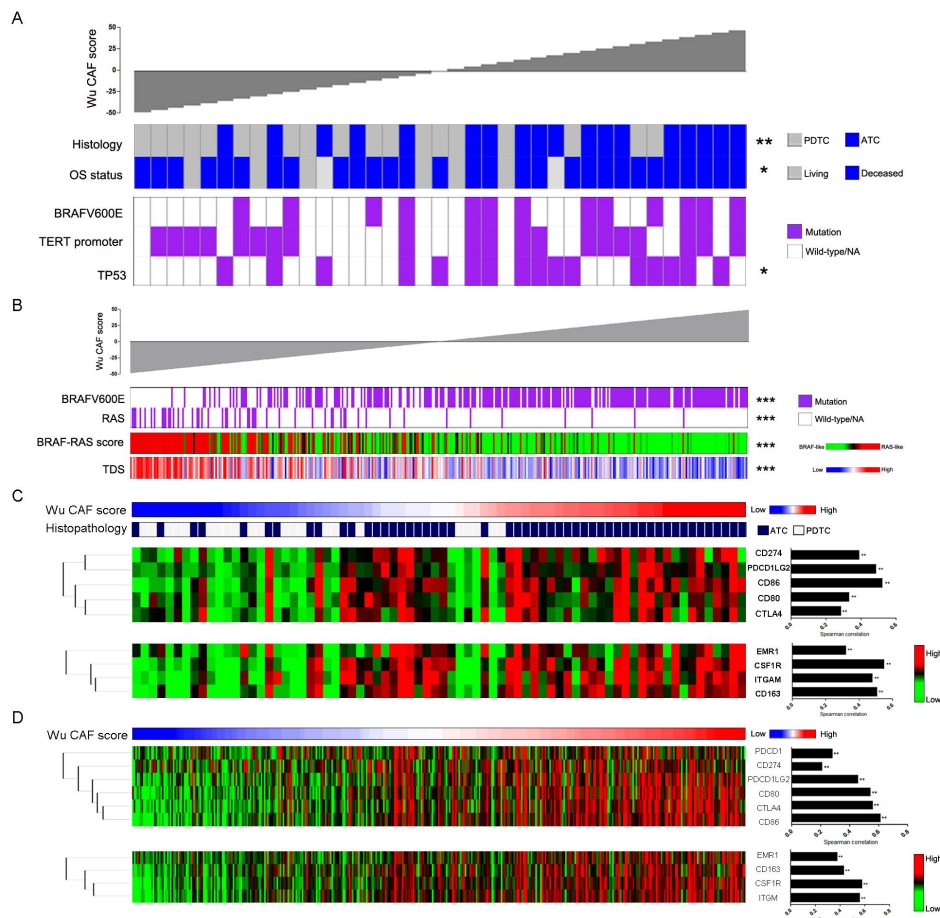
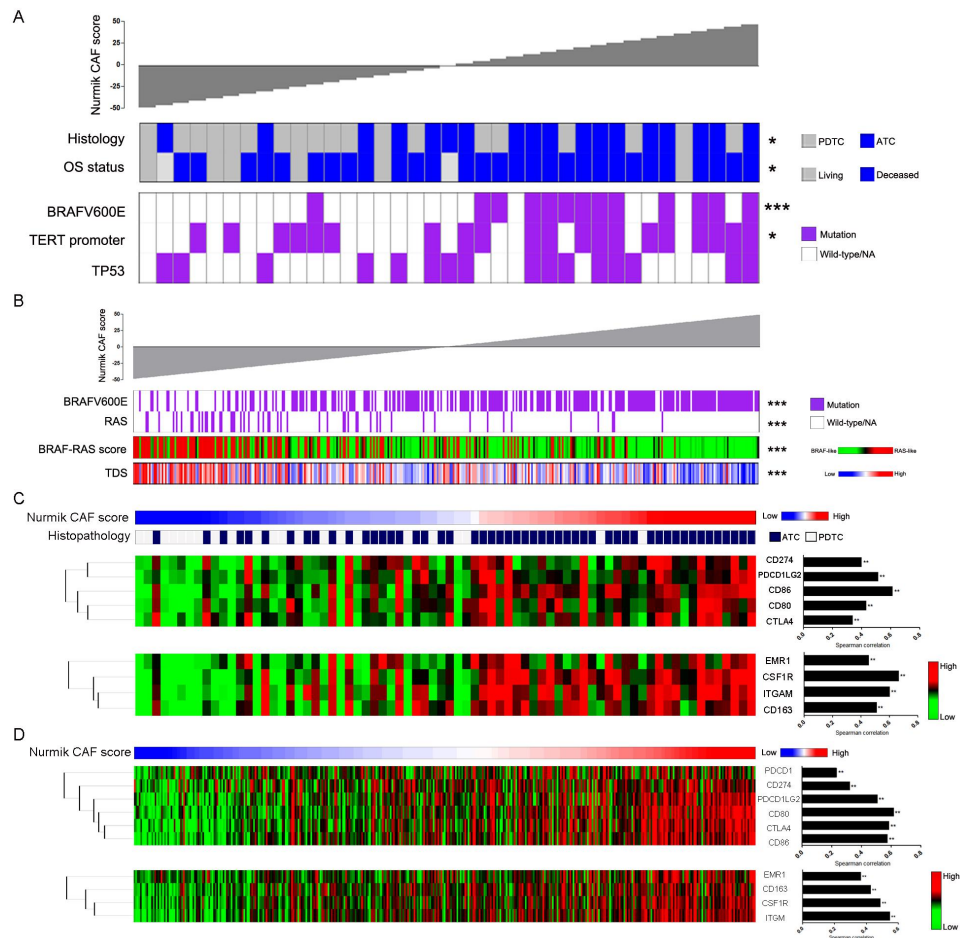


