

**Table 1.** Primers for primary PCR reaction

SNP	Region	Forward primer <sup>a</sup>	Reverse primer <sup>a</sup>	AMP_LEN (bp)
rs2051990	Intron 3	10mer-AATCTGGAAGAAAGTAAGCC	10mer-AAAAAGTAGGGAGAAATGC	81
rs7301906	Intron 3	10mer-AAGATAGCACCCCTGAATAGC	10mer-TGCGGTGTTTGTAGACTCAG	102
rs7304986	Intron 3	10mer-GGTGACAACAAGCAGTACTC	10mer-ATGACTAAGGAGCAATGCGG	112
rs7316184	Intron 3	10mer-GAATGCCACTTGGTCTGTTC	10mer-AAAGCCCCCATCTAGACATC	99
rs16929275	Intron 3	10mer-CTTCATAAAGTGCACACTGG	10mer-GCTGCTATAGATGTTGTGTG	91
rs16929276	Intron 3	10mer-CTTGACCTGAGCATGAGATG	10mer-TATGAGGTGATCCTCCAAGC	120
rs2302729	Intron 9	10mer-AGACTTGCTTCTTGAGTCCC	10mer-CTTCTAACCAACAGGGCCTC	106
rs215976	Exon	10mer-AGGAGGAGAAGATTGAGCTG	10mer-AGGAGACAGCTCCTCACCTT	99
rs216008	Exon	10mer-TCGCCATGAACATCCTCAAC	10mer-TGGGTTTGAAGGCAATGAGC	101
rs1051375	Exon	10mer-TCAACAACGCCAACAAACACC	10mer-GCCCGTGGCCCTCCACAGT	107
rs1544514	Exon	10mer-TGTTTCCTAGGAACGAGTGG	10mer-AGGAGTCCATAGGCGATTAC	104
rs2041135	3'UTR	10mer-CCTACCATATACTATTCAGTG	10mer-CAGCATCATTTTAATGCATC	120
rs2470433	3'UTR	10mer-GACCAGCAGTGCAACACAAG	10mer-GAAATGAAGTAGCCATCGCC	100
rs4765975	3'UTR	10mer-GTATACACAGACAAGGAGGG	10mer-TAATAGTAGGTTCTGATGG	93
rs7302540	3'UTR	10mer-TCCAGGTGCCACCTGACACA	10mer-TGGAGAACCTGGACTCTGG	120
rs7316246	3'UTR	10mer-AGTACTCTTTCACCTTCCC	10mer-ATGTGTTTCAGCTTACCCACC	107
rs7957163	3'UTR	10mer-TCTGGGATCCCTACAAAGTC	10mer-TTACTGGCTGCTACACAGGG	118
rs10466907	3'UTR	10mer-TTGTATTGGTATCTGGCTCC	10mer-TTTGTGAAGCCTCTTCTGGG	115
rs11062319	3'UTR	10mer-TGCCCTCTCCCAGCTCGCAG	10mer-TGTAGGGTCCTTTTGGTGAG	114
rs11353034	3'UTR	10mer-AATATGGAAACGGCCAGAC	10mer-CAAAGAGGCCACAAAAGGG	119
rs12809807	3'UTR	10mer-TCCAGGTGCCACCTGACACA	10mer-TGGAGAACCTGGACTCTGG	120

AMP\_LEN: Amplification length

<sup>a</sup>10mer represents ACGTTGGATG placed at 5'-end of each primer.

