Complete list of all 94 genes and 1,536 SNPs present on the COGS SNP Chip

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
2	1p36.13	HTR6	5-HT6	5-hydroxytryptamine (serotonin) receptor 6	14.3	1	rs9064	19881467	T	
3	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs517176	37067995	T	
4	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs570743	37076603	T	
5	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs3767045	37083256	T	
6	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs904896	37093554	T	
7	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs12067006	37097522	T	
8	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs1392745	37106082	T	
9	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs533337	37113564	T	
10	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs1587526	37135063	T	
11	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs1027599	37164007	T	
12	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs1334804	37167831	T	
13	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs7555221	37170848	T	
14	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs7517274	37174588	T	
15	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs1160752	37175999	T	
16	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs3767078	37177505	T	
17	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs3767087	37188856	T	
18	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs3767088	37189748	T	
19	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs535620	37192428	T	
20	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs10489412	37206210	T	
21	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs697923	37207734	T	
22	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs575605	37210363	T	
23	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs12066663	37228066	T	
24	1p34.3	GRIK3	GLUR7	glutamate receptor, ionotropic, kainate 3	238.7	1	rs12746787	37229889	T	
25	1p34.1	SLC6A9	GLYT1	solute carrier family 6, member 9 (glycine transporter)	35.0	1	rs1362153	44241618	T	
26	1p34.1	SLC6A9	GLYT1	solute carrier family 6, member 9 (glycine transporter)	35.0	1	rs6660227	44243365	T	
27	1p34.1	SLC6A9	GLYT1	solute carrier family 6, member 9 (glycine transporter)	35.0	1	rs6670336	44243903	T	
28	1p34.1	SLC6A9	GLYT1	solute carrier family 6, member 9 (glycine transporter)	35.0	1	rs2486000	44250594	T	
29	1p34.1	SLC6A9	GLYT1	solute carrier family 6, member 9 (glycine transporter)	35.0	1	rs6429644	44259867	T	
30	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs899974	53322775	T	
31	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1288403	53328371	T	
32	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs3766775	53340134	T	
33	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1288369	53348163	T	
34	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1288373	53351990	T	
35	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1769299	53358311	T	
36	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1769309	53363459	T	
37	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs3737989	53372666	T	
38	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1288367	53378472	T	
39	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs2486634	53383440	T	
40	1p32.3	SLC1A7	AAAT	solute carrier family 1, member 7 (glutamate transporter)	55.4	1	rs1679933	53384287	T	
41	1p21.2	GPR88	STRG	G protein-coupled receptor 88	3.9	1	rs2809823	100776350	T	
42	1q21.3	SNAPAP	SNAPIN	SNAP-associated protein	3.2	1	rs3795396	151902049	T	
43	1q22	CHRNB2		cholinergic receptor, nicotinic, beta 2	12.2	1	rs4845652	152804829	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
2				0.23	0.49	0.47	0.40
3				0.12	0.32	0.02	0.04
4				0.13	0.37		0.08
5			haplotype (Shibata et al. 2006)	0.03	0.00	0.11	0.03
6				0.20	0.26	0.22	0.11
7				0.22	0.45	0.00	0.02
8				0.03	0.47	0.10	0.09
9				0.04	0.20	0.02	0.01
10				0.05	0.43	0.11	0.15
11				0.07	0.30	0.09	0.10
12				0.10	0.33	0.13	0.11
13				0.03	0.21	0.00	0.00
14				0.40	0.00	0.19	0.26
15				0.35	0.28	0.13	0.19
16				0.01	0.00	0.03	0.07
17				0.07	0.15	0.03	0.07
18				0.24	0.00	0.38	0.43
19				0.33	0.48	0.06	0.12
20				0.12	0.39	0.00	0.03
21				0.25	0.05	0.08	0.06
22				0.30	0.00	0.03	0.09
23				0.01	0.26	0.01	0.00
24				0.02	0.00	0.00	0.00
25				0.12	0.41	0.31	0.30
26				0.03	0.19	0.01	0.00
27				0.02	0.13	0.01	0.00
28				0.14	0.04	0.27	0.17
29				0.08	0.05	0.22	0.06
30				0.07	0.31	0.19	0.22
31				0.10	0.23	0.36	0.29
32				0.29	0.23	0.34	0.26
33				0.42	0.13	0.32	0.22
34				0.06	0.41	0.44	0.30
35				0.43	0.48	0.42	0.30
36				0.42	0.11	0.16	0.08
37				0.17	0.23	0.26	0.31
38				0.17	0.35	0.32	0.23
39				0.38		0.33	0.40
40				0.40	0.31	0.40	0.33
41				0.48	0.12	0.23	0.24
42				0.47	0.30	0.31	0.36
43				0.09	0.19	0.13	0.10

	R
1	**Sequence**
2	GGACATGAGTCACACAGACACAATGTGAGTGTGCTCCCCCGTCATGCAACATCTGGACAC[A/C]ACTAACAGAGCATGGTGAATACATGCTGAATTGCATTCAGTATGGCTGTGAACTAGGCCT
3	ACCACACCCCCAGCTCCCCAAACTGAAGGTAAGAACAATTTAACCTGCTATAGCTCCATC[T/C]TTTGTTCCTCAGTCTCCAGATGCCCTGGTTGCTGGTTGAATCCTGCCTTGTACTCCAGAC
4	CGATCAGACAGAGCAGTGATTATACCCTCCATCCCCCATCTCTCATCTAAATTTCCCTCT[C/G]TCTATATTTACTGCCTACTTGTCTGTTTCCTCTTTCAAAAATCTTCTACTCACATCCGTA
5	TATAAATACGCTGCCTTCAGAGCAGCTGTAAAATGCCATTAATTTCGGGAAGTGCTTTGC[T/G]GATGGCATACATATTTAACAGCCAAAGCCCAGAGCATTAAAATGGTGCTCGCCTTAGTAA
6	GAGATGTCTAAGGGTTTTCATTTGGGATTTGTCAATGAAACTCCAGGGAACTGTGGACCC[A/C]TGACCTTGTGGGTTGAACTGTGAGTGTATGCATGGGTGCTGGGGGCATTCCGCAGGGAGA
7	GAGCGGCTCCCAAGGCCCTCCAGTCCTCAGCCCACCCTGCCCTGTCCCCCTTCTCCTCCC[T/C]TGCCACAGGTACATGATGTCCTGGTGAGCGAACAGGCCCAGAGGCCCTGGAGGTGACTCT
8	GTAAATATCCTATTAAAAGCATCTCTGCCTGGCTCAAGCCTCATTCCAAGGCCGGGGTGG[A/G]GGGTCGTTGAGTTGGTAAAATGGCAGGGCCTGAAGCTTTGGCCCCTCAGCCCTGCAGCCT
9	AAGGGTGTGGTTATAAGGAGAGGTGAAGAATTGGGGTCATGGCTGCAATCTCCCCCAAGG[A/G]GAATGGCTATTGAGAAGGCAGCCAGTGTTTGCCCCACGAGCTTTGTGCCTTATCTATTCT
10	GTCAAATGCTGCTTCTGCATTGATTCAGATGATCGCATTTTTTTCCTTTATTCTGTTACT[A/G]TGATGTATTATATTGATCAGTTGTTTTGAACCATCCTTGCATTCCAGGAATAAATTTTTC
11	CCAAGTGGACCAGGCCAGTGGGGACCAAGATAATTGGTAATGTTCAAGGTTCCTTAGCCA[T/C]GCTCCCACTACACCAGCACTGAGCACCCTTGCCTCCCCAAGGATGCAGGGACCCAGACAT
12	CTGAAATTCCAAAGGCAGGGACTCGAATATGGTGCTTCCCAGACTTTATTTGCTGGGTCT[T/C]TGGCCCCAGGAGATATTCACTGAGGAAAAAAACTAGAAAATCCCTGAAATAAAGAAAGCT
13	TTACAGCCAGTGGCACATCTTCTATTAAGAAGCTTCTTGGCTAAAATAAGATTGCTATTA[T/C]TTTCCAAACTGCCACTTGGAATCTGTCCACTCTACCTCCTAAATTAACTTGATTTTCTTC
14	CAAGATGGCACGGTTTTCCAAAGATGGAGTCTAGAAATCCCAAAGCATTTGATGATAACC[A/G]AAGAAAATTCTCAGGTTCAATTCTTGAAAGGTTATAGTTTGCAAGATCTTAGGAAAGCAG
15	TATGTGAGAGCCCTCCAGGTTGACTACATAAGGGTAGTTTCCTCCAACTGGCTTAATTCA[T/C]GGATGTAGTGGTCCCTGTACTATTACGAATTGATGGGACACTTGATTGTTCATTATAAAC
16	ACATCAGAACAGCAGCCTTTCTCCTGCAGGGTGCTGCAAGGGTGCTGGAGGAAGAAACTC[T/C]CTCAAACAAAGCAACAGAGAAAGACCCTGGACTTGGCTTTGCATACTCACAAGCAAAGAA
17	GTGGGGTGACACAGCAGAGGCACAGAGACTGTGGCCCAATTGGTACCCACATCCTGCTGC[A/G]CAACTTGCTTTGGTAAAGGCAAGAGGCTACATGCGATTTATCTGTTTGTTTATTCTTAGA
18	GGCCCCCTCTCCTCGGCAGCATGGCTTCTGTCCTACTTATGTCGAACTGGCAATGCTGGT[T/C]GCATGCAGATTAATGAGGCCACGGCTGAGGCCCTGCATTGGGGGACTGGCCTTGTTTCTA
19	GCATTCCTGTTGGGAAGCTCTCACCCCTCACCAAGCTCACCTCTCTCTAGCACACCTTAC[A/G]TCTGAGCTCCAGGATCTTGCCACTGCACTAGCCTAAGACGTCTTGGAATGCTGGCCCATG
20	GGAACAGAGGCCCAGATTCAGTGCCAGGTCCTCTGGTGTGTTTGCCACTAGGCCCTCTGT[T/C]GTACTGAGAAACTGAGCTGGCAGAGCACTGGGGTTCTGTGATGGTGGCAGACTCCCTGCC
21	TTTATGCAGGTCTCTACTCTCTCTACTCCAGTACTTATTCCATCATTAGGATTTTCATTC[T/C]GCACCTCCAGGGCCTAGCAACAGGCTTGGCACATGGTTAGTGCCAACAAATGTTGAATGA
22	CTGCAGGAAATTCCCAGGCCTCCCAGGCCCTGTGGATTCTCCTTCAGAAATCACAGCCTC[A/G]TTGGGATGCGGAGCACGTGGCGGAGCCCATGCCAAAGATGGATCAGGAGCCTCCGCGTGT
23	CATCCTGTACCAACAATACAGTGATAACCGTACCCCACTTTTACTGAGCAATCACTTCAT[A/C]CCAGGCACCATGCTAAGCCCCTCCCAGACATTATTCCTTTTGAGGCTCATTAAAATCCTA
24	CCAAAGGGAGCTCTTCCCAGGAACCTCACATTCCCCAGTTGAACTCCAAGATCCCTGAGG[A/G]CTGTAGCCCTGTTTCAGGTCATTTGCTTTCCCTGGCATCTGCTGAGGGTTCAGCCAAGGT
25	TTGGGCTCAGCCCAGGTCCTTGTTTGCACACTTCTCCCTTCAGGAATGCCTTTTCCTCAT[T/C]CTGTCAGGTGTCACCTCCTCCAGGAAGCCACCAGTGAGCATTTCACGTGCACCAATTAGC
26	TGTCTTTAAAACCAGGTAGGTATCACGACTGCCCAATTTCATGGACAAATGACTGTGAAC[A/G]ACCTCCCAAGGCCACAGCTAATATGCGACAGAGCCAGGATTTGGGAGGAGTCTGTGTGAC
27	CCCGGCACACCCAGCAACAGCAGCACCAGACGGGCGCAACACACACAGATTCTGATACAG[T/C]GACTGCTGCCTAGCTCCTTAACCTCTAAACGGCAGTTTCTGAGTCTGAAAATATGGATAC
28	GCTGGATTGAGAGCACAGGGTGGCTGCCCCACAAAGGTGTCTGTGCTGCAGTGCCCACCC[A/G]TCAGGCCTTGGTGCCTCCTTTGCCCACATTCCCACCTGGCCTATCCAAGGCGCTTGGGGC
29	ATAGAAGTGAGGATCCCATGGTAGGGGCCAGTGCCTGCTCCATGCATGCCAGGGCACAAA[T/C]AGAGCAGCAGAAGCCACGGAGAACTGGGATGGTCCAAGTGCATGGCTCACACACACGCCC
30	TGCTTGGGCTGGTGGGTCTGCCCTGAGCTGGCCCCTGACTCTCTTACATGTTCCACAGGA[T/C]GATGGACCGCCGGACTCTTTTCTGCAGCACACGCCTGTGTGCTGTGAGCCCCCCACTCTG
31	GGGTGGGTAGGAATGCCACACCAGGGAGCTCTCGGGGTCAAGTCCCTCCTCACAGTCCTG[A/C]AGCCCCATGGACCCCCATTCCTGGCCTCAGGAGAATCCCTGGGAACTGTGCAAACACCTG
32	CGCCTCGGTACACTCACACGCACACTCAGTACACTCACACGCCCGCCTCGGTACACTCAC[A/G]CTCTTTGTCTTGGTACACTCACATGTCCCACCTCAGTACACTCACACGCCCTGCCTCGGT
33	TTGTACTTGCTTCCCAGCTCCCAGCACAATGTCTTCACCCAGAGCAGCAGCTGAATACAG[T/C]GGAGCTGAATGGAAAGGAAGTGACTGTGCTCCTCCCAGGGCACCCCATCCATGCCTCTGC
34	CAGATTGAACCTTCTGAATTGGATCATGCCGCTTCTCTGTATAAAACTCATTTTCTGTGG[T/C]CTTTAGGATGCAACTTAGCTTTTGGCCTGGTTCACGGTGCACTTTGAGGCCGGTCCCCAC
35	TCTGGAGGCTGGAACTCCCTCCTAAGCCATCTGGCCACCACTCAGAGCCCAGGGATTGTG[T/G]ATCAAGAGATTGCAGTGATTAGAGACATTAACCCGCAGAGGCAGTGGGAAGGCCCAGCCT
36	GGCTGAGGAGGGCAAAACCATGGGAGGGGGGCCCCAATGCAGGTCCCGTCCAGATGATTC[A/G]TTCCTATACTAATGTAATGTGAGGCAGAATTTTCTAATTTTTGTCCAAGGCGTCTCTGTT
37	TCACCTGGAGACCACCAGTGGCAGGATCATCATCTTCAGCATCCTCATCAGGAGCTCTCC[A/G]GGGAACTGGAAGTAACTAATTTCCTGAAAACACAGTAAGAACTGGGGTTATAGCAAGAGA
38	TCTGGGGCCTACTTTGCCAAAGCTGCCTTTCCCATCTGTTTGGAAATGCAAATGTATTCC[A/G]GTCTGGATTAACCTGCCAGATAAATTGAAGGAAGGATGTAGAGGCTTAGAACAATTATTT
39	GATAGCCCCAGGTAGTTACTATGAAAGTCTTTACAGTAGCGGCTGTGTCGGAGGAAGTCA[C/G]CAAGTGGAGAATAGAGAATCCCACCCCTCCTCTGGAGCAGAGAACTCCCTGGGCCTGGTG
40	CAGCAGGGGTTGACTTATTTGCTAATGATTAATGATTAATGATTCGCCAGGGCTACAGGC[A/G]GGGCCAACCCAGCCTGGGAAGGCGGGGATAGGAAGGCTTCCCAGAGGAGACGTGGTTTAG
41	GCTGCAAGCCCAGGCGGGTGGGCAGGCAGGCAGCAGCAGCAAGAATGCTTGGCTGCAAAA[T/G]CAGAAGCTGAGCTCAAGAGGAGAGCACCCTGTGCTCAGAAGCAGGAGTGGTGGCTGATGT
42	AATCTCAGGACCAAAGTCTTTCAGAATCCCCAAATTCCTGACCCGTAAAGACCATATTCC[A/G]CTTTGCCTGCTGAGCAGCAGTATTCAAAAGAGTGGGGCAAAACAACTCAGTTCATATCTG
43	TCCCTTCTAGGTTCTTAGACACTATTAACCTCTTCTTCCTCTGTGCTTCCATCCATAGCA[T/C]TTCCTTTATATGTCTGTTAGAACAGCCATCACATTCTATAATAATTTGCTGCCAAACTGT

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
44	1q22	CHRNB2		cholinergic receptor, nicotinic, beta 2	12.2	1	rs2072659	152815145	T	
45	1q22	CHRNB2		cholinergic receptor, nicotinic, beta 2	12.2	1	rs3811450	152817656	T	
46	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs6660701	160307530	T	
47	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1337063	160325402	T	
48	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1415259	160351933	T	
49	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs7538490	160357954	T	
50	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs10458392	160358734	T	
51	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1572495	160365925	T	
52	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs10494368	160369894	T	
53	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4656355	160390421	T	
54	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs951121	160393068	T	
55	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1538018	160397105	T	
56	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs6427659	160408973	T	
57	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs7412698	160421843	T	
58	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4657165	160427626	T	
59	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1415263	160432667	T	
60	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4098275	160435746	T	
61	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4531275	160453174	T	
62	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs6683968	160458036	T	
63	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs7548168	160465166	T	
64	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs8179404	160467744	T	
65	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4657178	160477234	T	
66	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4145621	160485312	T	
67	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs4584372	160502061	T	
68	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs7528328	160514403	T	
69	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs6677154	160521288	T	
70	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs2819318	160547349	T	
71	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs2819328	160550681	T	
72	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs365522	160559210	T	
73	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs347300	160566447	T	
74	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs347311	160570531	T	
75	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs347313	160570900	T	
76	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1396225	160575345	T	
77	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs10800465	160576937	T	
78	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs3751286	160580009	T	
79	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs347273	160584137	T	
80	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs386231	160592447	T	
81	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs6681981	160598245	T	
82	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs1810354	160602346	T	
83	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs164149	160605205	T	
84	1q23.3	NOS1AP	CAPON	nitric oxide synthase 1 (neuronal) adaptor protein	298.7	1	rs737641	160605477	T	
85	1q23.3	RGS4		regulator of G-protein signaling 4	7.3	1	rs2661319	161306401		

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
44				0.06	0.04	0.21	0.21
45				0.08	0.13	0.11	0.22
46				0.38	0.46	0.33	0.41
47				0.05	0.37	0.13	0.14
48				0.37	0.34	0.31	0.39
49				0.30	0.31	0.44	0.49
50				0.22	0.05	0.48	0.43
51				0.08	0.35	0.14	0.14
52				0.11	0.35	0.14	0.14
53				0.38	0.04	0.26	0.23
54				0.18	0.41	0.17	0.18
55				0.25	0.09		0.19
56				0.07	0.43	0.00	0.00
57				0.33	0.22	0.28	0.33
58				0.06	0.00	0.02	0.03
59				0.38	0.49	0.46	0.44
60				0.16	0.25	0.13	0.12
61				0.27	0.48	0.48	0.41
62				0.29	0.48	0.48	0.40
63				0.05	0.12	0.00	0.00
64				0.21	0.40	0.15	0.16
65				0.23	0.39	0.49	0.48
66				0.45	0.05	0.31	0.27
67				0.20	0.36	0.48	0.43
68				0.13	0.33	0.39	0.36
69				0.14	0.35	0.47	0.48
70				0.45	0.43	0.44	0.47
71				0.07	0.39	0.07	0.12
72				0.30	0.20	0.31	0.36
73				0.38	0.14	0.30	0.34
74				0.28	0.01	0.06	0.19
75				0.43	0.18	0.14	0.24
76				0.38	0.02	0.07	0.20
77				0.31	0.20	0.43	0.46
78				0.04	0.01	0.07	0.16
79				0.10	0.34	0.07	0.16
80				0.31	0.43	0.25	0.24
81				0.42	0.08	0.41	0.47
82				0.11	0.49	0.02	0.17
83				0.44	0.44	0.35	0.29
84				0.01	0.11		0.44
85			p=0.005 (Chowdari et al. 2002), p=0.007 (Chen et al. 2004), p=0.03 (Talkowski et al. 2006), haplotype (Morris et al. 2004)			0.32	0.50

	R
1	**Sequence**
44	AGTGTTGGGTGGAGGATGGACGAGTGAGCTACCAGGAAGAGGGGCGCTGCCCCCACAGAT[C/G]CATCCTTTTGCTTCATCTGGAGTCCCTCCTCCCCCACGCCTCCATCCACACACAGCAGCT
45	GAAAGGGGTCAGTGTATATGAAAGGGTTACCTGGGCAGTGTCATTCCCTCCATCTCTGTA[T/C]GCAGCCCTTTGGGAACCATCACAATAAGGAAGAGGTGAGGGCAGAGGTGAAGGATCCACT
46	CCTCCCTGAGTGAGGAGTTCTGGCTTCTGAAACTGCAGTGGCGGTTCCCACTGCCCATCA[C/G]CAGGAAAGAGTGCTTTTTCTGTGGAACAGTGTTCTGCTCTTCCTTCAAGCCACTTGACCT
47	accaggtcttcctggagaaatgattgattccaggtctgagacacaaaatacacaagGAGT[A/G]GAAGAGAGATGAAGGGGAAGGAGAATGGCGAGAGGGAGAGAAAATCCCTGATACCAAAAG
48	CAATGATACCTGCTGCTGGTCTGCAAGCCACATTTGAGAGGCAAAGCTCTCACCATCCCA[A/G]ATTACATTTCTAGACAATTCCTCTTCCAAGAATCCCCTCACAAAAACCTACAACAACTCC
49	ATGTCTCCAAATGTCACAGCTGGTAGTGACAGATATGGCATCTCCATTTCCAGAGGAAGA[T/C]GGTGGAGGACACTAGTTTTGCCCTTTACAGCTGTGTGACTTTGGGCATATCATCTCCTGA
50	CCCCAGTGCCAAAAAGTGAAATAAACTCTTTGGTGGGCATGTAACAAAATAACTTCAATT[T/G]TTATTTCACACAGGATGACTAAATCTGAAATTGAATTATAGGGAAGAGTAGACAACCCTC
51	GATTTGCTAATGAAACAGAGATCAGGGACAGCTTCAGAGGATGCAGATTTGAGCTGAGCC[T/C]ATTAGGACAAATAGATCTATAGAAGCAAAGGATATTTAGGCAGGGAAAACGTGAGAGGTA
52	CCATTTATAGTTTTATCTAAAAGTCTATGAATGAAATCATACTCTCTTGCTGTCTTATTA[T/C]TCTAAAAGTGTGATATTTTATGTGAACTAGATTTTATAACAAGCTTTCCTTTTTATAATC
53	ATTAGTTAAAAAAGGTATATATTCTTTTTTTTTTTTTTTTGAGAGCACTAATATTTGCCA[A/G]TCACTTTTGTGTAGGACATTTTATTCTGTTTGATCTTTACTGAGAGCCAATTTTACAGTT
54	AAAAAAAGTCCCTTTTTAATTCACTTTTGACGAAGAGATAGGGAATATGTTGTCAGTAAT[A/G]TCACTATCATTATGAAAGTGATATCTCTGTTAATAGTAGCTACTATTAGGAATAGCTACT
55	CTTTATCCCTTTTTATAACTTTCTCCCTAAGTGGCCCCCCTCAGCACCATTTACTCCTTT[C/G]TCATTGTTCTCCTTTTCATCCTAAGTTCAGAGTTGGCAAGCCTACCTCAGAACAGCTGAA
56	ATGGCCATGACTCTGTGTTGCCAAATTACTTAACATTGCAAACTAGTGGCCTACAGGAAT[A/G]ATCTTGATGAGGCGGGTGGTTTAAGTGGAATGTCAGCAGGTGGTCATTGGAGATTATTGT
57	TGTGAGCTCATGTTTCATTCTGTGGTAACATAATTCCGCCCTACTTCCTAGAATCAGTGG[T/C]CATACAGATTACGTTTGCCTTTTGGTCAATAATCTGATGCCTTGAAGAACTCAAGTCTTG
58	TGTAAAGCAGCTCTTCTGTTGGCCTCACTTTGATTTTTCTCAGTGTGCCCCATACCACGG[A/G]CACTGTCCACACAGGAACATCAGATTGGAAAATATCCCTGAGTTCCCTAAGAGACAGGCA
59	AATGTGGTAAAATGGAAATCTGTCAACTGCTTCTGGGTTGGAAGGCAACATACTTGATGA[T/C]GATAAAGGAATTGGGAATGCCTAATGGTGACATTGGGGCTCACCATTTAGTGGGTTTTAT
60	AGTGGGGAAAAGAGGACAGCACCATTTATGGAATATCTGCTCCGCTGCTGCATGCCGGTT[A/G]CGTCCTCACTGTTGTTTTATTTATTCCTTTAAACCCTTGTAAGGCTCCATAGATGAAGTG
61	ATTTGAAAAGAGAAGTATAAACATTGTGATAAGAATGTTATAAGAACACTGACTGTGGAA[T/C]CAGGCAGCCTGGGTTCAAATCTTGGCATGACTATTACTGGCTGTGTGACCTTGGTCAACT
62	acacacacacacGGGTTAAGACCATGGTGTCTGGGTTCAAAGCCTGTCTCTATAACTCAC[T/G]AGCTTTTTTACTTAAGGCAGATTACTAAACTTCTCTAAGCTTCACTTTCCCTAATTTTCA
63	TTTTCTCTACCCCGGCTGCCTGCCAAAAGCAAACAAGTACTCTCTGGAGGAAGATAACAT[T/C]GTTCAGACCCTCAAATTAACGCTATCATTTTTCAAATACAATGTCTGGCAGTCAATAAAA
64	CATTTGGGTGTCTTCTTTGAAGAAATGTCTACTCAAGTCTTCTGCCCATTTTAAAATTGG[T/C]TTATTTGGCTTTTGTGTTGTTGAGCTGTACTTCTTATATAGTCTGGACATTAACCCTTTA
65	CAAATATTTACTGAGCACCTATTTGGTGCTGGGTGATATACTAAGTATTGGGGATTTCAC[T/C]TGGAGCAATTATGGCCCTGCCCTTGCAGAGTTCACAGTCTGATGGCGGGATACAGACGTG
66	TCGGGGACCCATCTCAATATGTTTTTTTCATCTTGACTTAAATCCAACTCTTCTTGTTTC[T/C]TTCTCCATCAAACCACAGCACCCCCCCCTTTCCTTTTATCAAGGGGTGATGGACAATAGA
67	CTTTATGAGAATACGCAGTTTCAATTTTATGTGGATTTGTGGGGTTCTTTGCCATGTATA[T/C]CTCATAAATCTGAGTTAAGTAACATTGATCCCATTTTACAGATGAGAAAACTGGGGCAGT
68	TCTCTTCTTCCTGATTCCTCAGTGCTGTTGCCAAGATTATGTTCAGGATTTGCACCTCTA[T/C]TTTTCACTCTTTTTAAAACCCTTAAGCACCCTCCTACTTTCTATGCAAAACTATAGTAAC
69	GGGTAAGAAATCATGATTAATAAAGGCCACAGAGAGAGTGAAACCAACAGGGAGGTGGAC[A/G]AAGCAAGAAAGAGAGATATGGTCAACTACAACATTCTTCCAGAAATATAAGACATTTAAG
70	CTCTCTGTTCGCTGACTCTCTCTCTCTCTTCTGGACCCATCTTCGCTTGTTTCTTCAGCA[T/C]CTTGAGCTGTGAACTATGCTCTGTCTCTCTGTCTTCCTGGATACCCTCTTTCTCCCTACA
71	TCATGAGAGAGCCCATAGACCTGCACAGCAGGAAACTGAAAATAGCTACCAAAGCAATCA[A/G]AATTAAACCTCTGGATCCGCCTCTCTGGGCCTGGCCCTAGAGGGCATCTTTTACACTAAT
72	TAGAGACATCTATGAAGACATCCAGGACTTGGAAACATAAGAGGAATAAAAAAATCCAGG[C/G]TTTCCAGGTGGCATAAATGTAACATGGGACTAATTTCTAGCCCAGGTATAGAGAAAACAA
73	ATCAGATTTTCTGAAAAGATGCTTTATCTGTTAAGGTTAAGTTAACCTTGGCTTACTGCC[A/G]TTCCTCTGTTCCTTCCACATCTCTGTGTCTTGTGGGCATGCCAGTTTGCATTCAAATCTG
74	TATGCATCTTTTGTCTTCAGGCCTCTTTAGCAGATGTTTAGGTACCTTGTCAAGTACCTT[C/G]TCAATAACACATGCCAGGGTCCAGATTTACTGATAGGTGTCCTATTCCCTACCCTAGCTC
75	GGAAGAGGGAGAAAAAGAAAAGCCATAGGCGCTGGAGATGAGAAAGTTTAGAGTTTGGGA[A/G]AGTGAAAGGCTCGTATGTGGCCTTGTGTAGGGGACCTGGGGAGGAGAGAAAAGGAAATAC
76	CAGAACCAAAGTTAAGTCCAAATGCAATGAACAGCTGTTCTCCTCAGCACACCTAATGTG[A/G]GTATCAACTTCATACCTAGCAGGAGTCAACATTTGATGAACTGCGGCAATGGTCATGAAA
77	ACTATGATAAAAATTGTTCCACCTTTCCTGCACTGCTTTTTCTTTTCTGTCTTAATTGCC[T/C]CTTGGTGCAGTGAATTCCATAGTCAGGATAAAACATTTCTTGAGCATTTACTATATGCCA
78	ACCACAGTGCTGAAACAATCAGTCAACTGAAAGGACAGATAGCAAATATGCCAGTTATGG[A/T]CTTAGCCCCAATTCTTCCCTCCCATGTGTAACAGAAGTAGTCAATATGCTTCAGAATCTT
79	ATGGGAGGAGTGAGGGAAGTAGTACTGAAAGAAAAGTATAGGAAGTGATCCTTATGGAAT[T/C]CCCACTGAGTCCCCAGGGAATCGTGAATCACATCAAACCCACTCCACCCAGCAGACCACT
80	AAACCTCCATGTGAGATAAGATATGAATGTTAAAGAGAGAGAGGTGCCCTGATATAAACC[A/G]CCTGGGAATCTAAGGGTAGAGCTATTGGTCAGTAATTTTGCTTCTGGGTTTAAAACATTT
81	TCTTCTAGGTATTGCTGGTACTCCACCATTGAACTTGGGTACCTGCAAAAAAAGCTTTCA[A/G]TTTTTTTCCTGGCTTCTGTAAGAGGGGACTTTTCCTTCACCCTCAATTCTAATTCTGACT
82	GCAGCCCATTTCTTTCTCAGAGAGCTTTTGCAATCAACAAACAGTATACTTGGCACCTAT[A/T]GGGTGTCATGGTCTCTGTGAGCTCTGTGGGAGACAGCAGATTGTTTCTTAGTTTACTACT
83	ATAACACTGCAGTTTGCATCTGTACCTTGTTGTCTAGGATAAAGACTTAATTCCCCGAAC[A/G]TATGACTCTAGCAGGTCTCAGCAATCTCTTCAGGCATTTGAAAATCTGTTAACAGCCACT
84	CACACATGTATATATAAACACATGTGTacacacacacacaaaacacacacacacacacCA[T/C]CTGATCCTATTTCCACTGACACCCTGATGCACCAAGGAAGGCTAACATAAAACTGAATTT
85	TGTAACATTTGCTTATAAGAACATAGAGAGTGAAAGTTACTGCACCACCACACGGAAAGC[A/G]TAGTGCCTTTCTGATGATGGAGCCAAACCTCATTCTGGGGTACCTTTCCTGAAACAAGTT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
86	1q23.3	RGS4		regulator of G-protein signaling 4	7.3	1	rs2842030	161307119	T	
87	1q23.3	RGS4		regulator of G-protein signaling 4	7.3	1	rs2940251	161314142	T	
88	1q31.3	ASPM		sp (abnormal spindle) homolog, microcephaly associated	62.6	1	rs10801589	195342817	T	
89	1q31.3	ASPM		sp (abnormal spindle) homolog, microcephaly associated	62.6	1	rs7551108	195365691	T	Thr119Ser
90	1q31.3	ASPM		sp (abnormal spindle) homolog, microcephaly associated	62.6	1	rs877897	195370598	T	
91	1q31.3	ASPM		sp (abnormal spindle) homolog, microcephaly associated	62.6	1	rs4326657	195385567	T	
92	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2082552	229834513	T	
93	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs12084975	229846734	T	
94	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1361519	229865965	T	
95	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs4366301	229872909	T	
96	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs6541281	229879757	T	
97	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1417584	229885673	T	
98	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs3738401	229896918		Arg264Gln
99	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs11122321	229902233	T	
100	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs4658935	229911421	T	
101	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1934909	229917902	T	
102	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs10495307	229946017	T	
103	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs10495308	229946190	T	
104	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2793092	229946963		
105	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs884158	229951395	T	
106	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2793091	229961231	T	
107	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2793085	229966500	T	
108	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs3738402	229969633	T	
109	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2492367	229973212	T	
110	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2812389	229977634	T	
111	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs10495310	229985399	T	
112	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs4658945	229985464	T	
113	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs11590192	229989468	T	
114	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1322783	229995698	T	
115	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2255340	230002773	T	
116	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs967244	230015269	T	
117	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1000731	230030114	T	
118	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs6667141	230031254	T	
119	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs7551537	230038840	T	
120	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs12731570	230048561	T	
121	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs12090070	230051472	T	
122	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs748583	230059461	T	
123	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs3081	230068955	T	
124	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1015101	230074317	T	
125	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs7534369	230082857	T	
126	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs11122362	230086482	T	
127	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1407599	230094534	T	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
86			p<0.05 (Fallin et al. 2005)	0.49	0.29	0.46	0.40
87				0.28	0.20	0.40	0.49
88				0.50	0.16	0.24	0.19
89				0.01	0.00	0.00	0.00
90				0.08	0.31	0.00	0.00
91				0.02	0.16	0.17	0.18
92				0.14	0.02	0.47	0.42
93				0.07	0.08	0.00	0.03
94				0.01	0.02	0.00	0.00
95				0.41	0.48	0.07	0.17
96				0.48	0.23	0.07	0.12
97				0.43	0.47	0.05	0.16
98			p=0.0001 (Zhang et al. 2006), haplotype (Hennah et al. 2003)	0.30	0.09	0.24	0.19
99				0.28	0.23	0.47	0.32
100				0.01	0.00	0.00	0.00
101				0.19	0.06	0.00	0.02
102				0.01			
103				0.21	0.20	0.46	0.42
104			p=0.0013 (Liu et al. 2006)	0.19	0.23	0.46	0.40
105				0.01	0.16	0.00	0.00
106			p=0.0071 (Liu et al. 2006)	0.30	0.21	0.48	0.47
107				0.13	0.36	0.31	0.28
108				0.02	0.04	0.23	0.20
109			haplotype (Chen et al. 2007)	0.08	0.25	0.09	0.16
110				0.49	0.20	0.47	0.48
111				0.08	0.25		0.21
112				0.24	0.32	0.33	0.30
113				0.41	0.34	0.41	0.41
114				0.13	0.19	0.15	0.12
115				0.19	0.29	0.39	0.41
116				0.14	0.21	0.18	0.14
117			haplotype (Hennah et al. 2003)	0.25	0.19	0.47	0.49
118				0.27	0.28	0.03	0.04
119				0.33	0.37	0.41	0.40
120				0.16	0.12	0.15	0.13
121				0.10	0.09	0.00	0.00
122				0.40	0.17	0.36	0.44
123				0.06	0.00	0.06	0.07
124				0.42	0.33	0.49	0.49
125							
126				0.13	0.13	0.39	0.31
127				0.35	0.25	0.09	0.18

Key appears on page 109.

	R
1	**Sequence**
86	TTCAAGCTTCACTTAACTTGCATATGAAATGAACCGTACAAAAATACAAGAGTGTCAGGA[T/G]AAAGTTATGCTCTGGTAAATATTTTGCAAAACAGATAAAAGATAATACTAGAGCTCTGTC
87	TTCTCGAATAATGAGTGTTTTTCAAAAGGTGGTCCTTGATATACATTATCTTCAGAAAAA[C/G]GGTCAGCCAATATTTTTTTTTATTTCTTTAATAGACAACCATAAAGAAGAAAGAAAGGAT
88	AGAGTTTCTCTGCTTGAGATATGGGCGCAGTCATGGAAAGAATGCAGTAGAGCAGTGTAA[T/C]TCAATCTTCAGTTTTCTGGTCAGATGATGAAACAAGGCAGCCCTGAGGAACTAGAGGGTA
89	AATGTGGAGAGAATGTAGGAGAGGCAGAGATACTTACCATCTCTATACAGGTGAGGAACA[C/G]TGGGGTGTCTATACTCAGCTGCTATATCAGGATTCCAAAGTAGGCGATTCAGAATAAACA
90	ACTTCTTAAACTAAGGTATTGAACAGTGGGGACAATATGCCCAAAGTGGGCAGGCCACAC[A/G]GGACTGATTGCATTGACTGATGAGAGAGAATAGAGAACAAAAAGTATATTTCAGTACTTT
91	CCTTTGGATCCACCCATTTCCAGAATATAAAATAGGAACACTTACTGACCACATTCTCAC[A/G]CTGGTTCCTAGATCCAAGGAACAAGGGCAATTATTGGAGAAAGGGCCAAGTGGAAGCCCC
92	AAACACCATAGAGTGTACTCACAAAAACCTAGATGGTATAGGCTATGACACACCTAAGCT[A/G]TATTGTATAGCTACTGTTCCTAGGCTACAAACCTGTGCAGCATGTTACTGTACTGAATAC
93	AATGGGTAAGAGTGTAGGCTGGCCTTTCACTTACCTTCCTGTGCTTTGCTCTTTACTGCT[A/G]GGGCTAGCAGCCGGAAAGCTACATATCCCAGGCTTTCTCGCCAGCTCATTTGCTGTTAAA
94	TTGTTAATCTTAGCTCATACAAAAGGCTTCCTAGTGGGGATGGAGCTTGAAGGAAAGCAT[C/G]AGATTTCAGGCAGGAGGGTGGAAAGTGATACAACCAAAGTGAGAATGTTCATTGCAAGTT
95	GGTGTTCCACCTCTAAAATTGGTTGAAATGAGGTATTGTATGGAAAAGGCTTTGGTAAAC[C/G]AGGAAGTGCTATACAAATGTCAAATATTAGTTTTTTCATTAGTTATATTGTTATTTTATG
96	AACTGATGAACAGATTTTCCTCCCACAAAGAAGGAAAAAGGGAGAAAATTCGTAGCTCTT[T/C]TCTCTTTTTAAAGACTGTGCTGGAAAATTCCAAAATGTTATCGGAATAAAGGAATGACTT
97	AACATCGAGGGATGGGCCTCCGGTATTGGTGCTTCTTGACACTATCCAGGTGATTCTAGG[A/G]GGCAGTCAGGACTGGAAGGCTTTGTTTTAAGGAAAAGTCCTATTTAACATCCTAGTACAC
98	AGATGGGAGCCAAAGCTGCCAGCTTGGACGGGCCTCACGAGGACCCGCGATGTCTCTCTC[A/G]GCCCTTCAGTCTCTTGGCTACACGGGTCTCTGCAGACTTGGCCCAGGCCGCAAGGAACAG
99	tgtctcttcttgacacagtcctcattacctgtgtgacctcattctctacagttttccctt[A/C]catcaatctgccccagatccagtggcattcttgctccctcttgcttttcatttcactttc
100	CCTCTTACTTTAAGTAAAAACTTAAAAATTGGGAGATGGGCTATACATTAAGACAAAAAT[A/C]CCATAGGAAGAGAATATGAACAAAATGTCATTTATTTAGTTTGGTTGCATTGTCTTAGCT
101	TGTGATAACCTATTGATGGGTTGAACTTTTCCTGAGCCCAGCACATAAAGCTCCCGGAAA[A/G]ACAGCCACAGTCAGAGACAATCAAAGGTTACTTTGGTCCCAGTAAAGATCAGACAAAAGT
102	TTTGAACGCTTGGTGTCAGTTAAGGAATGGGTACATTTCAGCATTATCCTAGAAGGTCTT[A/T]TCAGGCCAGACTCTACTGCGTATTTTAAGTGGGGTGTCTGAATTAGCTTCTGCAGTAACT
103	CTTGGACAGATGACCTTTTCTAGTATCCTTAGAATGAATTGTTGGTAAATGCTTAGTTTC[T/C]GGCTATAGGTTTCAATGCATATGACAAGTTTATGTGAATGTCTTTCACTTAACAGCCTCA
104	GATTCTCTCACTGGCCCTTATGTGGCAAGTTTTGGTTGTCTCTCACCCATTACATATATT[T/C]CACCTTTGTTTCTTATGGAAAAAAAACTATGCTTTCTGGCACCAAAAAAAAAAGTTGATT
105	GGACTGTAGGTGTTTGCTCTGTCAATAGGAGTTGATGAGGTCCTTCTGTTTATCTTTTCC[A/G]TGCAATAAGAAGTCCCTCCTGACTCTAGGCAGATTCAATCTGAGCAGGGGATACAGGGCT
106	AAACACATACATGCACACACACAATTTCGGTTACAAATAGGACCAGTTTTCACGTACATA[T/C]TGGTGAAGATCCAGTGGAAAAATGCACGGGGTGTATAGTTAGAGAAATGCAATGTATTCA
107	ACATCTGTGGCTCTGACACTTGGAGGCATAAACTCAGCATCCTAAAAAGGCCAAATTAAA[C/G]CTATCCCCTCCTTCCGTGGCATCTCCCACACAGCTAGATCTTGTCTGCCACCTTTGTACT
108	CAGGACAGCTTGCACGTGTCCATCACGAGACGAGACTGGCTTCTTCAGGAAAAGCAGCAG[T/C]TACAGGTGAGCAGGTGAAAGATCTTCAAGAAATATGATGGCATTTTTCTTTTCTTTGAGA
109	TTTGCCATGAGCAGGGTTAATTTATAAAATCTTGTCTCCTCATTCTCTACAGAAAGAAAT[T/C]GAAGCTCTCCAAGCAAGGATGTTTGTGCTGGAAGCCAAAGATCAACAGCTGAGAAGGGAA
110	TTACTCAACTTTCTAACATGCAATTGCAATATGCTTTGTTTCGTGGACAACGACCCAACA[A/G]CTTGAAAAGAAACTTCCTAATAGCATGTGACATTTCTGGATGTATCACTGGTGGAGACTT
111	CAGTTCTGGGTATTTATTTAAAAACTCAGTTGTTCCCATGGGAGCAACTGGACATTACTT[A/C]TTAAATAATCAGAATAAAGGGAGGGTAGTAATTGAAATGGAAATATGAAGTTGCCTTTGG
112	ATAATCAGAATAAAGGGAGGGTAGTAATTGAAATGGAAATATGAAGTTGCCTTTGGATCA[T/C]GTAACAGAATAAGCCTGGATGTAGTATCATTTTCCCCTTAGATCAAATTGTTGTATTTAA
113	TGCCTGGATCTAAAGCAAGTATTGGAAGTATTACTAAGAGAGGGTGTGGATTTAAGTATG[T/C]TCTAAGGCTCTTGAGATAGGCCTCCCTAAGGGACAGGATCTGGAGAAACCAAGTAAATAG
114	ATGAAGACATGGTTCCTGCCCTCAACCACTTACTGCTGCTAGAAATGCCAGAAAATGTAA[T/C]AGATGCTAGAAGAGGAGTGATTACTTGATTAAATGATGACCTGCAAAAGGAAAGGTCAAG
115	AATCATATGGCACACAGAGTACATTTAGTCTCTAAACTCTTCAAGAAACAGGAACTAGAA[A/G]TCCCAAATACGGTACTCACTTAAACACCTTGTGCTATATTATGTGCATATTAGTGAAACT
116	CAAGGTCTTGGTCTAAGCCTCATGGGATTAGATCTGAGGTCAAAATGCCTATAAAGTATT[A/G]ATCAAGGGCATTGTAGCATTTTCTCATGGCTTGGGTCTTGATATGAAT
117	CAGTGATCCAGCCCTCCCCAGTTACAGAAAAGCCTCAATGGAAAGTGGATTAGACACAGT[A/G]GCCATCCCCAAGTCCAAAACATAACAGGACTAAGGGCCCAGGGCAGCAAACACTAGCTCC
118	CTCGTAACTGTAGTTTGAGACAAATTTATCATTCCCAATCTACCAATGTGTGAAACTGAG[T/G]CTCAGTGAATTAACAGAGTGGCTCAAGTTTCTGTATATGGGAAGTAAAGAACTGGAATGA
119	TGAAACTGTCATCAGGGGCATGAAAAATGGGTTTGCAATAGTTCCCTGCCCTTCTCTGCA[T/C]AAACGATATACAGCATTTGATATTAAGGCAAATATCCTTTTCCATTGATGATGTGTAATC
120	GTAGGGGTGGGGAGTGAGCATCCACACTCGAGTGGCTGCAGATGCCATGAGACCCTCCAG[A/G]GATGACCAGGTCACTGTTAGGGCAGAGAGGAGGAGGCAGCTTTCAGAAGGAGCTGGGCAT
121	ACTTTGTACCTGCTGAGCTTCTTGATATGTGTTACGTTTACTTATCACAACAATCCTGCA[A/G]GGTGGAATTATTATCCTCATTTTTTTTTTTTTTTGAGACAGAATTTTGCTCTTGTTGCCT
122	AGCTGCAGGTTTTTCCCAGCAGGCTTGAACCCAAACCAGGGCCTTGAACATTCCCACACA[T/C]TGATAAAGGTATCTAAGCTTTTGCCCAAAACACTGAAAGAAACTGGCCCTGGCCCTGAGC
123	TTGAGCGCTGGGGGCTGAAGTCAGACTCTCTGGGTTCAAATCACAGTGCTGTGTCCTGCA[C/G]GCTGTCCTCAGGCAAGTTGCTGACTTCTCTGTGTCCAGG
124	GTGTCTCACCTGTCATAATTCAAAGGAGAGCCATGGACTGTGTGCGCTAGATTCACCTTC[A/G]GAGACTGGAGAGTCCCATCTCTGTACCACAGTGGACACCTGGACTTCCTCTGGCTTTCTC
125	ATTTTGTTATTTCTTAGTTTGAGAGCAGTTATTCAAATTAAAGTTTGAATATTTAAAAAA[A/T]TTTTGCTCTTGATTTTATTTCAAGTTAAAGCTTCTTAGGCATGTGTTTATTTGTAGGGCA
126	TTTTGAGAGATAAGAATCATCTCCTTTGGGGTGGGGCAGCTGCATTCCACACTCGGGACC[T/C]GGCCACTCAGTGCGGGGTGATGGTGCAGTTCCCAGGGACTGATGTACCTGCTCTGCAGTG
127	ATATACTGCTTCTTCTTCCTGACACCCACGTCCTCCACCTGTGGCATTAACATTATCCAA[A/C]ATTATGTGGCCATTCCCAGGTGTGTCAATAGTTTGTCAAGTATCAGCATTTTTCTCTTGG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
128	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs967433	230098438	T	
129	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs11577215	230103529	T	
130	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs10864702	230117276	T	
131	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2038636	230121872	T	
132	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2356710	230133586	T	
133	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821581	230143695	T	
134	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821585	230154072	T	
135	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs2772122	230157116	T	
136	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821597	230168887		
137	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs12060283	230173702	T	
138	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs4658971	230174437	T	
139	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821662	230187758	T	
140	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs843979	230197231	T	
141	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821661	230201820	T	
142	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821616	230211221	T	Ser704Cys
143	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821631	230214758	T	
144	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs821639	230216466	T	
145	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs3524	230225302	T	
146	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1160491	230228516	T	
147	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs9726024	230235123	T	
148	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1411771	230241398	T	
149	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs11122396	230241891	T	
150	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs1411775	230243925	T	
151	1q42.2	DISC1		disrupted in schizophrenia 1	414.5	1	rs9727641	230246966	T	
152	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs4852150	79591630	G	
153	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs10206130	79604099	G	
154	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6719738	79613746	G	
155	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs10520244	79614280	G	
156	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1864551	79620045	G	
157	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6716273	79622239	G	
158	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1367399	79627566	G	
159	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs880813	79629799	G	
160	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2566540	79639901	G	
161	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1971766	79644485	G	
162	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2566543	79651698	G	
163	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1549761	79664592	G	
164	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1430645	79666704	G	
165	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1549765	79670651	G	
166	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6750164	79676126	G	
167	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2566552	79684589	G	
168	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs4852153	79713047	G	
169	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs13400937	79718431	G	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
128				0.46	0.43	0.44	0.32
129				0.11	0.08	0.38	0.41
130				0.13	0.24	0.26	0.33
131				0.41	0.36	0.17	0.21
132				0.21	0.06	0.08	0.04
133				0.26	0.39	0.21	0.26
134				0.02	0.19	0.01	0.00
135				0.28	0.41	0.33	0.40
136			p=0.002 (Qu et al. 2007), haplotype (Callicott et al. 2005; DeRosse et al. 2007)	0.41	0.13	0.41	0.37
137				0.09	0.46	0.19	0.16
138			haplotype (Qu et al. 2007)	0.20	0.46		0.13
139							
140			p=0.01 (DeRosse et al. 2007), haplotype (Qu et al. 2007)	0.41	0.21	0.32	0.30
141				0.31	0.34	0.08	0.15
142			p=0.004 (Callicott et al. 2005), p=0.005 (Qu et al. 2007), p=0.002 (DeRosse et al. 2007), halpotype (Chen et al. 2007)	0.31	0.39	0.07	0.14
143				0.44	0.24	0.32	0.36
144				0.33	0.39	0.22	0.24
145				0.44	0.08	0.39	0.33
146				0.37	0.09	0.43	0.40
147				0.38	0.36	0.25	0.28
148				0.26	0.47	0.25	0.31
149				0.04	0.08	0.21	0.17
150				0.16	0.00	0.05	0.07
151				0.26	0.24	0.13	0.11
152				0.38	0.14	0.36	0.32
153				0.28	0.43	0.44	0.36
154				0.21	0.36	0.42	0.29
155				0.14	0.00	0.00	0.00
156				0.22	0.35	0.02	0.10
157		Y		0.47	0.28	0.43	0.37
158				0.22	0.28	0.39	0.37
159				0.28	0.48	0.42	0.47
160				0.20	0.32	0.41	0.34
161				0.38	0.38	0.47	0.48
162				0.09	0.03	0.36	0.33
163				0.18	0.45	0.36	0.32
164				0.22	0.23	0.34	0.33
165				0.10	0.18	0.41	0.34
166				0.32	0.47	0.48	0.44
167				0.14	0.03	0.35	0.33
168				0.28	0.22	0.49	0.28
169				0.18	0.10	0.37	0.24

	R
1	**Sequence**
128	ATCATACAGGCTGAAATGGTGTCATGTGATTCCAGAGGCCAAAAGGCTGGTGTGGAGTCA[T/C]GGCAACTTTCCTACCACTACATTCCCCCTTCCTATGAGTTTCATCGTACCAATGATGGCT
129	ACCAATTGGCAGTAACTGCTGCAGATAGTTCTCAAATGTTATTGCTTCCAATGGGGTGAA[C/G]TAAGTCATGCAGTGAGCCAATTCTCTTGCAAATGGCTGGCCTGTCTTCAAACGGCTATCA
130	ACTTTTGGTGGAGAGCAAATGATAGTCAAGACAGGAATGTGAGAATTGTGTATACTGTCC[T/C]GTACCAGTCAGGAGCCTAGCTTGGCTGCAGAAGAGGGCTAATAAAGAATGAAATAGGTGA
131	ACATGAATTTAAACCAAATCCCCACAGCAAAGTTCCCTGACCGGGCCAGAAAGACATACA[T/C]TTAGACTGCTGTGACAAAAACATCCACAGGAAAGCCAGCGTGCCTGGGAGAAACTCAGCT
132	GTTGACCAGAGGGGAGCAGGACCACCTGTGCTTTAAGGTCATCCTGATTTCCTGGTGGTC[A/G]TTAATACGAAAGAAGCTACACCAGGCTTGACTTCTCTGAGTCAGTGGTGTTCAGAGCCCT
133	CTTGCTCCTGGAATCTCACTGTTGCTTTATAAAGCAGAAAAAGGAAGGTAGGAAAGCCTC[T/C]CGGGGATGGGCACAGGCAGTGGGAATGTGGGAGCCGGCTGAGTGTTATGAATTAGCAGAA
134	TAACACATGCCAGATTCCATGTTAGGCACTGGGGCCACAGAGGTGAATATCACGCTGCCC[A/G]TGGGCTTAAGAAAATCAGGCTTGGTAACAGAAAGAGTCACATCAATAGATGACTAATAAA
135	CCAAGACTGTAGACAGGGAGTTTAGATTTTAAACTTCCGAATCAATACAGCCACAGACAC[A/G]CTGACGGAGAATAGAGCTCACCTTTTCCTCTCTTCTTACTCCCCTCCTCTTCCTTTCTTC
136	GGGGAGGGCTTGGCCCACTTGGTCCAGAGACATGAGTTTGCCATCAGGCAATAATGAATT[T/C]CTCCTGTACAATGGTTAGAGATATAAGATCCATTTCAACAGGAACCCATCTATAAAGTAA
137	CTTTTTAATGATTCGAGGAAGCGTCGTCAAGATTGTATGATAGTTTAATTTGCTAACATG[C/G]TATGAACCTGTTAGCTTCAGACACATGATTAATAAAAGTAAAACCCCTCATGGAATTTCT
138	TAACGAACATGCTGGTTATCAGCTGTGGTTTTGCAATGGAGGCGTTCCACCAGTGCAGAG[T/C]GGTAATTACGCTGCCCGGTCTCACTTTGCAAATGAACTGAAGCCTGTCTCTTTTAATTGA
139	actgagcatgtgccagtaatggtgaaaacatgcttttcataccattcagtctgcataata[A/G]cacactgaagggggtactactttattttctttcttttttttttttttttttggtgggtggg
140	AATTTAGTTTATATTCAGGTCTCCCTTAGAACACAATGGATAGCAACCCCTCCCTGGATT[C/G]TTAGTTAGAAGGTGATGAGATTAAGGCAATTAACCGATGACAATCCCCTTCATAGTTATA
141	ggggaagggagttggaggccaggagggaaggagagctctcccctggctgcttattgttag[T/C]agggctccaaatccagggcaggaataaacctagctgagctgcctttggttgcttggttgg
142	CATCCATCTGCCTCTCATCTTCTACAGACAGGCTTCCCCTGGCTTCCTGGAGCTGTAGGC[A/T]CTGGATAAGCAATCGACAAGCTTCCAAGTCAGCTTCCCACACTTTCCCAAGCAGTGGACA
143	GAAAACACAGGCAGGAAAACAAAAGCACCTTCCTAATGAGGCCCTTGTTATCATTTCCCC[A/G]TACCTTCTGTAGTCTAAAATCCTGGACCCGAATACAAACGGGAGTTTTCCTTCGTTAAAC
144	GAAATCAGCTTAAGACAAGGAGGACAAACATCTTCATTGTGGATCACCTTTTCCAGCTTT[T/C]TTTATGTGAAATTGAGTAAAAAGGAATGGAGATATTTAtgttgtggctcacagtatgata
145	ACAAATTCAGAGAGCTCAAGTCACCATGTTTGCTAAGAGAAGATCTGTCTGGCATTCTTT[T/C]GTGGGGCTGTTTTTCCAAGGCACAAGTTACAGGATCTCTCTCAGGCTTGTGCAGGAACCT
146	GGTCATTTCAAAGTGCTGCTTCCAGTATGTCAAGTCCCGAAGTGGATTTATCAAACAGAA[A/T]CCCTGAATCTTCCAGCTGTATCAATGGGCAAATTCAAAATTTAATAGGAATTCTAAAAAA
147	CTGCTTTTTTGAGGCCTATTCTTGCAATTAGGTGCAGTTAGCACCTCTATTCTAGTTTTG[A/G]AATTTGCCTAAATTGTCAATAGTTTTGGAATTTGCCTAAAATTTCTATTTGCCTAAAATT
148	GCTGGGGTCCAGGAAACAAAGCAAAAGCACAATATGTGAATGTGCTGATTGTGTTCCCTA[T/C]GGCTTTATCTCGAGCAAAATACACTCTACATATTTTAATAATAAGTATAATTAGCTTGTT
149	ATTTCCCTGCTGCAAATTTTGAAGTATTTGGGCAGGTGAGTCATGTTTTAACCACAAGCC[A/G]TAACTCATCTGTTGTCTTTGCTTGGTCTTAGAGTATCATTCAGAAAGTCCGCTAAGGGCC
150	TTTAATATTCACAGATGATGTTATTGTAAGCTGAAAACCCAAAAGAATCAACAGAAAAAC[A/G]TTTACACAATTAACACAATCAAAATCAACAGGCTTCATATATGCAGACAATAATTGGAAG
151	AAAATTTCTGCTATACGGAGTGAACAGAACCAATCTGAAGCAGGATGCAACCCAGTCAAG[T/C]GAGAACACTGTACTCAACCTAAAAAAGTGACTCTCAAGAGGTACCTGGTAATTCAGGTAG
152	TTAAAACAAAAATTATAAATGTAAGCCTAATTACAACAATACAAAAAACTATACATGAAT[A/C]CTTGGAACTTAAAGAGATAAATTTGTCTGGTCACTCTTTGGCCTGTAGTTTTTAGTTTAT
153	tctccacactggctcaaaaacatatacaccattgttttttttaactcttgcctattactt[T/G]atagtgtggttgtaccatggtttatttaatccttatttccatgtacattcagtttgtttg
154	AGGAGACCTTCTACATGTCATTGAAGTTCATCTAATATGCAGTCTCGCTCCTTGATGAAT[T/C]TGTATCTGATCCCTTAAAATGCTTCCATCTCATTCTCCTCCTAACTGCTATATCCCTTTA
155	GATGATGAGAGACACAAGTGGCCCCTAAACTGATTGAGATCTTAATAATGGCACATGTTC[T/C]TAATGGATTCAGAGATCTAGAGGAGCACCTATTGTGGGATACTAGTCCTAAGGAATGCTT
156	GAAGGCCATTGGAAATGCTGGAGGTGATAGAAGGTGATATCTGTGGTCCTGGGTCCTCTG[A/G]ATATAAAGTCATGAAGGCTAAATCACTGTAAACCTTTTTGACTGTATGAGGCCCTTGGAA
157	CTTAGGAGTTGATTAATAGGTTAAATAGTGGCTGGTGTCTCAGCTTATTAGAACATTTAC[A/G]ATTTGCATTTCCCCAATCTTCATAAttttttttttttttttgagacagagtctctctctgt
158	GGGTTGTATCTCAACAACTTGCCTATGTAATGATTCCTTTCCAGATTCAAGCCTTAAGGC[T/C]TGCTCAACAGTGCTTCCAGGCCAACTAATTTTTTAGAAATTTGTGGAATTTGTGAAAAGA
159	TCAGAAGTCAGGTAAGGCTGAATTCTGTCTTTATTATTTCAAATTCTCTGTTCCTTCCTC[A/C]GTTATATCATTTAAAAAAGATATAGGGATTGGAAACTTGGTTTGGCCATAGACTGTTTTT
160	GGAAAGAGCTCATACTGGAATTAGACTATCAGAGGGTGCTTTCCTGGTATGTGCCATTGA[A/T]TTTGAAATCTGGCAGTTTATGTGAATCACTTGGGAGCTTTTCAGTATGGTTGAGTTCTAG
161	AGTTTTCATTAATTTGGAAAAAACATACTTTGCTACATTGTACATTTGTCATTCAAAGTC[A/G]TTATAACAAATGCCATTAAAGGCTAGATTGCCTGGTATGTTAATGGTCCCAGGTTACATT
162	GCAATATTTTATATCTGCAGTGATAACAACCCAATTTGTTTTCTTCTGAACTATCTCTTT[T/G]ATGAATAGCCTAGAAAAATGTGGTTCACTAAATCATTAGAAGCACTGATTCTGGAGGATT
163	TAGCCTACAAAGCATTTCCTCAAAACAAGCAAACTTGAAATATAACCAAGTGTTACAAGC[T/G]TATTTCCAGTTTATGGGAATAATGAATGCTCAAAGATCAGGTTAAAGAAAACAATGAAGA
164	GAGTACAGGATGCCACAGAGGCCAACAACCCCTTCAGGGGTTCCATTTCCCTCCATGGGT[T/C]GGTTTCAGACTAACATCGACACTTTTGTTCTTCACAGAGTTTTAGGTCACAAATGCCCTT
165	TGAGACACATGATCCGGTAACAGATAATAACCCCTGGAAAAACCATGTGAAACGTTAATC[T/C]CTCAGACATCCTAGTAACAATTACGGAAAACAAAGTGTCATCAACAGTAAAATCATTGAC
166	acccataggcatcccaaattcagtacatctaaaattaaattcattatgctcccaattgtc[A/G]tattgcttctgtatttctatcttagtggatgcctgcactatcaacccaaatagcccaggg
167	CTGGCATTGGTTAAATGGTGAGGTCATGTGTGGGCATGAAAGCTCCATAGCCTGAGAGAG[A/C]GAGTCCACCAAAGAAGGGTTGGAGGACCCTGACTTGGGGGACAGCAGTGAAATAGGATGA
168	ATTCAGTTTGTCTAAATAAACTCCTAACCAGAAAATTTTAATGAAAAAAAATCCTCTAAA[A/G]TAACAATAAATATATTTCTTCTGTTTATCGACAAATAGCTAATGAGGATCAATAATGTTT
169	GCCCCACCAGACTTACCACCCGTGAAATAACATATTGAACACATTTCAGGAAGTTGAATT[T/G]TATCTTGGAAAAAAACAGATTTGGAACAAACTTTGGTTGAATTCCATTAACCTTGGAAAA

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
170	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1430642	79721176	G	
171	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs3795994	79726512	G	
172	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1511198	79737953	G	
173	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2861854	79743608	G	
174	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1567529	79745765	G	
175	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2861857	79759614	G	
176	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs4258819	79760823	G	
177	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6729255	79771489	G	
178	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1511182	79774055	G	
179	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6547259	79779235	G	
180	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1397693	79788862	G	
181	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs11689331	79802429	G	
182	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1397690	79805149	G	
183	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs4852514	79807254	G	
184	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs7565439	79816822	G	
185	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs11681484	79821666	G	
186	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs925404	79836197	G	
187	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs971476	79842175	G	
188	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs12713991	79844837	G	
189	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1397696	79850281	G	
190	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1159457	79855782	G	
191	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs10496232	79857271	G	
192	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2102547	79893363	G	
193	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1001112	79894431	G	
194	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6734305	79908334	G	
195	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2203051	79913587	G	
196	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2974154	79935364	G	
197	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs10496233	79935726	G	
198	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs13430537	79963829	G	
199	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2916508	79965305	G	
200	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs13414270	79968069	G	
201	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs989743	79970788	G	
202	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs13034462	79973002	G	
203	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs10496234	79973743	G	
204	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2974173	79975239	G	
205	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs974736	80019524	G	
206	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs540905	80066801	G	
207	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs482602	80081198	G	
208	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1368909	80082251	G	
209	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1434099	80082649	G	
210	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs417570	80086053	G	
211	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs450658	80089547	G	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
170				0.50	0.38	0.24	0.30
171				0.43	0.05	0.19	0.21
172				0.13	0.33	0.40	0.44
173				0.48	0.38	0.17	0.21
174				0.21	0.31	0.16	0.21
175				0.46	0.38	0.19	0.20
176		Y		0.28	0.49	0.08	0.16
177				0.38	0.41	0.09	0.12
178				0.24	0.19	0.43	0.49
179				0.21	0.19	0.49	0.41
180				0.18	0.38	0.38	0.38
181				0.22	0.09	0.24	0.27
182				0.20	0.05	0.08	0.08
183				0.06	0.00	0.00	0.00
184				0.26		0.22	0.28
185				0.43	0.38	0.34	0.46
186				0.33	0.14	0.32	0.21
187				0.13	0.18	0.42	0.44
188				0.49	0.00	0.05	0.00
189				0.25	0.15	0.25	0.31
190				0.05	0.05	0.00	0.01
191				0.07	0.36	0.42	0.30
192				0.49	0.00	0.03	0.00
193				0.45	0.27	0.19	0.14
194				0.46	0.28	0.41	0.40
195				0.40	0.18	0.10	0.10
196				0.19	0.08	0.16	0.10
197				0.27	0.28	0.09	0.13
198				0.26	0.20	0.41	0.30
199				0.11	0.00	0.17	0.12
200				0.27	0.49	0.31	0.30
201				0.18	0.03	0.20	0.12
202				0.09	0.13	0.04	0.06
203				0.43	0.34	0.44	0.36
204				0.27	0.13	0.07	0.07
205				0.07	0.23	0.03	0.01
206				0.29	0.33	0.21	0.34
207				0.15	0.23	0.03	0.04
208				0.47	0.18	0.15	0.38
209				0.50	0.13	0.08	0.10
210				0.25	0.36	0.14	0.23
211				0.29	0.28	0.14	0.36

	R
1	**Sequence**
170	AATATGTACTATACATTTTTCTGAAATACATAAATAAAAGTAAACCTGAAGTATAAATTA[T/C]GTTCTCTAAATAATACCAAGATGTCATGTGTTTTCAGGGTCTGGGGAAGTACTGAACAAA
171	GGTAATATAACTGACTCAACATCATACGTGCAGAGGTAGGTGAATTATCTCCACAGCTCT[A/C]TGATAATGACAGGCATTATCAGTCATTAGCTTCTTCTGAATTTGTATCAACTAAAGCTAG
172	TTAGTAATTTATTTTTTTCTAGGAACTGATTCCCTTCCTTTAGATGTTCATGCTTCATCA[C/G]TGCAGAGCCACACCTAATATTCTACTATACTTCTTTTAACCTTTCTTGTTTCGGGATTTA
173	TTGCTTTACTGTTTCCTGGCCTAGCCTTTAAATGTTCACGCTGTTCAGGCCTCCGACTTG[T/G]TTGGTACTCCTCCTTTCTTTCTTCTGCATTTTCTCCCCAGGTGATTCTACCCATCCCTAT
174	GCTGGCCAATACAAAGGAAATGAAATAGGAGAAAATTTTCATACACTTGTGAAATGAGAG[A/C]CCCAGGGTTTTAGAGATTGAAAGAACTTCTTTCTGGATTGAGAGTGGAAATCAAGGTAGG
175	ATACATTGTTATATAGAGATAAATACAACTGAGCTAAAAAAACCCCACAAATCTGAACAG[T/C]GGAGGGAGAGCCAGTGAAAGCAGTGGTGGCAGAAACATTCCATTATAGATGCAGAAAGTG
176	CCACTTTTACCATGAATGTTTTTGGTTTTGGTGTTGTTTTAAATGAGGCAGCAAATAAAC[A/G]AAACAGAAAATCTCGGGATTTAGAGATTTATCTTCCCTTAGGATATCCCTCCTTCATGAA
177	TCACACTTGTTTCTTGAATTTATACAGTAGGTTGTGTGTTCATATACTGAAAACATTCAC[C/G]TATTTATACATGGGGTTAACAGGTTGCATTAGGTGGTGAGAATATGGTTATTTTGTTTTT
178	TTGAGAATTGATGTTTATGTCCCTAATACCTAGAGTCTACACATTTTGCTGCATTTGCTT[C/G]ATGACATACCTATTCATTTTTCTGTTCATTCTTTCATCTATTTTTTCAAATTTCAAAGTG
179	AGAGGGGTGCCTATTACAATGGTTAAACTAAGTTTGCCCCTCTTCAGGAGAATAATATTT[C/G]GGGGTAATTCTTTCCCAAAATATTAGTGAAAATTGTTTGCTAGTTCACTCAGCACATAGT
180	CTGTAATCAAAGAGATAAAAGCCAACATAGGAATATTTATTACAGCTTTCAGAAGGGCAA[C/G]TTGAACTACTGGGGCAAGAGTGAAACACTGAAATAAGCATAGTACACTGTATAAGCACGC
181	CTACTGAATATGTTCGAATTTGGTTCTCAAATCAGAGGAAGTCCTCATTATTAGAAAAGT[A/G]TACTGCCACCATTGTGCATTATGGTTTTCAATTTAATAAATTTGAATGAAAATCTGAAAC
182	ccaaagtactggggttacaggcgtgagccaccgcgccAGCCCATTATTTCTTTAAAGTGG[T/C]GCTAGCATTGAACATGAACATCTTGAGTGGCTAATACTGAGTCCACTCAATCCCTTTATT
183	gtttcatcctgaaaccatccctcctccctccgacacattcccccggtggaaaaattgttg[T/C]ccatgaaactggtccctggtgccagaaaggttagggaccgctgGTGTAATGGGAGAATAA
184	TTGTCACCTCCCTTTGCGTCAGAATTTGTATAACTTTGTTGGTCTGCCTTTCTCTCTGAT[A/G]TGTACAACATACAACATACATATATCTTTAAATCTCACAAGTATTCTGCTTTAGGAAATA
185	GTAACATGATGGGAAAAAATGACACTTCAGGTGGGAGAAAAGGAAAATGTGCAGTAGTGT[A/G]GAGTGGCATGCATTGTCATAGGGTGGCAAGAGAACGGGCACGGCAACTCAGGGGAAGGAG
186	TCCCCTTCCTTATAGAAACTTCATTTTACAAGTGTTTCTCAGAGTGAAGTTCACAGACCA[T/C]CTGGTTCAGAATTCCCTGCGTGGGTATGGGAGGAGTCCATGAAAATTCATCTTGATAAGT
187	GGAGTGAAATTTGAGCTCAAGAACGTTTGTCTTTTTAAAGCATAAAAGTATTTAATAACA[T/C]TGGCTTTTGAAAAGCCCTTAAAATGTGCACGTATTTGTATGGGCTGCATAAAGGAAGAAG
188	AAAGAGACACTCAGTGTTAAAAATTGGAGCAGAATTAACTGAACAACATACAGTAAATTT[T/G]GCTAGCAATATTTATGAATCACCTTGTATTTAATAAGGACATTTTCATATTAAAGAATGT
189	GTGCCTATCCAATAATTACAACTGGGCCTTGTTTTGAAGCTGTCCTTAAGCATTAGTTAC[A/G]TTTTGAACTACTGGCCTCATAGCAGAAGTCTCTTAAATTCTTTCTTAAAGGATGAGTTGA
190	AATATTAAAAGATCCAGGGCTTTTGTTGCTTCTTCCAGAACTGTTTTCCAACTGTCATTC[A/C]TGCCTTGTCAACCATACCAAATGAGAGAAACCCAACACTGTCCATTTATCAGCAGCTGCT
191	TCATTACAAAAATATGATGCCATTGTTTCATTGTTTTTGAAATATGATTAACAAGCCAGT[A/G]AACAATAAGTTTGAAGTTTAGAACTACTTTATGATAAGTGGATTTAAATGCTTGAATGTG
192	ACCCAGCAGGTCTCTCAGGTTGGGGACTAGGTCTTTTATGCTTCAGGAGAAATCTGGGTG[A/G]CAAAGTACAGCATTTACTACAAATATCACTGCTAGATATGAACATAATATATTCAGATAA
193	ATCTGATGAAAGCTAAGGACCTTCTTTTAAGAAAAAAGCACACTCTTATAAAAATGTCTA[T/C]ATTAGTTTCCTAGAGTTTGCATGACAATGATATAAATGGGATACTTTAAAACAACAGAAA
194	TCTACTGTAAATAGAAGCAACTCTGTAGATGCCCCTGAAAGGAATATGTATCATTATATG[T/C]CATTGGGCACAAATATATGGTTTTTTTTAAAAGTCTTATGTGTCAACAATACTTAACAGA
195	GTAAATTTTAAACCTTATTTGTTTTCCATTGCTACTGATTACAGTTACCCCTTTTTACTT[T/G]TTTTGTTCTTAGAAAATGAAACTGATTTAAATATTAGCCAACAGTAAAGCTTTAGGAAAG
196	GTTAATTTTTCTTCTTTTCAGCAGGTTGTAGTGGCTAGAGGACATCAAAGGCTTTACCGT[A/G]GAAATGTTGCTCTGAGTTAGGTCTATAATCAAGTACATGAGATTGAACAAGAATGTATAT
197	AATCCTTATCAACATGAAATCACTTGTATCTGCTTAAAATGAGCTTTTAGTTTAATTTGC[T/G]TTGAATGAAATCATCTTCTATTTATCTTAGAATAATCTCAGAATTTAGTGTGAGTTTTCC
198	GTCCTGCCCTCCCAAAATTGAATTTGAAACACACTTCATATTAATAGTCACGAGTGTGTC[A/G]AACCCAGTTTTATGGGAGGCTGGATGCAGAAGTGTCTTAACATTTTATAGTTGATGAGAA
199	ATTCTCAACCACATTAAGCTGAAATGTTACCCTGGTATAGCAACTCTACATAAGTTCCCC[T/G]TCCTATTTTTACCTAATTTTCCCTACCTGCCTTTACCTTCTTACATTTTCTTCCCTTTTT
200	CTAATTAAAAAACCAAACATTTTCTAGGTCTAATTATGAAATCTTGAGAAATTTCAGTCA[T/C]TTTTTGGAAAATTTGATGTTTTTACATAATATAACTTTCTTGCACTGATTTTTTTGGCTC
201	ATGCTGTGAATGCCATTTTTAGTTTCACATTAAATATGAGATTTCTTCTGCTTTGTTGGT[C/G]TCTGAAGATTGCTCAGCGAGCACCTGGAATAAAGAGGAGCGAATGGCAGAAAGCGGGTAG
202	TGCAAATATTGACTTTAGACAGTCATGGCCATGAAACATTGTGTCCCTGCAAATAATCAC[T/G]AACCAAAGTTATACTAATTCATGCACGCCTATTCTCATTACCTGTATTAAAAAAAAAACC
203	CTGAGAAATCCTTGATGAGAAAATCTCATAGCAATCTCTCCCCAGATCACTTTTCACATA[T/C]GATAGGTAGTAAAAAAATATTTGAGAATAGTTGATTGTGCCAGACTGTTGTGTCTCATTA
204	GCTGAATATAAATTTATTATTCAGAAAAGAAGGGAAGGAAGGAACAGACAGAGGAACTCC[A/C]ATGAGGGCCAACACATGGATTAAACAGTGACTATGTACCTGAAAATGATAAACAGTTCAT
205	ATTAGATTTTAATTGGGTTTTAAAGCTAAGATGAATAGGTAGATAAGGTAGAATTGGTCA[A/G]AAACATACTAATGTAATAAAACCTTTGGTTCTCTAAGGCTCTTGCATTAAAGACCAGGCA
206	TTTAACAACTAACTTTAATTTACCACGGGAGATGTTGGTAAAAATTGTCAAGACCTCTTT[A/C]AGTTTTCAGCAAATGCCAATAGCAGCTTGGACATGATTGCTGCTAAGATGCCTTTAATGA
207	AAACTCTTTCTCTGCAATTTCTGATAGCTTTTGCCTTGTTTTCATATTGGCCTTCACTGC[T/C]AGCCACTTCCCTCAATTAACATCCTCTCCAAATCAATCATTGATATTATACTTCCTGCAA
208	TTTCTCCTGGGGATTAGTCTAATAATTGGCAGAGATAAGAATAAAGGCCAGGAATGTGTA[T/C]GTTTAACCAAGGAGTGTTTGCAATCTATTGCAAAGGGAGAGAGAAGAACTAGCTGAGCAA
209	TTAAATAACTCAGAATTTACTCATTTGTGAACATACCTCTCTGTACTTCCAAGTTATCTC[T/G]TTACCACACACAGAAATGTAAAAGCTTTAAACAATGTGTTTTTTAAGTGCTTAGTGACAA
210	AGCAAGAATGAGGCTTTCAAATCTCTTGTTTACCATCTCCTACCATGAGTTCCTATCACA[A/G]AAGTTTATCATGGTGAGCTTAACAGAGACAACTTAAGGGGAAAAAAACTTTTAGAGCACT
211	GGGTATTTTAATCAGTCCCTTATTTAGCACATGATACTGACTATCAACTTTTGTGCAGAA[C/G]AAGATGTTAGCATGGAGGAGCTGGCTTACAGAAAATATTTTAGACTTTCCGAGACACTGA

