Supplementary Online Content

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ANALYSIS OF DNA

Hybridization probes were prepared from genomic DNA pools as described and hybridized to the commercial version (samples 1 and 3) or early access (sample 2) StyI or NspI 500K microarrays (Affymetrix, Santa Clara, California) that were washed, stained, and scanned as described.[20] Allele frequencies for each single-nucleotide polymorphism (SNP) in each DNA pool were assessed on the basis of hybridization to the "perfect-match" cells on each of 4 arrays from replicate experiments, as described.[18,22] A t statistic for the differences between successful and unsuccessful abstainers was obtained as described,[18,21,22] and nominally significant SNPs were defined as those for which t values correspond to $P < .01$. We deleted data from SNPs on sex chromosomes and SNPs for which chromosomal positions could not be adequately determined using Map Viewer Build 36.1 (National Center for Biotechnology Information, Bethesda, Maryland)) or Netaffyx (Affymetrix).

The methods used herein have been found to generate correlations of 0.95 between pooled and individually determined genotype frequencies using these same array types.[18,20,21,27-29] When we have compared data for 7 randomly selected SNPs for which individual genotypes are available for 156 subjects from sample 1, we have identified strong correlations (with values up to 0.97) correlations between pool-to-pool variation noted in pooled and individually genotyped data (from Lerman et al[16]) for SNPs that display substantial pool-to-pool differences in allele frequency and more modest correlations for SNPs that display small pool-to-pool differences. In this additional validation study, the mean correlation between individually determined and pooled genotypes for this subsample was 0.74.

COMMENTS ON ANALYTIC APPROACHES

Genome-wide association (GWA) gains power to detect variants in more and more of the genome as more and more genetic markers (SNPs) are assayed. Because so many SNPs were assayed in such studies, however, stringent approaches to correct for the large number of multiple comparisons are needed. There is no clear-cut consensus about a single method that will produce only true results from any single sample. We have approached this problem by identifying nominally significant SNPs in each sample, identifying the clustering of such SNPs in each sample, and seeking small genomic areas in which clusters from at least 2 of the replicate samples studied herein provide clustered nominally significant SNPs. The criterion used to identify clustering—0.1 megabase separation between SNPs—is similar to that used in previous studies of addiction vulnerability,[18] and thus allows more direct comparison between these data and previously reported data. Other approaches to defining clustering are possible, including methods that rely on linkage disequilibrium assessed in different samples. We have used Monte Carlo simulation methods that do not make assumptions about the underlying distribution of data and provide empirical P values based on repeated random samples of the actual data sets produced in these studies.

Bonferroni corrections for multiple comparisons are also advocated by some investigators. In addition, false discovery rate corrections can be applied when multiple t tests are generated, as we do herein. Permutation analyses provide additional approaches. When we have applied these alternative approaches to prior GWA datasets,[18,19,21,22,30] they have provided results that have not significantly enhanced those derived from Monte Carlo methods.

Monte Carlo methods gain special power when we seek to assess the significance of the reproducible results from convergent data from multiple independent data sets that differ from each other in number of pools, etc. Under these circumstances, none of the available alternative methods appears to provide as tractable a means of assessing the significance of results obtained in multiple samples without assumptions about underlying distributions of the data as do Monte Carlo approaches. Based on each of these considerations, we have focused on the Monte Carlo approach as a primary analytic strategy a priori, and have carried these planned analyses forward as documented herein. We have used 10 000 Monte Carlo trials in circumstances in which moderately high significance is anticipated, and 100 000 trials in circumstances in which extremely high significance is anticipated, as noted in the text and tables.

eTable 1. Study Subjects[a]

Sample No.	No of Individuals	Abstinence Status		No. of Individuals/ Pool	No. of Pools	No. of Array Sets
		Successful	Unsuccessful			
1	266	126	140	14	19	76
2	134	55	79	18-19	7	28
3	150	60	90	15	10	40

[a] We included 550 individuals in this report. Allele frequencies were assessed using 4 independent array sets for each pool.

eTable 2. Genes Harboring Allelic Variants That Distinguish Successful vs Unsuccessful Abstainers in at Least 2 Samples[a]

Functional Class/ Gene Symbol	Description	Chr	Gene Start, bp	Gene End, bp	Strand[b]	Sample Nos.[c]												*P* Value[d]	References to Other GWA Studies[e]
						Clustered SNPs $P < .01$			5′			Within Gene			3′				
						1	2	3	1	2	3	1	2	3	1	2	3		
Cell adhesion																			
DAB1	Disabled homolog 1	1	57 236 167	58 488 799	−	7		2				7		2				.0117	
ASTN	Astrotactin	1	175 096 826	175 400 647	−		2	1					2	1				.0334	
USH2A	Usher syndrome 2A	1	213 862 859	214 66 3361	−		2	3					2	3				.0421	
CTNNA2	catenin (cadherin-associated protein), α 2	2	79 593 634	80 729 416	+		2	2					2	2				.1254	
CLSTN2	Calsyntenin 2	3	141 136 897	141 769 328	+	1	4	3					3	3	1	1		.0045	31
SEMA5A	Semaphorin 5A	5	9 091 850	9 599 158	−	5		1				5		1				.0087	
TRIO	Triple functional domain/PTPRF interacting	5	14 196 829	14 562 458	+		2	2					2	2				.0375	18
PTPRN2	Receptor protein tyrosine phosphatase N polypeptide 2	7	157 024 516	158 073 179	−	5	5					5	5					.0056	
CSMD1	CUB and Sushi multiple domains 1	8	2 782 789	4 839 736	−		10	5					10	5				.0049	18
SGCZ	Sarcoglycan zeta	8	13 991 744	15 140 163	−		3	5					3	5				.0191	18
PTPRD	Receptor protein tyrosine phosphatase D	9	8 307 268	9 008 735	−		2	8					2	8				.0028	18
TEK	TEK tyrosine kinase	9	27 099 286	27 220 172	+	2	2	3				1	2	3	1			.0011	
PCDH15	Protocadherin 15	10	55 250 866	56 231 057	−	3		4				3		4				.0175	
NRG3	Neuregulin 3	10	83 625 077	84 735 341	+		4	1					4	1				.0561	
DSCAML1	Down syndrome cell adhesion moleculelike 1	11	116 803 699	117 173 186	−		2	2					2	2				.0365	
NRXN3	Neurexin 3	14	77 939 846	79 400 515	+		2	3					2	3				.1002	21
ITGA11	Integrin α11	15	66 381 096	66 511 546	−		2	1					2	1				.0166	18
CDH13	Cadherin 13	16	81 218 079	82 387 702	+	8	3	7				8	3	7				.002	
LAMA1	Laminin α1	18	6 931 885	7 107 813	−		2	2					2	2				.0186	
PTPRT	Receptor protein tyrosine phosphatase T	20	40 134 806	41 251 971	−	5	6	5				5	6	5				.0024	
DSCAM	Down syndrome cell adhesion molecule	21	40 306 213	41 140 909	−	10	2					10	2					.0016	18
Enzymes																			
ST6GALNAC3	α-N-acneuraminyl-2,3-β-galactosyl 1,3)-N-acetyl-	1	76 312 992	76 869 220	+		2	4					2	4				.0143	

