Supplementary Material

Relationship Between *FERMT2*, *CELF1*, *COPI*, *CHRNA2*, and *ABCA7* Genetic Polymorphisms and Alzheimer's Disease Risk in the Southern Chinese Population

Supplementary Table 1. Primers of tested single nucleotide polymorphisms.

SNP	Forward Primers	Reverse Primers	Elongation Primers
rs4266886	TAAGTATATCCATACACTGGCATGG	GAGTCCAGTTATCCAAAGAGAAGAGT	TAAAGTGAGATCTTGCCATATATGCC
rs6572869	AGACTTCTCTGCTTTGACACAAATC	ACGAGGTTGTAAGTTTGGAGTCC	TGCAAATTTTATACCCACTTGTGC
rs1317149	GCTTCTAAGGCTCTGTGGACTACTC	TCAAGTCTGAGGCTTCTTTACTGC	CATATCATGGTCTAGTACTCAATGCAAC
rs11039280	GAGTTGTCTAGGAGCCTTCTGACTG	GACATTATGGTTAAGGTTTGTACTGTAGG	TCGCCCAGGCTAGAGTGCAGT
rs11604680	CCTCCTTACTCTGGTGAGGTCC	TCTAAGCAGGCTGAAGAGTGTCC	GGCTTGGTCTCTGACACTTCAAA
rs77336780	CAATCCTTCCTCCAAAGGAGCT	AGTGCTCCACCTGTTGTTCATG	GGATTTATGGAAGAACTTGAGAATC
rs7813641	GATCCATTGGTGTTGAACTCTAGC	TTGCTAACATAAGAATCCAGTGAAG	GAACTGTCTTTTCCATCATATACCTGA
rs9898218	TCTCCAGAATCACACTACAAGATGAG	GGACCACTGGGTTGAAGCATC	GTGGAGATGTTGCAGGATGC
rs3752242	TATGAGCAGCAAGGACATTCAG	GACACCGACAGGGAGAACTGG	AGGAGCTCTGGTGGCTCAGAT
rs667897	CTCACAGACAGAGTGGCTCAAAGC	GGCTGTGCTTCAGTCAGGAGTAG	CAAGGTAAACATCCGGTATGGTA
rs4147912	CTTTTCGGAGGAGCTACTGGTG	GGTCATTGTCATTGGCATCTGTG	CAACCAGCTATTAAGCCTCGTAG
rs2516049	CCTGKGGGAATCAGTGGACTTG	GGGAGAAGGAGTRGGAGCTGG	GGACAGTAGCACATGTGAGTCA
rs2741342	TAGTATATTCACACATCTGTGTAACATCAC	CACAGAAGTCTTCCGTGTTGATTG	TTTGCCTATTCTGCATATTCCATATCA
rs1109581	AGAGCTGCCAGGTAGATTGTGC	GGTAACTCCCACATTAGCACAGC	AAGGCCCTGCATGAGTTAACC
rs698842	CCAGGACTTCCCAACTTGAGAC	CTGGCCTCTATCACCTGTATCTTG	TGATTCTCATTTATTTGACCTGGCA
rs7116190	AAGGACTAGCCAGGTAGTTGTAAGC	CCAAGTATTCATGGAAGTCTCTGC	AGCTGATTGGAACTTGAATGTCTC
rs10742814	GTAGAAACAACAGAACAGTGCTGGG	GCTGCCTAATTATGGTAAGGTGC	AGTGGGAAGGTGGTGGGTGG

SNP, single nucleotide polymorphism

Supplementary Table 2. The alleles and genotype distribution of candidate genes in the controls and the AD cases.