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
212	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs427295	80092085	G	
213	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6753378	80096033	G	
214	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs921637	80112935	G	
215	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs6729700	80114681	G	
216	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1812391	80132155	G	
217	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs9973600	80136766	G	
218	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2121309	80139124	G	
219	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs7605424	80155080	G	
220	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs4852550	80159781	G	
221	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs716487	80164159	G	
222	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2902109	80171196	G	
223	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs3849389	80212764	G	
224	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2862019	80222952	G	
225	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1867805	80224823	G	
226	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs7605086	80228591	G	
227	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2078520	80246156	G	
228	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1443897	80266636	G	
229	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs894829	80266847	G	
230	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs980741	80277819	G	
231	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs1374118	80286561	G	
232	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs2597321	80321430	G	
233	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs310781	80323440	G	
234	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs160864	80331785	G	
235	2p12	CTNNA2	CAPR	catenin (cadherin-associated protein), alpha 2	1,135.8	2	rs318369	80342285	G	
236	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs3791878	171380437	T	
237	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs2241165	171386625	T	
238	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs3828275	171390986	T	
239	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs3791850	171416346	T	
240	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs769393	171417767	T	
241	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs7578661	171423379	T	
242	2q31.1	GAD1		glutamate decarboxylase 1	44.6	2	rs4297845	171427785	T	
243	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1836724	211953197	T	
244	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs3791682	211957951	T	
245	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1816532	211976485	T	
246	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs3791700	211983265	T	
247	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs3791703	211992598	T	
248	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs3791709	211995179	T	
249	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497944	212002670	T	
250	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2033647	212010372	T	
251	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1816531	212019978	T	
252	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2371271	212024933	T	
253	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1836749	212036235	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
212				0.14	0.04	0.08	0.10
213				0.32	0.28	0.17	0.39
214				0.42	0.32	0.14	0.14
215				0.48	0.17	0.18	0.18
216				0.23	0.06	0.12	0.12
217				0.41	0.30	0.11	0.12
218				0.43	0.20	0.11	0.13
219				0.32	0.24	0.21	0.27
220				0.43	0.08	0.18	0.16
221				0.22	0.42	0.31	0.36
222				0.14	0.16	0.43	0.42
223				0.48	0.13	0.13	0.16
224				0.48	0.03	0.18	0.17
225				0.39	0.42	0.26	0.31
226		Y		0.29	0.19	0.38	0.42
227				0.13	0.46	0.19	0.22
228				0.10	0.48	0.11	0.14
229				0.11	0.03	0.07	0.09
230				0.27	0.07	0.37	0.41
231				0.34	0.13	0.36	0.39
232				0.31	0.09	0.39	0.42
233				0.39	0.23	0.34	0.41
234				0.39	0.33	0.47	0.46
235				0.42	0.07	0.40	0.38
236				0.30	0.01	0.19	0.22
237			p=0.016 (Addington et al. 2005)	0.19	0.27	0.23	0.18
238				0.49	0.18	0.36	0.22
239			p=0.047 (Addington et al. 2005)	0.18	0.14	0.07	0.03
240				0.04	0.00	0.25	0.26
241				0.27	0.09	0.30	0.40
242				0.43	0.38	0.46	0.41
243				0.42	0.38	0.21	0.32
244				0.33	0.20	0.49	0.49
245				0.23	0.18	0.33	0.31
246				0.28	0.10	0.48	0.34
247				0.36	0.24	0.43	0.39
248				0.29	0.10	0.48	0.34
249				0.43	0.22	0.14	0.31
250				0.36	0.21	0.44	0.32
251				0.33	0.19	0.27	0.38
252				0.50	0.29	0.15	0.29
253				0.28	0.26	0.32	0.40

	R
1	**Sequence**
212	GCCCATAACTGTTTGGCCTTTTTCTTGCTGCCTTGGCACATCCTGGCTTTATCCACACCC[A/G]AGTCACCACCTCAGAAAGTGAGAGTCACACAGTACATAGTAGAGAACCTACCAGTAGAGT
213	TCTGTTTTAATTAGTCTCAGTAATAGATATGACAATAAGCAGGGCTCGTTCACAGCCATT[A/G]CATCAAGCAATGGAACCATCAGATCGCTGATCCTAACACCATGAAAGCTGTCACCCTGAA
214	TCTTCAGGGAAGTCTTTCCCTGATGTGCCAACCTGTTGGCCATAATAAAAGGTTTTACTT[A/G]TGGATAATACTGACAATATCCTGCATGAAATATGACTAAACAGAAAGCAGCTGGCAGTTA
215	AAAAAAAAAGCACTGAAAGAAAACATGGACAAATTCCTTTATGAACTTGAAGTAGAGAGG[T/C]GGCTTTTAAATATGACTGAAAATCCATTAATCATTAAAGGAAAGGATAAATCCAACCATA
216	ACTTTAAGTGTGAAAGCATATTGTTTATCCTTTAGAAAAGTGAATAATAATTTTTGCTGC[A/G]AAGTGGTATACCAGCACATTTGTCTATAAATTTACATTCTTGGATATTAGCAAAATTGCA
217	gtcacagctgctatgagtccacaaccatcagaaatccacatttctgatgaggattgtaca[T/G]cttcaagatggagcttctcttctgtgagttgagatgaatgcttcgtctctagccttctct
218	ATAAACGTTCTGCTATATTGTTTTGATATTTCCAGTTATTTTCTGAGAGTTTGCCACAAA[T/C]AGTGACGTGAGAAGGAGAAACTTTTAAAATGATTTTTGTTCTGAAGGAGTCCATAGGCCT
219	GAATGGCATTTCCCCATTTTGAAAGATGTAAGTAAAAACACTGTTTAACATCTGAAGTTC[A/G]TTTGCAAGAAGAGTAGATGAGCTAGAGAAGGTGGCAGAATGACAGTGTGACTCCCACTTT
220	GGGACGCTGTGAGATGCTGGTGAATTTGCTAGCTGGCGTGATGGATTGTCCCCTTACTTC[T/C]CTGCTTTCACTCCCCAACAGATGATTATTGTTCTCCTGTGCAAAGGACTGTGAGGACACT
221	GCCTGCAGGGGTTAGGACCATGCAGAAGATGGGCATGGGTATTCTACGCATCTCCAGTCA[A/G]ATTGAACATATTGGCTTAATGTC
222	TTTCTTCTTAGCTTCAGAGCATGAGGACGCTTGTGAAATACGTAGCAAGTGGCTCATGGG[A/G]CTCTTTCCAAATTGAGTTAGGATGTGTGTTCAGTTCTTGAACCTCATCTTATGCAGTGTG
223	gtgaaactctgtctcaaaaaaCATGTATATATAAATATATCTTGTGCAGTTTAATTTTCT[A/G]CTTGGATGATATGCCTGCTATTGTGATGTTTGAGGAAGTGAAGACGTCTTAGCACGTACT
224	cccttacctgtaagtcattgggaagttggagtcttcagcgttagctgctcacctcttctt[A/G]cttggtgccttgccataaatgcctcactttctctcactgcagtccctatgtcagtgtttg
225	TTGCTTAGGACGTAAAATTTTCATTTTCTATGTGGATAGGACTGTAACCCGCTGCACTAA[T/C]ATCACTACTGTCACATTTTGTCTACGTACCTCAAGCTTCCTACTATTTTTATAAGTAAGA
226	TTAGAGCGGATGTACAGGGGAAAGTTTTGTCTTCACGGAGTCAGTGTGGCTCATCTGTCT[T/G]TATTAAATGTCTAACAGTTACACTGAACAAGAATGACATTTTAAATAAGAGTAAGTACTG
227	TCAACAGAGACTTCTAGACTTCCACTTCttgtaatgcaggtatgaaaaaaatgcttcaaa[A/G]agcaattactaacacacttgaaacaaacaataaatagaaggccttatcaaagaaatggat
228	CTTTGCCATCCACAAAGGGAGAAAGGAGAGCACCAGCTGGAAGCTAATCTCCACAACAAT[T/C]GGCTCACAGACATTTCATAAATGTGTTCAACATCAACTCTTACACTCTTTTTTACTTATA
229	AAGGAGAGACATGAGAAATAAAGTAAAATCAATAAGGCAATGTGTCTCTAGGAGTTGACA[A/G]TTTTTTAGAGTGATGTATGAAGGCTCCAACATCTTTATTTCCAGAGTGAAGAAGATAATG
230	ACGATGTGAGTCTGAGCCCTGCCTTCACAGATCCTACTATCTAAGCAGCCATTAAGCAAG[A/T]AAGACAACATAAATAATTGACTACAGATTGTGAAAAGTGCTCTGAATAGAGATCTCATTG
231	TCCAAAGTTCTGACATCTTGAATATAACAACTGACACTAAAAGTTTTTTAAATTGATTCA[C/G]GACAATGCATTTAAAACATATTTATAAAGCACTTTATATAGATCATCAAGTGACTTTAGA
232	TGTAAGATCATTAAAATCTTCACTGTGGAGCCAAGGTTCAACCTGGGTTTTTAGGAAGAG[A/G]CAGGATTTAACTGTTTGAGGGAGTTAACATATAATGTAAAACATGGATGTGTTGGGTACA
233	GCAGAATGAAGAAAACACACCACCCAGAGTTACCATC[A/G]AGAAGAGAGAACAGACCCAGGCTGGCAGAGGAACAGCTCGGGCCAGACTGCTGTTCAGCT
234	GTACCCTTTTAATATCTCCTCAATGGTGTTTCTTCCCACACGTTTATGGACAATTTTAAG[T/G]AAGTCCTTAGTAGCACTGATGCAGGGCTTATTAGAACCCACATCTTGGTGTCCATCTAGT
235	GCCCTTAGGAAAAGCAATGGCTACTACAAGTGATCTCTTTATAACACTGGAGTTAGCTGA[A/G]ATTCAATTGGGTATTCAATTATTACCTCAGACCATATTGGTAGTGAAAGTCCCCAACCAC
236	TCTCCCCCAGTTTTTTTCTTTAGGGCAAAAATGTTGATGTCTGTGCGTGTCTGGGTGACA[A/C]CGTGTAGGCAGTGATTCCTTTACTGGTATTTACCGTGGTCCTCCCCCTCTCCCCAGGTGG
237	CCGACAGGCATATACTCTAAGCCCCCATCATACTCCCTTCCTGCTCCTGGCTTCAAATAT[A/G]GAACGGTGTCTCTGAGAGGCGGGGCACCCGGCGCCCCTCCGGGCCCGTAAGCGACCCCCG
238	CCGGCCCTACGACACGGCTTTAAACCTGCATCCCATTCCTTGGGCTGCACTTCCAGTAAT[A/G]TACTAGGAATCAGAATCCTCTCTAAATCCTGTAATTATTTTATGAATAGCACACTTACAC
239	TGAAGGATCTTTTCCCCTAGATAGAGCAATTGGCTCAGAATCATCCTGCCTCTGCTCTCC[T/C]TAGAGCTAAACCCTTGTTGTGAACTTTCAACCTCTTCATCGTGCTTAGGTCCTTTAGTTA
240	AACCTGGTTTCTTCTCTTGGCTCTTGCTGGCTACTGTGCTTCTTCTTTGATCAGTACTCA[A/G]GGTCTGTCAGCAACTGAACCTTTAAGGAAATTATTTAATTGAGTATTCCTTCATGTTTGC
241	TTTAAAGTCGGTAACTTTAGTTACCTAGAAAATTGGTTGTAGGGAACAGCTCTCTTGCCA[C/G]ATATGATTGGATAAATGAGGCATTGTTCTCCCTGGTGTGGAAGTAACATTGCCTTTGAGA
242	GTAGTGTACTGTGTATAGTTTTCTGTGGATTTTGACAAACCCATTCAGTCATGTATTAAT[A/G]ACTATCATCATGATCAAGGTCTACAACAGGTCTGTCACCCCAACGAATTTCCCATCCCCC
243	GATAGATCCAGAACCACAAAGCATCTGCACCACAAAAGGTGTTAGACTACCAAGCAGCTC[T/C]TGGTTTTCTGCATAGTATTAGTAGCACAGCTTAGGATGAGAATCCTTTCTCCAGTAACAT
244	CTGAAGCTTAATTCCACATCTATGTCTATAATATAGACTGCACATAGACATAAACACGCA[T/C]GTATTGTAAGTCCTCTGACAGTCCTCTCTTTTACTATATACACAAAGCCCTAAGCTATTC
245	AAGGAGGAGGCTCCAGAATTATAATACTTAGGTATTTAGTGGGGTCCATGGTGAAAGGTT[T/G]TGGGACCAAGCCAGGCATAATTGCAATCTCAGTGATACCAATGAGCATGAACACTCTGAG
246	ATATATATACACACATTGCCAATCTCTCCTCTTTTCCCGAATTGGAGGTCAGTTATAAAT[A/G]TCAGGCTGCTGCTTCAGTTTGGGTGAGGAGTAAAATCATTGTGATTTACCACGCTATGAG
247	ACAAATTTACTACTTCTTCATGCTCCGTACTGGTCAGTGAATACTGGATTACAGCACTTA[T/C]TATGCAGTCCCTCTATCTGTATGATTCTTTGATTAAGGTTTTCACTTCTTGAAAGCAGAA
248	AAGGAGTTGAAATTTAAATTTTGTGAAAATATGAGCAAAAGTTTGAAAAATGTTGTTTTA[A/T]TCGTAATGATCTGAGAAAGAAAGCAAGCTAGTGAAAGAAACGACTCAATTGGTAAGGCTT
249	TAGGCCTTTGAAATCATGAGGTTGGCTGCTCACCAAGGTGACACCAAGGTAACTCTATGA[C/G]AGAATCATGGTATTCAGTGAAAGGGAAGAGAAGACACATTGAAAGTAATTTCCCTACGGG
250	TTTTCGTCAATACCATTATTTGAAAATTAAGTCATTCTCTGTTCTTTTCCATAAGCAGTT[T/C]ATATGAGTTGATTCTAACCAGAGATTAAAATGTTAAATTCAATTCTAATACAATTTTCCT
251	TCACTGGTTTCATTAAATCCATTTATTCGGTACCATGACTTGTGAATGTTGCTTTGTTGT[A/T]TTACGCTTTCAGTGTTTTATAGAGGGTTTATAGTTTTCTTATGTTAAATGTTAATATATT
252	TATTAGATACTGGAAATATCAAGTTATCAGGAGTAAACTTCTATTAAACTTGGCTTGTTT[T/C]GTCTTATCATCACCATCACATTTCACTGCGAGTAGAAATTTTAGAAAAATCTCTTTTTCA
253	TTAATCAAGTGAGTAGCTTTGCAATTTGTACATGAACAAACCCTGCTGGAATTTGAGCCA[C/G]GAATCCTTGAAACTAAAAACTATAGCTCCGCTTTTTGTAATTGAAGGAGAATCACTGATT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
254	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4302167	212041668	T	
255	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4439896	212053703	T	
256	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4672614	212058333	T	
257	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4672615	212065237	T	
258	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4278873	212069319	T	
259	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4358067	212072729	T	
260	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10932379	212083593	T	
261	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435632	212086769	T	
262	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7599979	212091765	T	
263	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10932380	212098595	T	
264	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1851183	212112767	T	
265	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs953956	212121920	T	
266	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497945	212126355	T	
267	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497946	212126407	T	
268	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1879531	212147301	T	
269	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1818751	212162650	T	
270	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1972143	212170367	T	
271	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1851196	212178865	T	
272	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7601664	212201009	T	
273	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435644	212213909	T	
274	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435647	212215478	T	
275	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10932390	212220691	T	
276	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6708035	212224987	T	
277	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6730119	212227273	T	
278	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6719645	212233218	T	
279	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6719664	212233284	T	
280	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6725181	212238711	T	
281	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1818750	212243604	T	
282	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10173674	212253778	T	
283	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1829615	212256022	T	
284	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2371276	212263330	T	
285	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7425448	212266785	T	
286	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10205553	212268193	T	
287	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435659	212273140	T	
288	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs3923755	212274316	T	
289	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435660	212280184	T	
290	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6745717	212285476	T	
291	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs12162287	212288142	T	
292	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435665	212299886	T	
293	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7570613	212337824	T	
294	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs13008313	212350533	T	
295	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7423708	212354130	T	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
254				0.18	0.32	0.26	0.37
255				0.17	0.48		0.33
256				0.15	0.41	0.22	0.34
257				0.22	0.48	0.25	0.44
258				0.15	0.46	0.02	0.02
259				0.28	0.40	0.27	0.47
260				0.47	0.37	0.24	0.43
261				0.28	0.13	0.39	0.47
262		Y		0.23	0.32	0.14	0.17
263				0.30	0.33	0.14	0.18
264				0.27	0.05	0.14	0.16
265				0.08	0.48	0.02	0.01
266				0.19	0.36	0.06	0.07
267				0.01	0.28	0.05	0.04
268				0.18	0.33		0.15
269				0.15	0.42	0.08	0.08
270				0.10	0.30	0.08	0.09
271				0.10	0.39	0.23	0.17
272				0.09	0.38	0.28	0.28
273				0.01	0.08	0.00	0.00
274				0.02	0.20	0.00	0.00
275				0.20	0.03	0.28	0.34
276				0.21	0.37	0.00	0.00
277				0.43	0.33	0.08	0.11
278				0.26	0.04	0.38	0.30
279				0.08	0.28	0.00	0.00
280				0.10	0.41	0.05	0.08
281				0.04	0.00	0.00	0.00
282				0.47	0.36	0.00	0.01
283				0.49	0.27	0.05	0.08
284				0.50	0.37	0.11	0.12
285				0.15	0.14	0.05	0.03
286				0.48	0.30	0.14	0.10
287				0.44	0.26	0.33	0.31
288				0.46	0.33	0.16	0.23
289				0.41	0.39	0.08	0.10
290				0.19	0.26	0.06	0.02
291				0.28	0.05	0.47	0.48
292				0.11	0.16	0.32	0.38
293				0.26	0.09	0.39	0.47
294				0.45	0.23	0.35	0.40
295				0.28	0.33	0.19	0.09

	R
1	**Sequence**
254	CTTTGAGCAAATGAGGCTAATGAAAGAAAGCCACCGTGTTTGATGTTTAAGAGGACAGAT[T/G]TATAAACAGGAAAAAGTTAAAATGGGATTACTACTTTACACCTCCAACAAATAAAATAAC
255	TGGTGTTCCAGTGTTGCTACTGCCCCTATCTACCTGGTGAAATACTTTATCTCATTAGGC[A/G]TCACAGTTTTTATCCACCAAATGATAGGGAGTGAAATGTTTTGTTTATCTCTGTCATTTC
256	CAAGATGTAACAGTCTGCTTTCTGAGATCCTGCCTTTTTAATCTGTCATTAACCTTGTTC[A/G]TTTATCCTTTTTCTGTAGGAAAAACTATAGACCAGCAGGAGAGTATTCTTACTCTAATAA
257	CAGTGTGCCTCTAAGCACTTTCAAGGTAAGAAGAAGTCTTCACTAATTAATTCAGTTATT[T/C]TGATTTTGGGGGGAGCATTCAGGTTTTGGAGTAATATATAGATGGCAAAGTTTAAATCTT
258	GTTGAACCACTCCCATAAATAGACCCCTATATACAGTTCCCTACTTGACACTTCTGTTTG[A/G]GCCTCTAATATGTTATGTGTGCAAATCTGTGCTCCTAATAATCTCTGCCAAATCAGGCTA
259	ACTTCACTCATAAGCATCAGAATTTTAACAATAGGGTATTTTGCTTTGCTCTTTCTAGGT[A/G]AAGATACCCCCAAAAAGTTCTATTTCTGAGACTATATAAACTGTTCCCAAACCAAGGTGG
260	TTTACCTTTTTTTGAAGTTATCATTCAAAATACTCAGAATTCATGGATCTTTTCAGATGT[A/G]ATTATCTTGAAATTAGAAAATGTTTTCAATTATATATCTCTCTCTGAAAAGCTGTATGAT
261	TAACCCCTAACAGGAAGAAGAAATACAATACAGGCTCAGGGCTCCAGACTACTAAAACAA[A/G]TGATGAGGATAATAGCTAAGGTTTCTTTATATTTTTGGGGGGGATTAAAAAATTGATTAA
262	TATCCTGTGTCTGAGATGATTGATGTCATAATATAAACTCTGAAACATACAAAATGGCCA[A/T]AATTATTGAATGAATATTAAAGGGGTTTTTTTGTCAGGCTTAAATTTTGAAAATACAGGT
263	TTAGATGAGACTCTGAGATGTGCTGGCTTCAGGCACCAGGTCGGCCACACACTGGAGTAG[A/G]GCACCAAACAGGTTCTTGAAGTCCCCAATTTTAGGCCTTGGTTCTTGGATGACATTTCTG
264	GTGAATGTGATCCTCCCTAAGAGAGAAGGCAGAAATACAAAGGGAGGTTTTTTTATGTTC[A/T]TTGTATCACGTCTTAATGTTCCTCAAGCAATGGAACCATTCTTTCTTATGCTGAAAACTT
265	AAAATCACTGAACTAGACCTTCTGGGGCTCCTTCCTGCACCAACATTTCAATAGACTCTG[A/C]TAATCATTTTTAAAGATTCACCAGTTCCACAAAAGAAAATTTTCTTTTGGGTTCTTTNTG
266	TAGGAACCTGTGTAGGAAAGCATATGTGGATGAGAGACTCAGGTTCCTTGTTCCAAAGGC[A/C]AAAAATATTGAATATTAAACATGAGATTCCCTGCTCTCCTCAGCCTGGTATGGTCTATGA
267	CCAAAGGCAAAAAATATTGAATATTAAACATGAGATTCCCTGCTCTCCTCAGCCTGGTAT[A/G]GTCTATGAACAAATGCTAAATACTTTGTATCTGAAATTTTAAAAGTCATATTTTTAAATG
268	AGTTAACCCCAGGGAGAGCTAGCAGTATCTCTTCCCATCTCAACATATAACCATGAAGAG[A/T]TAAAAGATGGCTAAAGTAGATTTTGGCATTATAAGAGAACTTCAAAGACTACATAAATTT
269	ATTCAGAAGTATTAGGCAATACTTCTAAATAGATTTTTCAAATTTTTGACTGACATCATT[A/G]AAAAATTAGCTATTCGTTTTGATACGTATTCTCAGTTACAAGTTATTCTATATTATCAAT
270	ATATGTGTGGATTGAAAAAGAGTGTTAATAGATTCTGTACAAATGAATCCATTTATGTTA[T/G]TATGTTCTGATTATAAACTAATATACACTCATAGAAATGCAGAAAATATGTACAAATGAT
271	TGCCTTTCAAAACCAGATTCGCTGGGCTCCCATTGAGCTCCCAACTTGTAGGTAGCAGGA[A/G]AATTTAGACCAAGATCTTTTATATCAAGATTCTAAATTCAGTATTTCTTTTACCTAAGAG
272	CTGTGTGATTACAACACTAAGTTTTATCCTGTAAGCTTAGTCTTTCACTGCTGGTATAAT[A/G]AGATCATTGACTACTAATTTAATGATCCTAATTAAAACATGCATTCCTTGTCTGTTAGTT
273	AAAGTGACTAGACTCCCATGCCTATGGGAATATAATAAGGCCGATGATGCCTTAAAGGGA[T/C]GTGCAGAAATCAGCAGACAGACAATTAGAAGGGAGAAGTTTTTAGTTCTTTTTGATCTAT
274	CCTCTAAATATAGGAAAGCCTCAGGACTCAATCATTGGATTTCTTTACTTTCCTACTTAT[A/G]CCCTAGACAGGATGTACCATCCATCTCTTTATCTATGTAATGATAAGCAAGCATATTCAG
275	TATTTTTTGAATCTTAACACTTCTCTCCATTCACTCGAATTTCTGGCTCCCCAATTCCCT[C/G]ATTACTTATTCCAATAGTTTTAGCCAGCCATTCACATTGATAATACTAAATATTTACATT
276	TGTTTATTATACTTCAAGTTCTATTTTATTATACTGTAAGTCACTCAGTGAGTTTGAGTA[T/C]AATATTAACATTTTAGGGTCTCTAGAAGCTTTGGTAACAATGTCTGAGCATTTTGCTATC
277	ATCCAGGCTAAATCCTTCATGTAAATGTCAAACTTTCTCATAAACATCCCCTCACAAGTC[A/G]ATTGATTCTGACAAGTCAATGCAAGTGAAGAATGGAGTCACACTGCATTATATTTAAGTT
278	TGTAGGGCTTTAAAGAAGTAGTGAAGTTGCTAGATTAGTATTTTCAGTAAATCTCCTAGC[T/C]CTGTGGATACTAGTCAGCTGGCAGCCAGGCCGACTCATTTGGCACAAAGACTATTTTAGT
279	GATACTAGTCAGCTGGCAGCCAGGCCGACTCATTTGGCACAAAGACTATTTTAGTCCACG[T/C]AAGAGATGATGGACCAAACTAGGGAAATGGTAACTGTGTTGGAGGCAGAAGAACAGATTC
280	ATATCCTGTATGTGTGAAAACACTATAATAATGTATTTGTGCTTGAAATATTTTCCTTTT[T/C]GACATAAGCAGTTCCTGGGCCAACTGATTTCCATGTCATGACTCTAATGTGACTTAATTT
281	GCATGGAACTGATAAGCACATTGAGACTGGATGGTAAAATTGTGATTCCAAAGGTCTCAA[T/C]ACTACAGAACAATTCATTTAAGTACATTGAGCAATTCATTTAACATCTCTGAGATTATTT
282	TTTTAAAGCAGACTTAGATCTATCAACAAATCTTGCTACTTCTTGAATAATCTCTTTCAG[T/C]ATAGTTTAAGAGAGAAATGTGTGTGTATCTGTGTCTGTGTGCAGCAGTTTTATTGAAGTA
283	ATATTAAATTTAAAATATTTATATTATAAACCCAAAAGATAAAATAGTGAATCAAAAGTT[A/G]TAGAGCTCATAAGCCACATATGCAGAAAAACATAAATAGAAATAAAATAAAATCATTTTA
284	GAAGCTTCCTCTCCAATTTATGTCAAAGCATGTAACGAAAGATCAAAGCAGTCAGCCTTT[A/G]CCCTTCCACTTACTGTAAAGTGCTGTCACCTTTAGCAGAGGTAAGGGGAAGGGACAAGAG
285	AAACAACAGAAATTTATTCTCTCACAATTCTAGAGATCAGAAGTCCAAAATCCAGGTGTT[T/C]GCAGGCTAGTTTCTTCTTGGGCTCTCAGAGGGAGAATGTTCTATGGTCCTCCCCTAGCTT
286	TACCTTCCATTCCCTACTTATTAACTCTTTGGCCTGCTTCAATTCTGGACTCACTATAAA[A/G]TTGGATGATGTTGTCATCCAGAGAGTTCAGTTATTAGCAATTAACTATAGTTCTGAAATT
287	TTTTTTAAGGATGTGTTAGGAAACGAGAGTATAGCCCTGATTTAGGGAAACATTCATCAA[T/C]TGGTATTGAAGAAGATTCTATCTTATTGCCATGAATCATCTACTTTGGGGCATGTACACA
288	ATTTACATGTTTAATCGGCATCCCAGGTCATTTCAAGGATCCAATCAATTTGTGGAGATC[C/G]ACCCTATTGAATTCTCTGTTTGTTGTTTGGTTTCAGGGAGTTTCATAACAGAATAACAGA
289	TACTGAGAACACTTCCATGTTGCCAGGAATGAAATGAATTCTGGAATGTTAACATGAAGC[T/C]CAGTGGACCACAGATATTTTATACAGTTAATTTTAGAGACTCAGGACCCTTGTCAAATAA
290	ACACATACATAAGTCTTACAGAAATTTTATAAATCAATACTCCTCCTAACAACATAAAAT[T/C]ATCTATTTTCTACTTTCTTTGAAAATATCATTTTTAATGATTTTGAAATGCTGGTAACTT
291	AATTGATTACTCATTTTGTATGAAAAGAGAAGTTGCTTGACCTTAGAATATATATGAAGT[A/C]ATGAGCTTGTCCTGAGAGAAGAAATACTGGAAAATTTGAGAAGAAAGGGAATCTGGTGCA
292	CCCTCCATAAGTTGACCACCATCTCTGCCCTTCCAGGAATCACATTACTCTGTTTCTCAC[A/G]TCCAGCCAGATAGAAACACTACTTGCAATTAAGTTGTGATTCTCATTGCTTCTTCACAAG
293	TTTGTGTCACAACAAGGTCTGATTTCTAATGGGATTAATACAAATGCTCAGAAAGTTCAA[T/C]GGATTTTAGGAGGACAGGAATCCATTAGGCAAAGATGTTGAATGAGATCATTATAAAGAC
294	TGTCACTATCTCATGCCTGAAAGAAATTAGCATGGTTGACACCTATAATTCCACTAATTC[T/C]ACTATCCCTACGAGGTTTACCCCCATTACAGGGTTCCTGCCTAAATGAATCATCATCCAA
295	ATCTATTTTACCTAAATATTTTCATATAGAAGGAGTAACACAAGTTGGTAATGTAATAGA[T/G]GAGGTTTAATTGTACTCTATCTCGAGAATTCTATTTCAAGAAAGCTAGTTATATGTAATA

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
296	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7588431	212359230	T	
297	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435670	212364130	T	
298	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4673633	212366542	T	
299	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4672626	212378670	T	
300	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7583346	212386651	T	
301	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2118891	212387888	T	
302	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs991476	212411600	T	
303	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497952	212431603	T	
304	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1025752	212431704	T	
305	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1439252	212445389	T	
306	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs13390226	212448106	T	
307	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2068401	212452431	T	
308	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7600260	212457852	T	
309	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4292044	212469397	T	
310	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2043888	212477024	T	
311	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs11887994	212484167	T	
312	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs11896200	212491048	T	
313	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7603039	212497140	T	
314	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497953	212500610	T	
315	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7598440	212501443	T	
316	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1098066	212508207	T	
317	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs839530	212511010	T	
318	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs839525	212523542	T	
319	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs839517	212526022	T	
320	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497955	212526746	T	
321	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497956	212528430	T	
322	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs990741	212533818	T	
323	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs987320	212538445	T	
324	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2118890	212552847	T	
325	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521546	212558365	T	
326	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs12473886	212559616	T	
327	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1155683	212560914	T	
328	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1357124	212568293	T	
329	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1402714	212576359	T	
330	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521539	212597880	T	
331	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7607942	212604816	T	
332	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1546717	212610584	T	
333	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7582903	212617082	T	
334	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6712126	212624402	T	
335	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs9678219	212645894	T	
336	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521545	212646410	T	
337	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521553	212656660	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
296				0.41	0.35	0.24	0.13
297				0.31	0.31	0.05	0.06
298				0.19	0.22	0.34	0.36
299				0.09	0.22	0.13	0.09
300				0.30	0.02	0.38	0.44
301				0.08	0.00	0.26	0.30
302				0.18	0.13	0.26	0.30
303				0.21	0.14	0.22	0.24
304				0.42	0.47	0.45	0.42
305				0.36	0.04	0.47	0.44
306				0.07	0.30	0.01	0.02
307				0.47	0.28	0.35	0.33
308				0.13	0.23	0.00	0.00
309				0.05	0.00	0.00	0.00
310				0.14	0.00	0.00	0.00
311				0.27	0.46	0.21	0.12
312				0.04	0.33	0.00	0.00
313				0.21	0.27	0.40	0.48
314				0.06	0.04	0.00	0.00
315			p=0.005 (Silberberg et al. 2006)	0.47	0.05	0.48	0.46
316				0.19	0.12	0.38	0.39
317				0.12	0.29	0.10	0.07
318				0.20	0.31	0.10	0.09
319				0.30	0.48	0.39	0.39
320				0.07	0.00	0.00	0.00
321				0.04	0.21	0.00	0.00
322				0.26	0.19	0.39	0.39
323				0.08	0.01	0.28	0.29
324				0.15	0.38	0.02	0.01
325				0.11	0.00	0.00	0.00
326				0.14	0.28	0.46	0.44
327				0.18	0.27	0.46	0.46
328				0.40	0.36	0.44	0.40
329				0.03	0.43	0.47	0.46
330				0.01	0.39	0.00	0.00
331				0.37	0.01	0.02	0.03
332				0.10	0.18	0.08	0.03
333				0.28	0.22	0.08	0.04
334				0.13	0.43	0.17	0.04
335				0.13	0.35	0.08	0.04
336				0.12	0.45	0.00	0.00
337				0.36	0.16	0.17	0.04

Key appears on page 109.

	R
1	**Sequence**
296	TTCTAGGGAGTCATCAACCTAGAGGTTGCATTTAAAACCCTGAGAGTGTCTGAGATTACC[T/C]CTGGGGAGAAGACAGAGAAATAAATTGACTAAAGATAAAACCATAATAGTCAAAAAACAG
297	AGAATAGATACTAACCTGTAAGAAAGTTCTTAGAGATACAAATTATTTACTTGTTAGAAG[T/G]ACTGCCTAATGTTTCTGTCTTGGTTGACTACAGAGGCTTGACCGCATTTTTTAGATAAGA
298	CCAAGGCAGCAAAACCCATTTTCAAGATGAAGCCACAGAAAGCAGTTACAAGACTTTCTC[A/G]GACATAAAGCAATGTATCTTTCTCACTGTCATCACCTTAAGCCACACAAGTCTGTTGGCA
299	TTGTCACAGTCAGTCAATGTGGTCTTTTCAAAACCAAAATTAAATTGTTATAAGATGAAC[A/G]ACAAGGGTGGAACCAATACCAAAAATAGATAATTCAGAAGCTAGTATCTATGTCAAGATA
300	AGTTTTTTTCCCCTTTGACTCTGTATTACTATTCCTATCCTACAAGTGTGAAATCCAAGA[T/C]ATGTAGAAATTAACTGACTTACTTCAAGAAAGACAGGACAGTAAACTAGTTCTCATTGCC
301	GAAATCAGAGGTGTAGGCACAGCACCTGTGGTGTTTCCATCAGTTTGTAATGGTGTATTC[A/G]TGTGTATAAATGTGGCATATGTAATTAAGGTCCTGTGCCATAGCAACTGTAAGCACAGGC
302	AATATTATTGAATTTTGTTTACATACAATATAATGCCAATTTTACACTGACATTTTTGGA[T/C]ATACCCACATAAGCAGAAAATGCCTGAAACTGCAATAAGGATATGAATTGTATTTGTTTT
303	CATGGCTCACAAAAAGCCATTTTTTTTTTTATTTTGGCCAGCAATAAAATCCTTGGCTAGC[A/G]TTTCTCTGTTAGCTATAACAAAAACCTAGTTGTAAATAAGAAATAAAATTTTGAGACAGA
304	AATGAATAAATAATTAAAAGATACATTGCCTTTTGGAGTAGAACCACCATACAACATGCC[A/G]GATTGTTAATGGAAAGTATATTTCTATGTTACAGCTAACATCTGTCTCAAAATTTTATTT
305	TGTGTGTACCTATGTATGGTTTTGAGTGGAAGCCTATGCAAATGTCAGCAAAAGGCGGGG[A/G]TTCTTTTCAATTTTTCTTGAGAACACCAATTTTTCTGACAGTCTTGTCCTTTTTAAGATT
306	CTAAGGAACATGCAGATAACGTTTTTTTTTTTCCAAAGCAGACATATCTGCATTTCTTTG[A/G]TTGTTGGTTATTAATATTTCATTAATTTTCAAGCTACTGCAAATTCCCCTTGAGATATCA
307	TAAAATGATGTTTAACCTCATTGATAATCAAATACAAATTTAAATAAATATATCCTATGT[T/C]TTCATCTATTACACTAGCAAATGTCAAAATGGTTGTTATTGCCAGTTTGGCCAGGGTGTG
308	TAACATTGTATTTCACTTCTTTTTTTGGCTATGTTGAGCAAATTCCAAAAATTCTAAACA[A/T]AATTATAATAAAATTAGAGTCAACAATAGTATTACTCTATTCTCTTTTTTTCTGAAAAAT
309	TGACTAACCTCTTTCTTCCACATTCATACTTAGTCCATCATCAGTAAATCTTTTCCCTGT[A/G]AAGTAGAGCCCAAATTCAACAACTTTCAAAGAAATTTCTACTGCTGTCATCCTGGTCCAA
310	ATTAGCTAAATATAGTGCTATAAGAAGAATATTCTGAAAAGAAGATTGGCTGTTTAAAGA[T/C]AAAGGAACATCAGGGTCAGCCGCTAATGTCAAAGGCAAATAAATACTGTTCCAAGTATTG
311	ATTTCACAAACATTCTATAATGGGTAGTAAGTCAAAAATAAGTATTAATTTGAAGAGCCC[C/G]ACAGTCTTTTTTAAAAGTTGGCTTAATTTCTCTGATGCAAACATGGACATCTTCATTCTG
312	TAAGGGACCAACCTGACAGAACTTTGAAAGTCAAGATGAAGCCAGTGGCTGGATTGAAGA[T/C]GATTCTAGCTTAATGGAGGATATCACTCTTCAAATAGATGGGAATACAAATGGAGCTGAT
313	TATGCCATGACTCATAATAGGAAAGACTTGTCCCTATTAGTCCTCTAAAGCCCTGTGGCA[A/G]CTATGGACATCCAAAGGCTGTTGCTAGGAGTCCCATAGCACACACTAAAACTTAAAGGAT
314	TCCACATTAACAGAATGCCTTCAAGCAAAAAAGCATGACAGCCACATATGCTTTAAACTT[T/C]GGGAAACACAAATGTAGAGTGAGGAAGATAAAACCAGTCAAACAATCAGGTTCTACACTT
315	GCACCTGTTTGTTCACTGTTATCAAATGCCAGGCTGGGGGCTACCCCTGGTAAGAGGGCT[T/C]GGACTTCTTAAACCACAGAGCAACATAAACTCTCCTGTAGAAATCTTTTGTGTGCAAACA
316	GTTTACTTATCTTCAAAATAGAAAGAATCATAGTAACCTACAGTGATGGTTAACTTTAGA[T/C]GTCACCTTGACTGGATTAAGAAATACCCGGAAACCTGGTAAAGCTTTATTTTAGAGCATG
317	TAAAACATATTTAGAAGCAATGCATGCCATCCAGAACCCTGCTGACTCAAATATAAAATA[T/C]GGTTAAGGCCCAAATCAAAAATGACACATTCTGTATTCTACAATTTGATGATATAAGCCT
318	TAGGATTCTACTCTTCTATTGATTATTTGTAGCATGCTTATTCCTAAGAATTGTGTGACT[A/G]GGGGGAAAGAGTCTGAATAGAGGCTCACATATTTTATTTTTTATTATAAACCAACTAGAG
319	TAAGCATTGCTTTCCACTTTTCGATTCCATTCCATTCCACAGCCATTATTAAATGTTCAG[T/C]GCCAGAGTCTATATTTAGGGCCATAATATACACACATAAAGTATAAGGAACCATTTCTGA
320	TTATTAAAGCCTTGAATGCTTCAAAACTCTTCTAGCCCAAGGGACAATTTGTTTTGCTTA[T/C]GACATTTGATGATAGAAATCAAAAGATAATGGAAAACAAAAAAATAATTTCCCATACCAT
321	GCTGGAGGGTTAATAGTCCCCCTTCAGATCTCTACATTCCCAATTGATTCTTCATCTCCT[T/G]ACCTTATCAAGACTGTATTCCTGTATCATAGACTTATTACACTAGAGTTAGGTTTGTAAA
322	ttaaaattattttCACTTATTCGTTGGAACACCTTACAAGACATAGTGCCTGATGCAGAC[A/T]gatatctaatccccaatatgatggtatttggaggtggggcctttgggagatgattaagtc
323	CTCCGGTCTTTGAAGTAAAATAGAAGAAAGTGGAGATGTTACTTAGGCAAGCATCTTTCA[A/G]CACTAGAGCATTTATTCAAATGTGACTATATCAGGCAAATCTTTTATGAAGATGGCATAT
324	TGGATCAATCCCTAACTCAATAATGTTCATTAATTGGAATATTAGATGATTTATACATCT[A/T]TGCCCATTATGAACTCACCACATAGTTACTGAACCTCCATTTTCTTTTCAAATTACAGAC
325	CTTTTTCTTTACTCTTAATTTACTATCGAATCATTAGATTTTTCGGTATTTGTAATACTT[C/G]TGTTAAGTACAGTAAATTCAAGCATAAACATGGGAATATGCCTAAGATTGCTTTCTAGAA
326	CTTGAGAGTTAGCATAGCCTATTGGTTCAAGAACCTGGGCTCTAGGGCCAGATTTCCTAG[C/G]CTTGGAATTCTTTACTGTAATTTTCTCTGTGGCATAACAGGTACACTCAATGCATAGATT
327	GGAAGTTTTACTTAAAGTAATTTATACAGTTCAGAACTCGCCACTAAAGTTCAACATTTC[T/C]AAGAGCTATACCTTTCTGTGACTTCATTTTTCTCAAGTGACATTACAAATTTCTGGTATT
328	CCTGAGTTAAAATAACTGTCCTGGCTAATTTGAAAAATACATTTAATATTTTAGTTAGAG[C/G]AACTCTAATTGATGATTGCAATAGTTCTTATGTGTAAATTCGTTTAAAGTTTCTCAACGG
329	AAAAAAAATGCAGCTGAAAAGCAAATAATGATTTGAAAAACTGAGCTAAAGCGTTTTTTC[C/G]TATAACTCAATATGATGGAGCAAGTAAATAGAACAACATGAACAAAAGAGATACAGAGAA
330	ATATCAAAATGTAGTAACCAAGGACCTTGGATTCAGGACAATTTAGTTCACATTCCATGC[T/C]ATCCTTTCCTTGATGTGTGATATTCAGCAAATTACCAAGATTCCCTGAGCTGTCTTCTCT
331	TATCACAAAATTTTTAGAGAAGTCATTTTCTGACACTTTATATTAAATTGTGTGCAGAAA[A/G]GACTCAAGGAAAGACAAGTGATGGCAAAGATTATTATGGCAATTTCCCTAGTCACTAAAC
332	ATGTAAGTTAAAGTGGACACATTGGGTGTTCCAATGCAGAAGAATACAGAGAAATGCCAC[A/G]GGCTGAATATTTGGGCAAAGACTAACATTCTCTTGCTGACAAACATGTCTTTGTATTTTG
333	GTCTTAATTTTTGTTGTTGTTTTATTCTGAGTGCTTTATGTGCATTGTCTAGGGTCATAA[A/G]TTTAATTAGTGTCCAACTTAGTACTACACGGTAGTGTCTCCCAATAGTATATTTTTCCAT
334	AAATTGTTATCATTTGAGAGGTTTTATTTAAACATCATGAACTCACATAGTATTCACTAA[A/G]ACTTTTATTTTTAAGGTTCTCAAACCTATGCATTTAAAGAATAATTTTTAGCAATTTTCA
335	TGCAAATGAGTGAGTATCTGGAAGTTGAGATTAATGCTAAGAAACAAAGAAATATTGTTT[T/C]ATGAAAGCACACATCAAACAACAACAACAACAACAACAACTGGACTGAGGCTTGAGAAAA
336	TATATATTGTTCTGGCCACAATGGTGTGTGAATATTGTATATATACAGCCTCATAGAATC[A/C]CTGTCAAGACCCTTATTAAATATACAATTAACTTTCACCAATGGATTAATTAGTCTCATA
337	CTGGAGATAAATATTTTAAAGCAGTTTCCAGAATGCTTTACTTATGGGATTGTGCAATCC[A/T]ATGTTGTCAACCTATTTTGCCAGGTTTGTCTGGCATTGTTTTTTTTGGGGGGGAGGGGTG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
338	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7564926	212670237	T	
339	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2371438	212673776	T	
340	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2371440	212678711	T	
341	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs11903314	212688244	T	
342	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7426206	212692700	T	
343	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1568519	212714637	T	
344	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7579746	212725217	T	
345	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1357142	212725707	T	
346	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6737841	212729291	T	
347	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521657	212731683	T	
348	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521653	212736287	T	
349	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs939664	212746332	T	
350	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497961	212751316	T	
351	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521646	212752500	T	
352	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1915745	212753019	T	
353	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7608095	212778696	T	
354	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2049180	212789985	T	
355	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs9288446	212790272	T	
356	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1521641	212802134	T	
357	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1402770	212822805	T	
358	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1948875	212830963	T	
359	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1021916	212841067	T	
360	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2135161	212844992	T	
361	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1568516	212850372	T	
362	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs953831	212859060	T	
363	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1857795	212873152	T	
364	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1505344	212875519	T	
365	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1910866	212891941	T	
366	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7601515	212898738	T	
367	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1505366	212899634	T	
368	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1505374	212900905	T	
369	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1394785	212919219	T	
370	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1505360	212920375	T	
371	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497971	212933104	T	
372	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497972	212933541	T	
373	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs11892564	212934789	T	
374	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs4511675	212941984	T	
375	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1394795	212947747	T	
376	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7575393	212970360	T	
377	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1394796	212978672	T	
378	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1283310	212982136	T	
379	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs13383863	212992266	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
338				0.18	0.49	0.00	0.01
339				0.06	0.05	0.08	0.08
340				0.40			
341				0.03	0.16	0.00	0.00
342				0.35	0.24	0.22	0.11
343				0.09	0.29	0.00	0.00
344				0.03	0.19	0.00	0.00
345				0.28	0.03	0.31	0.22
346				0.01	0.03	0.00	0.00
347				0.31	0.00	0.00	0.00
348				0.33	0.38	0.09	0.09
349				0.35	0.23	0.10	0.09
350				0.10	0.17	0.00	0.00
351				0.40	0.12	0.13	0.22
352				0.23	0.13	0.00	0.00
353				0.33	0.38	0.09	0.20
354				0.50	0.33	0.12	0.22
355				0.20	0.27	0.11	0.16
356				0.44	0.34	0.13	0.21
357				0.24	0.41	0.00	0.00
358				0.46	0.03	0.13	0.23
359				0.01	0.01	0.07	0.24
360				0.11	0.22	0.00	0.00
361				0.03	0.15	0.00	0.00
362				0.09	0.39	0.01	0.03
363				0.02		0.00	0.00
364				0.31	0.06	0.11	0.14
365				0.18	0.30	0.25	0.20
366				0.19	0.48	0.24	0.24
367				0.03	0.24	0.23	0.19
368				0.07	0.03	0.24	0.19
369				0.29	0.41	0.17	0.13
370				0.43	0.06	0.17	0.16
371				0.18	0.03	0.05	0.04
372				0.07	0.36	0.07	0.03
373				0.21	0.24	0.07	0.03
374				0.30	0.35	0.10	0.10
375				0.08	0.00	0.00	0.01
376				0.16	0.41	0.13	0.10
377				0.23	0.32	0.05	0.02
378				0.48	0.13	0.17	0.09
379				0.08	0.18	0.08	0.02

	R
1	**Sequence**
338	TAATTTCATCATTGTTGTAACAATGTACAGGATGCTGCAGAAGGGAGAGGGGAAAAGTGT[A/G]CCATTACAATTTAGGAAGGCATAGTGTACTTTTATGAGGAGGTAACATGATACTGGAAAG
339	TATTCTGCCTGAGTAGGAGCAGGGAAGGTTTTAAAGAAAAGGTAAGTCTTGATCAAATAC[A/G]AACAATTTTGGCAGCATTTAGATAACTAGGCCTTGAGTCCTTTAGAGTCATTAAAGCAGA
340	CAAGCTATACAACACTGTCCTGACCTAATTGATATGGTTTAACTGTGTCCCCATCCAAAT[A/C]TCATCTTGAATCGTAGCTCTCACAATTCCCACGTGTTGTGGGAGGGACCCAGTTGGATGT
341	ACAGTTTTCACATTTTATTTTTACACTTTTGATCCTTAAATTATACTCTATGTGACCAAC[A/G]AGAGACCTTTAAAATTGATTTGGTCTCATGCAAAATTGTTCATCAAGTTTAAATCTGTCT
342	CCTTGGTAGTTGAATGTTAAACATAGTAAACTGGATTTCTCTTCCCAAAAAGAAATGCAA[A/G]AACTGGAGGTCAGAAGAAAGCTGGCATGAAAGGTGTTTACAGAGATAAGCATCAAGATTG
343	ATAAATGGCACCCCTTTCACTAACTCAGGCAAAAATCTAGTCAGTCAACTATTCTCTCTT[T/G]CCATAACCCAGTTATAAAAGCCACAAAACCATATGCAAATCCATCAGCTCTTTCTTCAGA
344	GAGTTCCTGTGGTCAAATCGGTCTCCATCATCTATTACTTTTGTGATCTTCGGCTAATTA[T/C]TTTACTCCTATTTGGTTTCCTTTATAAAAGGGAGTTATTAATAATGCCTTCCAGAATTAC
345	CCCATACATCTAACTGCCTATTGAATATCTCCACTCATAAGTTTAAAGGCCCTTCAAGTC[T/C]AACAGGTTCAAAATTAAAGTCATCCTTTTCCCAGAAGGAGCTTCTCCACTTGTGCTTCCT
346	GGGAAAAAAAGGAAAGGAAAGCAGGAACAGAAACACCTGTCAGTCATGAATGACTTATTG[A/G]CCCAGTTCATCAGCAGGGGAGCTGAATTTGATCAGTTCTGCCATGATTAGTGTCACTACA
347	AATAAACAGTGTATTCTCTAAGGAAAGAGACAATGTGCAATTCACTTTTGTGTCCACCAC[A/G]AGCTAGCCCAAGTCCACAACTCAGCAGAGGCTCATTAAATATCTGTCAATATGAGATGAA
348	TGTTTAGTTCCTTCACCCTTATTAATGAATAGTGCCTTTATATCATTTATGTTTTTTCAA[A/T]TGTCATATCCTGTGAAAAGAAAACCTTGGAAAAACACAGTTTTGGGTGATGGGAAACCTA
349	ATAATGCTTCAAGGCCTTTGCCTTTGCTACTCCCTCAGCCTGGGGTACTCTTCCCTAGCT[C/G]CAGGGCTTACTTCTTTCTGTTTCTGTTGTATGTTGCCTTTTCAGAGTAGTCACCTGTATA
350	TTTAAGGTTTTATTTTGGAAAAGCAATTAAGAGGACACTAAAGGATTTCAGACAAGAGAT[A/G]ATGTTAGGGCAAGATGATGATGCCCTAAAAATGAGAGTTATGTAAAGAAGGAGGAAAGTG
351	GGGTGAGCAACATGATCTCTAATTCTCACACCCAACAACCCATGGTAATCTTTTCTACTC[C/G]GTGTTAATATAGCTCTTTGTTATTCCTCTCTCCTAGAATTTATCTACC
352	TTATTTTGGCATGCAACGGCAATTATCACAATTCTCTTTCAAAAGGATCTGCATGGCTTT[A/G]TATTACCATTTTTTAGACATAAAATTTTTATGATAATATGCATCAAATAATTGTACCCCA
353	AAGCATTGTTACATATCAACAATAACAAATACACCATCTTTTACATGTAGGAGGGTCTTA[T/C]AGAAATAAGTAGTCAGATACTTAGGTAAATCATAGAGAGAAAATTTGAATTTTTAAAATT
354	TTCATTTTTAAACATTCCTTGCAATATCCTTCACATGTATGTGTTAAGATTGCAGATCAA[A/G]GCATCTGGTCTGTAATGCCTTGAGCACACAATAAAGAGAAAGGTAGCATCAGACAATTAG
355	TAAAAGGGTCTTCTGTGGAACTGATCAGAGCCAAAACCAAAATTTGTCTCCAATATCTTT[C/G]TGTCATCACCCACCAAAGCTTCTTAACATCTTTGCAAGTTCAAATGTTATTTAACCCTTA
356	TCTGTTTCCCTCTCTTCTAACTTTGTCATTCTCTATTATTGTTAAGGTTTCCCTCATTAT[A/G]TTTTCCACATTAGACTGTGTTCCTTAATTGCAACACTGTACATTATTCACCTATGTGTCA
357	CTGCATATGAAAAGAAATCAGCC[A/G]ACATTTTTTCTTATTTATGGCAAATCAAATACTGACTTATGTATATGAATATAGTAAAGA
358	GGGGTTTTGAAATATTGTTAAGCACATTATAAATGCTAAAATACTTCATAAACCACTTTT[A/G]TAAACAGGATGAATTGAGAGCTGTGAAA
359	TTTCTGCTCCCCCTCCCAAACTGCCTCAGCTTTTGTGAGATAACATTTATGGTTCCTACC[T/C]TCTTCTAGAGAATGCTAACTAGAAATTGCATCAGGCATTTGATATAGTGGTGATGTTTAA
360	CTTATAAGGATTAAAATTAACTGGTTACCAATTAACATTTTTTTTAAAAGACCTATGCCT[A/G]AGGCAGAAACTTTAGAATGTGAAAACAGAGCCTCTCCCAGTTTTCATAGCAATTAACCTC
361	TTTAATATTTTTTGATGTGTGTTTATTGAGCTAATATAATGGAACTTGCAACCACAACGG[A/T]TTCTACACGATTTCACCCCCGAATAAATAAGCACAACATATTCACCGTGAGTTCCCTGGA
362	ATAGTCAAATGTCATAATGGGCAACATGAGTTACACGTTGGCTCCCTTGAGTGTCTCCTC[A/G]TAATCACTTCAAATCTTACTGAGACCGAGATTTCAAAGCAAGAGGTACATATTAATTCAG
363	GTTCAGCAGAAGGGTACAGTGTTAGATGTAATTTGTTTATTGACAATCTCCAACAATGGT[T/G]CAGTGAACCAGCAAACACCACAAAAGTAATGAATCCTTTCCTCTTTTAAGTAATTATATG
364	AAGCCATCAAAATAAGGGGTGAATTAGAGTCCATTTTATTACCTCATATAATTGCAGTAC[A/G]ATAAAACATTGGCAAAATATGAGTTTCAGAATTTTCTAAGCAATCACCTTCTCTATTTTT
365	AGCTGGGATCACTGAATTTGGATTGAAAGTGTGGTATATCTATTATCCCAAGAACCTGAA[T/G]CAAAGAGAACACTGAAAAATGGTGAGGATTGGTCCCCACTGGCTCTCTGTAGCCATGGCA
366	TGCTTAGGAGAGGATGTAAGCAAAAGCCATGTTATCAAAACTGGGTTAAAATGCAGCACA[A/G]AGGTAAAGGTGTGAAATGGAGTATCATTACTAACCAAAGGTGCACTTTTGGGTTGGGGGA
367	CTATAGAAATGCTATTTTATATAAACATAGACGCCCTCAGTCCCTAATGCATAACCCTTT[T/G]TACCAACCAGGGCTTTGATTTTCATGCTGTCCCAAAGTTGCAGACATGTTCACGACACAG
368	TTTTGAAAAAAAAAATAAGGCATAGATACTCTTTCTGCTTTAATCACCCCTTTAATTCTCA[A/G]ATTGGGCCTAATGATTTAGTATTTGTCATCTAAATCCAAAACAGTTTTCCAGTTAACAAA
369	TTGTCAGGTGCATATCAACATTTATGTTGTCACCCTGGGCCAGCAAAACATTTAACAGAT[C/G]TGCTGTATCTATGTTTTCTAAGTATTTGATACCTATTTTTATATTTCCTCAATGATGGCC
370	AATTACAACTTTGATAAGTGATTTCAAAATATTCCTAACTTTGTAATTTCAAAAAAAAGG[T/G]CATTGGGAATCACTAATATACCCAAAATGAACTCTGAGGAAATGACAGATATTGGAGTGT
371	TGTGTTTGTAAAGGGATCTATTTGTGGAAAACTGACACCTCACTGTCCCTAACAAAGAAC[T/C]TTTCTATCACTTCAAAATGAAGGCATCCACAATGACCTACTATTCTTTACATCTAATAGA
372	GACTCTTGTAGCAACTTTTTTATTAGAATAATGCCTAATCTAATGTTTGGCATATCATGG[C/G]CTCTCAGTAAATGCTGCTAAATGACCAAACTTAGTAGCAACTGCTGATTTTTATTAATGA
373	TGATTCATCTACAATAAAATAATAACTTCTATTCGACAATGTCTGGCATGTGGTTGTCAC[A/G]TTAGCATTTGATTAATATGAAAAACAGCAGAAGTGTGAGTTTCACTCTGCGTTTTAAAAG
374	TCTCAGGCAGGCTGTAGGCCAACCTTCTGAATTAGAATCTACCTTGTAACACTATCCCCA[T/G]TGCACATTTGACAAGCACTGATCTAGGACTCATTAAGTTTCTAAAACAAAGGTTGCAAAA
375	GAAAGGTTCCTATTAGTTTGTCCTCGGCTTTGGAAACTAACAAATAAAGAAAATTGCATA[T/C]GATTTGGGGCAAGAAAATTTTCTTTAGTCACTGATTTACTCTGTGGCACAATCATAGCAG
376	GGCATGGTGGCACGCTCCTGCAGTCCCAGCTACTCAAGAGGCTGAGGCGAGAGTATCAGT[T/G]GAGCCTTAGAGGTCAAGGCTACAGTGAGCCATGATCTTGACACTGCACTCAGCCTGGGTG
377	GTGAGGATATATTTTCACAATTAATCATGCACATCTGTTTCCCTTAGATCTTCAAAGTTA[T/C]GAACATACTTCAATTATTTTTGTATGCTGGCTCCTAGGGAGCAGCCACACTTAGTAAGTA
378	TTCATTTTAATTAAGTATCCATTTTCATGTGCTTGAAACAGAAATGAATATAGCTTGGAC[A/G]GGGAACAGGTTATTTATAAAAAGGGAGATTTAAATGAGGGTAAAAATACATGGAAAGACA
379	TTTCAAGTCAATCTACGAATGACACTACATGCTGTAACATGTAATCACTAGATTTGGAAG[T/G]GGGAGGCAAAGAGTTGCCTGCATTTGAAAGTAGTGAAGACAAACATATTAAATAGGAAAA

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
380	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7570330	212997889	T	
381	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1505349	212999751	T	
382	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs2062930	213021330	T	
383	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1505372	213024715	T	
384	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs972489	213025126	T	
385	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs7564771	213031181	T	
386	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6435706	213046909	T	
387	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs10497974	213048055	T	
388	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs6752299	213056612	T	
389	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs979452	213061384	T	
390	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1384295	213093389	T	
391	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1351593	213102850	T	
392	2q34	ERBB4	HER4	v-erb-a erythroblastic leukemia viral oncogene homolog 4	1,156.5	2	rs1384292	213110886	T	
393	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1728818	11007992	T	
394	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1710887	11014960	T	
395	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1568074	11016308	T	
396	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1710891	11024133	T	
397	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs2697144	11026099	T	
398	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs2930154	11028389	T	
399	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs6778281	11028517	T	
400	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1170695	11030338	T	
401	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs9876005	11037763	T	
402	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1728802	11041520	T	
403	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs10510403	11041670	T	
404	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs11925331	11047167	T	
405	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs2675163	11050014	T	
406	3p25.3	SLC6A1	GAT1	solute carrier family 6, member 1 (GABA transporter)	46.5	3	rs1062246	11055169	T	
407	3p21.2	GRM2	MGLUR2	glutamate receptor, metabotropic 2	11.6	3	rs4687770	51730105	T	
408	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs2399496	115328703	T	
409	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs9824856	115335421	T	
410	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs2134655	115340891		
411	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs963468	115345577	T	
412	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs3773678	115352768	T	
413	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs2630349	115356062	T	
414	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs167771	115358965	T	
415	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs167770	115362252	T	
416	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs1486009	115371222	T	
417	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs6280	115373505		Gly9Ser
418	3q13.31	DRD3	D3DR	dopamine receptor D3	50.3	3	rs9825563	115382910	T	
419	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs4688043	121073938	T	
420	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs1381841	121161492	T	
421	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs11923854	121229259	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
380				0.18	0.04	0.00	0.00
381				0.18	0.00	0.00	0.00
382				0.48	0.48	0.01	0.04
383				0.30	0.25	0.01	0.04
384				0.19	0.06	0.00	0.00
385				0.21	0.08	0.00	0.00
386				0.01	0.25	0.03	0.04
387				0.02	0.34	0.00	0.00
388				0.03	0.25	0.02	0.04
389				0.25	0.05	0.01	0.00
390				0.42	0.07	0.14	0.07
391				0.13	0.25	0.09	0.03
392				0.47	0.17	0.13	0.06
393				0.29	0.44	0.45	0.47
394				0.48	0.20	0.36	0.46
395				0.48	0.28	0.47	0.50
396				0.46	0.42	0.46	0.40
397				0.23	0.16	0.35	0.36
398				0.23	0.00	0.18	0.17
399				0.09	0.20	0.11	0.13
400				0.31	0.43	0.35	0.40
401				0.02	0.35	0.11	0.14
402				0.09	0.00	0.17	0.13
403				0.17	0.18	0.30	0.23
404				0.04	0.45	0.40	0.32
405				0.24	0.11	0.38	0.32
406				0.34	0.28	0.41	0.44
407				0.18	0.49	0.36	0.40
408				0.50	0.31	0.33	0.44
409				0.03	0.38	0.01	0.01
410			p=0.022 (Talkowski et al. 2006), haplotype (Dominguez et al. 2007)	0.28	0.04	0.34	0.19
411			haplotype (Dominguez et al. 2007)	0.36	0.03	0.32	0.41
412				0.13	0.26	0.17	0.20
413				0.08	0.32	0.15	0.14
414				0.17	0.13	0.18	0.22
415				0.29	0.28	0.24	0.33
416				0.07	0.06	0.00	0.01
417			p=0.001 (Talkowski et al. 2006)	0.35	0.12	0.24	0.37
418				0.27	0.46	0.23	0.32
419				0.07	0.23	0.01	0.07
420				0.18	0.02	0.00	0.00
421				0.18	0.02	0.00	0.00

