

SUPPLEMENTARY MATERIAL [ONLINE ONLY]

Cholinergic Nicotinic Receptor Genes Implicated in a Nicotine Dependence Association Study Targeting 348 Candidate Genes with 3,713 SNPs

DNA Preparation. DNA was extracted from whole blood and EBV transformed cell lines on an AutoPure LS automated DNA extractor using the PuraGene Reagent System (GENTRA Systems). RNase was added to the WBC lysis stage with isopropanol precipitation of the DNA and resuspension in 1X TE Buffer (pH 8.0). DNA was quantified by optical density (OD) at 260nm on a DU-640 spectrophotometer (Beckman) and OD 260/280 absorbance ratios were between 1.8-2.0. DNA was aliquoted and stored frozen at -80⁰C until distributed to the genotyping labs.

Individual Genotype Cleaning. Concordance is computed independently for both reference and alternate allele feature sets, then a maximum is taken of the two values. For each allele at each offset for both the forward and reverse strand feature sets the identity of the brightest feature is noted. The concordance for a particular allele is computed as a ratio of the number of times the perfect match feature is the brightest to the total number of offsets over the forward and reverse strands. In the 24 feature SNP tiling each allele is represented by 6 features, distributed along 5 offsets and forward and reverse strands, with five perfect match probes and one mismatch. If N_{PM}^X is the number of times for allele X when the perfect match feature was brighter than the mismatch feature over all offsets and both strands, then:

$$concordance = \max\left(\frac{N_{PM}^{Ref}}{10}, \frac{N_{PM}^{Alt}}{10}\right)$$

SNP feature sets with concordance < 0.9 were discarded from further evaluation.

Let I^{TM} be the trimmed mean of perfect match intensities for a given allele and strand denoted by the subscript. The trimmed mean disregards the highest and the lowest intensity from the 5 perfect match intensities in the 24-feature tilings before computing the arithmetic mean. Let I^M be the mean of the mismatch intensity; since there is only one mismatch for each allele and strand no trimming is performed. We then define signal to background ratio (signal/background) to be the ratio between the amplitude of signal, computed from trimmed means of perfect match feature intensities, and amplitude of background, computed from means of mismatch feature intensities. The signal and background are computed as follows:

$$\text{signal} = \sqrt{((I_{PM,\text{Ref},\text{Fwd}}^{TM} + I_{PM,\text{Ref},\text{Rev}}^{TM})/2)^2 + ((I_{PM,\text{Alt},\text{Fwd}}^{TM} + I_{PM,\text{Alt},\text{Rev}}^{TM})/2)^2}$$

$$\text{background} = \sqrt{((I_{MM,\text{Ref},\text{Fwd}}^M + I_{MM,\text{Ref},\text{Rev}}^M)/2)^2 + ((I_{MM,\text{Alt},\text{Fwd}}^M + I_{MM,\text{Alt},\text{Rev}}^M)/2)^2}$$

SNP feature sets with signal/background < 1.5 were discarded from further evaluations. The number of saturated features was computed as the number of features that reached the highest intensity possible for the digitized numeric intensity value. SNPs with a nonzero number of saturated features were discarded from further evaluations.

As a final test, SNPs were tested for Hardy-Weinberg equilibrium (HWE). Those SNPs with an exact HWE p -value of less than 10^{-15} in either the cases or controls were discarded. SNPs with a HWE p -value between 10^{-15} and 10^{-4} were visually inspected and were discarded when problems with clustering were detected.

Table S1. Gender-specific odds ratios and 95% confidence intervals for SNPs in table 2. The odds ratios are based on the coefficient of the genotype term G in equation (2) and represent the increase in risk for every unit increase in G ; i.e., the risk follows a log-linear model (see table 8).