	galactosaminide α2, 6-sialyltransferase 3																		
REN	Renin	1	202 390 571	202 402 088	−		1	2		1				1			1	.0067	
CERKL	Ceramide kinase-like	2	182 109 650	182 229 996	−		1	3					1	3				.0079	
NEK11	NIMA-related kinase 11	3	132 228 417	132 551 993	+	7		7				7		6			1	.0016	
TNIK	TRAF2 and NCK interacting kinase	3	172 264 364	172 660 546	−		2	2					2	2				.0377	
LEPREL1	Leprecan-like 1	3	191 157 316	191 321 412	−		4	2					4	2				.006	
GALNT17	Polypeptide N-acetylgalactosaminyl-transferase 17	4	172 971 229	174 199 285	+		4	2					4	2				.058	
ADCY2	Adenylate cyclase 2	5	7 449 345	7 883 194	+	3		1				3					1	.0175	
PPP2R2B	Protein phosphatase 2 regulatory subunit B β isoform	5	145 949 260	146 441 207	−		5	8					5	8				.0007	
DPP6	Dipeptidyl-peptidase 6	7	154 060 464	154 316 928	+		2	1					2	1				.031	
PBK	PDZ-bnding kinase	8	27 723 057	27 751 268	−		1	3					1	3				.0038	
ST3GAL1	ST3 β-galactoside α-2,3-sialyltransferase 1	8	134 540 312	134 653 344	−		2	1					2	1				.0158	
MOBKL2B	MOB1-like 2B	9	27 315 207	27 519 850	−	1	2					1	2					.0082	
DAPK1	Death-associated protein kinase 1	9	89 302 576	89 513 369	+		2	3					2	3				.0105	
LYZL1	Lysozymelike 1	10	29 617 996	29 640 164	+		2	2			1		2				1	.0075	
PRKG1	cGMP-dependent protein kinase I	10	52 504 299	53 725 284	+	7	3	4			1	7	3	3				.0041	18
ADAM12	ADAM metallopeptidase domain 12	10	127 693 415	128 067 055	−		1	2					1	2				.0457	
FDX1	Ferredoxin 1	11	109 805 804	109 840 815	+		2	1		1			1				1	.01	
SERPINA2	Serpin peptidase inhibitor A 2	14	93 900 404	93 914 178	−		1	2		1				2				.0078	18
SERPINA1	Serpin peptidase inhibitor A 1	14	93 914 451	93 926 782	−		1	2					1				2	.008	18
AKAP13	A kinase anchor protein 13	15	83 724 875	84 093 590	+		5	2					5	2				.0065	18
ALDH3A2	Aldehyde dehydrogenase 3 A2	17	19 492 656	19 521 500	+	1	1			1					1			.0033	
ATP9A	Adenosine triphosphatase II 9A	20	49 646 721	49 818 315	−	1	1	2			1	1		1		1		.0026	
LARGE	Like-glycosyltransferase	22	31 999 063	32 646 410	−		4	4			1		4	3				.0067	
Transcriptional regulation																			

TDRD5	Tudor domain containing 5	1	177 827 648	177 927 021	+	2		1			1	2						.0064	
RARB	Retinoic acid receptor β	3	25 444 758	25 614 424	+		1	2					1	2				.0218	
SUPT3H	Suppressor of Ty 3 homolog	6	44 904 447	45 453 648	−		3	2					3	2				.0306	
CREB5	cAMP-responsive element binding protein 5	7	28 305 465	28 832 036	+	5		2				5		2				.0082	
GLIS3	GLIS family zinc finger 3	9	3 817 676	4 142 183	−		3	2					3	2				.0174	
BNC2	Basonuclin 2	9	16 399 501	16 860 786	−		3	6					3	6				.0027	
TACC2	Transforming acidic coiled-coil containing protein 2	10	123 738 679	124 004 047	+	1	1					1	1					.0141	
SOX5	SRY-box 5	12	23 576 498	24 606 647	−	2		2				2		2				.0514	
NPAS3	Neuronal PAS domain protein 3	14	32 478 200	33 340 702	+		5	1					5	1				.0239	18
PAX9	Paired box gene 9	14	36 200 656	36 215 621	+	1		2	1		2							.0026	
ZNF423	Zinc finger protein 423	16	48 082 022	48 418 419	−	3	3					3				3		.0044	
SALL4	Sal-like 4	20	49 833 988	49 852 421	−	1		1	1		1							.0039	
ERG	v-ets Erythroblastosis virus E26 oncogene like	21	38 675 671	38 955 488	−		2	2					2	1			1	.0293	
BCL2L13	Bcl2-like 13	22	16 501 485	16 591 991	+	3	1					3				1		.0037	
Receptors																			
GPR116	G protein–coupled receptor 116	6	46 928 294	46 990 825	−		2	1					2	1				.0114	
CD109	CD109 molecule	6	74 462 548	74 591 509	+	1		1				1		1				.0113	
GRIK2	Inotropic glutamate receptor kainate 2	6	101 953 675	102 623 474	+		2	2					2	2				.0648	
MTUS1	Mitochondrial tumor suppressor 1	8	17 545 583	17 702 666	−		3	3					3	3				.0049	
GRIN2A	Inotropic glutamate receptor N-methyl D-aspartate 2[a]	16	9 762 923	10 184 112	−		2	2		1				2		1		.0427	
GRIK1	Inotropic glutamate receptor kainate 1	21	29 831 125	30 234 153	−	3	4					3	4					.0028	
Channels																			
KCNN3	N-type potassium channel 3	1	152 946 526	153 109 378	−		1	2					1	2				.0224	
KCNK2	K-type potassium channel 2	1	213 245 765	213 477 059	+		4	2					1	2		3		.0069	
CACNA2D3	Voltage-dependent calcium channel	3	54 131 733	55 083 624	+	3	8					3	8					.0031	

