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Supplemental information

Expression and regulatory characteristics

of peripheral blood immune cells in primary

Sjögren's syndrome patients using single-cell transcriptomic

Jinkun Liu, Hongyan Gao, Chengyin Li, Fenglin Zhu, Miao Wang, Yanqiu Xu, and Bin Wu

Clinical characteristic, no. positive (%)	pSS(n=3)	HC(n=3)
Age (years) #	59.3(7)	57.3(4)
Sex, Female	3(100)	2(66.7)
Disease duration, years*	3(3.25)	NA
Labial salivary gland with focal lymphocytic	3(100)	NA
sialadenitis and focus score of \geq 1 foci/4 mm ²		
Ocualr staining scroe ≥ 5	NA	NA
Schirmer's test ≤5 mm/5 min in at least 1 eye	2(66.7)	NA
Unstimulated whole salivary flow rate \leq 0.1 ml/15 min	1(33.3)	NA
Anti-SSA/Ro positive	3(100)	0(0)
Articular	1(33.3)	0(0)
Rash involvement	0(0)	0(0)
Muscular involvement	0(0)	0(0)
Haematological	0(0)	0(0)
lymphadenopathy	1(33.3)	0(0)
nervous involvement	1(33.3)	0(0)
Pulmonary involvement	2(66.7)	0(0)
Laboratory characteristic		
RF (IU/ml) *	11(14.73)	NA
IgG (g/I) #	13.72(3.37)	NA
IgM (g/l) #	1.22(0.92)	NA
IgA (g/l) #	2.22 (1.23)	NA
Complement C3(mg/dl) #	1.00(0.04)	NA
Complement C4 (mg/dl) #	0.21(0.10)	NA
ESR (mm/hr) #	14.3(7.57)	NA
CRP (mg/l) #	0.54(0.35)	NA
ESSPRI#	15.99(10.69)	NA

Table S1. Clinical and laboratory features of patients with pSS and HC studied for scRNA-seq, related to STAR Methods.

*:median (range); #:mean(standard deviation); NA: not applicable; RF: Rheumatoid factor; ESR: Erythrocyte sedimentation rate; CRP: C-reactive protein.



Figure S1. Pseudotime reconstruction and developmental trajectory of cell subsets in monocytes inferred by Monocle3, related to Figure 3. (A) UMAP plot of CD14+ Mos, CD14+CD16+ Mos and CD16+ Mos across all samples. (B) Pseudotime single-cell trajectory reconstructed by Monocle3 for Mos. Pseudotime was shown numbers from one to three. (C) Pseudotemporal heat map showed gene expression dynamics for significant marker genes. (D)The expression of some genes in cell subsets was projected to UMAP map.



Figure S2. Subpopulation ratios and differentially expressed genes of the myeloid cell cluster, related to Figure 3. (A) Different genes induced myeloid cell in HCs and pSS patients. (B) Volcano plot showing significantly upregulated or downregulated genes in CD14+ Mos of pSS_3 patients compared with those of pSS_2 and pSS_1 patients. (C) Violin plots show increased expression of *FOLR3* in CD14+ Mos of pSS_3 patients. (D) Ten-sample integration after QC filtering of the GSE157278 dataset. (E) T-stochastic neighbour embedding (tSNE) plot of a single-cell profile. (F) The expression of marker genes for the cell types are defined above each panel. (G) Identification of monocyte subsets by marker genes.