

Description of Additional Supplementary Files

Supplementary Data 1

Significance of signature genes derived from scRNA-seq analysis of sorted Th cohort. These differential expression analyses were performed using the MAST method implemented in Seurat (two-sided test). P values were adjusted for multiple testing using the Benjamini–Hochberg method.

Supplementary Data 2

Differential expression analysis of TILs and PBMCs for clusters 18+21. Only genes with adjusted p-value < 0.05 are shown. These differential expression analyses were performed using the MAST method implemented in Seurat (two-sided test). P values were adjusted for multiple testing using the Benjamini–Hochberg method.

Supplementary Data 3

Differential expression analysis of clusters 13+26 and 18+21 among TILs. Only genes with adjusted p-value < 0.05 are shown. These differential expression analyses were performed using the MAST method implemented in Seurat (two-sided test). P values were adjusted for multiple testing using the Benjamini–Hochberg method.

Supplementary Data 4

Summary of the raw sequence data from scRNA-seq analysis (scRNA-seq surgery cohort n = 8 and sorted Th cohort n = 3).

Supplementary Data 5

Summary of the raw sequence data from scRNA-seq analysis of PBMC before treatment (scRNA-seq cohort 2, n=34 and scRNA-seq renal cell cancer patients, n = 3).