

Figure S1. Clustering of methylation data from tissue samples from individuals with obesity. Pearson's correlation coefficient-based heat-map representation of methylation status of autosomal CpG sites among different tissues.

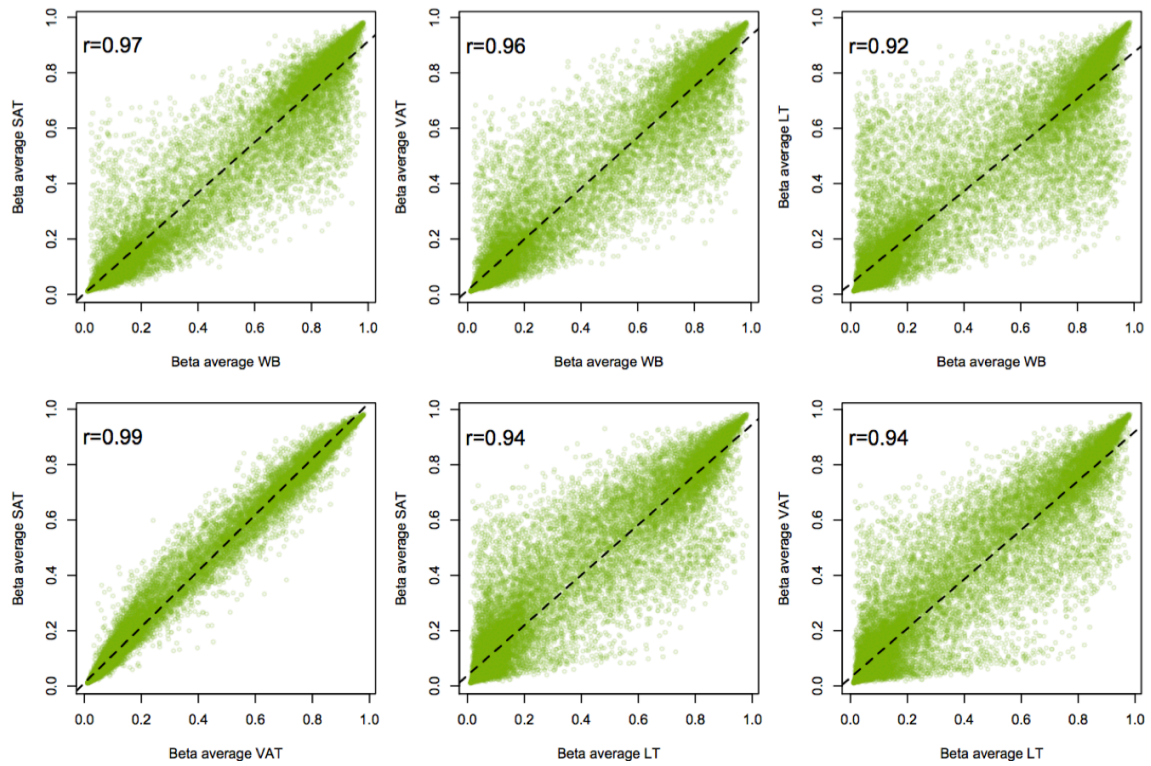


Figure S2. Comparison of methylation averages among tissue types. Scatter plots of comparison of DNA methylation levels between different tissue samples. Pearson's r values are denoted in the top left corner.

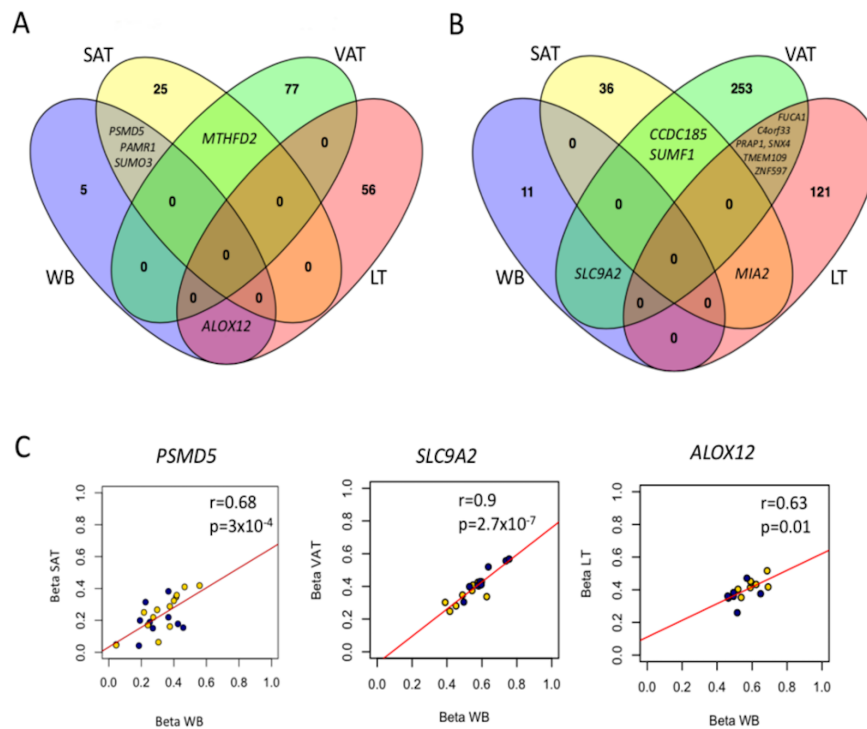


Figure S3. Comparison of DMCs between different tissues. (A) Venn diagram of positive DMCs. **(B)** Venn diagram of negative DMCs from WB. **(C)** Sites with correlation between WB and other tissues: *ALOX12* (cg03760483), *PSMD5* (cg09419670), and *SLC9A2* (cg20050113).

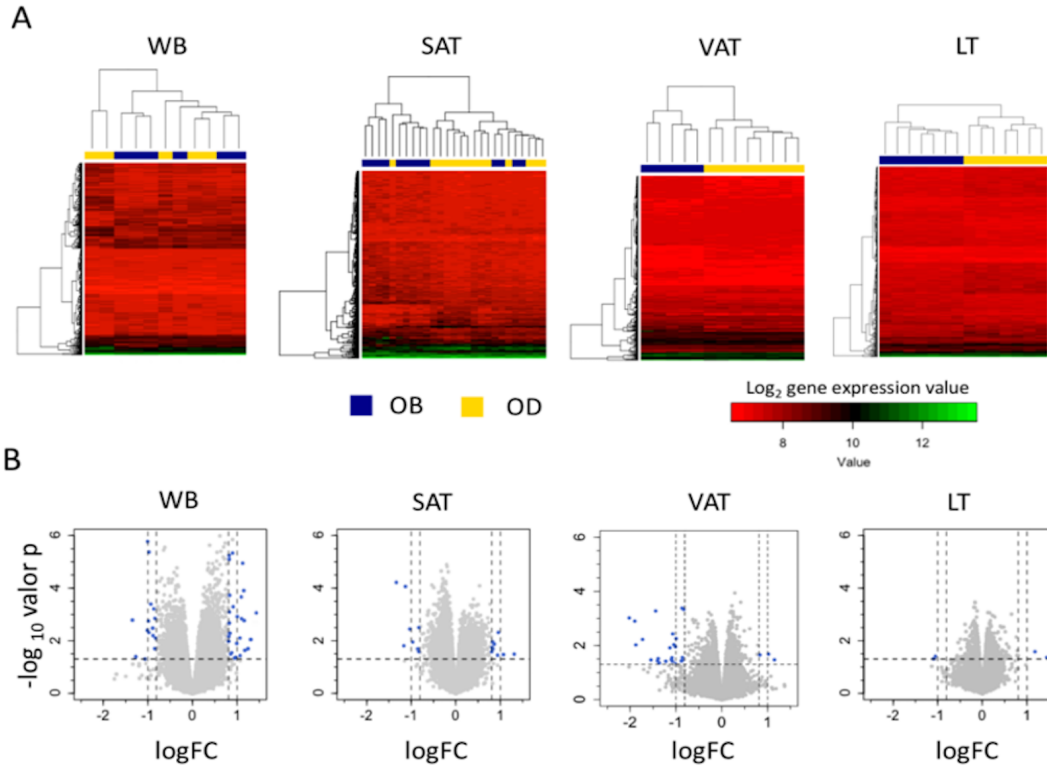


Figure S4. Differential gene expression. (A) Hierarchical clustering analysis of the top 500 identified probes that were differentially expressed between DO and NDO across tissues. The color bars at the top of the heat map indicate the patient status: yellow for DO, and blue for NDO. **(B)** Volcano plot of the log odds of differential expression vs. the log fold-change in gene expression between DO and NDO patients in WB, SAT, VAT, and LT. Probes with a $|\text{fold-change}| > 0.8$ and $p < 0.05$ are highlighted in blue.

Table S1. List of DMCs in WB in the comparison between the DO and NDO groups

Target ID	Symbol	CHR	CPG Island	Beta DO	Beta OB	Delta Beta	p-value
cg13105904	<i>KHNYN</i>	14	TRUE	0.22	0.12	0.1	0.009
cg09419670	<i>PSMD5*</i>	9	TRUE	0.37	0.28	0.09	0.008
cg21717724	<i>PSMD5</i>	9	TRUE	0.78	0.7	0.08	0.049
cg03760483	<i>ALOX12</i>	17	TRUE	0.52	0.45	0.07	0.003
cg21053323	<i>SUMO3</i>	21	TRUE	0.33	0.26	0.06	0.001
cg06873352	<i>STRADA</i>	17	TRUE	0.24	0.18	0.06	0.010
cg19728382	<i>STC2</i>	5	TRUE	0.58	0.53	0.05	0.009
cg19592945	<i>P2RXL1</i>	22	FALSE	0.48	0.43	0.05	0.033
cg14642338	<i>PAMR1</i>	11	FALSE	0.56	0.51	0.05	0.044
cg20050113	<i>SLC9A2</i>	2	TRUE	0.55	0.6	-0.05	0.048
cg06906435	<i>C14orf177</i>	14	FALSE	0.53	0.59	-0.05	0.039
cg02588309	<i>TTC33</i>	5	TRUE	0.34	0.39	-0.05	0.010
cg22686523	<i>FLJ25006</i>	17	FALSE	0.6	0.66	-0.06	0.048
cg13982505	<i>KCNJ13*</i>	2	FALSE	0.69	0.75	-0.06	0.019
cg13033054	<i>LINC00846</i>	21	FALSE	0.57	0.64	-0.06	0.026
cg23439277	<i>PLCE1*</i>	10	FALSE	0.63	0.69	-0.06	0.009
cg25853078	<i>OPCML*</i>	11	FALSE	0.47	0.54	-0.06	0.003
cg13383491	<i>GPR85*</i>	7	FALSE	0.47	0.55	-0.08	0.001
cg06771126	<i>HOP*</i>	4	FALSE	0.3	0.38	-0.08	0.012
cg25997474	<i>ADH1C*</i>	4	FALSE	0.58	0.66	-0.08	0.007
cg03606258	<i>GNAS</i>	20	TRUE	0.5	0.6	-0.1	0.038

*significant DMCs after adjusted by cell-type heterogeneity

Table S2. List of DMCs in SAT in the comparison between the DO and NDO groups

Target ID	Symbol	CHR	CPG Island	Beta DO	Beta OB	Delta Beta	p-value
cg17687883	<i>MTHFD2</i>	2	TRUE	0.2	0.07	0.14	0.011
cg09405083	<i>WBP1L</i>	10	FALSE	0.31	0.19	0.12	0.024
cg09419670	<i>PSMD5</i>	9	TRUE	0.27	0.19	0.08	0.024
cg14144305	<i>ALX4</i>	11	TRUE	0.34	0.26	0.08	0.007
cg04317399	<i>HOXA4</i>	7	TRUE	0.34	0.27	0.08	0.018
cg14642338	<i>PAMR1</i>	11	FALSE	0.47	0.4	0.07	0.006
cg00983520	<i>CPT1B</i>	22	TRUE	0.24	0.17	0.07	0.008
cg10190509	<i>CCL16</i>	17	FALSE	0.7	0.63	0.07	0.029
cg19393006	<i>TSC1</i>	9	FALSE	0.49	0.42	0.07	0.005
cg00186701	<i>TSPYL5</i>	8	TRUE	0.43	0.36	0.07	0.026

