**S4 Table. Top 20 increases and decreases in H3K4me3 methylation from ChIP-chip microarray analysis.**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Gene Symbol** | **Chromosome** | **Distance to TSS** | **MAT-score** | ***p*-value** |
| *Pcdha4-g* | chr18 | 781334 | -11.1605 | 9.36E-05 |
| *Pcdhga1* | chr18 | 72130 | -11.1605 | 9.36E-05 |
| *Pcdhga2* | chr18 | 64970 | -11.1605 | 9.36E-05 |
| *Pcdhga3* | chr18 | 59740 | -11.1605 | 9.36E-05 |
| *Pcdhgb1* | chr18 | 53617 | -11.1605 | 9.36E-05 |
| *Pcdhga4* | chr18 | 48675 | -11.1605 | 9.36E-05 |
| *Pcdhgb2* | chr18 | 44216 | -11.1605 | 9.36E-05 |
| *Pcdhga5* | chr18 | 39574 | -11.1605 | 9.36E-05 |
| *Pcdhga6* | chr18 | 26846 | -11.1605 | 9.36E-05 |
| *Pcdhga7* | chr18 | 19241 | -11.1605 | 9.36E-05 |
| *Pcdhgb4* | chr18 | 13521 | -11.1605 | 9.36E-05 |
| *Pcdhga8* | chr18 | 8369 | -11.1605 | 9.36E-05 |
| *Pcdhgb5* | chr18 | 2921 | -11.1605 | 9.36E-05 |
| *Pcdhga9* | chr18 | -2841 | -11.1605 | 9.36E-05 |
| *Pcdha4-g* | chr18 | 722971 | -8.17202 | 9.36E-05 |
| *Pcdhga1* | chr18 | 13767 | -8.17202 | 9.36E-05 |
| *Pcdhga2* | chr18 | 6607 | -8.17202 | 9.36E-05 |
| *Pcdhga3* | chr18 | 1377 | -8.17202 | 9.36E-05 |
| *Pcdhgb1* | chr18 | -4726 | -8.17202 | 9.36E-05 |
| *3110082I17Rik* | chr5 | 79747 | -7.15166 | 9.36E-05 |
| *Pou3f3os* | chr1 | -1404 | 5.41674 | 9.36E-05 |
| *Pou3f3* | chr1 | -896 | 5.41674 | 9.36E-05 |
| *2900092D14Rik* | chr1 | -4086 | 5.41674 | 9.36E-05 |
| *Olfr406* | chr11 | -2515 | 5.42421 | 9.36E-05 |
| *Serpinf2* | chr11 | -2463 | 5.45151 | 9.36E-05 |
| *Wdr81* | chr11 | 12733 | 5.45151 | 9.36E-05 |
| *Olfr391-ps* | chr11 | -2489 | 5.50726 | 9.36E-05 |
| *Olfr1370* | chr13 | -2489 | 5.55823 | 9.36E-05 |
| *Efcab6* | chr15 | 112908 | 5.61754 | 9.36E-05 |
| *Cyp2j12* | chr4 | -2379 | 5.7489 | 9.36E-05 |
| *1700109G14Rik* | chr14 | -1907 | 6.00292 | 9.36E-05 |
| *Arl11* | chr14 | -2491 | 6.00292 | 9.36E-05 |
| *Akap1* | chr11 | -2480 | 6.03939 | 9.36E-05 |
| *Flii* | chr11 | -577 | 6.21834 | 9.36E-05 |
| *Mief2* | chr11 | -579 | 6.21834 | 9.36E-05 |
| *Mir5100* | chr11 | -844 | 6.21834 | 9.36E-05 |
| *Tspan8* | chr10 | -2378 | 6.26893 | 9.36E-05 |
| *Mid1* | chrX | 294406 | 7.19251 | 9.36E-05 |
| *G530011O06Rik* | chrX | -687 | 7.19251 | 9.36E-05 |
| *Olfr284* | chr15 | -2489 | 7.1997 | 9.36E-05 |

The top and bottom 20 regions of differential histone methylation (RDHMs) according to MAT score are shown with the proximal gene including distance to the transcriptional start site (TSS).