

Table 1. Strongest regional common variant (MAF≥0.01) association results in IGAP (Stage 1), their associations in EADB, and combined analysis of IGAP and EADB (Stage 2)

Variant RSID	Chr	Basepair (hg19)	Genomic Region	EFF	REF	Stage 1: IGAP			EADB			Stage 2: IGAP + EADB Meta-Analysis		
						EAF	OR (95% CI)	P	EAF	OR (95% CI)	P	EAF	OR (95% CI)	P
rs7259620	19	45407788	<i>APOE</i> Region*	A	G	0.4397	0.67 (0.65, 0.69)	2.25E-199	0.4197	0.64 (0.62, 0.66)	1.20E-210	0.4308	0.66 (0.64, 0.67)	1.15E-401
rs6733839	2	127892810	<i>BINI</i> *	T	C	0.3836	1.18 (1.15, 1.21)	2.36E-35	0.3991	1.21 (1.18, 1.25)	5.12E-40	0.3906	1.19 (1.17, 1.22)	3.06E-73
rs7110631	11	85856187	<i>PICALM</i> *	C	G	0.318	0.88 (0.86, 0.90)	1.42E-20	0.3065	0.88 (0.85, 0.91)	2.77E-16	0.3130	0.88 (0.86, 0.90)	3.33E-35
rs679515	1	207750568	<i>CR1</i> *	T	C	0.1976	1.15 (1.12, 1.19)	5.69E-19	0.2030	1.16 (1.12, 1.20)	4.49E-17	0.2000	1.16 (1.13, 1.18)	2.62E-34
rs1582763	11	60021948	<i>MS4A</i> Region*	A	G	0.383	0.89 (0.87, 0.92)	3.63E-18	0.3597	0.90 (0.87, 0.92)	1.52E-13	0.3729	0.89 (0.88, 0.91)	4.08E-30
rs867230	8	27468503	<i>CLU</i> *	C	A	0.4052	0.89 (0.87, 0.92)	1.34E-17	0.3875	0.90 (0.87, 0.92)	2.75E-13	0.3973	0.90 (0.88, 0.91)	3.23E-29
rs11218343	11	121435587	<i>SORL1</i> *	C	T	0.0424	0.80 (0.75, 0.85)	1.10E-11	0.0391	0.86 (0.80, 0.92)	4.53E-5	0.0409	0.83 (0.79, 0.87)	6.69E-15
rs1385742	6	47595155	<i>CD2AP</i> *	A	T	0.3626	1.09 (1.06, 1.12)	7.41E-11	0.3577	1.06 (1.03, 1.10)	7.27E-5	0.3605	1.08 (1.06, 1.10)	5.37E-14
rs12151021	19	1050874	<i>ABCA7</i> *	A	G	0.3289	1.10 (1.07, 1.13)	7.46E-11	0.3306	1.15 (1.12, 1.18)	8.98E-20	0.3297	1.12 (1.10, 1.14)	5.24E-28
rs7920721	10	11720308	<i>USP6NL/ ECHDC3</i> *	G	A	0.3837	1.09 (1.06, 1.11)	4.59E-10	0.3908	1.07 (1.03, 1.10)	1.90E-5	0.3869	1.08 (1.06, 1.10)	7.11E-14
rs9323877	14	92934269	<i>SLC24A4</i> *	G	A	0.2422	1.09 (1.06, 1.13)	1.01E-9	0.2531	1.07 (1.04, 1.11)	1.70E-5	0.2470	1.08 (1.06, 1.11)	1.28E-13
rs7928419	11	47392114	<i>SPII</i> *	G	A	0.3399	0.92 (0.90, 0.95)	1.74E-9	0.3330	0.95 (0.92, 0.98)	0.00143	0.3369	0.94 (0.92, 0.95)	3.52E-11
rs2526377	17	56410041	<i>BZRAP1-AS1 (TSPOAPI-AS1)</i>	G	A	0.4479	0.93 (0.90, 0.95)	5.90E-9	0.4465	0.94 (0.91, 0.96)	1.07E-5	0.4473	0.93 (0.91, 0.95)	3.87E-13
rs11168036	5	139707439	<i>HBEGF</i>	T	G	0.4915	1.07 (1.05, 1.10)	1.95E-8	0.4873	0.99 (0.96, 1.01)	0.331	0.4996	0.95 (0.94, 0.97)	8.96E-07
rs73223431	8	27219987	<i>PTK2B</i> *	T	C	0.3596	1.08 (1.05, 1.10)	2.31E-8	0.3682	1.07 (1.04, 1.11)	1.198E-6	0.3634	1.08 (1.06, 1.10)	1.44E-13
rs114285994	16	19935763	<i>IQCK</i> *	A	G	0.1406	0.90 (0.87, 0.94)	3.53E-8	0.1223	0.98 (0.94, 1.02)	0.353	0.133	0.93 (0.91, 0.96)	1.54E-6
