Supplementary Material

Genome-Wide Association Study of Incident Dementia in a Community-Based Sample of Older Subjects

Supplementary Table 1. Any Dementia *APOE* Genotype Distribution

Genotype	Any Dementia (n=420)	Cognitively Normal (n=2,197)	Total (n=2,617)
E2/2	4 (0.95%)	18 (0.82%)	22 (0.84%)
E2/3	34 (8.10%)	279 (12.70%)	313 (11.96%)
E2/4	17 (4.05%)	43 (1.96%)	60 (2.29%)
E3/3	223 (53.10%)	1,442 (65.64%)	1,665 (63.62%)
E3/4	131 (31.20%)	391 (17.80%)	522 (19.94%)
E4/4	11 (2.62%)	24 (1.09%)	35 (1.34%)
Hardy-Weinberg p	0.13	0.88	0.43
Allele Frequency			
APOE*2	0.0702	0.0815	0.0797
APOE*3	0.7274	0.8089	0.7958
APOE*4	0.2024	0.1097	0.1246

Supplementary Table 2. Replication of AD-associated SNPs in the GEM sample

					GEM			Reported GWAS Results		
CHR	GENE	BP	SNP	Minor Allele	MAF	OR	p	MAF	OR	p
1	B4GALT3,ADAMTS4	161155392	rs4575098	A	0.2444	1.03 (0.86-1.23)	7.54E-01	0.239	1.02 (1.01–1.02)	2.1E - 10
1	CR1	207802552	rs4844610	A	0.193	1.04 (0.85-1.26)	7.14E-01	0.78	0.85 (0.83-0.88)	3.60E-24
2	INPP5D	233981912	rs10933431	G	0.2388	0.87 (0.73-1.05)	1.44E-01	0.223	0.91 (0.88–0.94)	3.4E - 09
2	BIN1,CYP27C1	127892810	rs6733839	T	0.3787	1.09 (0.93-1.27)	2.89E-01	0.407	1.20 (1.17–1.23)	2.1E - 44
2	PRKD3	37531939	rs17020490	C	0.142	1.04 (0.84-1.29)	7.16E-01	0.145	1.06 (1.04–1.08)	3.3E - 09
2	ADAM17,YWHAQ	9699011	rs72777026	G	0.1395	1.02 (0.81-1.27)	8.94E-01	0.144	1.06 (1.04–1.08)	2.7E - 08
3	MME	154801978	rs61762319	G	0.01948	0.81 (0.46-1.45)	4.85E-01	2.60E-02	1.16 (1.11–1.21)	2.2E - 11
3	GPR149,MME	154787511	rs16824536	A	0.05073	0.91 (0.63-1.3)	6.07E-01	5.40E-02	0.92 (0.89–0.95)	3.6E - 08
4	CLNK	11023682	rs10939105	A	0.2759	0.99 (0.83-1.18)	9.30E-01	0.772	0.99 (0.98-0.99)	1.90E-09
4	RHOH	40198846	rs2245466	G	0.322	0.94 (0.8-1.11)	4.83E-01	0.343	1.05 (1.03–1.06)	1.2E - 09
4	IDUA	987343	rs3822030	G	0.4307	0.96 (0.82-1.12)	5.98E-01	0.429	0.95 (0.94–0.96)	8.3E - 12
5	HAVCR2	156526331	rs6891966	A	0.229	1.11 (0.93-1.33)	2.54E-01	0.23	0.98 (0.97–0.99)	7.9E - 10
5	MEF2C-AS1	88223420	rs190982	G	0.3966	0.95 (0.81-1.11)	5.33E-01	0·408	0.92 (0.89–0.95)	3.2E - 08
5	TNIP1	150432388	rs871269	T	0.3376	0.95 (0.81-1.13)	5.75E-01	0.32	0.98 (0.97–0.99)	1.4E - 09
5	LOC100505878,MIR4280	86223195	rs62374257	C	0.2205	1.02 (0.85-1.23)	8.03E-01	0.23	1.07 (1.05–1.09)	1.4E - 15
6	CD2AP	47432637	rs9381563	C	0.3433	0.9 (0.77-1.06)	2.22E-01	0.656	0.93 (0.91-0.95)	5.80E-14
6	OR2B2,OR2B6	27883269	rs1497525	A	0.04147	1.64 (1.16-2.31)	**5.16E-03**	0.05–0.08	1.34 (1.15–1.56)	2.1E - 08
6	HS3ST5,FRK	114612895	rs785129	T	0.3445	1.22 (1.04-1.43)	**1.64E-02**	0.35	1.04 (1.03–1.06)	2.4E - 09
6	HLA-DRB1,HLA-DQA1	32559825	rs34855541	G	0.0978	0.84 (0.64-1.1)	2.02E-01	0.135	0.90 (0.87–0.92)	9.5E - 15
7	ZCWPW1	99932049	rs7384878	C	0.3083	1.02 (0.86-1.21)	8.27E-01	0.69		9.41E-16
7	NYAP1	100091795	rs12539172	T	0.3122	1.01 (0.85-1.19)	9.48E-01	0.714	1.09 (1.06-1.11)	9.3E-10
7	EPHA1	143107876	rs11762262	T	0.206	1.07 (0.88-1.29)	5.05E-01	0.425	1.01 (1.01-1.02)	3.60E-11
7	GPR141,NME8	37841534	rs2718058	G	0.3592	1.32 (1.13-1.55)	**4.14E-04**	0·373	0.93 (0.90–0.95)	4.8E - 09
7	ICA1	8244012	rs10952097	T	0.09703	0.78 (0.59-1.04)	8.85E-02	0.114	1.07 (1.05–1.10)	6.8E - 09
7	RPA3OS	7856894	rs6943429	T	0.4157	1.08 (0.92-1.26)	3.42E-01	0.42	1.05 (1.03–1.06)	1.0E - 10
7	LOC100996654,EGFR	54941328	rs76928645	T	0.1022	1.1 (0.86-1.41)	4.27E-01	0.103	0.93 (0.91–0.95)	1.6E - 10
7	PILRA	99971834	rs1859788	A	0.3056	1.01 (0.85-1.19)	9.42E-01	0.321	0.98 (0.98–0.99)	3.3E - 18

8	CTSB	11702122	rs1065712	C	0.05112	1.37 (0.99-1.89)	**5.53E-02**	5.30E-02	1.09 (1.06–1.12)	1.9E - 09
8	CLU	27467686	rs9331896	C	0.3976	1.09 (0.94-1.28)	2.63E-01	0.387	0.88 (0.85–0.90)	4.6E - 24
8	PTK2B	27219987	rs73223431	T	0.3453	0.96 (0.82-1.13)	6.21E-01	0.367	1.10 (1.07–1.13)	6.3E - 14
8	SHARPIN	145158607	rs34173062	A	0.0787	0.95 (0.71-1.27)	7.36E-01	8.10E-02	1.13 (1.09–1.16)	1.7E - 18
9	ABCA1	107665978	rs1800978	G	0.1269	1.04 (0.83-1.31)	7.25E-01	0.13	1.06 (1.04–1.08)	1.6E - 09
10	CCDC6	61645833	rs1171814	T	0.4742	0.78 (0.67-0.91)	**1.80E-03**	0.481	0.95 (0.93–0.97)	3.8E - 08
10	TSPAN14	82280137	rs1878036	T	0.1921	1.15 (0.95-1.39)	1.60E-01	0.207	1.07 (1.05–1.10)	2.7E - 09
10	USP6NL,ECHDC3	11720308	rs7920721	G	0.3702	1.08 (0.93-1.27)	3.16E-01	0.389	1.08 (1.05–1.11)	2.3E - 09
11	PICALM	85776544	rs867611	G	0.3248	0.82 (0.69-0.97)	**1.85E-02**	0.692	1.02 (1.02-1.02)	2.20E-18
11	MS4A2,MS4A6A	59936926	rs7933202	C	0.3931	0.85 (0.72-0.99)	**4.25E-02**	0.391	0.89 (0.87–0.92)	1.9E - 19
11	SORL1	121435587	rs11218343	C	0.04379	0.94 (0.64-1.38)	7.45E-01	0.04	0.80 (0.75–0.85)	2.9E - 12
11	SPI1	47380340	rs3740688	G	0.4539	1.02 (0.88-1.19)	8.05E-01	0.448	0.92 (0.89–0.94)	5.4E - 13
14	LINC00221,NONE	107121607	rs10131280	A	0.1358	0.83 (0.66-1.06)	1.28E-01	0.133	0.94 (0.92–0.96)	4.3E - 10
14	SLC24A4	92926952	rs10498633	T	0.2153	0.88 (0.73-1.07)	2.13E-01	0.217	0.91 (0.88–0.94)	5.5E - 09
14	FERMT2	53391680	rs17125924	G	0.09279	0.85 (0.65-1.12)	2.58E-01	9.90E-02	1.12 (1.08–1.15)	1.3E - 11
15	SPPL2A	50992311	rs12592778	A	0.1287	0.98 (0.8-1.19)	8.35E-01	0.133	0.94 (0.92–0.96)	4.2E − 09
15	TRIP4	64592270	rs77404765 (rs74615166: D'=1.0 R2=1.0)	C	0.02332	1.37 (0.82-2.29)	2.34E-01	0.02	1.31 (1.19–1.44)	9.7E − 09
15	APH1B	63569902	rs117618017	T	0.1258	1.3 (1.04-1.61)	**1.90E-02**	0.139	1.09 (1.06–1.12)	1.5E - 08
15	CTSH	79229199	rs12592898	A	0.1287	0.8 (0.63-1.02)	7.09E-02	0.133	0.94 (0.92–0.96)	4.2E - 09
15	ADAM10,FAM63B	59045774	rs593742	G	0.3084	1.11 (0.94-1.32)	2.13E-01	0.298	0.93 (0.91–0.95)	2.8E - 11
15	SNX1	64423506	rs3848143	G	0.213	1.06 (0.88-1.27)	5.74E-01	0.22	1.05 (1.04–1.07)	8.4E - 11
16	IQCK	19746982	rs16972322	T	0.1826	1.12 (0.91-1.37)	2.87E-01	0.18	0.92 0.89–0.95	2.4E−8
16	PLCG2	81773209	rs12444183	A	0.4288	1.17 (1-1.37)	**4.76E-02**	0.657	1.06 (1.04-1.08)	3.20E-08
16	WWOX,MAF	79608408	rs450674	C	0.3843	0.86 (0.73-1.01)	6.39E-02	0.373	0.96 (0.95–0.98)	3.2E - 08
16	IL34	70694000	rs4985556	A	0.1188	0.88 (0.69-1.13)	3.25E-01	8.80E-02	1.09 (1.05–1.12)	3.7E - 08
16	LINC00917,FENDRR	86454210	rs16941239	A	0.02469	1.15 (0.71-1.86)	5.72E-01	2.90E-02	1.13 (1.08–1.17)	1.3E - 08
16	PRDM7,NONE	90170095	rs56407236	A	0.06636	1.07 (0.79-1.44)	6.81E-01	6.90E-02	1.11 (1.08–1.14)	6.5E - 15
16	BCKDK	31122571	rs889555	T	0.2876	0.99 (0.83-1.17)	8.78E-01	0.29	0.95 (0.94–0.97)	3.2E - 08
16	WWOX,MAF	79355857	rs62039712	A	0.114	1 (0.79-1.27)	9.74E-01	9.40E-02	1.16 (1.09–1.24)	3.7E - 08