SNP	Alleles [n (%)]		p OR (95%CI)	Genotype [n (%)]			p	HWE p
rs6572869	G	A	0.35	GG	AG	AA		
CON	296 (71.2%)	120 (28.8%)	1.15	116 (55.8%)	64 (30.8%)	28 (13.5%)	**0.005**	0.18
AD	330 (68.2%)	154 (31.8%)	(0.87-1.53)	110 (45.5%)	110 (45.5%)	22 (9.1%)		
rs11604680	A	G	0.078	AA	AG	GG		
CON	306 (73.6%)	110 (26.4%)	1.31	117 (56.3%)	72 (34.6%)	19 (9.1%)	**0.007**	0.90
AD	329 (68%)	155 (32%)	(0.98-1.75)	105 (43.4%)	119 (49.2%)	18 (7.4%)		
rs1317149	G	A	0.35	GG	AG	AA		
CON	296 (71.2%)	120 (28.8%)	1.15	111 (53.4%)	74 (35.6%)	23 (11.1%)	**0.009**	0.93
AD	330 (68.2%)	154 (31.8%)	(0.87-1.53)	105 (43.4%)	120 (49.6%)	17 (7%)		
rs9898218	G	T	0.53	GG	GT	TT		
CON	320 (76.9%)	96 (23.1%)	1.11	132 (63.5%)	56 (26.9%)	20 (9.6%)	**0.005**	0.32
AD	363 (75%)	121 (25%)	(0.82-1.51)	133 (55.0%)	97 (40.1%)	12 (5%)		
rs2741342	G	A	**0.003**	GG	AG	AA		
CON	204 (49%)	212 (51%)	0.67	43 (20.7%)	118 (56.7%)	47 (22.6%)	**0.005**	0.33
AD	285 (58.9%)	199 (41.4%)	(0.52-0.88)	82 (33.9%)	121 (50.0%)	39 (16.1%)		
rs10742814	G	A	0.23	GG	AG	AA		
CON	267 (64.2%)	149 (35.8%)	0.84	91 (43.8%)	85 (40.9%)	32 (15.4%)	0.17	0.70
AD	330 (68.2%)	154 (31.8%)	(0.63-1.10)	111 (45.9%)	108 (44.6%)	23 (9.5%)		
rs11039280	G	A	**0.046**	GG	AG	AA		
CON	267 (64.2%)	149 (35.8%)	0.75	93 (44.7%)	81 (38.9%)	34 (16.3%)	0.064	0.18
AD	341 (70.5%)	143 (29.5%)	(0.57-0.99)	121 (50%)	99 (40.9%)	22 (9.1%)		
rs3752242	G	A	**0.037**	GG	AG	AA		
CON	251 (60.3%)	165 (39.7%)	0.74	77 (37.0%)	97 (46.6%)	34 (16.3%)	0.10	0.51
AD	325 (67.1%)	159 (32.9%)	(0.57-0.98)	113 (46.7%)	99 (40.9%)	30 (12.4%)		
rs4147912	C	A	0.16	CC	AC	AA		
CON	355 (84.9%)	61 (15.1%)	1.30	147 (70.7%)	59 (28.4%)	2 (1.0%)	0.30	0.23
AD	393 (81.2%)	91 (18.8%)	(0.91-1.85)	157 (64.9%)	79 (32.6%)	6 (2.5%)		
rs2516049	A	G	0.47	AA	AG	GG		
CON	318 (76.4%)	98 (23.6%)	0.89	124 (59.6%)	70 (33.7%)	14 (6.7%)	0.61	0.82
AD	380 (78.5%)	104 (21.5%)	(0.65-1.22)	149 (61.6%)	82 (33.9%)	11 (4.5%)		
rs1109581	G	A	0.34	GG	AG	AA		
CON	361 (86.8%)	55 (13.2%)	1.20	161 (77.4%)	39 (18.8%)	8 (3.8%)	0.24	0.10
AD	409 (84.5%)	75 (15.5%)	(0.83-1.75)	174 (71.9%)	61 (25.2%)	7 (2.9%)		
rs7116190	G	A	0.39	GG	AG	AA		
CON	335 (80.5%)	81 (19.5%)	0.86	136 (65.4%)	63 (30.3%)	9 (4.3%)	0.63	0.95
AD	401 (82.9%)	83 (17.1%)	(0.61-1.20)	166 (68.6%)	69 (28.5%)	7 (2.9%)		
rs667897	A	G	0.40	AA	AG	GG		
CON	271 (65.1%)	145 (34.9%)	0.88	93 (44.7%)	85 (40.9%)	30 (14.4%)	0.51	0.44

AD	329 (68%)	155 (32%)	(0.67-1.16)	113 (46.7%)	103 (42.6%)	26 (10.7%)		
rs4266886	C	T	0.78	CC	CT	TT		
CON	255 (61.3%)	161 (38.7%)	1.04	81 (38.9%)	93 (44.7%)	34 (16.3%)	0.69	0.10
AD	292 (60.3%)	192 (39.7%)	(0.80-1.36)	96 (39.7%)	100 (41.3%)	46 (19.0%)		
rs698842	T	A	0.23	TT	AT	AA		
CON	386 (92.8%)	30 (7.2%)	1.35	180 (86.5%)	26 (12.5%)	2 (1.0%)	0.33	0.89
AD	438 (90.5%)	46 (9.5%)	(0.84-2.18)	198 (81.8%)	42 (17.4%)	2 (0.8%)		
rs77336780	C	G	0.16	CC	CG	GG		
CON	360 (86.5%)	56 (13.5%)	1.31	160 (76.9%)	40 (19.2%)	8 (3.8%)	0.20	0.07
AD	402 (83.1%)	82 (16.9%)	(0.91-1.90)	169 (69.8%)	64 (26.4%)	9 (3.7%)		
rs7813641	T	A	0.33	TT	AT	AA		
CON	266 (63.9%)	150 (36.1%)	0.87	81 (38.9%)	104 (50.0%)	23 (11.1%)	0.35	0.82
AD	325 (67.1%)	159 (32.9%)	(0.66-1.14)	110 (45.5%)	105 (43.4%)	27 (11.2%)		

