Table 2 Associations with Individual Variants outside the *APOE* region

Name	gene	ADSP Discovery Meta			All Replication (ADGC+CHARGE +ADES-FR+FinnAD)			Discovery + All Replication		
		MAC (EA/CH)	best P	Model (group)	MAC	P Model 1	P Model 2	P Model 0	P Model 1	P Model 2
6:41129252:C:T (R47H)	TREM2	120/0	**4.8E-12**	0 (EA)	224	**1.6E-06**	**2.7E-06**	**3.2E-16**	**2.8E-10**	**1.6E-10**
7:154988675:G:A	AC099552.4	10/0	**1.2E-07**	2 (EA)	0	NA	NA	*1.3E-02*	*2.0E-07*	*1.2E-07*
7:99971313:T:C (rs2405442)	PILRA	6,219/219	**1.7E-07**	0 (EA)	22,798	5.3E-05	2.3E-05	**9.5E-10**	1.1E-06	5.0E-07
20:62729814:C:T (rs148484121)	OPRL1	61/4	5.8E-07	1 (all)	111	3.4E-01	5.6E-01	3.7E-03	1.4E-04	4.5E-04
11:59940599:T:A (rs7232)	MS4A6A	7,540/258	7.7E-07	0 (all)	20,963	**1.4E-11**	**3.1E-09**	**5.6E-17**	**3.8E-14**	**2.6E-11**
17:44828931:G:A (rs199533)	NSF	4,238/135	1.3E-06	0 (all)	11,120	2.5E-01	1.4E-02	2.1E-04	1.6E-02	1.9E-04
14:106235767:C:T (rs77307099)	IGHG3	6,200/176	1.9E-06	0 (all)	721	4.0E-01	3.5E-01	**1.4E-06**	1.3E-04	7.9E-05
14:106235766:G:A (rs78376194)	IGHG3	6,202/176	1.9E-06	0 (all)	719	4.2E-01	3.6E-01	**1.5E-06**	1.4E-04	8.5E-05
6:15638035:C:T (rs77460377)	DTNBP1	16/3	1.9E-06	2 (all)	35	8.5E-01	8.7E-01	8.7E-02	5.2E-03	3.0E-03
6:33041297:G:A (rs112178281)	HLA-DPA1	10/0	2.9E-06	1 (EA)	6	7.5E-01	9.2E-01	1.4E-01	2.1E-05	2.0E-05
11:59945745:T:C (rs12453)	MS4A6A	8,265/258	3.2E-06	0 (EA)	23,420	**4.7E-11**	**3.0E-08**	**1.4E-15**	**6.0E-13**	**1.2E-09**
3:195506101:T:A	MUC4	38/6	3.8E-06	1 (all)	0	NA	NA	*3.0E-04*	*3.8E-06*	*8.1E-06*
10:88446985:T:C (rs76615432)	LDB3	760/62	5.0E-06	1 (CH)	2,303	5.3E-01	5.9E-01	7.0E-01	6.3E-01	6.4E-01
19:1047507:AGGAGCAG:A	ABCA7	67/0	4.3E-06	0 (EA)	11	8.8E-02	9.7E-02	2.4E-04	1.6E-02	1.7E-02
14:106236128:T:A (rs12890612)	IGHG3	6,395/369	4.5E-06	0 (all)	1,473	8.5E-02	7.5E-02	**9.8E-07**	8.0E-05	6.4E-05
7:99799845:T:A (rs104395)	STAG3	5,248/248	5.5E-06	0 (EA)	15,948	3.0E-03	1.2E-03	**8.8E-07**	1.2E-04	4.0E-05

Table shows variants with $P < 6.1 \times 10^{-6}$ in EA, CH᾽ or combined strata in the discovery sample. Exome-wide significant results ($P < 3.1 \times 10^{-7}$) and suggestive results which improved in meta analysis of discovery + replication data are highlighted in bold. Results without variation data in the replication datasets are indicated in *italics*