Glaucoma-associated genes expressed in SC and the TM: Table 1 & Supp. dataset 2

Ben Thomson

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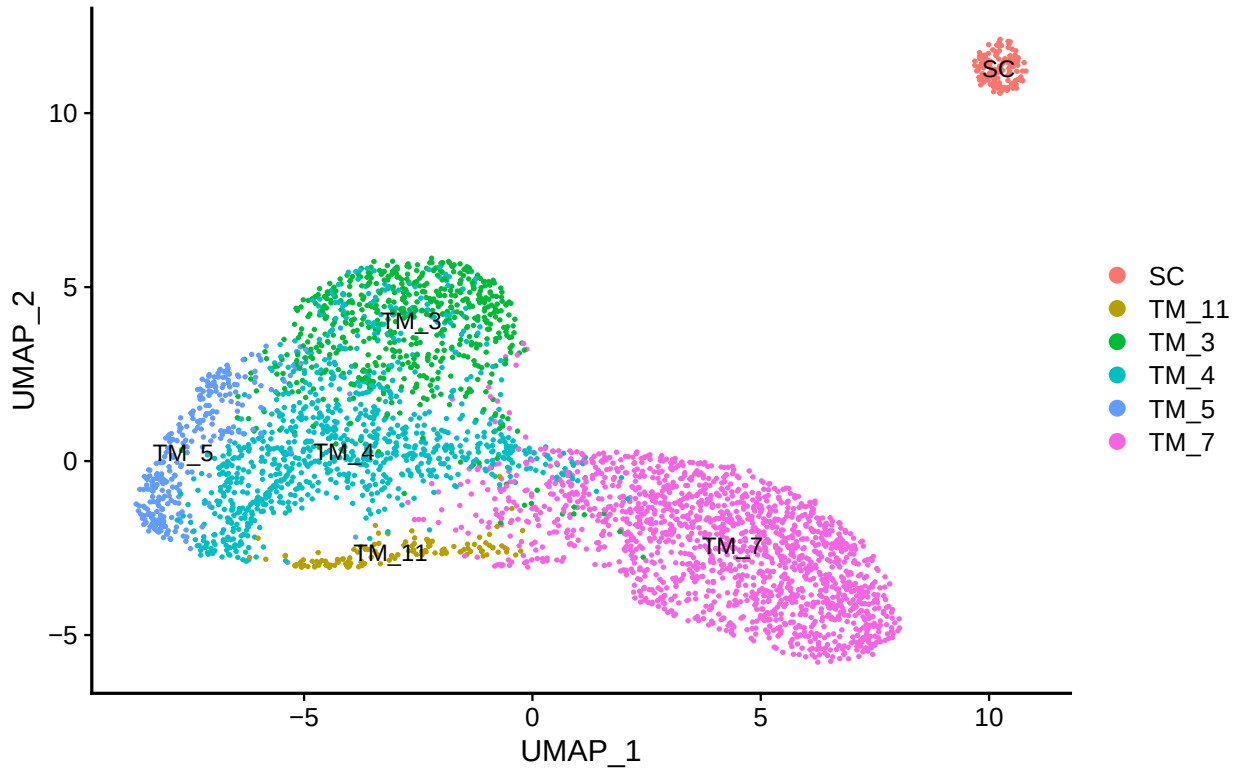
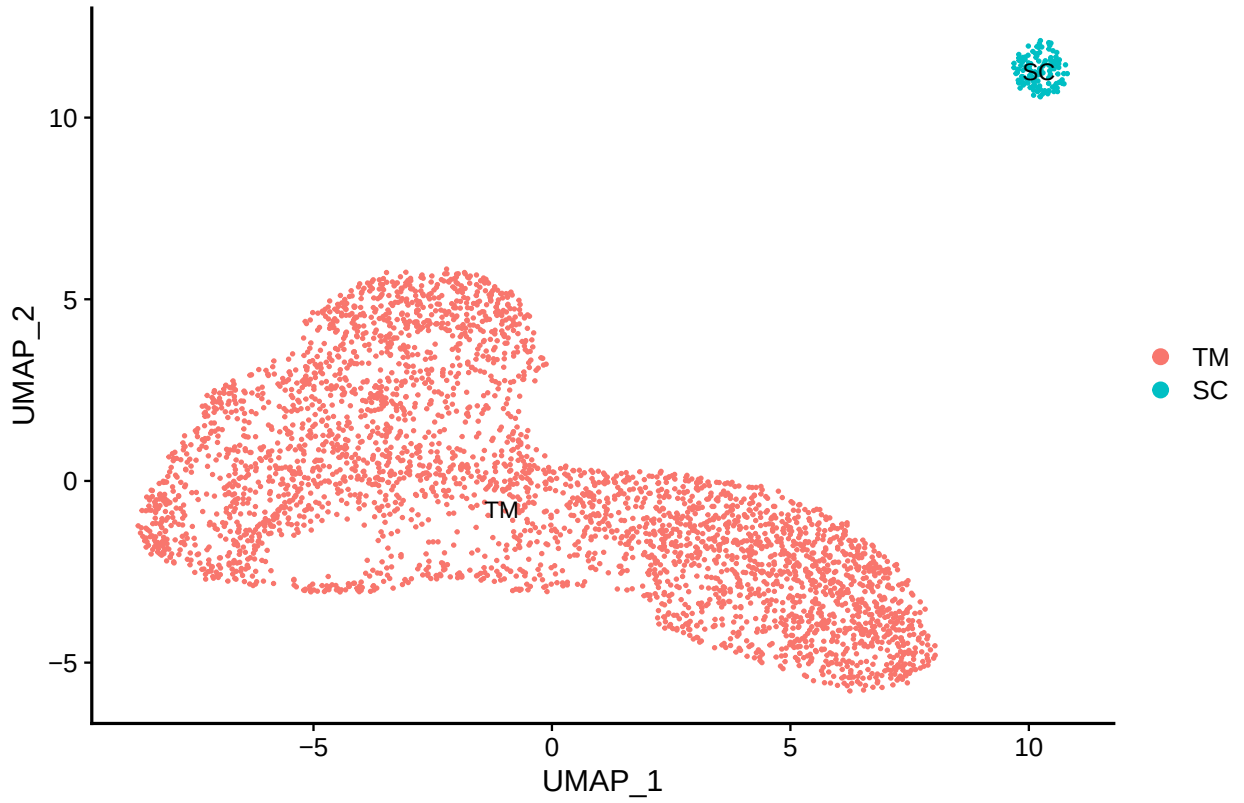
To identify key glaucoma genes expressed in the TM and SC endothelium, we generate a new dataset consisting of TM and SC cells. This dataset consists of the SC endothelial cluster as well as TM3-5, TM7 and the beam-like cluster TM11.

```
full.dataset <- readRDS("../data/full_dataset_10-2-20.rds.gz")
TM.dataset <- readRDS("../data/6wk_TM_subset_10-7-20.rds.gz")
EC.dataset <- readRDS("../data/6wk_endos_10-1-20.rds.gz")

full.dataset <- SetIdent(full.dataset, cells = Cells(TM.dataset),
  value = TM.dataset@active.ident)
full.dataset <- SetIdent(full.dataset, cells = Cells(EC.dataset),
  value = EC.dataset@active.ident)

SC_TM.dataset <- subset(full.dataset, idents = c("SC", "TM_3",
  "TM_4", "TM_5", "TM_7", "TM_11"))
keep(SC_TM.dataset, sure = T)

SC_TM.dataset <- RunUMAP(object = SC_TM.dataset, dims = 1:10,
  min.dist = 0.4, n.neighbors = 40, verbose = FALSE)


DimPlot(SC_TM.dataset, label = TRUE, pt.size = 0.5, label.size = 4) +
  coord_fixed() + theme(aspect.ratio = 0.7) + theme(axis.line = element_line(color = "black",
  size = 0.7))
```




```
SC_TM.dataset <- RenameIdents(SC_TM.dataset, TM_3 = "TM", TM_4 = "TM",
  TM_5 = "TM", TM_7 = "TM", TM_11 = "TM")

DimPlot(SC_TM.dataset, label = TRUE, pt.size = 0.5, label.size = 4) +
  coord_fixed() + theme(aspect.ratio = 0.7) + theme(axis.line = element_line(color = "black",
  size = 0.7))
```