**Table 2.** Primers and masses for SBE reaction

SNP	UEP_SEQ	UEP_MASS (Da)	EXT1_MASS (Da)	EXT2_MASS (Da)
rs2051990	aaggAAGCCAAAATGTGGAGTAT	7169.7	A, 7440.9	G, 7456.9
rs7301906	agaACCCTGAATAGCAATGTTGGT	7400.8	A, 7672	G, 7688
rs7304986	TACTCAATTCACCTGATTATTAC	7236.7	T, 7507.9	C, 7523.9
rs7316184	ttccGTTCTTGGGCCATTTATT	6673.3	C, 6920.5	T, 7000.4
rs16929275	aAACTGGACTCTTCACCA	5716.7	G, 5963.9	A, 6043.8
rs16929276	GAAGACCTGCGTTCT	4568	C, 4815.2	T, 4895.1
rs2302729	gCTTCAGACCCTTCCTG	5097.3	C, 5344.5	T, 5424.4
rs215976	ATCCATCACGGCTGA	4537	C, 4784.2	T, 4864.1
rs216008	CTCTTCACTGGCCTCTT	5063.3	C, 5310.5	T, 5390.4
rs1051375	ccccCCGGCTACCCCAGCAC	5928.8	A, 6200.1	G, 6216.1
rs1544514	ggctaATAATTTTTACGGTGGAAGC	7736	A, 8007.3	G, 8023.3
rs2041135	ATATTTGACATTTTAACCCCA	6339.2	T, 6610.4	C, 6626.4
rs2470433	CACAAGTGGTCAGAAAC	5212.4	A, 5483.6	G, 5499.6
rs4765975	ggatTAGAGTGACTCCCTTGGA	6790.4	A, 7061.6	T, 7117.5
rs7302540	AGCCCAAACCTCACT	4465.9	C, 4713.1	A, 4737.1
rs7316246	cTAGATCCTTGAGATGTCAG	6132	G, 6379.2	A, 6459.1
rs7957163	taAAATTCCTTAGATCCTGAGAA	7030.6	C, 7317.8	A, 7357.7
rs10466907	taTGGCTCCAGAAAGAAA	5540.6	G, 5787.8	T, 5811.9
rs11062319	caGGGCCCCGCCGCGCCTC	5751.7	C, 5998.9	T, 6078.8
rs11353034	ccacACGGCCCAGACTCCATC	6281.1	T, 6552.3	DEL, 6568.3
rs12809807	gagGGCTGCTGTGCAAAG	5604.6	A, 5875.9	G, 5891.9

UEP\_SEQ: SBE primer sequence; UEP\_MASS: SBE primer molecular weight; EXT1\_MASS: Extended SNP and extended product 1 molecular weight; EXT2\_MASS: Extended SNP and extended product 2 molecular weight.

**Table 3.** Clinical characteristics of patients with insomnia and the controls.

Variables	Case group	Control group	<i>P</i> -value
n	205	154	
Male (%)	127(61.9%)	87(56.5%)	0.358
Age (years)	52(18-78)	54(18-79)	0.081
SAS	39.22 ± 11.23		
SDS	43.35 ± 13.87		
Course of insomnia (years)	3.91±1.56		
PSQI total score	14.23±2.85		
BMI (kg/m <sup>2</sup> )	25.88±3.05	25.18±3.64	0.258
HbA1c (%)	7.15±3.13	5.08±2.12	0.015
SBP (mmHg)	139.12±9.62	123.57±10.15	<0.001
DBP (mmHg)	84.72±7.25	82.50±8.34	0.188

SAS: Self-rating anxiety scale; SDS: Self-rating depression scale; PSQI: Pittsburgh Sleep Quality Index; BMI: body weight index; SBP: Systolic blood pressure; DBP: diastolic blood pressure

**Table 4.** Genotype frequencies of twenty-one SNPs in the CACNA1C gene in the case-control cohort.

SNP ID	Major/minor allele	Group	AA[n (%)] <sup>a</sup>	AB[n (%)] <sup>a</sup>	BB[n (%)] <sup>a</sup>	P-value
rs2051990	A/G	Case	197(96.10)	7(3.41)	1(0.49)	0.240
		Control	151(98.05)	3(1.95)	0	
rs7301906	A/G	Case	203(99.02)	2(0.98)	0	1.000
		Control	153(99.35)	1(0.65)	0	
rs7304986	T/C	Case	198(96.59)	7(3.41)	0	0.609
		Control	151(98.05)	3(1.95)	0	
rs7316184	C/T	Case	198(96.59)	7(3.41)	0	0.609
		Control	151(98.05)	3(1.95)	0	
rs16929275	A/G	Case	198(96.59)	7(3.41)	0	0.609
		Control	151(98.05)	3(1.95)	0	
rs16929276	C/T	Case	198(96.59)	7(3.41)	0	0.609
		Control	151(98.05)	3(1.95)	0	
rs2302729	C/T	Case	89(43.42)	98(47.80)	18(8.78)	0.019
		Control	57(37.01)	68(44.16)	29(18.83)	
rs215976	C/T	Case	109(53.17)	83(40.49)	13(6.34)	0.270
		Control	72(46.75)	66(42.86)	16(10.39)	
rs216008	C/T	Case	91(44.39)	99(48.29)	15(7.32)	0.029
		Control	61(39.61)	68(44.16)	25(16.23)	
rs1051375	A/G	Case	91(44.39)	95(46.34)	19(9.27)	0.041
		Control	58(37.66)	68(44.16)	28(18.18)	
rs1544514	G/A	Case	172(83.90)	31(15.12)	2(0.98)	0.891
		Control	127(82.47)	27(17.53)	0	
rs2041135	C/T	Case	200(98.04)	3(1.47)	1(0.49)	0.257
		Control	153(99.35)	1(0.65)	0	
rs2470433	G/A	Case	197(96.10)	7(3.41)	1(0.49)	0.404
		Control	150(97.40)	4(2.60)	0	
rs4765975	A/T	Case	174(84.88)	30(14.63)	1(0.49)	0.876
		Control	129(83.77)	25(16.23)	0	
rs7302540	G/A	Case	203(99.02)	2(0.98)	0	0.509

