Meta-analysis of genetic association with diagnosed Alzheimer's disease identifies novel risk loci and implicates Abeta, Tau, immunity and lipid processing – Supplement

Contents

Supplementary Figure 1. Study design. 3

Supplementary Figure 2. Stage I discovery QQ Plot. 4

Supplementary *Figure 3. ECHDC3* locus 5

Supplementary Figure 4. *ACE* locus. 6

Supplementary Figure 5. *ADAM10* locus. 7

Supplementary Figure 6. *ADAMTS1* locus. 8

Supplementary Figure 7. *IQCK* locus. 9

Supplementary Figure 8. *SUCLG2P4* locus. 10

Supplementary Figure 9. *OARD1* locus. 11

Supplementary Table 2. Demographic description of datasets within each consortium. 13

Supplementary Table 3. Description of imputation properties and results by dataset. 14

Supplementary Table 4. Results for variants showing suggestive association with AD after Stage 2 or Stage 3 analysis. 15

Supplementary Table 5. GCTA conditional analysis results. 15

Supplementary Table 6. Rare variants with $P < 10^{-5}$ or common variants with $P < 5 \times 10^{-6}$ selected for replication Stage 3B genotyping. 16

Supplementary Table 7. Genes and non-coding features within the genome-wide significant loci (defined by LDLink LD boundaries). 17

Supplementary Table 8. Summary of eQTL associations for genome-wide significant loci across all tissues. 20

*Previously reported to be an eQTL gene for this locus in Alzheimer disease 20

Supplementary Table 9. Summary of eQTL associations for genome-wide significant loci across Alzheimer disease relevant tissues. 21

Supplementary Table 10 (see Excel Sheet). Complete list of eQTL's identified in search of databases. 25

Supplementary Table 11 (see Excel Sheet). Complete list of eQTL's identified in INFERNO analysis of GTEx. 25

Supplementary Table 12. Results of ALZbase and Barres Human RNA-Seq databases search for differentially expressed genes in AD for the genome-wide significant loci. 25

Supplementary Table 13. Top results of MAGMA pathway analysis for common and rare variant subsets. 25

Supplementary Table 14 (see Excel Sheet). MAGMA genome-wide pathway analysis results using all genes, excluding APOE region genes, and excluding APOE region genes and genome-wide significant genes. Results highlighted in red are pathways that are significant after FDR-correction in the 'all genes' analysis. 26

Supplementary Table 15 (see Excel Sheet). Gene-wide results for all significant pathway ($q<0.05$) in the MAGMA genome-wide pathway analysis. 26

Supplementary Table 16. Complete results of the Aβ-centered biological network pathway analysis using curated set of 335 genes from Campion et al[8]. 26

Supplementary Table 17 (see Excel sheet). Aβ-centered biological network pathway testing genes nominally significant only in: 1) common-only SNV testing, 2) rare-only SNV testing, and 3) both common-only and rare-only SNV testing. 28

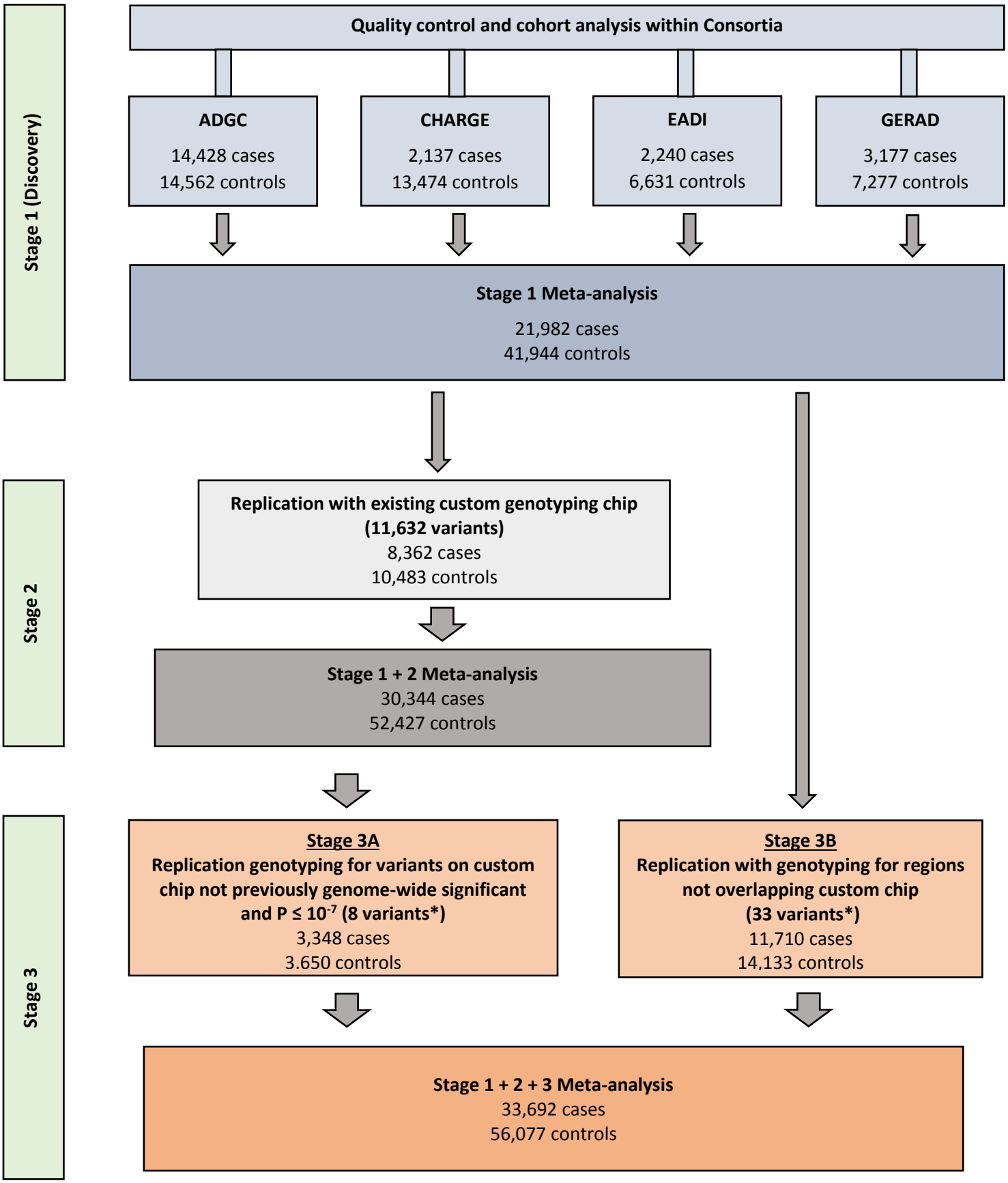
Supplementary Table 18 (see Excel Sheet). STRINGdb analysis of genes in genome-wide significant loci using the prioritized list of 68 genes in the genome-wide loci. 28

Supplementary Table 19 (see Excel Sheet). Results of Jensen diseases, Jensen tissues and Archs4 tissues analysis using Enrichr. 28

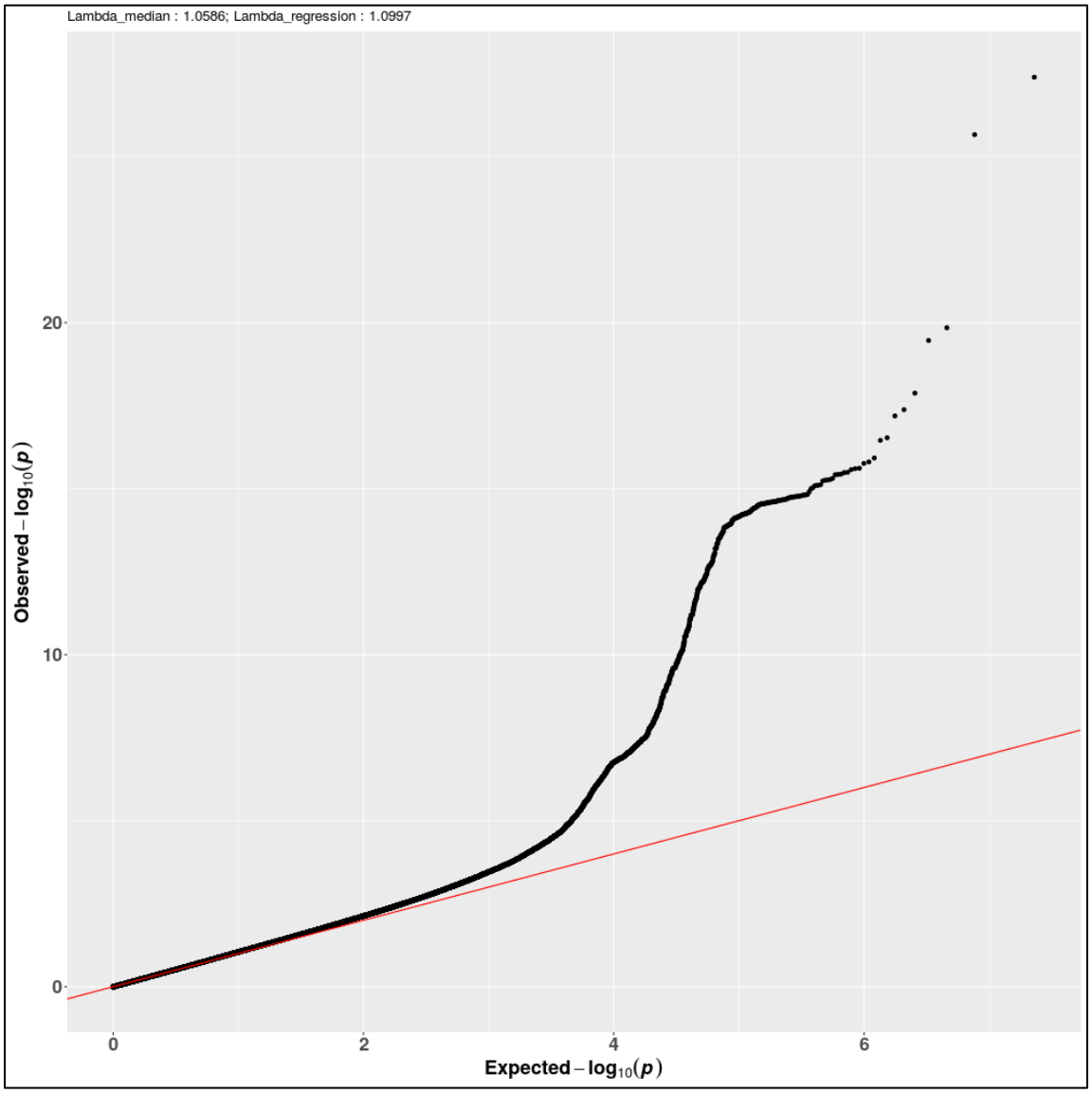
Supplementary Table 20. Full description of stage 2 datasets by center 29

Supplementary Table 21. Variants selected for genotyping in replication Stage 3A. 30