SNP	Gene	Primary p-value	Rank	Gender * Genotype p-value	Male OR	Female OR
rs6474413	<i>CHRNB3</i>	9.36E-05	1	1.12E-01	1.2 (0.9-1.5)	1.5 (1.3-1.9)
rs10958726	<i>CHRNB3</i>	1.33E-04	2	1.04E-01	1.2 (0.9-1.5)	1.5 (1.2-1.9)
rs578776	<i>CHRNA3</i>	3.08E-04	3	4.12E-01	1.5 (1.2-1.9)	1.3 (1.1-1.6)
rs6517442	<i>KCNJ6</i>	5.62E-04	4	6.17E-01	1.4 (1.1-1.7)	1.3 (1.1-1.5)
rs16969968	<i>CHRNA5</i>	6.42E-04	5	8.13E-01	1.3 (1.1-1.7)	1.3 (1.1-1.5)
rs3762611	<i>GABRA4</i>	9.22E-04	6	7.50E-02	2.1 (1.4-3.2)	1.3 (0.9-1.8)
rs1051730	<i>CHRNA3</i>	9.93E-04	7	1.00E+00	1.3 (1.0-1.6)	1.3 (1.1-1.5)
rs10508649	<i>PIP5K2A</i>	1.02E-03	8	1.09E-02	9.7 (2.1-44.2)	1.0 (0.3-3.1)
rs17041074	<i>DAO</i>	1.12E-03	9	3.70E-04	0.8 (0.6-1.0)	1.3 (1.1-1.6)
rs3762607	<i>GABRA4</i>	1.22E-03	10	3.43E-02	2.2 (1.4-3.3)	1.2 (0.9-1.6)
rs2767	<i>CHRND</i>	1.50E-03	11	1.08E-01	1.5 (1.2-1.8)	1.1 (1.0-1.4)
rs6772197	<i>DOCK3 (GRM2)</i>	1.66E-03	12	6.35E-04	1.6 (1.2-2.2)	0.9 (0.7-1.1)
rs3021529	<i>AVPRIA</i>	1.73E-03	13	8.96E-04	0.8 (0.5-1.0)	1.5 (1.1-1.9)
rs1206549	<i>CLTCL1</i>	1.75E-03	14	9.11E-01	1.4 (1.1-1.9)	1.4 (1.1-1.7)
rs637137	<i>CHRNA5</i>	2.82E-03	22	3.18E-01	1.5 (1.1-1.9)	1.2 (1.0-1.5)
rs3791729	<i>CHRND</i>	3.39E-03	25	3.10E-01	1.4 (1.1-1.7)	1.2 (1.0-1.4)
rs4531	<i>DBH</i>	5.10E-03	30	9.11E-01	1.5 (1.0-2.1)	1.5 (1.1-2.0)
rs3025382	<i>DBH</i>	5.14E-03	31	1.82E-01	1.6 (1.2-2.3)	1.2 (0.9-1.6)
rs7877	<i>FMO1</i>	6.33E-03	38	8.81E-01	1.3 (1.0-1.6)	1.3 (1.1-1.6)
rs6320	<i>HTR5A</i>	6.50E-03	39	1.61E-03	0.7 (0.6-1.0)	1.2 (1.0-1.5)
rs4802100	<i>CYP2B6</i>	6.76E-03	41	2.82E-02	0.9 (0.6-1.4)	1.6 (1.2-2.1)
rs2304297	<i>CHRNA6</i>	6.91E-03	42	1.59E-01	1.1 (0.8-1.4)	1.4 (1.1-1.7)
rs3760657	<i>CYP2B6</i>	6.98E-03	43	3.38E-02	0.9 (0.7-1.4)	1.6 (1.2-2.1)
rs2276560	<i>CHRNG</i>	7.42E-03	44	8.58E-02	1.5 (1.1-1.9)	1.1 (0.9-1.3)
rs742350	<i>FMO1</i>	8.45E-03	48	2.67E-01	1.2 (0.9-1.6)	1.5 (1.1-1.9)
rs684513	<i>CHRNA5</i>	8.72E-03	49	1.72E-01	1.5 (1.1-1.9)	1.2 (0.9-1.4)
rs510769	<i>OPRM1</i>	9.84E-03	58	1.38E-01	1.1 (0.8-1.4)	1.3 (1.1-1.6)
rs4245150	<i>DRD2</i>	1.08E-02	61	2.79E-03	0.8 (0.6-1.0)	1.2 (1.0-1.4)
rs3743078	<i>CHRNA3</i>	1.10E-02	63	1.54E-01	1.5 (1.1-2.0)	1.2 (0.9-1.4)
rs1657273	<i>HTR5A</i>	1.11E-02	64	3.06E-03	0.8 (0.6-1.0)	1.2 (1.0-1.5)
rs17602038	<i>DRD2</i>	1.17E-02	69	3.13E-03	0.8 (0.6-1.0)	1.2 (1.0-1.4)
rs3813567	<i>CHRNB4</i>	1.18E-02	70	9.10E-02	1.5 (1.1-2.0)	1.1 (0.9-1.4)

