00817367	TRUE	chr12:52400467-52401696	YES	0.038913	0.04225	1	1
cg13696940	TRUE	chr22:29709281-29712013	YES	0.039322	0.0426	0	1
cg18343290	FALSE		No	0.039523	0.04274	1	1
cg10177207	TRUE	chr2:220306855-220307096	YES	0.039587	0.04274	0	1
cg12060744	TRUE	chr19:58094739-58095764	YES	0.039854	0.04295	1	1

cg01046104	TRUE	chr19:58094739-58095764	YES	0.040097	0.04313	1	1
cg08806496	TRUE	chr5:92919558-92921430	YES	0.040205	0.04317	0	1
cg04011338	FALSE		YES	0.040843	0.04378	1	0
cg20341504	FALSE		No	0.041073	0.04394	0	1
cg06038655	TRUE	chr7:130417912-130419378	YES	0.041222	0.04402	1	1
cg22330512	TRUE	chr12:108522950-108523852	YES	0.041335	0.04407	1	1
cg22945605	TRUE	chr1:17865863-17866630	YES	0.041434	0.04409	1	1
cg08535600	TRUE	chr3:8808961-8811280	YES	0.041506	0.04409	1	1
cg22819616	TRUE	chr8:144952047-144952980	No	0.041854	0.04438	0	0
cg22280940	TRUE	chr8:48649766-48651653	YES	0.042148	0.04461	1	1
cg16495696	TRUE	chr15:90792559-90792929	YES	0.042396	0.0448	1	1
cg08773462	FALSE		No	0.042724	0.04503	1	0
cg02417684	TRUE	chr16:31483276-31483646	YES	0.04277	0.04503	1	1
cg13415795	FALSE		YES	0.043518	0.04574	1	0
cg24563094	TRUE	chr2:26395416-26395620	YES	0.043674	0.04582	1	1
cg16921014	TRUE	chr4:146402870-146403983	YES	0.044228	0.04632	1	1
cg11400774	TRUE	chr1:156051239-156051461	YES	0.044752	0.04679	1	1
cg22470850	TRUE	chr2:26396102-26397204	YES	0.045056	0.04702	1	1
cg16017578	TRUE	chr17:56031843-56033160	No	0.045352	0.04725	1	1
cg03574882	TRUE	chr7:151572761-151575106	YES	0.045835	0.04767	1	0
cg14951193	TRUE	chr19:4535069-4535339	YES	0.046648	0.04843	1	0
cg09795194	TRUE	chr17:19770306-19771508	YES	0.046828	0.04853	1	0
cg02017926	TRUE	chr12:123754049-123754373	YES	0.047133	0.04877	1	1
cg26706896	FALSE		No	0.047671	0.04924	1	1
cg15673034	TRUE	chr18:3498941-3499358	YES	0.048105	0.0496	1	1
cg03790804	TRUE	chr3:197807029-197808734	YES	0.048953	0.05039	0	1
cg21017887	TRUE	chr14:105398076-105400079	No	0.050024	0.0514	0	1

* TRUE – Probes within CpG Island, Shore or Shelf; FALSE- Probe outside of CpG Island

** Yes- The CpG is located in either promoter/ body/3'UTR region of a gene; No- Intergenic

$ Chip-seq peaks p<0.01; 0: indicates no enrichment; 1 indicates enrichment

Supplementary Table 3. Genetic networks affected by the differentially methylated TET2 signature genes

