Supplementary Online Content

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eTable. Results from logistic regression analyses on grandparental ages and autism risk only including inpatients

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eTable. Results From Logistic Regression Analyses on Grandparental Ages and Autism Risk Only Including Inpatients

SNP	Chromosome	Position	Gene	Location	Coding Status	Amino Acid Change	Major Allele	Minor Allele	MAF	HWE χ^2 Exact Test *P* Value
rs7539745	1	152,793,038	*CHRNB2*	Intron	−1	−1	G	C	0.141	0.239
rs7543174	1	152,794,296	*CHRNB2*	Intron	−1	−1	T	C	0.157	0.422
rs4845652	1	152,804,829	*CHRNB2*	Flanking 5' UTR	−1	−1	C	T	0.0883	0.661
rs2072658	1	152,806,849	*CHRNB2*	Flanking 5' UTR	−1	−1	G	A	0.0163	1
rs2072659	1	152,815,145	*CHRNB2*	3' UTR	−1	−1	C	G	0.104	0.845
rs2072660	1	152,815,345	*CHRNB2*	3' UTR	−1	−1	C	T	0.235	0.0291
rs2072661	1	152,815,504	*CHRNB2*	3' UTR	−1	−1	G	A	0.236	0.0304
rs3811450	1	152,817,656	*CHRNB2*	Flanking 3' UTR	−1	−1	C	T	0.0716	0.42
rs9616	1	152,822,357	*CHRNB2*	3' UTR	−1	−1	A	T	0.283	0.728
rs1127314	1	152,822,890	*CHRNB2*	3' UTR	−1	−1	A	G	0.298	0.128
rs1127313	1	152,823,049	*CHRNB2*	3' UTR	−1	−1	G	A	0.468	0.435
rs2131902	1	152,826,222	*CHRNB2*	Intron	−1	−1	T	C	0.308	0.158
rs3766927	1	152,830,765	*CHRNB2*	Flanking 5' UTR	−1	−1	C	T	0.298	0.128
rs12244716	10	134,978,372	*CALCYON*	Flanking 3' UTR	−1	−1	G	C	0.129	0.754
rs2275723	10	134,989,625	*CALCYON*	Intron	−1	−1	G	A	0.0954	0.836
rs10776672	10	135,007,945	*CALCYON*	Flanking 5' UTR	−1	−1	A	G	0.105	0.449
rs4838721	10	135,010,940	*CALCYON*	Intron	−1	−1	T	C	0.178	0.903
rs7932167	11	610,599	*DRD4*	Intron	−1	−1	T	G	0.22	0.355
rs12280580	11	616,220	*DRD4*	Flanking 3' UTR	−1	−1	C	G	0.288	0.142
rs4987059	11	626,433	*DRD4*	Flanking 5' UTR	−1	−1	G	A	0.0565	0.506
rs936461	11	626,496	*DRD4*	Flanking 5' UTR	−1	−1	G	A	0.358	0.479
rs10902188	11	644,043	*DRD4*	Coding	−1	−1	G	A	0.0877	0.263
rs6598007	11	646,523	*DRD4*	Intron	−1	−1	C	T	0.0595	0.105
rs4963126	11	646,845	*DRD4*	Intron	−1	−1	G	A	0.469	1
rs11603404	11	646,940	*DRD4*	Intron	−1	−1	G	A	0.135	0.223
rs11214589	11	112,750,258	*ANKK1*	Flanking 3' UTR	−1	−1	G	A	0.485	0.0811
rs4938010	11	112,750,776	*ANKK1*	Flanking 3' UTR	−1	−1	A	G	0.143	0.665