	α2/δ3																		
KCNIP4	Kv channel-interacting protein 4	4	20 339 337	21 155 377	−		6	2					6	2				.0095	
CACNB2	Voltage-dependent calcium channel β2	10	18 469 612	18 870 045	+		2	2					2	2				.0416	
ITPR2	Inositol 1,4,5-triphosphate receptor 2	12	26 377 193	26 877 398	−		6	3					6	3				.003	
Transporters																			
ATP8A1	Aminophospholipid transporter class type 8A 1	4	42 109 392	42 353 647	−	1		1				1		1				.0169	
SLC1A2	Solute carrier family 1/glial high affinity glutamate transporter 2	11	35 229 329	35 397 372	−		3	3					3	2			1	.0045	
MATE2	H$^+$/organic cation antiporter	17	19 522 220	19 560 515	−	1	1					1	1					.0047	
DNA/RNA																			
RBM19	RNA-binding motif protein 19	12	112 744 245	112 888 499	−	5		2				5		2				.0033	
A2BP1	Ataxin 2-binding protein 1	16	6 009 133	7 702 500	+	14		12				14		12				.0015	18
Ligands for receptors																			
OLFM3	Olfactomedin 3	1	102 040 718	102 235 136	−	1	7					1	7					.0006	
FGF12	Fibroblast growth factor 12	3	193 342 413	193 928 066	−		3	2					3	2				.0321	
TMTC2	Transmembrane and tetratricopeptide repeat containing 2	12	81 605 065	82 052 196	+	1		2						2	1			.0234	
THSD4	Thrombospondin type I domain containing 4	15	69 220 842	69 862 776	+	3	2	4				3	2	4				.0035	
Protein processing																			
PARK2	Parkin	6	161 689 661	163 068 793	−		6	2					6	2				.0236	
SORCS1	Sortilin-related VPS10 domain containing receptor 1	10	108 323 411	108 914 282	−		2	4		1	3		1	1				.0168	18
Intracellular signaling pathways																			
CHN2	Chimerin 2	7	29 200 646	29 520 469	+		2	2					2	2				.0314	18
PEBP4	Phosphatidylethanol-amine-binding	8	22 626 713	22 841 358	−	3		2				3		2				.0065	

	protein 4																		
NELL1	NEL-like 1	11	20 647 712	21 553 577	+		2	2					2	2				.0911	
EFCBP2	EF-hand calcium-binding protein 2	16	82 559 738	82 593 880	+	1		1						1	1			.0064	
BIK	Bcl2-interacting killer	22	41 836 701	41 855 662	+		1	2					1	1			1	.0087	
Structural proteins																			
KIAA1026	Kazrin	1	14 797 800	15 265 161	+	3		2	2		1	1		1				.013	
NPHS2	Podocin	1	177 786 299	177 811 691	−	1		2			2				1			.0038	
PKP1	Plakophilin 1	1	199 519 203	199 568 740	+		1	1					1	1				.0153	
ERC2	ELKS/RAB6-interacting/CAST family member 2	3	55 517 376	56 477 431	−		5	3					5	3				.0129	
MAGI1	Membrane-associated guanylate kinase, WW and PDZ domain containing 1	3	65 314 946	65 999 549	−	7		2				6		2	1			.006	
PARD3	Partitioning defective 3 homolog	10	34 440 103	35 143 929	−	4	2	2				4	2	2				.0077	
UNC13C	Unc13 homolog C	15	52 092 393	52 708 098	+		3	2					3	2				.0354	
SNAP25	Synaptosomal-associated protein	20	10 147 477	10 236 065	+		1	3					1	3				.0068	
MYO18B	Myosin XVIIIB	22	24 468 120	24 757 007	+		5	3					5	3				.0033	
Unknown function																			
TMEM108	Transmembrane protein 108	3	134 239 943	134 597 748	+	8	1		2	1		6						.0009	
C4orf22	Chromosome 4 open reading frame 22	4	81 475 898	82 103 928	+		1	1		1				1				.0836	
FLJ20184	Hypothetical protein FLJ20184	4	106 693 226	106 772 286	+		2	1					2	1				.0139	
C10orf64	Chromosome 10 open reading frame 64	10	49 563 518	49 686 269	+	1		2				1		2				.0078	
BTBD16	BTB domain containing 16	10	124 020 811	124 087 666	+	1	1			1		1						.0059	
LUZP2	Leucine zipper protein 2	11	24 475 132	25 060 762	+	3	1					3	1					.0217	
CCDC73	Coiled-coil domain containing 73	11	32 580 202	32 772 763	−	3	3		1			2	3					.0031	
FLJ42220	FLJ42220 protein	14	36 186 635	36 187 505	+	2		2							2		2	.003	
CCBE1	Collagen- and calcium-binding EGF domains 1	18	55 252 124	55 515 570	−	1		2						2	1			.0134	

Abbreviations: bp, base pair; cGMP, cyclic guanoisine monophosphate; chr, chromosome; GWA, genome-wide association; SNP, single-nucleotide polymorphism; SRY, sex-determining region Y, −, negative; +, positive.

[a] Chromosome number and initial chromosomal position for the gene come from the National Center for Biotechnology Information Map Viewer Build 36.1. Monte Carlo *P* values come from 10 000 simulation trials that each begins with random sampling from a database that contains all gene segments ±10 kilobases. These simulations assess the frequency of trials in which at least the observed numbers of nominally positive SNPs identified in each of the 3 samples studied herein was recorded to provide an empirical *P* value. Eight genes (noted in boldface) receive clustered, nominally highly significant association signals from each of the 3 samples studied herein. Other GWA studies with which the current results converge: (1) 639 000 SNP GWAs for dependence on at least 1 illegal substance in each of 2 samples with support from 100 000 SNP GWA for alcohol dependence and methamphetamine dependence[18]; (2) 10 000 SNP GWAs for dependence on at least 1 illegal substance in each of 2 samples[21]; and (3) 520 000 SNP GWAs for word recall memory.[31]

[b] Indicates chromosomal orientation of the gene (positive or negative strand).

[c] Indicates numbers of clustered SNPs from samples 1, 2, and 3, respectively, that display nominally highly significant ($P < .01$) allele frequency differences between successful and unsuccessful abstainers in the 10-kilobase (kb) 5′ flank of the gene, within the gene's exons or introns, or in the 10-kb 3′ flank of annotated exons.

[d] Indicates P values for each gene based on Monte Carlo simulations and the reference for other GWA studies that have identified the same gene.

