									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs157198	*EPB41*	1	29,076,494	Flanking 5' UTR	-	-	T	C	0.09	1.00	3.61×10^{-3}	0.08	1.00	0.73
rs157220	*EPB41*	1	29,083,883	Flanking 5' UTR	-	-	G	A	0.36	0.99	1.00	0.38	1.00	0.92
rs126014	*EPB41*	1	29,092,765	Flanking 3' UTR	-	-	A	G	0.37	0.99	0.91	0.38	0.97	1.00
rs150093	*EPB41*	1	29,101,418	Flanking 3' UTR	-	-	T	C	0.12	1.00	1.00	0.15	1.00	0.33
rs10915208	*EPB41*	1	29,102,916	Flanking 3' UTR	-	-	T	C	0.12	1.00	0.63	0.11	1.00	0.33
rs203298	*EPB41*	1	29,105,251	Flanking 3' UTR	-	-	C	G	0.09	1.00	0.23	0.08	1.00	0.51
rs203277	*EPB41*	1	29,107,918	Flanking 3' UTR	-	-	A	T	0.28	1.00	0.38	0.29	1.00	0.47
rs157194	*EPB41*	1	29,108,306	Flanking 3' UTR	-	-	A	G	0.11	1.00	0.30	0.11	1.00	0.30
rs203278	*EPB41*	1	29,114,784	Flanking 3' UTR	-	-	T	C	0.35	1.00	0.23	0.34	1.00	0.83
rs157208	*EPB41*	1	29,117,993	Flanking 3' UTR	-	-	T	C	0.24	0.99	0.89	0.23	0.99	0.89
rs150085	*EPB41*	1	29,120,374	Flanking 3' UTR	-	-	A	C	0.28	1.00	0.38	0.29	1.00	0.47
rs157213	*EPB41*	1	29,126,858	Flanking 3' UTR	-	-	C	G	0.11	1.00	0.30	0.11	1.00	0.60
rs150089	*EPB41*	1	29,131,901	Flanking 3' UTR	-	-	T	C	0.32	1.00	0.49	0.31	1.00	0.91
rs12038347	*EPB41*	1	29,141,303	Flanking 5' UTR	-	-	A	G	0.11	1.00	0.42	0.10	1.00	0.26
rs204057	*EPB41*	1	29,144,644	Flanking 5' UTR	-	-	C	A	0.23	1.00	1.00	0.23	1.00	0.89
rs204060	*EPB41*	1	29,152,213	Flanking 5' UTR	-	-	T	C	0.27	1.00	0.31	0.28	1.00	0.33
rs2985319	*EPB41*	1	29,162,203	Flanking 5' UTR	-	-	G	A	0.02	1.00	0.11	0.01	1.00	1.00
rs2985322	*EPB41*	1	29,169,054	Flanking 5' UTR	-	-	T	C	0.32	1.00	0.49	0.31	1.00	0.82
rs2985344	*EPB41*	1	29,176,902	Flanking 5' UTR	-	-	G	A	0.28	1.00	0.45	0.29	1.00	0.47
rs2762682	*EPB41*	1	29,182,405	Flanking 5' UTR	-	-	C	T	0.28	1.00	0.38	0.29	1.00	0.47
rs12021667	*EPB41*	1	29,183,661	Flanking 5' UTR	-	-	T	C	0.40	1.00	0.92	0.39	1.00	0.84
rs2762686	*EPB41*	1	29,188,832	Intron	-	-	G	C	0.11	1.00	0.30	0.11	1.00	0.60
rs2985329	*EPB41*	1	29,206,549	Intron	-	-	G	C	0.12	1.00	0.48	0.12	1.00	0.16
rs16837840	*EPB41*	1	29,207,867	Intron	-	-	A	C	0.11	1.00	0.79	0.10	1.00	0.27
rs2985331	*EPB41*	1	29,207,950	Intron	-	-	T	C	0.16	1.00	1.00	0.15	1.00	1.00
rs12072697	*EPB41*	1	29,209,878	Intron	-	-	G	A	0.09	1.00	0.23	0.09	1.00	0.52
rs2985332	*EPB41*	1	29,211,686	Intron	-	-	A	G	0.15	0.96	0.55	0.15	0.98	0.23
rs2985335	*EPB41*	1	29,218,234	Intron	-	-	G	A	0.12	1.00	0.63	0.12	1.00	0.16
rs11807517	*EPB41*	1	29,223,797	Intron	-	-	A	NA	0.00	1.00	NA	0.00	1.00	NA
rs10915216	*EPB41*	1	29,229,250	Intron	-	-	T	A	0.50	0.99	0.61	0.49	1.00	0.16
rs2486200	*EPB41*	1	29,236,572	Intron	-	-	T	C	0.23	1.00	0.31	0.22	1.00	0.11
rs12027267	*EPB41*	1	29,251,462	Intron	-	-	C	A	0.40	1.00	1.00	0.39	1.00	0.83
rs2788888	*EPB41*	1	29,252,579	Flanking 3' UTR	-	-	G	A	0.23	1.00	0.31	0.22	1.00	0.09
rs2153165	*EPB41*	1	29,258,073	Flanking 3' UTR	-	-	G	C	0.23	1.00	0.31	0.22	1.00	0.09
rs9426306	*EPB41*	1	29,261,001	Intron	-	-	C	T	0.12	1.00	0.48	0.12	1.00	0.16
rs12072831	*EPB41*	1	29,265,747	Intron	-	-	G	A	0.14	1.00	0.28	0.14	1.00	0.09
rs12130351	*EPB41*	1	29,269,534	Intron	-	-	C	T	0.07	1.00	0.68	0.06	1.00	0.22
rs6702335	*EPB41*	1	29,283,837	Intron	-	-	A	G	0.39	1.00	1.00	0.39	1.00	0.92
rs2254241	*EPB41*	1	29,290,620	Intron	-	-	G	A	0.12	1.00	0.47	0.12	1.00	0.15
rs12039988	*EPB41*	1	29,298,420	Flanking 3' UTR	-	-	G	A	0.39	1.00	0.92	0.39	1.00	0.83
rs4654390	*EPB41*	1	29,311,603	Intron	-	-	T	A	0.50	1.00	0.61	0.49	1.00	0.20
rs575710	*EPB41*	1	29,319,242	3' UTR	-	-	A	G	0.09	1.00	0.35	0.09	1.00	0.52
rs2452788	*EPB41*	1	29,319,398	3' UTR	-	-	G	A	0.14	0.96	0.30	0.14	0.97	0.21
rs484000	*EPB41*	1	29,324,724	Flanking 5' UTR	-	-	G	A	0.08	0.89	0.15	0.07	0.93	0.71
rs10914453	*HCRTR1*	1	31,847,623	Flanking 5' UTR	-	-	G	A	0.38	1.00	0.75	0.41	1.00	0.76
rs3753612	*HCRTR1*	1	31,854,997	Flanking 5' UTR	-	-	G	C	0.46	0.95	0.35	0.48	0.96	0.13
rs968335	*HCRTR1*	1	31,858,363	Intron	-	-	A	G	0.45	1.00	0.76	0.49	1.00	0.27
rs10914456	*HCRTR1*	1	31,860,758	Intron	-	-	C	T	0.41	0.95	0.24	0.45	0.95	0.12
rs7516785	*HCRTR1*	1	31,861,808	Coding Region	Nonsynonymous	R279Q (NP_001516)	G	NA	0.00	1.00	NA	0.00	1.00	NA
rs2271933	*HCRTR1*	1	31,865,112	Coding Region	Nonsynonymous	I408V (NP_001516)	G	A	0.40	1.00	0.92	0.43	1.00	0.68
rs6703093	*HCRTR1*	1	31,866,148	Flanking 3' UTR	-	-	T	C	0.46	1.00	0.68	0.48	1.00	0.23
rs10914457	*HCRTR1*	1	31,866,848	Flanking 3' UTR	-	-	C	A	0.45	0.95	0.10	0.39	0.96	0.29
rs10798880	*HCRTR1*	1	31,869,675	Intron	-	-	T	G	0.38	1.00	0.67	0.41	1.00	0.54
rs7546297	*HCRTR1*	1	31,879,081	Intron	-	-	G	A	0.37	1.00	0.67	0.41	1.00	0.54
rs7524405	*HCRTR1*	1	31,881,166	Intron	-	-	A	C	0.39	1.00	1.00	0.41	1.00	0.26
rs7539745	*CHRNB2*	1	152,793,038	Intron	-	-	G	C	0.13	1.00	0.49	0.15	1.00	0.34
rs7543174	*CHRNB2*	1	152,794,296	Intron	-	-	T	C	0.14	1.00	0.53	0.18	1.00	0.61
rs4845652	*CHRNB2*	1	152,804,829	Flanking 5' UTR	-	-	C	T	0.09	1.00	0.19	0.09	1.00	0.76
rs2072658	*CHRNB2*	1	152,806,849	Flanking 5' UTR	-	-	G	A	0.01	1.00	1.00	0.02	1.00	1.00
rs2072659	*CHRNB2*	1	152,815,145	3' UTR	-	-	C	G	0.11	0.95	0.59	0.10	0.96	0.40
rs2072660	*CHRNB2*	1	152,815,345	3' UTR	-	-	C	T	0.25	0.99	0.23	0.22	1.00	0.06
rs2072661	*CHRNB2*	1	152,815,504	3' UTR	-	-	G	A	0.26	1.00	0.19	0.22	1.00	0.08
rs3811450	*CHRNB2*	1	152,817,656	Flanking 3' UTR	-	-	C	T	0.08	1.00	0.71	0.07	1.00	1.00
rs9616	*CHRNB2*	1	152,822,357	3' UTR	-	-	A	T	0.29	1.00	1.00	0.27	1.00	0.71
rs1127314	*CHRNB2*	1	152,822,890	3' UTR	-	-	A	G	0.31	1.00	0.16	0.29	1.00	0.54
rs1127313	*CHRNB2*	1	152,823,049	3' UTR	-	-	G	A	0.46	1.00	0.08	0.47	1.00	0.55
rs2131902	*CHRNB2*	1	152,826,222	Intron	-	-	T	C	0.32	1.00	0.20	0.30	1.00	0.55
rs3766927	*CHRNB2*	1	152,830,765	Flanking 5' UTR	-	-	C	T	0.31	1.00	0.13	0.29	1.00	0.55
rs6700238	*NTRK1*	1	155,089,868	Intron	-	-	A	NA	0.00	0.98	NA	0.00	0.98	NA
rs1800878	*NTRK1*	1	155,100,893	Intron	-	-	G	T	0.02	1.00	1.00	0.03	1.00	0.30
rs1800879	*NTRK1*	1	155,104,765	Intron	-	-	C	T	0.38	1.00	0.92	0.36	1.00	0.83
rs6334	*NTRK1*	1	155,112,857	Coding Region	Synonymous	Q558Q (NP_002520)	G	A	0.21	1.00	0.88	0.23	1.00	0.32
rs6336	*NTRK1*	1	155,115,542	Coding Region	Nonsynonymous	H604Y (NP_002520)	C	T	0.06	1.00	0.63	0.05	1.00	1.00
rs2644596	*NTRK1*	1	155,118,938	Flanking 3' UTR	-	-	C	G	0.21	1.00	0.13	0.21	1.00	0.55
rs943551	*NTRK1*	1	155,122,121	Flanking 3' UTR	-	-	C	T	0.06	1.00	1.00	0.06	1.00	0.22
rs943552	*NTRK1*	1	155,122,242	Flanking 3' UTR	Nonsynonymous	A16V (XP_371320)	C	T	0.06	1.00	1.00	0.06	1.00	0.22
rs2768762	*NTRK1*	1	155,127,086	Flanking 3' UTR	-	-	T	G	0.21	1.00	0.55	0.19	1.00	0.52
rs2644620	*NTRK1*	1	155,127,792	Flanking 3' UTR	-	-	T	C	0.11	1.00	0.80	0.13	1.00	0.04
rs1186675	*KCNJ9*	1	158,305,708	Intron	-	-	G	A	0.12	1.00	0.63	0.12	1.00	0.10
rs4656874	*KCNJ9*	1	158,311,246	Flanking 5' UTR	-	-	C	T	0.28	1.00	0.71	0.30	1.00	0.55
rs4656876	*KCNJ9*	1	158,317,016	Flanking 5' UTR	-	-	G	C	0.45	1.00	0.92	0.47	1.00	0.19
rs2737703	*KCNJ9*	1	158,322,556	Intron	-	-	C	T	0.33	0.99	0.42	0.35	1.00	0.51
rs2753268	*KCNJ9*	1	158,324,876	3' UTR	-	-	G	A	0.28	1.00	0.71	0.29	1.00	0.63
rs2494211	*KCNJ9*	1	158,325,236	3' UTR	-	-	C	T	0.33	1.00	0.57	0.35	1.00	0.83
rs3180694	*KCNJ9*	1	158,328,008	3' UTR	-	-	C	T	0.11	1.00	0.45	0.12	1.00	0.24
rs12401728	*KCNJ9*	1	158,328,583	Intron	-	-	C	T	0.20	1.00	1.00	0.23	1.00	0.20
rs2369406	*KCNJ9*	1	158,331,042	Intron	-	-	C	T	0.46	1.00	0.92	0.42	1.00	0.76
rs11265320	*KCNJ9*	1	158,336,536	Flanking 5' UTR	-	-	C	T	0.45	1.00	0.61	0.47	1.00	0.14
rs1561289	*POMC*	2	25,222,544	Flanking 3' UTR	-	-	C	T	0.25	1.00	0.29	0.23	1.00	0.07
rs13428823	*POMC*	2	25,226,802	Flanking 3' UTR	-	-	A	G	0.36	1.00	0.74	0.36	1.00	0.83
rs3795955	*POMC*	2	25,228,609	Flanking 3' UTR	-	-	C	T	0.24	0.98	1.09×10^{-6}	0.26	0.99	1.33×10^{-5}
rs2164808	*POMC*	2	25,230,680	Flanking 3' UTR	Synonymous	Y1067Y (XP_039733)	C	T	0.39	1.00	0.14	0.42	1.00	0.92
rs2118404	*POMC*	2	25,230,833	Flanking 3' UTR	-	-	C	T	0.25	1.00	0.29	0.23	1.00	0.09
rs7589318	*POMC*	2	25,231,876	Flanking 3' UTR	-	-	G	A	0.29	0.99	0.04	0.29	1.00	0.72
rs1866146	*POMC*	2	25,234,077	Flanking 3' UTR	-	-	A	G	0.33	1.00	0.31	0.34	1.00	0.66
rs12473543	*POMC*	2	25,240,685	Intron	-	-	T	G	0.22	1.00	0.30	0.21	1.00	0.36
rs934778	*POMC*	2	25,242,728	Intron	-	-	A	G	0.32	1.00	0.30	0.34	1.00	0.82
rs3769671	*POMC*	2	25,243,657	Intron	-	-	A	C	0.04	0.99	1.00	0.04	0.99	1.00
rs6545976	*POMC*	2	25,248,154	Flanking 5' UTR	-	-	G	T	0.06	1.00	0.62	0.04	1.00	1.00
rs4665775	*POMC*	2	25,260,625	Flanking 5' UTR	-	-	A	G	0.20	0.98	0.27	0.20	0.98	0.88
rs16840214	*NR4A2*	2	156,875,018	Flanking 3' UTR	-	-	C	T	0.18	1.00	0.86	0.22	1.00	0.56
rs707127	*NR4A2*	2	156,877,056	Flanking 3' UTR	-	-	C	T	0.33	1.00	0.73	0.36	1.00	1.00
rs1528454	*NR4A2*	2	156,877,951	Flanking 3' UTR	-	-	T	C	0.26	1.00	0.90	0.29	1.00	0.81
rs1150143	*NR4A2*	2	156,885,862	Flanking 3' UTR	-	-	C	G	0.31	1.00	0.35	0.33	1.00	0.65
rs1150144	*NR4A2*	2	156,886,749	Flanking 3' UTR	-	-	A	G	0.28	1.00	0.21	0.30	1.00	0.63
rs12803	*NR4A2*	2	156,890,171	3' UTR	-	-	C	A	0.46	1.00	1.00	0.49	1.00	0.49
rs13428968	*NR4A2*	2	156,900,859	Flanking 5' UTR	-	-	T	C	0.17	1.00	0.59	0.18	1.00	0.50
rs834829	*NR4A2*	2	156,909,095	Flanking 5' UTR	-	-	G	A	0.28	1.00	0.53	0.30	1.00	0.55
rs834830	*NR4A2*	2	156,911,506	Flanking 5' UTR	-	-	A	G	0.20	1.00	0.06	0.22	1.00	0.47
rs2709371	*CREB1*	2	208,092,932	Flanking 5' UTR	-	-	A	G	0.21	1.00	0.55	0.18	1.00	0.62
rs2253206	*CREB1*	2	208,100,223	Flanking 5' UTR	-	-	G	A	0.44	0.99	0.22	0.48	0.99	0.76
rs2551640	*CREB1*	2	208,116,138	Intron	-	-	A	G	0.33	1.00	0.05	0.36	1.00	0.39
rs2551642	*CREB1*	2	208,121,742	Intron	-	-	C	A	0.20	1.00	0.88	0.18	1.00	1.00
rs2709402	*CREB1*	2	208,129,222	Intron	-	-	C	A	0.20	1.00	0.88	0.18	1.00	1.00
rs10932201	*CREB1*	2	208,134,502	Flanking 3' UTR	-	-	G	A	0.46	1.00	0.48	0.46	1.00	0.37
rs11904814	*CREB1*	2	208,135,043	Flanking 3' UTR	-	-	T	G	0.29	1.00	0.54	0.32	1.00	0.73

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs16839883	*CREB1*	2	208,137,587	Flanking 5' UTR	-	-	A	G	0.02	1.00	0.11	0.01	1.00	1.00
rs2551921	*CREB1*	2	208,143,800	Intron	-	-	T	C	0.20	1.00	0.88	0.18	1.00	1.00
rs2551923	*CREB1*	2	208,150,021	Intron	-	-	C	T	0.20	0.99	0.88	0.18	1.00	1.00
rs7369949	*CREB1*	2	208,159,033	Intron	-	-	T	C	0.34	1.00	0.14	0.36	1.00	0.39
rs13397461	*CREB1*	2	208,166,082	Intron	-	-	A	NA	0.00	1.00	NA	0.00	1.00	NA
rs2551928	*CREB1*	2	208,174,023	Flanking 3' UTR	-	-	G	A	0.21	1.00	0.88	0.18	1.00	0.87
rs1806584	*CREB1*	2	208,174,515	Flanking 3' UTR	-	-	A	G	0.20	0.99	0.88	0.18	1.00	1.00
rs1045780	*CREB1*	2	208,175,395	Flanking 3' UTR	-	-	G	A	0.20	1.00	0.88	0.18	1.00	1.00
rs2551931	*CREB1*	2	208,179,725	Flanking 3' UTR	-	-	G	A	0.20	0.99	0.64	0.18	0.99	1.00
rs7569963	*CREB1*	2	208,181,429	Flanking 3' UTR	-	-	G	A	0.26	1.00	0.36	0.30	1.00	0.72
rs10934253	*DRD3*	3	115,320,474	Flanking 3' UTR	-	-	A	T	0.02	1.00	0.13	0.02	1.00	0.21
rs1385884	*DRD3*	3	115,324,315	Flanking 3' UTR	-	-	T	A	0.42	1.00	0.61	0.43	1.00	0.84
rs2087017	*DRD3*	3	115,324,703	Flanking 3' UTR	-	-	A	G	0.43	1.00	0.61	0.43	1.00	0.84
rs2399496	*DRD3*	3	115,328,703	Flanking 3' UTR	-	-	A	T	0.48	1.00	0.54	0.47	1.00	1.00
rs2134655	*DRD3*	3	115,340,891	Flanking 3' UTR	-	-	C	T	0.27	1.00	1.00	0.28	1.00	0.18
rs963468	*DRD3*	3	115,345,577	Flanking 3' UTR	-	-	G	A	0.39	1.00	0.67	0.38	1.00	0.75
rs324035	*DRD3*	3	115,351,544	Intron	-	-	C	A	0.19	1.00	0.33	0.20	1.00	0.76
rs3773679	*DRD3*	3	115,352,025	Intron	-	-	C	T	0.39	1.00	1.00	0.38	1.00	0.83
rs3773678	*DRD3*	3	115,352,768	Intron	-	-	G	A	0.14	1.00	0.09	0.15	1.00	0.11
rs2630349	*DRD3*	3	115,356,062	Intron	-	-	G	A	0.06	1.00	0.04	0.07	1.00	0.02
rs2630350	*DRD3*	3	115,357,686	Intron	-	-	C	T	0.06	1.00	0.03	0.07	1.00	0.03
rs167771	*DRD3*	3	115,358,965	Intron	-	-	A	G	0.17	1.00	0.48	0.18	1.00	0.73
rs324032	*DRD3*	3	115,360,518	Intron	-	-	A	G	0.06	1.00	0.04	0.07	1.00	0.03
rs167770	*DRD3*	3	115,362,252	Intron	-	-	A	G	0.29	1.00	0.54	0.27	1.00	0.53
rs7625282	*DRD3*	3	115,364,217	Intron	-	-	A	G	0.27	1.00	0.90	0.25	1.00	0.28
rs324029	*DRD3*	3	115,364,313	Intron	-	-	G	A	0.29	1.00	0.63	0.27	1.00	0.53
rs7633291	*DRD3*	3	115,369,758	Intron	-	-	T	G	0.22	1.00	0.66	0.19	1.00	0.20
rs324022	*DRD3*	3	115,369,988	Intron	-	-	G	A	0.29	1.00	0.47	0.27	1.00	0.53
rs1486009	*DRD3*	3	115,371,222	Intron	-	-	A	G	0.06	1.00	1.00	0.05	1.00	1.00
rs6280	*DRD3*	3	115,373,505	Coding Region	Nonsynonymous	S9G (NP_387509)	T	C	0.34	1.00	1.00	0.33	0.99	1.00
rs324026	*DRD3*	3	115,373,732	Flanking 5' UTR	-	-	T	C	0.33	0.99	0.73	0.33	1.00	0.91
rs7638876	*DRD3*	3	115,376,990	Flanking 3' UTR	-	-	T	C	0.34	1.00	0.91	0.33	1.00	0.82