<i>rs893109</i>	<i>HTR5A</i>	1.24E-02	73	3.46E-03	0.8 (0.6-1.0)	1.2 (1.0-1.5)
<i>rs16864387</i>	<i>FMO4</i>	1.28E-02	74	3.82E-01	1.2 (0.9-1.7)	1.4 (1.1-1.9)
<i>rs6045733</i>	<i>PDYN</i>	1.55E-02	84	4.25E-03	1.3 (1.1-1.7)	0.9 (0.7-1.0)
<i>rs4953</i>	<i>CHRNB3</i>	1.61E-02	85	1.00E+00	1.6 (0.9-2.8)	1.7 (1.1-2.5)
<i>rs4952</i>	<i>CHRNB3</i>	1.63E-02	87	1.00E+00	1.6 (0.9-2.8)	1.7 (1.1-2.5)
<i>rs6749955</i>	<i>CHRNG</i>	1.70E-02	91	1.67E-01	1.4 (1.1-1.8)	1.1 (0.9-1.4)
<i>rs7517376</i>	<i>FMO1</i>	1.80E-02	95	3.78E-01	1.2 (0.9-1.6)	1.4 (1.1-1.8)

Table S2. Top associations with nicotine dependence showing results from the primary analysis side by side with results based on the U.S. sample only. The conventions are the same as for table 2.