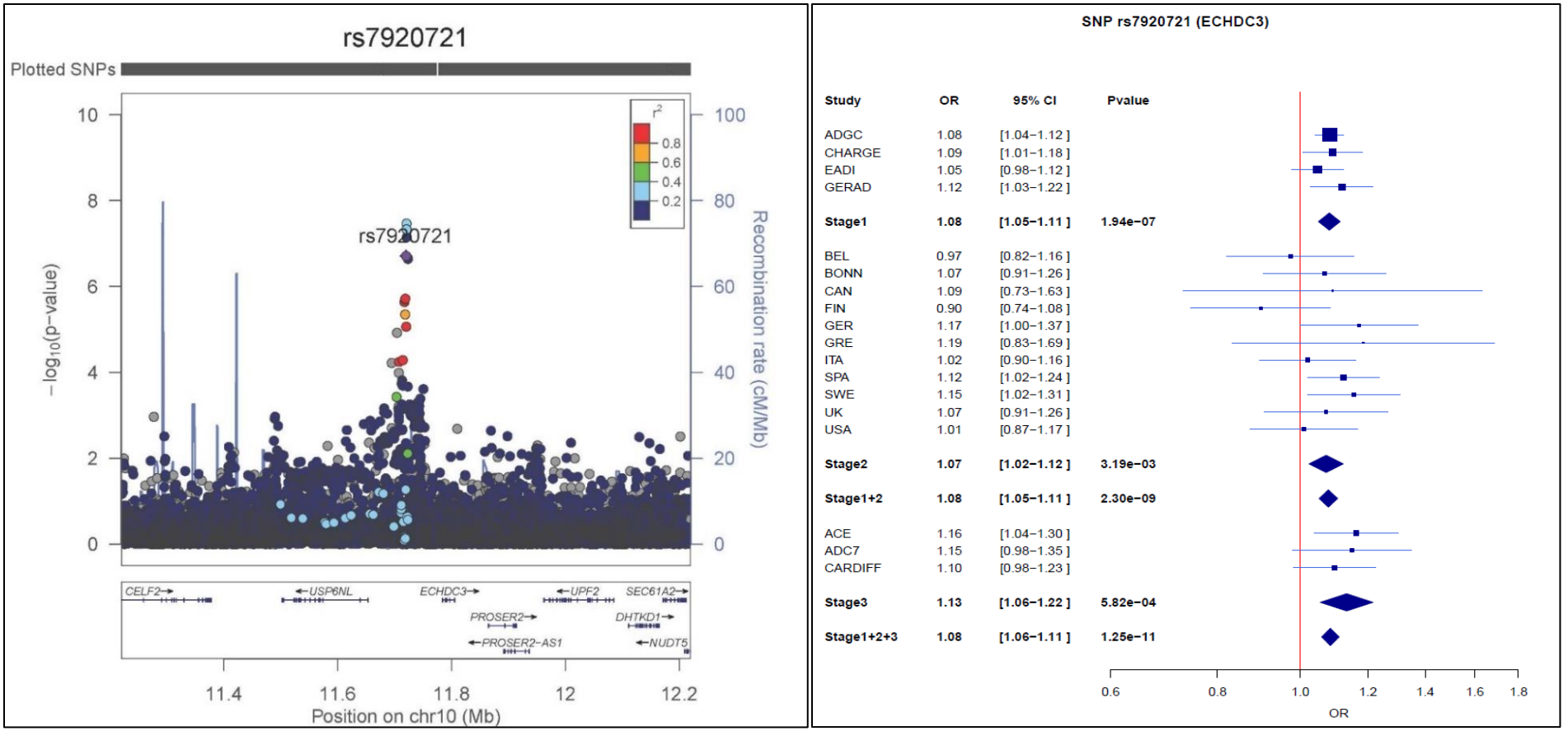
References 31



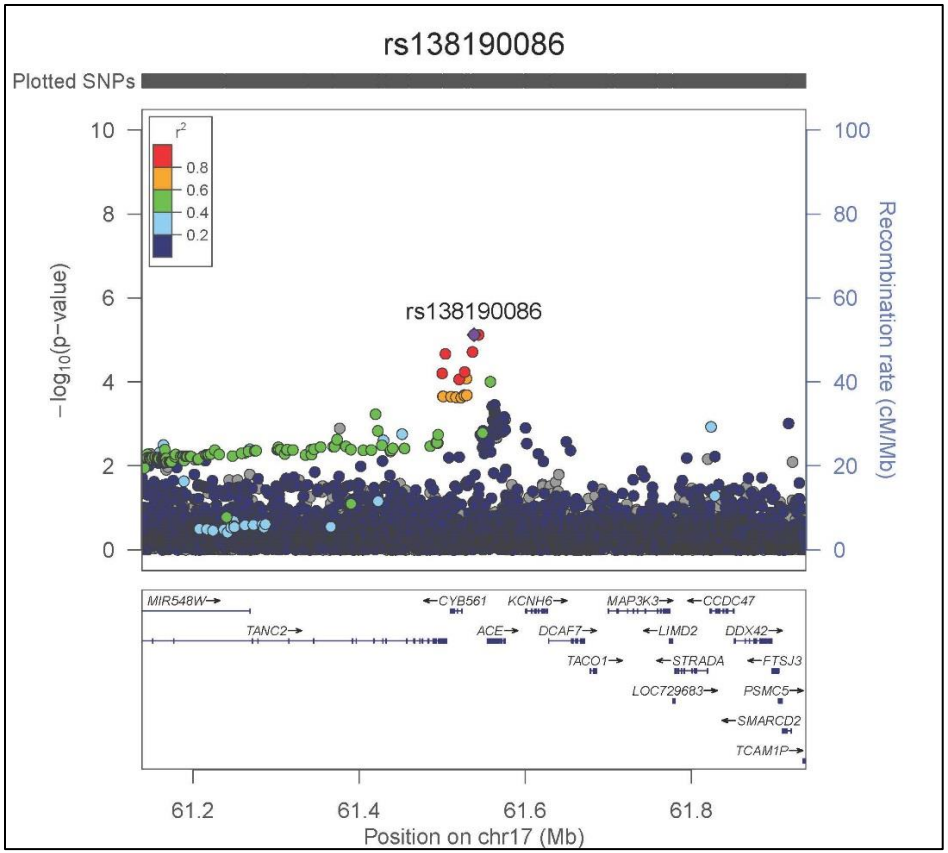
Supplementary Figure 1. Study design. Discovery meta-analysis in ADGC, CHARGE, EADI and GERAD followed by Stage I and II replication genotyping analysis. *Cases and controls are largely overlapping between the old and new genotyping.

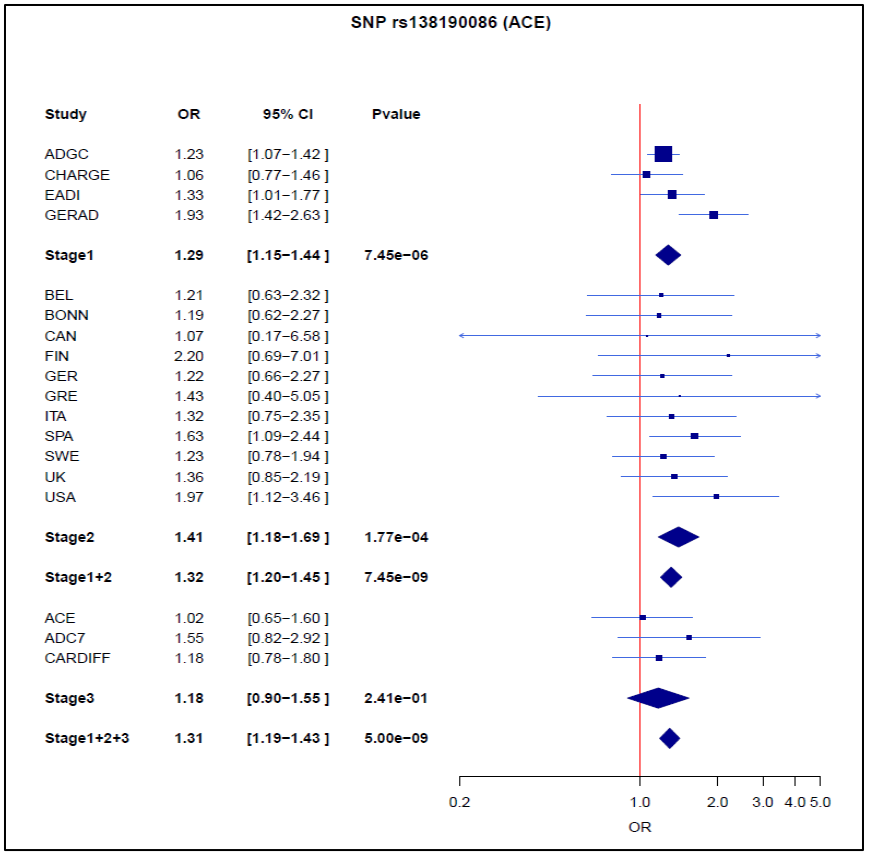


Supplementary Figure 2. Stage I discovery QQ Plot. QQ Plot of stage I discovery meta-analysis results (excludes the APOE locus).

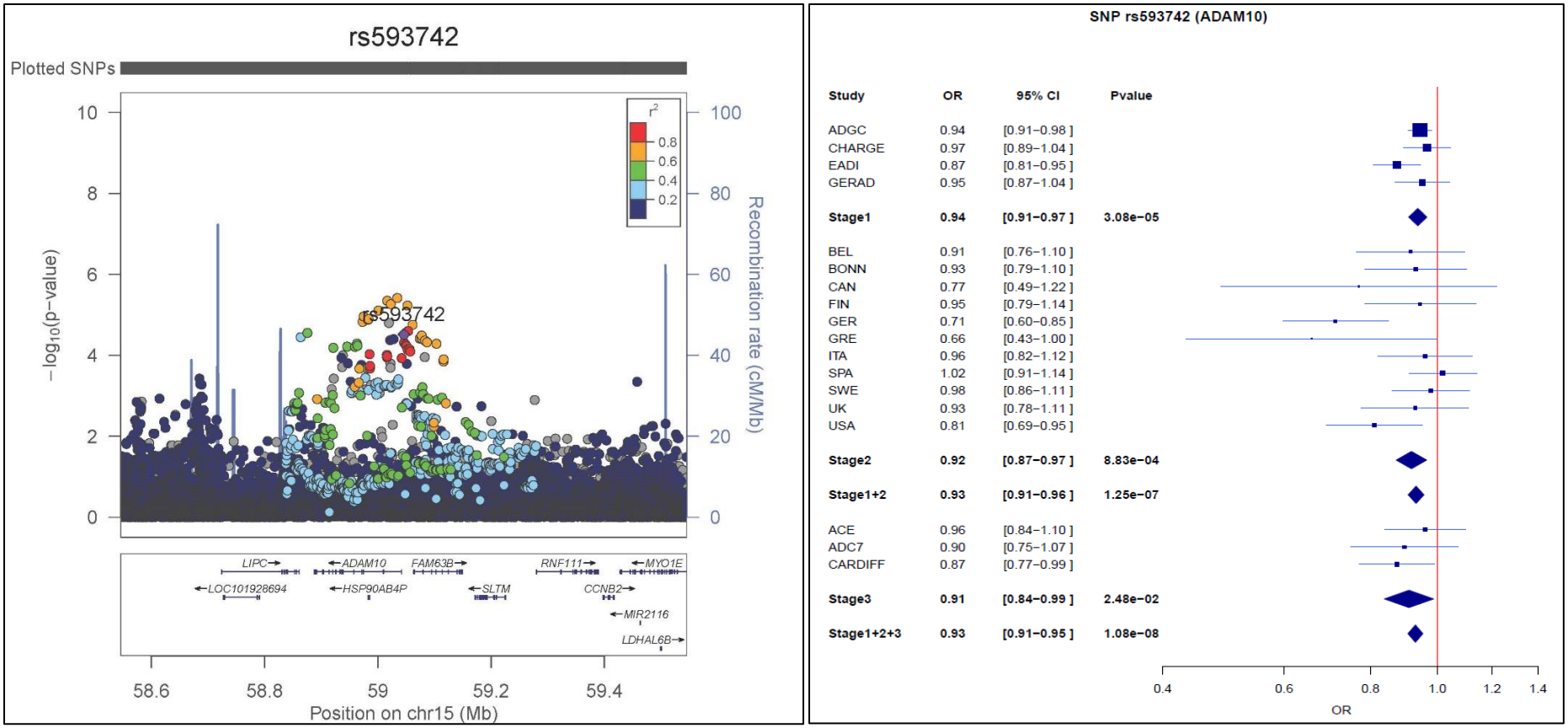


Supplementary Figure 3. *ECHDC3* locus. LocusZoom and forest plot of rs7920721 Stage 1 discovery results.

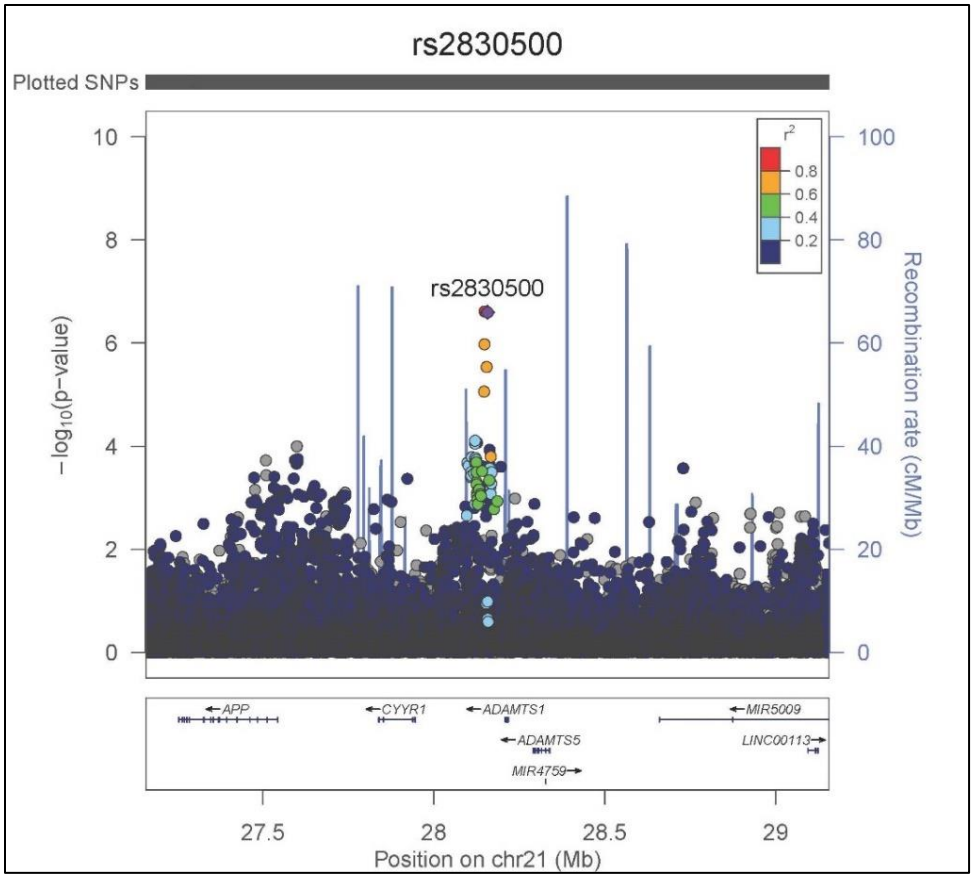


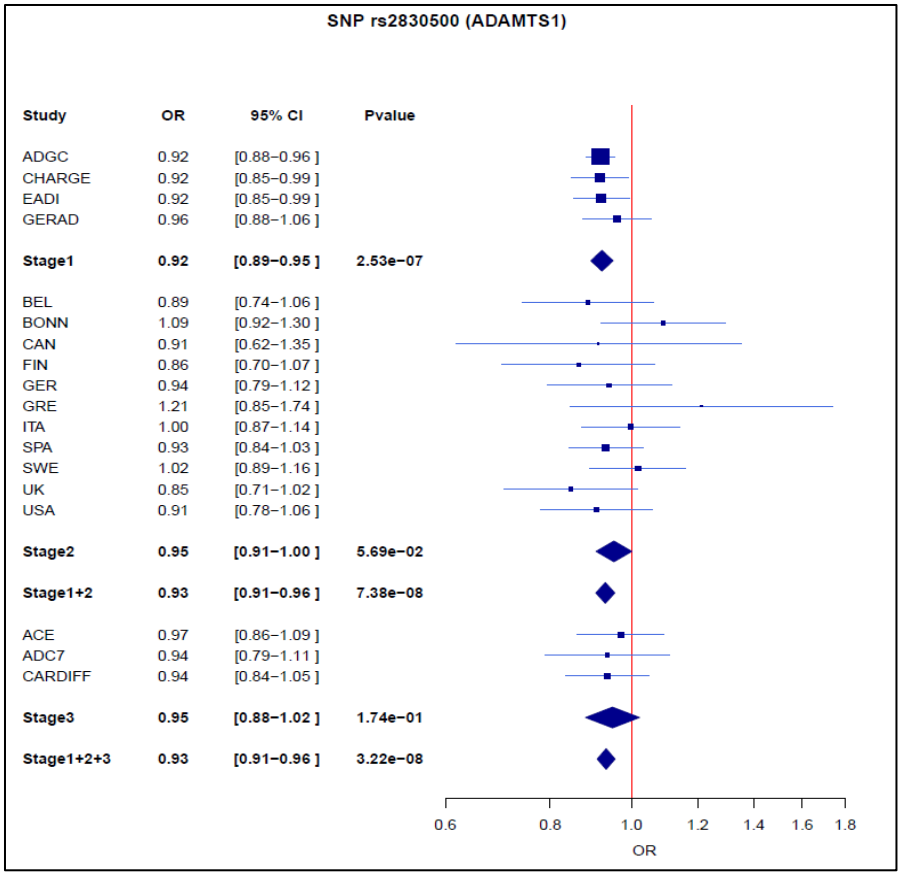


Supplementary Figure 4. *ACE* locus. LocusZoom and forest plot of rs138190086 Stage 1 discovery results.

