

SUPPLEMENTARY MATERIAL

Supplementary Table 1. Frequency of *APOE* alleles in study population.

<i>APOE</i> genotype	Study population (N=9,362)
$\epsilon 2/\epsilon 2$	63 (0.7)
$\epsilon 2/\epsilon 3$	1,208 (12.9)
$\epsilon 2/\epsilon 4$	250 (2.67)
$\epsilon 3/\epsilon 3$	5,467 (58.4)
$\epsilon 3/\epsilon 4$	2,161 (23.1)
$\epsilon 4/\epsilon 4$	213 (2.8)

Abbreviations: *APOE*, apolipoprotein E.

Data are presented as number (percentage) of participants.

Supplementary Table 2. Genetic variants included in the genetic risk score.

Chr	Rs-id	ALT- HRC	Assigned-gene	Locus discovered in:	Effect estimate	Maf	Weight ALT-HRC	R ² -RS1	R ² -RS2	R ² -RS3
19	rs4147929	G	<i>ABCA7</i>	Hollingsworth et al. , Naj et al.	Lambert et al. (2013)	0.19	-0.135	0.916	0.917	0.991
2	rs6733839	T	<i>BINI</i>	Seshadri et al.	Lambert et al. (2013)	0.409	0.188	0.960	0.911	0.962
20	rs7274581	C	<i>CASS4</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.083	-0.139	0.990	0.989	0.990
6	rs10948363	G	<i>CD2AP</i>	Hollingsworth et al. , Naj et al.	Lambert et al. (2013)	0.266	0.098	0.998	0.998	0.998
11	rs10838725	C	<i>CELF1</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.316	0.075	0.998	0.998	0.998
8	rs9331896	T	<i>CLU</i>	Harold et al. , Lambert et al. (2009)	Lambert et al. (2013)	0.379	0.146	0.902	0.974	0.901
1	rs6656401	G	<i>CRI</i>	Lambert et al. (2009)	Lambert et al. (2013)	0.197	-0.157	0.953	0.948	0.950
10	rs7920721	G	<i>ECHDC3</i>	Desikan et al.	Desikan et al.	0.387	-0.067	1.000	1.000	1.000
7	rs11771145	A	<i>EPHA1</i>	Hollingsworth et al. , Naj et al.	Lambert et al. (2013)	0.338	-0.102	0.998	0.998	0.999
14	rs17125944	C	<i>FERMT2</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.092	0.122	1.000	1.000	1.000
6	rs111418223	A	<i>HLA-DRB1/5</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.276	-0.108	0.314	0.312	0.314
4	rs13113697	G	<i>HS3ST1</i>	Desikan et al.	Desikan et al.	0.283	-0.067	0.999	0.998	0.999
2	rs35349669	T	<i>INPP5D</i>	Lambert et al.	Lambert et al. (2013)	0.488	0.066	0.975	0.973	0.976
17	rs118172952	G	<i>KANSL1</i>	Jun et al.	Lambert et al. (2013)	0.873	-0.151	0.710	0.700	0.708
5	rs190982	A	<i>MEF2C</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.408	0.080	0.979	0.934	0.978
11	rs983392	G	<i>MS4A6A</i>	Hollingsworth et al. , Naj et al.	Lambert et al. (2013)	0.403	-0.108	0.989	0.990	0.991
7	rs2718058	G	<i>NME8</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.373	-0.070	1.000	1.000	1.000
11	rs10792832	G	<i>PICALM</i>	Harold et al.	Lambert et al. (2013)	0.358	0.130	0.999	0.999	0.999
8	rs28834970	C	<i>PTK2B</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.366	0.096	0.993	0.990	0.994
14	rs10498633	T	<i>SLC24A4-RIN3</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.217	-0.104	0.999	0.999	1.000
11	rs11218343	C	<i>SORL1</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.039	-0.270	0.998	0.995	0.998
6	rs75932628	T	<i>TREM2</i>	Guerreiro et al. , Jonsson et al.	Ruiz et al.	0.0016	0.889	0.762	0.726	0.668
7	rs1476679	T	<i>ZCWPW1</i>	Lambert et al. (2013)	Lambert et al. (2013)	0.287	0.078	0.995	0.996	0.995

Ordered by assigned gene name. References: Harold et al.[1], Seshadri et al.[2], Hollingsworth et al.[3], Naj et al.[4], Lambert et al. (2009,2013)[5, 6], Jonsson et al.[7], and Ruiz et al.[8] Minor allele Frequency (Maf) of Rotterdam Study (RS) 1 is shown and is representative of the MAF in RS2 and RS3. R²= imputation quality. RS1= initial Rotterdam Study cohort, RS2=first extension Rotterdam Study, RS3=second extension. Rotterdam Study cohorts were imputed separately. Gene names are ncbi gene names assigned to the loci in the corresponding references.

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