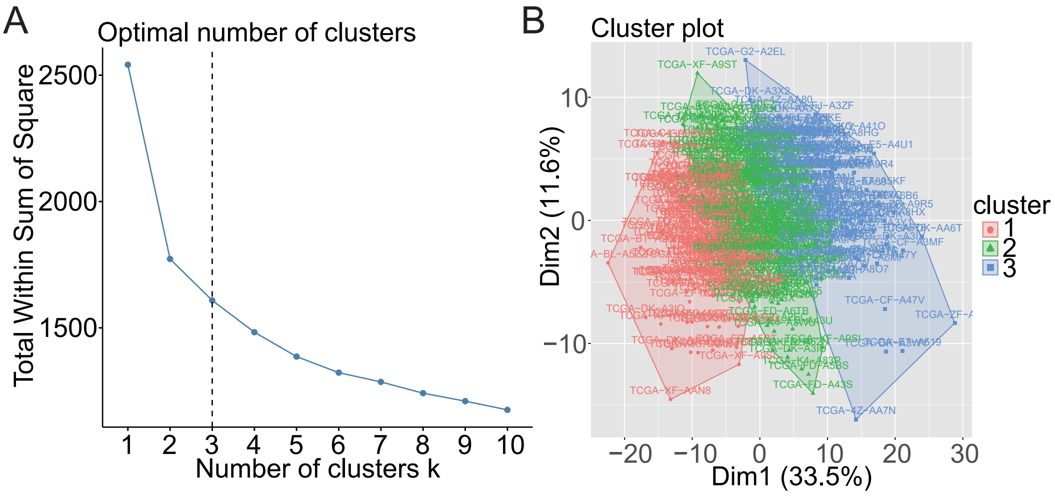

Figure S1 Identification of BC subtypes from TCGA. (A) The ideal number of clusters (K) was 3. (B) Cluster plot of 3 subtypes. BC, bladder cancer; TCGA, The Cancer Genome Atlas; Dim1, dimension 1; Dim2, Dimension 2.

