Supp. Table S1. Full results for all directly genotyped markers in ABCA1 in dementia cases vs. control

Marker	Assoc Allele	Case,Control Counts	Case,Control Freq.	Chi square	P value	SNP type	Strand
rs363717	A	2533:539, 3513:847	0.825, 0.806	4.20	4.03E-02	[A/G]	(-)
rs4149338	A	943:2121, 1299:3055	0.308, 0.298	0.76	3.84E-01	[A/G]	(+)
rs2482433	G	900:2134, 1252:3082	0.297, 0.289	0.52	4.71E-01	[A/G]	(+)
rs2740485	A	2823:253, 3962:398	0.918, 0.909	1.84	1.75E-01	[A/C]	(-)
rs2066881	A	2901:177, 4088:270	0.942, 0.938	0.63	4.27E-01	[A/G]	(-)
rs4149336	A	2566:510, 3614:742	0.834, 0.830	0.27	6.07E-01	[A/G]	(+)
rs2297406	G	2075:933, 2974:1340	0.690, 0.689	0.00	9.68E-01	[A/G]	(-)
rs2020927	G	363:2713, 509:3851	0.118, 0.117	0.03	8.67E-01	[A/G]	(+)
rs2230808	G	2408:660, 3398:960	0.785, 0.780	0.28	5.96E-01	[A/G]	(-)
rs2297404	G	2849:227, 4013:345	0.926, 0.921	0.73	3.92E-01	[C/G]	(-)
rs2777801	A	2770:290, 3907:437	0.905, 0.899	0.69	4.07E-01	[A/C]	(+)
rs2066716	G	2850:190, 3999:347	0.938, 0.920	7.98	4.70E-03	[A/G]	(-)
rs2297409	G	2524:538, 3553:793	0.824, 0.818	0.56	4.55E-01	[A/G]	(+)
rs33918808	C	2995:75, 4226:126	0.976, 0.971	1.40	2.37E-01	[C/G]	(+)
rs4149313	G	312:2756, 443:3917	0.102, 0.102	0.00	9.90E-01	[A/G]	(-)
rs2066717	A	156:2908, 217:4133	0.051, 0.050	0.04	8.42E-01	[A/G]	(+)
rs2065412	G	1469:1519, 1952:2372	0.492, 0.451	11.47	7.00E-04	[A/G]	(-)
rs2515601	A	2768:274, 3875:465	0.910, 0.893	5.79	1.62E-02	[A/G]	(+)
rs2472386	G	2157:889, 2966:1384	0.708, 0.682	5.82	1.58E-02	[A/G]	(+)
rs2274873	G	2725:265, 3834:410	0.911, 0.903	1.32	2.51E-01	[A/G]	(+)
rs4149291	C	2745:331, 3801:545	0.892, 0.875	5.48	1.92E-02	[C/G]	(+)
rs1175293	A	2884:184, 4083:265	0.940, 0.939	0.03	8.63E-01	[A/G]	(-)
rs2230806	G	2363:645, 3200:1096	0.786, 0.745	16.14	5.89E-05	[A/G]	(-)
rs2230805	G	2320:498, 3161:945	0.823, 0.770	28.92	7.55E-08	[A/G]	(-)
rs4149271	G	2465:601, 3451:903	0.804, 0.793	1.44	2.30E-01	[A/G]	(+)
rs11789603	G	2794:284, 3894:464	0.908, 0.894	4.02	4.49E-02	[A/G]	(-)
rs4149268	G	1963:1103, 2768:1588	0.640, 0.635	0.18	6.72E-01	[A/G]	(-)
rs3890182	A	404:2670, 553:3805	0.131, 0.127	0.33	5.66E-01	[A/G]	(+)
rs10120087	C	2769:301, 3891:465	0.902, 0.893	1.48	2.25E-01	[A/C]	(+)
rs2740487	A	1443:1617, 2024:2336	0.472, 0.464	0.39	5.32E-01	[A/G]	(+)
rs2777793	A	1380:1690, 1950:2398	0.450, 0.448	0.01	9.30E-01	[A/G]	(-)
rs3905001	G	2185:757, 3041:1149	0.743, 0.726	2.53	1.12E-01	[C/G]	(+)
rs2575879	C	1426:1638, 1956:2388	0.465, 0.450	1.66	1.98E-01	[C/G]	(+)
rs10820743	G	865:2193, 1177:3159	0.283, 0.271	1.17	2.80E-01	[A/G]	(-)
rs4149264	C	663:2401, 840:3518	0.216, 0.193	6.22	1.26E-02	[C/G]	(+)
rs4149262	T	268:2788, 373:3961	0.088, 0.086	0.06	8.06E-01	[A/T]	(+)
rs12350560	G	2824:246, 3907:433	0.920, 0.900	8.33	3.90E-03	[A/G]	(+)
rs2437811	A	2481:589, 3512:846	0.808, 0.806	0.06	8.07E-01	[A/G]	(-)
rs10991414	G	456:2536, 646:3614	0.152, 0.152	0.01	9.29E-01	[A/G]	(-)
rs2472377	G	1594:1366, 2269:2019	0.539, 0.529	0.62	4.32E-01	[A/G]	(-)
rs1800977	G	1955:1075, 2769:1561	0.645, 0.639	0.25	6.14E-01	[A/G]	(+)
rs2246293	G	1399:1557, 2007:2255	0.473, 0.471	0.04	8.43E-01	[C/G]	(+)
rs2043664	G	2203:871, 3113:1245	0.717, 0.714	0.05	8.26E-01	[A/G]	(+)
rs2487042	G	2351:667, 3351:981	0.779, 0.774	0.30	5.82E-01	[A/G]	(-)
rs2472496	G	1333:1711, 1882:2450	0.438, 0.434	0.09	7.67E-01	[A/G]	(+)