[e] Full references are found in the Reference List of the main article.

eTable 3. Chromosomal Regions Not Annotated as Containing Genes With at Least 2 Clustered Nominally Positive SNPs[a]

Chr	Base Pair Start[b]	Base Pair Stop[b]	No. of SNPs, Sample No.[c]		
			1	2	3
1	191 497 679	194 451 536	5	9	0
2	7 111 761	8 729 564	0	4	3
2	58 332 018	60 521 806	18	5	0
2	225 417 157	227 298 182	8	0	4
3	133 933 966	134 229 943	7	2	0
4	17 642 477	19 854 333	3	0	3
4	30 763 851	35 734 017	3	0	6
4	66 228 104	68 010 584	0	3	4
4	134 342 182	138 650 285	4	3	4
4	160 510 771	162 514 499	5	0	4
4	171 257 947	172 961 229	3	5	0
5	5 366 920	6 415 039	5	0	3
5	88 224 780	89 715 284	11	8	0
5	98 300 138	99 889 023	0	7	3
5	151 775 017	152 840 499	3	4	0
6	66 871 532	69 394 158	0	16	8
6	137 867 224	138 220 274	3	3	0
6	167 384 056	167 446 247	2	4	0
7	8 769 118	9 630 425	10	0	5
8	16 286 966	16 884 705	2	0	6
8	58 078 957	59 059 667	7	5	0
8	136 739 031	139 214 285	5	8	3
9	85 818 805	86 072 912	2	3	0
9	109 301 576	110 646 692	7	0	3
10	8 167 170	11 077 290	0	3	3
10	49 696 269	49 777 534	3	0	7
10	108 924 282	111 604 514	5	5	3
10	131 882 775	132 770 645	12	0	11
11	78 261 787	82 110 694	0	6	4
11	114 094 574	114 540 227	3	0	4
12	82 062 196	83 767 398	6	9	0
13	102 527 197	104 906 593	0	4	8
14	85 174 023	87 459 111	0	3	8
15	60 254 774	60 706 663	3	0	3
16	9 131 056	9 752 923	5	6	0
16	77 034 150	78 175 732	4	0	7
17	29 724 365	29 921 881	3	0	5
17	47 601 086	49 245 261	3	26	0
18	39 121 342	40 525 467	3	0	11
18	71 140 889	72 188 625	5	3	0
20	41 799 056	41 968 221	2	0	3

Abbreviations: chr, chromomsome; SNP, single-nucleotide polymorphism.

[a] Indicates nominally positive SNPs (within 0.1 megabase of each other) from at least 2 of the 3 samples described herein.

[b] Indicates base pair location for the beginning and end of the interval marked by the clustered nominally positive SNPs.

[c] Indicates the number of SNPs from samples 1, 2, and 3 that display nominal $P < .01$ values for the differences between successful vs unsuccessful abstainers that lie within the interval.

eTable 4. Results of Secondary Analyses That Identify Genes Based on Pooled Data From Placebo-, Bupropion-, and NRT-Treated Individuals From All 3 Samples[a]

				t Value		
Gene Symbol	**SNP[b]**	**Chr**	**Base Pair Location**	**NRT vs Placebo[c]**	**Bupropion vs Placebo[c]**	**Difference[d]**
NRT selective						
ARL6IP2	rs12468478	2	38 421 058	4.784	1.672	3.112
	rs11883614	2	38 429 139	4.266	2.486	1.780
	rs4589732	2	38 467 481	4.034	3.040	0.995
NRXN1	rs9677968	2	50 162 751	4.476	1.009	3.467
	rs921573	2	50 245 834	3.714	1.591	2.123
	rs11675607	2	50 277 378	3.910	1.441	2.469
	rs9309179	2	50 369 830	0.965	3.831	−2.866
HSPC159	rs10176971	2	64 530 626	4.150	0.995	3.155
	rs1426707	2	64 530 898	5.123	0.393	4.729
CTNNA2	rs17019221	2	80 615 263	4.208	0.601	3.606
	rs1434064	2	80 710 572	4.134	0.949	3.184
	rs216645	2	80 737 369	3.899	3.101	0.798
POLR1B	rs4849073	2	113 016 889	3.971	3.094	0.877
	rs4849074	2	113 017 468	3.737	0.001	3.736
RAB17	rs7595979	2	238 146 492	5.195	0.599	4.596
	rs1497129	2	238 151 184	4.681	2.933	1.748
	rs6431541	2	238 158 190	3.707	0.785	2.922
ARPP21	rs11129660	3	35 670 965	3.833	1.432	2.401
	rs9865772	3	35 769 904	5.745	1.433	4.312
CACNA2D3	rs4955861	3	54 586 203	3.807	3.360	0.447
	rs4955866	3	54 586 793	4.836	0.411	4.425
	rs666071	3	54 684 761	5.979	0.693	5.286
SYNPR	rs12374033	3	63 405 578	4.103	0.964	3.138
	rs17397636	3	63 476 495	4.554	2.488	2.067
	rs17338206	3	63 476 572	3.706	2.453	1.253
	rs17399554	3	63 542 394	2.037	4.457	−2.420
EPHB1	rs6762543	3	136 339 774	5.002	0.610	4.392
	rs10804635	3	136 361 774	4.100	3.694	0.406
	rs12636613	3	136 361 819	3.592	3.640	−0.047
CLSTN2	rs4683831	3	141 596 976	4.532	0.411	4.121
	rs6439919	3	141 648 020	4.091	0.535	3.556
	rs6810310	3	141 648 823	6.333	1.448	4.885
TMPRSS11D	rs13151552	4	68 360 369	4.318	0.766	3.552
	rs7671397	4	68 419 589	4.062	0.899	3.163
GRID2	rs1435480	4	94 907 655	3.852	0.321	3.530
	rs11932367	4	94 914 733	3.837	0.130	3.707
TRIM2	rs4696397	4	154 358 796	5.190	1.167	4.023
	rs17029639	4	154 368 893	4.493	0.807	3.686
	rs4696168	4	154 371 681	4.118	0.238	3.879
SDCCAG10	rs2915438	5	64 347 813	3.918	0.163	3.755
	rs2915441	5	64 351 549	5.418	0.166	5.252
KCNIP1	rs953601	5	169 997 291	5.586	0.177	5.409
	rs4867625	5	170 021 180	3.915	0.308	3.607
	rs872436	5	170 058 653	3.920	1.632	2.287
	rs984559	5	170 071 237	4.170	1.313	2.857