	R
1	**Sequence**
380	ATGAAAGTATAAGCACAAAGACAATTGATCAAATTATTAATTGTGGTCTTCTACTGGAGA[C/G]TATGACCCATGTCATTTTAGTTATACATAAAGAAAAATAATGGTGTAGGTGATACCTAAT
381	AGTAAAGCCTATATTTTAAAAATAACCATTACAGATTGTGAGTGCAGTCTAGGATCACAT[A/C]GCAGAACTAAAAGCTAACTGGCCCACCCACAAAGTAAATGTGAGACAGAGGGCTCGGGGT
382	TATTCTGTAACATCTTGTGCGATTAGCAAATGTAAGGCCGAAATGAATCTTTCAAACAGT[T/G]TATAAACAGTTTGATTTTCAAAATTATATAGACATTTCATTCTGATGTACGCAATTCATG
383	AGTCTGCAGTATAGTATTTTACTACATGGTTGATGTTCGGCTATACTTAAATGTTGGAAA[A/C]TATCGGAACATTACTTCAGATACTAGAGTTAATAATATTTGAAGTGGTGAAGTTTTAAAA
384	ATGTGTTAATAAAATATGCAAGGTCATTAGGCTGGCATGATTTAAAGAACCTTGGTAAGT[T/C]ATTCCCTCCCTTCATCCTCCCCCTTCATTCCACACATAACTTTCTGCTCTACTCATGACA
385	ATGTAAAAACAAAGCAGAAACATTGGAAAGCAAATGAGTGGAGCAGGAGAGAATGATTAC[A/G]ACAAAAAACTGTAATATCTTTTGAAAGGACCATGCAAAGGCAGCCAAGGGGAAAATTCCA
386	TTTCATGACAACATGAAATTTAACCATTATATGTTTTAATATCCATATTAATCCTGAATA[C/G]GAAAAAAGGTGGCTTTGACAAGTACTTCATAATAGCTAACAAAATTCAACCAATTGTAGA
387	TGAGCCACCACAATGGGACCATTCTCCATCTTATAGCCTCTATTTCTGTTGGTTGCGTCA[A/G]TATCACCTAAGCCCTCAAGTAGAAAGCTTACAAATCTCAATTCTTCTTTCTTCATAGTCT
388	ATAGTTCAGAAACTAAATGTTTTCTCTTCTCTTTGTCTAAAGAGAATATCTTGATTTAGG[A/C]CTTTAACTCCTTCTGGAACTCTTTCAAGAAGCCTCACCCATTGACTCTTTCTAAATCTGC
389	CAATATGCTAAAATAACATTGGCCTTTTAATTATAGTCATCCCTCTAGTTTTAACCTCTA[T/C]AGTCTGTCATCCATATTGTTGTAAAAATGATTTTCTAAATCACAAATCTCATCAGGTCAC
390	GGACAAACCATGAGCTATACCTTTAAGATAAAAACCTTTTAATGTAGTAGTTGAATTACC[A/G]AAATTTTTATGTGCAAGAATAGTAACCCAATAAAATAATTTTTACATGCAAATAACCTTA
391	ATCTCATGACTATGCCTTCCTTATTGTCCTTACTTTTGCTGATCCCTTTTCCTGGAATTT[A/G]TGGCTTACTTGGTGCTTTTACTTGGCCAAACTTTTGAATCTTTTAAGTTTTACTTTAAAT
392	GCTTTGCACCTGTGTGTGCTGCTGGCGACCGCTGCGCCCCCAGTCGCCCGAGCCTTGTGG[C/G]GTCAGACGCAACTCGCGCCCAGCCCGGGCAGCCGGAGTGCAGCAGGCGGGCGCGCCTCGG
393	ACTGTCCTAGGCTCCAGGGACAGAGCGATGGACAAGACAGGCCACAGCTTTCAAGGTGAT[C/G]CCAGTCCAGTATGGGAGACAGGCTTTCATCAAATAACCGCACAAACCCAGAATGACAAGC
394	GAGCCCAGATGAGGCCAGATCTGGTAGGAGGCAGAGCACAGAGCACTCAAAGATCGAGAC[T/G]TACAAGAGAGCGTGGGAAGGCACGGCTGTGAGGCTGGGGAGAAAAGGGCCGTAGCATCTT
395	ACAGGCTTGAGGCCCAGCAGAAGGCGGCTCTCCCACTTCTTTCTCAGGTCTGCAAGCCCA[A/G]GCCTCGGAGCCCTGCAGCTTTGGATCTGATTCCCAGCTCTGCCCTGTGTCAGTGGTATGA
396	TAATTAGGGGCCAGAACAGACGTTAGTAAACCACTGATCGTGTGAGCGAGACAAGCAGGA[T/C]TGGATCAGAGTGAAGTGGAGCTGGAAATTGGAGTCTGACTGTCCTGCTTGCACACAGAAG
397	TGGCCTGAACCTTATGGACTCCCAACTCCCAGCCAGCCGCATACTCTTACTCAAGAGATG[A/G]AGGAAAGCAGTTTCATGCCTTGGTATAAACCCCTCAGCTGCCTCAACGTACCTGAGAGGG
398	TGCCAATCTCTGAATGACAAGATGCTTTGTAGGGAAAGAAAACATGTACAGTTTGGAAGC[T/C]CTACATCAGAAGTGGCAAAATGGGTCAAAACTGGCCCTTGGGCTTGTTTTATTTGGCCTG
399	TCTTTGTGCTTGGTTTGGCCCCATTTTTATCAATGGCTTTAACACTTGGTCATAGAGCAT[A/C]CACTGAGGAAGGATGGGATATCCTGGGAATGTTTTACCATCTTCCTGCCTGGAGTGTCTT
400	CTCATCTATAAAATGGGAAGATAATAATAACTCCTTCCGAGGGTTATGGTGATGATTAAA[T/C]GAGATCATGTGTGTAAAGCATGTACAACTATGCCTGGCATATAGTTAGGGCTTAGGAAAT
401	accagataatgtggccatagtcgtcagcatcctggggcctggcacagagtggtcaagggg[A/G]agagtggatcagagaggcaaacggaggggaataaccagcataGCCAATTAGAATCACCTG
402	TGTTTAGAGTTAAAAAAAACGCAGTACATACAGGTTTGTTTCCCATTTTGTTCACTAAAC[A/G]TTGTTTTATTGCCTCATGAACAATTTGACGTTTTAATTGCACAAAACAGTCCCTCAGAAG
403	GAACCTCATTTTGTAAGAAAATGTGATTGCATCTGCAAAGGAGAGTTTCAGAGGAGCATT[A/G]AAGTAGGAACATCCCTGCATTTATGTGTTCGTCAGACAATTCTTGAGTGTCTACTATATA
404	cagacaaattagatgattttggagagtgtcaagtgccctggagaaaagaggacagcagca[T/C]agagaatggccagtagcacaggaggggcgctccctcagacaaggtagtcaagggaggtct
405	CATCAGGGAGAAACAGCCCCTGCCCAGGAAAGCCTTTGAAGGAATGGCTGGGATAGATGT[T/C]GAGTGGGAGGGACATTGAGAGTGGCAGGGGTGGAGGGGATCATCATGTCAGTCTCCTTTT
406	TGTAGAGAAAAAAAAATATGTGTACACATATGAACGCACAACATGCACATTCATCCTCAC[A/G]TGTGGCACGTAAGGTCTCATTTGATATTGTGTAGGAAATCTGAAGCCTTTTCCTGAGGTC
407	AAGAGTCACATTACAATGGCAGCTCTGATGATGGCCACCTTCCCACATTTGAGCCCTGTC[T/C]AGCAGCAGACCCTTGAGATAGAACACCAAGATCCAAGAGGAAGTGGTTACATTGGGCAAA
408	TCTTTCTTCAATAATAAATTAATCTTGGCTTACAGTCCCTTTTTTACCTATAAACTTAAA[A/T]TTTTTTTGACATTTTTGACTCTTTTGTAATAACACTTAGCTTAAAACACAAACACACTGG
409	AAAGCCAGATATTCACTTCATACCTCCATTCCCATGCAGCTAGAGCTCAGGCACATGCAC[A/C]AAGCCCAGTCAATTGCAGATTCACACCTGAGACTTTGAACTGGAACTTGTGAAGCAGGGA
410	TTTAGCTAAATTGGAGACACAAATCTGACACCGACTTTGGAATCTGCTAATTTTGGCTGC[A/G]CTTTGAAGGTAGGAAATCCAATCTCAAGAAAACATTGATAGTTGCCTCTAGAGCCTGCCT
411	TCATTCAGGCATCTTCAGAGTTTCCTTTGGCACCAGCACACCATGCTCTGCTGTATCAGG[A/G]TCTGTTGATGATGTGATATTTGCCTAGACTGCTGGGCCTCTGCTGGGAGTTAAGGCAACC
412	TGTTCAGTCATGGCAGCAGCAGGACTCAAGGCTCAGCCCCTCCTCCAAGGTGCCTCATAG[T/C]TACCACTAACAGCGAGGCCCTTGTAGACATATTGTACTAGAAGCCCCCGGCAGAGTCTAA
413	AGAGTTCTGTGAGGGCTGCTTTTCACCATCTTTTATTTGGTCAGACAGGGGGCTCAATAT[A/G]TCTTTAGTTCTGTGGACTCCCCTCCTGGAGTTGTTGAAGGAGAAAGCTTTTTGCAAATGA
414	CAATTTCATCTCTTCCCAGGTTGCCCCATACCCTTCTCATGCTCCAAAGTCTATCACAAT[A/G]ATCCTCTTTTCCATAAAGCCCTTTCACATTCCCACAGTCTGATTCAGTCACCCTTGAACT
415	CATTTTTCATAAAATTTACCTCCAAAGTAAAAATCTATCTGGCTTCAGCTTGTAAAGCTT[A/G]GAAACATTCTGAAACAACATTTATGGGAATCTATGTAAAATAAGTCTGTGCCAATGTGAC
416	AGAAAACCTATATGTACTACTACAGTGATTTCTTTAAGGCCTTTGGCAAGATTTCCTGTC[A/G]TTTTCTATAGTCTCACCTGCCCTTCTATGCTCAGTAGTAGAATAGGAGCACCAGTATATC
417	GTGGGCGGGCCTGGCTGGCACCTGTGGAGTTCTCTGCCCCACAGGTGTAGTTCAGGTGGC[T/C]ACTCAGCTGGCTCAGAGATGCCATAGCCCAGAGGGAGGTGCGTGATGCCAAGGGGCTTCC
418	GACCCCCGTGGTGAATGGGGAGGGATTGGTGTGGAAATAGAAGAGAAGCAGGGTAAATGA[A/G]GTGATCCTTTCTCTCTGGACTTCACTATAGGTGAAGATTAGCAATTGCTCCTTTTATCTG
419	CAAATTGGGACCTTCCTGAGAGTGAAGAGGCAAGCAATTAATAATTACACTGGACAAGCA[A/T]AAACTGGCACATAAGATCACCCTTGTCATTATATGTATTTAACGCTAAATTTTCCTAAAG
420	TTCAAAACTTACCCAGGATCCCAGCAATTGCACTCTTGGGCATATGTTTTATAGAAATAG[A/G]AATTTACGTTCACATTAAAACCGGCATATGAATGTTCAAAGCAGCTTTATTTAGAATAGC
421	AATATTCATGACATAAGATTACATGAAAAAGCAGAGTATATAGCTACAAATTGCTATATA[T/C]TGTGATCCCAATTTTGAAAACAAATGCTACACAAACACACCAAAAAGTAAACAGTTTTCT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
422	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs10934505	121250012	T	
423	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs968824	121255730	T	
424	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs334555	121286826	T	
425	3q13.33	GSK3B		glycogen synthase kinase 3 beta	267.7	3	rs3755557	121297647	T	
426	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4315750	46745942	G	
427	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4694834	46774165	G	
428	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs6818828	46787693	G	
429	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs6854637	46793476	G	
430	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs1866989	46795862	G	
431	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs1470207	46818137	G	
432	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs1946966	46832233	G	
433	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs6827925	46851302	G	
434	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs1542097	46856324	G	
435	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs3822110	46863626	G	
436	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs2044081	46913097	G	
437	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs1372497	46917095	G	
438	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs7672100	46960347	G	
439	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs2078610	46983811	G	
440	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4396966	46985892	G	
441	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs9683412	46997541	G	
442	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs13102109	46997899	G	
443	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4235146	46999617	G	
444	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4518219	46999789	G	
445	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4627835	47005024	G	
446	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs10000697	47010078	G	
447	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4599390	47030500	G	
448	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs728292	47052237	G	
449	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs6830892	47060562	G	
450	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4694846	47063555	G	
451	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs13107066	47073452	G	
452	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4695226	47077677	G	
453	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs7439087	47091757	G	
454	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs7679148	47111576	G	
455	4p12	GABRB1		gamma-aminobutyric acid (GABA) A receptor, beta 1	395.1	4	rs4591574	47118352	G	
456	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1513467	93464181	T	
457	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs13115966	93503757	T	
458	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6821502	93511369	T	
459	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2089990	93519211	T	
460	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1513460	93528549	T	
461	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6826363	93549155	T	
462	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs13109229	93551627	T	
463	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs5021051	93565766	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
422				0.06	0.36	0.50	0.49
423				0.25	0.33	0.01	0.07
424				0.20	0.00	0.00	0.00
425		Y		0.18	0.12	0.18	0.08
426				0.07	0.32	0.16	0.16
427				0.14	0.28	0.39	0.29
428				0.32	0.03	0.03	0.04
429				0.05	0.31	0.10	0.14
430				0.47	0.40	0.22	0.21
431				0.48	0.48	0.39	0.49
432				0.48	0.35	0.40	0.49
433				0.08	0.08	0.18	0.12
434				0.11	0.08	0.18	0.12
435				0.06	0.38	0.35	0.38
436				0.08	0.07	0.05	0.01
437				0.28	0.36	0.38	0.28
438				0.25	0.09		0.02
439				0.37	0.25	0.03	0.04
440				0.47	0.28	0.26	0.31
441				0.39	0.26	0.02	0.03
442				0.06	0.00	0.10	0.00
443				0.38	0.10	0.02	0.03
444				0.28	0.00	0.02	0.03
445				0.21	0.13	0.07	0.12
446				0.42	0.30	0.25	0.31
447				0.44	0.27	0.27	0.32
448				0.43	0.34	0.01	0.00
449				0.49	0.36	0.10	0.12
450				0.32	0.45	0.09	0.12
451				0.48	0.43	0.11	0.14
452				0.47	0.25	0.10	0.14
453				0.33	0.39	0.09	0.11
454				0.30	0.34	0.16	0.08
455				0.43	0.20	0.23	0.10
456				0.05	0.02	0.00	0.00
457				0.01	0.00	0.00	0.00
458				0.29	0.43	0.31	0.22
459				0.23	0.09		0.46
460				0.29	0.18	0.33	0.29
461				0.24	0.48	0.18	0.21
462				0.20	0.30	0.17	0.24
463				0.29	0.24	0.06	0.07

Key appears on page 109.

	R
1	**Sequence**
422	TAAGAGCATAAACTCTGGAGCCAGACAGCCTGGGTTAAATACTGGCTCTGCCACTTACTA[A/T]CTGTATTACTTTAGCCAAGTTTATTTATTTCAGTTCCCTGTGCCTCAGGCTCCTCATCTG
423	AATGTTCTAGGGAAGGAGAGAGAGGAGGGAATGAGAGATTGAACTAAGGATAAAATACCA[T/C]CATCTTGAACTTTCTAGAGAAATGTTTTTTATGCTTCTTGTTTGCTCTTTTTGTAAAAAT
424	GAATATGATATACAGTACGTTGCTCTTCTATATACATGTAATTATATCTTATTATTAAAA[C/G]TCTACCAACTCAAAGCTTCCCCCTTTCCTTCATAATTTAAGTAATGTATAGAATGTGAAA
425	TAATTTCTACCTGCAGAGTCATCTCTTTCTGTTAAGATGCTGTCTCCAGAAAGCACATGT[A/T]AAAGGACCTATATTTGATCAGATTACCTGGCTCTTGCTTTGAAACACTGATGAAGGACTT
426	GCAAATCCAAGTTTTCGTTGCTCCCTCCTTTGGCATCCATGTCATGGTTCATAAAGGAGG[A/C]AACACAATAGTTTTCCAGTCAGGTTTGCTAGCAAAGGCGATTTGTTTGTTTGAGTTCAAG
427	CTTTAGGTCACAAAATATTCAAAGGAGTTTTGTACAAAATAGTCATTAAGCCACCTAGAT[A/G]GCAAGGATGGCCTTATCATCTACCTGCAGCATAGTAGAAAAATAAAAACGAAATAGTTGG
428	CTACTCTTCTTTCATGAGCCACCTCAAATATCATTTCTTCTATGAGACATTTCCATACAA[A/T]GTCCATCATCTCCTCGAAGAATATACACTTCTTATACTCTGGTGTTGTTCTGTGTAATTC
429	CAAGTGGGTTGTTAAAAATGAAGACTTTTTCCCAGATGTGGTAAGAAGGAATAATGATCA[A/G]AGTCAGAGGAAGTCAGGGAATATGTGACAATGGAAGAAGAGTCAGAGATGTGATGTTGCA
430	ACTTCTAGGGTAATACAAAGTATACAGTACTCCCCTCCACGTTTGGCAATATAGGTAGCA[A/T]GATTGTGAAGATACATCCATGGTAAGGAATCTCTTTCTTGGGTTTGAAAATTCTATCAAA
431	ATTCTCTCTCCCCACCCCTGAGGCCACTGCCAGGGAATAGGAGATGGGTGGCATCGGAAA[A/T]TCAAGACTGTCTTTACTACTCTCTTCAGTGTCTCTTTCAGCGATATGAAGTTAAAAAACC
432	TTCTTTCTCTTTCAACCACTAAAATGTCTCAGTGGCGTCTCTTCTTTTGGCACACTTTGA[C/G]TAAGCTGTGCCAAAAGTGGAATCCCTGGTGCTGTGCCTTCTTTTTGTCTCTGCTTTCCGT
433	TAACATCTCTAGGTCTAAGATTTCTCAGCATACCTCCCTTTTTTCAGTTCAGGGAGGTGG[A/G]CTAGATGATTGTTTGAGGTTTCCTTGGCCTTTAATGTATGCAATTATTGGTAATGAGATT
434	TAATAGCAAAAGGATATTCACGTTTGACTGTTAGTCACACAATATCCTTTCTAAAGATAT[A/G]AAACCTCCTTCCACCTTACCTTCATGTAAAAAAAAAAAAATAACCCTCAGGCTACTTACA
435	CAGCCCTACCGATGCCCTCCCTTCTCTGCCCCCACTCCACCACCTTTTCCCATCTTACTG[T/C]TGCTTCAAAGTCTCCCTCAAATTCCACTTTCTCCATGAGAACTTTCACAGTTTTCCTAAC
436	ATCCTTTACCCTGTGTCTGAGACCAAT[T/C]ATAAAGTGACATACAGTTTTCTACCCCATTAGGAAAATAGTCATGGTGATTGTAGAAAAC
437	CCCAAACTGCCTTTCCTTTGTATATTATCATAAGTTGGCACTTTCTGAATAATTCTTTGC[T/C]CTCTTCTACTTTGATGTCTCTATTCTGCATTCTCCTGCTTCCTTCTCCCTGTTCCATGAA
438	ACTAAATCATTTCTAAAATACTGGGATTTTTAGAGAATGCTGGTTAAACACAGAGGAGTG[A/G]ATACATGAGTCAATCTCTGCCCACTCTTTAAACACCAAAATGATAGAGGAGAAATAAAAA
439	ATGGCTGGGGGATTTGTTGCCAAGACACAGCTGGGTTTAAACTACATCTTTCCCTACACC[T/G]CATTGGCCCAGAGTATGTTCTGTGAGCTATGTTTCTTGAACCTCAACTCTGGTCCTCATA
440	TTTGTTTTTTGCTTCTGAGCCAGGGAGACATGCGTATCAGCAACAGAGGAATTTTTTGAC[T/C]CTTCCCTGAGGATCCATTATTATCTGTGATGATGTGAAACAGAGACCATCAGTCCACAGA
441	AGACACTTAGTGTGCTTATAAATCCAGATCAACACTTTTGCCACAGGTTAATAGTAAACA[A/T]TGAAACCCAAAAACTCATAGTCCAAATATCAAACAGCTTTCCATTCCACTGAATACAAGA
442	GAAACAAAAAAAGAAACAAAAATCAGTAGAGGGAAGGAAAATAGAGAAATTCAGTCAGCA[A/T]ACTTAGGTTATGTTGACTCTTAGGTTTCATTTCTAGGAACCAAAAAGACACACCAACCTT
443	AGAGCCTTTCATTCAGATTAATTAATTACTGGAGTTAATTGGAACATTCAGGTTCCAATT[T/G]CAGGTTACCATAAACCTGAAAATGTTTATCATGACTTTTATTATTCTGAAGTGTAATGGT
444	TTCCCTTGTTAAGAAGTACATTTTTTAACTTTAACAATGTATGTGCTATGTGCTCACATG[T/C]TCTTTATGAATACAGTGTATTTAGGGGTTTGTTTTGTTGTTTTTAGTTTGAGAGGTGGTG
445	TGATGCCGATGAGGAAAAGGCATCTGATATTAAGATTCAATGCGAAGGAAACAGAATCCT[A/T]AGTATGATTACAAATATGCAAAAAGTCCACATAGGGGAAAAATGAAAAGACATACTACAA
446	GTTAATGCTTTTGCCTTTAGCTGGTTTTACCATCCTATACTTTCATTTGCTATCCACCAA[T/C]AAAAATATTTTCACACACCAGAATGAAAATCTTGAGTTTAAAAAACTAAAGACAGAATTA
447	AATCGTGCCATTGCACTCTAGCCTGGGCAACCAGTGTGAAACATCATCACCCCACCCCCC[A/C]AAAAAAAAGAATAGCTTGTCAAACAGAAATGAAGCACAGTCTATTTCTTTCAAACATAAA
448	TCTTCTATGCTTCCACTGTGCCTTTCCAGACCTTGATCATATCCTTTCAGAATGAAGGGA[T/C]TCAGTTTTCACAAATGAAAATAACCTTAGAAAGAATGTGAAGGTGGGGGTAGAGAATTGT
449	CTAATAAGGAAGGAATCCTGCTCCTTTCTTAATGTTTCCAAGTTAAGCTCCATCAGACCA[T/C]CTGGCAGTCATGGTACTTAGAGCATAAGAGGTGATTAATACCACCCTGGGATGTACTGAA
450	GGTAGACTTTTTCATGAGATGACATTCGTAATTTTCCTCCAAGTTTAGTTTCCATTATGA[T/C]GAAAAGTTGCAAGGTTTTCACTGTCATGGAAGAATTAAAACTGTGACTTAAGCTTCACAA
451	GCCTGGGCGACTGAGCGAGACTCCGTCTTAAAAACAAAAAACAAAAAAGAAGCCATAGAT[T/G]ATCTCAGCAGGAAGAAGTTCTTGGGAGGAGTAGAGGCACAAGCTAGGCTGACAGGATTTG
452	AAGTCTACAAACTAAGATATATGAAAATTCATTCTTTGGTTTTTATGATTTTATTTTAGA[A/C]TCTATGGTTCAGTCTGATAATGGCCATATACTTCCTCGATTCAGCAATTTTTCAGACACT
453	TTCATTTCCTCCTCCCTGGAAGTGAGCAGACTCAGCAGATCTGAGTTAAGTAGACAGACA[T/C]AGAAGCTGGTCTCAGCTGCTGAGTTCCTAAGGCTACCCCCTGCAATCCTATAAAAATGTG
454	AACACTTTCAGACAACTTTCTAAATGTAAATCAGCTCTGTATTGTGGTTAATTCCAGGAT[T/G]CAATGTGCAGGTGGAGGTGGGCATTGTAAAGGTATACAGCTCTGTCTTTAGGTCCAGCTT
455	AAGATTGGAAGCCAACTCTTGAGATTACCTAATGAAAACCTTCCATTTATAGATAAGGGA[T/C]CTGAGACCCAGACTTATCCAAGTCCATTTCTGAGTAGATAATAAAACTAGAATAATAACA
456	TCTAATACAATATAGTAGAGCACAGGTAAAAATGGATCCCATGTAATGAAAACAATTAAC[A/G]AATTCTACATAATCGGGCTATTTCTATCTCCTAGATAGCCCACATTAATAGGCCACATTA
457	AATGACTGAAAGGATTATTAAACTATGGTCAATTACTGATGATTTATAACACACAATTTA[T/C]GGTGATTCATTTTTTTTCTGGATACCTATCTTTGAATATGCTATTTTTAAAAATTATTTT
458	GGTTGCTTCATGAAGATTAAAATGAAAGCTGTAACCATAACAAAAAGTACAAGGTAAAGC[A/C]TCAAGAACTGATGTAGAAGCTGCAGCAGGTTATCCAGAAGACATAGCTAAAATAATTTAT
459	TCTGGTACCAAATATTTGTTTAAAAAAATGGAAAATACAATTTTAGCCTAAATAGTCATA[T/G]AAATGGGTCCTGGAGTAATTTCCTTTACAAAAATAGAAATATTGATAAACTTAATTATTA
460	ATTTTGCATGCAGTTGCAGTATTTTCCTGAAGTCACAATAGTATTCCCAATACCACGGTT[A/G]CAATAGTATCCCTGGCTCTCTCTCTGGTGAGCTACCACCTCATTTACCTTCCCACTGCCT
461	ATTGACTTCTTCTTTTCCTATTTTGATGCTTTTTATTTTATTTTCTCTCTTGCCTGATTG[T/C]TCCTGCTAGGACTTCCAGTGCTATGTTAAATAGGAGTGGTGAGAGTGAGCGTACTTGTCT
462	TCTTACAAAATAGAGATCAATCTCCAGCAAAATACAAGGCTTCACTGTATAAACTAAATA[T/C]GTTACTTTATTCTTAACGTTCTTTCATTTCCTACAATATTTAACCACCTTTTCCTGATTT
463	AAAGGGTGCTGTTTAGGACACATAGTAGCAAAATAAGGTAATCCATATTATATAGTGTTT[T/C]ACTTCTGACCACCTCTTCTGTAGTATGTTTGTGTAGCTTATTCTGTCTAGGCAACTGCCT

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
464	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6844474	93573071	T	
465	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7689616	93578476	T	
466	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs12647297	93621516	T	
467	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6811045	93622702	T	
468	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6532372	93628760	T	
469	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7659338	93647438	T	
470	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs13435785	93658446	T	
471	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs4692973	93669372	T	
472	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6815704	93693589	T	
473	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1450500	93698298	T	
474	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs921354	93703741	T	
475	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs11934085	93734189	T	
476	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7693534	93758663	T	
477	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs11734654	93788183	T	
478	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7694867	93792419	T	
479	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1479332	93809842	T	
480	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7692227	93828960	T	
481	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516911	93838020	T	
482	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2870642	93850739	T	
483	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1434786	93859480	T	
484	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6532381	93872361	T	
485	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516914	93879690	T	
486	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516916	93879981	T	
487	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2217789	93895487	T	
488	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs11931529	93918392	T	
489	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7671095	93926311	T	
490	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1369169	93959432	T	
491	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs4235037	93973122	T	
492	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1865431	93992250	T	
493	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs13147599	94003309	T	
494	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6532382	94005798	T	
495	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6818303	94041073	T	
496	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1902436	94098316	T	
497	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1378914	94117470	T	
498	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs729545	94120351	T	
499	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs12498874	94128750	T	
500	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs13142489	94135377	T	
501	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1039938	94137366	T	
502	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs11945434	94159989	T	
503	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1912718	94208915	T	
504	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs12506519	94233179	T	
505	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10021148	94257587	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
464				0.09	0.29	0.11	0.16
465				0.04	0.04	0.00	0.00
466				0.18	0.01	0.09	0.07
467				0.03	0.12	0.02	0.00
468				0.00	0.10	0.00	0.00
469				0.28	0.09	0.17	0.20
470				0.01	0.00	0.00	0.00
471				0.20	0.19	0.17	0.20
472				0.14	0.45	0.13	0.21
473				0.40	0.13		0.43
474				0.33	0.48	0.34	0.47
475				0.05	0.14	0.13	0.22
476				0.28	0.34	0.33	0.41
477				0.04	0.03	0.09	0.21
478				0.24	0.20	0.24	0.22
479				0.03	0.00	0.00	0.00
480				0.21	0.33	0.28	0.41
481				0.10	0.02	0.02	0.13
482				0.11	0.00	0.24	0.22
483				0.06	0.02		0.10
484				0.20	0.16		0.44
485				0.28	0.39	0.46	0.46
486				0.07	0.03	0.00	0.00
487				0.03	0.00	0.00	0.00
488				0.06	0.14	0.16	0.11
489				0.23	0.49	0.07	0.21
490				0.48	0.16	0.47	0.46
491				0.03	0.00	0.00	0.00
492				0.34	0.12	0.49	0.42
493				0.08	0.00	0.00	0.00
494				0.34	0.45	0.46	0.39
495				0.09	0.29	0.00	0.00
496				0.01	0.07	0.31	0.17
497				0.04	0.00	0.00	0.00
498				0.01	0.03	0.04	0.07
499				0.10	0.03	0.00	0.01
500				0.13	0.00	0.00	0.00
501				0.37	0.38	0.39	0.38
502				0.06	0.19	0.00	0.00
503				0.48	0.47	0.41	0.38
504				0.42	0.31	0.42	0.34
505				0.40	0.42	0.28	0.42

	R
1	**Sequence**
464	GCTGGGAATGTGCTGGGTCACACCTGAAGCCAGCAGGGTACTAGGTCTCCCCCAAGGCCT[A/G]CAATGAGTATTGCCTTCATCTGCTGATGTTTACTCAAAGCCCAAGGGCTCTTTATTCAGC
465	AACACTAAACCAACTATGTCACACAAAGCTTACTTTAAAAAAAGAAAGCAGAGGGACAGT[A/G]TGATGTATTTGTCATTAAAAGAAAAATAGGCTGCCAGGAATCTCGGAGCACATATACTCA
466	TAGAGAAGTATTACTCTTCTATTTTAAGAAATTACGGAAAGAAAAAGATAGAGGTAATTA[T/C]TCCAGGATAAGTGTTCATTTAATAGAATGGTAATAAGGAATTTATGTGAATCACAGACAC
467	ATGAAATAAAAATAATTATTCTATTCTTGCACCTTCTCCTTCTGGTTGAATTGGTCAAAG[A/G]CAAATAAGAATATAATTTGACTCCATTTAGTTATGTTAACTGTTTTAGAAAATACAATAG
468	GAAGCAAAATCTTTATGTTACTGGGAAATGGGAAACAAACTAATCTCCACAAGCAAGGCA[A/G]AATTCCACTGCTTCTGAGGTCAAAATGTAACCAAAAACCCTTCTGTCTCTGGGGTAGGCA
469	GCAGTATTTCACTTCAGTCCCCTTTGAAGAGTGTCATATATTTCCTGCAGGGATATTTCT[T/C]TGAAACTACAGAGCATATCACAGCTCCTTCTAAGATGATACACCACTTGGATGTCCTGAA
470	ATTCTTTGCCTGATAATTCTCCAAATTAGGAGTTAAGGTAAAGGTTAGCTCAACAGGCTT[A/G]TTGCTACTATAAATTAAATCCTGGCCCTGCCAAGATACAAAAGCTCAGAATATACCTGCA
471	AAACATAATGTGCTTTACAGGACTAATCATAATTCATCATTATCATGTACTTATCATATA[T/C]AGAAAGGACTGCCCTAGGCATTGAAGTTTTGGCAATAACCAGATTGCCCTTGTTTTTGAA
472	AAGAATGATGGTTTAATGTGTTGAACAGAATATACCATGAGCAAAAGCTTGTTGATTTGG[A/G]TAAGTCTCTACCTTGTTTCTTTAGGAGAATGTCATTTATGACTCCTCCTGCATTTGTATA
473	TTACATTTGGCCAGCCCTCTCTCAAATGCTTGCAATTGGGTAACATTGTTCCTGTGAGGG[A/G]AGGTCGAATATCACAGAGGTTATCTTATAAAACCTCATCATTTTTACAATGCCAAGATAT
474	ATAGCAGGAGAGGATTATGTATAGTTCTAATTTTACCACACTCCTCCTGAATACAATTCT[A/T]CCAGAAACACTTAATGCTTTTTTCTTTTTTATTCTTTAATGACTGCCTAGTATATTGTCT
475	TTTAAAAACCTTGAGAATTATAGGGGTGGAAAATTATATAAatctggttgaatattttca[T/C]aatttagatgaaataattgagacccagagaggttaaataattttccctagttcttctagg
476	aagtttgatagtgtgacaccttcagctttgttcattttgcttaagattgctttggctata[T/C]agatccttttgtggtttcatacaaagtttagagattttttccaattctgtgaagaatgt
477	AATATTCTGCTCATTTTGTTATACAGATTAAGGAAGTAAACAGATCCCCTTTACTTTGTA[A/C]CCTGTTAAAAATAATTTCATAAAATGAAGTTTCACTCATTGGGGACATTTTTTATCCTGA
478	AGATTGTCAATGTATTGGATGATGCCTGCCCACACTGGTGAGGGCAGATCTTCTTTACTC[A/G]GTCTACTGATTCATATGTTAATCTATCCAGAAACTCCCATATATTCACAGACAGAAATAA
479	GTCTGATCACTAGTTGATAGCTGCCTTTATTCAAGAAAATCTAAAGGAAAGGGCGCTATT[A/C]GTTTCAACAGTTGGCCCCACATGGAATAGGTGTATAATGGCTTTTGATTTGCAACTCTGG
480	TTGGAATAAACTTCCTCCAAACTTCTTTTAATGTTGATATTTTGACCTCTTCCCATGAAC[T/C]GTTAACGTTCTTAATGGTATCTAGAATGGTGAAATCTTTCTAGAAGGTTTCCAGTGTATT
481	GTCAGAGACAGGTTGGGTTGAAGGATGATGAGGTCAGGTTGCACCATTTGAAACAAAACC[A/G]TCAATGGAGTGTATCAGGAAGAAATTAAAATATAAACTGAGATAGCATGAGAGAAGTCTA
482	AATGCTCTCAACTTTTGCCAGGCCCTCTCTTAGCTTTTGTGCCATGTCCTGGTGACGACT[A/G]CACTTGAAATCCCTGGGCTACTGTACTTCTGTGCTATCCTTATTGAGAGAATGGCTTTCG
483	gggattacaggcatgagtcactgtgcctggccAAAAGACAGGTTCTTAACA[A/G]GACTACTTATGAAGTTATAAAACACTTTTAACAAATGCTATAACCATATGTTTATAGAAA
484	TTGTAGTCAACACCCCATCCCATTCATTTAAATTTTGCAAATAATTTCATCAGGAGTAAA[T/C]GTGAAAATGGACCTAGAGAATTGTGAGTATAATTTTTTTAGTGTTCTGTCATTGTGTGTA
485	GACCCCTTCTTTAAATCTGGCTGTCTTTGAAAACTTTTACCATTCATTAACACCTATATT[T/G]GAAAGTGGACAAAATAAATAAATGGGTGTTTGATTCTCAAACCAGTCCGTCCTGTGATTT
486	TTATAGGAGAAGAGGAAGAAAGGAAAAAGTGTTTCTGATTCTTCCTCTCATGTAACATTT[T/C]GACATAATTAAGTCTTATTCATTGGTACTGTATTTATAAATATTTCAAACTTAATAAGTA
487	TACTTATCTATACAATGATAGCTTCTTACAAGCAGAAACCTCTGTCTGATTTCTCACTGT[A/C]TCCCCAGTGCTAAGAGCAGTACCTGCCAAAAAAGTTATTTTTTTAGAAG
488	TTATGTTCCCATCTCAATGAGAACTTTTTCAACACCTCAAAGAGAAATACTTGATCCTCA[T/C]TTATACCTTCTCCATTGTTTTTTTTTAAATCGACAATTGCTCTTTATGTAATGAATTTTG
489	GTATGTATGTCACATGAATCTGTTGTCCTGAACTTTATTCCTGTGTCTTGAATTCATGCT[T/C]TTCTTTTAACCTTGCCTAAAACTTCTTGTATTTTATCTAAGTATCTGTTGGCTTCCTGTC
490	ATCTGAgattctcagtgctgtttatacatcacaatcacccatgggaggttttaaaactta[T/G]gctcagacatcatcacaaatctccaccacagacaaattcaaccccaattgctgagagagg
491	ATCAATTACAGTATTCATAGTGTTCATAAGAAATAAGACGTTAATTAGGTCATAGGGAAA[A/T]GTCAGTATAAACTGACTTTAAAAGGTATATTGAAAGATATGGTAGATGTTATGTTTACAA
492	GTGCAGAAGGGGAAGAAGCAGGCCTTTGGTCACAAATTTAAGTTGCATTAAAAACATTAT[T/C]AAAGTATTCATTACAGGCACAATGATAGGCAAATTAAAGACAATCTCGGGTAAGAGATGA
493	CTTAGAAACTGTCTTGGAGTTATGCGTTGTGCAGAACTTTAGAGTTTTTCTGTCTGATGA[A/G]AAAAGACTGAATTTTCATTTATCTTTTGATTTAGGCTTTTATTTTTTACACTTAACTTTG
494	GATCCTTGCTATCATATTCCCTTCAGGCTAAAGTGGTGTGTAAAATTTTCTCTAGATGAA[A/G]TATGTTGTGACTCAATTCACTCACAGTTTCACTCTTTGGCCAATTTGATATAGAGTACAA
495	AAAAAAAAAAAAAAAAAAAAGATAATGCCTTACAGTTTCATCCATATTGCTGCTGCAAAA[C/G]ACATGATTTCATGTTTTATGACTGAGTAGTATTCGTCTGTGTGTGTGTGTATTTCCCATT
496	ATGATATCACCTGTGTACAAAGACACTTTTAATTCTTCTACACCAGTAAGTATACCTTTA[T/C]TTCTCTTTGTATAATTGTGCTAGGACTTTCAGTAAAATCTTGAAAAAAGAGTGGTGAGAG
497	GCAGACCTACTGAATAATGGGAGACATTTTCCCTAAGGAGATGACATTTGATGGGAGAAC[T/C]GAAAAGCAAAAAGTAGTCAACCACAAAAATTTCTGGGAGAGGTACATTCTACATCAAAGG
498	ATTAATTACAAATATGTTGCAATAACTTCAAGAACCCAATTTTTGACTATTTTATCTTTA[T/C]ATTTGATTTATTAGTTTTGTAGATTCTTGATTTGTTTAGATAGGGTTGGGAGAGTAGAGT
499	CAGGTCACTAGATCCAGATCTCACTTGAAGAGAGAGGATTGCACAACCATGAATCAGAGA[A/T]CATTGGGGACAATCCTACAGGCTGCTTATCATGGTATTTATTACATTTTAACTGGATTAC
500	TAGTGGGCAGAGACATTTCTTCCTTCTCAGTGTATACAAATTTTATGCTTATCAGTAGAG[T/G]TGAGATTATTGGCTCACTTTTCCTCACAAGTGGATACATCTCTCTTCTTTATTCTCTCTC
501	GATGTAGTAGGTGATACAGTAGGAGTTATGTGGCAACATTTAGGCTTAACACTACCACAA[T/C]AAAATCATTATGTGTCAAGGCTGTGAAAGAGCTAGTGTGTTAGGAAGCATTATCCTTGAG
502	TGCTCTCTTTTTTGTATAAAATTCAAAACTTGGTCATCGTTTTAAGAGAGATATTAAAGG[C/G]TAACACATTGTATGATCGTATCAAAGTATCACATGTACCTCATGTACAGCCATTATACAT
503	CTTTCCTATTTACAAAAAAAAAAATTCAGTAATCTCGTGTTAGAGCTTTACCTCTTTTCT[A/C]TTCTGCGGGGAGGTGTGGGGGAAGAGAAGGTGTTAAATGTGATTTTATATACATCCATGT
504	AAGCATGTCCATTTTCAGTACTGCATAGCAGGTGCTGAGCTTGAATGACCTAAGCAAACT[A/C]CAACGAACACTTTCAGATTTCAGGTCAGCAAAGTCATCACCATTTGTTTATGGAACTTCT
505	AAATATCAGCTTTCAGGAACATTTTGCATGTGACAGCATGTGAGAATCAACATACATTTA[C/G]GTACAATCAGTCTGCTTTATTAACTGATTTTGTTTTTTGCAAATTCACCTATTCATTAAG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
506	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1354296	94294286	T	
507	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1155646	94339397	T	
508	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1875705	94361522	T	
509	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7697616	94375370	T	
510	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516413	94425654	T	
511	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs4524351	94435453	T	
512	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6854968	94452990	T	
513	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs3890316	94461921	T	
514	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1433666	94471383	T	
515	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2163959	94474279	T	
516	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2870699	94492353	T	
517	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1583337	94502359	T	
518	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1948016	94531366	T	
519	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1485012	94542392	T	
520	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1948017	94553839	T	
521	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1905733	94554163	T	
522	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516921	94596757	T	
523	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1485015	94609228	T	
524	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2200375	94610021	T	
525	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs4557232	94649460	T	
526	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs9307127	94653793	T	
527	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs4286488	94659049	T	
528	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6841321	94663865	T	
529	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1369465	94671971	T	
530	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1369464	94681259	T	
531	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs9991666	94693931	T	
532	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2196320	94722771	T	
533	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1435475	94747783	T	
534	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516926	94756177	T	
535	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1435476	94759989	T	
536	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1435477	94762390	T	
537	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516930	94776709	T	
538	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516931	94778088	T	
539	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516933	94789431	T	
540	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516938	94793386	T	
541	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516940	94813222	T	
542	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs11946557	94816124	T	
543	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1548037	94823482	T	
544	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs2196321	94832181	T	
545	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516941	94842434	T	
546	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs6850113	94853325	T	
547	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs1439543	94857136	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
506				0.45	0.23	0.24	0.34
507				0.43	0.38	0.15	0.27
508				0.46	0.28	0.46	0.39
509				0.08	0.33	0.40	0.32
510				0.40	0.21	0.15	0.39
511				0.35	0.05	0.19	0.39
512				0.34	0.43	0.42	0.46
513				0.27	0.35	0.09	0.10
514				0.44	0.28	0.33	0.36
515				0.09	0.25	0.02	0.07
516				0.42	0.23	0.35	0.32
517				0.48	0.18	0.38	0.39
518				0.35	0.38	0.40	0.35
519				0.09	0.34	0.01	0.06
520				0.10	0.37	0.01	0.06
521				0.02	0.00	0.00	0.00
522				0.02	0.11	0.00	0.00
523				0.33	0.02	0.10	0.18
524				0.20	0.16		0.41
525				0.17	0.33	0.46	0.38
526				0.28	0.01	0.08	0.19
527				0.26	0.00	0.33	0.29
528				0.28	0.08	0.00	0.00
529				0.33	0.02	0.39	0.30
530				0.04	0.42	0.00	0.03
531				0.43	0.43	0.13	0.32
532				0.23	0.00	0.05	0.19
533				0.03	0.19	0.07	0.07
534				0.27	0.33	0.00	0.01
535				0.12	0.44	0.06	0.03
536				0.46	0.26	0.35	0.33
537				0.24	0.24		
538				0.11	0.00	0.00	0.00
539				0.28	0.08	0.04	0.02
540				0.12	0.11	0.07	0.03
541				0.31	0.26	0.34	0.38
542				0.01	0.07	0.00	0.00
543				0.43	0.09	0.34	0.33
544				0.50		0.26	0.26
545				0.03	0.09	0.00	0.00
546				0.33	0.18	0.22	0.20
547				0.13	0.07	0.42	0.39

	R
1	**Sequence**
506	TATAGCAGCTATTCCTCCTATTAATTAAAATTCTATTCCTTCATTGTTACCAACTGATTA[A/G]GGTACAAGTTTTAGGAAAATAATAATTGAACAAATTCACCCTCAGGAGTAATGATACCAG
507	TGAGAATAAAGATTTAAAAATCATTGCCAGTGTCAGAAACCACTGTGTTACTGTCTTTAA[T/C]TCTCTGTGAGTTTCTGCTGGCATTGGGGTTTTCCTGGGCGTTTGCTGTGGTGATTTAAGG
508	CATCACCAAATCTCCACACTCACCTCCTCTACATGACAAGCTTTCAATATTTGACACCAT[T/C]TGTGGCTTGCTTTGAGATATCTTTCTTTTAGTTTTCATCACCTGGTATCGTTTCTAGGCT
509	CTCAACCTCTGATTCTCTTCTTTTAATTTTTCTACTCTTTGCTCTCTATATTTGATGTCC[A/G]CTGGTATTTCTATATCAAGTGGATGGATGaaattaaaacaaattttatttcatatttttt
510	TGTCAGCTATTTAGTATTGTTTCTAACATGTCAAATAGGACAGGCAAATTATCTTAAGAC[A/T]TGGGATTTAAACAAGTACTTCTTGATATTTCTTATTTTTTAATGCACATGTTTTATTTTT
511	GATTTAAAATAAATCATGGAGTGAGTGAAATCGAGAAAAACGAGGTCCAAATGTGGAGTC[T/C]TGGATTTTCCAACATTAAGAGGTAAGAAATATGAAGATAAAAGAGTACAGGAGACTGAAA
512	TAATATAAAAGCAAAACAAGAGCAAAGTGTTTCCATTAGTTCACTACCCATGTTTCTGCA[T/C]CTTAATCAGAGCGTTGTTAATATTTAAATATGCGTTTGAAGCCCCAAGTGTATAGGGAGG
513	acttctgggatattatattctctaggttttcattttcctcattCTAAATATCTTTCAGAT[A/G]GAAGTGACAGATTCTTTCTATGCTTTTAGATATCAGAAATTTCACATTTGTGATTAACTC
514	ACAATTGTTTTTGTGATTGTGTCTATTTTCTCAGAGAGAAATATTCAAGGAACATAGTGT[T/C]TCTGGAGTCTCCAGAATGAAGTGGAAAAGGGGGAAGCAGAGGATATAATACTGGAGAGAT
515	ACAAGCAACTTGGACTGGAATCAAAGTGACCTAGAAGAGCTACTTTCTACATCTTGCTAT[C/G]AATTCCCTAGGGCAAAGACATTATGTGGCAATATGTCCACATTAAAAGAAAGTATATCCT
516	TGACTTTGAAGCTTGCAGTCATTCTCTTGCTGTATGCTATAATTCCAAGCCAGGCATTCT[T/C]ATCAGAGGGACAGGTGGAGATCATTGAATCATAATCAAGGTTCATTGTTGTGAACTTTAA
517	AGAAGCAACGGTATAAAAAATATACTCACTGAGGCACAGGCTCACAGGAAAATCTAGTAT[T/C]GAGAAAAGTTACAAATTCTCTTTAGTGACCCAACACCTAACCTAAGCATAAGATTTCACT
518	CTAGGGAACACATTTTACAAATTGAACCTATCTTGCAGGTGGAAATACCATAAAGAAAAT[T/G]ATCATTGGAGAGATTACTGGCACACTGCATTCATTCACATGTCAAAGTGGAAAACATTCC
519	AGTCTCCTCTATTTAATACACCTATGCTAAGAAGCTTTGGCACACACTGCAAAAAGCACT[C/G]AACTTGCAGTCAAAAGGTATGACTTTTAGTATCGTACTAGTTTTTCTGCTTAATTGATCT
520	TAATCTTTAAAGCTTAAATTTTAAAAAGACAAAGTTTAACAGCAACCATTGAGGGTGAAT[T/C]ATTTATTGTTTTGCTCTCTTAACATACCTTTGGGGAATACAAATTAAAATAACAAGAACT
521	TGGAGGCATCAGTCTTTGGAAGAGTATTAACTTCTGGGACTGTCCTTGACTGATTTTTAG[T/C]TGGAGTATGTGTCATAATAATTCTATTAGATGAACTAAAGCTTTCAATCAATAGACTAAA
522	CAAGTAAGGAATGCAATAAATATTATTCTATTTTGAAACAGTGAGAGCCAAATAATTAAT[T/C]GGACAAGTTTAAAGAGTTGGGCAGATTGGATATTAAATAACAGAGCAATGACATTCTTTA
523	CTCCAAGATCTAGCCATAATGTTTTCTACTCTGCAGATCAGACACATATGGTTATCCATT[A/T]TGGAACACATGTTAACAAGTAAATCAAGAGATACGTCTCATTCCCAGCTGTATTTGTGGT
524	ATTTAGTTTTTCAGAAACGTCACTAATCTATACAACTATTTGCAATAACTACAGGGGACC[A/G]GTTGCACTATTTCCTGTGTCAACAGAAGATCTGACCTTGTTTTCCGATAGCTTAGAGATT
525	TCCAGGTAGAAATAACAAGGCTATTAGACGTGGAAAGGCAAAGATGGTGACAGATTTACA[A/G]AATTTAGGAGGTAAAATATACAGAACTTGATGAGAGTAGATGAGGTGGGGAAGTTAAAGA
526	CAAATGGTAGAATCCGTTCAATATTTTAGAATATTCCAGAAAATTCCAGAATCGCACTTT[C/G]TCTTCAGATAGGATGATTTAAATGCATTATTTTATGCAACAGATGTGTAGAGCAAAAAGG
527	gtcagccagtacaaaggccctgaggtagaagcatgcctagatgttccaagaatatgaagg[A/G]ggccagtatggattcagaaataagggataatatcagaagtgcaacaaggtcaagaggtaa
528	AAGATGAGTGTAGGTTGGCAGGAGGGGTGAGCATATTGCCAGGTGCTTACTGAGGTGTGG[A/G]GCCCCTCTTCATCCCTGACAGTGGCAGTGGAAGCTTGGCTAACAGCAATCTCACCAGCAG
529	aatatgaaaaataaaaataaTTCAGAATCAACCTTCCTGAGTTAATACAATGAACATAAT[A/G]TATTGTAATATGCAGAAATAAAATATGCAATCTGTAATATGTATATATATTGTAGTAATG
530	TACTTCAATTTCACTGAGTTAGGCTGTTTTCTCCATAGTGTCTCTCAACGACATTTCCTC[C/G]AGTTAGGTAAACAAATTCTGTCGGGCTGTCATATTCTTTTTCATTTGGGTTTTGGGAACT
531	AAGGAAGATTTGTCTAAGGTTCTATATAATTCACATTAATTTCTAACCTAGTACATTTAT[C/G]AGAAAAAGAAAATCGGAAATTAGTTTAGCATATATTTATCAAACACAGGAAGACTACTAA
532	AGACGTTGCTTTAGTTTTACAGTTTCTTCAGGTTTATCAGAAATAGAATGAGAAGTAGCG[A/T]TCATCTCAGACATTTGCCTAAAATAAATATAATTTCTGACACTTACAAAATGTATTTATC
533	TTCCTGGGAATGGAATTGCTGGACCAAAAGACATCTATGTATTTTTTAATTTGAATAGAT[A/G]TTGCTTTTGAAAAAGGCTATAACATTTTCCTGTTTCCACTAGCAATATGTGAGAGTACAC
534	CACTCAATGTATTTCCAAATTAGAGAAGGACATTTCTTCTTGTCTCACACTTTGAAAATG[A/G]TTTTATGATAGTCCAACATTTTAGCCATTCATAGTCATCTTGTAGTCATATGTCTAAAGG
535	TTTTTCTTAAAAGCCCAATTTTTTTTTACCTTAATACCGTGATCATATAGAACTGAGGAA[A/G]CTGCATGCTTTCTGTGGCCCTTGCCGTAAACTACATAGCATTATATTTCTTTACGTAACT
536	GGAGCTATAAGCAGGTCTGCAAGTTGGTTGCAAAGATCAGAGAAAAGAAGGAAACTATGG[A/G]ATAACTCTGTGGGTGAGAAATCAATGCAGACGAAACCTAACCAAGTGTTTTTCCTTCTCT
537	AATTATAAGACTCTCTCCAAAACTCTTTTATTCCCTTATAGTTAAATCACATTTTTAACA[T/C]TCAAAACACTCATTCTACTCAACAAACATAACGTCAAGACACTTTTTACTGTTTGAAAAA
538	TTGCCTCTTATCTATCCCATTTCATAGTTCTTTGAGCAGCTCAAATAAACTAACATCATA[A/G]TTGGTCAGACAGTCTACTCACATGTTAAACGTTTACTAATATGAAACAGAATCTGATACT
539	TCCTTTTGCCTGTATAGAATCCTTCTTATTGATCAACTCATTTCTCTAACTTGGCCTAAT[A/G]TCTCAAACAGTGCTTTGCCTATAGGAAATCAACAACATGATGTTAACTAATGCATTGGGT
540	ATACAGTGAAAATGGGGGGAAAAAGTTTGGAAACGTAAATTTGAGTTATAATAAAGGAAC[A/G]ATGTGAGAACAAAGTTGTTAGAACAATCTCTGAGTCTCCTCCACGCTGTCACATTTCCAC
541	TCTTTAAATAGCATAGAATACTATTTATCAGCGGTAGAACCAATTTAAATTACTTTCAGC[T/C]CTGATGAGAAATGGGAAGAGACTGAAGTACACTACACATTGGCATTTGTACAGTTGGCAG
542	TCCTAAGCAGAGGTTGGAAACAATTTTCACGCGTCACTGAAAGATAGCTTCCTTCAACTG[A/G]ATAATGTTAATGTTTATTGGCACTTAATAGCCTTAGACAGGACAGTATTTTGAAATTCAA
543	TTACATCACAAGAGTCTGTGTTCTGGAAGAATAATGCACTGAATTTTAATCATGATAATT[C/G]AGGCTTAGTATCTTTAAATACAACATAGCAGATGCAAGGTTAAATGGCAGTTTCAGTCTT
544	tgttgtcacttttttttgactttttttgacttcttgatttccatgattcctagaacaatact[A/G]agcatatgtaaaagtgttcaatgaatatttgttgaatgaatgaatATGGTTAGGACTATT
545	GGCTTTTTGTAAATAGATTCCATACACCAAGAATGTCTAGATTTCAATGCATTCTGCATT[A/C]AGTCCTTCTGTAAAACAAATAATTGTTTTGCTTATTAATCATAACTTTGGATATCTGTTT
546	TCAACTTATTAAAATTTGGGAAATTCTTTCCAAATAATTTAGATGTTAGACAATGAATTT[T/C]TAATGATTCTCAAGGTATTACTTCTTTAAAGTTGGAACAGAATGTGTAATAATCTTTTCT
547	TAGATCATTACTAAAAACGCATAGTCAGGGTCAAAATAGAGCTGGAATTCTTTTTACCTA[T/C]ATTTAAAAAGTATGCAGTGAAAAGTATTCAGGCTCAACTAGATAAAGAAGCTTTACAGAG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
548	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs4692990	94891726	T	
549	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs10516943	94894653	T	
550	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs7662498	94896866	T	
551	4q22.3	GRID2	GLURD2	glutamate receptor, ionotropic, delta 2	1,467.8	4	rs13101891	94899563	T	
552	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs40184	1448077	T	
553	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs11564773	1449813		
554	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs6869645	1457548	T	
555	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs6876225	1459036		
556	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs2550936	1464256		
557	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs6347	1464412	T	
558	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs11564759	1468291		
559	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs37022	1468629	T	
560	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs11564758	1473588		
561	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs463379	1484164	T	
562	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs403636	1491354	T	
563	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs2617605	1495521	T	
564	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs6350	1496199	T	
565	5p15.33	SLC6A3	DAT1	solute carrier family 6, member 3 (dopamine transporter)	52.6	5	rs2963238	1497427		
566	5q12.3	HTR1A	5-HT1A	5-hydroxytryptamine (serotonin) receptor 1A	1.3	5	rs1423691	63287418		
567	5q31.1	NEUROG1	NEUROD3	neurogenin 1	1.7	5	rs2344485	134896540	T	
568	5q31.1	NEUROG1	NEUROD3	neurogenin 1	1.7	5	rs2344484	134904530	T	
569	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs1985524	147827981	T	
570	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs10062444	147834255	T	
571	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs2005953	147847332	T	
572	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs6865878	147891909	T	
573	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs1432917	147901079	T	
574	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs2278392	147908418	T	
575	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs7731872	147927154	T	
576	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs4599527	147932732	T	
577	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs4489051	147934678	T	
578	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs1833710	147947939	T	
579	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs4280857	147952812	T	
580	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs7711800	147963048	T	
581	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs1011427	147968170	T	
582	5q32	HTR4	5-HT4	5-hydroxytryptamine (serotonin) receptor 4	203.1	5	rs2068190	147987206	T	
583	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs2241695	149583017	T	
584	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs2053053	149589586	T	
585	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs919741	149591881	T	
586	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs3822607	149591986	T	
587	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs3776825	149600864	T	
588	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs7701427	149613148	T	
589	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs2304042	149625000	T	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
548				0.19	0.00		0.27
549				0.02	0.23	0.00	0.00
550				0.04	0.03	0.00	0.00
551				0.18	0.22	0.05	0.07
552				0.44		0.14	0.32
553			haplotype (Greenwood et al. 2006)	0.04	0.18	0.01	0.02
554				0.05	0.18	0.02	0.06
555			haplotype (Greenwood et al. 2006)	0.05	0.20	0.00	0.04
556			haplotype (Greenwood et al. 2006)				
557			haplotype (Greenwood et al. 2006)	0.28	0.38	0.08	0.08
558			haplotype (Greenwood et al. 2006)				
559				0.23	0.44	0.44	0.44
560			haplotype (Greenwood et al. 2006)				
561				0.30	0.47		0.42
562				0.21	0.22	0.35	0.28
563				0.39	0.15	0.09	0.18
564				0.10	0.02	0.01	0.01
565			haplotype (Greenwood et al. 2006)				
566				0.48	0.18	0.13	0.13
567			haplotype (Fanous et al. 2007)	0.09	0.00	0.11	0.16
568			p=0.017 (Fanous et al. 2007)	0.34	0.16	0.29	0.37
569				0.39	0.48	0.18	0.11
570				0.03	0.33		0.16
571				0.42	0.30	0.47	0.48
572				0.01	0.04	0.00	0.00
573				0.08	0.48	0.35	0.22
574				0.11	0.50	0.35	0.22
575				0.01	0.09	0.00	0.00
576				0.17		0.36	0.22
577				0.03	0.20	0.02	0.02
578				0.10	0.27	0.17	0.18
579				0.06	0.04	0.00	0.01
580				0.50	0.45	0.41	0.46
581				0.09	0.32	0.42	0.32
582				0.48	0.33	0.24	0.31
583				0.49	0.16	0.28	0.37
584				0.46	0.16	0.13	0.16
585				0.30	0.02	0.10	0.08
586				0.48	0.03	0.49	0.40
587				0.40	0.27	0.40	0.38
588				0.13	0.26	0.33	0.27
589				0.37	0.03	0.25	0.22

	R
1	**Sequence**
548	TGGTTCTTGGGGGGAAATGCTCCTGTGGCATTATTGATTGCAGCCTTCATGAGAAGGACA[A/G]TGATTTACTGTGTTGCTTCCTGTGCAGCTGTGAATTTGCTGTACAGTGACAGGGCCTTCC
549	CACGTTACTCTTCTTTCTATGACAGTATGTCCATTTGTTATATATGGAATGCCATTATTT[T/G]CAGTGATCTATATAGCTTGAGTTTTAAATCAGTATACTTTTATCAAACGGTATACCTTTT
550	TGACTTCATCTAACCCTAATTACCCCCCAAAGGCCCCATCTCAAAATATCATTACAATGG[A/G]GCTTAGCGCTTCATCATATAAACTTTGGAGGGGCATAAACATTCAGTCCATAATAACATG
551	CATATATTTCAAATTTAAGGTTCATTTTCTACCAAATAACATGTCTATAAATTATGATGG[T/G]TCTTAGAGCCAACAAAAATTTCATCAAAATTTGAACATAAATGTTGTTCTAAATGTTAAA
552	CCACCACGCCAACCACAGTCTCGCGGCTTTTTAAAAAATCAAGTAATGATTGATTTGTAG[A/G]AGTTTGAGTGAGGCATCGGATCCCCGGCACCTGTCAAGGGTGTGTTGGTCCAGGCCCCCA
553	GAATCATGACATTCTCCTGGCTGGGGGAACAGGCACCGTGCCCAGCCCTGTGTGGGCATC[A/G]GAGGTGGTTCCCTCTGGTCCTGTCGGCGGATCTCTCCCCAGCCTCCTCATTCACAGCGGG
554	GTGCATCCCTGGACATGTCGGGCTTGCCTATCTGACATGGAGGTATTGCTGTAATGTGCT[T/C]TCTGTTATTGTTCAACTTCTTGCTAGATACCACCTTTCTTAGAAAGAACTATGCCTCCCC
555	CAGGCAGAGGTGAGTGGACAGCCCGACTCACCTCCAGCTTCCCCTCCCAACACAGAGGCG[A/C]GGCCCAAGTGCAGGACTCACAACGGACTGTGACAGGGGTCCAAGACCATGTGAGGTTTTT
556	AAGGTCTCCCAAATAATCACGGGGCTCGCCCAAGTCAAGGACAGGAGGTCTGGGGGCCGT[A/C]CGTGAGCCCAGGGATCTTGCCTAGCCCTGGGAGGGCAGGGCCCCCTCGGGTGGAAGGAAC
557	AGGGCCAGGGCTGATCTTCATCATCTACCCGGAAGCCATCGCCACGCTCCCTCTGTCCTC[A/G]GCCTGGGCCGTGGTCTTCTTCATCATGCTGCTCACCCTGGGTATCGACAGCGCCGTGAGT
558	CGCAGCACCAGCGCCCTTGGGAGTTCATGGGAAACACAGCCCCCGAGACCCCATGAGACC[T/C]GCCCAGTCAGGATCTGCATCTTAGCGAGGTCCCCGGGAGGTGTGTGCTCCTAGAGCTTCT
559	GTGCTTACTTTCTTTCACATCATGAGGCTAGAAACACGGTAAAAATACAAGGACAGTGTG[A/T]GCAGCAGAATGGCCAGGCAGACCACAAGCAGGCTTCACTGAGAGTGGGCGCTGGAAGGCA
560	GGGGCTCTGGCATTCCCAGGTTTCCATATGCATTGCCTGCCAGGGCTGAGAGGTGTCAGA[C/G]TTGCAGACACCAGGGTTCTTTCCTCGGGAAGCCAAATCCCAAGTACCTGTGATACAGCAC
561	CGGACTCTTCGACTCAGCCGTCATTTTGGAGAGGAGGAGAGGACGTTTGCGCGATTCTCC[C/G]CAGATCCAGTGTTTCCCGTCAGCCAGGGCGCTCCTGTTTGAGGGGCTCGCTTGCCTGGTT
562	GAGGAGGGCTGCAAAGTGTGGCCGCAGGAAGGAAGGCTCGTGGCCCTGCGGGCGGATCTT[T/G]GGAAGAGCTTGTTCACACTCACCTAGTCCTGGTGAGGAAGGAAAATTGCAAATCACAGAA
563	TCCAGAACCCAGCCACAGAGCCAGAAAGCGAAGATCGAGGCAGGGCCACCGGGGACGTCC[A/G]AGAACATTGGTGATCCCTTCCCAGGAGCCTCTTTGGGCCTCCCAGCCTCCCTGCCTGGCC
564	TAAGGAGCCCAATGCCGTGGGCCCGAAGGAGGTGGAGCTCATCCTTGTCAAGGAGCAGAA[T/C]GGAGTGCAGCTCACCAGCTCCACCCTCACCAACCCGCGGCAGAGCCCCGTGGAGGCCCAG
565	TGTCTGTGTGTCTGTGTGTGCGTGCGCTCGACTGAAACACGCTGCTGCTGGATCCAAATG[A/C]CAGAAGTCGCCCTGGCTGGGGCGGTGTAGACGCTCCTGCTCTCCTGCTCAGCGTTGCAGG
566	ATATAAGTTTGAATTTTTTGCCTTGTACCTACCCCTGGCCACCCTGTTGCAACTCTTTAA[T/C]GGTTAATGATTCTCTCCTCATTCTGATGCTCTCCTCCTTACTCTGCTCAAAACTTTCTTC
567	AAAATCTTTTTTTTCCCCACTGGATTCTTCTTTTCATGAATATAGTGATTTGGTGGCAAG[C/G]GTACAGAGGAAGATGGGAATGGGTTCAGGAAAATGTGTCCTGAACACAAAGCTGGTACAG
568	ACCCCAGGTTGAAGTGTTTCTGATAACCAGCAGAGAGGCTATTTGGCTCAACCTTGCTTT[T/C]ACAAAAGGGCTGGAAGGCTATGGACTCTAACTCCAAACGAGGACATACACATGGTCACTG
569	CATGTCTCTACTGACCTCTTCTCTTTGTTGGCTACATAAGCCCT[C/G]TCTTCCTGGTTTTGAGTTTTCCTAACACCTGCTGCCAGGCAGTTGGCTAACCACCAACCA
570	GCCATGCTAATTCAGGGAATGAAATGACGTAACCCCCCTAATGACATTCAATACGGAGAA[A/G]GACTAAATCGAAATTAAATTATCTGATCTCGACCAAGTTTTTAAAAGTACAGATAATGTC
571	CTGTGTGCGTAAGAATCAGCTGAGAGCAGTTTTTTAAAATGCAGATTGCTGCTCTCTCTG[C/G]CTCACTCCTGCCCTCCTACCCTCGCTGTCAAAGGTCTGGTATGGATCCTGGGAATCTGTA
572	TGTCCTCTGTATGTGCTATAACATGTCGTTATCTCTTAAGAGTGGGGTGCCACAAGGACA[C/G]CACTATGTTCTGGTGCATCCTATATGGACCAAAAACCACTGCATTGCCTTCCACTTTGCT
573	TATTCGTGTGTTTTTCTTTCTGGAACATAATAGCTGTTCCATGCATGTTTGGCTGAGCAC[A/T]GAATGCTGAGATGTGACTTGTGGTTGTTTGTATGACGCTGGGGTTGGTTTCTCTGTCCTC
574	ACGTCCTGCTCACAACGGCATCGATTTTTCACCTGTGCTGCATTTCTCTGGATAGGTAAG[A/G]ACAGAACAATGTGCATAGCGGAGCTCCATGCTGGAGACATGACTTGATGGATATTGGGCA
575	TCTTACAAGTTTATTTCTTGCAATAAAATCTTGTCTTCAATTTCCTGCCCTTATAGTCTA[T/C]GTGCTACACAAAATCTAGAGTTATACCTCTGAAATCAAAGGCAGACAATGTATGTTTTCC
576	AATTGTCATGGATAATGATAATCCAGTGATACTAAAACATATCTAGACAATTAACCAGAA[T/C]AATGAAGGTTTAGAATTATTCCCTGTGGCACAGGTAGAGCAGCTGAGGAAATGGAGATCT
577	CATAAAATAATTTTCTCTGGTTTCTGCTGCTAAAATGTCCTTATAGTGGAGCTTATAATA[A/T]CCCAAGAGGAAGCAAGCATGATAGGATAACTAATGAGTTTTCCACATAAGAGTCAACCTC
578	TCAACAATGCAAGTGTTGCAGAGATTAAATGAGACCAGTGCTGAGAAAAGTCTATCGGTC[T/C]TGCAACCACAGAGCTGACTGATGGTTCAGCAGGGGAGACTCAGCTGGTTGGTGGCAGAGC
579	TCATGGCTGTCTTATGGTTTCAATTTATTCTATTGTTTATTAATTTTAAACAATTATGTT[A/G]TAATCTCTCAAACTGGTATGCAATCTGAAGTACTTATAGTTAAAATTTTTCTGCTTTTGG
580	GTTAGTTTAACAAATATAAATCAATGCAATTCTCCATGTTAATAAAGGAGAATATTCATA[T/C]CACCACCTCAAAAAAAGCATTTGAAAAAATGTTATAATTACGATTTACAAAGAAAAAACT
581	ATTTTAGAGAAGCAGCTAATCTAGGCTTTGGTGGTCCACAAAAGCTTCTGAGAGATTGTG[T/C]CATAACTAGCCAAATGAAGTGGTGAAGAAGAATGCTCTCAGTAGCAAGAGAATGCCATT
582	ACTTTCTCTATCAACAGTGTAACTGACGTTTCTAGCCTCACCTTATCTCAAATGCCACCA[T/C]TGTTCATTGTATGTAATTACTGCAGTTCAAATCCTCAAAAGATGAATGCCAGAAAAAGCG
583	GCTGTTCCGGGACCACACTGGAGGAGGGGATGGGAGGGGCAGAGGAGATGCAACCGGGGG[T/C]CTCCTGTCTCACTTTCTTCACTTTCTCCACTCCCAGCAGCCCTCTCAATGGAGGCGCCCT
584	GCATGCACTTGTACACATGTGTGCACGTTTAAAACTGTGCACAAGGAGGGTGCGCAGGTG[T/C]GTGTGCATGTATATACCTGAGTGTTGCATAAAAGCATGGAAATAGGCTGTTAAGCTGGTC
585	TCTGTCTAAGCTGAAGCTTGGATTCTGCTCACTATGTATTTGGCTTTGAATGAATGAGAG[A/G]TGGTGGTGTCCTCATTTTACAGATGGGAAAACTGAGGCTCAGAACATCACACATCTAATA
586	AACAACCCTCGGAGAACACTATCATCTCCATTTCACAGACCTTCAAACCACCTTGTGGCC[T/C]GCAGTTGCACAGCTTGAGGACCTGGACAGTCATTTAAATAAACATCTGTCTAAGCTGAAG
587	CCTTCTGTGGAGGCCCCGGATGGAAGGCACAGGGCCTTGAGTTCAAAGGCCACTCCTGGC[T/C]CAACCATCACTTTGTAGCTCAGCCTCCTTCACTCCCTTGGATGGAGGAGGGAAGAAGTCC
588	GGCCCAACAGCATCTCCAGCCATACCCACTCAGGCAGGGGGTTCCCAGAGGCTTATGTGT[T/C]AACACAAATGGGTGCTGACCCCCAACACTTCTGCCAGCCCACCCCACTTACCAAACCATG
589	GCAGTGGAAAGAGGAAGAGGCCTGGGTTGCAGTGACTCAAGCACATCCCTCGCCCTCTCT[A/G]GCCTCCGTTTCCATGATTCTTAAATGTGAGGCTTCTCCGAGACTCCTCCAGGCCTGTTCC

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
590	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs959059	149630732	T	
591	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs874084	149631023	T	
592	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs3797616	149633197	T	
593	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs1897559	149636405	T	
594	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs10515639	149636619	T	
595	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs1432833	149641346	T	
596	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs3806947	149651516	T	
597	5q32	CAMK2A		calcium/calmodulin-dependent protein kinase II alpha	70.3	5	rs1432832	149653734	T	
598	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs592403	160652562	T	
599	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs3850733	160670895	T	
600	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs153296	160673511	T	
601	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs10515827	160687535	T	
602	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs252942	160688459	T	
603	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs187269	160689203		
604	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs252944	160690915		
605	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs194072	160691233		
606	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs1816072	160692234		
607	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs1816071	160692534		
608	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs967771	160694752	T	
609	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs2910298	160724310	T	
610	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs1422951	160766838	T	
611	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs10043074	160780542	T	
612	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs4498288	160807099	T	
613	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs2962420	160822562	T	
614	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs7724146	160827209	T	
615	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs2962406	160842679	T	
616	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs2962402	160870827	T	
617	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs6882041	160874978	T	
618	5q34	GABRB2		gamma-aminobutyric acid (GABA) A receptor, beta 2	254.3	5	rs4426954	160885609	T	
619	5q35.2	DRD1		dopamine receptor D1	3.5	5	rs5326	174802802	T	
620	6p24.3	MUTED		muted homolog	183.2	6	rs2815132	7974944	T	
621	6p24.3	MUTED		muted homolog	183.2	6	rs9379157	7993105	T	
622	6p24.3	MUTED		muted homolog	183.2	6	rs2294435	8002919	T	
623	6p24.3	MUTED		muted homolog	183.2	6	rs2815155	8010229	T	
624	6p24.3	MUTED		muted homolog	183.2	6	rs2326975	8014321	T	
625	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs1047631	15631080	T	
626	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs742106	15632459	T	
627	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs875462	15646415	T	
628	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs1040410	15655455	T	
629	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs7771339	15677985	T	
630	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs760666	15697100		
631	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs2619539	15728834		

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
590				0.03	0.38	0.00	0.00
591				0.18	0.47	0.37	0.27
592				0.02	0.00	0.07	0.04
593				0.13	0.01	0.04	0.01
594				0.19	0.33	0.35	0.34
595				0.14	0.45		0.44
596				0.04	0.24	0.10	0.20
597				0.33	0.23	0.28	0.20
598				0.30			
599				0.08	0.30	0.13	0.08
600				0.24	0.00	0.23	0.16
601		Y		0.19	0.00	0.00	0.00
602				0.29	0.37	0.23	0.26
603			p=0.0009 (Lo et al. 2004)	0.29	0.37		0.17
604			p=0.0003 (Lo et al. 2004)	0.10	0.13		0.13
605			p=0.0005 (Lo et al. 2004)	0.12	0.14	0.18	0.22
606			p=0.006 (Lo et al. 2007), p=0.027 (Lo et al. 2004), p=0.047 (Yu et al. 2006)				
607			p=0.0008 (Lo et al. 2004), p=0.005 (Lo et al. 2007), p=0.045 (Yu et al. 2006)				
608				0.24	0.00	0.06	0.18
609				0.13	0.00	0.06	0.02
610				0.28	0.41	0.36	0.21
611				0.15	0.42	0.28	0.20
612				0.01	0.00	0.00	0.00
613				0.37	0.29	0.50	0.46
614				0.18	0.08	0.23	0.14
615				0.26	0.31	0.44	0.30
616				0.01	0.00	0.12	0.09
617				0.31	0.25	0.44	0.28
618				0.41	0.18	0.39	0.46
619				0.13	0.18	0.24	0.24
620				0.48	0.18	0.24	0.24
621				0.04	0.03	0.10	0.21
622				0.18	0.16	0.16	0.17
623				0.46	0.15	0.23	0.18
624				0.06	0.17	0.23	0.20
625				0.20	0.17	0.00	0.02
626				0.34	0.16	0.44	0.38
627				0.20		0.00	0.00
628			haplotype (Fallin et al. 2005)	0.08	0.23	0.09	0.07
629				0.03	0.00	0.00	0.00
630			haplotype (Fallin et al. 2005; Straub et al. 2002)	0.20	0.12		0.00
631			p=0.006 (Straub et al. 2002), haplotype (Li et al. 2005)	0.47	0.28	0.36	0.34

