Supplemental information

Single-cell RNA sequencing depicts the local cell landscape in thyroid-associated ophthalmopathy

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Supporting Information

Fig. S1.

a

b

RASO1

Identity
COF MYF LPF

CEBPB

CEBPD

PPARG

CCL14

HLA-DRB1

Expression level

Expression level

Tagln

ACTA2

C

GO of DEG in each stromal cell clusters

vascular development
blood vessel development
blood vessel morphogenesis
angiogenesis
regulation of cell adhesion
Extracellular matrix organization
extracellular structure organization
external encapsulating structure organization
Molecules associated with elastic fibres
Elastin fibre formation
Smooth muscle development
Smooth muscle contraction
smooth muscle cell development
muscle cell differentiation
actin filament-based process

C

COF

MYF

LPF

FCGR3A

GZMK

GZMB

CD30

CD4

CD8A

NCR1

NCAM1

D

UMAP_1

Low

High

f

DEGs of CDF/Tm in TAO/HC comparison

DEGs of NK1 in TAO/HC comparison

DEGs of NK2 in TAO/HC comparison

Up
Stable
Down

CD40

CCL14

TGFBI

NFKB1

TNFRSF9

CD8A

CXCR4

FOS

IgG20

IGSF1

IGSF18

CCL14

TGFBI

CD8A

NFKB1

TNFRSF9

CD40

FOS

IgG20

IGSF1

IGSF18

CD8A

CXCR4

FOS

IgG20

IGSF1

IGSF18

CD8A

CXCR4

FOS

IgG20

IGSF1

IGSF18

CD8A

CXCR4

FOS

IgG20

IGSF1

IGSF18
Supplementary Fig. S1. Analysis of Gene Expression in Stromal Cells and T Cells. Related to Figures 1-5.

a. t-SNE plots segregated by different group. Each HC group (HC1, HC2) included five samples from healthy participants, TAO2 and TAO3 include three samples from TAO patients, while TAO1 and TAO4 include two samples from TAO patients. b. Heatmap showing scaled expression of top 10 highly expressed genes of OFs, ECs and peicytes in OCT. Violin plots showing the expression of CCL14, HLA-DRB1, TAGLN, and ACTA2 by OFs, ECs and peicytes. Color scheme is based on z-score distribution from –2 (blue) to 2 (red). c. Representative GO terms and KEGG pathway enriched by upregulated DEGs of OFs, ECs and peicytes in OCT. d. UMAP plots of canonical markers for NK&T cell subsets in OCT. e. Volcano plot showing DEGs of CD8+ Tm (left), NK1 (middle) subsets and NK2 (right) in TAO/HC comparison. f. Violin plot showing the expression of selected functional genes in NK&T cell subsets from HCs and TAO patients.
Fig. S2. Analysis of Gene Expression in Myeloid Cells. Related to Figures 6.

a. UMAP plots showing the expression of CSF3R and FCGR3B by OCT cells from HCs and TAO patients. 

b. Heatmap showing scaled expression of discriminative gene sets for neutrophils and other cells in OCT. Color scheme is based on z-score distribution from –2 (blue) to 2 (red).

c. Representative GO terms and KEGG pathway enriched by upregulated DEGs of neutrophils in OCT.

d. UMAP plots of canonical markers for mononuclear phagocyte subsets in OCT.

e. Pseudotime analysis of mononuclear phagocyte subsets in OCT exhibiting differentiation tendency from monocytes to DCs and macrophages.

f. Bar chart showing the relative proportion of mononuclear phagocyte subsets in OCT from HCs and TAO patients derived from scRNA-seq data.

g. UMAP plots showing the expression of MARCO, SIGLEC1, and STMN1 by mononuclear phagocyte subsets from HCs and TAO patients.

h. Violin plots showing the expression of IFNGR1, IFNGR2 and CD72 in mononuclear phagocyte subsets from HCs and TAO patients.

i. Violin plots showing the expression of selected functional genes in mononuclear phagocyte subsets from HCs and TAO patients.

j. Representative GO terms and KEGG pathway enriched by upregulated DEGs of CD16+ monocytes, CD14+ monocytes, and DCs in OCT during TAO.
Supplementary Fig. S3. The Cell-Cell Communication between MYF and Other Major Cell Subsets from TAO and HC. Related to Figures S7.
a. The interaction between MYF and other major cell subsets in OCT from TAO patients. b. The interaction between MYF and other major cell subsets in OCT from HC.
Supplementary Fig. S4. The Cell-Cell Communication between LPF and Other Major Cell Subsets from TAO and HC. Related to Figures 7.

**a.** The interaction between LPF and other major cell subsets in OCT from TAO patients.  
**b.** The interaction between LPF and other major cell subsets in OCT from HC.