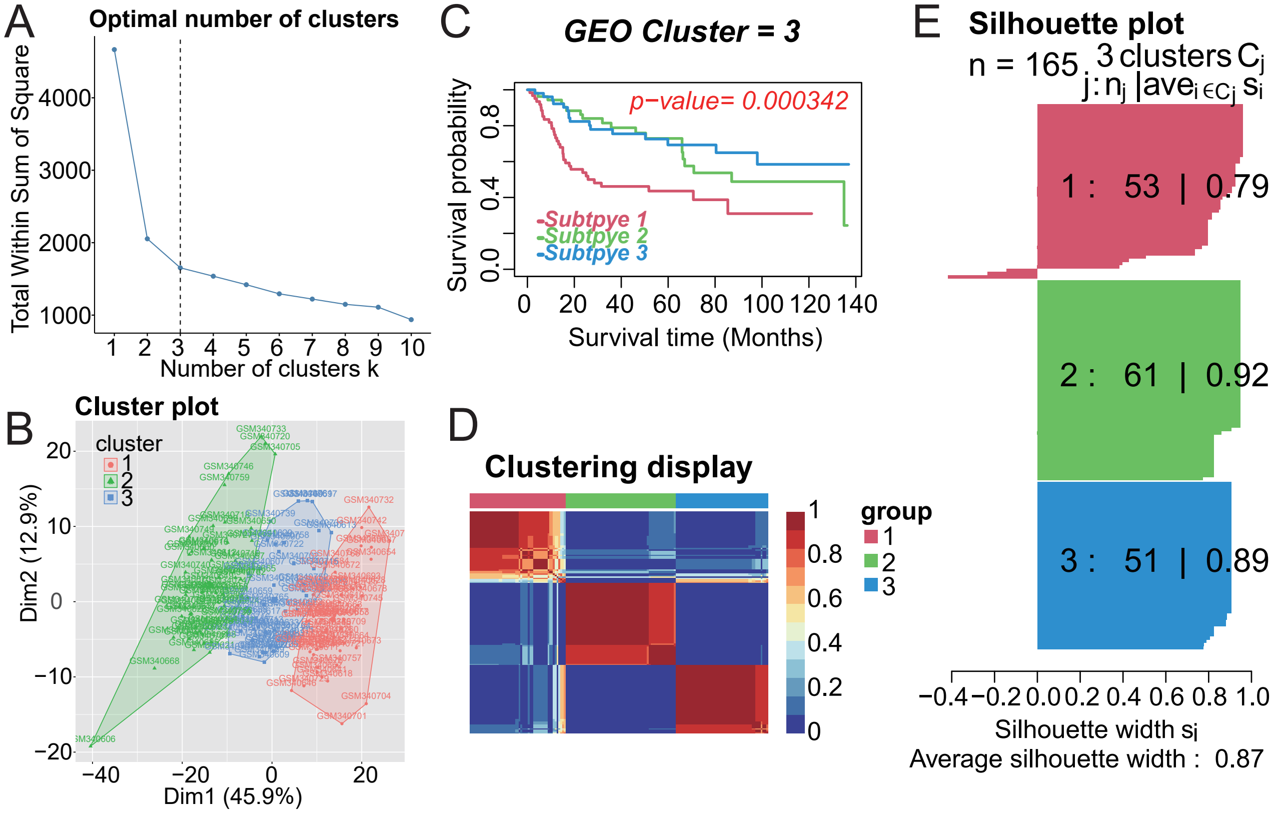

Figure S2 Identification of BC subtypes from GSE13507 was conducted. (A) The optimal number of clusters (K) was determined to be 3. (B) Visualization of the cluster results was performed. (C) Kaplan-Meier survival analysis for the three subtypes. (D) The NMF method was used to cluster BC samples. (E) Silhouette plot plots with a value of 0.87. BC, bladder cancer; NMF, nonnegative matrix factorization; GEO, gene expression omnibus; Dim1, dimension 1; Dim2, Dimension 2.

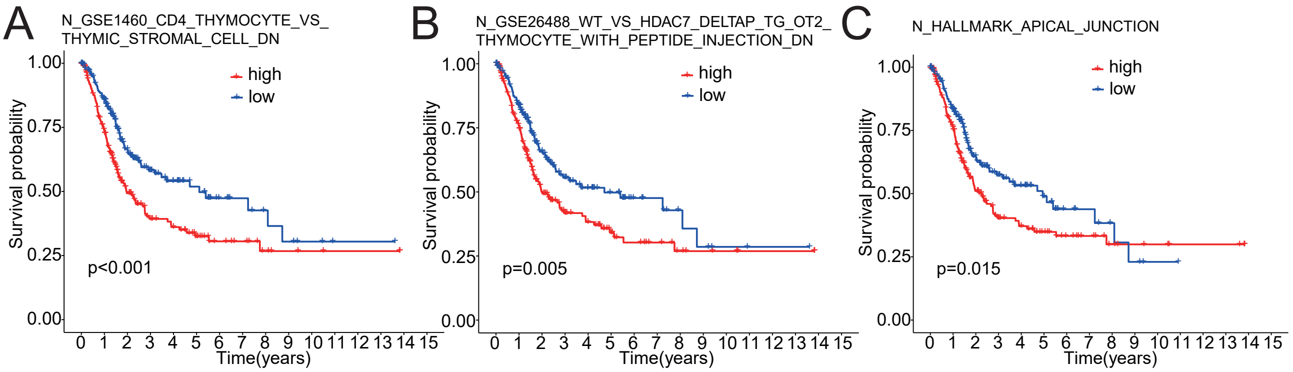

Figure S3 Kaplan-Meier survival analysis based on OS was performed for three prognostic gene sets in the model separately. OS, overall survival.