rs9825563	*DRD3*	3	115,382,910	Flanking 5' UTR	-	-	A	G	0.32	0.99	0.64	0.31	1.00	0.25
rs12639080	*DRD3*	3	115,386,481	Flanking 5' UTR	-	-	G	A	0.35	1.00	0.91	0.34	1.00	0.44
rs4678448	*NCK1*	3	138,053,879	Intron	-	-	C	T	0.33	1.00	0.91	0.28	1.00	0.09
rs1805300	*NCK1*	3	138,058,932	Flanking 3' UTR	-	-	G	A	0.33	1.00	0.91	0.28	1.00	0.09
rs938525	*NCK1*	3	138,064,643	Intron	-	-	T	C	0.32	1.00	0.82	0.28	1.00	0.14
rs9845460	*NCK1*	3	138,069,807	Intron	-	-	G	A	0.24	1.00	0.49	0.18	1.00	0.32
rs9818792	*NCK1*	3	138,072,010	Intron	-	-	T	C	0.32	1.00	0.73	0.28	1.00	0.17
rs12330283	*NCK1*	3	138,073,101	Intron	-	-	T	C	0.32	1.00	0.82	0.28	1.00	0.14
rs1865149	*NCK1*	3	138,078,300	Intron	-	-	A	G	0.32	1.00	0.82	0.28	1.00	0.14
rs2343662	*NCK1*	3	138,083,736	Intron	-	-	A	T	0.32	1.00	0.82	0.28	1.00	0.14
rs9846691	*NCK1*	3	138,088,961	Intron	-	-	C	T	0.32	1.00	0.82	0.28	1.00	0.14
rs6784005	*NCK1*	3	138,095,451	Intron	-	-	G	C	0.32	0.91	0.62	0.29	0.90	0.13
rs9824147	*NCK1*	3	138,100,688	Intron	-	-	A	T	0.04	1.00	1.00	0.02	1.00	1.00
rs9867325	*NCK1*	3	138,101,599	Intron	-	-	G	C	0.20	1.00	0.88	0.27	1.00	0.61
rs6761993	*NCK1*	3	138,108,592	Intron	-	-	T	C	0.39	0.99	0.67	0.38	1.00	0.17
rs9837990	*NCK1*	3	138,115,626	Intron	-	-	G	C	0.39	1.00	0.83	0.38	1.00	0.14
rs9881139	*NCK1*	3	138,116,730	Intron	-	-	G	A	0.39	1.00	0.75	0.38	1.00	0.14
rs4678274	*NCK1*	3	138,121,927	Intron	-	-	G	T	0.32	1.00	0.82	0.28	1.00	0.14
rs10935210	*NCK1*	3	138,133,843	Intron	-	-	G	A	0.32	1.00	0.82	0.28	1.00	0.17
rs6775389	*NCK1*	3	138,142,414	Intron	-	-	T	C	0.32	1.00	0.82	0.28	1.00	0.14
rs1433318	*NCK1*	3	138,149,144	Intron	-	-	T	C	0.32	1.00	0.91	0.28	1.00	0.17
rs835648	*NCK1*	3	138,154,194	Flanking 3' UTR	-	-	T	A	0.32	1.00	0.49	0.27	1.00	0.38
rs7648198	*NCK1*	3	138,154,451	Flanking 3' UTR	-	-	A	C	0.45	1.00	0.68	0.45	1.00	0.11
rs835637	*NCK1*	3	138,155,847	Flanking 5' UTR	-	-	A	T	0.47	1.00	1.00	0.45	1.00	0.23
rs835636	*NCK1*	3	138,157,190	Flanking 5' UTR	-	-	C	A	0.48	1.00	0.69	0.49	1.00	0.55
rs835634	*NCK1*	3	138,158,993	Flanking 5' UTR	-	-	C	T	0.44	1.00	0.26	0.42	1.00	0.84
rs12054220	*NCK1*	3	138,160,271	Intron	-	-	A	G	0.46	1.00	0.84	0.47	1.00	0.92
rs7655090	*DRD5*	4	9,374,973	Flanking 5' UTR	-	-	A	G	0.31	1.00	0.91	0.33	1.00	0.74
rs10939514	*DRD5*	4	9,382,294	Flanking 5' UTR	-	-	T	C	0.05	1.00	0.61	0.04	1.00	1.00
rs10939515	*DRD5*	4	9,382,394	Flanking 5' UTR	-	-	G	A	0.16	1.00	1.00	0.18	1.00	0.09
rs10033951	*DRD5*	4	9,388,678	Flanking 5' UTR	-	-	C	T	0.30	0.99	0.72	0.32	0.98	0.73
rs2867383	*DRD5*	4	9,397,033	Flanking 3' UTR	-	-	G	A	0.31	1.00	0.24	0.33	1.00	0.65
rs1850744	*DRD5*	4	9,399,810	Flanking 3' UTR	-	-	C	T	0.05	0.99	0.62	0.04	0.99	1.00
rs13106539	*DRD5*	4	9,406,801	Flanking 3' UTR	-	-	T	C	0.38	1.00	0.29	0.38	1.00	0.67
rs1519097	*DRD5*	4	9,411,951	Flanking 3' UTR	-	-	A	G	0.32	0.99	0.13	0.34	1.00	0.74
rs356219	*SNCA*	4	90,856,624	Flanking 3' UTR	-	-	A	G	0.36	1.00	0.28	0.39	1.00	0.29
rs11931074	*SNCA*	4	90,858,538	Flanking 3' UTR	-	-	G	T	0.08	1.00	0.73	0.08	1.00	0.07
rs356220	*SNCA*	4	90,860,363	Flanking 3' UTR	-	-	C	T	0.35	0.89	0.49	0.37	0.86	0.65
rs10003708	*SNCA*	4	90,862,074	Flanking 3' UTR	-	-	C	A	0.08	1.00	0.73	0.08	1.00	0.07
rs168552	*SNCA*	4	90,862,167	Flanking 3' UTR	-	-	T	C	0.29	1.00	0.39	0.31	1.00	0.64
rs3857051	*SNCA*	4	90,862,720	Flanking 3' UTR	-	-	A	G	0.08	1.00	0.73	0.08	1.00	0.07
rs356165	*SNCA*	4	90,865,909	3' UTR	-	-	A	G	0.38	0.96	0.13	0.41	0.95	0.06
rs10033209	*SNCA*	4	90,872,727	Intron	-	-	T	G	0.08	1.00	0.09	0.07	0.99	0.03
rs3775423	*SNCA*	4	90,876,514	Intron	-	-	C	T	0.08	1.00	0.72	0.07	1.00	0.06
rs356204	*SNCA*	4	90,882,565	Intron	-	-	C	T	0.44	0.93	0.83	0.46	0.94	0.12
rs356203	*SNCA*	4	90,885,064	Intron	-	-	T	C	0.37	1.00	0.28	0.39	1.00	0.21
rs356168	*SNCA*	4	90,893,454	Intron	-	-	A	G	0.46	1.00	0.84	0.48	1.00	0.16
rs356198	*SNCA*	4	90,901,527	Intron	-	-	C	T	0.20	1.00	0.35	0.18	1.00	0.06
rs6834765	*SNCA*	4	90,903,013	Intron	-	-	T	C	0.07	1.00	0.47	0.07	1.00	0.09
rs356164	*SNCA*	4	90,912,499	Intron	-	-	C	G	0.15	1.00	0.44	0.14	1.00	0.04
rs3822090	*SNCA*	4	90,923,899	Intron	-	-	C	T	0.13	1.00	0.39	0.11	1.00	0.61
rs2737033	*SNCA*	4	90,926,970	Intron	-	-	T	C	0.27	1.00	0.20	0.30	1.00	0.08
rs2737029	*SNCA*	4	90,930,793	Intron	-	-	T	C	0.40	0.99	0.35	0.41	1.00	0.18
rs10002435	*SNCA*	4	90,931,534	Intron	-	-	G	A	0.12	1.00	0.34	0.10	1.00	0.40
rs3775443	*SNCA*	4	90,934,697	Intron	-	-	T	G	0.07	1.00	0.71	0.05	1.00	1.00
rs6532190	*SNCA*	4	90,938,219	Intron	-	-	A	T	0.06	1.00	0.64	0.06	1.00	0.65
rs2583958	*SNCA*	4	90,939,388	Intron	-	-	T	C	0.26	1.00	0.12	0.30	1.00	0.12
rs17016188	*SNCA*	4	90,940,903	Intron	-	-	T	C	0.06	1.00	0.64	0.06	1.00	0.65
rs2619373	*SNCA*	4	90,941,456	Intron	-	-	G	A	0.26	1.00	0.12	0.30	1.00	0.12
rs17016190	*SNCA*	4	90,941,855	Intron	-	-	A	G	0.07	1.00	0.71	0.05	1.00	1.00
rs961386	*SNCA*	4	90,951,826	Intron	-	-	A	T	0.01	1.00	1.00	0.01	1.00	1.00
rs3822095	*SNCA*	4	90,955,540	Intron	-	-	T	C	0.37	1.00	0.24	0.38	1.00	0.60
rs2619372	*SNCA*	4	90,955,750	Intron	-	-	G	A	0.30	1.00	0.81	0.26	1.00	0.36
rs1812923	*SNCA*	4	90,958,562	Intron	-	-	C	A	0.43	1.00	0.26	0.45	1.00	1.00
rs2737020	*SNCA*	4	90,959,901	Intron	-	-	A	G	0.30	1.00	0.72	0.26	1.00	0.36
rs7356228	*SNCA*	4	90,962,878	Intron	-	-	C	G	0.37	1.00	0.24	0.39	1.00	0.60
rs2737015	*SNCA*	4	90,964,306	Intron	-	-	T	C	0.26	1.00	0.19	0.30	1.00	0.15
rs3113355	*SNCA*	4	90,964,368	Intron	-	-	T	A	0.23	1.00	0.77	0.21	1.00	0.10
rs6532191	*SNCA*	4	90,964,953	Intron	-	-	T	C	0.49	1.00	1.00	0.50	1.00	0.84
rs2583975	*SNCA*	4	90,967,511	Intron	-	-	C	T	0.22	1.00	0.55	0.20	1.00	0.12
rs13148411	*SNCA*	4	90,969,745	Flanking 5' UTR	-	-	A	G	0.26	1.00	0.19	0.30	1.00	0.19
rs10011157	*SNCA*	4	90,969,867	Flanking 5' UTR	-	-	T	C	0.23	1.00	0.77	0.21	1.00	0.09
rs2583981	*SNCA*	4	90,971,605	Flanking 5' UTR	-	-	A	T	0.27	1.00	0.16	0.30	1.00	0.19
rs2301134	*SNCA*	4	90,977,968	Flanking 5' UTR	-	-	A	G	0.50	1.00	0.92	0.49	1.00	0.55
rs3775085	*TDO2*	4	157,042,829	Flanking 5' UTR	-	-	A	C	0.08	1.00	0.34	0.10	1.00	0.42
rs3755910	*TDO2*	4	157,044,050	Flanking 5' UTR	-	-	C	A	0.02	1.00	1.00	0.03	1.00	0.07
rs2271537	*TDO2*	4	157,049,273	Intron	-	-	C	A	0.48	0.93	0.01	0.50	0.92	0.84
rs10517626	*TDO2*	4	157,050,894	Intron	-	-	G	T	0.11	1.00	0.79	0.10	1.00	0.17
rs2878125	*TDO2*	4	157,053,811	Intron	-	-	G	A	0.12	1.00	0.82	0.12	1.00	0.10
rs13152449	*TDO2*	4	157,055,252	Intron	-	-	A	G	0.10	1.00	0.59	0.10	1.00	0.57
rs11723579	*TDO2*	4	157,057,151	Intron	-	-	A	T	0.50	1.00	0.02	0.47	1.00	0.32
rs2292537	*TDO2*	4	157,058,912	Intron	-	-	T	C	0.09	1.00	1.00	0.09	1.00	0.14
rs2292536	*TDO2*	4	157,059,101	Intron	-	-	A	T	0.43	1.00	0.76	0.45	1.00	0.05
rs6856558	*TDO2*	4	157,059,403	Intron	-	-	C	T	0.36	1.00	0.58	0.38	1.00	0.03

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs9044	*TDO2*	4	157,065,537	3' UTR	-	-	A	G	0.46	1.00	0.27	0.49	1.00	0.16
rs6856354	*TDO2*	4	157,068,548	Intron	-	-	A	C	0.36	1.00	1.00	0.36	1.00	0.91
rs27074	*SLC6A3*	5	1,436,550	Flanking 3' UTR	-	-	C	T	0.09	1.00	0.75	0.10	1.00	0.41
rs11133762	*SLC6A3*	5	1,444,161	Flanking 3' UTR	-	-	C	T	0.01	1.00	1.00	0.01	1.00	1.00
rs10064525	*SLC6A3*	5	1,445,721	Flanking 3' UTR	-	-	T	G	0.06	0.99	0.66	0.08	0.99	0.49
rs40184	*SLC6A3*	5	1,448,077	Intron	-	-	C	T	0.48	0.98	0.05	0.47	1.00	1.00
rs11564767	*SLC6A3*	5	1,457,704	Intron	-	-	A	T	0.06	1.00	0.66	0.08	1.00	1.00
rs11564764	*SLC6A3*	5	1,458,806	Intron	-	-	C	T	0.06	1.00	0.34	0.07	1.00	0.68
rs3776511	*SLC6A3*	5	1,460,129	Intron	-	-	C	T	0.20	0.92	0.42	0.21	0.94	0.88
rs6347	*SLC6A3*	5	1,464,412	Coding Region	Synonymous	S405S (NP_001035)	T	C	0.26	0.98	0.69	0.27	0.99	0.71
rs37022	*SLC6A3*	5	1,468,629	Intron	-	-	A	T	0.17	0.99	0.86	0.16	1.00	0.35
rs10040882	*SLC6A3*	5	1,471,558	Intron	-	-	C	T	0.21	0.98	0.13	0.23	0.99	0.12
rs2975292	*SLC6A3*	5	1,472,932	Intron	-	-	G	C	0.35	0.95	0.37	0.37	0.96	0.59
rs458334	*SLC6A3*	5	1,483,093	Intron	-	-	A	G	0.43	1.00	0.06	0.43	1.00	0.48
rs456082	*SLC6A3*	5	1,483,515	Intron	-	-	A	G	0.21	0.99	0.54	0.20	1.00	0.75
rs11737901	*SLC6A3*	5	1,483,616	Intron	-	-	C	T	0.34	0.99	4.86×10^{-5}	0.32	1.00	0.49
rs409588	*SLC6A3*	5	1,483,834	Intron	-	-	G	T	0.20	1.00	0.54	0.20	1.00	0.64
rs4975646	*SLC6A3*	5	1,486,401	Intron	-	-	G	A	0.37	1.00	0.13	0.33	1.00	0.12
rs403636	*SLC6A3*	5	1,491,354	Intron	-	-	C	A	0.15	1.00	0.33	0.18	1.00	1.00
rs6350	*SLC6A3*	5	1,496,199	Coding Region	Synonymous	N38N (NP_001035)	G	A	0.06	1.00	0.66	0.05	1.00	1.00
rs11564753	*SLC6A3*	5	1,496,990	Intron	-	-	C	T	0.22	0.99	1.65×10^{-3}	0.21	1.00	3.63×10^{-3}
rs11564752	*SLC6A3*	5	1,497,985	Intron	-	-	C	A	0.06	0.96	1.00	0.05	0.97	7.98×10^{-4}
rs2975226	*SLC6A3*	5	1,498,616	Flanking 5' UTR	-	-	T	A	0.39	0.93	0.74	0.39	0.95	0.20
rs2652511	*SLC6A3*	5	1,499,389	Flanking 5' UTR	-	-	G	A	0.39	0.99	0.67	0.40	0.99	0.30
rs6413429	*SLC6A3*	5	1,500,027	Flanking 5' UTR	-	-	C	A	0.07	1.00	0.69	0.06	1.00	1.00
rs2652510	*SLC6A3*	5	1,500,860	Flanking 5' UTR	-	-	T	C	0.40	1.00	1.00	0.40	1.00	0.30
rs3756450	*SLC6A3*	5	1,501,148	Flanking 5' UTR	-	-	A	G	0.12	1.00	0.47	0.11	1.00	0.33
rs12652860	*SLC6A3*	5	1,506,772	Flanking 3' UTR	-	-	C	A	0.28	1.00	1.00	0.28	1.00	0.09
rs6859392	*HTR1A*	5	63,277,237	Flanking 3' UTR	-	-	G	C	0.31	1.00	1.00	0.30	1.00	0.64
rs10085024	*HTR1A*	5	63,284,120	Flanking 3' UTR	-	-	C	G	0.50	1.00	0.48	0.48	1.00	0.92
rs1364043	*HTR1A*	5	63,286,607	Flanking 3' UTR	-	-	T	G	0.25	1.00	0.59	0.21	1.00	0.14
rs6295	*HTR1A*	5	63,294,321	Flanking 5' UTR	-	-	C	G	0.49	1.00	0.55	0.48	1.00	0.84
rs10042486	*HTR1A*	5	63,297,085	Flanking 5' UTR	-	-	C	T	0.49	0.99	0.54	0.48	1.00	1.00
rs13436914	*HTR1A*	5	63,297,951	Flanking 5' UTR	-	-	T	C	1.27×10^{-3}	1.00	1.00	1.24×10^{-3}	1.00	1.00
rs11954565	*DRD1*	5	174,782,513	Flanking 3' UTR	-	-	A	G	0.34	0.99	0.05	0.36	0.99	0.51
rs1587176	*DRD1*	5	174,783,796	Flanking 3' UTR	-	-	T	G	0.19	1.00	0.74	0.15	0.99	0.57
rs1310277	*DRD1*	5	174,786,176	Flanking 3' UTR	-	-	G	A	0.12	1.00	0.34	0.13	1.00	0.40
rs11739696	*DRD1*	5	174,789,227	Flanking 3' UTR	-	-	G	A	0.37	1.00	0.33	0.37	1.00	0.75
rs2453737	*DRD1*	5	174,791,508	Flanking 3' UTR	-	-	T	C	0.37	1.00	0.10	0.38	1.00	0.83
rs6881740	*DRD1*	5	174,791,768	Flanking 3' UTR	-	-	C	G	0.35	1.00	0.12	0.36	0.99	0.83
rs11742274	*DRD1*	5	174,792,103	Flanking 3' UTR	-	-	C	G	0.19	1.00	0.75	0.19	1.00	0.33
rs265971	*DRD1*	5	174,793,017	Flanking 3' UTR	-	-	T	C	0.28	1.00	0.26	0.29	1.00	0.18
rs265972	*DRD1*	5	174,793,122	Flanking 3' UTR	-	-	A	G	0.47	1.00	0.61	0.48	1.00	0.69
rs265973	*DRD1*	5	174,793,305	Flanking 3' UTR	-	-	C	T	0.45	1.00	8.18×10^{-3}	0.45	1.00	0.84
rs265974	*DRD1*	5	174,793,846	Flanking 3' UTR	-	-	A	G	0.35	1.00	0.37	0.34	1.00	0.82
rs265975	*DRD1*	5	174,794,801	Flanking 3' UTR	-	-	C	T	0.34	1.00	0.58	0.34	1.00	0.91
rs265976	*DRD1*	5	174,795,026	Flanking 3' UTR	-	-	G	T	0.19	1.00	0.33	0.18	1.00	0.62
rs10476156	*DRD1*	5	174,795,276	Flanking 3' UTR	-	-	A	G	0.15	1.00	0.32	0.15	1.00	0.70
rs265977	*DRD1*	5	174,795,863	Flanking 3' UTR	-	-	C	T	0.17	0.99	0.38	0.17	1.00	0.86
rs863126	*DRD1*	5	174,795,954	Flanking 3' UTR	-	-	A	T	0.32	1.00	0.49	0.32	1.00	1.00
rs835616	*DRD1*	5	174,796,296	Flanking 3' UTR	-	-	G	A	0.38	0.99	0.07	0.35	0.99	0.74
rs835540	*DRD1*	5	174,796,497	Flanking 3' UTR	-	-	T	C	0.26	1.00	1.21×10^{-4}	0.25	1.00	5.41×10^{-3}
rs4867796	*DRD1*	5	174,798,127	Flanking 3' UTR	-	-	A	C	0.16	0.99	0.02	0.18	1.00	0.30
rs11746641	*DRD1*	5	174,798,697	Flanking 3' UTR	-	-	T	G	0.16	1.00	0.13	0.17	1.00	0.29
rs11749676	*DRD1*	5	174,798,904	Flanking 3' UTR	-	-	G	A	0.41	1.00	0.05	0.40	1.00	0.10
rs5326	*DRD1*	5	174,802,802	Intron	-	-	C	T	0.13	1.00	0.27	0.13	1.00	0.67
rs265981	*DRD1*	5	174,803,508	5' UTR	-	-	G	A	0.41	0.91	6.52×10^{-4}	0.40	0.88	5.89×10^{-4}
rs2168631	*DRD1*	5	174,808,608	Flanking 5' UTR	-	-	G	A	0.17	1.00	0.29	0.18	1.00	0.73
rs6878159	*DRD1*	5	174,809,007	Flanking 5' UTR	-	-	A	T	0.01	1.00	1.00	8.66×10^{-3}	1.00	1.00
rs267417	*DRD1*	5	174,813,120	Flanking 5' UTR	-	-	G	T	0.40	1.00	0.05	0.40	1.00	0.35
rs2471005	*DRD1*	5	174,814,813	Flanking 5' UTR	-	-	G	A	0.40	1.00	0.09	0.40	1.00	0.35
rs267400	*DRD1*	5	174,815,305	Flanking 5' UTR	-	-	C	T	0.41	1.00	0.76	0.42	1.00	0.76
rs11749035	*DRD1*	5	174,815,658	Flanking 5' UTR	-	-	C	T	0.16	1.00	0.12	0.16	1.00	0.59
rs267405	*DRD1*	5	174,817,158	Flanking 5' UTR	-	-	G	T	0.42	1.00	0.84	0.42	1.00	0.92
rs267406	*DRD1*	5	174,817,347	Flanking 5' UTR	-	-	G	T	0.42	1.00	0.92	0.42	1.00	0.92
rs10042051	*DRD1*	5	174,819,467	Flanking 5' UTR	-	-	A	G	0.02	1.00	1.00	9.90×10^{-3}	1.00	1.00
rs9396056	*HCRTR2*	6	55,141,716	Flanking 5' UTR	-	-	C	T	0.38	1.00	1.00	0.39	1.00	0.35
rs9357845	*HCRTR2*	6	55,142,145	Flanking 5' UTR	-	-	G	C	0.38	1.00	0.24	0.40	1.00	0.54