ID	Molecules in Network	Score	Focus Molecules	Top Functions
1	Alp, **BCAR1**, **CD9**, **CDH12**, Cg, **CPEB1**, **CYP26A1**, **DNMT3A**, **ERBB3**, ERK1/2, estrogen receptor, **ETS1**, **FAM59A**, **FGF9**, **FLNC**, **GJB2**, **HOXB9**, **HTATIP2**, **JAG1**, **JAG2**, **LRIG1**, **MAPK8IP1**, **MMP15**, Notch, **RUNX2**, **SATB2**, **SMAD1**, **SMAD3**, **SRCIN1**, **STUB1**, **SULF2**, **TGFB1I1**, **TMEFF1**, Vegf, **WNT1**	46	29	Tissue Morphology, Cellular Movement, Cellular Development
2	**BCR**, Calmodulin, **CAMK2N1**, **CARD10**, **CDH22**, **CEBPD**, Creb, **DGKZ**, **EPHB1**, ERK, Focal adhesion kinase, **GAD1 (includes EG:100006588)**, **HRH3**, Igm, **INSM1**, **INSM2**, Interferon alpha, **KCND3**, **LGI3**, **MAFB**, **NEUROG3**, NFkB (complex), **OXTR**, P38 MAPK, **PACSIN1**, **PDGFB**,PI3K (complex), Pka, **SIRPA**, **TIRAP**, **TNFSF11**, **TYRO3**, **UCP1**, **VSNL1**, **ZC3HAV1**	37	25	Hematological System Development and Function, Inflammatory Response, Hematopoiesis
3	**AOAH**, aspase, CHEK2, CLU, CSF3R, CYCS, DAPK1, **DLGAP1**, DNMT1, **EP400**, **ETS1**, **FAN1**, FGF8, **FRMD4A**, **FZD5**, GLB1, **ITPRIP**, **KCTD1**, LEF1, mir-21, MLH1, NANOG, PITX2, **PMEPA1**, PMS2, **PSD3**, **SLIT1**, **SOX7**, SPP1 (includes EG:100359743), **TBX1**, TP53 (includes EG:22059), TRRAP, **ULK2**, **WNT1**, ZIC3	19	16	Cell Death and Survival, Cell Cycle, Connective Tissue Development and Function, Cancer
4	AR, ARHGDIA, **ASAP2**, BIN1, CBX4, CDK11A/CDK11B, **CKAP4**, EED, **ESPN**, FIGLA, FKBP5, HDAC2, **HOXA7**, **HOXB7**, ITGB8, **MAP4K3**, MLL, **NMRK2**, NR3C1, **PITX3**, **PLEKHG5**, PTEN, PTK2B, PTP4A2, **RBMS2**, **RBPMS2**, RGS2 (includes EG:19735), RHOA, RHOB, SFTPC, **SMAD1**, **STUB1**, **TGFB1I1**, TSC22D3, **TTLL13**	17	15	Cellular Development, Cellular Growth and Proliferation, Cell Death and Survival

Genes associated with hematopoeitic development, differentiation, and hematological diseases as well as cell cycle regulation were enriched.
Genes typed in bold are present in our dataset.

Supplementary Table 4. Top 35 genes hypermethylated (β value difference >0.2) and downregulated (< -1.2 Fold) in *TET2*mut samples