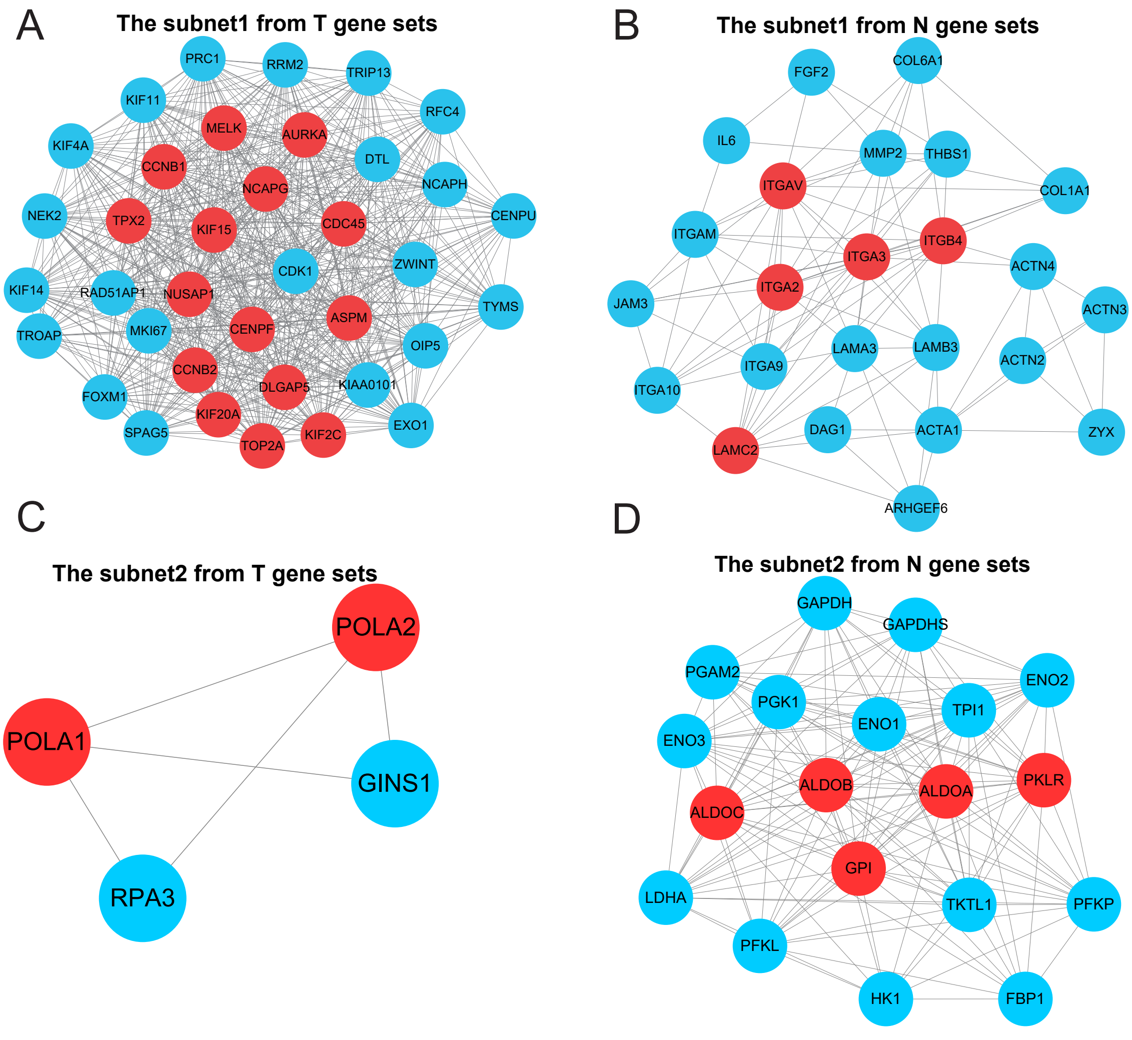

Figure S4 The (A,B) subnet1 and (C,D) subnet2 of PPI network by Cytoscape plugin MCODE of T and N gene sets. Red nodes indicate the hub genes. PPI, protein-protein interaction; MCODE, Molecular Complex Detection; T, tumor; N, normal; Subnet1, subnetwork 1; Subnet2, subnetwork 2.

