Table S2. Single Nucleotide Polymorphism discovery by genomic resequencing in seven α-like nAChR subunits (α2, α3, α4, α5, α6, α9, and α10) and three β-like nAChR subunits (β2, β3, and β4). Resequencing was performed on 192 individuals of Northern European descent. The individuals were chosen based on a high (n=72) and low (n=72) dependence scale and nonsmokers (n=48). Chromosomal positions ('Position') are based on the NCBI Human Genome Build 35 (May 2004). 'Imp.' designates annotation of SNP location, and 'Major' – 'Minor' allele assignments are based on the forward strand of the chromosome. Linkage disequilibrium groups ('LD Group') were determined using the ldSelect algorithm [68] at a threshold r^2 value of 0.64 on the 192 individuals across a gene or gene group (based on close proximity) and assigned a unique number. Genes are ordered by ascending chromosome number. The *P*-values are Fisher exact allele tests of high vs. low nicotine dependence with minor allele frequencies shown for these groups. The 'Genotyped' column indicates polymorphisms typed on the larger cohort.

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
CHRNB2: Chr 1	151353472	UTR	C	A		0.01	0.01	-	rs56205574	
	151353541	UTR	C	T	2	0.11	0.10	0.84	rs2280781	+
	151354912	intronic	A	T		0.04	0.02	0.45	rs8192484	
	151355288	intronic	G	A		0.01	0.01	-	rs55698310	
	151357563	non	G	C		0.01	0.01	-	rs55685423	
	151357605	synon	G	A		0.01	0.01	-	rs55857552	
	151357724	intronic	G	T	2	0.12	0.07	0.21	rs4845378	
	151357735	intronic	G	A		0.01	0.01	-	rs56146528	
	151361594	UTR	C	G		0.07	0.09	0.67	rs2072659	+
	151361794	UTR	C	T	1	0.30	0.20	0.07	rs2072660	+
	151361953	UTR	G	A	2	0.30	0.22	0.17	rs2072661	
	151362019	UTR	C	T	3	0.06	0.08	0.49	rs4292956	+

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	151362065	UTR	C	T	3	0.06	0.06	1.00	rs45490696	
CHRNA9: Chr 4										
	40178152	flank	C	A	4	0.30	0.28	0.89	rs372211	
	40178176	flank	A	T	4	0.30	0.28	0.79	rs4469116	+
	40178236	flank	A	T	4	0.30	0.28	0.70	rs4359945	
	40178241	flank	G	A		0.00	0.01	-	rs55725809	
	40178244	flank	C	T		0.01	0.03	0.68	rs6544304	
	40178451	synon	C	T	4	0.36	0.31	0.45	rs56241474	
	40178494	intronic	C	T		0.21	0.25	0.48	rs10015231	
	40178836	synon	C	T	6	0.40	0.41	0.90	rs10022491	+
	40178872	synon	C	T	4	0.31	0.28	0.70	rs56159866	
	40178896	synon	G	A		0.01	0.03	0.45	rs55974552	
	40178905	synon	G	A		<0.01	0.01	-	rs56171884	
	40178934	intronic	G	A		<0.01	0.01	-	rs56299220	
	40179007	intronic	G	A		0.03	0.05	0.54	rs55893318	
	40179152	intronic	T	C		<0.01	<0.01	1.00	rs55947729	
	40179971	intronic	-	A		0.06	0.04	0.57	rs10419703	
	40180010	intronic	A	G		<0.01	<0.01	-	rs55698633	
	40180065	intronic	G	C		0.06	0.04	0.79	rs6447332	
	40180178	synon	T	C		0.01	0.01	-	rs55998310	
	40180502	intronic	G	A	6	0.45	0.48	0.72	rs6819385	+
	40191579	intronic	G	A	4	0.36	0.33	0.69	rs7669882	+
	40191591	intronic	C	T	4	0.36	0.33	0.69	rs6447450	
	40191691	intronic	T	C	6	0.43	0.51	0.16	rs10029872	
	40192136	synon	G	A		<0.01	0.01	-	rs55665751	
	40192176	non	T	C		0.01	<0.01	-	rs56205779	
	40192387	intronic	C	A		0.01	<0.01	-	rs55660233	
	40192468	intronic	T	A		0.03	0.02	1.00	rs56078044	
	40196666	intronic	T	-	5	0.16	0.13	0.51	rs55692533	
	40196731	intronic	C	A	5	0.16	0.13	0.51	rs56012618	
	40196743	intronic	A	G	5	0.19	0.19	1.00	rs4861323	
	40196959	non	G	A		0.01	<0.01	-	rs56210055	
	40196969	non	C	T	5	0.17	0.14	0.52	rs55633891	
	40197161	non	A	G		<0.01	<0.01	-	rs56098158	
	40197220	non	C	T		0.01	<0.01	-	rs55962300	
	40197350	non	G	A	5	0.20	0.19	0.88	rs10009228	
	40197642	UTR	T	A		0.03	0.06	0.38	rs4861327	
	40197708	UTR	G	A	4	0.31	0.27	0.52	rs6819816	

