

Table 1 | Summary of discovery Stage 1, Stage 2 and overall meta-analyses results for identified loci reaching genome-wide significance after Stages 1 and 2

Variant ^a	Chr.	Position ^b	Closest gene ^c	Major/minor alleles	MAF ^d	OR	95% CI ^e	P	OR	95% CI ^e	P	OR	95% CI ^e	Meta P	I ² (%), P ^f
Previous genome-wide-significant loci still reaching significance															
rs48444610	1	207802552	CR1	C/A	0.187	1.16	1.12-1.20	8.2 × 10 ⁻¹⁶	1.20	1.13-1.27	3.8 × 10 ⁻¹⁰	1.17	1.13-1.21	3.6 × 10 ⁻²⁴	0, 8 × 10 ⁻¹
rs6733839	2	127892810	BIN1	C/T	0.407	1.18	1.15-1.22	4.0 × 10 ⁻²⁸	1.23	1.18-1.29	2.0 × 10 ⁻¹⁸	1.20	1.17-1.23	2.1 × 10 ⁻⁴⁴	15, 2 × 10 ⁻¹
rs10933431	2	233981912	INPP5D	C/G	0.223	0.90	0.87-0.94	2.6 × 10 ⁻⁷	0.92	0.87-0.97	3.2 × 10 ⁻³	0.91	0.88-0.94	3.4 × 10 ⁻⁹	0, 8 × 10 ⁻¹
rs9271058	6	32575406	HLA-DRB1	T/A	0.270	1.10	1.06-1.14	5.1 × 10 ⁻⁸	1.11	1.06-1.17	5.7 × 10 ⁻⁵	1.10	1.07-1.13	1.4 × 10 ⁻¹¹	10, 3 × 10 ⁻¹
rs75932628	6	41129252	TREM2	C/T	0.008	2.01	1.65-2.44	2.9 × 10 ⁻¹²	2.50	1.56-4.00	1.5 × 10 ⁻⁴	2.08	1.73-2.49	2.7 × 10 ⁻¹⁵	0, 6 × 10 ⁻¹
rs9473117	6	47431284	CD2AP	A/C	0.280	1.09	1.05-1.12	2.3 × 10 ⁻⁷	1.11	1.05-1.16	1.0 × 10 ⁻⁴	1.09	1.06-1.12	1.2 × 10 ⁻¹⁰	0, 6 × 10 ⁻¹
rs12539172	7	100091795	NYAP1 ^g	C/T	0.303	0.93	0.91-0.96	2.1 × 10 ⁻⁵	0.89	0.84-0.93	2.1 × 10 ⁻⁶	0.92	0.90-0.95	9.3 × 10 ⁻¹⁰	0, 8 × 10 ⁻¹
rs10808026	7	143099133	EPHA1	C/A	0.199	0.90	0.87-0.94	3.1 × 10 ⁻⁸	0.91	0.86-0.96	1.1 × 10 ⁻³	0.90	0.88-0.93	1.3 × 10 ⁻¹⁰	0, 5 × 10 ⁻¹
rs73223431	8	27219987	PTK2B	C/T	0.367	1.10	1.07-1.13	8.3 × 10 ⁻¹⁰	1.11	1.06-1.16	1.5 × 10 ⁻⁵	1.10	1.07-1.13	6.3 × 10 ⁻¹⁴	0, 6 × 10 ⁻¹
rs9331896	8	27467686	CLU	T/C	0.387	0.88	0.85-0.91	3.6 × 10 ⁻¹⁶	0.87	0.83-0.91	1.7 × 10 ⁻⁹	0.88	0.85-0.90	4.6 × 10 ⁻²⁴	3, 4 × 10 ⁻¹
rs3740688	11	47380340	SP1 ^h	T/G	0.448	0.91	0.89-0.94	9.7 × 10 ⁻¹¹	0.93	0.88-0.97	1.2 × 10 ⁻³	0.92	0.89-0.94	5.4 × 10 ⁻¹³	4, 4 × 10 ⁻¹