Table S1 The 109 differentially expressed gene sets were identified among three BC subtypes

N_GSE1460_CD4_THYMOCYTE_VS_THYMIC_STROMAL_CELL_DN
N_HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
N_GSE6259_CD4_TCELL_VS_CD8_TCELL_UP
N_GSE1460_INTRATHYMIC_T_PROGENITOR_VS_THYMIC_STROMAL_CELL_DN
N_GSE26488_WT_VS_HDAC7_DELTAP_TG_OT2_THYMOCYTE_WITH_PEPTIDE_INJECTION_DN
N_GSE4748_CTRL_VS_LPS_AND_CYANOBACTERIUM_LPSLIKE_STIM_DC_3H_UP
N_HALLMARK_APICAL_JUNCTION
N_GSE4748_CTRL_VS_LPS_STIM_DC_3H_UP
N_GSE1432_6H_VS_24H_IFNG_MICROGLIA_UP
N_GSE43955_1H_VS_20H_ACT_CD4_TCELL_WITH_TGFB_IL6_DN
N_GSE8868_SPLEEN_VS_INTESTINE_CD11B_POS_CD11C_NEG_DC_DN
N_GSE3982_DC_VS_BCELL_UP
N_GSE43955_1H_VS_42H_ACT_CD4_TCELL_WITH_TGFB_IL6_DN
N_GSE360_L_DONOVANI_VS_B_MALAYI_LOW_DOSE_DC_UP
N_HALLMARK_HYPOXIA
N_GSE43955_1H_VS_60H_ACT_CD4_TCELL_UP
N_GSE6269_HEALTHY_VS_STAPH_PNEUMO_INF_PBMC_DN
N_GSE6269_FLU_VS_STAPH_AUREUS_INF_PBMC_DN
N_GSE43955_TGFB_IL6_VS_TGFB_IL6_IL23_TH17_ACT_CD4_TCELL_52H_DN
T_GSE2706_UNSTIM_VS_2H_LPS_DC_UP
N_GSE19401_UNSTIM_VS_RETINOIC_ACID_AND_PAM2CSK4_STIM_FOLLICULAR_DC_DN
N_GSE22140_GERMFREE_VS_SPF_MOUSE_CD4_TCELL_DN
N_GSE24634_IL4_VS_CTRL_TREATED_NAIVE_CD4_TCELL_DAY7_DN
N_GSE2706_R848_VS_R848_AND_LPS_8H_STIM_DC_DN
N_GSE22196_HEALTHY_VS_OBESE_MOUSE_SKIN_GAMMADELTA_TCELL_DN
N_GSE9037_CTRL_VS_LPS_4H_STIM_IRAK4_KO_BMDM_DN
N_GSE22140_HEALTHY_VS_ARTHRITIC_GERMFREE_MOUSE_CD4_TCELL_DN
N_GSE19198_CTRL_VS_IL21_TREATED_TCELL_24H_UP
N_GSE19401_NAIVE_VS_IMMUNIZED_MOUSE_PLN_FOLLICULAR_DC_UP
N_GSE43955_TH0_VS_TGFB_IL6_TH17_ACT_CD4_TCELL_4H_UP
N_GSE9601_NFKB_INHIBITOR_VS_PI3K_INHIBITOR_TREATED_HCMV_INF_MONOCYTE_DN
N_GSE22140_GERMFREE_VS_SPF_ARTHRITIC_MOUSE_CD4_TCELL_UP
N_GSE3039_NKT_CELL_VS_B2_BCELL_DN
N_GSE9988_ANTI_TREM1_VS_CTRL_TREATED_MONOCYTES_UP
N_GSE36891_UNSTIM_VS_POLYIC_TLR3_STIM_PERITONEAL_MACROPHAGE_UP
N_GSE42021_CD24HI_TREG_VS_CD24HI_TCONV_THYMUS_DN
N_GSE27434_WT_VS_DNMT1_KO_TREG_DN

