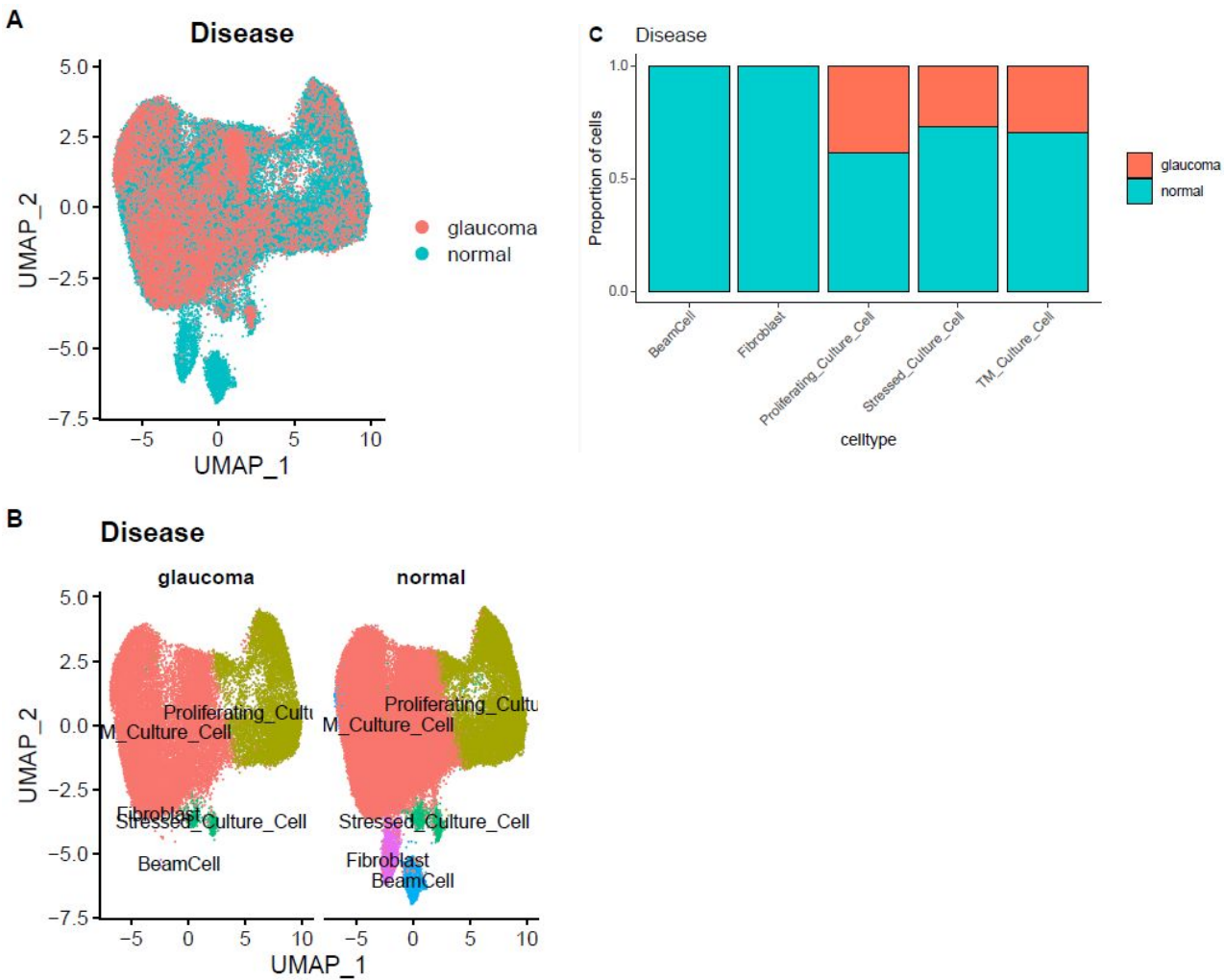




Supplementary figure 2. comparing norm(n=10) vs glaucoma(n=4) sample data

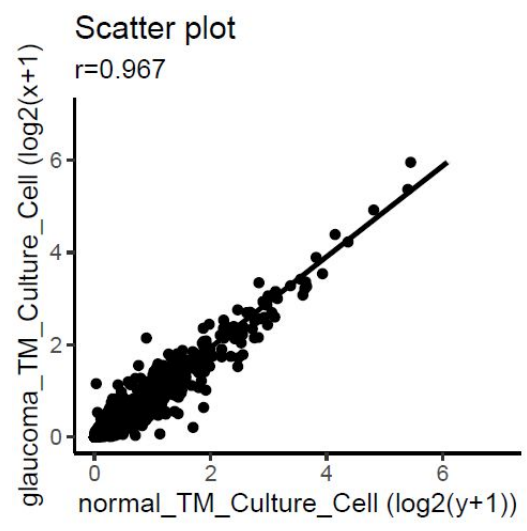


Supplementary table1. Number of cells assigned to individual cell clusters

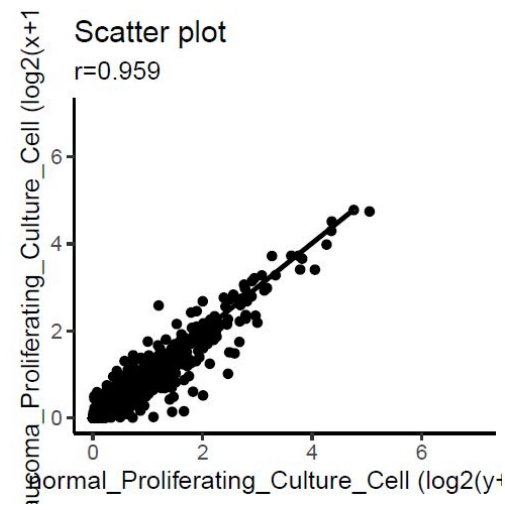
celltype	Normal cells		Glaucomatous cells		Total
	cells	Proportion (%)	cells	Proportion (%)	
TM_Culture_Cell	41591	73.1	17772	69.3	
Proliferating_Culture_Cell	11734	20.6	7457	29.1	
Stressed_Culture_Cell	1118	2	415	1.6	
BeamCell	1273	2.2	1	0	
Fibroblast	1178	2.1	4	0	
Total	56894	100	25649	100	82543

**Supplementary figure3. Scatter plots for correlation of highly variable genes (HVGs, n=2000) between normal and glaucoma**

