

Supplementary Information.

Supplemental Table S1: Previously reported genome-wide significant SNPs and their association results in the current study.

CHR	BP	SNP	Closest gene	Current Analysis					Previous GWAS				<i>power at 5% sig.level</i>
				Effect/Alt	Freq	OR	SE	<i>p</i> -value	Effect/Alt	OR	<i>p</i> -value	GWAS	
1	985377	rs113020870	<i>AGRN</i>	NA	NA	NA	NA	NA	C/T	1.90	3.8x10 ⁻⁰⁸	Wi	NA
1	109888432	rs141749679	<i>SORT1</i>	NA	NA	NA	NA	NA	C/T	1.38	7.5x10 ⁻⁰⁹	Be	NA
1	161155392	rs4575098	<i>ADAMTS4</i>	A/G	0.23	0.91	0.11	3.7x10 ⁻⁰¹	A/G	1.02	2.1x10 ⁻¹⁰	Ja	0.060
1	207802552	rs4844610	<i>CR1</i>	C/A	0.82	0.84	0.11	1.2x10 ⁻⁰¹	C/A	0.85	3.6x10 ⁻²⁴	Ku	0.105
2	9699011	rs72777026	<i>ADAM17</i>	G/A	0.14	0.87	0.13	2.7x10 ⁻⁰¹	G/A	1.06	2.7x10 ⁻⁰⁸	Be	0.084
2	37531939	rs17020490	<i>PRKD3</i>	C/T	0.14	0.97	0.13	8.1x10 ⁻⁰¹	C/T	1.06	3.3x10 ⁻⁰⁹	Be	0.084
2	106366056	rs143080277	<i>NCK2</i>	NA	NA	NA	NA	NA	C/T	1.47	2.1x10 ⁻¹³	Be	NA
2	127892810	rs6733839	<i>BIN1</i>	T/C	0.38	1.26	0.09	1.1x10⁻⁰²	T/C	1.2	2.4x10⁻⁶⁹	Ma	0.179

2	203743440	rs139643391	WDR12	NA	NA	NA	NA	NA	T/TC	0.94	1.1x10 ⁻⁰⁸	Be	NA
2	234068476	rs35349669	<i>INPP5D</i>	T/C	0.49	1.18	0.09	6.2x10 ⁻⁰²	T/C	1.07	3.6x10 ⁻¹¹	Ma	0.082
3	154787511	rs16824536	MME	A/G	0.06	0.97	0.19	8.9x10 ⁻⁰¹	A/G	0.92	3.6x10 ⁻⁰⁸	Be	0.099
3	154801978	rs61762319	MME	G/A	0.03	1.40	0.23	1.3x10 ⁻⁰¹	G/A	1.16	2.2x10 ⁻¹¹	Be	0.141
4	987343	rs3822030	IDUA	G/T	0.43	1.06	0.09	5.2x10 ⁻⁰¹	G/T	0.95	8.3x10 ⁻¹²	Be	0.075
4	11026028	rs6448453	<i>CLNK</i>	G/A	0.74	0.97	0.10	7.6x10 ⁻⁰¹	G/A	0.99	1.9x10 ⁻⁰⁹	Ja	0.053
4	40198846	rs2245466	RHOH	G/C	0.33	0.99	0.10	9.6x10 ⁻⁰¹	G/C	1.05	1.2x10 ⁻⁰⁹	Be	0.075
5	14724413	rs112403360	ANKH	A/T	0.08	1.25	0.15	1.5x10 ⁻⁰¹	A/T	1.09	2.3x10 ⁻⁰⁹	Be	0.103
5	86223195	rs62374257	COX7C	C/T	0.23	1.11	0.10	3.3x10 ⁻⁰¹	C/T	1.07	1.4x10 ⁻¹⁵	Be	0.090
5	88223420	rs190982	<i>MEF2C</i>	A/G	0.60	1	0.09	1	A/G	1.08	3.2x10 ⁻⁰⁸	La	0.082
5	150432388	rs871269	<i>TNIP1</i>	T/C	0.32	0.98	0.09	8.0x10 ⁻⁰¹	T/C	0.79	1.4x10 ⁻⁰⁹	Wi	0.273
5	156526331	rs6891966	<i>HAVCR2</i>	A/G	0.23	0.87	0.11	2.1x10 ⁻⁰¹	A/G	0.86	7.9x10 ⁻¹⁰	Wi	0.169
5	179628150	rs113706587	RASGEF1C	A/G	0.10	1.17	0.14	2.5x10 ⁻⁰¹	A/G	1.09	2.2x10 ⁻¹⁶	Be	0.105
6	32559825	rs34855541	<i>HLA-DRB1</i>	G/A	0.19	0.88	0.12	2.5x10 ⁻⁰¹	G/A	0.9	9.5x10 ⁻¹⁵	Ma	0.123
6	47432637	rs9381563	<i>CD2AP</i>	T/C	0.64	0.97	0.09	7.3x10 ⁻⁰¹	T/C	0.93	5.8x10 ⁻¹⁴	Ma	0.080
6	114612895	rs785129	HS3ST5	T/C	0.35	0.95	0.10	6.1x10 ⁻⁰¹	T/C	1.04	2.4x10 ⁻⁰⁹	Be	0.069

