

Supplementary Information

Table S1. Detailed data for the selection and exclusion of SNPs

SNPs	Neighboring gene	Referenced studies	Reported OR	MAF in China	Ref (validation in China)
rs78117248	ABCA7	1	2.07	0	
rs4147929	ABCA7	1, 2	1.15	0.2816	
rs3764650	ABCA7	3	1.23	0.267	
rs3752246	ABCA7	4	1.15	0.2767	
rs7412	APOE	1	~2 to 5	0.1068	
rs429358	APOE	1	~2 to 5	0.1019	
rs2588969	ARID5B	4	0.99/0.93	0.4757	
rs59335482	BIN1	1	1.2	NA	
rs7561528	BIN1	4, 3,	1.17/1.16	0.1214	
rs6733839	BIN1	1, 2	1.22	0.4223	
rs744373	BIN1	3, 5	1.17	0.3301	
rs7274581	CASS4	1, 2	0.88/1.14	0	
rs9349407	CD2AP	4, 3	1.11/1.12	0.1262	
rs9296559	CD2AP	3	1.1	0.1262	
rs10948363	CD2AP	1, 2, 3	1.1	0.1262	
rs3865444	CD33	1, 2, 4, 3	0.91/0.89	0.1796	
rs3826656	CD33	4	0.316	0.3155	
rs1532278	CLU	1, 4	0.89/1.20	0.1942	
rs11136000	CLU	3, 5	0.84	0.199	
rs7982	CLU	3	NA	0.1893	
rs9331888	CLU	3	NA	0.4757	
rs9331896	CLU	1, 2	1.16	0.1893	
rs2279590	CLU	3	NA	0.211	6,7
rs6656401	CR1	1, 3,8	1.18	0.0388	
rs6701713	CR1	4,5	1.16	0.335	
rs8093731	DSG2	2	0.91	0.0194	
rs11771145	EPHA1	1, 2, 3	1.11	0.4369	
rs11767557	EPHA1	4, 3	0.9/0.87	0.1408	9
rs597668	EXOC3L2	8	0.88/0.97	0.33	
rs17125944	FERMT2	1, 2	1.14	0.2524	
rs9271192	HLA-DRA/HLA-DRB5	1, 2	1.11	0.1796	
rs35349669	INPP5D	1, 2	1.08	0.0194	
rs190982	MEF2C	1, 2	0.93/1.08	0.1553	9
rs983392	MS4A	1,2, 3	1.11	0.0485	
rs670139	MS4A	3	1.08	0.4175	
rs4938933	MS4A	4	0.88	0.2621	
rs2718058	NME8	1, 2	0.93/1.08	0.2573	9,10

rs3851179	PICALM	3, 5	0.85	0.4563	
rs10792832	PICALM	1, 2	1.15	0.4612	
rs561655	PICALM	4	0.87	0.4854	
rs541458	PICALM	3	/	0.456	
rs28834970	PTK2B	1, 2	1.1	0.2282	
rs10498633	SCL24A4	1, 2	0.91/1.10	0.217	9,11
rs11218343	SORL1	1, 2, 3	0.77/1.30	0.3107	
rs3781834	SORL1	8	0.78	0.262	
rs2075650	TOMM40	5	2.53	0.1117	
rs75932628	TREM2	1, 3	2.26	0	
rs1476679	ZCWPW1	1, 2	0.91/1.10	0.3252	

MAF, minor allele frequency; MAF in CHB data set was from the 1000 Genomes database (<http://asia.ensembl.org/>); Ref (validation in China) means studies validating that the SNPs have no association with sAD in Chinese

Table S2. Detailed information on 35 SNPs in 18 genes

SNP	Neighbor Gene	Chr	Minor Allele	MAF (%)	HWE (<i>P</i> value)	Position
rs3752246	ABCA7	19	G	0.28	0.17	1056492
rs3764650	ABCA7	19	G	0.27	0.18	1046520
rs4147929	ABCA7	19	A	0.28	0.58	1063443
rs429358	APOE4	19	C	0.10	0.82	45411941
rs7412	APOE4	19	T	0.11	0.08	45412079
rs2588969	ARID5B	10	C	0.48	0.64	63611354
rs7561528	BIN1	2	A	0.12	0.29	127889637
rs6733839	BIN1	2	T	0.42	0.62	127892810
rs744373	BIN1	2	G	0.33	0.47	127894615
rs10948363	CD2AP	6	G	0.13	0.27	47487762
rs9296559	CD2AP	6	C	0.13	0.50	47452270
rs9349407	CD2AP	6	C	0.13	0.52	47453378
rs3826656	CD33	19	A	0.32	0.76	51726613
rs3865444	CD33	19	A	0.18	0.28	51727962
rs11136000	CLU	8	T	0.20	0.66	27464519
rs1532278	CLU	8	T	0.19	0.66	27466315
rs7982	CLU	8	A	0.19	0.30	27462481
rs9331888	CLU	8	G	0.48	0.03	27468862
rs9331896	CLU	8	C	0.19	0.77	27467686
rs6701713	CR1	1	A	0.34	1	207786289
rs11771145	EPHA1	7	G	0.44	0.92	143110762
rs597668	EXOC3L2	19	C	0.33	0.03	45708888
rs17125944	FERMT2	14	C	0.25	0.26	53400629
rs9271192	HLA-DRA	6	C	0.18	0.44	32578530
rs4938933	MS4A	11	C	0.26	0.35	60034429