rs9464203	*HCRTR2*	6	55,145,083	Flanking 5' UTR	-	-	G	A	0.22	1.00	0.55	0.21	1.00	0.22
rs9382460	*HCRTR2*	6	55,145,443	Flanking 5' UTR	-	-	C	A	0.16	1.00	0.86	0.19	1.00	0.34
rs9367621	*HCRTR2*	6	55,148,249	Intron	-	-	A	T	0.44	1.00	0.61	0.43	1.00	0.19
rs10456181	*HCRTR2*	6	55,148,655	Intron	-	-	G	A	0.34	1.00	0.74	0.36	1.00	0.67
rs4364482	*HCRTR2*	6	55,148,947	Intron	-	-	G	A	0.20	1.00	0.34	0.19	1.00	0.26
rs6927478	*HCRTR2*	6	55,152,345	Intron	-	-	T	G	0.37	1.00	0.75	0.39	1.00	0.75
rs9370399	*HCRTR2*	6	55,152,984	Intron	-	-	A	C	0.49	1.00	0.13	0.44	1.00	0.48
rs7768760	*HCRTR2*	6	55,153,334	Intron	-	-	T	G	0.47	1.00	0.31	0.46	1.00	0.62
rs7775745	*HCRTR2*	6	55,158,466	Intron	-	-	G	A	0.45	1.00	0.03	0.43	1.00	1.00
rs3134689	*HCRTR2*	6	55,162,711	Intron	-	-	A	G	0.20	1.00	0.64	0.19	1.00	0.26
rs4712099	*HCRTR2*	6	55,163,157	Intron	-	-	G	A	0.17	1.00	0.37	0.18	1.00	0.87
rs4236127	*HCRTR2*	6	55,164,136	Intron	-	-	T	C	0.19	1.00	0.52	0.17	1.00	0.60
rs9475195	*HCRTR2*	6	55,168,977	Intron	-	-	T	C	0.38	1.00	0.29	0.41	1.00	0.36
rs3134696	*HCRTR2*	6	55,170,060	Intron	-	-	T	C	0.21	1.00	0.76	0.19	1.00	0.26
rs3122148	*HCRTR2*	6	55,173,948	Intron	-	-	A	G	0.21	1.00	0.88	0.19	1.00	0.33
rs10498801	*HCRTR2*	6	55,174,923	Intron	-	-	G	A	0.19	1.00	0.52	0.18	1.00	0.61
rs12111375	*HCRTR2*	6	55,176,953	Intron	-	-	T	C	0.48	0.88	0.00	0.49	0.91	2.79×10^{-5}
rs9367622	*HCRTR2*	6	55,177,132	Intron	-	-	T	C	0.16	1.00	0.57	0.15	1.00	0.17
rs3134705	*HCRTR2*	6	55,182,315	Intron	-	-	G	A	0.41	1.00	0.04	0.38	1.00	0.09
rs3122153	*HCRTR2*	6	55,184,612	Intron	-	-	T	G	0.23	1.00	1.00	0.20	1.00	0.27
rs4142972	*HCRTR2*	6	55,184,896	Intron	-	-	G	A	0.17	1.00	0.73	0.18	1.00	0.51
rs3122154	*HCRTR2*	6	55,186,417	Intron	-	-	C	T	0.21	0.99	0.28	0.20	1.00	0.35
rs12662510	*HCRTR2*	6	55,187,850	Intron	-	-	A	G	0.15	0.98	0.56	0.15	0.99	0.17
rs9370403	*HCRTR2*	6	55,189,315	Intron	-	-	G	C	0.20	0.97	0.20	0.19	0.96	0.74
rs3134710	*HCRTR2*	6	55,190,420	Intron	-	-	A	T	0.25	1.00	0.08	0.25	1.00	0.43
rs3122156	*HCRTR2*	6	55,190,766	Intron	-	-	T	G	0.25	1.00	0.11	0.25	1.00	0.29
rs4311511	*HCRTR2*	6	55,198,566	Intron	-	-	A	G	0.30	0.99	0.54	0.28	0.99	0.32
rs4311512	*HCRTR2*	6	55,198,654	Intron	-	-	A	G	0.29	1.00	0.54	0.27	1.00	0.26
rs9382467	*HCRTR2*	6	55,198,914	Intron	-	-	A	T	0.48	1.00	0.69	0.45	1.00	0.42
rs9349768	*HCRTR2*	6	55,199,409	Intron	-	-	A	T	0.22	1.00	0.06	0.22	1.00	0.20
rs7771240	*HCRTR2*	6	55,201,790	Intron	-	-	T	C	0.29	1.00	0.27	0.27	1.00	0.32
rs9357850	*HCRTR2*	6	55,204,783	Intron	-	-	C	T	0.22	1.00	0.03	0.23	1.00	0.12
rs9475210	*HCRTR2*	6	55,210,529	Intron	-	-	G	A	0.07	1.00	0.42	0.05	1.00	1.00
rs4074181	*HCRTR2*	6	55,211,426	Intron	-	-	C	T	0.22	1.00	0.03	0.22	1.00	0.08
rs3134711	*HCRTR2*	6	55,211,851	Intron	-	-	G	A	0.29	1.00	0.27	0.27	1.00	0.17
rs7741664	*HCRTR2*	6	55,213,260	Intron	-	-	T	C	0.26	1.00	0.05	0.25	1.00	0.19
rs9357853	*HCRTR2*	6	55,213,660	Intron	-	-	T	C	0.26	1.00	0.03	0.26	1.00	0.07
rs3122167	*HCRTR2*	6	55,220,774	Intron	-	-	T	C	0.30	1.00	0.47	0.28	1.00	0.13
rs3122169	*HCRTR2*	6	55,221,370	Intron	-	-	A	C	0.19	1.00	0.87	0.18	1.00	0.17
rs2811239	*HCRTR2*	6	55,229,913	Intron	-	-	G	A	0.19	1.00	0.62	0.17	1.00	0.16
rs2653342	*HCRTR2*	6	55,239,096	Intron	-	-	G	A	0.16	1.00	0.58	0.15	1.00	0.35
rs2653343	*HCRTR2*	6	55,241,285	Intron	-	-	A	T	0.20	1.00	0.52	0.18	1.00	0.40
rs2134294	*HCRTR2*	6	55,242,206	Intron	-	-	C	T	0.47	1.00	0.76	0.43	1.00	0.48
rs7452651	*HCRTR2*	6	55,243,472	Intron	-	-	G	A	0.23	1.00	0.07	0.22	1.00	0.06
rs2653346	*HCRTR2*	6	55,244,249	Intron	-	-	G	A	0.04	1.00	1.00	0.02	1.00	1.00
rs6929837	*HCRTR2*	6	55,244,576	Intron	-	-	T	A	0.20	1.00	0.52	0.18	1.00	0.40
rs2653348	*HCRTR2*	6	55,247,827	Intron	-	-	C	T	0.44	1.00	0.30	0.41	1.00	0.54

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs2653349	*HCRTR2*	6	55,250,296	Coding Region	Nonsynonymous	I308V (NP_001517)	G	A	0.20	1.00	0.52	0.18	1.00	0.31
rs2653350	*HCRTR2*	6	55,252,061	Intron	-	-	A	G	0.46	1.00	0.48	0.42	1.00	0.54
rs2811228	*HCRTR2*	6	55,260,768	Flanking 3' UTR	-	-	C	A	0.42	1.00	0.35	0.38	1.00	0.60
rs10456702	*HCRTR2*	6	55,261,975	Flanking 3' UTR	-	-	A	G	0.49	1.00	0.69	0.44	1.00	0.61
rs2653357	*HCRTR2*	6	55,264,698	Flanking 3' UTR	-	-	G	A	0.42	1.00	0.35	0.38	1.00	0.60
rs12203487	*HTR1B*	6	78,215,602	Flanking 3' UTR	-	-	T	A	0.11	1.00	0.29	0.12	1.00	0.49
rs1145831	*HTR1B*	6	78,217,292	Flanking 3' UTR	-	-	T	C	0.21	1.00	0.88	0.23	1.00	0.57
rs12527054	*HTR1B*	6	78,220,647	Flanking 3' UTR	-	-	T	C	0.08	1.00	1.00	0.07	1.00	0.71
rs9350712	*HTR1B*	6	78,220,836	Flanking 3' UTR	-	-	A	T	0.44	1.00	0.41	0.44	1.00	0.27
rs12527143	*HTR1B*	6	78,221,317	Flanking 3' UTR	-	-	T	C	0.19	1.00	0.09	0.19	1.00	0.52
rs9359271	*HTR1B*	6	78,222,839	Flanking 3' UTR	-	-	A	C	0.27	1.00	1.00	0.29	1.00	0.47
rs2000292	*HTR1B*	6	78,223,664	Flanking 3' UTR	-	-	G	A	0.28	1.00	0.80	0.28	1.00	0.05
rs13212041	*HTR1B*	6	78,227,843	Flanking 3' UTR	-	-	T	C	0.17	1.00	0.86	0.19	1.00	1.00
rs6297	*HTR1B*	6	78,228,660	Flanking 3' UTR	-	-	T	C	0.12	1.00	0.49	0.13	1.00	0.83
rs6296	*HTR1B*	6	78,228,979	Coding Region	Synonymous	V287V (NP_000854)	C	G	0.28	1.00	0.11	0.28	1.00	0.22
rs130060	*HTR1B*	6	78,229,469	Coding Region	Nonsynonymous	F124C (NP_000854)	A	C	0.02	1.00	1.00	8.66×10^{-3}	1.00	1.00
rs130058	*HTR1B*	6	78,230,000	Flanking 5' UTR	-	-	T	A	0.31	1.00	0.64	0.28	1.00	0.90
rs11568817	*HTR1B*	6	78,230,101	Flanking 5' UTR	-	-	A	C	0.47	1.00	0.92	0.43	1.00	0.69
rs1228814	*HTR1B*	6	78,230,539	Flanking 5' UTR	-	-	G	T	0.46	0.98	0.92	0.43	0.98	0.54
rs4140535	*HTR1B*	6	78,231,771	Flanking 5' UTR	-	-	G	A	0.38	1.00	0.20	0.38	1.00	0.75
rs10806098	*HTR1B*	6	78,232,728	Flanking 5' UTR	-	-	G	A	0.29	1.00	0.22	0.28	1.00	0.22
rs1213365	*HTR1B*	6	78,233,274	Flanking 5' UTR	-	-	G	C	0.47	0.92	0.60	0.49	0.93	0.54
rs1213366	*HTR1B*	6	78,233,589	Flanking 5' UTR	-	-	A	G	0.46	1.00	0.84	0.43	1.00	0.68
rs1213369	*HTR1B*	6	78,234,976	Flanking 5' UTR	-	-	C	G	0.42	1.00	0.41	0.43	1.00	0.76
rs1213370	*HTR1B*	6	78,235,516	Flanking 5' UTR	-	-	C	G	0.45	1.00	1.00	0.47	1.00	1.00
rs1213371	*HTR1B*	6	78,236,764	Flanking 5' UTR	-	-	C	T	0.46	1.00	1.00	0.43	0.99	0.76
rs1936158	*HTR1B*	6	78,241,094	Flanking 5' UTR	-	-	G	T	0.40	1.00	0.12	0.41	1.00	0.84
rs12173930	*HTR1B*	6	78,243,153	Flanking 5' UTR	-	-	C	T	0.11	0.99	0.80	0.13	1.00	1.00
rs2798949	*HTR1B*	6	78,246,853	Flanking 5' UTR	-	-	G	A	0.37	1.00	0.45	0.34	1.00	0.91
rs9352483	*HTR1B*	6	78,246,975	Flanking 5' UTR	-	-	G	A	0.14	1.00	0.67	0.15	1.00	0.44
rs4543330	*HTR1B*	6	78,247,352	Flanking 5' UTR	-	-	A	C	0.15	1.00	0.56	0.15	1.00	0.16
rs1343491	*HTR1B*	6	78,247,981	Flanking 5' UTR	-	-	C	T	0.08	1.00	1.00	0.09	1.00	1.00
rs6938321	*CNR1*	6	88,892,773	Flanking 3' UTR	-	-	T	C	0.12	1.00	0.34	0.11	1.00	0.20
rs9353524	*CNR1*	6	88,894,335	Flanking 3' UTR	-	-	C	G	0.22	0.99	0.66	0.21	1.00	0.18
rs10485171	*CNR1*	6	88,900,109	Flanking 3' UTR	-	-	A	G	0.41	1.00	0.40	0.43	1.00	0.84
rs806365	*CNR1*	6	88,902,668	Flanking 3' UTR	-	-	C	T	0.46	1.00	0.10	0.44	0.99	0.42
rs7766029	*CNR1*	6	88,904,154	Flanking 3' UTR	-	-	C	T	0.50	1.00	0.55	0.48	1.00	0.77
rs806366	*CNR1*	6	88,904,308	Flanking 3' UTR	-	-	C	T	0.49	1.00	0.84	0.49	1.00	0.55
rs806368	*CNR1*	6	88,906,819	3' UTR	-	-	T	C	0.23	0.99	0.89	0.21	0.99	0.14
rs1049353	*CNR1*	6	88,910,354	Coding Region	Synonymous	T392T (NP_149421)	C	T	0.25	0.99	1.00	0.26	1.00	0.70
rs806369	*CNR1*	6	88,912,897	Flanking 5' UTR	-	-	C	T	0.31	1.00	0.35	0.30	1.00	0.72
rs806371	*CNR1*	6	88,913,082	Flanking 5' UTR	-	-	T	G	0.13	1.00	1.00	0.13	1.00	1.00
rs806374	*CNR1*	6	88,914,039	Flanking 5' UTR	-	-	T	C	0.35	1.00	0.37	0.35	1.00	0.19
rs806375	*CNR1*	6	88,915,240	Flanking 5' UTR	-	-	A	T	0.49	1.00	0.27	0.42	1.00	0.76
rs806376	*CNR1*	6	88,915,367	Flanking 5' UTR	-	-	T	C	0.47	1.00	0.42	0.47	1.00	0.84
rs806377	*CNR1*	6	88,915,442	Flanking 5' UTR	-	-	C	T	0.44	1.00	0.47	0.49	1.00	0.92
rs806378	*CNR1*	6	88,916,270	Flanking 5' UTR	-	-	C	T	0.30	0.99	0.03	0.25	0.98	0.89
rs2023239	*CNR1*	6	88,917,201	Flanking 5' UTR	-	-	T	C	0.18	1.00	1.00	0.17	1.00	0.72
rs806379	*CNR1*	6	88,917,986	Flanking 5' UTR	-	-	A	T	0.48	1.00	0.61	0.46	1.00	0.48
rs6454672	*CNR1*	6	88,918,289	Flanking 5' UTR	-	-	T	C	0.14	1.00	0.67	0.13	1.00	0.67
rs9444584	*CNR1*	6	88,919,278	Flanking 5' UTR	-	-	C	T	0.21	1.00	0.23	0.19	1.00	0.20
rs806381	*CNR1*	6	88,922,620	Flanking 5' UTR	-	-	A	G	0.36	1.00	0.74	0.30	0.99	0.91
rs6454673	*CNR1*	6	88,927,768	Flanking 5' UTR	-	-	G	A	0.33	1.00	0.30	0.28	1.00	0.62
rs1413753	*EPB41L2*	6	131,192,197	Flanking 3' UTR	-	-	C	T	0.31	1.00	0.05	0.32	1.00	0.17
rs2281487	*EPB41L2*	6	131,192,810	Flanking 3' UTR	-	-	T	C	0.41	1.00	0.25	0.40	1.00	1.00
rs1413755	*EPB41L2*	6	131,195,892	Flanking 3' UTR	-	-	C	T	0.38	0.99	0.13	0.37	1.00	0.91
rs6938735	*EPB41L2*	6	131,196,596	Flanking 3' UTR	-	-	T	C	0.30	1.00	8.64×10^{-3}	0.30	1.00	0.35
rs2236081	*EPB41L2*	6	131,196,716	Flanking 3' UTR	-	-	T	C	0.28	1.00	0.38	0.28	1.00	0.09
rs6975	*EPB41L2*	6	131,197,795	Flanking 3' UTR	-	-	G	T	0.24	1.00	0.28	0.27	1.00	0.06
rs3734186	*EPB41L2*	6	131,199,378	Flanking 3' UTR	-	-	T	C	0.03	1.00	1.00	0.03	1.00	1.00
rs988749	*EPB41L2*	6	131,201,181	Flanking 3' UTR	-	-	T	G	0.29	1.00	0.03	0.29	1.00	0.81
rs17059669	*EPB41L2*	6	131,201,485	Flanking 3' UTR	-	-	G	A	0.01	1.00	1.00	0.02	1.00	1.00
rs6935267	*EPB41L2*	6	131,204,791	Intron	-	-	G	T	0.18	1.00	0.01	0.17	1.00	0.86
rs6919007	*EPB41L2*	6	131,206,179	Intron	-	-	A	T	0.38	1.00	0.02	0.36	1.00	0.83
rs4897468	*EPB41L2*	6	131,206,765	Intron	-	-	T	C	0.39	1.00	0.04	0.36	1.00	0.91
rs4075265	*EPB41L2*	6	131,208,150	Intron	-	-	C	T	0.31	1.00	4.15×10^{-3}	0.31	1.00	0.35
rs10499174	*EPB41L2*	6	131,209,689	Intron	-	-	T	G	0.03	1.00	0.37	0.01	1.00	1.00
rs9402292	*EPB41L2*	6	131,211,966	Intron	-	-	A	G	0.38	0.99	0.02	0.36	1.00	0.83
rs928592	*EPB41L2*	6	131,219,792	Intron	-	-	G	A	0.27	1.00	0.04	0.30	1.00	0.02
rs10457561	*EPB41L2*	6	131,223,025	Intron	-	-	T	C	0.14	1.00	0.69	0.17	1.00	0.21
rs6569709	*EPB41L2*	6	131,223,739	Intron	-	-	C	T	0.31	1.00	8.98×10^{-3}	0.31	1.00	0.56
rs933063	*EPB41L2*	6	131,225,408	Intron	-	-	C	T	0.30	1.00	0.09	0.33	1.00	0.31
rs3777432	*EPB41L2*	6	131,225,509	Intron	-	-	G	A	0.15	1.00	0.54	0.17	1.00	0.15
rs915172	*EPB41L2*	6	131,226,463	Intron	-	-	T	G	0.29	1.00	0.47	0.32	1.00	0.07
rs7775013	*EPB41L2*	6	131,228,271	Intron	-	-	T	G	0.39	1.00	0.11	0.36	1.00	0.91
rs17059736	*EPB41L2*	6	131,232,531	Coding Region	-	-	G	A	0.12	1.00	0.63	0.14	1.00	0.40
rs3777438	*EPB41L2*	6	131,241,795	Intron	-	-	C	A	0.17	0.97	0.86	0.17	0.98	0.37
rs3822859	*EPB41L2*	6	131,248,402	Intron	-	-	A	T	0.01	1.00	1.00	0.02	1.00	1.00
rs3798249	*EPB41L2*	6	131,249,136	Intron	-	-	T	C	0.48	1.00	0.54	0.49	1.00	0.49
rs2839942	*EPB41L2*	6	131,250,191	Intron	-	-	G	A	0.31	1.00	0.10	0.32	1.00	0.42
rs12206057	*EPB41L2*	6	131,254,210	Intron	-	-	A	T	0.17	1.00	0.72	0.17	1.00	0.38
rs4897472	*EPB41L2*	6	131,254,831	Intron	-	-	A	G	0.48	1.00	0.48	0.49	1.00	0.49
rs4897473	*EPB41L2*	6	131,256,964	Intron	-	-	C	T	0.36	1.00	0.74	0.33	1.00	0.82
rs10499177	*EPB41L2*	6	131,257,514	Intron	-	-	A	G	0.07	1.00	0.44	0.10	1.00	0.40
rs2068147	*EPB41L2*	6	131,263,595	Intron	-	-	C	T	0.48	1.00	0.48	0.49	1.00	0.49
rs3777450	*EPB41L2*	6	131,269,439	Intron	-	-	T	C	0.03	1.00	1.00	0.02	1.00	1.00
rs1999474	*EPB41L2*	6	131,279,395	Intron	-	-	T	C	0.28	0.99	0.06	0.27	1.00	0.90
rs12528626	*EPB41L2*	6	131,291,090	Intron	-	-	A	G	0.07	1.00	0.44	0.09	1.00	0.23
rs3777457	*EPB41L2*	6	131,291,580	Intron	-	-	G	A	0.17	1.00	0.72	0.17	1.00	0.22
rs7766004	*EPB41L2*	6	131,295,666	Intron	-	-	G	A	0.28	1.00	0.10	0.27	1.00	0.90
rs3822864	*EPB41L2*	6	131,295,963	Intron	-	-	G	A	0.03	1.00	1.00	0.02	1.00	1.00
rs9321260	*EPB41L2*	6	131,305,235	Intron	-	-	A	T	0.18	1.00	1.00	0.19	1.00	0.75
rs3777463	*EPB41L2*	6	131,307,487	Intron	-	-	A	G	0.03	1.00	1.00	0.02	1.00	1.00
rs3777464	*EPB41L2*	6	131,308,450	Intron	-	-	A	G	0.08	1.00	0.32	0.11	1.00	0.80
rs3777466	*EPB41L2*	6	131,309,919	Intron	-	-	A	G	0.46	1.00	0.76	0.46	1.00	1.00
rs9492767	*EPB41L2*	6	131,314,703	Intron	-	-	T	C	0.17	0.99	1.00	0.19	1.00	0.41
rs9375785	*EPB41L2*	6	131,316,601	Intron	-	-	C	T	0.16	1.00	1.00	0.18	1.00	0.24
rs2297853	*EPB41L2*	6	131,318,638	Intron	-	-	G	T	0.34	1.00	0.37	0.36	1.00	0.67
rs6941712	*EPB41L2*	6	131,323,903	Intron	-	-	T	C	0.11	1.00	0.80	0.13	1.00	0.65
rs2105250	*EPB41L2*	6	131,325,875	Intron	-	-	A	T	0.28	1.00	0.17	0.27	1.00	1.00
rs2095961	*EPB41L2*	6	131,325,953	Intron	-	-	C	T	0.34	1.00	0.37	0.36	1.00	0.59
rs12527605	*EPB41L2*	6	131,326,069	Intron	-	-	C	T	0.07	1.00	0.42	0.09	1.00	0.23
rs12210856	*OPRM1*	6	154,399,679	Flanking 5' UTR	-	-	T	G	0.05	1.00	0.61	0.03	1.00	1.00
rs1799972	*OPRM1*	6	154,402,389	Coding Region	Nonsynonymous	A6V (NP_000905)	C	T	6.36×10^{-3}	1.00	1.00	1.24×10^{-3}	1.00	1.00