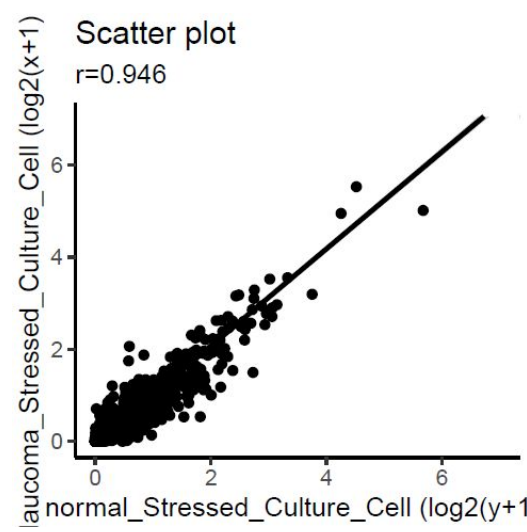
**A. TM culture cell**



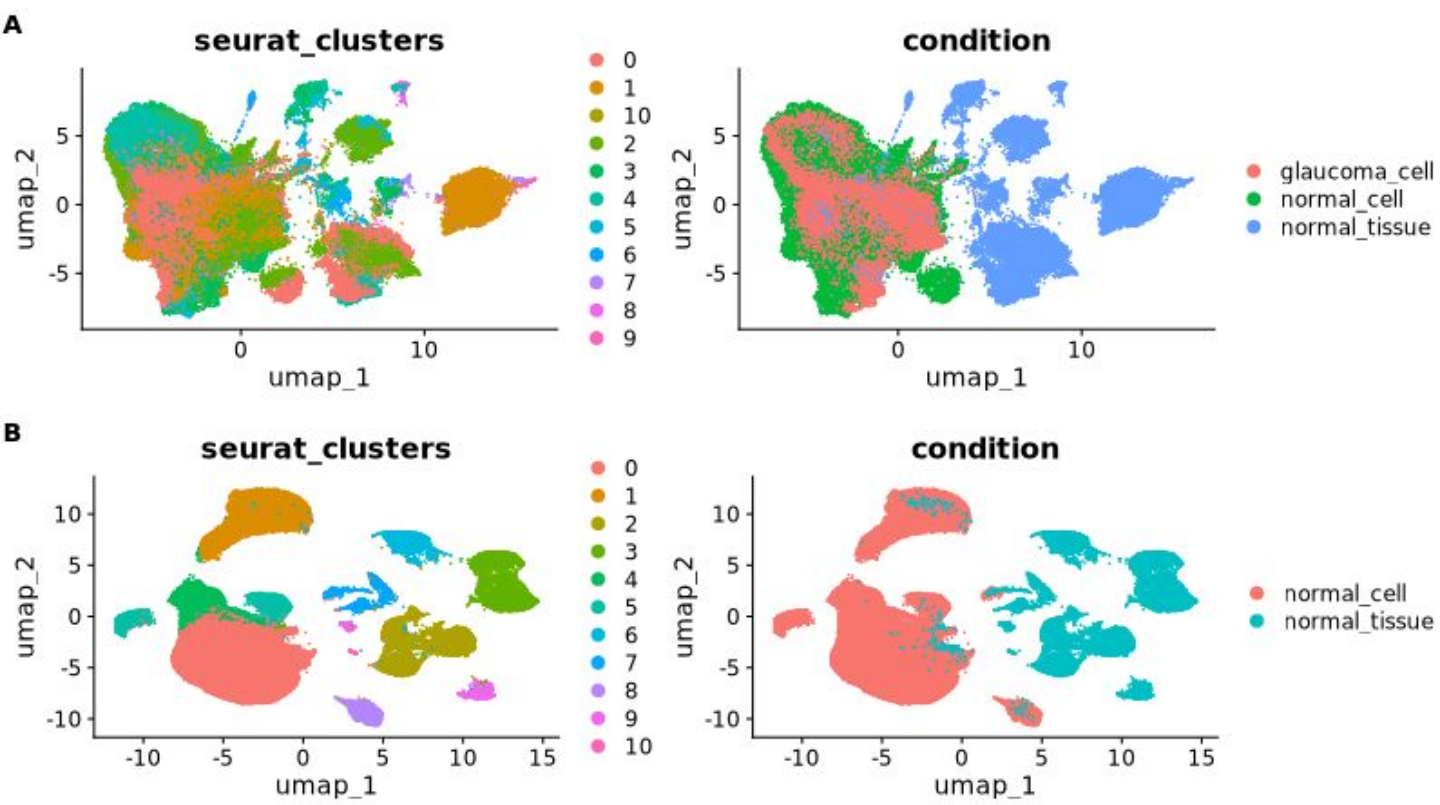
**B. Proliferating Culture Cells**



**C. Stressed culture cell**



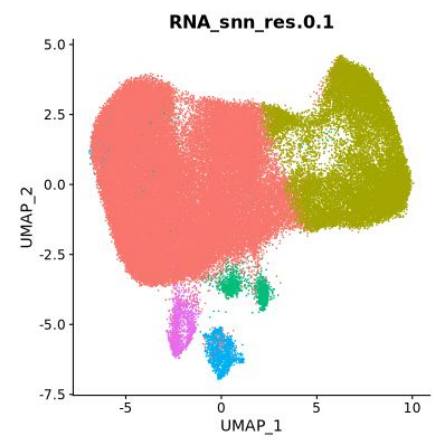
Supplementary figure 4. Sub-group analysis: superimpose normal\_cells to normal TM tissue data



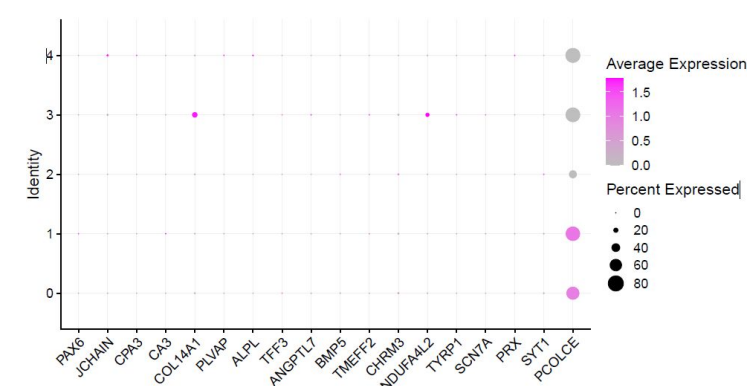
A. Data integration and clustering for 3 groups: glaucomatous cells, normal cells, and normal tissues from Chen lab. B. Data integration and clustering for 2 groups: normal cells, and normal tissues.

