TABLE 1. PCR primers for amplification of the promoter region and whole coding region of the human 5-HT_{1A} receptor gene

Primer Name	Primer sequence	Primer Position	PCR product (bp)	Annealing temperature
5HT1A-AF	5'-GGAGTAGTTGGAATTCCCTCC	-855~-835	283	60°C
5HT1A-AR	5'-TGTGAGTCGCTTCGAAAGCGA	-573~-593		
5HT1A-BF	5'-CAGAGGAAAGAGGCACTCCTC	-664~-644	311	61°C
5HT1A-BR	5'-CCCACTAGCAAACAGTCTCCA	-354~-374		
5HT1A-CF	5'-GCTTCTCGGTTCTAGATATTTC	-402~-381	269	60°C
5HT1A-CR	5'-AGTTCTTACTGCTTCGGCGAA	-134~-154		
5HT1A-DF	5'-AAAGCTGCTCCTCGGAGATAC	-177~-157	222	66°C
5HT1A-DR	5'-TGGTGATGTGGTGTTGTTGCC	45~25		
5HT1A-EF	5'-ATGGATGTGCTCAGCCCTGGT	1~21	216	64°C
5HT1A-ER	5'-ATTGGCCACGTTCTGCAGGGA	216~196		
5HT1A-FF	5'-TCCCTGCAGAACGTGGCCAAT	196~216	237	55°C
5HT1A-FR	5'-GTAGTCGATGGGGTCCGTGAT	432~412		
5HT1A-GF	5'-ATCTTGCACCTGTGCGCCATC	370~390	276	58°C
5HT1A-GR	5'-CCCATAGAGAACCAGCATGAG	645~625		
5HT1A-HF	5'-GGAGCTTTCTACATCCCGCTG	601~621	306	62°C
5HT1A-HR	5'-CTCTTTGGAGTTGCCCACTCG	906~886		
5HT1A-IF	5'-CTGGAGGTGATCGAGGTGCAC	865~885	213	64°C
5HT1A-IR	5'-GGGCAGCCAGCAGAGGATGAA	1077~1057		
5HT1A-JF	5'-GGAAAAATGAGCGCAACGCCG	965~985	343	55°C
5HT1A-JR	5'-ACGGATCCTGTAGCCTCGACT	1307~1287		

TABLE 2. PCR primers for amplification of the promoter region and whole coding region of the human AP-2 gene