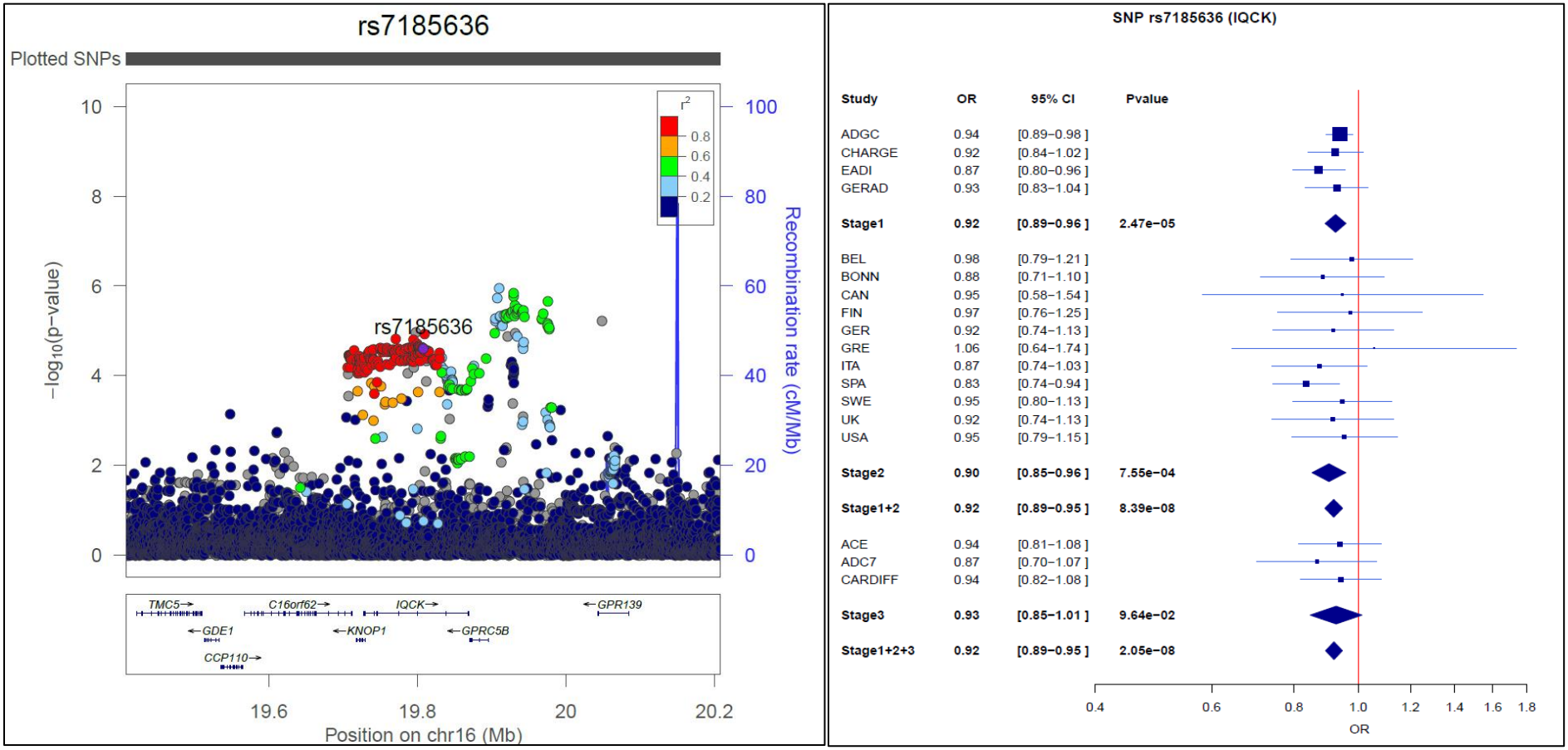


Supplementary Figure 5. ***ADAM10*** **locus.** LocusZoom and forest plot of rs593742 Stage 1 discovery results.

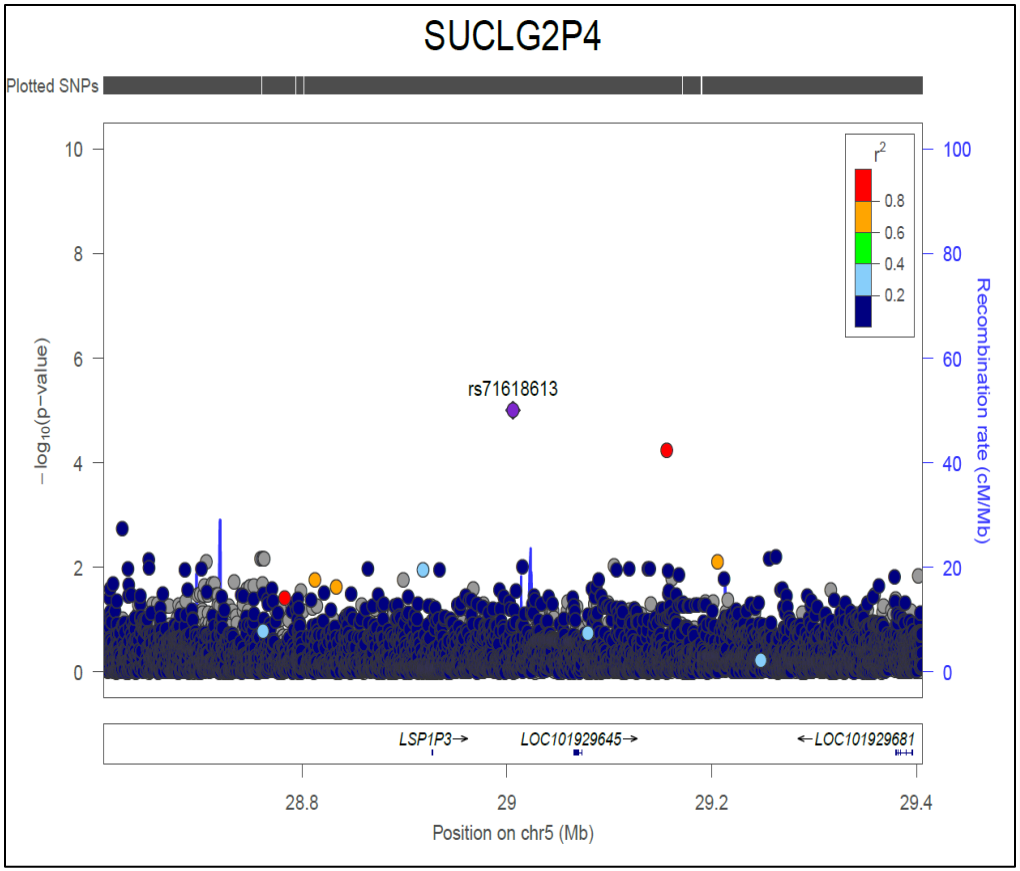


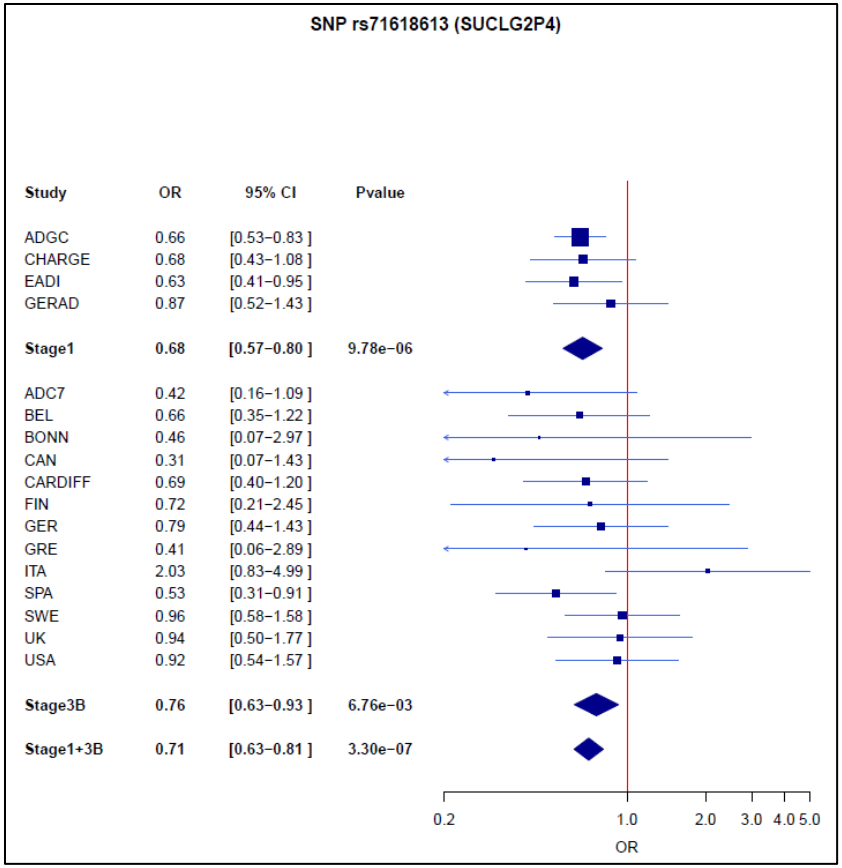


Supplementary Figure 6. *ADAMTS1* locus. LocusZoom and forest plot of rs2830500 Stage 1 discovery results.

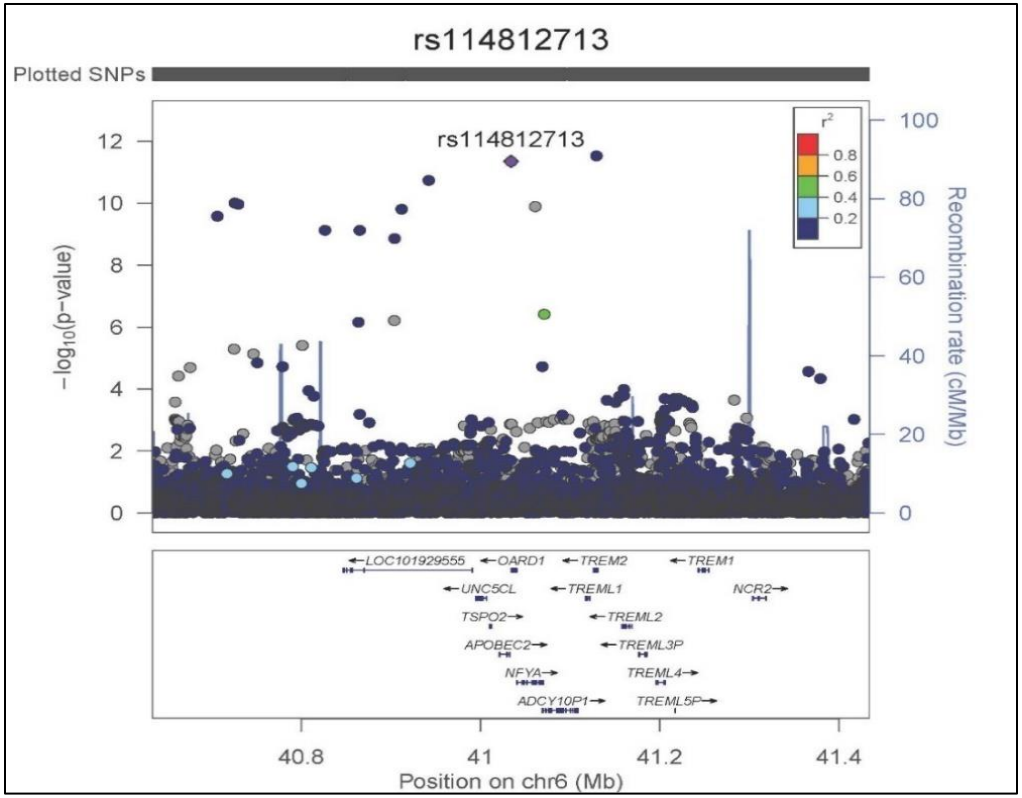


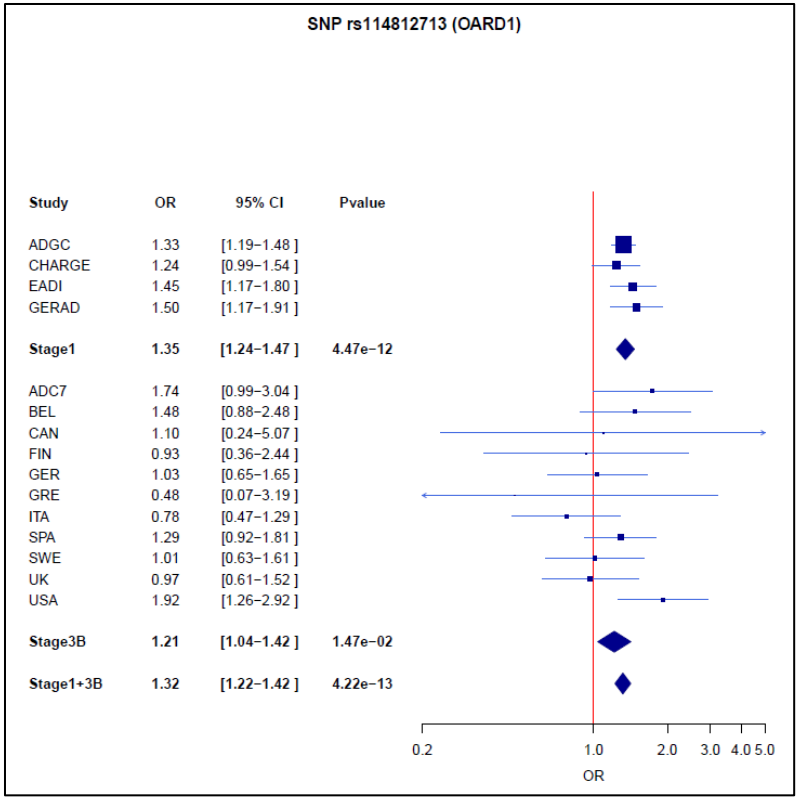
Supplementary Figure 7. *IQCK* locus. LocusZoom and forest plot of rs7185636 (*IQCK* region).





Supplementary Figure 8. *SUCLG2P4* locus. LocusZoom and forest plot of rs71618613 Stage 1 discovery results.





Supplementary Figure 9. *OARD1* locus. LocusZoom and forest plot of rs114812713 Stage 1 discovery results.

