|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Supplementary. Distribution of methylation haplotype block in different gene regions | | | | |
|  | Obeserved counts | Expectation counts | Fold-Change | P-value\* |
| Promoter | 34427 | 68758 | 1.88 | <1.0\*10-3 |
| UTR5 | 34427 | 50143 | 1.14 | <1.0\*10-3 |
| Enhancer | 34425 | 95165 | 0.57 | <1.0\*10-3 |
| mir | 749 | 1073 | 0.44 | <1.0\*10-3 |
| Intron | 309504 | 256163 | 0.41 | <1.0\*10-3 |
| Downstream | 34427 | 41270 | 0.26 | <1.0\*10-3 |
| Exon | 343931 | 207330 | 0.24 | <1.0\*10-3 |
| UTR3 | 34427 | 39283 | 0.15 | <1.0\*10-3 |
| \* genomic locations of methylation haplotype blocks were randomly permuted among defined gene regions with 1000 iteration. The emperical P-values were estimated. | | | | |