rs12539172	7	100091795	<i>NYAP1</i> *	T	C	0.3135	0.93 (0.90, 0.95)	1.32E-7	0.3100	0.92 (0.89, 0.95)	5.243E-7	0.312	0.93 (0.91, 0.95)	3.594E-13
rs3135348	6	32394098	<i>HLA-DRB1/5</i> *	A	G	0.4248	1.07 (1.04, 1.10)	2.25E-7	NA	NA	NA	0.4248	1.07 (1.04, 1.10)	2.11E-7
rs10753507	1	21152380	<i>EIF4G3</i>	T	A	0.4038	0.93 (0.91, 0.96)	2.72E-7	0.4013	0.97 (0.94, 1.00)	0.0229	0.4027	0.95 (0.93, 0.97)	9.47E-8
rs11735125	4	66237551	<i>EPHA5</i>	G	C	0.0225	1.24 (1.14, 1.34)	3.68E-7	0.0243	1.00 (0.91, 1.09)	0.991	0.0233	1.12 (1.06, 1.19)	1.51E-4
rs17462136	20	54987216	<i>CASS4</i> *	C	G	0.0919	0.89 (0.85, 0.93)	3.92E-7	0.0800	0.83 (0.78, 0.87)	1.15E-12	0.0870	0.86 (0.83, 0.89)	2.91E-17
rs8107367	19	18564705	<i>ELL</i>	G	A	0.3337	1.07 (1.04, 1.10)	5.55E-7	0.3319	1.01 (0.98, 1.04)	0.483	0.3329	1.04 (1.02, 1.07)	2.15E-5
rs1943782	11	102357848	<i>LOC102723838</i>	A	G	0.0845	1.12 (1.07, 1.17)	7.39E-7	0.0860	1.02 (0.97, 1.08)	0.362	0.0851	1.08 (1.04, 1.12)	1.50E-5
rs140016620	16	70713787	<i>MTSSL1/IL34</i>	G	A	0.0653	1.14 (1.08, 1.19)	9.31E-7	0.0628	1.09 (1.03, 1.16)	0.00345	0.0642	1.12 (1.07, 1.16)	1.80E-8
rs56402156	7	143103481	<i>EPHA1</i> *	A	G	0.2002	0.93 (0.90, 0.95)	1.26E-6	0.1838	0.92 (0.89, 0.96)	9.71E-6	0.1932	0.92 (0.90, 0.95)	5.72E-11
rs1001158	4	11038456	<i>CLNK</i>	G	A	0.2825	1.07 (1.04, 1.10)	2.03E-6	0.2841	1.07 (1.04, 1.10)	2.63E-5	0.2832	1.07 (1.05, 1.09)	2.24E-10
rs10858815	12	89391846	<i>LOC728084/ LINC02458</i>	C	A	0.0411	0.85 (0.80, 0.91)	2.07E-6	0.0424	0.99 (0.92, 1.06)	0.766	0.0417	0.91 (0.87, 0.96)	2.28E-4
rs3896609	15	51057868	<i>SPPL2A</i> *	A	C	0.1855	0.92 (0.89, 0.95)	2.11E-6	0.1863	0.98 (0.94, 1.01)	0.181	0.1859	0.95 (0.92, 0.97)	1.02E-5
rs72985631	2	232829502	<i>DIS3L2/ INPP5D</i> *	A	G	0.0242	0.82 (0.76, 0.89)	3.01E-6	0.0211	0.98 (0.89, 1.08)	0.694	0.0229	0.88 (0.83, 0.94)	1.34E-5
rs12580654	12	52268547	<i>ANKRD33</i>	C	G	0.1061	1.10 (1.06, 1.15)	3.48E-6	0.1034	1.02 (0.98, 1.07)	0.352	0.1049	1.07 (1.03, 1.10)	4.56E-5
rs143867193	17	61503610	<i>TANC2/ACE</i> *	T	C	0.0163	1.27 (1.15, 1.40)	3.56E-6	0.0146	1.10 (0.98, 1.24)	0.0923	0.0156	1.19 (1.11, 1.29)	3.91E-6
rs6966331	7	37883793	<i>NME8</i> *	T	C	0.3523	0.94 (0.92, 0.97)	6.09E-6	0.3480	0.94 (0.91, 0.97)	2.88E-5	0.3504	0.94 (0.92, 0.96)	7.14E-10
rs11028038	11	24605495	<i>LUZP2</i>	C	T	0.2165	1.07 (1.04, 1.10)	7.29E-6	0.2143	0.97 (0.94, 1.00)	0.0828	0.2156	1.03 (1.00, 1.05)	0.0270
rs11236918	11	76448286	<i>GUCY2EP/ TSKU</i>	A	C	0.1122	1.09 (1.05, 1.13)	8.13E-6	0.1150	1.01 (0.96, 1.05)	0.78793	0.1134	1.05 (1.02, 1.09)	3.97E-4
rs9960448	18	57986377	<i>MC4R</i>	T	G	0.2904	0.94 (0.91, 0.97)	8.24E-6	0.2773	1.00 (0.97, 1.03)	0.9519	0.2848	0.96 (0.94, 0.98)	6.46E-4