SNP	Gene	Function	Cat ^a	Risk Allele	US-only Risk Allele	Primary p-value	US-only p-value	Primary Rank	US-only Rank	Primary FDR	US-only FDR
rs6474413	<i>CHRN B3</i>	<i>FP</i>	A	T (0.81/0.76)	T (0.81/0.76)	9.36E-05	3.23E-03	1	19	0.056	0.228
rs10958726	<i>CHRN B3</i>	<i>LD BIN</i>	A	T (0.81/0.76)	T (0.81/0.77)	1.33E-04	4.69E-03	2	27	0.056	0.228
rs578776	<i>CHRNA3</i>	<i>UTR</i>	A	G (0.78/0.72)	G (0.78/0.71)	3.08E-04	8.48E-05	3	1	0.086	0.071
rs6517442	<i>KCNJ6</i>	<i>FP</i>	B	C (0.34/0.28)	C (0.35/0.28)	5.62E-04	6.93E-04	4	5	0.344	0.228
rs16969968	<i>CHRNA5</i>	<i>NONSYN</i>	A	A (0.38/0.32)	A (0.38/0.32)	6.42E-04	7.32E-04	5	7	0.134	0.176
rs3762611	<i>GABRA4</i>	<i>FP</i>	B	G (0.93/0.91)	G (0.94/0.91)	9.22E-04	5.29E-03	6	31	0.344	0.533
rs1051730	<i>CHRNA3</i>	<i>SYNON</i>	A	A (0.38/0.32)	A (0.38/0.32)	9.93E-04	8.41E-04	7	10	0.166	0.176
rs10508649	<i>PIP5K2A</i>	<i>SYNON</i>	B	T (1.00/0.99)	T (1.00/0.99)	1.02E-03	3.44E-04	8	2	0.344	0.228
rs17041074	<i>DAO</i>	<i>INTRON</i>	B	A (0.27/0.26)	A (0.27/0.27)	1.12E-03	1.90E-03	9	13	0.344	0.349
rs3762607	<i>GABRA4</i>	<i>FP</i>	B	A (0.93/0.91)	A (0.94/0.91)	1.22E-03	6.16E-03	10	40	0.344	0.565
rs2767	<i>CHRND</i>	<i>UTR</i>	A	G (0.39/0.34)	G (0.39/0.34)	1.50E-03	4.87E-03	11	28	0.209	0.228
rs6772197	(<i>GRM2</i>)	<i>INTRON</i>	B	A (0.84/0.83)	A (0.85/0.83)	1.66E-03	7.39E-03	12	47	0.384	0.599
rs3021529	<i>AVPRIA</i>	<i>UTR</i>	B	G (0.86/0.85)	G (0.87/0.86)	1.73E-03	5.96E-02	13	298	0.384	0.867
rs1206549	<i>CLTC L1</i>	<i>INTRON</i>	B	G (0.86/0.82)	G (0.87/0.82)	1.75E-03	4.35E-04	14	3	0.384	0.228
rs637137	<i>CHRNA5</i>	<i>INTRON</i>	A	T (0.81/0.76)	T (0.80/0.75)	2.82E-03	2.80E-03	22	16	0.336	0.228
rs3791729	<i>CHRND</i>	<i>INTRON</i>	A	A (0.36/0.32)	A (0.37/0.32)	3.39E-03	1.70E-02	25	113	0.344	0.325
rs4531	<i>DBH</i>	<i>NONSYN</i>	A	G (0.93/0.91)	G (0.93/0.91)	5.10E-03	2.34E-02	30	143	0.344	0.383
rs3025382	<i>DBH</i>	<i>INTRON</i>	A	G (0.9/0.88)	G (0.92/0.88)	5.14E-03	8.17E-04	31	9	0.344	0.176
rs7877	<i>FMO1</i>	<i>UTR</i>	A	C (0.74/0.70)	C (0.74/0.70)	6.33E-03	8.46E-03	38	59	0.344	0.228
rs6320	<i>HTR5A</i>	<i>SYNON</i>	A	T (0.72/0.71)	T (0.72/0.71)	6.50E-03	6.04E-03	39	38	0.344	0.228
rs4802100	<i>CYP2A7P1</i>	<i>FP</i>	A	G (0.10/0.08)	G (0.10/0.09)	6.76E-03	5.28E-02	41	263	0.344	0.533
rs2304297	<i>CHRNA6</i>	<i>UTR</i>	A	G (0.79/0.75)	G (0.79/0.75)	6.91E-03	1.38E-02	42	95	0.344	0.295
rs3760657	<i>CYP2A7P1</i>	<i>FP</i>	A	G (0.10/0.08)	G (0.10/0.09)	6.98E-03	5.50E-02	43	277	0.344	0.540
rs2276560	<i>CHRNG</i>	<i>LD BIN</i>	A	T (0.77/0.74)	T (0.77/0.74)	7.42E-03	1.04E-02	44	72	0.344	0.256
rs742350	<i>FMO1</i>	<i>SYNON</i>	A	C (0.87/0.84)	C (0.87/0.84)	8.45E-03	5.51E-03	48	33	0.344	0.228
rs684513	<i>CHRNA5</i>	<i>INTRON</i>	A	C (0.82/0.78)	C (0.81/0.77)	8.72E-03	8.15E-03	49	54	0.344	0.228
rs510769	<i>OPRM1</i>	<i>INTRON</i>	A	T (0.27/0.24)	T (0.27/0.24)	9.84E-03	2.84E-02	58	167	0.344	0.410
rs4245150	<i>DRD2</i>	<i>LD BIN</i>	A	G (0.37/0.36)	G (0.37/0.36)	1.08E-02	1.29E-02	61	87	0.344	0.284
rs3743078	<i>CHRNA3</i>	<i>INTRON</i>	A	G (0.83/0.79)	G (0.82/0.79)	1.10E-02	1.98E-02	63	128	0.344	0.349
rs1657273	<i>HTR5A</i>	<i>LD BIN</i>	A	G (0.69/0.68)	G (0.69/0.68)	1.11E-02	7.74E-03	64	50	0.344	0.228
rs17602038	<i>DRD2</i>	<i>LD BIN</i>	A	C (0.37/0.36)	C (0.37/0.36)	1.17E-02	1.43E-02	69	98	0.344	0.298
rs3813567	<i>CHRN B4</i>	<i>FP</i>	A	A (0.83/0.79)	A (0.83/0.79)	1.18E-02	1.18E-02	70	81	0.344	0.274
rs893109	<i>HTR5A</i>	<i>LD BIN</i>	A	G (0.69/0.68)	G (0.69/0.68)	1.24E-02	7.84E-03	73	52	0.344	0.228