	rs1363713	5	170 095 672	5.213	1.642	3.571
FLJ37396	rs9374067	6	109 690 736	3.698	0.915	2.784
	rs932222	6	109 693 371	4.903	2.026	2.877
ARHGAP18	rs1894642	6	130 057 024	4.342	1.181	3.160
	rs763132	6	130 062 040	3.924	0.741	3.183
VIL2	rs6455600	6	159 117 280	3.977	0.388	3.588
	rs6455601	6	159 137 292	5.881	1.891	3.990
DNAH11	rs4392794	7	21 702 815	7.131	0.691	6.440
	rs12700327	7	21 729 025	3.691	0.761	2.929
	rs1174962	7	21 817 682	4.580	2.373	2.206
TEK	rs7865623	9	27 142 209	2.949	3.942	−0.993
	rs7037246	9	27 219 544	4.270	0.488	3.782
	rs857	9	27 219 786	3.762	0.346	3.416
PTGES	rs4474069	9	131 540 940	6.085	0.328	5.757
	rs7035496	9	131 563 434	4.526	0.407	4.118
AKR1C4	rs3750571	10	5 237 434	5.092	1.345	3.747
	rs4881413	10	5 248 450	4.136	0.189	3.947
ITIH5	rs12416004	10	7 650 219	4.065	1.366	2.699
	rs11255241	10	7 700 496	3.929	0.364	3.565
	rs11255242	10	7 701 120	3.912	0.055	3.857
CAMK1D	rs1644391	10	12 908 310	4.322	1.415	2.906
	rs1757070	10	12 918 360	4.092	1.479	2.613
PARD3	rs1660622	10	34 496 515	4.955	0.077	4.878
	rs629039	10	34 528 370	3.919	1.600	2.318
	rs678188	10	34 535 295	4.264	0.168	4.096
	rs1778871	10	34 575 027	5.635	0.084	5.551
	rs1778870	10	34 615 285	5.075	1.109	3.966
	rs16935302	10	34 629 748	3.971	0.276	3.695
PCDH15	rs10825324	10	55 840 119	3.789	1.854	1.935
	rs12146398	10	55 842 860	4.352	0.643	3.709
	rs11004281	10	55 843 065	3.902	0.967	2.935
C10orf107	rs16916501	10	63 122 152	4.272	1.194	3.079
	rs2448396	10	63 199 744	8.979	3.302	5.677
ADAM12	rs7920207	10	127 721 299	3.713	0.668	3.045
	rs2292692	10	127 727 920	4.161	0.830	3.331
	rs1710288	10	127 731 276	3.741	2.567	1.174
SPON1	rs7116230	11	13 992 156	3.997	0.390	3.607
	rs11023051	11	13 992 537	4.279	2.374	1.905
	rs11023054	11	14 005 230	3.582	3.859	−0.277
	rs10832165	11	14 005 260	5.154	3.991	1.164
	rs11023055	11	14 005 745	6.811	2.741	4.070
	rs11023059	11	14 020 968	4.108	1.401	2.707
	rs1528640	11	14 027 404	4.659	1.719	2.940
	rs11023067	11	14 031 836	4.029	1.253	2.775
	rs1406356	11	14 034 087	4.334	1.715	2.619
NELL1	rs10766758	11	20 970 702	4.001	0.671	3.330
	rs1516757	11	21 037 853	6.197	2.648	3.549
	rs1516748	11	21 046 745	5.359	2.744	2.615
	rs1945413	11	21 418 450	3.822	0.070	3.753
	rs6483772	11	21 459 570	4.311	3.028	1.283
	rs4279993	11	21 483 019	1.444	3.926	−2.482

STS-1	rs7930792	11	122 086 935	3.806	0.137	3.669
	rs11218769	11	122 092 818	3.864	0.394	3.471
	rs4936742	11	122 146 296	3.420	3.765	−0.344
C12orf36	rs4763340	12	13 421 760	4.820	2.408	2.411
	rs1993508	12	13 423 598	4.470	1.218	3.252
NOS1	rs9658498	12	116 131 245	3.727	1.099	2.627
	rs3741476	12	116 134 855	3.779	0.889	2.891
	rs733334	12	116 195 409	4.943	1.400	3.543
	rs17509231	12	116 257 043	3.950	2.840	1.110
CRYL1	rs17081647	13	19 875 507	3.696	0.049	3.646
	rs9315607	13	19 939 654	3.896	2.703	1.193
TUBGCP3	rs7139689	13	112 259 301	3.997	0.266	3.730
	rs9550153	13	112 282 279	4.233	0.704	3.529
	rs9577820	13	112 296 262	6.210	2.687	3.524
ZNF597	rs171634	16	3 418 867	6.294	1.204	5.090
	rs37824	16	3 426 237	5.303	1.919	3.384
XYLT1	rs9923657	16	17 121 806	4.660	1.508	3.152
	rs9939115	16	17 128 060	3.759	0.364	3.396
	rs9807009	16	17 133 351	4.181	1.786	2.395
	rs4782031	16	17 141 541	4.684	0.285	4.399
CA10	rs981577	17	47 262 912	3.830	2.074	1.756
	rs7215201	17	47 304 239	6.164	2.733	3.431
	rs203018	17	47 390 503	3.851	2.378	1.472
LAMA3	rs11878083	18	19 691 466	6.432	0.579	5.854
	rs8092476	18	19 692 630	6.176	0.362	5.814
	rs8093042	18	19 695 482	4.083	0.755	3.328
	rs8087837	18	19 731 580	5.206	0.193	5.013
	rs1154238	18	19 769 389	5.449	0.391	5.058
	rs1786045	18	19 791 960	4.520	0.272	4.249
CSF2RB	rs4821566	22	35 639 007	6.519	3.537	2.982
	rs9607397	22	35 640 488	5.631	2.669	2.962
Nonselective						
NPHP4	rs4908559	1	5 878 404	3.199	3.752	−0.553
	rs2282281	1	5 882 943	2.546	6.496	−3.950
	rs3747987	1	5 900 385	2.624	4.241	−1.616
	rs4908639	1	5 972 849	5.879	2.324	3.555
KCTD3	rs4846828	1	213 818 026	4.641	3.832	0.809
	rs2646806	1	213 868 035	2.301	3.746	−1.445
USH2A	rs2646806	1	213 868 035	2.301	3.746	−1.445
	rs2646821	1	213 916 631	4.245	1.225	3.020
	rs17046325	1	213 961 146	4.321	0.191	4.130
OBSCN	rs2144300	1	226 601 651	4.199	1.777	2.422
	rs17315646	1	226 602 042	4.243	2.355	1.888
	rs4846914	1	226 602 426	3.744	1.334	2.410
	rs609526	1	226 615 641	4.603	2.836	1.767
GALNT2	rs4459095	1	228 292 315	3.896	1.204	2.692
	rs872624	1	228 381 635	3.696	4.153	−0.457
RNF144	rs4669112	2	6 979 250	0.298	3.791	−3.493
	rs771315	2	7 048 121	4.322	1.980	2.342
	rs3772017	2	7 048 443	3.920	0.001	3.919
RBJ	rs6545814	2	25 042 967	2.592	3.729	−1.138