SNP, single nucleotide polymorphism; AD, Alzheimer's disease; CON, healthy controls; OR, odds ratio; CI, confidence interval;

HWE, Hardy-Weinberg equilibrium

Bold indicates statistically significant values.

Supplementary Table 3. Association of SNP of candidate genes with AD risk in four genetic models.

Gene	SNP	dominant model (adjusted)			Recessive model (adjusted)		
		p	OR	95%CI	p	OR	95%CI
FERMT2	rs6572869	**0.022**	1.55	1.07-2.26	0.13	0.63	0.35-1.14
CELF1	rs11604680	**0.007**	1.68	1.15-2.44	0.53	0.81	0.41-1.56
CELF1	rs1317149	**0.033**	1.50	1.03-2.19	0.13	0.6	0.31-1.16
COPI	rs9898218	0.065	1.43	0.98-2.10	0.073	0.51	0.24-1.07
CHRNA2	rs2741342	**0.002**	0.5	0.33-0.77	0.068	0.64	0.4-1.03
CELF1	rs10742814	0.61	0.91	0.62-1.32	**0.039**	0.55	0.31-0.97
CELF1	rs11039280	0.26	0.81	0.56-1.17	**0.016**	0.49	0.28-0.88
ABCA7	rs3752242	**0.047**	0.68	0.47-0.99	0.26	0.73	0.43-1.26
ABCA7	rs4147912	0.25	1.26	0.85-1.89	0.28	2.46	0.49-12.40
HLA-DRB1	rs2516049	0.68	0.92	0.63-1.35	0.38	0.69	0.30-1.57
ADGRF4	rs1109581	0.22	1.31	0.85-2.02	0.59	0.75	0.27-2.12
MS4A	rs7116190	0.41	0.85	0.57-1.26	0.41	0.66	0.24-1.80
MS4A	rs667897	0.65	0.92	0.63-1.33	0.24	0.71	0.40-1.25
CR1	rs4266886	0.99	1	0.68-1.47	0.46	1.21	0.74-1.97
NRXN1	rs698842	0.17	1.44	0.86-2.43	0.80	0.78	0.11-5.59
OR51I1	rs77336780	0.075	1.47	0.96-2.26	0.93	1.05	0.39-2.79
CSMD1	rs7813641	0.18	0.77	0.53-1.13	0.99	1.01	0.56-1.82
Gene	SNP	additive model (adjusted)			overdominant model (adjusted)		
		p	OR	95%CI	p	OR	95%CI
FERMT2	rs6572869	0.33	1.15	0.87-1.51	**0.001**	1.96	1.32-2.92
CELF1	rs11604680	0.065	1.32	0.98-1.78	**0.002**	1.82	1.24-2.67
CELF1	rs1317149	0.33	1.16	0.87-1.55	**0.003**	1.80	1.23-2.64
COPI	rs9898218	0.48	1.11	0.83-1.50	**0.004**	1.81	1.21-2.71
CHRNA2	rs2741342	**0.002**	0.64	0.48-0.85	0.16	0.77	0.53-1.11
CELF1	rs10742814	0.17	0.83	0.63-1.09	0.39	1.18	0.81-1.72
CELF1	rs11039280	**0.048**	0.76	0.58-0.99	0.63	1.1	0.75-1.61
ABCA7	rs3752242	**0.049**	0.76	0.58-1.00	0.23	0.80	0.55-1.16
ABCA7	rs4147912	0.18	1.29	0.89-1.87	0.40	1.19	0.79-1.79
HLA-DRB1	rs2516049	0.50	0.90	0.66-1.23	0.99	1	0.67-1.48
ADGRF4	rs1109581	0.40	1.17	0.82-1.68	0.13	1.43	0.91-2.25
MS4A	rs7116190	0.33	0.84	0.60-1.18	0.60	0.90	0.60-1.35
MS4A	rs667897	0.36	0.88	0.67-1.16	0.74	1.07	0.73-1.56
CR1	rs4266886	0.69	1.05	0.81-1.36	0.56	0.89	0.61-1.30
NRXN1	rs698842	0.22	1.35	0.835-2.180	0.14	1.50	0.88-2.55
OR51I1	rs77336780	0.13	1.31	0.92-1.87	0.068	1.52	0.97-2.39
CSMD1	rs7813641	0.32	0.87	0.65-1.15	0.18	0.78	0.53-1.13

AD, Alzheimer's disease; SNP, single nucleotide polymorphism; OR, odds ratio; CI, confidence interval; p value was adjusted for gender and age. Bold indicates statistically significant values.