	R
1	**Sequence**
590	TTGCCCCAGTGGGAGAGAGGGTCAGGCACCAAGGTGGTCCCTGGATGCTGGGGATCTCGG[A/G]TTAGTTCACCACACTCTCGAGGCACATTCACACACACACTTGCACGTTGACCAAAAGAGA
591	CAGCAGAGGGGGTGGCTGGGGTTAGGGTGAGGGTCTCTGAAGGACCAGGAGCCCCACGTG[C/G]TATACAGTCAGTATGAAAAGTCCAAGCTTGTGGAAGGCTGGGAACTAGAGACAGGGTGGG
592	CTACTCAAAGAATAAAATCTAAAAATGTTCAGAGACCTGGATTCCACGGTTCTAACACTA[T/C]GTGATTCTAATGTTTTACAGCATGATGAGCCCGACTTTGATGACGTTGGCAGGCTCCTCT
593	TCCTGCACCCTGGAGCTCACAACCTTCCCTGCTTCCTGCCCTTCTCTTCCTGGAGTTCTC[A/G]GAACCTTGCCCAGATGTGGCCACTTTAAGCTTCTTTCTCATAGGGCTTTTGAGAATCATG
594	GGGATGGTTGGACGGGGGAGGGAGGGATGAGTATAATTTCTCCATTAGAGAGGCAAAACT[T/C]CATTCTAGGTAAAGACCTTAGATCAGTGATTATCAAATTGGCTGCCTCAGAATCCCCTGG
595	ATGGACCTCAAGGTCGGACCCCCTCTAACCTGAGAGTACTGGGTATTGGAAAAAGCAATG[A/G]CTATGAATCAGCAGTCCTGGGTTCAAAGTCTTGGCCCCAGTTTCTTCAGCTTTGGAATAG
596	GAGGGTTATCCAGATGTCTCCAGGGGGCCCCTGCAAGTAGGGTAGTGAGTCAGGGACTTC[A/G]TGGGGTTGGAGAATACCAACAAGCAGATAACATGTCCTGCAAGTGAGAGGACTAGCAAGG
597	GGCCCTGCAGGACCCTGGGGCACTTGGGCATATGTGTGTGGGCTGTGGAAGGTGGGATTT[C/G]AGTCAGCTGTCACAATGCCACTGGGGCTACAATCACCCATGCAGGAACCCAGCCCTGGTC
598	TTGTTTTTCTCAGACGAAGTCAGCTGTCCCTGCAATTTTTGTCCCTATAATTTTATTTCT[T/G]AATTTAATAGAGTATTTCAAGAGAAGGATTTGTTCATCACTTTAAAGGATTCATGGTCCT
599	GAGCTTTTCAGAGACTTAGCTAGGCTGAGTAACCCTGGCTTCTTGAATTCAAATTGGATT[A/C]TATGGCTGCCAATAATAGAACTGAAGAAAGATATTTTAAAACAGCTTCACACGCAATCTG
600	TCACAAAGTTTGGGAGGCACATCACCAATGTGTTGATCAGCAAATATTTATTAAACTAAT[C/G]CTCTTGGAGACCAAGCCAACAGTTAAGAGCACGGGCAGTCCTGAACATAATCAAACCTAC
601	GGGACATTCTTGATAAGAAATGGGGTGGTATTATTCATGATGCTGACACAAAGGACAGCA[T/C]CGCATAATCAGGAGCAATGTGGACCTCCTCTAACCTTTCATGCTGGGTGAACAAAGAAAT
602	TCCTATAGTTTTTACAATGAAAGATGTCTCCAGACAATGCCTAATGTCCTCTGGGAGAAG[A/G]AAATGACCCTGTTTTGAGAACCACTGAAAAATACTAAATAATCTCTGGTATCTTTTTTGT
603	TGAGTTAGAAGCTTCCATATGGTTTGCTCCAAATACAACTCAATGGCAGAGATTATTTAT[A/G]CTTTGCTATCCTTGAAATTAATTTGAAGTTAGAAATATCAAAACATCAAGGAAATAATCA
604	CCTAGGATAGGGAATGGATATAGGTATAAATTAGCTTACAGTGATCACTGAACGTTTGAT[C/G]CCTTCTTTTAATTAAATTTTTGTATTTATAGTTATATATCTAGTGCGGGGTTAAAACGTG
605	GTGGAGAGAGCTTTTATATCAAGGTTGGATTTGGGGGAGAGTACACAGTCCATTACCATG[A/G]TCTCGGAAAAATCATTGTGGGTACATTGCAAGACAGGATGGGAAGAATCGTGAGAAGACT
606	ATAGTGTTTAAGGGCCTGGATTCCTGAGTCAGAAAGATTCTCATTCCAATGGCAACTCTA[T/C]AACTTTCCATCTGTGTGATCTTGACCTCTGAGCTTTGTCTATTTTCACATCACTATTTTG
607	GATCATCCGTAGTTGAAATGATGAAGAGAAAATTGAAACTGGAAAATGTCTCAAAATGAC[A/G]GCTATAAAGAGGACACGAGAAATGTAAGATACCTGTATCTAAAGCAAGACCAAGGTTTTA
608	GAACAATTGAAAGAATGAAAAAAAGAACTGTCCCAAATTGTCCTAACAATTACAGAGGAG[A/G]GGTATGTTTGATTCACTCTATGAGGCTGAGTAGGGAAGAGCTGGAATTC
609	TGGCTTATGGCATGTAATAATTACAGTGACTAGAATGGTACTTCTTTAGGTTAAGTGGCT[A/T]ATTATCAGTCAGCCAGAAGGATCTAATGTAAATATTTGAGGGAAAGAAGTATCAAAAGTT
610	GAGGGAGGAGGGGGCATGATGAGGCCATGTAGTTGACATTGGTATTGTGTAGCTGAGCTG[A/G]CACAGAATACAGCAGAGTATCCCCCTGACTATTCCTATTTCAAAGATATATAATACTTTC
611	TTTGTGTTGGGATTTTGGGGTTAAGGGAATGAAAGTTCCTACCACCTTAAATGAACTTCC[T/C]CCTTTCTATCATTTTGATGTCAGCTCATCATAACCCACCTAAGGAGCCTTCTCCCACCAC
612	GGCTAGTGGGAACAATTCAACATGGAATTAGTATCTTTCTCTAGGGATTTATGGTCATTT[A/G]GCATTTTGTTGCCTTTTATTCTGTCCATAAGAGTGCAGATAATGAGCTACTTCTGAGAAG
613	TGGATCAAGGAGCACCCAGAAGTGGTTTATTTGGGGTTTTTCAGTTTGAATAAACCAACT[A/C]TGAGACAAGTTCCCAAAGGTGGAGTTGTCAAATGTGAAGGATAGCCTTGTAATATTAAAG
614	GGGTAGAATGTTTTAACTTTAGGCATTTTAGAAAAGTATTTCAGTTTTTTTGTCAGTATT[T/C]CCACTTTTCAAAAATATGACACAACAGGACTGATTTCCAAAGATTGGAATACCAAACTAT
615	CCCACTAGTTCCTACTCATTACACAGTCAAATGAGTTTGAGAAATGCTGAGTTACACAAG[A/T]TTAAGAAATTTCTTTGCTGTAGGACTTATTGGTAGCCATTAAATTAATGTGCATAGCAAA
616	TAAAGGTCAACTTTTAGATATAAACATAACAGAGTTTTATGCAGTTTAGAAAAGAAAAGA[A/G]CAAGATTATTTAGGAACTTTGATCTGTCTTTTTAACCGCTCCTTCTCTCTTTTGATGTAG
617	TATTATTAGAAAATATGTTCTTTTCTATTCGGGGGATAGTTTGCAAAACAGATCTTTTTA[T/C]TTTGGAAAATGAATGAGTATATTATTGCCTACAACTGTAGCTATGAGAAACTCAATTTTA
618	AAGGCTGGCCTAGTTGATATAAATTCTTTTCTCCTACAATTTCTGAGCTTTTGCCTTCTT[T/C]TCAAAGGTACATTTGATATAACCAACACAGGAGTTACAATTCAATGAAAGACTTTCTAAA
619	CATGGAATGTTGGTGAGGCCCTCTGCCAGGGAAGCAATCTGGCTGTGCAAAGTGCTGCCT[A/G]GTGGGGAGGACTCCTGGAAATCTGACTGACCCCTATTCCCTGCTTAGGAACTTGAGGGGT
620	gaggttcgttccccaggtcccctgggaacagaggctgcctagccagccttcccacactaa[T/C]gagatatccctttgcggacctcccccattcaagatgagtggcattctgatcgtttactag
621	GGTTGTATACTCTCAACAGCATCTTGGTAGCATTCTGTCTTTGTTTACTAGCAGAAATAC[T/C]CTATGAGGAGAAACTGCCCCCAACAACAACTTGGTTACTCTGAGTAATGTTCACATACAA
622	ATTCTAATGTGGGTTAAATTGATCAAGAGAAAATTCCTCCAAAGGCAGCACAGGAATTTC[A/G]CTTGATCTCCTGATTCCTTGTTTTTGGTTAGATTACTAGAGACACTGTCAGGTTAAAACA
623	CTACTGTATAGCAAAGCCAATTAGCTGGGGGCTGTTTCCCTACTATGCCATGAGTGTGGC[T/C]GACTATTCCTGCCTTTCTTTTTAGACACCTGTTTCCTAGAATGCTTCTCTTGCTCCCTCT
624	CTTCCAGCCACCTGATTACAAATTCCAAAGCTTCTTTGGTGCAGTCGATAAACTAGTCTG[T/C]TCATGTAATGTAAGTTCTCCTTCTCCCCCATCCCCATTTTTCCTGACCTTCTGCAACACA
625	GCTGTATGCGGAATTCCACCTGGAAAGCCAGGTTGTTTTATAGAGGTTCTTGATTTTTAC[A/G]TAATTGCCAATAATGTGTGAGAAACTTAAAGAACAGCTAACAATAAAGTGTGAGGACGGT
626	CTCCACTCCGGTAACTTTGGTGAGTTGAGAGCTTTCTTGTTTGTTTTCCCTCCTTTACCA[T/C]CCAGAAATCCATTTGAGTCTGCTCCTTGTGGTTAAGGACTGGCGTTTGCAGGGAGGTGCG
627	ACTCCTTAAAGGGGAACATCTGGGTGAGCCTGGCCTAGCTAGGCTTGTGAAGGGCA[T/C]TGGGCCTTCTTGGAGAAAGATGTGAAGCGTGACAGGGATTTGACACAGGGCCATTATCTG
628	TAGTCCTGTAGGTGATTTTGATGCTGCCAAATGTGGAGAACCACTGGTTTTCTGTCTGTA[T/C]AACCCTTTTGAATGGACTCTTTAATAAATAATTTTCACTCACAGACGCTGGCAGTTGGTT
629	GCCAAGCTCTGTACTTCCTGAGAACCTCTGAACACATAGTTTCTTCTGCATAGAAATTTC[A/G]TGCCCACTCGTTACTCATATTGGTTCTCTCCTTTTTGTCCTTTAGTCTCAGACTTAATAG
630	ATATATAATTTGAATATAATATAGAAATAATAGAAATAAGTACACTAAGGTGGGAGTAAT[T/C]AACCAGAGAGAGGTCATGACACTTGATCTGAATGACGAGTACTCACTGGGCTAGAAAGGA
631	GAAGCAATATTCAGCTCATTCTGTTATAACTAGTCTGACATGGTCTTAAAATGTATAAAA[C/G]ACTATCATAGCTAATAGGATTATTTAAAAGGCTGTTTCATTTTGATTAGTGATAAAAACT

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
632	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs3213207	15736081		
633	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs1011313	15741411	T	
634	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs6459409	15744832	T	
635	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs2619528	15757808		
636	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs2619522	15761628		
637	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs1018381	15765049		
638	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs1474605	15766191	T	
639	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs1997679	15766884	T	
640	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs909706	15768850		
641	6p22.3	DTNBP1	Dysbindin	dystrobrevin binding protein 1	140.2	6	rs9476886	15769440	T	
642	6p22.1	MOG		myelin oligodendrocyte glycoprotein	15.4	6	rs29254	29731573	T	
643	6p22.1	MOG		myelin oligodendrocyte glycoprotein	15.4	6	rs29234	29732091	T	
644	6p22.1	MOG		myelin oligodendrocyte glycoprotein	15.4	6	rs2256266	29740297	T	
645	6p22.1	MOG		myelin oligodendrocyte glycoprotein	15.4	6	rs2747419	29750173	T	
646	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs204991	32269344	T	
647	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs2071286	32287874	T	
648	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs379464	32294326	T	
649	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs422951	32296361	T	Thr320Ala
650	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs520692	32296618		
651	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs2071282	32296921	T	Pro204Leu
652	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs915894	32298368		Lys117Gln
653	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs3134931	32298598	T	
654	6p21.32	NOTCH4		notch homolog 4	33.3	6	rs532385	32303337	T	
655	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs7762948	34094069	T	
656	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs2229901	34098425	T	
657	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs7772436	34099346	T	
658	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs2451383	34113047	T	
659	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs9469690	34120889	T	
660	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs3778068	34136383	T	
661	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs1906953	34144424	T	
662	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs2499689	34149284	T	
663	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs2451341	34149425	T	
664	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs1565364	34156504	T	
665	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs1873249	34161402	T	
666	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs874631	34170783	T	
667	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs2499713	34171329	T	
668	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs733457	34176386	T	
669	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs747373	34188002	T	
670	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs2499722	34191437	T	
671	6p21.31	GRM4	MGLUR4	glutamate receptor, metabotropic 4	133.8	6	rs937031	34193665	T	
672	6q14.1	HTR1B	5-HT1DB	5-hydroxytryptamine (serotonin) receptor 1B	1.3	6	rs6296	78228979		
673	6q23.2	TAAR6	TRAR4	trace amine associated receptor 6	1.0	6	rs8192624	132933946	T	Val265Ile

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
632			p=0.00009 (Straub et al. 2002), p=0.005 (Schwab et al. 2003), p=0.17 (van den Ord et al. 2003), p=0.020 (Li et al. 2005), p=0.036 (Stefanis et al. 2007)	0.12	0.03		0.01
633			p=0.009 (Schwab et al. 2003), haplotype (Straub et al. 2002; Funke et al. 2004)	0.07	0.00	0.19	0.23
634				0.17	0.08	0.27	0.29
635			p=0.002 (Li et al. 2005), p=0.013 (van den Ord et al. 2003), p=0.014 (Schwab et al. 2003), p=0.047 (Straub et al. 2002)	0.19	0.37	0.09	0.07
636			p=0.005 (Stefanis et al. 2007), p=0.015 (Funke et al. 2004), p=0.030 (Schwab et al. 2003), p=0.047 (Straub et al. 2002), p=0.066 (van den Ord et al. 2003)	0.18	0.36		0.08
637			p=0.0006 (Funke et al. 2004), p=0.026 (Stefanis et al. 2007), haplotype (Straub et al. 2002; Schwab et al. 2003; van den Ord et al. 2003)	0.08	0.31	0.09	0.06
638				0.19	0.36	0.09	0.07
639				0.28	0.43	0.09	0.06
640			haplotype (Straub et al. 2002; Li et al. 2005; Funke et al. 2004)				
641				0.25	0.47	0.42	0.34
642				0.04	0.00	0.02	0.14
643				0.05	0.17	0.02	0.01
644				0.31	0.05	0.22	0.28
645				0.03	0.04		0.00
646				0.14	0.16	0.21	0.33
647				0.20	0.01	0.29	0.16
648				0.01	0.23	0.08	0.10
649			haplotype (Wang et al. 2006; Zhang et al. 2004)	0.37	0.27	0.27	0.22
650			p=0.002 (Wang et al. 2006), p=0.017 (Zhang et al. 2004)	0.07	0.25	0.25	0.18
651		Y		0.03	0.00	0.09	0.06
652			haplotype (Wang et al. 2006)	0.35	0.36		0.48
653				0.22	0.43	0.44	0.42
654				0.13	0.39	0.42	0.42
655				0.04	0.42	0.04	0.05
656				0.18	0.26	0.27	0.42
657				0.06	0.28	0.03	0.04
658				0.23	0.23	0.31	0.50
659				0.16	0.49	0.24	0.32
660				0.38	0.33	0.43	0.43
661				0.10	0.39	0.40	0.46
662				0.03	0.21	0.06	0.16
663				0.01	0.17	0.06	0.14
664				0.23	0.33	0.44	0.42
665				0.48	0.23	0.23	0.28
666				0.09	0.05	0.26	0.24
667				0.07	0.01	0.19	0.14
668				0.41	0.27	0.36	0.48
669				0.02	0.16	0.01	0.02
670				0.43	0.34	0.43	0.43
671				0.03	0.23	0.10	0.12
672				0.34	0.24		0.46
673				0.08	0.03	0.07	0.03

	R
1	**Sequence**
632	CATGGTATATTCTAAATGTATTAGGGAACTTTTCTTTGAAGACTTCCTTTCGTAAAGCCA[A/G]TAATTACCCGTTAATTATGTTTTATGTTTGTTTTCTTTTTGGTTGTTAGTGGTAGTTTTT
633	ACAATAACACTTAAAAGTTGATATGACTCCTTAATTCACAGGCTACAGAATGGATGTTGC[A/G]TTAGTGGGCATGAAAACAATGTTAATTAACAGTTGCTTGTGTGCAGTAACTTGGCGTCTC
634	TGCCAACTTCTTAGGAAGCCAGACAGGTTTCCTTGTTGACTCCTTTAGCCAACAGGTACA[T/C]TTTTTTTCCCCCTAGCTTAAGCTTTCACCAGGGGGATGTAGCCACCTCAAAGTCCAAAGA
635	TGTAATATACATAGCATAAAATGTATCTTAACCATTCTTAAGCTTAGTAGTGCTGAGTAC[A/G]TTCACATGGTTGTGCATCCAATCCCAAAAACTCTTTTCATCTTGCAAAATGGAAACTCTG
636	TAGAGGGGAGGAGACTGCTAGAATTAAATAGCTGGCAGAAGCAGTGAGTGAGAGCTGACA[T/G]CCAGGTGACCAATGGTAGAGAAAGAAAATTTAGGAAAGGTAGACATAAGAGCCCAAACAA
637	AATGATGTAGACAGTTGGAAATTGAGTTACAAGTAAATGAAACGTCATGCAGGTTCCGCA[T/C]GCTGTTGAATCACCGGCAGATCTCAGCAGTCATTGTAGTACTCAATG
638	GCAAAGCAGAATGAACAGAATGTTAAAGATACAAATAGTGTGGTATGTGAGTCCGAAGAA[A/G]GAGTCATTAGTTAGGATGCATTTACAGAAGGCTTCAAAGAGGAAGGGGTTTCTAAAACTA
639	ATACCAAAGTACATACTTCGAAGCCACTCTGGTCTTTGACTTTTACCTTTTGAGCTGTTA[T/C]GACCAAAGGCCTCAGGATTGAGGTATTTAGGCATGCAAACCCTTCAGGGAACTGAAAATC
640	GAGATCAGGGTAACCCTAAACGTTTAGAGTTAGTTAAGGAGAGACATGCCAAAGGGATCT[A/G]GTTAGAACCCCTTGGAAACTGACTTGACTTCTTAAAGATGCCGTAGTCTGGGGCCATTTT
641	TTTGGCTAACATCTTTCTCATTAGAAATTTAAAACGAGGCTGGGCGCAGTGACTAATACC[T/C]ATAATCCCACCACTTCAGGAAGCCTAGGAGGGAGGATCTCTTGTACCCAGGAGTTGGAGG
642	TTGGACACAAGCAATGTTTGGCTACTCTGGTGCTGTGTGGTTGAAAGTCA[A/G]GATTGCAGGGGTCAATCCCATGGAAAAAGTGGCCGCTGTGGATCTCTGGC
643	TCCTCAGTGTCACAGGGGAGAGTGAGATCTGGAATGGAAAATGACCTTTCTCTCACCTCT[T/G]GGCTCAGCTGAGAATTGCAAGTGTGAGACCAGCATTGGTAGCAGGTTCCAAAAATAGACT
644	ACAGGTGTGAGCCACCATGCCCGCTGTAAACTACCTTCTTAAAAGCTCTAGAAGAGGGCT[T/C]TTAACCTTTTGTTGTGTGTCATGCACCTTCCGCAAGCTGATGAAGTTGATAGACCCATCT
645	GGCTAGAAATAAGAAGAAAAAAAGAAAAAATTGGCTTTTCAAATTAGAAGCAAATAAAAA[T/G]TTAACTGGAATCTTTCAACACTGTCAGAAATGTAAATTTTAACTTACAACAACACTTCTT
646	CATATCTATATCTCTTATGCCCAAAATAAACTTTCCCCTGCCCCTTGTCTGCACTAAACT[A/G]TAAGTTTCCAAAATGAACCCTTCCCGTACTCTATTTGGTACACATCTTGTCTCCTGAATA
647	TCTGTCCTGATCATCATAACCCAGGCAGAGTGGACCACACTTAATCCAGCTACACTCAAC[A/G]CATTTCACCCCACCCCACTCACTTCGATGTCACGCCACCCTCTTTGTAAAAGAACACTAA
648	GAGATCCCAAAGTGGAGGAATTTGAAGTGCATCTGGGAAGCTTGTTGCTCCTATATTTGT[T/C]CCGTTGCTTTGGGTTCATCCTGGTCTCCACTGTTTCATCCTGAATTGAGGTGGGATCAAC
649	TCGTCCCCTCCCCAACCCCCTGCAGGCTGGGACTGCTCCGAAGATGTGGATGAGTGTGAG[A/G]CCCAGGGTCCCCCTCACTGCAGAAACGGGGGCACCTGCCAGAACTCTGCTGGTAGCTTTC
650	TCTCCGTTGGAGCCTCCTCCCACAGCTGATCCATGACCCTGTCAGGTTTCATAGGCCCGG[A/G]CTGTGAGGTGAATCCAGACAACTGTGTCAGCCACCAATGTCAGAATGGGGGCACTTGCCA
651	CGGGCTTCGAGGGCCATGCCTGTGAACGTGATGTCAACGAGTGCTTCCAGGACCCAGGAC[T/C]CTGCCCCAAAGGCACCTCCTGCCATAACACCCTGGGCTCCTTCCAGTGCCTCTGCCCTGT
652	TTGACACCCAGCTTCTTGTGCACTTGCCTCCCTGGCTTCACTGGTGAGAGATGCCAGGCC[A/C]AGCTTGAAGACCCTTGTCCTCCCTCCTTCTGTTCCAAAGGGGCCGCTGCCACATCCAGG
653	AAGGAGATGAAGGGAAACAAATGAAGGCAGAGGAGGGAGTGGGCAAGAATAGGAAGAGGG[A/G]CCAGTGATGTGAGTTTTCCTCTCCTCCCCTGCCCAGGTGTGCCCCTGGCTTCCTGGGTGA
654	CAGGGGGTATACAATGAAAGAAAATCCCTTTAATAAAATGAATCTCTATTTGATGAAATA[T/C]TGTAGGAAAAAGGGTCATTTCCCAGAGGGAACTATCTGTATCCCTGGCATGCTGCAGTTC
655	GCTCTGTTTAACTCATTATGGAAATTTTCCCGATATACAGGAAGGAGAGCAGGATAAAGA[T/C]TGCCCGCTCAAGAATCATCCACTTTTGGCCACGTTGGCTTCAGCTCTGCTGCTCCCTGCC
656	TGCCTGCCCGTGGGCACCCACGGACGTGGCTTGGTGCTGAGGATAGCAGAGCCCCCAGCC[A/G]TCACTGCTGGCAGCCTGGGCAAACCGGGTGAGCAACAGGAGGACGAGGGGCCGGGGCGGT
657	CCCCAGATCCCCAGGGCCCTCTGAGCACCTACCCTTTCTACTTCTTGGTGCCCCTGTCTC[T/C]CTCAGTCTTGAGCCCCCCTTTTCTGCCCCTGTCCCTCTGGCCCTTACTCCACACCAGGAC
658	TCTTTACATCTTGCTCTAAATTAGTGCTACCCACAGTTACACGTCCCTGAAGACACAATG[A/G]CTGTGAGCAATAGAGCCACACGAGTGTTGTCACACCCTACTGAATATGTTACAATATTCT
659	CTCAGGCCCTTCCCTTGTGCCCCACAGGAAACAACGACAGGACCTAGGTGACTCCCCTGG[A/C]GGGGTAGCGGGGCATGTAGGGGAGGGGTGGGGGATACTGCAGGAACCACAAACCCTCACT
660	CATCTGAGCTGAAGGTGTCCTCAAAAACAGCAGGCCTGGAGTGAGGCACATAGCTGGGTG[C/G]GGTGTGGGAGCCTAATCTTACCAGGCTTTGGGATGGGAGTAGGGGGCAGGAAGTCAGGGA
661	AGACCCATCCCCCCGCACCACCACTTGTGGGATGTGCCTATCTCATGCAGTCAGCCTGGG[T/C]GGGCTGAAAGGAAAGGCCTCCCGTAAGAGGAGCCGGCTTGTGCCCTGCCTCACCCACTCC
662	CACCATACACAGTCAGATACGCACCACACACAAATACACATAACCACACACAGAGTCACA[A/G]ATACACCACACACAGACACAGGTAACCCTGGACAGTCACATATAACAAGCCTGCCTGACC
663	AAGCACAAGCAGGCGGTGCCCACCGTGAAGCGTCCACACCCCCACCCTCACACTGCCTGG[T/C]GGCTCTCACACAGTCACCGCACGTGAACAAAGCACCCCTCCAGCCCATCTCTTCTTAACT
664	GCACCAGAGGAGTGGCTGCCAGGGGATTCAGGCCTCCCAGACCACTTTCAGAAAGGGGCC[C/G]TCACAGCTCATACTTGGTCACGCAGGAGTCACACGTGACTTGAGGGATCCTGATCCACTT
665	AGAGAGCTAAAGAAGAAGTGAGTAGTTGGGGGCTGGATTTTGCAATTAACcattcattca[A/G]caaacatttattgagcaactactatgtgccagggctgtgttagatgctggagatgcagcg
666	CCCCCCACCCTCTGGGAGAATGCAGTGTGTGCCGTGGGCCAGGGCCAGTGTGCCAGGGCC[T/C]CACTCTGGATTTGGGCCAGGGTCTGAAGGCTTCTAACGAGTCTGGCCCCACAGGGGATGC
667	AGCTGTCTCCTAAGGCTGTGAGGGTCACATGAGGGAATTCAAGCAAAGCACTCAGAACAG[T/C]GCCTGGCAGGCGGTAAGCACTAAGGGTCAGCTCTTAGGGGAGCTGCCATTCCTCCCGCTA
668	TTGACCAGGGTTTACTGAGCACCCACTGAGTGCTCTGCATGATCCCTGCCTTCATGGAGC[T/G]GACATCCGAGTGGGAGAGACAATCAATAGTGAATGAATACACACAGAGCTAATGCTGGGT
669	AGAGCTGTAAGCAGGGAGATGCTGCCTCCCTGGGGCGGGGGAGAGGAGGAAAAGAAAGGG[C/G]CTATTTAATTTAATTCCGTGTTTTATCGCTCGTTGGATAAATAACCTTCATTAAGATGGA
670	GAAAGAGCCTTTCTAGCTTCCCAAAGGGGCCCTGGGACAAGCCTTGCTGGGTTTTGGGCC[T/C]AACTCCAATCCTCTGTCTGCTCCCAGCCCTCCCTAAATAACTGTGCAGCGCGAGGCTGGA
671	TGGCATTCAATGGCTAGGTCATCACCCAAGGGGCCCTCGCATCTTTCATATACTATGTCT[T/C]GCTGGTGGCTGGTTGGATGTGAGATCTTGGGGCTGCTTACCTGGCTGCATCTATGTATTT
672	CACCTCTATTAACTCGCGGGTTCCCGACGTGCCCAGCGAATCCGGATCTCCTGTGTATGT[C/G]AACCAAGTCAAAGTGCGAGTCTCCGACGCCCTGCTGGAAAAGAAGAAACTCATGGCCGCT
673	TACAAAGCCAGAGTGGCCAGGAGAGAGAGAAAAGCAGCTAAAACCCTGGGGGTCACAGTG[A/G]TAGCATTTATGATTTCATGGTTACCATATAGCATTGATTCATTAATTGATGCCTTTATGG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
674	6q23.2	TAAR6	TRAR4	trace amine associated receptor 6	1.0	6	rs8192625	132934025	T	Cys291Tyr
675	6q23.2	TAAR6	TRAR4	trace amine associated receptor 6	1.0	6	rs7772821	132934199	T	
676	6q23.2	TAAR6	TRAR4	trace amine associated receptor 6	1.0	6	rs4305745	132935405		
677	6q23.2	TAAR6	TRAR4	trace amine associated receptor 6	1.0	6	rs6903874	132938603		
678	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs12216492	146418311	T	
679	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs4896857	146488865	T	
680	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs4607452	146529796	T	
681	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs4895691	146564647	T	
682	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs4272232	146605615	T	
683	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs7744909	146607938	T	
684	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs7750079	146643446	T	
685	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362956	146668721	T	
686	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs941901	146698944	T	
687	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362862	146702961	T	
688	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs1983635	146707365	T	
689	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362836	146708451	T	
690	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs61914	146717958	T	
691	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs725186	146718101	T	
692	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362895	146721019	T	
693	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362848	146724178	T	
694	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs9403775	146728202	T	
695	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs2300620	146745874	T	
696	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362925	146757695	T	
697	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362854	146758161	T	
698	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs362936	146762519	T	Gly884Glu
699	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs979775	146767662	T	
700	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs7755078	146768262	T	
701	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs2300626	146771510	T	
702	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs3804295	146781896	T	
703	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs2284796	146788588	T	
704	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs2941	146796825	T	Val929Ile
705	6q24.3	GRM1	MGLUR1	glutamate receptor, metabotropic 1	409.8	6	rs7770466	146800958	T	
706	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs488133	152167137	T	
707	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs532010	152172611	T	
708	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs11155813	152191128	T	
709	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs9479130	152210149	T	
710	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs1709182	152217050	T	
711	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs9340820	152217518	T	
712	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs1709183	152235689	T	
713	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs9340835	152241624	T	
714	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs6557170	152244797	T	
715	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs7761846	152254201	T	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
674			p=0.040 (Duan et al. 2004), haplotype (Pae et al. 2006)	0.07	0.13	0.07	0.03
675				0.20	0.25	0.33	0.14
676			p=0.001 (Duan et al. 2004)	0.42	0.50	0.35	0.33
677			p=0.003 (Duan et al. 2004), p=0.010 (Pae et al. 2006)	0.17	0.43	0.27	0.12
678				0.12	0.00	0.04	0.06
679				0.07	0.36	0.09	0.08
680				0.09	0.26	0.18	0.11
681				0.01	0.38	0.01	0.03
682				0.39	0.00	0.44	0.46
683				0.03	0.24	0.16	0.10
684				0.03	0.38	0.09	0.01
685				0.02	0.00	0.00	0.00
686				0.22	0.14	0.16	0.10
687				0.01	0.00	0.05	0.01
688				0.35	0.00	0.05	0.08
689				0.29	0.03	0.02	0.04
690				0.44	0.35	0.33	0.49
691		Y		0.20	0.08	0.26	0.17
692				0.15	0.12	0.26	0.12
693				0.09	0.00	0.24	0.37
694				0.11	0.44	0.27	0.27
695				0.16	0.15	0.36	0.47
696				0.01	0.00	0.23	0.11
697				0.38	0.33	0.30	0.43
698		Y		0.03	0.00	0.00	0.00
699				0.15	0.00	0.00	0.00
700				0.38	0.04	0.08	0.11
701				0.03	0.45	0.38	0.29
702				0.49	0.06	0.46	0.47
703				0.03	0.00	0.41	0.34
704				0.04	0.00	0.00	0.01
705				0.03	0.24	0.00	0.00
706				0.32	0.00	0.09	0.09
707				0.32	0.45	0.38	0.37
708				0.12	0.45	0.28	0.29
709				0.41	0.47	0.38	0.37
710				0.37	0.07	0.01	0.02
711				0.03	0.16	0.31	0.28
712				0.28	0.35	0.40	0.47
713				0.37	0.27	0.23	0.21
714				0.21	0.06	0.46	0.49
715				0.08	0.48	0.10	0.09

	R
1	**Sequence**
674	GGTTACCATATAGCATTGATTCATTAATTGATGCCTTTATGGGCTTTATAACCCCTGCCT[A/G]TATTTATGAGATTTGCTGTTGGTGTGCTTATTATAACTCAGCCATGAATCCTTTGATTTA
675	AGGTTTTAAAGAACAGTTCAGCAACCATGAATTTGTTTTCTGAACATATATAAGCAGTTG[T/G]ATAGACGAAGTTCAGGATACCTTTAAAATTACCAAGCGAAATGAGTTTTTAAAAATCAAG
676	TCTATGTCCTTTCTTCCCCAAATCCATAACCCCCATGTAGTCATGAGAAAAATGTCAGAC[A/G]AAACTTTATCGGGAATATTCTGCATAATATTTGATCAGTATTTCTCAAAACTGTCAGTCA
677	AGATATTTAGCATTTAGAGTTTCTCTCATAAGTCAGTGGTTCTTGATAATTTTTAGATCA[T/C]AGTCACATTGAAATATGCTGAAATCTATGTATTCTTTCTCTAGAAAAATGCACACAATCA
678	CCATTAAACAATTTTTCCTGAGAATGAGAAATTTCATCCAAAATCAAAGTTATTCCAAAA[T/C]CATGACTTTCAATTCCTAACATGTCGTGTTAACTTTATTATTCTTTCTTTTATAGATATC
679	TCTGTTTTTTAAAATTCTGACGAAGTGATATATTTCTATTCATTTCTAGTTACAGCCAGA[A/G]ACTAGAGAAAAATGATTTTCAGAACCAAAAATTTCTGCTTTATATTTTTGTGGAGACCTT
680	TTATATGTGCTCTTCAAATTAGCTTTACTAAATTCACCAATTTTATGTGTTTATTTGATG[C/G]ATTTTGATAACTCTACGCAGTGACATAAGCACCAAAGCAATCATGATGTAGAATGCTTGC
681	CTTTACAAGTGAAGAGGCTAAGGCTTCAAGAAGTTACATGACTTGCCTAAAAATCACATA[A/G]CTAGTAAGTGATTGTGCCACTTGTAAGTTGTGCAACTTGTAAGTTGAACCCACAATGTCT
682	TATATTGCAAGCTCTTTGTTGTAATGCCGCTCTATCTGAAGGCCTAGAATATTTTCCCTT[T/C]TCCATTTCCCCTCCTCTTTAAAAAAGAATTTTACAGCACACCAGACATGAGAGACTTTGT
683	TAAAGTGATAAATTGTTCTTTTGTTCTCAAGGTTAATTGCAGTCCCTATGCCCTGTTTAC[A/G]CTTTAACGACTCCCAATGGGAGCAAGCAAACAAACAATTGAAAATATAAATTTAATTGTA
684	CATGCACATTTTCTACATAATGGATTGTATCCCCTTTCTCTTATTTTTACTCATTACTTC[A/G]TTTACATTTAGTTTGTTTGAAAGCAAGTTCTCATTCTCTCACTCAGGCAGGAGTGCAGTG
685	CTCTTGACCTAGAGAGGCTTGCCATCTCTTTGGGCAAATCAAAACAGATC[A/G]CATACATGAAATAGACAAATAACAATAGAGGACAACGAGTTTTTGCAGGG
686	TCCAACTCTCCCACTCCACATCCAAACTGATTGTGAGGTGTATTAGTCCATTCTTAAGCT[C/G]CTATAGAGACATACCCAAGACTGGGTAATTTATAAAGAAAAAGAGGTTTAATGGATTTAC
687	AATCATTTCTGCCTTCACTTTAGATTCTGTGAGCTTTCAGGGGGCACTACTGAAAAATCA[A/G]TGCCAGGTATGTACTTAGAGAAGCTTCTGTTAATGGTTTTCCTGTTGACCTAGCCCATAG
688	GCATTTGTTTTATCAACAGATGTTACTAAGACCTCCTTGCCTGTGTGCTCTTGATAACAT[T/C]AATCTTCCTAAATTCTGGGATAGATATTGACTAAAGTTTCACTAGCCATGAGTTTTTATT
689	ATGAAAATAGAGATACTCAGAAAGGACATACCATTGCTTGGGATTCAAAGAGGACCATAA[T/C]AGCATAAACTTTGAAGCTTTCTTACATATCTAAAGGAAAGCATCCTTCCTATCACCCATA
690	ATGTGAGTAATTTCCATTTTCATTTCCAGGAATTTTTGTGTTTTATTTCAGATTACATTA[A/T]TACAGCTTCTCACATACAAAGAAGGCTTTGCTGCAATGCTGGCTCTAGAATGTCTTTTTC
691	GAGTGATATCCAAGTGAGAATTAACTGTGGGCTGCTGGCTCACACTCATCCTGTTGATCA[A/G]TGACACTAATCTACACCTCTGATATCTTTCCATTTTAGATTCATTAGAGCTATAGAACCT
692	TCATTTTCCGTTTCTCTACCTAGTCCTTTGATTCTTTTGAAACTGGCATTTTTTTCTACA[A/C]AAGACAGCGTCCCCACTTTCTAACTATTTTCAGGAGCTATTTGGAGGGTGGGTGGGGCAA
693	TAGCAGTCATAACAGCAATGTCTAGAACTCTCCGAGTGCTGATAGCCAAGGGCCCAAGAC[A/G]CAAGTACAGCCAAAGAGAGTCTGGGGCAACAGATAAAATCTGAACAGTGTTATGCAAGCA
694	ATATCATTAATTTATCCACAACCACTATGAGTAATGCCCACACCTTCACCACTCCCACTC[A/T]GACCTATATCTGTGCTGTTCTCTTGGTCACTGAACTTTTTTGTTATTACCTCAGATCCAG
695	TGATACTATGGGGAGGGAGCATAATTTCAGTGTAAATTAATAAAGTCTGAGTCTAGAGGG[T/G]TGACTATGAAGATAGAAAGGATAAATTTCATCTTACAGATATTATATGGCAAAAGTACAC
696	ACCTAGTAATAAATCATAGAGAGGCACAACCATATACAATCCATCTGGAGATGCTCAAAG[A/G]TTTCTTTTGCAATTTTATCAATGTCCCATACATTTTTTTCCAAATTAATTTAATTACAAA
697	ATTCAACTAATTCAGGAGGTCTAAGCCTACCTACAGAGGGAGAGAATATGGTCCTTTTTA[A/T]GTTAGTTGTTGAGTCTATTTCAGAACTATTTGAAAGTTTCCTAAAGTTTTTTCTTCATCT
698	CCGCTCCAACACTTTCCTCAACATCTTCCGAAGAAAGAAGGCAGGGGCAG[A/G]GAATGCCAAGTGAGTTATCTGACCTGTTTGTCTCTCTTTTCTCTTCCTTT
699	GTACTTTTTCTATAAATCACAAGGTGCAATAAAGGTTTTTGTGAAGTTTCATCATCATGT[A/G]TAAGCTTTAGGGGAAGAAACTGACTTATAGAAAGACCAGTTAATAGAGTGCCACAGTAAT
700	GCAGTAGACAAAGGTTATCAAAAAGAATGTGGGAAATAAAAGGATGCAATATTATGGAAA[A/C]CAAGGAGACCTTGTATTAATGCGCTCAGGTTGTCAAAACAAAATACCACCAACTGAGCTG
701	TCTAGAAACTGGGGATATGCCTTAGCCTTATGCATTCATTATATTCGTGCTATAAAAAAT[A/G]GAGGAGCTGTAAGTCTGCTGGAAGTGGAGGCATGCTACTGTTACTCCGTGTGAGATGTGT
702	CAATTCCAACATGTTTGTCAAGTTCCTGTACAATTCACATTGCAATGTAGGCGAAATCTC[A/G]GTACCTCTCCTGTGATCCTTTTTACTCCTTATATGTTATTAATGTTAATTCTAATCTCCC
703	TCACCCTAAGCATCTTGTACCTGAAATTCTTTTCTATGACAGGCAGCCCGCTTATGTGGC[A/G]TGACAGCCAGACAGCTTTATCCCATCACCTTCTGCAGTGCTAGCTGACTCATGGGAAATG
704	ATGTGGCACCGCCTCTCTGTGCACGTGAAGACCAATGAGACGGCCTGCAACCAAACAGCC[A/G]TCATCAAGCCCCTCACTAAAAGTTACCAAGGCTCTGGCAAGAGCCTGACCTTTTCAGATA
705	CATTGGTTCCCCAAACAAAGGAGTCTCTGTTATTCACATTTTCTGCTATGAGATTCCTGC[A/G]AAGTAGGGCATTTCCCAAGTATCACTTGAAAAGAGAATATGATGGTACAAGGACCACACG
706	ACTTCTTGGGCTAACTTTGATTGTAAGTCTCTGAACAATCAAAGCCTGTGAGGAGACAGC[T/C]AACCTTCTTATTCTTCCTATGTCAATAGTGAACAATTGCAGATCCCCTTTCCTTTCCTTC
707	TGTTTTAACCCTAAATTAAAACAAGTAAAATTAATTTGAAATATGCCAACCTTTAAAAGT[T/C]TTGTTCATTGTTTGTCTTTTGAGTAAAGACAGCTTGGATCTGCGTGGCTGTGGGATGCTC
708	TTGAACTTAAGAAAATTCAAATGATGCATTGGCTGCCTCCTATTTATTACATGCTGCTCA[T/C]AGGCATAACAGCATAGTCTAACAAGTATAAAACCTGTGTAACTGTAGCTTTCAGTGCAGT
709	CTGGATAGCTCCTTTAACAGCTGTGGCCGGTAAGCAGGCACTTATTTGCTAAAGAACTCA[A/C]GCCCATTTAGCTGGCTTCATCTGCTTTGTAGAGCTCTGTTAAAAAGAGTTCCTATTTCTC
710	TACTACACTATGTCAGCACTATATAGGTTATCTTGTAACCTGCTTGCCTGGCTATTTGGC[T/C]GAAAAATAACAACATGTAAGGAAAATCTATTTCATAAGTCTAACATTTACTTTGTAA
711	AATCATGTATTAGGAAGTACAGAGTGAATGAGTAGAGAATTTCTAAATTAGCACCCAAGG[T/G]TGGGTGGCTAGATTATGTTTATAAATATGAACTTTTGTATTAAGTGCAATGATTTAAAAG
712	GCAATACTTTGACTTATATGACAAGGATGAAATGCACAGTCCAACTCCCCAGCCACAACG[A/G]TACAAGGGAACAGAAGTCTTGTCCTGCCTTACACTCTGAGAAAGATATTGACTTTCTGCA
713	ACTTCCTTAGTCTAAATTCAGGACATTTCCCCAAGATATGTAAGAATTTAGACTTATGCA[A/G]ACAGACTTTATAAAAACATGCCAATATTTATTAGTTTGTGAATTTTAATATTCTGCTCCC
714	TAAATAAATAAATAAATAAATAAAGTAACGGATTCATTTAGTGTTTCAGAAGGATACTGA[A/G]GGGAGGGAAGGGCTGATGATGGTGCTACCTGCTGATTGTAATAGGGAAAAGCCCGTTTCT
715	AAGGGTTTATCTTGTTTGTACAATTTTCTTTTGCAAAAATAAATGATTCTTGATATGATG[T/C]AAGGACTTTTTCCGTAGATAGAACCTATAAAATGCAGAACTTTGGGGCAGTAATTATATG

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
716	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs4870062	152279311	T	
717	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs3020377	152314091	T	
718	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs3020317	152320434	T	
719	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs1884051	152324972	T	
720	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs985694	152328318	T	
721	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs1884052	152333059	T	
722	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs1884054	152333259	T	
723	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs3020407	152348954	T	
724	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs7757956	152358833	T	
725	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs9340949	152360403	T	
726	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs9340954	152361865	T	
727	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs3020368	152412883	T	
728	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs7764672	152434661	T	
729	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs13192678	152447603	T	
730	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs3778090	152449721	T	
731	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs2474148	152454597	T	
732	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs3020383	152458472	T	
733	6q25.1	ESR1	NR3A1	estrogen receptor 1	295.7	6	rs1543403	152470397	T	
734	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs2073535	21432682	T	
735	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs2282888	21442657	T	
736	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs10233357	21456570	T	
737	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs4722032	21458066	T	
738	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs3807643	21476387	T	
739	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs2282896	21479247	T	
740	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs6943809	21484906	T	
741	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs1011168	21496283	T	
742	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs3807641	21496629		
743	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs12668354	21498416		
744	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs12673091	21504592	T	
745	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs1018954	21516416	T	
746	7p15.3	SP4	SPR-1	Sp4 transcription factor	86.5	7	rs11974306	21523887		
747	7p14.3	CRHR2	CRF2	corticotropin releasing hormone receptor 2	47.5	7	rs2240403	30661727	T	
748	7p14.3	CRHR2	CRF2	corticotropin releasing hormone receptor 2	47.5	7	rs2190242	30676000	T	
749	7p14.3	CRHR2	CRF2	corticotropin releasing hormone receptor 2	47.5	7	rs2284217	30680133	T	
750	7p14.3	CRHR2	CRF2	corticotropin releasing hormone receptor 2	47.5	7	rs2267717	30683568	T	
751	7p14.3	CRHR2	CRF2	corticotropin releasing hormone receptor 2	47.5	7	rs4723002	30692226	T	
752	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2073549	86111520	T	
753	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs701332	86115570	T	
754	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs274614	86116023	T	
755	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs724224	86163556	T	
756	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs1527765	86173887	T	
757	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2189816	86179382	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
716				0.28	0.40	0.44	0.40
717				0.30	0.23	0.21	0.19
718				0.12	0.23	0.40	0.39
719				0.30	0.42	0.50	0.46
720				0.12	0.13	0.49	0.42
721				0.09	0.03	0.35	0.30
722				0.29	0.08	0.28	0.32
723				0.28	0.09	0.31	0.40
724				0.19	0.33	0.11	0.03
725				0.02	0.00	0.08	0.14
726				0.28	0.39	0.44	0.47
727				0.13	0.13	0.13	0.02
728							
729				0.08	0.47	0.22	0.36
730				0.04	0.10	0.21	0.31
731				0.36	0.35	0.38	0.48
732				0.10	0.01	0.14	0.03
733				0.45	0.46	0.22	0.44
734				0.01	0.00	0.10	0.08
735				0.33	0.08	0.08	0.11
736				0.04	0.36	0.35	0.41
737				0.07	0.00	0.00	0.00
738				0.03	0.09	0.19	0.10
739				0.02	0.16	0.48	0.48
740				0.21	0.27	0.19	0.18
741				0.35	0.04	0.07	0.03
742				0.04	0.10	0.48	0.47
743			haplotype (Zhou et al. 2009)	0.30	0.08	0.09	0.10
744			haplotype (Zhou et al. 2009)	0.31	0.47	0.17	0.21
745				0.44	0.27	0.08	0.11
746			haplotype (Zhou et al. 2009)	0.48	0.13		
747				0.08	0.11		0.17
748				0.20	0.23	0.42	0.48
749				0.19	0.39	0.41	0.47
750				0.10	0.22		
751				0.07	0.18	0.20	0.14
752				0.01	0.00	0.06	0.00
753				0.23	0.27	0.06	0.05
754				0.38	0.42	0.19	0.14
755				0.44	0.08	0.25	0.21
756				0.08	0.02	0.11	0.10
757				0.17	0.00	0.00	0.00

	R
1	**Sequence**
716	AGAGACCTAGACACAGTTCTTATTAAGAAATTTTTTAATTTAGGTGGCATATTTCAGAGA[T/G]AAATTCTCTGCTTGGGGCAATAGGTACCTCCTTTGGAATAAGCATGGTGAGAAAGAATTG
717	TTTGAATTCATCCTGGTATGCTGTGTGAGCTGGGGCTCCAATGTCGTTTTCCTACAGATG[A/G]CTCCACAGTTGTTTCGGTTTCATTCGAACAGCCTCCTACAGAAGTATTTTTCAGACTTCT
718	TGTTACAGTTAAGAAAAAAAAAATTCTAGGTATTGACCCCTGCCAGTTTTCGGAGTTAATA[T/C]TAACTAGTGATTTGGGGCTACATTTAAGTGCTTTAAGCTATCCTACAAGCTTAAAGTAGT
719	GGGAGTAGGATCCACTAGCTTGCTGCTTGTCTCTTATAATTAGGATCAAGAGCTTCTGCC[A/G]TCTTCTAGGCATTCTGCTGCTTCAAGGGAGTCTCTGAGATTGGGTTCTGCATGGATGTAT
720	TCTTCTCATCCACTCTATCTCATTACCTAAAAGGTTATCCTTAGAGCTTTATATAATACA[T/C]CCCTGAAGTTTAGATCATTTTATTGCCTCCCAATTGTTGAGAGTAAGGAATTTAGTACAT
721	TACTGGCTTAGCACAGTGCTCGGCATTCAGTAAATAAGGTTAAGGAAGGCCAGTGATATA[C/G]AGTAGTAGAAAACAGCAGTTAATGAAGGCTTGCTTTCTGTCACAGGTTCCTCTCCTCCAG
722	CCCTCCCACAAGCATATACAAATTTTATGGAAACAGACAAAAATTTGTAGGGAAGCAAAT[A/C]CCTTCAAGGTTGAGTCTTTCTGGTCTTCTAGAAGGTAAGCTTGGTGATGGGGCAGTCACA
723	GTTGTGTTTTGATGTGTGTGGTCTGGGTGAGCGGCTCAGTGCTGCTGCTGTGGAGAAGGC[A/G]TGATATGGAAGGGATGTGACTGTCCTTCTTCATCTTCATAACGGGGCCAGGACTGGGGTG
724	GCTTTCTCATGGTGTCTCCACTATGAAGTAGCTGAGCTGAGATCTCACCCAAGGCCCTGC[A/T]GGGTTCAGGCCACACTCTTAAGTACTCACAGCTGCATCACACTGAATATCATCTCCCTGC
725	GTAGGTACTTCAAATGGACAAGTATAACACATTATGACTGCTAATATGGATGCATTGGGA[A/G]GAAAATAAGCCCTAAGAAGCAATATGCAGAAAAGCTATGATTGCTGGAGACAGATAGATC
726	GAGTTACATCATCTGTTCCAAACACCCTTGTAATGGTTGTATCAGCGTCAATGTCTGAGT[T/G]GCTGTCCTGGTTCTCCTGGCCAGTCCTCAGCTGGCCATGCCTGTTCAGGCACCAGAGAAA
727	CTTTTTTGCTTTTGTCCCCCCATTTCACTGGAAATCTATCCACTGGGCACCACTGTTGGT[T/C]GGCTTCCTTTCATAGATTCCTTTATGTTTCAAATTTTAAAAAGACAATAATAGCAACAAA
728	acacgtaagtgatttctctttcaggattataaataacatttgttttgcatttttttcata[T/C]atcttttgctcacttttcattgttactttgtatatgttgctagaaattgatttgctggtg
729	AAAAACAGTTATTCAACATGAAAACTCTTTTTCAGACAAAGTTCTACAAAGTCTATTTCT[T/C]ACAAGTAGGACTTTGGCAAGGATTGTGCAACTGACAATTCAAAGTCATTTATTCCGTGGT
730	TTATACACACTAGTCTAACAATACACATTTGCTCAAGGATTGGGTTACGAGCAGGCTCTT[T/C]ACCTTTCAGGTGAACAATTACACATCAGGAGAAGGATGGAAGTTTCCTATCTATGAACAA
731	GTCGCTGAGGTCCCAGCACGGTGTGCCTTCACACCGTGCAAACAATAAGAAGAGAAGAGA[T/G]GCACACATGTCACCTTTCCAGGCAGGGACATCCAAGCTGTTTGAGTCTCCATTCTGTGAT
732	CTCATGTCCACTGACATTTCATTGGCCAAGCAAGCATGTGGGGTGTCCAGAGTCAAAGAG[C/G]GACATGTTGCCGGGGTCATGACTATTTCTGAGCAATAATCTAACCTATCATAGCTCAGAT
733	ACTCTAATTCTTTAAACATGGTTTCCTTCAGATATTTAAGCATATTTATAATAGCTACAT[C/G]AAGTCTTTGCTAAATCCAGCATCTGGGAAACACATAGTTTCTTTTGACCTCTGCTATTCC
734	CAGGAGACAAAAATGCCCAAGGCTGAGTGTGAAGCCCAGGTAAGAAGTGAGACAATGGCT[T/C]TGAGCCTGGGGTGTAAGCATGCCTTGTTCCCAAGGCCAGTATTTACATGTGGGGTCACTT
735	GTTGTAACCTTTTGATACTGCTGCTAAAGTCTATTTATAAAGGCATTTTGTGTTTTTACT[A/G]TTTGAAGTGAAAGCAGAAATATGGGTCGAAGATTCTGCACTGCTACATTAAGTCAATCCT
736	TTTAGGGGGCTTTTTTGGTGGGCATAGTAATATTGAGGTAAATATACATGCTTTGGGGTG[A/C]AATAGGTTTCTGTTATATTCTCTTTCATTGGGCCTTCATATAAGTATTGGATCCAGTTTG
737	GAATTCTGAGACTCCCAACATGCCAGGCAGGTGGCTGCAGTCATGCCAGCTGTAGTCATG[C/G]CGGCTGAGACCTGGGTGCGTGGGGTTGCTAACCAATTCCGATACATGCCCAGAATTAGAA
738	AAGAAAGAGGCCATCTGTGTGGTTTTTATGTCATTTGTCCTTTGGCTACCAAGGTTCCTG[A/G]CACACTGAAAGTACTTAATGAATGTTTCTTAAATAAAGCGAATGATAATCTAAAATCTAT
739	TAAATGTTATTGAGCACGAAAGTGAGATGATCAGAACACTACTTTTTTATTTTTCTGGCA[A/G]CAGTGTGAAGGATGAGAAAGGAGGGAAAGCTCAATTTAGGTTGGTAGAGGCACAGATTGA
740	TTTATTTTTCATTATGGAATTGTCTCTTTATATATTCTACATACAAATTCCTTATCAGAT[A/G]TACAATTTGAAAATATTGTCTCCTGGCTGGGCGCAGTGGCTCACGCCTGTAATCCCAGCA
741	CTCTGGACAAGTTTACTTATTTGTTTTCTTAAGTATCTAAATGAGGACAATGAAAAGCAA[A/T]CTATAGCAGGCAATTGAGAAATGAAGTGAAAACTTGAATTTGAATAACAGTGTATCATAT
742	GTTCTGCACTTACACCACGACTGGGACCACCTTCAGAGTAGAAGTGGCAAGACAGAAAAA[T/C]GATGTTGATTTACCTCAGATTTCTTGGAAAACAGACTCTATTTTCTAGTTCCCCTAGCCA
743	ATATATTTTGAAAAGTTAGATATATACCAACCACTACAGAGAGGGTGGGTGGAGATACTC[A/C]CCTAAATGTCTCCTATATATAGGACTGATAATTATTATAGACTTTAATAATTTTGTAAAT
744	ccaagggcaactATCTACTTTTACCCCCAGGTAAATGATACTGGAAAATGTAGGGTACTC[A/G]TGAAAAGACTTTAGATATTCTAGGCCGCGTAGGTAAGAAAGAGTGTAGGAGGGACTGATA
745	AAACAACATTTCAGTCCCTTAAGTAACAATTTTAGAGGGAAGATCTACGGCTAACAGTTA[A/T]TCATTGTGCACATCAGGATAAACCAGTTAACCAAATTTTGATATGCCTCATTTATTATAC
746	AAACCAATTACTGAAAAACAGAAACAGCTGCTCATGTGTTGTTCACTAACTTTTGTGGGT[A/T]TATGTGTGGATGATTTTCTATATTTAAAAGCATTCTCTATATTTAGAAATATATGTGTTA
747	AGAGCAGCCTCAGGAAAGCTCACTGTGGGGCCCCCATCTGGTCACAGGCCCCACCTGGAA[T/C]GACTGCAGGAAGGAGTTGAAATAGATGAACATGATCTGTGACAGGTCGTCCTCCCCGGGA
748	tcccagcctaactgtcctgacccatctccagcattctACATGGCCACTGGCATTGGCACA[A/C]ATAGGTTTGGCACATACCCTCTTTGTGTGGATCCACCACTTAAAGCACCTCCTCCTTCTT
749	TGGGTGGGAAAGGCATCCCCAGGGCCCTTTGCTGGTGCTGTCTGGGATTCAGGCCAGGGA[A/G]CTTGGATTCCATTTCTTAGTGTTATATGGACACAGCTCTCTGAGCCTCGACTGCCTGTTC
750	GGGGAGAGGTGGGAGGAAAATGGAATATAAGTGCCCCACTTCTGGCCAAACCACTTCCAT[A/G]CTAATCCACTTCCTTTCGGCCTACAGACAGGGAGACAGGCCCACAAAAGGGATGAGACTT
751	TATTGCAAAGAAGGTTCTTCATGATCATCGTCCCCCATCCTCACCCTCCTGCTTCATTTG[A/G]AAGGCCCTCCAGAACAATGTGTCACTACCAGAAACCATTCGCTATCTCTGTTCCTTGTTT
752	AGTCGGCAAATCTACCCTGGCTTTTCGTATAAAAATCCTCTCGTCTAGGTACCCTGGCTC[A/T]CTGAAGACTCTGCAGATATACCCTTATAAGAGGGAGGGTGGGGGAGGGAAAAGAACGAGA
753	TGACCTATGTGAATATTAAGGTGGTACTTTCTGAGGAATGTTCTATGTGGATGCACATTA[T/C]GAGACATTTTCATTGCAAATTTGTTTGCAACAGAACCCTGTCAACGCCCACACTACAAGG
754	TAAAAATAGAAAAGCCTGAAAAAAAAAACATAAAAAAACAGGTTTTCACTTTGTTCACTT[A/G]AAATCTTGTTCCAAGACATCCGTGTGTAGGCTTCTTTAAGATTCTTAAGCAAATATCTTG
755	TTACTATTGTCACATTGTTTTCTCCTACCTCTGACCTTCCTGTTTCTCTCTTATAAGGAA[A/C]CTTGTAATTGCTTTGAGCCCACTTGGATAATGCGGGATAATCTCCCATCACTCTTTCTTA
756	AGGAGATGACACTAATGGAAATGTAGAGTCAAAGGAGTGCAAGGCTCACATGGAAGCATA[T/C]GGATCCGGGAGCTAAGAGCCAAGTGCACAGTTGTTGAATGAGGGAGAGAGGAGAGGTTAC
757	AAGAAAACCTCAGAGGTAGTCTTAACTTCTCTCTCTCCTCAAAGTCTAGTCCTCAAATTC[T/C]GCTTACTTTACCTTTGACTTGCCCCTTAACCTCCTCTTCACTCCTGCTCTTCTCTATAAC

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
758	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2214653	86183431	T	
759	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2237548	86198886	T	
760	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2237552	86211311	T	
761	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs6943659	86233862	T	
762	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2282965	86239740	T	
763	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs6465084	86241411		
764	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs10487052	86248625	T	
765	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2237562	86260168	T	
766	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs1468412	86271387		
767	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2299222	86280340	T	
768	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2299223	86285216	T	
769	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs2299227	86289908	T	
770	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs10952891	86305187	T	
771	7q21.12	GRM3	MGLUR3	glutamate receptor, metabotropic 3	221.0	7	rs10487055	86333978	T	
772	7q22.1	RELN		reelin	517.7	7	rs737373	102902878	T	
773	7q22.1	RELN		reelin	517.7	7	rs736707	102917639	T	
774	7q22.1	RELN		reelin	517.7	7	rs2528856	102930031	T	
775	7q22.1	RELN		reelin	517.7	7	rs2528858	102938847	T	
776	7q22.1	RELN		reelin	517.7	7	rs2075039	102949958	T	
777	7q22.1	RELN		reelin	517.7	7	rs2256504	102953131	T	
778	7q22.1	RELN		reelin	517.7	7	rs2237622	102957006	T	
779	7q22.1	RELN		reelin	517.7	7	rs10487160	102962491	T	
780	7q22.1	RELN		reelin	517.7	7	rs1008126	102962680	T	
781	7q22.1	RELN		reelin	517.7	7	rs362754	102969462	T	
782	7q22.1	RELN		reelin	517.7	7	rs362719	102973113	T	
783	7q22.1	RELN		reelin	517.7	7	rs362777	102977433	T	
784	7q22.1	RELN		reelin	517.7	7	rs362721	102978664	T	
785	7q22.1	RELN		reelin	517.7	7	rs2247776	102986955	T	
786	7q22.1	RELN		reelin	517.7	7	rs2229860	102993063	T	Pro157Arg
787	7q22.1	RELN		reelin	517.7	7	rs123712	103018526	T	
788	7q22.1	RELN		reelin	517.7	7	rs362685	103034019	T	
789	7q22.1	RELN		reelin	517.7	7	rs977639	103047145	T	
790	7q22.1	RELN		reelin	517.7	7	rs362698	103064528	T	
791	7q22.1	RELN		reelin	517.7	7	rs6958081	103079061	T	
792	7q22.1	RELN		reelin	517.7	7	rs1860686	103079680	T	
793	7q22.1	RELN		reelin	517.7	7	rs727531	103088691	T	
794	7q22.1	RELN		reelin	517.7	7	rs1012065	103098311	T	
795	7q22.1	RELN		reelin	517.7	7	rs1541329	103108339	T	
796	7q22.1	RELN		reelin	517.7	7	rs12666897	103113430	T	
797	7q22.1	RELN		reelin	517.7	7	rs1858782	103131063	T	
798	7q22.1	RELN		reelin	517.7	7	rs496907	103149720	T	
799	7q22.1	RELN		reelin	517.7	7	rs10487166	103162502	T	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
758				0.42	0.01	0.35	0.32
759				0.26	0.14	0.26	0.22
760				0.02	0.07	0.11	0.02
761				0.35	0.15	0.23	0.22
762				0.24	0.15	0.14	0.14
763			p=0.009 (Egan et al. 2004)	0.25	0.30		0.13
764				0.27	0.33	0.09	0.20
765			haplotype (Chen et al. 2005)	0.28	0.28	0.16	0.21
766			p=0.00001 (Egan et al. 2004), p=0.011 (Fujii et al. 2003), haplotype (Chen et al. 2005)	0.28	0.34	0.15	0.24
767				0.02	0.00	0.08	0.03
768					0.02	0.08	0.04
769				0.04	0.00	0.05	0.00
770				0.09	0.13	0.00	0.01
771				0.09			
772				0.09	0.39		0.21
773				0.23	0.47	0.43	0.42
774				0.31	0.47	0.31	0.46
775				0.05	0.20	0.09	0.18
776				0.03	0.03	0.13	0.07
777				0.09			
778				0.16	0.09	0.40	0.22
779				0.05	0.34	0.22	0.44
780				0.27	0.43	0.23	0.21
781				0.04	0.00	0.07	0.01
782				0.14	0.26	0.34	0.37
783				0.06	0.29		0.23
784				0.45	0.16	0.16	0.23
785				0.11			
786				0.01	0.00	0.00	0.00
787				0.32	0.08	0.33	0.26
788				0.05	0.00	0.08	0.13
789				0.13	0.33	0.10	0.12
790				0.18	0.04	0.18	0.26
791				0.37	0.32	0.47	0.41
792				0.10	0.14	0.01	0.03
793				0.32	0.30	0.42	0.31
794				0.18	0.45	0.11	0.16
795				0.45	0.48	0.44	0.46
796				0.17	0.15	0.09	0.13
797				0.16	0.45	0.16	0.26
798				0.35	0.00	0.31	0.22
799				0.09	0.07	0.08	0.09

	R
1	**Sequence**
758	GAGATAAAGATCCTCAAATGTATTCCCAATGTCATCTAGAAAACTCCTAAGAAAGTCAAG[A/G]TGGGGCTCAGGGTTTATGGTCATCACACTTGACCTTCTTTAATGATAAGATGATGTAAAG
759	TCTTGGACAAATTATCCCTTTCATTCTTAATTTTCTTATTTAAAAATATTGTCAGATTGG[A/G]TTGGCTATACCTATCTCCTAGGATTTTTGAAAATAGGTTTGAGAGTGTAAAGGGTAACAG
760	TTATTAGCATCATCTTACAGATAAGAAAACAGAGATGCCAAGAGCTGTTCAAGACCCTAA[A/C]GCAAATGGGCAATGTTACCTCTCTAATCTAGCTCCTCTCCTTATGAATCCACTATACGAA
761	TTCATCATTTTCCCAATCCCCAGAAAGATTGGTTTCATGAAAACTCCCACTGGTAGAAAG[T/C]ACAAGAACTAGAACTCAGATAGATCTTTTGTACTTCTGTGTTCTTTTAACTACCCCATGT
762	GTGGGACAAAATTGCCCCCATCGTCCTCACTCCCATTCTTTACACATGTGCCACAGATGC[T/C]TTGATTTGAGAGCAGCTCTAGGGGTTCCATTCCAATTGTACTTAGACCAACTATTCCAGA
763	TTAAACCTATGATATTTTGCCTTAATGACACAAAGTTCTCTTTCCAAATTACCATTAAAT[A/G]TGTGCCTTTTTCATGGATTGATATGTACAATTTCAGTATTTCAATATGGAAAGAGCAGCG
764	TTTGTTCACTTCTGAGGAATTCTGAATTGGAATCTAAACAGGATAAACCACTTAATAATC[T/C]GTCTTTGACTTTAGCCACCCTTAGATTTCTGGCACTTGCTGAACTGCAATATTGAATTTT
765	GAAGAAATCTTACTCCCAGGGCTTCACTTATATGTGAAGAGGACAATTCCCTGTTACTGA[T/C]GGACTCATCATAACAGGACTGAATAGTATGTACAGCTAAGCTAAGACAGTTTTCTTTTTT
766	CACATTCTTGGATCATTGCACAGTGATATGTTCCTTCAGCTTGCAATGTTATAGGCAGTA[A/T]AATGATTGTTATCTCATAATGCATAAAAATTGCACTGGAGGCAAAACCAGTCTCCAGTTA
767	TCTAGTCACAGTGCCCCTCATTATCATCAGAACTTCTAGAGTTATTTCAGAGTTCCAATA[T/C]TGTTTTTAATCTTCTAATTTAAAAGTACAACATAAAAATAAATTGTATTGTGTTTCAAGT
768	AGAGGCAGAAAGAGAATTTGAATCTACTGCAGTAGATCAATGCAATACATGCACACACAC[A/T]TGCACACATATATACAACATACGCTGAGCCTACCTCCTTAGACATTATCTTATGTTGCAG
769	GATTGCAAAGGGATAGAGCGAGAGATATGAATGGTGAATGGGAAGTGGGCCAGATTGTGT[A/G]GGACTGTGAAATTCATACTTTGTGATACTTTATTATGTAGGATGTAGTTCCATGATACAC
770	TCTAAGAAAAGAGTAAAGATTGGCAGTGAAATAGAAGCACACAGTAGTAGAACAGAGTAC[A/G]TGGCATAGAAATGGGTGATCAGAGGGGTGGTGTATGTTGGCAAGACAAACATGATGAGCA
771	AGATGGGTTGTGCAGAGACATGGCTGATGCCTCAAACAATCAAACTGATTATGTATCTTT[T/C]CAAACAAGACAATTAGGCGTGTATATAAATCTTCAGAAAACTGTGTTTTTGAGAGGGCTG
772	TTCTACGTGTTCAAGTATTACATTTTCTTTG[A/T]TTACTCCCTCTATAAGTGAACTTTTTTTTTTTTACTTTGAACTCTCATAGTGCTCATTTC
773	AGACATTTGGGAAGCCCTTTTCTCACAAATAGTCCCCTCTCCCAGAGGCTGGAGGCAGGA[T/C]GCAGCCATGGAAGTAACAACCTACTGAATCCCTTCTGCTCTCTGTGGTTCTTTCAGTGCA
774	GGGACACTGGGAACTGTGCGTAAGCACTTTATTCAAAGACTCTTTATGTTTCACAAGATT[T/C]GTTTAGTCAGACTATCTGATTAATACAGTCTAGGTGCACCTGTTATTTTCTTTTGTGTAT
775	ACTGCTCATATTATATACACTCTATAGACAAAACACTAATATAAATACATTGTTTCAGGA[A/G]CATAAATACTAGGAGGATTGAGATATATGCCCTTTGTCTGATATTAGTACACACACAACC
776	GAGAGAGGAAAAGTCAACATCAGACAAAGCCCCTGCAAGCTTGTTCTCAAATTAGTGAAG[A/G]CTACTCTTTTCCTAGTCCAAGATGATGAAAAGTTACTGATTTTCAGAGAGCTTGCCAGAA
777	attcctttttgttcaacatcgtagacttcatggacagcacctagagcttagtgggtgttc[T/C]aAACGTCCAGGAAGTTCGTATCCAGGGGCTTCCATTCTCACAGTAAGCAATGTGGAAATG
778	CTGCAGACATTAAGTAGCTTCCACGGTGTGGCTAAAACCACCTGGGTTTCCAAAGTGTAG[A/T]TAATCTTTAAAGAAGGTGGTATCAGTTAGGTCATTAGGGCTAGTAGAAGGGAATAGATAA
779	ATTTTATTAAGCCCTGATCCCTTTCCATAGAGACAAGAATGAAAGGTTTTTCACATAAAA[T/G]AATGCTTCAGGTGATAATTCTCAAGATAATGTCCATAATAAAATTTTAAAAGCAGACATA
780	GAAAACAGTGGCTGCATCACTTGGCTTCTCCAACTTAATTCAGAGATGCCCAGACAAGTC[A/G]TTTAAAATAGGCCCATTGGATACAGAATAGACTGAAACAGAGTCTGTTTTCTGCTAGTGA
781	GAGACAATTACTTATTTGGGAACACCTAATAATTTCTAAATTAGAGAACTCAGCTGCTAA[T/C]AAAAATCTGAAATAAGGAACATCAAATTAAACTATATGCATTAAAGTGGGATAATGATAA
782	AAGCTAATCAACAGAACAATATACCTTCAAAGTATGCACATCTGATCAATGAACAATGGG[A/C]AGCTTCTACCTATGCTCAACACCCAAGAAATAGAAAACATTTGCCATTTCAGGAACAAAA
783	ACAAGGATCATAAACTTCTGTTGCTAAGTCCCCCACACTTTCTGAGTGAAGTCCATGCCA[T/C]TCCCCAGTATCTTTCCAATAAGTTCTTTCACCTTTTTGGTAAGCCTCTTTATATTTCTTG
784	ATTTTAAATATCCACTGATCTGCTTGAGAACAGAGGAAGAAACGTCAGGTGGAAATTTCC[T/C]CATGATAAAGTGGCAAGTGAACGATGACTTCAGGAATAAACTGTCAAAGGAGAAACAAAT
785	ATATGTCGGATTCTAAAACGTCTATCCTTTATGAGATACCAGTGTTTTGTTTATTAAACT[A/G]TCTTTTGGTTTGGGGAGAAAAATATCCAGATAATGCCAAATGTAGAATTTGAGAATTATT
786	AGCTCCAGTATTCTCTGAACAATGGCAAGGACTGGCATCTTGTCACCGAAGAGTGTGTTC[C/G]TCCAACCATTGGCTGTCTGCATTACACGGAAAGTTCAATTTACACCTCGGAAAGATTCCA
787	TAACTGTCCTTTCTTTTCTATTTTCTCTTCTGATCTTTATAGGGAAGCTATATTTTGGTC[A/C]TACAGTTGAAGTTATTACACATCTAGAGCTTTCCTCCACATTCTGTTATACATAGCGTTG
788	GTTTGCTAAAACAGTAAGTCAGTGAGTGGATGAACAGGTCAGTAAAGGGC[A/T]GCCTGCTTATGGCTTCTGTAGGTGACGGAATGAAGAATGTACTAGTAGTT
789	GTTGAAGTCCAGATTCCATTTTCAGCCCGGCCACTTGCCTGTGTCTCCTGTGGAACTAGG[T/C]CAATTTACCCAACATTCCAGATGCCAGCAGCTAATTCCAAAAACTTTAACAAATATATAG
790	TTTTATTCATAACACTCATTAAATTTATAAAAGAAACAGCATAAAGCACTTCCAATAAGA[T/C]ACCCAGAATAAATTTTTTCTAAGAACAAATGTTAAAATACATGTTATGTTCGTGATAGGA
791	GTCCAATTTCAAAATTTAACTTTCTTCCATTTTTTCTATGCTGCATTTCTCTATAAGTAG[T/C]GTGGCAATAACCACAGAACTGCCATATAGAATTTAAGTTCATGCAGTCCAAAATATAAGT
792	TCTCTTTCACTAAAGTCTGACCAGCTTTCAAAGGGCAATCAGTTAAATTACTGCTATAAA[T/C]AAACTATGTTTCAAAGACAACAAATGGTAACTTGAGTTTGTGCTCTTGAGTTTGATAGGT
793	TATTAACCTAAATTTCTCAGCTTCCTACTACAAAAGAGTTATGCAATGATGAGATATTCA[T/G]GAAAACAAAGGCTCACCTTGATGACTATTTTTGGGGGGAAGCTGGGAAAAAGAAATCGCT
794	TTCTGAATGACTATATGCCAACAGTTTAACAGTGAAGAATGGGAATTAGCATGGGGGGGA[A/G]ATTTTAGACTTTTACTTTGCTCATTTTCTTTGCAGTAAGCAAATAATTTCCAGGAAAAAG
795	TGTCAAAGCTCTGGACTCCACCAAAGCTCTTTGATCTGGGAGAGGAGTGCACTGTTCTTA[C/G]AAGAGCTAGAAGGGACCAGAAACCACTGTTTCTTTTTTTCCCTCTAGGGTCTCCCCAGCC
796	TACTAGTAGGTTACCGATTTCTAAAGTCCCTTAAGTATGGCTCTTATGTGTTTCTCTTTG[T/G]CAATCAAAAATATTTTCCTACTTTGCCACTAAATGGATTTCCTTTACTTGAGAAGCAGAA
797	ACACAAACCCTCCAAATTGCAATCCCACTATCCCATAGACTTTGGTCAGCAGAATAAGCT[T/C]TGTTCTTGCCCAGATGGAAATGGCTCCTTGATTCTGCCTAGGGTAAGATGAGGAAAGAGT
798	TACACTTGTTAATAAGTCAAAGAAAACTCTTTCATCAAAAAAACCATTATTTTTGTTTTT[T/C]CTAACACTTTACTTATGATCACACATGGACTTCTGAACTGTCTGTAAATTGTTGTAGGTA
799	AGGGAAAAATTCCAATTCTATAAAAACAATGTGCATTTCAAGGAATGTTTATCATTTTGA[T/C]GGTGAACATTTATTTTGAAAATTTACAATAACTTTTCTTAAAAACTGTTTTTTCAATTAT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
800	7q22.1	RELN		reelin	517.7	7	rs471360	103168085	T	
801	7q22.1	RELN		reelin	517.7	7	rs634500	103178645	T	
802	7q22.1	RELN		reelin	517.7	7	rs4446675	103184569	T	
803	7q22.1	RELN		reelin	517.7	7	rs694894	103184640	T	
804	7q22.1	RELN		reelin	517.7	7	rs10487169	103184694	T	
805	7q22.1	RELN		reelin	517.7	7	rs2283029	103185455	T	
806	7q22.1	RELN		reelin	517.7	7	rs663302	103185721	T	
807	7q22.1	RELN		reelin	517.7	7	rs10487172	103189479	T	
808	7q22.1	RELN		reelin	517.7	7	rs141473	103194962	T	
809	7q22.1	RELN		reelin	517.7	7	rs262340	103205478	T	
810	7q22.1	RELN		reelin	517.7	7	rs262342	103206219	T	
811	7q22.1	RELN		reelin	517.7	7	rs1510846	103208938	T	
812	7q22.1	RELN		reelin	517.7	7	rs262355	103213351	T	
813	7q22.1	RELN		reelin	517.7	7	rs1404431	103223839	T	
814	7q22.1	RELN		reelin	517.7	7	rs39327	103231907	T	
815	7q22.1	RELN		reelin	517.7	7	rs39330	103236791	T	
816	7q22.1	RELN		reelin	517.7	7	rs6465937	103240727	T	
817	7q22.1	RELN		reelin	517.7	7	rs39343	103251234	T	
818	7q22.1	RELN		reelin	517.7	7	rs39379	103266305	T	
819	7q22.1	RELN		reelin	517.7	7	rs39383	103267479	T	
820	7q22.1	RELN		reelin	517.7	7	rs1848959	103268966	T	
821	7q22.1	RELN		reelin	517.7	7	rs2299394	103299179	T	
822	7q22.1	RELN		reelin	517.7	7	rs2299395	103316276	T	
823	7q22.1	RELN		reelin	517.7	7	rs802786	103333644	T	
824	7q22.1	RELN		reelin	517.7	7	rs802787	103336960	T	
825	7q22.1	RELN		reelin	517.7	7	rs2299403	103343150	T	
826	7q22.1	RELN		reelin	517.7	7	rs10487174	103355110	T	
827	7q22.1	RELN		reelin	517.7	7	rs10487175	103360382	T	
828	7q22.1	RELN		reelin	517.7	7	rs3735630	103361697	T	
829	7q22.1	RELN		reelin	517.7	7	rs6965133	103368862	T	
830	7q22.1	RELN		reelin	517.7	7	rs7808549	103370996	T	
831	7q22.1	RELN		reelin	517.7	7	rs876425	103371937	T	
832	7q22.1	RELN		reelin	517.7	7	rs10237086	103402273	T	
833	7q22.1	RELN		reelin	517.7	7	rs10487180	103406534	T	
834	7q36.1	KCNH2	HERG	potassium voltage-gated channel, subfamily H, member 2	33.1	7	rs4725982	150268796	T	
835	7q36.1	KCNH2	HERG	potassium voltage-gated channel, subfamily H, member 2	33.1	7	rs6947240	150288142	T	
836	7q36.1	KCNH2	HERG	potassium voltage-gated channel, subfamily H, member 2	33.1	7	rs2968857	150293263	T	
837	7q36.1	KCNH2	HERG	potassium voltage-gated channel, subfamily H, member 2	33.1	7	rs748693	150302370	T	
838	7q36.1	KCNH2	HERG	potassium voltage-gated channel, subfamily H, member 2	33.1	7	rs11771844	150306843	T	
839	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs17092104	20049834		Val392Leu
840	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs903997	20049996	T	
841	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs6992927	20074325	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
800				0.11	0.45	0.05	0.09
801				0.43	0.12	0.37	0.35
802				0.05	0.03	0.08	0.06
803				0.29	0.10	0.24	0.45
804				0.03	0.05	0.07	0.09
805				0.14	0.28	0.10	0.08
806				0.35			
807				0.14	0.02		0.35
808				0.36	0.17	0.43	0.40
809				0.31	0.39	0.48	0.48
810				0.41	0.31	0.09	0.07
811				0.20	0.36	0.49	0.48
812				0.41	0.28	0.24	0.29
813				0.22	0.09	0.30	0.27
814				0.18	0.30	0.13	0.10
815				0.45	0.28		0.29
816				0.37	0.18	0.49	0.49
817				0.31	0.44		0.30
818				0.22	0.18	0.09	0.13
819				0.43	0.39	0.21	0.24
820				0.18	0.19	0.28	0.23
821				0.08	0.03	0.39	0.39
822				0.10	0.04	0.38	0.38
823				0.21	0.00	0.13	0.24
824				0.42	0.26	0.44	0.42
825				0.21	0.46	0.38	0.31
826				0.40	0.47	0.47	0.50
827				0.03	0.25	0.26	0.21
828				0.50	0.48	0.22	0.26
829				0.21	0.03	0.43	0.37
830				0.18	0.29	0.49	0.39
831				0.43			
832				0.43	0.15	0.40	0.36
833				0.08	0.02	0.16	0.17
834				0.22	0.25	0.28	0.36
835				0.25	0.03	0.00	0.02
836				0.35	0.08	0.13	0.18
837				0.30	0.08	0.17	0.20
838				0.04	0.00	0.00	0.00
839			haplotype (Richards et al. 2006)	0.08	0.00		0.04
840				0.26	0.04	0.33	0.42
841				0.25	0.03	0.27	0.23

Key appears on page 109.