Supplementary figure 5. Further sub-clustering of hTM cell data and assessing cell types using published known cell markers

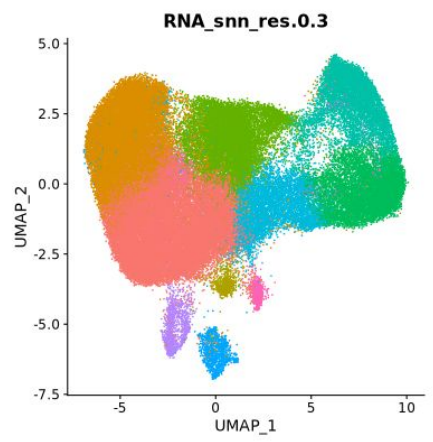
A. rs=0.1



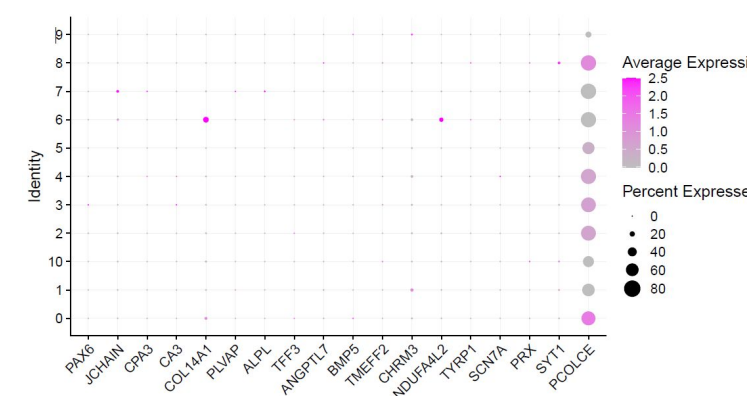
Known cell markers from Sanes group in Table4\*



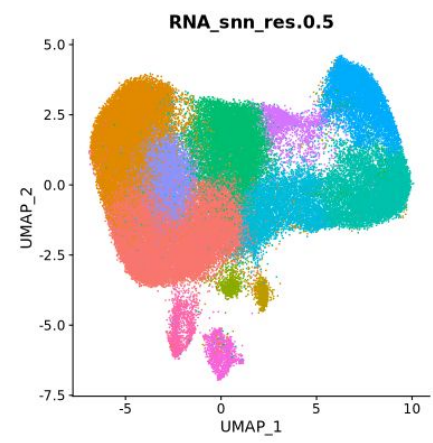
B. rs=0.3



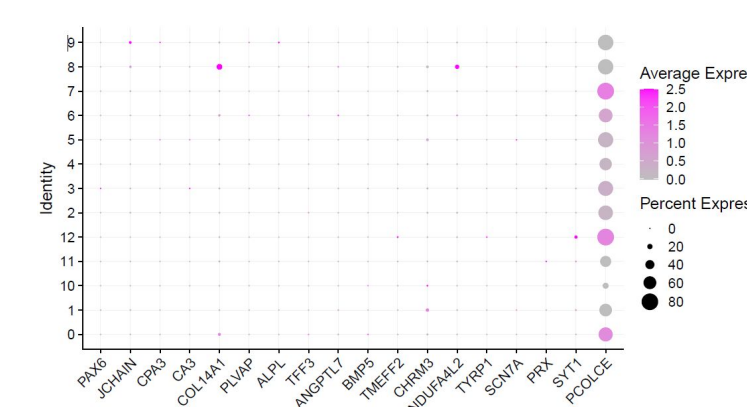
Known cell markers from Sanes group in Table4\*



C. rs=0.5



Known cell markers from Sanes group in Table4\*



\* Known cell markers: To assess the cell type reported cell markers used from publication (Cell Atlas of Human Trabecular Meshwork and Aqueous Outflow Structures, Zyl et al., 2000).