<i>rs16864387</i>	<i>FMO4</i>	<i>UTR</i>	A	T (0.87/0.84)	T (0.88/0.84)	1.28E-02	7.58E-03	74	48	0.344	0.228
<i>rs6045733</i>	<i>PDYN</i>	<i>LD BIN</i>	A	G (0.66/0.65)	G (0.66/0.65)	1.55E-02	1.56E-02	84	108	0.384	0.318
<i>rs4953</i>	<i>CHRN B3</i>	<i>SYNON</i>	A	G (0.97/0.95)	G (0.97/0.95)	1.61E-02	2.67E-02	85	160	0.384	0.410
<i>rs4952</i>	<i>CHRN B3</i>	<i>SYNON</i>	A	C (0.97/0.95)	C (0.97/0.95)	1.63E-02	2.71E-02	87	163	0.384	0.410
<i>rs6749955</i>	<i>CHRNG</i>	<i>LD BIN</i>	A	T (0.77/0.73)	T (0.77/0.73)	1.70E-02	2.09E-02	91	135	0.384	0.349
<i>rs7517376</i>	<i>FMO1</i>	<i>SYNON</i>	A	A (0.87/0.84)	A (0.88/0.84)	1.80E-02	7.74E-03	95	51	0.384	0.228

^aCategory.

Table S3. Top associations with nicotine dependence based on the U.S. sample only. The *p*-value for the U.S. sample uses the same logistic regression model as for the primary analysis with the “site” term omitted. Only results where the weighted FDR in the U.S. sample is less than 40% are shown. LD estimates used for bins are from the U.S. sample. The conventions are the same as for table 2.