Supplementary Table 4. The allele and genotype distribution of candidate genes in *APOE* ε4 carriers.

SNP	N	Alleles [n (%)]		p OR (95%CI)	Genotype [n (%)]			p	HWE p
rs6572869		G	A	**0.012**	GG	AG	AA		
CON	61	96 (78.7%)	26 (21.3%)	1.93	38 (62.3%)	20 (32.8%)	3 (4.9%)	**0.032**	0.99
AD	131	172 (65.6%)	90 (34.4%)	1.17-3.19	56 (42.7%)	60 (45.8%)	15 (11.5%)		
rs11604680		A	G	0.066	AA	AG	GG		
CON	61	96 (78.7%)	26 (21.3%)	1.62	40 (65.6%)	16 (26.2%)	5 (8.2%)	**0.041**	0.88
AD	131	182 (69.5%)	80 (30.5%)	0.98-2.69	62 (47.3%)	58 (44.3%)	11 (8.4%)		
rs1317149		G	A	0.18	GG	AG	AA		
CON	61	94 (77%)	28 (23%)	1.42	38 (62.3%)	18 (29.5%)	5 (8.2%)	0.19	0.88
AD	131	184 (70.2%)	78 (29.8%)	0.87-2.34	64 (48.9%)	56 (42.7%)	11 (8.4%)		
rs9898218		G	T	0.61	GG	GT	TT		
CON	61	91 (74.6%)	31 (25.4%)	0.87	38 (62.3%)	15 (24.6%)	8 (13.1%)	**0.008**	0.89
AD	131	202 (77.1%)	60 (22.9%)	0.53-1.44	75 (57.3%)	52 (39.7%)	4 (3.1%)		
rs2741342		G	A	0.061	GG	AG	AA		
CON	61	60 (49.2%)	62 (50.8%)	0.66	12 (19.7%)	36 (59%)	13 (21.3%)	0.13	0.24
AD	131	156 (59.5%)	106 (40.5%)	0.43-1.01	43 (32.8%)	70 (53.4%)	18 (13.7%)		
rs10742814		G	A	**0.041**	GG	AG	AA		
CON	61	68 (55.7%)	54 (44.3%)	0.63	23 (37.7%)	22 (36.1%)	16 (26.2%)	**0.024**	0.44
AD	131	175 (66.8%)	87 (33.2%)	0.40-0.97	58 (44.3%)	59 (45%)	14 (10.7%)		
rs11039280		G	A	**0.023**	GG	AG	AA		
CON	61	68 (55.7%)	54 (44.3%)	0.59	23 (37.7%)	22 (36.1%)	16 (26.2%)	**0.023**	0.26
AD	131	178 (67.9%)	84 (32.1%)	0.38-0.92	61 (46.6%)	56 (42.7%)	14 (10.7%)		
rs3752242		G	A	**0.004**	GG	AG	AA		
CON	61	68 (55.7%)	54 (44.3%)	0.52	22 (36.1%)	24 (39.3%)	15 (24.6%)	**0.021**	0.08
AD	131	186 (71%)	76 (29%)	0.33-0.80	69 (52.7%)	48 (36.6%)	14 (10.7%)		
rs4147912		C	A	**0.018**	CC	AC	AA		
CON	61	110 (90.2%)	12 (9.8%)	2.22	50 (82%)	10 (16.4%)	1 (1.6%)	**0.039**	0.99
AD	131	211 (80.5%)	51 (19.5%)	1.13-4.33	84 (64.1%)	43 (32.8%)	4 (3.1%)		
rs2516049		A	G	0.43	AA	AG	GG		
CON	61	91 (74.6%)	31 (25.4%)	0.80	39 (63.9%)	13 (21.3%)	9 (14.8%)	**0.024**	0.11
AD	131	206 (78.6%)	56 (21.4%)	0.48-1.32	81 (61.8%)	44 (33.6%)	6 (4.6%)		
rs1109581		G	A	0.46	GG	AG	AA		
CON	61	99 (81.1%)	23 (18.9%)	0.78	41 (67.2%)	17 (27.9%)	3 (4.9%)	0.67	0.33
AD	131	222 (84.7%)	40 (15.3%)	0.44-1.36	96 (73.3%)	30 (22.9%)	5 (3.8%)		
rs7116190		G	A	0.66	GG	AG	AA		
CON	61	104 (85.2%)	18 (14.8%)	1.17	44 (72.1%)	16 (26.2%)	1 (1.6%)	0.89	0.87
AD	131	218 (83.2%)	44 (16.8%)	0.64-2.12	90 (68.7%)	38 (29.0%)	3 (2.3%)		
rs667897		A	G	0.41	AA	AG	GG		
CON	61	81 (66.4%)	41 (33.6%)	0.82	27 (44.3%)	27 (44.3%)	7 (11.5%)	0.72	0.99