17	ZNF594	5138980	rs113260531	A	0.1295	1.08 (0.86-1.36)	5.26E-01	0.117	1.02 (1.01-1.03)	9.20E-10
17	RP11-81K2.1	47450775	rs28394864	A	0.4573	0.98 (0.84-1.14)	7.87E-01	0.471	1.01 (1.01-1.02)	1.90E-08
17	TSPOAP1	56398006	rs2526380	G	0.4249	0.92 (0.79-1.07)	2.87E-01	0.449	0.97 (0.96-0.98)	2.60E-08
17	MYO15A	18059454	rs2242595	A	0.1179	0.8 (0.62-1.03)	8.31E-02	0.112	0.94 (0.92–0.96)	1.1E - 09
17	CYB561,ACE	61538148	rs138190086	A	0.01794	1.45 (0.87-2.42)	1.53E-01	1.70E-02	1.25 (1.16–1.35)	1.9E - 09
17	BZRAP1-AS1	56409089	rs2632516	C	0.4433	0.91 (0.78-1.06)	2.20E-01	0.44–0.60	0.92 (0.91–0.94)	4.4E - 08
17	BZRAP1	56398006	rs2526380	G	0.4423	0.92 (0.79-1.07)	2.87E-01	0.44	0.97 (0.96–0.98)	2.6E - 08
17	FAM171A2,ITGA2B	42442344	rs708382	C	0.3812	0.96 (0.82-1.13)	6.56E-01	0.39	1.02 (1.01–1.02)	2.0E - 09
18	DSG2	29088958	rs8093731	T	0.009067	0.58 (0.26-1.31)	1.90E-01	0.017	0.73 (0.62–0.86)	1.0E−04
18	ALPK2	56189459	rs76726049	C	0.01929	0.85 (0.48-1.49)	5.62E-01	1.10E-02	1.06 (1.04–1.08)	3.3E - 08
19	APOE	45411941	rs429358	C	0.1242	2.22 (1.8-2.73)	**9.36E-14**	0.216	3.32 (3.20–3.45)	1.2E - 881
19	ABCA7	1056492	rs3752246	G	0.1744	1.27 (1.05-1.55)	**1.49E-02**	0.182	1.15 (1.11–1.18)	3.1E - 16
19	LILRA5	54825174	rs1761461	A	0.4981	0.91 (0.78-1.06)	2.44E-01	0.49	1.01 (1.01–1.02)	1.6E - 09
19	NFIC	3405592	rs9749589	A	0.1526	1.09 (0.89-1.34)	4.12E-01	0.02–0.16	0.76 (0.69–0.83)	1.5E - 08
19	FBXO46,LOC388553	46241841	rs76320948	T	0.03549	0.88 (0.57-1.36)	5.60E-01	4.60E-02	0.97 (0.96–0.98)	4.6E - 08
19	CD33	51727962	rs3865444	A	0.3177	1 (0.84-1.18)	9.68E-01	0.336	0.99 (0.98–0.99)	6.3E - 09
20	CASS4	54998544	rs6014724	G	0.09877	0.81 (0.61-1.06)	1.28E-01	8.80E-02	0.89 (0.87–0.93)	1.1E - 10
20	RBCK1	393978	rs1358782	A	0.2527	0.91 (0.75-1.09)	2.95E-01	0.246	0.95 (0.94–0.97)	1.6E - 08
20	SLC2A4RG	62374441	rs6742	T	0.2058	0.94 (0.77-1.14)	5.32E-01	0.221	0.95 (0.93–0.97)	2.6E - 09
21	CYYR1,ADAMTS1	28156856	rs2830500	A	0.3316	1.03 (0.86-1.23)	8.31E-01	0.336	0.93 (0.91–0.95)	2.6E - 08

Supplementary Table 3. Genome-wide Significant SNPs on Chromosome 19 and 12 in Any Dementia GWAS Analysis

CHR	**SNP**	**BP**	**A1**	**MAF-Cases**	**MAF-Controls**	**OR (95% CI)**	***p***	**LOC**	**GENE/LOCUS**
19	rs429358	45411941	C	0.19930	0.10990	2.086 (1.703-2.554)	1.191E-12	Exonic	*APOE*
19	rs769449	45410002	A	0.15570	0.08908	1.919 (1.538-2.394)	7.536E-09	Intronic	*APOE*
19	rs4420638	45422946	G	0.22290	0.14370	1.731 (1.434-2.089)	1.121E-08	Downstream	*APOC1*
19	rs12721051	45422160	G	0.22170	0.14350	1.725 (1.429-2.083)	1.378E-08	Intronic	*APOC1*
19	rs6857	45392254	T	0.21460	0.13920	1.717 (1.418-2.079)	3.175E-08	3' UTR	*NECTIN2*
12	rs148377161	28830097	T	0.04717	0.01632	3.237 (2.160-4.852)	1.282E-08	Intergenic	*CCDC91/ LOC105369711*
12	rs192213585	28918097	C	0.04717	0.01677	3.166 (2.115-4.740)	2.176E-08	Intergenic	*CCDC91/ LOC105369711*
12	rs148760255	28755421	G	0.04363	0.01519	3.247 (2.133-4.943)	3.953E-08	Intergenic	*CCDC91/ LOC105369711*

Supplementary Table 4. Any Dementia Sex-Stratified Analysis

			Any Dementia Males				Any Dementia Females					
CHR	**SNP**	**BP**	**MAF-Cases**	**MAF-Controls**	**OR (95% CI)**	***p***	**MAF-Cases**	**MAF-Controls**	**OR (95% CI)**	***p***	**LOC**	**GENE/LOCUS**
1	rs140076909	98808256	0.05656	0.01507	4.1250 (2.419-7.033)	1.938E-07	0.01232	0.01994	0.6042 (0.2384-1.531)	0.28820	Intergenic	*SNX7* *LOC729987*
7	rs117803234	7155404	0.06787	0.01954	3.5890 (2.233-5.771)	1.325E-07	0.00985	0.02863	0.3348 (0.1204-0.931)	3.599E-02	Intergenic	*C1GALT1* *LOC100131257*
12	rs148760255	28755421	0.04299	0.01792	2.646 (1.507-4.645)	6.996E-04	0.04433	0.01176	4.269 (2.238-8.145)	1.064E-05	Intergenic	*CCDC91* *FAR2*
12	rs148377161	28830097	0.04299	0.01832	2.573 (1.469-4.508)	9.547E-04	0.05172	0.01380	4.196 (2.309-7.624)	2.510E-06	Intergenic	*CCDC91* *FAR2*
12	rs192213585	28918097	0.04525	0.01832	2.737 (1.576-4.755)	3.503E-04	0.04926	0.01483	3.747 (2.059-6.820)	1.541E-05	Intergenic	*CCDC91* *FAR2*
19	rs429358	45411941	0.16970	0.10750	1.729 (1.299-2.301)	1.745E-04	0.23150	0.11300	2.582 (1.9230-3.4670)	2.845E-10	Exonic	*APOE*
19	rs769449	45410002	0.12900	0.08876	1.5260 (1.113-2.093)	8.724E-03	0.18470	0.08947	2.468 (1.7950-3.3940)	2.703E-08	Intronic	*APOE*
19	rs12721051	45422160	0.18550	0.14130	1.40 (1.07-1.833)	1.429E-02	0.26110	0.14620	2.145 (1.6370-2.8110)	3.195E-08	Intronic	*APOC1*
19	rs4420638	45422946	0.18780	0.14130	1.405 (1.073-1.838)	1.326E-02	0.26110	0.14670	2.137 (1.6310-2.8010)	3.713E-08	Downstream	*APOC1*

