Supplementary Materials

Supplementary Table 1: AD-associated genes based on a FDR 10% cutoff and the most-significant SNP responsible for the identification of the gene as AD-related.

	Most-significant SNP within 5 kb							
GENE	rsID	CHR	bp	p-value	nSNP	EFFn	$p_{corrected}$	FDR
APOC1	rs4420638	19	45,422,946	<1E-300	4	4	<1E-300	<1E-300
TOMM40	rs6857	19	45,392,254	2.03E-200	9	5	1.02E-199	1.63E-195
PVRL2	rs6857	19	45,392,254	2.03E-200	39	14	2.84E-199	3.04E-195
APOE	rs10119	19	45,406,673	6.24E-125	5	4	2.50E-124	2.00E-120
BCAM	rs10402271	19	45,329,214	8.72E-44	8	6	5.23E-43	3.36E-39
EIF5AP3	rs1114832	19	45,636,201	3.21E-18	4	2	6.41E-18	3.43E-14
LRRC68	rs1114832	19	45,636,201	3.21E-18	34	7	2.24E-17	1.03E-13
NKPD1	rs1048699	19	45,650,386	6.15E-18	7	5	3.07E-17	1.23E-13
BCL3	rs8100239	19	45,253,104	2.01E-14	3	3	6.03E-14	2.15E-10
MS4A4A	rs10792263	11	60,079,651	2.88E-11	38	9	2.59E-10	8.33E-07
MS4A6E	rs4939338	11	60,099,225	2.58E-11	44	13	3.35E-10	9.76E-07
CLPTM1	rs16979595	19	45,477,381	8.47E-10	31	5	4.23E-09	1.13E-05
CR1	rs6656401	1	207,692,049	3.41E-10	80	17	5.79E-09	1.43E-05
EXOC3L2	rs10415983	19	45,711,598	1.26E-09	18	6	7.55E-09	1.73E-05
MS4A4E	rs1426250	11	60,001,325	1.75E-09	50	6	1.05E-08	2.25E-05
MS4A6A	rs17602572	11	59,948,374	4.09E-09	15	3	1.23E-08	2.46E-05
PICALM	rs669813	11	85,762,244	1.37E-09	126	17	2.33E-08	4.41E-05
RELB	rs10424046	19	45,536,036	6.25E-08	8	4	2.50E-07	4.43E-04
CLASRP	rs1560725	19	45,543,787	1.31E-07	10	2	2.63E-07	4.43E-04
APOC2	rs5167	19	45,448,465	1.28E-07	15	4	5.12E-07	7.47E-04
APOC4	rs5167	19	45,448,465	1.28E-07	11	4	5.12E-07	7.47E-04
APOC4-APOC2	rs5167	19	45,448,465	1.28E-07	15	4	5.12E-07	7.47E-04
CD33	rs3865444	19	51,727,962	1.07E-07	18	7	7.47E-07	1.04E-03
MIR4531	rs203709	19	45,161,566	4.52E-07	4	2	9.04E-07	1.18E-03
CLU	rs1532278	8	27,466,315	8.34E-08	25	11	9.17E-07	1.18E-03
PVR	rs7255066	19	45,146,103	1.80E-07	11	6	1.08E-06	1.33E-03
MS4A2	rs2847655	11	59,865,671	2.35E-07	28	7	1.65E-06	1.96E-03
EPHA1	rs11767557	7	143,109,139	2.43E-07	16	9	2.19E-06	2.51E-03
LOC285965	rs11767557	7	143,109,139	2.43E-07	129	20	4.86E-06	5.38E-03
ABCA7	rs3752246	19	1,056,492	5.79E-07	27	10	5.79E-06	6.19E-03
GEMIN7	rs7250924	19	45,585,706	2.08E-06	5	3	6.25E-06	6.46E-03

rsID—SNP ID for the most significant SNP in or near the gene; CHR—chromosome; bp—HG 19 base-pair position; p-value—significance of the most-significant SNP within or near the gene; nSNP—The number of SNPs examined within 5 kb of the gene; EFFn—The effective number of independent tests as calculated using the Li and Ji method; $p_{corrected}$—The gene-level significance which has been corrected for EFFn; FDR—the Benjamini Hochberg false discovery rate for the gene.