Abbreviations: Chr, chromosome; EFF, Effect allele; REF, reference allele; EAF, effect allele frequency; OR, Odds ratio; CI, Confidence interval; *P*, P-value

Shaded box indicates genome-wide significance within analysis stage

* Loci with prior associations in IGAP [Lambert et al. (2013) or Kunkle et al. (2019)]

Table 2. Strongest common variant (MAF≥0.01) association results by genomic region in Stage 2 and Stage 3. Variants depicted had $P<10^{-5}$ in IGAP (Stage 1) analysis (n=3,345 variants) and had the strongest regional association in meta-analysis of IGAP+EADB (Stage 2). UKBB AD-proxy association results and meta-analysis of IGAP, EADB, and UKBB (Stage 3) are also shown.

Variant RSID	Chr	Basepair (hg19)	Genomic Region	EFF	REF	Stage 2: IGAP + EADB Meta-Analysis			UKB			Stage 3: IGAP + EADB + UKB Meta-Analysis		
						EAF	OR (95% CI)	P	EAF	OR (95% CI)	P	EAF	OR (95% CI)	P
rs112019714	19	45404857	<i>APOE</i> Region*	C	T	0.0384	2.51 (2.39, 2.63)	2.25E-306	0.0258	1.55 (1.48, 1.62)	2.97E-86	0.0332	1.92 (1.86, 1.99)	1.78E-344
rs6733839	2	127892810	<i>BIN1</i> *	T	C	0.3906	1.19 (1.17, 1.22)	3.06E-73	0.3893	1.07 (1.05, 1.09)	1.97E-16	0.3915	1.12 (1.11, 1.14)	4.66E-73
rs10792832	11	85867875	<i>PICALM</i> *	A	G	0.3621	0.88 (0.87, 0.90)	6.48E-36	0.3731	0.96 (0.94, 0.98)	2.25E-6	0.3675	0.93 (0.91, 0.94)	6.04E-32
rs679515	1	207750568	<i>CR1</i> *	T	C	0.2000	1.16 (1.13, 1.18)	2.62E-34	0.1754	1.05 (1.03, 1.07)	2.59E-6	0.1870	1.10 (1.08, 1.11)	2.19E-31
rs1582763	11	60021948	<i>MS4A</i> Region*	A	G	0.3729	0.89 (0.88, 0.91)	4.08E-30	0.3821	0.96 (0.94, 0.98)	2.25E-6	0.3773	0.93 (0.92, 0.94)	2.66E-28
rs867230	8	27468503	<i>CLU</i> *	C	A	0.3973	0.90 (0.88, 0.91)	3.23E-29	0.4135	0.96 (0.95, 0.98)	9.38E-6	0.4057	0.93 (0.92, 0.95)	1.43E-26
rs3752246	19	1056492	<i>ABCA7</i> *	G	C	0.1851	1.12 (1.10, 1.15)	2.55E-20	0.1762	1.02 (0.99, 1.04)	0.166	0.1802	1.06 (1.04, 1.08)	1.77E-12