7	7856894	rs6943429	UMAD1	T/C	0.41	1.10	0.09	3.1x10 ⁻⁰¹	T/C	1.05	1.0x10 ⁻¹⁰	Be	0.073
7	8244012	rs10952097	ICA1	T/C	0.11	0.97	0.14	8.1x10 ⁻⁰¹	T/C	1.07	6.8x10 ⁻⁰⁹	Be	0.090
7	12269593	rs13237518	TMEM106B	A/C	0.41	0.86	0.09	1.1x10 ⁻⁰¹	A/C	0.96	4.9x10 ⁻¹¹	Be	0.069
7	28168750	rs1160871	JAZF1	NA	NA	NA	NA	NA	G/GTCTT	0.95	9.8x10 ⁻⁰⁹	Be	NA
7	37841534	rs2718058	<i>GPR141</i>	G/A	0.37	0.92	0.09	3.4x10 ⁻⁰¹	G/A	0.93	4.8x10 ⁻⁰⁹	La	0.090
7	54941328	rs76928645	SEC61G	T/C	0.10	0.66	0.17	1.5x10⁻⁰²	T/C	0.93	1.6x10⁻¹⁰	Be	0.094
7	100004446	rs1476679	<i>ZCWPW1</i>	T/C	0.69	1.09	0.10	3.9x10 ⁻⁰¹	T/C	1.1	9.9x10 ⁻¹⁹	Ma	0.085
7	143099133	rs10808026	<i>EPHA1</i>	A/C	0.22	0.93	0.11	4.8x10 ⁻⁰¹	A/C	0.91	1.1x10 ⁻¹⁴	Ma	0.112
8	11702122	rs1065712	CTSB	C/G	0.05	1.14	0.20	5.1x10 ⁻⁰¹	C/G	1.09	1.9x10 ⁻⁰⁹	Be	0.100
8	27464929	rs4236673	<i>CLU</i>	G/A	0.60	1.17	0.09	8.7x10 ⁻⁰²	G/A	1.12	1.1x10 ⁻²⁸	Ma	0.101
8	145158607	rs34173062	SHARPIN	A/G	0.07	0.93	0.19	7.2x10 ⁻⁰¹	A/G	1.13	1.7x10 ⁻¹⁶	Be	0.134
9	107665978	rs1800978	ABCA1	G/C	0.12	0.78	0.15	8.7x10 ⁻⁰²	G/C	1.06	1.6x10 ⁻⁰⁹	Be	0.084
10	11720308	rs7920721	<i>ECHDC3</i>	G/A	0.38	1.02	0.09	8.3x10 ⁻⁰¹	G/A	1.08	1.8x10 ⁻¹¹	Ku	0.091
10	61784928	rs7068231	ANK3	T/G	0.40	1.03	0.09	7.7x10 ⁻⁰¹	T/G	0.95	3.3x10 ⁻¹³	Be	0.076
10	82253984	rs6586028	TSPAN14	C/T	0.21	0.89	0.11	3.0x10 ⁻⁰¹	C/T	0.93	2.0x10 ⁻¹⁹	Be	0.094
10	98026407	rs6584063	BLNK	G/A	0.04	0.70	0.26	1.6x10 ⁻⁰¹	G/A	0.89	6.7x10 ⁻¹¹	Be	0.120