Table S1 (*continued*)

Table S1 (*continued*)

N_GSE30971_CTRL_VS_LPS_STIM_MACROPHAGE_WBP7_KO_4H_UP
N_GSE45365_NK_CELL_VS_CD11B_DC_DN
N_GSE22886_DAY0_VS_DAY1_MONOCYTE_IN_CULTURE_DN
N_GSE19923_E2A_KO_VS_HEB_AND_E2A_KO_DP_THYMOCYTE_UP
N_GSE30971_CTRL_VS_LPS_STIM_MACROPHAGE_WBP7_HET_2H_UP
N_GSE42021_TREG_PLN_VS_CD24INT_TREG_THYMUS_UP
N_GSE2706_R848_VS_LPS_8H_STIM_DC_DN
N_GSE13946_CTRL_VS_DSS_COLITIS_GD_TCELL_FROM_COLON_UP
N_GSE25123_WT_VS_PPARG_KO_MACROPHAGE_UP
N_GSE30971_CTRL_VS_LPS_STIM_MACROPHAGE_WBP7_KO_2H_UP
N_HALLMARK_COMPLEMENT
N_HALLMARK_INFLAMMATORY_RESPONSE
N_HALLMARK_TNFA_SIGNALING_VIA_NFKB
N_GSE42021_TCONV_PLN_VS_TREG_PRECURSORS_THYMUS_DN
N_GSE23502_WT_VS_HDC_KO_MYELOID_DERIVED_SUPPRESSOR_CELL_BM_DN
N_GSE30971_WBP7_HET_VS_KO_MACROPHAGE_2H_LPS_STIM_DN
N_GSE30971_WBP7_HET_VS_KO_MACROPHAGE_DN
N_GSE2706_UNSTIM_VS_2H_R848_DC_DN
N_GSE15330_LYMPHOID_MULTIPOTENT_VS_MEGAKARYOCYTE_ERYTHROID_PROGENITOR_IKAROS_KO_DN
N_GSE14386_UNTREATED_VS_IFNA_TREATED_ACT_PBMC_MS_PATIENT_DN
N_GSE41176_UNSTIM_VS_ANTI_IGM_STIM_BCELL_1H_UP
N_GSE29617_CTRL_VS_DAY7_TIV_FLU_VACCINE_PBMC_2008_UP
N_GSE3982_CTRL_VS_LPS_4H_MAC_DN
N_GSE9988_LPS_VS_CTRL_TREATED_MONOCYTE_UP
N_GSE2706_UNSTIM_VS_2H_LPS_DC_DN
N_GSE35685_CD34POS_CD38NEG_VS_CD34POS_CD10POS_BONE_MARROW_DN
N_GSE9988_LOW_LPS_VS_VEHICLE_TREATED_MONOCYTE_UP
N_GSE9988_LOW_LPS_VS_CTRL_TREATED_MONOCYTE_UP
N_GSE9988_ANTI_TREM1_VS_LPS_MONOCYTE_DN
N_GSE9988_LPS_VS_VEHICLE_TREATED_MONOCYTE_UP
N_GSE9988_ANTI_TREM1_VS_LOW_LPS_MONOCYTE_DN
N_GSE2706_UNSTIM_VS_2H_LPS_AND_R848_DC_DN
N_GSE9988_ANTI_TREM1_VS_ANTI_TREM1_AND_LPS_MONOCYTE_DN
T_GSE32164_RESTING_DIFFERENTIATED_VS_ALTERNATIVELY_ACT_M2_MACROPHAGE_UP
T_GSE24634_TEFF_VS_TCONV_DAY10_IN_CULTURE_UP
T_GSE25088_WT_VS_STAT6_KO_MACROPHAGE_DN

Table S1 (*continued*)

Table S1 (*continued*)