rs1799971	*OPRM1*	6	154,402,490	Coding Region	Nonsynonymous	N40D (NP_000905)	A	G	0.12	1.00	0.81	0.13	1.00	0.83
rs510769	*OPRM1*	6	154,403,712	Intron	-	-	C	T	0.25	1.00	0.51	0.24	1.00	0.89
rs477292	*OPRM1*	6	154,405,080	Intron	-	-	C	T	0.22	1.00	0.46	0.21	1.00	0.88
rs557748	*OPRM1*	6	154,405,995	Intron	-	-	G	A	0.21	1.00	0.55	0.21	1.00	1.00
rs514980	*OPRM1*	6	154,409,860	Intron	-	-	T	C	0.21	1.00	0.65	0.20	1.00	0.76
rs4870266	*OPRM1*	6	154,410,691	Intron	-	-	G	A	0.06	1.00	1.00	0.08	1.00	0.50
rs607759	*OPRM1*	6	154,414,130	Intron	-	-	C	T	0.22	1.00	0.65	0.21	1.00	0.88
rs610231	*OPRM1*	6	154,420,170	Intron	-	-	A	G	0.12	0.99	1.00	0.12	1.00	0.47
rs3823010	*OPRM1*	6	154,420,845	Intron	-	-	G	A	0.16	1.00	1.00	0.15	1.00	0.57
rs7773995	*OPRM1*	6	154,424,060	Intron	-	-	C	T	0.16	1.00	1.00	0.15	1.00	0.57
rs495491	*OPRM1*	6	154,424,235	Intron	-	-	A	G	0.26	1.00	0.30	0.23	1.00	0.89

									Male			**Female**		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs589046	*OPRM1*	6	154,434,831	Intron	-	-	C	T	0.26	1.00	0.24	0.23	1.00	0.78
rs1381376	*OPRM1*	6	154,434,951	Intron	-	-	C	T	0.16	1.00	1.00	0.15	1.00	0.55
rs3778151	*OPRM1*	6	154,435,373	Intron	-	-	T	C	0.16	1.00	0.85	0.15	1.00	0.56
rs17209711	*OPRM1*	6	154,438,148	Intron	-	-	T	A	0.16	1.00	0.70	0.14	1.00	0.42
rs3778155	*OPRM1*	6	154,445,511	Intron	-	-	C	T	0.16	0.97	0.57	0.16	0.97	0.56
rs3778158	*OPRM1*	6	154,447,423	Intron	-	-	A	T	0.15	1.00	1.00	0.15	1.00	0.55
rs563649	*OPRM1*	6	154,449,660	Intron	-	-	C	T	0.10	1.00	0.57	0.08	1.00	0.72
rs9322446	*OPRM1*	6	154,450,395	Intron	-	-	G	A	0.14	1.00	0.14	0.16	1.00	0.85
rs9479757	*OPRM1*	6	154,453,037	Flanking 3' UTR	-	-	G	A	0.10	1.00	0.77	0.09	1.00	0.54
rs2075572	*OPRM1*	6	154,453,697	Flanking 5' UTR	-	-	C	G	0.45	1.00	0.84	0.40	1.00	0.35
rs510587	*OPRM1*	6	154,455,121	Flanking 3' UTR	-	-	G	A	0.05	1.00	1.00	0.05	1.00	0.29
rs9282821	*OPRM1*	6	154,456,068	Flanking 5' UTR	-	-	C	A	0.44	1.00	0.76	0.39	1.00	0.41
rs540825	*OPRM1*	6	154,456,139	Coding Region	-	-	T	A	0.26	1.00	0.52	0.24	1.00	0.89
rs548646	*OPRM1*	6	154,459,840	Flanking 3' UTR	-	-	C	T	0.35	1.00	1.00	0.33	1.00	0.50
rs3798683	*OPRM1*	6	154,460,107	Flanking 3' UTR	-	-	G	A	0.14	1.00	0.68	0.16	1.00	0.57
rs599548	*OPRM1*	6	154,460,254	Flanking 3' UTR	-	-	G	A	0.13	1.00	0.51	0.13	1.00	0.27
rs9322447	*OPRM1*	6	154,466,013	Flanking 3' UTR	-	-	G	A	0.49	1.00	0.42	0.46	1.00	0.84
rs618207	*OPRM1*	6	154,466,362	Flanking 3' UTR	-	-	G	A	0.35	1.00	1.00	0.33	1.00	0.43
rs1853384	*OPRM1*	6	154,466,651	Flanking 3' UTR	-	-	C	T	0.35	1.00	1.00	0.33	1.00	0.43
rs623956	*OPRM1*	6	154,471,718	Flanking 5' UTR	-	-	A	G	0.25	0.95	0.59	0.24	0.95	0.78
rs504932	*OPRM1*	6	154,472,161	Flanking 5' UTR	-	-	A	G	0.25	1.00	0.51	0.24	1.00	1.00
rs609148	*OPRM1*	6	154,472,707	Flanking 5' UTR	-	-	G	A	0.25	1.00	0.51	0.24	1.00	1.00
rs606148	*OPRM1*	6	154,477,679	Flanking 5' UTR	-	-	C	A	0.10	1.00	1.00	0.09	1.00	0.55
rs632395	*OPRM1*	6	154,478,944	Flanking 5' UTR	-	-	G	A	0.10	1.00	1.00	0.09	1.00	0.55
rs648893	*OPRM1*	6	154,480,321	Flanking 5' UTR	-	-	A	G	0.25	0.99	0.50	0.24	1.00	1.00
rs1323041	*OPRM1*	6	154,480,873	Flanking 5' UTR	-	-	G	A	0.49	1.00	0.48	0.46	1.00	0.84
rs512053	*OPRM1*	6	154,481,209	Flanking 5' UTR	-	-	G	T	0.08	1.00	0.72	0.09	1.00	0.06
rs642489	*OPRM1*	6	154,484,368	Flanking 3' UTR	-	-	G	T	0.25	1.00	0.51	0.24	1.00	1.00
rs613341	*OPRM1*	6	154,484,971	Flanking 3' UTR	-	-	C	T	0.09	1.00	1.00	0.09	1.00	0.52
rs10485058	*OPRM1*	6	154,486,907	Flanking 3' UTR	-	-	A	G	0.14	1.00	0.40	0.15	1.00	1.00
rs613355	*OPRM1*	6	154,491,542	Flanking 3' UTR	-	-	A	C	0.36	1.00	1.00	0.33	1.00	0.37
rs3735275	*DDC*	7	50,484,765	5' UTR	-	-	A	G	0.15	1.00	0.33	0.19	1.00	1.00
rs4947510	*DDC*	7	50,492,914	Flanking 3' UTR	-	-	G	A	0.27	1.00	0.16	0.32	1.00	0.21
rs4947511	*DDC*	7	50,493,367	Flanking 3' UTR	-	-	G	A	5.08×10^{-3}	1.00	1.00	4.95×10^{-3}	1.00	1.00
rs11575553	*DDC*	7	50,493,713	3' UTR	-	-	G	A	0.10	1.00	0.26	0.11	1.00	0.61
rs4947535	*DDC*	7	50,499,175	Intron	-	-	A	T	0.27	1.00	0.25	0.30	1.00	0.15
rs730092	*DDC*	7	50,503,248	Intron	-	-	G	C	0.40	1.00	0.21	0.45	1.00	0.31
rs11238131	*DDC*	7	50,506,083	Intron	-	-	C	T	0.27	1.00	0.25	0.30	1.00	0.15
rs7803247	*DDC*	7	50,508,237	Intron	-	-	C	T	0.40	0.99	0.21	0.45	1.00	0.31
rs11771818	*DDC*	7	50,509,669	Intron	-	-	G	A	0.13	1.00	0.27	0.13	1.00	0.83
rs11772714	*DDC*	7	50,510,337	Intron	-	-	A	G	0.19	1.00	0.51	0.21	1.00	0.65
rs11238133	*DDC*	7	50,510,408	Intron	-	-	C	A	0.30	0.97	0.07	0.36	0.98	8.49×10^{-3}
rs732215	*DDC*	7	50,511,557	Intron	-	-	A	C	0.47	1.00	0.92	0.42	1.00	0.61
rs896309	*DDC*	7	50,512,516	Intron	-	-	G	A	0.19	1.00	0.51	0.21	1.00	0.76
rs4579483	*DDC*	7	50,513,594	Intron	-	-	T	C	0.39	1.00	0.34	0.43	1.00	0.42
rs11575453	*DDC*	7	50,515,359	Intron	-	-	C	T	0.08	1.00	0.09	0.08	1.00	0.18
rs4947577	*DDC*	7	50,516,103	Intron	-	-	C	G	0.39	0.99	0.53	0.43	1.00	0.54
rs17152020	*DDC*	7	50,517,353	Intron	-	-	T	A	0.20	1.00	0.76	0.22	1.00	0.89
rs1451372	*DDC*	7	50,521,365	Intron	-	-	G	C	0.39	1.00	0.46	0.43	1.00	0.48
rs7790758	*DDC*	7	50,529,038	Intron	-	-	A	G	0.19	1.00	0.51	0.21	1.00	0.76
rs4602840	*DDC*	7	50,530,315	Intron	-	-	C	A	0.12	1.00	0.23	0.14	1.00	0.04
rs1037351	*DDC*	7	50,532,898	Intron	-	-	T	C	0.34	1.00	0.65	0.35	1.00	0.38
rs11575383	*DDC*	7	50,535,184	Intron	-	-	C	A	0.07	1.00	0.25	0.07	1.00	0.12
rs896307	*DDC*	7	50,536,554	Intron	-	-	C	T	0.19	1.00	0.51	0.21	1.00	0.77
rs880028	*DDC*	7	50,537,630	Intron	-	-	A	G	0.20	0.99	1.00	0.22	1.00	0.89
rs4947584	*DDC*	7	50,540,203	Intron	-	-	A	T	0.35	0.99	0.83	0.37	1.00	0.29
rs6592961	*DDC*	7	50,540,384	Intron	-	-	G	A	0.21	1.00	0.88	0.23	1.00	0.89
rs12718574	*DDC*	7	50,541,342	Intron	-	-	G	C	0.45	1.00	1.00	0.41	1.00	0.76
rs1817074	*DDC*	7	50,541,506	Intron	-	-	T	C	0.36	1.00	0.51	0.38	1.00	0.67
rs17635123	*DDC*	7	50,543,469	Intron	-	-	T	C	0.12	1.00	0.22	0.14	1.00	0.09
rs1470750	*DDC*	7	50,544,142	Intron	-	-	C	G	0.43	1.00	0.47	0.39	1.00	0.53
rs2100280	*DDC*	7	50,548,330	Intron	-	-	A	G	0.25	0.97	0.68	0.27	0.99	0.10
rs1451368	*DDC*	7	50,555,261	Intron	-	-	C	T	0.26	1.00	0.36	0.28	1.00	0.21
rs10244632	*DDC*	7	50,566,197	Intron	-	-	C	T	0.27	0.96	0.07	0.30	0.96	0.14
rs11575321	*DDC*	7	50,572,601	Intron	-	-	C	G	0.10	1.00	0.25	0.12	1.00	0.03
rs11575313	*DDC*	7	50,573,662	Intron	-	-	T	C	0.10	1.00	0.24	0.12	1.00	0.03
rs10268819	*DDC*	7	50,577,565	Intron	-	-	C	T	0.14	0.94	0.27	0.13	0.95	0.82
rs3807552	*DDC*	7	50,578,236	Intron	-	-	G	A	0.20	0.88	0.40	0.21	0.92	0.53
rs3779078	*DDC*	7	50,578,412	Intron	-	-	C	T	0.19	1.00	1.00	0.21	1.00	0.88
rs6264	*DDC*	7	50,579,229	Coding Region	Nonsynonymous	V17M (NP_000781)	C	NA	0.00	1.00	NA	0.00	1.00	NA
rs2044859	*DDC*	7	50,580,056	Intron	-	-	A	G	0.34	1.00	1.00	0.37	1.00	0.91
rs7786398	*DDC*	7	50,580,400	Intron	-	-	A	G	0.44	1.00	1.00	0.48	1.00	0.49
rs10276473	*DDC*	7	50,580,491	Intron	-	-	G	T	0.20	1.00	0.87	0.21	1.00	0.46
rs11765748	*DDC*	7	50,583,110	Intron	-	-	A	T	0.48	1.00	0.36	0.49	1.00	0.84
rs7456339	*DDC*	7	50,583,334	Intron	-	-	A	G	0.13	1.00	0.02	0.15	1.00	0.04
rs10499695	*DDC*	7	50,586,098	Intron	-	-	C	T	0.49	1.00	0.42	0.49	1.00	1.00
rs4947644	*DDC*	7	50,586,370	Intron	-	-	T	C	0.49	1.00	0.42	0.48	1.00	0.92
rs2329340	*DDC*	7	50,587,723	Intron	-	-	C	T	0.32	1.00	0.82	0.34	1.00	0.58
rs10227616	*PRKAR2B*	7	106,462,434	Flanking 5' UTR	-	-	C	A	0.32	1.00	0.82	0.34	1.00	0.22
rs1544582	*PRKAR2B*	7	106,475,074	Intron	-	-	A	G	0.48	1.00	0.69	0.45	1.00	0.42
rs2237649	*PRKAR2B*	7	106,481,518	Intron	-	-	G	A	0.48	1.00	0.84	0.45	1.00	0.37
rs1476879	*PRKAR2B*	7	106,485,977	Intron	-	-	T	A	0.48	1.00	1.00	0.46	1.00	0.32
rs6957586	*PRKAR2B*	7	106,489,869	Intron	-	-	A	G	0.32	1.00	1.00	0.34	1.00	0.32
rs11766415	*PRKAR2B*	7	106,496,001	Intron	-	-	A	G	0.42	1.00	0.18	0.42	1.00	0.42
rs3801969	*PRKAR2B*	7	106,498,728	Intron	-	-	G	T	0.45	1.00	0.36	0.44	1.00	0.27
rs2536503	*PRKAR2B*	7	106,501,051	Intron	-	-	G	A	0.13	1.00	1.00	0.12	1.00	0.81
rs2536504	*PRKAR2B*	7	106,501,141	Intron	-	-	C	T	0.34	1.00	0.22	0.34	1.00	0.38
rs6960842	*PRKAR2B*	7	106,502,556	Intron	-	-	C	G	0.42	1.00	0.47	0.43	1.00	0.31
rs17340577	*PRKAR2B*	7	106,506,649	Intron	-	-	C	T	0.07	0.99	0.71	0.09	0.99	0.53
rs2299419	*PRKAR2B*	7	106,506,772	Intron	-	-	T	C	0.09	1.00	1.00	0.09	1.00	0.76
rs2251838	*PRKAR2B*	7	106,507,403	Intron	-	-	A	G	0.35	1.00	0.18	0.35	1.00	0.23
rs12154324	*PRKAR2B*	7	106,508,168	Intron	-	-	G	A	0.08	1.00	0.75	0.09	1.00	0.76
rs7778076	*PRKAR2B*	7	106,510,244	Intron	-	-	A	G	0.09	1.00	0.75	0.09	1.00	0.77
rs6466156	*PRKAR2B*	7	106,519,170	Intron	-	-	A	G	0.36	1.00	0.08	0.35	1.00	0.66
rs6466157	*PRKAR2B*	7	106,519,537	Intron	-	-	T	C	0.49	1.00	0.37	0.49	1.00	0.20
rs717099	*PRKAR2B*	7	106,528,174	Intron	-	-	A	G	0.47	1.00	0.03	0.46	1.00	0.48
rs6955387	*PRKAR2B*	7	106,535,275	Intron	-	-	G	C	0.40	1.00	0.04	0.39	1.00	0.83
rs12055940	*PRKAR2B*	7	106,538,782	Intron	-	-	C	T	0.09	1.00	1.00	0.09	1.00	0.77
rs2250121	*PRKAR2B*	7	106,540,484	Intron	-	-	A	G	0.09	1.00	1.00	0.10	1.00	0.77
rs2237652	*PRKAR2B*	7	106,547,212	Intron	-	-	T	C	0.49	1.00	0.31	0.49	1.00	0.27
rs9656135	*PRKAR2B*	7	106,555,592	Intron	-	-	C	T	0.08	1.00	0.75	0.08	1.00	1.00
rs17153861	*PRKAR2B*	7	106,556,875	Intron	-	-	G	A	0.09	1.00	1.00	0.09	1.00	0.76
rs2191917	*PRKAR2B*	7	106,560,944	Intron	-	-	T	G	0.09	1.00	1.00	0.09	1.00	0.77
rs1860803	*PRKAR2B*	7	106,567,076	Intron	-	-	T	G	0.43	0.99	0.18	0.41	1.00	0.84
rs3729876	*PRKAR2B*	7	106,574,188	Intron	-	-	C	T	0.18	1.00	0.23	0.21	1.00	0.88
rs6977868	*PRKAR2B*	7	106,577,791	Intron	-	-	G	T	0.18	1.00	0.30	0.20	1.00	1.00
rs11767623	*PRKAR2B*	7	106,579,568	Intron	-	-	T	C	0.18	1.00	0.23	0.20	1.00	0.88
rs12705406	*PRKAR2B*	7	106,579,790	Intron	-	-	G	A	0.12	1.00	0.24	0.15	1.00	0.69
rs257384	*PRKAR2B*	7	106,592,630	Flanking 3' UTR	-	-	C	T	0.44	1.00	0.47	0.44	1.00	0.55
rs257387	*PRKAR2B*	7	106,595,716	Flanking 5' UTR	-	-	G	A	0.18	1.00	0.30	0.20	1.00	1.00
rs2303928	*CDK5*	7	150,370,263	Intron	-	-	C	G	0.39	1.00	0.46	0.40	1.00	0.12
rs2069459	*CDK5*	7	150,382,523	Intron	-	-	C	A	0.39	1.00	0.07	0.37	1.00	0.06
rs891507	*CDK5*	7	150,382,999	Intron	-	-	C	T	0.15	0.97	0.69	0.15	0.98	0.44
rs2069454	*CDK5*	7	150,383,915	Intron	-	-	C	G	0.15	0.92	0.83	0.12	0.93	0.81
rs2069443	*CDK5*	7	150,386,106	Flanking 5' UTR	-	-	T	G	0.26	1.00	0.24	0.26	1.00	0.52
rs1549760	*CDK5*	7	150,386,772	Flanking 5' UTR	-	-	C	T	0.23	1.00	0.47	0.23	1.00	0.39

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs3793336	*CDK5*	7	150,393,804	Intron	-	-	A	G	0.14	0.78	0.48	0.14	0.79	0.17
rs2303933	*CDK5*	7	150,397,732	Intron	-	-	G	A	0.40	1.00	0.67	0.41	1.00	0.54
rs2303937	*CDK5*	7	150,399,719	Coding Region	Synonymous	T734T (NP_003031)	G	A	0.45	1.00	0.36	0.44	1.00	0.48
rs11765015	*CDK5*	7	150,401,765	Intron	-	-	G	A	0.28	0.99	0.71	0.26	1.00	0.61
rs4733065	*CHRNA2*	8	27,363,921	Intron	-	-	G	A	0.46	0.98	0.36	0.46	0.99	0.55
rs2278319	*CHRNA2*	8	27,364,878	Intron	-	-	C	T	0.24	1.00	0.68	0.25	1.00	0.24
rs1106359	*CHRNA2*	8	27,365,256	Intron	-	-	T	C	0.42	1.00	0.92	0.40	1.00	0.08
rs1879184	*CHRNA2*	8	27,367,620	Coding Region	Synonymous	T876T (NP_775268)	C	T	0.13	1.00	0.65	0.14	1.00	0.41
rs10093964	*CHRNA2*	8	27,367,957	Intron	-	-	C	T	0.43	0.99	0.92	0.41	1.00	0.08
rs1879182	*CHRNA2*	8	27,371,793	Coding Region	Synonymous	A960A (NP_775268)	G	A	0.13	1.00	0.65	0.14	1.00	0.41
rs748283	*CHRNA2*	8	27,373,112	Flanking 3' UTR	-	-	C	A	0.49	1.00	0.42	0.49	1.00	0.20
rs1057137	*CHRNA2*	8	27,373,362	Flanking 3' UTR	-	-	G	T	0.40	0.98	0.67	0.39	1.00	0.11
rs735421	*CHRNA2*	8	27,375,209	Intron	-	-	A	G	0.29	0.99	0.54	0.31	1.00	0.73
rs891394	*CHRNA2*	8	27,375,686	Intron	-	-	C	G	0.25	1.00	1.00	0.27	1.00	0.06
rs3735757	*CHRNA2*	8	27,377,514	Intron	-	-	C	G	0.13	1.00	1.00	0.14	0.99	0.67
rs2322581	*CHRNA2*	8	27,379,524	Intron	-	-	T	G	0.17	1.00	0.72	0.15	1.00	0.57
rs891398	*CHRNA2*	8	27,380,739	Coding Region	Nonsynonymous	T125A (NP_000733)	T	C	0.47	1.00	0.55	0.48	1.00	0.76
rs891399	*CHRNA2*	8	27,381,340	Intron	-	-	G	A	0.13	1.00	0.65	0.13	1.00	0.83
rs2565062	*CHRNA2*	8	27,381,857	Intron	-	-	G	A	0.13	1.00	0.65	0.13	1.00	1.00
rs2472554	*CHRNA2*	8	27,384,271	Intron	-	-	C	G	0.30	1.00	0.15	0.31	1.00	0.82
rs2472553	*CHRNA2*	8	27,384,428	Coding Region	Nonsynonymous	T22I (NP_000733)	G	A	0.13	1.00	0.65	0.13	1.00	1.00
rs7815010	*CHRNA2*	8	27,386,013	Intron	-	-	C	T	0.25	1.00	0.89	0.25	1.00	0.69
rs2741339	*CHRNA2*	8	27,390,886	Intron	-	-	A	G	0.28	1.00	0.61	0.26	1.00	1.00
rs2565059	*CHRNA2*	8	27,392,895	Flanking 5' UTR	-	-	G	A	0.18	1.00	1.00	0.19	1.00	0.74
rs2565055	*CHRNA2*	8	27,393,297	Flanking 5' UTR	-	-	G	T	0.24	1.00	1.00	0.24	1.00	0.59