	rs2384061	2	25 047 271	5.058	5.099	−0.042
REEP1	rs9917140	2	86 304 323	0.014	3.681	−3.666
	rs10175330	2	86 325 772	2.496	3.748	−1.252
	rs11691807	2	86 394 679	4.328	1.751	2.576
ALS2CR19	rs2289025	2	205 794 726	0.864	5.499	−4.635
	rs1434160	2	205 813 311	0.822	3.725	−2.903
	rs6738364	2	205 849 770	3.922	0.218	3.704
	rs7593566	2	205 921 326	3.737	2.157	1.580
ITGA9	rs6419832	3	37 593 101	5.141	3.874	1.267
	rs2212035	3	37 599 249	4.273	4.668	−0.395
	rs9857453	3	37 600 754	4.433	3.612	0.821
	rs1155741	3	37 602 116	3.796	2.264	1.532
	rs6550486	3	37 603 958	4.789	4.393	0.395
FSTL1	rs4676776	3	121 589 229	2.348	6.686	−4.338
	rs1733329	3	121 589 510	4.419	2.104	2.315
	rs4676698	3	121 589 903	2.916	3.766	−0.850
	rs1700	3	121 597 327	3.990	0.948	3.042
	rs1147695	3	121 602 136	5.685	3.617	2.068
	rs9880550	3	121 605 314	2.198	4.305	−2.107
MIRN198	rs4676776	3	121 589 229	2.348	6.686	−4.338
	rs1733329	3	121 589 510	4.419	2.104	2.315
	rs4676698	3	121 589 903	2.916	3.766	−0.850
	rs1700	3	121 597 327	3.990	0.948	3.042
	rs1147695	3	121 602 136	5.685	3.617	2.068
	rs9880550	3	121 605 314	2.198	4.305	−2.107
TM4SF1	rs6440605	3	150 573 605	4.364	4.638	−0.275
	rs6808255	3	150 574 454	3.935	2.993	0.942
JAKMIP1	rs11940459	4	6 143 916	3.754	1.484	2.270
	rs16838127	4	6 174 478	3.485	4.704	−1.219
	rs16838138	4	6 176 773	4.347	2.413	1.934
SYNPO2	rs10857061	4	120 138 941	0.150	5.660	−5.510
	rs13117019	4	120 169 338	3.827	2.370	1.457
	rs10518319	4	120 169 800	7.450	4.540	2.910
SEMA5A	rs1024487	5	9 410 007	4.320	2.395	1.926
	rs1205718	5	9 410 103	3.696	2.116	1.580
	rs13174956	5	9 489 697	4.744	1.267	3.477
PLCXD3	rs6872806	5	41 371 807	5.104	1.133	3.971
	rs7725517	5	41 391 870	4.091	3.206	0.886
	rs16871303	5	41 412 396	4.233	4.872	−0.639
	rs9654393	5	41 449 453	3.701	1.126	2.575
FLJ46010	rs39565	5	65 565 268	0.791	4.098	−3.307
	rs2997131	5	65 655 130	4.812	1.433	3.379
	rs7708487	5	65 685 580	3.772	2.020	1.752
KCTD16	rs960963	5	143 683 708	4.067	1.356	2.711
	rs244536	5	143 695 682	4.096	1.623	2.472
	rs244525	5	143 708 284	4.596	0.477	4.119
	rs1023679	5	143 746 359	4.015	1.360	2.655
	rs145716	5	143 827 411	3.754	1.486	2.268
GRIA1	rs10070447	5	153 159 007	0.968	5.169	−4.201
	rs13354399	5	153 169 624	3.135	3.664	−0.529
C6orf170	rs1273745	6	121 506 710	4.453	1.026	3.426

	rs1273746	6	121 506 916	4.001	2.788	1.213
	rs12717175	6	121 576 730	4.105	1.935	2.170
	rs463	7	43 076 024	4.271	0.353	3.919
AUTS2	rs7793102	7	69 593 327	4.710	0.237	4.472
	rs10265371	7	69 633 026	0.118	3.685	−3.567
	rs4718991	7	69 650 784	2.529	3.962	−1.433
	rs6957385	7	69 661 080	6.560	1.491	5.069
TRIM24	rs3778705	7	137 720 145	4.343	0.782	3.561
	rs6956225	7	137 792 501	2.964	4.963	−1.999
DENND1A	rs7023669	9	125 284 313	1.961	5.022	−3.061
	rs1891034	9	125 311 953	4.592	1.348	3.244
	rs522894	9	125 379 159	4.077	1.496	2.581
SFMBT2	rs2462696	10	7 248 868	1.715	3.730	−2.014
	rs2762608	10	7 269 445	1.541	3.582	−2.042
	rs2692840	10	7 299 452	4.787	0.328	4.459
CUGBP2	rs7907550	10	11 171 558	0.104	4.050	−3.946
	rs636416	10	11 259 496	4.023	0.867	3.157
	rs658469	10	11 261 372	2.222	3.723	−1.500
	rs1058349	10	11 342 383	4.635	1.607	3.028
	rs10795859	10	11 385 712	5.872	3.367	2.505
MYPN	rs1906719	10	69 584 587	4.145	3.364	0.781
	rs7079385	10	69 628 981	3.971	2.833	1.138
	rs10998021	10	69 638 195	4.743	3.374	1.369
PNLIPRP3	rs17094718	10	118 175 653	3.871	0.193	3.679
	rs1897511	10	118 176 259	1.066	4.204	−3.138
TXNL2	rs4750788	10	131 815 840	0.366	4.489	−4.123
	rs16910144	10	131 838 548	3.796	2.826	0.970
FLJ46154	rs288464	11	31 019 531	4.069	2.326	1.743
	rs208064	11	31 114 971	0.472	5.145	−4.673
SLC1A2	rs4756208	11	35 276 660	5.195	2.748	2.447
	rs10836389	11	35 372 547	1.393	3.594	−2.201
FDX1	rs4753891	11	109 803 757	4.464	1.984	2.480
	rs935135	11	109 835 105	3.836	1.050	2.786
IGSF4	rs1124848	11	114 591 158	4.994	3.820	1.174
	rs11215464	11	114 661 446	4.401	3.489	0.913
	rs10891823	11	114 663 444	6.506	1.462	5.044
HNT	rs11222888	11	131 426 061	1.308	4.751	−3.443
	rs9667087	11	131 489 352	4.411	0.493	3.918
	rs10894503	11	131 489 763	3.792	1.559	2.233
	rs10791209	11	131 513 590	3.717	1.105	2.612
EFCAB4B	rs10848906	12	3 638 966	4.737	4.076	0.661
	rs242028	12	3 656 976	0.860	5.014	−4.153
	rs4766163	12	3 690 519	3.979	0.399	3.580
GRIN2B	rs9971835	12	13 953 134	1.094	3.637	−2.543
	rs10772719	12	13 959 964	4.523	2.270	2.253
	rs219920	12	13 992 578	3.794	2.233	1.561
PLEKHA5	rs1514831	12	19 195 039	3.871	1.751	2.120
	rs10841162	12	19 208 349	4.370	1.810	2.560
	rs16915248	12	19 275 480	4.227	1.075	3.152
ITPR2	rs11048476	12	26 393 579	4.377	1.523	2.853
	rs2171520	12	26 395 604	4.568	0.014	4.554