T_GSE3982_MEMORY_CD4_TCELL_VS_TH2_DN
T_GSE3982_NKCELL_VS_TH1_DN
T_GSE3982_EFF_MEMORY_CD4_TCELL_VS_TH2_DN
T_GSE36826_WT_VS_IL1R_KO_SKIN_STAPH_AUREUS_INF_UP
T_GOLDRATH_EFF_VS_MEMORY_CD8_TCELL_UP
T_GSE3982_CENT_MEMORY_CD4_TCELL_VS_TH2_DN
T_GSE26156_DOUBLE_POSITIVE_VS_CD4_SINGLE_POSITIVE_THYMOCYTE_DN
T_GSE30962_ACUTE_VS_CHRONIC_LCMV_PRIMARY_INF_CD8_TCELL_DN
T_GSE45365_HEALTHY_VS_MCMV_INFECTION_CD11B_DC_DN
T_GSE11386_NAIVE_VS_MEMORY_BCELL_UP
T_GSE16451_CTRL_VS_WEST_EQUINE_ENC_VIRUS_IMMATURE_NEURON_CELL_LINE_DN
T_GSE13485_CTRL_VS_DAY7_YF17D_VACCINE_PBMC_DN
T_KAECH_DAY8_EFF_VS_MEMORY_CD8_TCELL_UP
T_GSE13485_DAY3_VS_DAY7_YF17D_VACCINE_PBMC_DN
T_GSE10239_NAIVE_VS_KLRG1HIGH_EFF_CD8_TCELL_DN
T_GSE45365_HEALTHY_VS_MCMV_INFECTION_CD11B_DC_IFNAR_KO_DN
T_GSE24634_IL4_VS_CTRL_TREATED_NAIVE_CD4_TCELL_DAY7_UP
T_GSE28726_NAIVE_VS_ACTIVATED_CD4_TCELL_DN
T_GSE2405_S_AUREUS_VS_UNTREATED_NEUTROPHIL_DN
T_GSE45365_WT_VS_IFNAR_KO_BCELL_MCMV_INFECTION_DN
T_GSE40274_CTRL_VS_EOS_TRANSDUCED_ACTIVATED_CD4_TCELL_UP
T_GSE13547_CTRL_VS_ANTI_IGM_STIM_BCELL_2H_UP
T_GSE13547_2H_VS_12_H_ANTI_IGM_STIM_ZFX_KO_BCELL_DN
T_GSE28726_NAIVE_CD4_TCELL_VS_NAIVE_VA24NEG_NKTCELL_UP
T_GSE39110_DAY3_VS_DAY6_POST_IMMUNIZATION_CD8_TCELL_WITH_IL2_TREATMENT_UP
T_GSE45365_WT_VS_IFNAR_KO_CD11B_DC_MCMV_INFECTION_DN
T_GSE12845_IGD_POS_BLOOD_VS_PRE_GC_TONSIL_BCELL_DN
T_GSE25088_WT_VS_STAT6_KO_MACROPHAGE_IL4_STIM_DN
T_GSE13547_2H_VS_12_H_ANTI_IGM_STIM_BCELL_UP
T_GSE39110_DAY3_VS_DAY6_POST_IMMUNIZATION_CD8_TCELL_DN
T_GSE14415_TCONV_VS_FOXP3_KO_INDUCED_TREG_DN
T_GSE14415_INDUCED_VS_NATURAL_TREG_DN
T_GSE13547_CTRL_VS_ANTI_IGM_STIM_BCELL_12H_UP
T_GSE24634_TEFF_VS_TCONV_DAY7_IN_CULTURE_UP
T_GSE14415_NATURAL_TREG_VS_TCONV_DN
T_GSE15750_DAY6_VS_DAY10_EFF_CD8_TCELL_UP

BC, bladder cancer.

