Table S1. Primary information for *MTHFR* rs1801133 C>T, rs3753584 A>G, rs4845882 G>A, rs4846048 A>G and rs9651118 T>C polymorphisms

Genotyped SNPs	*MTHFR* rs9651118 T>C	*MTHFR* rs4846048 A>G	*MTHFR* rs1801133 C>T	*MTHFR* rs4845882 G>A	*MTHFR* rs3753584 A>G
Chromosome	1	1	1	1	1
Function	intron	intron	missense	intron	nearGene-5
ChrPos (Genome Build 36.3)	11784801	11768839	11778965	11765754	11787173
Regulome DB Score[a]	5	3a	4	1f	4
TFBS[b]	Y	—	—	—	Y
Splicing (ESE or ESS)	—	—	—	—	Y
miRNA (miRanda)	—	Y	—	—	—
nsSNP	—	—	Y	—	—
MAF[c] for Chinese in database	0.382	0.105	0.439	0.198	0.093
MAF in our controls (n = 608)	0.353	0.102	0.444	0.175	0.067
P value for HWE[d] test in our controls	0.456	0.097	0.033	0.066	0.764
Genotyping method[e]	LDR	LDR	LDR	LDR	LDR
% Genotyping value	96.59%	98.19%	97.65%	98.93%	97.65%

[a]http://www.regulomedb.org/; [b]TFBS: Transcription Factor Binding Site (http://snpinfo.niehs.nih.gov/snpinfo/snpfunc.htm); [c]MAF: minor allele frequency; [d]HWE: Hardy-Weinberg equilibrium; [e]LDR: ligation detection reaction.