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	40197827	UTR	C	T		0.05	0.04	0.78	rs56291234	
CHRNA2: Chr 8										
	27374308	UTR	C	T	10	0.44	0.45	0.88	rs2292974	
	27374342	UTR	C	A	10	0.41	0.45	0.56	rs2292975	+
	27374461	UTR	G	A	7	0.15	0.20	0.34	rs2292976	
	27374552	UTR	G	C	7	0.14	0.20	0.34	rs2292977	
	27375209	intronic	A	G		0.27	0.29	0.87	rs735421	+
	27376443	non	G	T		<0.01	0.01	-	rs56344740	
	27376553	synon	G	A		0.03	0.01	0.45	rs56298562	
	27376814	non	G	C		<0.01	0.01	-	rs56339365	
	27376892	non	C	T		<0.01	<0.01	-	rs56371471	
	27377043	synon	G	A		<0.01	0.01	-	rs56189058	
	27377106	synon	G	A		0.02	0.01	0.62	rs56229264	
	27380739	non	T	C	9	0.48	0.48	1.00	rs891398	+
	27380761	synon	G	A	7	0.13	0.13	1.00	rs2565061	+
	27380841	intronic	C	T		0.00	0.01	1.00	rs55698463	
	27381108	intronic	G	T	7	0.14	0.15	0.87	rs2099166	
	27382758	intronic	GG	-	9	0.47	0.46	1.00	rs3832545	
	27384184	intronic	C	T	7	0.11	0.12	1.00	rs2565066	
	27384271	intronic	C	G		0.33	0.28	0.37	rs2472554	+
	27384326	intronic	G	A		0.01	0.01	-	rs55965307	
	27384428	non	G	A	7	0.13	0.13	1.00	rs2472553	+
	27384537	UTR	G	T	8	0.01	0.00	-	rs12114756	
	27384705	intronic	C	A		<0.01	0.01	-	rs55954528	
	27392419	UTR	G	T	8	0.01	<0.01	-	rs55934039	
	27392545	UTR	G	A		<0.01	0.02	0.11	rs55726427	
	27392664	UTR	C	T		<0.01	0.01	-	rs56032736	
	27392684	flank	A	T	8	0.01	<0.01	-	rs2565060	
	27392699	flank	T	C	8	0.01	<0.01	-	rs34206731	
	27392703	flank	C	T	8	0.01	<0.01	-	rs56278204	
CHRNB3: Chr 8										
	42671628	flank	G	T		<0.01	0.01	-	rs56279199	
	42671687	flank	G	C		0.01	0.01	-	rs41272375	
	42671790	UTR	A	G		0.19	0.25	0.31	rs4950	+
	42672020	intronic	A	T		0.01	0.02	0.36	rs55920715	
	42683143	non	T	G		<0.01	0.01	-	rs56357313	
	42684671	intronic	T	-		<0.01	0.01	-	rs55786845	
	42704851	intronic	T	C	12	0.08	0.05	0.47	rs55817013	

