**Supplementary Data**

**Protein-Protein Interaction (PPI) Network**

The Overexpressed DEGs were imported into STRING database with minimum required interaction score more than 0.4 to construct PPI network(Szklarczyk et al., 2019). The data of nodes from the PPI network was further analyzed by Cytoscape software (version 3.7.2)(Shannon et al., 2003). In addition, Molecular Complex Detection (MCODE) (Bader and Hogue, 2003)was used to find densely connected regions by selecting clusters with node numbers greater than 10.

**Supplementary Data 1.** A gene list of immune and stromal signatures.

**Supplementary Figure 1.** Distribution of immune/stromal scores in T stage (A) and lymph node status (B).

**Supplementary Figure 2.** PPI network of DEGs and module identification. (A) The PPI network of 67 overexpressed DEGs. (B-C) Module 1 (B) and module 2 (C) were the top two modules (> 10 nodes) in the PPI network (A). The color of nodes indicated the combine scores.

**References**

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