SNP	Gene	Function	Cat ^a	LD Bin ID	Min r^2	U.S.-only Risk Allele	U.S.-only p-value	Primary p-value	U.S.-only Rank	Primary Rank	U.S.-only FDR	Primary FDR
rs578776	<i>CHRNA3</i>	UTR	A	.		G (0.78/0.71)	8.48E-05	3.08E-04	1	3	0.071	0.086
rs10508649	<i>PIP5K2A</i>	SYNON	B	.		T (1.00/0.99)	3.44E-04	1.02E-03	2	8	0.228	0.344
rs1206549	<i>CLTCL1</i>	INTRON	B	22-5	0.994	G (0.87/0.82)	4.35E-04	1.75E-03	3	14	0.228	0.384
rs807429	<i>CLTCL1</i>	INTRON	B	22-5	0.994	A (0.87/0.82)	4.89E-04	1.93E-03	4	15	0.228	0.402
rs6517442	<i>KCNJ6</i>	FP	B	.		C (0.35/0.28)	6.93E-04	5.62E-04	5	4	0.228	0.344
rs2180529	<i>SNX5</i>	LD BIN	B	20-6	0.920	T (0.30/0.27)	7.28E-04	4.87E-03	6	28	0.228	0.505
rs16969968	<i>CHRNA5</i>	NONSYN	A	15-12	0.989	A (0.38/0.32)	7.32E-04	6.42E-04	7	5	0.176	0.134
rs10246819	<i>CHRM2</i>	LD BIN	B	7-49	0.867	C (0.56/0.54)	7.99E-04	3.33E-03	8	24	0.228	0.471
rs3025382	<i>DBH</i>	INTRON	A	.		G (0.92/0.88)	8.17E-04	5.14E-03	9	31	0.176	0.344
rs1051730	<i>CHRNA3</i>	SYNON	A	15-12	0.989	A (0.38/0.32)	8.41E-04	9.93E-04	10	7	0.176	0.166
rs1061418	<i>GABRE</i>	UTR	B	.		A (0.14/0.12)	8.43E-04	6.15E-03	11	36	0.228	0.570
rs1378650	<i>CHRM2</i>	LD BIN	B	.		G (0.56/0.51)	1.67E-03	1.78E-02	12	93	0.325	0.744
rs17041074	<i>DAO</i>	INTRON	B	.		A (0.27/0.27)	1.90E-03	1.12E-03	13	9	0.349	0.344
rs17636651	<i>CAMK2D</i>	FP	B	.		G (0.95/0.93)	2.02E-03	1.39E-02	14	79	0.349	0.693
rs3803431	<i>ALDH1A3</i>	SYNON	B	.		C (0.97/0.95)	2.51E-03	2.78E-02	15	137	0.398	0.783
rs637137	<i>CHRNA5</i>	INTRON	A	15-3	0.805	T (0.80/0.75)	2.80E-03	2.82E-03	16	22	0.228	0.336
rs16143	<i>NPY</i>	UTR	A	7-1	0.803	T (0.28/0.26)	3.21E-03	2.49E-02	18	126	0.228	0.446
rs6474413	<i>CHRNB3</i>	FP	A	8-21	0.988	T (0.81/0.76)	3.23E-03	9.36E-05	19	1	0.228	0.056
rs16142	<i>NPY</i>	UTR	A	7-1	0.803	G (0.28/0.26)	4.46E-03	3.31E-02	26	173	0.228	0.471
rs10958726	<i>CHRNB3</i>	LD BIN	A	8-21	0.988	T (0.81/0.77)	4.69E-03	1.33E-04	27	2	0.228	0.056
rs2767	<i>CHRND</i>	UTR	A	2-68	0.877	G (0.39/0.34)	4.87E-03	1.50E-03	28	11	0.228	0.209
rs16478	<i>NPY</i>	UTR	A	7-1	0.803	A (0.28/0.26)	5.31E-03	3.80E-02	32	194	0.228	0.495
rs742350	<i>FMO1</i>	SYNON	A	1-7	0.974	C (0.87/0.84)	5.51E-03	8.45E-03	33	48	0.228	0.344
rs2302761	<i>CHRNBI</i>	INTRON	A	17-8	0.933	C (0.83/0.78)	5.64E-03	4.61E-02	34	238	0.228	0.504
rs7210231	<i>CHRNBI</i>	INTRON	A	17-8	0.933	C (0.82/0.77)	5.74E-03	4.18E-02	35	218	0.228	0.498
rs6320	<i>HTR5A</i>	SYNON	A	.		T (0.72/0.71)	6.04E-03	6.50E-03	38	39	0.228	0.344
rs16149	<i>NPY</i>	FP	A	7-1	0.803	A (0.28/0.26)	6.12E-03	3.51E-02	39	183	0.228	0.480
rs16138	<i>NPY</i>	INTRON	A	.		C (0.28/0.26)	6.19E-03	4.42E-02	41	227	0.228	0.504
rs2236196	<i>CHRNA4</i>	UTR	A	.		G (0.28/0.23)	6.68E-03	2.63E-02	42	132	0.228	0.446
rs16864387	<i>FMO4</i>	UTR	A	1-7	0.974	T (0.88/0.84)	7.58E-03	1.28E-02	48	74	0.228	0.344