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Supplementary Table 1: Continued

GENE	Most-significant SNP within 5 kb				nSNP	EFFn	$p_{corrected}$	FDR
	rsID	CHR	bp	p-value				
SIGLEC22P	rs3852865	19	51,714,065	1.35E-06	15	5	6.76E-06	6.78E-03
PTK2B	rs17447007	8	27,230,637	3.56E-07	200	26	9.25E-06	9.00E-03
BLOC1S3	rs12460041	19	45,677,315	5.53E-06	3	2	1.11E-05	0.010
LOC100421517	rs2396825	6	47,568,696	2.22E-06	9	5	1.11E-05	0.010
CD2AP	rs9349407	6	47,453,378	1.03E-06	116	13	1.34E-05	0.012
TRAPPC6A	rs12460041	19	45,677,315	5.53E-06	6	3	1.66E-05	0.014
HBEGF	rs2282802	5	139,712,239	3.05E-06	19	6	1.83E-05	0.015
CEACAM16	rs2965164	19	45,202,052	3.08E-06	12	7	2.16E-05	0.018
YWHAZP9	rs558678	11	59,852,113	7.19E-06	13	4	2.87E-05	0.023
MIR142	rs2632516	17	56,409,089	1.15E-05	5	3	3.45E-05	0.027
SORL1	rs1792124	11	121,441,520	1.29E-06	155	30	3.88E-05	0.030
LOC100289298	rs1476679	7	100,004,446	2.02E-05	5	2	4.05E-05	0.030
MS4A3	rs528823	11	59,837,097	8.80E-06	22	5	4.40E-05	0.032
MTSS1L	rs4985556	16	70,694,000	7.44E-06	16	7	5.20E-05	0.037
MIR4736	rs2632516	17	56,409,089	1.15E-05	6	5	5.75E-05	0.040
IL34	rs4985556	16	70,694,000	7.44E-06	43	8	5.95E-05	0.041
CEACAM19	rs2289494	19	45,186,965	1.28E-05	12	5	6.39E-05	0.043
BIN1	rs1060743	2	127,826,533	4.85E-06	85	15	7.27E-05	0.048
LOC100506779	rs2526380	17	56,398,006	8.23E-06	21	9	7.41E-05	0.048
BZRAP1	rs2526380	17	56,398,006	8.23E-06	35	10	8.23E-05	0.052
CCDC116	rs5754467	22	21,985,094	2.25E-05	8	4	8.98E-05	0.054
YDJC	rs5754467	22	21,985,094	2.25E-05	11	4	8.98E-05	0.054
PILRA	rs2405442	7	99,971,313	3.25E-05	11	3	9.74E-05	0.058
ZCWPW1	rs1476679	7	100,004,446	2.02E-05	13	6	1.21E-04	0.071
REPIN1	rs4725336	7	150,067,445	3.11E-05	10	4	1.24E-04	0.071
ZNF296	rs3786509	19	45,570,051	0.0001553	1	1	1.55E-04	0.087
SPPL2A	rs12440864	15	51,005,957	2.12E-05	51	8	1.70E-04	0.094
CCDC83	rs7927222	11	85,627,108	1.47E-05	67	12	1.76E-04	0.096

rsID—SNP ID for the most significant SNP in or near the gene; CHR—chromosome; bp—HG 19 base-pair position; p-value—significance of the most-significant SNP within or near the gene; nSNP—The number of SNPs examined within 5 kb of the gene; EFFn—The effective number of independent tests as calculated using the Li and Ji method; $p_{corrected}$—The gene-level significance based on the peak SNP significance corrected for EFFn; FDR—the Benjamini Hochberg false discovery rate for the gene.

Supplementary Table 2: Genes significantly associated with AD according to the AlzGene database (http://www.alzgene.org).

ABCA7	DAPK1	MS4A6A
ACE	ECE1	MTHFR
ADAM10	ENTPD7	NEDD9
APOC1	EPHA1	OTC
APOC4	EXOC3L2	PCDH11X
APOE	GAB2	PGBD1
ARID5B	GAPDHS	PICALM
BCAM	GRN	PRNP
BIN1	GWA_14q32.13	PVRL2
CALHM1	IDE	SORCS1
CCR2	IL1A	SORL1
CD2AP	IL1B	TF
CD33	IL33	TFAM
CH25H	IL8	THRA
CHRNB2	LDLR	TNF
CLU	LOC439999	TNK1
CR1	LOC651924	TOMM40
CST3	MS4A4E	hCG2039140