10	124172912	rs7908662	PLEKHA1	G/A	0.48	1.10	0.09	2.8x10 ⁻⁰¹	G/A	0.96	2.6x10 ⁻⁰⁹	Be	0.068
11	47380340	rs3740688	<i>SPI1</i>	T/G	0.55	1.1	0.09	3.0x10 ⁻⁰¹	T/G	1.09	5.5x10 ⁻¹³	Ku	0.089
11	59936926	rs7933202	<i>MS4A6A</i>	C/A	0.40	0.86	0.09	8.8x10 ⁻⁰²	C/A	0.89	1.9x10 ⁻¹⁹	Ku	0.122
11	85867875	rs10792832	<i>PICALM</i>	G/A	0.63	1.04	0.09	7.0x10 ⁻⁰¹	G/A	1.13	5.1x10 ⁻³⁶	Ma	0.102
11	121435587	rs11218343	<i>SORL1</i>	C/T	0.04	0.41	0.33	7.3x10⁻⁰³	C/T	0.81	4.6x10⁻¹⁷	Ma	0.211
12	113719788	rs6489896	TPCN1	C/T	0.07	0.99	0.17	9.6x10 ⁻⁰¹	C/T	1.08	1.8x10 ⁻⁰⁹	Be	0.096
14	53391680	rs17125924	<i>FERMT2</i>	G/A	0.09	0.95	0.15	7.3x10 ⁻⁰¹	G/A	1.12	1.3x10 ⁻¹¹	Ma	0.128
14	92938855	rs12590654	<i>SLC24A4</i>	A/G	0.34	0.89	0.10	2.2x10 ⁻⁰¹	A/G	0.92	8.2x10 ⁻¹²	Ma	0.099
14	106228095	rs7157106	IGH gene cluster	A/G	0.35	0.99	0.09	9.4x10 ⁻⁰¹	A/G	1.05	2.0x10 ⁻⁰⁸	Be	0.075
14	107121607	rs10131280	IGH gene cluster	A/G	0.13	0.84	0.14	2.0x10 ⁻⁰¹	A/G	0.94	4.3x10 ⁻¹⁰	Be	0.087
15	51001534	rs59685680	<i>SPPL2A</i>	G/T	0.20	0.94	0.11	5.8x10 ⁻⁰¹	G/T	0.93	9.2x10 ⁻⁰⁹	Ma	0.095
15	59045774	rs593742	<i>ADAM10</i>	G/A	0.31	0.95	0.10	6.3x10 ⁻⁰¹	G/A	0.93	2.8x10 ⁻¹¹	Ma	0.092
15	63569902	rs117618017	<i>APH1B</i>	T/C	0.15	1.3	0.12	2.4x10⁻⁰²	T/C	1.02	3.3x10⁻⁰⁸	Ja	0.060
15	64423506	rs3848143	<i>SNX1</i>	G/A	0.20	1.23	0.10	4.8x10⁻⁰²	G/A	1.05	8.4x10⁻¹¹	Be	0.077