rs670139	MS4A	11	T	0.42	0.34	59971795
rs10792832	PICALM	11	A	0.46	0.56	85867875
rs3851179	PICALM	11	T	0.46	0.38	85868640
rs541458	PICALM	11	T	0.46	0.64	85788351
rs561655	PICALM	11	G	0.49	0.85	85800279
rs28834970	PTK2B	8	C	0.23	0.48	27195121
rs11218343	SORL1	11	C	0.31	0.58	121435587
rs3781834	SORL1	11	G	0.26	0.19	121445940
rs2075650	TOMM40	19	G	0.11	0.35	45395619
rs1476679	ZCWPW1	7	C	0.33	0.26	100004446

SNP, single-nucleotide polymorphism; Chr, chromosome; MAF, minor allele frequency; HWE, Hardy-Weinberg equilibrium; MAF in CHB data set was from the 1000 Genomes database (<http://asia.ensembl.org/>) ; HWE test was performed in the control group.

Table S3. Allele distribution of SNPs in our study groups

SNP	Neighboring Gene	Risk allele	Risk allele frequency		OR (95% CI)	<i>P</i> value
			sAD	Control		
rs4147929	ABCA7	A	0.33	0.30	1.13(0.93-1.38)	0.23
rs3764650	ABCA7	G	0.32	0.30	1.11(0.91-1.36)	0.31
rs3752246	ABCA7	G	0.34	0.32	1.08(0.89-1.31)	0.45
rs429358	APOE4	C	0.25	0.12	2.55(1.99-3.28)	0.00
rs7412	APOE4	T	0.05	0.07	0.62(0.42-0.92)	0.02
rs2588969	ARID5B	C	0.49	0.48	1.02(0.85-1.23)	0.85
rs6733839	BIN1	T	0.45	0.38	1.30(1.08-1.57)	0.01
rs7561528	BIN1	A	0.13	0.10	1.38(1.03-1.85)	0.03
rs744373	BIN1	G	0.36	0.34	1.07(0.88-1.30)	0.49
rs9296559	CD2AP	C	0.13	0.12	1.15(0.87-1.52)	0.32
rs10948363	CD2AP	G	0.13	0.12	1.14(0.87-1.51)	0.36
rs9349407	CD2AP	C	0.13	0.12	1.13(0.86-1.49)	0.40
rs3865444	CD33	A	0.17	0.22	0.72(0.57-0.91)	0.01
rs3826656	CD33	A	0.30	0.34	0.81(0.66-0.98)	0.03
rs1532278	CLU	T	0.18	0.20	0.90(0.71-1.13)	0.37
rs9331896	CLU	C	0.19	0.20	0.90(0.71-1.13)	0.37
rs11136000	CLU	T	0.19	0.20	0.92(0.73-1.16)	0.51
rs9331888	CLU	G	0.50	0.49	1.07(0.88-1.29)	0.53
rs7982	CLU	A	0.18	0.19	0.93(0.74-1.18)	0.59
rs6701713	CR1	A	0.35	0.36	0.95(0.78-1.15)	0.59
rs11771145	EPHA1	G	0.48	0.43	1.25(1.04-1.50)	0.02
rs597668	EXOC3L2	C	0.35	0.35	1.03(0.85-1.25)	0.77
rs17125944	FERMT2	C	0.23	0.21	1.10(0.88-1.38)	0.43
rs9271192	HLA-DRA	C	0.21	0.19	1.13(0.90-1.43)	0.31

