**Table S3.** The genetic model selection of SNPs at *MTHFD* gene

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **SNPs** | **Genotypes** | **Control (n)** | **Case (n)** | ***Z*HWDTT||** | **GMS** |
| rs1950902 | GG/GA/AA | 72/242/190 | 46/200/218 | 0.267 | addictive |
| rs2236225 | GG/GA/AA | 332/152/20 | 286/158/20 | -0.562 | addictive |
| rs2236222 | AA/GA/GG | 318/164/22 | 254/166/44 | 1.612 | addictive |
| rs11849530 | AA/GA/GG | 230/206/68 | 216/176/72 | 1.137 | addictive |
| rs1256142 | GG/GA/AA | 108/246/150 | 78/256/130 | -2.085 | dominant |

Abbreviations: SNPs = single nucleotide polymorphisms; MTHFD = methylenetetrahydrofolate dehydrogenase; GMS = genetic model selection.

||We classified the genetic model into the recessive model if *Z*HWDTT > c, the dominant model if *Z*HWDTT < -c, and in the addictive model if otherwise, where we chose c = Φ-1(0.95) = 1.645.