Description of Additional Supplementary Files

Supplementary Data 1: Summary statistics for the discovery whole exome sequencing study from Hong Kong, Japan, Singapore, and Vietnam

QV-cases: Number of qualifying rare variants* in persons with primary angle-closure glaucoma

QV-controls: Number of qualifying rare variants in unaffected individuals

NonQV-cases: Number of persons with primary angle-closure glaucoma who were not carrying qualifying rare variants.

NonQV-controls: Number of unaffected individuals who were not not carrying qualifying rare variants.

Odds Ratio: Odds of primary angle-closure glaucoma for carriers of qualifying rare variants compared to non-carriers; calculated for each gene from the gene-based burden test.

L95: Lower boundary of the 95% confidence interval of the Odds Ratio

U95: Upper boundary of the 95% confidence interval of the Odds Ratio

$\boldsymbol{P}$-$_{CMH}$: *P*-value obtained from stratified meta-analysis of Hong Kong, Japan, Singapore, and Vietnam case-control studies using the Cochran Mantel-Haenszel method

$\boldsymbol{P}$-$_{PCA+VC}$: *P*-value obtained from meta-analysis of Hong Kong, Japan, Singapore, and Vietnam case-control studies after adjusting for ancestry principal components and exome-wide variant count (total exome variant count).

Genes surpassing exome-wide significance ($P < 2.5 \times 10^{-6}$) are highlighted in red.

*Qualifying rare variants are defined as mis-sense variants with allele frequency less than 1% and having a CADD score >10. Variants with such a CADD score are predicted to be within the top 10% most deleterious substitutions that can occur in the human genome.