**Supplementary Figures**

**A table with numbers and numbers

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**Fig. S1.** Colocalizing eQTLs and sQTLs in GTEx tissues and retina with genome-wide significant loci in EUR ML endophenotype meta-analyses. Genes with at least one significant colocalization result (CLPP>0.01) are shown for e/sQTLs tested across selected GTEx tissues and peripheral retina for the genome-wide significant loci from the EUR and the cross-ancestry endophenotype meta-analyses. Bubble size is proportional to the maximum colocalization posterior probability (CLPP) of all e/sVariants tested for the given gene, QTL type and tissue combination. Points are color-coded by the relative direction of effect between the QTL and the GWAS meta-analysis.

A graph with blue dots and white lines

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a)

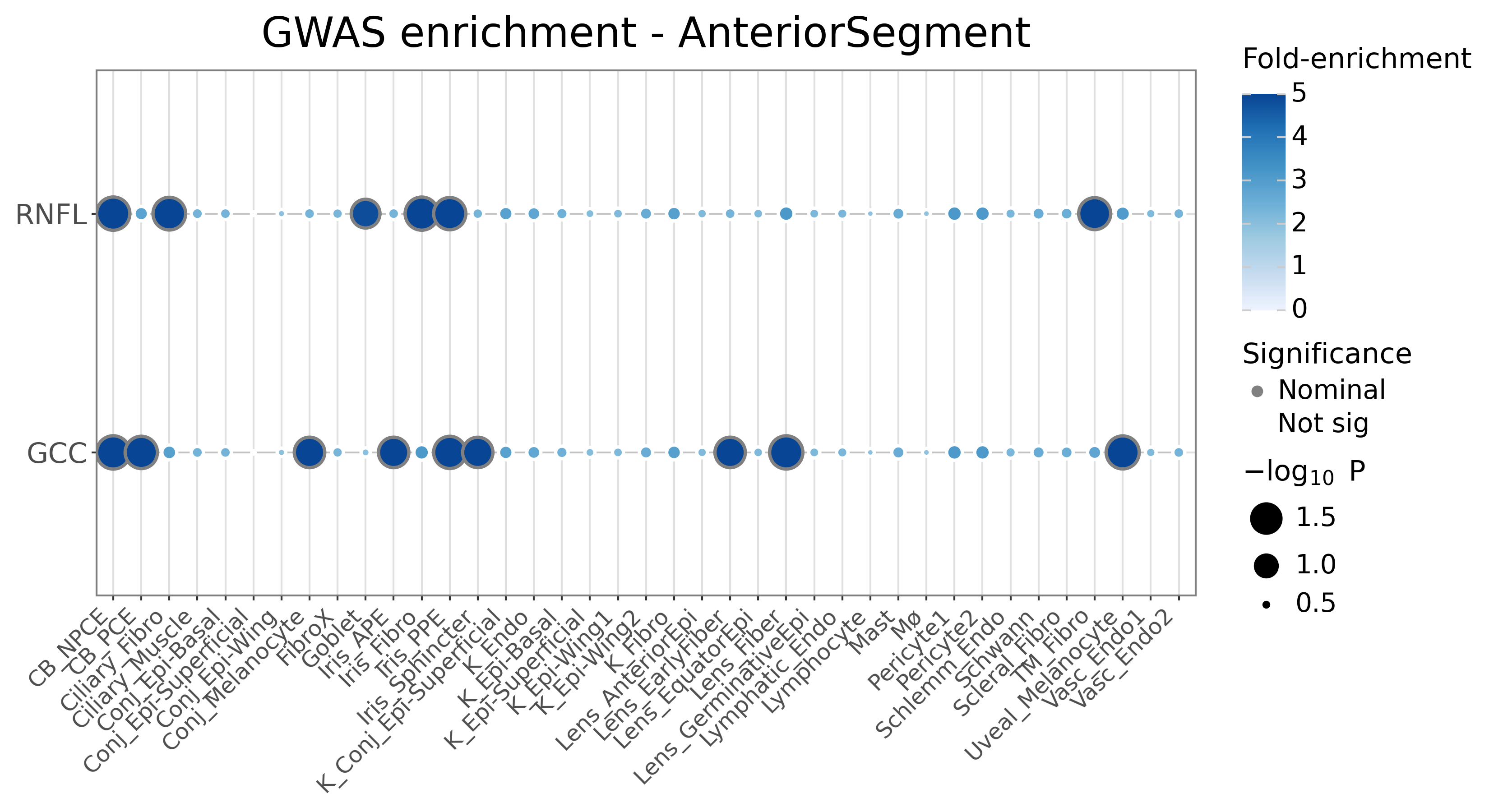
b)

**Fig. S2.** Cross-ancestry GWAS enrichment in specific cell types in a) optic nerve head, and b) anterior segment using ECLIPSER.

b)

a)

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**Fig. S3.** EUR GWAS enrichment in specific cell types in a) optic nerve head, and b) anterior segment using ECLIPSER.

A diagram of a graph

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**Fig. S4.** Single-cell expression of genes in various cell types in a) anterior segment, b) optic nerve head, optic nerve and surrounding posterior tissues, and c) retina. Single nucleus RNA-seq for the anterior segment was taken from van Zyl et al., 2022 *(48)* and for the optic nerve head and surrounding posterior tissues from Monavarfeshani, Yan, *et al.,* 2023 *(49)*.