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AD	131	185 (70.6%)	77 (29.4%)	0.52-1.30	65 (49.6%)	55 (42%)	11 (8.4%)		
rs4266886		C	T	0.91	CC	CT	TT		
CON	61	71 (58.2%)	51 (41.8%)	0.96	24 (39.3%)	23 (37.7%)	14 (23%)	0.83	0.08
AD	131	155 (59.2%)	107 (40.8%)	0.62-1.49	50 (38.2%)	55 (42%)	26 (19.8%)		
rs698842		T	A	0.18	TT	AT	AA		
CON	61	115 (94.3%)	7 (5.7%)	1.89	55 (90.2%)	5 (8.2%)	1 (1.6%)	0.18	0.91
AD	131	235 (89.7%)	27 (10.3%)	0.80-4.46	105 (80.2%)	25 (19.1%)	1 (0.8%)		
rs77336780		C	G	0.57	CC	CG	GG		
CON	61	102 (83.6%)	20 (16.4%)	1.20	45 (73.8%)	12 (19.7%)	4 (6.6%)	0.37	0.22
AD	131	212 (80.9%)	50 (19.1%)	0.68-2.13	87 (66.4%)	38 (29%)	6 (4.6%)		
rs7813641		T	A	0.73	TT	AT	AA		
CON	61	83 (68%)	39 (32%)	1.11	26 (42.6%)	31 (50.8%)	4 (6.6%)	0.24	0.99
AD	131	172 (65.6%)	90 (34.4%)	0.70-1.76	59 (45%)	54 (41.2%)	18 (13.7%)		

SNP, single nucleotide polymorphism; *APOE*, apolipoprotein E; CON, healthy controls; OR, odds ratio, CI, confidence interval

HWE, Hardy-Weinberg equilibrium; N, number.

Bold indicates statistically significant values.

Supplementary Table 5. Association of SNPs of candidate genes with AD in *APOE* ε4 carriers in four genetic model.