rs754672	11	112,754,346	*ANKK1*	Flanking 3' UTR	−1	−1	T	C	0.474	0.722
rs3897584	11	112,754,935	*ANKK1*	Flanking 3' UTR	−1	−1	C	G	0.336	0.204
rs10891545	11	112,763,275	*ANKK1*	Flanking 5' UTR	−1	−1	T	C	0.14	1
rs4938012	11	112,764,864	*ANKK1*	Intron	−1	−1	G	A	0.33	0.336
rs7123797	11	112,767,781	*ANKK1*	Intron	−1	−1	G	A	0.336	0.0566
rs12360992	11	112,768,110	*ANKK1*	Intron	−1	−1	C	A	0.469	0.776
rs4590907	11	112,768,580	*ANKK1*	Intron	−1	−1	T	G	0.137	0.881

rs17115439	11	112,769,482	*ANKK1*	Coding	−1	−1	C	T	0.333	0.426
rs11214596	11	112,769,721	*ANKK1*	Intron	−1	−1	G	C	0.469	0.831
rs4938015	11	112,769,854	*ANKK1*	Intron	−1	−1	C	T	0.332	0.426
rs7118900	11	112,772,031	*ANKK1*	Coding	NONSYN	A239T (NP_848605)	G	A	0.198	0.738
rs4938016	11	112,775,225	*ANKK1*	Coding	NONSYN	G442R (NP_848605)	C	G	0.304	0.867
rs2734849	11	112,775,370	*ANKK1*	Coding	NONSYN	H490R (NP_848605)	G	A	0.5	1
rs2734848	11	112,775,584	*ANKK1*	Coding	SYNON	Y561Y (NP_848605)	T	C	0.16	0.893
rs7104979	11	112,775,688	*ANKK1*	Coding	NONSYN	P596L (NP_848605)	C	T	6.30E−04	1
rs11214601	11	112,777,972	*ANKK1*	Flanking 3' UTR	−1	−1	C	T	0.169	0.707
rs1003641	11	112,778,846	*ANKK1*	Flanking 3' UTR	−1	−1	G	A	0.29	0.931
rs12422191	11	112,779,220	*ANKK1*	Flanking 3' UTR	−1	−1	G	A	0.0816	0.811
rs10891549	11	112,783,657	*ANKK1*	Flanking 3' UTR	−1	−1	C	T	0.461	0.83
rs2734841	11	112,786,986	*ANKK1*	Intron	−1	−1	C	A	0.29	0.797
rs1124491	11	112,787,300	*ANKK1*	Intron	−1	−1	G	A	0.169	0.707
rs1124492	11	112,787,485	*ANKK1*	Intron	−1	−1	C	A	0.114	0.598
rs6277	11	112,788,669	*ANKK1*	Coding	SYNON	P290P (NP_057658)	A	G	0.461	1
rs1076560	11	112,788,898	*ANKK1*	Intron	−1	−1	C	A	0.17	0.707
rs2440390	11	112,792,088	*DRD2*	Intron	−1	−1	C	T	0.122	0.741
rs1079727	11	112,794,392	*DRD2*	Intron	−1	−1	T	C	0.167	0.371
rs2734833	11	112,798,130	*DRD2*	Intron	−1	−1	A	G	0.399	0.823
rs1076562	11	112,801,218	*DRD2*	Intron	−1	−1	G	A	0.236	0.624
rs2471851	11	112,806,279	*DRD2*	Intron	−1	−1	A	C	0.167	0.523
rs7122246	11	112,809,667	*DRD2*	Intron	−1	−1	A	G	0.404	0.768
rs4436578	11	112,811,975	*DRD2*	Intron	−1	−1	T	C	0.123	0.101
rs4587762	11	112,812,103	*DRD2*	Intron	−1	−1	A	G	0.408	0.769
rs4586205	11	112,812,339	*DRD2*	Intron	−1	−1	T	G	0.243	0.7
rs4620755	11	112,814,829	*DRD2*	Intron	−1	−1	G	A	0.119	0.124
rs7125415	11	112,815,891	*DRD2*	Intron	−1	−1	C	T	0.0946	0.409