rs2741335	*CHRNA2*	8	27,393,708	Flanking 5' UTR	-	-	A	C	0.26	1.00	0.90	0.27	1.00	1.00
rs6558000	*CHRNA2*	8	27,395,271	Flanking 5' UTR	-	-	T	C	0.08	1.00	0.72	0.07	1.00	0.25
rs7017417	*CHRNA2*	8	27,401,222	Flanking 5' UTR	-	-	A	G	0.10	1.00	0.26	0.10	1.00	1.00
rs9314348	*CHRNA2*	8	27,401,343	Flanking 5' UTR	-	-	T	C	0.10	1.00	0.27	0.10	1.00	1.00
rs7003694	*CHRNA2*	8	27,403,111	Flanking 5' UTR	-	-	T	C	0.09	1.00	0.35	0.09	1.00	1.00
rs7017612	*CHRNA6;CHRNB3*	8	42,718,402	Flanking 3' UTR	-	-	A	C	0.21	0.99	0.54	0.18	1.00	0.18
rs9298628	*CHRNA6*	8	42,725,148	Flanking 3' UTR	-	-	C	T	0.20	0.99	0.75	0.19	1.00	0.63
rs2304297	*CHRNA6*	8	42,727,356	3' UTR	-	-	G	C	0.24	1.00	0.78	0.22	1.00	0.89
rs2196128	*CHRNA6*	8	42,737,443	Intron	-	-	T	C	0.22	1.00	0.89	0.21	1.00	1.00
rs16891620	*CHRNA6*	8	42,744,820	Flanking 5' UTR	-	-	C	A	0.11	1.00	0.79	0.12	1.00	0.63
rs10107450	*CHRNA6*	8	42,749,052	Flanking 5' UTR	-	-	C	T	0.23	1.00	1.00	0.22	1.00	0.88
rs6474419	*CHRNA6*	8	42,754,456	Flanking 5' UTR	-	-	A	G	0.04	1.00	1.00	0.03	1.00	1.00
rs10988625	*FREQ*	9	131,967,389	Flanking 5' UTR	-	-	G	A	0.06	1.00	0.39	0.07	1.00	0.15
rs12378342	*FREQ*	9	131,970,164	Flanking 5' UTR	-	-	T	C	0.08	1.00	0.15	0.07	1.00	1.00
rs9802616	*FREQ*	9	131,970,944	Flanking 5' UTR	-	-	T	A	0.16	1.00	0.58	0.16	1.00	0.37
rs917690	*FREQ*	9	131,974,002	Flanking 5' UTR	-	-	T	G	0.10	0.96	0.38	0.10	0.96	1.00
rs3780708	*FREQ*	9	131,975,772	Intron	-	-	C	T	0.34	0.98	1.00	0.35	0.99	0.91
rs1017112	*FREQ*	9	131,976,625	Intron	-	-	T	C	0.17	1.00	1.00	0.18	1.00	0.14
rs4837479	*FREQ*	9	131,979,828	Intron	-	-	C	T	0.16	1.00	1.00	0.16	1.00	0.14
rs3780711	*FREQ*	9	131,982,864	Intron	-	-	T	C	0.12	0.97	0.64	0.13	0.97	5.92×10^{-4}
rs7849345	*FREQ*	9	131,984,366	Intron	-	-	C	T	0.48	1.00	0.69	0.50	0.99	0.27
rs10819610	*FREQ*	9	131,986,436	Intron	-	-	G	T	0.27	1.00	0.07	0.29	1.00	0.90
rs3824544	*FREQ*	9	131,988,371	Intron	-	-	C	T	0.25	0.98	0.59	0.23	1.00	0.16
rs7862394	*FREQ*	9	131,989,685	Intron	-	-	A	G	0.32	1.00	0.29	0.31	1.00	0.64
rs10819611	*FREQ*	9	131,995,274	Intron	-	-	T	C	0.32	1.00	0.30	0.31	1.00	0.24
rs1009502	*FREQ*	9	131,996,050	Intron	-	-	G	A	0.32	0.98	0.13	0.32	0.96	0.56
rs1342043	*FREQ*	9	131,998,126	Intron	-	-	T	C	0.14	0.99	0.09	0.15	1.00	0.25
rs7856531	*FREQ*	9	132,000,447	Intron	-	-	T	G	0.47	1.00	0.76	0.48	1.00	0.69
rs7037293	*FREQ*	9	132,002,538	Intron	-	-	G	A	0.13	0.99	0.12	0.15	0.99	0.85
rs7045735	*FREQ*	9	132,004,454	Intron	-	-	A	G	0.39	0.95	0.39	0.42	0.97	0.41
rs7024495	*FREQ*	9	132,007,017	Intron	-	-	G	A	0.48	1.00	0.62	0.50	1.00	0.84
rs7023210	*FREQ*	9	132,011,977	Intron	-	-	T	C	0.48	1.00	0.69	0.49	1.00	0.92
rs947513	*FREQ*	9	132,013,809	Intron	-	-	A	G	0.45	1.00	0.76	0.45	1.00	0.92
rs10819615	*FREQ*	9	132,014,745	Intron	-	-	C	T	0.37	0.99	0.39	0.34	0.99	0.82
rs3897499	*FREQ*	9	132,014,885	Intron	-	-	A	T	0.36	0.99	0.58	0.34	0.99	0.09
rs4240446	*FREQ*	9	132,018,220	Intron	-	-	G	A	0.14	0.96	0.08	0.15	0.95	0.16
rs10988645	*FREQ*	9	132,019,357	Intron	-	-	G	A	0.30	1.00	0.09	0.28	1.00	0.62
rs3829905	*FREQ*	9	132,024,932	Intron	-	-	C	T	0.36	0.85	0.55	0.35	0.88	0.24
rs2277200	*FREQ*	9	132,028,530	Coding Region	Synonymous	G172G (NP_055101)	T	G	0.33	1.00	0.17	0.31	1.00	0.49
rs2900286	*FREQ*	9	132,030,234	Intron	-	-	G	C	0.33	1.00	0.25	0.31	1.00	0.49
rs7873936	*FREQ*	9	132,032,983	Intron	-	-	G	A	0.19	1.00	0.32	0.17	1.00	0.72
rs7852859	*FREQ*	9	132,034,981	Intron	-	-	A	G	0.12	1.00	0.10	0.12	1.00	0.63
rs1054879	*FREQ*	9	132,035,589	3' UTR	-	-	A	G	0.45	1.00	0.31	0.48	1.00	0.55
rs13710	*FREQ*	9	132,037,596	3' UTR	-	-	T	C	0.33	1.00	0.73	0.29	1.00	0.72
rs709611	*FREQ*	9	132,038,180	3' UTR	-	-	C	T	0.31	0.99	0.81	0.28	1.00	0.32
rs7867364	*FREQ*	9	132,040,103	Flanking 3' UTR	-	-	C	T	0.18	1.00	0.49	0.17	1.00	0.48
rs7863731	*FREQ*	9	132,042,626	Flanking 3' UTR	-	-	C	T	0.37	0.99	0.83	0.38	0.98	0.52
rs1557123	*FREQ*	9	132,042,979	Flanking 3' UTR	-	-	C	G	0.08	1.00	0.08	0.08	1.00	0.17
rs7867693	*FREQ*	9	132,043,625	Flanking 3' UTR	-	-	G	A	0.13	1.00	0.65	0.12	1.00	0.49
rs7868148	*FREQ*	9	132,043,755	Flanking 3' UTR	-	-	G	A	0.27	1.00	0.20	0.27	1.00	1.00
rs10819621	*FREQ*	9	132,045,353	Flanking 3' UTR	-	-	T	C	0.15	1.00	0.44	0.15	1.00	0.85
rs10988653	*FREQ*	9	132,046,295	Flanking 3' UTR	-	-	T	C	0.39	1.00	0.20	0.38	1.00	0.67
rs2519765	*DBH*	9	135,484,246	Flanking 5' UTR	-	-	C	T	0.30	0.99	0.63	0.35	1.00	0.38
rs2519148	*DBH*	9	135,484,387	Flanking 5' UTR	-	-	G	A	0.50	0.99	0.84	0.47	0.99	0.27
rs2519147	*DBH*	9	135,485,139	Flanking 5' UTR	-	-	A	G	0.34	1.00	0.91	0.38	1.00	0.75
rs1076153	*DBH*	9	135,487,964	Flanking 5' UTR	-	-	G	T	0.21	0.99	0.17	0.20	1.00	0.36
rs1076150	*DBH*	9	135,488,582	Flanking 5' UTR	-	-	C	T	0.49	0.96	0.26	0.47	0.97	0.01
rs1611115	*DBH*	9	135,490,336	Flanking 5' UTR	-	-	C	T	0.20	1.00	0.27	0.18	1.00	1.00
rs2797849	*DBH*	9	135,491,762	Intron	-	-	G	C	0.35	1.00	0.91	0.39	0.99	0.92
rs2519143	*DBH*	9	135,492,149	Intron	-	-	G	A	0.18	1.00	0.40	0.16	1.00	0.71
rs3025388	*DBH*	9	135,493,077	Intron	-	-	A	G	0.17	0.94	0.27	0.15	0.96	0.17
rs2007153	*DBH*	9	135,493,640	Intron	-	-	C	T	0.35	1.00	0.74	0.32	1.00	1.00
rs2519155	*DBH*	9	135,494,419	Intron	-	-	T	C	0.35	1.00	0.91	0.39	1.00	0.92
rs1611118	*DBH*	9	135,494,744	Intron	-	-	C	T	0.05	1.00	0.61	0.05	1.00	1.00
rs1108580	*DBH*	9	135,494,935	Intron	Synonymous	E148E (NP_000778)	G	A	0.47	0.93	0.75	0.44	0.94	0.08
rs1108581	*DBH*	9	135,495,062	Intron	-	-	A	G	0.18	1.00	0.13	0.17	1.00	0.73
rs5320	*DBH*	9	135,497,294	Coding Region	Nonsynonymous	A197T (NP_000778)	G	A	0.07	0.92	0.68	0.05	0.93	0.60
rs5324	*DBH*	9	135,498,479	Coding Region	Nonsynonymous	D276N (NP_000778)	G	A	1.27×10^{-3}	1.00	1.00	1.24×10^{-3}	1.00	1.00
rs3025399	*DBH*	9	135,498,795	Intron	-	-	A	C	0.03	1.00	0.35	0.04	1.00	1.00
rs1611123	*DBH*	9	135,498,904	Intron	-	-	C	T	0.47	1.00	0.48	0.50	1.00	0.09
rs2797855	*DBH*	9	135,500,715	Intron	-	-	G	C	0.40	1.00	0.53	0.45	1.00	0.48
rs1541333	*DBH*	9	135,501,206	Intron	-	-	G	C	0.46	1.00	0.92	0.43	1.00	0.04
rs1541332	*DBH*	9	135,501,337	Intron	-	-	G	A	0.48	0.99	0.48	0.42	1.00	0.84
rs2519154	*DBH*	9	135,502,096	Intron	-	-	T	C	0.43	1.00	0.47	0.40	1.00	0.92
rs2797853	*DBH*	9	135,502,336	Intron	-	-	C	T	0.35	1.00	0.05	0.37	1.00	0.39
rs6479643	*DBH*	9	135,504,489	Intron	-	-	G	C	0.36	1.00	0.83	0.38	1.00	0.40
rs77905	*DBH*	9	135,507,918	Coding Region	Synonymous	T456T (NP_000778)	A	G	0.46	0.99	0.54	0.48	1.00	0.42
rs2097628	*DBH*	9	135,509,523	Intron	-	-	T	C	0.03	1.00	1.00	0.02	1.00	1.00
rs2073833	*DBH*	9	135,510,103	Intron	-	-	G	C	0.40	0.97	0.83	0.41	0.98	0.15
rs6271	*DBH*	9	135,512,095	Coding Region	Nonsynonymous	R535C (NP_000778)	C	T	0.08	0.99	1.00	0.08	0.99	0.28
rs10993948	*DBH*	9	135,512,723	Intron	-	-	G	C	0.03	1.00	1.00	0.02	1.00	1.00
rs10993949	*DBH*	9	135,512,806	Intron	-	-	A	G	0.03	1.00	1.00	0.02	1.00	1.00
rs3025425	*DBH*	9	135,512,987	Intron	-	-	C	T	0.03	1.00	1.00	0.02	1.00	1.00
rs129883	*DBH*	9	135,514,632	Flanking 3' UTR	-	-	C	G	0.34	1.00	0.91	0.37	1.00	0.13
rs129915	*DBH*	9	135,514,739	Flanking 3' UTR	-	-	A	G	0.27	0.93	0.23	0.29	0.93	0.13
rs129884	*DBH*	9	135,514,907	Flanking 3' UTR	-	-	G	A	0.17	1.00	0.86	0.17	1.00	0.48
rs129886	*DBH*	9	135,518,542	3' UTR	-	-	C	T	0.18	0.99	0.61	0.18	1.00	1.00
rs2073835	*DBH*	9	135,522,004	Intron	-	-	G	A	0.29	0.96	0.26	0.31	0.98	0.08
rs12244716	*CALY*	10	134,978,372	Flanking 3' UTR	-	-	G	C	0.14	0.99	1.00	0.12	1.00	0.81
rs2275723	*CALY*	10	134,989,625	Intron	-	-	G	A	0.10	0.99	0.78	0.09	0.99	1.00
rs2298122	*CALY*	10	134,991,562	Intron	-	-	T	G	0.19	0.93	1.00	0.17	0.95	1.00

									Male			Female		
SNP	Gene Region	Chromosome	Position	Location	Coding Status	Amino Acid Change	Major Allele	Minor Allele	MAF	Call Rate	HWE Chi-square Exact P	MAF	Call Rate	HWE Chi-square Exact P
rs11101694	*CALY*	10	134,996,704	Intron	-	-	T	C	0.13	0.91	1.00	0.12	0.94	1.00
rs10776672	*CALY*	10	135,007,945	Flanking 5' UTR	-	-	A	G	0.11	1.00	0.79	0.10	1.00	0.42
rs4838721	*CALY*	10	135,010,940	Intron	-	-	T	C	0.19	1.00	0.74	0.17	1.00	0.86
rs7932167	*DRD4*	11	610,599	Intron	-	-	T	G	0.23	1.00	0.77	0.21	1.00	0.30
rs12280580	*DRD4*	11	616,220	Flanking 3' UTR	-	-	C	G	0.30	1.00	0.07	0.28	1.00	0.81
rs4987059	*DRD4*	11	626,433	Flanking 5' UTR	-	-	G	A	0.06	1.00	1.00	0.05	1.00	0.62
rs936461	*DRD4*	11	626,496	Flanking 5' UTR	-	-	G	A	0.36	0.96	0.26	0.36	0.96	0.03
rs1800443	*DRD4*	11	629,830	Coding Region	Nonsynonymous	V194G (NP_000788)	T	NA	0.00	1.00	NA	0.00	1.00	NA
rs11246226	*DRD4*	11	631,191	Flanking 3' UTR	-	-	A	C	0.50	0.90	0.92	0.48	0.93	0.68
rs936465	*DRD4*	11	633,568	Flanking 3' UTR	-	-	C	G	0.47	0.88	0.83	0.45	0.92	0.46
rs10902188	*DRD4*	11	644,043	Coding Region	-	-	G	A	0.09	1.00	0.76	0.09	1.00	0.34
rs6598007	*DRD4*	11	646,523	Intron	-	-	C	T	0.06	1.00	0.38	0.06	1.00	0.38
rs4963126	*DRD4*	11	646,845	Intron	-	-	G	A	0.45	1.00	0.22	0.49	1.00	0.23
rs11603404	*DRD4*	11	646,940	Intron	-	-	G	A	0.13	1.00	1.00	0.14	1.00	0.15
rs1004446	*TH*	11	2,126,719	Flanking 3' UTR	-	-	G	A	0.37	1.00	0.59	0.38	1.00	0.21
rs7924316	*TH*	11	2,130,023	Flanking 3' UTR	-	-	G	T	0.49	0.99	0.16	0.48	1.00	0.69
rs3842748	*TH*	11	2,137,971	Intron	-	-	G	C	0.22	0.97	0.76	0.24	0.98	0.41
rs2070762	*TH*	11	2,142,911	Intron	-	-	G	A	0.50	0.99	0.92	0.50	1.00	0.49
rs6356	*TH*	11	2,147,527	Coding Region	Nonsynonymous	V108M (NP_954987)	C	T	0.37	1.00	1.00	0.35	1.00	0.74
rs10770140	*TH*	11	2,150,173	Flanking 5' UTR	-	-	T	C	0.35	0.99	0.91	0.41	0.99	0.84
rs10770141	*TH*	11	2,150,416	Flanking 5' UTR	-	-	G	A	0.35	1.00	0.51	0.41	1.00	0.84
rs10743149	*TH*	11	2,150,751	Flanking 5' UTR	-	-	C	T	0.12	1.00	0.64	0.13	1.00	0.65
rs10840495	*TH*	11	2,152,413	Flanking 5' UTR	-	-	G	A	0.34	0.86	0.34	0.38	0.88	0.91
rs11042978	*TH*	11	2,154,994	Flanking 5' UTR	-	-	G	T	0.48	0.99	0.36	0.46	1.00	0.69
rs6578993	*TH*	11	2,157,739	Flanking 5' UTR	-	-	C	T	0.16	1.00	0.35	0.15	1.00	0.03
rs11043001	*TH*	11	2,159,621	Flanking 5' UTR	-	-	G	A	0.17	1.00	0.59	0.16	1.00	8.89×10^{-3}
rs11043003	*TH*	11	2,159,730	Flanking 5' UTR	-	-	T	C	0.23	1.00	0.20	0.27	1.00	0.32
rs11043016	*TH*	11	2,162,603	Flanking 5' UTR	-	-	T	C	0.24	1.00	0.27	0.27	0.99	0.26
rs11564703	*TH*	11	2,163,785	Flanking 5' UTR	-	-	A	G	0.41	0.99	0.21	0.44	0.99	0.48
rs12419948	*BDNF*	11	27,623,560	Flanking 3' UTR	-	-	T	A	0.21	1.00	0.36	0.19	1.00	0.52
rs1519479	*BDNF*	11	27,624,107	Flanking 3' UTR	-	-	T	C	0.48	1.00	0.22	0.47	1.00	0.32
rs11030098	*BDNF*	11	27,628,869	Flanking 3' UTR	-	-	C	G	1.27×10^{-3}	1.00	1.00	3.71×10^{-3}	1.00	1.00
rs1519480	*BDNF*	11	27,632,288	Flanking 3' UTR	-	-	T	C	0.31	1.00	0.82	0.27	1.00	0.80
rs7124442	*BDNF*	11	27,633,617	3' UTR	-	-	T	C	0.30	0.97	1.00	0.26	0.98	0.70
rs6265	*BDNF*	11	27,636,492	Coding Region	Nonsynonymous	M66V (NP_733931)	C	T	0.19	1.00	0.52	0.18	1.00	0.73
rs11030101	*BDNF*	11	27,637,320	Flanking 5' UTR	-	-	A	T	0.46	1.00	0.16	0.48	1.00	0.76
rs11030104	*BDNF*	11	27,641,093	Flanking 5' UTR	-	-	A	G	0.21	1.00	0.29	0.20	1.00	0.28
rs1401635	*BDNF*	11	27,650,567	Flanking 5' UTR	-	-	G	C	0.30	1.00	1.00	0.27	1.00	0.70
rs12291063	*BDNF*	11	27,650,677	Flanking 5' UTR	-	-	T	C	1.27×10^{-3}	1.00	1.00	3.71×10^{-3}	1.00	1.00
rs2049045	*BDNF*	11	27,650,817	Flanking 5' UTR	-	-	G	C	0.19	1.00	0.62	0.17	1.00	0.72
rs11030107	*BDNF*	11	27,651,411	Flanking 5' UTR	-	-	A	G	0.26	0.98	0.43	0.22	0.98	1.00
rs10835210	*BDNF*	11	27,652,486	Flanking 5' UTR	-	-	C	A	0.42	1.00	0.05	0.48	1.00	1.00
rs7103873	*BDNF*	11	27,656,893	Flanking 5' UTR	-	-	G	C	0.46	1.00	0.22	0.48	1.00	0.69
rs6484320	*BDNF*	11	27,659,764	Flanking 3' UTR	-	-	A	T	0.22	1.00	0.38	0.20	1.00	0.03
rs1013402	*BDNF*	11	27,668,957	Flanking 3' UTR	-	-	A	G	0.31	1.00	0.91	0.27	1.00	0.45
rs988748	*BDNF*	11	27,681,321	Flanking 5' UTR	-	-	G	C	0.22	1.00	0.38	0.21	1.00	0.05
rs10767664	*BDNF*	11	27,682,562	Flanking 5' UTR	-	-	A	T	0.22	0.99	0.37	0.20	1.00	0.03
rs2030324	*BDNF*	11	27,683,491	Flanking 5' UTR	-	-	G	A	0.48	1.00	0.36	0.47	1.00	0.55
rs11030119	*BDNF*	11	27,684,678	Flanking 5' UTR	-	-	G	A	0.29	1.00	0.90	0.26	1.00	0.30
rs7934165	*BDNF*	11	27,688,559	Flanking 5' UTR	-	-	A	G	0.48	0.99	0.48	0.47	0.99	0.69
rs11030121	*BDNF*	11	27,692,783	Flanking 3' UTR	-	-	C	T	0.30	1.00	0.90	0.27	1.00	0.37
rs12273363	*BDNF*	11	27,701,435	Flanking 5' UTR	-	-	T	C	0.20	0.99	0.06	0.16	0.99	0.86
rs908867	*BDNF*	11	27,702,340	Flanking 5' UTR	-	-	C	T	0.09	1.00	0.36	0.10	1.00	1.00
rs1491850	*BDNF*	11	27,706,301	Flanking 5' UTR	-	-	T	C	0.43	0.99	0.05	0.37	1.00	0.24
rs2049048	*BDNF*	11	27,707,162	Flanking 5' UTR	-	-	G	A	0.16	1.00	0.71	0.13	1.00	0.13
rs11214589	*ANKK1*	11	112,750,258	Flanking 3' UTR	-	-	G	A	0.48	0.95	0.54	0.49	0.95	0.08
rs4938010	*ANKK1*	11	112,750,776	Flanking 3' UTR	-	-	A	G	0.14	1.00	0.67	0.15	1.00	0.24
