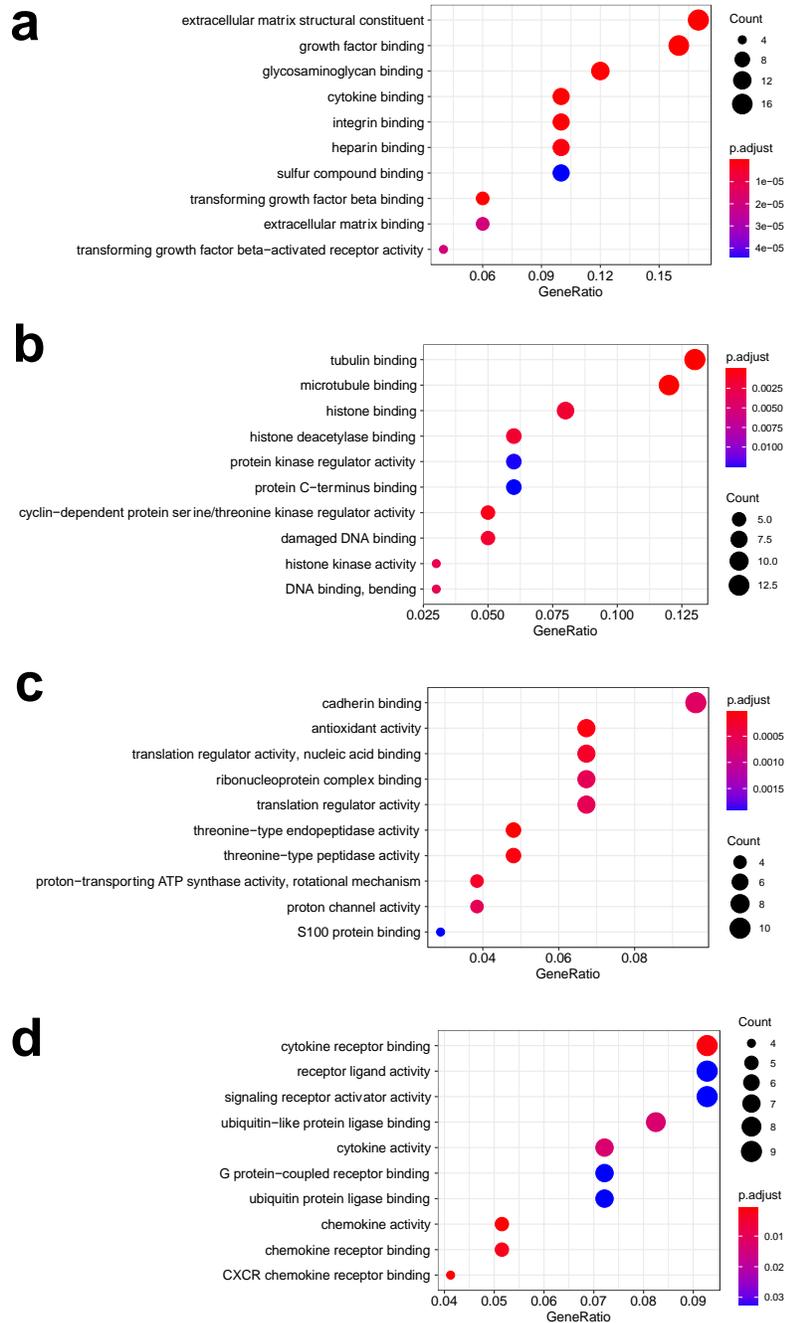


Supplemental Materials

Supplemental Figure S1



Supplemental Figure S1: Gene ontology molecular function analysis of cluster markers for each BOEC subpopulation. (a) ‘Vascular remodeling’ population; **(b)** ‘Proliferative’ population; **(c)** ‘Energetically primed’ population; **(d)** ‘Activated’ population. The top 10 enriched processes based on adjusted p values (p.adjust) are shown, with ‘count’ indicating the number of genes underlying each term.

Supplemental Table S1: Demographics of wet AMD and normal donors from whom blood outgrowth endothelial cells (BOECs) were derived.

Disease status	Age	Genotypes		
		ARMS2, rs10490924 (risk allele: T)	HTRA1, rs11200638 (risk allele: A)	CFH, rs800292 (risk allele: G)
Wet AMD	71	TT	AA	GA
	86	TT	AA	AA
Normal control	46	GG	GG	GA

Additional Table S2: Key resources used in this study.

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Biological samples		
PBMC	This paper	N/A
Chemicals, peptides, and recombinant proteins		
TRITC-Phalloidin	Merck	90228
Critical commercial assays		
Chromium Single Cell 3' v3 Reagent Kit	10X Genomics	PN-1000075
Experimental models: Cell lines		
Patient-derived BOECs	This paper	N/A
Software and algorithms		
Seurat v 4.1.1	References 91 and 92 in Main Manuscript	https://satijalab.org/seurat/
clusterProfiler v 4.2.2	Reference 96 in Main Manuscript	https://github.com/YuLab-SMU/clusterProfiler
ReactomePA v 1.38.0	Reference 97 in Main Manuscript	https://github.com/YuLab-SMU/ReactomePA
ZEN BLUE	ZEISS	https://www.zeiss.com/microscopy/int/products/microscope-software/zen.html
Others		
Confocal LSM800	Airyscan Microscope ZEISS	N/A