

Supplementary Table S14. Summary of p-values obtained from t-tests comparing methylation percentages detected by DREAM analysis.

Gene	Total Smal sites	CB vs Adult	Adult vs MDS	Adult vs AML	MDS vs AML
<i>ASIC2</i>	4	0.082	0.233	0.008	0.002
<i>CDH4</i>	10	0.205	0.302	0.010	0.009
<i>CDH13</i>	4	0.018	0.019	0.002	0.001
<i>COLEC12</i>	4	0.039	0.002	0.0004	0.0003
<i>CRB3</i>	1	0.001	0.162	0.009	0.229
<i>ELOVL2</i>	2	0.121	0.802	0.117	0.046
<i>EN2</i>	4	0.022	0.232	0.013	0.007
<i>ESR1</i>	5	0.004	0.153	0.012	0.632
<i>FBN1</i>	5	0.011	0.197	0.017	0.014
<i>GATA5</i>	11	0.080	0.014	0.002	0.009
<i>GPR37</i>	4	0.004	0.135	0.007	0.003
<i>HAND2</i>	5	0.0002	0.009	0.020	0.070
<i>HOXC12</i>	3	0.0002	0.004	0.0002	0.001
<i>HS3ST2</i>	2	0.149	0.208	0.028	0.014
<i>KCNMA1</i>	4	0.172	0.156	0.042	0.158
<i>KLF14</i>	2	0.002	0.045	0.001	0.046
<i>KY</i>	1	0.069	0.0001	0.079	0.027
<i>NTPX2</i>	4	0.019	0.025	0.0002	0.001
<i>PAX3</i>	2	0.108	0.083	0.007	0.208
<i>PGR</i>	4	0.138	0.012	0.0003	0.001
<i>PRDM5</i>	5	0.102	0.265	0.006	0.002
<i>SOX11</i>	11	<0.0001	0.005	<0.0001	0.0002
<i>TLX3</i>	10	0.002	0.005	<0.0001	0.0005
<i>TMEFF2</i>	3	0.234	0.506	0.067	0.036
<i>TMEM229A</i>	2	0.099	0.206	0.028	0.054
<i>WT1</i>	3	0.086	0.845	0.036	0.011
Ave of 26 genes	115	0.0001	0.003	<0.0001	<0.0001
<i>ESPNL</i>	3	0.001	0.315	0.130	0.006