Primer name	Primer sequence	Primer position	Region	PCR product (bp)	Annealing temperature
AP2PUF	5'-GAATTGTGCTCAGTTCAGGTAG	-1959 ~ -1938	promoter	327	58°C
AP2PUR	5'-TCATCTGGGGCTTGTTTCTCG	-1633 ~ -1653			
AP2PMF	5'-CACCCAGGAAACCTTAGCCTG	-1052 ~-1032	promoter	313	66°C
AP2PMR	5'-AGACCGGCGAAGTCACTCCAG	-740 ~-760			
AP2PO-PF	5'-CAGCTCGGATCGTGGTAGCAG	-669 ~-649	promoter	261	58°C
AP2PO-PR	5'-CTCTCTACGCCGCGAACTTGC	-409 ~-429			
AP2PD-PF	5'-GAGCTCGAGGAAGGTTTTATC	-478 ~-458	promoter	213	58°C
AP2PD-PR	5'-GAGATCTCCCTCTAATGGTAG	-266 ~-286			
AP2STRPF	5'-CTACCATTAGAGGGAGATCTC	-286 ~ -266	promoter & partial exon 1	322	58°C
AP2STRPR	5'-CTCGTACTTGATATTATCCGTC	36 ~ 15			
AP2STRPF	5'-CTACCATTAGAGGGAGATCTC	-286 ~ -266	exon 1	366	58°C
AP2EX1PR	5'-TGACCGCACGGATGATCGAG	80 ~61			
AP2EX2UF	5'-CAACGGGAACGGGCCATTTCC	4438 ~ 4458	upper region of exon 2	324	64°C
AP2EX2UR	5'-TGCAGGGGGTTCAGGCTGTAG	4761 ~ 4741			
AP2EX2DF	5'-GTCGCAAGATCCTTACTCCCAC	4708 ~ 4729	down region of exon 2	311	62°C
AP2EX2DR	5'-CTGTGTTCCCTCGGCTGGTTG	5018 ~ 4998			
AP2EX3PF	5'-CACTTACATCCATGTGTATC	8011 ~ 8030	exon 3	216	58°C
AP2EX3PR	5'-TGCCTATCTATTTGCTAATTC	8226 ~ 8206			
AP2EX4PF	5'-GACGCCCAACACGCGGCCTC	10098 ~ 10117	exon 4	348	71°C
AP2EX4PR	5'-GTTTCGGTCGCCGCCACCGC	10445 ~ 10426			
AP2EX5PF	5'-GTGGTGCAGAGAACCCAATG	12273 ~ 12292	exon 5	212	58°C
AP2EX5PR	5'-GAAGTTCCTTCTAGTTAGCAAG	12484 ~ 12463			
AP2BEX5F	5'-CGTTACCCTGCTCACATCAC	12421 ~ 12440	AP-2B-specific region	307	58°C
AP2BEX5R	5'-GGAGAATGTGCAGTTCTTAAAC	12727 ~ 12706			
AP2EX6PF	5'-CACTCTTCATTCTCTCGCAC	14259 ~ 14278	exon 6	251	58°C
AP2EX6PR	5'-TTTGGTTTCTCTTTCTCTTGAC	14509 ~ 14481			
AP2EX7UF	5'-CTACTAGTGCTGCCCATAGTG	16041 ~ 16061	upper region of exon 7	278	62°C
AP2EX7UR	5'-TGAGGTACATTTTGTCCATGGC	16318 ~ 16297			
AP2EX7DF	5'-TCACGGCCCTGCAGAACTATC	16259 ~ 16279	down region of exon 7	215	62°C
AP2EX7DR	5'-GCTGATCCCGGAGCTGTCAC	16473 ~ 16454			

TABLE 3. PCR primers for amplification of the promoter region in the human CREB gene

Primer name	Primer sequence	Primer position	PCR product (bp)	Annealing temperature
CREB-UF	5'-CCTGCTGTAGAAAACAGGCTG	-1034 ~ -1014	244	66°C
CREB-UR	5'-CGAGACTCCGCGGAAAAACC	-791 ~ -810		
CREB-MF	5'-TCAAGAGCAGAGCCAGGGCAG	-602 ~-582	238	66°C
CREB-MR	5'-GAAGGCGAAGGCGGGCTGAG	-365 ~-384		
CREB-DF	5'-GTCGCCCGAAGAAACCCGAAG	-340 ~ -320	327	62°C
CREB-DR	5'-GTACAAGCTCCTCCGTCACTG	-14 ~ -34		

TABLE 4. Detection of DNA sequence variants in the human $5HT_{1A}$ receptor gene

	Variant name	Nucleotide change	Primer Pair	Gel condition for SSCP analysis	Restriction enzyme	References
Promoter region	-581C→A	-581C→A	HT1A-BF HT1A-BR	7% PAG (49:1, A:B ratio) 10% glycerol	*Mbo*II	present study
	-480delA	-480delA	HT1A-BF HT1A-BR	7% PAG (49:1, A:B ratio) 10% glycerol	not available	present study
	-321G→C	-321G→C	HT1A-CF HT1A-CR	10% PAG (99:1, A:B ratio)	*Nla*IV	present study
	-152C→G	-152C→G	HT1A-DF HT1A-DR	10% PAG (99:1, A:B ratio)	*Hae*III	present study
	-51T→C	-51T→C	HT1A-DF HT1A-DR	10% PAG (99:1, A:B ratio)	*Tfi*I	present study
Coding region	Gly272Asp	GGT 815 GAT	HT1A-HF HT1A-HR	8% PAG (49:1, A:B ratio) 10% glycerol	*Fok*I	present study
	Pro16Leu	CCG 47 CTG	HT1A-EF HT1A-ER	10% PAG (99:1, A:B ratio)	*Msp*I	Harada et al., 1996
	294G→A	GTG 294 GTA Val98 (silent)	HT1A-FF HT1A-FR	10% PAG (99:1, A:B ratio)	*Rsa*I	Xie et al., 1995
	549C→T	CCC 549 CCT Pro183 (silent)	HT1A-GF HT1A-GR	10% PAG (49:1, A:B ratio) 10% glycerol	not available	Erdmann et al., 1995

PAG, polyacrylamide gel; A:B ratio, acrylamide:bisacrylamide ratio.