rs4938933	MS4A	C	0.30	0.27	1.11(0.90-1.36)	0.32
rs670139	MS4A	T	0.42	0.44	0.95(0.79-1.14)	0.57
rs561655	PICALM	G	0.43	0.49	0.78(0.65-0.94)	0.01
rs541458	PICALM	T	0.47	0.53	0.79(0.65-0.95)	0.01
rs10792832	PICALM	A	0.35	0.40	0.81(0.67-0.98)	0.03
rs3851179	PICALM	T	0.35	0.39	0.81(0.67-0.99)	0.04
rs28834970	PTK2B	C	0.26	0.27	0.92(0.74-1.13)	0.42
rs11218343	SORL1	C	0.26	0.31	0.78(0.64-0.96)	0.02
rs3781834	SORL1	G	0.19	0.23	0.79(0.63-0.99)	0.04
rs2075650	TOMM40	G	0.23	0.11	2.32(1.79-3.00)	0.00
rs1476679	ZCWPW1	C	0.32	0.29	1.14(0.93-1.40)	0.20

SNP, single nucleotide polymorphism; sAD, sporadic Alzheimer's disease; OR, odds ratio; CI, confidence interval; OR and 95% CI adjusted for age, sex, and APOE ε4 status

Table S4. Genotype frequencies of 35 SNPs in our study groups

SNP	Neighboring Gene	Genotype	Number of Samples		P value	OR (95% CI)
			sAD	Control		
rs4147929	ABCA7	GG/GC/CC	57/199/203	54/188/218	0.3797	1.14(0.93-1.40)
rs3764650	ABCA7	GG/GT/TT	48/196/217	46/180/237	0.3236	1.11(0.90-1.35)
rs3752246	ABCA7	AA/AG/GG	52/202/207	45/190/228	0.1927	1.09(0.90-1.33)
rs429358	APOE	CC/CT/TT	42/149/268	7/94/358	0.0015 22	3.94(1.69-9.18)
rs7412	APOE	TT/TC/CC	3/37/419	5/57/395	0.0713 8	0.69(0.47-1.03)
rs2588969	ARID5B	AA/AG/GG	55/203/203	51/199/213	0.5271	1.04(0.86-1.25)
rs6733839	BIN1	AA/AG/GG	7/106/348	2/87/374	0.0717 8	1.28(1.05-1.55)
rs7561528	BIN1	TT/TC/CC	91/233/137	71/214/177	0.0137 3	1.33(0.98-1.80)
rs744373	BIN1	GG/GA/AA	54/211/182	57/198/201	0.463	1.08(0.88-1.32)
rs9296559	CD2AP	GG/GA/AA	5/113/343	9/93/361	0.5241	1.11(0.83-1.48)
rs1094836 3	CD2AP	CC/CT/TT	5/113/343	8/94/361	0.4751	1.10(0.82-1.46)
rs9349407	CD2AP	CC/CG/GG	5/113/343	8/96/359	0.583	1.08(0.81-1.45)
rs3865444	CD33	AA/AG/GG	35/200/226	56/206/201	0.0043 65	0.66(0.51-0.85)
rs3826656	CD33	AA/AC/CC	12/129/320	18/168/277	0.0011 73	0.74(0.60-0.91)
rs1532278	CLU	TT/TC/CC	14/146/300	20/145/295	0.6193	0.92(0.72-1.17)
rs9331896	CLU	TT/TC/CC	12/144/300	20/145/294	0.4858	0.91(0.72-1.16)
rs1113600 0	CLU	AA/AG/GG	13/143/305	21/138/304	0.737	0.94(0.74-1.20)

rs9331888	CLU	GG/GC/CC	125/195/12 2	116/200/13 0	0.5919	1.05(0.88-1.26)
rs7982	CLU	CC/CT/TT	12/147/302	20/147/296	0.4689	0.96(0.75-1.22)
rs6701713	CR1	GG/GA/AA	31/192/238	34/194/235	0.8289	0.92(0.75-1.13)
rs1177114 5	EPHA1	GG/GA/AA	102/242/11 7	86/226/151	0.0432 3	1.22(1.01-1.49)
rs597668	EXOC3L2	CC/CT/TT	59/212/190	66/188/209	0.8591	1.02(0.84-1.24)
rs1712594 4	FERMT2	CC/CT/TT	33/143/282	24/145/293	0.536	1.07(0.86-1.34)
rs9271192	HLA-DRA	CC/CA/AA	26/138/297	13/146/304	0.7274	1.04(0.82-1.32)
rs4938933	MS4A	CC/CA/AA	52/191/211	43/200/216	0.3601	1.12(0.91-1.38)
rs670139	MS4A	TT/TG/GG	65/255/139	81/237/142	0.6013	0.95(0.77-1.16)
rs561655	PICALM	AA/AG/GG	64/196/201	70/228/162	0.0152 4	0.75(0.62-0.91)
rs541458	PICALM	TT/TC/CC	62/197/202	67/231/165	0.0185 3	0.77(0.64-0.92)
rs1079283 2	PICALM	CC/CT/TT	108/215/13 8	131/226/10 6	0.0054 82	0.78(0.64-0.95)
rs3851179	PICALM	GG/GA/AA	90/217/154	113/229/12 1	0.0032 73	0.79(0.65-0.96)
rs2883497 0	PTK2B	CC/CT/TT	35/161/256	37/175/245	0.4243	0.92(0.74-1.13)
rs1121834 3	SORL1	CC/CT/TT	18/197/246	40/202/221	0.0912 4	0.83(0.66-1.03)
rs3781834	SORL1	GG/GA/AA	9/153/299	29/153/281	0.0599 8	0.80(0.63-1.01)
rs2075650	TOMM40	GG/GA/AA	33/144/281	8/89/362	0.0829 1	1.57(0.94-2.61)
rs1476679	ZCWPW1	CC/CT/TT	46/203/212	34/202/227	0.282	1.12(0.91-1.38)