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	42706222	synon	C	T	12	0.06	0.04	0.57	rs4952	
	42706709	non	G	A		0.01	0.01	-	rs56198260	
	42706816	synon	G	C	12	0.06	0.04	0.57	rs4953	+
	42710763	intronic	G	A		<0.01	<0.01	-	rs55924223	
	42710995	UTR	G	A		0.01	0.01	-	rs56313404	
CHRNA6: Chr 8										
	42726938	flank	T	A	11	0.17	0.22	0.29	rs7832639	
	42726994	UTR	G	A		0.01	<0.01	-	rs55776131	
	42727068	UTR	T	C		0.03	0.00	0.06	rs41265262	
	42727243	UTR	C	T		0.01	0.00	-	rs56044754	
	42727356	UTR	G	C	11	0.21	0.28	0.17	rs2304297	
	42727538	non	C	T		0.00	0.00	-	rs55662044	
	42727720	intronic	G	A	11	0.14	0.23	0.07	rs7845663	
	42730880	stop	C	A		<0.01	0.01	-	rs56315032	
	42731021	frameshift	T	-		0.01	<0.01	-	rs56229628	
	42731443	intronic	G	A	11	0.14	0.24	0.04	rs7000412	
	42731535	intronic	C	A	11	0.14	0.24	0.05	rs7001753	
	42733291	intronic	T	C		0.00	0.01	-	rs55984829	
	42733535	intronic	C	A	11	0.16	0.25	0.08	rs892413	+
	42739158	intronic	C	G	11	0.15	0.24	0.05	rs1072003	+
	42739555	intronic	C	T		0.01	<0.01	-	rs56238139	
	42739561	intronic	C	A		0.01	0.03	0.21	rs11985288	
	42742951	flank	ATG	-		0.02	0.01	0.62	rs56376656	
CHRNA10: Chr 11										
	3643303	flank	G	A		0.13	0.11	0.70	rs56084560	
	3643385	flank	C	T	14	0.05	0.05	1.00	rs12269960	
	3643435	UTR	C	G		<0.01	0.01	-	rs12711988	
	3643520	UTR	C	G	16	<0.01	0.02	0.25	rs12221525	
	3643625	UTR	T	A	14	0.06	0.06	1.00	rs55798582	
	3644005	non	G	A		<0.01	0.01	-	rs2231548	
	3644050	non	A	G		<0.01	<0.01	-	rs55650071	
	3644052	non	G	T		0.01	<0.01	-	rs56054950	
	3644202	non	T	G	14	0.06	0.06	1.00	rs2231547	
	3644227	non	C	T	14	0.06	0.06	1.00	rs2231546	
	3644561	intronic	A	G	13	0.29	0.27	0.79	rs2741862	+
	3644640	intronic	TTTA	-		0.01	<0.01	0.50	rs55839829	
	3644804	intronic	G	A	13	0.36	0.35	0.88	rs2741861	
	3644856	intronic	G	C	17	<0.01	0.01	-	rs56101595	

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	3646686	intronic	A	G		<0.01	0.01	-	rs55836061	
	3646697	intronic	G	A		0.01	<0.01	-	rs55933520	
	3646759	intronic	G	A	13	0.01	<0.01	-	rs2741868	+
	3646854	intronic	T	C	13	0.35	0.36	0.80	rs2672211	
	3647134	non	G	T	15	0.04	0.02	0.50	rs55719530	
	3647174	intronic	T	A	15	0.04	0.02	0.50	rs56167171	
	3647338	intronic	CT	-		0.18	0.15	0.63	rs3996926	
	3647347	intronic	A	-	17	<0.01	0.01	1.00	rs55794740	
	3647439	intronic	A	C		0.01	0.04	0.45	rs11028916	
	3647450	intronic	14nts[1]	-		<0.01	<0.01	-	rs56081677	
	3647789	intronic	T	A		<0.01	0.01	-	rs55716405	
	3647913	intronic	G	C		<0.01	<0.01	-	rs55966314	
	3647993	intronic	C	T		0.18	0.12	0.23	rs2672213	+
	3648013	intronic	T	G	18	<0.01	<0.01	-	rs16942496	
	3648088	intronic	T	C	13	0.33	0.34	0.90	rs2672214	
	3649205	flank	A	G	18	<0.01	0.01	-	rs55982775	
	3649219	flank	G	T	16	<0.01	0.03	0.12	rs2231536	
	3649354	flank	C	G		<0.01	0.01	-	rs55886645	
CHRNA5: Chr 15										
	76644934	flank	G	A		<0.01	0.01	-	rs56182392	
	76644951	flank	T	A	21	0.22	0.22	1.00	rs503464	
	76644994	UTR	T	G	20	0.49	0.38	0.10	rs55853698	
	76645041	UTR	C	G	20	0.49	0.38	0.11	rs55781567	
	76651079	intronic	C	T		0.02	0.02	1.00	rs56219480	
	76651199	intronic	G	A		<0.01	<0.01	-	rs55758640	
	76660174	intronic	C	T	21	0.18	0.22	0.45	rs569207	+
	76660327	non	T	G		<0.01	<0.01	-	rs56351164	
	76665596	intronic	G	A	20	0.53	0.32	0.002	rs951266	
	76665620	intronic	C	T		<0.01	0.02	0.20	rs56160480	
	76665737	intronic	A	G		0.01	<0.01	-	rs56211565	
	76666023	intronic	A	C		<0.01	0.01	-	rs56257539	
	76666113	intronic	C	T		0.01	0.01	-	rs55982512	
	76666297	intronic	A	G	19	0.31	0.45	0.03	rs555018	+
	76667536	intronic	C	T	19	0.31	0.35	0.60	rs647041	
	76667632	intronic	G	C	22	0.05	0.06	0.60	rs12898919	
	76667748	non	A	G	24	0.01	0.00	-	rs56023835	
	76667807	non	G	A		0.04	0.02	0.45	rs2229961	+