Enterz-Id	Gene Name	Gene Detail	Functional Genomic distribution	β-value diff.(Tet2mut vs Tet2 wt)	Expression Fold Change	Pearson. Corr.
2047	EPHB1	EPH receptor B1	Promoter	0.412961	-1.38005	-0.02381
2113	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1	Body	0.375849	-1.24208	-0.02381
5443	POMC	Proopiomelanocortin	Promoter	0.538493	-1.51781	-0.57143
7574	ZNF26	zinc finger protein 26	Promoter	0.466784	-1.29062	-0.57143
8099	CDK2AP1	cyclin-dependent kinase 2 associated protein 1	Body	0.603602	-1.32463	-0.11905
8445	DYRK2	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	Promoter	0.418542	-1.20419	-0.07143
8600	TNFSF11	tumor necrosis factor (ligand) superfamily, member 11	Promoter	0.305845	-1.49934	-0.2619
8706	B3GALNT1	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	Promoter	0.526885	-1.50246	0.214286
8874	ARHGEF7	Rho guanine nucleotide exchange factor (GEF) 7	Promoter	0.590279	-1.52321	-0.29048
9455	HOMER2	homer homolog 2 (Drosophila)	Body	0.464126	-1.62323	-0.35714
9638	FEZ1	fasciculation and elongation protein zeta 1 (zygin I)	Promoter	0.477806	-1.38889	-0.19048
9706	ULK2	unc-51-like kinase 2	Promoter	0.438478	-1.47446	-0.2381
9929	JOSD1	Josephin domain containing 1	Promoter	0.273092	-1.3119	-0.38095
10160	FARP1	FERM, RhoGEF (ARHGEF) and pleckstrin domain protein 1 (chondrocyte-derived)	Promoter	0.562678	-1.41433	-0.02381
10553	HTATIP2	HIV-1 Tat interactive protein 2, 30kDa	Promoter	0.317632	-1.21381	0.047619
22909	FAN1	FANCD2/FANCI-associated nuclease 1	Promoter	0.506296	-1.24072	-0.66667
26108	PYGO1	pygopus homolog 1 (Drosophila)	Body	0.451437	-2.56199	-0.2381
55366	LGR4	leucine-rich repeat-containing G protein-coupled receptor 4	Promoter	0.512544	-1.37405	-0.69048
56829	ZC3HAV1	zinc finger CCCH-type, antiviral	3'UTR	0.368085	-1.2749	-0.88095
59348	ZNF350	zinc finger protein 350	Promoter	0.481225	-2.58233	-0.54762
79047	KCTD15	potassium channel tetramerisation domain containing 15	Promoter	0.433789	-1.20181	-0.04762
79596	RNF219	ring finger protein 219	Promoter	0.518075	-1.33124	-0.57143
84101	USP44	ubiquitin specific peptidase 44	Promoter	0.61217	-1.40315	-0.69048
84451	KIAA1804	mixed lineage kinase 4	Promoter	0.345757	-1.20278	-0.69048
85415	RHPN2	rhophilin, Rho GTPase binding protein 2	Body	0.255424	-1.49271	-0.38095

93517	SDR42E1	short chain dehydrogenase	Promoter	0.542368	-2.01244	-0.80952
152573	SHISA3	shisa homolog 3 (Xenopus laevis)	Body	0.494514	-1.50897	-0.30952
160622	GRASP	GRP1-associated scaffold protein	Promoter	0.589405	-2.16077	0.166667
166614	DCLK2	doublecortin-like kinase 2	Promoter	0.565693	-2.12449	-0.66667
284307	ZIK1	zinc finger protein interacting with K protein 1 homolog	Promoter	0.467432	-1.97665	-0.88095
348840	ANKRD18DP	Ankyrin repeat domain 18	Promoter	0.639283	-1.34193	-0.83333
390927	ZNF793	zinc finger protein 793	Promoter	0.527175	-1.27379	-0.38095
400720	ZNF772	zinc finger protein 772	Promoter	0.496242	-1.27794	-0.59524
441212	RP9P	retinitis pigmentosa 9 pseudogene	Body	0.455395	-1.40611	-0.33333
728392	LOC728392	NLR family, pyrin domain containing 1	Promoter	0.473732	-1.45675	-0.33333

Supplementary Table 5: Clinical characteristics according to *TET2* mutation status in DLBCL patients.

	***TET2* Mut n=12**	***TET2* wt n=88**	**P value**
Sex: Female	4	34	0,523
Male	7	49	
Missing data	1	5	
Age (year), Mean	68	59	0,086*
IPI			
0-2. no. of patients	7	54	0,223
3-5, no. of patients	4	24	
Missing data	1	10	
LDH			
Above normal level	5	47	0,223
Within normal level	6	32	
Missing data	1	9	
Performance score			
0-2	10	75	0,481
3-4	1	7	
Missing data	1	6	
Clinical Stage			
I-II, no. of patients	5	41	0,604
III-IV no. of patients	6	43	
Missing data	1	4	

*****P value determined by One-Way Anova test, other P values determined by Pearson Chi-square test.