Next, a list of all genes expressed in each cluster was generated and compared to a curated list of glaucoma-associated loci.

```
glaucoma.genes <- read.csv("../data/glaucoma_loci.csv", stringsAsFactors = FALSE)

sc.exp <- AverageExpression(subset(SC_TM.dataset, idents = "SC"),
  verbose = FALSE)$RNA
sc.exp <- subset(sc.exp, subset = SC > 0.3)
setDT(sc.exp, keep.rownames = "gene")[]
SC <- sc.exp[sc.exp$gene %in% glaucoma.genes$Gene, ]
SC <- SC %>% dplyr::rename(SC = "gene")

TM.exp <- AverageExpression(subset(SC_TM.dataset, idents = "TM"),
  verbose = FALSE)$RNA
TM.exp <- subset(TM.exp, subset = TM > 0.3)
setDT(TM.exp, keep.rownames = "gene")[]
TM <- TM.exp[TM.exp$gene %in% glaucoma.genes$Gene, ]
TM <- TM %>% dplyr::rename(TM = "gene")


SC_list <- as.list(SC[, 1])
TM_list <- as.list(TM[, 1])
```

```
Shared <- intersect(SC_list$SC, TM_list$TM)


# identify non universal GC genes
SC_list <- as.data.table(setdiff(SC_list$SC, Shared))
setnames(SC_list, "SC")
TM_list <- as.data.table(setdiff(TM_list$TM, Shared))
setnames(TM_list, "TM")

Shared <- as.data.table(Shared)
setnames(Shared, "Shared genes")


gene.table <- plyr::ldply(c(SC_list, TM_list, Shared), rbind)
write.csv(t(gene.table), file = "../datasets/SC_TM_exp__GC_genes_12-1-20.csv")

# now export list of all genes expressed in TM and SC
# populations
write.csv(sc.exp, file = "../datasets/SC_exp_genes_all_12-1-20.csv")
write.csv(TM.exp, file = "../datasets/tm_exp_genes_all_12-1-20.csv")
```

```
kbl(t(gene.table)) %>% kable_minimal()
```

.id	SC	TM	Shared genes
1	Tek	Myoc	Tmco1
2	Kdr	Tgfb2	Fmnl2
3	Tgfbr3	Fbn1	Abca1
4	Flt1	Svep1	Atxn2
5	Cav2	Bicc1	Cav1
6	Cttnbp2	Col6a2	Fermt2
7	Bmp4	Dcn	Ets1
8	Flt4	Vegfc	Arhgef12
9	Gas7	Cdh11	Stag1
10	NA	Loxl2	Foxc1
11	NA	Loxl1	Vegfa
12	NA	Col12a1	Cyp1b1
13	NA	Efemp1	NA
14	NA	Adamts2	NA
15	NA	Gmds	NA
16	NA	Angpt1	NA
17	NA	Thbs2	NA
18	NA	Ltbp1	NA