Supplementary Table 5. Suggestive SNPs Among AD *APOE*4* Carriers

			AD E4 Carrier					
CHR	**SNP**	**BP**	**MAF-Cases**	**MAF-Controls**	**OR (95% CI)**	p	**LOC**	**GENE/LOCUS**
1	rs488959	37430810	0.3212	0.2758	1.936 (1.445-2.593)	9.51E-06	Intronic	*GRIK3*
1	rs697923	37435147	0.3225	0.2727	1.963 (1.464-2.632)	6.54E-06	Intronic	*GRIK3*
1	rs11263955	37438380	0.3212	0.2722	1.974 (1.472-2.647)	5.48E-06	Intronic	*GRIK3*
2	rs77731149	69481923	0.06865	0.05190	3.733 (2.119-6.574)	5.09E-06	Intergenic	*ANTXR1* *LOC100421347*
6	rs73039501	167289534	0.07772	0.04669	3.665 (2.172-6.183)	1.14E-06	Intergenic	*RPS6KA2* *RPS6KA2-AS1*
7	rs10254077	46723871	0.0842	0.0612	3.191 (1.947-5.228)	4.11E-06	Intergenic	*LOC730338*
7	rs1473245	46730919	0.11400	0.09701	2.52 (1.673-3.796)	9.76E-06	Intronic	*LOC730338*
7	rs700748	46733679	0.11530	0.09723	2.52 (1.673-3.796)	9.76E-06	Intronic	*LOC730338*
7	rs11973225	46734636	0.11270	0.09701	2.52 (1.673-3.796)	9.76E-06	Intronic	*LOC730338*
7	rs59656959	46747168	0.07661	0.09974	2.787 (1.774-4.377)	8.62E-06	Intergenic	*LOC730338*
7	rs56071734	46748230	0.09585	0.07570	2.84 (1.805-4.467)	6.37E-06	Intergenic	*LOC730338*
7	rs856547	46748582	0.09974	0.07661	2.787 (1.774-4.377)	8.62E-06	Intergenic	*LOC730338*
7	rs74362872	46788622	0.08161	0.06120	3.189 (1.924-5.284)	6.78E-06	Intergenic	*LOC730338*

9	rs117770454	27496245	0.1114	0.0757	2.844 (1.853-4.367)	1.76E-06	Intronic Downstream	*MOB3B* *LOC105376001*
9	rs12553951	27512234	0.10750	0.07457	2.718 (1.765-4.186)	5.63E-06	Intronic	*MOB3B*
11	rs4331058	101411993	0.3653	0.3119	1.915 (1.437-2.552)	9.14E-06	Intronic	*TRPC6*
11	rs34548246	101415271	0.3653	0.3107	1.915 (1.437-2.552)	9.14E-06	Intronic	*TRPC6*
11	rs118121717	109176047	0.05959	0.03921	3.555 (2.042-6.189)	7.36E-06	Intergenic	*C11orf87* *RNA5SP349*
13	rs117421253	93091326	0.02591	0.01360	7.604 (3.124-18.51)	7.82E-06	Intronic	*GPC5*
13	rs9517934	100595522	0.4443	0.3989	1.896 (1.445-2.488)	3.97E-06	Intronic	*LOC101927437*
18	rs72987909	75113020	0.3355	0.2922	2.077 (1.546-2.79)	1.24E-06	Intergenic	*LOC107985171*
20	rs117000803	54827154	0.04275	0.01972	7.045 (3.064-16.2)	4.32E-06	Intergenic	*MC3R*
22	rs1669114	22035951	0.2047	0.2536	0.4237 (0.2926-0.6136)	5.51E-06	Intronic	*PPIL2*
22	rs861830	22041601	0.2073	0.2548	0.4347 (0.3009-0.6278)	8.93E-06	Intronic	*PPIL2*

Supplementary Table 6. Suggestive SNPs Among AD Non-*APOE*4* Carriers

			AD Non-E4 Carrier					
CHR	**SNP**	**BP**	**MAF-Cases**	**MAF-Controls**	**OR (95% CI)**	p	**LOC**	**GENE/LOCUS**
1	rs74500357	5425805	0.08679	0.04669	2.24 (1.567-3.156)	7.62E-06	Intergenic	*LOC107984911* *LOC105376686* *LOC105376682*
1	rs12735762	157244976	0.4132	0.4884	0.6276 (0.5109-0.7711)	9.18E-06	Exonic Intronic	*LINC02772* *LOC105371456*
1	rs17578989	234737989	0.4093	0.3579	1.619 (1.326-1.977)	2.24E-06	Intergenic	*IRF2BP2*
1	rs4636	234744413	0.4093	0.3583	1.607 (1.316-1.963)	3.33E-06	Exonic	*IRF2BP2*
1	rs6695708	234747692	0.4093	0.3592	1.612 (1.318-1.97)	3.19E-06	Upstream	*IRF2BP2*
1	rs35581844	234751563	0.4093	0.3592	1.625 (1.33-1.986)	2.1E-06	Intergenic	*IRF2BP2*
2	rs147929195	15683329	0.04922	0.02221	2.895 (1.836-4.565)	4.78E-06	Intronic	*NBAS*
2	rs188995929	223037743	0.01295	0.00204	9.42 (3.579-24.8)	5.57E-06	Intergenic	*PAX3* *LOC107985991*
2	rs10177231	238333762	0.01813	0.00476	6.513 (2.899-14.63)	5.69E-06	Intronic	*COL6A3*
2	rs13410386	238337833	0.01684	0.00476	6.513 (2.899-14.63)	5.69E-06	Intronic	*COL6A3*
3	rs13077785	95097192	0.3886	0.3203	1.594 (1.304-1.948)	5.32E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs1516610	95106563	0.3199	0.2579	1.609 (1.308-1.979)	6.61E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs491667	95113450	0.3990	0.3323	1.575 (1.292-1.921)	7.1E-06	Intergenic	*RPS18P6* *MTHFD2P1*

3	rs2222255	95125919	0.3614	0.2962	1.59 (1.297-1.948)	7.82E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs2203839	95126043	0.4106	0.3420	1.566 (1.286-1.907)	7.84E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs2222254	95126310	0.3808	0.3146	1.564 (1.283-1.907)	9.71E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs12490147	95127525	0.3316	0.2679	1.602 (1.304-1.968)	7.04E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs13063764	95133452	0.3368	0.2709	1.608 (1.309-1.975)	5.89E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs524360	95138590	0.4171	0.3445	1.58 (1.298-1.925)	5.31E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs494331	95139548	0.4145	0.3422	1.581 (1.299-1.925)	5.07E-06	Intergenic	*RPS18P6* *MTHFD2P1*
3	rs189342591	98206694	0.014250	0.002947	8.781 (3.363-22.93)	9.14E-06	Intergenic	*OR5K2* *OR5K1*
4	rs147649359	53897690	0.01554	0.00340	8.534 (3.482-20.92)	2.77E-06	Intronic	*SCFD2*
4	rs184984767	53911523	0.019430	0.005666	5.934 (2.848-12.37)	1.99E-06	Intronic	*SCFD2*
4	rs189488810	130509770	0.015540	0.005213	6.07 (2.785-13.23)	5.72E-06	Intergenic	*LINC02466* *LOC105377417*
4	rs114014858	162780079	0.04793	0.02743	2.743 (1.764-4.266)	7.52E-06	Intronic	*FSTL5*
4	rs111618415	171369795	0.02720	0.01201	5.367 (2.852-10.1)	**1.89E-07**	Intergenic	*LINC02512* *HSP90AA6P*
4	rs75810822	171473359	0.025910	0.009066	5.456 (2.768-10.75)	9.5E-07	Intergenic	*LINC02512* *HSP90AA6P*
4	rs77062504	186614058	0.03368	0.01247	3.566 (2.037-6.244)	8.63E-06	Intronic	*SORBS2*
4	rs28516669	186621344	0.03368	0.01247	3.566 (2.037-6.244)	8.63E-06	Intronic	*SORBS2*