rs4936270	11	112,823,618	*DRD2*	Intron	−1	−1	C	T	0.0999	0.234
rs4274224	11	112,824,662	*DRD2*	Intron	−1	−1	A	G	0.466	0.831
rs4245148	11	112,825,629	*DRD2*	Intron	−1	−1	C	T	0.101	0.243
rs4460839	11	112,827,006	*DRD2*	Intron	−1	−1	T	C	0.0955	0.146
rs7122454	11	112,832,678	*DRD2*	Intron	−1	−1	G	C	0.148	0.675
rs7131056	11	112,834,984	*DRD2*	Intron	−1	−1	C	A	0.434	0.885
rs11214611	11	112,835,429	*DRD2*	Intron	−1	−1	A	G	0.149	0.677
rs10891552	11	112,838,881	*DRD2*	Intron	−1	−1	A	T	0.0388	0.626
rs4630328	11	112,839,419	*DRD2*	Intron	−1	−1	G	A	0.363	0.647
rs11214613	11	112,840,469	*DRD2*	Intron	−1	−1	G	A	0.0903	0.278
rs4938019	11	112,846,601	*DRD2*	Intron	−1	−1	T	C	0.152	0.891
rs1799978	11	112,851,561	*DRD2*	Flanking 5' UTR	−1	−1	T	C	0.0533	1
rs10891556	11	112,857,971	*DRD2*	Flanking 5' UTR	−1	−1	G	T	0.174	1
rs6589377	11	112,860,946	*DRD2*	Flanking 5' UTR	−1	−1	A	G	0.364	0.703
rs1514246	15	30,106,782	*CHRNA7*	Flanking 5' UTR	−1	−1	C	A	0.256	0.352

rs868437	15	30,111,569	*CHRNA7*	Intron	−1	−1	T	C	0.275	0.479
rs883473	15	30,112,968	*CHRNA7*	Intron	−1	−1	G	A	0.289	0.545
rs4779563	15	30,124,529	*CHRNA7*	Intron	−1	−1	C	T	0.232	1
rs1913456	15	30,133,241	*CHRNA7*	Intron	−1	−1	A	T	0.185	0.557
rs4779969	15	30,136,223	*CHRNA7*	Intron	−1	−1	C	A	0.0477	0.416
rs8027814	15	30,137,964	*CHRNA7*	Intron	−1	−1	A	G	0.274	0.421
rs2175886	15	30,143,239	*CHRNA7*	Intron	−1	−1	T	C	0.448	0.0441
rs11071530	15	30,147,264	*CHRNA7*	Intron	−1	−1	G	A	0.0899	0.127
rs6494211	15	30,164,880	*CHRNA7*	Intron	−1	−1	A	T	0.326	0.0519
rs8033518	15	30,168,901	*CHRNA7*	Intron	−1	−1	G	A	0.0471	0.25
rs2133965	15	30,171,846	*CHRNA7*	Intron	−1	−1	G	A	0.0628	0.229
rs7175581	15	30,172,759	*CHRNA7*	Intron	−1	−1	G	A	0.418	0.512
rs4779565	15	30,177,362	*CHRNA7*	Intron	−1	−1	G	T	0.421	0.513
rs8035668	15	30,178,638	*CHRNA7*	Intron	−1	−1	A	G	0.203	0.827
rs9788657	15	30,182,318	*CHRNA7*	Intron	−1	−1	C	A	0.202	0.741
rs6494223	15	30,183,749	*CHRNA7*	Intron	−1	−1	C	T	0.38	0.822
rs8030315	15	30,184,411	*CHRNA7*	Intron	−1	−1	C	T	0.2	0.912
rs9788679	15	30,186,609	*CHRNA7*	Intron	−1	−1	C	A	0.194	0.571
rs10438342	15	30,189,338	*CHRNA7*	Intron	−1	−1	G	A	0.374	0.762
rs11852956	15	30,190,622	*CHRNA7*	Intron	−1	−1	T	C	0.224	0.185
rs1039394	15	30,195,021	*CHRNA7*	Intron	−1	−1	C	G	0.0581	0.177