Supplementary Figure-S1 Correlations of the CAF score with DDTC, thyroid differentiation score (TDS) and BRAF-RAS score. (A) Comparison analyses of the CAF score among normal thyroid (NT) tissues, PTCs and dedifferentiated thyroid cancers (DDTCs). (B) Predictive effects of the CAF score for low-TDS patients in PTC. (C) Linear correlations of the CAF score with TDS. (D) Linear correlations of the CAF score with BRAF-RAS score. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure-S2 Correlations of the CAF score with genetic mutations and markers of tumor microenvironment based on the Wu CAF signature in thyroid cancer. (A) The DDTC patients from the GSE76039 cohort were ranked by histological subtypes, OS status, $BRAF^{V600E}$ mutation, $TERT$ promoter mutation and $TP53$ mutation based on the CAF scores. (B) The PTC patients from the TCGA cohort were ranked by $BRAF^{V600E}$ mutation, RAS mutation, BRAF-RAS score and thyroid differentiation score (TDS) based on the CAF scores. (C) The DDTC patients were ranked by the CAF score, histopathological subtypes, immune checkpoint markers and activated tumor-associated macrophage markers. (D) The PTC patients were ranked by the CAF score, immune checkpoint markers and activated tumor-associated macrophage markers. Spearman's correlation was performed to analyse the linear correlation of the CAF score with expression value of immune microenvironment markers. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.



Supplementary Figure-S3 Correlations of the CAF score with genetic mutations and markers of tumor microenvironment based on the Nurmik CAF signature in thyroid cancer. (A) The DDTC patients from the GSE76039 cohort were ranked by histological subtypes, OS status, *BRAF*^{V600E} mutation, *TERT* promoter mutation and *TP53* mutation based on the CAF score. (B) The PTC patients from the TCGA cohort were ranked by *BRAF*^{V600E} mutation, *RAS* mutation, BRAF-RAS score and thyroid differentiation score (TDS) based on the CAF score. (C) The DDTC patients were ranked by the CAF score, histopathological subtypes, immune checkpoint markers and activated tumor-associated macrophage markers. (D) The PTC patients were ranked by the CAF score, immune checkpoint markers and activated tumor-associated macrophage markers. Spearman's correlation was performed to analyse the linear correlation of the CAF score with expression value of immune microenvironment markers. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$.

Supplementary Table-S1. Genes of the three CAF signatures used in this study

Study, author	Year	Gene ID
Xiaofen Wu	2017	BMP4
		MGP
		TGFBI
Martin Nurmik	2020	SPHK1
		FAP
		α -SMA/ACTA2
		MFAP5
		COL11A1
		TNNC1
		PDPN
		ITGA11
		NG2/CSPG4
		DCN
Alexandre Calon	2015	PDPN
		FAP

Supplementary Table-S2. Gene expression profiles of the three CAF signatures in the FUSCC cohort