4	rs76819555	186651744	0.03238	0.01179	3.815 (2.136-6.811)	6.01E-06	Intronic	*SORBS2*
5	rs190418844	12108973	0.018130	0.003626	7.463 (3.223-17.28)	2.71E-06	Intergenic	*RNU6-679P* *CTNND2*
5	rs2968128	12163091	0.018130	0.003853	6.851 (3.02-15.54)	4.14E-06	Intergenic	*RNU6-679P* *CTNND2*
5	rs2907292	12202427	0.020730	0.003853	7.512 (3.356-16.82)	9.35E-07	Intergenic	*RNU6-679P* *CTNND2*
5	rs190244925	13277544	0.012950	0.002267	9.791 (3.564-26.9)	9.66E-06	Intergenic	*RPS23P5* *LOC105374660* *LOC105374659*
5	rs527611067	13346976	0.012950	0.002267	9.791 (3.564-26.9)	9.66E-06	Intergenic	*RPS23P5* *LOC105374660* *LOC105374659*
5	rs187039392	13507743	0.014250	0.002267	13.37 (4.753-37.64)	**8.98E-07**	Intronic	*LOC105374660*
5	rs534653341	13611354	0.01295	0.00204	12.05 (4.198-34.6)	3.73E-06	Intergenic	*RPL29P13* *LOC105374660* *NENFP3* *DNAH5*
5	rs114804794	75698863	0.011660	0.002947	8.527 (3.311-21.96)	9E-06	Upstream	*IQGAP2*
5	rs115573891	75712057	0.01166	0.00272	8.527 (3.311-21.96)	9E-06	Intronic	*IQGAP2*
5	rs71581242	115977629	0.06218	0.03604	2.435 (1.662-3.567)	4.89E-06	Intergenic	*SEMA6A* *SEMA6A-AS2* *RPS17P2*
5	rs13154525	116055905	0.06477	0.03762	2.361 (1.626-3.428)	6.3E-06	Intergenic	*RPS17P2* *LINC02214*
5	rs77801218	149704854	0.10230	0.06936	2.035 (1.488-2.783)	8.62E-06	Intergenic	*LOC105378225* *ARSI*
5	rs79048160	149705793	0.10230	0.06958	2.034 (1.487-2.781)	8.74E-06	Intergenic	*LOC105378225* *ARSI*

5	rs75972093	158104737	0.020730	0.005213	6.418 (3.034-13.58)	1.16E-06	Intergenic	*EBF1* *LINC02227*
5	rs143255859	179397609	0.03497	0.01428	3.278 (1.949-5.514)	7.63E-06	Intronic	*RNF130*
6	rs78883162	49239776	0.02073	0.00816	4.683 (2.376-9.23)	8.19E-06	Intergenic	*RNU7-65P* *EEF1A1P42*
6	rs79437694	130261681	0.010360	0.002267	15.66 (4.774-51.33)	5.62E-06	Intronic	*LOC105377999*
7	rs139786718	1921843	0.03368	0.01632	3.373 (2.004-5.675)	4.68E-06	Intronic	*MAD1L1*
7	rs4731788	130986966	0.4262	0.4923	0.616 (0.5005-0.7581)	4.74E-06	Intronic	*MKLN1*
7	rs10954315	130991609	0.4301	0.4934	0.6224 (0.5062-0.7653)	6.93E-06	Intronic	*MKLN1*
7	rs4731790	130992047	0.4288	0.4925	0.6224 (0.5062-0.7654)	6.96E-06	Intronic	*MKLN1*
8	rs112102340	96387711	0.06865	0.03581	2.483 (1.674-3.683)	6.11E-06	Intronic	*C8orf37-AS1*
8	rs77972768	139199114	0.02850	0.01224	3.781 (2.097-6.816)	9.77E-06	Intronic	*FAM135B*
8	rs79286235	139199560	0.02850	0.01133	4.125 (2.267-7.503)	3.47E-06	Intronic	*FAM135B*
8	rs11992577	139201200	0.02850	0.01201	3.781 (2.097-6.816)	9.77E-06	Intronic	*FAM135B*
8	rs78168498	139201871	0.02850	0.01156	3.819 (2.116-6.893)	8.7E-06	Intronic	*FAM135B*
8	rs75982628	139206991	0.02720	0.01065	3.97 (2.155-7.315)	9.75E-06	Intronic	*FAM135B*
9	rs140005165	94663660	0.012950	0.001813	13 (4.282-39.44)	5.97E-06	Intronic	*ROR2*
9	rs117247154	135217116	0.07124	0.03762	2.458 (1.693-3.568)	2.27E-06	Intronic	*SETX*

9	rs149384840	139412885	0.02202	0.00748	4.929 (2.471-9.83)	5.95E-06	Intronic	*NOTCH1*
10	rs150783484	52729827	0.03756	0.01723	3.494 (2.087-5.852)	1.98E-06	Intergenic	*MIX23P2* *PRKG1*
11	rs79193402	64677105	0.04663	0.02108	2.819 (1.783-4.457)	9.26E-06	Intronic	*ATG2A*
11	rs1869446	68872284	0.2798	0.2149	1.667 (1.342-2.072)	3.93E-06	Intergenic	*TPCN2* *LOC107984344*
11	rs1551304	68876587	0.3329	0.2543	1.652 (1.339-2.039)	2.85E-06	Intergenic	*TPCN2* *LOC107984344*
11	rs10896430	68877162	0.2940	0.2228	1.684 (1.358-2.089)	2.05E-06	Intergenic	*TPCN2* *LOC107984344*
11	rs12365981	68877592	0.3316	0.2536	1.638 (1.328-2.022)	4.17E-06	Intergenic	*TPCN2* *LOC107984344*
11	rs11228503	68879044	0.3212	0.2446	1.645 (1.332-2.032)	3.85E-06	Intergenic	*TPCN2* *LOC107984344*
11	rs509243	70023419	0.05181	0.02131	2.881 (1.814-4.574)	7.3E-06	Intronic Upstream	*ANO1* *LOC101928473*
11	rs151107956	70033070	0.05181	0.02085	2.976 (1.871-4.733)	4.1E-06	Intronic	*ANO1*
11	rs492812	70037637	0.05181	0.02131	2.884 (1.816-4.58)	7.14E-06	Intergenic	*FADD* *ANO1*
11	rs149743840	70049228	0.03627	0.01292	3.492 (2.019-6.041)	7.72E-06	Upstream	*FADD*
12	rs556343211	12576021	0.01813	0.00408	8.66 (3.665-20.46)	**8.61E-07**	Intronic	*BORCS5*
13	rs73181031	37933766	0.019430	0.005666	5.062 (2.477-10.35)	8.71E-06	Intergenic	*LOC105377814* *LINC01048*
13	rs117887196	50857743	0.01554	0.00544	5.983 (2.773-12.91)	5.13E-06	Intronic	*DLEU1*
13	rs9516960	98212585	0.01554	0.00544	6.245 (2.782-14.02)	9.02E-06	Intronic	*LOC105370324*

15	rs546851015	94948144	0.011660	0.001587	13.56 (4.344-42.31)	7.15E-06	Intronic	*MCTP2*
18	rs147426078	49388643	0.014250	0.003853	7.995 (3.251-19.66)	5.94E-06	Intergenic	*RPS8P3* *LOC105372121* *LOC100422053*
19	rs536700624	5050994	0.01813	0.00408	6.016 (2.733-13.24)	8.26E-06	Intronic	*KDM4B*
20	rs3092540	45410725	0.2293	0.1908	1.682 (1.336-2.118)	9.71E-06	Intergenic	*SLC2A10*
20	rs78962860	50476411	0.04534	0.01904	3.144 (1.963-5.034)	1.86E-06	Intronic	*LINC01429*
20	rs117029867	51914871	0.024610	0.009066	4.403 (2.292-8.459)	8.58E-06	Intronic	*TSHZ2*
20	rs151122369	61337472	0.02073	0.00612	5.325 (2.653-10.69)	2.54E-06	Intergenic	*NTSR1* *LOC107987285*