15	79229199	rs12592898	CTSH	A/G	0.13	0.94	0.13	6.1x10 ⁻⁰¹	A/G	0.94	4.2x10 ⁻⁰⁹	Be	0.087
16	19808163	rs7185636	<i>IQCK</i>	C/T	0.17	0.72	0.13	9.0x10⁻⁰³	C/T	0.92	2.4x10⁻⁰⁸	Ku	0.103
16	30021402	rs1140239	DOC2A	NA	NA	NA	NA	NA	T/C	0.94	2.6x10 ⁻¹³	Be	NA
16	31133100	rs59735493	<i>KAT8</i>	A/G	0.28	1.01	0.10	9.0x10 ⁻⁰¹	A/G	0.99	4.0x10 ⁻⁰⁸	Ja	0.055
16	70694000	rs4985556	<i>IL34</i>	A/C	0.11	0.98	0.14	8.7x10 ⁻⁰¹	A/C	1.09	3.7x10 ⁻⁰⁸	Ma	0.105
16	79355857	rs62039712	<i>WWOX</i>	A/G	0.12	0.88	0.14	3.8x10 ⁻⁰¹	A/G	1.16	3.7x10 ⁻⁰⁸	Ku	0.166
16	79608408	rs450674	MAF	C/T	0.40	0.87	0.09	1.3x10 ⁻⁰¹	C/T	0.96	3.2x10 ⁻⁰⁸	Be	0.070
16	81773209	rs12444183	<i>PLCG2</i>	G/A	0.61	0.98	0.09	8.5x10 ⁻⁰¹	G/A	1.06	3.2x10 ⁻⁰⁸	Ma	0.073
16	86454210	rs16941239	FOXF1	A/T	0.02	1.56	0.25	7.5x10 ⁻⁰²	A/T	1.13	1.3x10 ⁻⁰⁸	Be	0.113
16	90170095	rs56407236	PRDM7	A/G	0.07	0.91	0.18	5.8x10 ⁻⁰¹	A/G	1.11	6.5x10 ⁻¹⁵	Be	0.118
17	1631350	rs35048651	WDR81	NA	NA	NA	NA	NA	T/TGAG	1.06	7.7x10 ⁻¹¹	Be	NA
17	5137047	rs7225151	<i>SCIMP</i>	A/G	0.12	1	0.14	9.8x10 ⁻⁰¹	A/G	1.1	6.1x10 ⁻¹²	Ma	0.113
17	18059454	rs2242595	MYO15A	A/G	0.12	0.81	0.14	1.5x10 ⁻⁰¹	A/G	0.94	1.1x10 ⁻⁰⁹	Be	0.087
17	42430244	rs5848	GRN	T/C	0.27	1.02	0.10	8.7x10 ⁻⁰¹	T/C	1.07	2.4x10 ⁻²⁰	Be	0.088
17	42442344	rs708382	<i>GRN</i>	C/T	0.39	1.02	0.09	7.9x10 ⁻⁰¹	C/T	1.31	2.0x10 ⁻⁰⁹	Wi	0.275
17	47450775	rs28394864	<i>RP11-81K2.1</i>	A/G	0.46	1.07	0.09	4.3x10 ⁻⁰¹	A/G	1.01	1.9x10 ⁻⁰⁸	Ja	0.054