cg09025324	<i>SART2</i>	6	TRUE	0.2	0.14	0.06	0.03
cg08321346	<i>ANKMY1</i>	2	TRUE	0.21	0.14	0.06	0.034
cg25316898	<i>C18orf21</i>	18	TRUE	0.17	0.1	0.06	0.047
cg00648883	<i>EEF1DP3</i>	13	FALSE	0.36	0.3	0.06	0.028
cg17903316	<i>LOXHD1</i>	18	FALSE	0.36	0.3	0.06	0.047
cg26154999	<i>FAM124B</i>	2	TRUE	0.36	0.31	0.06	0.038
cg10098888	<i>IRS1</i>	2	TRUE	0.17	0.11	0.06	0.017
cg01193293	<i>SIGLEC7</i>	19	FALSE	0.52	0.46	0.06	0.05
cg22062068	<i>HNRNPG-T</i>	11	TRUE	0.55	0.5	0.06	0.043
cg12782180	<i>LEP</i>	7	TRUE	0.3	0.25	0.06	0.008
cg21053323	<i>SUMO3</i>	21	TRUE	0.19	0.13	0.06	0.042
cg00929606	<i>ZNF3</i>	7	TRUE	0.31	0.26	0.05	0.023
cg21019522	<i>SLC22A18</i>	11	FALSE	0.3	0.24	0.05	0.017
cg24664957	<i>VPS37B</i>	12	TRUE	0.51	0.46	0.05	0.003
cg11405695	<i>ATAD3C</i>	1	FALSE	0.53	0.48	0.05	0.028
cg06476606	<i>IFIT2</i>	10	FALSE	0.15	0.09	0.05	0.017
cg03160637	<i>DDB1</i>	11	TRUE	0.15	0.1	0.05	0.031
cg22222251	<i>WBSCR19</i>	7	FALSE	0.67	0.62	0.05	0.008
cg14679202	<i>L3MBTL2</i>	22	TRUE	0.39	0.34	0.05	0.027
cg03811411	<i>SGCD</i>	5	FALSE	0.65	0.7	-0.05	0.018
cg16504670	<i>DEF8</i>	16	TRUE	0.77	0.82	-0.05	0.009
cg05654163	<i>SLC39A2</i>	14	FALSE	0.62	0.67	-0.05	0.011
cg03190825	<i>CYP4F11</i>	19	FALSE	0.43	0.48	-0.05	0.023
cg21011830	<i>RPL18A</i>	19	TRUE	0.06	0.11	-0.05	0.011
cg04452713	<i>DST</i>	6	TRUE	0.26	0.31	-0.05	0.003
cg06563300	<i>SLC17A8</i>	12	FALSE	0.21	0.26	-0.05	0.018
cg07039113	<i>S100A9</i>	1	FALSE	0.73	0.78	-0.05	0.004
cg14290291	<i>MZT2B</i>	2	FALSE	0.43	0.48	-0.05	0.001
cg06112415	<i>CGREF1</i>	2	TRUE	0.37	0.42	-0.05	<0.001
cg24603941	<i>MIA2</i>	14	FALSE	0.68	0.74	-0.05	0.003
cg13980719	<i>TNP1</i>	2	FALSE	0.5	0.55	-0.05	0.022
cg24041453	<i>CCDC11</i>	18	TRUE	0.13	0.19	-0.05	0.024
cg01031251	<i>RPS6KA1</i>	1	TRUE	0.57	0.62	-0.05	0.004
cg05333568	<i>CCDC185</i>	1	TRUE	0.28	0.34	-0.05	0.043
cg04893119	<i>PI15</i>	8	FALSE	0.57	0.63	-0.05	0.031
cg03573747	<i>ADIPOQ</i>	3	FALSE	0.73	0.78	-0.06	0.006
cg00626466	<i>GNS</i>	12	TRUE	0.54	0.59	-0.06	0.022
cg05885720	<i>EMP1</i>	12	FALSE	0.63	0.69	-0.06	0.007
cg20781967	<i>NINJ2</i>	12	FALSE	0.34	0.4	-0.06	0.032

cg24833277	<i>FAM83A</i>	8	TRUE	0.64	0.7	-0.06	0.041
cg21048669	<i>CLEC3A</i>	16	FALSE	0.48	0.53	-0.06	0.026
cg27525902	<i>FGF7</i>	15	FALSE	0.52	0.58	-0.06	0.028
cg21550483	<i>CLEC10A</i>	17	FALSE	0.39	0.44	-0.06	0.043
cg19592945	<i>P2RXL1</i>	22	FALSE	0.34	0.4	-0.06	0.047
cg18847227	<i>SUMF1</i>	3	TRUE	0.42	0.48	-0.06	0.006
cg21686987	<i>CTRB1</i>	16	FALSE	0.75	0.81	-0.06	<0.001
cg03793778	<i>LGALS7</i>	19	FALSE	0.57	0.63	-0.06	0.044
cg18344063	<i>MGAT4C</i>	12	FALSE	0.57	0.64	-0.06	0.047
cg21832243	<i>TTC3</i>	21	FALSE	0.3	0.36	-0.06	0.038
cg00673191	<i>DOPEY2</i>	21	FALSE	0.3	0.36	-0.06	0.038
cg15302379	<i>KAZALD1</i>	10	TRUE	0.56	0.62	-0.07	0.001
cg21126707	<i>MYF5</i>	12	TRUE	0.5	0.57	-0.07	0.001
cg05293216	<i>FANCG</i>	9	TRUE	0.6	0.67	-0.07	0.01
cg26185508	<i>CDCP2</i>	1	TRUE	0.41	0.48	-0.07	0.025
cg07221454	<i>MS4A10</i>	11	FALSE	0.62	0.69	-0.07	0.041
cg15149938	<i>C22orf34</i>	22	FALSE	0.64	0.71	-0.07	0.007
cg02276665	<i>CTNNA1</i>	5	TRUE	0.39	0.47	-0.09	<0.001
cg02288165	<i>SN</i>	20	FALSE	0.33	0.42	-0.09	0.006

Table S3. List of DMCs in VAT in the comparison between the DO and NDO groups

Target ID	Symbol	CHR	CPG Island	Beta DO	Beta OB	Delta Beta	<i>p</i> -value
cg17687883	<i>MTHFD2</i>	2	TRUE	0.21	0.06	0.16	0.009
cg02964385	<i>STK38</i>	6	FALSE	0.58	0.42	0.16	0.036
cg15235832	<i>ACTR2</i>	2	TRUE	0.27	0.14	0.13	0.002
cg17872476	<i>VTI1A</i>	10	FALSE	0.40	0.28	0.12	0.001
cg22438810	<i>LCN2</i>	9	FALSE	0.66	0.54	0.11	0.023
cg01734338	<i>KCNQ1</i>	11	TRUE	0.74	0.63	0.11	0.001
cg04570669	<i>APIN</i>	4	FALSE	0.56	0.46	0.11	<0.001
cg11237738	<i>LINC01587</i>	4	FALSE	0.70	0.59	0.10	0.008
cg14074641	<i>ABCC12</i>	16	FALSE	0.39	0.30	0.09	0.003
cg01120761	<i>CLEC4C</i>	12	FALSE	0.77	0.68	0.09	0.040
cg02719634	<i>SLC22A18A5</i>	11	FALSE	0.84	0.75	0.09	0.032
cg20622019	<i>ADA</i>	20	TRUE	0.37	0.28	0.09	0.039
cg21755709	<i>PDXK</i>	21	TRUE	0.71	0.62	0.09	0.004
cg14732540	<i>BRDT</i>	1	TRUE	0.86	0.77	0.09	0.008
cg13906813	<i>HLA-DPA1</i>	6	FALSE	0.57	0.48	0.09	0.029
cg21781546	<i>ZNF142</i>	2	FALSE	0.70	0.63	0.08	<0.001
cg27212977	<i>DEFA6</i>	8	FALSE	0.81	0.73	0.08	<0.001
cg12218747	<i>SETD4</i>	21	TRUE	0.68	0.61	0.08	0.007
cg17994910	<i>CCDC30</i>	1	FALSE	0.49	0.41	0.08	0.013
cg17758148	<i>JMY</i>	5	FALSE	0.42	0.34	0.08	0.036
cg04601137	<i>ADAMTSL5</i>	19	FALSE	0.40	0.32	0.08	0.021
cg17496921	<i>TSPAN16</i>	19	FALSE	0.31	0.24	0.07	0.035
cg11376198	<i>AFAR3</i>	1	TRUE	0.22	0.14	0.07	0.030
cg21784940	<i>REPIN1</i>	7	FALSE	0.43	0.35	0.07	0.001
cg25112853	<i>HSC20</i>	22	FALSE	0.57	0.50	0.07	0.030
cg15792367	<i>KLK11</i>	19	FALSE	0.58	0.50	0.07	0.021
cg13525683	<i>TIAF1</i>	17	TRUE	0.73	0.66	0.07	0.010
cg13044136	<i>AES</i>	19	TRUE	0.16	0.09	0.07	0.011
cg11147886	<i>NFAT5</i>	16	FALSE	0.73	0.66	0.07	0.046
cg24612198	<i>CD3E</i>	11	FALSE	0.58	0.51	0.07	<0.001
cg18236297	<i>CYSLTR2</i>	13	FALSE	0.53	0.46	0.07	0.035
cg09325101	<i>OSTbeta</i>	15	FALSE	0.25	0.18	0.07	0.048
cg01817393	<i>GNAS</i>	20	TRUE	0.28	0.22	0.07	0.013
cg11584936	<i>BNIPL</i>	1	FALSE	0.67	0.60	0.07	0.045
cg08666623	<i>ST6GALNAC2</i>	17	FALSE	0.22	0.15	0.07	0.028
cg21644628	<i>HEATR3</i>	16	FALSE	0.63	0.56	0.07	0.009

cg19468534	<i>NUSAP1</i>	15	FALSE	0.55	0.49	0.07	<0.001
cg19103704	<i>FCGBP</i>	19	FALSE	0.46	0.39	0.07	0.024
cg27044702	<i>TPSAB1</i>	16	FALSE	0.70	0.64	0.07	0.042
cg00943909	<i>GNAS</i>	20	TRUE	0.51	0.44	0.07	0.029
cg04008843	<i>TTR</i>	18	FALSE	0.51	0.45	0.06	0.006
cg11151665	<i>PSG6</i>	19	FALSE	0.81	0.75	0.06	<0.001
cg19740969	<i>CXCL9</i>	4	FALSE	0.74	0.68	0.06	0.007
cg15862544	<i>EGFL4</i>	19	FALSE	0.83	0.77	0.06	0.021
cg23154064	<i>FAM208A</i>	3	FALSE	0.59	0.53	0.06	0.001
cg19279346	<i>LILRB2</i>	19	FALSE	0.68	0.62	0.06	0.005
cg09559551	<i>RSC1A1</i>	1	FALSE	0.78	0.72	0.06	0.024
cg02212280	<i>MMP1</i>	11	FALSE	0.80	0.74	0.06	<0.001
cg20812929	<i>DHRS4L2</i>	14	TRUE	0.31	0.25	0.06	0.022
cg08046471	<i>CXCL11</i>	4	FALSE	0.72	0.66	0.06	0.025
cg27016609	<i>STON1</i>	2	FALSE	0.49	0.44	0.06	0.001
cg26981881	<i>DEC1</i>	9	FALSE	0.73	0.67	0.06	0.039
cg09873510	<i>NLN</i>	5	FALSE	0.67	0.62	0.06	0.015
cg13982505	<i>KCNJ13</i>	2	FALSE	0.71	0.66	0.06	0.003
cg25803423	<i>C14orf119</i>	14	TRUE	0.15	0.09	0.06	0.028
cg27383744	<i>BRCA1</i>	17	TRUE	0.84	0.79	0.06	0.001
cg27661264	<i>GNAS</i>	20	TRUE	0.28	0.22	0.05	0.030
cg08972170	<i>Ells1</i>	7	TRUE	0.73	0.67	0.05	0.036
cg06776256	<i>GPRC5A</i>	12	TRUE	0.33	0.28	0.05	0.044
cg11003133	<i>AIM2</i>	1	FALSE	0.86	0.81	0.05	0.032
cg17606194	<i>SYCE1</i>	10	TRUE	0.47	0.41	0.05	0.037
cg14837082	<i>HRH1</i>	3	FALSE	0.65	0.60	0.05	0.015
cg11251498	<i>INDOL1</i>	8	FALSE	0.21	0.16	0.05	0.002
cg20895028	<i>CDH26</i>	20	FALSE	0.79	0.74	0.05	<0.001
cg16879115	<i>APOBEC1</i>	12	FALSE	0.70	0.65	0.05	0.021
cg25743584	<i>TIAF1</i>	17	FALSE	0.69	0.64	0.05	0.001
cg09964921	<i>KCNE1</i>	21	FALSE	0.78	0.73	0.05	0.002
cg22726338	<i>AKNAD1</i>	1	FALSE	0.68	0.62	0.05	0.011
cg27090087	<i>TINAG</i>	6	FALSE	0.51	0.45	0.05	0.032
cg17896229	<i>PROKR2</i>	20	TRUE	0.61	0.56	0.05	0.005
cg25372103	<i>DLL1</i>	6	TRUE	0.28	0.23	0.05	0.003
cg02131853	<i>TMEM156</i>	4	FALSE	0.70	0.65	0.05	<0.001
cg25420952	<i>AMBP</i>	9	FALSE	0.79	0.74	0.05	0.049
cg25650811	<i>CCDC129</i>	7	TRUE	0.59	0.54	0.05	0.008
cg20891917	<i>IFRD1</i>	7	FALSE	0.86	0.81	0.05	0.001