SUPPLEMENTARY TABLES

Supplementary Table 1. Description of the consortium data sets used for Stage 1 discovery, Stage 2 replication and Stage 3 replication

		Alzheimer's disease cases			Controls		
	Consortium	***N***	**Percent female**	**Mean AAO (s.d)**	***N***	**Percent female**	**Mean AAE (s.d)**
Discovery	ADGC	14,428	59.3	71.1 (17.3)	14,562	59.3	76.2 (9.9)
	CHARGE	2,137	67.3	82.6 (12)	13,474	55.8	76.7 (8.2)
	EADI	2,240	65.0	75.4 (9.1)	6,631	60.6	78.9 (7.0)
	GERAD	3,177	64.0	73.0 (0.2)	7,277	51.8	51.0 (0.1)
	N	21,982			41,944		

	Country	***N***	**Percent female**	**Mean AAO (s.d)**	***N***	**Percent female**	**Mean AAE (s.d.)**
Stage 2*	Belgium	878	66.1	75.4 (8.6)	661	59.5	65.7 (14.3)
	Finland	422	68.0	71.4 (6.9)	562	59.3	69.1 (6.2)
	Germany	972	63.9	73.0 (8.6)	2,378	53.1	69.5 (10.1)
	Greece	256	63.3	69.2 (8.0)	229	34.1	49.3 (16.4)
	Hungary	125	68.0	74.9 (6.8)	100	69.0	74.4 (6.5)
	Italy	1,729	66.5	71.5 (8.7)	720	55.7	70.0 (10.4)
	Spain	2,121	66.3	75.0 (8.3)	1,921	55.3	70.2 (10.8)
	Sweden	797	61.7	76.8 (8.1)	1,506	62.8	70.6 (8.7)
	UK	490	67.6	74.6 (8.7)	1,066	29.2	73.8 (6.5)
	USA	572	61.9	83.5 (7.6)	1,340	54.0	79.3 (6.8)
	N	8,362			10,483		

	Country	***N***	**Percent female**	**Mean AAO (s.d)**	***N***	**Percent female**	**Mean AAE (s.d.)**
Stage 3*	Spain	932	71.0	77.7 (7.9)	1,813	68.4	54.6 (12.1)
	UK	1,902	57.8	73.8 (12.9)	1,047	64.8	77.2 (7.9)
	USA (ADC7)	514	51.3	73.90 (8.3)	790	63.6	72.3 (7.7)
	N	3,348			3,650		

AAO, age at onset; AAE, age at examination.

***Stage 2 and Stage 3 datasets were combined for genotyping of 33 replication variants not present on the 2013 custom chip**

Supplementary Table 2. Demographic description of datasets within each consortium.

Consortium		AD cases			Controls		
		N	% female	Mean AA (SD)	*N*	% female	Mean AAE (SD)
ADGC	ACT	532	62.6	78.8 (12.7)	1571	55.6	81.7 (5.9)
	ADC1	1549	54.3	71.6 (11.0)	512	59.2	76.8 (8.8)
	ADC2	727	50.8	61.4 (29.5)	156	67.9	75.8 (7.9)
	ADC3	894	54.7	58.6 (32.8)	586	63.0	72.8 (17.5)
	ADC4	304	55.3	73.4 (7.0)	377	63.9	75.7 (8.1)
	ADC5	286	53.1	73.7 (7.0)	505	65.5	77.6 (9.0)
	ADC6	213	58.2	73.9 (7.6)	338	66.6	74.6 (9.0)
	ADNI	268	42.2	75.3 (7.1)	173	40.5	78.6 (5.5)
	BIOCARD	6	33.3	73.8 (6.1)	112	62.5	68.0 (5.5)
	CHAP	27	63.0	84.8 (7.6)	144	52.8	81.8 (6.6)
	EAS	9	44.4	85.2 (4.9)	141	41.1	84.4 (5.2)
	GenADA	666	56.9	72.8 (13.5)	712	63.9	74.2 (7.0)
	MAYO	658	57.4	73.6 (4.8)	1046	51.1	72.9 (4.4)
	MIRAGE	491	63.3	69.9 (11.5)	738	58.8	70.8 (12.1)
	MTC	256	57.0	73.6 (11.8)	189	61.4	70.9 (9.7)
	NIALOAD	1798	65.0	73.1 (9.3)	1568	60.2	73.8 (9.3)
	NBB	80	71.3	74.5 (7.5)	48	56.3	81.5 (9.4)
	OHSU	132	62.1	85.9 (5.7)	153	54.9	83.9 (7.6)
	PFIZER	696	53.7	73.7 (5.0)	762	54.1	77.2 (4.9)
	RMAYO	13	23.1	78.5 (9.0)	233	41.6	79.2 (5.8)
	ROSMAP	295	70.5	85.6 (6.2)	769	72.0	82.2 (7.1)
	ROSMAP2	59	78.0	81.9 (6.9)	217	76.0	80.8 (7.2)
	TARC1	323	61.6	74.0 (7.1)	181	65.2	73.9 (8.2)
	TGEN2	668	64.8	67.2 (22.9)	365	48.5	80.0 (8.7)
	UKS	596	57.4	72.2 (6.6)	170	51.2	64.1 (3.0)
	UMCWRMSSM	1177	64.5	71.1 (17.4)	1126	61.3	73.5 (10.6)
	UPITT	1255	62.9	66.8 (22.4)	829	63.3	75.5 (6.0)
	WASHU	339	57.2	69.1 (21.5)	187	60.4	76.9 (8.4)
	WASHU2	38	57.9	73.4 (7.3)	94	46.8	51.7 (35.2)
	WHICAP	73	72.6	83.9 (7.8)	560	60.4	81.7 (6.7)
CHARGE	AGES	95	51.6	81.5 (0.1)	2708	59.2	75.7 (0.1)
	ASPS	277	57.8	76.4 (8.3)	169	58.0	66.4 (10.8)
	CHS	450	66.0	81.9 (5.2)	1702	60.3	81.1 (5.2)
	FHS	330	64.0	86.1 (7.2)	3910	49.0	74.0 (9.5)
	ROTTERDAM	985	73.2		4985	57.6	78.0 (7.6)
EADI		2240	65.0	75.4 (9.1)	6631	60.6	78.9 (7.0)
GERAD	MRC	1,008	70.3	80.9 (6.5)	873	61.6	75.9 (6.3)
	ARUK	939	61.0	76.6 (9.6)	82	59.8	77.9 (7.6)
	BONN	551	63.7	72.9 (8.3)	37	64.9	79.5 (3.6)
	WASHU	423	56.0	82.1 (9.0)	156	65.4	78.5 (9.7)
	NIMH	127	63.0	80.1 (6.1)	-	-	-
	UCL:PRION	82	59.8	63.6 (9.9)	-	-	-
	UCL:LASER	47	74.5	80.6(7.9)	-	-	-
	1958BC	-	-	-	5,342	49.8	45.0 (0.0)
	KORA	-	-	-	434	49.1	56.0 (7.2)
	HNR	-	-	-	353	52.9	54.6 (5.3)
	MAYO[1]	-	-	-	-	-	-
TOTALS		21982			41944		

[1] **MAYO study is part of both ADGC and GERAD consortia. For the purposes of this meta-analysis, MAYO was removed from the GERAD dataset and included in the ADGC dataset only.**

Supplementary Table 3. Description of imputation properties and results by dataset.

Cohort	Genotyping Chip	Imputation software	*N* SNPs analyzed*	Analysis Software and Properties		
				GWAS Software	Number of PC's for adjustment	Genomic Inflation factor (I)
ACT	Illumina 660	IMPUTE2	16,424,562	SNPTest	3	0.97
ADC1	Illumina 660	IMPUTE2	17,238,284	SNPTest	3	0.96
ADC2	Illumina 660	IMPUTE2	14,480,888	SNPTest	3	0.96
ADC3	Illumina OmniExpress	IMPUTE2	15,717.417	SNPTest	3	0.98
ADC4	Illumina OmniExpress	IMPUTE2	14,289,060	SNPTest	3	0.98
ADC5	Illumina OmniExpress	IMPUTE2	14,414,187	SNPTest	3	0.98
ADC6	Illumina OmniExpress	IMPUTE2	13,674,194	SNPTest	3	0.98
ADNI	Illumina 610	IMPUTE2	13,138,557	SNPTest	2	0.98
BIOCARD	Illumina OmniExpress	IMPUTE2	9,906,615	SNPTest	3	0.94
CHAP	Illumina OmniExpress	IMPUTE2	10,753,247	SNPTest	3	0.94
EAS	Illumina OmniExpress	IMPUTE2	10,665,402	SNPTest	3	0.91
GenADA	Affymetrix 500/Illumina 550/Illumina 1M	IMPUTE2	15,785,004	SNPTest	2	0.95
MAYO	Illumina HapMap300	IMPUTE2	12,734,320	SNPTest	4	1.00
MIRAGE	Illumina 610/Illumina 330	IMPUTE2	16,564,164	GWAF	3	0.99
MTC	Illumina OmniExpress	IMPUTE2	10,084,974	SNPTest	3	0.94
NIALOAD	Illumina 610	IMPUTE2	13,844,168	GWAF	2	0.98
NBB	Illumina 1M	IMPUTE2	10,198,532	SNPTest	3	0.95
OHSU	Illumina HumanCNV370v1_C	IMPUTE2	11,955,295	SNPTest	2	0.98
PFIZER	Illumina 550	IMPUTE2	16,237,067	SNPTest	3	0.99
RMAYO	Illumina OmniExpress	IMPUTE2	11,275,229	SNPTest	3	0.89
ROSMAP	Affymetrix 6.0	IMPUTE2	14,554,245	SNPTest	2	0.98
ROSMAP2	Illumina OmniExpress	IMPUTE2	11,644,798	SNPTest	3	0.97
TARC1	Affymetrix 6.0	IMPUTE2	13,461,662	SNPTest	3	0.98
TGEN2	Affymetrix 1M	IMPUTE2	14,303,739	SNPTest	2	0.98
UKS	Illumina 550	IMPUTE2	13,648,502	SNPTest	3	1.02
UMCWRMSSM	Illumina Human660/1M Duo/Affymetrix 6.0	IMPUTE2	13,073,899	SNPTest	4	1.01
UPITT	Illumina Omni-Quad	IMPUTE2	16,383,317	SNPTest	3	1.01
WASHU	Illumina Human610	IMPUTE2	13,400,901	SNPTest	3	0.98
WASHU2	Illumina OmniExpress	IMPUTE2	10,045,921	SNPTest	3	1.01
WHICAP	Illumina OmniExpress	IMPUTE2	13,987,587	SNPTest	3	0.94
AGES	Illumina 370CNV Duo BeadChip	Minimac	9,597,323	SNPTest	2	0.99
ASPS	Illumina 610	Minimac	12,014,637	SNPTest	3	1.02
CHS	Illumina 370CNV Duo BeadChip	Minimac	8,589,517	R	2	0.96
FHS	Affymetrix 500	Minimac	9,372,016	GWAF	2	1.00
ROTTERDAM	Illumina 550	Minimac	11,949,047	SNPTest	2	1.00
EADI	Illumina 610	IMPUTE2	19,365,337	SNPTest	4	1.02
GERAD	Illumina 300/Illumina 550/Illumina 610	Minimac	12,637,856	SNPTest	3	1.12

*Before quality filters for presence in 30% cases and 30% controls and rare variant imputation quality score ≥ 0.70

Supplementary Table 4. Results for variants showing suggestive association with AD after Stage 2 or Stage 3 analysis.

rsID	Chr:Position	MAF	Closest Gene(s)*	Variant type †	Discovery OR [95% CI]	Discovery *P*-value	Stage 2 OR [95% CI]	Stage 2 *P*-value	Stage 3 OR [95% CI]	Stage 3 *P*-value	Combined OR [95% CI]	Combined *P*-value
rs182921547	4:32834210	0.033	*LOC101927363*, *MAPRE1P2*	intergenic	1.38 [1.21-1.58]	1.1×10^{-6}	1.29 [0.74-2.25]	0.378	--	--	1.38 [1.21-1.56]	7.6×10^{-7}
rs71618613	5:29005985	0.010	*SUCLG2P4*, *LOC101929645*	downstream gene variant	0.68 [0.57-0.80]	9.7×10^{-6}	0.76 [0.63-0.93]	0.006	--	--	0.71 [0.63-0.81]	3.3×10^{-7}
rs35868327	5:52665230	0.013	*LOC257396,FST*	Intergenic variant	0.69 [0.59-0.80]	7.8×10^{-6}	0.58 [0.29-1.17]	0.126	--	--	0.68 [0.59-0.79]	2.6×10^{-7}
rs4723711	7:37844263	0.355	*LOC100420413*, *NME8*	intron variant	0.95 [0.92-0.98]	2.7×10^{-4}	0.91 [0.87-0.95]	9.5×10^{-5}				2.8×10^{-7}
rs4735340	8:95976251	0.476	*NDUFAF6*	intron variant	0.95 [0.92-0.98]	1.2×10^{-4}	0.92 [0.88-0.96]	2.6×10^{-4}	--	--	0.93 [0.92-0.96]	2.1×10^{-7}
rs10751667	11:941941	0.359	*AP2A2*	intron variant	0.94 [0.92-0.97]	1.4×10^{-4}	0.93 [0.89-0.97]	1.3×10^{-3}	--	--	0.94 [0.92-0.96]	8.1×10^{-7}
rs7295246	12:43967677	0.413	*ADAMTS20*	upstream gene variant	1.06 [1.03-1.09]	1.2×10^{-4}	1.09 [1.04-1.14]	3.7×10^{-4}	1.02 [0.95-1.10]	0.54	1.06 [1.04-1.09]	4.0×10^{-7}
rs10467994	15:51008687	0.333	*SPPL2A*	intron variant	1.05 [1.02-1.08]	4.4×10^{-4}	0.91 [0.87-0.95]	7.7×10^{-5}	--	--	1.06 [1.04-1.09]	3.4×10^{-7}
rs62039712	16:79355857	0.115	*WWOX,MAF*	intergenic variant	1.17 [1.10-1.23]	1.1×10^{-7}	1.13 [0.84-1.51]	0.434	--	--	1.16 [1.10-1.23]	8.7×10^{-8}
rs2632516	17:56409089	0.440	*MIR142 / BZRAP1-AS1***	non-coding transcript exonic	0.93 [0.90-0.96]	3.6×10^{-7}	0.96 [0.92-1.01]	0.116	--	--	0.94 [0.92-0.96]	1.4×10^{-7}
rs8111708	19:18558876	0.342	*ELL*	intron variant	1.07 [1.04-1.10]	3.9×10^{-6}	1.05 [1.00-1.10]	0.031	--	--	1.06 [1.04-1.09]	5.0 x 10-7

† Based on Ensembl Transcripts

* Intergenic variants list the two genes on each side of the variant

** Variant is annotated to both gene features

Supplementary Table 5. GCTA conditional analysis results.

