**Supplemental figures**

**Figure S1** Quantile-quantile and cluster plots

**Top row** Quantile-quantile plots for the exome-wide discovery meta-analysis. Known genes are in orange. The genomic control coefficient ($\lambda_{GC}$) is reported. Middle panel: Variants near *APOE* excluded **Bottom row** Cluster plots for SNPs in *SKAP2* and *TM2D3* demonstrate appropriate calling of the rare variant genotypes.