rs17462136	20	54987216	<i>CASS4</i> *	C	G	0.0870	0.86 (0.83, 0.89)	2.91E-17	0.0875	0.96 (0.94, 0.99)	0.0118	0.087	0.92 (0.90, 0.94)	1.42E-13
rs9473123	6	47475339	<i>CD2AP</i> *	A	G	0.2699	1.08 (1.06, 1.11)	3.55E-14	0.2765	1.02 (1.00, 1.04)	0.0154	0.2741	1.05 (1.03, 1.06)	1.17E-11
rs7912495	10	11718713	<i>USP6NL/ECHDC3</i> *	G	A	0.4675	1.07 (1.05, 1.10)	5.81E-14	0.4533	1.03 (1.01, 1.05)	3.07E-4	0.4600	1.05 (1.04, 1.06)	2.18E-14
rs3993878	14	92931983	<i>SLC24A4</i> *	G	A	0.2562	1.09 (1.06, 1.11)	7.80E-14	0.2360	1.02 (1.00, 1.04)	0.0391	0.2452	1.05 (1.03, 1.06)	8.51E-11
rs73223431	8	27219987	<i>PTK2B</i> *	T	C	0.3634	1.08 (1.06, 1.10)	1.44E-13	0.3660	1.04 (1.02, 1.05)	2.67E-5	0.3657	1.05 (1.04, 1.07)	1.12E-15
rs117618017	15	63569902	<i>APH1B</i>	T	C	0.1400	1.12 (1.08, 1.15)	2.10E-13	0.1393	1.04 (1.02, 1.06)	8.79E-4	0.1401	1.07 (1.05, 1.09)	9.62E-13
rs2526378	17	56404349	<i>BZRAP1-AS1 (TSPOAP1-AS1)</i>	G	A	0.4526	0.93 (0.91, 0.95)	2.31E-13	0.4487	0.99 (0.97, 1.00)	0.158	0.4501	0.96 (0.95, 0.98)	4.86E-9
rs12539172	7	100091795	<i>NYAPI</i> *	T	C	0.3120	0.93 (0.91, 0.95)	3.59E-13	0.3264	0.96 (0.94, 0.97)	2.41E-7	0.3194	0.94 (0.93, 0.96)	5.87E-18
rs6586028	10	82253984	<i>TSPAN14</i>	C	T	0.2017	0.92 (0.90, 0.94)	2.33E-12	0.2055	0.97 (0.95, 0.99)	0.00215	0.2034	0.95 (0.93, 0.96)	5.74E-12
rs2830500	21	28156856	<i>ADAMTS1</i> *	A	C	0.3123	0.93 (0.91, 0.95)	3.41E-11	0.2924	0.99 (0.97, 1.01)	0.317	0.3009	0.97 (0.95, 0.98)	2.97E-7
rs75045569	7	143109208	<i>EPHA1</i> *	G	T	0.1625	0.92 (0.89, 0.94)	4.47E-11	0.1851	0.96 (0.94, 0.98)	3.32E-5	0.1753	0.94 (0.93, 0.96)	1.43E-13
rs9275313	6	32665759	<i>HLA-DRB1/5</i> *	T	G	0.0983	0.90 (0.87, 0.93)	5.37E-11	0.1047	0.94 (0.92, 0.97)	1.61E-5	0.1016	0.92 (0.91, 0.94)	5.48E-14
rs11039202	11	47382426	<i>SPI1</i> *	T	A	0.3255	0.94 (0.92, 0.95)	6.28E-11	0.3227	1.00 (0.98, 1.01)	0.5877	0.3238	0.97 (0.96, 0.98)	2.59E-6
rs2904297	4	11040290	<i>CLNK</i>	C	T	0.2846	1.07 (1.05, 1.09)	1.20E-10	0.2650	1.04 (1.02, 1.06)	3.44E-5	0.2742	1.05 (1.04, 1.07)	1.92E-13
