**Table S2 Distribution of the CpG islands at different genomic regions\***

|  |  |  |  |
| --- | --- | --- | --- |
|  | All CpG islands in the methylation array | Hypermethyalted CpG islands | Hypomethylated CpG islands |
| Promoter (<=1000 bp) | 35.30% | 11.50% | 15.40% |
| Promoter (1000-2000 bp) | 2.00% | 3.10% | 2.30% |
| Promoter (2000-3000 bp) | 0.80% | 4.20% | 0.70% |
| Downstream (<=1000 bp) | 1.00% | 1.00% | 2.10% |
| Downstream (1000-2000 bp) | 0.80% | 0.00% | 1.70% |
| Downstream (2000-3000 bp) | 0.60% | 2.10% | 0.90% |
| 5'UTR | 12.40% | 5.20% | 4.30% |
| 3'UTR | 2.00% | 7.30% | 4.30% |
| Coding Exon | 12.60% | 27.10% | 20.70% |
| Intron | 20.80% | 15.60% | 31.5% |
| Distal Intergenic | 11.80% | 22.90% | 16.2% |

\*Reference genes in the genome assembly hg18 were used to calculate the distribution of the CpG islands.