rs16956223	15	30,198,075	*CHRNA7*	Intron	−1	−1	G	A	0.163	0.796
rs1392808	15	30,198,807	*CHRNA7*	Intron	−1	−1	C	A	0.16	0.598
rs904952	15	30,206,037	*CHRNA7*	Intron	−1	−1	T	C	0.485	0.776
rs7402321	15	30,207,700	*CHRNA7*	Intron	−1	−1	C	T	0.373	0.218
rs7175359	15	30,212,239	*CHRNA7*	Intron	−1	−1	C	T	0.482	0.62
rs2651418	15	30,226,573	*CHRNA7*	Intron	−1	−1	T	C	0.498	0.355
rs2611605	15	30,228,925	*CHRNA7*	Intron	−1	−1	C	T	0.193	0.82
rs7178176	15	30,231,105	*CHRNA7*	Intron	−1	−1	C	T	0.248	0.506
rs2337980	15	30,231,488	*CHRNA7*	Intron	−1	−1	C	T	0.443	0.35
rs7164518	15	30,249,900	*CHRNA7*	Flanking 3' UTR	−1	−1	A	G	0.174	0.804
rs4275821	15	76,636,596	*CHRNA5*	Flanking 3' UTR	−1	−1	T	C	0.362	0.4
rs2036527	15	76,638,670	*CHRNA5*	Flanking 5' UTR	−1	−1	G	A	0.407	0.66
rs684513	15	76,645,455	*CHRNA5*	Intron	−1	−1	C	G	0.162	1
rs871058	15	76,645,546	*CHRNA5*	Intron	−1	−1	G	A	0.348	0.391
rs667282	15	76,650,527	*CHRNA5*	Intron	−1	−1	T	C	0.182	0.635
rs601079	15	76,656,634	*CHRNA5*	Intron	−1	−1	A	T	0.414	1
rs637137	15	76,661,031	*CHRNA5*	Intron	−1	−1	T	A	0.182	0.635
rs692780	15	76,663,560	*CHRNA5*	Intron	−1	−1	G	C	0.365	0.879
rs555018	15	76,666,297	*CHRNA3;CHRNA5*	Intron	−1	−1	A	G	0.412	1
rs647041	15	76,667,536	*CHRNA3;CHRNA5*	Intron	−1	−1	C	T	0.413	0.884
rs514743	15	76,671,282	*CHRNA3;CHRNA5*	Intron	−1	−1	A	T	0.369	0.82
rs578776	15	76,675,455	*CHRNA3;CHRNA5*	3' UTR	−1	−1	G	A	0.223	0.54

rs6495307	15	76,677,376	*CHRNA3;CHRNA5*	Intron	−1	−1	C	T	0.415	0.942
rs1051730	15	76,681,394	*CHRNA3;CHRNA5*	Coding	SYNON	Y215Y (NP_000734)	G	A	0.396	0.235
rs3743078	15	76,681,814	*CHRNA3;CHRNA5*	Intron	−1	−1	G	C	0.185	0.64
rs1317286	15	76,683,184	*CHRNA3;CHRNA5*	Intron	−1	−1	A	G	0.404	0.659
rs938682	15	76,683,602	*CHRNA3*	Intron	−1	−1	A	G	0.181	0.72
rs4887069	15	76,696,125	*CHRNA3;CHRNB4*	Intron	−1	−1	A	G	0.186	0.64
rs3743075	15	76,696,507	*CHRNA3;CHRNB4*	Coding	SYNON	K97K (NP_000734)	C	T	0.366	1
rs3743073	15	76,696,594	*CHRNA3;CHRNB4*	Intron	−1	−1	T	G	0.37	0.939
rs1878399	15	76,699,058	*CHRNA3;CHRNB4*	Intron	−1	−1	C	G	0.418	0.827
rs6495309	15	76,702,300	*CHRNA3;CHRNB4*	Flanking 3' UTR	−1	−1	C	T	0.172	0.456
rs1948	15	76,704,454	*CHRNA3;CHRNB4*	3' UTR	−1	−1	G	A	0.341	0.53
rs7178270	15	76,708,132	*CHRNA3;CHRNB4*	Intron	−1	−1	C	G	0.392	0.552