LOCUS	SNP	Chr	Basepair	Freq	Beta	SE	P	N	Freq_geno	bJ	bJ_se	pJ	LD_r
BIN1	rs4663096	2	127861766	0.1759	0.1246	0.0187	2.88E-11	68302.5	0.173395	0.103623	0.018816	3.65E-08	0.11
BIN1	rs6733839	2	127892810	0.4067	0.1693	0.0154	4.02E-28	60421.4	0.404105	0.160078	0.015506	5.51E-25	0
TREM2	rs114812713	6	41034000	0.0301	0.298	0.0431	4.47E-12	63837.4	0.0262434	0.239265	0.046545	2.74E-07	0.44
TREM2	rs75932628	6	41129252	0.0082	0.6989	0.1001	2.95E-12	42466.6	0.00569907	0.529187	0.107465	8.47E-07	-0.06
TREM2	rs3857580	6	41216334	0.5795	0.0536	0.0144	0.000199	68551.3	0.566761	0.066938	0.014513	3.98E-06	0
PTK2B	rs73223431	8	27219987	0.3669	0.0936	0.0153	8.34E-10	63678.1	0.36164	0.091696	0.015306	2.09E-09	0.01
CLU	rs867230	8	27468503	0.6029	0.1333	0.0158	3.49E-17	57897	0.614787	0.131888	0.015811	7.35E-17	0
ABCA7	rs12151021	19	1050874	0.3247	0.1071	0.0169	2.56E-10	55281.7	0.31123	0.128068	0.017523	2.70E-13	-0.28
ABCA7	rs4147918	19	1058176	0.9616	0.1033	0.0379	0.006484	65312.2	0.962218	0.178792	0.039284	5.33E-06	0

Supplementary Table 6. Rare variants with P < 10^{-5} or common variants with P < 5 x 10^{-6} selected for replication Stage 3B genotyping.

Chr:Position[a]	rsID	IQS[b]	Studies in stage 3B[c]	VEP Consequence[d]	Closest gene(s)[e]	MAF[f]	Stage 1 Discovery (n=63,926)		Stage 3B (n=25,871)		Overall Stages 1 + 3B (n=90,836)		
							OR [95% CI][g]	P-value	OR [95% CI][g]	P-value	OR [95% CI][g]	P-value	I^2 (%) P value[h]
1:72221591	rs190217640	0.946	1	intron variant	*NEGR1,NEGR1-IT1*	0.009	0.69[0.58-0.81]	5.78 x10^{-6}	0.88[0.38-2.03]	0.763	0.69[0.59-0.81]	6.51 x 10^{-6}	22, 8 x 10^{-1}
2:186808552	rs67839872	0.991	13	intergenic variant	*FSIP2,AC097500.2*	0.089	1.12[1.07-1.18]	4.61 x 10^{-6}	1.01[0.94-1.09]	0.801	1.09[1.04-1.13]	8.11 x 10^{-5}	11, 2 x 10^{-1}
3:34413128	rs76695866	0.807	13	intron variant	*AC018359.1*	0.037	1.20[1.11-1.30]	6.15 x 10^{-6}	1.08[0.97-1.21]	0.150	1.16[1.09-1.23]	6.59 x 10^{-6}	3, 4 x 10^{-1}
3:101227435	rs6806784	0.458		intron variant	*FAM172BP,SENP7*	0.016	1.62[1.35-1.95]	2.93 x 10^{-7}	0.60[0.29-1.25]	0.172	1.53[1.28-1.83]	3.56 x 10^{-6}	9, 3 x 10^{-1}
4:32834210	rs182921547	0.513	1	intergenic variant	*PCDH7*	0.034	1.38[1.21-1.58]	1.10 x 10^{-6}	1.29[0.74-2.25]	0.378	1.38[1.21-1.56]	7.60 x 10^{-7}	0, 9 x 10^{-1}
4:66245059	rs28660482	0.958	13	intron variant	*EPHA5*	0.024	1.25[1.14-1.37]	2.90 x 10^{-6}	1.03[0.90-1.18]	0.682	1.17[1.09-1.27]	4.16 x 10^{-5}	15, 2 x 10^{-1}
4:104176240	rs6822989	0.937	3	upstream gene variant	*CENPE,TACR3*	0.008	1.55[1.29-1.86]	3.48 x 10^{-6}	0.87[0.61-1.25]	0.456	1.37[1.17-1.62]	1.52 x 10^{-4}	28, 5 x 10^{-1}
4:110145870	rs7686421	0.979	3	intron variant	*COL25A1*	0.045	1.17[1.09-1.25]	7.92 x 10^{-6}	0.78[0.65-0.94]	0.008	1.11[1.04-1.19]	1.04 x 10^{-3}	0, 5 x 10^{-1}
5:29005985	rs71618613	0.691	13	downstream gene variant	*SUCLG2P4*	0.010	0.68[0.57-0.80]	9.78 x 10^{-6}	0.76[0.63-0.93]	0.006	0.71[0.63-0.81]	3.30 x 10^{-7}	0, 9 x 10^{-1}
5:52665230	rs35868327	0.688	1	regulatory region variant	*LOC257396,FST*	0.013	0.69[0.59-0.80]	7.78 x 10^{-7}	0.58[0.29-1.17]	0.126	0.68[0.59-0.79]	2.60 x 10^{-7}	0, 9 x 10^{-1}
5:138997756	rs19213255	0.726	1	intron variant	*UBE2D2*	0.021	0.76[0.67-0.86]	7.08 x 10^{-6}	0.65[0.31-1.37]	0.257	0.75[0.67-0.85]	3.93 x 10^{-6}	0, 9 x 10^{-1}
6:41034000	rs114812713	0.943	11	3-prime UTR variant	*OARD1*	0.030	1.35[1.24-1.47]	4.47 x 10^{-12}	1.21[1.04-1.42]	0.014	1.32[1.22-1.42]	4.22 x 10^{-13}	0, 6 x 10^{-1}
6:108880646	rs76185277	0.743	13	upstream gene variant	*FOXO3*	0.036	1.23[1.12-1.34]	8.60 x 10^{-6}	0.94[0.83-1.07]	0.346	1.12[1.04-1.21]	2.10 x 10^{-3}	11, 3 x 10^{-1}
7:6908860	rs187857322	0.529	1	upstream gene variant	*CCZ1B*	0.013	1.61[1.31-1.98]	6.49 x 10^{-6}	2.22[0.80-6.14]	0.126	1.63[1.33-2.00]	2.32 x 10^{-6}	0, 6 x 10^{-1}
7:127426090	rs117240937	0.714	13	intron variant	*SND1*	0.017	0.73[0.64-0.83]	3.35 x 10^{-6}	1.02[0.86-1.22]	0.795	0.82[0.74-0.92]	3.49 x 10^{-4}	12, 3 x 10^{-1}
8:10054330	rs187804459	0.839	1	intron variant	*MSRA*	0.007	1.61[1.31-1.98]	5.14 x 10^{-6}	0.62[0.24-1.58]	0.312	1.54[1.26-1.89]	2.25 x 10^{-5}	32, 2 x 10^{-1}
8:71013736	rs6981871	0.874	11	downstream gene variant	*PRDM14,NCOA2*	0.001	5.00[2.47-10.13]	7.84 x 10^{-6}	1.18[0.65-2.16]	0.590	2.17[1.37-3.43]	9.27 x 10^{-4}	27, 1 x 10^{-1}
8:74290338	rs192326911	0.539	1	intergenic variant	*AK128216,STAU2*	0.010	1.63[1.32-2.02]	7.47 x 10^{-6}	3.27[0.71-15.06]	0.128	1.65[1.34-2.04]	3.36 x 10^{-6}	0, 9 x 10^{-1}
8:98364076	rs16895579	0.983	3	intergenic variant	*LOC101927066*	0.045	1.17[1.09-1.25]	6.90 x 10^{-6}	1.02[0.83-1.25]	0.830	1.15[1.08-1.23]	1.50 x 10^{-5}	0, 5 x 10^{-1}
10:113349717	rs201852095	0.759	1	intergenic variant	*ADRA2A,GPAM*	0.262	1.09[1.05-1.13]	4.70 x 10^{-6}	0.94[0.77-1.16]	0.567	1.09[1.05-1.13]	1.06 x 10^{-5}	0, 7 x 10^{-1}
11:11548181	rs148178636	0.95	12	intron variant	*GALNT18*	0.003	1.91[1.44-2.54]	7.62 x 10^{-6}	1.26[0.82-1.92]	0.293	1.68[1.33-2.13]	1.67 x 10^{-5}	29, 7 x 10^{-1}
11:46699124	rs8914	1	13	3-prime UTR variant	*ARHGAP1,ATG13, ZNF408*	0.115	1.12[1.07-1.17]	6.64 x 10^{-7}	1.03[0.97-1.10]	0.334	1.09[1.05-1.13]	3.50 x 10^{-6}	14, 2 x 10^{-1}
11:46804761	rs11038990	0.931	13	non-coding transcript exon variant	*MIR5582,SNORD67, F2,CKAP5*	0.113	1.13[1.08-1.19]	2.44 x 10^{-7}	1.04[0.97-1.11]	0.290	1.10[1.06-1.14]	1.48 x 10^{-6}	10, 3 x 10^{-1}
12:127222883	rs117394726	0.68	12	intron variant	*LOC100996671, LINC00943, LINC00944*	0.040	1.25[1.14-1.36]	2.46 x 10^{-6}	1.03[0.92-1.15]	0.608	1.15[1.07-1.24]	7.68 x 10^{-5}	2, 4 x 10^{-1}
13:39624822	rs190094306	0.528	1	downstream gene variant	*NHLRC3,PROSER1*	0.012	1.64[1.33-2.02]	3.84 x 10^{-6}	1.27[0.52-3.09]	0.603	1.62[1.32-1.99]	3.92 x 10^{-6}	0, 9 x 10^{-1}
14:34443925	rs35833468	0.737	1	intron variant	*EGLN3*	0.435	0.92[0.89-0.95]	6.35 x 10^{-7}	1.14[0.94-1.38]	0.183	0.92[0.89-0.96]	2.96 x 10^{-6}	0, 7 x 10^{-1}
15:31441761	rs192098867	0.932	1	intron variant	*TRPM1*	0.015	0.76[0.68-0.86]	6.90 x 10^{-6}	0.87[0.47-1.61]	0.647	0.77[0.68-0.86]	6.72 x 10^{-6}	0, 7 x 10^{-1}
16:79355857	rs62039712	0.697	1	intergenic variant	*WWOX,MAF*	0.116	1.17[1.10-1.23]	1.17 x 10^{-7}	1.13[0.84-1.51]	0.434	1.16[1.10-1.23]	8.78 x 10^{-8}	21, 1 x 10^{-1}
17:73028843	rs7218004	0.982	11	non-coding transcript exon variant	*ICT1,CDR2L,ATP5H, KCTD2*	0.024	1.23[1.12-1.35]	8.54 x 10^{-6}	0.99[0.85-1.15]	0.891	1.16[1.07-1.26]	1.87 x 10^{-4}	0, 8 x 10^{-1}
18:22967911	rs143606322	0.493	13	intergenic variant	*ZNF521,SS18*	0.011	0.57[0.45-0.73]	6.16 x 10^{-6}	1.35[1.07-1.69]	0.010	0.90[0.76-1.07]	0.2244	43, 5 x 10^{-3}
19:18558876	rs8111708	0.989	13	intron variant	*ISYNA1,ELL,SSBP4*	0.343	1.07[1.04-1.10]	3.95 x 10^{-6}	1.05[1.00-1.10]	0.031	1.06[1.04-1.09]	5.08 x 10^{-7}	13, 2 x 10^{-1}
21:37069610	rs909441	0.748	13	intron variant	*MIR802 (within RUNX1)*	0.061	0.85[0.79-0.91]	4.55 x 10^{-6}	0.97[0.89-1.06]	0.541	0.89[0.85-0.94]	5.60 x 10^{-5}	14, 2 x 10^{-1}
22:21926584	rs138727474	0.782	1	intron variant	*UBE2L3,RIMBP3B, RIMBP3C*	0.027	0.78[0.70-0.87]	3.90 x 10^{-6}	1.56[0.93-2.60]	0.089	0.80[0.72-0.89]	3.01 x 10^{-5}	0, 5 x 10^{-1}

[a]Build 37, assembly hg19.
[b]Imputation Quality Score
[c]SNPs failed in sequenom
dEnsembl Variant Effect Predictor consequence[1]
[e]Based on position of top SNP in reference to the refSeq assembly
[f]Average in the discovery sample.
[g]Calculated with respect to the minor allele.
[h]Cochran's *Q* test

Supplementary Table 7. Genes and non-coding features within the genome-wide significant loci (defined by LDLink LD boundaries).