Supplementary Table 7. Suggestive SNPs Among Any Dementia *APOE*4* Carrier

CHR	SNP	BP	MAF-Cases	MAF-Controls	OR (95% CI)	p	LOC	GENE
1	rs488959	37430810	0.3255	0.2758	1.945 (1.457 - 2.598)	6.51E-06	intronic	GRIK3
1	rs697923	37435147	0.3231	0.2727	1.945 (1.456 - 2.598)	6.75E-06	intronic	GRIK3
1	rs11263955	37438380	0.3208	0.2722	1.925 (1.442 - 2.57)	9.01E-06	intronic	GRIK3
6	rs73039501	1.67E+08	0.07665	0.04669	3.559 (2.114 - 5.992)	1.79E-06	intergenic	RPS6KA2,RPS6KA2-AS1
7	rs10254077	46723871	0.08255	0.0612	3.08 (1.888 - 5.024)	6.64E-06	intergenic	IGFBP3,TNS3
9	rs117770454	27496245	0.1061	0.0757	2.807 (1.837 - 4.289)	1.82E-06	intronic	MOB3B
9	rs12553951	27512234	0.1026	0.07457	2.687 (1.753 - 4.118)	5.67E-06	intronic	MOB3B
11	rs77000724	82275804	0.05425	0.02947	4.142 (2.237 - 7.67)	6.15E-06	intergenic	LOC101928989,FAM181B
11	rs118121717	1.09E+08	0.05778	0.03921	3.627 (2.099 - 6.265)	3.85E-06	intergenic	DDX10,C11orf87
13	rs9517934	1.01E+08	0.4469	0.3989	1.928 (1.473 - 2.524)	1.75E-06	ncRNA_intronic	LOC101927437
18	rs4799989	35542361	0.1686	0.2233	0.4118 (0.2793 - 0.607)	7.40E-06	intergenic	MIR4318,LINC00669
18	rs72987909	75113020	0.3337	0.2922	2.022 (1.513 - 2.702)	1.92E-06	intergenic	GALR1,LINC01029
20	rs117000803	54827154	0.04363	0.01972	6.568 (2.856 - 15.11)	9.47E-06	intergenic	MC3R,FAM210B
22	rs1669114	22035951	0.204	0.2536	0.4399 (0.3073 - 0.6298)	7.27E-06	intronic	PPIL2

Supplementary Table 8. Suggestive SNPs Among Any Dementia Non-*APOE*4* Carriers

CHR	**SNP**	**BP**	**MAF-Cases**	**MAF-Controls**	**OR (95% CI)**	**p**	**LOC**	**GENE**
1	rs144675968	1.77E+08	0.04245	0.02289	3.043 (1.926 - 4.808)	1.85E-06	intergenic	BRINP2,LOC101928778
1	rs141675993	1.77E+08	0.04127	0.02357	2.964 (1.864 - 4.715)	4.44E-06	intergenic	BRINP2,LOC101928778
1	rs17578989	2.35E+08	0.4163	0.3579	1.646 (1.362 - 1.989)	2.47E-07	intergenic	LINC01354,IRF2BP2
1	rs4636	2.35E+08	0.4163	0.3583	1.636 (1.353 - 1.977)	3.63E-07	exonic	IRF2BP2
1	rs6695708	2.35E+08	0.4163	0.3592	1.639 (1.355 - 1.983)	3.59E-07	intergenic	IRF2BP2,LINC00184
1	rs35581844	2.35E+08	0.4163	0.3592	1.653 (1.367 – 2)	**2.22E-07**	intergenic	IRF2BP2,LINC00184
1	rs10797557	2.35E+08	0.3927	0.3416	1.605 (1.322 - 1.949)	1.72E-06	intergenic	IRF2BP2,LINC00184
1	rs3850718	2.35E+08	0.3962	0.3438	1.613 (1.33 - 1.957)	1.23E-06	intergenic	IRF2BP2,LINC00184
1	rs12736461	2.35E+08	0.3986	0.3447	1.619 (1.332 - 1.967)	1.25E-06	intergenic	IRF2BP2,LINC00184
1	rs17519958	2.35E+08	0.3821	0.3377	1.57 (1.29 - 1.91)	6.48E-06	intergenic	IRF2BP2,LINC00184
1	rs7536996	2.35E+08	0.3868	0.3375	1.577 (1.295 - 1.919)	5.52E-06	intergenic	IRF2BP2,LINC00184
1	rs11802387	2.42E+08	0.09788	0.06596	2.005 (1.479 - 2.717)	7.42E-06	intronic	PLD5
3	rs140323454	85581142	0.04835	0.01813	2.915 (1.817 - 4.678)	9.19E-06	intronic	CADM2
3	rs62261694	85723238	0.05071	0.01881	2.992 (1.876 - 4.772)	4.20E-06	intronic	CADM2
4	rs181391253	290470	0.02123	0.009973	4 (2.166 - 7.39)	9.52E-06	upstream	ZNF732
4	rs29001236	1E+08	0.05307	0.02448	2.982 (1.933 - 4.598)	**7.74E-07**	ncRNA_intronic	LOC100507053
4	rs114014858	1.63E+08	0.04717	0.02743	2.617 (1.714 - 3.996)	8.36E-06	intronic	FSTL5
4	rs111618415	1.71E+08	0.02476	0.01201	4.607 (2.464 - 8.614)	1.73E-06	intergenic	AADAT,LOC100506122
4	rs75810822	1.71E+08	0.02358	0.009066	4.642 (2.375 - 9.074)	7.14E-06	intergenic	AADAT,LOC100506122

4	rs76819555	1.87E+08	0.03066	0.01179	3.588 (2.037 - 6.319)	9.72E-06	intronic	SORBS2
5	rs77801218	1.5E+08	0.1014	0.06936	2.023 (1.5 - 2.728)	3.84E-06	intergenic	ARSI,TCOF1
5	rs80347489	1.5E+08	0.1014	0.06981	2.012 (1.493 - 2.713)	4.52E-06	intergenic	ARSI,TCOF1
5	rs79048160	1.5E+08	0.1014	0.06958	2.022 (1.5 - 2.727)	3.88E-06	intergenic	ARSI,TCOF1
5	rs77026648	1.54E+08	0.02476	0.01065	3.933 (2.168 - 7.134)	6.57E-06	intergenic	HAND1,MIR3141
6	rs139600027	24922133	0.04363	0.01859	3.267 (2.024 - 5.273)	1.26E-06	intronic	FAM65B
6	rs78883162	49239776	0.02241	0.00816	4.669 (2.445 - 8.917)	3.04E-06	intergenic	PTCHD4,MUT
7	rs73669600	125510	0.03774	0.02063	2.955 (1.866 - 4.679)	3.84E-06	intergenic	NONE,LOC100507642
7	rs4731786	1.31E+08	0.4493	0.4887	1.564 (1.289 - 1.898)	5.68E-06	intronic	MKLN1
7	rs4731788	1.31E+08	0.4304	0.4923	0.6204 (0.5099 - 0.7549)	1.86E-06	intronic	MKLN1
7	rs10954315	1.31E+08	0.4351	0.4934	0.626 (0.5149 - 0.7612)	2.65E-06	intronic	MKLN1
7	rs4731790	1.31E+08	0.434	0.4925	0.6264 (0.5152 - 0.7616)	2.73E-06	intronic	MKLN1
8	rs1472162	19607661	0.375	0.3126	1.56 (1.29 - 1.887)	4.64E-06	intergenic	CSGALNACT1,INTS10
8	rs79286235	1.39E+08	0.02712	0.01133	3.803 (2.119 - 6.825)	7.56E-06	intronic	FAM135B
9	rs34399954	1.13E+08	0.04599	0.02607	2.636 (1.735 - 4.006)	5.61E-06	intergenic	SVEP1,MUSK
9	rs35142681	1.13E+08	0.04835	0.02675	2.64 (1.737 - 4.01)	5.38E-06	exonic	MUSK
10	rs17753457	28970843	0.06132	0.03808	2.257 (1.579 - 3.225)	7.99E-06	intronic	BAMBI
10	rs150783484	52729827	0.03774	0.01723	3.377 (2.052 - 5.556)	1.68E-06	intergenic	A1CF,PRKG1
11	rs1869446	68872284	0.2783	0.2149	1.626 (1.322 - 2)	4.09E-06	intergenic	TPCN2,LOC338694
11	rs1551304	68876587	0.3278	0.2543	1.577 (1.291 - 1.926)	8.37E-06	intergenic	TPCN2,LOC338694
11	rs10896430	68877162	0.2913	0.2228	1.636 (1.333 - 2.008)	2.54E-06	intergenic	TPCN2,LOC338694
11	rs11228503	68879044	0.3172	0.2446	1.576 (1.289 - 1.927)	9.47E-06	intergenic	TPCN2,LOC338694