rs950776	15	76,713,073	*CHRNB4*	Intron	−1	−1	T	C	0.342	0.694
rs12441998	15	76,716,427	*CHRNB4*	Intron	−1	−1	A	G	0.177	1
rs1316971	15	76,717,565	*CHRNB4*	Intron	−1	−1	G	A	0.177	1
rs11633223	15	76,722,531	*CHRNB4*	Flanking 5' UTR	−1	−1	T	C	0.378	0.291
rs3971872	15	76,729,090	*CHRNB4*	Flanking 5' UTR	−1	−1	C	T	0.0902	0.828
rs4603829	20	61,439,336	*CHRNA4*	Flanking 3' UTR	−1	−1	T	C	0.358	0.442
rs4809538	20	61,440,620	*CHRNA4*	Flanking 3' UTR	−1	−1	G	A	0.227	1
rs4522666	20	61,444,924	*CHRNA4*	Flanking 3' UTR	−1	−1	A	G	0.362	0.939
rs2236196	20	61,448,000	*CHRNA4*	Intron	−1	−1	A	G	0.262	0.784
rs3787137	20	61,449,544	*CHRNA4*	Intron	−1	−1	A	G	0.414	1
rs1044396	20	61,451,578	*CHRNA4*	Coding	SYNON	S543S (NP_000735)	A	G	0.449	0.884
rs755203	20	61,464,708	*CHRNA4*	Flanking 5' UTR	−1	−1	A	G	0.432	1
rs4809549	20	61,472,553	*CHRNA4*	Flanking 5' UTR	−1	−1	G	C	0.476	0.67
rs4485648	22	18,299,405	*COMT*	Intron	−1	−1	T	C	0.188	0.908
rs8140265	22	18,301,641	*COMT*	Flanking 5' UTR	−1	−1	G	A	0.29	0.931
rs8137828	22	18,303,406	*COMT*	Flanking 3' UTR	−1	−1	C	T	0.468	0.831
rs2871047	22	18,306,331	*COMT*	Flanking 5' UTR	−1	−1	G	A	0.0555	0.294
rs6518592	22	18,307,146	*COMT*	Flanking 5' UTR	−1	−1	C	A	0.427	1
rs737865	22	18,310,121	*COMT*	Intron	−1	−1	A	G	0.293	1
rs1544325	22	18,311,668	*COMT*	Intron	−1	−1	G	A	0.43	0.614
rs174675	22	18,314,051	*COMT*	Intron	−1	−1	C	T	0.274	1
rs5993883	22	18,317,638	*COMT*	Intron	−1	−1	G	T	0.479	0.723
rs5992500	22	18,321,947	*COMT*	Intron	−1	−1	C	T	2.50E−03	1
rs7290221	22	18,322,680	*COMT*	Intron	−1	−1	G	C	0.491	1
rs740603	22	18,325,177	*COMT*	Intron	−1	−1	G	A	0.483	0.832
rs4646312	22	18,328,337	*COMT*	Intron	−1	−1	T	C	0.391	0.371
rs165656	22	18,328,863	*COMT*	Intron	−1	−1	C	G	0.475	0.225
rs4633	22	18,330,235	*COMT*	Coding	SYNON	H12H (NP_009294)	T	C	0.482	0.356
rs2239393	22	18,330,428	*COMT*	Flanking 3' UTR	−1	−1	A	G	0.396	0.46
rs4646316	22	18,332,132	*COMT*	Intron	−1	−1	C	T	0.218	0.532
rs165774	22	18,332,561	*COMT*	Intron	−1	−1	G	A	0.322	0.745

rs174696	22	18,333,176	*COMT*	Intron	−1	−1	T	C	0.216	0.677
rs174697	22	18,333,832	*COMT*	Intron	−1	−1	G	A	0.0521	0.467
rs174699	22	18,334,458	*COMT*	Intron	−1	−1	T	C	0.0514	0.458
rs165599	22	18,336,781	*COMT*	Flanking 3' UTR	−1	−1	A	G	0.325	0.375
rs165824	22	18,339,366	*COMT*	Intron	−1	−1	A	G	0.0818	0.0846