Top Associated SNV	Position	Lead SNV Gene	LD Block (GRCh37)	Gene(s) and Gene Features in LD Block†	Additional Potential cis-eQTL genes and non-coding features within 500kb of LD block*
rs4844610	1:207802552	*CR1**	1:207679307-207850539	***CR1***, ***CR1L***, *AL691452.1, RP11-78B10.2*	***C1orf116***, ***YOD1***, ***PFKFB2***, ***C4BPB***, ***CD55***, ***CR2***, ***CD46***, ***C1orf132***, *MIR29C, MIR29B2,* ***LOC148696***, ***CD34***, ***PLXNA2***, *RP11-164O23.8, RP11-164O23.7, RP11-6J21.2, RP11-357P18.2, RP11-357P18.3, RP11-328D5.1*
rs6733839	2:127892810	*BIN1*	2:127882182-127894615		***GYPC***, ***LOC101929926***, ***BIN1***, ***CYP27C1***, ***ERCC3***, ***MAP3K2***, ***PROC***, *MIR4783,* ***IWS1***, ***MYO7B***, ***LOC105373609***, *RNU6-675P, AC114783.1, RNU7-182P, RP11-521O16.1, RP11-521O16.2, RNU6-1147P, AC068282.3, AC010976.2, RNU4-48P, RP11-286H15.1*
rs10933431	2:233981912	*INPP5D*	2:233976593-233981912	***INPP5D***	***EFHD1***, ***GIGYF2***, ***KCNJ13***, ***C2orf82***, ***NGEF***, ***LOC101928881***, ***NEU2***, ***ATG16L1***, ***SCARNA5***, ***SCARNA6***, ***SAG***, ***DGKD***, ***USP40***, *AC073254.1, RN7SL359P, snoU13, AC064852.4, RNU6-107P, Y_RNA, AC106876.2, RP11-400N9.1*
rs9275152	6: 32652196	*HLA-DQB1*	6:32395036-32636434	***HLA-DRA***, ***HLA-DRB5***, ***HLA-DRB6***, ***HLA-DRB1***, ***HLA-DQA1***, ***HLA-DQB1***, ***HLA-DQB1-AS1***, *RNU1-61P*	***C2***, ***C2-AS1***, ***CFB***, ***NELFE***, *MIR1236,* ***SKIV2L***, ***DXO***, ***STK19***, ***C4B_2***, ***C4A***, ***C4B***, ***CYP21A2***, ***CYP21A1P***, ***TNXA***, ***TNXB***, ***STK19***, ***ATF6B***, ***FKBPL***, ***PRRT1***, ***LOC100507547***, ***PPT2***, ***PPT2-EGFL8***, ***AGPAT1***, *MIR6721,* ***RNF5***, ***RNF5P1***, *MIR6833,* ***AGER***, ***PBX2***, ***GPSM3***, ***NOTCH4***, ***LOC101929163***, ***C6orf10***, ***HCG23***, ***BTNL2***, *MIR3135B,* ***HLA-DOB***, ***TAP2***, ***PSMB8***, ***PSMB8-AS1***, ***TAP1***, ***PSMB9***, ***LOC100294145***, ***HLA-DMB***, ***HLA-DMA***, ***BRD2***, ***HLA-DOA***, ***HLA-DPA1***, ***HLA-DPB1***, ***HLA-DPB2***, ***HCG24***, ***COL11A2***, *LINC00951,* ***TDRG1***, *Xxbac-BPG116M5.17,* ***C4A-AS1***, *AL645922.1,* ***C4B-AS1***, *RNA5SP206,* ***EGFL8***, *XXbac-BPG300A18.13, XXbac-BPG154L12.5, XXbac-BPG154L12.4, RNU6-603P, XXbac-BPG254F23.7, XXbac-BPG246D15.9, AL645941.1, XXbac-BPG181M17.5, XXbac-BPG181M17.6, BRD2-IT1*
rs75932628	6:41129252	*TREM2**	6:40706366-41365821	***LOC101929555***, ***UNC5CL***, ***TSPO2***, ***APOBEC2***, ***OARD1***, ***NFYA***, ***ADCY10P1***, ***TREML1***, ***TREM2***, ***TREML2***, ***TREML3P***, ***TREML4***, ***TREML5P***, ***TREM1***, ***NCR2***, *RNA5SP207, RNU6-643P, AL136967.1, RP1-149M18.3*	***LRFN2***, *LINC01276,* ***FOXP4-AS1***, ***FOXP4***, *MIR4641,* ***MDFI***, ***TFEB***, ***PGC***, ***FRS3***, ***PRICKLE4***, ***TOMM6***, ***USP49***, *RP11-552E20.1, RP11-552E20.4,* ***TDRG1***, *RNU-250P, RP11-121P10.1, RP3-462C17.1, RP11-570K4.1, RP1-149M18.4, AL035588.1, RP11-298J23.5, RP11-298J23.8, RP11-298J23.9, SNORA8, RP5-973N23.4*
rs9473117	6:47431284	*CD2AP*	6:47412916-47628558	***CD2AP***, ***ADGRF2***, *AL355353.1, RP11-385F7.1*	***ADGRF5***, ***ADGRF1***, ***TNFRSF21***, ***ADGRF4***, ***OPN5***, ***PTCHD4***, *Y_RNA, RN7SKP116, RP11-550C4.6, RNU1-105P*
rs12539172	7:100091795	*NYAP1*	7:99932049-100190116	***PMS2P1***, ***STAG3L5P-PVRIG2P-PILRB***, ***STAG3L5P***, ***PVRIG2P***, *MIR6840,* ***PILRB***, ***PILRA***, ***ZCWPW1***, ***MEPCE***, ***PPP1R35***, ***C7orf61***, ***TSC22D4***, ***NYAP1***, ***AGFG2***, ***SAP25***, ***LRCH4***, ***ZASP***, ***FBXO24***, ***PCOLCE-AS1***, *RP11-758P17.2, RP11-758P17.3, RN7SL161P,* ***TSC22D4***, *AC092849.1, RP11-44M6.1, RN7SL416P*	***CYP3A43***, ***CYP3A43***, ***OR2AE1***, ***TRIM4***, ***GJC3***, ***AZGP1***, ***AZGP1P1***, ***ZKSCAN1***, ***ZNF3***, ***COPS6***, ***MCM7***, *MIR25, MIR93, MIR106B,* ***AP4M1***, ***TAF6***, ***CNPY4***, ***MBLAC1***, ***LAMTOR4***, ***C7orf43***, *MIR4658,* ***GAL3ST4***, ***GPC2***, ***STAG3***, ***GATS***, ***PVRIG***, ***SPDYE3***, ***PCOLCE***, ***MOSPD3***, ***TFR2***, ***ACTL6B***, ***LOC105375429***, ***GNB2***, ***POP7***, ***EPO***, ***ZAN***, ***EPHB4***, ***SLC12A9-AS1***, ***SLC12A9***, ***TRIP6***, *MIR6875,* ***SRRT***, ***UFSP1***, ***ACHE***, ***MUC3A***, ***MUC12***, *LOC102724094, MUC17, RP11-506M12.1, AC073842.19, AC005071.1, Y_RNA, RP11-758P17.2, RP11758P17.3, RP11-44M6.7, RN7SL750P, RP11-126L15.4, RN7SL549P, RP11-395B7.2, RP11-395B7.4*

rs11762262	7:143107876	*EPHA1*	7:143099107-143109208	***EPHA1***, ***EPHA1-AS1***	***TRPV5***, *C7orf34*, ***KEL***, ***OR9A2***, ***OR6V1***, ***OR6W1P***, ***PIP***, ***TAS2R39***, ***TAS2R40***, ***LOC105375545***, ***GSTK1***, ***TMEM139***, ***CASP2***, ***CLCN1***, ***FAM131B***, ***LOC100507507***, ***ZYX***, *MIR5892*, ***TAS2R60***, ***TAS2R41***, ***OR10AC1***, ***CTAGE15***, ***TCAF2***, ***TCAF2P1***, ***CTAGE6***, ***LOC154761***, ***TCAF1***, *RP11-556I13.2, RP11-556I13.1, AC073342.12, AC073342.12, RN7SL535P, RN7SL481P, RP11-563K23.1, AC093673.5, RNU6-267P*
rs73223431	8:27219987	*PTK2B*	8:27195121-27238052	***PTK2B***	***ADRA1A***, ***STMN4***, ***TRIM35***, *MIR6842*, ***CHRNA2***, ***EPHX2***, ***CLU***, *MIR6843*, ***SCARA3***, *MIR3622B*, ***CCDC25***, ***ESCO2***, ***PBK***, ***SCARA5***, *MIR548H4, RP11-521M14.2, RP11-521M14.1, RNU6-1086P, RP11-16P20.4, RP11-16P20.3, RNU6-1276P, AC090150.1, RP11-521M14.1, MIR2622A, RP11-16P20.3, snoU13*
rs9331896	8:27467686	*CLU*	8:27456253-27468503	***CLU***, *MIR6843*	***STMN4***, ***TRIM35***, ***PTK2B***, *MIR6842*, ***CHRNA2***, ***EPHX2***, ***SCARA3***, *MIR3622B, MIR3622A*, ***CCDC25***, ***ESCO2***, ***PBK***, ***SCARA5***, ***STMN4***, ***TRIM35***, ***PTK2B***, *MIR4287*, ***NUGGC***, ***ELP3***, *RP11-521M14.1, MIR2622A, RP11-16P20.3, snoU13, RNU6-1276P, RP11-597M17.1*
rs7920721	10:11720308	*ECHDC3*	10:11703491-11723257	*RP11-138I18.2*	***CELF2***, ***CELF2-AS1***, ***USP6NL***, ***ECHDC3***, ***PROSER2***, ***PROSER2-AS1***, ***UPF2***, ***DHTKD1***, ***SEC61A2***, *MIR548AK*, ***NUDT5***, *RP3-323N1.2, RP11-544P1.3, PR11-138I18.1, RP11-138I18.2, RNU6-1095P, snoU13*
rs3740688	11:47380340	*SPI1**	11:47372377-47466790	***MYBPC3***, ***SPI1***, *MIR4487*, ***SLC39A13***, ***PSMC3***, ***RAPSN***, *RP11-750H9.5, AC090559.2, RNU6-1302P*	***LRP4-AS1***, ***LRP4***, ***C11orf49***, ***ARFGAP2***, ***PACSIN3***, *MIR6745*, ***DDB2***, ***ACP2***, ***NR1H3***, ***MADD***, ***LOC101928943***, ***CELF1***, ***PTPMT1***, ***KBTBD4***, ***NDUFS3***, ***FAM180B***, ***C1QTNF4***, ***MTCH2***, ***AGBL2***, ***FNBP4***, ***NUP160***, *RP11-390K5.3, RP11-390K5.6, RN7SL772P, RP11-17G12.2, RP11-17G12.3, RP11-750H9.5, AC090559.1, RP11-750H9.7, RN7SL652P, RNU5E-10P, RP11-76I23.7, Y_RNA, snoU13, RNA5SP340*
rs793322	11:59936926	*MS4A2*	11:59856028-60097777	***MS4A2***, ***MS4A6A***, *MIR6503, AP001257.1*, ***MS4A4E***, ***MS4A4A***	***OSBP***, *MIR3162*, ***PATL1***, ***OR10V1***, ***OR10V2P***, ***STX3***, ***MRPL16***, ***GIF***, ***TCN1***, ***OOSP1***, ***MS4A3***, ***MS4A7***, ***MS4A14***, ***MS4A5***, ***MS4A1***, ***MS4A12***, ***MS4A13***, *LINC00301*, ***MS4A8***, ***MS4A18***, ***MS4A15***, ***MS4A10***, *MIR3162, AP000442.1, AP000640.2, RN7SKP192, AP000640.10, RP11-736I10.1, RP11-804A23.1*
rs3851179	11:85868640	*PICALM*	11:85670385-85868640	***PICALM***, *snoU13, RNU6-560P*	***DLG2***, ***TMEM126B***, ***TMEM126A***, ***CREBZF***, ***CCDC89***, ***SYTL2***, ***CCDC83***, ***EED***, *MIR6755*, ***HIKESHI***, ***CCDC81***, ***ME3***, *RNU6-1292P, AP000974.1, RP11-700A24.1, RP11-90K17.2, RNU6-560P, RP11-12D16.2, RN7SL225P, RP11-317J19.1, RP11-762L8.6*
rs11218343	11:121435587	*SORL1**	11:121433926-121461593	***SORL1***	***TBCEL***, ***TECTA***, ***SC5D***, *MIR100HG, RNU6-256P, RP11-166D19.1*
rs17125924	14:53391680	*FERMT2*	14:53293307-53462216	***FERMT2***	***PTGER2***, ***TXNDC16***, ***GPR137C***, ***ERO1A***, ***PSMC6***, ***STYX***, ***GNPNAT1***, ***DDHD1***, ***LOC101927620***, *RP11-841O20.2, RP11-589M4.1, RP11-589M4.3, RP11-368P15.3, AL356020.1, RP11-547D23.1, AL163953.3*
rs12881735	14:92932828	*SLC24A4*	14:92926952-92957176	***SLC24A4***	***TRIP11***, ***ATXN3***, ***NDUFB1***, ***CPSF2***, ***RIN3***, ***LGMN***, ***GOLGA5***, ***LINC02287***, ***CHGA***, ***ITPK1***, *RP11-472N19.3, RNU6-366P, RP11-862G15.1, RP11-862G15.2*
rs593742	15:59045774	*ADAM10**	15:58873555-59120077	***ADAM10***, ***HSP90AB4P***, ***LOC101928725***, ***MINDY2***, *RP11-50C13.1, snoU13, RN7SKP95*, ***U3***, *RP11-30K9.6*, ***FAM63B***, *RP11-30K9.4*	***AQP9***, ***LIPC***, ***LIPC-AS1***, ***SLTM***, ***RNF111***, ***CCNB2***, ***MYO1E***, ***MIR2116***, ***LDHAL6B***, ***ALDH1A2***, *RP11-355N15.1, RP11-355N15.3, RP11-355N15.2, RP11-50C13.2, snoU13, RP11-30K9.5, AC025918.2, RP11-59H7.4, RP11-59H7.3*, ***C15orf31***, *AC092756.1, RP11-429D19.1*

rs7185636	16:19808163	*IQCK*	16:19706199-19867021	***C16orf62*, *KNOP1*, *IQCK***, *AC002550.5, CTD-2380F24.1*	***SYT17*, *CLEC19A*, *TMC5*, *GDE1*, *CCP110*, *GPRC5B*, *GPR139*, *GP2*, *UMOD***, *AC003003.5, CTA-363E6.1, CTA-363E6.2, CTA-363E6.3, CTA-363E6.5, CTA-363E6.6, RNU4-46P, CTA-363E6.7, CTA-363E6.8, AC002550.6, AC002550.5, CTD-2380F24.1, AC134300.1, RP11-204E4.3*
rs138190086	17:61538148	*ACE*	17:61499732-61543566	***TANC2*, *CYB561***, *RP11-269G24.3, RP11-269G24.4, RP11-269G24.6*	***ACE***, *MIR633,* ***KCNH6*, *DCAF7*, *TACO1*, *MAP3K3*, *LIMD2*, *LOC729683*, *STRADA*, *CCDC47*, *DDX42*, *FTSJ3*, *PSMC5*, *SMARCD2*, *TCAM1P*, *CSH2*, *GH2*, *CSH1*, *CSHL1*, *GH1*, *CD79B*, *SCN4A***, *RP11-180P8.1, RP11-180P8.3, RP11-180P8.3, RP11-556O9.2, AC037445.1, AC015923.1, RP11-269G24.2, CTD-2501B8.1, RNU6-288P, RP11-51F16.1, RP11-51F16.8, RN7SL805P*
rs3752246	19:1056492	*ABCA7**	19:1050130-1075979	***ABCA7*, *ARHGAP45*, *HMHA1***	***BSG*, *HCN2*, *POLRMT*, *FGF22*, *RNF126*, *FSTL3*, *PRSS57*, *PALM*, *MISP*, *PTBP1***, *MIR4745,* ***PLPPR3***, *MIR3187,* ***AZU1*, *PRTN3*, *ELANE*, *CFD*, *MED16***, *RNU6-2,* ***R3HDM4*, *KISS1R*, *ARID3A*, *WDR18*, *GRIN3B*, *TMEM259*, *CNN2*, *POLR2E*, *GPX4*, *SBNO2*, *STK11*, *CBARP*, *ATP5D*, *MIDN*, *CIRBP-AS1*, *CIRBP*, *C19orf24*, *EFNA2*, *MUM1*, *NDUFS7*, *GAMT*, *DAZAP1*, *RPS15*, *APC2*, *C19orf25*, *PCSK4*, *REEP6*, *ADAMTSL5*, *PLK5*, *MEX3D***, *AC009005.2, AC004449.6, AC004156.3, AC006273.4, AC006273.5, AC005391.2, LLNLR-260G6.1, AC004528.1, LLNLR-284B4.2, LLNR-284B4.1, AC011558.5, AC004221.2, AC005330.2, AC004623.3, AC004623.2, LLNLR-307A6.1, AC005329.7, CTB-26B13.5, CTB-25B13.12, CTB-25B13.9, AC027307.2, AC027307.1, RN7SL477P*
rs6024870	20:54997568	*CASS4*	20:54979828-55025377	***CSTF1*, *CASS4***	***CBLN4*, *MC3R*, *FAM210B*, *AURKA*, *RTFDC1*, *GCNT7*, *FAM209A*, *FAM209B*, *LINC01716*, *TFAP2C***, *RNA5SP487, RP11-380D15.3, AL121914.1, snoU13, RP5-1153D9.5, RP5-843L14.1, RNU6-1146P, RN7SL170P, AL133232.1, RP5-897D18.1, RNU6-929P*
rs2830500	21:28156856	*ADAMTS1*	21:28146668-28166355		***CYYR1-AS1*, *CYYR1*, *ADAMTS1*, *ADAMTS5***, *MIR4759, AP001595.1, AP001596.6, KB-1466C5.1, AP001601.2*

†Protein coding genes are bolded

*Strong evidence evidence supports this gene as the risk gene for this locus

Supplementary Table 8. Summary of eQTL associations for genome-wide significant loci across all tissues. Complete results can be found in Supplementary Tables 13 and 14.