Gene	SNP	dominant model (adjusted)			Recessive model (adjusted)		
		p	**OR**	**95%CI**	**p**	**OR**	**95%CI**
FERMT2	rs6572869	**0.009**	2.33	1.23-4.40	0.2	2.32	0.64-8.39
CELF1	rs11604680	**0.016**	2.20	1.16-4.17	0.95	1.03	0.34-3.15
CELF1	rs1317149	0.058	1.85	0.98-3.47	0.95	1.03	0.34-3.15
COPI	rs9898218	0.45	1.28	0.68-2.40	**0.023**	0.23	0.065-0.81
CHRNA2	rs2741342	**0.028**	0.43	0.20-0.91	0.15	0.56	0.25-1.24
CELF1	rs10742814	0.39	0.76	0.40-1.43	**0.004**	0.30	0.13-0.68
CELF1	rs11039280	0.24	0.68	0.36-1.29	**0.004**	0.30	0.13-0.68
ABCA7	rs3752242	**0.042**	0.52	0.28-0.98	**0.035**	0.40	0.17-0.94
ABCA7	rs4147912	**0.034**	2.28	1.06-4.87	0.68	1.60	0.17-14.74
HLA-DRB1	rs2516049	0.69	1.14	0.60-2.16	**0.033**	0.30	0.10-0.91
ADGRF4	rs1109581	0.33	0.72	0.37-1.40	0.81	0.83	0.19-3.66
MS4A	rs7116190	0.84	1.07	0.54-2.13	0.86	1.24	0.12-12.37
MS4A	rs667897	0.37	0.75	0.40-1.40	0.43	0.66	0.24-1.84
CR1	rs4266886	0.70	1.13	0.60-2.15	0.77	0.90	0.42-1.90
NRXN1	rs698842	0.12	2.13	0.82-5.51	0.50	0.38	0.023-6.22
OR51I1	rs77336780	0.33	1.40	0.71-2.77	0.6	0.70	0.19-2.64
CSMD1	rs7813641	0.73	0.90	0.48-1.67	0.14	2.36	0.75-7.48
Gene	**SNP**	additive model (adjusted)			overdominant model (adjusted)		
		p	**OR**	**95%CI**	**p**	**OR**	**95%CI**
FERMT2	rs6572869	**0.01**	1.99	1.17-3.36	0.058	1.88	0.98-3.61
CELF1	rs11604680	0.058	1.64	0.98-2.74	**0.015**	2.32	1.18-4.56
CELF1	rs1317149	0.14	1.47	0.89-2.43	0.056	1.90	0.98-3.69
COPI	rs9898218	0.72	0.91	0.56-1.50	**0.044**	2.02	1.02-4.02
CHRNA2	rs2741342	**0.021**	0.57	0.35-0.92	0.33	0.73	0.39-1.38
CELF1	rs10742814	**0.036**	0.63	0.41-0.97	0.19	1.55	0.81-2.95
CELF1	rs11039280	**0.022**	0.60	0.39-0.93	0.32	1.39	0.73-2.64
ABCA7	rs3752242	**0.015**	0.59	0.38-0.90	0.57	0.83	0.43-1.59
ABCA7	rs4147912	**0.046**	2.03	1.01-4.07	**0.043**	2.24	1.02-4.91
HLA-DRB1	rs2516049	0.52	0.86	0.53-1.38	0.084	1.89	0.92-3.88
ADGRF4	rs1109581	0.38	0.78	0.46-1.35	0.36	0.72	0.36-1.46
MS4A	rs7116190	0.82	1.07	0.58-2.00	0.89	1.05	0.52-2.12
MS4A	rs667897	0.30	0.78	0.49-1.25	0.66	0.87	0.47-1.62
CR1	rs4266886	0.93	1.02	0.67-1.54	0.54	1.22	0.65-2.32
NRXN1	rs698842	0.21	1.74	0.73-4.14	0.079	2.50	0.90-6.93
OR51I1	rs77336780	0.57	1.17	0.68-2.02	0.20	1.63	0.78-3.43
CSMD1	rs7813641	0.66	1.11	0.70-1.76	0.19	0.66	0.36-1.23

SNP, single nucleotide polymorphism; *APOE*, apolipoprotein E; OR, odds ratio, CI, confidence interval

p value was adjusted for gender and age. Bold indicates statistically significant values.

Supplementary Table 6. The allele and genotype distribution of candidate genes in *APOE* ε4 non-carriers.