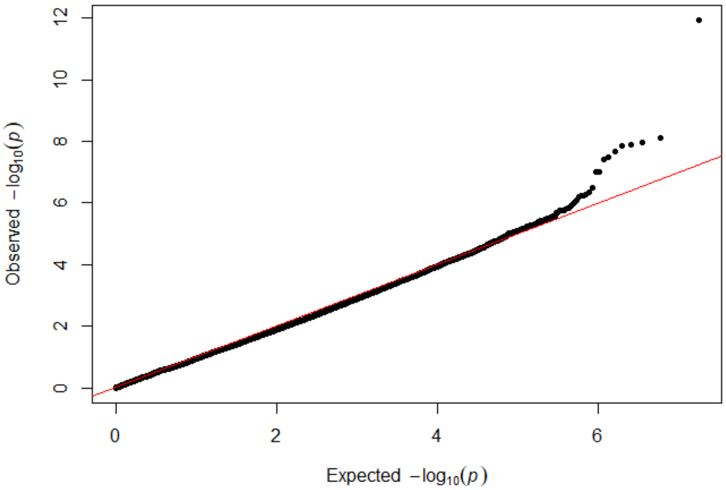
11	rs1981412	71138710	0.1993	0.274	0.5731 (0.4508 - 0.7286)	5.53E-06	intergenic	FLJ42102,DHCR7
11	rs12797951	71143266	0.2028	0.2761	0.5839 (0.4605 - 0.7404)	8.93E-06	intergenic	FLJ42102,DHCR7
11	rs2040323	71172783	0.1922	0.2675	0.5809 (0.4566 - 0.739)	9.80E-06	intronic	NADSYN1
11	rs12278461	71182185	0.1922	0.2695	0.5691 (0.4472 - 0.7242)	4.54E-06	intronic	NADSYN1
11	rs732934	71186476	0.1946	0.2711	0.5809 (0.4576 - 0.7375)	8.14E-06	intronic	NADSYN1
11	rs4944062	71187294	0.1922	0.269	0.5759 (0.4528 - 0.7325)	6.88E-06	intronic	NADSYN1
11	rs3794060	71187679	0.1946	0.2711	0.5734 (0.451 - 0.7291)	5.64E-06	intronic	NADSYN1
11	rs12807827	71203790	0.1969	0.2733	0.5823 (0.459 - 0.7388)	8.52E-06	intronic	NADSYN1
11	rs4945008	71221248	0.1969	0.2743	0.5788 (0.4562 - 0.7344)	6.75E-06	intergenic	NADSYN1,KRTAP5-7
11	rs7126108	1.23E+08	0.1085	0.07185	1.961 (1.46 - 2.635)	7.84E-06	intergenic	LOC341056,HSPA8
12	rs192213585	28918097	0.04717	0.01677	3.204 (1.935 - 5.305)	5.99E-06	intergenic	CCDC91,FAR2
13	rs633542	86312573	0.2394	0.3166	0.579 (0.4613 - 0.7267)	2.43E-06	intergenic	LINC00351,SLITRK6
13	rs635071	86312630	0.2394	0.3182	0.575 (0.4584 - 0.7213)	1.70E-06	intergenic	LINC00351,SLITRK6
13	rs1927741	86315007	0.237	0.3153	0.5836 (0.4652 - 0.7321)	3.24E-06	intergenic	LINC00351,SLITRK6
17	rs117893494	56244180	0.04009	0.02108	2.878 (1.82 - 4.551)	6.10E-06	intergenic	MSX2P1,OR4D2
18	rs80107944	75219486	0.237	0.1874	1.648 (1.327 - 2.048)	6.33E-06	intergenic	GALR1,LINC01029
19	rs28481768	32727750	0.04009	0.01904	2.924 (1.829 - 4.677)	7.51E-06	intergenic	LOC101927411,ZNF507
19	rs77021364	42308310	0.1474	0.1022	1.829 (1.409 - 2.373)	5.65E-06	intronic	CEACAM3
20	rs117029867	51914871	0.02594	0.009066	4.33 (2.322 - 8.073)	4.01E-06	intronic	TSHZ2
20	rs6070926	58297267	0.2795	0.2226	1.637 (1.325 - 2.022)	5.02E-06	intronic	PHACTR3

Supplementary Table 9. Summary of Bioinformatics Analyses

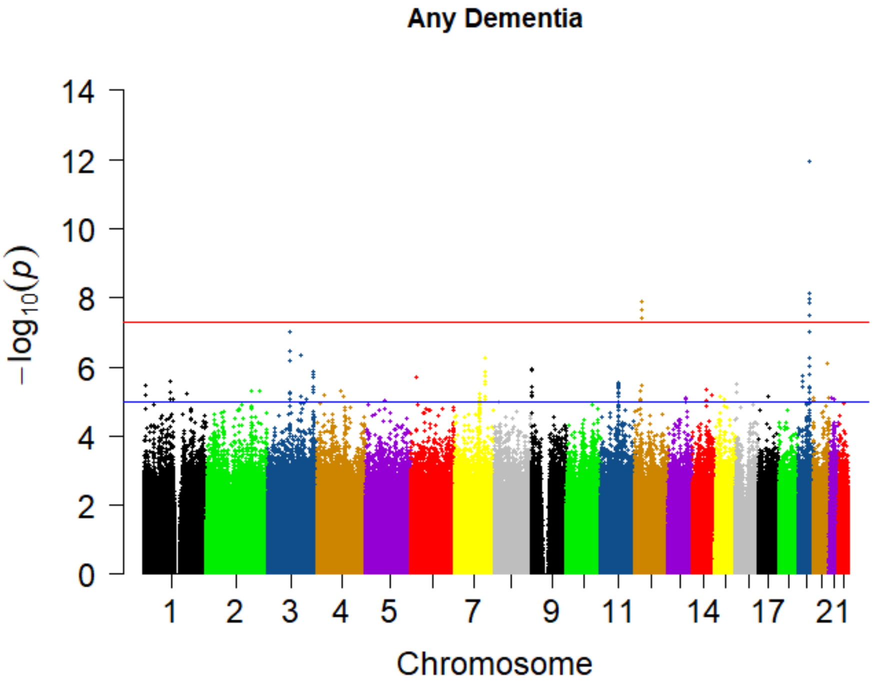
CHR	SNP	p	GTEx	RegulomeDB Rank (Probability Score)	CADD Score
1	rs140076909	3.723e-08	No significant eQTLs	4 (0.60906)	4.318
1	***rs192741543**	4.035e-06	No significant eQTLs	5 (0.13454)	0.640
1	***rs184006746**	6.263e-06	No significant eQTLs	3a (0.65177)	3.493
1	***rs78196091**	4.402e-06	No significant eQTLs	6 (0.47449)	0.162
7	rs117803234	6.936e-08	No significant eQTLs	6 (0.073)	1.393
12	rs148760255	2.087E-08	No significant eQTLs	5 (0.58955)	2.289
12	rs148377161	1.661E-08	No significant eQTLs	6 (0.0)	1.382
12	rs192213585	2.664E-08	No significant eQTLS	5 (0.58955)	2.399
12	****rs147253910**	2.254e-06	No significant eQTLS	5 (0.13454)	2.975

*SNPs in bold letters are in linkage disequilibrium ($R^2 = 0.73, 0.76, 0.67$) with the top SNP on chromosome 1

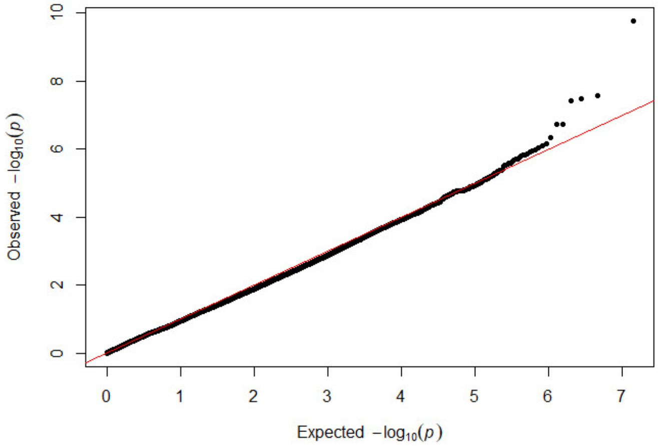
** SNPs in bold letters are in linkage disequilibrium ($R^2 = 0.74$) with the top SNPs on chromosome 12



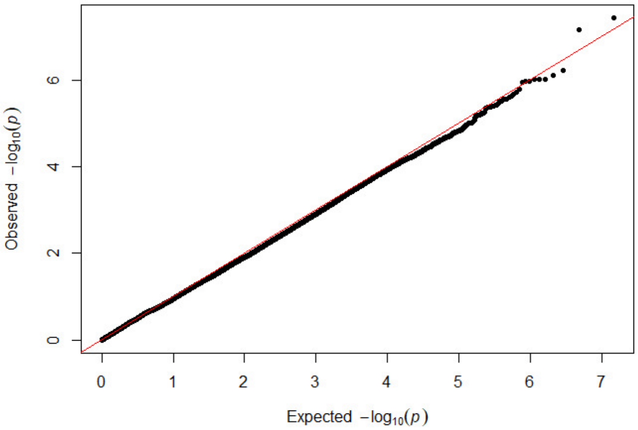
Supplementary Figure 1. Quantile-quantile plot showing observed versus expected p-values for the Any Dementia analysis.



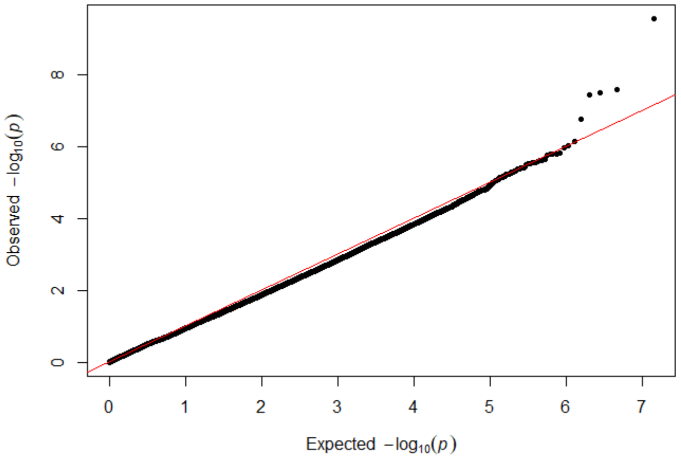
Supplementary Figure 2. Manhattan plot showing genome-wide p-values for the association with any form of dementia. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.