rs165815	22	18,339,473	*COMT*	Coding	NONSYN	Q906R (NP_001661)	T	C	0.144	0.474
rs5993891	22	18,339,746	*COMT*	Intron	−1	−1	C	T	0.0569	0.506
rs2240713	22	18,341,101	*COMT*	Intron	−1	−1	C	T	0.0524	0.161
rs887199	22	18,341,955	*COMT*	Intron	−1	−1	G	A	0.145	0.32
rs887200	22	18,343,666	*COMT*	Intron	−1	−1	T	C	0.129	1
rs10934253	3	115,320,474	*DRD3*	Flanking 3' UTR	−1	−1	A	T	0.0219	0.0509
rs1385884	3	115,324,315	*DRD3*	Flanking 3' UTR	−1	−1	T	A	0.428	0.563
rs2087017	3	115,324,703	*DRD3*	Flanking 3' UTR	−1	−1	A	G	0.429	0.613
rs2399496	3	115,328,703	*DRD3*	Flanking 3' UTR	−1	−1	A	T	0.474	0.67
rs2134655	3	115,340,891	*DRD3*	Flanking 3' UTR	−1	−1	C	T	0.273	0.326
rs963468	3	115,345,577	*DRD3*	Flanking 3' UTR	−1	−1	G	A	0.388	0.551
rs324035	3	115,351,544	*DRD3*	Intron	−1	−1	C	A	0.197	0.372
rs3773679	3	115,352,025	*DRD3*	Intron	−1	−1	C	T	0.386	0.823
rs3773678	3	115,352,768	*DRD3*	Intron	−1	−1	G	A	0.143	0.02
rs2630349	3	115,356,062	*DRD3*	Intron	−1	−1	G	A	0.0634	2.70E−03
rs2630350	3	115,357,686	*DRD3*	Intron	−1	−1	C	T	0.0633	2.70E−03
rs167771	3	115,358,965	*DRD3*	Intron	−1	−1	A	G	0.176	0.463
rs324032	3	115,360,518	*DRD3*	Intron	−1	−1	A	G	0.0639	3.10E−03
rs167770	3	115,362,252	*DRD3*	Intron	−1	−1	A	G	0.281	0.38
rs7625282	3	115,364,217	*DRD3*	Intron	−1	−1	A	G	0.259	0.52
rs324029	3	115,364,313	*DRD3*	Intron	−1	−1	G	A	0.282	0.432
rs7633291	3	115,369,758	*DRD3*	Intron	−1	−1	T	G	0.205	0.233
rs324022	3	115,369,988	*DRD3*	Intron	−1	−1	G	A	0.282	0.337
rs1486009	3	115,371,222	*DRD3*	Intron	−1	−1	A	G	0.0545	1
rs6280	3	115,373,505	*DRD3*	Coding	NONSYN	S9G (NP_387509)	T	C	0.335	1
rs324026	3	115,373,732	*DRD3*	Flanking 5' UTR	−1	−1	T	C	0.33	0.873
rs7638876	3	115,376,990	*DRD3*	Flanking 3' UTR	−1	−1	T	C	0.339	0.812
rs9825563	3	115,382,910	*DRD3*	Flanking 5' UTR	−1	−1	A	G	0.315	0.25
rs12639080	3	115,386,481	*DRD3*	Flanking 5' UTR	−1	−1	G	A	0.344	0.695
rs7655090	4	9,374,973	*DRD5*	Flanking 5' UTR	−1	−1	A	G	0.318	0.935
rs10939514	4	9,382,294	*DRD5*	Flanking 5' UTR	−1	−1	T	C	0.0476	0.25
rs10939515	4	9,382,394	*DRD5*	Flanking 5' UTR	−1	−1	G	A	0.17	0.21
rs10033951	4	9,388,678	*DRD5*	Flanking 5' UTR	−1	−1	C	T	0.31	1
rs2867383	4	9,397,033	*DRD5*	Flanking 3' UTR	−1	−1	G	A	0.319	0.626
rs1850744	4	9,399,810	*DRD5*	Flanking 3' UTR	−1	−1	C	T	0.0475	0.251