[1] Major Allele: TCAGTACCCAACAG

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	76668142	intronic	G	A	22	0.06	0.07	0.79	rs12903575	+
	76669007	intronic	T	C		<0.01	<0.01	-	rs56186290	
	76669059	intronic	C	T		0.01	<0.01	-	rs56201623	
	76669159	intronic	T	C		0.01	0.01	-	rs56134824	
	76669276	non	C	T		0.00	0.01	-	rs55863434	
	76669980	non	G	A	20	0.50	0.34	0.008	rs16969968	+
	76673043	UTR	C	T	19	0.28	0.38	0.09	rs615470	
	76673204	UTR	G	A		<0.01	<0.01	-	rs8192483	
	76673213	UTR	G	A		<0.01	0.02	0.22	rs55783657	
	76673253	UTR	C	T	20	0.51	0.32	0.003	rs8192482	
	76673282	UTR	A	G	21	0.20	0.27	0.24	rs564585	
	76673903	flank	G	A		<0.01	0.01	-	rs55989223	
	76673947	flank	C	T		<0.01	0.01	-	rs56255741	
	76674002	flank	G	A	20	0.49	0.34	0.01	rs4887067	
CHRNA3: Chr 15										
	76674415	flank	A	C		0.01	<0.01	-	rs55919839	
	76674493	flank	T	G	22	0.04	0.06	0.44	rs12899226	
	76674550	flank	G	A		<0.01	0.01	-	rs55736590	
	76674770	UTR	TCTC	-	19	0.29	0.38	0.13	rs56297775	
	76674887	UTR	G	A	19	0.29	0.38	0.13	rs660652	
	76675049	UTR	G	A	19	0.29	0.38	0.13	rs472054	
	76675098	UTR	13nts[2]	-		<0.01	<0.01	-	rs55948826	
	76675213	UTR	G	A		<0.01	0.01	-	rs56148181	
	76675293	UTR	3(C)	7(C)	21	0.1	0.2	0.60	rs10637216	
	76675406	UTR	G	A		0.01	0.01	1.00	rs56113144	
	76675455	UTR	G	A		0.21	0.26	0.40	rs578776	+
	76675568	UTR	10nts[3]	-		<0.01	0.01	-	rs55820134	
	76675663	UTR	A	G	24	0.01	<0.01	-	rs56256191	
	76680842	synon	G	A		0.01	0.01	-	rs56403513	
	76680914	synon	G	A		0.01	<0.01	-	rs56179957	
	76681338	non	G	A		0.01	<0.01	-	rs56371320	
	76681394	synon	G	A	20	0.49	0.36	0.02	rs1051730	+
	76681412	synon	G	T		0.01	0.01	-	rs55958820	
	76681475	synon	A	G		0.01	0.01	-	rs8192480	
	76696453	synon	C	T		0.06	0.01	0.10	rs8192479	
	76696507	synon	C	T	19	0.28	0.37	0.13	rs3743075	

[2] Major Allele: ATGCTGTGGTCCA
[3] Major Allele: TAGGGTAACG

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	76696535	intronic	A	G	19	0.29	0.38	0.13	rs3743074	
	76696594	intronic	T	G	19	0.29	0.38	0.13	rs3743073	
	76696612	intronic	G	A		0.01	<0.01	-	rs41280050	
	76698094	intronic	-	A	22	0.03	0.06	0.41	rs34844435	
	76698135	intronic	G	A		<0.01	0.01	-	rs56409843	
	76698236	synon	T	C	20	0.54	0.42	0.03	rs8040868	
	76698285	non	C	T	22	0.04	0.06	0.59	rs8192475	+
	76700428	flank	VNTR[4]						rs55787222	
CHRNB4: Chr 15										
	76703677	flank	G	C	19	0.29	0.39	0.08	rs2904130	
	76704371	UTR	C	T		0.02	0.01	0.67	rs55952530	
	76704454	UTR	G	A	19	0.27	0.38	0.05	rs1948	
	76708372	non	C	A		<0.01	<0.01	-	rs56258098	
	76708398	non	G	A		0.01	<0.01	-	rs56317523	+
	76708657	non	G	A		0.01	0.01	-	rs56235003	
	76708817	synon	G	A	23	0.01	0.01	-	rs3743072	
	76708862	synon	G	A		0.00	0.01	-	rs55859769	
	76709249	synon	G	A		0.05	0.04	1.00	rs55919125	
	76709284	non	T	C	23	<0.01	0.01	-	rs56218866	+
	76709288	synon	G	A		0.01	<0.01	-	rs55851389	
	76709295	non	C	T		0.01	0.02	0.62	rs56095004	+
	76710560	non	G	A	22	0.04	0.07	0.29	rs12914008	
	76710776	intronic	C	G		0.01	<0.01	-	rs55647022	
	76710900	intronic	T	G	21	0.16	0.22	0.23	rs28534575	
	76711042	intronic	C	T	20	0.48	0.28	0.001	rs17487223	
	76713781	intronic	C	G	21	0.17	0.22	0.43	rs12440014	
	76714644	intronic	T	G		0.01	0.01	-	rs12440298	
	76714827	intronic	T	C		<0.01	0.01	-	rs56011563	
	76715319	intronic	T	G		0.20	0.21	1.00	rs12441088	
CHRNA4: Chr 20										
	61446974	UTR	C	T	26	0.06	0.06	1.00	rs45476096	+
	61447364	UTR	T	C	26	0.06	0.06	1.00	rs41283006	
	61447445	UTR	C	T		<0.01	<0.01	-	rs55985535	
	61447459	UTR	C	T	26	0.06	0.06	1.00	rs41283008	
	61447493	UTR	G	C	26	0.06	0.06	1.00	rs41283010	
	61447553	UTR	C	T		0.01	0.01	-	rs55715203	