rs7933202	11	59936926	MS4A2	A/C	0.391	0.89	0.86-0.92	2.2 × 10 ⁻¹⁵	0.90	0.86-0.95	1.6 × 10 ⁻⁵	0.89	0.87-0.92	1.9 × 10 ⁻¹⁹	27, 5 × 10 ⁻²
rs3851179	11	85868640	PICALM	C/T	0.356	0.89	0.86-0.91	5.8 × 10 ⁻¹⁶	0.85	0.81-0.89	6.1 × 10 ⁻¹¹	0.88	0.86-0.90	6.0 × 10 ⁻²⁵	0, 8 × 10 ⁻¹
rs11218343	11	121435587	SORL1	T/C	0.040	0.81	0.76-0.88	2.7 × 10 ⁻⁸	0.77	0.68-0.87	1.8 × 10 ⁻⁵	0.80	0.75-0.85	2.9 × 10 ⁻¹²	7, 3 × 10 ⁻¹
rs17125924	14	53391680	FERMT2	A/G	0.093	1.13	1.08-1.19	6.6 × 10 ⁻⁷	1.15	1.06-1.25	5.0 × 10 ⁻⁴	1.14	1.09-1.18	1.4 × 10 ⁻⁹	8, 3 × 10 ⁻¹
rs12881735	14	92932828	SLC24A4	T/C	0.221	0.92	0.88-0.95	4.9 × 10 ⁻⁷	0.92	0.87-0.97	4.3 × 10 ⁻³	0.92	0.89-0.94	7.4 × 10 ⁻⁹	0, 6 × 10 ⁻¹
rs3752246	19	1056492	ABCA7	C/G	0.182	1.13	1.09-1.18	6.6 × 10 ⁻¹⁰	1.18	1.11-1.25	4.7 × 10 ⁻⁸	1.15	1.11-1.18	3.1 × 10 ⁻¹⁶	0, 5 × 10 ⁻¹
rs429358	19	45411941	APOE	T/C	0.216	3.32	3.20-3.45	1.2 × 10 ⁻⁸⁸ⁱ	APOE region not carried forward to replication stage						
rs6024870	20	54997568	CASS4	G/A	0.088	0.88	0.84-0.93	1.1 × 10 ⁻⁶	0.90	0.82-0.97	9.0 × 10 ⁻³	0.88	0.85-0.92	3.5 × 10 ⁻⁸	0, 9 × 10 ⁻¹
New genome-wide-significant loci reaching significance															
rs7920721	10	11720308	ECHDC3	A/G	0.389	1.08	1.05-1.11	1.9 × 10 ⁻⁷	1.07	1.02-1.12	3.2 × 10 ⁻³	1.08	1.05-1.11	2.3 × 10 ⁻⁹	0, 8 × 10 ⁻¹
rs138190086	17	61538148	ACE	G/A	0.020	1.29	1.15-1.44	7.5 × 10 ⁻⁶	1.41	1.18-1.69	1.8 × 10 ⁻⁴	1.32	1.20-1.45	7.5 × 10 ⁻⁹	0, 9 × 10 ⁻¹
Previous genome-wide-significant loci not reaching significance															
rs190982	5	88223420	MEF2C	A/G	0.390	0.95	0.92-0.97	2.8 × 10 ⁻⁴	0.93	0.89-0.98	2.7 × 10 ⁻³	0.94	0.92-0.97	2.8 × 10 ⁻⁶	0, 6 × 10 ⁻¹
rs4723711	7	37844263	NME8	A/T	0.356	0.95	0.92-0.98	2.7 × 10 ⁻⁴	0.91	0.87-0.95	1.0 × 10 ⁻⁴	0.94	0.91-0.96	2.8 × 10 ⁻⁷	0, 5 × 10 ⁻¹