rs754672	*ANKK1*	11	112,754,346	Flanking 3' UTR	-	-	T	C	0.46	1.00	0.42	0.48	1.00	0.84
rs3897584	*ANKK1*	11	112,754,935	Flanking 3' UTR	-	-	C	G	0.34	1.00	0.18	0.34	1.00	0.74
rs10891545	*ANKK1*	11	112,763,275	Flanking 5' UTR	-	-	T	C	0.13	1.00	0.65	0.15	1.00	0.70
rs4938012	*ANKK1*	11	112,764,864	Intron	-	-	G	A	0.33	1.00	0.09	0.33	1.00	0.82
rs7123797	*ANKK1*	11	112,767,781	Intron	-	-	G	A	0.34	1.00	0.02	0.34	1.00	0.74
rs12360992	*ANKK1*	11	112,768,110	Intron	-	-	C	A	0.46	1.00	0.61	0.48	1.00	0.92
rs4590907	*ANKK1*	11	112,768,580	Intron	-	-	T	G	0.13	1.00	0.65	0.15	1.00	0.84
rs17115439	*ANKK1*	11	112,769,482	Coding Region	-	-	C	T	0.33	1.00	0.11	0.33	1.00	0.74
rs11214596	*ANKK1*	11	112,769,721	Intron	-	-	G	C	0.46	1.00	0.61	0.48	1.00	0.92
rs4938015	*ANKK1*	11	112,769,854	Intron	-	-	C	T	0.33	1.00	0.11	0.33	1.00	0.65
rs7118900	*ANKK1*	11	112,772,031	Coding Region	Nonsynonymous	A239T (NP_848605)	G	A	0.20	1.00	1.00	0.19	0.99	0.63
rs4938016	*ANKK1*	11	112,775,225	Coding Region	Nonsynonymous	G442R (NP_848605)	C	G	0.30	1.00	1.00	0.31	1.00	0.91
rs2734849	*ANKK1*	11	112,775,370	Coding Region	Nonsynonymous	H490R (NP_848605)	G	A	0.50	1.00	0.76	0.50	1.00	0.84
rs2734848	*ANKK1*	11	112,775,584	Coding Region	Synonymous	Y561Y (NP_848605)	T	C	0.16	0.95	0.70	0.16	0.97	1.00
rs7104979	*ANKK1*	11	112,775,688	Coding Region	Nonsynonymous	P596L (NP_848605)	C	T	1.27×10^{-3}	1.00	1.00	0.00	1.00	NA
rs1800497	*ANKK1*	11	112,776,038	Coding Region	Nonsynonymous	E713K (NP_848605)	G	A	0.21	0.94	0.53	0.20	0.96	0.88
rs11214601	*ANKK1*	11	112,777,972	Flanking 3' UTR	-	-	C	T	0.17	1.00	1.00	0.17	1.00	0.60
rs1003641	*ANKK1*	11	112,778,846	Flanking 3' UTR	-	-	G	A	0.28	1.00	0.90	0.30	1.00	1.00
rs12422191	*ANKK1*	11	112,779,220	Flanking 3' UTR	-	-	G	A	0.08	1.00	0.72	0.09	1.00	0.34
rs10891549	*ANKK1*	11	112,783,657	Flanking 3' UTR	-	-	C	T	0.45	0.99	0.68	0.47	0.99	0.92
rs2734841	*ANKK1*	11	112,786,986	Intron	-	-	C	A	0.28	0.99	0.80	0.30	1.00	1.00
rs1124491	*ANKK1*	11	112,787,300	Intron	-	-	G	A	0.17	1.00	1.00	0.17	1.00	0.60
rs1124492	*ANKK1*	11	112,787,485	Intron	-	-	C	A	0.11	1.00	0.60	0.12	1.00	0.15
rs6277	*ANKK1*	11	112,788,669	Coding Region	Synonymous	P290P (NP_057658)	A	G	0.45	0.99	0.92	0.47	0.99	1.00
rs1076560	*ANKK1*	11	112,788,898	Intron	-	-	C	A	0.17	1.00	1.00	0.17	1.00	0.60
rs2440390	*DRD2*	11	112,792,088	Intron	-	-	C	T	0.12	1.00	0.48	0.12	1.00	1.00
rs1079727	*DRD2*	11	112,794,392	Intron	-	-	T	C	0.16	1.00	1.00	0.17	1.00	0.29
rs2734833	*DRD2*	11	112,798,130	Intron	-	-	A	G	0.39	0.98	0.91	0.41	0.99	0.61
rs1076562	*DRD2*	11	112,801,218	Intron	-	-	G	A	0.23	1.00	0.57	0.25	1.00	0.23
rs2471851	*DRD2*	11	112,806,279	Intron	-	-	A	C	0.16	1.00	0.86	0.17	1.00	0.29
rs7122246	*DRD2*	11	112,809,667	Intron	-	-	A	G	0.39	1.00	0.92	0.41	1.00	0.61
rs4436578	*DRD2*	11	112,811,975	Intron	-	-	T	C	0.11	1.00	1.00	0.13	1.00	0.05
rs4587762	*DRD2*	11	112,812,103	Intron	-	-	A	G	0.40	1.00	0.92	0.42	1.00	0.76
rs4586205	*DRD2*	11	112,812,339	Intron	-	-	T	G	0.24	1.00	0.68	0.25	1.00	0.29
rs4620755	*DRD2*	11	112,814,829	Intron	-	-	G	A	0.11	1.00	0.80	0.13	1.00	0.04
rs7125415	*DRD2*	11	112,815,891	Intron	-	-	C	T	0.09	1.00	1.00	0.10	1.00	0.28
rs4936270	*DRD2*	11	112,823,618	Intron	-	-	C	T	0.09	0.99	1.00	0.11	1.00	0.14
rs4274224	*DRD2*	11	112,824,662	Intron	-	-	A	G	0.47	1.00	0.48	0.46	1.00	0.84
rs4245148	*DRD2*	11	112,825,629	Intron	-	-	C	T	0.09	1.00	1.00	0.12	1.00	0.22
rs4460839	*DRD2*	11	112,827,006	Intron	-	-	T	C	0.08	1.00	0.75	0.11	1.00	0.11
rs7122454	*DRD2*	11	112,832,678	Intron	-	-	G	C	0.15	1.00	0.85	0.14	1.00	0.31
rs7131056	*DRD2*	11	112,834,984	Intron	-	-	C	A	0.41	1.00	0.75	0.46	1.00	0.84
rs11214611	*DRD2*	11	112,835,429	Intron	-	-	A	G	0.15	1.00	0.70	0.14	1.00	0.31
rs10891552	*DRD2*	11	112,838,881	Intron	-	-	A	T	0.05	1.00	1.00	0.03	1.00	1.00
rs4630328	*DRD2*	11	112,839,419	Intron	-	-	G	A	0.38	1.00	0.59	0.35	1.00	1.00
rs11214613	*DRD2*	11	112,840,469	Intron	-	-	G	A	0.08	1.00	1.00	0.10	1.00	0.10
rs4938019	*DRD2*	11	112,846,601	Intron	-	-	T	C	0.16	1.00	0.57	0.15	1.00	0.31
rs1799978	*DRD2*	11	112,851,561	Flanking 5' UTR	-	-	T	C	0.06	1.00	0.63	0.05	1.00	0.61
rs10891556	*DRD2*	11	112,857,971	Flanking 5' UTR	-	-	G	T	0.18	0.98	0.22	0.17	0.99	0.29
rs6589377	*DRD2*	11	112,860,946	Flanking 5' UTR	-	-	A	G	0.38	1.00	0.59	0.35	1.00	1.00
rs2110113	*CALM1*	14	89,922,506	Flanking 5' UTR	-	-	A	G	0.12	1.00	0.45	0.12	1.00	0.35
rs3814847	*CALM1*	14	89,931,789	Flanking 5' UTR	-	-	C	G	0.37	1.00	0.28	0.34	1.00	0.58
rs12885713	*CALM1*	14	89,933,110	Flanking 5' UTR	-	-	T	C	0.45	1.00	0.08	0.43	1.00	0.68
rs3213718	*CALM1*	14	89,939,666	Intron	-	-	T	C	0.43	1.00	0.12	0.41	1.00	1.00
rs5871	*CALM1*	14	89,941,231	3' UTR	-	-	T	C	0.07	1.00	0.44	0.07	1.00	0.71
rs3814843	*CALM1*	14	89,942,766	3' UTR	-	-	T	G	0.04	1.00	1.00	0.04	1.00	1.00
rs8006462	*CALM1*	14	89,948,429	Flanking 3' UTR	-	-	C	T	0.34	0.99	0.06	0.32	1.00	0.49
rs2896135	*CALM1*	14	89,950,493	Flanking 3' UTR	-	-	A	G	0.42	1.00	0.12	0.38	1.00	0.75

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs876259	*CALM1*	14	89,952,709	Flanking 3' UTR	-	-	T	G	0.07	1.00	0.04	0.06	1.00	0.67
rs12895068	*CALM1*	14	89,957,031	Flanking 3' UTR	-	-	A	T	0.07	1.00	0.01	0.06	1.00	0.66
rs1514246	*CHRNA7*	15	30,106,782	Flanking 5' UTR	-	-	C	A	0.26	0.99	0.18	0.26	0.99	1.00
rs868437	*CHRNA7*	15	30,111,569	Intron	-	-	T	C	0.28	1.00	0.45	0.27	1.00	0.80
rs883473	*CHRNA7*	15	30,112,968	Intron	-	-	G	A	0.29	0.99	0.47	0.29	1.00	0.81
rs4779563	*CHRNA7*	15	30,124,529	Intron	-	-	C	T	0.24	0.99	0.58	0.23	1.00	0.67
rs1913456	*CHRNA7*	15	30,133,241	Intron	-	-	A	T	0.19	1.00	0.51	0.18	1.00	0.74
rs4779969	*CHRNA7*	15	30,136,223	Intron	-	-	C	A	0.05	0.99	0.22	0.05	1.00	0.60
rs8027814	*CHRNA7*	15	30,137,964	Intron	-	-	A	G	0.28	0.99	0.31	0.27	0.99	0.90
rs2175886	*CHRNA7*	15	30,143,239	Intron	-	-	T	C	0.44	0.99	0.18	0.45	0.99	0.13
rs11071530	*CHRNA7*	15	30,147,264	Intron	-	-	G	A	0.09	0.99	0.22	0.09	1.00	0.35
rs6494211	*CHRNA7*	15	30,164,880	Intron	-	-	A	T	0.32	0.99	0.08	0.33	0.99	0.37
rs1514248	*CHRNA7*	15	30,164,975	Intron	-	-	T	C	0.11	0.93	3.08×10^{-4}	0.11	0.93	4.05×10^{-4}
rs8033518	*CHRNA7*	15	30,168,901	Intron	-	-	G	A	0.05	1.00	0.22	0.05	1.00	0.58
rs2133965	*CHRNA7*	15	30,171,846	Intron	-	-	G	A	0.06	0.99	0.66	0.06	1.00	0.19
rs7175581	*CHRNA7*	15	30,172,759	Intron	-	-	G	A	0.42	0.99	0.26	0.41	1.00	0.84
rs4779565	*CHRNA7*	15	30,177,362	Intron	-	-	G	T	0.42	0.99	0.35	0.43	1.00	1.00
rs8035668	*CHRNA7*	15	30,178,638	Intron	-	-	A	G	0.22	1.00	1.00	0.19	1.00	0.63
rs9788657	*CHRNA7*	15	30,182,318	Intron	-	-	C	A	0.21	0.99	1.00	0.19	0.99	0.63
rs6494223	*CHRNA7*	15	30,183,749	Intron	-	-	C	T	0.37	1.00	0.28	0.39	1.00	0.47
rs8030315	*CHRNA7*	15	30,184,411	Intron	-	-	C	T	0.21	0.99	0.88	0.19	0.99	0.74
rs9788679	*CHRNA7*	15	30,186,609	Intron	-	-	C	A	0.20	0.99	1.00	0.18	0.99	0.40
rs10438342	*CHRNA7*	15	30,189,338	Intron	-	-	G	A	0.38	0.99	0.91	0.37	0.99	0.52
rs11852956	*CHRNA7*	15	30,190,622	Intron	-	-	T	C	0.22	1.00	0.56	0.23	1.00	0.25
rs1039394	*CHRNA7*	15	30,195,021	Intron	-	-	C	G	0.06	0.99	0.20	0.05	0.99	0.29
rs16956223	*CHRNA7*	15	30,198,075	Intron	-	-	G	A	0.17	1.00	1.00	0.16	1.00	0.70
rs1392808	*CHRNA7*	15	30,198,807	Intron	-	-	C	A	0.17	0.99	1.00	0.15	0.99	0.56
rs904952	*CHRNA7*	15	30,206,037	Intron	-	-	T	C	0.49	0.99	0.31	0.48	0.99	0.55
rs7402321	*CHRNA7*	15	30,207,700	Intron	-	-	C	T	0.37	0.96	0.38	0.38	0.97	0.39
rs7175359	*CHRNA7*	15	30,212,239	Intron	-	-	C	T	0.49	0.99	0.27	0.47	1.00	0.69
rs2651418	*CHRNA7*	15	30,226,573	Intron	-	-	T	C	0.49	0.98	0.13	0.49	0.99	0.84
rs2611605	*CHRNA7*	15	30,228,925	Intron	-	-	C	T	0.18	0.99	0.87	0.20	1.00	0.88
rs7178176	*CHRNA7*	15	30,231,105	Intron	-	-	C	T	0.25	1.00	1.00	0.25	1.00	0.42
rs2337980	*CHRNA7*	15	30,231,488	Intron	-	-	C	T	0.45	0.99	0.42	0.43	1.00	0.68
rs7164518	*CHRNA7*	15	30,249,900	Flanking 3' UTR	-	-	A	G	0.18	0.99	1.00	0.17	0.99	0.72
rs4275821	*CHRNA5*	15	76,636,596	Flanking 3' UTR	-	-	T	C	0.35	1.00	0.22	0.38	1.00	1.00
rs2036527	*CHRNA5*	15	76,638,670	Flanking 5' UTR	-	-	G	A	0.41	1.00	0.68	0.40	1.00	0.30
rs684513	*CHRNA5*	15	76,645,455	Intron	-	-	C	G	0.17	0.99	0.60	0.15	1.00	0.69
rs871058	*CHRNA5*	15	76,645,546	Intron	-	-	G	A	0.33	1.00	0.09	0.37	1.00	0.75
rs667282	*CHRNA5*	15	76,650,527	Intron	-	-	T	C	0.20	1.00	0.22	0.16	1.00	0.58
rs601079	*CHRNA5*	15	76,656,634	Intron	-	-	A	T	0.39	1.00	1.00	0.44	1.00	1.00
rs637137	*CHRNA5*	15	76,661,031	Intron	-	-	T	A	0.20	1.00	0.27	0.16	1.00	0.58
rs692780	*CHRNA5*	15	76,663,560	Intron	-	-	G	C	0.35	1.00	0.37	0.38	1.00	0.60
rs555018	*CHRNA3;CHRNA5*	15	76,666,297	Intron	-	-	A	G	0.39	1.00	1.00	0.44	1.00	0.92
rs647041	*CHRNA3;CHRNA5*	15	76,667,536	Intron	-	-	C	T	0.39	1.00	0.83	0.44	1.00	1.00
rs514743	*CHRNA3;CHRNA5*	15	76,671,282	Intron	-	-	A	T	0.35	1.00	0.44	0.39	1.00	0.68
rs578776	*CHRNA3;CHRNA5*	15	76,675,455	3' UTR	-	-	G	A	0.24	1.00	0.13	0.21	1.00	0.65
rs6495307	*CHRNA3;CHRNA5*	15	76,677,376	Intron	-	-	C	T	0.39	1.00	1.00	0.44	1.00	1.00
rs1051730	*CHRNA3;CHRNA5*	15	76,681,394	Coding Region	Synonymous	Y215Y (NP_000734)	G	A	0.40	0.99	0.83	0.39	0.99	0.17
rs3743078	*CHRNA3;CHRNA5*	15	76,681,814	Intron	-	-	G	C	0.21	1.00	0.36	0.16	1.00	0.86
rs3743077	*CHRNA3;CHRNA5*	15	76,681,951	Intron	-	-	C	T	0.36	0.94	0.65	0.42	0.95	0.92
rs1317286	*CHRNA3;CHRNA5*	15	76,683,184	Intron	-	-	A	G	0.41	0.99	0.83	0.40	1.00	0.41
rs938682	*CHRNA3*	15	76,683,602	Intron	-	-	A	G	0.20	1.00	0.27	0.16	1.00	0.58
rs4887069	*CHRNA3;CHRNB4*	15	76,696,125	Intron	-	-	A	G	0.20	0.99	0.43	0.17	1.00	0.86
rs3743075	*CHRNA3;CHRNB4*	15	76,696,507	Coding Region	Synonymous	K97K (NP_000734)	C	T	0.35	1.00	0.37	0.38	1.00	0.34
rs3743073	*CHRNA3;CHRNB4*	15	76,696,594	Intron	-	-	T	G	0.35	0.99	0.27	0.39	1.00	0.46
rs1878399	*CHRNA3;CHRNB4*	15	76,699,058	Intron	-	-	C	G	0.39	0.99	0.83	0.44	1.00	1.00
rs6495309	*CHRNA3;CHRNB4*	15	76,702,300	Flanking 3' UTR	-	-	C	T	0.19	1.00	0.08	0.15	1.00	0.44
rs1948	*CHRNA3;CHRNB4*	15	76,704,454	3' UTR	-	-	G	A	0.33	1.00	0.65	0.35	1.00	0.16
rs7178270	*CHRNA3;CHRNB4*	15	76,708,132	Intron	-	-	C	G	0.37	1.00	0.91	0.42	1.00	0.54
rs950776	*CHRNB4*	15	76,713,073	Intron	-	-	T	C	0.33	1.00	0.43	0.35	1.00	0.16
rs12441998	*CHRNB4*	15	76,716,427	Intron	-	-	A	G	0.18	1.00	0.74	0.17	1.00	0.72
rs1316971	*CHRNB4*	15	76,717,565	Intron	-	-	G	A	0.18	1.00	0.74	0.17	1.00	0.72
rs11633223	*CHRNB4*	15	76,722,531	Flanking 5' UTR	-	-	T	C	0.36	1.00	1.00	0.39	1.00	0.12
rs3971872	*CHRNB4*	15	76,729,090	Flanking 5' UTR	-	-	C	T	0.09	1.00	0.55	0.09	1.00	1.00
rs2191416	*CREBBP*	16	3,710,730	Flanking 5' UTR	-	-	G	A	0.26	1.00	0.05	0.24	1.00	0.07
rs9392	*CREBBP*	16	3,715,170	Flanking 3' UTR	-	-	G	A	0.23	1.00	0.08	0.22	1.00	0.56
rs130008	*CREBBP*	16	3,721,953	Intron	-	-	C	G	0.03	1.00	1.00	0.02	1.00	1.00
rs130016	*CREBBP*	16	3,730,308	Intron	-	-	C	T	0.50	1.00	0.00	0.50	1.00	0.00
rs129968	*CREBBP*	16	3,731,262	Intron	-	-	G	A	0.36	0.96	1.00	0.35	0.98	0.32
rs3025684	*CREBBP*	16	3,735,364	Intron	-	-	G	A	0.03	0.98	1.00	0.02	0.97	1.00
rs129963	*CREBBP*	16	3,736,148	Intron	-	-	C	T	0.46	1.00	0.76	0.44	1.00	0.84
rs11864123	*CREBBP*	16	3,744,325	Intron	-	-	T	A	0.02	1.00	1.00	0.01	1.00	1.00
rs886528	*CREBBP*	16	3,751,557	Intron	-	-	A	G	0.44	0.99	0.92	0.46	1.00	0.37
rs13380693	*CREBBP*	16	3,757,049	Intron	-	-	T	C	0.02	1.00	0.16	0.02	1.00	1.00
rs12051375	*CREBBP*	16	3,767,554	Intron	-	-	G	A	5.08×10^{-3}	1.00	1.00	8.66×10^{-3}	1.00	1.00
rs130002	*CREBBP*	16	3,767,932	Intron	-	-	T	C	5.08×10^{-3}	1.00	1.00	8.66×10^{-3}	1.00	1.00
rs8052927	*CREBBP*	16	3,768,586	Intron	-	-	G	T	0.02	1.00	1.00	0.02	1.00	1.00
rs130021	*CREBBP*	16	3,772,472	Intron	-	-	A	G	0.35	1.00	0.51	0.37	1.00	0.83
rs130025	*CREBBP*	16	3,772,960	Intron	-	-	C	A	0.02	1.00	1.00	0.01	1.00	1.00
rs8046065	*CREBBP*	16	3,778,299	Intron	-	-	C	T	0.12	1.00	0.82	0.12	1.00	0.82
rs3789033	*CREBBP*	16	3,779,536	Intron	-	-	T	C	0.22	1.00	0.66	0.24	1.00	0.49
rs8047652	*CREBBP*	16	3,789,559	Intron	-	-	G	T	0.02	1.00	0.18	0.02	1.00	1.00
rs13334803	*CREBBP*	16	3,798,348	Intron	-	-	T	A	0.02	1.00	0.11	0.01	1.00	1.00
rs130046	*CREBBP*	16	3,803,947	Intron	-	-	A	C	0.02	1.00	0.13	0.01	1.00	1.00
rs11644593	*CREBBP*	16	3,811,287	Intron	-	-	G	A	0.10	1.00	0.40	0.11	1.00	0.79
rs1296720	*CREBBP*	16	3,813,643	Intron	-	-	A	C	0.20	1.00	0.35	0.18	1.00	0.41
rs4567717	*CREBBP*	16	3,838,834	Intron	-	-	A	C	0.02	1.00	0.10	0.01	1.00	1.00
rs2540038	*CREBBP*	16	3,848,845	Intron	-	-	G	A	0.01	1.00	1.00	9.93×10^{-3}	1.00	1.00
rs2239316	*CREBBP*	16	3,853,996	Intron	-	-	A	G	0.26	1.00	0.69	0.27	1.00	0.90
rs7202140	*CREBBP*	16	3,864,655	Intron	-	-	C	G	0.02	1.00	0.20	0.02	1.00	1.00