rs13106539	4	9,406,801	*DRD5*	Flanking 3' UTR	−1	−1	T	C	0.38	0.259
rs1519097	4	9,411,951	*DRD5*	Flanking 3' UTR	−1	−1	A	G	0.33	0.199
rs11954565	5	174,782,513	*DRD1*	Flanking 3' UTR	−1	−1	A	G	0.348	0.433

rs1587176	5	174,783,796	*DRD1*	Flanking 3' UTR	−1	−1	T	G	0.172	0.531
rs1310277	5	174,786,176	*DRD1*	Flanking 3' UTR	−1	−1	G	A	0.128	1
rs11739696	5	174,789,227	*DRD1*	Flanking 3' UTR	−1	−1	G	A	0.37	0.363
rs2453737	5	174,791,508	*DRD1*	Flanking 3' UTR	−1	−1	T	C	0.372	0.197
rs6881740	5	174,791,768	*DRD1*	Flanking 3' UTR	−1	−1	C	G	0.355	0.245
rs11742274	5	174,792,103	*DRD1*	Flanking 3' UTR	−1	−1	C	G	0.192	0.649
rs265971	5	174,793,017	*DRD1*	Flanking 3' UTR	−1	−1	T	C	0.284	0.0811
rs265972	5	174,793,122	*DRD1*	Flanking 3' UTR	−1	−1	A	G	0.473	0.523
rs265973	5	174,793,305	*DRD1*	Flanking 3' UTR	−1	−1	C	T	0.451	0.1
rs265974	5	174,793,846	*DRD1*	Flanking 3' UTR	−1	−1	A	G	0.342	0.431
rs265975	5	174,794,801	*DRD1*	Flanking 3' UTR	−1	−1	C	T	0.344	0.814
rs265976	5	174,795,026	*DRD1*	Flanking 3' UTR	−1	−1	G	T	0.189	0.73
rs10476156	5	174,795,276	*DRD1*	Flanking 3' UTR	−1	−1	A	G	0.151	0.783
rs265977	5	174,795,863	*DRD1*	Flanking 3' UTR	−1	−1	C	T	0.172	0.71
rs863126	5	174,795,954	*DRD1*	Flanking 3' UTR	−1	−1	A	T	0.323	0.628
rs835616	5	174,796,296	*DRD1*	Flanking 3' UTR	−1	−1	G	A	0.365	0.125
rs835540	5	174,796,497	*DRD1*	Flanking 3' UTR	−1	−1	T	C	0.256	2.60E−06
rs4867796	5	174,798,127	*DRD1*	Flanking 3' UTR	−1	−1	A	C	0.17	0.45
rs11746641	5	174,798,697	*DRD1*	Flanking 3' UTR	−1	−1	T	G	0.163	0.796
rs11749676	5	174,798,904	*DRD1*	Flanking 3' UTR	−1	−1	G	A	0.409	0.0102
rs5326	5	174,802,802	*DRD1*	Intron	−1	−1	C	T	0.132	0.644
rs2168631	5	174,808,608	*DRD1*	Flanking 5' UTR	−1	−1	G	A	0.175	0.712
rs6878159	5	174,809,007	*DRD1*	Flanking 5' UTR	−1	−1	A	T	0.0113	1
rs267417	5	174,813,120	*DRD1*	Flanking 5' UTR	−1	−1	G	T	0.4	0.039
rs2471005	5	174,814,813	*DRD1*	Flanking 5' UTR	−1	−1	G	A	0.4	0.0649
rs267400	5	174,815,305	*DRD1*	Flanking 5' UTR	−1	−1	C	T	0.418	1
rs11749035	5	174,815,658	*DRD1*	Flanking 5' UTR	−1	−1	C	T	0.16	0.511
rs267405	5	174,817,158	*DRD1*	Flanking 5' UTR	−1	−1	G	T	0.418	1
rs267406	5	174,817,347	*DRD1*	Flanking 5' UTR	−1	−1	G	T	0.418	1
rs10042051	5	174,819,467	*DRD1*	Flanking 5' UTR	−1	−1	A	G	0.0132	1
rs4733065	8	27,363,921	*CHRNA2*	Intron	−1	−1	G	A	0.461	0.283