17	56398006	rs2526380	<i>BZRAP1</i>	G/C	0.43	1.04	0.09	6.4x10 ⁻⁰¹	G/C	0.97	2.6x10 ⁻⁰⁸	Ja	0.064
17	61538148	rs138190086	<i>CYB561</i>	A/G	0.02	0.99	0.33	9.7x10 ⁻⁰¹	A/G	1.25	1.9x10 ⁻⁰⁹	Ma	0.187
18	56189459	rs76726049	<i>ALPK2</i>	C/T	0.02	0.9	0.38	7.8x10 ⁻⁰¹	C/T	1.06	3.3x10 ⁻⁰⁸	Ja	0.072
19	1056492	rs3752246	<i>ABCA7</i>	C/G	0.83	0.92	0.11	4.3x10 ⁻⁰¹	C/G	0.87	3.1x10 ⁻¹⁶	Ku	0.094
19	1854254	rs149080927	<i>KLF16</i>	NA	NA	NA	NA	NA	G/GC	1.05	5.1x10 ⁻¹⁰	Be	NA
19	45411941	rs429358	<i>APOE</i>	NA	NA	NA	NA	NA	T/C	3.32	1.2x10 ⁻⁸⁸¹	Ku	NA
19	49213504	rs2452170	<i>NTN5</i>	A/G	0.53	1.16	0.09	1.0x10 ⁻⁰¹	A/G	1.24	1.7x10 ⁻⁰⁸	Wi	0.181
19	50453317	rs9304690	<i>SIGLEC11</i>	T/C	0.25	1.08	0.10	4.2x10 ⁻⁰¹	T/C	1.05	4.7x10 ⁻⁰⁹	Be	0.076
19	51728477	rs12459419	<i>CD33</i>	T/C	0.33	0.75	0.10	3.5x10⁻⁰³	T/C	0.99	6.3x10⁻⁰⁹	Ma	0.055
19	54771451	rs587709	<i>LILRB2</i>	C/T	0.27	1.31	0.10	5.1x10⁻⁰³	C/T	1.05	3.6x10⁻¹¹	Be	0.076
19	54825174	rs1761461	<i>LILRB2</i>	C/A	0.50	0.84	0.09	5.2x10 ⁻⁰²	C/A	0.84	1.6x10 ⁻⁰⁹	Wi	0.166
20	393978	rs1358782	<i>RBCK1</i>	A/G	0.23	1.04	0.10	7.3x10 ⁻⁰¹	A/G	0.95	1.6x10 ⁻⁰⁸	Be	0.079
20	54983075	rs6069736	<i>CSTF1</i>	T/C	0.09	0.81	0.17	2.0x10 ⁻⁰¹	T/C	0.89	2.0x10 ⁻¹⁰	Ma	0.132
20	62374441	rs6742	<i>SLC2A4RG</i>	T/C	0.22	1.00	0.11	9.8x10 ⁻⁰¹	T/C	0.95	2.6x10 ⁻⁰⁹	Be	0.079
21	27473875	rs2154481	<i>APP</i>	C/T	0.48	0.89	0.09	1.9x10 ⁻⁰¹	C/T	0.95	1.0x10 ⁻¹²	Be	0.074

21	28156856	rs2830500	<i>ADAMTS1</i>	A/C	0.29	0.84	0.10	9.2×10^{-02}	A/C	0.93	2.6×10^{-08}	Ku	0.092
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CHR –chromosome; BP –base-pair position in build37; SNP –single nucleotide polymorphism, closest gene –genes were annotated with assembly hg19; effect/non-effect –effect and non-effect alleles; freq- frequency of reference allele in the UK Biobank *APOE-ε4* homozygotes individuals; OR, SE, p-value –odds ratio, standard error and p-value of the current and previous reported AD GWAS association studies; GWAS –corresponding GWAS study (Ma = Marioni et al., Ku = Kunkle et al., Ja = Jansen et al., La = Lambert et al., Wi = Wightman et al., Be = Bellenguez et al 2021); power at 5% sig.level - power to detect the reported effect size in $\epsilon 4\epsilon 4$ homozygous sample of UK Biobank at 5% significance level. No proxy SNP with $R^2 > 0.7$ was found for rs184384746 (closest gene *HESX1*), rs187370608 (*UNC5CL*) or rs114360492 (*CNTNAP2*). Starred SNPs were present on the genotyping array (rather than imputed). Replicated loci are shown in bold.