TABLE 5. Genotype and allele frequencies of the 5-HT_{1A} receptor gene variants in schizophrenic patients and controls

Samples	Genotype distribution											
	Pro16Leu			294G→A			549C→T			Gly272Asp		
	Pro/Pro	Pro/Leu	Leu/Leu	G/G	G/A	A/A	C/C	C/T	T/T	Gly/Gly	Gly/Asp	Asp/Asp
Schizophrenia n=61	58 (95.1%)	3 (4.9%)	0 (0%)	59 (96.7%)	2 (3.3%)	0 (0.0%)	59 (96.7%)	2 (3.3%)	0 (0%)	55 (90.2%)	5 (8.2%)	1 (1.6%)
Control n=100	92 (92.0%)	8 (8.0%)	0 (0%)	91 (91.0%)	9 (9.0%)	0 (0.0%)	93 (93.0%)	7 (7.0%)	0 (0%)	95 (95.0%)	5 (5.0%)	0 (0%)
P value*	P=0.5360			P=0.2091			P=0.4847			P=0.3347		
OR	0.595 [0.152-2.335]			0.343 [0.072-1.643]			0.450 [0.090-2.243]			2.073 [0.604-7.111]		
	Allele frequency											
	Pro16	Leu16		294G	294A		549C	549T		Gly272	Asp272	
Schizophrenia n=61	0.975	0.025		0.984	0.016		0.984	0.016		0.943	0.057	
Control n=100	0.960	0.040		0.955	0.045		0.965	0.035		0.975	0.025	
P value*	P=0.5433			P=0.2173			P=0.4913			P=0.2231		
OR	0.605 [0.157-2.326]			0.354 [0.075-1.666]			0.460 [0.094-2.250]			2.374 [0.736-7.655]		

*P values were calculated by Fisher's exact test. OR, odds ratio; 95% confidence intervals are given in square brackets.

TABLE 6. Detection of DNA sequence variants in the promoter region of the human AP-2 gene

Nucleotide change	Primer set	Gel condition for SSCP analysis	Restriction enzyme
-1769G→A	AP2PUF AP2PUR	7% PAG (49:1, A:B ratio)	not available
-803G→T	AP2PMF AP2PMR	7% PAG (49:1, A:B ratio)	not available
-90G→C	AP2STRPF AP2STRPR	10% PAG (99:1, A:B ratio)	*Msp* I

PAG, polyacrylamide gel; A:B ratio, acrylamide:bisacrylamide ratio.

TABLE 7. Polymorphic status between the -90 and -803 loci of the AP-2 gene in schizophrenics (a) and controls (b)

a)

-803 \ -90	GG	GC	CC	total
GG	35	1	0	36
GT	0	38	1	39
TT	0	0	12	12
total	35	39	13	87

(delta value=0.2268, χ^2=157.259, df=1, P<0.000001)

b)

-803 \ -90	GG	GC	CC	total
GG	43	1	0	44
GT	0	49	0	49
TT	0	1	6	7
total	43	51	6	100

(delta value=0.2107, χ^2=159.198, df=1, P<0.000001)

TABLE 8. Genotype and allele frequencies at the-90 and -803 loci of the AP-2 gene in schizophrenics including subtypes and course specifiers, and controls.