cg15344028	<i>ICOS</i>	2	FALSE	0.74	0.69	0.05	0.031
cg23580000	<i>ADCY7</i>	16	TRUE	0.87	0.82	0.05	0.040
cg00182461	<i>PPIL3</i>	2	TRUE	0.14	0.09	0.05	0.004
cg15674997	<i>GRM6</i>	5	TRUE	0.35	0.40	-0.05	0.001
cg10316764	<i>TAOK2</i>	16	TRUE	0.35	0.40	-0.05	0.038
cg12958778	<i>TBC1D14</i>	4	TRUE	0.47	0.52	-0.05	0.033
cg06637774	<i>P2RY6</i>	11	TRUE	0.24	0.29	-0.05	0.025
cg16601861	<i>ALDH1A1</i>	9	FALSE	0.34	0.39	-0.05	0.043
cg25509184	<i>CFTR</i>	7	TRUE	0.57	0.62	-0.05	0.024
cg00968931	<i>MRPL54</i>	19	FALSE	0.69	0.74	-0.05	0.025
cg17692403	<i>R3HDML</i>	20	FALSE	0.13	0.18	-0.05	0.006
cg00666746	<i>SYDE1</i>	19	TRUE	0.11	0.16	-0.05	0.001
cg10929387	<i>ITIH4</i>	3	FALSE	0.82	0.87	-0.05	0.017
cg09354267	<i>ATG5</i>	6	TRUE	0.28	0.34	-0.05	0.049
cg25938646	<i>SLITRK1</i>	13	TRUE	0.42	0.47	-0.05	0.023
cg00296685	<i>GTF2H4</i>	6	TRUE	0.44	0.49	-0.05	0.004
cg25356886	<i>CRYGD</i>	2	TRUE	0.42	0.47	-0.05	0.005
cg02337166	<i>NR1D1</i>	17	FALSE	0.10	0.15	-0.05	0.036
cg07880854	<i>FBLN7</i>	2	FALSE	0.17	0.22	-0.05	0.007
cg09893305	<i>HAPLN1</i>	5	FALSE	0.50	0.55	-0.05	0.040
cg27465566	<i>TRIO</i>	5	TRUE	0.30	0.35	-0.05	0.007
cg19903229	<i>C14orf105</i>	14	FALSE	0.57	0.62	-0.05	0.013
cg10537269	<i>TIMM9</i>	14	TRUE	0.20	0.25	-0.05	0.041
cg15343119	<i>GALR1</i>	18	TRUE	0.19	0.24	-0.05	0.004
cg08041019	<i>ATXN2</i>	12	TRUE	0.23	0.29	-0.05	0.005
cg10731149	<i>CYBRD1</i>	2	TRUE	0.59	0.64	-0.05	0.010
cg07657236	<i>KCNH8</i>	3	TRUE	0.18	0.24	-0.05	0.002
cg00567749	<i>CSPG2</i>	5	TRUE	0.34	0.40	-0.05	0.015
cg08445039	<i>FKBP9</i>	7	TRUE	0.13	0.18	-0.05	0.033
cg03464655	<i>SLC38A11</i>	2	TRUE	0.22	0.27	-0.05	0.026
cg10742801	<i>PRAP1</i>	10	FALSE	0.29	0.34	-0.05	0.007
cg02065387	<i>GABRA1</i>	5	FALSE	0.56	0.62	-0.05	0.047
cg22193702	<i>PADI1</i>	1	FALSE	0.82	0.87	-0.05	0.047
cg19188060	<i>PSMD2</i>	3	TRUE	0.13	0.19	-0.05	<0.001
cg09604428	<i>PB1</i>	3	FALSE	0.88	0.93	-0.05	0.025
cg02318535	<i>PPM1E</i>	17	TRUE	0.78	0.83	-0.05	0.048
cg09788239	<i>PCQAP</i>	22	TRUE	0.12	0.17	-0.05	0.003
cg03743584	<i>PRAP1</i>	10	FALSE	0.18	0.23	-0.05	0.020
cg08223748	<i>MEF2C</i>	5	TRUE	0.25	0.30	-0.05	0.008

cg07536847	PAX7	1	TRUE	0.16	0.21	-0.05	0.006
cg16468910	SNX4	3	TRUE	0.27	0.33	-0.05	0.022
cg16046951	MKKS	20	TRUE	0.21	0.26	-0.05	0.025
cg16168311	APOA1BP	1	TRUE	0.10	0.15	-0.05	0.001
cg16608652	B3GALT2	1	FALSE	0.81	0.86	-0.05	0.038
cg08261177	ALDH16A1	19	TRUE	0.07	0.12	-0.05	0.010
cg15014458	LYPD3	19	FALSE	0.24	0.30	-0.05	0.037
cg18411898	RPRM	2	TRUE	0.38	0.43	-0.05	0.002
cg17509872	CNOT7	8	FALSE	0.28	0.34	-0.05	0.018
cg15109571	SUFU	10	TRUE	0.07	0.13	-0.05	0.001
cg02727285	RELB	19	TRUE	0.38	0.43	-0.05	0.035
cg26815021	SFRS2	17	TRUE	0.17	0.23	-0.05	<0.001
cg08207256	DNM2	19	TRUE	0.17	0.22	-0.05	0.003
cg11885098	EFNA2	19	TRUE	0.23	0.28	-0.05	0.009
cg24958765	RAB4B	19	TRUE	0.15	0.20	-0.05	0.009
cg00021527	TAF15	17	TRUE	0.09	0.15	-0.05	0.010
cg19948393	ANKRD33	12	TRUE	0.48	0.54	-0.05	0.030
cg08054038	PVRL2	19	TRUE	0.46	0.51	-0.05	0.003
cg22430790	FRMD6	14	TRUE	0.20	0.25	-0.06	0.001
cg09209002	SAS10	4	TRUE	0.09	0.14	-0.06	0.027
cg18001427	RWDD2B	21	TRUE	0.16	0.22	-0.06	0.032
cg16195804	C12orf65	12	TRUE	0.16	0.21	-0.06	0.008
cg06150803	TNFRSF19	13	FALSE	0.23	0.28	-0.06	0.004
cg17166812	NDUFS2	1	FALSE	0.24	0.29	-0.06	0.041
cg23061257	YIPF1	1	TRUE	0.25	0.31	-0.06	0.019
cg06543018	RBP1	3	TRUE	0.19	0.25	-0.06	0.017
cg15350194	FAM70B	13	TRUE	0.28	0.34	-0.06	0.003
cg01190915	MT2A	16	TRUE	0.38	0.44	-0.06	0.036
cg02630888	FBXL5	4	TRUE	0.64	0.70	-0.06	0.034
cg20513206	C19orf47	19	TRUE	0.65	0.70	-0.06	0.048
cg12619509	DNASE1L2	16	TRUE	0.25	0.31	-0.06	<0.001
cg20867633	GOLT1A	1	TRUE	0.33	0.39	-0.06	0.002
cg20449692	CLDN11	3	TRUE	0.06	0.12	-0.06	0.002
cg23771929	FREQ	9	TRUE	0.19	0.25	-0.06	0.013
cg05154390	MRPS15	1	TRUE	0.17	0.23	-0.06	0.014
cg01333131	CDC42BPB	14	TRUE	0.13	0.19	-0.06	0.010
cg09164559	KIAA1279	10	TRUE	0.24	0.30	-0.06	0.047
cg08361238	PTGFRN	1	TRUE	0.38	0.44	-0.06	0.037
cg24083641	MGC46496	4	TRUE	0.40	0.45	-0.06	0.013

cg02586730	<i>EFEMP2</i>	11	TRUE	0.38	0.44	-0.06	0.044
cg05856931	<i>MSI2</i>	17	TRUE	0.52	0.57	-0.06	0.003
cg07425555	<i>FLJ23447</i>	19	FALSE	0.27	0.33	-0.06	0.002
cg24450312	<i>RASSF5</i>	1	TRUE	0.16	0.22	-0.06	0.001
cg14892768	<i>AXL</i>	19	FALSE	0.16	0.21	-0.06	0.008
cg03942271	<i>AUH</i>	9	TRUE	0.26	0.32	-0.06	0.019
cg14191360	<i>MET</i>	7	TRUE	0.60	0.66	-0.06	0.047
cg03532005	<i>PSPH</i>	7	TRUE	0.24	0.30	-0.06	0.002
cg11503011	<i>EBF</i>	5	FALSE	0.16	0.22	-0.06	0.001
cg05179880	<i>PDCD7</i>	15	TRUE	0.22	0.28	-0.06	0.021
cg00066816	<i>IL12B</i>	5	TRUE	0.35	0.41	-0.06	0.029
cg04759439	<i>CAST1</i>	3	TRUE	0.19	0.25	-0.06	<0.001
cg04065065	<i>PIGO</i>	9	TRUE	0.20	0.26	-0.06	<0.001
cg11976166	<i>TGFB2</i>	1	TRUE	0.19	0.25	-0.06	0.001
cg08697665	<i>RARRES1</i>	3	TRUE	0.33	0.39	-0.06	0.011
cg22134325	<i>NPAS4</i>	11	TRUE	0.17	0.23	-0.06	0.012
cg08216808	<i>ARPC2</i>	2	FALSE	0.22	0.28	-0.06	0.009
cg14166009	<i>HKR1</i>	19	TRUE	0.18	0.23	-0.06	0.013
cg25482967	<i>MRPS10</i>	6	TRUE	0.31	0.36	-0.06	0.010
cg02214188	<i>BDH2</i>	4	FALSE	0.47	0.52	-0.06	0.004
cg16152813	<i>FAM57B</i>	16	FALSE	0.16	0.22	-0.06	0.001
cg11466908	<i>AUH</i>	9	TRUE	0.09	0.15	-0.06	<0.001
cg04371779	<i>GPATCH2L</i>	14	TRUE	0.09	0.15	-0.06	0.008
cg02401978	<i>ZNF746</i>	7	FALSE	0.53	0.58	-0.06	0.040
cg01457653	<i>FBXL8</i>	16	TRUE	0.09	0.14	-0.06	0.024
cg09310112	<i>JMJD2B</i>	19	TRUE	0.09	0.15	-0.06	0.022
cg11418559	<i>ZNF593</i>	1	TRUE	0.27	0.33	-0.06	0.025
cg27069753	<i>ELA3B</i>	1	FALSE	0.51	0.57	-0.06	0.020
cg17593391	<i>RRAGC</i>	1	TRUE	0.26	0.32	-0.06	0.046
cg08749917	<i>RTP1</i>	3	FALSE	0.43	0.49	-0.06	0.029
cg07036530	<i>GPR26</i>	10	TRUE	0.29	0.35	-0.06	0.012
cg21151355	<i>GJB3</i>	1	FALSE	0.24	0.30	-0.06	0.008
cg17166338	<i>TERT</i>	5	TRUE	0.48	0.54	-0.06	0.026
cg19350340	<i>ASPM</i>	1	TRUE	0.32	0.38	-0.06	0.008
cg22986999	<i>MRGPRF</i>	11	TRUE	0.28	0.34	-0.06	0.042
cg27112247	<i>TMED2</i>	12	TRUE	0.53	0.59	-0.06	<0.001
cg01200177	<i>POLR2D</i>	2	TRUE	0.31	0.37	-0.06	0.011
cg11052143	<i>ALS2CR11</i>	2	TRUE	0.18	0.25	-0.06	0.025
cg03682712	<i>LOXL1</i>	15	TRUE	0.10	0.16	-0.06	0.016

cg20119051	<i>R3HDM1</i>	2	TRUE	0.48	0.54	-0.06	0.001
cg10927536	<i>SRRD</i>	22	TRUE	0.35	0.41	-0.06	0.019
cg04845628	<i>MINA</i>	3	TRUE	0.63	0.69	-0.06	0.001
cg05194726	<i>NRIP2</i>	12	FALSE	0.11	0.17	-0.06	0.017
cg11412582	<i>HERC2</i>	15	TRUE	0.12	0.18	-0.06	0.024
cg23769143	<i>TIMP4</i>	3	FALSE	0.18	0.25	-0.06	0.032
cg12256080	<i>ABT1</i>	6	TRUE	0.09	0.15	-0.06	0.004
cg11730100	<i>FEN1</i>	11	TRUE	0.23	0.29	-0.06	0.002
cg25225238	<i>GRM3</i>	7	FALSE	0.33	0.39	-0.06	0.039
cg12324629	<i>ULK2</i>	17	TRUE	0.37	0.44	-0.06	0.029
cg04532952	<i>CA4</i>	17	TRUE	0.14	0.20	-0.06	0.002
cg15557833	<i>MFSD8</i>	4	TRUE	0.25	0.32	-0.06	<0.001
cg07884019	<i>HMP19</i>	5	FALSE	0.28	0.34	-0.06	0.047
cg11177693	<i>ZNF513</i>	2	TRUE	0.56	0.62	-0.06	0.020
cg21759080	<i>STX5A</i>	11	TRUE	0.13	0.19	-0.06	0.021
cg24674220	<i>GMEB2</i>	20	FALSE	0.71	0.77	-0.06	0.045
cg03098721	<i>TTL7</i>	1	TRUE	0.58	0.64	-0.06	0.024
cg25982743	<i>TIMP4</i>	3	TRUE	0.14	0.21	-0.06	0.001
cg20856064	<i>PH-4</i>	3	TRUE	0.17	0.23	-0.06	<0.001
cg24792360	<i>FUCA1</i>	1	TRUE	0.41	0.48	-0.06	0.038
cg03513163	<i>PCDHB1</i>	5	TRUE	0.29	0.35	-0.06	0.032
cg05587474	<i>MOV10</i>	1	TRUE	0.38	0.45	-0.06	<0.001
cg17327630	<i>ZNF212</i>	7	TRUE	0.17	0.23	-0.07	0.007
cg00647741	<i>ZNF274</i>	19	FALSE	0.43	0.49	-0.07	0.043
cg11536940	<i>PGCP</i>	8	TRUE	0.25	0.32	-0.07	0.038
cg17865752	<i>CCNT2</i>	2	TRUE	0.30	0.36	-0.07	0.019
cg19974223	<i>ANKRD33</i>	12	TRUE	0.60	0.66	-0.07	0.013
cg21493666	<i>PPME1</i>	11	TRUE	0.20	0.26	-0.07	0.005
cg05303448	<i>AACS</i>	12	TRUE	0.22	0.29	-0.07	0.001
cg10994379	<i>CAPSL</i>	5	FALSE	0.37	0.44	-0.07	0.050
cg00571634	<i>WDR5B</i>	3	TRUE	0.41	0.48	-0.07	0.003
cg14920846	<i>NAV1</i>	1	TRUE	0.42	0.48	-0.07	0.025
cg08707819	<i>RCOR1</i>	14	TRUE	0.35	0.42	-0.07	0.001
cg24362726	<i>C4orf33</i>	4	FALSE	0.64	0.71	-0.07	0.048
cg26431343	<i>HSPC117</i>	22	FALSE	0.48	0.55	-0.07	0.005
cg11908570	<i>KIAA0040</i>	1	TRUE	0.24	0.31	-0.07	0.001
cg22972055	<i>UNC84A</i>	7	TRUE	0.68	0.75	-0.07	0.019
cg17783509	<i>PHOX2B</i>	4	FALSE	0.30	0.37	-0.07	0.009
cg23547429	<i>SLC43A3</i>	11	FALSE	0.20	0.26	-0.07	<0.001