Marker	Assoc Allele	Case,Control Counts	Case,Control Freq.	Chi square	P value	SNP type	Strand
rs3887137	A	362:2656, 498:3708	0.120, 0.118	0.04	8.42E-01	[A/G]	(-)

All results are based upon simple allele counts in 2x2 chi-square contingency tables. The threshold for significance considering 46 tests and strict Bonferroni correction is P = 1.1E-03. For each associated allele and SNP type, strand is shown relative to the reference sequence of the human genome.

Supp. Table S2. Haplotype frequencies in cases and controls for directly typed variants in ABCA1

Haplotype	Case,Control Ratio Counts	Case,Control Freq.	Chi Square	P Value
Block 3 (markers 8-12)				
AGGAG	2206:869,3030:1319	0.717, 0.697	3.675	5.52E-02
AAGCG	269:2806,412:3937	0.088, 0.095	1.083	2.98E-01
GACAG	227:2848,342:4007	0.074, 0.079	0.575	4.48E-01
AGGAA	193:2882,347:4003	0.063, 0.080	7.697	5.50E-03
GAGAG	119:2956,149:4200	0.039, 0.034	1.009	3.15E-01
AAGAG	33:3042,40:4309	0.011, 0.009	0.504	4.78E-01
Block 5 (markers 15-20)				
AGGAGG	1506:1563,1958:2387	0.491, 0.451	11.706	6.00E-04
AGAAGG	662:2407,1004:3341	0.216, 0.231	2.367	1.24E-01
AGAGAG	280:2790,467:3878	0.091, 0.108	5.344	2.08E-02
AGAAAA	288:2781,450:3896	0.094, 0.104	1.833	1.76E-01
GGAAAG	154:2915,225:4121	0.050, 0.052	0.095	7.58E-01
GAAAAG	158:2911,212:4134	0.052, 0.049	0.303	5.82E-01
Block 6 (markers 21-24)				
CAGG	2178:897,2897:1458	0.708, 0.665	15.462	8.42E-05
CAAA	325:2750,557:3798	0.106, 0.128	8.443	3.70E-03
GAAA	260:2815,449:3906	0.085, 0.103	7.208	7.30E-03
CGGG	183:2892,265:4090	0.060, 0.061	0.054	8.16E-01
GAAG	51:3024,81:4274	0.017, 0.019	0.335	5.63E-01
Block 8 (markers 31-33)				
GCA	1384:1693,1888:2471	0.450, 0.433	2.031	1.54E-01
AGG	773:2304,1062:3297	0.251, 0.244	0.567	4.52E-01
AGA	565:2512,822:3537	0.184, 0.189	0.294	5.88E-01
GGA	207:2870,387:3972	0.067, 0.089	11.328	8.00E-04
GGG	98:2979,121:4238	0.032, 0.028	1.038	3.08E-01
ACA	45:3032,71:4288	0.015, 0.016	0.316	5.74E-01
Block 9 (markers 34-37)				
GAGA	1303:1774,1864:2493	0.423, 0.428	0.147	7.02E-01
CAGA	666:2411,840:3517	0.217, 0.193	6.22	1.26E-02
GAGG	591:2487,844:3513	0.192, 0.194	0.034	8.53E-01
GAAA	247:2831,434:3923	0.080, 0.100	8.266	4.00E-03
GTGA	270:2807,373:3984	0.088, 0.086	0.102	7.49E-01

Only blocks in which one or more haplotypes were significant at $p < 0.05$ are shown. The illustration below shows block locations and intervals, defined by LD of solid splines. Eleven blocks were predicted and are shown from left to right as bounded regions. Both rs2230805 and rs2230806 occur in block 6. Shading for LD is according to D'. Marker numbering for blocks is according to Supp. Table S1. The threshold for significance considering 48 independent haplotype tests is P = 1.1E-03.