	rs1532067	12	26 493 700	4.583	2.041	2.542
YAF2	rs12371615	12	40 850 256	4.059	1.492	2.568
	rs10880264	12	40 872 802	4.385	2.994	1.391
	rs10785334	12	40 906 644	4.152	0.322	3.830
BTBD11	rs4964569	12	106 253 978	1.425	4.195	−2.770
	rs1426467	12	106 274 715	4.188	1.277	2.911
	rs7957618	12	106 332 823	3.764	1.406	2.358
	rs10778561	12	106 364 091	0.483	4.720	−4.238
OAS2	rs2525846	12	111 916 273	4.091	2.530	1.561
	rs1732778	12	111 919 645	4.987	2.520	2.467
	rs1293778	12	111 929 847	5.343	3.340	2.004
NPAS3	rs17101083	14	32 965 666	2.768	4.013	−1.245
	rs967440	14	32 977 498	3.962	2.184	1.778
	rs12887949	14	33 048 257	4.631	3.865	0.767
RGS6	rs2332712	14	71 607 946	2.458	4.929	−2.471
	rs17108294	14	71 693 707	3.774	4.481	−0.706
	rs20838	14	71 714 279	1.098	3.642	−2.544
	rs1076317	14	71 802 071	5.979	1.989	3.989
	rs1568404	14	71 806 722	4.292	2.615	1.677
	rs12184980	14	71 815 012	3.896	1.795	2.101
DPF3	rs758913	14	72 334 214	2.896	4.010	−1.114
	rs4243643	14	72 364 297	4.368	1.596	2.772
	rs2333006	14	72 427 007	3.732	2.449	1.282
MYO1E	rs17190785	15	57 243 929	4.969	0.388	4.581
	rs2242321	15	57 253 509	1.444	3.755	−2.311
	rs11854052	15	57 254 345	5.345	0.610	4.735
A2BP1	rs17139303	16	6 055 552	1.882	3.982	−2.101
	rs2035593	16	6 101 996	3.779	0.580	3.199
	rs9646295	16	6 110 094	3.989	1.862	2.126
TNRC6A	rs16973968	16	24 664 039	2.149	3.709	−1.561
	rs12596320	16	24 725 006	5.856	0.660	5.196
CDH13	rs7187677	16	81 674 862	3.785	0.465	3.320
	rs13339002	16	81 738 358	1.125	3.874	−2.749
	rs889730	16	81 814 806	4.170	0.643	3.527
	rs4782805	16	82 095 671	2.143	3.787	−1.644
	rs4074373	16	82 113 026	0.752	4.070	−3.318
	rs4782814	16	82 127 288	4.220	0.993	3.227
WFDC1	rs39547	16	82 877 290	1.907	3.800	−1.893
	rs8051764	16	82 898 397	3.389	3.785	−0.397
GLP2R	rs2047664	17	9 669 336	3.758	0.132	3.626
	rs4791901	17	9 722 679	3.832	1.306	2.526
	rs2240737	17	9 731 884	3.692	1.685	2.007
GAS7	rs16959082	17	9 801 736	3.907	1.038	2.869
	rs16959192	17	9 830 867	4.247	0.768	3.478
SCAP1	rs12948653	17	43 614 253	3.850	0.537	3.314
	rs10514935	17	43 615 673	3.819	3.821	−0.002
	rs9905961	17	43 711 363	4.335	3.317	1.019
GP6	rs11668169	19	60 227 294	3.852	1.318	2.533
	rs1671214	19	60 244 635	4.721	1.028	3.693
C20orf85	rs6513369	20	56 168 677	3.466	4.087	−0.621
	rs884341	20	56 170 080	2.983	4.114	−1.131