cg14435807	<i>LOXL1</i>	15	TRUE	0.13	0.20	-0.07	0.002
cg05257610	<i>NDUFAF7</i>	2	FALSE	0.57	0.64	-0.07	0.039
cg01860753	<i>RASSF5</i>	1	TRUE	0.22	0.29	-0.07	0.012
cg12271671	<i>FGL2</i>	7	FALSE	0.29	0.35	-0.07	0.016
cg07129274	<i>HIST1H2AL</i>	6	TRUE	0.27	0.34	-0.07	0.012
cg02860543	<i>IGF2BP3</i>	7	TRUE	0.42	0.49	-0.07	0.043
cg25345738	<i>PWP1</i>	12	FALSE	0.16	0.22	-0.07	0.018
cg01718365	<i>AOF2</i>	1	TRUE	0.24	0.31	-0.07	0.008
cg01288089	<i>CXCL10</i>	4	FALSE	0.25	0.32	-0.07	<0.001
cg02147791	<i>SAP18</i>	13	TRUE	0.22	0.29	-0.07	0.035
cg09404633	<i>LMOD1</i>	1	TRUE	0.21	0.28	-0.07	0.001
cg15868302	<i>FOXD2</i>	1	TRUE	0.42	0.49	-0.07	0.018
cg09047884	<i>TLL1</i>	22	TRUE	0.58	0.65	-0.07	0.001
cg02849695	<i>CCDC19</i>	1	TRUE	0.24	0.31	-0.07	0.001
cg07693270	<i>RPL39L</i>	3	TRUE	0.41	0.48	-0.07	<0.001
cg03160508	<i>RHOD</i>	11	TRUE	0.18	0.25	-0.07	0.015
cg18632102	<i>CNOT8</i>	5	TRUE	0.37	0.44	-0.07	0.020
cg20426860	<i>FLJ20422</i>	19	TRUE	0.18	0.25	-0.07	0.006
cg24088408	<i>E2F1</i>	20	TRUE	0.53	0.61	-0.07	0.027
cg21422208	<i>RFT1</i>	3	TRUE	0.28	0.35	-0.07	0.011
cg19453250	<i>STAT1P1</i>	18	FALSE	0.31	0.38	-0.07	0.007
cg18847227	<i>SUMF1</i>	3	TRUE	0.39	0.47	-0.07	0.015
cg27239157	<i>MCF2L2</i>	3	TRUE	0.41	0.48	-0.07	<0.001
cg15815843	<i>MFAP5</i>	12	FALSE	0.72	0.79	-0.07	0.017
cg20773127	<i>ENPEP</i>	4	TRUE	0.41	0.48	-0.07	0.037
cg03876622	<i>CSDA</i>	12	TRUE	0.21	0.29	-0.07	0.017
cg14036856	<i>MGC52423</i>	1	FALSE	0.62	0.69	-0.07	0.025
cg17387870	<i>CHFR</i>	12	TRUE	0.24	0.31	-0.07	0.017
cg11672225	<i>RNF185</i>	22	TRUE	0.20	0.27	-0.07	0.006
cg01337047	<i>DSG1</i>	18	FALSE	0.46	0.53	-0.07	0.048
cg08713365	<i>C20orf98</i>	20	TRUE	0.08	0.16	-0.07	0.017
cg14711201	<i>SKP2</i>	5	TRUE	0.14	0.21	-0.07	0.001
cg07460665	<i>CALCOCO2</i>	17	TRUE	0.16	0.23	-0.07	0.002
cg19759064	<i>PHKG1</i>	7	FALSE	0.29	0.36	-0.07	0.046
cg11816577	<i>YWHAE</i>	17	TRUE	0.15	0.23	-0.07	0.047
cg18977436	<i>FGF14</i>	13	FALSE	0.32	0.39	-0.08	0.006
cg26924825	<i>LCAT</i>	16	FALSE	0.54	0.62	-0.08	0.039
cg15881727	<i>ZBED4</i>	22	TRUE	0.11	0.18	-0.08	0.001
cg00674922	<i>SATB1</i>	3	TRUE	0.39	0.46	-0.08	0.005

cg05624932	<i>CRISPLD1</i>	8	TRUE	0.35	0.42	-0.08	0.031
cg17378989	<i>ERCC1</i>	19	TRUE	0.32	0.40	-0.08	0.020
cg27394046	<i>XRN2</i>	20	TRUE	0.51	0.59	-0.08	0.027
cg05333568	<i>CCDC185</i>	1	TRUE	0.26	0.34	-0.08	0.019
cg16121444	<i>NME7</i>	1	TRUE	0.16	0.23	-0.08	0.025
cg01919208	<i>LAMB2</i>	3	TRUE	0.16	0.24	-0.08	0.009
cg20055101	<i>ZNF206</i>	16	FALSE	0.33	0.41	-0.08	0.041
cg10217449	<i>GNPDA2</i>	4	TRUE	0.45	0.53	-0.08	0.018
cg18964732	<i>TMCO1</i>	1	TRUE	0.16	0.24	-0.08	0.002
cg21993406	<i>CENPH</i>	5	FALSE	0.32	0.40	-0.08	0.039
cg01446393	<i>FAM107A</i>	3	FALSE	0.58	0.66	-0.08	0.045
cg26284390	<i>NFKBIZ</i>	3	TRUE	0.25	0.33	-0.08	0.026
cg13549845	<i>GRID2</i>	4	TRUE	0.48	0.56	-0.08	0.011
cg00984602	<i>SRF</i>	6	TRUE	0.20	0.28	-0.08	0.001
cg26486702	<i>USP21</i>	1	TRUE	0.23	0.31	-0.08	0.022
cg05420896	<i>DCC</i>	18	TRUE	0.29	0.37	-0.08	0.007
cg10841258	<i>CTTNBP2NL</i>	1	TRUE	0.23	0.31	-0.08	0.037
cg12148581	<i>RPL14</i>	3	TRUE	0.41	0.49	-0.08	0.028
cg18053607	<i>PIB5PA</i>	22	FALSE	0.22	0.30	-0.08	0.045
cg12435611	<i>BRIP1</i>	17	TRUE	0.28	0.36	-0.08	0.014
cg19972619	<i>MYC</i>	8	TRUE	0.08	0.16	-0.08	0.005
cg24333473	<i>ZNF597</i>	16	TRUE	0.23	0.31	-0.08	0.032
cg05681757	<i>FGD4</i>	12	FALSE	0.34	0.43	-0.09	0.001
cg16858125	<i>ELOVL1</i>	1	TRUE	0.45	0.54	-0.09	0.018
cg21374864	<i>TOR1A</i>	9	TRUE	0.30	0.39	-0.09	0.012
cg06363129	<i>SOSTDC1</i>	7	FALSE	0.34	0.42	-0.09	0.001
cg03813905	<i>NDUFB9</i>	8	TRUE	0.28	0.37	-0.09	0.011
cg01185080	<i>ZNF710</i>	15	TRUE	0.25	0.34	-0.09	0.005
cg25162921	<i>MTAP</i>	9	TRUE	0.24	0.33	-0.09	0.004
cg23904249	<i>MGC2574</i>	11	TRUE	0.59	0.68	-0.09	0.001
cg08005849	<i>HGF</i>	7	FALSE	0.38	0.47	-0.09	0.005
cg12477119	<i>CRKRS</i>	17	TRUE	0.30	0.39	-0.09	0.003
cg04561804	<i>TLOC1</i>	3	FALSE	0.30	0.39	-0.09	0.025
cg09494546	<i>SLC16A4</i>	1	FALSE	0.58	0.67	-0.09	0.017
cg24115040	<i>DLX5</i>	7	TRUE	0.42	0.51	-0.09	0.021
cg16706631	<i>HIST1H4E</i>	6	TRUE	0.29	0.38	-0.09	0.038
cg06609049	<i>THOP1</i>	19	TRUE	0.36	0.45	-0.09	0.016
cg08586737	<i>GCC1</i>	7	TRUE	0.30	0.39	-0.09	0.038
cg27546682	<i>STK40</i>	1	TRUE	0.29	0.38	-0.09	0.004

cg15298323	ACAT2	6	TRUE	0.62	0.71	-0.09	0.001
cg01745657	PLCXD2	3	TRUE	0.28	0.37	-0.09	0.005
cg04975920	TSPAN1	1	FALSE	0.47	0.56	-0.09	0.047
cg20050113	SLC9A2	2	TRUE	0.35	0.44	-0.09	0.016
cg03787486	ADH5	4	TRUE	0.24	0.34	-0.09	<0.001
cg01985396	DAAM2	6	FALSE	0.26	0.35	-0.10	<0.001
cg15780361	ALS2CR11	2	TRUE	0.33	0.43	-0.10	0.006
cg22496254	HCAP-G	4	FALSE	0.56	0.65	-0.10	0.035
cg23242898	DCC	18	TRUE	0.57	0.67	-0.10	0.011
cg06493080	HOXB7	17	TRUE	0.35	0.45	-0.10	0.038
cg10735607	TMEM109	11	TRUE	0.53	0.63	-0.10	0.048
cg19573166	SLC22A17	14	FALSE	0.47	0.57	-0.10	0.035
cg27413025	CYP20A1	2	TRUE	0.28	0.38	-0.10	<0.001
cg24745738	EDNRB	13	TRUE	0.22	0.32	-0.10	0.001
cg10003443	FOXA2	20	TRUE	0.36	0.46	-0.10	0.010
cg07455279	NDUFA3	19	TRUE	0.21	0.31	-0.10	0.046
cg27202708	CCDC185	1	TRUE	0.27	0.38	-0.11	0.001
cg03882305	TRIM50C	7	TRUE	0.38	0.49	-0.11	0.003
cg26777475	PCOLCE	7	FALSE	0.44	0.55	-0.11	0.048
cg04689061	PKIA	8	TRUE	0.31	0.42	-0.11	0.025
cg03454353	ZFP37	9	TRUE	0.45	0.56	-0.11	<0.001
cg20229788	GCKR	2	FALSE	0.37	0.49	-0.11	0.005
cg23970338	TSFM	12	TRUE	0.13	0.25	-0.12	0.010
cg21168622	ZNF350	19	TRUE	0.24	0.36	-0.12	0.032
cg22502502	TRIM38	6	FALSE	0.28	0.40	-0.12	0.002
cg08965324	LTA4H	12	TRUE	0.32	0.45	-0.13	0.032
cg20587336	ARMC1	8	TRUE	0.35	0.49	-0.14	0.006
cg07713361	APOL1	22	FALSE	0.41	0.55	-0.14	0.003
cg12992720	EDG4	19	TRUE	0.25	0.39	-0.14	0.001
cg25125453	SPTLC3	20	FALSE	0.44	0.58	-0.15	0.002
cg08942800	CRISP2	6	TRUE	0.36	0.52	-0.17	0.017

Table S4. List of DMCs in LT in the comparison between the DO and NDO groups

Target ID	Symbol	CHR	CPG Island	Beta DO	Beta OB	Delta Beta	p-value
cg10296238	<i>SPATC1L</i>	21	TRUE	0.59	0.47	0.12	0.029
cg18145505	<i>GREM1</i>	15	TRUE	0.35	0.23	0.12	0.013
cg23002761	<i>FBLIM1</i>	1	TRUE	0.31	0.19	0.11	0.026
cg10746737	<i>HLA-DRB5</i>	6	FALSE	0.71	0.61	0.11	0.018
cg09794131	<i>HYDIN</i>	16	TRUE	0.34	0.23	0.11	0.030
cg07747299	<i>SPATC1L</i>	21	TRUE	0.56	0.46	0.10	0.040
cg06851207	<i>FLJ10781</i>	19	TRUE	0.72	0.62	0.09	0.028
cg06361108	<i>CCNF</i>	16	TRUE	0.21	0.13	0.09	0.009
cg25902889	<i>FSD1</i>	19	FALSE	0.62	0.53	0.09	0.009
cg17483510	<i>GNB4</i>	3	TRUE	0.45	0.36	0.08	0.011
cg26764244	<i>GNG12</i>	1	TRUE	0.28	0.20	0.08	0.034
cg16670497	<i>GSTM2</i>	1	TRUE	0.44	0.36	0.08	0.024
cg17179881	<i>BIK</i>	22	TRUE	0.62	0.54	0.08	0.017
cg12699145	<i>TMC7</i>	16	TRUE	0.29	0.21	0.08	0.009
cg07404485	<i>PON1</i>	7	FALSE	0.38	0.31	0.08	0.002
cg06268694	<i>CELSR1</i>	22	TRUE	0.30	0.23	0.07	0.026
cg26577529	<i>KRT6E</i>	12	FALSE	0.73	0.65	0.07	0.016
cg04557383	<i>MT1H</i>	16	TRUE	0.43	0.35	0.07	0.005
cg19297232	<i>SMPD3</i>	16	TRUE	0.59	0.52	0.07	0.029
cg22039287	<i>RIT2</i>	18	FALSE	0.61	0.53	0.07	0.006
cg22609784	<i>MSX1</i>	4	TRUE	0.55	0.48	0.07	0.001
cg07640473	<i>SEMA3F</i>	3	TRUE	0.51	0.44	0.07	0.029
cg10447080	<i>FILIP1</i>	6	FALSE	0.37	0.30	0.07	0.012
cg18055394	<i>EPHA3</i>	3	TRUE	0.34	0.27	0.07	0.041
cg03283421	<i>CUZD1</i>	10	FALSE	0.72	0.65	0.07	0.034
cg08137040	<i>ZNF800</i>	7	TRUE	0.35	0.28	0.07	0.003
cg15534366	<i>CDH4</i>	20	FALSE	0.52	0.46	0.07	0.012
cg00563926	<i>TGFBR3</i>	1	TRUE	0.27	0.21	0.06	0.047
cg26525091	<i>MADCAM1</i>	19	TRUE	0.24	0.18	0.06	0.004
cg00949442	<i>ABCA3</i>	16	TRUE	0.24	0.18	0.06	0.002
cg06147863	<i>SPI1</i>	11	FALSE	0.67	0.61	0.06	0.001
cg07914866	<i>IRAK3</i>	12	TRUE	0.33	0.27	0.06	0.010
cg13391638	<i>FLJ13576</i>	7	TRUE	0.41	0.35	0.06	0.028
cg21974239	<i>MAPK12</i>	22	TRUE	0.22	0.16	0.06	0.007
cg00489401	<i>FLT4</i>	5	TRUE	0.20	0.14	0.06	0.021
cg15778232	<i>PHB2</i>	12	FALSE	0.63	0.57	0.06	0.019