[4] Variable Nucleotide Repeat Frequencies: 4(GGCG) 0.510, 2(GGCG) 0.465, 5(GGCG) 0.025

Gene: Chromosome	Position	Imp.	Major	Minor	LD Group	Freq. High	Freq. Low	P value	refSNP ID	Genotyped
	61447587	UTR	C	T		0.01	0.01	-	rs56339657	
	61447666	UTR	G	A		0.00	0.01	-	rs56164905	
	61447762	UTR	G	T		0.02	0.04	0.72	rs45607838	
	61447779	UTR	A	G		0.08	0.10	0.84	rs45624232	
	61447817	UTR	G	A	26	0.06	0.06	1.00	rs45556643	
	61451397	intronic	G	A		<0.01	0.01	-	rs56160350	
	61451435	intronic	T	C	29	0.17	0.17	1.00	rs3827020	
	61451438	intronic	G	A		0.10	0.05	0.24	rs45442394	
	61451546	non	G	A	31	<0.01	0.01	-	rs56000199	
	61451548	synon	T	C	30	0.41	0.42	1.00	rs1044397	+
	61451578	synon	A	G	30	0.41	0.41	1.00	rs1044396	+
	61451759	non	C	T		<0.01	0.02	0.25	rs55855125	
	61451806	synon	G	A		<0.01	<0.01	-	rs45569837	
	61451855	non	G	A	31	<0.01	0.01	-	rs55915440	
	61451980	synon	G	A	27	0.05	0.05	1.00	rs2229960	
	61451998	synon	A	C	28	0.13	0.10	0.55	rs2229959	
	61452004	synon	C	G		<0.01	0.01	-	rs56142348	
	61452201	non	G	A		0.01	<0.01	-	rs56175056	
	61452529	synon	G	A	27	0.05	0.05	1.00	rs1044394	+
	61452568	synon	G	A	28	0.13	0.10	0.43	rs1044393	+
	61452846	intronic	G	A	26	0.06	0.06	1.00	rs56151028	
	61452940	intronic	C	T	28	0.14	0.11	0.70	rs13041103	
	61452956	intronic	C	T	25	0.12	0.07	0.26	rs55731226	
	61452958	intronic	T	C		0.04	0.02	0.50	rs55786941	
	61452967	intronic	C	-	27	0.03	0.04	0.72	rs55869461	
	61457989	intronic	G	-	25	0.27	0.08	0.13	rs56305048	
	61458015	intronic	C	T		0.08	0.00	0.49	rs56148915	
	61458016	intronic	G	A	25	0.21	0.08	0.42	rs56019702	
	61458019	intronic	A	G		<0.01	<0.01	-	rs55683444	
	61458266	intronic	C	T	25	0.41	0.46	0.81	rs2273502	+
	61461175	intronic	G	T		0.04	0.04	0.77	rs45539234	
	61461318	intronic	C	T	27	0.04	0.04	1.00	rs6090384	
	61461322	intronic	C	T	25	0.09	0.06	0.26	rs2273505	
	61461383	synon	G	A	25	0.09	0.06	0.26	rs2273506	
	61461585	intronic	G	A	29	0.21	0.18	0.65	rs3818204	+
	61461665	intronic	G	C		0.17	0.17	1.00	rs13044665	