	R
1	**Sequence**
800	TATTACCCAAGTTGTTGACCCTGGAGAAAGAATAAAGGTCTAATGTGGGAAGGAGGCTTA[T/C]TTTTACTGCTTATATTTTTGGATTATTTGAAATTTTAACCACATAAATTTTTAAATTTTT
801	CTAGAAGAACTTTGGGCATGTCAAGTGCAATATTTTCACCAACTGTAGAGTTCATATTTC[T/C]GCTGAATAGATGATGAATAAGTAAACTCACTTTCATGGCTGGCTACGGTGTAAGTGTGCT
802	CATTTAGTATGCAAAACTTAATGCAAGGAAAAGTACAAATTTTCCTGAAAAAGATTCACG[C/G]ATATGTGGCATAAAAATGGGCCAAAGCCTAGTAAAGTACCGGGCCTAGAAGCTTATTTTA
803	TAAAAATGGGCCAAAGCCTAGTAAAGTACTGGGCCTAGAAGCTTATTTTAATCATTTCTC[A/G]ATAAATGACCATATCAATCTAGTTTTATGTAGTCTAAACAAATTTTCTAAGCCCGTAGGA
804	TTTCTCGATAAATGACCATATCAATCTAGTTTTATGTAGTCTAAACAAATTTTCTAAGCC[T/C]GTAGGAAGTTCACCATCTTTTCCACATTTACTGAGGTAAATGCACCACGGAAAAATTAAA
805	CCAAAGGTGTGCACAGAGGGAGATGCACTAGGGATGGGAACCCTGCTACTTGTCAGAGGA[T/C]ACTGAATTGAAGAGAGAGGAAGATAGGCTGGAGTTGTTCTGTACCCAGAGAGATCACTGT
806	TTTTCAGAAGTGAATATTTTTTCTGTAAGGTAGGATGTTCAACTAGGAATGAATGTTCGG[A/C]TAGGATGAATCTAGGAATATCCAATTCTGTTAAGAGTTCCCTGTTAGAAAGTGCATGTGA
807	GTGAGCCACCATGCCTGGCCAAATTTTAATTTTTAAAAAATTGTTACTGTGTAGCAACTT[T/C]TAAAAATCCTAGACCTTTGAGAACTTGAAGAGATGAAGTTCATAGATGGAGCAGATGTGA
808	AGTATATGTGTTCTTTCCAAGGTTTTCAGGGAATTTAGGCAGTAGTGATAATCTTGTTTA[T/C]TAGGGCTGTGGTTCCTGAGGGTTTTTAATGTTTGATCTTTTTTTAACTTTAAGAATCTAC
809	CATCCTGATTGAATTGTAAGTAGACCCTAGTGTCAGTCCCCGTGGACCCAAGTCTCTGAA[A/G]GTAATCTGATAAATTAATCCATGTTGAAGTGTTAATGGGTGATATCACTTCAAGCTAACA
810	TCTTATTGGTCCACAAGCCTACTTGTCATTGTGCCAGCCTATGCTCCCATGAACACGATC[A/G]GCCAAATTATCAAAATAAGATTCAGGTAACAGAGGTTTCACCTTTTCTCTAAATATCAGA
811	AGCCATCCGCACTGCACTCCTTAGGGTGGGATTAATGTCAATATGGCAAGCCTATTTGAA[T/C]GTATTTAGAGCTGTCAAATAATTCATGGTGGTTTACCCACAGAATCACAGCATTTATTTC
812	CAATTTTAAGGTTCAAACAGCAGATCTGGAATCAGAAGATGTGGGTTTGCACCACAGCTC[A/T]ATGATTTATGTTGATCTTATATGAGTGTTAATTTTCTGAGATAGGACTAGAAATGTTGTG
813	GTAATATGGAAATCAGTATTCTGTATGACCTAATTTAAAGGGATAAGTGCTTGAGTACAT[A/G]CACTCAGTTCAGTGTTCCAAAATAATTTACTGCATATAACTCCAGGGATATTTAAATTAT
814	ATCAATCATGCAGGTATGTTAGACATAATTTAGAATAATTCTTATATGTACTTGAAATAA[T/C]CTTACTTTTAACCCCAAACTGAATCAACTTTTTAAAAATTTTCCATAAACAAATGCAAGA
815	TCCCTCAGAATTGGAAAGGCAATGCTCCTCAGAATTGTAATGCACTGACTTCTAGCTTTC[A/T]GTGTGGCTTGAGAAGCCCAAGGCCATTCCCATTCTTAACGCTTTCTAGGGAAGAAACTTT
816	CCAGATACCTTTTAAATTTTGTCTTATTCTTCATCGGTTTTTTGCAACAAACATCTCTCC[T/G]TTTAGTATCATCTGAGAACTTAATTAACTTGCTCTTTTCCCTCTGTTTTAGGTCAATGAT
817	ACATTAGTGTATAATTTGGAGGGAAAAGGAAATCAGTATTAAAGTTTTCAAATGTCATCA[A/G]ATTATTTTGCAAGAAGGTTATGGGCTCAGTTGACTGTTAAAAATGTAAATGTAAAGAACA
818	GGACTTTGTTTTCCTTTTTGGCCAGGCAGACTCCTGCAGACTTGTCATTTTCCATACACC[T/G]GATCCCTGCTTTATGCCTGACCAGAGGGGAGTGGCAGCTCCTGAGTCACGCTATTGAGTC
819	tgcttcataaatattaacttatttaaggcccttcacaaccctatgaagtaggagtgttac[A/G]ttcttcattttactaattaagacactgagaaaatagagtgatatggtttgatactatgtc
820	ATGATTTTAAAACATCCATACTTTATTAAAGGAATCATGGCTTTACAGAGTGATATTGAT[T/G]GTTGGTACAGAAATTACAGCAAAGTTATGATTCTTTTTTAAGATGTTTGTACACAATATG
821	TAGATCACAAAATCTTTAACTACCAAGAATGTATTTCCCAAGCAAGAGACTACATTTGCC[A/G]TATTAATAGGACAGTCATGGATTTTTAGGTCTCTAGTTTCAGAGGAAGCATGACCACTTT
822	ATCATTTAACAAGGTTTCTAAGGACCATTTATTTAGCATTTTGCTAAAGAGATGGCCTCA[A/G]AATCTAGTAAAGAAGACTCCCTGGCAGAGCCACTACTTGCCTGTCCTTGGCCTTCGTAGA
823	GTTTTAATAGAGGAGGTAAGTATGGAAGGGGGCCCTAAAAGATGGCAGAGGATTTGCCCC[A/G]GAGACCGAGCCAGAAAGAATTCCAAGGGACACAAACAAGGGCAGTAGACGTTTAAAAGAG
824	CTGCTGCTAATGCCCTGGGGAGTATGGGCCTTGGCGATAATTAGCAAGTTTGTAATAGGT[T/G]CTACTTAGTCTTAATGTGAAGGATAATGAAAAGTTAGCATACAGGCCCTGCATTTCTATG
825	TCTTTCCAATAGAATAGAAGTCCTCACACTTTAACATGGATCAACATCACCTGGAGTGTT[T/G]ATTTCAAAAAATGATCACAGGATCCCACCACTAGAATTTCTGATTCACTGTGTTTGAAGT
826	TGCTGACATCGAAATTCACAAAATAAATGTTAAATTCACAAAATAATGTCAAATAAATGA[T/C]GTTCAGGTACTAGCACAGATAGTTGCTCTAATATGCTACAACTGAATTCTAAGATTTTCA
827	TGGAGTCAGAATGGCTAGCAGCAACAGAAAAGGGCACTTCACTGACATAGGATTCCCATT[A/C]ATCTAGAGGCAAaagcaagctaccaaagtgggcaactgaaacttaatcatcaggtaaaac
828	GTCATGGTATGGATGAAAAAATAGGCACTATTGAGAACACTTAAAGAACAAGAACCGAAG[A/G]TTTTTGGCTGTTTCTCATCATCTCATGGAAAGGTGGGCAGGGATCAGGGTGCCACAGAAC
829	GACACGAGACTGGTACAATTTCTCTAAGACATACTACCCCTCAGAAGAGCTTAGACTTCC[A/G]TAACTGTCACCTTGGGAGAGTTTTAACACATCTAGAAAAAGAGAAAGATGTATTCAAGTT
830	CCAAGTTGGAGATAAGATGGGACACCACTTGTATTAAAATTGTGACAGCTGCCCTGAGCC[A/G]GAAACACATTTACATCCTGACCACCGGCCTGTTAGAATAATCATGTAAAGCTTTGTGCAG
831	GATCTAGGAGTCCCAGTCACTGTTCACCTACTGTCCTCCACACGCCTAGTATTTCTATGT[A/G]GAAAAAAAATCAGTTTTTTCTTATGATTTATTCTTATTCTTATGGTTTATTAATTAATTT
832	TCCTTGGAAACATTCATGTTAATTTCCATAAGTTTGGAGCCTCCGATCCTCTTAACTTAT[A/G]GGATATCAATACATGTAATTTAATGAAGATGCAGAATTCTCAGCTGCTGTTCCCTTTGTA
833	CTGTTAACAGTCTGGCATAAACCACTTACATTTGAAATAAAAATTCTAAAAGTTGTAATA[A/C]CTGCATCAGGTGAAATCACGTTAGTCTCATGGCTTCCTACCCTCCCCACCCTGGAGGCTC
834	TGTCCACCACCAGGGGAAAAGGTAGATCCCACAGACCCGAATCTGGAACTGCAAAGCCCC[T/C]GGTGTAACCTCCCTCAGCCTTGACCATCGAAGGACAAATGAACAACCACCCAGAGGACGG
835	TCCTCCCTATCTCATTTCCTCATATCCTCCCAGCACCTCTGCCTTTCCCTCAAGCGAGGC[A/G]CTGTAGCACAGTGCTTAAGCCCACAGACTTTAGGCCTACGATCTCTGGGTTCATAGCCCG
836	GCAGCATCTCCAGACAGACTCCTCCACCACCCCTTCCAGCCTGAGACCCAGCCAGCAATC[T/C]ATGGGATCATTTATAGGGTCTTGGGGGCCGCTGTAGTCATCTAGACCCACCCAAATCCAC
837	CCCTAAGGTAGATAGGGGCCTGTGCCCGGATGTCAGCGCACAACTGCCAATCTGACCTTT[A/G]ACCTCCATCCACGCACGTACCTGCCATCCCAGCTCGGTCTAACTCTAGTCCAACTTGCTC
838	CCTCGAAGACGAGCCCGGAGTCAAGGGAGACCCTGGAAATAGGAAAAGCAAGACAATCTG[A/G]AGGCCCCAGAGCAGCAGAGCTCTGAAATAAGGGAGGGTTAAACTTAGAAGGGGCACGCCC
839	AGTCCTGATGACTCTTCCTCCTTCCCCATGCAGGTTCCTCTGGCTCACAATATTTTTGGT[C/G]TCATTGGCCCCAATGCAGGGCTTGGCCTTGCCATAGGTAAGAAGTGCCCTCAAAGAAAAC
840	GCGCTGGTCAAGTTTTCATATCCTTAAAATGGAGGTATAGATTCTTTTCCATGAGAAAGT[C/G]TGAGAGTGCAGGAGGATGATGTATGTGGCCAATAGTGCACTCTGAATAAATGCATTTCAT
841	AGTGAAAGCATGTAGCTTGTCAATTAAGTTGTATGAGGGAGGAGCCTCAAAGAAAGGGTA[A/G]TTTTATCGTTTGGGGCTTGGGTTTCCAAGCCCAGAAAATCGGAGTCTGTATCCTGGCTGT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
842	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs1390938	20080993		Thr136Ile
843	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs2270637	20081107	T	Thr98Ser
844	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs2270641	20082746	T	Pro4Thr
845	8p21.3	SLC18A1	VMAT1	solute carrier family 18, member 1 (vesicular monoamine)	38.4	8	rs7820517	20088916	T	
846	8p21.3	PPP3CC	CALNA3	protein phosphatase 3, catalytic subunit, gamma isoform (calcineurin A gamma)	100.0	8	rs7837713	22375143	T	
847	8p21.3	PPP3CC	CALNA3	protein phosphatase 3, catalytic subunit, gamma isoform (calcineurin A gamma)	100.0	8	rs2443502	22396444	T	
848	8p21.3	PPP3CC	CALNA3	protein phosphatase 3, catalytic subunit, gamma isoform (calcineurin A gamma)	100.0	8	rs2469749	22413543	T	
849	8p21.2	EBF2		early B-cell factor 2	200.8	8	rs4568629	25785669	G	
850	8p21.2	EBF2		early B-cell factor 2	200.8	8	rs10106488	25793729	G	
851	8p21.2	EBF2		early B-cell factor 2	200.8	8	rs11781208	25796328	G	
852	8p21.2	EBF2		early B-cell factor 2	200.8	8	rs10503779	25799345	G	
853	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4281084	31614916	T	
854	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7819063	31618950	T	
855	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10113797	31629879	T	
856	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7840792	31632615	T	
857	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs9297175	31660834	T	
858	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4403369	31664440	T	
859	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4733271	31686548	T	
860	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs12155594	31726137	T	
861	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1827536	31732659	T	
862	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs13270788	31750525	T	
863	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503888	31753095	T	
864	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503889	31762338	T	
865	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10087212	31773072	T	
866	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2062817	31781972	T	
867	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10081404	31794013	T	
868	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6987310	31795172	T	
869	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs776401	31836504	T	
870	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503895	31853189	T	
871	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs776387	31857593	T	
872	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1875722	31879970	T	
873	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs884530	31889125	T	
874	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1481625	31899469	T	
875	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7002063	31923076	T	
876	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1462878	31945845	T	
877	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs327325	31988398	T	
878	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10954818	31995681	T	
879	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1462906	32016134	T	
880	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10954822	32026808	T	
881	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs956203	32030300	T	
882	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs9297185	32063570	T	
883	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503899	32066776	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
842			haplotype (Richards et al. 2006)	0.25	0.03	0.27	0.22
843			p=0.010 (Richards et al. 2006)	0.23	0.25	0.24	0.20
844			haplotype (Richards et al. 2006)	0.37	0.11	0.34	0.27
845				0.13	0.25	0.32	0.34
846				0.08	0.09	0.05	0.13
847				0.49	0.14	0.36	0.31
848				0.32	0.17	0.39	0.32
849				0.48	0.09	0.42	0.26
850				0.49	0.36	0.16	0.14
851				0.49	0.08	0.16	0.16
852				0.33	0.10	0.24	0.14
853				0.23	0.21	0.26	0.28
854				0.19	0.35	0.01	0.01
855				0.47	0.38	0.22	0.29
856				0.01	0.42	0.02	0.04
857				0.01	0.45	0.00	0.00
858				0.13	0.35	0.08	0.18
859				0.23	0.37	0.08	0.16
860				0.19	0.00	0.00	0.00
861				0.01	0.10	0.00	0.00
862				0.41	0.15	0.15	0.21
863				0.07	0.00	0.00	0.00
864				0.10	0.00		0.00
865				0.32	0.49	0.08	0.17
866				0.28	0.05	0.21	0.34
867				0.01	0.06	0.00	0.00
868				0.17	0.02	0.01	0.01
869				0.27	0.21	0.03	0.14
870				0.28	0.06	0.07	0.16
871				0.45	0.48	0.11	0.30
872				0.34	0.03	0.21	0.34
873				0.09	0.38	0.03	0.00
874				0.23	0.14	0.03	0.14
875				0.23	0.08	0.18	0.27
876				0.20	0.33	0.30	0.39
877				0.33	0.37	0.26	0.38
878				0.29	0.06	0.24	0.36
879				0.02	0.17	0.00	0.00
880				0.15	0.00	0.44	0.47
881				0.38	0.05	0.22	0.36
882				0.29	0.33	0.26	0.33
883				0.48	0.02	0.09	0.09

Key appears on page 109.

	R
1	**Sequence**
842	AATGGGTTGACCAGAAGTTGCATCACAGCCTTTGAAGCAAACAGAACCCCGACCCGGGTA[A/G]TCTCTTCCTCCAAGAAACCTGTGCCTTGCAAGCAGTTGTTTTTATGAGCTGAGATGGCTT
843	ATGGCTTCAGTGGCTGGAGGTGGGATGGTGCTGGCAGTGTCATTCATCCATGCTATTCCA[C/G]TAGGTACGCTTTCTTCAACAGCCACGGTGTTGTTGTTGAAGAAGGAGAAGATGGTGGAAA
844	GCACCAGCTGCCGGGACGCTCTCCCCTCCTTCAGCAACCGCTGGGGAGCATCCAGAATGG[T/G]CCGGAGCATGGTGATGGCCGGACTGGGGCAGTCTTCCCCTGCGGGCTCTTAGGGAAGGTC
845	GTGGTTGGCATACAACATCCTCAGACGGACAGCTTTTTCTCCGGGCCAAATAATATCTAT[A/T]ACCCAATTACATGTACCCTGGGCTGTGGCTGACATGGCCTGGCAGAGGAGACGGCCCTGT
846	AAAACATCTGTAGTCAAAAATAAGTTACACTGATTTAGCTTGCTGCAGGAAGGAATAACA[T/C]ACATCAGAAGAGCTGTGGGACCTCTCAAAAGGATAGAGTTAGGAAAGAGGACATACAGGA
847	AGTTATAGGAGCAGATGAAAAAGTTGGAGAGAGTCACCTTCTAGCCAAGCAAAAAGATAC[A/G]CTTTTTCAAGTGGAGAAAGAACAGAAGGGAATAATATATGACTTGCAATCATGTACAGTG
848	ATTGGTTGAGTTCATTTGAATGAATGAGCATCTGTGATTTGTATGTTTAGAACACACTCT[T/C]GAAAAAGAATTTCTGGGTTAGGGGGCAGGCACATTTTAAAGACTTTTGGCATACTCTAAA
849	CTTAACAATTACAGCCTTGACACTGCAGGCTGGAGGTCATTTATGCTCTTGACCAGCAGG[A/G]GCACTGATTGCAAAGATGGCAACATCAAGGCCTGGTTGCTTTTTTTAAAAAAAATGTGAG
850	GCATATTGACACACAAACATTTTCCTTTTACGTAATCACATCTTTTGCTTGATGGTGCCT[A/G]TCTTTGGCCTCAATGTTCACAAGTCTCAAAATGATAATTATTCTTTAAACCTGTAATCTT
851	TCTCCAATAGCCTGAGCATAGAGCTCAATGTTGAGCACAGAGTGCACTGCTCAATAAATA[T/C]ACACGTCATGCAAAAGTCGTTAATGTCTCAGCACATGAAGAAAACAGAGATATTTTACGA
852	agcagcatgaaaacggactaatacaCATGCCTAGCACATGTAGGGTAAGTTCTAGTTTAA[A/G]TACAAAATGCATTGCCACAGCTGTCAGACAAGCTTTTGGTCCTGCAGGAATGTGCTCACC
853	AAATTGCCAACTTGCAGAATCTTGGGCTAAATGAACCAACAGGTCACCAAATGTTGAAGT[A/G]GTTTGTCATATAGTGACAGATAACTGATACAAATCTGGAAGGTAGAGAGGAAGAAAGTGT
854	AGCAGAGTCTGCCTGTGATGGAGAGTGTGTCAGTTCTTTTAAATTTGTGTCTGGTGGGGG[T/C]CAATTATTTAAATTTCTGGTTGGCATTTGTGGTGGTTAAGTCCTGCTGTTAATTAATACC
855	AATATGATGACTTAGAGATATGTTTATATTACATTGTCAAGTGAAAAGTGTTGTATAATA[T/C]ATGTGTGATTGActtttctttctttgcttttccttttcttttctctttctctctctCTGT
856	GAAGGTGAGGAATAGCAGAAAGGACAGTCAGCACAAAGGAAGCAAAAATGGGGTCTGAGA[A/G]GTAAGGAACAATCAGACGATTCTAGACTTCCAGGATTCCAGATTTTATCTTAAAAACAGG
857	tgtaggttcatttattgcaacaaaggtaccactgtgctgggggatgaccatcgtgaggga[A/G]gctgtgcatgtgggtggggcaggggctatatgggaactctcactactttctgttctatgt
858	AAGCAAACAAACAAACCCCAAAGAATAGTCAAGCAGCTGAGACATTCAGTAGCCTTGTAG[A/G]CAAAACAAGACATATTCTTATTGTTGGAGTATAGTTGTGTAAGGCCTGTAGCCCCTTTCT
859	GTCTTTATAAAGTTTTGATATTAGTGTTACTCTTTTTTGTAGAGGAAAGAATAATTTTTT[A/T]AAATTTTTCCTTGTTCTGGGGCTATTTTAAAATGCTGGAATTCACTGTTCTTTAAAAATG
860	ACATTGGAAGAATGGTTAAGTAAATTGTGCATTATACAATACAATGCAGCATTATGCAGC[T/C]ATTAAAAACTATGTTTATGAAAACTTCTCCATGACAGAGGATAGTACATAAGTTTAAATG
861	CAGGTATATTGGTTAATCATACATAAAGCCCTAGGAAGCAGAGCAAGGATTCATTAACCC[A/G]CAGGCAAGGTTAAATAAAGTACTTCCTGAACACAGTGAGGTTCAAGAAACACGTTATTTA
862	ATCAAGGACTACCGTAATTTCATACCAGGAAGAAAACTGTCAAAATATGTCATGAGTCCA[A/G]CTAAAAACCTAGCTCAAACCATCATAGTCTCTCATCCAAACTACTAAATTGACTTCCTAA
863	TCTTTGTGTTTTAAAATGTGTCTGATGCTGTCTTCTTCATAGTTTGTTAGGAGCACTAAA[T/C]GAATAGTAGAAAGCCTGCCAGAAAGTGATTTAGTCTGAATCTATAAAGCTGTTTCTGAGC
864	TAATTCAGAAGTGCACACAGGACTCCAGGTTTGAGTATGGGAGTTGTCCTTCAAGGATTG[A/G]CAGTTGAAGCATTCACCAGAGCATGGATGTGTTTTCTGAGCAAGAGCTGTCAATAATTAG
865	GTAGACACTCAAGAAATTGTATTCACAGCATAAACATGTTTATTGTTGTGGAGTGATTTT[C/G]TATGAAATGTTACAAGGAAAATATATATTTTAAACCAACAAGTAATCTTTGCAAAAAAAA
866	GTCTCAGCAGTAACAGTCCCAGTAGTAACAATGGAGAAGCATTTCCTTTCTCCAATACCA[T/C]AAATGCATGATGGGATGGGTAGTTTTCTATCAACTTGGCTAGGCTATCATGTCCCATTAT
867	ATTGATTTAGATGTTATGAAAATTAAATAAGTTCCAAAAGGCAGAAGATAGGCTATACAC[A/G]TATTTTTAAAAATTTGTCATTGTTCAAACAATATTGAATATAAAATTGAAATGTCCCTCA
868	CAGCAAATACGTAATCCACAAGAATGTTATAAGAAAGATATTTATCAAGCCTCTAAAAAA[A/G]AAGAAAGTAATCAAAAGATAAGGATGCATAAATATCTTAAGACTACTCATGACATCAAGG
869	GTGAAGCTGTTATTTTCATCACAATGTGATCTATACCTAATGATTACATTACCTGTACAT[T/C]TGAAGCTCGTTCGTAAACCATCGTCCCCTGAGAGTATACCTAACATAGGAAATACTATAT
870	GGAAGAAATGAATTGATCACAGAAGCATCTAGAGCTAGGACCAATTAAAAGTCAGTTAGT[T/G]TATATGACCTATTTGAAGATTTCTCAACAATCTTGACCTATTGCTTAAGAGCACAACATT
871	AGAAATGGGTCTAATAGTACCTATCACACAAGATTTTCTGTGAAGATTTTGTGAGATCCT[A/G]TATATTAAGCACCCAGTGCATAGGTGTTCTCAATGTTAAATCCCCTCTCCATGTCTGAAC
872	ATGAGAGGGAGAACAAGGTAGAAGTTCTACTCCCTTTTATGACCTGGACTGTAGCATTAT[T/C]CCTGTTACGTTCTATTGGACGAAAGTGAGTCACTAAAACTGGTCCATACCTCCCAATGGA
873	AAATAAGGTATCATTAATTGAATGCCTCCTCTAGGTTTTAAGCCACATCATtttaacact[T/C]acaacaagtctatcaggtaggtatgatttttaccattttcagataaggaaattaggggtc
874	AAGGTAGATAAAAGTCATTTAACCACATAGTCCACTGAGAAGAAAATCAAATGAGGGCTG[A/T]TTTATTGATGTATATTTTGGACATCCCTTCTCAATTCCACATTTAGTGACATCATGTTGG
875	AAGAGAAGACCTTCTGCAGACATCTGTGGAATTTCTCTGGGCTGCCCCCACAACTCGATC[A/G]CCATTGTTTTATTTTACCTTTTTGGTTTTTTGCCTAGTGTTTCATTCACTTCCCTCCATA
876	GAACAGCTTCTCTTATCGTGTCAATTGCCACATTTATGCCAGCTGGTTGCAGAAGTGGCA[T/C]ATCCCTCAAACTAAAAACCAGGGCCCACTTTGATGCTGCTATACAGATAGAAAAAAACCA
877	GGATACGTAAAGGCTGCTGCTGTTGCTTTGCGAATTGAACATGAACGTGCAAATGGAACC[A/T]GCCTCTTGAAGGATGCTCTAAAACCTTGGGCTTGCTAAATTGGCTGTCATTGTAAGAAAA
878	TAAAATGCTTTTTATTTTCATCTATTTTCTTTCACACAGCAGTACTTTATCTTCTTTTAT[A/G]TTCCACTAAATGTATGAAATGTATGTTGTTTTTTCACTGTCATGTTGATGGAGATATGGG
879	AAGCTGGAACTGTATGGTTATATTCACAAATTCTGGGATGTTTGTTTTGGCTTTGTGTTA[T/C]AATTGCAGCTACGAAACTAAAAGTGAACAAATTGCTTTCTCATTTAATTTCTTTTTATCA
880	GAGGAAACAAATTTAAGGCAAGATTCTGAATGACAGTTCTGTATTCTACAAACCTTTGCT[A/G]ATGAAAGGGAAGATGATGATTTTCAATGTAGGTCATGGCCTGAAGTGGAGAATTTCTGAA
881	GCCTGGTATTCTGACTAGCCCTGAGGACTCATGGCAAGTGATGAAATGGACACAGCCCTC[A/G]CACACCTTTTGGTCAAATATGGAGACTTAGCGGCCACAGAGCATCATTTCTAGAGTCAAT
882	AGCTCTGGGAATGTGAGCATCAGTTATGAATATAGGTCATCTCAGTTTGTGCACAGCACA[T/C]TTTCTGTCAGTCCAATATAAACTTGTATGAGTAGATCTGTTTATTGTGATAACTACAACT
883	GATATAGAAGGAAGATTGAGTTTAAGAGTATCAGCAGCAAAGTGACAGAAACGCTCATAC[A/G]TTAAAAACTAAAAATTAGACTTAATTGGTTATAGGTGGGAGGAGCCTATTACTTTTGGTG

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
884	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs11776959	32068406	T	
885	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs9297186	32079918	T	
886	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1481756	32086787	T	
887	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1481762	32110769	T	
888	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1481763	32113352	T	
889	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6468085	32120207	T	
890	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1383964	32123716	T	
891	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4733299	32136282	T	
892	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7002832	32173915	T	
893	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10110401	32175992	T	
894	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7001060	32186009	T	
895	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6468090	32195591	T	
896	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs12549243	32200083	T	
897	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs11782156	32216518	T	
898	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1351510	32223600	T	
899	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs12680804	32235936	T	
900	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1531746	32238717	T	
901	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1159631	32244856	T	
902	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1481758	32251340	T	
903	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7822564	32252424	T	
904	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs901561	32263004	T	
905	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs11782374	32269498	T	
906	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503903	32272475	T	
907	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7818821	32272706	T	
908	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6468095	32284018	T	
909	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503904	32284229	T	
910	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7005124	32287272	T	
911	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503905	32287870	T	
912	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4317533	32290309	T	
913	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503906	32291504	T	
914	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503907	32291552	T	
915	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1545961	32292898	T	
916	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1386440	32297073	T	
917	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7010701	32301673	T	
918	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1948098	32304474	T	
919	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2008626	32308921	T	
920	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1565031	32320677	T	
921	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10091429	32324547	T	
922	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs1714420	32340954	T	
923	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7834123	32342748	T	
924	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6468099	32346583	T	
925	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6992907	32347468	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
884				0.44	0.16	0.24	0.17
885				0.08	0.38	0.21	0.34
886				0.42	0.36	0.22	0.17
887				0.45	0.22	0.39	0.48
888				0.46	0.25	0.09	0.08
889				0.13	0.17	0.18	0.28
890				0.45	0.19	0.11	0.11
891				0.07	0.00	0.23	0.29
892				0.08	0.00	0.00	0.00
893				0.01	0.14	0.03	0.02
894				0.09	0.13	0.27	0.29
895				0.22	0.02	0.47	0.49
896				0.07	0.06	0.21	0.28
897				0.46	0.28	0.14	0.18
898				0.30	0.02	0.40	0.49
899				0.13	0.30		0.21
900				0.37	0.04	0.25	0.33
901				0.03	0.00	0.00	0.00
902				0.20	0.07	0.50	0.43
903				0.38	0.13	0.19	0.14
904				0.38	0.02	0.15	0.18
905				0.08	0.00	0.00	0.00
906				0.07	0.04	0.01	0.02
907				0.23	0.39		0.08
908				0.17	0.14	0.16	0.24
909				0.09	0.00	0.07	0.10
910				0.43	0.11	0.14	0.14
911				0.07	0.00	0.09	0.13
912				0.41	0.28	0.31	0.40
913				0.17	0.02	0.14	0.07
914				0.37	0.23	0.16	0.19
915				0.38	0.04	0.35	0.40
916				0.31	0.33	0.24	0.26
917				0.12	0.33	0.00	0.00
918				0.35	0.22	0.22	0.19
919				0.04	0.23	0.00	0.00
920				0.15	0.18	0.05	0.10
921				0.35	0.33	0.47	0.32
922				0.08	0.31	0.46	0.41
923				0.08	0.21	0.00	0.00
924				0.29	0.28	0.01	0.01
925				0.43	0.48	0.33	0.26

	R
1	**Sequence**
884	AAAAAGAAGTAATTGGATGAGGTGATTTATGTAATTCCTACAACCTCTCAGTGCTAACAA[A/G]GCAACATTCAATGACATTTACAATGATCATGGTGGCAAGTTGGGAGAGAGAAAGGGCATT
885	TTAGTGGGAGTAATAGCATTGAATGCCCTCCATGCTCACTGGAACTTCATCCACAATTAC[A/C]ATGTCTTGGTGGCTTTCTAAGTTTTTTTTTAATTTTTAATTTCTAATTTTTGTAGGTACA
886	TTCCCTGAAGCTTTCTCATCAACACCAAGAAGCTGAAGGGGAAAATGAAAGTTCCCCTTC[A/G]GTTCCCCTCAATTCAAGAGTAATTGAGACCAACATCATTCATGGATATTAATAATATGAC
887	TACGAAAACTAGATTTATGAAAAGGCCCATGGATTTTACATCTATTATATCATCTCCTGT[T/C]GGTTTGAGAATGAAATGTTTGTTTTGCTAATATGTTTTTCTGATTAAGAAGTGGAGGCAG
888	ATATTCAGATTCCTTAAGCGCATGGTTCCTCTCCTATAATACAAACCTCTTGCAGGTACT[T/G]TTGTCACCTGGCCCTTTTCATATCACCCTGTGAGGAGTGGGGCCCAGAGAACCTACACAA
889	AAGTCAACTGTTGGTCCACCAGGCCTCTAAGCTGCAGCCTCTGTCAGCTTGGGGACAGTG[A/G]GATCCATGTGACTTGCCTGCTACTGCCCTTGATTGGGCAGATCACAGAGCAGATGGCCTG
890	CACAAAAGGGTTGAGACCTTTAATTAATCAAAAAATTGACCATTCCTTGAACCTTGATTG[T/C]TTGGTATCATTAACAAAGGACATGAGACAACATGTTCAAGCTTTATAATTTGCTGGAAAT
891	AGCTTAGCCACGATCGTATAAAACAATAAATGTTGGTTAATTTCTAAAGTACATTGATTG[T/C]TTTAGTTTTTGTTTTAAGAAAAAGGCTTGGCCGGGCGCGGTGGCTCACGCCTGTAATCCC
892	GTCTTAGGCTTCCTCTTATAGTCTAGCATGATATTATTCTATTTCATCTTTTTTTATATG[T/C]TTGCTCCCTTGAGTGTTTTAGAATGAGACTGCTAGATTTTATGTTTCTAAAGCTGGTTTT
893	ATATATCTTAATATATATATATATCTTATTTATATGTCTTATTTCATTGTTATGAAAACC[T/G]AGCTTTCTTTCCTTCTATCCTTTCAATATTATGCTACTTGTATTTAGTATTTACATTGTA
894	ATTTTTGTTTTCTTATACATACCTTCCAATATTGTCCAAATTTTCAATAATAAGCATGCA[T/G]AGCCTAATATATCATGTAGATGAGTGCAAAATGAACACAGAGATTAAGATCATGGGCTTT
895	TAAAGTCTGATAATTTAATTTGTCTAAAGTTTTCCTTTTAACACGACCAAGAGTCACAGA[T/C]TGCTTAGTCTGGAGAAGCTACTCTTGGCTCTATGCAGTCCACAAAAAATGACATTTAGAA
896	ATCAATCAAAGAGAGACAATGGCATTCTCTCAAAGATCAGATGTTTTGTAGTGCAACTAT[A/G]TTGTTCTGTTTTTCTTTACTTCAATTATCAGATAGACAGGAAAAAATACAACAAAATAGC
897	AATGTTAAGCAATAAAACTTTAGGAAACAAACAGGAGAAAATGATGAGGACCTAAAGCTA[T/G]GTGAAGAACTTCTAGACTTGATACTAAAAGTATGATTTTCATTTTAAATGAATTTTAAAA
898	AATTTTGCTTTGTGGTGCTTCCCTGAAAGCTCTTACAAATCTAGCTGTAGTGCTTTGTCT[T/C]AACAAAGGATTATCTCAGAGCCCCATGGCAAAGCTCTATGCCAGGTACTTTTCATTTGGG
899	AGCCAAAACATATCAGGTACAAACAAATAGTGGAGTTAAAAATCAAACATGGACCATCTG[C/G]CTCTGTAGTCCAGGCCCTTAACCACTACATTATATAACCTCTTGAGAGAGGAAAACTTAG
900	CTTGTTCCCCACCCAAAATCTATTGAATCAGAATCTCTAGGGAGTGAGGACCAACAGTTG[T/C]GCTTTTAACACCTCCACTCCCCCCTTGTATTGGACGGTAAAGGCCAGAAAAGATTACCTT
901	GTCACCCAAAATTCCATGGGAAAATGCACGATGGTTTTCTATGAAATTGGTGCATAAATA[T/C]AGGTATAACATAAGGAAGAGATGAACATCAGCTCCATTTTAGGAGAGAAGAAAACAAATT
902	AGTTATGTTACATGCAACTCCAAAGCCTCCACAGCTGTTGTCTCTACTCTCCATTCAAAA[T/C]AATGCACGTGCAACTTTCCCTTGTGGCTGGCTTCGTCCTCCACACACCAATGCTTTGTGT
903	CAAAATAACACAAAATGCTTGCTCTCATGAACCTGGAGACAGACGGTAAGAATATACAGC[A/G]ATAGGCAACATGGTAGGTGGGGATGAGTGCTCTGAATTAAAATAAGGCAGGACACAGAGA
904	AAGTTAATTGACTACAGACATATGCAAGAGAGCTCTCAATTGAGCCATAAGATCTTTTGG[A/G]ATGTGGGTGTTTACAAGGTAGCTATAAGCACTCTCATAAGTACTGCACCTGTGAATCATG
905	TTGGTGATATGAAGAAAACCATATGTGATAGATTCTAAATATATAACCACAAAAGCCAAA[A/C]TGACGGTTTGGAACATCTCAGCAACTATTATTGATTACTACAGTTGAAGAGGTTGAATCA
906	AGAGTGAACCCACAGAAGAGATTCTGATGAAACTGAAAGTGGATTGGTAGGAAAATTGCT[T/G]TACAATAATCTCTACTACTTGCTTTTCATGTAGGGGTTTGGGAATTAGTCTCTTATTTCT
907	GAAGACATTTCCTATGATGGCATTTTGGTCTTTCTATCTCCAGGGAAGTCAAGTGATTGG[A/G]AAGAATTTTAAAGAGACTTGGGCTGAGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTT
908	CCTTTTGCTTTTACAACTTAAATTTAATTGAAATTTTAATCCCTAGCAGGTTTTTAATAA[T/C]GGGCAGCTTTTGAGACATTAAAAAACATTGCTCTCACTTCCCAGATAAGGAGGTTGTCCA
909	GTGTAGTCAACTTCCCCTTATGGAATCCATTGATAAATCATGGCAAAAGGAAACCACTCT[A/G]TGGAAATAACGTCTAAAGGAGACCCTCTTTATCCCGGAGAGGAAAACCAGAGAGCAGTCA
910	TGCTAATGCCCTCAAACAAGGCAAACATTTTGTGAATAATTTTTAGATAATATATGACGG[T/G]TTGGATCTTTGGTTTTGTTGTTTTGAATGGAATGCATAGAAAAAAGAACTTGTTTCAACA
911	ACCTCATTTGAAAGTCCAGGCTTCTCAGCTTGATGTCCAAGGTTCTCCATGACACATATC[T/C]TCTTGAGCACTTCACTTCATGCCCCGACCAAGCTTGGACTTCTTCCCCCTCACATGCTTG
912	AGCATCACAGTATAAAGACTTAAGTTCTAAGAGTTGATATTGCTGTAGATGTTGGGAATG[A/G]AATCTTAGGAGTAACCTTTACCGGAGGCAACTTCTACTGCCCTTGCTACCTTTGGTGTGA
913	TAGCATTGTGCTGATGCAATTCTGTTCCAGATAACCGAGGGAGGGAATGGCGGTCCTCGC[A/G]TGAAGACTAAGTAGACGTGCTATTACCCTCCTCGGTTGGCTCCAGCAATAAGCCTAATGA
914	GGCGGTCCTCGCGTGAAGACTAAGTAGACGTGCTATTACCCTCCTCGGTTGGCTCCAGCA[A/G]TAAGCCTAATGACCTCTACAAAGCTGTTCTGTAATACAGAAGTAAACACTTACTCTGCAC
915	ACAGTGTCCAGCAGACTGGCAGGGACCTGATATGAACATCACAGAGGAAAAAAACACATA[T/C]GAAACAATTAATGCTTGCCATTGGGCCAAATGCTTTGTATGTGTTATTTCATTTATATTT
916	GCTCACAGTCGTACAGCTCTTAAGTAGCAGACCTGGGCTTAAAACCAGGTTATCCTGGGT[T/C]CAAAATCTTAGGTTCTTTCACATATCCTATTCTTCCTCCTGGGGCTAAGGTCACGCACTA
917	GGATTCTGGGAATCAAATAATTCTTCCCAGCACCAAACTTTGATGAGAGAATACTTTAAT[A/G]TCTGTGGTTGCAGAATAAATATGATTCACTCTGAGGATTCTGCACTGCAATTGAATATGT
918	ATATTGAAGCTAGTTTTAAGATACAGTCTAAGCAGAAAAGAGCAGAGACTATAACTTTCC[A/G]TGGCAGAAGCACTCCAAGACTCAAGATGCTAAAGCAATGTTGTGACTGATTTCTTTTTCT
919	TGACCTAGCCTTGAATATCTCATTTAGGAAGTTACACACGTGTCTGGGCTTTTCAAAATG[T/C]TTGCATGCCATTAATCAGCATCTTACATCAGCTTGCTCAATGAATGATGACTATGTCAAA
920	GACCTAATAAGCAGATTTGCAGAGCCATAACCTTGCTGGCTTATGTCAGCTCGAAGTAAA[A/G]GGGGAGGTGGTAGTGGTGAATCTGTTTTTATTACTCAGTGTTTAATCATAATGAATCAGA
921	TAGTCTCAATACATATTAACAGAAAGTCAGTGTCAACTCACCTGCACCTCACACAGTAAA[T/C]TGATTTAGGCATCTCAGATTCCTAAACTCTCTAGGTTAACACCTCATATAGTAATGAAAG
922	TCTACAAGATTAACACAAGTATATAGTTATATAATTTTCAAGATCAAAATATAGAAAAGT[T/C]CCACAACCCCTCATAATTTCTTCATTCACCTTGTAAATAACTCCTCCCAATCCCAACCCC
923	AATATTTTAGACTTCATGGATGATACAGTCTTGGGGCAGCTACTCAACTCTGGCCTTGGG[T/C]GAAAAAGCAGCCACAGACAGCACAAAAACCAATGGGCATAACTGTGATCCGGTAAAGCTG
924	GGTATTGAGAAGAAGATGGTTTCCTCTTGGAACTTGGCCAACTGGCTCACAGCGAACGTG[C/G]TGTGGACTCTTACCAGCTCTCTCTAGTATGCTAAGGGCCCCCAACCAGGGACCCTGAAGG
925	ATTGGTAGCAAATGGACTGTTACGAGAGCAAATGATATTTTGCAGAGCTGAGAGTGTGAC[T/C]TGTCTTCAATTATTTGAATCCCTATCCTACAAAAGCATTGAAAAAGGAAGATCTGGAGCC

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
926	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503913	32353655	T	
927	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2347508	32358707	T	
928	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2347509	32360960	T	
929	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4373483	32361621	T	
930	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs939077	32365080	T	
931	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6986716	32367281	T	
932	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10101959	32372076	T	
933	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503914	32400369	T	
934	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs9918832	32402139	T	
935	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs11782671	32410143	T	
936	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2347501	32413693	T	
937	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10103930	32425497	T	
938	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7842667	32446897	T	
939	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7001605	32466789	T	
940	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4733342	32468778	T	
941	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7844425	32495159	T	
942	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4733348	32496353	T	
943	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10113593	32510900	T	
944	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503919	32519284	T	
945	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7000590	32520170	T	
946	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4733130	32526536	T	
947	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2439312	32531901	T	
948	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs11776203	32538661	T	
949	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10104033	32542822	T	
950	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503920	32548231	T	
951	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7826436	32559476	T	
952	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503921	32560877	T	
953	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs3924999	32572900	T	Arg38Gln
954	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10954864	32581039	T	
955	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2439282	32582243	T	
956	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2439281	32585096	T	
957	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6996203	32587559	T	
958	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs12547858	32606595	T	
959	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2439273	32609852	T	
960	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10098373	32612127	T	
961	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7825588	32623943	T	
962	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs13259346	32630548	T	
963	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2466052	32631182	T	
964	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2466046	32636704	T	
965	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2439324	32638195	T	
966	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs6468122	32658869	T	
967	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs9297195	32658983	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
926				0.15	0.16	0.21	0.18
927				0.04	0.18	0.00	0.00
928				0.06	0.13	0.48	0.40
929				0.43	0.45	0.48	0.40
930				0.47	0.18	0.30	0.23
931				0.16	0.38	0.35	0.24
932				0.33	0.25	0.00	0.00
933				0.18	0.01	0.00	0.00
934				0.22	0.26	0.28	0.21
935				0.28	0.46	0.30	0.24
936				0.19	0.45	0.16	0.17
937				0.42	0.47	0.18	0.16
938				0.29	0.38	0.03	0.09
939				0.43	0.43	0.17	0.20
940				0.13	0.09	0.11	0.12
941				0.33	0.14	0.18	0.13
942				0.13	0.00	0.14	0.11
943				0.02	0.18	0.38	0.36
944				0.18	0.03	0.00	0.01
945				0.34	0.47	0.06	0.10
946				0.42	0.13	0.28	0.13
947				0.22	0.38	0.08	0.18
948				0.25	0.00	0.09	0.02
949				0.40	0.43	0.19	0.12
950				0.30	0.09	0.28	0.16
951				0.27	0.25	0.25	0.14
952				0.22	0.23	0.24	0.16
953				0.36	0.02	0.19	0.21
954				0.49	0.39	0.18	0.18
955				0.13	0.41	0.01	0.03
956				0.43	0.10	0.15	0.14
957				0.08	0.00	0.00	0.00
958				0.19	0.00	0.22	0.12
959				0.18	0.24	0.05	0.11
960				0.49	0.43	0.16	0.14
961				0.08	0.18	0.00	0.00
962				0.46	0.13	0.15	0.12
963				0.03	0.17	0.33	0.33
964				0.43	0.33	0.25	0.19
965				0.02	0.09	0.00	0.00
966				0.33	0.10	0.15	0.10
967				0.15	0.18	0.00	0.00

	R
1	**Sequence**
926	TGCTTTGGAATGGAGTTTATTGCCCACTAAAGATGCTAAGCTGGAAAAATATAAATTGGG[A/G]CTATCCATTGGCTAAATTCCCTGCCCTGAGGAGCAGGCCTGTCTCCAGTGGGAGGAAGAA
927	TGATAATACTGGGGGACCAAATTACCTTTTAAAATTATATTTAAGCCTACTAAACAACAA[T/C]TTCTGAGTTAACAATATTAAGACAAATAAAGAATGACATGGCTCACAATTATAAATCAGC
928	GTAATGAGAATGCATAGCCCCACTTCGTCTGGTAAATTGGGACTGTAATTCTTACTTTGT[T/C]TTAGCCCACAGGATGATATGTATAGAAAGTGAGTTATAAACTGTAAATGAagctgggcac
929	AACTCTGGAGTACTGATTAACATCATTGTCTAGCAGTTGAAAGCTCTCTGATAACCTTGG[A/G]GAGTGCTAGATAGAATAGATACAATTTTGCCTTTTGATTTTCCTTTGCCCAAACAAGTGG
930	GGAAATTTCATTTCATGTTGCTCATTGACTACGCTGAACCTGGCTTTCAGGTCACCTGGG[A/C]ATTAGAATCCTCATCCGAAAGTCTGTTTTTGTTTTTTTCCAAGTGACTGAATCGTAACAA
931	GTTCTCCTGGGGTCTCTGGTGTCCCTGATTCTGGAAATGCTTTCCTGTCTCTTCTCTCTA[A/C]CCCATTTCACTTAGATAAGTCCTATTTATCCTTGAGATTTCTCATAGGTGGCAGTCTTTT
932	GAAATCAGTGGTGAGAAGAATGGCTATAAGGAATGGGCTCTACAATTACTGTCACTCTCA[C/G]CAAAAGAGAACGCAAGGAATGCATATTTCATCTCATGGCGACCTGAGGATCGTCCTCAAT
933	GCCTCACACTTCATCAGAGGCCATTTCATCTTTATTACACAGCCACACACAAGGCAGCAT[T/C]TTCTCCTTTCACTGATGGATTATTTCAAGATTTATAAGGTCTGGTCTACATGAAAGCAAA
934	TTATTGAAAAGCAGCTATTGTTTTAAGTCCTTTGCATATACATTTCTATGATTTACTATA[T/C]ATCAGTAGCATTTCTCCAACCCATCTTGGCTAGGCAAGCACCACTGAATATGAAGGAGGC
935	AGTGCCAAGAGGTGAGGTCAGGGCAGGGGCTCTTGCACATGGCACATACTATCTGCCCCA[T/C]AGCTATTTTGACTTGGACAGTCATTGTGCTGGGTGGTAAAAATTCCAGTGGGCTGGGTAG
936	AATTAAGCATGAGTCCCATCACTGAGATAACAGTCTTTCTTGGACAGAGTTATGCCAGGT[T/C]TTTTTCTATGTAAAGCAGTCATCTATTAGGCTGTCGTTGGTCTGTCAAGATGAAACTGTG
937	AATAGGAATAAAATATCGAGGGCTTAAATTAGTGTAATCTCTCAAGATCTTGAATTTGAC[A/G]TTTTCATAATTTTTACTTAATCATAGCTCCTGGGGATTGGAATTACTCTTTTAGCTGGCC
938	GATACAAGCAAATTAATTAAGGAATAAGATCAAAGAATATTGGGAAATGTTTAATCCACT[T/C]GGTGTGGGAAAAGGACTTTTTTGTTTGTTTGTTTTTGAGACGGAGTCTTGCTCTGTCGCC
939	TTAAAATAATAACTCATAATGGCTCTCCAAATGTCTGTAAAAGCATTTCACTTAACAATA[C/G]CTGGCAAATATTATGTCAGTGGAAAATACAGCCAAGTTTTGGCTCATCCAAAATGTTGTC
940	AAAAAGCTGTTTTAGTTGGCTCCAAGAATGTCTCTGGGAATTATAATGTATTCATAGAAA[T/C]GAGTGTGGAGTGCCCACTTGCACAATGGAAGATCCACAATAATACACCTGGATCTGATAG
941	AAAAGATAAAAAAAATAGAACCACCACCAAATATAAATATTTATTTCCATATCTCACAAT[T/G]TTTTCCTAGGCCATTGCTGGTGACAGACTTTCCAGTCCTTTTCAGAACTTACTCATCACA
942	GGAAAGCAGGACCTATTTGTTAAAACAAAAAGAAATAGCTCTGTATTCAAGAGTAGTTTT[T/C]TCAATGGATACTTTGCCCGTAAACATTAAAACTCACTAACACTTAAAATAAATAGATTTG
943	CAAAGAACTTATCACATGTTTATGTATAAGTTTAAATGCATTGAATGTCAAAAATGCAGA[T/C]AGCGCTTTGATCAAGGACATTTTAGCAATGTATTCAGACAGGATCTTTATTTTCTAGGGT
944	TGCAGAGCAAATTCAGGAAAAAAAAGTAATTATGCTTCTTCGCATTTTATCATTTTATAA[A/C]CTCACCTTTTAGAGAAGGTATTGAGAGATTATACTGATTAGTCCAGATTTTTATTTTACA
945	CTGTTCTATTTAGGTTCATTCTATCCAAAGTATTTAGTGCTTACCAGATGCAAAGTACAG[T/C]TAGGAATTCTAATGGATAGAAATATAAAATAAATGGATACAAGGTTATATAATCTCTGCC
946	CTCAAGAGCAGCGGCAGGGATTCCTAAAGGTCAGCGAAGCAGATGAAATCTAGTCCAGTG[T/C]CAGGAATCAGCTCTGCCCCAAACAAGTTCTACAAACTTTTGGCTTAACAGTTCTATTTTT
947	TTTGGGGAATAGCAGTGTGATGCTCCTGGAGCACCCTCTGGAGGCCAGAAAAAGGTGACA[T/C]GGGGCATAGGAAGAATGAAGAGAATTCTGATCATCTCTGCTCTTATGTAGAGGCCGAACT
948	ATGCCTTTATGCAGGAAACTCTGAAAACAAGCAAGAGATCTTTGTGGGCTCTCTGTAAAT[T/G]ATGTGCATGCAAAAAAGCATCCTCAGTGCTTGTCCCTTGACAGCTGCTCTGAGACCACTG
949	ATATTTTTCAGGTTGTTATTTATTTCTTTTAGCAGAGTAAGCCTAGTTGTTTCATAATTT[C/G]TGTGTGGTAATTTCAGTTTGTGTTGGTTCTCACTCTCTATGCCTTGGTTCCTTCTGTGCT
950	GTTATAGTCTTCATAAATATTTTTATAGCCAGTAACATAAAACAATAAAGACAGTGCTCC[A/G]AATTAAAGATACAGCAATGACATGACATCTACATTTGAAACTAGTAATAATGGATGCCGG
951	CCAAAGGGCTGGGATTACAGGCGTGAGACACGGCGCCCAGCCTGAGCTCTCTATATTTTA[A/G]TTTCCTTTAATAACATGATCAGTTCCACCCATGAATTTAATTAATTCCTTATGAGTTTGC
952	GTTTACAAAGTACTTTCATACATGATCTCATTGTTCAGCACGAAAAAAGCTGTACACAAG[A/T]TGGTGCAATCCAAGTAAGGTCTCCAGTGTAGCTAATAGTAGGGTAAGGAAAACGATATGT
953	TCACACCGAAGGACTAGTTTGGAACCTGCAGCCGATTCCTGGCTTTTCATCTCTTTCAAT[T/C]GGGGAGGCAAGGCTAAAAGAAGAAAAGAGAATGAAAAACAACTCTGATCACCAGGCAATC
954	AAGCAAACATCCAGATATTTTATTCATTCATTCACACATTTATTCAATAATGTCTGAAGA[C/G]AAAGCATAGCCTGATGTATGCTCCACGAGACTAGCAAGAAGTTGACATTATAGCTACACT
955	CCCAATTGGTAAATTTTCTTACTTTTCTATATCCAAATGCCATCAGCCACTAGGGTTTAG[A/G]AAGAGAAAAATGTATAAAATCATTTCCTACAAGTCTGTTAAGGACACTTACTGAAGGTTA
956	AAAACAAAAAAAACCTGGGTTCATATCTCCTTTTGCTGTTAAATATCTCTGTGATCCTGA[A/G]TAAGTCTGTTTTCTATGCTGTCTTTTATTCTTTTTTAATACAATGAAGGGGTTGGATAAG
957	AGTAATTATTAAAATAAAATTAGATCATAAAAGTCTTCTGCAATGAAACTCATTGTTTAG[A/T]TCTATCTGGATTAGTGACTAAATATAAACGAAATGATTAAAAAATTAGGAAATTCCCCTT
958	ATTTTTTTGTTGGATTATCATTTTTTAAGTTGTACACATTTACAATGAAAAGAAAACCAC[T/C]TTCACTTTAAATCATGGGCACAGATATTTAAGTATTTTAAAATCAAAGTTTTAAAAAACT
959	AGGATGAGAATGAGTTTTAGAATTAAACTTACAAGCTATCATCTTTCTAAATGAATGAGC[T/C]GCTCAGAGATGAACTGATGGTAACTAAAGAAATCAATAATAAAATGATCAGGATGAACAT
960	AACTGATGTATATATATTACTTGGCACAATGTCTGACCTGTTTCTGTTTTTCACAGTCAG[C/G]CTTCTCTTCCATTTTCTAAGGTGACTCGGACCTTACCACTCTAAAAATTCAAATCATGCC
961	TGGCTGGGGATACTGATTTTACTCAGACCAGCCTGCAGCTCTAGAGTGTGGGTAGAGAGC[A/G]GGGAGTGGGGGTTGGGAGAGGGGGAGGAAAGAGAGAGAGGAGAGAGGACGGGCTTGGATG
962	TACCAAATACTGAACACTTGCCCAGCAATGTCCTTTAACTGACAGCAATCCCACCTCTGC[T/C]ACCAACAGGCTGAGTAGCCAGGGGTGATTCACCATATGGCACTATCTAATCAAACCATTG
963	CAAAGGTAAGGATGACTTCAGTTTTAGTCTCAGCACTGCTACTGATTGGTTGTAGTGACA[T/C]TGGGCAAGTCACTTCACTTTTCCAGACCTGCCTTTTCTCACTTAGGAAGTGACACAAATA
964	AGGAAGTTTGGGGTTCTGCTGCAGGCGTGTCTTCAATATCACAAGAGAGTTTATGAGATA[T/C]GTGCTTTGTAAATATTGGTGCTATGGTGTCCTCAAGAAATGAAAATAAAAGTAATTTGTG
965	TACACATATATGATTGTCCATGTCAATGTCAACAGATGGCATTTTGCCAGAGAGGGCAGC[A/G]TTTTTATTCAAACCATCCATGTCGCTCTATTTCTGACTGACAGGTAGATTGATGATTATC
966	GAAACTGTCTGCAAATAAACATGTATAATGATTTTAGTGTATATGACATGAAACAGACGG[T/C]GACCCATTTATTAAGGTCCATTACACAGATATAGGAGGGACTTTAAAGGCATCACAAAAT
967	ACAAAATACTTGCCAGGAAGTAAATGTTGACTATTTCCAAATCTCAGTGCAAAATGAGAT[A/G]GATAACGTTAACATGCACATGGAGTAATACATTCTTTAAGTACCTATTCAGTGAGGACCT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
968	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4445183	32681985	T	
969	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10095556	32686855	T	
970	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2976525	32692525	T	
971	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7844475	32711671	T	
972	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs2976532	32713793	T	
973	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7007436	32721934	T	
974	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs4512342	32727416	T	
975	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs10503929	32733525	T	Met(289/286/294)Thr
976	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7005288	32740009	T	
977	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs3735782	32744399	T	
978	8p12	NRG1	GGF, HRG, NDF	neuregulin 1	1,124.6	8	rs7812718	32746598	T	
979	8p11.21	CHRNB3		cholinergic receptor, nicotinic, beta 3	40.8	8	rs1530847	42667396	T	
980	8p11.21	CHRNB3		cholinergic receptor, nicotinic, beta 3	40.8	8	rs7844824	42672170	T	
981	8p11.21	CHRNB3		cholinergic receptor, nicotinic, beta 3	40.8	8	rs7012713	42711460	T	
982	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs3824473	103374598	T	
983	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs1407877	103395276	T	
984	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs3739724	103396260	T	
985	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs6479056	103399082	T	
986	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs1323432	103402758	T	
987	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs942141	103411557	T	
988	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs10125230	103417353	T	
989	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs12685902	103420991	T	
990	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs2181561	103427933	T	
991	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs2031202	103432195	T	
992	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs10512284	103433635	T	
993	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs4742820	103434406	T	
994	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs4743478	103440270	T	
995	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs2417282	103448043	T	
996	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs1323413	103466545	T	
997	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs766551	103467877	T	
998	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs1337679	103495146	T	
999	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs2152868	103496167	T	
1000	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs1337697	103518748	T	
1001	9q31.1	GRIN3A	NMDAR-L	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	169.2	9	rs4743484	103519301	T	
1002	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs1076153	135487964	T	
1003	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs1076150	135488582	T	
1004	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs1611115	135490336	T	
1005	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs2797849	135491762	T	
1006	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs3025388	135493077	T	
1007	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs2007153	135493640	T	
1008	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs1108581	135495062	T	
1009	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs3025399	135498795	T	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
968				0.39	0.17	0.11	0.07
969				0.23	0.48	0.00	0.00
970				0.08	0.43	0.30	0.31
971				0.01	0.09	0.00	0.00
972				0.48	0.05	0.00	0.00
973				0.24	0.36	0.38	0.37
974				0.13	0.08	0.39	0.36
975				0.23	0.00	0.00	0.00
976				0.19	0.07	0.48	0.43
977				0.47	0.24	0.49	0.43
978				0.08	0.25	0.00	0.00
979				0.15	0.46	0.14	0.20
980				0.02	0.00	0.00	0.00
981				0.08	0.00	0.00	0.00
982				0.18	0.28	0.22	0.30
983				0.12	0.18	0.36	0.20
984				0.11	0.17	0.25	0.28
985				0.27	0.09	0.07	0.13
986				0.08	0.03	0.00	0.00
987				0.38	0.38	0.41	0.49
988				0.19	0.09	0.06	0.11
989				0.44	0.42	0.44	0.47
990				0.07	0.00	0.09	0.20
991				0.18	0.40	0.41	0.47
992				0.23	0.04	0.09	0.01
993				0.41	0.50	0.31	0.48
994				0.09	0.07	0.13	0.31
995				0.03	0.21	0.14	0.26
996				0.09	0.28	0.15	0.01
997							
998				0.08	0.27	0.15	0.01
999				0.17	0.08	0.48	0.40
1000				0.48	0.44	0.34	0.40
1001				0.22	0.00	0.08	0.02
1002				0.18	0.26	0.32	0.40
1003				0.48	0.49	0.07	0.12
1004				0.18	0.13	0.16	0.22
1005				0.41	0.35	0.00	0.00
1006				0.11	0.43	0.15	0.17
1007				0.29	0.49	0.31	0.39
1008				0.14	0.48	0.16	0.17
1009				0.05	0.00	0.08	0.11

