

Supplemental Figure S2 of Genome-wide RNA sequencing of human trabecular meshwork cells treated with TGF- β 1 : relevance to pseudoexfoliation glaucoma

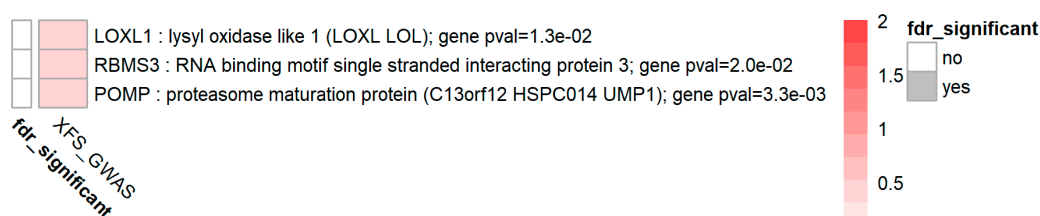


Figure S2. Genes associated with XFS from genome-wide association studies (GWAS). Heatmap showing genes with nominal p-value $p < 0.05$ for genes associated with genome-wide association studies for pseudoexfoliation syndrome (XFS). Heatmap colours correspond to fold change expressed as \log_2FC which has been limited to a range of $[0, 2]$ for clarity. The annotation bar on the left shows if the genome-wide false discovery rate has an $FDR < 0.05$ (in which FDR is the BH corrected p-value) for a particular gene which is the case for none of the genes shown.