rs2278319	8	27,364,878	*CHRNA2*	Intron	−1	−1	C	T	0.247	0.254
rs1106359	8	27,365,256	*CHRNA2*	Intron	−1	−1	T	C	0.41	0.242
rs1879184	8	27,367,620	*CHRNA2*	Coding	SYNON	T876T (NP_775268)	C	T	0.133	0.76
rs10093964	8	27,367,957	*CHRNA2*	Intron	−1	−1	C	T	0.419	0.19
rs1879182	8	27,371,793	*CHRNA2*	Coding	SYNON	A960A (NP_775268)	G	A	0.133	0.76
rs748283	8	27,373,112	*CHRNA2*	Flanking 3' UTR	−1	−1	C	A	0.491	0.138
rs1057137	8	27,373,362	*CHRNA2*	Flanking 3' UTR	−1	−1	G	T	0.395	0.413
rs735421	8	27,375,209	*CHRNA2*	Intron	−1	−1	A	G	0.304	0.867
rs891394	8	27,375,686	*CHRNA2*	Intron	−1	−1	C	G	0.263	0.201
rs3735757	8	27,377,514	*CHRNA2*	Intron	−1	−1	C	G	0.133	1
rs2322581	8	27,379,524	*CHRNA2*	Intron	−1	−1	T	G	0.162	1
rs891398	8	27,380,739	*CHRNA2*	Coding	NONSYN	T125A (NP_000733)	T	C	0.474	0.887

rs891399	8	27,381,340	*CHRNA2*	Intron	−1	−1	G	A	0.129	0.532
rs2565062	8	27,381,857	*CHRNA2*	Intron	−1	−1	G	A	0.129	0.635
rs2472554	8	27,384,271	*CHRNA2*	Intron	−1	−1	C	G	0.306	0.244
rs2472553	8	27,384,428	*CHRNA2*	Coding	NONSYN	T22I (NP_000733)	G	A	0.128	0.634
rs7815010	8	27,386,013	*CHRNA2*	Intron	−1	−1	C	T	0.249	0.925
rs2741339	8	27,390,886	*CHRNA2*	Intron	−1	−1	A	G	0.268	0.719
rs2565059	8	27,392,895	*CHRNA2*	Flanking 5' UTR	−1	−1	G	A	0.184	0.813
rs2565055	8	27,393,297	*CHRNA2*	Flanking 5' UTR	−1	−1	G	T	0.241	0.771
rs2741335	8	27,393,708	*CHRNA2*	Flanking 5' UTR	−1	−1	A	C	0.264	0.928
rs6558000	8	27,395,271	*CHRNA2*	Flanking 5' UTR	−1	−1	T	C	0.0746	0.612
rs7017417	8	27,401,222	*CHRNA2*	Flanking 5' UTR	−1	−1	A	G	0.101	0.435
rs9314348	8	27,401,343	*CHRNA2*	Flanking 5' UTR	−1	−1	T	C	0.102	0.44
rs7003694	8	27,403,111	*CHRNA2*	Flanking 5' UTR	−1	−1	T	C	0.0921	0.529
rs7017612	8	42,718,402	*CHRNA6;CHRNB3*	Flanking 3' UTR	−1	−1	A	C	0.197	0.655
rs9298628	8	42,725,148	*CHRNA6*	Flanking 3' UTR	−1	−1	C	T	0.195	0.822
rs2304297	8	42,727,356	*CHRNA6*	3' UTR	−1	−1	G	C	0.229	1
rs2196128	8	42,737,443	*CHRNA6*	Intron	−1	−1	T	C	0.216	1
rs16891620	8	42,744,820	*CHRNA6*	Flanking 5' UTR	−1	−1	C	A	0.112	0.859
rs10107450	8	42,749,052	*CHRNA6*	Flanking 5' UTR	−1	−1	C	T	0.222	0.918
rs6474419	8	42,754,456	*CHRNA6*	Flanking 5' UTR	−1	−1	A	G	0.0357	0.619

Abbreviations: HWE, Hardy-Weinberg equilibrium; MAF, minor allele frequency; SNP, single-nucleotide polymorphism; UTR, untranslated region.