



Supplementary Figure S6. Expression profile of selected genes in the tumor (red) and normal tissues (blue) across different cancers. The X-axis represents normal and tumor samples and Y-axis represents median expression ($\log_2(\text{TPM} + 1)$). The median expression values are the $\log_2(\text{TPM} + 1)$ values. ACC: Adrenocortical carcinoma, BLCA: Bladder Urothelial Carcinoma, BRCA: breast invasive carcinoma, CESC: cervical squamous cell carcinoma and endocervical adenocarcinoma, COAD: colon adenocarcinoma, EUSC: Lymphoid Neoplasm Diffuse Large B-cell Lymphoma, ESCA: esophageal carcinoma, GBMLGG: Glioblastoma multiforme, HNSC: Head and neck squamous cell carcinoma, KIRC: Kidney renal clear cell carcinoma, LIHC: Liver Hepatocellular Carcinoma, LUAD: lung adenocarcinoma, LUSC: lung squamous cell carcinoma, PAAD: Pancreatic adenocarcinoma, PRAD: Prostate adenocarcinoma, READ: Rectum adenocarcinoma, STAD: stomach adenocarcinoma, THCA: Thyroid carcinoma, TCGA: Testicular Germ Cell Tumors, TPM: Transcripts per Million.