**Table S1 Expression data of genes hypomethylated at core promoter regions\***

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Gene ID | Mean Expression (malignant) | STD # (malignant) | Mean Expression (benign) | STD (benign) | Statistical power$ |
| *ADCY3* | 7078.00 | 5184.37 | 1783.10 | 595.82 | 62.1% |
| *ANGPTL1* | 101.68 | 26.46 | 112.25 | 19.28 | 11.2% |
| *C1orf113* | 106.89 | 24.38 | 146.26 | 20.02 | 79.7% |
| *C4BPA* | 101.17 | 48.48 | 100.15 | 14.03 | 5.0% |
| *C7orf65* | 131.99 | 15.68 | 149.28 | 19.38 | 34.1% |
| *DIAPH3* | 258.70 | 71.88 | 155.59 | 36.19 | 81.7% |
| *DLC1* | 222.92 | 261.24 | 134.51 | 37.49 | 11.6% |
| *GAS7* | 823.42 | 702.44 | 197.93 | 60.22 | 51.0% |
| *LAG3* | 1304.50 | 2141.89 | 141.43 | 42.57 | 22.9% |
| *LOC100130872* | 114.37 | 22.93 | 127.86 | 25.17 | 14.4% |
| *LRRC32* | 1812.00 | 2759.81 | 525.27 | 194.96 | 18.0% |
| *MAMDC2* | 556.99 | 769.76 | 214.45 | 77.56 | 16.8% |
| *MSLNL* | 112.08 | 19.76 | 127.50 | 16.11 | 27.2% |
| *SLC1A5* | 559.40 | 358.29 | 296.07 | 108.23 | 35.0% |
| *SPON2* | 539.70 | 759.96 | 133.55 | 38.78 | 22.3% |

\*Hypomethylated gene promoters were selected based on the criteria defined in Methods.

#STD: standard deviation.

$Statistical power was calculated using the mean and STD values of malignant and benign groups (two-tailed test, alpha error level 5%).