cg13975369	<i>TSGA14</i>	7	TRUE	0.32	0.26	0.06	0.010
cg14620221	<i>OR8B8</i>	11	FALSE	0.80	0.74	0.06	0.018
cg08946332	<i>ALOX12</i>	17	TRUE	0.87	0.81	0.06	0.016
cg27038439	<i>MSX1</i>	4	TRUE	0.75	0.70	0.06	0.044
cg12499211	<i>SH2D2A</i>	1	TRUE	0.44	0.38	0.06	0.049
cg24789869	<i>DDX11</i>	12	TRUE	0.12	0.07	0.06	0.001
cg26069745	<i>HOXA2</i>	7	TRUE	0.25	0.19	0.06	0.021
cg27063525	<i>NUS1</i>	6	TRUE	0.17	0.11	0.06	0.049
cg03760483	<i>ALOX12</i>	17	TRUE	0.43	0.37	0.06	0.043
cg18815943	<i>FOXE3</i>	1	TRUE	0.13	0.07	0.06	0.001
cg07637239	<i>KCNK18</i>	10	FALSE	0.52	0.46	0.06	0.018
cg09328024	<i>DYRK3</i>	1	TRUE	0.28	0.22	0.06	0.022
cg00043004	<i>NOXO1</i>	16	TRUE	0.16	0.11	0.06	0.006
cg18501026	<i>DOCK3</i>	3	TRUE	0.23	0.17	0.06	0.002
cg19777470	<i>CRABP1</i>	15	TRUE	0.25	0.20	0.06	0.013
cg13707560	<i>NME5</i>	5	TRUE	0.42	0.37	0.05	0.026
cg09606564	<i>MFAP4</i>	17	FALSE	0.34	0.29	0.05	0.036
cg19428417	<i>RRAD</i>	16	TRUE	0.52	0.47	0.05	0.025
cg09238677	<i>C3AR1</i>	12	FALSE	0.47	0.41	0.05	0.047
cg00328227	<i>C1orf59</i>	1	TRUE	0.53	0.48	0.05	0.048
cg16352283	<i>FAM46B</i>	1	TRUE	0.52	0.47	0.05	0.031
cg21096915	<i>MGC16291</i>	10	TRUE	0.17	0.22	-0.05	0.013
cg19149785	<i>KLK8</i>	19	TRUE	0.65	0.70	-0.05	0.044
cg16330965	<i>SNAPC5</i>	15	TRUE	0.23	0.28	-0.05	0.012
cg06690548	<i>SLC7A11</i>	4	TRUE	0.73	0.78	-0.05	0.005
cg13817266	<i>HSPA6</i>	1	TRUE	0.35	0.40	-0.05	0.047
cg02104644	<i>SYT7</i>	11	TRUE	0.11	0.16	-0.05	0.046
cg10735607	<i>TMEM109</i>	11	TRUE	0.48	0.53	-0.05	0.013
cg15619125	<i>MAMDC4</i>	9	FALSE	0.44	0.49	-0.05	0.037
cg00754253	<i>HRASLS5</i>	11	FALSE	0.33	0.38	-0.05	0.035
cg13823701	<i>TNXB</i>	6	FALSE	0.27	0.33	-0.05	0.049
cg26125600	<i>PF4V1</i>	4	FALSE	0.38	0.43	-0.05	0.003
cg26205432	<i>PLN</i>	6	FALSE	0.56	0.61	-0.05	0.032
cg15784615	<i>LTBR</i>	12	FALSE	0.22	0.27	-0.05	0.013
cg14861570	<i>MMD</i>	17	FALSE	0.26	0.32	-0.05	0.001
cg09547190	<i>C9orf89</i>	9	TRUE	0.38	0.44	-0.05	0.009
cg23685580	<i>CATSPER2</i>	15	TRUE	0.81	0.87	-0.05	0.027
cg18940763	<i>XBP1</i>	22	TRUE	0.13	0.19	-0.05	0.013
cg05341115	<i>HYAL4</i>	7	FALSE	0.67	0.72	-0.05	0.001

cg14532519	<i>TCF20</i>	22	FALSE	0.58	0.63	-0.05	0.019
cg24603941	<i>MIA2</i>	14	FALSE	0.51	0.57	-0.05	0.023
cg12815142	<i>SPAG7</i>	17	TRUE	0.30	0.36	-0.05	0.037
cg04991214	<i>PFDN2</i>	1	FALSE	0.50	0.56	-0.05	0.050
cg14882700	<i>OTOP1</i>	4	TRUE	0.20	0.26	-0.05	0.037
cg06948408	<i>TMEM125</i>	1	TRUE	0.18	0.23	-0.05	0.017
cg18184219	<i>CEP170</i>	1	FALSE	0.73	0.79	-0.05	0.031
cg02741177	<i>PROL1</i>	4	FALSE	0.65	0.70	-0.05	0.005
cg03964111	<i>LR8</i>	7	FALSE	0.17	0.22	-0.05	0.003
cg17122311	<i>IL27</i>	16	FALSE	0.46	0.51	-0.05	0.040
cg10742801	<i>PRAP1</i>	10	FALSE	0.29	0.34	-0.05	0.006
cg01035422	<i>PLIN</i>	15	FALSE	0.70	0.76	-0.05	0.018
cg01895214	<i>LOC654342</i>	2	TRUE	0.49	0.54	-0.05	0.001
cg01040850	<i>MR1</i>	1	FALSE	0.53	0.59	-0.05	0.046
cg14851685	<i>CYP4F22</i>	19	FALSE	0.60	0.65	-0.05	0.036
cg05507459	<i>NXNL2</i>	9	TRUE	0.29	0.34	-0.05	0.001
cg00135393	<i>FGG</i>	4	FALSE	0.31	0.37	-0.05	0.036
cg25017250	<i>APOC4</i>	19	TRUE	0.28	0.34	-0.05	0.038
cg13431205	<i>RB1</i>	13	TRUE	0.51	0.57	-0.05	0.039
cg10574499	<i>UNQ2446</i>	16	FALSE	0.28	0.34	-0.06	0.037
cg02655623	<i>HSA277841</i>	17	FALSE	0.61	0.67	-0.06	0.003
cg03894103	<i>PREPL</i>	2	FALSE	0.70	0.76	-0.06	0.033
cg07514381	<i>LRRC2</i>	3	FALSE	0.69	0.75	-0.06	0.042
cg14477619	<i>NPC1L1</i>	7	FALSE	0.41	0.47	-0.06	0.013
cg04106785	<i>CDK5R1</i>	17	TRUE	0.32	0.37	-0.06	0.010
cg17229388	<i>MGC35169</i>	13	TRUE	0.70	0.76	-0.06	0.022
cg13849691	<i>ACSL5</i>	10	TRUE	0.78	0.84	-0.06	0.050
cg06048973	<i>ACTC</i>	15	FALSE	0.50	0.55	-0.06	0.044
cg08137716	<i>TTLL6</i>	17	FALSE	0.71	0.76	-0.06	0.022
cg24652919	<i>WDR58</i>	16	FALSE	0.64	0.69	-0.06	0.039
cg20199333	<i>F2</i>	11	FALSE	0.48	0.54	-0.06	0.016
cg24898863	<i>S100A8</i>	1	FALSE	0.23	0.29	-0.06	0.002
cg20099806	<i>CCDC47</i>	17	FALSE	0.25	0.31	-0.06	0.004
cg18294158	<i>ORC5L</i>	7	FALSE	0.66	0.72	-0.06	0.007
cg15398520	<i>LPAL2</i>	6	FALSE	0.35	0.41	-0.06	0.027
cg25677709	<i>NDST1</i>	5	FALSE	0.50	0.56	-0.06	0.016
cg24269657	<i>F7</i>	13	FALSE	0.41	0.46	-0.06	0.006
cg00466492	<i>CTXN1</i>	19	TRUE	0.76	0.81	-0.06	0.025
cg01484156	<i>NCALD</i>	8	FALSE	0.34	0.40	-0.06	<0.001

cg20584011	<i>ZDHHC11</i>	5	TRUE	0.72	0.78	-0.06	0.002
cg16153267	<i>RB1</i>	13	TRUE	0.56	0.61	-0.06	0.008
cg22337624	<i>DHX38</i>	16	FALSE	0.27	0.33	-0.06	0.003
cg06850526	<i>MGC15523</i>	17	TRUE	0.27	0.33	-0.06	0.039
cg18901980	<i>KRT25A</i>	17	FALSE	0.68	0.74	-0.06	0.003
cg16639185	<i>LGTN</i>	1	TRUE	0.33	0.39	-0.06	0.031
cg10303487	<i>DPYS</i>	8	TRUE	0.07	0.13	-0.06	0.033
cg00579402	<i>FUT6</i>	19	FALSE	0.52	0.58	-0.06	0.034
cg04837071	<i>NOXA1</i>	9	TRUE	0.53	0.59	-0.06	0.033
cg12694870	<i>HPD</i>	12	FALSE	0.38	0.44	-0.06	0.027
cg07233761	<i>ESM1</i>	5	TRUE	0.27	0.33	-0.06	0.031
cg22171829	<i>PDK4</i>	7	TRUE	0.12	0.18	-0.06	0.037
cg15201291	<i>CYP2C8</i>	10	FALSE	0.53	0.60	-0.06	0.014
cg05985767	<i>ANPEP</i>	15	TRUE	0.36	0.42	-0.06	0.008
cg07163603	<i>HLA-A</i>	6	FALSE	0.34	0.40	-0.06	0.032
cg24920358	<i>PPIE</i>	1	TRUE	0.32	0.38	-0.06	0.046
cg03835296	<i>SLC17A1</i>	6	FALSE	0.32	0.38	-0.07	0.014
cg12542604	<i>ANKS1A</i>	6	TRUE	0.14	0.20	-0.07	0.020
cg07745725	<i>PSG3</i>	19	FALSE	0.55	0.62	-0.07	0.008
cg02523400	<i>SERPIND1</i>	22	FALSE	0.34	0.40	-0.07	0.048
cg24792360	<i>FUCA1</i>	1	TRUE	0.34	0.41	-0.07	0.011
cg27420123	<i>FSHB</i>	11	FALSE	0.34	0.41	-0.07	0.007
cg23834593	<i>HNF4A</i>	20	FALSE	0.37	0.44	-0.07	0.029
cg10414946	<i>MS4A2</i>	11	FALSE	0.47	0.54	-0.07	0.020
cg07150830	<i>NOS2A</i>	17	FALSE	0.52	0.59	-0.07	0.020
cg25514304	<i>PSEN2</i>	1	FALSE	0.42	0.49	-0.07	0.041
cg15783800	<i>HAK</i>	18	TRUE	0.36	0.43	-0.07	0.007
cg27440834	<i>SNX4</i>	3	FALSE	0.56	0.63	-0.07	0.038
cg02735486	<i>ANK2</i>	4	TRUE	0.46	0.53	-0.07	0.030
cg15149645	<i>P8</i>	16	FALSE	0.17	0.24	-0.07	0.003
cg13614083	<i>KCNAB2</i>	1	TRUE	0.51	0.58	-0.07	0.032
cg12003230	<i>LINC00313</i>	21	FALSE	0.48	0.55	-0.07	0.017
cg02399455	<i>SRI</i>	7	FALSE	0.54	0.61	-0.07	0.025
cg15357639	<i>OGG1</i>	3	TRUE	0.78	0.85	-0.07	0.013
cg07109801	<i>NDUFAF3</i>	3	TRUE	0.50	0.57	-0.07	0.018
cg19464944	<i>FCGR1A</i>	1	FALSE	0.31	0.39	-0.07	0.038
cg20615832	<i>PF4V1</i>	4	TRUE	0.28	0.35	-0.07	0.022
cg23322523	<i>TRIM55</i>	8	FALSE	0.26	0.33	-0.07	0.013
cg05976325	<i>LOC284912</i>	22	FALSE	0.51	0.58	-0.07	0.038