rs3781831	11	121436004	<i>SORL1</i> *	A	G	0.0223	0.81 (0.76, 0.86)	1.66E-10	0.0209	0.96 (0.90, 1.01)	0.134	0.0215	0.89 (0.85, 0.93)	7.75E-8
rs9926151	16	19815411	<i>IQCK</i> *	A	G	0.1752	0.92 (0.90, 0.95)	3.34E-10	0.1725	1.00 (0.98, 1.02)	0.878	0.1736	0.97 (0.95, 0.98)	2.51E-5
rs6966331	7	37883793	<i>NME8</i> *	T	C	0.3504	0.94 (0.92, 0.96)	7.14E-10	0.3385	0.98 (0.97, 1.00)	0.0645	0.3434	0.96 (0.95, 0.98)	4.81E-8
rs34173062	8	145158607	<i>SHARPIN</i>	A	G	0.0857	1.13 (1.09, 1.18)	1.56E-9	0.0717	1.08 (1.04, 1.11)	5.96E-6	0.0777	1.10 (1.07, 1.13)	2.67E-13
rs11538963	16	70696272	<i>MTSS1L/IL34</i>	C	T	0.0890	1.11 (1.07, 1.14)	7.80E-9	--	--	--	0.0890	1.11 (1.07, 1.14)	7.80E-9
rs875121	19	50451508	<i>ATF5/SIGLEC11</i>	C	A	0.2438	1.07 (1.04, 1.09)	1.03E-8	0.2475	1.03 (1.01, 1.05)	0.00481	0.2464	1.04 (1.03, 1.06)	4.84E-9
rs185105129	17	61548353	<i>ACE</i> *	T	C	0.0141	1.28 (1.17, 1.39)	1.29E-8	0.0166	1.12 (1.05, 1.19)	2.58E-4	0.016	1.17 (1.12, 1.23)	2.96E-10
rs114812713	6	41034000	<i>UNC5CL/OARD1</i> *	C	G	0.0236	1.20 (1.12, 1.27)	1.85E-8	0.0267	1.06 (1.01, 1.11)	0.0274	0.0256	1.11 (1.07, 1.16)	1.57E-7
rs12407731	1	21254789	<i>EIF4G3</i>	T	C	0.4476	0.95 (0.94, 0.97)	4.72E-7	0.4371	0.98 (0.96, 1.00)	0.0148	0.4412	0.97 (0.96, 0.98)	2.58E-7
rs3131610	15	50800095	<i>USP50</i>	A	G	0.2540	0.95 (0.93, 0.97)	6.14E-7	0.2502	0.97 (0.96, 0.99)	0.00649	0.2514	0.96 (0.95, 0.98)	9.73E-8
rs7268	5	139712550	<i>HBEGF</i>	A	C	0.4530	1.05 (1.03, 1.07)	9.33E-7	0.4379	1.02 (1.00, 1.04)	0.0244	0.4447	1.03 (1.02, 1.04)	9.29E-7
rs10411009	19	18606266	<i>ELL</i>	G	A	0.3370	1.06 (1.04, 1.09)	4.20E-6	0.3519	1.00 (0.99, 1.02)	0.769	0.3476	1.02 (1.01, 1.03)	0.00595
rs62039712	16	79355857	<i>WWOX</i> *	A	G	0.1186	1.08 (1.05, 1.12)	4.68E-6	0.1215	1.01 (0.99, 1.04)	0.391	0.1205	1.04 (1.02, 1.06)	5.03E-4
rs12774458	10	7623127	<i>ITIH5</i>	G	A	0.3654	0.95 (0.93, 0.97)	7.53E-6	0.3446	1.00 (0.98, 1.02)	0.795	0.3525	0.98 (0.97, 1.00)	0.0113

