Table e-2. Power calculations

Nearest Gene	SNP	Minor Allele	Control MAF	AD risk OR	Detectable OR in PCA+Posterior AD	Observed OR in PCA+Posterior AD
APOE	**rs429358**	**C**	**0.123**	**4.36**	**1.63**	**4.74 (3.37-6.67)**
CLU	**rs11136000**	**A**	**0.412**	**0.82**	**0.69**	**0.68 (0.49-0.93)**
BIN1	**rs744373**	**G**	**0.273**	**1.17**	**1.47**	**1.42 (1.03-1.96)**
APOE	**rs7412**	**T**	**0.080**	**0.25**	**0.42**	**0.46 (0.20-1.07)**
ABCA7	rs3764650	C	0.078	1.23	1.78	0.98 (0.57-1.70)
PICALM	rs3851179	A	0.367	0.80	0.68	1.23 (0.90-1.68)
CD2AP	rs9349407	C	0.267	1.11	1.48	0.72 (0.50-1.05)
CR1	rs3818361	A	0.194	1.15	1.52	1.19 (0.82-1.71)
MS4A6A	rs610932	A	0.434	0.87	0.69	0.88 (0.64-1.20)
CD33	rs3865444	A	0.318	0.92	0.66	0.88 (0.64-1.21)
EPHA1	rs11767557	G	0.203	0.87	0.61	0.93 (0.63-1.38)

Table e-2. Power calculations

Given the minor allele frequencies (MAF) of the tested variants in controls and published OR estimates for AD risk, we estimated the effect sizes that would be detectable in our Combined Case- Control cohort, with 80% power and α=0.05. Observed OR estimates in our combined cohort is depicted in this table for comparison.