cg13520715	<i>LINC00479</i>	21	FALSE	0.70	0.77	-0.07	0.022
cg25657700	<i>SNRPN</i>	15	TRUE	0.54	0.62	-0.07	0.026
cg04994456	<i>RNF186</i>	1	FALSE	0.40	0.48	-0.08	0.010
cg19554294	<i>VN1R2</i>	19	FALSE	0.51	0.58	-0.08	0.010
cg18429742	<i>ZDHHC11</i>	5	TRUE	0.64	0.72	-0.08	0.016
cg13705284	<i>ACOX2</i>	3	FALSE	0.19	0.27	-0.08	0.012
cg13726463	<i>COX6A2</i>	16	TRUE	0.51	0.58	-0.08	0.004
cg26955850	<i>OXT</i>	20	TRUE	0.37	0.45	-0.08	0.050
cg04662594	<i>EPB49</i>	8	FALSE	0.32	0.40	-0.08	0.002
cg20131968	<i>CCDC47</i>	17	FALSE	0.33	0.42	-0.08	0.020
cg03743584	<i>PRAP1</i>	10	FALSE	0.19	0.27	-0.08	0.003
cg06784466	<i>FPRL2</i>	19	FALSE	0.39	0.48	-0.08	0.008
cg11108890	<i>VAMP5</i>	2	TRUE	0.10	0.18	-0.08	0.040
cg26631477	<i>GPR125</i>	4	TRUE	0.19	0.27	-0.08	<0.001
cg02142461	<i>LYAR</i>	4	FALSE	0.72	0.80	-0.08	0.013
cg03533858	<i>MORN1</i>	1	FALSE	0.43	0.51	-0.08	0.029
cg08510456	<i>BSN</i>	3	TRUE	0.39	0.47	-0.08	0.039
cg06194808	<i>MGC9712</i>	7	FALSE	0.48	0.57	-0.09	0.008
cg25598083	<i>ACOT2</i>	14	FALSE	0.48	0.57	-0.09	0.025
cg07251788	<i>CLTCL1</i>	22	TRUE	0.42	0.51	-0.09	0.028
cg18678121	<i>SEC61A2</i>	10	TRUE	0.50	0.60	-0.09	0.011
cg03733371	<i>LIPH</i>	3	FALSE	0.44	0.54	-0.10	0.047
cg02192965	<i>SLC3A1</i>	2	FALSE	0.60	0.70	-0.10	0.023
cg24333473	<i>ZNF597</i>	16	TRUE	0.37	0.47	-0.10	0.042
cg17264470	<i>FGF21</i>	19	FALSE	0.76	0.87	-0.11	0.016
cg22730830	<i>PRSS21</i>	16	TRUE	0.57	0.68	-0.11	0.003
cg24362726	<i>C4orf33</i>	4	FALSE	0.31	0.42	-0.11	0.039
cg01600189	<i>FLJ20444</i>	9	TRUE	0.18	0.30	-0.11	0.005
cg24092914	<i>VHL</i>	3	TRUE	0.46	0.58	-0.12	0.021
cg26267561	<i>OXT</i>	20	TRUE	0.68	0.84	-0.15	0.001
cg20655558	<i>DNAJB7</i>	22	FALSE	0.56	0.72	-0.16	0.035
cg23349790	<i>IGSF21</i>	1	TRUE	0.12	0.30	-0.18	<0.001

Table S5 . Gene ontology enrichment analysis using the genes with DMCs in SAT

GO term	Fold enrichment	Count	p value	Genes
Regulation of cellular ketone metabolic process	22.1	4	0.001	<i>LEP, CPT1B, IRS1, ADIPOQ</i>
Regulation of carbohydrate biosynthetic process	44.9	3	0.002	<i>LEP, IRS1, ADIPOQ</i>
Muscle organ development	7.5	5	0.004	<i>CPT1B, TSC1, MYF5, SGCD, ALX4</i>
Regulation of lipid metabolic process	11.2	4	0.005	<i>LEP, CPT1B, IRS1, ADIPOQ</i>
Regulation of glucose metabolic process	27	3	0.005	<i>LEP, IRS1, ADIPOQ</i>
Fatty acid catabolic process	26.2	3	0.006	<i>LEP, CPT1B, ADIPOQ</i>
Regulation of cellular carbohydrate metabolic process	24.8	3	0.006	<i>LEP, IRS1, ADIPOQ</i>
Regulation of carbohydrate metabolic process	24.2	3	0.006	<i>LEP, IRS1, ADIPOQ</i>
Regulation of fatty acid metabolic process	19.3	3	0.010	<i>CPT1B, IRS1, ADIPOQ</i>
Embryonic skeletal system morphogenesis	16.6	3	0.013	<i>HOXA4, MYF5, ALX4</i>
Skeletal system development	4.9	5	0.017	<i>HOXA4, CLEC3A, KAZALD1, MYF5, ALX4</i>
Development of primary female sexual characteristics	13.7	3	0.019	<i>LEP, FGF7, FANCG</i>
Cell adhesion	3.1	7	0.020	<i>TSC1, MYF5, SIGLEC7, LGALS7, NINJ2, CTNNA1, DST</i>
Biological adhesion	3.1	7	0.020	<i>TSC1, MYF5, SIGLEC7, LGALS7, NINJ2, CTNNA1, DST</i>
Cellular lipid catabolic process	12.4	3	0.023	<i>LEP, CPT1B, ADIPOQ</i>
Regulation of gluconeogenesis	78.7	2	0.025	<i>LEP, ADIPOQ</i>
Negative regulation of response to stimulus	9.4	3	0.038	<i>LEP, IRS1, ADIPOQ</i>
Response to insulin stimulus	9.4	3	0.038	<i>LEP, TSC1, IRS1</i>
Phosphatidylcholine biosynthetic process	44.9	2	0.043	<i>CPT1B, FGF7</i>
Organic acid catabolic process	8.5	3	0.046	<i>LEP, CPT1B, ADIPOQ</i>
Carboxylic acid catabolic process	8.5	3	0.046	<i>LEP, CPT1B, ADIPOQ</i>
Skeletal system morphogenesis	8.4	3	0.047	<i>HOXA4, MYF5, ALX4</i>

Table S6 . Gene ontology enrichment analysis using the genes with DMCs in VAT

GO term	Fold enrichment	Count	p value	Genes
Regulation of apoptosis	1.9	26	0.003	<i>DCC, MEF2C, ADA, TGFB2, EDNRB, ATG5, PAX7, GRID2, TNFRSF19, MYC, TERT, ERCC1, FGD4, CD3E, SKP2, TRIO, HGF, CSDA, YWHAE, BRCA1, JMY, KCNH8, IL12B, TIAF1, PDCD7, DNM2</i>
Regulation of programmed cell death	1.9	26	0.003	<i>DCC, MEF2C, ADA, TGFB2, EDNRB, ATG5, PAX7, GRID2, TNFRSF19, MYC, TERT, ERCC1, FGD4, CD3E, SKP2, TRIO, HGF, CSDA, YWHAE, BRCA1, JMY, KCNH8, IL12B, TIAF1, PDCD7, DNM2</i>
Regulation of cell death	1.9	26	0.003	<i>DCC, MEF2C, ADA, TGFB2, EDNRB, ATG5, PAX7, GRID2, TNFRSF19, MYC, TERT, ERCC1, FGD4, CD3E, SKP2, TRIO, HGF, CSDA, YWHAE, BRCA1, JMY, KCNH8, IL12B, TIAF1, PDCD7, DNM2</i>
Negative regulation of lyase activity	5.3	5	0.014	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6</i>
Negative regulation of adenylate cyclase activity	5.3	5	0.014	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6</i>
Negative regulation of cyclase activity	5.3	5	0.014	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6</i>
Negative regulation of neuron differentiation	7.1	4	0.018	<i>PHOX2B, FOXA2, DLL1, ASPM</i>
Negative regulation of apoptosis	2.1	13	0.019	<i>MEF2C, SKP2, HGF, CSDA, ADA, EDNRB, ATG5, PAX7, KCNH8, TIAF1, MYC, ERCC1, TERT</i>
DNA catabolic process	4.9	5	0.019	<i>GTF2H4, DNASE1L2, MYC, XRN2, ERCC1</i>
Negative regulation of programmed cell death	2.1	13	0.02	<i>MEF2C, SKP2, HGF, CSDA, ADA, EDNRB, ATG5, PAX7, KCNH8, TIAF1, MYC, ERCC1, TERT</i>
Negative regulation of cell death	2.1	13	0.021	<i>MEF2C, SKP2, HGF, CSDA, ADA, EDNRB, ATG5, PAX7, KCNH8, TIAF1, MYC, ERCC1, TERT</i>
Regulation of adenylate cyclase activity	3.6	6	0.024	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Regulation of cell cycle	2.1	12	0.027	<i>E2F1, CCNT2, SKP2, RPRM, BRIP1, NUSAP1, HERC2, CHFR, PKIA, MYC, BRCA1, TGFB2</i>
Regulation of cyclase activity	3.5	6	0.027	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Regulation of camp biosynthetic process	3.5	6	0.029	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Regulation of lyase activity	3.5	6	0.029	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Regulation of camp metabolic process	3.4	6	0.032	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>

Positive regulation of apoptosis	1.9	14	0.033	<i>DCC, CD3E, SKP2, TRIO, YWHAE, BRCA1, TGFB2, JMY, TNFRSF19, IL12B, MYC, PDCD7, DNM2, FGD4</i>
Hepatocyte growth factor receptor signaling pathway	58.3	2	0.034	<i>MET, HGF</i>
Positive regulation of programmed cell death	1.9	14	0.035	<i>DCC, CD3E, SKP2, TRIO, YWHAE, BRCA1, TGFB2, JMY, TNFRSF19, IL12B, MYC, PDCD7, DNM2, FGD4</i>
Positive regulation of cell death	1.9	14	0.036	<i>DCC, CD3E, SKP2, TRIO, YWHAE, BRCA1, TGFB2, JMY, TNFRSF19, IL12B, MYC, PDCD7, DNM2, FGD4</i>
Lymphocyte activation during immune response	9.7	3	0.037	<i>RELB, IL12B, ADA</i>
Cell death	1.6	20	0.039	<i>E2F1, MEF2C, DCC, TAOK2, FGF14, TRIO, YWHAE, BRCA1, RRAGC, TGFB2, ATXN2, BNIPL, RASSF5, APOL1, ATG5, TNFRSF19, TIAF1, MYC, PDCD7, FGD4</i>
Regulation of nucleotide biosynthetic process	3.2	6	0.04	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Regulation of cyclic nucleotide biosynthetic process	3.2	6	0.04	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Death	1.6	20	0.042	<i>E2F1, MEF2C, DCC, TAOK2, FGF14, TRIO, YWHAE, BRCA1, RRAGC, TGFB2, ATXN2, BNIPL, RASSF5, APOL1, ATG5, TNFRSF19, TIAF1, MYC, PDCD7, FGD4</i>
Regulation of cyclic nucleotide metabolic process	3.1	6	0.044	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Cell migration	2.1	10	0.047	<i>DCC, PHOX2B, EDNRB, TAOK2, MET, ENPEP, IL12B, SRF, YWHAE, TGFB2</i>
Second-messenger-mediated signaling	2.2	9	0.048	<i>EDNRB, P2RY6, HRH1, ADCY7, GALR1, GRM6, HIST1H4E, GNAS, FEN1</i>
Regulation of nucleotide metabolic process	3	6	0.049	<i>EDNRB, GRM3, ADCY7, GALR1, GRM6, GNAS</i>
Regulation of survival gene product expression	8.3	3	0.049	<i>MEF2C, SKP2, MYC</i>

Table S7 . Gene ontology enrichment analysis using the genes with DMCs in LT

GO term	Fold Enrichment	Count	p value	Genes
Response to wounding	2.9	13	0.002	<i>C3AR1, KLK8, S100A8, NDST1, IL27, F7, SYT7, EPHA3, FGG, HNF4A, F2, MS4A2, SERPIND1</i>
Regulation of cell growth	4.2	7	0.006	<i>HNF4A, SEMA3F, RB1, ESM1, GREM1, CDH4, ALOX12</i>
Regulation of body fluid levels	5	6	0.007	<i>FGG, HNF4A, OXT, F2, SERPIND1, F7</i>
Regulation of cell size	4	7	0.008	<i>HNF4A, SEMA3F, TGFBR3, RB1, GREM1, CDH4, ALOX12</i>
Regulation of cellular component size	3.4	8	0.008	<i>HNF4A, SEMA3F, TGFBR3, RB1, EPB49, GREM1, CDH4, ALOX12</i>
Blood coagulation	5.7	5	0.011	<i>FGG, HNF4A, F2, SERPIND1, F7</i>
Coagulation	5.7	5	0.011	<i>FGG, HNF4A, F2, SERPIND1, F7</i>
Homeostatic process	2.2	14	0.011	<i>SRI, C3AR1, OXT, CCDC47, RB1, EPHA3, HNF4A, APOC4, PLN, F2, NPC1L1, TGFBR3, DYRK3, MT1H</i>
Hemostasis	5.4	5	0.013	<i>FGG, HNF4A, F2, SERPIND1, F7</i>
Regulation of homeostatic process	5.1	5	0.016	<i>KLK8, OXT, F2, SPI1, MS4A2</i>
Di-, tri-valent inorganic cation homeostasis	3.4	7	0.016	<i>SRI, C3AR1, OXT, PLN, F2, CCDC47, MT1H</i>
Superoxide metabolic process	14	3	0.019	<i>NOXO1, NOXA1, ALOX12</i>
Wound healing	3.7	6	0.023	<i>FGG, HNF4A, F2, SERPIND1, F7, SYT7</i>
Regulation of nervous system development	3.6	6	0.024	<i>HOXA2, CDK5R1, KLK8, SEMA3F, OXT, CDH4</i>
Regulation of cell morphogenesis	4.5	5	0.025	<i>KLK8, SEMA3F, TGFBR3, FBLIM1, CDH4</i>
Regulation of neuron differentiation	4.4	5	0.027	<i>HOXA2, CDK5R1, KLK8, SEMA3F, CDH4</i>
Regulation of cell morphogenesis involved in differentiation	6.1	4	0.028	<i>KLK8, SEMA3F, TGFBR3, CDH4</i>
Chemical homeostasis	2.3	10	0.030	<i>SRI, C3AR1, HNF4A, APOC4,</i>

