

GSM4909281 (T1), GSM4909283 (T2) and GSM4909284 (T3) datasets were obtained for analysis. Quality control was screened by the percentage of mitochondria genes (< 10%) according to each sample (Supplementary Fig.1a-1b). The top 2,000 highly variable genes in the scRNA-Seq data were selected using “vst” of Seurat (Supplementary Fig. 1c).