SNP ID	Major/minor allele	Group	AA[n (%)] <sup>a</sup>	AB[n (%)] <sup>a</sup>	BB[n (%)] <sup>a</sup>	P-value
rs7316246	G/A	Control	154(100.00)	0	0	0.995
		Case	174(84.88)	30(14.63)	1(0.49)	
rs7957163	C/A	Control	130(84.42)	24(15.58)	0	0.995
		Case	174(84.88)	30(14.63)	1(0.49)	
rs10466907	T/G	Control	130(84.42)	24(15.58)	0	0.906
		Case	175(85.36)	29(14.15)	1(0.49)	
rs11062319	T/C	Control	130(84.42)	24(15.58)	0	0.183
		Case	189(92.19)	15(7.32)	1(0.49)	
rs11353034	T/DEL	Control	146(94.80)	7(4.55)	1(0.65)	0.906
		Case	175(85.36)	29(14.15)	1(0.49)	
rs12809807	C/A	Control	130(84.42)	24(15.58)	0	0.961
		Case	174(84.88)	31(15.12)	0	
		Control	131(85.06)	23(14.94)	0	

<sup>a</sup> A: represents major genotype or wild genotype, B: represents minor or mutant genotype, AA: represents the wild-type homozygote, AB: represents the heterozygote, BB: represents the mutant homozygote.

**Table 5.** Estimated effects for three selected SNPs in univariable analyses and stepwise multivariate logistic regressions and risk factor-adjusted analyses of insomnia

SNP	Model	Univariable analyses		Multivariate analyses		FDR (BH) thresholds <sup>b</sup>
		OR((95% CI)	<i>P</i> -value	AOR <sup>a</sup> (95% CI)	<i>P</i> -value	
rs216008	CC vs. CT vs. TT				0.019	0.0023
	Dominant (CC vs. CT+TT)	0.882(0.537-1.256)	0.364	0.883(0.531-1.265)	0.372	0.0023
	Recessive (CC+CT vs. TT)	0.407(0.207-0.803)	0.008	0.405(0.206-0.801)	0.009	0.0023
	Additive (CC vs. TT)	0.402(0.196-0.824)	0.011	0.400(0.192-0.829)	0.015	0.0023
rs2302729	CC vs. CT vs. TT				0.029	0.0047
	Dominant (CC vs. CT+TT)	0.766(0.499-1.175)	0.222	0.769(0.492-1.183)	0.239	0.0047
	Recessive (CC+CT vs. TT)	0.415(0.221-0.779)	0.005	0.414(0.220-0.771)	0.004	0.0047
	Additive (CC vs. TT)	0.398(0.202-0.781)	0.007	0.395(0.201-0.778)	0.011	0.0047
rs1051375	AA vs. AG vs. GG				0.041	0.0071
	Dominant (AA vs. AG+GG)	0.757(0.494-1.160)	0.200	0.760(0.490-1.173)	0.225	0.0071
	Recessive (AA+AG vs. GG)	0.460(0.246-0.859)	0.013	0.462(0.242-0.868)	0.021	0.0071
	Additive (AA vs. GG)	0.432(0.221-0.845)	0.013	0.430(0.215-0.854)	0.019	0.0071

**AOR:** Adjusted odds ratio; **CI:** Confidence interval; **FDR:** false discovery rate;

<sup>a</sup> logistic regression analyses adjusted for age and gender, BMI, history of hypertension, and HbA1c;

<sup>b</sup> the FDR adjusting for multiple comparisons among 21 polymorphisms, FDR (BH) thresholds for each of the 21 individual SNPs was calculated as described (Benjamini et al. 2001), any P-value is smaller than the FDR threshold is where the null hypothesis is rejected.

**Table 6.** Haplotype analysis of CACNA1C gene in cases and controls

Block	Haplotype	Case, Control Frequencies	<i>P</i> value	OR ( 95%CI )
Block 1	rs2302729-rs1051375			
	CA	0.668, 0.584	0.0211	1.433(1.055-1.945)
	TG	0.319, 0.396	0.0335	0.716(0.523-0.975)
Block 2	rs7316264-rs12809807- rs10466907-rs4765975-rs7957163			
	GCTAC	0.922, 0.919	0.8784	1.044(0.605-1.800)
	AAGTA	0.073, 0.075	0.9392	0.978(0.556-1.720)

Haplotype frequencies were analyzed using Haploview v4.2 software. Haplotypes with frequencies >1% in all subjects were listed.