	rs6015215	20	56 178 326	0.083	5.618	−5.535
FBXO7	rs5754110	22	31 202 798	1.199	4.045	−2.846
	rs2267179	22	31 210 334	4.207	1.015	3.192
	rs738981	22	31 211 339	4.727	0.420	4.307
LARGE	rs2267293	22	32 536 110	3.856	1.429	2.427
	rs1894428	22	32 550 739	3.804	2.137	1.667
	rs1894429	22	32 550 994	5.594	1.918	3.675
Bupropion selective						
CACNA1E	rs3935384	1	179 760 627	1.044	3.589	−2.545
	rs12091137	1	179 807 389	1.201	4.322	−3.121
	rs12086466	1	179 807 435	1.865	4.237	−2.372
	rs723015	1	179 808 238	4.159	2.780	1.380
	rs10797838	1	179 808 677	1.424	3.995	−2.570
	rs10797839	1	179 809 454	1.304	4.688	−3.384
	rs10752898	1	179 809 553	1.349	4.015	−2.666
	rs2027085	1	179 840 268	1.566	4.141	−2.575
NAG	rs2049718	2	15 469 187	1.877	3.781	−1.904
	rs2031011	2	15 498 988	0.027	3.865	−3.838
	rs7568678	2	15 546 801	3.856	1.006	2.850
	rs2241237	2	15 606 755	3.998	3.414	0.584
	rs6710456	2	15 620 537	1.751	4.164	−2.412
	rs11694485	2	15 626 752	2.252	5.297	−3.045
GALNT13	rs10931861	2	154 650 478	2.824	3.950	−1.125
	rs12693888	2	154 668 170	2.445	3.953	−1.509
	rs1013694	2	154 686 856	3.003	3.838	−0.836
	rs7608978	2	154 715 317	0.068	5.751	−5.683
PLCL1	rs1607373	2	198 626 038	1.771	4.354	−2.583
	rs1518360	2	198 640 809	2.437	4.515	−2.078
	rs10177758	2	198 684 423	2.001	3.640	−1.640
	rs1371664	2	198 729 971	4.978	3.165	1.813
GALNT17	rs336006	4	173 735 675	0.300	4.024	−3.724
	rs10004745	4	173 769 727	0.797	3.710	−2.913
	rs1455126	4	173 842 252	1.330	3.994	−2.663
SIL1	rs7731574	5	138 482 091	0.658	4.368	−3.710
	rs13160445	5	138 545 134	1.567	3.672	−2.105
SDK1	rs12672248	7	3 333 145	1.936	4.888	−2.952
	rs10085602	7	3 406 258	2.864	6.486	−3.622
	rs2341447	7	3 476 429	0.642	3.628	−2.986
GPR37	rs12540261	7	124 180 788	0.294	3.583	−3.289
	rs12535807	7	124 185 384	0.020	3.684	−3.664
POT1	rs7806530	7	124 253 835	2.179	3.982	−1.803
	rs10269342	7	124 287 796	1.751	4.123	−2.372
C9orf47	rs10991722	9	90 797 821	1.242	5.038	−3.796
	rs10820820	9	90 810 753	0.230	7.271	−7.041
EDG3	rs10991722	9	90 797 821	1.242	5.038	−3.796
	rs10820820	9	90 810 753	0.230	7.271	−7.041
SUFU	rs4919652	10	104 264 147	3.885	0.414	3.472
	rs10786684	10	104 313 018	0.436	4.572	−4.136
	rs10786685	10	104 313 093	0.218	4.554	−4.336
	rs4917976	10	104 350 508	0.300	3.814	−3.514

	rs7075269	10	104 355 714	1.462	4.040	−2.578
	rs7907417	10	104 360 652	0.218	3.892	−3.674
BRWD2	rs10788126	10	122 647 189	0.322	6.938	−6.615
	rs6585674	10	122 648 007	0.346	4.593	−4.247
	rs1530116	10	122 657 012	0.167	3.960	−3.793
TUB	rs4758287	11	8 056 489	1.045	4.309	−3.264
	rs11041740	11	8 074 094	0.118	4.705	−4.587
	rs1055233	11	8 084 071	0.208	4.100	−3.892
	rs4343012	11	8 089 751	1.284	4.875	−3.591
	rs10734629	11	8 143 253	2.098	5.753	−3.654
RIC3	rs1055233	11	8 084 071	0.208	4.100	−3.892
	rs4343012	11	8 089 751	1.284	4.875	−3.591
	rs10839984	11	8 137 470	1.203	4.538	−3.336
NCAM1	rs6589354	11	112 383 757	1.983	3.853	−1.870
	rs12794745	11	112 456 919	2.520	4.552	−2.032
	rs11214501	11	112 490 687	0.209	4.292	−4.083
	rs4937993	11	112 509 872	0.300	3.911	−3.611
	rs10891510	11	112 513 370	2.199	4.366	−2.167
OR8F1P	rs4935872	11	123 581 205	2.018	3.730	−1.712
	rs4936911	11	123 581 430	2.754	4.861	−2.108
	rs10893162	11	123 581 479	1.518	6.045	−4.527
	rs10893168	11	123 584 949	1.727	4.214	−2.487
	rs2512284	11	123 591 632	4.030	2.751	1.279
OR8G3P	rs4935872	11	123 581 205	2.018	3.730	−1.712
	rs4936911	11	123 581 430	2.754	4.861	−2.108
	rs10893162	11	123 581 479	1.518	6.045	−4.527
	rs10893168	11	123 584 949	1.727	4.214	−2.487
	rs2512284	11	123 591 632	4.030	2.751	1.279
OR8D1	rs10893205	11	123 677 775	2.606	5.512	−2.906
	rs10893206	11	123 680 084	1.069	3.704	−2.634
	rs7107539	11	123 685 492	2.121	3.629	−1.508
	rs7107539	11	123 685 492	2.121	3.629	−1.508
OAS1	rs4766674	12	111 827 921	3.054	6.153	−3.098
	rs10774679	12	111 837 468	2.179	3.925	−1.746
POSTN	rs7995907	13	37 033 780	1.297	4.473	−3.177
	rs9576309	13	37 059 563	1.000	4.275	−3.275
VGCNL1	rs11069434	13	100 681 085	1.042	3.676	−2.635
	rs1333758	13	100 695 884	2.781	5.693	−2.912
	rs509933	13	100 768 557	3.133	4.536	−1.403
KIAA0672	rs7223372	17	12 713 626	1.548	4.808	−3.260
	rs7209847	17	12 745 275	1.926	4.274	−2.348
	rs6502214	17	12 749 964	3.720	2.413	1.306
DOK6	rs10084092	18	65 430 704	1.232	4.870	−3.638
	rs10871647	18	65 466 878	1.992	4.060	−2.068
	rs4243315	18	65 484 826	2.386	4.238	−1.852
PEPD	rs1477336	19	38 638 733	4.466	3.459	1.007
	rs17761012	19	38 642 117	1.600	3.877	−2.277
	rs3786922	19	38 698 220	2.443	4.525	−2.082
CYP2A7P1	rs10419393	19	46 096 036	2.804	3.745	−0.941
	rs3844443	19	46 123 775	1.149	4.630	−3.481
	rs7251950	19	46 174 582	1.139	4.052	−2.914

Abbreviations: chr, chromomome; NRT, nicotine replacement therapy; SNP, single-nucleotide polymorphism.

[a] We determined SNPs that displayed t values corresponding to $P < .005$ for the differences in successful abstinence for NRT vs placebo treatment ($t > 3.69$), bupropion hydrochloride vs placebo treatment ($t > 3.58$), or both. Genes identified by at least 2 such SNPs were identified as noted in the "Methods" section of the text, and those for which most SNPs were NRT, those for which most SNPs were bupropion specific, and those for which there was no clear treatment specificity are listed. The SNPs listed in this table as identifying the genes listed herein cluster within small chromosomal regions to extents much greater than that expected by chance (Monte Carlo $P < .00001$).

[b] Indicates clustered SNPs that identify the genes.

[c] Indicates the differences in allelic frequencies between the active therapy vs placebo.

[d] Indicates the difference between the t values in the 2 preceding columns.