SUPPLEMENTARY TABLES

Supplementary Table 1. The list of cell surface markers used to identify cell cluster.

Cells	Markers
Epithelial	PECAM1, CD34, VWF, EPCAM, SFN, KRT19
Fibroblasts	ACTA2, MCAM, MYLK, MYL9, FAP, THY1
Immune cells	PTPRC, CD3G, CD3E, CD79A, BLNK, CD68, CSF1R, MARCO, CD207
B cell	CD79A, CD79B, CD19, MS4A1, MZB1
T cell	CD3D, CD3E, CD3G, CD2
Macrophages	HLA-DMB, HLA-DQA1, HLA-DRB5, CD68, AIF1, CD74, CYBB, DOK3, KYNU, METRNL, MS4A6A, MS4A7, PIM1, PLAC8, PLBD1, PLTP, S100A11, SH3BGRL, SPINT2, SYNGR2, TREM1, CCL2, CD93, CIB1, CREM, SAMHD1, TMEM123, DSE, FGR, FOSL2
	FPR3, GPR65, ITGA4, PTPN7, SAMHD1, TGFBI, THBD
	VOPP1
Dendritic cell (DC)	HLA-DPB1, HLA-DQB1, HLA-DRA, HLA-DPA1, CD1E, CD83

Supplementary Table 2. 219 TAMRG signature.

Gene symbol
ABI3, ADAP2, AIF1, ALOX5AP, AOAH, APBB1IP, APOBR, APOL6, ARHGAP30, ARHGAP9, ARHGDIB, BIN2, BTK, C1orf162, C1QA, C1QB, C1QC, C3AR1, CCR1, CCR5, CD14, CD163, CD180, CD2, CD300A, CD37, CD3E, CD4, CD48, CD53, CD79A, CD84, CD86, CLEC7A, CMPK2, CSF1R, CSF2RA, CSF2RB, CTSS, CXCL10, CYBB, CYTH4, CYTIP, DDX60, DOCK2, DOK2, DOK3, ETV7, EVI2A, EVI2B, FAM78A, FCER1G, FCGR1A, FCGR2A, FCGR2B, FCGR3A, FERMT3, FGL2, FPR3, FYB1, GBP4, GIMAP4, GIMAP6, GNA15, GPR65, GPR84, HAVCR2, HCK, IFI35, IFI44, IFI44L, IFIH1, IFIT2, IFIT3, IGHA1, IGHG1, IGHG2, IGHG3, IGHGP, IGHM, IGHV1-18, IGHV1-2, IGHV1-46, IGHV1-69, IGHV1-69D, IGHV3-11, IGHV3-15, IGHV3-21, IGHV3-23, IGHV3-30, IGHV3-33, IGHV3-48, IGHV3-49, IGHV3-53, IGHV3-66, IGHV3-7, IGHV3-74, IGHV4-28, IGHV4-31, IGHV4-34, IGHV4-39, IGHV4-59, IGHV4-61, IGHV5-51, IGKC, IGKV1-12, IGKV1-16, IGKV1-17, IGKV1-27, IGKV1-39, IGKV1-5, IGKV1-6, IGKV1-8, IGKV1-9, IGKV3-11, IGKV3-15, IGKV3-20, IGKV3D-20, IGKV4-1, IGLC2, IGLC3, IGLL5, IGLV1-40, IGLV1-44, IGLV1-47, IGLV1-51, IGLV2-11, IGLV2-14, IGLV2-23, IGLV2-8, IGLV3-1, IGLV3-19, IGLV3-21, IGLV3-25, IGLV4-69, IGLV6-57, IGSF6, IKZF1, IL10RA, IL2RB, IL2RG, ITGAL, ITGAM, ITGAX, ITGB2, JCHAIN, LAIR1, LAPTM5, LAT2, LCP2, LILRB1, LILRB2, LILRB4, LPXN, LRRC25, LSP1, LY86, MNDA, MPEG1, MPP1, MS4A4A, MS4A6A, MS4A7, MSR1, MX1, MYO1F, MZB1, NCF1, NCF2, NCF4, NCKAP1L, NFAM1, NPL, OAS1, OAS2, OAS3, OASL, OSCAR, PARP12, PARP14, PARP9, PCED1B-AS1, PDCD1LG2, PLEK, PLSCR1, PTPRC, RAC2, RASAL3, RCSD1, RNASE6, RSAD2, SAMD9, SAMD9L, SAMSN1, SASH3, SELPLG, SLA, SLAMF7, SLAMF8, SLC37A2, SLCO2B1, SP100, SPI1, SRGN, STX11, TAGAP, TAP1, TBXAS1, TLR2, TLR7, TNFAIP8L2, TNFSF13B, TRIM22, TRPV2, TYMP, TYROBP, UBE2L6, VSIG4,WAS

Supplementary Table 3. Univariate and multivariate Cox proportional hazards analyses of risk score and clinicopathological variables in the TCGA training set.

Variable	TCGA training set (*n* = 375)			
	Univariate analysis		Multivariate analysis	
	HR (95% CI)	*P* value	HR (95% CI)	*P* value
Age	1.02 (1.008–1.032)	0.001	1.017 (1.005–1.030)	0.0059
Stage	2.115 (0.938–4.766)	0.04	1.71 (0.755–3.874)	0.198
Grade	1.183 (0.820–1.706)	0.4	–	–
M(M1/M0/Mx)	1.262 (0.90–1.77)	0.18	–	–
N(N1/N0/Nx)	1.428 (0.836–2.439)	0.19	–	–
Residual	1.609 (1.210–2.139)	0.002	1.464 (1.095–1.958)	0.01
Risk score	1.604 (1.38–1.865)	3e-07	1.596 (1.366–1.865)	4.07e-09

Abbreviations: HR: hazard ratio; CI: confidence interval; M: metastasis; N: lymph node.

Supplementary Table 4. C-index (standard error) of the prognostic signatures and clinical characteristics in the nine datasets.

Study	Training set	Validation set (average)	Overall
Our study	0.614 (0.022)	0.611 (0.028)	0.613
Crijns 2009 [45]	0.54 (0.021)	0.560 (0.023)	0.55
Denkert 2009 [46]	0.566 (0.021)	0.541 (0.023)	0.554
Hernandez 2010 [47]	0.526 (0.021)	0.510 (0.023)	0.518
Kang 2012 [48]	0.542 (0.021)	0.514 (0.023)	0.528
Kernagis 2012 [49]	0.54 (0.021)	0.561 (0.023)	0.55
Konstantinopoulos 2010 [50]	0.495 (0.021)	0.529 (0.023)	0.512
Sabatier 2011 [51]	0.555 (0.021)	0.543 (0.023)	0.549
Yoshihara 2012 [52]	0.592 (0.021)	0.576 (0.023)	0.584

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