<i>rs1657273</i>	<i>HTR5A</i>	<i>LD BIN</i>	A	7-29	0.974 G (0.69/0.68)	7.74E-03	1.11E-02	50	64	0.228	0.344
<i>rs7517376</i>	<i>FMO1</i>	<i>SYNON</i>	A	1-7	0.974 A (0.88/0.84)	7.74E-03	1.80E-02	51	95	0.228	0.384
<i>rs893109</i>	<i>HTR5A</i>	<i>LD BIN</i>	A	7-29	0.974 G (0.69/0.68)	7.84E-03	1.24E-02	52	73	0.228	0.344
<i>rs684513</i>	<i>CHRNA5</i>	<i>INTRON</i>	A	15-3	0.805 C (0.81/0.77)	8.15E-03	8.72E-03	54	49	0.228	0.344
<i>rs7877</i>	<i>FMO1</i>	<i>UTR</i>	A	1-62	0.887 C (0.74/0.70)	8.46E-03	6.33E-03	59	38	0.228	0.344
<i>rs740602</i>	<i>COMT</i>	<i>SYNON</i>	A	.	G (1.00/0.99)	9.53E-03	3.43E-02	62	180	0.249	0.477
<i>rs16159</i>	<i>NPY</i>	<i>LD BIN</i>	A	7-1	0.803 T (0.31/0.29)	9.83E-03	7.43E-02	63	373	0.249	0.614
<i>rs2276560</i>	<i>CHRNG</i>	<i>LD BIN</i>	A	2-63	0.931 T (0.77/0.74)	1.04E-02	7.42E-03	72	44	0.256	0.344
<i>rs7215056</i>	<i>CHRNBI</i>	<i>INTRON</i>	A	17-8	0.933 C (0.82/0.78)	1.07E-02	6.09E-02	73	295	0.256	0.570
<i>rs3813567</i>	<i>CHRNFB</i>	<i>FP</i>	A	.	A (0.83/0.79)	1.18E-02	1.18E-02	81	70	0.274	0.344
<i>rs17149039</i>	<i>NPY</i>	<i>LD BIN</i>	A	7-1	0.803 G (0.33/0.31)	1.27E-02	8.45E-02	85	428	0.284	0.632
<i>rs4245150</i>	<i>DRD2</i>	<i>LD BIN</i>	A	11-8	0.997 G (0.37/0.36)	1.29E-02	1.08E-02	87	61	0.284	0.344
<i>rs2304297</i>	<i>CHRNA6</i>	<i>UTR</i>	A	8-52	0.830 G (0.79/0.75)	1.38E-02	6.91E-03	95	42	0.295	0.344
<i>rs17602038</i>	<i>DRD2</i>	<i>LD BIN</i>	A	11-8	0.997 C (0.37/0.36)	1.43E-02	1.17E-02	98	69	0.298	0.344
<i>rs6045733</i>	<i>PDYN</i>	<i>LD BIN</i>	A	20-34	0.803 G (0.66/0.65)	1.56E-02	1.55E-02	108	84	0.318	0.384
<i>rs3791729</i>	<i>CHRND</i>	<i>INTRON</i>	A	2-68	0.877 A (0.37/0.32)	1.70E-02	3.39E-03	113	25	0.325	0.344
<i>rs12056414</i>	<i>OPRK1</i>	<i>INTRON</i>	A	8-14	1.000 A (0.09/0.07)	1.71E-02	3.71E-02	116	191	0.325	0.492
<i>rs3743078</i>	<i>CHRNA3</i>	<i>INTRON</i>	A	15-3	0.805 G (0.82/0.79)	1.98E-02	1.10E-02	128	63	0.349	0.344
<i>rs16148</i>	<i>NPY</i>	<i>FP</i>	A	7-1	0.803 C (0.35/0.33)	2.01E-02	1.14E-01	130	556	0.349	0.676
<i>rs6045819</i>	<i>PDYN</i>	<i>SYNON</i>	A	20-29	0.859 A (0.90/0.88)	2.05E-02	2.98E-02	133	159	0.349	0.470
<i>rs6749955</i>	<i>CHRNG</i>	<i>LD BIN</i>	A	2-63	0.931 T (0.77/0.73)	2.09E-02	1.70E-02	135	91	0.349	0.384
<i>rs4531</i>	<i>DBH</i>	<i>NONSYN</i>	A	.	G (0.93/0.91)	2.34E-02	5.10E-03	143	30	0.383	0.344
<i>rs12056411</i>	<i>OPRK1</i>	<i>INTRON</i>	A	8-14	1.000 A (0.09/0.07)	2.53E-02	5.21E-02	154	263	0.398	0.522

^a Category.