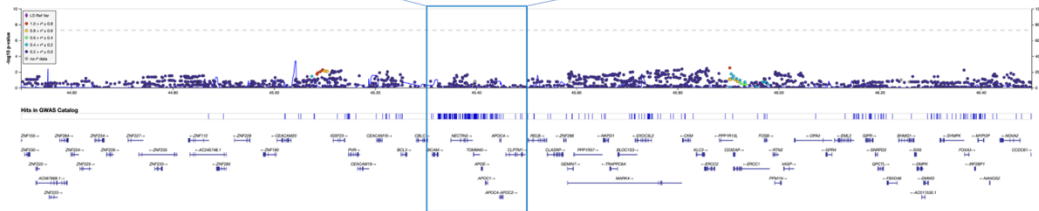
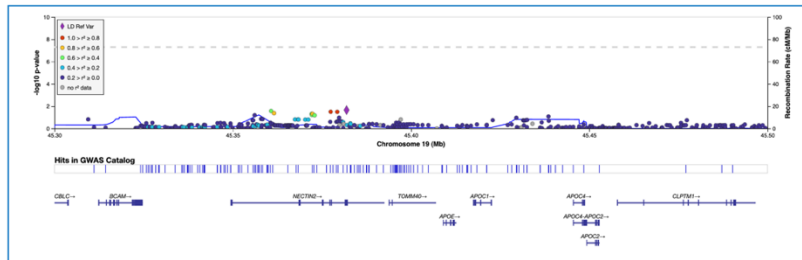
Supplemental Table S2. Allele frequencies of GWAS significant SNPs in DAB1, depending upon AD case-control status and APOE-ε4 genotype.

N APOE-ε4 alleles	AD status	rs17541203_C	rs197111_T	rs78921149_T	rs112437613_T	rs17115257_G	rs58359668_T
0	0	0.067	0.069	0.066	0.066	0.081	0.081
	1	0.066	0.066	0.064	0.064	0.081	0.081
1	0	0.066	0.068	0.065	0.065	0.080	0.08
	1	0.069	0.072	0.069	0.069	0.086	0.086
2	0	0.063	0.065	0.062	0.061	0.076	0.076
	1	0.12	0.12	0.12	0.12	0.14	0.14

N APOE-ε4 alleles –number of APOE- ε4 alleles (coded 0,1,2); AD –Alzheimer’s disease; AD status – coded AD case -1 and control -0; rs-number _SNP rs number and corresponding minor allele.

1 **Figure S1.** LocusZoom plot showing SNP associations in the *APOE* region (chromosome 19:
2 44.5-46.5 Mb).

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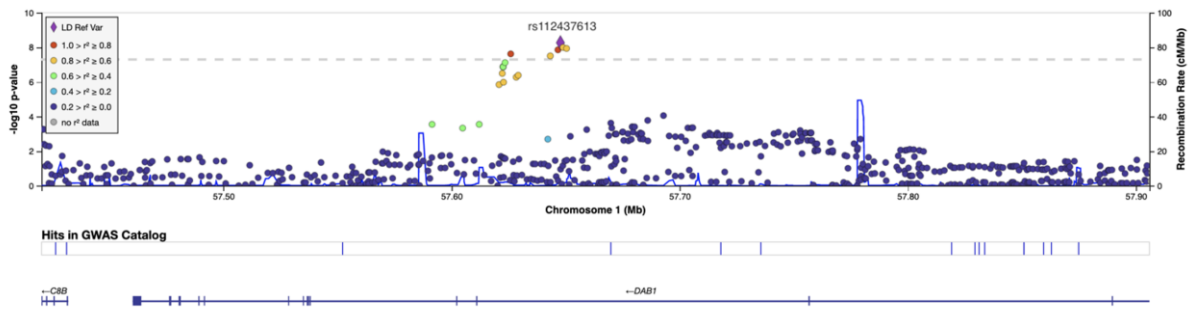
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9 **Figure S2.** LocusZoom plot showing SNP associations in the *DAB1* gene.

