Supplementary Figures

A large cross-ancestry meta-analysis of genome-wide association studies identifies 69 novel risk loci for primary open-angle glaucoma and includes a genetic link with Alzheimer's disease

Supplementary Figure 1. QQ and Manhattan plots.

A) European meta-analysis.
B) Cross-ancestry meta-analysis.
C) Male-stratified meta-analysis.
D) Female-stratified meta-analysis.
E) NTG-stratified meta-analysis.
F) HTG-stratified meta-analysis.
Supplementary Figure 2. Correlation of SNP effect estimates between European POAG meta-analysis and each of the replication datasets. The X-axis shows effect estimates in log(OR) scale for the European genome-wide significant SNPs. The Y-axis shows estimates for the same SNPs in UKBB self-reports (panel A), Asians (panel B), and Africans (panel C). The previously-identified risk loci are shown in red and the novel loci in blue. Horizontal grey bars on each dot represent the 95% confidence intervals (CIs) for the effect estimates in Europeans, and vertical grey bars shows the 95% CIs in the replication datasets. The blue line is the linear regression line best fitting the data.

A) European POAG vs. UKBB self-reports.  

B) European POAG vs. Asians.  

C) European POAG vs. Africans.
Supplementary Figure 3. LocusZoom plots for the genome-wide significant SNPs from the cross-ancestry meta-analysis. On each row, the plots show the same region in Europeans (first plot), Asians (second plot), and Africans (third plot). However, there are only two plots per row for the last four rows (X chromosome loci) because X chromosome data was not available for the African studies. The index SNPs are the most significant SNPs in the cross-ancestry meta-analysis while P-value of associations and LD structures are shown for each ancestry separately.
Supplementary Figure 4. Enrichment of the expression of the significant genes identified by MAGMA in GTEX tissues. The horizontal line indicates the significance threshold (P<1e-03), Bonferroni-corrected for 53 GTEX tissues tested.

A) Results from the European meta-analysis.

B) Results from the cross-ancestry meta-analysis.
**Supplementary Figure 5. Chromatin and eQTL interactions for the POAG risk loci.** The interactions are shown for each chromosome separately. Orange lines show chromatin interactions and green lines eQTL interactions. Green genes are the eQTL-mapped genes, orange genes are mapped by chromatin interactions, and red genes by both. The outer layers are Manhattan plots with the most significant SNPs shown.

**Chromosome 1**
Chromosome 3
Chromosome 4
Chromosome 8
Chromosome 10
Chromosome 11
Chromosome 16
Chromosome 21
Chromosome 22
Supplementary Figure 6. Gene expression heatmaps in eye tissues.

A) Gene expression of the novel POAG risk genes.