S100A16 is a potential prognostic marker for PC
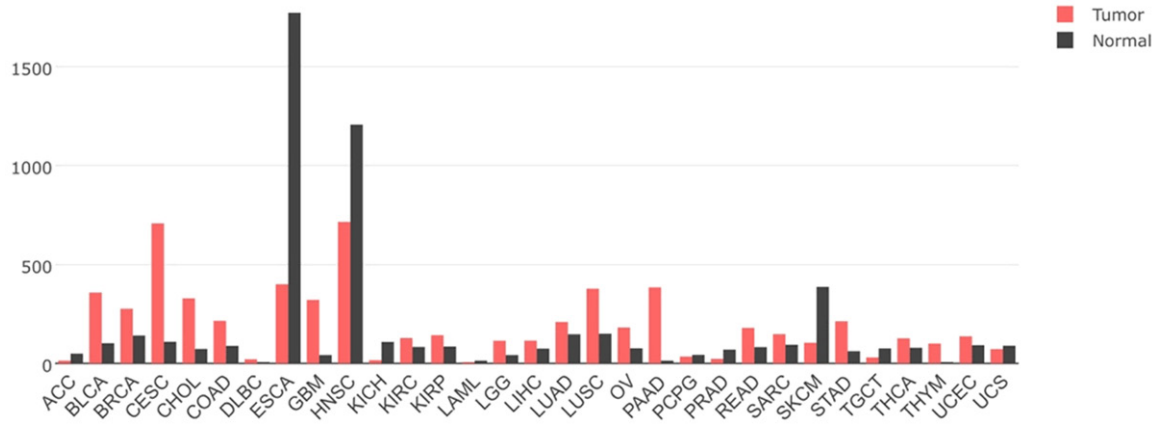

Figure S1. The S100A16 expression profile across tumor samples and paired normal tissues. The height of bar represents the median expression of certain tumor type or normal tissue. In order to understand the expression of S100A16 in various tumors and normal tisues, GEPIA database (http://gepia.cancer-pku.cn) was used to analyze its expression. It is obvious that the expression level of S100A16 in PAAD is much higher than that in the paired normal tissues.

Figure S2. A representative heatmap of dysregulated genes in PAAD. The dysregulated genes in PAAD were investigated by comparing the RNA sequencing data between tumor samples and normal samples.