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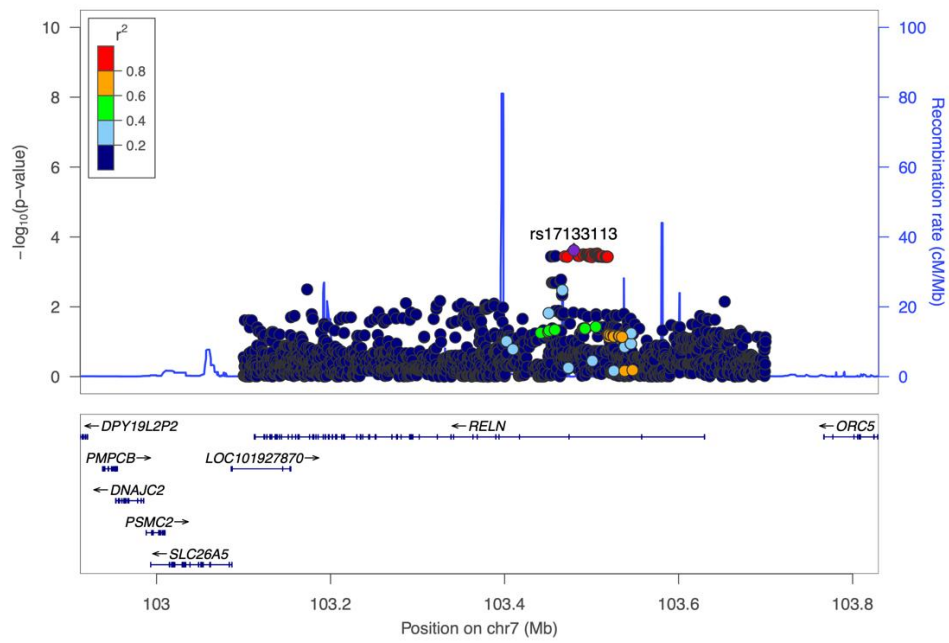
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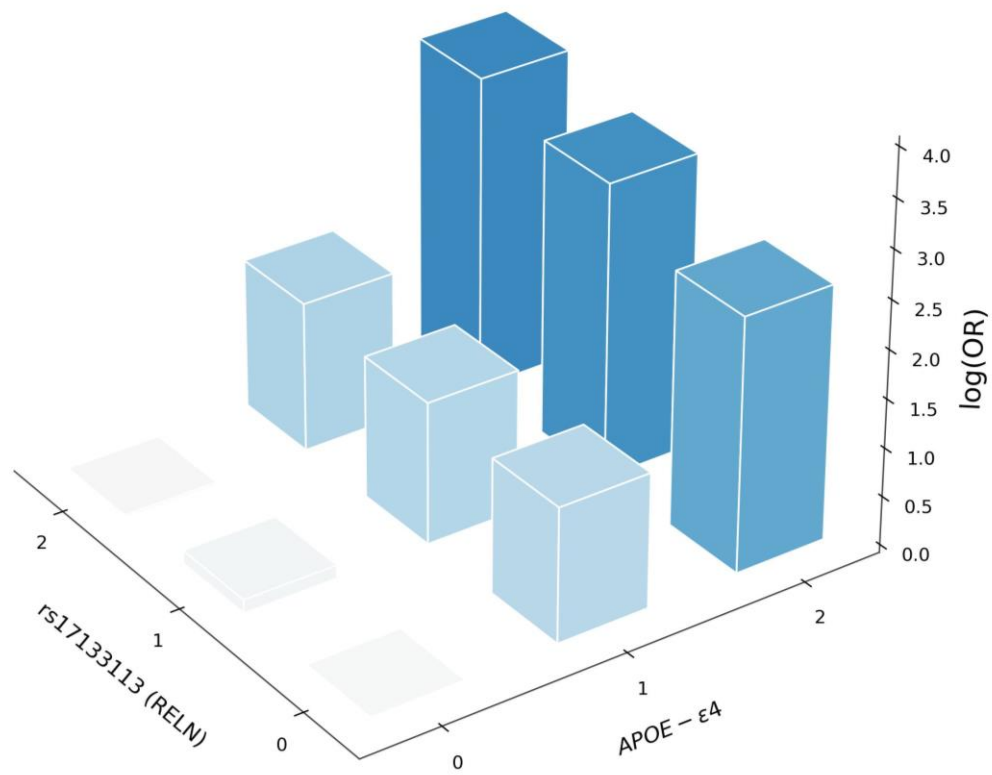
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23 **Figure S3:** LocusZoom plot showing SNP associations in the *RELN* gene.



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31 **Figure S4:** Epistatic effect between *APOE*- ϵ 4 and rs17133113 (*RELN*) in the whole sample of
32 the UK Biobank aged 65+ (N=229,748).



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