rs2526687	*CREBBP*	16	3,872,726	Flanking 5' UTR	-	-	G	A	0.01	1.00	1.00	9.90×10^{-3}	1.00	1.00
rs12453682	*PPP1R1B*	17	35,023,531	Flanking 5' UTR	-	-	T	C	0.31	1.00	0.29	0.33	1.00	0.50
rs1877032	*PPP1R1B*	17	35,024,590	Flanking 5' UTR	-	-	T	C	0.10	0.92	1.00	0.08	0.91	0.72
rs1874228	*PPP1R1B*	17	35,028,800	Flanking 5' UTR	-	-	G	A	0.25	0.99	0.69	0.29	0.99	0.09
rs879606	*PPP1R1B*	17	35,035,375	Flanking 5' UTR	-	-	G	A	0.16	1.00	0.46	0.20	1.00	1.00
rs1495099	*PPP1R1B*	17	35,037,990	Flanking 5' UTR	-	-	G	C	0.29	0.99	0.72	0.31	0.99	0.03
rs907094	*PPP1R1B*	17	35,043,897	Intron	-	-	A	G	0.23	1.00	0.67	0.26	1.00	0.09
rs1874224	*PPP1R1B*	17	35,049,186	Intron	-	-	T	G	0.02	1.00	1.00	8.66×10^{-3}	1.00	1.00
rs9892427	*PPP1R1B*	17	35,058,384	Intron	-	-	T	C	0.07	1.00	0.26	0.06	1.00	0.38
rs9972882	*PPP1R1B*	17	35,061,224	Intron	-	-	C	A	0.25	1.00	1.00	0.29	1.00	1.00
rs12953076	*CRHR1*	17	41,209,781	Flanking 5' UTR	-	-	C	T	0.19	1.00	0.10	0.16	1.00	0.85
rs4074461	*CRHR1*	17	41,210,922	Flanking 5' UTR	-	-	T	G	0.43	1.00	0.18	0.49	0.99	0.55
rs12944712	*CRHR1*	17	41,226,918	Intron	-	-	G	A	0.45	1.00	0.54	0.41	1.00	0.61
rs4792887	*CRHR1*	17	41,232,791	Intron	-	-	C	T	0.12	1.00	0.22	0.11	1.00	0.12
rs16940646	*CRHR1*	17	41,235,682	Intron	-	-	A	C	0.12	1.00	0.23	0.11	1.00	0.12
rs242924	*CRHR1*	17	41,241,147	Intron	-	-	G	T	0.42	1.00	0.22	0.47	1.00	0.76
rs242942	*CRHR1*	17	41,247,413	Intron	-	-	C	T	0.13	1.00	0.36	0.12	1.00	0.63
rs81189	*CRHR1*	17	41,250,579	Intron	-	-	G	C	0.46	1.00	1.00	0.50	1.00	0.20
rs242939	*CRHR1*	17	41,251,360	Intron	-	-	T	C	0.08	1.00	0.75	0.08	1.00	0.73
rs1876829	*CRHR1*	17	41,267,224	Intron	-	-	T	C	0.22	0.94	0.13	0.20	0.95	0.34
rs1876828	*CRHR1*	17	41,267,306	Intron	-	-	C	T	0.22	0.95	0.13	0.21	0.96	0.35
rs878887	*CRHR1*	17	41,268,363	3' UTR	-	-	C	T	0.22	0.99	0.24	0.20	0.98	0.27
rs10445364	*CRHR1*	17	41,272,136	Flanking 3' UTR	-	-	G	A	0.22	1.00	0.11	0.20	1.00	0.44
rs4792825	*CRHR1*	17	41,275,461	Flanking 5' UTR	-	-	A	G	0.12	1.00	0.81	0.11	1.00	1.00

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs17690326	*CRHR1*	17	41,276,754	Flanking 5' UTR	-	-	T	C	0.22	1.00	0.14	0.20	1.00	0.44
rs242944	*CRHR1*	17	41,278,960	Coding Region	Nonsynonymous	R303H (NP_787078)	A	G	0.45	1.00	0.08	0.41	1.00	0.08
rs9909443	*GRB2*	17	70,819,941	Flanking 3' UTR	-	-	C	T	0.27	1.00	0.37	0.25	1.00	0.69
rs4559942	*GRB2*	17	70,820,864	Flanking 3' UTR	-	-	A	G	0.28	1.00	0.53	0.26	1.00	0.70
rs6501775	*GRB2*	17	70,822,168	Flanking 3' UTR	-	-	C	T	0.05	0.99	0.22	0.05	1.00	0.61
rs8081778	*GRB2*	17	70,823,867	Flanking 3' UTR	-	-	C	T	0.19	1.00	0.62	0.19	1.00	0.25
rs7219	*GRB2*	17	70,826,963	3' UTR	-	-	T	C	0.29	0.99	0.62	0.26	1.00	0.61
rs8079197	*GRB2*	17	70,828,274	Intron	-	-	C	G	0.28	1.00	0.53	0.26	1.00	0.61
rs12946365	*GRB2*	17	70,829,239	Intron	-	-	T	C	0.28	1.00	0.53	0.26	1.00	0.61
rs12600908	*GRB2*	17	70,839,969	Flanking 3' UTR	-	-	G	A	0.15	1.00	0.54	0.12	1.00	0.64
rs4789170	*GRB2*	17	70,844,389	Intron	-	-	C	T	0.27	1.00	0.61	0.25	1.00	0.51
rs9912608	*GRB2*	17	70,848,626	Intron	-	-	C	G	0.27	1.00	0.60	0.25	1.00	0.51
rs4789172	*GRB2*	17	70,853,307	Intron	-	-	T	C	0.48	1.00	0.09	0.49	1.00	0.37
rs1369299	*GRB2*	17	70,858,920	Intron	-	-	C	T	0.18	1.00	1.00	0.18	1.00	0.24
rs4789176	*GRB2*	17	70,864,463	Intron	-	-	T	A	0.18	1.00	1.00	0.18	1.00	0.40
rs4350602	*GRB2*	17	70,867,364	Intron	-	-	T	C	0.30	1.00	0.81	0.29	1.00	0.40
rs9902966	*GRB2*	17	70,873,742	Intron	-	-	T	C	0.20	1.00	0.52	0.19	1.00	0.33
rs4789178	*GRB2*	17	70,879,837	Intron	-	-	G	C	0.20	1.00	0.63	0.19	1.00	0.33
rs4789182	*GRB2*	17	70,886,540	Intron	-	-	A	G	0.32	1.00	0.64	0.30	1.00	0.55
rs2053156	*GRB2*	17	70,890,035	Intron	-	-	T	G	0.20	1.00	0.63	0.19	1.00	0.33
rs9909076	*GRB2*	17	70,896,404	Intron	-	-	T	G	0.20	1.00	0.63	0.19	1.00	0.33
rs4788891	*GRB2*	17	70,902,740	Intron	-	-	G	A	0.20	1.00	0.63	0.19	1.00	0.41
rs4789189	*GRB2*	17	70,909,580	Intron	-	-	G	C	0.20	0.99	0.75	0.19	1.00	0.33
rs9908820	*GRB2*	17	70,920,414	Flanking 5' UTR	-	-	G	A	0.33	1.00	0.21	0.30	1.00	0.56
rs8065441	*GRB2*	17	70,922,042	Flanking 5' UTR	-	-	G	C	0.13	1.00	0.08	0.14	1.00	0.20
rs12608148	*ADCYAP1*	18	879,159	Flanking 5' UTR	-	-	G	A	0.27	1.00	0.52	0.31	1.00	0.73
rs4797325	*ADCYAP1*	18	879,905	Flanking 5' UTR	-	-	G	A	0.42	0.99	1.00	0.42	0.98	0.92
rs1599789	*ADCYAP1*	18	881,312	Flanking 5' UTR	-	-	A	G	0.27	1.00	0.09	0.24	1.00	0.41
rs2040176	*ADCYAP1*	18	882,467	Flanking 5' UTR	-	-	T	C	0.11	1.00	0.45	0.12	1.00	0.81
rs1916610	*ADCYAP1*	18	882,847	Flanking 5' UTR	-	-	C	T	0.46	1.00	0.31	0.46	1.00	0.37
rs11081411	*ADCYAP1*	18	883,205	Flanking 5' UTR	-	-	A	G	0.17	0.99	3.29×10^{-3}	0.13	1.00	0.03
rs11665625	*ADCYAP1*	18	890,332	Flanking 5' UTR	-	-	G	A	0.47	1.00	0.84	0.44	1.00	0.69
rs12961210	*ADCYAP1*	18	890,523	Flanking 5' UTR	-	-	T	G	0.32	0.99	0.91	0.32	1.00	1.00
rs9635870	*ADCYAP1*	18	890,765	Flanking 5' UTR	-	-	G	A	0.30	0.98	2.39×10^{-3}	0.27	0.99	1.65×10^{-8}
rs2846579	*ADCYAP1*	18	891,897	Flanking 5' UTR	-	-	C	T	0.11	1.00	0.45	0.12	1.00	1.00
rs2846583	*ADCYAP1*	18	892,965	Flanking 5' UTR	-	-	A	T	0.28	1.00	0.71	0.31	1.00	0.73
rs2846584	*ADCYAP1*	18	894,054	Flanking 5' UTR	-	-	C	T	0.27	1.00	0.80	0.30	1.00	0.72
rs8192595	*ADCYAP1*	18	897,521	Intron	-	-	A	G	0.10	1.00	0.23	0.09	1.00	1.00
rs11659736	*ADCYAP1*	18	905,937	Flanking 3' UTR	-	-	C	T	0.37	1.00	0.75	0.37	1.00	0.24
rs7228988	*ADCYAP1*	18	907,957	Flanking 3' UTR	-	-	A	G	0.31	1.00	0.48	0.31	1.00	0.10
rs11663172	*ADCYAP1*	18	910,173	Flanking 3' UTR	-	-	G	A	0.41	1.00	0.84	0.42	1.00	0.05
rs17501755	*ADCYAP1*	18	910,497	Flanking 3' UTR	-	-	T	C	0.30	1.00	0.48	0.32	1.00	0.91
rs12373400	*ADCYAP1*	18	913,096	Flanking 3' UTR	-	-	A	G	0.39	1.00	0.52	0.40	1.00	0.15
rs10853372	*ADCYAP1*	18	913,261	Flanking 3' UTR	-	-	G	A	0.40	1.00	0.60	0.39	1.00	6.44×10^{-3}
rs16952813	*ADCYAP1*	18	914,630	Flanking 3' UTR	-	-	G	A	0.08	1.00	0.50	0.08	1.00	0.50
rs17501915	*ADCYAP1*	18	915,250	Flanking 3' UTR	-	-	G	A	0.30	1.00	0.40	0.32	1.00	0.91
rs4798767	*ADCYAP1*	18	917,475	Flanking 3' UTR	-	-	A	T	0.41	1.00	0.68	0.39	1.00	4.83×10^{-3}
rs11660066	*ADCYAP1*	18	918,035	Flanking 3' UTR	-	-	C	T	0.08	1.00	0.50	0.08	1.00	0.50
rs11667211	*KLF16*	19	1,790,483	Intron	-	-	C	T	0.16	1.00	0.02	0.15	1.00	1.00
rs893539	*KLF16*	19	1,794,493	Intron	-	-	G	A	0.24	0.99	0.58	0.25	0.99	0.43
rs1609761	*KLF16*	19	1,798,698	Intron	-	-	A	C	0.20	0.99	0.42	0.22	1.00	0.37
rs893541	*KLF16*	19	1,809,183	Intron	-	-	T	C	0.17	1.00	1.00	0.19	1.00	0.10
rs3810417	*KLF16*	19	1,815,601	Flanking 5' UTR	-	-	C	T	0.16	0.99	0.85	0.18	1.00	0.09
rs10401329	*KLF16*	19	1,822,699	Flanking 3' UTR	-	-	G	A	0.13	0.95	0.64	0.13	0.96	0.04
rs10423854	*FOSB*	19	50,647,512	Flanking 5' UTR	-	-	A	G	0.43	1.00	0.30	0.41	1.00	0.92
rs10415949	*FOSB*	19	50,654,639	Flanking 5' UTR	-	-	A	G	0.23	1.00	0.89	0.24	1.00	0.27
rs2238687	*FOSB*	19	50,665,006	Intron	-	-	G	C	0.14	1.00	0.67	0.14	1.00	0.29
rs2276469	*FOSB*	19	50,666,433	Intron	-	-	T	C	0.44	0.91	0.83	0.46	0.94	0.92
rs708905	*FOSB*	19	50,669,312	3' UTR	-	-	G	C	0.14	0.99	1.00	0.13	0.99	0.03
rs6509214	*FOSB*	19	50,673,655	Flanking 3' UTR	-	-	G	T	0.32	1.00	0.49	0.34	1.00	0.10
rs4511641	*FOSB*	19	50,685,408	Intron	-	-	C	A	0.45	1.00	0.61	0.44	1.00	0.84
rs6142508	*EPB41L1*	20	34,160,719	Flanking 5' UTR	-	-	A	G	0.16	1.00	0.86	0.18	1.00	0.24
rs2746103	*EPB41L1*	20	34,167,348	Flanking 3' UTR	-	-	T	G	0.23	1.00	0.31	0.23	1.00	0.39
rs6141600	*EPB41L1*	20	34,175,724	Flanking 3' UTR	-	-	T	C	0.30	0.96	0.09	0.27	0.98	0.61
rs6121156	*EPB41L1*	20	34,176,747	Flanking 3' UTR	-	-	A	G	3.81×10^{-3}	1.00	1.00	1.24×10^{-3}	1.00	1.00
rs6142512	*EPB41L1*	20	34,178,851	Flanking 3' UTR	-	-	A	G	0.16	1.00	0.86	0.18	1.00	0.32
rs1474976	*EPB41L1*	20	34,195,786	Flanking 5' UTR	-	-	A	C	0.09	1.00	0.76	0.12	1.00	0.63
rs6121163	*EPB41L1*	20	34,200,451	Flanking 5' UTR	-	-	T	G	0.06	1.00	0.38	0.05	1.00	0.20
rs7266316	*EPB41L1*	20	34,203,883	Flanking 5' UTR	-	-	C	T	0.00	1.00	NA	1.24×10^{-3}	1.00	1.00
rs6060831	*EPB41L1*	20	34,209,464	Intron	-	-	T	C	1.27×10^{-3}	1.00	1.00	0.00	1.00	NA
rs6058429	*EPB41L1*	20	34,219,275	Intron	-	-	A	G	0.06	1.00	0.38	0.05	1.00	0.23
rs6060845	*EPB41L1*	20	34,233,225	Intron	-	-	A	G	0.24	1.00	0.49	0.25	1.00	0.60
rs2247688	*EPB41L1*	20	34,238,965	Intron	-	-	A	G	0.24	1.00	0.49	0.25	1.00	0.43
rs6121179	*EPB41L1*	20	34,256,911	Intron	-	-	A	G	0.18	1.00	0.40	0.19	0.99	0.10
rs6119707	*EPB41L1*	20	34,267,901	Flanking 3' UTR	-	-	A	NA	0.00	0.99	NA	0.00	1.00	NA
rs11700361	*EPB41L1*	20	34,285,729	Flanking 3' UTR	-	-	C	T	0.16	1.00	0.71	0.18	1.00	0.13
rs709050	*EPB41L1*	20	34,292,023	Intron	-	-	G	A	0.19	1.00	0.52	0.19	1.00	0.52
rs965808	*GNAS*	20	56,841,821	Flanking 5' UTR	-	-	A	C	0.24	1.00	0.89	0.25	1.00	0.23
rs3761264	*GNAS*	20	56,846,766	Flanking 5' UTR	-	-	C	T	0.43	1.00	0.61	0.45	1.00	0.09
rs6064714	*GNAS*	20	56,847,535	Flanking 5' UTR	-	-	A	G	0.14	1.00	0.84	0.13	1.00	0.27
rs1800900	*GNAS*	20	56,848,505	5' UTR	-	-	G	A	0.39	0.94	0.74	0.39	0.96	0.03
rs4810147	*GNAS*	20	56,855,022	Flanking 3' UTR	-	-	G	A	0.47	1.00	0.42	0.47	1.00	0.02
rs6015389	*GNAS*	20	56,860,121	Flanking 5' UTR	-	-	T	C	0.36	0.99	0.51	0.34	0.99	0.15
rs6026561	*GNAS*	20	56,860,527	Flanking 5' UTR	-	-	T	C	0.36	0.99	0.51	0.34	1.00	0.09
rs8125112	*GNAS*	20	56,864,560	Flanking 3' UTR	-	-	T	C	0.15	0.97	1.00	0.14	0.98	0.22
rs6064716	*GNAS*	20	56,877,541	Flanking 3' UTR	-	-	G	C	0.12	1.00	0.48	0.12	1.00	0.24
rs2145288	*GNAS*	20	56,877,604	Flanking 3' UTR	-	-	A	C	0.27	1.00	0.80	0.29	1.00	0.05
rs6026567	*GNAS*	20	56,878,310	Flanking 3' UTR	-	-	A	G	0.43	1.00	0.10	0.42	1.00	0.48
rs12625436	*GNAS*	20	56,878,608	Flanking 3' UTR	-	-	G	A	0.40	1.00	0.06	0.40	1.00	0.30
rs7271854	*GNAS*	20	56,880,417	Flanking 3' UTR	-	-	C	T	0.40	0.97	0.83	0.38	0.99	0.14
rs4810148	*GNAS*	20	56,881,306	Flanking 3' UTR	-	-	T	C	0.35	1.00	0.66	0.33	1.00	0.57
rs2180696	*GNAS*	20	56,887,299	Flanking 5' UTR	-	-	C	G	0.41	1.00	0.75	0.39	1.00	0.92
rs6026574	*GNAS*	20	56,889,890	Flanking 5' UTR	-	-	A	T	0.35	0.99	1.00	0.38	1.00	0.34
rs4812042	*GNAS*	20	56,895,310	Flanking 5' UTR	-	-	A	G	0.40	1.00	0.83	0.42	1.00	0.61
rs6092704	*GNAS*	20	56,901,873	Flanking 3' UTR	-	-	A	C	0.12	1.00	0.46	0.08	1.00	0.34
rs2057291	*GNAS*	20	56,905,438	Intron	-	-	G	A	0.36	1.00	0.83	0.38	1.00	0.60
rs6128461	*GNAS*	20	56,910,485	Intron	-	-	C	T	0.39	1.00	0.83	0.41	1.00	0.30
rs7121	*GNAS*	20	56,912,202	Coding Region	Synonymous	I117I (NP_536351)	T	C	0.48	1.00	0.61	0.48	1.00	0.43
rs3730168	*GNAS*	20	56,912,334	Intron	-	-	G	A	0.34	1.00	0.74	0.35	1.00	0.74
rs6026593	*GNAS*	20	56,912,528	Intron	-	-	A	G	0.12	1.00	0.63	0.10	1.00	0.05
rs919197	*GNAS*	20	56,914,328	Intron	-	-	C	T	0.46	1.00	0.92	0.45	1.00	0.76
rs3787493	*GNAS*	20	56,914,543	Intron	-	-	G	A	0.45	1.00	0.92	0.44	1.00	0.69
rs234630	*GNAS*	20	56,917,050	Intron	-	-	T	C	0.31	1.00	0.91	0.34	1.00	0.22
rs234628	*GNAS*	20	56,919,006	Intron	-	-	C	T	0.42	1.00	0.84	0.41	1.00	0.54
rs234627	*GNAS*	20	56,920,375	Flanking 3' UTR	-	-	C	T	0.30	1.00	0.91	0.32	1.00	0.43
rs234623	*GNAS*	20	56,922,359	Flanking 3' UTR	-	-	A	G	0.45	1.00	0.92	0.46	1.00	0.92
rs234621	*GNAS*	20	56,923,643	Flanking 3' UTR	-	-	C	A	0.31	1.00	0.81	0.34	1.00	0.66
rs151331	*GNAS*	20	56,925,899	Flanking 3' UTR	-	-	G	A	0.31	1.00	1.00	0.35	1.00	0.58
rs4603829	*CHRNA4*	20	61,439,336	Flanking 3' UTR	-	-	T	C	0.35	1.00	0.82	0.37	1.00	0.46
rs4809538	*CHRNA4*	20	61,440,620	Flanking 3' UTR	-	-	G	A	0.22	1.00	1.00	0.23	1.00	0.89
rs4522666	*CHRNA4*	20	61,444,924	Flanking 3' UTR	-	-	A	G	0.37	1.00	0.39	0.36	1.00	0.45
rs2236196	*CHRNA4*	20	61,448,000	Intron	-	-	A	G	0.28	1.00	0.80	0.25	1.00	0.50
rs3787137	*CHRNA4*	20	61,449,544	Intron	-	-	A	G	0.42	0.98	0.60	0.41	0.98	0.54
rs3787138	*CHRNA4*	20	61,449,668	Intron	-	-	A	G	0.13	0.92	1.00	0.11	0.94	0.30
rs1044396	*CHRNA4*	20	61,451,578	Coding Region	Synonymous	S543S (NP_000735)	A	G	0.45	0.96	0.47	0.44	0.97	0.61

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs2273504	*CHRNA4*	20	61,458,505	Intron	-	-	G	A	0.16	0.90	0.84	0.18	0.91	1.00
rs6010918	*CHRNA4*	20	61,459,945	Intron	-	-	G	A	0.06	0.92	0.63	0.04	0.95	0.02
rs2273505	*CHRNA4*	20	61,461,322	Intron	-	-	C	T	0.07	0.91	1.00	0.07	0.94	0.08
rs755203	*CHRNA4*	20	61,464,708	Flanking 5' UTR	-	-	A	G	0.44	0.99	0.92	0.42	0.99	0.92
rs4809549	*CHRNA4*	20	61,472,553	Flanking 5' UTR	-	-	G	C	0.47	1.00	0.76	0.48	1.00	0.37
rs7281533	*CLIC6*	21	34,969,460	Intron	-	-	T	C	0.21	1.00	0.65	0.23	1.00	0.39
rs2409531	*CLIC6*	21	34,975,371	Intron	-	-	A	G	0.21	1.00	0.65	0.23	1.00	0.39
rs7281040	*CLIC6*	21	34,978,271	Intron	-	-	C	T	0.21	1.00	0.54	0.23	1.00	0.39
rs2834578	*CLIC6*	21	34,981,479	Intron	-	-	C	T	0.40	1.00	0.04	0.39	1.00	0.25
