**Availability of data and material**

The autonomic nervous system related genes were collected through the Molecular Signatures Database (MSigDB) by taking “Autonomic Nervous System” as key words. The GOBP\_AUTONOMIC\_NERVOUS\_SYSTEM\_DEVELOPMENT data set contains a total of 46 genes related to Autonomic Nervous System (https://www.gsea-msigdb.org/gsea/msigdb/human/geneset/GOBP\_AUTONOMIC\_NERVOUS\_SYSTEM\_DEVELOPMENT.html).

Two datasets with clear tumor immunotherapy efficacy, including SKCM related data set GSE115978 and BCC related data set GSE123813 were downloaded from the GEO database (https://www.ncbi.nlm.nih.gov/geo/) through R package GEOquery.

Thirty-four scRNA-Seq datasets contained stromal or immune cells were collected from the TISCH database (http://tisch.comp-genomics.org/), comprising 345 patients and 663760 cells. The datasets cover 17 cancer types including BCC, SKCM, Breast Cancer (BRCA), Cholangiocarcinoma (CHOL), colorectal Cancer (CRC), Glioma (GBM), HNSC, Liver Hepatocellular Cancer (LIHC), Medulloblastoma (MB), Merkel Cell Carcinoma (MCC), Multiple Myeloma (MM), Neuroendocrine Tumor, Non-small Cell Lung Cancer (NSCLC), Ovarian Serous Cystadenocarcinoma (OV), Pancreatic Adenocarcinoma (PAAD), STAD and Uveal Melanoma (UVM).

The pan-cancer transcriptome data set of The Cancer Genome Atlas (TCGA) was downloaded from the UCSC Xena database (http://xena.ucsc.edu). TMB and MSI data were downloaded from the cBioPortal database (http://cbioportal.org). The relevant clinicopathological information of 30 different cancer types was downloaded through R package TCGAbiolink. The survival data all met the following criteria containing mRNA expression and clinical data. All patients had completed standardized diagnosis and treatment, who survived for more than 30 days.

Eight ICI related RNA-Seq datasets consisting of four SKCM related datasets (Hugo 2016 (PMID: 26997480), Liu 2019 (PMID: 31792460), Gide 2019 (PMID: 30753825), Riaz 2017 (PMID: 29033130)), two Urothelial Carcinoma (UC) related datasets (Mariathasan 2018 (PMID: 29443960), Synder 2017 (PMID: 28552987)), one GBM related data set (Zhao 2019 (PMID: 30742119)), and one Renal Cell Carcinoma (RCC) related data set (Braun 2020 (PMID: 32472114)). The data set Hugo 2016 of SKCM contained 27 pre-treated tumor samples from 26 patients, and the data set Zhao 2019 GBM included 34 pre-treated tumor samples from 17 patients. For these two data groups, one tumor sample was randomly selected for each patient. Seven pan-cancer signatures (IPRES.Sig (PMID: 26997480), INFG.Sig (PMID: 28650338), T.cell.inflamed.Sig (PMID: 28650338), PDL1.Sig (PMID: 22658127), LRRC15.CAF.Sig (PMID: 31699795), NLRP3.Sig (PMID: 33212483), Cytotoxic.Sig (PMID: 25594174)) and four SKCM specific signatures (CRMA.Sig (PMID: 29656892), ImmuCells.Sig (PMID: 33033253), IMS.Sig (PMID: 33542239), TRS.Sig (PMID: 34804045)) gene lists were collected . The codes and algorithms of the above 11 signatures were derived from the original studies, such as ssGSEA of NLRP3.Sig and cancer classification of ImmuneCell.Sig.