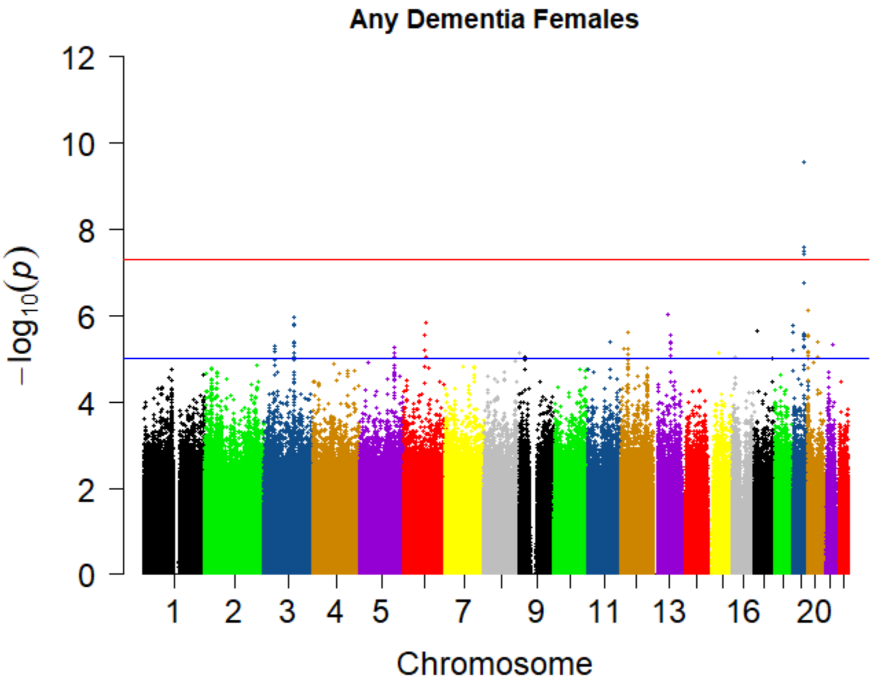
Supplementary Figure 3. Quantile-quantile plot showing observed versus expected *P*-values for AD Females analysis.



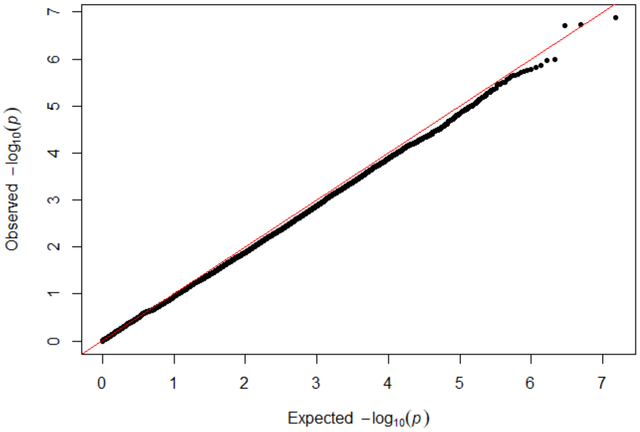
Supplementary Figure 4. Quantile-quantile plot showing observed versus expected *P*-values for AD Males analysis.



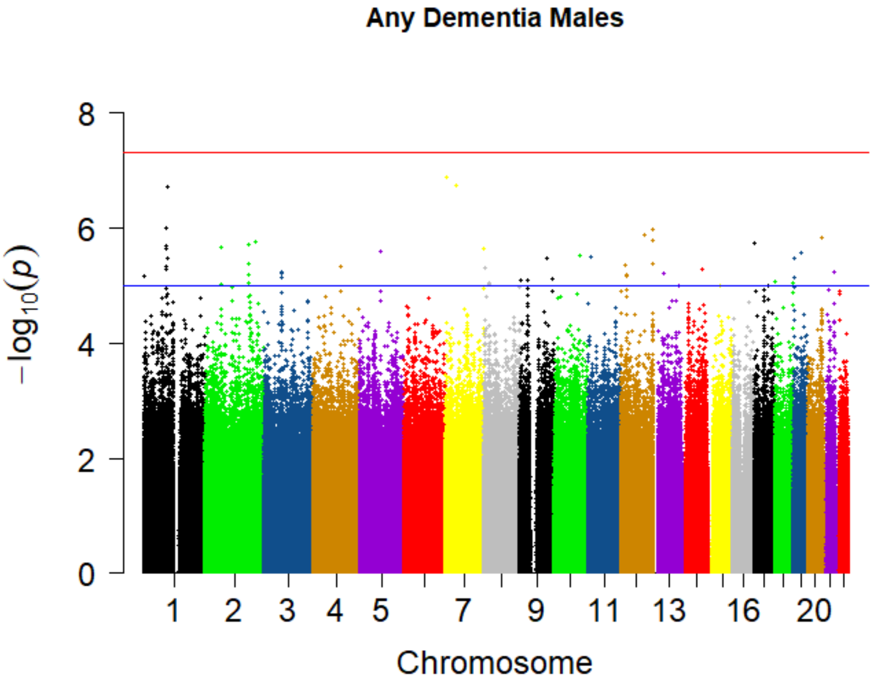
Supplementary Figure 5. Quantile-quantile plot showing observed versus expected *P*-values for the Any Dementia females analysis.



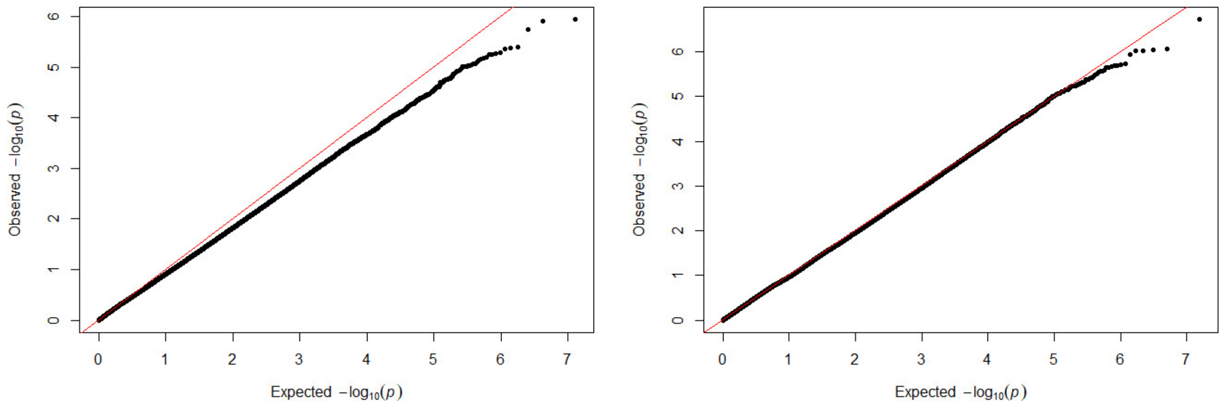
Supplementary Figure 6. Manhattan plot showing genome-wide p-values for the association of any form of dementia in females. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.



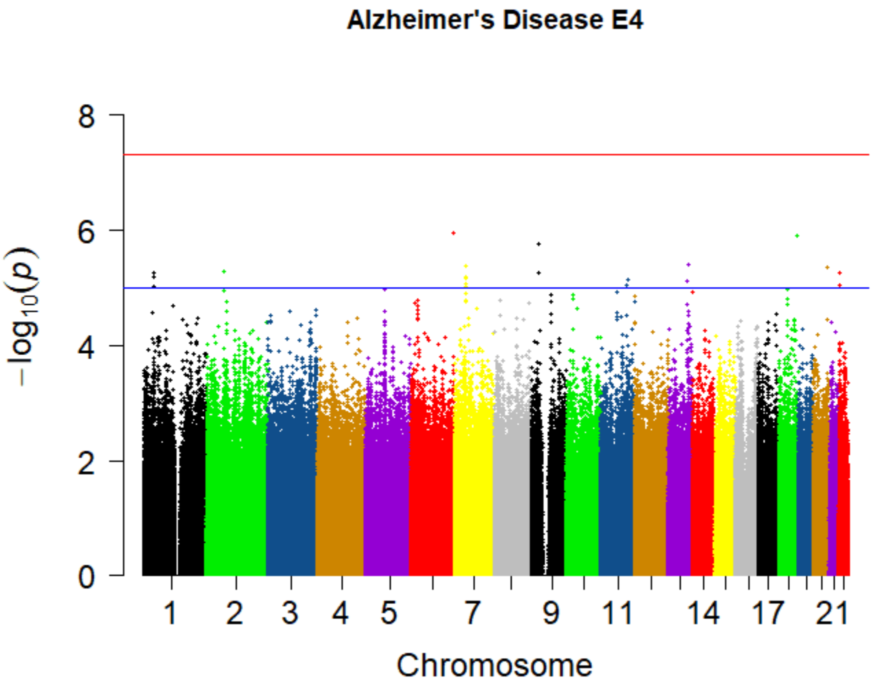
Supplementary Figure 7. Quantile-quantile plot showing observed versus expected *P*-values for the Any Dementia Males analysis.



