**Supplementary Material**

**Figure S1 Results of t-SNE dimensional reduction in GSE81861**

A) Colorectal tumor tissue and normal mucosa were separated distinctly by t-SNE algorithm. B) Different cell populations were separated distinctly by t-SNE algorithm.
Figure S2 Hub gene expressions respectively in different cell populations.

A) BMP5 was activated in both tumor epithelial cells and T cells. The mean expression in 2 cell populations were displayed in histogram. B) The cell population-expression scatter diagrams of BMP5. BMP5 were expressed in both tumor epithelial and T cells. C) The cell population-expression scatter diagrams of HOXC6. HOXC6 were expressed only in epithelial cells. D) The cell population-expression scatter diagrams of HOXC8. HOXC8 were expressed only in epithelial cells.
### Table S1: Cluster of Epithelial cells

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Note: logFC.x is log2(Fold change) of cluster x vs. gene high expression cluster
Table S4: Significant upregulated marker genes in low pathologic-stage-related cluster of T cells

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Note: logFC.x is log2(Fold change) of cluster x vs. gene high expression cluster
Table S5: Results of spearman correlation analysis with the 84 pathologic-stage-related genes

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Table S6: gene expression signatures reference for different cell categories

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Table S7: Results of CIBERSORT with CRC patients in TCGA
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**Table S8: Results of GSEA associated with high-low C1/C2 ratio**

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