Supplemental material: Transcriptome datasets selection criteria

The selection criteria for transcriptome datasets of peripheral blood were as follows: 1) Patients were SjS cases, and controls were non-SjS controls; 2) Transcriptome analyses of whole blood or peripheral blood mononuclear cells (PBMCs); 3) Transcriptome analyses were performed using microarrays or RNA-seq; 4) Five samples were the minimal size of each group. Five transcriptome datasets of peripheral blood were finally included **(Supplementary Table 1)**.

The selection criteria for transcriptome datasets of glandular tissues were as follows: 1) Patients were SjS cases, and controls were non-SjS controls; 2) Transcriptome analyses of salivary glandular tissues; 3) Transcriptome analyses were performed using microarrays or RNA-seq; 4) Two samples were the minimal size of each group. One glandular transcriptome study of four SjS patients and four non-SjS controls from our research team were also used. Six transcriptome datasets of glandular tissues were finally included **(Supplementary Table 2)**.

There was only one transcriptome dataset of salivary epithelial cells for patients with SjS and non-SjS controls (GSE97614). GSE97614 provided transcriptome analysis of human salivary epithelial cells from nine patients with SjS and three non-SjS controls. Among those nine SjS patients, six had heavy immune infiltrations (FS $\geq$2) in salivary glands, while the other three had moderate immune infiltrations (FS <2) in salivary glands.

To identify genes expressed mainly in salivary glandular epithelial cells, single-cell RNA-sequencing (scRNA-seq) data of salivary glands from GEO database were analyzed. GSE132867 provided a 10 × scRNA-seq transcriptomic analysis of the murine parotid gland. The count matrix of GSE132867 was downloaded from GEO database and was used in this study.