	R
1	**Sequence**
968	AAGTCTCATCAATGAAATTAGTAATCTGTGGGGACAAACATGCCATTAGTGCCTGTCATT[T/C]GAGATTTGTGATCATTGACGTGCTTTTTATGGCATCTGAAAATATTAGTTTGACTTTAAA
969	TATATTTTTTGTCTCAAGAGGTTCTGAGAACATGTGTGCCTGTATTTCAAATTTTAAATG[A/G]GTGAAGATAAGGCTTGGCATAGTCAATTGAATAAAATTTAGTAAAAAATCAACGGAATAC
970	AGTATAATGCTAGGCATGAAAGGCATGAGGAAATGATGGGAGCCTCCAGACAGAAAAGGT[A/C]TCCCACTGGTGACTGATTTCTATTCAGAGACAATGCCATCCCTGTGATTGAAGCTCCAAC
971	CATTTAACAGATATAGACAGCATTTGTGAGAGCAAGTGGTGGGACTCATGTGGATCTAGA[T/C]AGTGCGCTCTTCAGACGACTGTGTCCTCTATTTCTTTCATGTCCTCATATATCTAGAATC
972	GAATGATGACTAGAGAGAGAGGAAATATCAGCTGTATTTTTTTTTCTTCCTCTTGTTCCT[A/G]ATCAAGGGAGGGTTTGATGAAAATGAAGCTGAGAAGAGAAAGGATGTCTAAGGATGGTTT
973	AACTTCTCTTTTAGACCATTTGCTTTTTCAGAAGATATCATTTTAAAATAACCACTATGT[T/G]TTTGTGAAGTTCAGAGTGTGATTCCTTAAATAACTTCTTTAGTATGCTTTCAATGCCACT
974	TCACACTGTCAAAGTAAAAGAAAAATATATGAGTATACAAAATTTGGACACACTTTTTTG[T/G]AAGGCCTTCATCCTACATAGTTGGGATTGAAGACCAGTCTCTGGGGAGTAAGGAGCTGTG
975	AACAGCGGAAAAAGCTGCATGACCGTCTTCGGCAGAGCCTTCGGTCTGAACGAAACAATA[T/C]GATGAACATTGCCAATGGGCCTCACCATCCTAACCCACCCCCCGAGAATGTCCAGCTGGT
976	GAGCATTATCAGACATAACATGATAGAAGGTAACAGGGTACAGCCAACCCTTGAGGCATC[A/G]TGAAAGAGATTGACCAAAGACTGATATAGCTGTGGGTTTTGGAAGAGAGATAGACCAAAG
977	AAGTTTATCCAGGGTAACTTGCTCACTAACTATTCCTTTTTATGGCCTGGGGTTAAAGGG[A/C]GCATGGCTCACACTGGTGAAAATAAGGAAGGCCTGGTCTTATCTTGTATTAATAATACTG
978	TGTCCTAACGATGAATGATAAAAGGACTTGATGTTCACAATTTGGGGTTATAAGGCAGGT[C/G]TGAAATCTGGAGACTCAAGATGCTGGAAGGAGTGGAAAGTTTCGATGACTTTATATGAAT
979	TGGATTAAAGTGTTATCCTGCCCAGTGGTGGATGTAATAAGATTTAAACCAAAACAATTA[T/C]CTCTAGAGTGAAATTTTAGGCATCAAGAGATGAGAGGTTATTTAGGAGGGCAGTGAGAAT
980	ATGTTTTTGTCATTTGCTGCGTTTCTCCTTCTGAATCACTATGAGCTTGGTAAGAAAATA[T/C]AAAAGCAGGAAAAACATTATTGAATGCACTGAGCATTACTCAGAGAATTGTTCAAATATT
981	TGCTTGTTAGCAATGGGCCAGGCAAATCTCAACAAGGGTTTGGGGATTACACTGGCAGGA[T/C]AGCTGGCACTGCACACTTAACAATAACACAGATTCCAAGTTGCCTGGCCTACCGAAGCAG
982	GACTGTTTAGTAAGAGCATGCTTACACCCTACTGTGAAAAGGGGAGGGGATGTGGTAAGC[A/G]GAAACAGAAGACAGGCAGCAGAGGCATTAAAAATGCATACCATGCTTTCAGAACAAAAGC
983	CAGAATGCATGTGTCTCTTCCCACGCATTTATGTCATGTTGGTAGCTTTAGATCAGCCAT[A/G]GTGAGAAAAGAACAAAAGCTTTTAGTTGTTTTTGTTTTGTTTTGGAGAATTTGTTTACCA
984	TTTTTGAACTTTTAAAGTTCTAGTTTGGTCTTTGAATCAAAACAAAGTAAAAGATGTTTA[T/C]AAAAGCCATTTCCTTTTCTTTCCCCACTATGCTCATTTGACTTGCTCTTCCCCCTATAGG
985	GAGAGCTTCAAGATGGCCACAGCAGAACATTAAACCAAGTACGGGACCTTATGAGACTGC[A/G]TGGGCCACATGCCCATGAAGCTGGCCCTGCAAGGAGTTGGGCCCATTGACCTCTCTGTGC
986	cagtcacactggcattctttcagttcctcctacttgttttgttcctcctgccctagggcc[T/C]ctttgcacatggagtttcttctacctggaacactcattccttcccagaA
987	ACATTTCTGGATTTGAATCCTGTCTCTACTATTAACAGCTGAATTACTTAACTGCTCTTA[A/C]GTCTGAGTCTCCTCATCTATGAATGGGTATGATAAAACCTGCCATCCCATTTTGTTCTAA
988	ATAGTAAAAAAAAAAACCCAAACCCTTTTTTTTTTTGCCTTCAACATGATTGAGGAAGAG[A/T]GATTAAAAATATAGTTCATTTTTCATGGATAAAGACTAAAAGATTGTCAAGCATCCAAAG
989	CTCATTTTTAAATTGCTGACTCAACTGAGCAGCCTGAGTTGCTTTCATTATTACTAGAAA[T/C]GTGGCTTTGCAATAAAGACAGGGTTGACTATTTTGTGGTTGATGAATGAAGCAAAATGGA
990	TTTTTTATTGTCATATTGCTACCACAAATATTTGTGGAATATTGGCAAGTGATAACTTGT[T/G]GCTACGTAGCTGTCAAGGTACATTATGGTACTGTGGCAGTCGAACTTTGATTGGAGAAAC
991	AGACAAAAGACTTTACATAGAAAAATTTGACCTAGGTCTTGAAAAATTAATAGATGTTGG[A/G]CAGACAATGCTGATAAATGTGCCTTGCGCAAGCCATACGACTGCAATTTGCTACTATGAG
992	TTTTATGGTCTATGACCAGGATTTTTAGGGAAATCCTGCTTTTCTGGGTCTCATTTTCTT[T/C]TCTGAATGCACCAGCACATCGTTCCTTTCCAAAGCATGGAAGGAATCAGGGAACCAGCAG
993	CTAGACCTGTAACACCCTCCCATTATACCTACAGTTTCACATAGCACTGACAACACTTGG[A/G]ATTATTTTTATAATTTGCCTTCCCTGCTAGATTGTAAGTTTCCATGAGGATGGTGCCCAT
994	CTGTGAAATAGCACTGCAGTACTCATTTCCTGAGCCTCTGGATGTACCTCGGTATTTTTC[T/C]GTCTCATTTATTGTAATGAAAGTGTAGAGCCTATCATCATGGTCTCCAACTGAAGTATCT
995	TACATATTCAGATCATTTGCCCATTTTAAAATTAGATTATTTGCTTTTGTTTTGGCTACA[T/G]AATTGTTTGAGATCCTTTTATAACCTGGTTATTAATCCCCTGTTGAATGAATAGTTTGCA
996	TTAACTCTTTTTGCTAGAATAATTTATTTTACAATAAAAGTAATATATGTTGCTTCTCAC[A/G]GCCTCCTACCAACTCATCTGGGAAGCAAGCTC
997	TCCATAGGCACTAAATTCTCCCTGATTAAAATTAAAATGCTATCAAAGTGAATTTGAAAA[A/G]TGAAAAGGGAATTTTGAAAAATACTCAAAAAATTAAATCACATAAACCTATTACTTTCAA
998	GCTGTGCCACCTTGGGAAAATTACTCACTTTTTCTGAACCTTGATTTTGTCTTCTATTAA[A/C]GGGGGATGATCATTGCAGTCACCTCATGAGGCCATTGTGAGGATGAAATAAAATAATATG
999	ATTAAAGAATATATAACAGAGCAGTACAATATAATGAATGTTTCAGAAGGCAGGATTATC[A/C]CTGCATGGTGCAGTTGACATAATATTGCTGGCAATGCTAGGTATGGTCTATTTCATTGCA
1000	CGCCTCACTGCCTGGCTGAGTAATGGAAGATGGCATAGGATAGGCCTGTAATCATAACAA[C/G]TACAGTTCCTTTAAGGTACAGCTAGAAAGAGCTAGAATAAGTATATAATGTAAAGGACAG
1001	tgttaaaaAGAAAACAGATATATGAGGTCATAGCATATAATATAGTGGAATTCAGTGAGG[T/C]TAAAATTCTATACTTTAAAAACTACCAAATGTGATTTTTTTTTCCCAGGTGGTTCCTGGT
1002	GGGAGTGGCCTGGCCTGTTCACTCACCCAGCTCCAGTCTGCACCACCGTCGCTCCACTTG[T/G]GGTTGTCACTGCCTGAGGTTAGGACGTCAGCAGAAGCCAGCCTCATGTGGCAGAGGCGAT
1003	GCACACCTTGTCAGCCAAGGTCAGAAAAATTCCACTGGAGTCAAGAGGAAGGGACGCTCA[A/G]ATGAAAAATGCAACCGCAGAGAAAATCTGCGGAGACTGGGGCCGGGCGGGAGGGAGCGAA
1004	GGGGTGGAGCTGGAGGGATCAAGCAGAATGTCCTGAAGGCAGCTGCCCTCAGTCTACTTG[T/C]GGGAGAGGACAGGAGGGAGAGGTGCCGTGGTGAGACTGACCCTCGGGCCCACGGGTGGAT
1005	CCCCATCTGGCCGTCTTTCTGCACTCACCCTCCTTAACCCAGAAAGTTCTTCTGTCACCT[C/G]TCAGTGTTTGAGTTGACTCTGCTCTGAGCCAAGTCTGCACCCCGAGCTTGGGCATCATGG
1006	CCTGCATTTCCCGGCTGCTAGGGAAGCCAGAGGAAGCCAGGTGACTTTGCCTTTCCGTGC[A/G]CTGGCAAGGTTAATTTGCACAACAAATTCCTACGAAAGCAAATGTCAGCCTTATTATTCC
1007	ATTGAAGGCTCAAACAGATGGTCAGAGTTGTTTACACCTGTCCTGCCCTCCAACATTCAC[A/G]CGTGTGTGAGAATCATATTCCTAACATTCCGACCCACACCAAGCCCATATCCCTAGCTAC
1008	ATGTCATAGTACCTTTCCTGTCCCTGATAAGTCTGGGGCCTGGGCCTGGCCAGCTATGAC[A/G]GAGAGAAAGCCAAGGAGGATGGCCAGAGGCAGTGGTGGGGCCAAAGCACTTAGGATGGTC
1009	CACAGAAACGCAAGTGCCSCAGGACCTTATGCCCTCAGTGGGTCCTGATTCTGTTTCCCA[A/C]CTGGAGTCAGGGTTTTGTGTACAGGTGGTCCCAGGGCT

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1010	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs1541333	135501206	T	
1011	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs2519154	135502096	T	
1012	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs2797853	135502336	T	
1013	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs77905	135507918	T	
1014	9q34.2	DBH		dopamine beta-hydroxylase	23.0	9	rs2073833	135510103	T	
1015	9q34.3	GRIN1	NMDAR1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	30.4	9	rs11146020	139152905		
1016	9q34.3	GRIN1	NMDAR1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	30.4	9	rs2301364	139154356	T	
1017	9q34.3	GRIN1	NMDAR1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	30.4	9	rs10870198	139162141	T	
1018	9q34.3	GRIN1	NMDAR1	glutamate receptor, ionotropic, N-methyl D-aspartate 1	30.4	9	rs12238250	139166503	T	
1019	10p12.1	GAD2		glutamate decarboxylase 2	88.3	10	rs3781117	26552050	T	
1020	10p12.1	GAD2		glutamate decarboxylase 2	88.3	10	rs2839673	26553557	T	Gly232Glu
1021	10p12.1	GAD2		glutamate decarboxylase 2	88.3	10	rs8190646	26560513	T	
1022	10p12.1	GAD2		glutamate decarboxylase 2	88.3	10	rs11015008	26567596	T	
1023	10p12.1	GAD2		glutamate decarboxylase 2	88.3	10	rs4747550	26625608	T	
1024	10p12.1	GAD2		glutamate decarboxylase 2	88.3	10	rs876848	26636502	T	
1025	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2616673	87357346	G	
1026	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1876883	87365358	G	
1027	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2457450	87372875	G	
1028	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs10788462	87408436	G	
1029	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7097285	87420101	G	
1030	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4547037	87424453	G	
1031	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs12255557	87426328	G	
1032	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2356728	87484397	G	
1033	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2949374	87491059	G	
1034	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs3011703	87509023	G	
1035	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2140661	87512489	G	
1036	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1917155	87529467	G	
1037	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2949385	87533376	G	
1038	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1106789	87543389	G	
1039	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1917146	87558623	G	
1040	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7902997	87564546	G	
1041	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1112487	87589036	G	
1042	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1880386	87601923	G	
1043	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1880385	87605302	G	
1044	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs11599415	87607771	G	
1045	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7895098	87640358	G	
1046	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1917143	87646055	G	
1047	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2222546	87652091	G	
1048	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs6585987	87655958	G	
1049	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2882832	87660812	G	
1050	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2352099	87674661	G	
1051	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs12245750	87678254	G	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1010				0.46	0.36	0.07	0.07
1011				0.38	0.25	0.07	0.07
1012				0.43	0.00	0.00	0.00
1013				0.46	0.38	0.18	0.07
1014				0.34	0.36	0.46	0.41
1015			p=0.000001 (Zhao et al. 2006)				
1016				0.13	0.14	0.23	0.13
1017				0.43	0.24	0.05	0.10
1018				0.08	0.08	0.05	0.09
1019				0.17	0.00		0.31
1020				0.01	0.00	0.00	0.00
1021				0.13	0.19	0.02	0.06
1022				0.15	0.00	0.24	0.19
1023				0.17	0.41	0.43	0.39
1024				0.32	0.43	0.33	0.36
1025				0.21	0.00	0.18	0.16
1026				0.14	0.19	0.00	0.00
1027				0.34	0.37	0.38	0.37
1028				0.45	0.12	0.42	0.40
1029				0.19	0.33	0.26	0.23
1030				0.30	0.33	0.05	0.04
1031				0.14	0.13	0.13	0.16
1032				0.48	0.17	0.31	0.29
1033				0.28	0.35	0.26	0.23
1034				0.33	0.48	0.18	0.11
1035				0.48	0.20	0.31	0.29
1036				0.49	0.19	0.32	0.31
1037				0.38	0.42	0.19	0.11
1038				0.15	0.47	0.24	0.28
1039				0.26	0.01	0.00	0.01
1040				0.22	0.49	0.36	0.34
1041				0.10	0.18	0.06	0.06
1042		Y		0.16	0.22	0.00	0.00
1043				0.48	0.08	0.44	0.44
1044				0.12	0.00	0.00	0.00
1045				0.19	0.30	0.11	0.14
1046				0.26	0.35	0.21	0.18
1047				0.31	0.37	0.21	0.19
1048				0.09	0.38	0.00	0.00
1049				0.34	0.17	0.21	0.21
1050				0.37	0.23	0.38	0.27
1051				0.23	0.12	0.38	0.27

	R
1	**Sequence**
1010	GGGTGGTCTGGAGGGGCTGTGCAGCAGGAGGCTCTGCCCCCTGGGTTATGTACAGGAAAG[C/G]GATGTCAGGCGGCAAGGAGTGTGAAATTGACAAGGGGTTTTAATTCACAGGGAAGAGGCT
1011	CTACTTTGATTTATGTCCTGCAGACCCAAGGAACCCACCTACCAAGCTGACATCTCAGGA[A/G]CAATTTGAGTGAGAATGTGGCCCCCCAGGAGGAGGGCCAGCGTTGCAGGTCTAGCCCCCG
1012	TAAGTGCTTTGATGTTCTTCTTCCACGTTCAAAGGAACCTAAGCTGGAAATCAGCCTGCA[A/G]GACGGTGACAACCTGCAGGGTGTGGTCTGGGCAAAGAAGAGGGCATGGAACTCCCATCTG
1013	CCTGGGCAGGTGCAGGGGGAAGCGGGGGTGACTTACCACTGTGGCCAGCTCCCGGTCTTC[T/C]GTGTTGTACGTGCAGGAGGTGATGAGCACATCTCCCTGAGGAAAAGCCAATGTGACCATC
1014	GGGGAGCTGCCCTCCCCTTTGATCCCACCTGGTGCTGTGATGTGGCCACTGCCAAGAGGA[C/G]GACATGGGCCAGGGAAGCCACAGAACTGCCCACGGGGACGCTGGCACCGAGGGCCTCAAC
1015	GGCCTGGCTGAGCACATGCGGCAGCCACGGTCACCCTCCCTATTCCTCTTAGCCCGAGGA[C/G]GGGGGTCCCAAGTTACATGGCCACGCAGATGGGGCCTCTCCCTCATTTCTGAACCTTGTG
1016	TGGAGTGTGTCAGTGTGGGGGTGGGCATTCCGGGTAAGAGAGTAGAAGCGCCTGTCCAGC[T/C]ACATGCCCGCCCTGCAGAGCTTTAAACAGGACGGGGCCTGGGGCCATCTTTGTTTCTGCT
1017	ACTGCTGGGGCCACACAGCAGGTGCACGGCAGGGTGGGGGCGGCAGGTGGGGCTCCCTCC[A/G]AACGGTGGACGCGGACAGGGCCTCCTTTTCTCCCGAGAGCGACCGTTTCCAAGAGCACAG
1018	TGCTGGGATTACAGGAGTGAGCCACCGTGCCCAGCCACTTGTGGCCTCTTCTGTTATTTT[A/C]TGAATTGTTTACACTTCCCTTACTCATCACAGAGCTTGAGAGAAATTCTGTAGCTGTGAT
1019	TGTTTTATCAACAAGATACAGAAAGATATACTCAATCGACTGATTAGTCCATCGCAAGGC[T/C]TATCTAATTAACTTCTAGATTCCTCTAAAACTCTCTAAATGGATTGACATCCACACTCTC
1020	ATGAGAGAAATCATTGGCTGGCCAG[A/G]GGGCTCTGGCGATGGGATATTTTCT
1021	ATCTTTTGGGGTTTTATTTTGTGAAATGTCCTTCTTCAACGTATAGGGGTCACATTGGGC[A/G]AAAACCACACAGCCTAAAATTACTTAGTATTTACTTTCTGTTGCTGCTGGAACAAATGAT
1022	GTGTGACTAATAAGATAGCAGCTTCACAGACGTGCCTGTGTACAGATCCACATCACCTGC[A/G]AATCACACAGTCTCTAAAAATGTGTCTGGGAGGTCCCCTCCCCTCCAGATCATTATAATT
1023	GGAGGGGCAGCAAGTGGGCTGTGCCAATGTTTACCAAACAAGAATCAAAAGGGCTGGTCT[A/G]TTGATCACCTCTTGTGTTTCTGGTTCTTTATCTTCTTATTTTAATTTTTTTTATTCTTGA
1024	CTCTGCTCCAGCCTTTCCTCTCTCCCAAGCCTCTCCATTTCATAGACATAGATTGTTA[T/C]GCCTGTGAACCACCCGCATCCTCACAGTGTGTTTTTATAGCATTACTGTTTAATTTTGGG
1025	CTCAGGAGATGGTGGGCAGTTTTTCAAAGCATCAGGAGAAAGAGTTCTGATCAGTTCAAT[A/C]GCAGATGTTTTAGGGAGGGCAATGAGAGCGAACCGACAATGACTTCACATCGTGGGTGGT
1026	CATGTAAGACACAGAATGTGGCTGTGCATTCAGTGACTTAGTTGTTAAGATACATGTGCA[T/C]TTATATGGTTTGGGGTCATGCTTAGATTGCCCCAGAACACTACAGACCTCTCTCATGGCA
1027	AAATAAATGAATTTGGGGACCCAAAGAAAGCCTCAGCACTGCCTTTTACTCAGCATGGAG[T/G]TGAAAGAGAAAGGCTGAGGAAGCTCTAGGATGCCAAGGAAGTGAAGACGACATTTAGGAA
1028	GCACAGAGTCATGGGAACATGAAGTTGAACCTGTCCCAGCTTAGCAGACAAGGAACTGGG[A/G]CTGTGGGCAAAGAGGGAGGGTTCATGGGAAGGGTGAGGCTGAGGCTGAGGCTTAAGGAGA
1029	CTGAAATGGGCACCAATGCTGAGACTTGCATTAGAAACAGAGCAGTGAGGATTCTGCCTG[A/C]CCCCTGAATGGGATTTCAATGGGCTTTTTAAACAAGCCCACTGTATTTCTATCTTGAATA
1030	ACCTGTTCTTTCTGTCACACAACTTAGTACAAGAGAAGTTAAGAGTGAAAATTGCAGGTT[T/G]TTTTTTTTTTTGGTGTGCAGCATAAATCCATCCATAGCAGAGTCAAATGGATTACCTGAC
1031	CAGCTTAAGTTCTGTTTGTAGGAATCCCAACTACAGGCAAGAAAGCTTCGCAGTCAAACA[T/C]ACCACAATGGAGACGCAGCTTCCAATGAGCCTGCCCTAGCCCTAGAACAGCAAAGGGAAG
1032	CAAACACATCAAAGTTCAACTATGTTCCAGGATTCAGGATCCTTCATATTGGGTAGGAAA[C/G]TTTATTATTCCCTCACATCAGACAGAAGCCAAGTGCCCCAGGCTGAGTGAATCTCCCCAT
1033	TTAGAGTGGTTGAAAGTTCCTGGGTTGGATTTTGTCTTTTGCATGATTTTGTGTTGGAAA[T/C]TTACTTTAAGACTTCTAGTCATGGTAAAGTATTTGAATAATAAATATATATTTTTTTAAA
1034	TCACTGAGGGCCTTTCCCTCTCCCTGCAACCCTGGTGCTCCTTTCCAGGCATCCCAGTAT[A/G]ATGGACCATAGACATTTACTGTTGGATTCTGGACCAGTCCTTGGGCAGCTGCACCCTTAA
1035	CACAACAGGCACTCACTTCTTCCCACGCTCCAAACTGAGTTGATCACTTGTGCATTGTTA[T/C]GACTTCAAGACAGGGGGACTTTCTTCTCTTCCCCATTGCCCTCTCTCTTCCTGGTTTCTC
1036	CGAGGTTAATTACATCATCTAAAGAGGTCCTAACTGCCCCTTCCAGGCATGTTCTATGAG[T/C]TTGCCCCTGAATGAGCAGTCACTAATACCTCCTAATCTCACACAACAGGCACTGGCAATG
1037	TAAACCAGAATGAAAATGACATACCTTTGTAGGAGCCAAGGATCTTGCTAAAAACACTTC[T/G]TCCTTGTGTCATGAGGTGAGCTGAGGATTACCACTGGTGGGAACAGGGATCACTTTAGAA
1038	TCTGATGGTCTCTGCAGGGCTTCACCATTTGGCATCTCTGCTACGCTCACTGATAGTAAC[A/G]TTTACAAGGTACGGCACATACAAAATACTCCACAAATGATAGCTATTACTACCATGGTAA
1039	AATGTACTATTACACATATTAAAAAACAGAAAATGACTGATAATCAAGAGATAAAATAGT[A/C]AATAGAATTAAGACCTTAAAAGGTAAAGATATTGAGTGAACAGACCAGCATTTAAAAATA
1040	GATAACCCTCATATCTATTAAAGTTATTAAATTTGTAGTTAAAAACCTTTCAAAAGGCCC[T/C]TATAGTTTCACTGATGGATCAGGAAGAAATAATACCAATTCTGCACAATTTCTTCTAGAA
1041	tgccatgtggcaatgagaagatgtttattctgttgtttttgggtagagaggtctgtagat[A/G]tccataagttctatttgatccagtgctgagttcaggtcttgaatatcttaatttcctctc
1042	TTTATTTTAAAATGTATCTTTTTGTCATTTTAAAATCTGCCCTTAATAACTGCATATCCT[A/G]GTTGTTATCTGTCTGCCTAGCAGCTTATCGCTGCTAAGGGGAAGTTATCTGGAAAGCAGG
1043	AGAAAGCTGGATTTGAAGTGAATTGAGTAATCTATGGATGATTTGTTAGAGTGAATTCAC[T/C]TTTAGAGGCTTCAAAAGAGCATTTAGGGAAATCCATAGCGTTAGGAATTTAGTCACAATG
1044	CTGAAGTCTGAGATGAGCCAATAGGAGGTGCAAGGCATCACAAACATCTGCCCCGTCATG[T/C]CTGTCCAGCCCTCAAGGGCCATTCCCAGCATGTCACATCCAGGCAGAGCTGACTGCCTCC
1045	GTAAATTCTCACTGTGCCTCCAAAACCAAAAGGAAATTGTAAGTGATAATCCATTGCTCT[A/G]TCTATGCTGGAGTTAGAACCAGAACCAGCTCTTCCACGGTGAGGTAAATGTCTCCTGTTG
1046	GATCTACCCAATATAATAATCAGAACTTTTACTTGGCTTGATGCGGAAATTTTGACCCTT[A/T]AAGGACAAAAATCAACATGTATCTTCCATTAAGTTAGAGCTGGGCTGGTTCAAAGGCAGT
1047	GATTCATATCCTGGGTGGGACAAAGCAGTACAGCGAGAGCTTTCATCACACTATGCAGAA[C/G]AGCATGCGATTGAAAAACGTATAAATTATTTATTTATGGAATTTTCCACTTAATACTTTT
1048	AATTTAAGTCCTAATGATAGAGGGTTAATAAATCAAGAGAACATAAAAATCCTAAGCATT[T/C]ATGCCCCTTGAAATAAAGCTTCCAAATATATTAAGCAATAACTGGTAAAACTGAAAGGAG
1049	ATCCATTTGCAGGGATGACCCATGAGATATGAACGCAATAGTAAGAAGTAAATAAGGGTA[T/C]AAATGTGGGGTCAGGGTCATCCTGCAGAGGGCTGCAGCAGGCTGGATGAAGTGGGCAGAT
1050	GGATGGCAGAAGCGCCCGCTCACAGCCCCGGGGGAATGAAGATTCATTACAGATCATTTG[T/C]GGATCCTTCAGATGAAATAGAGGCAGCTTCCAGGGCTGTGCAGGGAGTGCAATTTACTAT
1051	GAATCGGCACTGGCAGGCTTGGCCTGCAGACACCAAGTCACTCCAGCTGCAGAACTGGTG[A/T]CCTGTGAAGGCTGGGAGCTGGGCCAAAAGTGGCACGACAGGAAGCTCCCTTTCCCCCTTG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1052	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7924131	87684856	G	
1053	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1418396	87690805	G	
1054	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7906886	87696511	G	
1055	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2153828	87705134	G	
1056	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7912559	87724804	G	
1057	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4244970	87732575	G	
1058	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4393254	87734378	G	
1059	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs10509525	87735846	G	
1060	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2352464	87737769	G	
1061	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2001321	87745432	G	
1062	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7089658	87760259	G	
1063	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs10788476	87766857	G	
1064	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs12256782	87788988	G	
1065	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs10788478	87797370	G	
1066	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4934146	87810686	G	
1067	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs12266132	87813079	G	
1068	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2001697	87815478	G	
1069	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4934150	87855354	G	
1070	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4460754	87861881	G	
1071	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs884700	87884268	G	
1072	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs10509531	87887983	G	
1073	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs12262754	87919062	G	
1074	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4934159	87936653	G	
1075	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1902667	87939219	G	
1076	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2607829	87941666	G	
1077	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2607830	87957082	G	
1078	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2607840	87960202	G	
1079	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs11201945	87965746	G	
1080	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2814346	87994907	G	
1081	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2814351	87998880	G	
1082	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2814352	88004329	G	
1083	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1902664	88007496	G	
1084	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1947568	88008808	G	
1085	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2607863	88014423	G	
1086	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1870167	88019566	G	
1087	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs2217224	88059396	G	
1088	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs1896526	88059468	G	
1089	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7904985	88106459	G	
1090	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs4933391	88111974	G	
1091	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs7089364	88113931	G	
1092	10q23.2	GRID1		glutamate receptor, ionotropic, delta 1	766.9	10	rs3814614	88118261	G	
1093	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs2420203	92497843	T	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1052				0.46	0.31	0.46	0.34
1053				0.15	0.30	0.38	0.40
1054				0.46	0.30	0.50	0.43
1055				0.08	0.08	0.25	0.36
1056				0.49	0.20	0.50	0.40
1057				0.49	0.27	0.34	0.24
1058				0.05	0.01	0.00	0.00
1059				0.45	0.19	0.34	0.24
1060		Y		0.27	0.28	0.15	0.18
1061				0.24	0.30	0.14	0.12
1062				0.25	0.26		0.13
1063				0.43	0.13	0.42	0.43
1064				0.18	0.41	0.11	0.16
1065				0.47	0.13	0.47	0.37
1066				0.14	0.02	0.00	0.00
1067				0.05	0.10	0.10	0.13
1068				0.24	0.09	0.11	0.11
1069				0.17	0.39	0.19	0.23
1070				0.08	0.20	0.00	0.00
1071				0.23	0.37	0.18	0.22
1072				0.31	0.17	0.31	0.32
1073				0.15	0.40	0.17	0.12
1074				0.16	0.13	0.07	0.03
1075				0.50	0.02	0.26	0.34
1076				0.24	0.43	0.49	0.48
1077				0.27	0.23	0.14	0.10
1078				0.23	0.23	0.11	0.07
1079				0.19	0.22	0.09	0.06
1080				0.16	0.04	0.49	0.39
1081			p=0.010 (Fallin et al. 2005)	0.13	0.38	0.43	0.44
1082				0.18	0.38	0.43	0.41
1083				0.13	0.37	0.43	0.41
1084				0.33	0.08	0.41	0.37
1085				0.08	0.00	0.00	0.00
1086				0.17	0.46	0.46	0.42
1087				0.33	0.07		0.35
1088				0.07	0.33	0.00	0.02
1089				0.32	0.08	0.15	0.20
1090				0.36	0.00	0.30	0.26
1091				0.15	0.27		0.43
1092				0.45	0.14	0.35	0.30
1093				0.14	0.36	0.28	0.31

	R
1	**Sequence**
1052	TTACATGCTGACCATGACGGGTCCCGGCTAACAGCTCTATACAGATTACTTCCCTGAATC[C/G]TTACAGTAGCCACTTCATCAGGGGTACTATTGTCTCAGTTATTAAAGATGAGACAGCAGA
1053	GGGGAGACTGGAGAAGAATTGTATGTATTAAGGACCCACATATATCAGGTGCTTTTCATC[A/C]ATCTGTGATGTGTGATGTGTATTCATTTATTCTTCCCACCTTAGGAGGGTTGGTCTTCAT
1054	TCTGAGAAATTGTCTTCAGTTTCATTTTGCACTGTGATGCCAACAAGCCCAGTGTTCTCA[A/G]GCATCCAGGAAGGTAGACATAAGGGGCCTCCCAGAACCCCACCCACACTCCCCAGTGTGG
1055	GCTGGACCCTCTACCACTGATTCCACCCATTTTACTCCCAGAGGAGGCCATTGCGTCCAG[A/G]TTCTTGGCACTTCCATAAGTTGTCTCGCATGCTGGAGGCTGGCTATCCTGATGCAGGTTC
1056	CCCTGCTTAAAATTCTGTGTTTCTCCATGTTCTCTACAAGGGTTTCATCCAGAGCCTCAT[A/G]CAAATCTAAATATGCCACCTTAGACATTCCCATTCTCATCATTTGCCCAAATGAATTTGT
1057	CTATCATCTCTATGTTTTGGGAAGAACTTTTTCCCTAAGTGGCTATTGTCACTGAAAAAG[A/G]AACTCCCTCAGCCCAAGTTTCTCAGCAAGGGCAACCCACAGGCAAAAACAGGAAAACTCA
1058	GAAGTGCAAGGAGCCTTGGTCCTGGCCAAATCCCAGCATATCCCAGCACCTGGAAAGAAA[T/C]ATCAGAGCAAAACGGCCCTCAGAAGCTCTTTCAGACACCAGAAGGATGCAGGCAGAGAGG
1059	TACTGCATTCAAGGTGCTCAATAAATCCTGTTTAATAAAATTCTGTAGCACTAAGCACAA[T/C]GAGGAGGGAAGTTCTGCATGCCTCCCAGGTGTTCGTAACTTACGGATGGATTGGGTGGAT
1060	AGATGAATAATTGGAGATGGAGGGGGCATGCCAGATATTCATTTCTATTCAGCAGGTCTT[T/C]TGTTTTTGAGCTGGAATTTAATGCGGGTCTCTGTGTTAGGTACAGGGGATTTGGTGGTGA
1061	GTTCTTGCTCTGCTGCACACTTTTGTGGCTGCATCTGCCTCTAGGGCAAGGGGTCAAGAG[T/G]GTTAGAGGATAAAAGCTTGGTAAACTTACAGCCAGTTTGGTATTCTTTGAATTCTTGTTT
1062	TGTTGGCAGGAGTGGGACTGGGATTCCAGAAAGTAAAGTTTAAATTGATTTCTGAATATG[A/G]AAAGGAAGTAATGAGGCCGGGTATGGTGGTTCATTCCTATAATCCTAGCACTTTGGGAGG
1063	TACAGAGATCAAAGGTTACAGACACAAAGTATTGGACCTGCTGCTAAGTATTCCTGGTTT[C/G]CAATTTGACCCCAACCACTTACTTGCTATGTGTGATAAAACATTTGTTTGAGACAATAAC
1064	ATTCCTCACTCCTAACCTCTCTATGGTCATTTTCCCCTATTCCTCCACCCTCAACCTTGG[A/C]AGTTCTGGAGTTCATGACACAGCTCATGTCAATTCACCACTCTGTGAATAAATAGTTCCA
1065	CTTGCCTTCAAATTGTTATGAAGTAAACATTAAGGACTGAGGAGATCAAAGAAGCTCTGG[A/G]TTAATTGGAACCCAGCAATGATGCTGGAGATGATTTTTGGGTTAATCTCGGAGGAGCCAC
1066	TGGGTATCCACCTCCCAACAGAGCTGGCAGGCACTAGCAGATCAGTTGACTCTACAATGC[A/G]CCCCTTTCCAAAGAGAAGGCAGAGCAGCCTCCACCCCGCAGGACTCCCTATGCCTCCCCA
1067	GTGGAAAACCCACAGGTGCTAGAGAAACATACGCCAGCCGCTGGGAAGCATAAAGGAGCT[T/C]ATGGTGAACTGGACAATGGAGAACATGGACTGATGGGAAATGCCAGAACGGGAACCTGAG
1068	ATTATTTATACCCCTCTAATTTGGAGCAGCAAGACTGACCACGAGGCAGCCTCAGCCCTC[T/C]TATGTCTGGCATGACAAGGATGGTGACAATCAAATGCTTGCAGCTCCAAGGAGAAGTGAT
1069	TTCAATGAAAGCAGAGCCCTAGGGGCCAGCTGCCCCTCCCCAGCAGTGTCCGGGGCACAC[A/G]GAGCCTTCATTCCCCATTCAGCAAGCACTGAAGCCTCTTCTGTGTGCCAAGCACCAGAGC
1070	GTCTTAGATGACTCAACACAGGAGTTGTCCAAGTCATCCCAGGTGAGGACACAGCACCTC[A/G]TCCCTATGACTAGGGACAGGGGACACAGTGCTGGGACCTAGGACCCCAGGTCAAGCCAGG
1071	AAGCCTGACCTGGAGAAGAACAACAATAAGACATGTAAACTGTAGGGCGTTAACCTCTAA[T/C]ACCCTGAAAAGGACCCCAAGAACACATCAGTCCTGAAGTCTGGATTTCCTGCCCCAGGCT
1072	TCTCTGTTCGAGGTTGGAGCCTTCTAATGAAGACAGGGCCCATCAGTTTAAGAATCCATT[A/G]GTTAGTAAAGAATCCATTCATTTGTAAAGAATCCATTAATTTGAGAAGAAACTAGAAATA
1073	GCAAGTACTGTTGAGCTTGTCAAGCCACGCTGTAGCCCCAGGGGCAGTGGTATGCTAGGA[A/G]AGGTTTAACTGGCTCTCTGGAAGTAAATAAACCCCTGACTTGTAGCATTTACCAACTTCC
1074	CACAAGAGAGTCCAGCAGATCTGATCTATTCATTTAGAGAGAAGCAAACTGAGGTAGAGA[C/G]ACTAACTCCCAGGCAGAAGCAACTGTTCCTCTGGACTAGCTTTAGAGGTTTAAGCTGGGG
1075	TCCCAGAAGTCCTGACACAGCCTCCTCATTACTCCCCTGCCTGTGGTCTCCTTTTCCCCA[C/G]CATCCCTACCCTCTacacacacacacacacgcacacacacacacatcacatgcacacaTT
1076	GGAGTGGGCCATGTGTTCCTGATGGCACCCCTGCTGATCCATCCTGCGTCGCTGGGACAC[A/G]GAGGTCTTGAGGGAGTGATGAGAGAAAGGCCAGGGAGAGACAGACCTTGGAGGCCCTGTG
1077	ATGAAGCAGTTGTTCCAGAAGGATTATTCAAAAGCCACTTGACAATAACAAAGAAAGACG[T/C]TCCCGCCACTCAGGCAGTTACCACGGGTGTGGAGGAGGAACACAGCGGACGCTCCAGCAG
1078	CCAAGGAAGGGGCAGGAGGCTGACATCTGTTCAGCATCTTGTGCACTGTGAGGCATTGGC[A/G]CTTGCTATCAGCGTCCTAAGTCAGTGCTCTCGTAGCTCTGCTGGGTAGAGATTCTTATTC
1079	CTTCACGTGCCCCATGCTCTCTACATGTAGACATGCCCATTCTAATCTCTATCTTTGCAC[A/G]TGCTGATTCCCTTTTCCTGAAATGCTCTTCCTCCCCTACTTTGCCTTTCACACTTCCACT
1080	TGGCCTGGTACAGAGCCTGGGGCTCCCTGTAGACCAACTGGCCTGTGTCCAGCTCCCAAT[A/G]CCTGGAAACTCCTCTCCTGGGCTCTGGGGGAGTGGATTAAGCCAGGGGAGGGAAGAGGGG
1081	GTCCACAAGGGCTCCCAGAAAACCCTCCTGTTCCCAAATACCTTCCCCTTCTGACAGCCA[T/C]GATGCCTGGAAAGCCACGATTAGGTGGGGAGAGGGTCCCATACTGAGATCTCCCTATTTC
1082	CCTTAGAATCACCTGGGTAGCTTTCAAAACCCTTGATACTCACGTTGCAGCCCCATAGTG[T/C]GGGAGCCTGGAGTCAGTGTTCACACACTCCTGGATGATTCATGCAGCTGGGGCCACACCC
1083	GAGTTGGCGCTCATGTCATCTTCACACTTAGTCTGCCTTCTCCCAGGCCCTCTCTGTGTT[T/C]CTCAGCCATGCCCCATGATGAGTTCTGTGTCCCATACACCTGCCTGGCTATTCCCTTCTA
1084	CAGCACATGTTGGCCTGTGTCCAGCCATCAGCGCCCACCTTTTTGAGGCCACAGCTGCTC[T/C]GTTTTCCTCATCAGAGGTTCTCTCTTTTTCTTTGAAATTTAAGCATTGTTCAGTTATGAA
1085	CTGTTGCTCTGAAGGAGGCAGGGGCTGGGCCTGCAGCTGCCTGGGCAGAGCGGCTCCTGC[A/G]TGGGACATGGCTCTTCTCTCTGGTTACAGACTCACCACTTCGCTCCCAACCTACCTCCAC
1086	AGTGAAATGGGACCTTGTATTACAGGCATCTTTCAGGGTTTCCATGGAGTACACCTAGGC[A/G]ATGGTCAATAAATGTGGGTCCCATATCTTAGAGGGCTTAGAGGGACAGCAAAAAGCAAAA
1087	GTTCTTTGACGGCAGTGACCATGGAGGTCAGAGGCCACACTGCTAGCAATTCAAGTCCCC[T/C]ATAAAGATCACTGGGAGAACAAAAGCTGCCATCTCTAGTTCAGAGTTCCTCCCACGCGGT
1088	ACAAATATACTTCAGAAGGAAGGACATTGAAGGCTATTGATCCCATTCTACTTATTGGAC[C/G]TTCCTTAGATGGTTCTTTGACGGCAGTGACCATGGAGGTCAGAGGCCACACTGCTAGCAA
1089	CTGGGAGTTTTGGATTGTTTGTTACTGCAGCATAACTTAGTCTCCCCTGACTCATACAAC[A/G]GGAAACACAGAACAAAACCAAAGGGTGGAGACCCACAGGCACAGCCATGGGTAACCAAGT
1090	GAGATGGGGTTTGTGGAACCAGTGTCAAGGGAACAGGTGGCACTGTGAAAGTTGTAGCTT[A/G]TCACCCCAGGTCCCCACCCCATTTAGGGTTCCTTCCGCTAAGAAGGCCCTGCCCTCCCCT
1091	GAACCCTCTCCCCGCTTCCCTTGGCCCGAGGGTCAAGGCACTCGCAGACCGATGATTGCC[A/G]GGTGGTGGGAAGTCTGAACTGGGATTTCAGCTTGGCGGGGTAGATTAAGGCTCTCCGATC
1092	TTCTCCCTACAGCATTTCAGCCAGTGAATGGTAGAATTTTGCAGGAATAAGAATTAGAGG[T/C]GTAGAGGGTTTTGAGATGCGGGGTGGGTCAGGTTTCACTACTCAAGGACCCTAAGACAGG
1093	TTGCTTCCTTGAAAGTCACTAAGACTTCTTAGACCAATTCTTGGTTCTCACCTGCCAAGA[T/C]GGGCAGGAACATTTCCTAAAAGCTCCTGTGGCTCTTTTTCTTTTATTTTTTAGAGGCGAG

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1094	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs7086484	92523709	T	
1095	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs12779003	92532245	T	
1096	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs12412496	92536145		
1097	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs11596518	92544991	T	
1098	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs10785973	92588151	T	
1099	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs2226116	92590219	T	
1100	10q23.31	HTR7	5-HT7	5-hydroxytryptamine (serotonin) receptor 7	117.1	10	rs12259062	92600025	T	
1101	10q24.31	BLOC1S2	BLOS2	biogenesis of lysosome-related organelles complex-1, subunit 2	12.7	10	rs12254005	102028675		
1102	10q24.31	BLOC1S2	BLOS2	biogenesis of lysosome-related organelles complex-1, subunit 2	12.7	10	rs2305386	102038259		
1103	10q25.2	ADRA2A		adrenergic, alpha-2A, receptor	3.7	10	rs521674	112825580	T	
1104	10q25.2	ADRA2A		adrenergic, alpha-2A, receptor	3.7	10	rs3750625	112829591	T	
1105	11p15.5	DRD4	D4DR	dopamine receptor D4	3.4	11	rs3758653	626399	T	
1106	11p15.5	DRD4	D4DR	dopamine receptor D4	3.4	11	rs936465	633568	T	
1107	11p15.5	TH		tyrosine hydroxylase	7.9	11	rs3842748	2137971	T	
1108	11p15.5	TH		tyrosine hydroxylase	7.9	11	rs2070762	2142911	T	
1109	11p14.1	BDNF		brain-derived neurotrophic factor	66.9	11	rs6265	27636492		Val66Met
1110	11p14.1	BDNF		brain-derived neurotrophic factor	66.9	11	rs925948	27637280	T	
1111	11p14.1	BDNF		brain-derived neurotrophic factor	66.9	11	rs2049046	27680351	T	
1112	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs3818275	35265359	T	
1113	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs10488816	35267994	T	
1114	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs2281634	35270749	T	
1115	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs2273688	35295319	T	
1116	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs4083481	35308455	T	
1117	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs4756213	35320142	T	
1118	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs2025111	35332773	T	
1119	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs1320443	35337365	T	
1120	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs7931955	35341795	T	
1121	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs1885345	35349177	T	
1122	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs911562	35355929	T	
1123	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs4593985	35359700	T	
1124	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs7108848	35365917	T	
1125	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs10836389	35372547	T	
1126	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs2421897	35394439	T	
1127	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs1923292	35394755	T	
1128	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs1923293	35395679	T	
1129	11p13	SLC1A2	EAAT2, GLT-1	solute carrier family 1, member 2 (glial high affinity glutamate transporter)	168.0	11	rs1923295	35399184	T	
1130	11q12.3	CHRM1		cholinergic receptor, muscarinic 1	12.9	11	rs4963323	62431179	T	
1131	11q12.3	CHRM1		cholinergic receptor, muscarinic 1	12.9	11	rs2067477	62434882	T	
1132	11q12.3	CHRM1		cholinergic receptor, muscarinic 1	12.9	11	rs544978	62441806	T	
1133	11q12.3	CHRM1		cholinergic receptor, muscarinic 1	12.9	11	rs2075748	62444845	T	
1134	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs308884	87883972	T	
1135	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs6483229	87903521	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1094				0.25	0.48	0.31	0.22
1095				0.01	0.04	0.00	0.00
1096			p=0.005 (Ikeda et al. 2006)	0.22	0.43	0.30	0.21
1097				0.20	0.01	0.23	0.22
1098				0.33	0.00	0.27	0.31
1099				0.17	0.00	0.00	0.00
1100				0.34	0.03	0.48	0.38
1101				0.50	0.37	0.24	0.22
1102				0.07	0.09	0.13	0.02
1103				0.28	0.19	0.32	0.31
1104				0.07	0.15	0.31	0.21
1105				0.21	0.19	0.16	0.21
1106				0.43	0.47	0.24	0.20
1107				0.25	0.21	0.02	0.08
1108				0.48	0.17	0.47	0.46
1109			p=0.005 (Neves-Periera et al. 2005)	0.18	0.00	0.34	0.37
1110				0.01	0.00	0.00	0.00
1111				0.41	0.44	0.46	0.33
1112				0.38	0.38	0.15	0.28
1113				0.26	0.30	0.35	0.19
1114				0.07	0.14	0.11	0.21
1115				0.28	0.08	0.02	0.09
1116				0.28	0.02	0.35	0.16
1117				0.41	0.43	0.26	0.37
1118				0.41	0.14	0.41	0.27
1119				0.13	0.26	0.21	0.22
1120				0.14	0.36	0.15	0.18
1121				0.27	0.07	0.05	0.06
1122				0.48	0.50	0.23	0.28
1123				0.24	0.14	0.40	0.42
1124				0.15	0.29	0.01	0.04
1125				0.14	0.26	0.36	0.39
1126				0.01	0.30	0.13	0.16
1127				0.44	0.16	0.47	0.47
1128				0.03	0.43	0.13	0.16
1129				0.40			
1130				0.15	0.00	0.25	0.21
1131				0.10	0.00	0.06	0.14
1132				0.29	0.14	0.24	0.13
1133				0.25	0.04	0.15	0.24
1134				0.17	0.33	0.32	0.27
1135				0.37	0.48	0.32	0.38

Key appears on page 109.

	R
1	**Sequence**
1094	ATGGGAGTGCAGAGGTGTTCTTCTTTTACAGCAATTGAAAATAAGGCTATTTTTTTTTCC[A/G]ATCTGCCAACTATATGACTGCTGACATTTGTGATACATTCCTTTCACATCCTCTGTTCAG
1095	GGGATGATGATGATGATGATGATGGCAATGATGAAGTTAAATCTCTTCAAAACATCTTTG[A/G]AATTCCTGACTTCCTTGAGCAATCAAACCTGCTAGAATCATGCCCCATCACCTTTCCTAT
1096	CTCTATGCAGGCCACTGATTTTTTTTCCCACATATGTATTTTGGGGAATTTGAAGCTAAC[A/G]AGGAAGCCAGATGTGGTGCCTGAGCTAACACTTCCACGTGTATTTGTTCCTAATATCTAA
1097	TATGGTAGTTCTATTTTTAATTTTTTGAGAAACCCCCATACTTTTTTCCATAATAACTGT[A/G]TCAATTTACAAACCAACAACAATGCACAAGGATTCTCTTTTCTCCTAAATAAAAAACAAG
1098	ATACACCTCCAAGACAGATCCGGAATTTCTCCAGTTGTCTCTGTCTCCACTACTCCAACC[A/C]AGTCCAAGCTACGATTACCTCTTGCCTTGACTAACGTAGAAGCCTTCCCATTGGTCTCCA
1099	CACACAGGATTCCCTTCTCTTGGTTGCGGTGGCTGCTGTAAGTGTTGGGTGTTGAGGACA[A/C]TTGCATTGCATACTGCAGCTAAGTTTTCTGCATGTTTGGGGTAGGAGAATGAAGCAGCCT
1100	CAGTTTTGAGGAAAGAACATTTAAAGTTCTGAACTAGCCAGGGGTGGAAGTCATTGGGCT[A/G]AAATCCTAAGAAGGCTACATCCTAGAAAGAGGCATCTGCCAGTGGCAGAGCTCTAACAGA
1101	TTAAGGCCATGAGTTCGAGACCAGCCTGGGCAACACAGCAAGGCCTTGTTTCAAAAACAA[A/T]TTTTTTAAAGTAGCTGGATGTGATGGTGCACACCTGTAGTCCCAGGTACTCAGGAGGCTG
1102	ATGTCTTCCTACTTCCCAGTGAATCCTATTCTTATCCTTTGTGCATCCCAAGATTTGTTG[T/C]TAGCACCCATGGGTTTCTCGTTTTCCCCCACAGAGGTTCCCTATAAAAGAGAAGAGGAAG
1103	CCCCCACCGCTATTCTTATCAGAGAGAACATGGAAAATATTCTACTCCCTCTTCCCCTTA[A/T]TGAAGGATGCTGTGTGTACATCTGAATGGGGGTGGGATGCGGGGCGGGAGTGGAGTCTAG
1104	CTAATTCCCCTTCCATTCCCAACTCTCTCTCTCTTTTTGAAGAAAAATGCTAAGGGCAGC[A/C]CTGCCTGCCCTCCCCATCCCCCGCTGTAAATATACACTATTTTTGATAGCACACATGGGG
1105	GACTACAGAAAATACCTCTCAGGTCACAGGTCACCCCTCTTTGGTGAAGAGTCCATAGAA[T/C]TCTCTGCTGCGCTTTGCAAGCACTTTCTCTTCTRCACGTTTGGAACCTACCCCGGCCTGT
1106	CTGTGTTCTCTGCACACAGAAGGCTCCATGGCTGTGGCTGCCTTGGGGCGAGAAAGTACA[C/G]ACTCAGCAACAGCTCAGCAGGCACCTGGGGTAGGGTGGCAGCGCCAGGAGGAACCTGCAC
1107	CCCCGGGGCGGGGGAAGGAGGTGGGACATGTGGGCGTTGGGGCCTGTAGGTCCACACCCA[C/G]TGTGGGTGACCCTCCCTCTAACCTGGGTCCAGCCCGGCTGGAGATGGGTGGGAGTGCGAC
1108	TGGCCTTGAGCAGGGCTGGACCTGTGAGCCCAGGTCACAGATGAGAAAACCGACCCCTGG[T/C]TGCAGCAGCCCCCACACAGCAGGGACACCATCCGTGAGAAGGACCCCAGCGTCTGGGGAG
1109	GTGAATGGGCCCAAGGCAGGTTCAAGAGGCTTGACATCATTGGCTGACACTTTCGAACAC[A/G]TGATAGAAGAGCTGTTGGATGAGGACCAGAAAGTTCGGCCCAATGAAGAAAACAATAAGG
1110	AATAGCACAATAAAACAGCAGTTGGGGAACTATAAGGAGCCTTTAAATTGACTTTTTTTT[T/C]CCTCTTCCCACAGAGATACTCTATTATAGCAAAGAAGAAAGATAATTTCATTGAGCCATC
1111	GGAGGGACCTTCATTTTAACACTCACCCAGGTGATTTTTATGCTCCGAGGAGGTCCAGGG[A/T]CTCCAAGTTAAGTACGGTACTGCTGTCTTATTCTTTATTCTAAATTTTAAGGTCTGCACA
1112	TTTTTTTTTTGCAACCCAATTAATATGGGCAATCAGATGCACTTCAATATCGAATCCAAG[A/G]TGGAAACAGTGGCCAAAAGAAAAAATCTTCAAGCTCTGAGTATATCTCCAAAACCAGAAC
1113	CAGTAAATTTTTAAGACAAATGTCAAGTGAAGAGGAGGATTATTTGCAACTTGTGACACA[T/C]GAGCTAATATTCTTATACAAAAAGAGAGCTTGAAAATCAATCAGGAAGGGACGAATACCT
1114	TAAGGGAAGTGGTCCAAAGTAAAAAATAACATGAACTTTTCTCAGCAAAAGTCTTTTTTT[A/G]TACAGAAGAGCCAAGCGTTTTCCTCAGTGTGCGGTACAGAGGAGGCCCAGGTTCTGAATC
1115	GGGCCCTGTCTGCCCAGGCTTCAGTGATATAATTTTCCTCCTTACCTCCTCTAGCCATTC[A/G]TTCTCCTTTGGATTCTAGTAGTTCTTAAATTTTTTGCAAATAAATATCTTGTGAGAGTGT
1116	ACCTATGCCCTTCAGTTTTTCAAAGGCAGGGCAGAAGCCTCAGCTCTGGTAGAATCTGAC[A/G]TGCTGGAGGTTGAAAGTGAGAAAGGCAGTCTTTGATGGGCTTAGGGGAGTGGGGAAGTGA
1117	CTGATATGGAAAAATATCTAAGATGTATTTAAGAAGTTGAAAATTGCATATGCATGTGTA[T/C]ATTTATAATGTTTGGAAAGAAATTCTGGAAAGAAAAGTTAAAAAATGATAGGCAAGGATT
1118	ATGTCTGGACACATTTTTGGTTTTGCTGCAAATCACCCCCCAAAACAAAGAATTATTTTG[A/C]CCCAAATGCCAATAGGGCCGAGGTCGAGAAACCCTATCCCAACAGATGTCAGGGAGGCAG
1119	CTGCAATTCATGAATTTTCATTTGTGTCAATTTCTTCACAGTGATGGCTGAAGACACTAA[A/C]ATTAGAACCTGTAGAAAGAACATGAGGCTGAAAGTAGAGGACATATTCATTAAGGACTGC
1120	GTCAGCCAGTTGCTTTATACTGAGTTCTTCCAGCAACTCTCTGCACGGAATTATTATTAT[C/G]TCCATCTTCTTGATGAGGCAAAGAGAGAGAAAATAACTTGCTCCAGGACACGTGGCTGAC
1121	AGGGTGGCATCTTCCTCTCTCATTCATGGGGTGAGTTTTGAGCTGTTTTCTTGCAGAGAC[A/G]ATGGGTGGAGTTGACTCATCTGTGTTCACTTTGGTCCAGCACCTGTAGGCCAGGTGGCTA
1122	ATTATTCCATTGACTTTGCCTGTCGTATTTGTCAAATCCAGATAATTCAGACCCTGAACA[A/G]AAAGAAACGTTTTTGTTTTGTTTTCTCATTTTACATACTGACATGTTCTAGCTTATCTAG
1123	CCTTACCCATAAAGATCACCCCTTCTTTCTCTTTGAGTTTGAGTCCCACCAAGAACAGCC[T/C]GAAAAATCTTCAATAGCTGTCAATTTTTAAAAACATCAGAGGGACACTGAAGTACAAGCC
1124	TAAGCATCAGGACCTTAAAATAAGGGAACCAAAATGCCTTTCTCAGCTTCCCACTGCACC[T/C]TTCTGGAAGGAGGAGGAAGTGACAAAAAAAAACAAAAACAAACAAAATCATTTCTAGACT
1125	GTGTCCACAGATGGGGGGACACACCAATTTGGCAGCCTGAGCCTGCTGGAGTGAAAGGCC[A/G]CTTTTCAAAAATATGGAAGTGCAAATAGCTCATTTAACTCCCCTGATGAAAAAAAAATCC
1126	ATAGGGAATACCATCTTTTCAGAAAGATTCCAAGACTTGGCAAAGCTTTGGGGTTATCAT[C/G]TGAAAATGATGTGTGCTGGGCATGGCTGGTGCAGATTACTGGCTTTCTCTCAAACTTTTG
1127	AAATAAATGTGAACCAGAATGGTCAGTTTCCCATATTATCCTATTCCCCAAACATTCTGG[A/G]TCAAACAAAGTTGAACTGAAAATATATAAATTGAAAGCATATAACTATATTGCTATTTTT
1128	TATAAAAGCCTTTTTAACTAAACATGGTAAGACACTGATCTTGATCCATATGGGCTCCTA[T/G]TATCTATTTCTAGAGATCTGTTTTAGCACAAGGTACCACCCTCCTTGTACACAGGTGTCT
1129	AAATCTCTGCTTACCTCCTTCCTTTACTCTCCTTTCCAAAATCTGAATCCAAACGTCATC[T/C]TCCATCCATGCCTTTCTCCATCTCTCCCCTCCCCCCTTCTCTCTCAATCCTGTCTGCACC
1130	AGGGCTGTGAGGGAGCAGTGGTAAGGGAGGGGCCCTCTTAGGAACTTGAGCTCACAACCC[C/G]GTAAGCTGTGCTGGTGGGAAGGGGATATGGGGTTTGGATCCTTCCAAACAGGAAGGTCCA
1131	TGCTGACCTCATCATCGGTACCTTCTCCATGAACCTCTATACCACGTACCTGCTCATGGG[A/C]CACTGGGCTCTGGGCACGCTGGCTTGTGACCTCTGGCTGGCCCTGGACTATGTGGCCAGC
1132	AGGAGGGGCTTCTCTCCAGGACTGTGGCCTCCTGATGAAGGCTGTTAGAAGGCTTTAATA[A/C]TATCACTAATACTCCTTACACATAATAGCAGCAAAGAAAAATTACTCATATTATAGTAAC
1133	GCCAGGAAGCAGCCCTTGCCACCAGCATCCTGTGGGAGGTTGACCCCCATCTTGATGGGG[A/G]TGCCAGTCCCAGAACCTCCTGTCCTCCCTCAGGGCACCCTGAAACCCACCACCCCCGTCC
1134	AGAAAAGGATGGCTTTCTGCCAGAGTTTCTCAGATTGTGAAAGAATCTGAGAAACAAAGT[A/G]CTTCAGATTTACTTTGGGAGCAGAAGAACAGAATGCTTGTCAAAAGCATAGATCCTTGGA
1135	ACCAATATCTACTGAATATTGGATTACTGAAATTTCTATATTGGCTATGTGATTCAGAAT[A/G]CATAAATGAGTGCAGAATGAAGTGAAAGACTAGAAGAAAATAAACAAGTTTAAATAATAA

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1136	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs10501667	87904955	T	
1137	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs178244	87908693	T	
1138	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs905645	87910401	T	
1139	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs308892	87911831	T	
1140	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs2131068	87920854	T	
1141	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs308793	87923538	T	
1142	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs308787	87925352	T	
1143	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs719182	87929030	T	
1144	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs10501669	87933883	T	
1145	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs308873	87936450	T	
1146	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs10501670	87938932	T	
1147	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs308875	87942090	T	
1148	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs2133395	87961055	T	
1149	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1504088	87965452	T	
1150	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs3816649	87977813	T	
1151	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1354411	88016449	T	
1152	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1499043	88032310	T	
1153	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs904462	88070572	T	
1154	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs6483387	88079083	T	
1155	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs3763964	88079420	T	
1156	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs2219746	88082538	T	
1157	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1993842	88091682	T	
1158	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs2169662	88093542	T	
1159	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1532548	88096475	T	
1160	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1499177	88097077	T	
1161	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs904493	88104997	T	
1162	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1000061	88115425	T	
1163	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs10501680	88117162	T	
1164	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1903851	88120139	T	
1165	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1903841	88173280	T	
1166	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs645327	88228434	T	
1167	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs547644	88277389	T	
1168	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs167569	88281729	T	
1169	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs1508673	88287173	T	
1170	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs10830200	88385087	T	
1171	11q14.3	GRM5	MGLUR5	glutamate receptor, metabotropic 5	540.2	11	rs7126679	88393493	T	
1172	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs7944570	112350798	G	
1173	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs12575544	112424195	G	
1174	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs2509377	112431469	G	
1175	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs7933413	112464115	G	
1176	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs10502168	112500642	G	
1177	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs1245119	112506871	G	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
1136				0.29	0.03	0.43	0.49
1137				0.39	0.20	0.27	0.32
1138				0.13	0.00	0.00	0.00
1139				0.38	0.07	0.24	0.22
1140				0.01	0.00	0.00	0.02
1141				0.43	0.40	0.50	0.46
1142				0.18	0.38	0.07	0.08
1143				0.17	0.00	0.00	0.00
1144				0.02	0.23	0.00	0.00
1145				0.20	0.00	0.00	0.00
1146				0.28	0.19	0.07	0.14
1147				0.48	0.05	0.46	0.50
1148				0.35	0.06	0.41	0.50
1149				0.30	0.39	0.28	0.41
1150				0.09	0.31	0.16	0.11
1151				0.05	0.49	0.34	0.30
1152				0.02	0.03	0.18	0.20
1153				0.08	0.20	0.47	0.43
1154				0.06	0.43	0.38	0.32
1155				0.02	0.05	0.17	0.15
1156		Y		0.31	0.35	0.13	0.14
1157				0.05	0.46	0.25	0.21
1158				0.01	0.02	0.16	0.10
1159				0.06	0.00	0.00	0.00
1160				0.38	0.23	0.50	0.46
1161				0.25	0.29	0.47	0.38
1162				0.40	0.36	0.44	0.41
1163		Y		0.12	0.20		0.02
1164				0.17	0.28	0.19	0.21
1165				0.37	0.24		0.48
1166				0.32	0.08	0.01	0.00
1167				0.04	0.08	0.01	0.00
1168				0.03	0.08	0.01	0.00
1169				0.03	0.24	0.32	0.27
1170				0.40	0.41	0.38	0.47
1171				0.36	0.13	0.48	0.33
1172				0.15	0.11	0.36	0.40
1173				0.21	0.28	0.28	0.41
1174				0.48	0.29	0.09	0.20
1175				0.22	0.23	0.48	0.41
1176				0.11	0.00	0.19	0.10
1177				0.42	0.38	0.43	0.46

	R
1	**Sequence**
1136	TGTGAAAGCGAGTTGGAAAATGTTGCATATTTCACATATGTCTTATGTGTAAATTTTAGT[A/G]ACTCAATATGGAATGGACACTAATGAGGCAGGAGGGTAAGTCTGGGGAGTAAGTGGGTAG
1137	ACTAACAAATACTTTAGTGTTACTTAGATGTTTGTGTTCTTTTAAATAATGCTCCTTTCT[A/G]TATGTACCATTTATATAAAATAAGTGTGAGAGTTAATAAGTTAGATTTGTAAGGAGCAAA
1138	TTGATCAGAGGAAAATTCTAGATGAAGGCAGAAGGGAAGTCATTATGGATCTTTAGGTTA[A/G]AGGGAAACAGTGAAGCCAAATTTAAAAAGATCAATATTATGCAGTACTATTGCAAGGTAA
1139	GAGGAATCAGTCTTCCTATCCAAAAGGGTAGAAAGGGCTCAAGTAAAAGCATAGGCAGTG[T/G]CTCAAGCCAAGGAGATTATGGGGAAAAAAAATGATAAGGTTTGAAAAATAGTACAGTTAC
1140	ATCCTTTTCTCTAGCCCTTTGGCTAAAATAAGTTTTCTACCTTTTCTCAATCACCTGGAC[A/T]CACATTTTTGGTCTCACCTTCTATGTCCCAACTCCTTCCCTTCCCCACCTCCCACAAGGC
1141	GAAAGACATTTGGGAAATTATCATCATTACAACTTGATTTCAGTTAGGAATCTTCCTATT[T/G]AAGCCTCTTGATAAACTGAATAAATGACTGTCCATTTCCCTGTTTTCTTTTTTTATCCCC
1142	TCTTTGGGCAACTCCAGTGAGAAAGCCTTTCTGCCCAAGATGCACTCAGCTTGTGTAGCA[A/G]TAATCAAAGACTACCACTGTGGGTTTGCACAGAGAGCTCAATGTAAGCAGCAGAGACAAA
1143	CTTTTCACTAATCCTGGGGTCATCTCATGACCCCACCTAATAGACAGTCCTGGTGACAAT[T/C]TGAGTAGGTTACATGACTTTACTCTTTAGAATGCTACTGACATGGAAATATTTGACTTCA
1144	GCCTTGGAAGATGAGTAGGATCTGGAGAGATAGAAGGAAAAGGTGGAGGACTCTAAAGAA[A/C]GAGAAATAGCATGAACATCACTTCATGCAGACTAATAATGCCTGAAGGAAATATAAGCCA
1145	AATTTTAATATGCTATTGAGCCCATCTCTTGGGATGTCATGTGGGCTTAAATAGGTAAAT[A/C]AAGTCTCTGGATGTAGGTCTTTGGTGGAGAAGCATCTACCATGCTCGACCCAGCCCTGTT
1146	ATTTGAAATCTACATATCTTCCATTTATTTATCTAGATTTTAGAAATACTGTTAAATTTC[A/G]GAAGAGTTAGCAGGGCTGATGTCTTGACCAGCTCTTTTGATTACACATTACACTTCTTAA
1147	AATGTGCAACCAAAGTTGAGAACCATTGTTCTAGGAGGATCATTCCTGTCAGTTAGACTT[T/G]AAAGAAAATGGACTTGAGATAGCTTCACTGAGTAAGTAGGAAAGGAGGCAAGTAATCTGG
1148	TAAAGAAGTGTTAGACAAAGCATTGTTTGCAAAATCTAGGGAGATAATGGAGTACACTTT[A/G]ATTTGTTATTCTGTGTGAGCTATGATCTAAGTTATTGGCTCTTTCCAACTTTAAAAATTT
1149	TTTGTGAATTTCAGGTGTTTATTAAAATAAATTCATGCCCTTTTCCAAGAAGAATTCCAA[T/C]ATTACAATCTCTTTTTGAATCAATAGTGATAACTTAATATGTTTTCCTCTGATAATTTAG
1150	TCTCTAATTACAGGTAACCCATTATTCAGTACCCAGGAATGTCGCGAGAGTAGATTTGTA[T/C]CTCAAAGCTATGCTTAATTTGTTTCCCAACAGGTTCTCTGACTCTGAAAACACATCATGT
1151	CCTTTTCTCACACTAGATTACTGTTCTCTCCAAATACAATCTTGAAAATGTTAATGTGGT[A/G]CAAGGATGAGGAATCTCAAATCTGGGTGTTAGCTGTAGCAGTTATTTAATTTAATTTTAT
1152	ATGGTGTAAGGTATAAATCTTTACAGATGTATAATTACCATTTTTCTCTCATATTTTTGA[A/G]TGCCAACAGCTATTGCACAGCAAACAAAAACATACATACAATAATACAACAGAGTAGGTT
1153	AGGTTTTATAACTTTTATTAATTTCCTAAAGGATGAACAATTCAAAAATCAGGGATCATA[A/G]CACTGACAAAAGCTCTAAAGTAATAGATTTCTCTTTGTATGCAAGTGAACTCTTTAAATA
1154	GATCTTCGAGTACTGATCAATATCTGTGATCTTTGAAGGTCCAGTTGTGTTACCATTCCC[A/G]GAAGCAGTCCCTAAGCCCTCACCCTTCCTCACTCAAGATTTAGGGCTTCTTCTCTACTAT
1155	ATCATCTAACCCAGGAAATTTTGGAAGGTGCTATTAATAATTTTCCTGTGATGATAGGTA[T/C]GAACCTGGATGGATGGTCACCTTATTTTTAAAACTGCTTTCTAAGGTGATTTTTCTAATG
1156	GGCTGTTTGCCTGGACTCACCCTAAGTCAACAGAGGCTGTATTTCCATCACCATTTCCGG[A/G]CAAGCTTGTGCTTCTGGCATCATCTCCATGTGCCCTGGGGGCAAATTTAGCTGAGTTTTG
1157	GCTTAACTCATAGTATATATTGGCTAACAACTGAACATGCACGTGGAATCCTTTCTCAAA[T/G]AAGTCACAGATTCTGTAAAAGACTTCACTGAGAAATTGACTTTTGATTAAATGTTTGTTT
1158	ATTTTAGAAAAAGTTAAAAATAATATTGGAGAGCGTCCTTCTGTCTAATCTCCATTAAAA[T/C]TGTTATGTGCCCTGTGCAAAAGCCATTTATATGGACAGACTCACACAGGTTTGCAGGAAA
1159	GAGTACACAAAGGTTGACACTGCTGTTTAAAACCTCAATGATAAGGGGAAGGAATGTTCC[A/G]CAGTGAAAAGTTGTTATCTAGTTGCTTGAGTGTTCAGAGGTTTCCCACATCTTTTGTAGA
1160	AAGGTCAGTGCAGAGGAGACCTGAAGAAAGAATATGATTTTAACAGGTGAAGATTGGGTA[A/G]GAAAGAAGATACCTTTCCACTATCAGGGATGGTATGTGCTTAGGCTCAGTGGCAGATTAG
1161	CACACTGTACATGTCTCTATCATAGCACTTAGCAAACTAAACTAAAACCAATTGTTGAAA[T/C]GTAGTCTCCTGTTTGACTGAAAATTCCCTGAATGCAAGATTACTTTATTAATTTCTACAC
1162	AGCAACTGGGAGTCTCATATCCTCTCTTGGTGACTCTCCAGGTATTTATTGTTCCTTTCT[A/G]TGAAGAGCCTATGAGGAGAGGGAGAAATCATGTTACACAGAGAAAGTCCTTCAAAGTACG
1163	AGCAATACATTACAAACAGACAGGGAGACATTAACAGCTAGACATTCTGTGCAGCAAACC[A/T]TTATTTATGACAAGGTCACCTTTGCTTTAAGTAGATATTCAGCAGTCATTGCATAATAGG
1164	ACCATGTCAATGTGAATACAGCATAACAAGCTGGGTAACACATTCCTTAGACTTAAGCAT[T/C]GGAGATAAACAGATTATGACTGAAACTGACCTAAGACTTGGAGTAGATATAGAACGAAGA
1165	TCTACAGTACTTAAAAAAAAAACCTTCTAGATTACTTGCAAAACAATATCAAAATTTTTG[T/C]TTATCTATTTCCAGTAGTAAATTTTGTGTTCCTGAAGGACAAGAATCATATTGTGTTTAC
1166	CTGATTATACTCATGATTTATTTGATGCTGAAAACTTGGTTAAAAATATAAACAACGATG[T/C]TGAATTTTTTCTTAGGAAACATAGCTCACTTTAAATAATGTGTTTTATCATGGGATTTCT
1167	TTGAATACCACACTTATGGTTCAGAGACTCCTGGGATTCCACCGAAAAAGAAAAGGGAGT[A/G]TACAAGCTAAAGCTATTTCCAGTGTTTAAAAGAAACTAAGGGATACAATATATTAATTGC
1168	TGATTAGGGTTTCTGACCATCAGAGTACTAATATAAGGCAACTAAGAATGCTAGAATAAC[A/G]GGTTTCCTTGCAGTATGGAGAGAAGGGACCACCATATGCATATAGGTAAACTCACACTTT
1169	TCTTTGATCTCTCACAAGAATCTCACTAAACTCCATTAGGATAGAGAACTTGATGTGATT[T/G]GTCACTACTATATCTCCAGTTCTTGGGAGAGAGAATGCTTGATGTGTAGGAACTATTTCT
1170	CAAAGTAAGAGTAGACTTTTTGTTGCCATGGAGATTTCGGAAATGAAGGTAAAATGTATC[T/C]GCATATAATACTTGCAAATAAAGATCTGTAGGGGTAGCAGGAATTCCTCATGCCAATGAA
1171	TGGTCTACATGTCCTAGACACAGAACCGGAGGAACCATCGATTCCAGCTTCATGCCTATC[T/C]GGTTTTTGATGAATTAATGATCCATTATCCCTGTGAGACCATTCATTACATATTATTCTA
1172	ACAGTTTGTGTGTGTGTGTGTGTGTGTATGTATGTGTGTGTGTGTTTGAATTAGTGGTAT[C/G]AGAGGCTCTATTGACTTTAATTTTGGAGCAGACTCAGAACCCACTGATGACCTATCTCCT
1173	AAATAGACTATTTGGATTGGCATTGCTATCTGTTCCAAGAATGTTGTTTTTGACAGAAAC[A/G]TTGAAAACTTTTAAAACAATGTTAAAACAATGGGTATTTAGGTGGTTAGCAAGTTATTTT
1174	AGGCTACCTAGCTAAAATAGCAAGGAGTGGGTTGAGAACAGCAGGAATATGTTAAGGGAA[A/G]AAGGAATATGTTTCTGTGCAAATATTACCATACAATCTTAATCTTTTTATCTTCCTGGAT
1175	TCTTGAGTTTATTTGATTTTGAAGTTGCTTCATCAGAAATGAATAAATAGACTTAAAGAG[A/G]GAAATACCACAAGCTTTAAACATAAACACTAAGTAGATTGACATCTTGTCTCTAACTTCA
1176	TGGAAGGGCTTTCCTTGGATTATAACTTATCAAAAGATACCAGAGCAATAAGGTATAATA[A/C]GTCAAGGAAAAAAGAATTCCCATTTTTCCTGTGTGTGTGTTCATTGGGCTCTCACTACAGCA
1177	AATAGAAAAGAAAAGGTCTCTAGTAGTTTTCCTCATAGTCCAACCAGTGCTGCAAGGAGA[C/G]AGTTACTATGAACAATTCGACGAAGGACTGCAACAATACCACCATTCTACCTTAGGAAGA