Abbreviations: Chr, chromosome; EFF, Effect allele; REF, reference allele; EAF, effect allele frequency; OR, Odds ratio; CI, Confidence interval; P , P-value

Shaded box indicates genome-wide significance within analysis stage

* Loci with prior associations in IGAP [Lambert et al. (2013) or Kunkle et al. (2019)]

Table 3. All strongest rare variant (MAF<0.01) association results in IGAP (Stage 1) [no filtering on LD], their associations in EADB, and combined analysis of IGAP and EADB (Stage 2)

Variant RSID	Chr	Basepair (hg19)	Genomic Region	EFF	REF	Stage 1: IGAP			EADB			Stage 2: IGAP + EADB Meta-Analysis		
						EAF	OR (95% CI)	P	EAF	OR (95% CI)	P	EAF	OR (95% CI)	P
rs547509922	19	45331261	<i>APOE</i> Region (intergenic)	T	C	0.0048	2.80 (2.31, 3.40)	1.12E-25	0.0053	2.26 (1.83, 2.78)	2.01E-15	0.0051	2.54 (2.2, 2.92)	5.04E-38
rs559118614	19	45554058	<i>APOE</i> Region (<i>CLASRP</i>)	G	T	0.0094	2.04 (1.77, 2.35)	1.88E-22	0.0097	2.42 (2.06, 2.84)	5.64E-29	0.0095	2.2 (1.98, 2.44)	1.83E-47
rs75932628	6	41129252	<i>TREM2</i>	T	C	0.0043	2.45 (1.99, 3.02)	3.72E-17	0.0028	2.14 (1.58, 2.89)	2.97E-07	0.0038	2.34 (1.97, 2.78)	2.15E-22
rs187370608	6	40942196	<i>TREM2</i> (upstream)	A	G	0.0042	2.19 (1.78, 2.70)	2.34E-13	0.0029	2.10 (1.57, 2.81)	2.77E-07	0.0038	2.16 (1.82, 2.56)	8.70E-19
rs143202663	6	40865240	<i>TREM2</i> (upstream)	C	T	0.0040	2.11 (1.71, 2.61)	2.59E-12	0.0027	2.18 (1.63, 2.90)	4.41E-08	0.0036	2.14 (1.80, 2.53)	1.83E-18
rs145342536	6	40911888	<i>TREM2</i> (upstream)	A	T	0.0046	1.99 (1.64, 2.41)	4.13E-12	0.0029	2.07 (1.56, 2.75)	2.14E-07	0.0040	2.01 (1.71, 2.36)	1.14E-17
rs12664332	6	40904030	<i>TREM2</i> (upstream)	A	G	0.0045	1.95 (1.61, 2.37)	1.57E-11	0.0029	2.10 (1.58, 2.79)	1.31E-07	0.0040	2.00 (1.70, 2.34)	2.98E-17
rs112952132	19	45198060	<i>APOE</i> Region (intergenic)	T	C	0.0084	0.60 (0.52, 0.70)	7.41E-11	0.0085	0.74 (0.63, 0.87)	2.93E-4	0.0084	0.66 (0.59, 0.74)	5.40E-13