Locus	cis-eQTL Gene
CR1	*CR1*, CD55*
BIN1	*BIN1, SAP130*
INPP5D	no eQTLs found
HLA-DQB1	*AGPAT1, ATF6B, BAT2, BRD2, C4A, CYP21A1P, CYP21A2, HCG23, HLA-DOB, HLA-DPB2, HLA-DQA1, HLA-DQA2, HLA-DQB1, HLA-DQB1-AS1, HLA-DQB2, HLA-DRB1, HLA-DRB3, HLA-DRB5, HLA-DRB6, MICB, NOTCH4, PRRT1, PSMB9, RPL32P1, SNORA38, SNORD48, TAP2, TAPBP, TNXA, TNXB, XXbac-BPG254F23.6, XXbac-BPG300A18.13*
TREM2	no eQTLs found
CD2AP	*CD2AP, GPR111, RP11-385F7.1*
NYAP1	*AGFG2, AP4M1, C7orf43, CNPY4, EPHB4, GAL3ST4, GATS*, GIGYF1, GPC2, NYAP1, PILRA, PILRB*, PMS2P1, PVIRG, STAG3, STAGL5P-PVRIG2P-PILRB, TRIM4*, ZKSCAN1*
EPHA1	*ARHGEF35, EPHA1, EHPA1-AS1, FAM115D, OR2A7, TAS2R60*
PTK2B	*PTK2B*, SCARA3, TASR60*
CLU	*CLU**
ECHDC3	*RP11-138I18.2*
SPI1	*C11orf49, C1QTNF4*, CELF1*, CUGBP1, FAM180B, FNBP4*, MADD*, MDK, MTCH2*, MYBPC3*, NR1H3, NUP160*, PSMC3, PTPMT1*, RAPSN, RP11-750H9.5, SLC39A13, SPI1**
MS4A2	*ARFGAP2, C11orf49, MS4A2, MS4A4A*, MS4A6A**
PICALM	*PICALM*, SYTL2*
SORL1	no eQTLs found
FERMT2	*FERMT2, GNG2, STYX*
SLC24A4	*SLC24A4, RIN3*
ADAM10	*ADAM10, FAM63B*
IQCK	*AC002550.5, C16orf88, CTD-2194A8.2, CTD-2380F24.1, GPRC5B, IQCK, KNOP1, DEF8*
ACE	no eQTLs found
ABCA7	*ABCA7, CNN2, HMHA1, POLR2E*
CASS4	*CASS4, CSTF1, FAM209B, RPL39P*
ADAMTS1	*ADAMTS1*

*Previously reported to be an eQTL gene for this locus in Alzheimer disease

Supplementary Table 9. Summary of eQTL associations for genome-wide significant loci across Alzheimer disease relevant tissues. Complete results can be found in Supplementary Table 12 and 13. Studies searched include Fairfax et al. 2012[2], Grundberg et al. 2012[3], Lappalainen et al. 2013[4], Ramasamy et al. 2014 (BRAINEAC)[5], Jansen et al. 2017[6], GTEx via INFERNO and SCANdb, and Zeller et al. 2010[7].

Locus	cis-eQTL Gene	Tissue(s)	Source(s)
CR1	*CD55*	Blood	Jansen 2017
	CR1	Lymphoblasts	Grundberg 2012
BIN1	*BIN1*	Monocytes, Blood, Lymphoblasts, Cerebral Cortex	Zeller 2010, Jansen 2017, Fairfax 2012, Lappalainen 2013, Ramasamy 2014
	SAP130	Temporal Cortex	Ramasamy 2014
INPP5D	no eQTLs found		
HLA-DQB1	*AGPAT1*	Frontal Cortex	Ramasamy 2014
	BAT2, SNORA38	Cerebral Cortex	Ramasamy 2014
	BRD2	Frontal Cortex	Ramasamy 2014
	CYP21A1P	Blood	GTEx
	HCG23	Cortex	GTEx
	HLA-DOB	Monocytes	Zeller 2010, Fairffax 2012
	HLA-DQA1	Monocytes, Lymphoblasts, Anterior Cingulate Cortex, Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hippocampus, Hypothalamus, Nucleaus accumbens Basal Ganglia, Cells EBV-transformed lymphocytes, Blood	Zeller 2010, Lappalanienen 2013, GTEx
	HLA-DQA2	Cerebral Cortex, Hippocampus, Temporal Cortex, Thalamus, Caudate Basal Ganglia, Cerebellum, Frontal Cortex, Hippocampus, Hypothalamus, Nucleus Accumbens Basal Ganglia, EBV-transformed Lymphocytes, Blood	Ramasamy 2014, GTEx
	HLA-DQB1	Monocytes, Lymphoblasts, Anterior Cingulate Cortex, Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hippocampus, Hypothalamus, Nucleaus accumbens Basal Ganglia, Cells EBV-transformed Lymphocytes, Blood	Zeller 2010, Lappalanienen 2013, GTEx
	HLA-DQB1-AS1	Anterior Cingulate Cortex, Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hippocampus, Hypothalamus, Nucleaus accumbens Basal Ganglia, Cells EBV-transformed Lymphocytes, Blood	GTEx

	HLA-DQB2	Cortex, Hippocampus, Hypothalamus, EBV-transformed Lymphocytes, Blood	GTEx
	HLA-DRB1	Monocytes, Anterior Cingulate Cortex, Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hippocampus, Hypothalamus, Nucleaus accumbens Basal Ganglia, Cells EBV-transformed Lymphocytes, Blood, Putamen Basal Ganglia, Transformed Fibroblasts	Zeller 2010, GTEx
	HLA-DRB3	Monocytes	Zeller 2010
	HLA-DRB5	Monocytes, Anterior Cingulate Cortex, Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hippocampus, Hypothalamus, Nucleaus accumbens Basal Ganglia, Cells EBV-transformed Lymphocytes, Blood, Putamen Basal Ganglia, Transformed Fibroblasts	Zeller 2010, GTEx
	HLA-DRB6	Monocytes, Cerebellar Hemisphere, Blood	Zeller 2010, GTEx
	NOTCH4	Adipose	Grundberg 2012
	PSMB9	Lymphoblasts	Grundberg 2012
	SNORD48	Transformed Fibroblasts	GTEx
	XXbac-BPG254F23.6	EBV-transformed Lymphocytes, Blood	GTEx
	XXbac-BPG300A18.13	EBV-transformed Lymphocytes, Blood	GTEx
	TAPBP	Frontal Cortex	Ramasamy 2014
	TAP2	Monocytes, Lymphoblasts	Zeller 2010, Ramasamy 2014
	TNXB, ATF6B, TNXA	Occipital Cortex	Ramasamy 2014
TREM2	no eQTLs found		
CD2AP	*CD2AP*	Transformed Fibroblasts, Cerebellar Hemisphere, Cerebellum	GTEx
	RP11-385F7.1		GTEx
NYAP1	*AGFG2*	Cerebellum	GTEx
	AP4M1	Monocytes	Fairfax 2012
	CNPY4	B-cell	Fairfax 2012
	C7orf43	Blood	Jansen 2017
	EPHB4	Blood	Jansen 2017
	GAL3ST4	Blood	Jansen 2017
	GATS	Monocytes, Lymphoblasts	Zeller 2010, Grundberg 2012

	GIGYF1	Transformed Fibroblasts	GTEx
	PILRA	Blood, Transformed Fibroblasts	Jansen 2017, GTEx
	PILRB	Blood, Lymphoblasts, B-cell, Adipose	Jansen 2017, Zeller 2010, Grundberg 2012, Fairfax 2012
	PMS2P1	Transformed Fibroblasts	GTEx
	PVIRG	Blood, B-cell	Jansen 2017, Fairfax 2012
	STAG3L5P-PVRIG2P-PILRB	Blood	GTEx
	TRIM4	Blood, Monocytes	Jansen 2017, Zeller 2010
	ZKSCAN1	Blood	Jansen 2017
EPHA1	*EPHA1-AS1*	Blood	GTEx
	FAM115D	Blood	GTEx
PTK2B	*PTK2B*	Monocytes	Zeller 2010
	TASR60	Blood	GTEx
	PTK2B	Monocytes	Fairfax 2012
	SCARA3	Skin	Grundberg 2012
CLU	no eQTLs found		
ECHDC3	no eQTLs found		
SPI1	*C11orf49*	Temporal Cortex	Ramasamy 2014
	C1QTNF4	Adipose, EBV-transformed Lymphocytes, Transformed Fibroblasts, Blood	Grundberg 2012, GTEx
	CELF1	Liver	Grundberg 2012
	CELF1, CUGBP1	Thalamus	Ramasamy 2014
	FAM180B	Cerebellum	GTEx
	FNBP4	Transformed Fibroblasts	GTEx
	MADD	Blood	Jansen 2017
	MDK	Cerebral Cortex	Ramasamy 2014
	MTCH2	Blood, Cerebral Cortex, Skin, Cortex, Nucleus Accumbens Basal Ganglia	Jansen 2017, Ramasamy 2014, Grundberg 2012, GTEx
	MYBPC3	Blood, Monocytes	Jansen 2017, Zeller 2010
	NR1H3	Blood, Monocytes	Grundberg 2012, Zeller 2010
	NUP160	Cerebral Cortex, Temporal Cortex	Ramasamy 2014
	PSMC3	Transformed Fibroblasts	GTEx
	PTPMT1	Monocytes	Fairfax 2012
	RP11-750H9.5	Cerebellar Hemisphere	GTEx
	SLC39A13	Frontal Cortex, Temporal Cortex	Ramasamy 2014

	SPI1	Lymphoblasts, Monocytes	Grundberg 2012, Zeller 2010
MS4A2	*ARFGAP2*	Temporal Cortex	Ramasamy 2014
	C11orf49	Thalamus	Ramasamy 2014
	MS4A4A	Blood, Monocytes	Jansen 2017, Zeller 2010, Fairfax 2012
	MS4A6A	Blood	GTEx
PICALM	*SYTL2*	Lymphoblasts	Grundberg 2012
SORL1	no eQTLs found		
FERMT2	*GNG2*	Blood	Jansen 2017
	STYX	Blood, Transformed Fibroblasts	Jansen 2017, GTEx
SLC24A4	*SLC24A4*	Blood, Monocytes	Jansen 2017, Zeller 2010
	RIN3	Transformed Fibroblasts	GTEx
ADAM10	*ADAM10*	Blood	Jansen 2017
	FAM63B	Blood	Jansen 2017, GTEx
IQCK	*AC002550.5*	Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hypothalamus, Nucleaus accumbens Basal Ganglia, Putamen Basal Ganglia, EBV-transformed Lymphocytes, Blood	GTEx
	C16orf88	Blood, Lymphoblasts	Jansen 2017, Grundberg 2012
	CTD-2380F24.1	Caudate Basal Ganglia, Cerebellum, Cortex, Hypothalamus, Nucleus Accumbens Basal Ganglia	GTEx
	DEF8	Monocytes	Zeller 2010
	GPRC5B	Lymphoblasts	Fairfax 2012
	IQCK	Cerebral Cortex, Nucleus Accumbens Basal Ganglia	Ramasamy 2012, Grundberg 2012, GTEx
	KNOP1	Anterior Cingulate Cortex, Caudate Basal Ganglia, Cerebellar Hemisphere, Cerebellum, Cortex, Frontal Cortex, Hippocampus, Hypothalamus, Nucleaus accumbens Basal Ganglia, Putamen Basal Ganglia, EBV-transformed Lymphocytes, Transformed Fibroblasts, Blood	GTEx
ACE	no eQTLs found		
ABCA7	*CNN2*	Blood	Jansen 2017
	HMHA1	Cerebellar Hemisphere, Transformed Fibroblasts	GTEx
	POLR2E	Monocytes, Temporal Cortex, Cerebellar Hemisphere	Fairfax 2012, Ramasamy 2014
CASS4	*CASS4*	Transformed Fibroblasts	GTEx

	CSTF1	Transformed Fibroblasts	GTEx
	FAM209B	Blood	GTEx
	RPL39P	Transformed Fibroblasts, Blood	GTEx
ADAMTS1	*ADAMTS1*	Blood	Jansen 2017

Supplementary Table 10 (see Excel Sheet). Complete list of eQTL's identified in search of databases.

Supplementary Table 11 (see Excel Sheet). Complete list of eQTL's identified in INFERNO analysis of GTEx.

Supplementary Table 12. Results of ALZbase and Barres Human RNA-Seq databases search for differentially expressed genes in AD for the genome-wide significant loci.
Summary results for eQTL search are also presented in the 'Brain-related eQTL and non-Brain eQTL columns.

Supplementary Table 13. Top results of MAGMA pathway analysis for common and rare variant subsets.

