Figure legends

**Supplementary Figure 1. Hierarchical clustering and principle component analysis of CD8\(^+\) TILs from CRC advanced and early stages.** Differentially expressed genes with fold change <2 and p value<0.05, were subjected to CLC analysis to perform clustering. Hierarchical clustering of CD8\(^+\) TILs from 18 CRC patients based on DEGs. Each column represents a sample and each row represents a transcript. Expression level of each gene in a single sample is depicted according to color scale (A). PCA based on DEGs in CD8\(^+\) TILs from CRC patients with advanced and early stages (B).

**Supplementary Figure 2. Identification of differentially expressed genes in tumor-infiltrating CD8\(^+\) T cells from CRC patients in stage pairwise comparisons.** Volcano plots show genes that were significantly upregulated (in red) or downregulated (in green), or remained unchanged (in gray) when comparing stage II versus I (A), III vs I (B), IV versus I (C), III versus II (D), IV versus II (E) and IV versus III (F). The number of downregulated and upregulated genes is indicated in each plot.

**Supplementary Figure 3: Common functional pathways in CD8\(^+\) TILs between disease stages.** Venn diagrams based on functional annotations of upregulated (A) and downregulated (B) genes. Tables show the name of upregulated or downregulated pathways corresponding to each cluster.

**Supplementary Figure 4: Association between poor prognosis CD8\(^+\) T cell gene signature and anatomical CRC location, gender or age.** Supporting data for the evaluation of poor prognosis CD8\(^+\) T cell gene signature (denoted as ppCD8sig) in TCGA CRC dataset. Distribution of patients with high, intermediate, or low ppCD8sig scores across the different anatomical location of their colon cancer; left-sided colon cancer patients (splenic flexure, descending and sigmoid colon) and right-sided colon cancers (hepatic flexure, ascending colon and the cecum) (A). The association between ppCD8sig and sex (B) or patient age (C) using Chi-squared (\(\chi^2\)) test. H.: hepatic; A.: ascending; S.: splenic; D.: descending; n.s.: not significant.

**Supplementary Figure 5: Protein-protein interaction (PPI) networks in the poor prognosis CD8sig score.** PPI networks based on differentially expressed genes in CD8\(^+\) TILs from patients with high ppCD8sig score vs low ppCD8sig score. PPI networks based on upregulated (B) and downregulated (C) genes in in CD8\(^+\) TILs from patients with high ppCD8sig score compared with those with low scores.