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
1178	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs4937993	112509872	G	
1179	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs1261878	112513530	G	
1180	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs10502169	112523618	G	
1181	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs10502170	112545328	G	
1182	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs2043602	112548936	G	
1183	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs2196456	112561921	G	
1184	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs1943620	112570503	G	
1185	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs1836796	112578570	G	
1186	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs1821693	112582751	G	
1187	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs2850303	112596440	G	
1188	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs646558	112611117		
1189	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs2303377	112616711		
1190	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs620291	112619068	G	
1191	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs605843	112630444	G	
1192	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs7951404	112634337	G	
1193	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs618114	112650283	G	
1194	11q23.1	NCAM1		neural cell adhesion molecule 1	316.4	11	rs668204	112654852	G	
1195	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs6279	112786283	T	
1196	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs1076563	112801119	T	
1197	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs7125415	112815891	T	
1198	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs4648318	112818599	T	
1199	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs4274224	112824662	T	
1200	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs7131056	112834984	T	
1201	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs4350392	112840927	T	
1202	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs1799978	112851561	T	
1203	11q23.2	DRD2	D2R	dopamine receptor D2	65.6	11	rs12364283	112852165	T	
1204	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs6589829	120036183	T	
1205	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs7928347	120041103	T	
1206	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs10502240	120053122	T	
1207	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs4445646	120061551	T	
1208	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs7126415	120071745	T	
1209	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs11217976	120077744	T	
1210	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs3133855	120090061	T	
1211	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs1939664	120090510	T	
1212	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs949298	120113295	T	
1213	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs1945010	120122714	T	
1214	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2156762	120129549	T	
1215	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs3133864	120133222	T	
1216	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs10502242	120146214	T	
1217	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs7948804	120148017	T	
1218	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs948028	120149657	T	
1219	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2852217	120152436	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1178				0.46	0.19	0.21	0.23
1179				0.30	0.01	0.14	0.17
1180				0.12	0.12	0.30	0.23
1181				0.13	0.31		0.38
1182				0.40	0.47	0.44	0.48
1183				0.28	0.01	0.15	0.18
1184			p=0.037 (Sullivan et al. 2007)	0.33	0.25	0.47	0.40
1185			p=0.007 (Sullivan et al. 2007)	0.45	0.01	0.26	0.34
1186			p=0.036 (Sullivan et al. 2007)	0.42	0.27	0.27	0.34
1187				0.49	0.07	0.28	0.36
1188			haplotype (Atz et al. 2007)	0.22	0.42	0.23	0.24
1189			haplotype (Atz et al. 2007)	0.33	0.22	0.41	0.41
1190		Y		0.18	0.18	0.15	0.16
1191				0.24	0.48	0.33	0.29
1192				0.08	0.08	0.00	0.00
1193				0.39	0.16	0.10	0.16
1194				0.08	0.03	0.06	0.09
1195				0.30	0.34	0.47	0.47
1196				0.34	0.14	0.06	0.06
1197				0.07	0.15		0.35
1198				0.18	0.50	0.46	0.47
1199				0.46	0.18	0.34	0.27
1200				0.45	0.26	0.47	0.47
1201				0.12	0.08	0.35	0.38
1202				0.03	0.13	0.11	0.14
1203				0.08	0.01	0.00	0.01
1204				0.36	0.18	0.27	0.27
1205				0.27	0.23	0.42	0.21
1206				0.17	0.26	0.06	0.01
1207				0.33	0.14	0.44	0.42
1208				0.46	0.23	0.44	0.43
1209				0.02	0.00	0.00	0.00
1210				0.35	0.41	0.46	0.43
1211				0.46	0.24	0.38	0.34
1212				0.23	0.22	0.44	0.49
1213				0.33	0.18	0.43	0.46
1214				0.33	0.20	0.14	0.18
1215				0.22	0.02	0.02	0.03
1216				0.03	0.25	0.00	0.00
1217				0.08	0.40	0.11	0.18
1218			haplotype (Pickard et al. 2006)	0.15	0.17	0.12	0.17
1219			haplotype (Pickard et al. 2006)	0.26	0.10	0.42	0.37

	R
1	**Sequence**
1178	AGAGGCCATTTAGGTTCTTTGCCAAATGAGAAAATTTGTAATTTTGTATCTGCTAATCAC[A/G]TCCACCTACCATATATTCTTTTTTCTCTCTTTGCCTATTTTCGGTGGCAAAAAAAAAACA
1179	ATTGCAGTGTTTCATTTAAAGCTTTTAAAGTACAGAAGGCTCTAATAATGAGTTTTGCCA[A/C]AATCAGTCTTTGAAGAAAGTAATTTTGACATGTAGGTTTCATATTTTTGGAGATGTCTTA
1180	GTAGTTTCTGAACAACCCCAGAAGCTTGTAACAGGGACAGCTCCTCTACAAATACGTAAC[A/G]CAGCCAGATAGGACATATCATTTATGGGGCATCACCTCAGTGCCAGATGCTATATGGTGA
1181	AGATTGGCTCCACATTAATAATGCAGAGAGAAAAGATGTTTGCTTAGAAAAAGCTAGAAC[A/G]TGAACTGTGATTTGCCTTCTCCTGACCCTGTGGCAGCTCCTCAAAAATATAGTTCAAGCT
1182	TAAAATTGCCTATTACTTAAAAATCTAAAACTCAGTAGACCCTGTGTGGA[A/G]GCTGGAGCTGCCACGAGCAGTATTTTTGAAAAGTAAAACTTGACAACATCATGGGAAAAA
1183	AAATAACCTGAAAATCATATTATGACCGTTGTTTTCTGAGATTCACACCAGTCTAATGGT[T/C]CCCAAATGCAGCGGGGGCAGGCTCTGGACCAGGGGCAGGTTATCTGGTTAagaatcacct
1184	TATGAGTGTAAAGAGCCCAAGGGTCTCCTTCAAGTGCATTTGGTTTAGAGATGTCTATAT[A/G]TTATCTGAAAGTTGTCTGTATGGCTCGTCTTTATACCAGGAAGCTCCGTTTTCTTTATCC
1185	CCTAGACTTCCTCTGTAGTCAAGGTGAAGTCTAGATGACAGATTTGCTATGTTGAGGCAG[A/C]TTTTTGCAAAAGGAAGGAAGAGGCCCTGGCTCTTAAATGGCCATACTATTGACCCTGTAA
1186	AGTTGGACATTACTGCTCCCAGTGGTTAAATGGTTAACACCAATTCGAATGCATCAGCTA[T/C]AACAAAGAGTGCCATTTCTCTGGGACTGTGATAAACAACCTTGTACAAAACTGTTTTTTA
1187	GGATTTTATAAGGCAGCTTATCATAGATATACTAATGCCATTTAATGCTCATGCATTTTA[T/C]AACTCTTTGCATGCATTCTGTTAAAATCAAATTTTTATTGCCAAAAAGGAACAAAGCAAG
1188	CATGGGCCAGCTCAGGGTTCCCCACTGCCCCCAGGGAGAAGAAGGTGGGCTGGGAAAAGG[T/G]GGGCAGCTGGCTTTACTTACGGACTGGCTGCGTCTTGAACTCGGAGGCCGCGCTGATCTC
1189	TTTTTTTCATTCAGTATCTGTGTGCCTCAATGATCTTTTTTCCCCACCTTCATTTTTCTT[T/C]CTTCAGCGGCATCTGCTAGCTCGTCTACCCCTGTTCCATTGTCTCCACCAGATAGTGAGT
1190	CAGAAGGAGGGACAGCAAAGCGAAAGCCGGGAAGGAGATGCTGTTCTTTTGTGTCCTCAG[C/G]GTTTGCCTAATCCTTGGCTATTTTTAACTAGAGAGTCGATTTGGAAAAGCCTCCTCATGC
1191	TTCCTTTGATACGAGGAGGAACCAGAGAGAAGGCTAAGGAAGAGCCCACTACTTATCATC[A/G]TAGGGCCAGCAGCATGCTGATCACCTGGGCGCTTTTTAGACCTGTAACAAGATCCTTCCA
1192	GCCCACTGTTGGACTTGACAGCAGAACTTAGTCCCGAGGTACCTCCATCTATTTGCTGCC[A/G]TTGTAGAGACCAGGTCACACTGCATGGAATAGAAAAACCTTATTCAGTCCAACAGATGTT
1193	GAGTGGCTGGGAAGACTCGGGGCTCCCCAGCATCAAATGGCTGCTGGGTCTCAAAGTTCA[A/G]GAGAAAGTCCTTAACCTTTCAGGTTTGTAAGTGTCTTGCCAAAATTCAGTGGCACCAGCT
1194	TTTAGAATAAGCGCCATGTCATTACCTTATTGCTGAAATCTTGAAGCTCAGGTGTTGACT[A/G]TTACTACGATTAGGTCTGATGGTATCGCACACCCAGGATGCCAACAGCGCCAACTCCCGC
1195	CTTCCTCTGGGGCTCTAGGGTTGCTGGAGCCTGAGTCAGGGCCCAGAGGCTGAGTTTTCT[C/G]TTTGTGGGGCTTGGCGTGGAGCAGGCGGTGGGGAGAGATGGACAGTTCACACCCTGCAAG
1196	TGGTTCTGTAGCTCACATTCTAGGAGAAACAACAGCCAATTAATCAAGCAATTACATCTA[A/C]GGGTGATAGGGAGTAGGAAATGGAACAGGGAGAGAGATACATAACCTAGTTCAGGTATTC
1197	AAATGACTCACCCAGGTTCATAGAGCCTATTGCTTTCAGAACCAGGATTGCAATTAAGGT[T/C]TCTAGACAGGTCCCCTGCTTTATCCTACAGGGCTCTCTGACTCCTGGAAAGGGCTCAATC
1198	GCTGCAAAGGTAATTAGATGATCAATCGTAGAAAGTCTAAAGCAAATGGAACCTTTAGGG[A/G]GAGAGATTTGTGTTTGCTGTGTCCCATGGAATATCAGCAGGGAAGAAAAGGAACCTAAAG
1199	TCTGTCTCTTCCTCAAGCTCATTGTCACTTCCGAGAGGGGACTGGGGTCAGGCCTCATTC[A/G]GGTTCCCTAGAGTGGAAAGGATTGGTAAGGAGCTGGGTAGCTCTCCTTGGCCACCTCTAA
1200	TAGAAAATATGATCTGGGGCAGCATGGAAATATTGTATCAGACAGATCTAGGCTCAAATA[A/C]CAGCTTCAGTTCTCACCACCTGTGTGGCCTTGATTAACACTTTACTTTCTATCTCTGAGT
1201	GAGTTCTGGCGAATTTAAGATATCTTTTCAGGTCTTTCAAGCCTTCCTACCTCCACTGCC[A/C]CTCCCTAGATCAGGCTGCCAGCATTGCTGTCCTGAACAACTGCAAACTCTCCTAGGTACT
1202	AGTCCTCAAAGGAGAAGACTGGCGAGCAGACGGTGAGGACCCAGCCTGCAATCACAGCTT[A/G]TTACTCTGGGTGTGGGTGGGAGCGCAGTGGGCGGTCGAGGGTTGCGTTCCCGCCTCAAAA
1203	CTTTCTCTTTCTTTTCTTTCTTCTGCAGCAATTAGTTACCAACTGTCCTCAGTTTGCCAG[A/G]TTCTGTGTCAGATTCAGAAGTCACACACAGAAAGAAAACCAGGCCCCTGATCCCGCACCC
1204	GGATGGTGGGGCAGCTGCCTAGCTGGAGCCTGGGACTCACGTGCCCCCAACCCCCTCTCT[T/C]GCAGAGTTATGTCATGCCCAGGCCAGCAGGGGGCTCCATGAGGATTCATAGAAGATGCCC
1205	AGACAAGGGAAAAGGATAAAAAACACCAGTTTCTTATCCTGTTATGCTGTGTATTAAATA[T/C]ATCTAATCCACCGAGATTCAAATATACCAGCTGAATTCTTTGCCTTGTAGAGGATTCACC
1206	GAGACAGCTGGGAAGGGGCTGTGTAACAGGAAGTATTTTATCACGTTGATTTAGTAATCT[T/C]GCCACTCCTAACATGTCAGGGCACTAAAGGAGTAGCCTGAGAGCTGAGTGTGATCTGAGC
1207	CCATGTCCCTGGGGCAGGCCGGCTTTTTCTCCATGCACACACCTGGACCTAGGCATTCTT[T/C]TCCCTATCAAACTCATTTTTTTGAAGACCACCAACCCAATGGCATTTTCTTGGTCTTCCT
1208	TGATTGGCCCTGCAGAGGCCTGGCAGGTTGGCAGTTGGAGCCGCCATGCAGATAACTGAG[C/G]GCAGCCAAGGACCCAACTGAGTGCAGCCTCTGGAAGGAGCAATTGAAGGGACAAGACCAG
1209	catttaggaggctcttgcagtaatccaggtgagagaggttgctggcttgtccaggatgca[A/G]cagtaaaggtggtaagaaaggttggaattctggatagattttgaaggtaaagccaacaga
1210	TCACCGCTATTGAAAGGCTGGGAGAGCATAGCATACACTTTTGCATCCACATGGTGTCTC[A/G]ACACAGCTAAGTCCTCAGTCATAACAACAGCAACTATGGATAGCACCTTTAGACTTTAGT
1211	GAGGACACAGAAGATTAAGCACTTACTGAAAAGTATCAAATGTGTCCTAATAGAGGAAGT[A/T]TGAAGTACTACAGCGTCCCATAGCAAGGCCCTGTGACCTGGTCTGGGAGTTAAGGATGGC
1212	ATGGATCCAAAGTCTAGACATTAGACATTGAGCACCAATAGCTGCTAATACTAAAAACAG[A/G]GCAAAAAGCAGGCATTGTGTGTTCCTAATGAAGTGCATAGCTTTGGCTAAAAGAATAGAA
1213	TGTCATCATCAGGAATGACAGATTCCTCAGAGAAGAGGCAGAGCTCAGGTTTCCCATCTT[T/C]TCTAAGCACGTCACTCAGTAGGATTTCAAATACAGACAACTCTTGAATGAATGCAGTCAC
1214	GAGACTACATACCCTATTTTCCTTTTTTGGCAAAACAGTCATCATTTTCAATTCAACAAA[T/C]ATATGAGTAGTTATTCTACATCCAGCCCAATCTTAGGTGCTGTGGGGGAGACAACAGGTA
1215	AGACACAGCCAGAGAGAGACAGAGCTGAGGTTTGGCTAAAAGCCCATGCTACTCCCATTG[A/G]CCACACCACCTTCTGGACGCCCCAAGGCAGGTATCCTGGCCCAGCAGACACAACCTCACT
1216	AAATTCTACAGCACAGAGCTGCCTGGGTGATGGTGGCATGATAAAATTACCTTAACTCCC[A/G]GCATCTGTTTATGCCACATAGTGAAAGTTAATGAGGGCTGACCCTCAGCAAAACTGGGAA
1217	AAAAAAGCCAAAAGGACAGGACTGCCCAAAGCCTTTGGGGCAGGACCACTCAGAGCCTTG[T/C]GGGCTCAGCCTCTGCCCCAGTGTGTCTAGAAGGCAGGAACTCTGCCCTAACAGGTCTAGC
1218	GGCCACGCCCTTGGTGAAATGAGGACTGTAAAACAGCTGACTCATAGGTAGAGGGGATAA[A/C]CTGGGCTCTGAGTTAGAAAAAATTGTCCCCTGGGACTTTATAACCACAGACTACTCTCAA
1219	GGACACCCTCCATGTCTGCTGCAGTCTTTGTCCTGAAGGCAGGAGATCACTGGATGCTCT[T/C]AGAGGGGAATTAGGCTGTAAGAACAATGTATTGCTTTGTAACAAGTTATCCCAAGACTTA

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1220	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs1815771	120161689	T	
1221	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs879602	120161782	T	
1222	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs3133860	120166388	T	
1223	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs1954787	120168573	T	
1224	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs1939670	120184769	T	
1225	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs7105286	120192444	T	
1226	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs4935752	120194329		
1227	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs6589846	120205357	T	
1228	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs7121233	120222363	T	
1229	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs11218030	120225204	T	
1230	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs4331110	120235879	T	
1231	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs4344499	120239629	T	
1232	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs3802912	120243607	T	
1233	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs12577602	120260428	T	
1234	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs7111184	120276273	T	
1235	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2156635	120276878	T	
1236	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2156634	120281211	T	
1237	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2156633	120292102	T	
1238	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs949295	120295062	T	
1239	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs10502243	120300651	T	
1240	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs949054	120301098	T	
1241	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2852241	120302794	T	
1242	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs10892647	120309501	T	
1243	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs602104	120314593	T	
1244	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs2298724	120328931	T	
1245	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs672176	120334459	T	
1246	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs734167	120334569	T	
1247	11q23.3	GRIK4	KA1	glutamate receptor, ionotropic, kainate 4	325.9	11	rs4936570	120339783	T	
1248	11q24.2	FEZ1		fasciculation and elongation protein zeta 1	50.5	11	rs6590145	124823126	T	
1249	11q24.2	FEZ1		fasciculation and elongation protein zeta 1	50.5	11	rs11220083	124833570	T	
1250	11q24.2	FEZ1		fasciculation and elongation protein zeta 1	50.5	11	rs12223186	124836849	T	
1251	11q24.2	FEZ1		fasciculation and elongation protein zeta 1	50.5	11	rs2849222	124858699	T	
1252	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805502	13605448		
1253	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs890	13606575		
1254	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805247	13607242		His1399His
1255	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1806201	13608775		Thr888Thr
1256	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs4764011	13611689	G	
1257	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2268092	13612439	G	
1258	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1806209	13612543	G	
1259	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1806194	13614394	G	
1260	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2193147	13624088	G	
1261	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805470	13627299	G	

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1220				0.12	0.00	0.06	0.01
1221			haplotype (Pickard et al. 2006)	0.18	0.05	0.11	0.01
1222				0.10	0.40	0.03	0.19
1223			haplotype (Pickard et al. 2006)	0.47	0.06	0.03	0.19
1224				0.09	0.32	0.00	0.00
1225				0.41	0.35	0.43	0.46
1226			p=0.001 (Pickard et al. 2006)	0.36	0.05	0.43	0.44
1227			p=0.004 (Pickard et al. 2006)	0.33	0.24	0.48	0.47
1228				0.38	0.05	0.47	0.44
1229				0.14	0.02	0.44	0.33
1230			haplotype (Pickard et al. 2006)	0.40	0.44	0.39	0.29
1231				0.20	0.33	0.39	0.29
1232				0.33	0.19	0.40	0.49
1233				0.10	0.42	0.46	0.43
1234			haplotype (Pickard et al. 2006)	0.31	0.32	0.18	0.29
1235			haplotype (Pickard et al. 2006)	0.41	0.25	0.34	0.38
1236				0.16	0.04	0.06	0.09
1237				0.31	0.38	0.06	0.08
1238				0.43	0.23	0.47	0.46
1239				0.17	0.36	0.02	0.00
1240			haplotype (Pickard et al. 2006)	0.18	0.06	0.43	0.42
1241				0.07	0.13	0.00	0.02
1242				0.27	0.13	0.36	0.39
1243				0.21	0.18	0.02	0.00
1244				0.31		0.28	0.26
1245				0.37	0.49	0.02	0.00
1246				0.22	0.01	0.36	0.38
1247				0.27	0.46	0.24	0.31
1248				0.09	0.12	0.30	0.27
1249				0.01	0.01	0.00	0.00
1250				0.50	0.29	0.30	0.40
1251				0.23	0.45	0.11	0.07
1252			haplotype (Ohtsuki et al. 2001)	0.20	0.45		0.16
1253			p=0.044 (Di Maria et al. 2004)	0.50	0.09		0.21
1254			p=0.017 (Li and He 2007), haplotype (Ohtsuki et al. 2001)	0.10	0.40		0.16
1255		Y	p=0.070 (Ohtsuki et al. 2001)	0.22	0.07	0.47	0.46
1256				0.43	0.46	0.01	0.04
1257				0.09	0.03	0.14	0.17
1258				0.12	0.08	0.23	0.26
1259				0.43	0.02	0.01	0.04
1260				0.38	0.00	0.01	0.04
1261		Y		0.18	0.38	0.00	0.00

Key appears on page 109.

	R
1	**Sequence**
1220	GCACTTGGGGTGTTTCCGGTTTACACAGCAGTCCCGTGACACAGGGAAATGGTTCTCTGC[A/G]GCGCCTGAGCAGCTTGATTCTGTGCATGCCTCCGCGTCTCCATGCGCATCCTCCTGGTGG
1221	TGAAGTGTGATGGGCTTGGCAACCCCGCTGAGTGGGGGCTCTGTGTGTGCCAAAAGGGCC[A/G]GGAGGGCAGGTTAGCTGGGGATGAGCACAGAGCCACCAGGAGGATGCGCATGGAGACGCG
1222	TGTTTTTTTGTTCAGGTGGTCTCTTCCTGGAACGTACTCAGCTGTTTTTTAAAACCCATG[A/T]CCAAATCCTACCTAATAACCCTCATTCTCATACCCCATTCCCACCGTGCCCCAGGTAAGC
1223	AGTGGACTGGTTTGAGAAATTTTGAGGAAGTACAACCAAAAGCAATTGGAGACTGGTTAT[T/C]GGAAGGTGCGGAATTGGGTGAAGGCACGATGCCTGGGTAGCTGGTGCTGCTATTAACTAA
1224	CCCCACGGGGCTCACAGAGATGTGCACTGGGGAGGGCTGGGAGAACTCAGAGTCCTTCAC[A/G]CGGAAGCACTTCCCGATGCTGCAGCCTGAATGGAGCAGAGGGTGCAGTCTCCCTCTGAGC
1225	GAGGCTCAGCCTTCCAGAAGCTCTAGTCTCAGGAGGACACAGTTCTTAGAAACAGGAGGA[A/G]CACTTGCTGCAGGAGGGACTGGATGCCTCCTCAGTGAGCCGCTCCTGCCAGGGCAGGAGC
1226	TCTGTTTGTTATTCACTTTAGACAGAGTGGATGGGATACAAAATACAAGCGGGAAGAAAG[A/C]TCCGTTATGACACAGATCAATGTCACTCTTTAGAATTGCCTTTCATAACTCACCAGACTC
1227	TAAAAAAAAAATTAAATTCAGGCTGCCAAACAAAACGGGGATGTGATTTGAACTTCATCA[T/G]CAACTTAGCTGCGAGTGCCGggaccctaaactcctgagggcagggactgtatgtgacccg
1228	GTCTATTAATGTGAGGTGTGGCAGCCCAGAGGAGAGAGCATGTAGTTCTTCTTTGGGAGT[T/C]TGGATGAGGGTTTACAGATATGGCTTCCCTTACTGAAGCATGGGTTAGAGATGGCAATTG
1229	GTGCATATAAAATACATCAAACTGAAATAAGAACAAGACCCTGGAGACTACTGTGGTTCA[A/G]TATCTCTGGACACATAATGGAAATGCTCCCCTTTGACTGCCCAGGCCTTCTATCTAATAG
1230	TCCAGTTTGCACGTGTAAGCTAATGAAGCTGGGCTCTGGGTAGGTGAGCTGAGGCCTGTA[A/G]CCTGAGGCCTTGGCAGTGTCTGGAGCTGTGTGGCAAGGATGCAAGGGTGGCGCCAGGGGC
1231	TGGTGAGTTTTTAAAATAGGAGCGATGCCTGTCTCTGATAAGACATGCCCAGAGGCAAAG[T/G]CATATCTAGACATCTATACACTTGGCATCTAATTAGTACTTGGCCAACACGGTGACCTTG
1232	CTGTCGGCCACCTGGCAGGTATGGCCTGGGGGCATGGACTGATCTTGCTTTCCTGGTTAC[T/C]TCTCAGTTCAGCCACTCCTCTCTCAGTGCCCTTAGAACGGGGCTCCCTCTCCAGAAAGCT
1233	AACCACGCAAAGACCGGCCCATGCCAGCCAGGCGGGGTGCACACCAGCTGTACCAGGCTG[T/G]CCACTCAGGGCTTCAGGATGGCCTCCCCACAGCCTCTCCCTCTCCTGCCTCTCTCCTTCC
1234	GGGTTGGGTCCATAGAGCTTAGGAACTTGAATGCCAGGCTACTAAGTTTCCCTTCACTGT[T/G]AGGAGATGGGGTCACTGAACATTTTCATTCattcatttatttatgtgatgactgtttatt
1235	CGGATGGATAGAAGAGGACAGATCCAGAAGATTTTTAGAGACTAAGAAGACAGCGGGAAG[C/G]AGGTCCCAGCAATCACACTGGGTGCTGCACCCCCTCCCCCAAAGTGGACTCAGCCAGGCT
1236	CTCGTAGCGGTCATTGCCTTCCATCTCCTGGTGGTTCCCCTTCAGCATTAAATATGGGTT[T/C]TCCTGCAGCAAAACTGGGCAGCTGTCATTCTCATCTTAGCCCTGGTGTCTCACCCGCGTG
1237	CTAGCACTCCTGGGCGTTAGCTTCTTGGGGCTCTGTTTTCTTAGTCTGAAAAACGAGGTG[A/G]TCATAAGAAGTCCAGTTTCCAGATAAGAGGGTTGAGGACAGAAGTGTCAGCCAAATGTCC
1238	ACATTTCAGACCTCACACCGTTCCCTCTGCCGGCAACTCTCTCCTCCTTGTCGCCTGTCA[A/G]ATTCCTACTTGTCTATCAAGGTCTGACTTGACGGCACTTCCCTGAGAGGCATTGCAGTGG
1239	TTCTCCTCATCTCTAAATAGGTTACTGCCAACCTTAGACGTTGCTGTGGGTCTCAAGAAC[A/G]ATCTGTGAAAAAACAGTTTTGGGGTATGACTATTGATGGGCATATGAGCCATGTCAACAA
1240	CACGGGCCTGTTATTAGGACTGTTTTTGTTGGGTAAAATAAAGTACCACCAACTTCTGTG[A/G]GCATCGCCCACAGCCATAGAGAACTTCTAGAGGCCTTCCCTGTGCTCCTTCTCTGTTCCC
1241	TAATGGGCCCCTCTCCTCGAGACACTCTGGCTCATTATACTGCTTTATTTTCTTCACAGC[A/G]GAAATCATGACCTGAAATTGTCTTGTTTATTTACCAGTTTACCTGTTGATTGTCTAGAGT
1242	AATAAATGACTTGTCCAAGGTCATACAACAGGTAAGTGAGTGCGAGTCCAGGTAGTTCTA[A/G]GCCACACTGAAAACTAAGTTCAGTTACCCCCTCTACTGCCTTAATAGCCCCTTATTGATA
1243	CCCCACTTTCTTTGCAGTGTTTGTACGTAGTCATTCAGAACTGATTAGCCTGTTTGTAGA[T/C]TGTTGGACCACACTTCACTTTTCTTATTTCATCTTTTGCATCAACTGATCGACCAGCATT
1244	TTCCCAActcctcctccccctctcctcctccccacccccctccccATGCAGTTCCCAGAGG[T/C]GGACACGAGGTGGCGGTGTAAGGACAGGGAAGGGAAGAGGAGAGTACCGAGCCACCAGGA
1245	TTTGGTCCGTTCCATGGAGGAGTGGGAGGTCAGAAGACAGGGCCATCGTGGCCTACCTCG[A/G]CCTCCTCACCCAGAGCACGTGATAGAAAACACCATGTCGCTGGAGAGAATGCCAGTTTGA
1246	GCACAAGCGGCTCAGTGCAAACCCATCGGCTCTGCTGAGAAAGGGAATGATGCCCGCTTC[T/C]GGAGGGCTCAGTGGAGCCTCGCTCCTGTGTCAAAGGGCATTTTCAGTTGTCAAACTGGCA
1247	CCTCAGTTATCTAATTCATAAAATTAGGTTTCTAATACCTACATTATGGGGTTGGGAGGA[T/C]TAAACCTGATAATCTAGTTAGGTGCCTTACCTCAGTGTCTCACACTGAGCCTACCTTGGG
1248	CTTTAAAATAACATGGGAGGGGAGAAGTTGGGTAGAGGCGTAAATGAAATAAGCCTGGCC[C/G]GGACTTAATAACTGTTGATGCCAGCTCATCAGTACCTGAGAGTGTATTATGCCATTTCCT
1249	ACAGTCATAATTACTATAAACCTGTGTCAGAGAGTTAAGAGGATGGCCTCTGGAGTTAAC[C/G]TACCTGGCTTCAAATGTTAGCTTCACCCCTTATGGCTTCTGCATGGACTAAGCACAAATA
1250	CAGGTCTTTAGATGAGTTTTGTCCCAACCTTCACCTTTGTCTGTTCTCCATGGATGGACT[A/G]AAGTCCCCGAGGCCAGCATTGTACTCTTTGAGGTGGTTTCTTCACAGTGGGCTGGACCAA
1251	AATGCAGTGATGTAAAGAGTAGTCCTGCAGTGACCTTTCCAGCGGGTGTGGTGCCTTGGA[A/G]TTTTGTCTTGGAGAAAGCAAATCCTATTTGCTTCTTGGCTCTAGAATGCTAATGGCACTT
1252	TACATGTATATCTTTTTTTATTCCTCAATGGTACAATCTGAGAGGGAAACAAGGTGTTGC[A/G]GGAAGGTAGAAGGGCTTCTACCAAGAGTGTTCACTCTGGGCTCAAGTCACATTCCCAGGG
1253	GAGTGAAGCTGGGAGAACCAAAAAGAGGCTATGTGAGCACAAAGGTAGCTTTTCCCAAAC[T/G]GATCTTTTCATTTAGGTGAGGAAGCAAAAGCATCTATGTGAGACCATTTAGCACACTGCT
1254	CGGCCTGGCTTTCGACGCCCCCGCCACCGTGGGCTGCCTGAAGAAGTAGGATTTGCTGCC[A/G]TGGAGCAAGCACTGGTCGTCCCCAAAAGTGGGGATGAAAGGGTTTTGCGTGACCCGGTCA
1255	CATGTTCTTGGCCGTGCGCAGCAGGCGCAGGATGTTGGAGTGTGTGTTGTTCATGGTTGC[A/G]GTGGGGGAGTTCATTACAGACTGGCGCTCCTCGATCGCCACCCCATGGATGCAGCTGTAG
1256	TTAATGCCATTACATATTAATTCATCAACGTACTTAGTAAGCATTCAATAAAAATTTCAC[A/G]TGAGTACCGCAGGCGATATGAACACATGAGACGTTGCTCCCGCTCTCCATTATCTAGCCT
1257	GACCTTTTTCCACTTCACCAGATGCTAGGAAGTAGGAGGAAGTAGGAAGAGGTCCCAGAC[A/T]AAAGGAAAGTAAAAGAAACCATGTGCCCTAGAATGCATCTAATTCTAGACAAGCAAAATT
1258	TCTAGACAAGCAAAATTCTGAAAAATCTCATGGAGAAAATTGCCTATTCCCATAGTTCTA[C/G]TTTGGCTAAAAAATTGAACTTTGCTTGCATAATCTGACTAAAGTTTTGGCAACTTTTGCA
1259	AGTAAGGTTTAAGTTGGAACTCTGCCAGAATCTAAAGCCTAAATCCCAGGCTGTTCTTTA[T/C]GTGCTTTTGGGTTGAAAGGAGGAGTTCTTTTCTTCCCACTGGGAATGATGAGAATGTAAG
1260	ATGTTAACGCCCCATCGCCACCCTTCCAAAGCCAATCCATCCTCCCTGCCAGCTTCAATT[T/C]AGCCTCCTTCTAGAAGCCTTTCAGGAAATTTATATGTCAATGGCGTGCACCTCTGTGGTC
1261	TCCTATATTAACTATATTAACTTTAACATATCATAACCTGCACCTTGAGGTTTTAAGTGT[T/C]TGGCAAAGTCTTGTGTCTGGCCATAAAATATCACATCAGTAGCACACATTTAAAGGGCAT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
1262	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs7970177	13630255	G	
1263	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805490	13632338	G	
1264	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2268097	13644099	G	
1265	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805513	13644916	G	
1266	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs11611022	13673187	G	
1267	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805543	13675580	G	
1268	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805545	13679765	G	
1269	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1805552	13682595	G	
1270	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs980365	13711294	G	
1271	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2268102	13713506	G	
1272	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2284406	13716683	G	
1273	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2192972	13723783	G	
1274	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1158541	13737940	G	
1275	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2192975	13740061	G	
1276	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10492134	13750149	G	
1277	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2300253	13753218	G	
1278	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2284411	13757439	G	
1279	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs741327	13768808	G	
1280	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2268120	13769155	G	
1281	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10845837	13771435	G	
1282	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2216128	13774281	G	
1283	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2268122	13788728	G	
1284	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10492137	13817153	G	
1285	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10845840	13822124	G	
1286	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2268127	13832115	G	
1287	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2284418	13834895	G	
1288	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs220557	13839047	G	
1289	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs220558	13839332	G	
1290	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2300266	13843034	G	
1291	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2300267	13843198	G	
1292	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs220567	13845670	G	
1293	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs220599	13866565	G	
1294	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2160733	13872994	G	
1295	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2284425	13880286	G	
1296	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2300273	13881701	G	
1297	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2193509	13887540	G	
1298	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1120905	13895444	G	
1299	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2193511	13896054	G	
1300	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2284428	13901181	G	
1301	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1160295	13901691	G	
1302	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10772713	13903800	G	
1303	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2300279	13907309	G	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
1262				0.08	0.20	0.22	0.16
1263				0.27	0.08	0.35	0.31
1264				0.36	0.12	0.24	0.19
1265				0.08	0.01	0.00	0.00
1266				0.11	0.08	0.01	0.00
1267				0.34	0.01	0.01	0.03
1268				0.31	0.08	0.46	0.47
1269				0.26	0.05	0.34	0.33
1270				0.32	0.11	0.25	0.19
1271				0.41	0.25	0.24	0.17
1272				0.28	0.12	0.39	0.30
1273				0.24	0.15	0.23	0.18
1274				0.41	0.31	0.34	0.33
1275				0.37	0.49	0.36	0.27
1276				0.38	0.01	0.02	0.01
1277				0.47	0.28	0.36	0.37
1278				0.30	0.36	0.17	0.14
1279				0.22	0.46	0.50	0.34
1280				0.07	0.00	0.22	0.17
1281				0.26	0.26	0.22	0.17
1282				0.30	0.12	0.27	0.19
1283				0.13	0.00	0.34	0.33
1284				0.27	0.18	0.01	0.00
1285				0.41	0.49	0.01	0.00
1286				0.30	0.13	0.47	0.44
1287				0.16	0.03	0.13	0.17
1288				0.39	0.42	0.41	0.49
1289				0.40	0.38	0.42	0.49
1290				0.08	0.08	0.21	0.14
1291				0.43	0.13	0.38	0.48
1292				0.37	0.31	0.15	0.33
1293				0.40	0.44	0.40	0.48
1294				0.23	0.01	0.02	0.02
1295				0.28	0.10	0.19	0.38
1296				0.48	0.46	0.22	0.43
1297				0.45	0.48	0.38	0.47
1298				0.40	0.35	0.40	0.46
1299				0.33	0.41	0.24	0.15
1300		Y		0.12	0.13	0.19	0.13
1301				0.31	0.00	0.00	0.00
1302				0.38	0.38	0.21	0.14
1303				0.31	0.06	0.16	0.09

	R
1	**Sequence**
1262	TTATAATGCAAACATAATTATTATAAGGTGACTGCTACAAAAGTGAAATATCAATAACCA[T/C]GTTGGTAGAAAAATGAAGTTCAATTTTTCCAGTTGACTAAGGGTTAAGCCAAAAAACTTA
1263	GAACTCCATGATAATTCTATCATGAGACCAGGCCACTGAATCCTTTTCATGGTCTGAAAT[A/G]TGCATCTCATGTTCTCTTTGTCAATGGATTACAGAGAAGGTAGCCTACTTCAAAATTCTT
1264	GAGGCCACATAGGGAAGCTATAGACAAATTCAATGATTCCAACAGTTAAAAGAAGTGCTC[A/G]CTAGCCTCTCCCACATCCAGAACATTCCAAATCTGAAAGGACAACATCCCATGCTGTGTA
1265	ATGAGAAGAGTGCATTAGTGTTTTTCTGCACAAAGGAATTGTGAAAATGA[T/C]ACATCTCACAGAAACATGTCCTCAATTCCCTTCGATAAGGACATCACTAC
1266	ACATTAAAGAGACACATAAGAATTACTGAGGCAATGAGGGAGCACAAATGGAAGAGGTCA[A/G]AGTCATTTAAAATACATTATAATTTTAGAAGCCTAGACCACAAAGAAAAAAAAAGGCTTG
1267	TGACTGCCCATGGGATGTTGGCACATAAACTTGCAGAGACTGATTCTCTAACTGTAAAAT[A/G]TGAGGGTAAAAACATTTGCCAAAATACCCTCATATAGGTTTGAGAGAAACTAAGGTGAAA
1268	CTGCTTTGCAATGAAGACAATTTTCTAATTGGAATCAACAGACACCCAGTGTCTGCAGTC[T/C]CTGTTGGAAATAGCAGACGTAAGTAGCAATCAAAAGGTAGAGTACAAGCACAGAAGGATT
1269	GATTTTGAGCTCAGTGATTTTTGTTTTTGCAAGAAGTAAACCAAAACCAAGACATGTCCA[T/C]GTGAATGCATAAGTACATACTGAATGAATGTGAATGGAAATGTCCATGCAAACAGAAGGG
1270	TTTCATTTTCTTGAAAGTTGAGGGCTTGTAAAATTCAGACTCACGTTCCCAAGGAGTCAT[A/G]TGACTACTGCTCAGTATGAGACCCTTTCCAGCGCTGTTTCTATTCTGTGGTTCATACATG
1271	GTTGTGTCTCAGAGGAGAAAGTGAACAGCTGATCTCCACACTTGGTACAATTATTCTTCA[T/C]ACATTTAAAGAGAATAAGTCATCACCTCATTGCCTTTTTTTTCTTTCCCTTAACAACCCC
1272	ACTAAATCCTCCCTGGACCAAGGGGACTTTCTGAAGCAGCATTAGGCGTCTTGAGGATGA[T/C]GTCCTGGGGACGAGGATAACAGTGGAAGGACCAATACAACTTTCCATGATGCAATCTCAC
1273	TGAATGATTAATCTATATGCTGCTGACAGATATGAATGATGAAAGGATACTTTGGAGAAG[A/C]ATATTTTGTATATTGTCATAAAATTTTACTAATGTTTTTGATAAGTGTAAAATATGTGAG
1274	TCCTCACCACTGCTTGGCAAGGCAGAGAGTAGGGGAGTCACCGGAGAAGGGGAAGGAGGG[A/G]TGTATGCTTCCTCTGATGGTTTCCATGCCTGTCTACACAAGACAACCACCCAGGGAGATT
1275	ACATCCATCCACTCTTCACAATAGTCTCAGATTATTCTCCAGCATGCAATCATCATTTCC[A/G]CTACTGGGGTTCAGGTTTGCATTGTTTCCCTTATCTACACTATGAGCCGCTTAACTTGTC
1276	AATGAAGGGTTGTTATTAGTGAGGTAGTAATCATTTGCTATCCATGCCCACAGTAGACAA[C/G]ACAGGAGCAAACAAATTAAATTACATCAGGAAAGATTTCAATTAGACATAAGGAAGAACC
1277	ATGAGAAACCCAGGTTTACATAAATAAAGAAGTGATTTTTCTTTCATCTTGTGAAGTATG[T/C]CTTCAAAATCCAAACTTACTGGTTCTGGTTCCAGATAAGATGGAGTGAACACATGCCAAT
1278	ATCCTTGGTTGAAACCATTTTAAGTTAACAACATGACTTTTTTCCCCTACTCTTGGTCCA[T/C]TTGATGCTCTCCTTTTATGCTCCTAGCAGACATAATTAGCAGACACTGATGATGTCATTC
1279	AAAAAGAGATCAGAAGATTAAGAAGGTGGGAATGTTAAAATGGAAGTATTAATTTTATGT[A/G]AGACTGAAAATTGATTACCTGACTCTGTCCTAAGATGCATTTCTGAAGGCTCTCCTAGGA
1280	ACCTCCAAAAATTATTGCCAGATGCATTCTACTATGGTGTCTAGGACATAGCAGGTCCCC[A/G]GCAGATAATTTGCTCCTCCTTTTCTTCCCCCTTCATCTGAAACAGTAAATTCAGATGTCA
1281	TCATTTTATAAATAAGGAGAGTAAGACACAAAGAAACTAAGTGACATATGCCACGACAAG[C/G]TAGGGTGTGGACTGCCATGCAAGTCTTCTGATTTCCAGTTTAATGTTTTTGTTGCTATAC
1282	CCCAGCCTGGGGATGGCACCTTTATGAGGAACAGTGAGGAAGTGGCCTGGGGATGCTTCA[T/C]GATAGGAGGAAGGAAATTATCTGAGTCTCTCAGTCTGAAGTGTTTTACTGATGTTGGAAT
1283	AAGGTAAAGGCAAGAAAGGTTTTAAAAGCTTTAAATGAAAGCTGGCTAAAGAAGAGAGGG[T/G]CAGCAAAAGATCAATGAACAAAACACCCAATAAAGAAAGAGACAGAAAAGAATAAAGAAA
1284	TATTCTCATTTAACAAAGTCTCAGCCTCCATTCTCACCCACATCCTCAAAGGTGAAGTAA[A/G]TGCTCTAAGGTCCATCCTCTGGAAGGGCCCAGAGATACCATGGACTATAGATGGGTGGAT
1285	CTCCTAAATTTTTTACAATATCTGTGGTCTACTTTTTCTCAGTCTCTTTCCAATTTCCTA[T/C]GTCTGCCTTGATTGTCTGCTATGGTTCTACCTAAAACAATTGAAATTCAAAGTCAAGCCT
1286	AGCTAGTTATTTAGAAATCCAAAAGCATTCTCCCATTGATCCAATGTAATAAATGGGGAT[T/C]GCAACCCCAGACCAGCCTGCAAATACCAACTTATCTCAAATACACCAGGAAGATTCTTCA
1287	CCTCTGTGGAGAATCACTTCTTTTCTTTCAGTTGGTTTGAAGGGGCATGGTCACTGTTCA[T/C]TGGTGCTGAGTAGTGATTTTATAAAATACACAGTAGGAACTTCAGACTTAGAAAGGAGGC
1288	AGCCATGACAATCTAATTCAGGTTTTGTCCTCCCAGGAGGTGATCAGTGAGTCCAGATGG[A/C]CACCAAGCTACCTCATTGTCCTGGGCATCGAAGCCAGACTGCACTGCAGGTGTGTGCTGA
1289	CACTCATGAGAATTCAGAATGACTAGGATACATAATCATGACATAATTAGAACCAAACAA[A/G]AAAAGTTTAACAAGAACAAATGAGCTTAGTAAAAATAAGCTGTGTCCATCTATATTGGGT
1290	GAACATTTCAACAGGAAAAAAACCAAACTAGATGGATCTTAGAACATGTCCTCATGACGA[T/G]CTCTGTTCTGAAGGGTCTGTCATTCCAGCATTGAAGGCCTCCTTACATTCAAAAAGGTGC
1291	TTCCCACAACCACTAGTATTCAACATATATTCATTGAATGAATTAATTAATGTTAGTGTT[T/C]GACATTTGTTAAATCCAAGAAAATACTGACAAGTTTGGGTACTGGGACTGCAATTTGTAG
1292	AAGAATTTCAAAGAAAGAGAGCAAGAAGTCAAGAGAGTACATCTAGGAGGTACAACACCA[C/G]AGGCCCAGAACAGAGAAGGACAGAGAAACTTGTACTGTCCCAGTGGGGCCTGTAGAAATG
1293	CCCTAAGGTAGGTCCACCCTCTCAGTTAGGCAGTAGTAAAAGATCTAAACATAATCAATC[A/G]GGCACATTGTATGTAGCTGTGAGGGTTAGAAGTACAAAATGTAGTTGTGAGGGTTAGAAG
1294	AGTTATTTATGGTGGGAGGGTAATTTCAGATTGCCACACTCCCTCATGGCTGGAAGTGAA[A/C]GTATCACAATTTTTGTTTCTAATGTTCAAATCAGATCATATAGTTCCTGCTTATAAACCT
1295	GAAATTTCATACAGCGAAGCTGCAAGTCCTGAACTGGATCTTTTCTCTCTGATCTGGGCA[T/G]GTTGGGGACTGCATTTGTATGTAGTTAACCTGTATCTTCAGAAAGATTCTCCCAAAGCCA
1296	GCATGGTGCCTGGCCCATTTGCAGGCTGGCAATCAGAAGGGCGCCCTTCTCAGCCAAGCA[T/C]TGGACAGAGTGTTTAGTGAGGTAAGGCATTTCCTTCTATGTTAACCATACATGGCTGGCA
1297	AATTTTGGTTGACATCTGATTGCTGATTACTATGAGTGTGATCTTCCAGACAACTGTGTC[T/C]GCATCAAGTACCCCTAGGGGTCATTCCCATTTGATTCTGTGTTAATATTTTTATAATTTT
1298	ACTCCCACTGAATATCAGAGACAAGAGAGTTGTTGAACTGACATCTGATGGTGGATTTCA[T/G]CGTCTCTAATTCCACTGACTTTCTTTGTCATTTTCATGGTGTTTCCTCCCTTCTGTTTTC
1299	GCAATGAGAATACAGGAATGGTAAGAATAAAAGGCAAAGAGGTTGGAAGGAGATGGAAGG[A/G]GTATGCAGACAGTAGATCTGTGAAGGCAAAAGAAGTGGAGCGATGCAGATGGAAGACAGC
1300	GACCCACCCATGTTCTAAATTCTATACATTCTCATTGCTGCTGTCACCAAATCTGTGACA[A/G]ATCTAATTACTCTTGTCATCATAATTTTTGTGACTAGCACTAAAAGGGTCAACAGTATTC
1301	AAAAATCACCCTCATACATTCCCAAACATCTTCTAAGAATCCCTAAAAGGGAAGATACCA[A/G]TAGAGAGGAATAAGTTGAAAGTTAAGAAAAAAAGAAAATAACTGATGAACCAAGATCCTA
1302	CCCAAAATATAGTTCAAGTAGGGAAAATTGGAGAGAAGAAACTGAACTCCAGGTAATTTT[A/G]TCCTGGCTTTTTTTTCTTACTCCCTCATCGTATGCACTGGGAAAAAGTCTTAAAGTCAAG
1303	CCTCCTTATTTGGCGGAGAGAAAGACATGATGGAATATTTGGGTGTGGTAGCAATGAAGG[A/C]AGGAGCAAGGGGAAAGTGATGAGAGGAGGTCTCATTACAGTGACCTAGAAGAATTCACTT

Key appears on page 109.

Complete list of all 94 genes and 1,536 SNPs present on the COGS SNP Chip

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1304	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs7301328	13910044		Pro122Pro
1305	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10845852	13918404	G	
1306	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10772715	13929270	G	
1307	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs10492141	13936517	G	
1308	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs11055673	13945279	G	
1309	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs4764038	13953904	G	
1310	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2216344	13961423	G	
1311	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs2160729	13963111	G	
1312	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs219891	13977415	G	
1313	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs219904	13984155	G	
1314	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs219912	13986655	G	
1315	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs219934	14004982	G	
1316	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs12829455	14005924	G	
1317	12p13.1	GRIN2B	NMDAR2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	418.9	12	rs1895056	14029302	G	
1318	12q13.2	BLOC1S1	BLOS1	biogenesis of lysosome-related organelles complex-1, subunit 1	3.7	12	rs4457792	54396053	T	
1319	12q13.2	BLOC1S1	BLOS1	biogenesis of lysosome-related organelles complex-1, subunit 1	3.7	12	rs941022	54397591	T	
1320	12q13.2	BLOC1S1	BLOS1	biogenesis of lysosome-related organelles complex-1, subunit 1	3.7	12	rs3138136	54403837	T	
1321	12q22	EEA1		early endosome antigen 1	153.9	12	rs10507017	91689067	T	
1322	12q22	EEA1		early endosome antigen 1	153.9	12	rs10507018	91699244	T	
1323	12q22	EEA1		early endosome antigen 1	153.9	12	rs11106700	91713188	T	
1324	12q22	EEA1		early endosome antigen 1	153.9	12	rs1995169	91769607	T	
1325	12q22	EEA1		early endosome antigen 1	153.9	12	rs7965897	91783407	T	
1326	12q24.11	DAO	DAAO	D-amino-acid oxidase	20.8	12	rs2070587	107801872	T	
1327	12q24.11	DAO	DAAO	D-amino-acid oxidase	20.8	12	rs6539458	107804967	T	
1328	12q24.11	DAO	DAAO	D-amino-acid oxidase	20.8	12	rs3741775	107807732	T	
1329	12q24.11	DAO	DAAO	D-amino-acid oxidase	20.8	12	rs11830725	107811857	T	
1330	12q24.11	DAO	DAAO	D-amino-acid oxidase	20.8	12	rs3918347	107817449	T	
1331	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs7333412	46301361	T	
1332	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs3125	46306852	T	
1333	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs977003	46313002	T	
1334	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs1923886	46321292	T	
1335	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs2296972	46326472	T	
1336	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs9316233	46331356	T	
1337	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs659734	46333284	T	
1338	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs1928042	46335217	T	
1339	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs582385	46343995	T	
1340	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs985933	46353864	T	
1341	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs9534505	46358745	T	
1342	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs2070036	46364951	T	
1343	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs2070037	46365071	T	
1344	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs6313	46367941		Ser34Ser
1345	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs1328685	46369891	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1304			p=0.020 (Ohtsuki et al. 2001)	0.29	0.44		0.49
1305				0.13	0.33	0.15	0.09
1306				0.35	0.17	0.34	0.46
1307		Y		0.28	0.13	0.19	0.14
1308				0.18	0.00	0.23	0.17
1309				0.33	0.24	0.01	0.00
1310				0.44	0.49	0.47	0.41
1311				0.37	0.23	0.01	0.04
1312				0.07	0.17	0.11	0.03
1313				0.48	0.48	0.50	0.37
1314				0.41	0.33	0.05	0.06
1315				0.48	0.47	0.47	0.41
1316				0.45	0.24	0.06	0.06
1317				0.26	0.00	0.00	0.01
1318	Y			0.04	0.38	0.01	0.03
1319				0.45	0.11	0.06	0.09
1320				0.08	0.02	0.00	0.00
1321				0.12	0.11	0.00	0.01
1322				0.13	0.01	0.00	0.02
1323				0.38	0.18	0.03	0.08
1324				0.03	0.08	0.00	0.00
1325				0.02	0.12	0.01	0.00
1326			haplotype (Liu et al. 2004)	0.18	0.38	0.32	0.31
1327				0.04	0.03	0.00	0.00
1328			p=0.000001 (Liu et al. 2004), p=021 (Schumacher et al. 2004), p=0.048 (Stefanis et al. 2007)	0.37	0.00	0.33	0.43
1329				0.07	0.43	0.00	0.00
1330				0.31	0.38	0.36	0.43
1331			p=0.025 (Dominguez et al. 2007)	0.18	0.48	0.21	0.12
1332				0.11	0.05	0.21	0.12
1333				0.45	0.15	0.25	0.13
1334				0.45	0.03	0.41	0.48
1335			p=0.023 (Dominguez et al. 2007)	0.29	0.23	0.49	0.48
1336				0.21	0.42	0.34	0.27
1337			p=0.034 (Dominguez et al. 2007)	0.07	0.18	0.00	0.00
1338				0.24	0.33	0.05	0.08
1339				0.18	0.20	0.01	0.02
1340				0.36	0.48	0.43	0.42
1341				0.11	0.24	0.03	0.09
1342				0.03	0.01	0.33	0.24
1343				0.19	0.02	0.44	0.41
1344			p<0.001 (Baritaki et al. 2004), p=0.020 Golimbet et al. 2007)	0.45	0.35		0.48
1345				0.13	0.33	0.07	0.08

	R
1	**Sequence**
1304	GCAGCCCCTTTTTACCTTATCTGCCATTATCATAGAGGAGCCCCCGTGGATGCCCAGGAT[C/G]GGGGTGAGAGTCTGTGCTGAAATGAAATCGAGGATCTGGGCGATGGCTTCCTGGTCTGTG
1305	AGCAATATTTCTGCTACATCTTTCCTGGAACCTCTCCCGAGTAAGAGCCTTCTCATTCTT[A/C]GTTCAACCAGACCTGTCACCTGGGCTCCTTCTTGTCCTTACAGCACTTCCAGTGGCTCAA
1306	AACCTCCCAAAGAGGTTATAGCTATTCGTGTAGAAGATAATCAGGCCATAAAAAAATGCT[A/G]CAGACAAGATAATAGATTTGAAACTGATGAGGGGTAAAACACAGTAAGATGTGAAAAAAG
1307	ATAATGACAGAAGGGAAGAAAAAAACCAGAAGTCCCATCTCCCAATGGCCGAGTTCTAAT[T/C]TGTATTTTATGCTTATATGTCAAATCCAATATAATGTCCTTACAGTTTTCCAGTCTTGGT
1308	TAACTGAAGTTCTCTAAGATTCAAATTTAATAGATAACGCCAAACAATTTTTTCAAATTG[A/G]GCCAATTAAATTTCCACAAGCAGTGTAGAAGTATTCCTCTTCTACATTCTCACCAACATT
1309	CACTTGTCCTTAAAATGGGACAAAGACTAGAAAGACTCGGGAAGAAAAAGGATAAGAAAG[T/G]GCCTTAAGGTGTGAAGGAATATCTAGCAGCAATAAAGGTAAATGTGACGAGGAAGTAAAT
1310	ACCAGTCCAAGCACATCATGTCCCTCTGGGTCACATCCCATTAAAACAAGGCTCCAAATG[A/G]GGTCCCACTAATAAAACCCCATAACCCTGCTAATCAAAACTGCTTATTTTACAAGCCCCA
1311	TGTCTTTTTGGAACAATTAGCTTGAAAGTCAGCTTTCTTTGTCTAGGATCCTTCTCAATC[T/C]TTCCACCCACTCAAAACTATTAGCAGTTCAACTAACTTATTTTCATTTACTTCATGTATT
1312	CCTGTTAGTCATCAGCTCATGCTAAGTCTCTTATTTCTTCCCACCACCTCTGCAAATAGT[A/C]CCTTTAACAAACTCTCTTCAATTAAACCCTTTGAGTATGCCATTGTCTCCCTGCCAGCAC
1313	CCACAGAAAGTACACAGAATACAAAACTAGAAAGGGTTGAGTGTGCCTGTGCATTAGGTA[T/C]GGCATCAAGGCAGGAGCTGGGAAGTAACCACAGTGACCTGTAAACCTGTAAGTGCAGGTC
1314	GGCACTATTTGGGAAGCTAAGTTGTACAACTGAATAATGTAATTAAATGTAATTCATTCC[A/G]AATGTTAAGGGCTAGAATGTCTTCTCAAAATTAATGAAAACTCAATTCATTTGGAAATAA
1315	TTCCTGATGTCAGGGAAGACAGGAAGTATTGTGTGACAGCAAAGTCCGTAATGAAGAGAC[A/G]GATTGGGTCAGGACAAAGGCAGTTGTAGCTGTAAAGAACAAAACAAAGTCCCCTCTGAAG
1316	AAAATCTAAGAGTAGTTATTTCCACAGCATGAGGAGCTGTGTGCATAAAATTAGAGGGTT[A/G]AGAGCATTTATTTAATCAACCCACCACATCTTCTAGAAACGTAGGTCCAGCGGAATGGCA
1317	TCAGCAAACGCAAAGCCTATGCCTTGCCTGGCCAACAACAACAAAAAAAGTATGTTTATC[T/C]GGCAACATCTTTCAGATCAAACACGGTACCAAAGGCTGGAGCCTGAAGTTTATACAATTT
1318	AACACTTCACCTGCCCTCCGCAACCCTCTACCTCTCTTCCCCGCCAAGATCTTCACCCAA[C/G]GTCTCAAGAGGGCGGTTCCCAACCTCACGTGACACAGCGGTCACGTGACATGGCCCCGGG
1319	GGGTCACTTAGGGTCAAGAGACAATGTTCTTTGCTTTTTCCCAAGTCTTTGGCTGTTACT[T/G]GCATTCTCATTTAGGGCTGGGGCAGGGTGTGGTCCCTAGAGACCCAATAGGAAGGTAAGA
1320	TATAGGGAGGGGACTTTGAGGGACATGGGTTGGGGAGCTGAGAAAGTTACCACAGACCAG[A/G]GACAAGAGTTTTGACGGAGATGCCTACTGCCCCGGGACAAGGGTCAAGTGGGGTAGAGGG
1321	AATAATTATTATCATGGCAGGATATATACTATTAACTACATTCAAGGAACTAGTTCTTAG[A/G]GTCAGATTATTGCATCAAAGGGAAGTCCACAAACTTCCATTTCAGAATCGTACCTTTTGC
1322	CACCATCACCACACCCACAGAACATTTTTAAATTAAATTTCAGGAACTGAACCATTTAGA[A/G]TTTACCAAGAATTTCAGGGAATATACACTGCAGAGTAATATCCTGTCAGCTAACAGGAAT
1323	TCCCTCAGAACCAAATTTAACCATATTGGTCATCTGTTTTTAGAAAATACCAACATCAAC[A/T]CAAATCTCTTCAGCAAAGCTTCTTTGATCACCCAACCTTCAGTAGAATTATGTCCCATCA
1324	GTTTGCTCCAGGTTGGATGTAGTTAATTTATATATTTATTGAGAGCTAAATAAAGGAAAG[A/G]AAGTCAAGGACAGATCCAAGATTATTAAGTCTTGGGAGAGTATTAGAGATGTATGGTTCC
1325	AGTTTGGATATCTACAATGATAACAAGTTTTCTAGTCAGTAAATGTCCTTGCTAACCTAC[A/G]GCTAACACAGTAAAGGCCTAAAATTAATGTGTAGCCCCATAAAATATAAAAAACAAACAT
1326	GGGCCACAGGCCCGAGTTGCCAGGAGCTGAGGTCTGCGGGAGGAGAGTTGTGAGTGAAGA[T/G]GAGGGAAAGTTGAATTTGGCTCTTCTGGGCACAAATAATTCTCTTGTTCTGCCTCAGCAG
1327	gagggtctaggaaatgtaggtgagctgtgtgcccagggggaggaggaaaagttgtaggag[T/C]ggcaagtcgatgtctgccacCAGTGTTTACAAGGAGGGGTGCTTGCAGCCAGACTGAACA
1328	GGGGTCATACAGACTGGTTGGAATCCCAGTTTGGCCACTTGGCTGTGTGACCTTAGGAAG[T/G]CACTTAGCCTCTCTGAAACTCAGTATCTTCATCTACAAAACAATATGGTGATATGGAGCT
1329	TCTGCTTCCTTTCTGACTTCTTTTGGGAGGTTCCAGGAAGATTTCCCCCATCCAAAGAAC[T/C]GTTTTACAACCACTTTTATATTCAGAGTTGTGCAGGAGCCTCATAACAGCCTATGAACAG
1330	CCATGGCAAGGAAAGTAATGCCCTCTTCCACTCCTCAGATGGCTCTGGCATTTTCAGGGA[A/G]CAGTCATGTCTGATCTCAAGTTCCACACAGGCTCCATAGCAGGCAGGGGCAGTGGTGGCT
1331	TCCCATATAAAAGATAAAGTTGTCATTTATTTGAAATCCATCTAGAGAATTTAAGAAAAC[A/G]TGAGGGTTCTGCATTCCAGATTATCCTTGGCACCTGAAGCAGTGCCTTGGTTCAACAAGG
1332	AAAAAAAAATATGAGATTGGAAAAAATTAGACAAGTCTAGTGGAACCAACGATCATATCT[C/G]TATGCCTCATTTTATTCTGTCAATGAAAAGCGGGGTTCAATGCTACAAAATGTGTGCTTG
1333	ACAATTCAAGATGAGATTTGGGTGGAGACACAGAATGAAACCATATCAATTGGTGTAATT[T/G]AGTGCTTATTAGTCATATTAGGGGCTAGAATTTTTCTGCCCATCTAAGGAAAGATCTATC
1334	CACTCGCTCACCCCCCACCTTTCCTTATCCCAGTAAATGGTCCTACCATCTATCCAGATA[T/C]ACAGCTTAAAAACTTAGGAGTCTCTTTCCATTATCCTGCCTTTGCAAAAGACTCACCAGC
1335	CTAAGGTGTGGTAGCTGAGGAACACCTAAGCTTGTGCTATTTGTAATGCTGCTTATTAGA[T/G]ACATCGCTGATCCTCCTGTCAACTCCAGTTAATGTTTCTGTCCCATTCAAGTTGAAAATG
1336	CCCAAATAATCAGATATCTAAAATCTTGTGTTGAAGAGAAGTACCTATAATTTGCCCAAG[C/G]CTTCAAGATGCTATCACATGGCTGATTCCTCTCATTCTTCAAGTTTCAGCTGAGATGAAA
1337	TTCTTGCCTCTGAGCTTTTCTCCTCATTCCCCTCTGAATCTAGCTGCTTTCCGTTTATGA[T/C]TTCAGTTCAATTTCCTACCAGCTATTATGAGATAACTAGGACCTTTTAAAGAATAAATTT
1338	TCACCTTATTTGACTAATTTTGACTAATTGTTGAGAAAATAAGTCTGAATTAAAGAGTCA[A/C]AATTGCAGTTTATTTCAGAGAAATTTTTATTCTCCAATGCACATGGTAACTAGTGTTATA
1339	AGGATATGTCTAGAATTAAATTACATTTTGATAATTCTTTCCAGCTCTATAATTCCATTT[T/C]CTACTGTTGGGTTTCAACACCTAAAATTGTCAGCAAGCCTCTGAACAAAGATGCTTTTGT
1340	CTGAGGAATCCACTTGAGATTGTCTCTCCTGGGACCCTCCAGGTTTATGCCCAACTCCTT[T/C]ATACGGCTATTAGTCAGCCTAAGAAGTACATGTCAGAGACTATTCAGGCAACCAGGACAG
1341	AAGGTGAGAAAATAGCCTGGGGAGAGTCAAACAAAAAAGATAGAGTAATATTAGTACCAC[A/G]TAAAGCAGAATTCAAGGTCCCAAACCTGTCCTTGGGGTCAGGGAGAGAAAAAGCAATTGG
1342	ACTATGATAAGCTAGCACTGGCTGATGAATGCAGGGTTTGAAAATTTCTAGTGTCTGGAG[T/G]TATGTGAGTGTGGCACGGTAAGCTTGGATGGTCTCTATTTGGGGGTTCTCTTTCTTCCCC
1343	CCTTACGCCTGGCAAAACATTTCTTTTGTTAATGGCTTATGTCAAAATTTGTGTTTTGGC[T/C]CCTCTTCTGGAGCACCTCTCACACTGTACTGTCAGGATTTAGTCACATATTTCTCTGGAT
1344	TACGAACTCCCTAATGCAATTAAATGATGACACCAGGCTCTACAGTAATGACTTTAACTC[T/C]GGAGAAGCTAACACTTCTGATGCATTTAACTGGACAGTCGACTCTGAAAATCGAACCAAC
1345	TTTCCTCAATAGTTGGGTTTTGCTACAGTTCTATCACCTTCTGTTCTTCACATTCTCCCT[A/G]GACAAATTCAACCACTCTCATGCCTTCAATATGTTTGTGGCCAAGTCTGTACCTTCATAG

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1346	13q14.2	HTR2A	5-HT2A	5-hydroxytryptamine (serotonin)receptor 2A	62.7	13	rs4142900	46371551	T	
1347	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs1341402	104913510		
1348	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs1341403	104914808	T	
1349	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs2391191	104917447		Arg30Lys
1350	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs1539070	104922458	T	
1351	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs3916968	104925530	T	
1352	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs701567	104939996	T	
1353	13q33.2	DAOA	G72	D-amino oxidase activator	24.8	13	rs778294	104940236	T	
1354	14q32.33	AKT1	PKB	v-akt murine thymoma viral oncogene homolog 1	26.4	14	rs2498804	104304140	T	
1355	14q32.33	AKT1	PKB	v-akt murine thymoma viral oncogene homolog 1	26.4	14	rs2494732	104310237		
1356	14q32.33	AKT1	PKB	v-akt murine thymoma viral oncogene homolog 1	26.4	14	rs2494738	104317731	T	
1357	14q32.33	AKT1	PKB	v-akt murine thymoma viral oncogene homolog 1	26.4	14	rs2494743	104322765	T	
1358	14q32.33	AKT1	PKB	v-akt murine thymoma viral oncogene homolog 1	26.4	14	rs1130214	104330779	T	
1359	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs3087454	30108259		
1360	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs6494165	30108578		
1361	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs3826029	30108777		
1362	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs885071	30111868		
1363	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs883473	30112968		
1364	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs8037484	30134166		
1365	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs4779970	30137170		
1366	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs12593470	30148531		
1367	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs982574	30161315		
1368	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs12914788	30163729		
1369	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs2133965	30171846		
1370	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs8035668	30178638		
1371	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs9788657	30182318		
1372	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs8028396	30184013		
1373	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs10438342	30189338		
1374	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs11858834	30190213		
1375	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs12915695	30190637		
1376	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs16956223	30198075		
1377	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs7170028	30212293		
1378	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs1909884	30226590		
1379	15q13.3	CHRNA7		cholinergic receptor, nicotinic, alpha 7	138.5	15	rs2337980	30231488		
1380	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs2267770	9773460	T	
1381	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs10492827	9776259	T	
1382	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs9933832	9856135	T	
1383	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs2267795	9878376	T	
1384	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs968301	9881867	T	
1385	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs7189130	9886053	T	
1386	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs9938172	9909920	T	
1387	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs4782039	9914468	T	

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
1346				0.43	0.32	0.16	0.28
1347			p=0.008 (Hattori et al. 2003), p=0.048 (Schumacher et al. 2004)	0.36	0.00		0.00
1348				0.34	0.30	0.30	0.50
1349			p=0.032 (Chumakov et al. 2002), p=0.031 (Addington et al. 2004), p=0.037 (Schumacher et al. 2004), p=0.045 (Hall et al. 2004), haplotype (Yue et al. 2007)	0.34	0.08	0.31	0.48
1350				0.15	0.28	0.00	0.00
1351				0.22	0.32	0.17	0.23
1352				0.49	0.25	0.39	0.40
1353			p=0.018 (Hattori et al. 2003), p=0.025 (Ma et al. 2006), haplotype (Korostishevsky et al. 2006; Yue et al. 2007)	0.40	0.23	0.15	0.11
1354				0.33	0.21	0.40	0.39
1355			p=0.004 (Ikeda et al. 2004), haplotype (Bajestan et al. 2006)	0.39	0.48		
1356				0.11	0.06	0.40	0.41
1357				0.09	0.50	0.34	0.26
1358			p=0.011 (Schwab et al. 2005)	0.28	0.41	0.07	0.10
1359			p=0.0009 Stephens et al. 2009				
1360				0.06	0.03	0.09	0.21
1361							
1362				0.19	0.43		0.38
1363				0.30	0.22	0.11	0.14
1364				0.25	0.13		
1365				0.06	0.31		
1366				0.04	0.01		0.02
1367				0.10	0.48	0.17	0.23
1368				0.10	0.18		0.23
1369				0.06	0.48	0.17	0.23
1370				0.18	0.30	0.05	0.06
1371				0.17	0.26		0.06
1372				0.43	0.18		0.43
1373				0.30	0.28	0.05	0.08
1374				0.18	0.10		0.04
1375				0.30	0.02		0.08
1376				0.16	0.02		0.03
1377				0.48	0.31		0.29
1378				0.32	0.47	0.18	0.31
1379				0.43	0.45	0.17	0.26
1380				0.42	0.39	0.15	0.18
1381				0.23	0.01	0.00	0.00
1382				0.29	0.39	0.11	0.08
1383				0.26	0.38	0.10	0.11
1384				0.34	0.04	0.49	0.31
1385				0.21	0.38	0.06	0.04
1386				0.32	0.44	0.06	0.04
1387				0.24		0.05	0.01

Key appears on page 109.