Pathway	N genes in pathway in dataset	Common SNVs *P**	Common SNVs q-value	Rare SNVs *P**	Rare SNVs q-value	Pathway description
GO:65005	20	1.45E-07*	9.53E-04	6.76E-02	8.42E-01	protein-lipid complex assembly
GO:1902003	10	4.56E-07*	1.49E-03	4.94E-02	8.42E-01	regulation of beta-amyloid formation
GO:32994	39	1.16E-06*	2.54E-03	1.78E-02	8.17E-01	protein-lipid complex
GO:1902991	12	3.54E-06*	5.80E-03	5.66E-02	8.42E-01	regulation of amyloid precursor protein catabolic process

GO:43691	17	5.55E-06*	6.75E-03	3.08E-02	8.17E-01	reverse cholesterol transport
GO:71825	35	6.18E-06*	6.75E-03	1.27E-01	8.42E-01	protein-lipid complex subunit organization
GO:34377	18	1.64E-05*	1.53E-02	1.82E-01	8.42E-01	plasma lipoprotein particle assembly
GO:48156	10	3.19E-05*	2.61E-02	7.77E-01	8.54E-01	tau protein binding
GO:2253	382	6.32E-05*	4.60E-02	2.09E-01	8.42E-01	activation of immune response
MGI:9940	36	6.68E-02	4.56E-01	7.36E-05	5.45E-01	abnormal_hippocampus_pyramidal_cell_morphology
GO:2764	367	7.93E-05	5.19E-02	2.03E-01	8.42E-01	immune response-regulating signaling pathway
GO:50	11	7.53E-01	5.61E-01	1.15E-04	5.45E-01	urea cycle
GO:1990777	37	1.53E-04	8.35E-02	3.10E-02	8.17E-01	lipoprotein particle
GO:34358	37	1.53E-04	8.35E-02	3.10E-02	8.17E-01	plasma lipoprotein particle
GO:71827	33	1.82E-04	9.17E-02	2.50E-01	8.42E-01	plasma lipoprotein particle organization
MGI:8284	44	1.84E-01	4.99E-01	1.86E-04	5.68E-01	abnormal_hippocampus_pyramidal_cell_layer
GO:43205	14	6.59E-01	5.52E-01	2.98E-04	5.68E-01	fibril
GO:1527	10	9.43E-01	5.87E-01	3.18E-04	5.68E-01	microfibril
BIOCARTA:62	18	3.76E-04	1.58E-01	1.28E-01	8.42E-01	BIOCARTA_NDKDYNAMIN_PATHWAY
GO:42605	21	3.84E-04	1.58E-01	5.75E-01	8.48E-01	peptide antigen binding
GO:42987	10	3.86E-04	1.58E-01	7.59E-02	8.42E-01	amyloid precursor protein catabolic process
GO:70016	13	5.65E-01	5.38E-01	4.02E-04	5.68E-01	armadillo repeat domain binding
GO:2768	285	4.62E-04	1.78E-01	8.59E-02	8.42E-01	immune response-regulating cell surface receptor signaling pathway
MGI:1727	38	5.95E-01	5.44E-01	4.72E-04	5.68E-01	abnormal_embryo_implantation
GO:19627	12	5.44E-01	5.37E-01	5.17E-04	5.68E-01	urea metabolic process
GO:32460	12	5.23E-04	1.88E-01	6.29E-02	8.42E-01	negative regulation of protein oligomerization
GO:43407	69	5.56E-04	1.88E-01	6.48E-01	8.50E-01	negative regulation of MAP kinase activity
GO:48259	70	5.74E-04	1.88E-01	6.12E-01	8.48E-01	regulation of receptor-mediated endocytosis
GO:18298	10	6.30E-04	1.95E-01	1.89E-01	8.42E-01	protein-chromophore linkage
REACTOME:248	11	3.27E-02	4.11E-01	6.60E-04	5.68E-01	REACT:CONDENSATION_OF_PROMETAPHASE_CHROMOSOMES
MGI:8474	20	4.47E-01	5.23E-01	6.62E-04	5.68E-01	absent_spleen_germinal_center
GO:16722	15	4.38E-01	5.22E-01	6.70E-04	5.68E-01	oxidoreductase activity, oxidizing metal ions
GO:6959	141	6.76E-04	1.95E-01	4.00E-02	8.42E-01	humoral immune response
GO:2757	335	6.85E-04	1.95E-01	2.14E-01	8.42E-01	immune response-activating signal transduction
GO:34364	25	7.26E-04	1.97E-01	1.05E-01	8.42E-01	high-density lipoprotein particle
GO:2455	35	7.52E-04	1.97E-01	1.38E-02	7.91E-01	humoral immune response mediated by circulating immunoglobulin
PAN-PW:4396	10	3.05E-01	5.14E-01	7.78E-04	5.68E-01	Vitamin_D_metabolism_and_pathway
GO:46209	17	1.31E-01	4.81E-01	8.31E-04	5.68E-01	nitric oxide metabolic process
MGI:188	326	8.40E-04	2.12E-01	6.34E-01	8.48E-01	abnormal_circulating_glucose_level
GO:30669	46	8.81E-04	2.14E-01	4.63E-01	8.48E-01	clathrin-coated endocytic vesicle membrane
GO:45334	61	9.68E-04	2.26E-01	4.08E-01	8.48E-01	clathrin-coated endocytic vesicle
REACTOME:1132	172	7.42E-01	5.60E-01	9.87E-04	5.68E-01	REACT:SIGNALING_BY_PDGF
MGI:8227	12	6.84E-01	5.56E-01	9.94E-04	5.68E-01	absent_anterior_commissure

*Significant after FDR-correction (q-value≤0.05)

Supplementary Table 14 (see Excel Sheet). MAGMA genome-wide pathway analysis results using all genes, excluding APOE region genes, and excluding APOE region genes and genome-wide significant genes. Results highlighted in red are pathways that are significant after FDR-correction in the 'all genes' analysis.

Supplementary Table 15 (see Excel Sheet). Gene-wide results for all significant pathway (q<0.05) in the MAGMA genome-wide pathway analysis.

Supplementary Table 16. Complete results of the Aβ-centered biological network pathway analysis using curated set of 335 genes from Campion et al[8].

Category	Subcategory	N Genes	Common SNVs *P* 0kb	Common SNVs *P* 35kb-10kb	Rare SNVs *P* 0kb	Rare SNVs *P* 35kb-10kb
Aβ -centered biological network (all genes)	--	331	2.27E-04*	1.54E-04*	8.26E-01	5.19E-01

Clearance and degradation of Aβ	--	74	2.18E-04*	3.27E-03	3.13E-01	5.11E-01
Clearance and degradation of Aβ	Microglia	47	2.24E-04*	1.83E-02	2.49E-01	6.87E-01
Aggregation of Aβ	--	35	7.09E-04*	9.93E-03	9.02E-02	1.68E-01
Aggregation of Aβ	Miscellaneous	21	1.08E-03*	3.38E-02	9.53E-02	1.90E-01
APP processing and trafficking	Clathrin/caveolin-dependent endocytosis	10	1.19E-03	1.15E-02	3.64E-01	1.84E-01
Mediator of Aβ toxicity	--	51	3.82E-02	4.69E-02	5.89E-01	5.70E-01
Mediator of Aβ toxicity	Calcium homeostasis	6	6.90E-02	1.21E-01	3.96E-01	2.54E-01
Mediator of Aβ toxicity	Miscellaneous	3	7.61E-02	2.35E-02	9.79E-01	7.61E-01
Clearance and degradation of Aβ	Enzymatic degradation of Aβ	15	7.77E-02	2.63E-02	6.10E-01	2.95E-01
Mediator of Aβ toxicity	Tau toxicity	20	9.03E-02	3.48E-01	7.17E-01	6.85E-01
Aggregation of Aβ	Chaperone	9	1.52E-01	3.09E-01	1.98E-01	1.13E-02
Aggregation of Aβ	Heparan sulfate proteoglycan	5	1.65E-01	2.41E-02	6.04E-01	9.86E-01
APP processing and trafficking	Cholesterol metabolism	8	2.03E-01	4.49E-01	7.26E-01	3.06E-01
Clearance and degradation of Aβ	ERAD/proteasome	1	2.05E-01	2.09E-01	8.02E-01	6.06E-01
APP processing and trafficking	Internalization of APP	16	2.38E-01	7.17E-02	3.31E-01	8.47E-01
APP processing and trafficking	Early secretory pathway	10	2.52E-01	2.74E-01	4.26E-01	7.14E-01
Mediator of Aβ toxicity	Synaptic toxicity	19	3.37E-01	2.51E-01	2.80E-01	3.94E-01
APP processing and trafficking	β-secretase cleavage	27	3.39E-01	2.16E-01	6.71E-01	3.72E-01
APP processing and trafficking	Miscellaneous	12	3.75E-01	3.81E-01	9.91E-01	9.72E-01
Clearance and degradation of Aβ	Miscellaneous	1	3.78E-01	1.68E-01	N/A	8.98E-01
APP processing and trafficking	Aβ-cleavage (other)	2	3.94E-01	6.27E-01	5.76E-02	2.43E-01
Clearance and degradation of Aβ	Blood brain barrier	8	4.08E-01	3.95E-01	3.16E-01	2.45E-01
APP processing and trafficking	--	170	4.80E-01	1.38E-01	9.72E-01	6.42E-01
Mediator of Aβ toxicity	Tau toxicity	1	5.16E-01	5.73E-01	1.35E-01	1.66E-01
APP processing and trafficking	Axonal transport	4	6.22E-01	1.86E-01	9.00E-01	8.00E-01
APP processing and trafficking	Endosomes/retromer	26	6.44E-01	7.41E-01	4.95E-01	3.00E-01
APP processing and trafficking	α-secretase cleavage	12	6.73E-01	6.00E-01	8.08E-01	5.39E-01
Clearance and degradation of Aβ	Autophagy	2	8.32E-01	8.13E-01	4.35E-01	4.24E-01
APP processing and trafficking	Endoplasmic reticulum	4	8.39E-01	6.58E-01	7.89E-01	6.53E-01
APP processing and trafficking	ERAD/proteasome	5	8.96E-01	5.93E-01	7.46E-01	4.88E-01
Mediator of Aβ toxicity	Mitochondrial toxicity	2	9.37E-01	1.47E-01	5.42E-01	6.06E-01
APP processing and trafficking	γ-secretase cleavage	34	9.61E-01	7.15E-01	9.20E-01	4.65E-01

[†]Significant after Bonferroni correction for 32 pathway sets tested.

Supplementary Table 17 (see Excel sheet). Aβ-centered biological network pathway testing genes nominally significant only in: 1) common-only SNV testing, 2) rare-only SNV testing, and 3) both common-only and rare-only SNV testing.

Supplementary Table 18 (see Excel Sheet). STRINGdb analysis of genes in genome-wide significant loci using the prioritized list of 68 genes in the genome-wide loci.

Supplementary Table 19 (see Excel Sheet). Results of Jensen diseases, Jensen tissues and Archs4 tissues analysis using Enrichr.

Supplementary Table 20. Full description of stage 2 datasets by center

Country	Center	Consortium	AD Cases				Controls		
			N	% Women	Mean Age (s.d.)	Mean AAO (s.d)	N	% Women	Mean AAE (s.d.)
Belgium	Antwerp	EADI	878	66.1	78.8 (8.2)	75.4 (8.5)	661	59.5	65.7 (14.3)
Finland	Kuopio	EADI	422	68.0	71.4 (6.9)	71.4 (6.9)	562	59.3	69.1 (6.2)
Germany	Bonn 1	GERAD	530	61.7	73.3 (8.6)	73.3 (8.6)	1,096	52.4	64.8 (10.9)
Germany	Bonn 2	GERAD	7	57.1	76.0 (8.7)	70.0 (3.9)	490	67.6	79.6 (3.2)
Germany	Essen	GERAD	150	65.3	81.5 (6.6)	76.0 (6.9)	262	60.3	76.2 (6.0)
Germany	Munich	GERAD	285	67.4	73.4 (8.7)	70.7 (8.7)	530	37.7	66.6 (3.4)
Greece	Thessaloniki	GERAD	256	63.3	73.1 (7.9)	69.2 (8.0)	220	34.1	49.3 (16.4)
Hungary	Budapest	ADGC	125	68.0	78.9 (7.3)	74.9 (6.8)	100	69.0	74.4 (6.5)
Italy	Cagliari	EADI	130	73.1	77.3 (6.8)	74.9 (6.5)	110	55.5	65.7 (7.8)
Italy	Florence	EADI	441	60.1	70.7 (8.4)	67.1 (8.5)	77	54.5	64.0 (13.1)
Italy	Milan	EADI	314	67.5	78.1 (7.6)	73.3 (7.5)	165	60.6	69.8 (11.1)
Italy	Perugia	EADI	124	73.4	78.8 (6.8)	-	79	51.9	74.4 (6.2)
Italy	Pisa	EADI	27	77.8	74.1 (8.7)	72.1 (8.7)	10	70.0	52.6 (22.2)
Italy	Rome	EADI	388	70.9	75.7 (7.5)	73.1 (7.8)	42	61.9	68.6 (6.5)
Italy	San Giovanni Rotonda	EADI	139	64.7	78.8 (6.9)	78.5 (7.4)	80	33.8	76.3 (7.0)
Italy	Tronia	EADI	166	60.8	77.6 (8.0)	71.7 (8.3)	157	61.8	72.1 (8.3)
Spain	Barcelona 1	CHARGE	475	73.7	80.2 (6.7)	78.9 (6.7)	478	64.6	63.3 (9.4)
Spain	Barcelona 2	EADI	280	71.4	77.1 (5.4)	77.1 (5.4)	200	20.0	75.5 (5.2)
Spain	Las Palmas de Gran Canaria	EADI	255	68.2	80.9 (6.8)	75.8 (7.0)	294	36.4	70.1 (5.9)
Spain	Madrid	EADI	92	60.9	70.1 (9.6)	68.4 (9.9)	153	61.4	67.7 (14.4)
Spain	Oviedo	EADI	242	62.8	81.1 (7.1)	78.1 (6.8)	169	66.3	73.3 (8.2)
Spain	Pamplone	GERAD	421	59.4	74.9 (9.2)	69.2 (9.2)	338	59.8	67.1 (10.9)
Spain	Santander	EADI	356	63.2	76.6 (6.9)	73.7 (7.0)	289	68.5	80.9 (7.5)
Sweden	Stockholm	EADI	514	61.3	69.6 (9.3)	87.0 (5.6)	1,272	62.8	69.8 (8.9)
Sweden	Uppsala	EADI	283	62.5	76.5 (8.0)	76.5 (8.0)	234	62.8	74.8 (6.3)
UK	Belfast	GERAD	178	68.5	76.8 (7.3)	72.7 (6.6)	186	69.9	74.1 (9.0)
UK	Bristol	GERAD	12	58.3	82.1 (9.6)	69.4 (10.7)	7	42.9	78.6 (8.4)
UK	Caerphilly	GERAD	30	0.0	74.3 (4.1)	-	519	0.0	72.1 (4.0)
UK	Southampton	GERAD	107	66.4	83.8 (7.3)	78.6 (7.8)	79	55.7	74.0 (7.9)
UK	Nottingham	GERAD	163	50.3	76.3 (9.4)	72.9 (8.7)	275	48.7	76.7 (6.7)
USA	Jacksonville	GERAD	572	61.9	83.5 (7.6)	83.5 (7.6)	1,340	54.0	79.3 (6.8)

Supplementary Table 21. Variants selected for genotyping in replication Stage 3A.

Chr:Position[b]	rsID	Imputation quality score	VEP Consequence*	Closest gene(s)[c]	MAF[d]
5:88223420	rs190982	0.89	intron variant	*MEF2C*	0.390
7:37844263	rs4723711	0.99	intron variant	*NME8*	0.355
10:11720308	rs7920721	0.85	upstream gene variant	*ECHDC3*	0.389
12:43967677	rs7295246	0.97	upstream gene variant	*ADAMTS20*	0.414
15:59045774	rs593742	0.98	upstream gene variant	*ADAM10*	0.295
16:19808163	rs7185636	0.99	intron variant	*IQCK*	0.180
17:61543566	rs189894386	0.782	intergenic variant	*TANC2,ACE,CYB561*	0.018
21:28156856	rs2830500	0.96	intergenic variant	*ADAMTS1*	0.308

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