SNP	N	Alleles [n (%)]		p OR (95%CI)	Genotype [n (%)]			p	HWE p
rs6572869		G	A	0.5	GG	AG	AA		
CON	147	200 (68%)	94 (32%)	0.86	78 (53.1%)	44 (29.9%)	25 (17.0%)	**0.006**	0.07
AD	111	158 (71.2%)	64 (28.8%)	0.59-1.26	54 (48.6%)	50 (45%)	7 (6.3%)		
rs11604680		A	G	0.21	AA	AG	GG		
CON	147	210 (71.4%)	84 (28.6%)	1.28	77 (52.4%)	56 (38.1%)	14 (9.5%)	**0.027**	0.59
AD	111	147 (66.2%)	75 (33.8%)	0.88-1.86	43 (38.7%)	61 (55%)	7 (6.3%)		
rs1317149		G	A	0.51	GG	AG	AA		
CON	147	202 (68.7%)	92 (31.3%)	1.14	73 (49.7%)	56 (38.1%)	18 (12.2%)	**0.005**	0.64
AD	111	146 (65.8%)	76 (34.2%)	0.79-1.66	41 (36.9%)	64 (57.7%)	6 (5.4%)		
rs9898218		G	T	0.18	GG	GT	TT		
CON	147	229 (77.9%)	65 (22.1%)	1.34	94 (63.9%)	41 (27.9%)	12 (8.2%)	0.11	0.3
AD	111	161 (72.5%)	61 (27.5%)	0.89-2.00	58 (52.3%)	45 (40.5%)	8 (7.2%)		
rs2741342		G	A	**0.041**	GG	AG	AA		
CON	147	144 (49.0%)	150 (51.0%)	0.69	31 (21.1%)	82 (55.8%)	34 (23.1%)	**0.043**	0.86
AD	111	129 (58.1%)	93 (41.9%)	0.49-0.98	39 (35.1%)	51 (45.9%)	21 (18.9%)		
rs10742814		G	A	0.63	GG	AG	AA		
CON	147	199 (67.7%)	95 (32.3%)	0.91	68 (46.3%)	63 (42.9%)	16 (10.9%)	0.78	0.99
AD	111	155 (69.8%)	67 (30.2%)	0.62-1.32	53 (47.7%)	49 (44.1%)	9 (8.1%)		
rs11039280		G	A	0.17	GG	AG	AA		
CON	147	199 (67.7%)	95 (32.3%)	0.76	70 (47.6%)	59 (40.1%)	18 (12.2%)	0.35	0.67
AD	111	163 (73.4%)	59 (26.6%)	0.52-1.12	60 (54.1%)	43 (38.7%)	8 (7.2%)		
rs3752242		G	A	1	GG	AG	AA		
CON	147	183 (62.2%)	111 (37.8%)	0.98	55 (37.4%)	73 (49.7%)	19 (12.9%)	0.85	0.93
AD	111	139 (62.6%)	83 (37.4%)	0.69-1.41	44 (39.6%)	51 (45.9%)	16 (14.4%)		
rs4147912		C	A	0.91	CC	AC	AA		
CON	147	243 (82.7%)	51 (17.3%)	1.05	97 (66%)	49 (33.3%)	1 (0.7%)	0.76	0.1
AD	111	182 (82.0%)	40 (18.0%)	0.66-1.65	73 (65.8%)	36 (32.4%)	2 (1.8%)		
rs2516049		A	G	0.83	AA	AG	GG		
CON	147	227 (77.2%)	67 (22.8%)	0.94	85 (57.8%)	57 (38.8%)	5 (3.4%)	0.69	0.6
AD	111	174 (78.4%)	48 (21.6%)	0.61-1.42	68 (61.3%)	38 (34.2%)	5 (4.5%)		
rs1109581		G	A	0.11	GG	AG	AA		
CON	147	262 (89.1%)	32 (10.9%)	1.53	120 (81.6)	22 (15%)	5 (3.4%)	**0.028**	0.34
AD	111	187 (84.2%)	35 (15.8%)	0.92-2.56	78 (70.3%)	31 (27.9%)	2 (1.8%)		
rs7116190		G	A	0.32	GG	AG	AA		
CON	147	231 (78.6%)	63 (21.4%)	0.78	92 (62.6%)	47 (32.0%)	8 (5.4%)	0.60	0.75
AD	111	183 (82.4%)	39 (17.6%)	0.50-1.22	76 (68.5%)	31 (27.9%)	4 (3.6%)		
rs667897		A	G	1	AA	AG	GG		
CON	147	190 (64.6%)	104 (35.4)	0.99	66 (44.9%)	58 (39.5%)	23 (15.6%)	0.78	0.27

	N								
AD	111	144 (64.9%)	78 (35.1%)	0.69-1.43	48 (43.2%)	48 (43.2%)	15 (13.5%)		
rs4266886		C	T	0.86	CC	CT	TT		
CON	147	184 (62.6%)	110 (37.4)	1.04	57 (38.8%)	70 (47.6%)	20 (13.6%)	0.44	0.71
AD	111	137 (61.7%)	85 (38.3%)	0.73-1.49	46 (41.4%)	45 (40.5%)	20 (18.0%)		
rs698842		T	A	0.87	TT	AT	AA		
CON	147	271 (92.2%)	23 (7.8%)	1.10	125 (85%)	21 (14.3%)	1 (0.7%)	0.93	0.97
AD	111	203 (91.4%)	19 (8.6%)	0.59-2.08	93 (83.8%)	17 (15.3%)	1 (0.9%)		
rs77336780		C	G	0.51	CC	CG	GG		
CON	147	258 (87.8%)	36 (12.2%)	1.21	115 (78.2)	28 (19.0%)	4 (2.7%)	0.70	0.4
AD	111	190 (85.6%)	32 (14.4%)	0.72-2.01	82 (73.9%)	26 (23.4%)	3 (2.7%)		
rs7813641		T	A	0.14	TT	AT	AA		
CON	147	183 (62.2%)	111 (37.8)	0.74	55 (37.4%)	73 (49.7%)	19 (12.9%)	0.29	0.65
AD	111	153 (68.9%)	69 (31.1%)	0.51-1.08	51 (45.9%)	51 (45.9%)	9 (8.1%)		

SNP, single nucleotide polymorphism; *APOE*, apolipoprotein E; CON, healthy controls; OR, odds ratio, CI, confidence interval

HWE, Hardy-Weinberg equilibrium; N, number.