	R
1	**Sequence**
1346	ATTAAGATGAATTGATTATTAAAAAGGAGAACCAGGGAGAAACTTAGAACCTCTCATTTT[T/G]TCTTGTTACTTTGTTTATTGGGATACCAATTTAATTTTATTAAAGATAGCAGAGGGAAAT
1347	CACACACACACACACATCTTCAACATTTGTTAACATTAACATTCATTTTGTTTCCTGTTA[T/C]GCATGTGTATATGTGCTTTTATTTAATAATGTTAGTTAACATTTCCTTTTTCTGTAAATA
1348	GTGAGATCCCTGAGAAAGGAGACTTTGTTTGTTTTGTTCCCCACAGTGCCTCAGTGTCTG[A/C]AATAGCACCTGGTAAATCATAGGGACTTCTGAAATACTTTCTGAATGGATAAATGAGTGG
1349	TTTCTTTAATTTTTAGATCCAGATATACATTGGGTAAAATCTACTTCATAGGTTTTCAAA[A/G]GAGCATTCTTCTGAGCAAATCTGAAAACTCTCTAAACTCTATTGGTATGTTACTCTTTAT
1350	TACCTTGTGGTCAACACCGGAGGAAAGGCCCCTTGACAGGGAAAAGGAATCTTCCCAACA[C/G]TCACACAGGGAAGGGACGAGAGGACTATTTCATCGTGAGGTTTGGAGCTTTGGAAAGGCT
1351	GCATTCATGGATCCAATTACGTTTTTTGTCATGGTAAAAGCCACAGTGGATATATTAAAT[A/G]AGAGTGTGGTTTAAGAATGAAGGCCCAGGAGTCTGGAGATCTGGTTTCTAAGGCTGACTT
1352	CACAACTACATATTTGGATATAATTTCAAAGAAAGACTGTGAAAAAGCATAAAGAATTGT[A/G]GGAATTGCCTGAGAATTGAGGACGTTCATCTGCAATGCCTGTAAGGCTTACATTAAACAA
1353	TCTTGCCATGAAGACTTTTCCAACATGGCTGCTTACTTCTTCAAGCCTGTAAGGAGATCC[A/G]GTCTCAGTTGGCCAGGTCTTGTGAAAGGTAACCTCATCACCGGAGTCAAGTGTCATCACC
1354	CATCATGCTCTTTCCAGCACAAGGCCGGCCTGGAAGGGAGGAAGATAATAAAAGTGACTT[T/G]AGCACTTAGACCTCCCATGTTTCAGCAGGTGTGGGTAACTGAAGGCTCTGCAGGTCTCTG
1355	AGGACCGCCTGGYGSAGGGGCAGGTGCAGCCTGGGGATGAGGGGATGGAGGTGTAGCCTG[T/C]AGCTGGGATGGGCGGCCCTCACCTCTGCTTGGGGTCCTTCTTGAGCAGCCCTGAAAGCAA
1356	CTGGGTGTGCCAGGACAGATGTGCCTGGGATGCCTGAGTCCCAGGGGGCAGGCGCGGTAC[A/G]GGAGCTGTTTCTTAGGGCCAGCGACAGAAACGGCCCTGGGTCAACGGGAAGGCAGACTCG
1357	CAACCAGGCTGGGGTGGGGGCAGGGGAGGGGCCACACAACGGAGGCCAGCTGACCCCACT[T/C]GGCTGGAGCCCCCAGGTCTGTGGGTGAAATACATCCACTGCTCCTCCCGGCACAAGCCCT
1358	CAGACCGGCAGGGGCGCTGTGGTTTAGGAGGGGCCTGGGGTTTCTCCCAGGAGGTTTTTG[T/G]GCTTGCGCTGGAGGGCTCTGGACTCCCGTTTGCGCCAGTGGCCTGCATCCTGGTCCTGTC
1359	CTAAGAGCCCTGTCTTCCCTTCTAGAAGAGCATGAGCCCATGGGGCCAAGGGAATTTATT[T/G]ATTTTTTCTGGAGTATGGCTATCAGGATCACATTCCTGAAACCAGAACTGCTTCTTTACC
1360	TGTCCGGACTGCTAGAAGTGGTAGGGGGACTCAAGAGCCAGATGAAGCTAAGGGCACGCC[T/G]GTCTGCTCTCCAGGGACCCCTGGCGTCCCTTTCTCCTGGCAGAATGACTGCTATCCTTTG
1361	CCCAACTATTTGATTTGGAAGAATAACGCAGTATATTGCCCTTGCCATGAAGTGTCTTAA[A/G]TGTATTACTGTTAATGTACACATGTTTAAACAAAGGGTCAGCATAGGCTTTCATAACTGC
1362	GCCAAGGCTCAAGATGCTTAAGAAACTTACCTAACAGCAGCCATCCAGAAACCAACACAG[A/C]CAGAACCCACCGAAGATCCCAAGTACAAATCCTGAGCTCTTTAAAGCAACTGAGGAACTG
1363	TTTAAATAAATTAAATGACTTTGTTCTGCCGAAGTTACCAAGTCTAAAGGAAGCAGCAGA[T/C]GAAAGACAAAGGACTTGTCCGATGTTGGTTTTCCTCATAGCCCTACCTCTAATCACAGAG
1364	aaagtctagttttgcccttctctggaactctgtataagaggaatcacccaagcacacagc[A/G]tgcgttctttgggatctggctttttggttcatttttatttttgtgagccacccaagttg
1365	TGCAGAGTTTTCCTTTAAAAATAAAAAGTGCTACTTTTTAAGCCTTTGATCAAATGTTGA[T/C]ACTCCTCAACTTTGTGACTGAATCATTTAGGACAATATTTTAAATTTGCCTAAAATATCT
1366	acttgaaTGGCTTTCGTCTGCTAGCTAATGGACACCTTTTTTGTGATACCCTTGTTTCTT[T/G]TGTATAATTTTAAAACAACTACATAAAGCAATAATTAAAATCTGACTGACATTAGACTTA
1367	aacaagagaaaaaaagttccattatatttacccatatttttacttgccatatttttccct[C/G]ctttctctccactcttccttcttttaatgtttcctttcaatctattgaactttagctatt
1368	CAGAAAAACAAACATGTTGGAAAACTGCAAGTTTAATCAGATTCTACAGGACTTCTTAGA[A/C]TCCTTGTGACAGCAATATGAACTAAGAATTGGTAGGAGGGGTTATAGTTCTTTCTGTTTA
1369	AAGTAGCCTGGAAAAAAGCCCAAATAAGAAGGGCATGCTTCTCATGAGTTCTTTATATTA[T/C]ACTATATAAGTCTTGGATCAAATTAAGCATGATTTCAAAGATGAGCTAATAAAATAACAG
1370	ATCCTTTGGGCAGTGCAGTTGGAGGAGGGTGATCTGATCATATGGATGGTCAGAAAGTCC[A/G]GTGTGAAGATGAGTAGAGGACAGCCTCTGTGTGTGTGCACCTGCGTGTGCATAGGGGCAG
1371	CTAGGTGTAGTAACATGAGTAGTTGGACATGAAAGCCACTTTGTTAAAGCAATGTTACTC[A/C]ATCTTTGAACTTCTTCTAGGTTATATGCCAAAAATAATGTAGTTTTTATCAAATGTATCA
1372	TATCCTGTTTCATTTTTCTCCCAAAGGCTTCTCACCATGTAACCCGCTTTGTGTTCACTC[A/G]TCTATCTGTTCATTGGTTCTGAGTCTTCATCACCCTTAGAATGTGTGCACAGTGTGGGGG
1373	CATACACAGGACACTGGACTAGCATAAAGGCTGTGATCTGGCCGGGGAGGGGATGAGCCC[A/G]TGGTTTACGCAGTGGGGTGTGCGGGGTGTGGGGAGGCAGCGTACAGCTCTGGCTGTGCCT
1374	tctcagcagctctgaaaatttttccccctcctttgatgttgttttcgtaactttgcgtca[A/G]attattttggtctaaaatcaaattgaaatctatgtgaattgaggcatttatttgtctcac
1375	AGCACCTGATCCTCGGAGGGATGACCCCAGACGTGGGTATTCCTCTGGCAAAAGTCACTC[A/G]ATAACCTCAATTAAGGCCTGGCCGTGAGCTTGTGTGAGTGCTTCCTGAGTCTTCACCTGC
1376	TGTTTTAAAGCAGTGAGTGGAGCCAGCCAACCTATGTTTGCATCTTCAAAGTCATCCTCC[A/G]AACTGTCCATCTCACTCTCCCAGGTCTCATCATGGTCGCTCTTGCTGTTTGTTTTTAATT
1377	TAGGGCTCTACCCCTGTGACCTGATTTAACCCTGGTCAGCTCTTGCTTATCGTTTTTAGC[T/C]GTATTACCTCCTTATCGTTTTTCTTGTATTTATGCTGTCATAGCAAGTGGCATTTTTCTG
1378	AGTTGGCATATTAAATTGAATGTAACATGGGATATTATAACAACTGGATATGGCATAGGA[T/C]GGATTACAGCAAAGCTATAAGTAACATGGGAGAAGATTAACACAGCAGATATCCAGTTTC
1379	CTGCAGGGGCCATAGTGGCCAAAATGAGGGGAGCTTTACTCTGGGGTGCTGGTACTTTGA[T/C]TGGCTGCCTGTGTTTTTTTGAGGTGGTTTATTTTTCTTTACCAGTAGGGCTGTGTTTTAA
1380	AAAAAATAGGAAATCCATCCCTTTCCAGTTCCTCACCCACAAAAATGGGTGCTGATCAAT[T/C]GGTTGTGTAGGTAAAGGGATGAGAAGAGGGTATCTTGATTCAATTCCTTTTCTTCCAACA
1381	AAGCTGGGGGGTGGGATGGACCACATAATGCTCTCTGTGCCCTTCTAACTCACTCTATCT[A/G]TGATTCCAAGAACGCAAGTCCAGGGAGAAGGTTCAGCTCTCCATGGAGACTCTCTTATAT
1382	ATCAGCATTCCTGACTCATAAAAGCTATTCTGAAGTGTGAGCCAATACCAGGGTTGCACC[A/G]CATTTCCTCCAGCAGTGCTTCCAGGAGTAAGGTTTCAATCCATTTCCTCCAGCAGTGCTT
1383	GTCATACCCCCAACTTCCACTCAACTTCCAAGGCAGATACCATCCCTGTGAATCTCCACA[A/T]CCTATATGAAAATTTCCATCATTCATCCTAGGAACTGTGCAAAGTACTGGAACAAGCACT
1384	ACTTTTAAAGGGGTCATGTGATTGGGTGAGGCTCGCCCCAATAATCTCCTTGTTGAGTAA[T/C]TCAAAGTCAACTGAGAAGTCCTTTCTGCCATGTGGCCTAATAAAACCAAGGAGTGACAGC
1385	GGTAGAATAAGTAGTTCAGCCTAGAGCAATCCAATTTATTACTCAAGGCTCAACTCCAAT[A/G]CCTCTAGCTTTACAAAGAATTTCTCTAAGTGAGAAATTCTCACTTAGAGAAtttcttttt
1386	GGAGAGTAGGAGGAAGAGAAAGAGGGAACAAAGGAGGAGAAAGAGGAAAAGAAGAGAAGT[T/C]AAAGAGAAGAAAACCCAGGGGAAGAAGGAGAAGAAGAAGACAGACCAACAGGAGAGTAAA
1387	GATTTCTCTCCACTTCTTTGGAGGGTCCCTTCCACTGATAGCTTAAAGTGTCAGCAAGAG[T/C]TTCCTTTCACTGAACCACAGTTATTTCCTTGAAGCTTCAACCCACTAGCTCTAGTTCTCT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1388	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs2315510	9928092	T	
1389	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs11074504	9941777	T	
1390	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs10500369	9944975	T	
1391	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1875209	9945555	T	
1392	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs4782090	9955433	T	
1393	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs884918	9967327	T	
1394	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs3104703	9972637	T	
1395	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs11641062	9990252	T	
1396	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs2243716	9995650	T	
1397	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs3848328	10002888	T	
1398	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1237957	10004371	T	
1399	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs844395	10010407	T	
1400	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1969060	10024638	T	
1401	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs8052800	10040290	T	
1402	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs7197547	10043745	T	
1403	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs2352740	10064582	T	
1404	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs9302409	10072531	T	
1405	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs6497676	10087724	T	
1406	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1448239	10094936	T	
1407	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs2352748	10106606	T	
1408	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs4782262	10120001	T	
1409	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1375071	10131081	T	
1410	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1070487	10143493	T	
1411	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1345424	10158160	T	
1412	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs4587976	10163636	T	
1413	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1650420	10175831	T	
1414	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1868291	10176699	T	
1415	16p13.2	GRIN2A	NMDAR2A	glutamate receptor, ionotropic, N-methyl D-aspartate 2A	421.2	16	rs1071504	10187517	T	
1416	16p13.11	NDE1		nuclear distribution gene E (nudE) homolog 1	74.9	16	rs4781678	15654613	G	
1417	16p13.11	NDE1		nuclear distribution gene E (nudE) homolog 1	74.9	16	rs2242549	15705711	G	
1418	16p13.11	NDE1		nuclear distribution gene E (nudE) homolog 1	74.9	16	rs881803	15709835	G	
1419	16p13.11	NDE1		nuclear distribution gene E (nudE) homolog 1	74.9	16	rs2075512	15721446	G	
1420	16p13.11	NDE1		nuclear distribution gene E (nudE) homolog 1	74.9	16	rs2075511	15725642	G	
1421	17p13.3	YWHAE	14-3-3E	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	55.7	17	rs9393	1195142	T	
1422	17p13.3	YWHAE	14-3-3E	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	55.7	17	rs7266	1195216	T	
1423	17p13.3	YWHAE	14-3-3E	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	55.7	17	rs8078073	1215433	T	
1424	17p13.3	YWHAE	14-3-3E	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	55.7	17	rs10521111	1228614	T	
1425	17p13.3	YWHAE	14-3-3E	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	55.7	17	rs4790084	1229729	T	
1426	17p13.3	YWHAE	14-3-3E	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon	55.7	17	rs9912147	1231072	T	
1427	17p13.3	PAFAH1B1	LIS1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit	92.0	17	rs8068673	2449136	G	
1428	17p13.3	PAFAH1B1	LIS1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit	92.0	17	rs1266475	2482070	G	
1429	17p13.3	PAFAH1B1	LIS1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit	92.0	17	rs8081803	2511759	G	

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
1388				0.11	0.19	0.00	0.00
1389				0.42	0.48	0.17	0.24
1390				0.22	0.16	0.08	0.02
1391				0.29	0.07	0.23	0.27
1392				0.10	0.00	0.32	0.40
1393				0.44	0.42	0.44	0.47
1394				0.50	0.35	0.39	0.41
1395				0.42	0.24	0.32	0.32
1396				0.11	0.09	0.24	0.38
1397				0.28	0.42	0.39	0.43
1398				0.10	0.04	0.27	0.40
1399				0.42	0.43	0.42	0.49
1400				0.17	0.47	0.48	0.44
1401				0.49	0.29	0.10	0.10
1402				0.44	0.38	0.02	0.10
1403				0.32	0.37	0.01	0.02
1404				0.13	0.37	0.00	0.00
1405				0.38	0.31	0.42	0.46
1406				0.15	0.39	0.17	0.02
1407				0.25	0.25	0.45	0.46
1408				0.08	0.36	0.15	0.01
1409				0.35	0.25	0.27	0.24
1410				0.41	0.37	0.15	0.13
1411				0.34	0.20	0.34	0.41
1412				0.41	0.36	0.25	0.14
1413				0.29	0.48	0.44	0.44
1414				0.04	0.18		
1415				0.36	0.41	0.10	0.10
1416				0.49	0.13	0.35	0.34
1417				0.48	0.28	0.40	0.38
1418				0.39	0.28	0.40	0.40
1419				0.47	0.13	0.48	0.43
1420				0.43	0.23	0.27	0.26
1421				0.07	0.13	0.34	0.16
1422				0.09	0.00	0.00	0.00
1423				0.23	0.49	0.00	0.00
1424				0.14	0.00	0.00	0.00
1425				0.39	0.33	0.46	0.39
1426				0.50	0.04	0.49	0.44
1427				0.30	0.30	0.14	0.14
1428				0.32	0.22	0.14	0.14
1429				0.26	0.12	0.01	0.07

	R
1	**Sequence**
1388	GGGATAAAATACTTTAAAAAGCCCTGGAGGTAACATGGATAAATAAACCAACCCAGGTGG[T/G]GACTAAGGTGTACTGCGCAGAGATGACAGTCACTTCCAGCTTCCAGTTGATCATTAGCAG
1389	TAATTAAATTAATTAAAGTGGGTAATAGATTTAAAGACTTTGGATAATTATTGTTTTCCC[T/G]ACAGTAGCTTTTGCAGAAATCTAATATTCTTGAATTGATTAACCATTTTAAATCACATCT
1390	AAGGTTACAAAGCCCATCCACACCCATTATCTCTTTGATCCTAACTACTCAAGAGATAAC[A/G]CAAGTGGCATAACACTCATGGATGGCATTTCTCCTAAAGACACAGGATGAGAGGTTAAAT
1391	GAGGTAACTCAGCAACGATCCAGAGAGACTCCTGGGGAATTTGCATTCTCCTGTTGAGGA[T/C]TGCCCTTGTGAGCCCTGGTAAGCCCTGATGTGCTTTCTGTTACTCTCATAGTGTATCAAC
1392	ACTGGGGTCAGGGGGCTCCTCCTCCTGCTTTCTTTTTTCCCCATTCCCCAATGTCCTCTA[A/T]GTCAATCCTTCTGTCCTAGACAGAGAAACTTGTGCCAGAAAACACAGGATATCCTAAAAT
1393	ATATTGACTATCTGGGCTTTTAAATAAAACACTTGCCAATTGCTGCTTTACAATACTTTC[T/C]GGTAGCTTATCAAAATAATCTTGGGATCTTTTAAATATGCAGCACCTTAAGCCCAGAATC
1394	ATAGAAAAGCCTAATTTTCAGTAAAACAGAAGCTTCCACTTCTTCCCTGATATAACAATT[T/G]CCCTTGGGTATGTCAACTCAAAACTCAACCACCATGCTTTGTGAAATCCAAGCCACATAA
1395	TTTTGATGGAATGTAGCCCAAGATCCCCCAGAACAGAACCATGATAACCAGACAGGAGGA[C/G]GGTCCTACAACTAACTCTCATTTTCCCTTCAAGCCAATATTGAAGACTTGATATCTTGGT
1396	CCTGTCAGAATGCAAAGCCCATTTGTCAGTTCCTGGATAGTTTCTTTCAGCTATTTCAAG[A/G]GGTGACCTGGGTTACTTCCCCCATCTTCTCTGTACTCAGGCCTTGTAGCTCCTTCTCTCT
1397	GATTTTGCTCCTTCCAACTCTCTGCCCTACATACCCTCTGCTGAAACTATCTTATGGCTG[A/G]TGCCCCATCGTGAACACAACATGGGAACCTGCCAACATTCCACAAGTGCTTCCATGCATG
1398	ATTCATCAGTACTTTGTAAAATGGAATAAACTTTTAAGCATTAACTAGCAGAAAAATCTG[C/G]CATATTGCTGCTGAGTGAGTGTGTAGCAACTGACAATTATGGACAGTAGAACTCAAACTA
1399	AGCTTACACTCTGATGGAGAGAGACAGGCAATACACTAATACAGATGAAAATACGTTATA[T/C]GTCAAGTGCTGATAAAGTCCCGTATTTATGCTGGAATTTGGGTGAATCATGTCAATTTGC
1400	AATAGATTATGTAATATTTATTCAATGTATTTTACTTGTCTGTTGTTTATAGAGCCCTGC[T/C]TCAGTTGGATGAGTTATTTCAGATTTGGAAGTGTCTCGTTCTCTAGCTTGGGAATGCAGC
1401	AAACAAAAAAAACAAAAACCCACCCTAGATATTGCCAAATGTCCCCTGGCCTAGATAATT[C/G]CAACTAGTCCTTCAAAAATCAGGGCAGTGTCACCTCCTCCAGGAAGCCCCCTGGCCCCCT
1402	TTGGATCACTCACTCTGAGGAAGTTGGCTGCCATGACATGAGGGACTTCAAGCAGCCCCA[T/C]GGAGAGGTTCTCAAAATCAATAAATGAGGCCCCCTGCCAGCAGCCTCGGAAACAAGCCAT
1403	GCTAAACACTGGGTATACATGGATATAAAAATGGGAATAGACACTGGGGATGATGATAAG[T/C]GTGAGGAGAGCAAGGCTGAAAAACTACCTGTTGTGAACTATGCTCACTACTTGGATGATG
1404	CAGCTTAAGTAATACCTACATAAAAGAACCATGCCTAGCACATGGCTGAATGTTGAATAC[T/C]GTTGCATGGAAATTTGGGATTTCTAGTTAGAGGCTTTATAAAGGTAGAATCATGCAGACA
1405	CAGGAATGCTCAACAGATGTGGATAATGAGTATGGAGGAGCAATGATGCCAAAAATAATT[A/G]TTCCTTGGGCCTTCTAGATCTTCTCACTTCCCCTGAGGAGAGATTGTGCATTCTGCCTAC
1406	GGTTTTTTGTTTTTTTTTTTCACTTTGTTGCCCGGGTATTCCCTAAAACACCCAGAGACT[C/G]TAGCTCTTAAATATAAGGCTGATTAAAGCTGATCGATGCCACCTGACTATAATACTGTCA
1407	CCCCTGACAAAAAGCCTAAGGATCCTCACCCAGCAATGCTGACCACGACCATTAAAACAT[A/G]AAGCCCACCCCCAAAGAGGAAAATCCTTGCCCTTTAATGAAGCTGCCAAAAACCTCCAAA
1408	GGGCACAATCTATGTCTTCCAGTCCTGGTATGGCGGAGAAGAAAAGATTCAAGTAGCAGA[T/C]AGACTGCTGTATCTAAAAACTTGGGTTCTTTTCCCAGCTCCATCTTAAACTGTGCAGAAA
1409	TTGGTCTGAGATATAAGCAGGAGATTATGGTGCTCCTTCTAGGCCACAGCAAGCAATTGA[T/C]TTTAATTCTAGGTAAAATGGAAAGCTGGAGGAAGATTTTAATAAAGATGCATGTGATTCA
1410	GCTACCTGTTCTGAGTTATAGGAAATATCCCAAAGCGCCCATGTCCTACCATTCCAGGGT[A/G]CAAAAGAGCACGAACCCACAAGAAGATATTGGAAGATTTACTGAGCCACAGGGAAATGAG
1411	CAATGACATGTTTCACACTTGTATTTCTTCTTACAGTTTTCAGGGTTTTCATACACCTTA[T/C]TTCATTCGATCCTAATAAGAACCCTGAGAGGTAGATTTCAACTGTGCTTTCCAAAAGTAA
1412	TGTCCAGAAAGGGAGCCCACATGAGAAGAACAAAGTCAGTGTTAGAGCAGGTGGAGGTCT[C/G]GGTTCTGAGCTGAGGTGTCTTGACTCCACTGAGGCTCAGTTACAGAAGAGGAGTGAGGAG
1413	TTCTTCTCTGATTGCTCTAGCATCTTTCCTTCTTCAGTTGTGAAGTCCTTCATTTGTAGA[A/G]TCAGTTAGTTGGATGTTCACATATGTTCTTTAATTTTTGTTTGTGAACTTATTTTCAAGG
1414	TATTGTGCTTTGCCCTCTGTGGACTTTCTTAGAGGATTCAAGATTTTCTTTAATTCTGGA[A/G]AAAATCTCAGCCGCTATCTGTTGGATTCTTTCTTTCCATCATTCTTTCTATTCTCTCCTT
1415	GGTATTCAGGGTTTTAAGTTATTCATGATCAGACTTATAGAAAGATAAATCAAACTGATA[T/C]GGCCTCTTTTGAATAGAGAAAGAAGGCAGCCCTTCATTGGAAGGGACACTGTGCCTCTAA
1416	CAACTGCATCGTTTTCCATTCAGTCCTCTGTTGACATTGAGGTTTCCAGTTTTCCACATT[A/C]GTGAATGATGGTGTGCATCTTTGAACATGGGTCCTTGCCTGCCTAAGTATTTTTGTAGGT
1417	AGCCTGACATATTGAAAAGCAGATCGTCTTGCTTTGAAAAACCTTCTCCACCCACCCCCG[A/C]AACCAATTTCAGCTGATTAAATTCAATCACTCATGCCTTAAGACTGGCAATGATTTGTTG
1418	ACTGCATCTTGACGAGATGGCAGAGGCTGTGTGTGTAGCTTGGATTTTTCTTCCTTTCAT[A/G]CCAAAAGCCACTCTTACGTGGTTAGGGCACTCAGCAGTGCTGTCCTCCCTTGTCCAGTGA
1419	GGGTGACACTAGGAGCTTGGGGCATGGGTGGAGGGAGGGCACAGTTCCCCTCAGGCCACC[A/G]AAGTCAGCAGAGCGGGCTCCAGGAAGCAAGCCTGCACCTGCCATTGGTGTGGGTTCAGCT
1420	GAAGAGGTTCCAGAAGGAGATCGAGAACCTCACCCAGCAGTACGAGGAGAAGGCGGCCGC[T/G]TATGATAAACTGGAAAAGACCAAGAACAGGCTTCAGCAGGAGCTGGACGACCTGGTTGTT
1421	CCAGATGTGGCAAGATCACCATTAGCAAATGGAAATTACATTTGAAAGCCATTAGACTTA[T/C]AGGTGATGCAAGCATCTAAGAGAGAGGTTAATCACACTATAGAGGCATAAGTGGTATCAG
1422	CCAGCTTTTAGGTTCTTTAAGACACTAACAGGACTACATAGAGGCTTTTTCAGCATTACT[A/G]TGTCGTCTCCGTGCCAGATGTGGCAAGATCACCATTAGCAAATGGAAATTACATTTGAAA
1423	TCTCATTAAATAAGGTAATTAGGCACACCTAACTATTTTCCAGCAAAAAAAAATGAGCTG[T/C]CAGTTTAAGAGAAAGATTAAGAATTTACAGGTTCTAAAATGTATTGTCTCACAAATAAAT
1424	TATTGCTCCTGAAATGGTCTGAGTCAGGCTTTTTAGACATGCTTTTTAGTACAGAACTGA[T/C]GCTTCCCAGATTATTTGTCAGTGTGATAGAGAAGGTGCGTGATAATCGTTTTAGAAAAAA
1425	AATCATATTTTCTTAGAAAAACAAAATGCAAGAATAGTGATCACTAGTTCTACTCAATTA[A/G]GATGAGCAAAAGGCTGGGATGTACCCTGGAGCGTGTTACGATGAGTTATGAAGGAAGGAG
1426	TTCTAGCCACAGCTTGCCTGATTAGACTGTAACTCTTCCATAGTAGGTATTATAAGTAAC[C/G]ATTTTATTACTCACAAGGGGAAAGTTGTTCCCCATACATGCTAAAGAAATACATATTGAT
1427	CTTCTTGTTGAAACTTACCTAGATAGGACTAATCTGCATTTGTCAAGGATACTTCTGGAA[T/C]GGTACTCTCTATTGTCTTTTAACATTGTCATAAACGTTTCTCTAGAACTTTCTAAATATT
1428	CCCATTACCCAGCCTCAACAGTTAGCAATTCAAAGCCTGTCTTGTTTCATGTATCTCTCT[T/C]ATTCACTGTCATTACCCAAGTCACAGACATGATATTATTTTACTTCGATTTGATGTAGCT
1429	CTTTAAATGGGTCTAGTAAGAAAACATCTCAGTTCATCAGCCTTTGACTTAACCTTGTTT[T/C]TTCTTCATATGAGCAATGAAATTAAAATGGTTACGGAACTCTTAGAACTTTTTCATTCTT

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	Cytoband	Gene Name	Gene Alias	Description	Size (kb)	Chrom	SNP ID	Position (bp)	htSNP*	Coding
1430	17p13.3	PAFAH1B1	LIS1	platelet-activating factor acetylhydrolase, isoform Ib, alpha subunit	92.0	17	rs2317297	2523841	G	
1431	17p13.1	DLG4	PSD95	discs, large homolog 4	29.8	17	rs11650232	7029647	T	
1432	17p13.1	DLG4	PSD95	discs, large homolog 4	29.8	17	rs314253	7032374	T	
1433	17p13.1	DLG4	PSD95	discs, large homolog 4	29.8	17	rs222853	7054704	T	
1434	17p13.1	DLG4	PSD95	discs, large homolog 4	29.8	17	rs507506	7059046	T	
1435	17p13.1	NDEL1	NUDEL	nuclear distribution gene E (nudE) homolog like 1	44.8	17	rs1391768	8281591	G	
1436	17q11.2	SLC6A4	SERT, 5HTT	solute carrier family 6, member 4 (serotonin transporter)	37.8	17	rs2054847	25556139	T	
1437	17q11.2	SLC6A4	SERT, 5HTT	solute carrier family 6, member 4 (serotonin transporter)	37.8	17	rs140700	25567515	T	
1438	17q11.2	SLC6A4	SERT, 5HTT	solute carrier family 6, member 4 (serotonin transporter)	37.8	17	rs6355	25572936	T	Gly56Ala
1439	17q11.2	SLC6A4	SERT, 5HTT	solute carrier family 6, member 4 (serotonin transporter)	37.8	17	rs8073965	25583308	T	
1440	17q11.2	SLC6A4	SERT, 5HTT	solute carrier family 6, member 4 (serotonin transporter)	37.8	17	rs2020933	25585881	T	
1441	17q11.2	SLC6A4	SERT, 5HTT	solute carrier family 6, member 4 (serotonin transporter)	37.8	17	rs4392119	25589489	T	
1442	17q12	PPP1R1B	DARPP-32	protein phosphatase 1, regulatory subunit 1B (dopamine and cAMP regulated phosphoprotein)	9.7	17	rs4795390	35035136		
1443	17q12	PPP1R1B	DARPP-32	protein phosphatase 1, regulatory subunit 1B (dopamine and cAMP regulated phosphoprotein)	9.7	17	rs879606	35035375		
1444	17q12	PPP1R1B	DARPP-32	protein phosphatase 1, regulatory subunit 1B (dopamine and cAMP regulated phosphoprotein)	9.7	17	rs907094	35043897		
1445	17q12	PPP1R1B	DARPP-32	protein phosphatase 1, regulatory subunit 1B (dopamine and cAMP regulated phosphoprotein)	9.7	17	rs3764352	35044465		
1446	17q21.31	CRHR1	CRF1	corticotropin releasing hormone receptor 1	51.5	17	rs4792882	41225048	T	
1447	17q21.31	CRHR1	CRF1	corticotropin releasing hormone receptor 1	51.5	17	rs4792887	41232791	T	
1448	17q21.31	CRHR1	CRF1	corticotropin releasing hormone receptor 1	51.5	17	rs81189	41250579	T	
1449	17q21.31	CRHR1	CRF1	corticotropin releasing hormone receptor 1	51.5	17	rs242939	41251360	T	
1450	19q13.12	MAG		myelin-associated glycoprotein	21.7	19	rs10432275	40481735	T	
1451	19q13.12	MAG		myelin-associated glycoprotein	21.7	19	rs11669734	40486615	T	
1452	19q13.31	APOE		apolipoprotein E	3.6	19	rs405509	50100676	T	
1453	20q11.23	SLC32A1	VGAT	solute carrier family 32, member 1 (vesicular GABA transporter)	4.9	20	rs6092935	36783319	T	
1454	20q11.23	SLC32A1	VGAT	solute carrier family 32, member 1 (vesicular GABA transporter)	4.9	20	rs1322183	36791688	T	
1455	20q11.23	SLC32A1	VGAT	solute carrier family 32, member 1 (vesicular GABA transporter)	4.9	20	rs1321099	36792059	T	
1456	20q11.23	SLC32A1	VGAT	solute carrier family 32, member 1 (vesicular GABA transporter)	4.9	20	rs1406857	36795846	T	
1457	20q13.33	CHRNA4		cholinergic receptor, nicotinic, alpha 4	30.7	20	rs4522666	61444924	T	
1458	20q13.33	CHRNA4		cholinergic receptor, nicotinic, alpha 4	30.7	20	rs3787138	61449668	T	
1459	20q13.33	CHRNA4		cholinergic receptor, nicotinic, alpha 4	30.7	20	rs755204	61464609	T	
1460	20q13.33	CHRNA4		cholinergic receptor, nicotinic, alpha 4	30.7	20	rs755203	61464708	T	
1461	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs385440	17281090	T	
1462	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs9618419	17287405	T	
1463	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs5746640	17291157	T	
1464	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs2241305	17292429	T	
1465	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs2016108	17295963	T	
1466	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs367766	17297031	T	
1467	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs759406	17297748	T	
1468	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs4819757	17300516	T	
1469	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs8137125	17303183	T	
1470	22q11.21	PRODH		proline dehydrogenase 1	23.8	22	rs9604911	17304956	T	
1471	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs2072123	17406613		Ala473Val

	K	L	M	N	O	P	Q
1	Prom**	TFBS**	Association (reference)	MAF_CEU	MAF_YRI	MAF_JPT	MAF_HCB
1430				0.06	0.46	0.13	0.08
1431				0.46	0.03	0.00	0.00
1432				0.35	0.48	0.49	0.46
1433				0.06	0.02	0.23	0.20
1434				0.47	0.40	0.42	0.46
1435				0.41	0.49	0.24	0.48
1436				0.40	0.02	0.17	0.19
1437				0.10	0.04	0.10	0.06
1438				0.03	0.00	0.00	0.00
1439				0.01	0.00	0.00	0.00
1440				0.05	0.39	0.01	0.07
1441				0.02	0.00	0.00	0.00
1442			haplotype (Meyer-Lindenberg et al. 2007)				
1443			p=0.001 (Meyer-Lindenberg et al. 2007)	0.13			
1444			haplotype (Meyer-Lindenberg et al. 2007)	0.15	0.14	0.38	0.43
1445			p=0.049 (Meyer-Lindenberg et al. 2007)				
1446				0.03	0.00	0.00	0.00
1447				0.07	0.30	0.00	0.00
1448				0.46	0.39	0.17	0.16
1449				0.07	0.32	0.00	0.00
1450				0.38	0.23	0.32	0.32
1451				0.22	0.00	0.17	0.19
1452				0.50	0.24	0.25	0.34
1453				0.23	0.18	0.05	0.11
1454				0.46	0.03	0.38	0.33
1455				0.06	0.40	0.46	0.47
1456				0.35	0.06	0.36	0.44
1457				0.38	0.08	0.41	0.46
1458				0.09	0.50	0.04	0.16
1459				0.03	0.16	0.05	0.14
1460				0.38	0.03	0.44	0.34
1461				0.08	0.38	0.03	0.09
1462				0.15	0.23	0.03	0.08
1463				0.36	0.48	0.22	0.29
1464				0.10	0.24		
1465				0.26	0.33	0.27	0.18
1466				0.35	0.00	0.00	0.00
1467				0.15	0.33	0.02	0.03
1468				0.39	0.05	0.18	0.01
1469				0.09	0.42	0.03	0.02
1470				0.27	0.27	0.35	0.31
1471			p=0.003 (Shifman et al. 2006)	0.39	0.42	0.26	0.34

	R
1	**Sequence**
1430	AAGTTACTAGTTTTACTCAGATTAGTAGAGCATAGCTTTTTTCCAATATGGCTGGAAATA[T/C]TTTTAAGTGTGCATTTAGTTTTGAAAGATTTTATTTCTTATACATATTTTATCTTCTAGA
1431	TGCGCCAGGGCAAGGGAAGAGGGGGACCACCAGTGCTGAAAGGAGCAGACGGGCCTCTGC[A/G]CACAAGTTTAAATCTGAGCTGACACAACCCACCCCAAGGGCTTCAATATCCCATCTCTGC
1432	GCAAAAGGGCATTTTTTGTAGCCACTCCTGACTAAAGTTGAGAGTTTCATGCAAAAGACC[A/G]ACCCAGGGGTAGTGATTCTGTGGATGGCATGGCCGTCCAAGCCTAAAGTAGTCCAAGAAT
1433	AGCTTTGGTCCTAATTTACCTTGCAGGGAATTGGAGGCCTTGTGAAGGAAGAGTGGATAG[T/C]GGAGAGCGGCTTCCACCCCTTCCCCCAGGTCTCAATTCTGGGGCTTGCCCCTCAGCTTGT
1434	AAGATGGAAGACTCAGGCAGAGCTGGGGAGCTCAACGACCGCAAAGCCTGAGCACTCCCT[A/G]CCCCATCCAGCATTTGGGGAAGCAGGAGCCATGTGCCCCCTGCAGGCTCCTCTTGGGCTA
1435	TTAACTCTTCAAAGTTGATCATAAACACGGTCTCTCTTTGATTCTATCAGACTTCTTTTT[T/C]ACTTTATGGAGTGCTCAGAAACTTACGTCAGAAGTAATTTTAAGCTTTAGTAACCAAATT
1436	GTCTTTTAAAAAATTGTAATAAAATATTATTTATTTTGATTTTGGCTCCTGCTGAAATGT[T/C]GTGCCTGAGGTGAGTGCCTCCATGTGCCCTGGGGCTTGGGGCTGTTCGTTTCTGTCAATT
1437	ACCCTGAATCCCGATCCCTGTGTGACTCCAAGGGTTGTGATCTTTCTGCCACACCACCTC[A/G]CCCTCCTTTCTCAAGGTCTTCAAGAATAAAAGACACTGACATCCATTGACCCACCTCCCT
1438	ACAAAGTGGAGTCCGGGCAAATATCCAATGGGTACTCAGCAGTTCCAAGTCCTGGTGCGG[C/G]AGATGACACACGGCACTCTATCCCAGCGACCACCACCACCCTAGTGGCTGAGCT
1439	TTCAACAGTTCAGTAACAAAGGAAATGAAATGCTCTTTTTTCCTGTATACACACAGAAAG[T/G]TCACACCAAAACCCAAGACGGCAAAGGCCCACGTACTTGCCCCCTCCTGCTAGCTGCCCA
1440	GACATTACAAAGACTTTGTGTATGTATTTTTACCATCAGTTTTGTCCAGAAAAGTGAACC[A/T]GGTCAATGGATTATTTATGAGCCTGCTAGCTAACTCTCATCATAGGAAGACGAGAGCAAA
1441	CAACTGGCCCAGACCCTCCCCCTCTCTCTAAACAGGTGTTTCTCTTCCTCCTGCCCTGGG[T/C]ACCATCCCACAGAGAGGCCAGGCCCACCTGCAGGTCCTCACCTCCACAGAGCCAGCCTCT
1442	GCCTGGGCCATGCCCTTCCCATACCCCTTCTTCCTTTCAGGACCTCCTTATTTACCCTCC[C/G]AAGGCACTGCCAAACAGGTCTTTGCCACTCCCCACCACACCCCATCTTCGACAGAGGTTC
1443	GGGTGGGCTGATGTGGAGCTGGATGGCCAGGACATCCCACTCCTATGAGCAACACTCTGG[A/G]CCTCCTGCCACCCTTTCCCTCACCCCCAGAGTGGGCCCTGACCCCAATTCCAGAAGATTC
1444	GCGTGTATGAGACACTGAACTAGAAGGGGACGTCCTCGTATACTCAAGGAGGACCCACAG[T/C]TAATCCACATGTCACAGGCCCCTCAGCTTACCAGACTGCCTGATGACCTTCAGGACTTCA
1445	TGCAGGCAGGAGGCCCAAGGCCTTTTGTTTGTGTGGAAGAGCTGACAGCTTCTAGTAGGG[A/G]TGGTTGACTCTTCAGTATTCCCATAAATAATGAGACTAAAAAGGTTAATGGGCCGGGCTG
1446	cacacacacacacacacacacacacacacacacacGCTGGTACCCTGGCGAGTGAGCTAC[T/G]TTGCAGTGTTTGTAACACCCGCACCTGCCACCTCCCTCAGAAGCCACTGTGTGGTCACCA
1447	GGCCAGCAGATGGAAAGTGTGGGCTGGGGCCCTTGCCTCTGGGGTCACCAGGTACATCTT[T/C]GATCTTGGCCACACTGGAGAGTCAAGGGCTTCTCTGGGCCCCGAGTCAGGGTCCGCCAGA
1448	GTGTGCACCCTTGGGTCCTTGTGGTCTTGAACTCAGAGTCCCAAGAGGGCACAGGGGTGA[C/G]CCCAGACACCATGTAGTTTACTCCAAGACTCACTGTGTGACCTCCCAGCACATTGTTGCC
1449	CCACAGACAGCCTGGCCGGCCCCACCCAGCAGCCTGAACACGGAGGCCACACAAGAGTGG[A/G]TTCCAAGTGAAGGAGTGACCAACTCAGATCTGAAACCTGAGGCTGGGCGGTGGCGCTGGG
1450	CTGCACACATACCATACACAAAAACCACACACTACACACATACATCACAAACACACCACA[T/C]ACTACACAAACCACACACATCACACTACACACATGCACCACACACCCACACCACACACAC
1451	CAGCCATCACTCCAGGTTGTAGCAGCCAAGTCACAGTTTTGACTCCCCTTCCTTAAGCAA[T/C]TCCCTCTGGAATATCGCCTTCCTGTTTCCATTTCCCCTGCTTCCTCCCAAGTTCCTGTTG
1452	TAGAGGTCTTTTGACCACCCCCCACAGTCCCCAGGAAGGGAGGACACCTCGCCCAGTAAT[A/C]CAGACACCCTCCTCCATTCTGGGGGCCAAGCGTGGAAGGGGAATGTGGAGGCTGCCGCCC
1453	TCAAAGACAGAAGAGCGTACATTCCAACTCACTCAACCCCCAGATCCAATCGCAGGCTTT[T/C]TCTTGTGCACTCCCATTTCCACCCCCAGCCCCACAACGAGAACTGGCTGTTGAGTATAGT
1454	CTCTCTGTTTTGAGGTTGGAAGTTGAGAGCTTCCACCAAATTCTCAGATGGACCCGCCCC[A/C]AGGGGAGAGATTCGAACAAACCTCGACCTGGCAGCTGAGGGGGCCGCTACAGCACTCTCC
1455	CTGTTGATTCTAGAGTCAGATCTCTTTGCTATGGCTGTGCAAACCCCACCTTGGATTGCA[C/G]GGCAGGGTTCTCCTGGGTGGCAGATGCCTCCTGCCGGGCCAGATTGGCTCGTGGCTCTGG
1456	GGGGAAAGGCCAAATAAAGATTGCTTTGATGAGCTTGTGGACACCTGAGGTTCAATCCTG[T/C]TGGGGACCCTCCAAGATACCTTGTGGAATAGACCTAAAATGGTCCCATCACAGGACAGGA
1457	GTGCAAACCCCTGACAATCCCACTACCAGGTGTTCCGTCCTAAGCAGCGAGCTTCCAACC[A/G]TGGGTCAAGAAATCAGTTTTGTGGGTTGCATCCAGCCTTTCCTACAGACTGAAATAGAAG
1458	GGGCCTGGGCACACTGTGGGGACAGTGCCGCCTCCTGCTCTGATTGTTTATAGCAATCCC[A/G]GGTCTCCTGATGGTGTTAAACTGAACCAAAACGGCCGCATTTATCTACGGGAAGCCTGAA
1459	AGCCCAAAACTACATCTGAGGCCAGCAGGAGGCCGGGGTGCAGACCCTAAAGCCAGATGG[T/C]CTGGGTTGGAATCCCAGTACTGACTGTGAGCTTCGGCAAGTCGCTCGGCCTCTCCGCACC
1460	CCGTCAGCAGGGTGGGTGGCAGACACCCATGGCTCCAGGAAAGAGTTCAGGAAAGTAGAC[T/C]TGGGATCTCCCAGGAGGCTGTCCCAGTGAGGGCACGTCAGCCCAAAACTACATCTGAGGC
1461	CTCCTCCATCCTGTGCAGGTGAAGCCAGGAACTGAGGGCCAGTTCCAGGACACTGTCCCC[A/G]GTGCAGGGATACAGGGCTCCTGTCCCAGCTCTGAGCCTGTCCTGCCATCCCAGGTGCCCC
1462	GGGCGGGAAAGTGCCACCCTGAGGCCCAGGCTAAACCTCTCTCAGTATTCCCAGCCCACA[T/G]GAACCCTCTCACCCGTCTGTGCAGGGCTGGGAGGGAGGGCCACCTGGACAAGCAGCACAG
1463	ACCGAGTCTCTCAGGAACCTCTGACGCAAGCGCAGGCTCCTGCCCCCGTGCAGCCAGCCC[A/G]CAGTCCCACCCTGTCCTCCAGGCCAGCCCTCCTGCAGCATTCTTGCCCCTGACACTTCTT
1464	CGGTGGGTGAACACTAAGCTGGGGCAGGAGCCAGAGGGCTGGGTTCTGACCACACTTGGG[T/C]CCCTCACTGTTCAGCCCCTTCCTGAGGGGCCCCACTGCCTCCCAGAAGGCATCTCCTCTC
1465	AGAGAGTTGGACAAGGGCGGGGTGTGGACCCCCATGCTCTGCTTGTTTCAATAGGCATCA[T/C]GTCCCCAGGGACAGCCACCCAGAGCTGAGGTGGAGGCTGAGGGGGTGGTCAGGGTCTTCC
1466	ACCAGAGGCGCCTGAGAGGAAAATCCCATTGTGAAACCAAGTCCCCACCCAGACTCCTTC[T/C]GAGAACACACAGGCCATTGGTTATTCAACAGGCAGCTCAGCAAAGGCTGCAGCCAAGAGC
1467	AGCCTCCTCCATCAGGTCAGCAAGTTTGTGTAAACAGCCAGGTAGCACAGACTCTCAGTC[A/G]GGCCACACCCTCCCTGCCACAACGGCTTCACTCTGCCTCAGTAGGGCCATAGTAATTAGA
1468	GGGCAACTGTCGACTGCCGCACGGGGCCACGCAGTCTCCCTCTACCTAACTGCTCGCCTC[T/C]GCACGGCCAGCACTAAATGAAGGGGCGGGAGCCCAGGCTGCACTGACTCCAGGGATGCTT
1469	GTTTGAGGGGCTTCCCATTTTTCCCCAACAGTGTTCTCAGAGTGGCCGTGTCTGGGAAGC[T/G]GCTGGGTCCCGGGGTTTGAATTCCGGGGTTCCAGGCTATGAGCCCTACACCAGGATTCTC
1470	TATGGTTCGTTTTATATGAAGAGTTCAGAATAGACAAATCGATAGAGACAGAAGTCACAC[T/G]AAGACAAGCCCATAGTGGAGCCTGGTGAGTATGGCACTGGCAGTGGTGCCTGGAGGTGGA
1471	CCGTACCTGCCTCTGACACCCCTCTGTCTCTTCCTGCAGACGATGATGCTTTTGAGCCTG[T/C]GGAGGTCAGCCTGCCAGCCCCTGGGGATGGTGGGAGTGAAGGTGCATTACTCCGGCGCCT

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1472	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs2238735	17426677	T	
1473	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs2238754	17438146	T	
1474	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs2854659	17463552	T	
1475	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs10483100	17465202	T	
1476	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs2800972	17473085	T	
1477	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs807743	17483598	T	
1478	22q11.21	DGCR2	DGS-C	DiGeorge syndrome critical region gene 2	86.2	22	rs807759	17493686		
1479	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs737865	18310121		
1480	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs174675	18314051	T	
1481	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs5993883	18317638	T	
1482	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs740603	18325177	T	
1483	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs740601	18330763	T	
1484	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs4680	18331271		Val158Met
1485	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs4646316	18332132	T	
1486	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs165774	18332561	T	
1487	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs174696	18333176	T	
1488	22q11.21	COMT		catechol-O-methyltransferase	28.1	22	rs174697	18333832	T	
1489	22q11.21	ZDHHC8	ZNF378	zinc finger, DHHC-type containing 8	16.2	22	rs175174	18507554	T	
1490	22q11.21	ZDHHC8	ZNF378	zinc finger, DHHC-type containing 8	16.2	22	rs2286930	18508880	T	
1491	22q11.23	ADORA2A		adenosine A2a receptor	14.8	22	rs3761422	23156672	G	
1492	22q11.23	ADORA2A		adenosine A2a receptor	14.8	22	rs2236624	23166024	G	
1493	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs576895	24261580		
1494	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs558934	24264721		
1495	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs5761116	24280750		
1496	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs2283811	24305450	T	
1497	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs1008673	24324013	T	
1498	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs5761149	24376900	T	
1499	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs11913984	24389030	T	
1500	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs6004737	24395034	T	
1501	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs718163	24411873	T	
1502	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs5761159	24432308	T	
1503	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs9608416	24441018	T	
1504	22q11.23	ADRBK2	GRK3	adrenergic, beta, receptor kinase 2	159.0	22	rs6519621	24441816	T	
1505	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs4820239	35288854		
1506	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs2267341	35306921		
1507	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs2283981	35316038		
1508	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs3788521	35322433		
1509	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs738977	35338874		
1510	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs738518	35449746		
1511	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs3484	35526817		
1512	22q12.3	CACNG2		calcium channel, voltage-dependent, gamma subunit 2	138.8	22	rs736720	35532777		
1513	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs7881868	113753140		

Key appears on page 109.

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
1472				0.01	0.00	0.07	0.06
1473				0.08	0.00	0.39	0.17
1474				0.18	0.43	0.18	0.18
1475				0.21	0.08	0.05	0.13
1476				0.44	0.28	0.33	0.40
1477				0.28	0.46	0.24	0.28
1478			p=0.0002 (Shifman et al. 2006)	0.47	0.43	0.33	0.41
1479			haplotype (Funke et al. 2005; Chen et al. 2004; Meyer-Lindenberg et al. 2006)	0.13			
1480				0.26	0.37	0.42	0.42
1481				0.48	0.48	0.49	0.38
1482				0.48	0.42	0.49	0.44
1483				0.41			
1484			p<0.001 (Meyer-Lindenberg et al. 2006), p=0.001 (Schurhoff et al. 2007), p=0.046 (Chen et al. 2004), haplotype (Funke et al. 2005)	0.48	0.29	0.24	0.26
1485				0.22	0.15	0.41	0.36
1486				0.34	0.22	0.13	0.18
1487				0.19	0.34	0.47	0.46
1488				0.03	0.22	0.34	0.34
1489			p=0.0005 (Mukai et al. 2004), haplotype (Chen et al. 2004)	0.33	0.47	0.44	0.32
1490				0.03	0.05	0.10	0.04
1491				0.37	0.34	0.32	0.34
1492				0.21	0.01	0.21	0.31
1493			haplotype (Barrett et al. 2007)	0.26	0.30	0.40	0.33
1494			haplotype (Barrett et al. 2007)	0.23	0.19	0.36	0.39
1495			haplotype (Barrett et al. 2007)	0.12	0.04	0.23	0.23
1496				0.11	0.04	0.43	0.33
1497				0.32	0.00	0.00	0.00
1498				0.01	0.00	0.00	0.00
1499				0.03	0.43	0.05	0.01
1500				0.02	0.40	0.05	0.01
1501				0.27	0.13	0.35	0.43
1502				0.33	0.10	0.34	0.39
1503				0.35	0.10	0.25	0.28
1504				0.03	0.48	0.01	0.01
1505				0.23	0.08		0.30
1506			p=0.003 Liang et al. 2005	0.38	0.44	0.18	0.21
1507			p=0.003 Liang et al. 2005	0.35	0.38		0.21
1508				0.09	0.19	0.09	0.07
1509				0.21	0.42	0.02	0.02
1510			p=0.005 Liang et al. 2005	0.22	0.49	0.46	0.48
1511				0.48	0.40		0.35
1512				0.45	0.34	0.15	0.16
1513				0.16	0.12	0.06	0.03

Key appears on page 109.

	R
1	**Sequence**
1472	GCTGGGGAGTGGTAGGTGATGAGGGTAGTGAAGGAAGGGGCTGCTGGCCTTGATGGAACT[A/G]TGATTTCTATGAGAAACGAGAGCTGTGAACAAGGGAGCAGAGGTGAAAAGGACCCCCAGC
1473	AGGTCACATGGGCACCAAAGACCAGGTTGTTACATGTTGACTGAGTGAAGTCATCTGCCC[T/C]CTGGGGTGGGAGACCAGGTGAAATATTTCAGAAACATAACCAGAAAGCCAAATGGTGATA
1474	AATTATAAATCCAGGGCTTGCCCCATGACTGGTACTGAAGCACTATTTGATGAGTAAATC[A/T]GCAATTGGGACATGCTCTTCTGGCCTAATGTCTGTCTTCCTCAGCCACAATTAACCATTA
1475	CCACACTTAGTGTCCATAACTCAAACACACTTGAAGAATACTTCTTCTCTCCATACTCTA[T/C]GCATGTCTGGGAAAGGCTCCAAAGGCCCAAACAGCCTTCCTCTTTGAGAAGTGCCCATCT
1476	CAGGCCTCTGGCAAGCACCCATTCTGAACAGGTGCTGCCCAGTGGGGAAGGGAGCGATGC[A/G]CGCTCTGGAAGGCACACTGTACTCCGGGGCCCCAGAGGGACTTCGGGACCAGATAGCTTC
1477	ACATCTCTATAAAGCTCTGTTACGATGTCCATGTTCCAAATGAGGAAACTGAAGAGTGAG[C/G]AGTAGAACAGATTGAGCCTAGGCAGTGTGGCTCTAGAGCCCATGCTCTTAAGCCACCATA
1478	ACGCCCCCAAGTGCGGTGCTGGGGTCGGGAAAGGGCAGGGAGAGGACAGGACCAAGAAGC[A/G]TGCCGAGGTACCCCTGTAGAGGAGCGCAGGCTTTATCTGCAGTTGGGACTGAGGGTCTGG
1479	CTACGGTCCCTCAGGCTTGGAGGGTCACTTTAAACAATAAAAAGCAACAGGACACAAAAA[T/C]CCCTGGCTGGAAAAATCCAAAAAGCAGGTCTGTTAGCAGGGCAGGCCCGGAGTGACTTCC
1480	ACACAGTGAGACTCCATCTCAAAAAAAGAAATAAGGAAATGCTGTCAGAAGCCTACCCCA[T/C]GGTACCTGTCATGGGCCTTTTCATTGGTCCCTTTTTGTTGAAGATGAAGCACTTTGCCCT
1481	GTCTATTATTTAACTTCACTTAGTATGACTCTGAGGTTGAAAGTTACTGAAAACATCTTG[T/G]AAGCTTTTTTAGGCCAATATATTATCAAACGCAATTAACAAAACACAACTCACTAGTTTA
1482	GGTGTCAAGCCCAGCTGCCTGTGTCCTGGCCGCACTGTGAGGCACTGAGGATGCCCTCAC[A/G]CGTGCATCTGCATGTGGCGTGCATGTGGCAAGCATGTGCAGGTGCTGTGTGGGCACGATC
1483	TTTTCCACCCTTCCTGGCTGGCCCCAGTGTGTCCTAACACAGAGCTGCCCTCTCTGAATC[A/C]CCGAACCGCCCACCTTGGGGCCCTGGGGCGGCACTAGTTCCCTGAGTCACTCCGTGAGCC
1484	ACCATCGAGATCAACCCCGACTGTGCCGCCATCACCCAGCGGATGGTGGATTTCGCTGGC[A/G]TGAAGGACAAGGTGTGCATGCCTGACCCGTTGTCAGACCTGGAAAAAGGGCCGGCTGTGG
1485	AGGTGCAAAATGGGTGGCAGAAGTGGGGTGCACACCCCAGACCAGACACCAGGGCAGAAA[T/C]GGCACAGGACCAAGGAGATGGGGTGGGGAAGGGCCGCTCTGGGCCCAGCCTGCTCTCCCC
1486	TCCACCTGGTGCTCGCTCACCTGCAGCTCTCCCAGAAACTGGACACTGCTGTTAGCAGCC[A/G]GACTAGGAGCACGAGGGGCACAGCCCCCATGCCTGGCTAGGTAGGGCCGCTGGACCCTGG
1487	GCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGCGTCCGGCCGTATTCCAGCTTT[T/C]AAAACAACAAAAAACAACAAAAACTTTTCTGGAAAGATCCCTGTCAGCCTTGTGGAGTGT
1488	CCTGGCTCTTGTGAGGGTCTAGCCATCCCCTCAGTGGGTTCTGTGAGCATCGGAGGCACG[A/G]GGGGTGAGGGGCTCAGGAGCAGGTTGCAATTCAAAATCAAGGGCTGCTTTGAGGAGGCCT
1489	AAGGCTTGGTTCCTGCCCAGGGATCCCCAGTGGGCAGGTGGCCGTCCCTAGGTTGGGAGG[A/G]GGTTTGTCCACAGGCACCTGCTCTGTGCTGCTGCGATGGGGTCTGCGGTGTCCTGGCCTG
1490	GTTCAGCAGTGACCTGCAGACCCCGCGCCCAGGCAGTGCTGGTGAGGTTGGGGCAGCCAC[A/G]ACTAGGGAGGGATATGGGTTGACCCTCCTCTGACCTCAGTCTGACAGTGGTCTGCATCCC
1491	TGGGTGATGGGACTGGGGAGTCCTCCTTCACTTTGGCAGACGTGTTATGTTCCACCTTGT[T/C]TGCCCCCAGCAAGGCCCTTGAATCTGGAGCGTGGTCTGGGGCTGCATCAGCCTTCTAGCC
1492	CAAGTCAAATGGCAAATGGGGAAGAGAAGACAGGGTATGGAGTACAAGAGGCCTAGATCC[T/C]CTATAGGTCTGATCTGGCTGGTGCTGCCCCTAGCCAGTAAAGCCACCCTCCAGACCCCTT
1493	cactgttaaatTAGGTGGTAGCTTGGGGATCTCTGAGACATCTTCTTATCTAAAGGTACC[T/C]CTCTCACCAAGCTTCCAGTGTCTCTGAACCCCACATTAGATATGCATTTCTGAACCCATC
1494	TGATTTTCATACTAAGAAATAAATAACAATTATGATGGCCATAATCTATGGAGTGTTTGC[C/G]ATATGTCACACTGCTTCCATATGTGACCTCCTTTATATCTCCCCACAATTCTAGGAGGAA
1495	TGTTTAGAAAAATTAAGGCCTGGATGGACAGAGCTATCATTTGTTTGCTTCCTCTCATTT[T/C]TATTTAAAGCAGTTTATAAAGAAAGTCCTCCAGAAAAATCCAGCCGGCTCCCCACCCCCA
1496	GGCTTGAGCCTCTGTGCCCGACCAATGAATGAGGGGACTTCTTTTTTTATTTTTATTATT[A/T]TTTTTTTGAGATGGTGTCTCACTCTGTCCCCCAGGCTGGAGTGTAGTGGCATGATCTCAG
1497	AGAAGGTGTATGGTACCAGGTGACATTTGGATCTCCACAAAGAAATATAGAGTACCTGCA[A/G]TAATGTAAAAGCCATCGAATGTAAAGACATTGCATGTCTAAAGCCAAAACAATGCAAATA
1498	ATGTTTGAATCTATATTCACTTTTAAAGTCTACTTAATGGTGGTCATTTTTTCCCCTTTA[A/G]AATATATTAAATAGTTGATTTGGGGAGGAAAACTTATTCTGAATATTAACAGTGGTGAAA
1499	CCTGACATTAATTCTTAGGGGTATTTTTGTGTATTTTCTCTTATTTGATGGAAATTTTAT[C/G]TTTTTACAACCCCATTATCAGTTTGTTGATGAATGTATGCATTTAGGGCCCAAACAATCC
1500	GATTTTCTGCAGCCATTACAATTTTCTGTAAATAAATTATTTTTAAAGTTGATTTGTTAA[T/C]TTCCATCAAATTAGAAAAAAGAATTCATGTCAGGTGATAAGTTTGGAGCTTTGATTTTGA
1501	ttacaggcgtgagccaccgtgcccggctAGATCTGGTTTTAAATCAAACACTCAGAACAT[A/G]ATAAAACTTCAAGTGAACTTAAAAAAAAAAAAAAAAAAAACTAGGCATGTGAGTTGTGAATT
1502	GGAAGAAGTACGGCGGGTATGGGTGTGCATTTGTGTGCAAGTGTGCAGCTCAATGCCCAG[T/G]CCTGTGTCTCATCCCCCAGCCACACACACTGTGGTGAGCTGGAGCTCAGCATGCTGGCTC
1503	TTTTCATTTTGCACTGGGGCCCGAGAAGTATGTAGCTGGTCCTGGCGAGGAACTTAGCAC[A/G]ACATGTCACTTGTCAAGAGAGGTAAATGTCTCCCATTCAAGTACTAACCAGGCCCAACCC
1504	AATAGGTTACTTTGGTAGCAGCATCTTGGTATAGGATTCCTTGGTCTTATCTGATGATTT[T/C]CCTGTGGCATTTAAAGTGTCTTCAATTCTGGATGACTTACTCTTTATATAAACGTTGCCA
1505	CTTGTCTGAGGAAGCCACCTTTCCATCACAGAGACCCCCTGCAGCTCACTGGGACCTTCC[A/G]CTACTCCCTCCAACCTTCAAGCCCAGCTCTCACCTCTCACAACGGTTTTGCTTTGTTTTT
1506	CACAGGGACCCACATACACACAGACATGTGCAAACACACAAGCGCTTACACATTCAGACA[T/C]AGACACTCAAACACACAGACATGCGGGTACCGAAAGACACAGAACACAGCACAGACTCAT
1507	AGGCATCTTTATAAAGAATCTGTGCAGGAGTGAGGCTCAGAGAGCAGTACTGACATGCCC[T/C]GAGGCGTCCCACAAATTGAGGACAGAGCTTCACCCAGCAGGGCCCCAGCTGCATCCTGGT
1508	TTGGATGGTTTGCAACAACAGAACGTGTGGCATCCTATGAGTTTGATCGTTCTCTCGTTC[C/G]TTCATTCATTCTTTCAGTGGGTAGTTTCTTTCTTTTTTTGTTTTTTGGGAAGGAGGGAGG
1509	GAATGAACTTTGGAAATCACAGCATTAGCGGGAAAGGATGTGTCTAATGGATGAAATACC[T/C]GCAGCCGGTAAACCACTGGTAAAAAGCATCCTCTCCCAAGCTTAGGACAAAAGACTTCTT
1510	ATGAAATGGAATGGGCTCAGACCAGGAGCCAGTGTTTGAATGCCGCTGTGAGACAAAGGG[T/C]GAGTGACTTCACCTGCTGAAACCTCCGCTTCCTTCTCTGAATGACAGAATGCCTCCATTT
1511	CAGGGGATGGGGGAGTAAAAAATAACATAAACGAACTGAACAGAAATGCAGGAGGGTGGC[A/G]AGAGGGGCCGAGATTGGGTGTTCAGGGCAGAGAGGTGGAAGACCAGGGGCAGTCAGTGCT
1512	GTTCTGGGGCTCACTCTGTACCAGGCACCGCACGGTGTGTTATTCCATTTCATCCTCGTC[A/G]GCTCTCTTATCTTCATTTTGTTTACAGAGAAACTGAGGCTGAGTGTCACTGTGTCACTCA
1513	TTTGATCATGCTTTATGTGTTTGGGGAAATTTTTGATGTTTAAAACATGTCAAATATTAA[T/C]GTCCTTGCACCAAATTTATTTGTCCTACTGCAAAAATATAGCTGGCTAATATTTATTTCA

Key appears on page 109.

	A	B	C	D	E	F	G	H	I	J
1	**Cytoband**	**Gene Name**	**Gene Alias**	**Description**	**Size (kb)**	**Chrom**	**SNP ID**	**Position (bp)**	**htSNP***	**Coding**
1514	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs2192372	113798029		
1515	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs5988087	113841112		
1516	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs6318	113871991		
1517	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs2428707	113906615		
1518	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs2497504	113930668		
1519	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs4243981	113963054		
1520	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs4272555	113989881		
1521	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs5946017	114018929		
1522	Xq23	HTR2C	5-HT2C	5-hydroxytryptamine (serotonin) receptor 2C	326.1	X	rs1801412	114048960		
1523	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs1491793	151084760		
1524	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs6653441	151103823		
1525	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs5925135	151120197		
1526	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs994424	151132436		
1527	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs2194897	151163760		
1528	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs5970247	151177001		
1529	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs1492302	151207321		
1530	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs6627574	151221892		
1531	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs1492293	151243408		
1532	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs6653443	151259417		
1533	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs389292	151292110		
1534	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs6526104	151314578		
1535	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs11094580	151343175		
1536	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs7065528	151355822		
1537	Xq28	GABRA3		gamma-aminobutyric acid (GABA) A receptor, alpha 3	285.6	X	rs6627595	151368659		
1538										
1539	Key: htSNP=haplotype tagging SNP; Coding=nonsynonymous or synonymous coding sequence variant ; Prom=promoter variant; TFBS=transcription factor binding site variant;									
1540	MAF=minor allele frequency; CEU=CEPH/Caucasian; YRI=Yoruban/African; JPT=Japanese; HCB=Chinese									
1541	*T=TAGGER SNP selection method (de Bakker et al. 2005); G=Gabriel SNP selection method (Gabriel et al. 2002); **Y=yes									

	K	L	M	N	O	P	Q
1	**Prom****	**TFBS****	**Association (reference)**	**MAF_CEU**	**MAF_YRI**	**MAF_JPT**	**MAF_HCB**
1514				0.46	0.48	0.15	0.18
1515				0.16	0.32	0.06	0.03
1516				0.16	0.47	0.06	0.03
1517				0.14	0.39	0.03	0.03
1518				0.14	0.44	0.03	0.03
1519				0.14	0.47	0.03	0.03
1520				0.14	0.46	0.03	0.03
1521				0.14	0.46	0.03	0.03
1522				0.13	0.00	0.08	0.02
1523				0.23	0.14	0.07	0.10
1524				0.23	0.36	0.07	0.10
1525				0.22	0.49	0.24	0.38
1526				0.22	0.38	0.41	0.40
1527				0.21	0.37	0.40	0.42
1528				0.13	0.43	0.25	0.12
1529				0.10	0.21	0.06	0.11
1530				0.13	0.42	0.30	0.28
1531				0.13	0.36	0.30	0.28
1532				0.13	0.44	0.30	0.29
1533				0.37	0.04	0.21	0.32
1534				0.43	0.28	0.25	0.27
1535				0.43	0.10	0.23	0.27
1536				0.18	0.42	0.48	0.33
1537				0.48	0.42	0.36	0.41
1538							
1539							
1540							
1541							

Key appears on page 109.

	R
1	**Sequence**
1514	ATGATGAAATGGAACAAGAAAAAATTGTCTCCCAGCAAATATTTAGACATGTGACATTTT[A/G]TGTTTTTAAAGGTCATTGATATTTTAGGGTATTTATCTTAACTACTTAATATTTTTAATT
1515	CTACCCTGCAGAAAGAGAAGCCTCAAGGATGTTTTGCTGATGGGATCTGAATCAATATAA[T/C]GGCTTTAAATGAATTGGACATGCTCATTTTACCCACATCTACTTCCCTGATTTTTCTGAA
1516	GATTGTTTTTTTTTTTCTTAATTTTCAGTGTGCACCTAATTGGCCTATTGGTTTGGCAAT[C/G]TGATATTTCTGTGAGCCCAGTAGCAGCTATAGTAACTGACATTTTCAATACCTCCGATGG
1517	TAGGCAGGTGTTAATAGAGTCTGAACTGAACTGAAATAAAATTATTTTGAGTAAAGCTAT[A/G]GTTCTAAAACAGTGTGTATCAGCTAGGACCATGTACAGTACTAATAAGTACACAATAACT
1518	TAGTAGGCAATACTTACATGTTGCTTACTATGTGCCAGGCACTGTTACAGGTGCTTTGTC[C/G]TCATACACGATTCCTTATATCCCATACCTAAGGTGCCTTAGTCCGCATATCAAGTGAGGC
1519	TTTTTTTCTATTGACTTAGAAATCACTCTACATTAATGACATAGTCAAAGAGATTTTACT[T/C]TTGTTCTCTTGTAAATAAAATACCAGATTAAAGGTATGCTTAATGTGATAAAGTAAAGCC
1520	AACAAGATCAAGACTTCTATTTAATCTTCACTAATATCATCTAAATATTTTGACTCTGGG[T/C]TTATTGATCAAATACATTTAAGTTTTAAGATTGTTCTATTGTAGATTGTTCTGCCTGTGT
1521	GGTGCTGATGTCTTCTATTTAATACTATTATTGTATTCCTATTTCTCCCATCAGTTTTGG[T/G]AATACTTGCTTTATATATTTGTGCTTCAGAGTTGAGAGCATATATATTTACCATTGTTAT
1522	CAGAAGTGGAAGGATAATGAGATGTAATACACCAAATAGCTTTTCACTTCTTAAGGACAG[T/G]GTTCAAATTCTGATTATTACAACAAGCAAACTGAAATTAGTGTTTTCATTCTGGTCCTTA
1523	ATCTCCTCAATTTAGGATCCAACTTTTCCCATGCTAGAACTGGAGTTGGGGCACTAATGA[A/T]CCTGTGTCACATCAAGGGAGACCCTGCCACATGGA
1524	GAATTTCTCCCGGGTTATGTTTTACTGCAGTTCGATAAATCAGTTATTATAACCTCCATC[A/C]ATGTTCATTCTTCTATAGCTATGTTAATATCTCTTGTCTGACTGACATCCCTTGTCCTTC
1525	CTATCCGGGTCCAGTGTGAAATTGTCAAAGGGACAATGGAAAGACACTTTTGTATATTCA[T/C]GAGTATTCACAACTTAGATCATTTCTATGGGTGGAACTTACAAGTGGACTTTTAGAAAGC
1526	CAGTCTTTTCTCACTAGACTGTAAGCTCAATGAGGTGATGAGGCCTCAGATGTTTTATGA[T/C]CGCTGTATCTTCACTATCTAATATGATGCCTTGATATTTGTTGAACGGGTAACTGATTAA
1527	ATAAGTTCTGTTGTTTATAAATTACCCAGTCTAAGGTGTTTTATTATAGCAGTTCAAATG[C/G]ATTAAGACAGTGCCCATTTGCCTTCGACCCACGGAGAGTGACACTTCTGGAAAGTGAGGT
1528	GAGAAAGTGTTTCTACTGAAATGTAGCAACCTCAAAATTCTAATCATATGTGGGATTGAC[A/G]TCCGAATATATACTGTCTGCCTGATCTGAAGTTTACAAGCTGAAAACTTAACACAAAAAT
1529	TAGCCAGAAAATGGGGCTAGACATCAAGGCATAGTGGTCCCCGTGTAGAACACTGGAGTC[A/G]TGTCAAATATCCCTGCTTTTGCCTGGGCTTGGAATAGAGGCCTGTGGATGGTAACATAAA
1530	GTAGTTTTTCAACCCTTTCCCCACTGCCTCCCCCCATTCTCTTGTAGTCCCCAGGGTCTA[T/C]TGTTTTCATCTTTATGTCTGTGTATGCCCTATGTTTAGCTCCCACCTGTAAGTGAGAACT
1531	TATCTGTTTTTCCAAAGCTTACGTATTTTTGTTTACCAGTCTGACCCAGAATTTTACTGC[T/C]GATTGATATTGATATTAGCCTTAATAAAGAAAGTATTCTATATAACTAATTAAGCCTATC
1532	TATTATCTCACTTTCTGTGTAATACAAAACTGTTCAATGGCATATTTCCACTTCTTTGTG[A/C]TTTCATTGACATACATTTTCCTTGTACATATATTACAAGCTACACAATACATGGTTATTA
1533	ATCTCATTTTTTCAATGCCACGTTGAAACCATCTCTCATCTATGCATGTGCACCACAGTC[T/C]TTCTTATTTGAGGTTCATGCCTCCTATCTGTATCACTCTCTGCCTTTCAATCTTACGTCT
1534	TTAATGATGGGTGAGCAATATCTATGATGTATACACAGAGAATCAATTAGTATACACATA[A/C]AATACACAAGCAGTTGGCTATCCTTCAGGAGTGGTATCCATTCAGACGCATGTCCCTATC
1535	TATTAATTTGAAAGTTAGCTATTTTAGGGTTGTGGGAAAAGAACATGATTCATAGGGATT[A/G]TAATAAGAACAATTTTTGTATTGTGTATCTTTATTTTTCATTTTATTTTTGAACTGTGTG
1536	ACATACTCTTGTCAACAAATGGGGCTGGAAAAACTGGACATACATAAGGAAAAATATATT[A/G]TATATGCCTGGAACATTACCTTGCTCCAAAGGCAAAAGTCATCTAAACATGCACCAAAGA
1537	GTTTTTAAAAGGTGCAGTTTGGAGCATGTTGGGTGGATGAGGCTATAAAAAGTGAAGTAC[C/G]ATTTTCAAGGAAAGGAAGCTGACCAATCAAAGTCTTTTGGGCAGCCCCTCCAGAAATCCA
1538	
1539	
1540	
1541	