Supplementary material

Table S1. PCR-RFLP primer sequences of 7 SNPs for NNMT gene polymorphisms

SNP_ID	Primer Forward	Primer Reverse
rs694539	ACGTTGGATGGTCCTAGAGTCCTA	ACGTTGGATGCAGCCATCTCAAATG
rs2256292	GAATCC	GATGC
rs2301128	ACGTTGGATGTTTAAGGTCTAGGA	ACGTTGGATGCCATGTAACAGACTT
rs10891645	GAAGG	TCTGG
rs2155806	ACGTTGGATGTTATTCCCCAATCCA	ACGTTGGATGTTTTTACCTTCTCCTA
	GGGTG	GACC
	ACGTTGGATGTGATACTATCAACCT	ACGTTGGATGGAGTGTATATTGTTCA
	GCCTG	GTTG
	ACGTTGGATGCAGCAATATTAGGT	ACGTTGGATGCGTAGATTACAGACT
	TCACCG	TTGGG
	ACGTTGGATGCTTAGCTCCTTGAAT	ACGTTGGATGGAGGGAAAGGACAA
	GGCAC	ATTGAC
	ACGTTGGATGCTGCTTGCTTCAGT	ACGTTGGATGAGCTCCTCCAAAAAG
	CTGGTT	GAGTC

Table S2. Distribution of NNMT genotypes and alleles between cases and controls

SNP	Haplotype /Allele	Cases	Controls	Chi^2	*P*-value	OR(95%CI)
rs694539	AA	2(0.048)	7(0.081)			
	AG	21(0.500)	46(0.535)			
	GG	19(0.452)	33(0.384)	0.8509	0.6535	
	A	25(0.298)	60(0.349)			
	G	59(0.702)	112(0.651)	0.6675	0.4139	0.791(0.450-1.389)
rs2256292	CC	5(0.119)	10(0.116)			
	CG	18(0.429)	44(0.512)			
	GG	19(0.452)	32(0.372)	0.8603	0.6504	
	C	28(0.333)	64(0.372)			
	G	56(0.667)	108(0.628)	0.3683	0.5439	0.844(0.487-1.461)
rs2301128	AA	0(0.000)	1(0.012)			
	AG	7(0.167)	18(0.209)			
	GG	35(0.833)	67(0.779)	0.8553	0.6521	
	A	7(0.083)	20(0.116)			
	G	77(0.917)	152(0.884)	0.6493	0.4204	0.691(0.280-1.705)
rs10891645	AC	5(0.119)	10(0.116)			
	CC	37(0.881)	76(0.884)	0.0021	0.9635	
	A	5(0.060)	10(0.058)			
	C	79(0.940)	162(0.942)	0.002	0.9647	1.025(0.339-3.101)
rs2155806	CC	2(0.048)	0(0.000)			

	CT	9(0.214)	23(0.267)			
	TT	31(0.738)	63(0.733)	4.4154	0.11	
	C	13(0.155)	23(0.134)			
	T	71(0.845)	149(0.866)	0.2068	0.6493	0.843(0.404-1.761)
rs1941398	CC	24(0.571)	55(0.640)			
	CG	14(0.333)	30(0.349)			
	GG	4(0.095)	1(0.012)	5.2819	0.0713	
	C	62(0.738)	140(0.814)			
	G	22(0.262)	32(0.186)	1.9512	0.1624	0.644(0.347~1.197)
rs2604279	CC	2(0.048)	0(0.000)			
	CT	12(0.286)	21(0.244)			
	TT	28(0.667)	65(0.756)	4.5927	0.1006	
	C	16(0.190)	21(0.122)			
	T	68(0.810)	151(0.878)	2.1345	0.144	0.591(0.290-1.203)

Table S3.Frequency and analysis of observed haplotypes (rs2256292, rs2301128, rs10891645) in patients with SZ and in healthy controls

Haplotype	**Case(freq%)**	**Control(freq%)**	***P*-value**	**Odds Ratio (95%CI)**
Total				
CAC	7.9	11.6	0.3579	0.651(0.259-1.636)
CGC	25.0	25.5	0.9407	0.977(0.536-1.784)
GGA	5.5	5.8	0.9268	0.948(0.304-2.958)
GGC	61.2	57.0	0.4973	1.203(0.705-2.052)
Female				
CAC	9.5	12.3	0.6375	0.753(0.231-2.457)
CGC	21.4	29.2	0.3343	0.660(0.283-1.540)
GGA	4.8	4.7	0.9908	1.010(0.188-5.420)
GGC	64.3	53.8	0.2445	1.547(0.740-3.236)
Male				
CAC	5.2	10.6	0.3424	0.474(0.099-2.278)
CGC	28.6	16.1	0.1091	2.135(0.835-5.461)
GGA	5.2	4	0.7517	1.434(0.215-8.390)
GGC	59.1	65.7	0.5676	0.791(0.354-1.769)

All those frequency less than 0.03 will be ignored in analysis