Bold indicates statistically significant values.

Supplementary Table 7. Association of SNPs of candidate genes with AD in *APOE* ε4 non-carriers in four genetic model.

Gene	SNP	dominant model (adjusted)			Recessive model (adjusted)		
		p	**OR**	**95%CI**	**p**	**OR**	**95%CI**
FERMT2	rs6572869	0.43	1.22	0.74-2.01	**0.014**	0.33	0.14-0.80
CELF1	rs11604680	**0.028**	1.76	1.06-2.92	0.38	0.65	0.25-1.68
CELF1	rs1317149	**0.038**	1.72	1.03-2.86	0.062	0.4	0.15-1.05
COPI	rs9898218	0.066	1.61	0.97-2.66	0.82	0.90	0.35-2.29
CHRNA2	rs2741342	**0.017**	0.51	0.29-0.89	0.41	0.77	0.42-1.43
CELF1	rs10742814	0.77	0.93	0.57-1.52	0.35	0.66	0.28-1.58
CELF1	rs11039280	0.31	0.77	0.47-1.27	0.16	0.53	0.22-1.28
ABCA7	rs3752242	0.69	0.90	0.54-1.50	0.81	1.09	0.53-2.25
ABCA7	rs4147912	0.94	1.02	0.61-1.72	0.45	2.53	0.22-28.51
HLA-DRB1	rs2516049	0.61	0.87	0.53-1.45	0.69	1.30	0.36-4.67
ADGRF4	rs1109581	**0.04**	1.85	1.03-3.32	0.40	0.49	0.092-2.58
MS4A	rs7116190	0.37	0.79	0.47-1.33	0.53	0.67	0.20-2.31
MS4A	rs667897	0.76	1.08	0.66-1.78	0.63	0.84	0.41-1.70
CR1	rs4266886	0.71	0.91	0.55-1.50	0.35	1.38	0.70-2.73
NRXN1	rs698842	0.69	1.15	0.58-2.28	0.87	1.27	0.078-20.64
OR51I1	rs77336780	0.35	1.32	0.74-2.36	0.93	1.07	0.23-4.93
CSMD1	rs7813641	0.19	0.72	0.43-1.18	0.25	0.61	0.26-1.41
Gene	SNP	additive model (adjusted)			overdominant model (adjusted)		
		p	**OR**	**95%CI**	**p**	**OR**	**95%CI**
FERMT2	rs6572869	0.53	0.89	0.62-1.28	**0.011**	1.97	1.17-3.33
CELF1	rs11604680	0.18	1.31	0.88-1.94	**0.007**	1.99	1.20-3.30
CELF1	rs1317149	0.46	1.16	0.79-1.70	**0.002**	2.29	1.37-3.82
COPI	rs9898218	0.18	1.30	0.88-1.92	**0.04**	1.74	1.03-2.94
CHRNA2	rs2741342	**0.044**	0.69	0.48-0.99	0.14	0.69	0.42-1.14
CELF1	rs10742814	0.52	0.88	0.60-1.29	0.80	1.07	0.65-1.76
CELF1	rs11039280	0.16	0.76	0.52-1.11	0.87	0.96	0.58-1.59
ABCA7	rs3752242	0.87	0.97	0.67-1.4	0.59	0.87	0.53-1.43
ABCA7	rs4147912	0.81	1.06	0.65-1.74	0.92	0.97	0.58-1.65
HLA-DRB1	rs2516049	0.76	0.93	0.60-1.45	0.49	0.83	0.49-1.40
ADGRF4	rs1109581	0.14	1.45	0.88-2.39	**0.013**	2.18	1.18-4.04
MS4A	rs7116190	0.33	0.80	0.52-1.25	0.52	0.84	0.49-1.44
MS4A	rs667897	0.98	1.00	0.70-1.41	0.51	1.18	0.72-1.96
CR1	rs4266886	0.83	1.04	0.73-1.48	0.29	0.76	0.46-1.26
NRXN1	rs698842	0.68	1.14	0.61-2.15	0.71	1.14	0.57-2.30
OR51I1	rs77336780	0.41	1.23	0.75-2.03	0.35	1.34	0.73-2.45
CSMD1	rs7813641	0.13	0.74	0.50-1.09	0.57	0.87	0.53-1.43

SNP, single nucleotide polymorphism; *APOE*, apolipoprotein E; OR: odds ratio, CI: confidence interval

p value was adjusted for gender and age. Bold indicates statistically significant values.