Subjects (numbers)		-90 locus Genotypes GG (%)	GC (%)	CC (%)	Alleles G (%)	C (%)	-803 locus Genotypes GG (%)	GT (%)	TT (%)	Alleles G (%)	T (%)
Schizophrenics (87)		35 (40)	39 (45)	13 (15)	109 (63)	65 (37)	36 (41)	39 (45)	12 (14)	111 (64)	63 (36)
		χ^2=4.12, P=0.128			P=0.275		χ^2=2.36, P=0.307			P=0.381	
Subtypes	Paranoid type (18)	11 (61)	5 (28)	2 (11)	27 (75)	9 (25)	11 (61)	5 (28)	2 (11)	27 (75)	9 (25)
		χ^2=3.41, P=0.181			P=0.556		χ^2=2.80, P=0.247			P=0.556	
	Disorganized type (28)	7 (25)	16 (57)	5 (18)	30 (54)	26 (46)	7 (25)	16 (57)	5 (18)	30 (54)	26 (46)
		χ^2=5.55, P=0.062			P=0.056		χ^2=5.02, P=0.081			P=0.056	
	Catatonic type & Undifferentiated type (13)	5 (39)	6 (46)	2 (15)	16 (62)	10 (38)	6 (46)	5 (39)	2 (15)	17 (65)	9 (35)
		χ^2=1.54, P=0.463			P=0.507		χ^2=1.30, P=0.523			P=0.824	
	Residual type (28)	12 (43)	12 (43)	4 (14)	36 (64)	20 (36)	12 (43)	13 (46)	3 (11)	37 (66)	19 (34)
		χ^2=2.22, P=0.330			P=0.628		χ^2=0.423, P=0.810			P=0.748	
Course	Episodic (53)	21 (39)	20 (38)	12 (23)	62 (58)	44 (42)	22 (41)	20 (38)	11 (21)	64 (60)	42 (40)
		χ^2=9.56, P=0.008[1)]			P=0.101		χ^2=6.60, P=0.037[2)]			P=0.166	
	Continuous (19)	7 (37)	12 (63)	0 (0)	26 (68)	12 (32)	7 (37)	12 (63)	0 (0)	26 (68)	12 (32)
		χ^2=1.73, P=0.421			P=1.000		χ^2=2.15, P=0.342			P=1.000	
	Single episode & Other or unspecified pattern (15)	7 (47)	7 (47)	1 (6)	21 (70)	9 (30)	7 (47)	7 (47)	1 (6)	21 (70)	9 (30)
		χ^2=0.098, P=0.952			P=1.000		χ^2=0.038, P=0.981			P=1.000	
Controls (100)		43 (43)	51 (51)	6 (6)	137 (69)	63 (31)	44 (44)	49 (49)	7 (7)	137 (69)	63 (31)

P values after the Bonferroni correction were [1)] P=0.064, [2)] P=0.296.

TABLE 9. Condition for detection of DNA sequence variants in the promoter region of the human CREB gene, and genotype distribution and allele frequency

Nucleotide change	-933T→C			-413G→A		
Primer set	CREB-UF CREB-UR			CREB-MF CREB-MR		
Gel condition for SSCP analysis	7% PAG (49:1, A:B ratio) 10% glycerol			7% PAG (49:1, A:B ratio) 10% glycerol		
Restriction enzyme	not available			*Hph* I		
	Genotype distribution					
	T/T	T/C	C/C	G/G	G/A	A/A
Schizophrenia n=80	79 (98.8%)	1 (1.2%)	0 (0%)	79 (98.8%)	1 (1.2%)	0 (0%)
Control n=100	100 (100%)	0 (0%)	0 (0%)	100 (100%)	0 (0%)	0 (0%)
P value	P=0.44			P=0.44		
	Allele frequency					
	-933T		-933C	-413G		-413A
Schizophrenia n=80	0.994		0.006	0.994		0.006
Control n=100	1.000		0	1.000		0
P value	P=1.00			P=1.00		

P values were caluculated by Fisher's exact test.

PAG, polyacrylamide gel; A:B ratio, acrylamide:bisacrylamide ratio.

TABLE 10. Clinical characteristics of schizophrenic patients possessing the variants in the promoter region of the human CREB gene

Variant	-933T→C	-413G→A
Age	24	40
Age at onset	13	15
Sex	Female	Male
Family history	Uncle	None
Subtype	Undifferentiated type	Disorganized type
Longitudinal course	Episodic with interepisode residual symptoms	Continuous with prominent negative symptoms
Characteristic symptoms	•Auditory hallucinations •Persecutory delusions •Visual hallucinations •Conversion symptoms •Intellectual impairment (IQ 54 by WAIS-R testing)	•Auditory hallucinations •Passivity experiences •Disorganized speech •Affective flattening
EEG	slow wave abnormal	within normal limits
CT	within normal limits	not performed
MRI	within normal limits	not performed
Neurological examination	within normal limits	within normal limits