^aVariants showing the best level of association after meta-analysis of Stages 1 and 2. ^bBuild 37, assembly hg19. ^cBased on position of top SNP in reference to the RefSeq assembly. ^dAverage in the discovery sample. ^eCalculated with respect to the minor allele. ^fCochran's Q test. ^gPreviously the ZCWPW1 locus. ^hPreviously the CELF1 locus. ⁱChr., chromosome; CI, confidence interval; OR, odds ratio; I², heterogeneity estimate.

Table 2 | Summary of discovery Stage 1, Stage 2, Stage 3 (A and B), and overall meta-analysis results of potential novel loci

Stage 3A					Stage 1 + 2 (n = 82,771)			Stage 3A (n = 11,666)			Overall (n = 94,437)			
SNP ^a	Chr.	Position ^b	Closest gene ^c	Major/ minor allele	MAF ^e	OR	95% CI ^f	P	OR	95% CI ^f	P	OR	95% CI ^f	Meta P
rs4735340	8	95976251	NDUFAF6	T/A	0.476	0.94	0.92–0.96	3.4 × 10 ^{−7}	0.92	0.83–1.02	9.7 × 10 ^{−2}	0.94	0.92–0.96	9.2 × 10 ^{−8}
rs7920721 ^g	10	11720308	ECHDC3	A/G	0.390	1.08	1.05–1.11	2.3 × 10 ^{−9}	1.11	1.04–1.18	1.5 × 10 ^{−3}	1.08	1.06–1.11	1.8 × 10 ^{−11}
rs7295246	12	43967677	ADAMTS20	T/G	0.413	1.07	1.04–1.09	2.7 × 10 ^{−7}	1.02	0.96–1.09	4.5 × 10 ^{−1}	1.06	1.04–1.08	3.9 × 10 ^{−7}
rs10467994	15	51008687	SPPL2A	T/C	0.333	0.94	0.91–0.96	3.9 × 10 ^{−7}	0.97	0.87–1.08	6.2 × 10 ^{−1}	0.94	0.92–0.96	4.3 × 10 ^{−7}
rs593742	15	59045774	ADAM10	A/G	0.295	0.93	0.91–0.96	1.3 × 10 ^{−7}	0.91	0.85–0.98	1.5 × 10 ^{−2}	0.93	0.91–0.95	6.8 × 10 ^{−9}
rs7185636	16	19808163	IQCK	T/C	0.180	0.92	0.89–0.95	8.4 × 10 ^{−8}	0.94	0.86–1.01	1.1 × 10 ^{−1}	0.92	0.89–0.95	2.4 × 10 ^{−8}
rs2632516	17	56409089	MIR142/TSPDAP1-AS1 ^d	G/C	0.440	0.94	0.92–0.96	2.3 × 10 ^{−7}	0.91	0.82–1.01	7.5 × 10 ^{−2}	0.94	0.91–0.96	5.3 × 10 ^{−8}
rs138190086	17	61538148	ACE	G/A	0.020	1.32	1.20–1.45	7.5 × 10 ^{−9}	1.17	0.92–1.48	2.1 × 10 ^{−1}	1.30	1.19–1.42	5.3 × 10 ^{−9}
rs2830500	21	28156856	ADAMTS1	C/A	0.308	0.93	0.91–0.96	7.4 × 10 ^{−8}	0.95	0.89–1.02	1.3 × 10 ^{−1}	0.93	0.91–0.96	2.6 × 10 ^{−8}
Stage 3B					Stage 1 (n = 63,926)			Stage 3B (n = 30,511) ^h			Overall (n = 94,437) ^h			
SNP ^a	Chr.	Position ^b	Closest gene ^c	Major/minor allele	MAF ^e	OR	95% CI ^f	P	OR	95% CI ^f	P	OR	95% CI ^f	Meta P
rs71618613	5	29005985	SUCLG2P4	A/C	0.010	0.68	0.57–0.80	9.8 × 10 ^{−6}	0.76	0.63–0.93	6.8 × 10 ^{−3}	0.71	0.63–0.81	3.3 × 10 ^{−7}
rs35868327	5	52665230	FST	T/A	0.013	0.69	0.59–0.80	7.8 × 10 ^{−7}	0.58	0.29–1.17	1.2 × 10 ^{−1}	0.68	0.59–0.79	2.6 × 10 ^{−7}
rs114812713	6	41034000	OARD1	G/C	0.030	1.35	1.24–1.47	4.5 × 10 ^{−12}	1.23	1.06–1.42	7.2 × 10 ^{−3}	1.32	1.22–1.42	2.1 × 10 ^{−13}
rs62039712	16	79355857	WWOX	G/A	0.116	1.17	1.10–1.23	1.2 × 10 ^{−7}	1.14	0.96–1.36	1.3 × 10 ^{−1}	1.16	1.10–1.23	3.7 × 10 ^{−8}