SNP, single nucleotide polymorphism; sAD, sporadic Alzheimer's disease; OR, odds ratio; CI, confidence interval; OR and 95% CI adjusted for age, sex, and APOE ϵ 4 status

Table S5 Correlations between PRSs and CSF biomarkers

Biomarkers	sAD		Cognitively Normal Participants	
	(n = 60)		(n = 200)	
	ρ	<i>P</i> value	ρ	<i>P</i> value
CSF A β 42	0.15	0.28	-0.15	0.043
CSF A β 42/ A β 40	0.08	0.54	-0.18	0.011
CSF T-tau	-0.10	0.44	0.08	0.28
CSF P-tau	-0.06	0.67	0.08	0.27

sAD, sporadic Alzheimer's disease; CSF, cerebrospinal fluid. Spearman correlation coefficients (ρ) were used to assess the correlations.

References

1. Cuyvers E, Sleegers K. Genetic variations underlying Alzheimer's disease: evidence from genome-wide association studies and beyond. *The Lancet Neurology*. 2016;15(8):857-868.
2. Lambert J-C, Ibrahim-Verbaas CA, Harold D, et al. Meta-analysis of 74,046 individuals identifies 11 new susceptibility loci for Alzheimer's disease. *Nature Genetics*. 2013;45(12):1452-1458.
3. Karch CM, Goate AM. Alzheimer's Disease Risk Genes and Mechanisms of Disease Pathogenesis. *Biological Psychiatry*. 2015;77(1):43-51.
4. Naj AC, Jun G, Beecham GW, et al. Common variants at MS4A4/MS4A6E, CD2AP, CD33 and EPHA1 are associated with late-onset Alzheimer's disease. *Nat Genet*. May 2011;43(5):436-441.
5. Harold D, Abraham R, Hollingworth P, et al. Genome-wide association study identifies variants at CLU and PICALM associated with Alzheimer's disease. *Nat Genet*. Oct 2009;41(10):1088-1093.
6. Zhang S, Li X, Ma G, et al. CLU rs9331888 Polymorphism Contributes to Alzheimer's Disease Susceptibility in Caucasian But Not East Asian Populations. *Mol Neurobiol*. Apr 2016;53(3):1446-1451.
7. Yu JT, Li L, Zhu QX, et al. Implication of CLU gene polymorphisms in Chinese patients with Alzheimer's disease. *Clinica chimica acta; international journal of clinical chemistry*. Oct 09 2010;411(19-20):1516-1519.
8. Toft M, Miyashita A, Koike A, et al. SORL1 Is Genetically Associated with Late-Onset Alzheimer's Disease in Japanese, Koreans and Caucasians. *PLoS ONE*. 2013;8(4).
9. Xiao Q, Liu ZJ, Tao S, et al. Risk prediction for sporadic Alzheimer's disease using genetic risk score in the Han Chinese population. *Oncotarget*. Nov 10 2015;6(35):36955-36964.
10. Liu Y, Yu JT, Wang HF, et al. Association between NME8 locus polymorphism and cognitive decline, cerebrospinal fluid and neuroimaging biomarkers in Alzheimer's disease. *PLoS One*. 2014;9(12):e114777.
11. Lu H, Zhu XC, Wang HF, et al. Lack of Association Between SLC24A4 Polymorphism and Late-onset Alzheimer's Disease in Han Chinese. *Curr Neurovasc Res*. 2016;13(3):239-243.