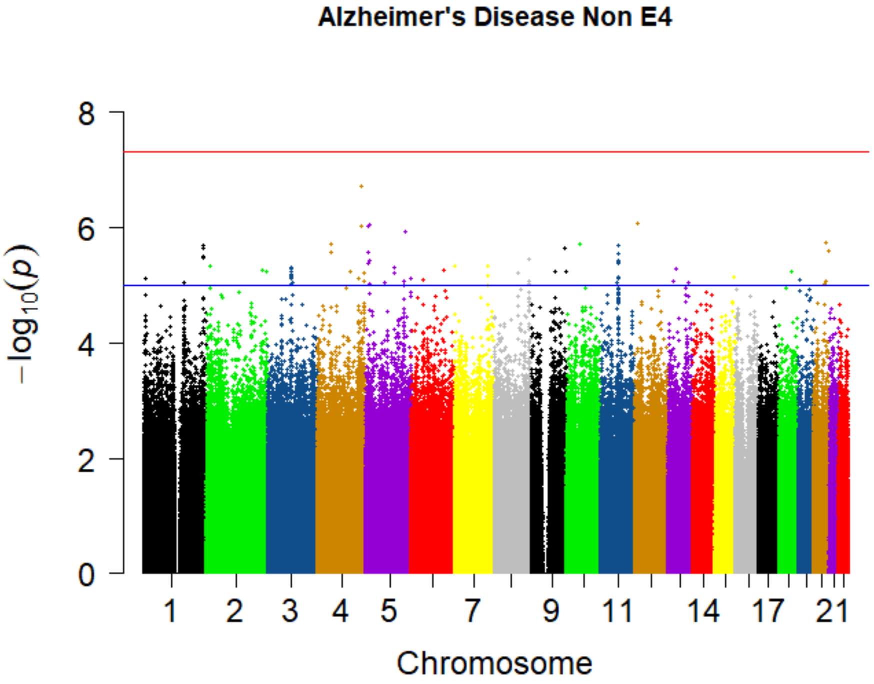
Supplementary Figure 8. Manhattan plot showing genome-wide p-values for the association of any form of dementia in males. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.



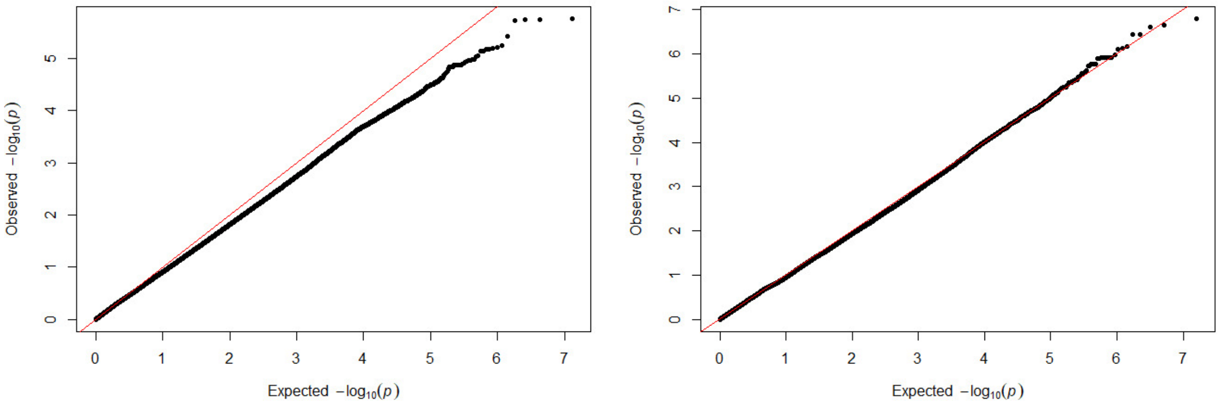
Supplementary Figure 9. Quantile-quantile plots showing observed versus expected p-values for AD *APOE*4* (left) and non-*APOE*4* (right) carrier analyses.



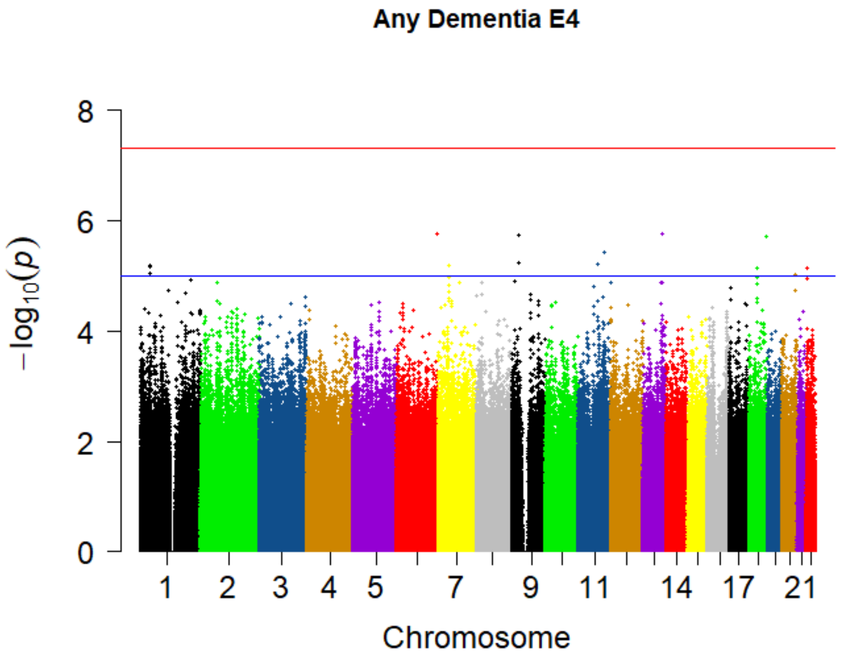
Supplementary Figure 10. Manhattan plot showing genome-wide p-values for the association with Alzheimer’s disease in *APOE*4* carriers. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.



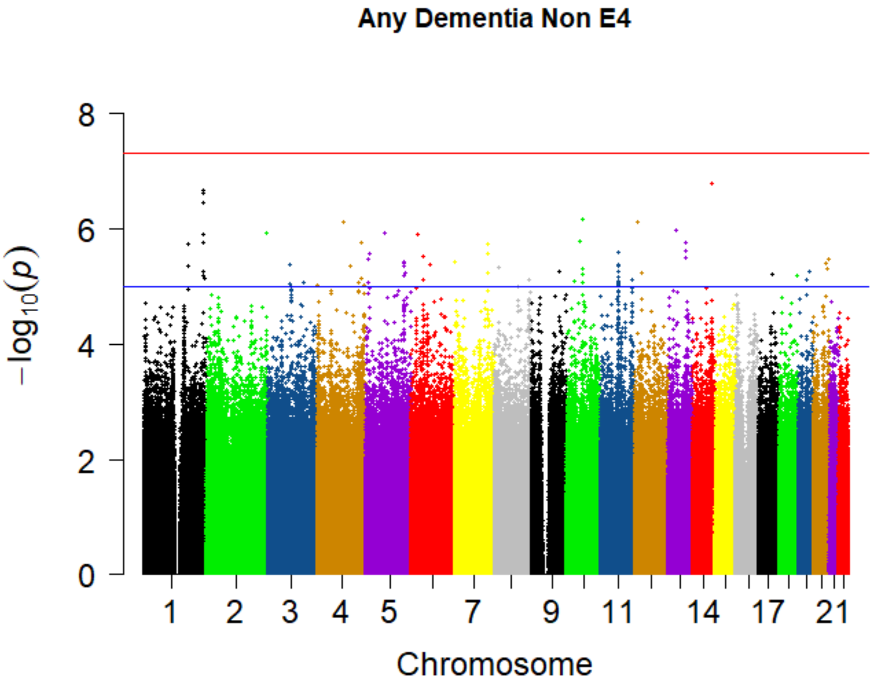
Supplementary Figure 11. Manhattan plot showing genome-wide p-values for the association with Alzheimer's disease in non-*APOE*4* carriers. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.



Supplementary Figure 12. Quantile-quantile plots showing observed versus expected p-values for Any Dementia *APOE*4* (left) and non-*APOE*4* (right) carrier analyses.



Supplementary Figure 13. Manhattan plot showing genome-wide p-values for the association with any form of dementia in *APOE*4* carriers. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.



Supplementary Figure 14. Manhattan plot showing genome-wide p-values for the association with any form of dementia in non-*APOE*4* carriers. The threshold for genome-wide significance (p<5E-08) is indicated by the red line and the threshold for suggestive significance (p<1E-05) is indicated by the blue line.