rs78905796	19	45132679	<i>APOE</i> Region (<i>IGSF23</i>)	A	G	0.0052	1.78 (1.48, 2.14)	1.01E-9	0.0049	1.79 (1.44, 2.23)	1.47E-7	0.005	1.78 (1.55, 2.05)	1.13E-15
rs540038005	15	61371352	<i>RORA</i>	T	C	0.00084	3.60 (2.27, 5.71)	5.40E-8	0.00087	0.80 (0.49, 1.31)	0.370	0.0009	1.79 (1.28, 2.51)	7.25E-4
rs551336410	15	61373788	<i>RORA</i>	T	C	0.00091	3.34 (2.14, 5.23)	1.29E-7	0.00090	0.77 (0.47, 1.26)	0.297	0.0009	1.71 (1.23, 2.38)	0.00141
rs192675224	6	40706366	<i>TREM2</i> (upstream)	A	G	0.0033	1.85 (1.46, 2.35)	3.15E-7	0.0023	1.70 (1.26, 2.29)	4.65E-4	0.0029	1.79 (1.49, 2.16)	7.57E-10
rs150085726	6	40729544	<i>TREM2</i> (upstream)	A	G	0.0033	1.86 (1.47, 2.37)	3.24E-7	0.0022	1.76 (1.29, 2.40)	2.91E-4	0.0029	1.82 (1.51, 2.20)	4.84E-10
rs143080277	2	106366056	<i>NCK2</i>	C	T	0.0052	1.65 (1.36, 2.01)	3.66E-7	0.0056	1.32 (1.08, 1.61)	0.00576	0.0054	1.48 (1.29, 1.70)	2.69E-8
rs17035636	3	36859000	<i>LINC02033/TRANK1</i> (downstream)	C	T	0.0016	0.43 (0.31, 0.62)	2.64E-6	0.0026	0.85 (0.62, 1.16)	0.302	0.0021	0.63 (0.5, 0.79)	8.62E-5
rs182464045	2	207595819	<i>DYTN/MDH1B</i>	T	C	0.0013	2.40 (1.66, 3.47)	3.14E-6	0.0022	1.08 (0.79, 1.46)	0.635	0.0018	1.49 (1.18, 1.89)	8.55E-4
rs78774825	8	81473635	<i>ZBTB10/ZNF704</i>	T	G	0.0025	1.90 (1.45, 2.50)	3.81E-6	0.0035	0.97 (0.74, 1.27)	0.831	0.003	1.36 (1.12, 1.65)	0.00189
rs114999466	16	76230037	<i>CNTNAP4</i> (upstream)	G	A	0.0069	0.69 (0.59, 0.81)	3.91E-6	0.0085	0.82 (0.70, 0.96)	0.0114	0.0077	0.75 (0.67, 0.84)	4.51E-7
rs552075630	2	10693329	<i>ODC1/NOL10</i>	T	G	0.0051	1.57 (1.29, 1.91)	5.82E-6	0.0051	1.07 (0.86, 1.33)	0.525	0.0051	1.33 (1.15, 1.53)	1.44E-4
rs112120395	21	21159556	<i>LINC00320</i>	G	T	0.0055	1.52 (1.27, 1.83)	6.09E-6	0.0054	0.90 (0.74, 1.09)	0.267	0.0055	1.19 (1.04, 1.36)	0.0107
rs527488596	3	90428380	<i>EPHA3</i> (downstream)	A	T	0.0055	0.65 (0.53, 0.78)	6.32E-6	NA	NA	NA	0.0055	0.65 (0.53, 0.78)	6.32E-6
rs145472714	18	66411495	<i>CCDC102B</i>	G	T	0.0077	0.70 (0.60, 0.82)	9.24E-6	0.0047	0.92 (0.73, 1.17)	0.506	0.0068	0.76 (0.67, 0.87)	5.46E-5

