|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Probe | Gene | Chr | Start | End | Feature | Case (n=10) | Control (n=10) | Meth.Diff | *P* value |
| cg25020666 | YWHAG† | 7 | 75957850 | 75957850 | 3'UTR | 0.503±0.064 | 0.370±0.108 | 0.133 | 0.003\*\* |
| cg19360943 | ING4† | 12 | 6762431 | 6762431 | Body | 0.955±0.007 | 0.761±0.218 | 0.194 | 0.009\*\* |
| cg17416644 | BRSK2† | 11 | 1474841 | 1474841 | Body | 0.848±0.082 | 0.604±0.180 | 0.244 | <0.001\*\* |
| cg06231783 | BRSK2† | 11 | 1475048 | 1475048 | Body | 0.375±0.042 | 0.257±0.142 | 0.118 | 0.017\* |
| cg12064373 | BRSK2† | 11 | 1457153 | 1457153 | Body | 0.568±0.106 | 0.400±0.164 | 0.168 | 0.011\* |
| cg25271479 | BRSK2† | 11 | 1457346 | 1457346 | Body | 0.342±0.079 | 0.206±0.145 | 0.136 | 0.014\* |
| cg06696596 | GJA1† | 6 | 122391246 | 122391246 | IGR | 0.575±0.121 | 0.463±0.118 | 0.112 | 0.043\* |
| - | DAPK1‡ | 9 | 90112562 | 90112787 | UTR5 | 0.064±0.023 | 0.039±0.020 | 0.025 | 0.026 |
| - | TNFAIP8‡ | 5 | 118603742 | 118603908 | upstream | 0.058±0.012 | 0.038±0.016 | 0.020 | 0.050 |
| cg10912203 | TNFSF8‡ | 9 | 117656513 | 117656772 | Intronic | 0.911±0.052 | 0.792±0.115 | 0.119 | 0.006 |
| cg0642321 | GZMM‡ | 19 | 551401 | 551401 | intergenic | 0.758±0.082 | 0.614±0.166 | 0.144 | 0.020 |
| - | HOXA5‡ | 7 | 27183133 | 27184188 | Exonic | 0.789±0.071 | 0.721±0.097 | 0.068 | 0.001 |

**Supplementary Table 1 The differences of DNA methylation of apoptosis associated genes between the case group and the control group in the results of Methylation 850K BeadChip (mean±SD).**

Notes：Chr, Chromosome; Meth.Diff =The methylation level of case-The methylation level of control; †indicates intrinsic apoptosis-associated genes; ‡ indicates extrinsic apoptosis-associated genes \* *P*<0.05, \*\* *P*<0.01