				<i>OXT, PLN, F2, NPC1L1, CCDC47, MT1H</i>
Regulation of cell development	3.4	6	0.031	<i>HOXA2, CDK5R1, KLK8, SEMA3F, TGFBR3, CDH4</i>
Negative regulation of cellular component organization	4.1	5	0.033	<i>IRAK3, KLK8, SEMA3F, TGFBR3, EPB49</i>
Calcium ion transport	4.1	5	0.033	<i>SRI, CATSPER2, PLN, F2, PSEN2</i>
Response to prostaglandin stimulus	58.3	2	0.034	<i>OXT, TGFBR3</i>
Response to prostaglandin E stimulus	58.3	2	0.034	<i>OXT, TGFBR3</i>
Muscle organ development	3.3	6	0.034	<i>SRI, MSX1, MAPK12, PLN, VAMP5, TGFBR3</i>
Cation homeostasis	2.9	7	0.035	<i>SRI, C3AR1, OXT, PLN, F2, CCDC47, MT1H</i>
Negative regulation of cell growth	5.1	4	0.044	<i>HNF4A, SEMA3F, RB1, GREM1</i>
Cellular di-, tri-valent inorganic cation homeostasis	3.1	6	0.044	<i>SRI, C3AR1, OXT, PLN, F2, MT1H</i>
Myeloid cell differentiation	5	4	0.045	<i>PSEN2, TGFBR3, DYRK3, RB1</i>

Table S8. Differential gene expression in WB in the comparison between DO and NDO groups

Symbol	Accession	logFC	p value
<i>RAP1GAP</i>	NM_002885.1	1.430	0.001
<i>UTS2</i>	NM_006786.2	1.307	0.009
<i>AMFR</i>	NM_001144.4	1.245	0.020
<i>NFIX</i>	NM_002501.2	1.175	0.023
<i>LOC100131164</i>	XM_001721919.1	1.160	0.002
<i>MCOLN1</i>	NM_020533.1	1.152	<0.001
<i>C16ORF35</i>	NM_001039476.1	1.126	<0.001
<i>RNF182</i>	NM_152737.2	1.101	0.001
<i>SLC4A1</i>	NM_000342.2	1.096	<0.001
<i>HSPC157</i>	NR_023918.1	1.068	0.037
<i>SOCS1</i>	NM_003745.1	1.064	0.008
<i>KRT1</i>	NM_006121.3	1.004	0.001
<i>USF1</i>	NM_007122.3	0.993	0.013

<i>UTS2</i>	NM_021995.1	0.969	0.043
<i>C17ORF97</i>	NM_001013672.3	0.948	0.045
<i>ZDHHC19</i>	NM_001039617.1	0.912	0.001
<i>C16ORF35</i>	NM_012075.1	0.899	<0.001
<i>RBM38</i>	NM_017495.4	0.880	0.029
<i>CMBL</i>	NM_138809.3	0.853	0.032
<i>VWCE</i>	NM_152718.2	0.841	0.005
<i>LOC100128714</i>	XM_001722756.1	0.833	<0.001
<i>TSTA3</i>	NM_003313.2	0.828	0.001
<i>NR1D1</i>	NM_021724.2	0.827	0.002
<i>TMEM86B</i>	NM_173804.3	0.827	0.005
<i>ACSL6</i>	NM_001009185.1	0.823	<0.001
<i>TRIM58</i>	NM_015431.3	0.821	0.002
<i>SCARNA17</i>	NR_003003.2	0.820	<0.001
<i>PLEK2</i>	NM_016445.1	0.813	0.007
<i>SLC6A10P</i>	NR_003083.2	0.810	0.010
<i>SLC22A16</i>	NM_033125.2	-0.843	0.001
<i>NAPSA</i>	NM_004851.1	-0.849	0.020
<i>LACTB2</i>	NM_016027.1	-0.870	0.001
<i>LOC653071</i>	XM_930721.1	-0.885	0.006
<i>ODF2L</i>	NM_001007022.1	-0.893	0.003
<i>SPAST</i>	NM_199436.1	-0.935	0.000
<i>ORM2</i>	NM_000608.2	-0.975	<0.001
<i>COPG2</i>	NM_012133.2	-0.977	0.005
<i>NKX3-1</i>	NM_006167.2	-0.988	0.002
<i>LOC283547</i>	XM_378454.3	-1.007	<0.001
<i>PLCB1</i>	NM_015192.2	-1.013	0.004
<i>ORM1</i>	NM_000607.1	-1.067	0.050
<i>MFF</i>	NM_020194.4	-1.273	0.040
<i>LOC253039</i>	NR_024408.1	-1.348	0.002

Table S9. Differential gene expression in SAT in the comparison between DO and NDO groups

Symbol	Accession	logFC	p value
<i>CCL20</i>	NM_004591.1	1.310	0.032
<i>SLAMF1</i>	NM_003037.1	1.068	0.034
<i>AMFR</i>	NM_001144.4	0.955	0.005
<i>PTX3</i>	NM_002852.2	0.937	0.035
<i>ACTA1</i>	NM_001100.3	0.862	0.013
<i>LIPG</i>	NM_006033.2	0.831	0.021
<i>TNC</i>	NM_002160.2	0.828	0.011
<i>EDN1</i>	NM_001955.2	0.815	0.018
<i>SERPINA3</i>	NM_001085.4	0.809	0.026
<i>LOC645313</i>	XR_017585.2	-0.829	0.026
<i>MS4A4A</i>	NM_148975.1	-0.829	0.003
<i>ITGB1BP1</i>	NM_022334.3	-0.854	0.020
<i>MIR1974</i>	NR_031738.1	-0.966	0.011
<i>SEL1L2</i>	NM_025229.1	-1.032	0.004
<i>STMN2</i>	NM_007029.2	-1.127	<0.001
<i>LOC644936</i>	NR_004845.1	-1.164	0.016
<i>STMN2</i>	NM_007029.2	-1.333	<0.001

Table S10. Differential gene expression in VAT in the comparison between DO and NDO groups

Symbol	Accession	logFC	p value
<i>AMFR</i>	NM_001144.4	1.149	0.034
<i>G3BP2</i>	NM_203504.1	1.020	0.021
<i>G3BP2</i>	NM_203504.1	0.829	0.022
<i>GZMH</i>	NM_033423.3	-0.832	<0.001
<i>RNU1A3</i>	NR_004430.1	-0.860	0.028
<i>DHRS9</i>	NM_005771.3	-0.860	0.036
<i>LOC648984</i>	XM_938063.1	-0.868	<0.001
<i>CCL18</i>	NM_002988.2	-0.884	0.037
<i>NR4A3</i>	NM_173199.1	-0.996	0.006
<i>ACP5</i>	NM_001611.2	-1.011	0.011
<i>RNU1-3</i>	NR_004408.1	-1.015	0.046
<i>ALAS2</i>	NM_001037968.1	-1.047	0.009
<i>HBE1</i>	NM_005330.3	-1.070	0.004
<i>RNU1G2</i>	NR_004426.1	-1.081	0.038
<i>RNU1-5</i>	NR_004400.1	-1.088	0.028
<i>HSPA1B</i>	NM_005346.3	-1.100	0.034
<i>DEFB1</i>	NM_005218.3	-1.133	0.012
<i>KLF4</i>	NM_004235.3	-1.225	0.038
<i>KLF4</i>	NM_004235.3	-1.366	0.044
<i>JUN</i>	NM_002228.3	-1.389	0.031
<i>LOC644936</i>	NR_004845.1	-1.402	0.037
<i>HBD</i>	NM_000519.3	-1.443	0.001
<i>NR4A2</i>	NM_006186.2	-1.547	0.034
<i>HBA1</i>	NM_000558.3	-1.731	0.006
<i>LOC731682</i>	XM_001129369.1	-1.877	0.010
<i>HBG2</i>	NM_000184.2	-1.899	0.001
<i>HBG1</i>	NM_000559.2	-2.020	0.001
<i>FOS</i>	NM_005252.2	-2.757	0.021
<i>FOSB</i>	NM_006732.1	-3.175	0.024

Table S11. Differential gene expression in LT in the comparison between DO and NDO groups

Symbol	Accession	logFC	p value
<i>HLA-DRB1</i>	NM_002124.1	1.447	0.043
<i>PLA2G2A</i>	NM_000300.2	1.179	0.026
<i>LOC729708</i>	XM_001725700.1	-1.053	0.039
<i>LOC100132564</i>	XM_001713808.1	-1.091	0.049

Table S12. List of genes with correlation between alteration of DNA methylation and differential gene expression in WB

Symbol	Target ID	Delta Beta	p value (Delta Beta)	log FC	p value (logFC)
<i>BRDT</i>	cg14732540	0.086	0.008	-0.132	0.007
<i>PSG6</i>	cg11151665	0.064	<0.001	-0.125	0.029
<i>PPP2R2D</i>	cg21750602	0.039	0.044	-0.196	0.029
<i>GPR175</i>	cg13728650	0.031	0.006	-0.193	0.037
<i>KRT13</i>	cg10742225	0.027	0.017	-0.132	0.015
<i>C21orf94</i>	cg17266238	0.025	0.032	-0.140	0.047
<i>PSG6</i>	cg17642353	0.022	0.040	-0.125	0.029
<i>HBQ1</i>	cg17714030	0.019	0.008	-0.570	0.001
<i>HBD</i>	cg20609368	0.016	0.041	-1.443	0.001
<i>SLC7A6OS</i>	cg27077685	0.010	0.025	-0.283	0.024
<i>STEAP3</i>	cg04749104	0.010	0.038	-0.176	0.010
<i>THSD1</i>	cg16114640	0.009	0.013	-0.169	0.004
<i>PRMT2</i>	cg06725035	0.008	0.018	-0.295	0.007
<i>ASAH1</i>	cg13563405	-0.004	0.048	0.164	0.004
<i>TTC9C</i>	cg24515202	-0.004	0.027	0.195	0.049
<i>APBA1</i>	cg15840658	-0.005	0.037	0.138	0.037
<i>APBA1</i>	cg15623573	-0.005	0.048	0.138	0.037
<i>BCKDHB</i>	cg15256539	-0.006	0.020	0.191	0.048
<i>BCKDHB</i>	cg15256539	-0.006	0.020	0.284	0.009
<i>PPM1J</i>	cg12687922	-0.006	0.024	0.092	0.039
<i>RET</i>	cg05621401	-0.008	0.014	0.155	0.035
<i>LARGE</i>	cg05670348	-0.008	0.028	0.301	0.019
<i>MEIS2</i>	cg02917381	-0.008	0.005	0.109	0.027
<i>RBKS</i>	cg06869899	-0.009	0.017	0.176	0.036
<i>MBD6</i>	cg25107978	-0.012	0.015	0.334	0.043

<i>ERCC8</i>	cg11649654	-0.012	0.047	0.239	0.001
<i>PPP1R3D</i>	cg08966023	-0.013	0.044	0.165	0.045
<i>GOSR1</i>	cg19098314	-0.014	0.002	0.139	0.033
<i>RFK</i>	cg13789236	-0.014	0.009	0.127	0.032
<i>PLEKHA1</i>	cg01246254	-0.020	<0.001	0.282	0.040
<i>IRX3</i>	cg24662961	-0.020	0.003	0.774	0.021
<i>DPH2</i>	cg25955969	-0.026	0.035	0.163	0.026
<i>IGF2</i>	cg02166532	-0.027	0.008	0.132	0.024
<i>LRPPRC</i>	cg26538116	-0.027	0.013	0.227	0.024
<i>SNX16</i>	cg06027949	-0.034	0.011	0.435	0.032
<i>FLJ44060</i>	cg08489623	-0.041	0.032	0.128	0.034
<i>CRB3</i>	cg03258472	-0.046	0.026	0.173	0.033
<i>BARHL2</i>	cg17241310	-0.046	0.036	0.255	0.004
<i>C14orf105</i>	cg19903229	-0.051	0.013	0.132	0.012
<i>SNX4</i>	cg16468910	-0.054	0.022	0.212	0.015
<i>HMP19</i>	cg07884019	-0.062	0.047	0.119	0.031
<i>EDNRB</i>	cg24745738	-0.101	0.001	0.193	0.026

Table S13. List of genes with correlation between alteration of DNA methylation and differential gene expression in SAT

Symbol	Target ID	Delta Beta	<i>p</i> value (Delta Beta)	log FC	<i>p</i> value (logFC)
<i>LEP</i>	cg12782180	0.056	0.008	-0.352	0.022
<i>ZNF3</i>	cg00929606	0.054	0.023	-0.142	0.001
<i>CAPSL</i>	cg24202119	0.028	0.040	-0.166	0.006
<i>KCNQ1</i>	cg17229197	0.026	0.019	-0.293	<0.001
<i>KCNQ1</i>	cg27491887	0.024	0.037	-0.293	<0.001
<i>C1QC</i>	cg11393848	0.023	0.029	-0.600	0.007
<i>CTSE</i>	cg04457794	0.015	0.021	-0.232	0.018
<i>CLTA</i>	cg26966384	0.015	0.035	-0.206	0.003
<i>CLTA</i>	cg26966384	0.015	0.035	-0.174	0.027
<i>NIT1</i>	cg10053203	0.015	0.010	-0.284	0.006
<i>ST7L</i>	cg01183669	0.015	0.009	-0.145	0.031
<i>OPRM1</i>	cg14262937	0.014	0.022	-0.129	0.013
<i>OPRM1</i>	cg14262937	0.014	0.022	-0.198	<0.001
<i>PTGER3</i>	cg12739034	0.012	0.009	-0.635	0.001
<i>DHFR</i>	cg16161425	0.011	0.040	-0.170	0.047