rs2236610	*CLIC6*	21	34,982,538	Intron	-	-	C	G	0.17	0.99	0.14	0.17	0.97	0.73
rs2834586	*CLIC6*	21	34,986,352	Intron	-	-	G	A	0.19	1.00	0.25	0.19	1.00	0.26
rs2834587	*CLIC6*	21	34,986,503	Intron	-	-	G	C	0.35	1.00	0.82	0.35	1.00	0.83
rs2186287	*CLIC6*	21	34,990,935	Intron	-	-	C	A	0.34	0.98	0.37	0.35	1.00	1.00
rs2834590	*CLIC6*	21	34,991,708	Intron	-	-	G	A	0.16	1.00	0.46	0.16	1.00	0.10
rs2070367	*CLIC6*	21	35,001,362	Intron	-	-	G	A	0.21	1.00	0.10	0.20	1.00	0.28
rs6517254	*CLIC6*	21	35,002,160	Coding Region	Synonymous	F511F (NP_444507)	C	T	0.38	1.00	0.52	0.38	1.00	0.92
rs3819041	*CLIC6*	21	35,003,496	Intron	-	-	C	G	0.42	1.00	0.15	0.40	1.00	0.15
rs2834600	*CLIC6*	21	35,007,972	Intron	-	-	C	T	0.13	1.00	0.04	0.14	1.00	0.06
rs2834603	*CLIC6*	21	35,014,793	Flanking 3' UTR	-	-	A	G	0.08	1.00	0.06	0.05	1.00	1.00
rs2834604	*CLIC6*	21	35,014,932	Flanking 3' UTR	-	-	C	T	0.33	1.00	0.26	0.37	1.00	0.24
rs2834605	*CLIC6*	21	35,019,400	Flanking 3' UTR	-	-	T	C	0.12	1.00	0.06	0.14	1.00	1.68×10^{-3}
rs11088294	*CLIC6*	21	35,020,213	Flanking 3' UTR	-	-	G	A	0.24	0.99	0.07	0.27	1.00	0.45
rs1107470	*CLIC6*	21	35,021,758	Flanking 3' UTR	-	-	T	A	0.21	1.00	0.65	0.19	1.00	0.52
rs4485648	*COMT*	22	18,299,405	Intron	-	-	T	C	0.20	1.00	0.34	0.18	1.00	0.17
rs8140265	*COMT*	22	18,301,641	Flanking 5' UTR	-	-	G	A	0.31	1.00	1.00	0.27	1.00	1.00
rs8137828	*COMT*	22	18,303,406	Flanking 3' UTR	-	-	C	T	0.44	1.00	0.92	0.50	1.00	1.00
rs2871047	*COMT*	22	18,306,331	Flanking 5' UTR	-	-	G	A	0.05	0.99	0.10	0.06	0.99	1.00
rs6518592	*COMT*	22	18,307,146	Flanking 5' UTR	-	-	C	A	0.40	1.00	0.92	0.45	1.00	0.92
rs737865	*COMT*	22	18,310,121	Intron	-	-	A	G	0.31	1.00	1.00	0.28	1.00	0.90
rs1544325	*COMT*	22	18,311,668	Intron	-	-	G	A	0.40	1.00	0.68	0.46	1.00	0.92
rs174675	*COMT*	22	18,314,051	Intron	-	-	C	T	0.28	1.00	0.90	0.27	1.00	0.80
rs5993883	*COMT*	22	18,317,638	Intron	-	-	G	T	0.45	1.00	0.26	0.50	1.00	0.55
rs5992500	*COMT*	22	18,321,947	Intron	-	-	C	T	5.10×10^{-3}	0.99	1.00	0.00	1.00	NA
rs7290221	*COMT*	22	18,322,680	Intron	-	-	G	C	0.47	1.00	1.00	0.48	1.00	1.00
rs740603	*COMT*	22	18,325,177	Intron	-	-	G	A	0.46	1.00	0.92	0.49	1.00	0.69
rs4646312	*COMT*	22	18,328,337	Intron	-	-	T	C	0.40	0.99	0.60	0.38	1.00	0.46
rs165656	*COMT*	22	18,328,863	Intron	-	-	C	G	0.49	0.99	0.16	0.46	0.99	0.76
rs4633	*COMT*	22	18,330,235	Coding Region	Synonymous	H12H (NP_009294)	T	C	0.50	0.99	0.19	0.47	1.00	1.00
rs2239393	*COMT*	22	18,330,428	Flanking 3' UTR	-	-	A	G	0.41	0.99	0.84	0.38	1.00	0.40
rs4646316	*COMT*	22	18,332,132	Intron	-	-	C	T	0.22	0.99	0.88	0.21	1.00	0.55
rs165774	*COMT*	22	18,332,561	Intron	-	-	G	A	0.30	0.99	0.48	0.34	0.99	0.27
rs174696	*COMT*	22	18,333,176	Intron	-	-	T	C	0.23	1.00	0.48	0.20	1.00	0.88
rs174697	*COMT*	22	18,333,832	Intron	-	-	G	A	0.05	1.00	1.00	0.05	1.00	0.25
rs174699	*COMT*	22	18,334,458	Intron	-	-	T	C	0.06	1.00	1.00	0.05	1.00	0.21
rs165599	*COMT*	22	18,336,781	Flanking 3' UTR	-	-	A	G	0.35	1.00	0.91	0.30	1.00	0.24
rs165824	*COMT*	22	18,339,366	Intron	-	-	A	G	0.09	0.95	0.75	0.08	0.96	0.02
rs165815	*COMT*	22	18,339,473	Coding Region	Nonsynonymous	Q906R (NP_001661)	T	C	0.16	1.00	0.57	0.13	1.00	0.67
rs5993891	*COMT*	22	18,339,746	Intron	-	-	C	T	0.06	0.99	0.38	0.05	0.99	1.00
rs2240713	*COMT*	22	18,341,101	Intron	-	-	C	T	0.06	0.99	0.62	0.05	1.00	0.61
rs887199	*COMT*	22	18,341,955	Intron	-	-	G	A	0.16	1.00	0.45	0.13	1.00	0.67
rs887200	*COMT*	22	18,343,666	Intron	-	-	T	C	0.14	0.97	0.83	0.12	0.99	1.00
rs17759568	*MAPK1*	22	20,440,627	Flanking 3' UTR	-	-	A	G	0.04	1.00	1.00	0.04	1.00	0.49
rs2276005	*MAPK1*	22	20,443,688	Flanking 3' UTR	-	-	T	G	0.04	1.00	1.00	0.04	1.00	0.12
rs13515	*MAPK1*	22	20,445,886	3' UTR	-	-	C	T	0.21	0.99	0.29	0.18	1.00	0.25
rs1063311	*MAPK1*	22	20,446,467	3' UTR	Nonsynonymous	R100C (XP_498872)	C	T	0.46	0.99	0.61	0.43	0.99	0.26
rs5755074	*MAPK1*	22	20,451,327	Flanking 3' UTR	-	-	C	T	0.04	1.00	1.00	0.04	1.00	0.12
rs2266966	*MAPK1*	22	20,451,554	Flanking 3' UTR	-	-	T	C	0.46	1.00	0.54	0.43	1.00	0.22
rs17759598	*MAPK1*	22	20,452,149	Flanking 3' UTR	-	-	T	C	0.17	1.00	0.72	0.14	1.00	0.84
rs2298432	*MAPK1*	22	20,453,189	Flanking 3' UTR	-	-	C	A	0.36	1.00	0.27	0.35	1.00	0.66
rs4821263	*MAPK1*	22	20,457,490	Intron	-	-	C	T	0.04	1.00	1.00	0.04	1.00	0.12
rs743409	*MAPK1*	22	20,459,215	Intron	-	-	G	A	0.44	1.00	0.92	0.47	1.00	0.02
rs2283791	*MAPK1*	22	20,460,945	Intron	-	-	C	G	0.46	0.99	0.68	0.43	1.00	0.22
rs9607272	*MAPK1*	22	20,466,398	Intron	-	-	T	G	0.25	1.00	0.03	0.24	1.00	0.42
rs11704205	*MAPK1*	22	20,475,253	Intron	-	-	C	T	0.45	1.00	0.84	0.47	1.00	0.04
rs5999550	*MAPK1*	22	20,481,286	Intron	-	-	G	C	0.45	1.00	0.84	0.47	1.00	0.04
rs2298434	*MAPK1*	22	20,483,239	Intron	-	-	G	A	0.04	1.00	1.00	0.04	1.00	0.12
rs9610355	*MAPK1*	22	20,493,633	Intron	-	-	G	A	0.04	1.00	1.00	0.04	1.00	0.12
rs3788332	*MAPK1*	22	20,501,567	Intron	-	-	A	G	0.45	1.00	0.84	0.47	1.00	0.05
rs5999704	*MAPK1*	22	20,508,791	Intron	-	-	G	T	0.00	1.00	NA	1.24×10^{-3}	1.00	1.00
rs1892848	*MAPK1*	22	20,516,562	Intron	-	-	C	T	0.45	1.00	0.84	0.47	1.00	0.04
rs9610375	*MAPK1*	22	20,517,093	Intron	-	-	G	T	0.49	0.98	0.61	0.48	0.99	0.06
rs5755694	*MAPK1*	22	20,530,530	Intron	-	-	C	T	0.43	1.00	0.76	0.45	1.00	0.02
rs8136867	*MAPK1*	22	20,534,793	Intron	-	-	A	G	0.43	1.00	0.68	0.45	1.00	0.02
rs2876981	*MAPK1*	22	20,535,611	Intron	-	-	A	C	0.42	1.00	0.47	0.39	1.00	0.47
rs9610470	*MAPK1*	22	20,539,139	Intron	-	-	T	C	0.26	1.00	0.05	0.25	1.00	0.60
rs4821401	*MAPK1*	22	20,544,572	Intron	-	-	T	C	0.04	1.00	1.00	0.04	1.00	0.12
rs5755745	*MAPK1*	22	20,550,816	Intron	-	-	T	C	0.04	1.00	1.00	0.04	1.00	0.15
rs5999891	*MAPK1*	22	20,557,038	Flanking 5' UTR	-	-	A	C	0.00	1.00	NA	1.24×10^{-3}	1.00	1.00
rs9612225	*GNAZ*	22	21,736,619	Flanking 5' UTR	-	-	G	A	0.26	0.99	0.44	0.25	1.00	1.00
rs13054331	*GNAZ*	22	21,737,063	Flanking 5' UTR	-	-	G	A	0.26	1.00	0.44	0.25	1.00	0.89
rs9624019	*GNAZ*	22	21,737,301	Flanking 5' UTR	-	-	A	C	0.09	1.00	1.00	0.11	1.00	0.46
rs3788337	*GNAZ*	22	21,742,017	Flanking 5' UTR	-	-	G	A	0.36	1.00	0.83	0.37	1.00	0.67
rs3788339	*GNAZ*	22	21,747,677	Intron	-	-	A	G	0.10	1.00	0.78	0.13	1.00	0.66
rs3788341	*GNAZ*	22	21,747,758	Intron	-	-	A	G	0.47	1.00	0.61	0.49	1.00	0.42
rs9306383	*GNAZ*	22	21,751,058	Intron	-	-	A	C	0.43	0.99	0.41	0.45	1.00	0.69
rs3827315	*GNAZ*	22	21,752,890	Intron	-	-	T	C	0.28	1.00	0.90	0.29	1.00	0.02
rs5751579	*GNAZ*	22	21,759,224	Intron	-	-	C	T	0.26	1.00	0.80	0.28	1.00	0.08
rs1858746	*GNAZ*	22	21,763,804	Intron	-	-	T	C	0.28	0.96	0.80	0.28	0.99	0.14
rs5751583	*GNAZ*	22	21,764,327	Intron	-	-	G	A	0.06	1.00	0.14	0.07	1.00	1.00
rs3810614	*GNAZ*	22	21,767,271	Intron	-	-	G	A	0.28	0.98	0.70	0.29	0.99	0.04
rs739362	*GNAZ*	22	21,774,067	Intron	-	-	G	C	0.27	0.93	0.60	0.28	0.96	0.06
rs2266999	*GNAZ*	22	21,781,775	Intron	-	-	G	C	0.27	1.00	0.80	0.28	0.99	0.08
rs2283802	*GNAZ*	22	21,784,722	Intron	-	-	C	T	0.26	1.00	1.00	0.27	0.99	0.17
rs13054985	*GNAZ*	22	21,788,577	Intron	-	-	A	G	0.44	1.00	0.05	0.44	1.00	0.76
rs885964	*GNAZ*	22	21,791,003	Intron	-	-	C	G	0.44	1.00	0.04	0.43	0.99	0.61
rs5759593	*GNAZ*	22	21,794,457	Intron	-	-	G	A	0.39	1.00	0.02	0.40	1.00	0.18
rs4820537	*GNAZ*	22	21,794,810	Intron	-	-	G	A	0.48	0.99	0.31	0.49	1.00	0.16
rs9612234	*GNAZ*	22	21,797,080	3' UTR	-	-	T	C	0.44	1.00	0.04	0.44	1.00	0.54
rs756632	*GNAZ*	22	21,799,918	Flanking 3' UTR	-	-	C	T	0.15	0.99	0.33	0.13	1.00	0.26
rs9612237	*GNAZ*	22	21,802,954	Flanking 3' UTR	-	-	C	T	0.43	1.00	0.02	0.43	1.00	0.36
rs760973	*PRKCABP*	22	36,777,212	Flanking 5' UTR	-	-	A	C	0.42	1.00	0.21	0.43	1.00	0.54
rs4821733	*PRKCABP*	22	36,779,340	Flanking 5' UTR	-	-	A	G	0.42	1.00	1.00	0.43	1.00	0.19
rs737662	*PRKCABP*	22	36,782,311	Flanking 5' UTR	-	-	C	G	0.31	0.99	0.64	0.33	0.99	0.50
rs3952	*PRKCABP*	22	36,786,544	Intron	-	-	A	G	0.32	1.00	0.73	0.33	1.00	0.37
rs2076370	*PRKCABP*	22	36,793,914	Intron	-	-	G	A	0.39	0.98	0.39	0.38	0.99	0.45
rs760975	*PRKCABP*	22	36,797,730	Intron	-	-	C	G	0.38	0.99	0.39	0.39	1.00	0.60
rs7289911	*PRKCABP*	22	36,798,578	Intron	-	-	G	A	0.02	0.99	1.00	0.03	1.00	1.00
rs2012859	*PRKCABP*	22	36,803,652	Flanking 3' UTR	-	-	G	A	0.30	0.99	0.81	0.29	1.00	0.55
rs2076371	*PRKCABP*	22	36,804,642	Coding Region	Nonsynonymous	V405A (NP_037488)	G	A	0.28	1.00	0.90	0.28	1.00	0.53
rs1004764	*PRKCABP*	22	36,804,798	Intron	-	-	A	G	0.39	1.00	0.53	0.38	1.00	0.67
rs2076372	*PRKCABP*	22	36,804,911	Intron	-	-	C	T	0.28	1.00	0.16	0.25	1.00	1.00
rs8135665	*PRKCABP*	22	36,806,222	Intron	-	-	C	T	0.20	0.99	0.27	0.21	0.99	0.07
rs5756908	*PRKCABP*	22	36,806,525	Intron	-	-	C	T	0.50	1.00	0.36	0.48	1.00	0.92
rs2267366	*PRKCABP*	22	36,810,605	Flanking 3' UTR	-	-	T	C	0.13	1.00	0.66	0.16	1.00	0.58
rs5905613	*MAOA*	X	43,392,244	Flanking 5' UTR	-	-	C	T	0.30	1.00	0.53	0.27	1.00	0.53

									Male			Female		
SNP	**Gene Region**	**Chromosome**	**Position**	**Location**	**Coding Status**	**Amino Acid Change**	**Major Allele**	**Minor Allele**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**	**MAF**	**Call Rate**	**HWE Chi-square Exact P**
rs4824657	*MAOA*	X	43,397,246	Flanking 5' UTR	-	-	C	G	0.30	0.96	0.30	0.27	0.96	0.30
rs3788862	*MAOA*	X	43,402,308	Intron	-	-	G	A	0.30	1.00	0.71	0.27	1.00	0.71
rs5906883	*MAOA*	X	43,411,887	Intron	-	-	C	A	0.30	1.00	1.00	0.28	1.00	1.00
rs1465108	*MAOA*	X	43,423,153	Intron	-	-	G	A	0.30	1.00	0.80	0.28	1.00	0.80
rs5906957	*MAOA*	X	43,432,254	Intron	-	-	G	A	0.26	1.00	0.16	0.23	1.00	0.16
rs909525	*MAOA*	X	43,438,146	Intron	-	-	T	C	0.35	1.00	0.56	0.31	1.00	0.56
rs2283725	*MAOA*	X	43,444,920	Intron	-	-	G	A	0.35	1.00	0.49	0.31	1.00	0.49
rs3027399	*MAOA*	X	43,477,666	Intron	-	-	G	C	0.02	0.99	0.09	0.08	1.00	0.09
rs2205718	*MAOA*	X	43,482,409	Intron	-	-	G	T	0.31	1.00	0.90	0.29	1.00	0.90
rs2072743	*MAOA*	X	43,484,465	Intron	-	-	C	T	0.36	0.99	0.57	0.33	1.00	0.57
rs979606	*MAOA*	X	43,486,086	Intron	-	-	T	C	0.31	1.00	0.90	0.29	1.00	0.90
rs3027409	*MAOA*	X	43,491,977	Flanking 3' UTR	-	-	T	G	0.05	1.00	1.00	0.04	1.00	1.00
rs2064070	*MAOA*	X	43,493,626	Flanking 3' UTR	-	-	T	A	0.31	0.99	0.81	0.30	1.00	0.81
rs6609257	*MAOA*	X	43,497,652	Flanking 3' UTR	-	-	A	G	0.44	1.00	0.26	0.40	1.00	0.26
rs3027415	*MAOA*	X	43,499,385	Flanking 3' UTR	-	-	T	C	0.21	1.00	0.34	0.24	1.00	0.34
rs3027416	*MAOA*	X	43,499,578	Flanking 3' UTR	-	-	A	T	0.00	0.98	1.00	4.98×10^{-3}	1.00	1.00
rs3027421	*MAOB*	X	43,504,669	Flanking 3' UTR	-	-	G	C	0.00	1.00	1.00	7.43×10^{-3}	1.00	1.00
rs3027431	*MAOB*	X	43,508,028	Flanking 3' UTR	-	-	G	A	1.27×10^{-3}	1.00	1.00	9.90×10^{-3}	1.00	1.00
rs12558036	*MAOB*	X	43,508,224	Flanking 3' UTR	-	-	C	G	0.00	1.00	1.00	7.43×10^{-3}	1.00	1.00
rs1040398	*MAOB*	X	43,510,375	Flanking 3' UTR	-	-	A	G	1.27×10^{-3}	1.00	1.00	7.43×10^{-3}	1.00	1.00
rs1799836	*MAOB*	X	43,512,943	Intron	-	-	T	C	0.44	1.00	0.69	0.48	1.00	0.69
rs10521432	*MAOB*	X	43,518,684	Intron	-	-	G	A	0.27	1.00	0.16	0.30	1.00	0.16
rs7888450	*MAOB*	X	43,518,947	Intron	-	-	T	C	1.27×10^{-3}	1.00	1.00	4.95×10^{-3}	1.00	1.00
rs17310637	*MAOB*	X	43,524,923	Intron	-	-	C	G	0.00	1.00	1.00	4.95×10^{-3}	1.00	1.00
rs12007768	*MAOB*	X	43,530,940	Intron	-	-	G	NA	0.00	1.00	NA	0.00	1.00	NA
rs2311013	*MAOB*	X	43,536,455	Intron	-	-	T	A	0.04	1.00	1.00	0.03	1.00	1.00
rs5905449	*MAOB*	X	43,540,597	Intron	-	-	G	A	0.20	0.99	0.35	0.25	1.00	0.35
rs3027459	*MAOB*	X	43,546,221	Intron	-	-	C	NA	0.00	1.00	NA	0.00	1.00	NA
rs736944	*MAOB*	X	43,559,979	Intron	-	-	C	T	0.16	1.00	1.00	0.18	1.00	1.00
rs17146716	*MAOB*	X	43,564,576	Intron	-	-	A	G	1.27×10^{-3}	1.00	1.00	4.95×10^{-3}	1.00	1.00
rs6651806	*MAOB*	X	43,573,908	Intron	-	-	A	C	0.28	1.00	0.25	0.31	1.00	0.25
rs5952795	*MAOB*	X	43,582,223	Intron	-	-	G	NA	0.00	1.00	NA	0.00	1.00	NA
rs4824562	*MAOB*	X	43,588,734	Intron	-	-	T	C	0.15	1.00	1.00	0.16	1.00	1.00
rs5952330	*MAOB*	X	43,589,225	Intron	-	-	A	G	0.00	1.00	1.00	3.71×10^{-3}	1.00	1.00
rs5952799	*MAOB*	X	43,589,787	Intron	-	-	C	T	0.15	0.94	0.71	0.16	0.99	0.71
rs5952813	*MAOB*	X	43,599,701	Intron	-	-	G	C	0.00	1.00	1.00	3.71×10^{-3}	1.00	1.00
rs5952340	*MAOB*	X	43,605,747	Intron	-	-	T	NA	0.00	1.00	NA	0.00	1.00	NA
rs5905512	*MAOB*	X	43,611,338	Intron	-	-	A	G	0.48	1.00	0.69	0.49	1.00	0.69
rs5952352	*MAOB*	X	43,613,532	Intron	-	-	C	G	0.00	1.00	1.00	3.71×10^{-3}	1.00	1.00
rs2070822	*FLNA*	X	153,232,642	Intron	-	-	A	G	0.22	0.96	0.07	0.24	0.96	0.07
rs2070827	*FLNA*	X	153,235,897	Intron	-	-	G	A	0.10	0.97	0.58	0.10	0.99	0.58
rs5945185	*FLNA*	X	153,244,670	Intron	-	-	T	G	0.20	0.96	0.03	0.23	0.98	0.03
rs1064816	*FLNA*	X	153,248,322	Coding Region	Nonsynonymous	V320A (NP_001447)	A	G	0.22	0.93	1.00	0.24	0.95	1.00
rs17428	*FLNA*	X	153,263,157	Flanking 3' UTR	-	-	C	T	0.19	0.97	0.04	0.22	0.98	0.04