## SUPPLEMENTARY TABLES

**Supplementary Table 1. Suggestive SNPs in GWAS.**

| CHR | BP | SNP | MAF | Closest Gene | SNP Type/Location | *P* values |
|---|---|---|---|---|---|---|
| 17 | 18055903 | rs74361457 | 0.017 | *MYO15A* | intron | 9.52E-07 |
| 17 | 80461935 | rs8078417 | 0.31 | *NARF* | intergenic | 1.75E-06 |
| 7 | 66903871 | rs62465226 | 0.354 | *LOC105375337* | intergenic | 2.51E-06 |
| 7 | 66904395 | rs6948216 | 0.393 | *LOC105375337* | intergenic | 2.51E-06 |
| 7 | 66908992 | rs4618582 | 0.404 | *LOC105375337* | intergenic | 2.51E-06 |
| 7 | 66902955 | rs7785167 | 0.413 | *STAG3L4* | intergenic | 3.16E-06 |
| 7 | 66898482 | rs4357188 | 0.355 | *STAG3L4* | intergenic | 4.05E-06 |
| 7 | 66901317 | rs12666354 | 0.358 | *LOC105375337* | intergenic | 4.05E-06 |
| 17 | 18227081 | rs921986 | 0.323 | *SMCR8* | intron | 6.27E-06 |
| 17 | 18164404 | rs2605142 | 0.2963 | *MIEF2* | intron | 8.30E-06 |
| 17 | 18228605 | rs4925172 | 0.324 | *SMCR8* | intron | 9.11E-06 |
| 17 | 18231998 | rs1979276 | 0.324 | *SHMT1* | intron | 9.11E-06 |
| 7 | 66896600 | rs6460344 | 0.127 | *LOC105375337* | intergenic | 9.35E-06 |

Abbreviations: BP, base pair (variant position); CHR, chromosome; MAF, minor allele frequency; SNP, single nucleotide polymorphism

**Supplementary Table 2. Baseline demographic characteristics and rs16840041 genotypes as predictors of time to clinical disease progression.**

| Characteristic | Hazard ratio (95% CI) | Wald $\chi^2$ 1 | p value |
|---|---|---|---|
| genotype | 1.63(1.12–2.36) | 6.60 | 0.010 |
| age | 1.03(1.01–1.05) | 6.66 | 0.010 |
| diagnosis | 1.45(1.24–1.70) | 20.63 | <0.001 |
| *APOE4* + | 1.72(1.36–2.05) | 24.04 | <0.001 |

Cox proportional hazard models were used to assess the ability of demographic variables (age, diagnosis, and *APOE4* status) to predict clinical disease progression of AD over the 1-10 year follow-up period.
Abbreviations: CI, confidence intervals; *APOE*, apolipoprotein E.