Table S2 The 20 representative prognosis-related gene sets in BC subtypes are identified by univariate Cox regression analysis

id	HR	HR.95L	HR.95H	pvalue
N_GSE1460_CD4_THYMOCYTE_VS_THYMIC_STROMAL_CELL_DN	1,955.7124	52.861109	72,355.861	3.90E-05
N_HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	10.094612	2.4250258	42.020661	0.0014862
N_GSE6259_CD4_TCELL_VS_CD8_TCELL_UP	1,240.9502	24.347049	63,250.267	0.0003829
N_GSE1460_INTRATHYMIC_T_PROGENITOR_VS_THYMIC_STROMAL_CELL_DN	388.4133	16.241028	9,289.1219	0.0002323
N_GSE26488_WT_VS_HDAC7_DELTAP_TG_OT2_THYMOCYTE_WITH_PEPTIDE_INJECTION_DN	12,414.218	82.565572	1,866,550.4	0.0002282
N_GSE4748_CTRL_VS_LPS_AND_CYANOBACTERIUM_LPSLIKE_STIM_DC_3H_UP	444.2844	8.9548426	22,042.669	0.00221
N_HALLMARK_APICAL_JUNCTION	201.6031	4.8516776	8,377.2696	0.0052625
N_GSE4748_CTRL_VS_LPS_STIM_DC_3H_UP	474.04836	13.815365	16,266.081	0.0006364
N_GSE1432_6H_VS_24H_IFNG_MICROGLIA_UP	463.08245	3.6617548	58,563.549	0.0129344
N_GSE8868_SPLEEN_VS_INTESTINE_CD11B_POS_CD11C_NEG_DC_DN	1,457.3729	6.0379319	351,765.42	0.0092597
N_GSE3982_DC_VS_BCELL_UP	125.63682	2.3850326	6,618.1946	0.0168613
N_GSE43955_1H_VS_42H_ACT_CD4_TCELL_WITH_TGFB_IL6_DN	469.4618	2.8868703	76,343.709	0.0178805
N_HALLMARK_HYPOXIA	86.822483	1.5269002	4,936.8936	0.0303676
T_GSE2706_UNSTIM_VS_2H_LPS_DC_UP	0.000419	1.54E-06	0.1142713	0.0065673
N_GSE9988_ANTI_TREM1_VS_CTRL_TREATED_MONOCYTES_UP	37.43445	1.0495922	1,335.1262	0.0469772
N_GSE36891_UNSTIM_VS_POLYIC_TLR3_STIM_PERITONEAL_MACROPHAGE_UP	24.76714	1.2664715	484.34664	0.0343714
T_GSE32164_RESTING_DIFFERENTIATED_VS_ALTERNATIVELY_ACT_M2_MACROPHAGE_UP	157.48352	2.2281883	11,130.594	0.0198728
T_GSE25088_WT_VS_STAT6_KO_MACROPHAGE_DN	52.396331	1.9097451	1,437.5612	0.0191375
T_GSE3982_MEMORY_CD4_TCELL_VS_TH2_DN	98.194238	1.241716	7,765.1478	0.0396812
T_GSE45365_HEALTHY_VS_MCMV_INFECTION_CD11B_DC_DN	29.851438	1.1207532	795.09775	0.0425563

BC, bladder cancer.

Table S3 A prognostic model containing seven gene sets was established by the LASSO analysis

Gene	Coef
N_GSE1460_CD4_THYMOCYTE_VS_THYMIC_STROMAL_CELL_DN	9.4789547
N_GSE26488_WT_VS_HDAC7_DELTAP_TG_OT2_THYMOCYTE_WITH_PEPTIDE_INJECTION_DN	4.7435145
N_HALLMARK_APICAL_JUNCTION	–0.56884
N_GSE1432_6H_VS_24H_IFNG_MICROGLIA_UP	–5.037914
N_GSE43955_1H_VS_42H_ACT_CD4_TCELL_WITH_TGFB_IL6_DN	–2.133411
N_HALLMARK_HYPOXIA	–1.829146
T_GSE25088_WT_VS_STAT6_KO_MACROPHAGE_DN	3.0210103

LASSO, least absolute shrinkage and selection operator.