<i>PTPRO</i>	cg27196745	0.008	0.043	-0.447	0.011
<i>POFUT1</i>	cg25811820	0.006	0.016	-0.078	0.048
<i>ULBP1</i>	cg25589890	0.006	0.041	-0.173	0.015
<i>SFRS3</i>	cg08027745	0.005	0.044	-0.406	0.017
<i>TSC22D4</i>	cg08487374	0.005	0.016	-0.292	0.010
<i>CCDC5</i>	cg18307767	0.004	0.046	-0.219	0.047
<i>POP5</i>	cg07236358	0.004	0.042	-0.310	0.031
<i>F5</i>	cg09891761	-0.004	0.032	0.559	0.007
<i>DICER1</i>	cg16184930	-0.005	0.016	0.146	0.011
<i>GUCY1A2</i>	cg23984434	-0.005	0.030	0.131	0.021
<i>USP48</i>	cg20956373	-0.005	0.028	0.347	0.048
<i>MLL5</i>	cg05566397	-0.006	0.045	0.542	0.008
<i>AMPH</i>	cg10293925	-0.007	0.002	0.660	0.011
<i>YWHAB</i>	cg07064406	-0.008	0.047	0.156	0.045
<i>ZNF273</i>	cg05306735	-0.013	0.016	0.189	0.032
<i>CUGBP2</i>	cg15777781	-0.015	0.014	0.338	0.014
<i>LRRC39</i>	cg26117431	-0.015	0.009	0.129	0.005
<i>TUB</i>	cg15480475	-0.015	0.019	0.427	0.041
<i>TOMM34</i>	cg11454415	-0.017	0.014	0.325	0.017
<i>DNM1L</i>	cg27387222	-0.017	0.017	0.327	0.025
<i>CLN8</i>	cg23833896	-0.020	0.006	0.227	0.023
<i>C1orf124</i>	cg15459773	-0.021	0.046	0.183	0.005
<i>C1orf124</i>	cg15459773	-0.021	0.046	0.233	0.031
<i>C11orf47</i>	cg18103150	-0.021	0.012	0.211	0.031
<i>PDE4D</i>	cg05992340	-0.022	0.008	0.405	0.033
<i>SCT</i>	cg05782292	-0.025	0.048	0.075	0.038
<i>TCAP</i>	cg01680823	-0.026	0.049	0.228	0.011
<i>ADRA1D</i>	cg09614401	-0.030	0.039	0.102	0.017
<i>BVES</i>	cg20624391	-0.034	0.023	0.073	0.045
<i>NR2E3</i>	cg18860847	-0.034	0.038	0.098	0.016
<i>SYNJ2</i>	cg13645811	-0.034	0.001	0.553	0.002
<i>RIMS3</i>	cg08394377	-0.036	0.016	0.291	0.030
<i>RUNX2</i>	cg05996042	-0.037	0.003	0.123	0.042
<i>ADPRHL1</i>	cg00463202	-0.045	0.010	0.091	0.007
<i>P4HA3</i>	cg25599211	-0.048	0.015	0.085	0.025
<i>DST</i>	cg04452713	-0.051	0.003	0.319	0.024
<i>MGAT4C</i>	cg18344063	-0.062	0.047	0.121	0.038

Table S14. List of genes with correlation between alteration of DNA methylation and differential gene expression in VAT

Symbol	Target ID	Delta Beta	p value (Delta Beta)	log FC	p value (logFC)
<i>BRDT</i>	cg14732540	0.086	0.008	-0.132	0.007
<i>PSG6</i>	cg11151665	0.064	<0.001	-0.125	0.029
<i>PPP2R2D</i>	cg21750602	0.039	0.044	-0.196	0.029
<i>GPR175</i>	cg13728650	0.031	0.006	-0.193	0.037
<i>KRT13</i>	cg10742225	0.027	0.017	-0.132	0.015
<i>C21orf94</i>	cg17266238	0.025	0.032	-0.140	0.047
<i>PSG6</i>	cg17642353	0.022	0.040	-0.125	0.029
<i>HBQ1</i>	cg17714030	0.019	0.008	-0.570	0.001
<i>HBD</i>	cg20609368	0.016	0.041	-1.443	0.001
<i>SLC7A6OS</i>	cg27077685	0.010	0.025	-0.283	0.024
<i>STEAP3</i>	cg04749104	0.010	0.038	-0.176	0.010
<i>THSD1</i>	cg16114640	0.009	0.013	-0.169	0.004
<i>PRMT2</i>	cg06725035	0.008	0.018	-0.295	0.007
<i>ASAH1</i>	cg13563405	-0.004	0.048	0.164	0.004
<i>TTC9C</i>	cg24515202	-0.004	0.027	0.195	0.049
<i>APBA1</i>	cg15840658	-0.005	0.037	0.138	0.037
<i>APBA1</i>	cg15623573	-0.005	0.048	0.138	0.037
<i>BCKDHB</i>	cg15256539	-0.006	0.020	0.191	0.048
<i>BCKDHB</i>	cg15256539	-0.006	0.020	0.284	0.009
<i>PPM1J</i>	cg12687922	-0.006	0.024	0.092	0.039
<i>RET</i>	cg05621401	-0.008	0.014	0.155	0.035
<i>LARGE</i>	cg05670348	-0.008	0.028	0.301	0.019
<i>MEIS2</i>	cg02917381	-0.008	0.005	0.109	0.027
<i>RBKS</i>	cg06869899	-0.009	0.017	0.176	0.036
<i>MBD6</i>	cg25107978	-0.012	0.015	0.334	0.043
<i>ERCC8</i>	cg11649654	-0.012	0.047	0.239	0.001
<i>PPP1R3D</i>	cg08966023	-0.013	0.044	0.165	0.045
<i>GOSR1</i>	cg19098314	-0.014	0.002	0.139	0.033
<i>RFK</i>	cg13789236	-0.014	0.009	0.127	0.032
<i>PLEKHA1</i>	cg01246254	-0.020	<0.001	0.282	0.040
<i>IRX3</i>	cg24662961	-0.020	0.003	0.774	0.021
<i>DPH2</i>	cg25955969	-0.026	0.035	0.163	0.026
<i>IGF2</i>	cg02166532	-0.027	0.008	0.132	0.024
<i>LRPPRC</i>	cg26538116	-0.027	0.013	0.227	0.024
<i>SNX16</i>	cg06027949	-0.034	0.011	0.435	0.032

<i>FLJ44060</i>	cg08489623	-0.041	0.032	0.128	0.034
<i>CRB3</i>	cg03258472	-0.046	0.026	0.173	0.033
<i>BARHL2</i>	cg17241310	-0.046	0.036	0.255	0.004
<i>C14orf105</i>	cg19903229	-0.051	0.013	0.132	0.012
<i>SNX4</i>	cg16468910	-0.054	0.022	0.212	0.015
<i>HMP19</i>	cg07884019	-0.062	0.047	0.119	0.031
<i>EDNRB</i>	cg24745738	-0.101	0.001	0.193	0.026

Table S15. List of genes with correlation between alteration of DNA methylation and differential gene expression in LT

Symbol	Target ID	Delta Beta	<i>p</i> value (Delta Beta)	log FC	<i>p</i> value (logFC)
<i>SLC12A8</i>	cg14391622	0.049	0.021	-0.353	0.034
<i>CACNB4</i>	cg18272264	0.042	0.011	-0.152	0.033
<i>FAM3B</i>	cg03158400	0.040	0.040	-0.128	0.037
<i>SYK</i>	cg10025443	0.038	0.022	-0.133	0.047
<i>CTBS</i>	cg08380539	0.004	0.046	-0.263	0.020
<i>MARCH8</i>	cg02702510	-0.011	0.027	0.070	0.041
<i>SON</i>	cg26265060	-0.027	0.050	0.064	0.050
<i>KCNJ1</i>	cg14481339	-0.033	0.022	0.096	0.034
<i>TMEM92</i>	cg25949363	-0.035	0.038	0.116	0.031
<i>PLA2G2A</i>	cg11037787	-0.042	0.025	1.179	0.026
<i>NRG4</i>	cg13044277	-0.043	0.028	0.236	0.036
<i>PNLIPRP1</i>	cg27600794	-0.044	0.021	0.110	0.014
<i>SYT7</i>	cg02104644	-0.051	0.046	0.138	0.033
<i>LTBR</i>	cg15784615	-0.052	0.013	0.250	0.028
<i>CATSPER2</i>	cg23685580	-0.052	0.027	0.078	0.032
<i>LPAL2</i>	cg15398520	-0.058	0.027	0.107	0.010
<i>NCALD</i>	cg01484156	-0.059	<0.001	0.266	0.013
<i>ZDHHC11</i>	cg20584011	-0.059	0.002	0.763	0.007
<i>LGTN</i>	cg16639185	-0.060	0.031	0.241	0.031
<i>ZDHHC11</i>	cg18429742	-0.078	0.016	0.763	0.007
<i>OXT</i>	cg26955850	-0.080	0.050	0.802	0.037
<i>PRSS21</i>	cg22730830	-0.113	0.003	0.132	0.012
<i>OXT</i>	cg26267561	-0.154	0.001	0.802	0.037

Table S16. Gene ontology enrichment analysis using the genes with correlation between alteration of DNA methylation and differential gene expression

Tissue	Term	Count	p value	Genes
WB	GO:0042981~regulation of apoptosis	9	0.011	<i>MSH6, CASP9, SNCB, DEDD, PLEKHG5, HSPA5, IGFBP3, CLN8, GCH1</i>
	GO:0043067~regulation of programmed cell death	9	0.012	<i>MSH6, CASP9, SNCB, DEDD, PLEKHG5, HSPA5, IGFBP3, CLN8, GCH1</i>
	GO:0010941~regulation of cell death	9	0.012	<i>MSH6, CASP9, SNCB, DEDD, PLEKHG5, HSPA5, IGFBP3, CLN8, GCH1</i>
	GO:0009416~response to light stimulus	4	0.016	<i>MSH6, CASP9, NR2E3, SCARA3</i>
	GO:0009411~response to UV	3	0.022	<i>MSH6, CASP9, SCARA3</i>
	GO:0043065~positive regulation of apoptosis	6	0.024	<i>MSH6, CASP9, DEDD, PLEKHG5, IGFBP3, GCH1</i>
	GO:0043068~positive regulation of programmed cell death	6	0.025	<i>MSH6, CASP9, DEDD, PLEKHG5, IGFBP3, GCH1</i>
	GO:0006979~response to oxidative stress	4	0.025	<i>UCP2, TXNRD2, SCARA3, CLN8</i>
	GO:0010942~positive regulation of cell death	6	0.025	<i>MSH6, CASP9, DEDD, PLEKHG5, IGFBP3, GCH1</i>
	GO:0050884~neuromuscular process controlling posture	2	0.034	<i>CLN8, GCH1</i>
	GO:0045773~positive regulation of axon extension	2	0.034	<i>LIMK1, MAPT</i>
	GO:0009314~response to radiation	4	0.041	<i>MSH6, CASP9, NR2E3, SCARA3</i>
	GO:0000305~response to oxygen radical	2	0.041	<i>UCP2, TXNRD2</i>
SAT	GO:0007005~mitochondrion organization	4	0.007	<i>DNM1L, SYNJ2, CLN8, TOMM34</i>
	GO:0008015~blood circulation	4	0.015	<i>F5, TCAP, KCNQ1, ADRA1D</i>
	GO:0003013~circulatory system process	4	0.015	<i>F5, TCAP, KCNQ1, ADRA1D</i>
	GO:0040029~regulation of gene expression, epigenetic	3	0.020	<i>MLL5, DICER1, KCNQ1</i>
	GO:0007188~G-protein signaling, coupled to cAMP nucleotide second messenger	3	0.024	<i>OPRM1, PTGER3, ADRA1D</i>
	GO:0019933~cAMP-mediated signaling	3	0.029	<i>OPRM1, PTGER3, ADRA1D</i>

	GO:0007187~G-protein signaling, coupled to cyclic nucleotide second messenger	3	0.041	<i>OPRM1, PTGER3, ADRA1D</i>
VAT	GO:0007497~posterior midgut development	2	0.004	<i>EDNRB, RET</i>
	GO:0048484~enteric nervous system development	2	0.020	<i>EDNRB, RET</i>
	GO:0015671~oxygen transport	2	0.027	<i>HBQ1, HBD</i>
LT	GO:0046903~secretion	5	0.000	<i>OXT, FAM3B, CACNB4, SYK, KCNJ1</i>
	GO:0003001~generation of a signal involved in cell-cell signaling	3	0.004	<i>FAM3B, CACNB4, SYK</i>
	GO:0030001~metal ion transport	4	0.016	<i>SLC12A8, CATSPER2, CACNB4, KCNJ1</i>
	GO:0006812~cation transport	4	0.026	<i>SLC12A8, CATSPER2, CACNB4, KCNJ1</i>
	GO:0048584~positive regulation of response to stimulus	3	0.031	<i>PLA2G2A, CACNB4, SYK</i>
	GO:0007267~cell-cell signaling	4	0.032	<i>OXT, FAM3B, CACNB4, SYK</i>
	GO:0050851~antigen receptor-mediated signaling pathway	2	0.038	<i>CACNB4, SYK</i>
	GO:0051094~positive regulation of developmental process	3	0.042	<i>OXT, PLA2G2A, SYK</i>
	GO:0002429~immune response-activating cell surface receptor signaling pathway	2	0.045	<i>CACNB4, SYK</i>