Abbreviations: Chr, chromosome; EFF, Effect allele; REF, reference allele; EAF, effect allele frequency; OR, Odds ratio; CI, Confidence interval; *P*, P-value

Shaded box indicates genome-wide significance within analysis stage

Table 4. Strongest rare variant (MAF<0.01) association results by genomic region in Stage 2 and Stage 3. Variants depicted had $P<10^{-5}$ in IGAP (Stage 1) analysis (n=372 variants) and had the strongest regional association in meta-analysis of IGAP+EADB (Stage 2). Variants in close proximity with similar allele frequencies were not included. UKBB AD-proxy association results and meta-analysis of IGAP, EADB, and UKBB (Stage 3) are also shown.

Variant RSID	Chr	Basepair (hg19)	Genomic Region	EFF	REF	Stage 2: IGAP + EADB Meta-Analysis			UKBB			Stage 3: IGAP + EADB + UKBB Meta-Analysis		
						EAF	OR (95% CI)	P	EAF	OR (95% CI)	P	EAF	OR (95% CI)	P
rs183427010	19	45366498	<i>APOE</i> Region (<i>PVRL2</i>)	A	G	0.0093	2.81 (2.51, 3.13)	5.32E-75	0.0055	1.53 (1.39, 1.69)	1.82E-17	0.0075	2.00 (1.86, 2.15)	1.53E-76
rs75932628	6	41129252	<i>TREM2</i>	T	C	0.0038	2.34 (1.97, 2.78)	2.15E-22	0.0025	1.45 (1.25, 1.69)	9.00E-7	0.0032	1.79 (1.60, 2.00)	5.59E-24
rs143080277	2	106366056	<i>NCK2</i>	C	T	0.0054	1.48 (1.29, 1.70)	2.69E-08	0.0041	1.34 (1.18, 1.52)	3.22E-6	0.0048	1.40 (1.28, 1.54)	7.17E-13
rs921719566	16	76230037	<i>CNTNAP4</i> (upstream)	G	A	0.0077	0.75 (0.67, 0.84)	4.51E-7	0.0066	1.02 (0.93, 1.13)	0.651	0.0071	0.89 (0.83, 0.96)	0.00252
rs1032524620	5	140854118	<i>PCDHGA/B</i> (gene family cluster)	G	C	0.0003	5.14 (2.66, 9.96)	1.17E-6	--	--	--	0.0003	5.14 (2.66, 9.96)	1.17E-6
rs778473798	5	66025094	<i>MAST4</i>	T	G	0.0003	13.8 (4.72, 40.4)	1.65E-6	--	--	--	0.0003	13.8 (4.72, 40.4)	1.65E-6
rs779452860	19	24444215	<i>ZNF254</i> (downstream)	G	T	0.0006	3.62 (2.14, 6.15)	1.79E-6	--	--	--	0.0006	3.62 (2.14, 6.15)	1.79E-6
rs1004589836	18	59553737	<i>RNF152</i>	C	A	0.0004	3.93 (2.20, 7.02)	3.81E-6	--	--	--	0.0004	3.93 (2.20, 7.02)	3.81E-6
rs570907469	2	158285821	<i>CYTIP</i>	A	G	0.0026	1.79 (1.40, 2.29)	3.88E-6	0.0025	1.04 (0.88, 1.22)	0.677	0.0025	1.23 (1.07, 1.41)	0.00338
rs749016100	7	91966514	<i>ANKIB1</i>	G	A	0.0004	4.39 (2.34, 8.22)	3.93E-6	--	--	--	0.0004	4.39 (2.34, 8.22)	3.93E-6
rs527488596	3	90428380	<i>EPHA3</i> (downstream)	A	T	0.0055	0.65 (0.53, 0.78)	6.32E-6	0.0057	0.98 (0.88, 1.1)	0.784	0.0056	0.88 (0.80, 0.97)	0.0113
rs776752144	10	36231917	<i>PCAT5</i> (downstream)	G	T	0.0002	13.1 (4.28, 40.0)	6.43E-6	--	--	--	0.0002	13.1 (4.28, 40.0)	6.43E-6
rs958893222	3	104387013	<i>ALCAM</i> (upstream)	A	G	0.0003	7.51 (3.13, 18.0)	6.51E-6	--	--	--	0.0003	7.51 (3.13, 18.0)	6.51E-6
rs779246720	10	92032063	<i>HTR7</i> (downstream)	A	G	0.0013	0.46 (0.33, 0.65)	6.73E-6	--	--	--	0.0013	0.46 (0.33, 0.65)	6.73E-6
rs536943899	3	28624836	<i>ZCWPW2</i> (downstream)	C	T	0.0017	1.79 (1.39, 2.31)	6.98E-6	0.0025	1.00 (0.85, 1.19)	0.955	0.0022	1.20 (1.04, 1.38)	0.0109
rs190394847	21	45550148	<i>PWP2</i>	A	G	0.001	2.90 (1.82, 4.61)	7.61E-6	0.0012	0.90 (0.70, 1.17)	0.440	0.0011	1.19 (0.95, 1.50)	0.130
rs146698767	21	45544573	<i>PWP2</i>	A	G	0.0013	2.49 (1.67, 3.71)	8.21E-6	0.0015	0.91 (0.72, 1.14)	0.397	0.0014	1.16 (0.95, 1.42)	0.135
rs559275238	19	45939260	<i>ERCC1</i>	G	T	0.0067	1.54 (1.27, 1.85)	8.45E-6	0.0080	1.06 (0.96, 1.16)	0.263	0.0078	1.14 (1.05, 1.24)	0.00282
rs138181035	19	44863163	<i>ZFP112</i>	T	C	0.0037	0.67 (0.57, 0.80)	8.60E-6	0.0043	0.98 (0.86, 1.13)	0.806	0.0041	0.85 (0.76, 0.95)	0.00329

Abbreviations: Chr, chromosome; EFF, Effect allele; REF, reference allele; EAF, effect allele frequency; OR, Odds ratio; CI, Confidence interval; *P*, P-value

Shaded box indicates genome-wide significance within analysis stage