CAF signature	NT1	NT2	NT3	NT4	NT5	PTC1	PTC2	PTC3	PTC4	PTC5	DDTC1	DDTC2	DDTC3	DDTC4	DDTC5
Wu															
MGP	67.72093026	107.7244784	147.6317897	100.217512	352.3428403	54.52420543	19.88099667	10.97174766	151.4559851	75.20430575	30.82467664	1.773269359	5.867657711	107.6121609	135.182382
SPHK1	2.153683481	2.219300908	1.203868224	2.291832486	3.740262603	11.02379366	6.083673885	17.08590159	3.542197494	7.005052859	60.82563445	24.51280292	96.85958726	54.13917828	14.01448048
BMP4	6.507451108	5.398120305	7.261060374	2.969060817	11.58658418	4.03359141	2.40739927	0.577042723	5.870666388	5.239395442	1.433249516	0.671489714	6.727515328	3.800996437	1.67980407
TGFBI	2.597233927	13.12244825	6.462300573	4.319521567	15.28795104	4.840047398	20.67108345	6.583968377	8.601719663	5.24714606	397.5254258	318.8203057	154.4925965	27.87351992	14.12462585
Nurmik															
FAP	1.194851794	2.844740255	0.886484783	1.909860405	3.650135793	1.433730389	10.22251372	0.410746215	1.63615789	0.686455037	7.437553098	66.13975774	2.848043775	10.03860934	3.818230906
ITGA11	0.70976239	0.883250564	1.123923179	0.766822445	3.418301553	1.055885037	5.957955157	0.616199925	1.982969927	1.414150974	1.928168311	2.473028149	13.42653241	7.063453737	2.118049657
MFAP5	1.193498515	1.803877846	0.288743726	1.836366023	17.92617493	0.028019476	6.004758786	0.12542558	0.247233468	0.017651882	5.401614348	0.058381803	0.186487964	3.508794001	2.452395854
CSPG4	4.817137652	1.28886892	2.207558207	2.987104611	11.03458734	2.028944684	2.988562053	5.84969623	10.69634177	8.402242771	35.44595924	8.32484723	25.92976101	4.245337047	7.682520085
ACTA2	59.42431685	27.06682659	50.61065584	34.35177709	453.557658	50.22839004	50.83546991	67.82260384	102.0569004	96.0091639	117.3704778	15.29833697	27.31904584	61.63015644	56.36184708
COL11A1	0.130967484	0.091859347	0.112116268	0.017391277	0.271856506	0.903013375	40.92985143	2.303580201	0.230395813	0.068540474	2.529582136	0.510053934	0.467888985	26.43311592	4.858868235
PDPN	0.689640261	2.330967935	1.455579074	0.80735903	2.118880135	0.205452087	1.538954149	0.229919958	1.072592878	0.258863945	47.37861032	61.84462556	1.327973435	24.90653122	1.63299252
TNNC1	1.624545554	1.851591304	5.649765469	0.175276322	1.757658745	0.986848262	1.559153976	1.12891648	0.516004927	8.772888411	0	0.114233996	0.449102324	0.2004542	1.64052392
Calon															
FAP	1.194851794	2.844740255	0.886484783	1.909860405	3.650135793	1.433730389	10.22251372	0.410746215	1.63615789	0.686455037	7.437553098	66.13975774	2.848043775	10.03860934	3.818230906
DCN	33.64805358	36.85757636	39.77660691	25.26793356	76.31068212	4.890310903	24.56319598	1.276550563	21.8470869	0.715818857	5.81129647	1.891677297	3.188094618	10.4980324	18.25824489
PDPN	0.689640261	2.330967935	1.455579074	0.80735903	2.118880135	0.205452087	1.538954149	0.229919958	1.072592878	0.258863945	47.37861032	61.84462556	1.327973435	24.90653122	1.63299252

Supplementary Table-S3. Clinicopathological characteristics and genetic alterations of PTC patients in the TCGA cohort

Variables	TCGA (N=502)	
	N	%
Age (years), mean \pm SD (range)	47.18 \pm 15.85 (15-89)	
Gender		
Male	135	26.90
Female	366	72.90
NA	1	0.20
Multifocality		
Unifocal	265	52.80
Multifocal	226	45.00
NA	11	2.20
Coexistent HT		
Yes	65	12.90
No	397	79.10
NA	40	8.00
Histological subtypes		
Low-risk		
Classical	356	70.92
Follicular	100	19.92
Mixed papillary and follicular variant	1	0.20
Encapsulated follicular	1	0.20
Columnar cell variant	1	0.20
High-risk		
Tall cell variant	36	7.17
Diffuse sclerosing variant	4	0.80
Cribriform morular variant	2	0.40
NA	1	0.20
ETE		
Yes	331	65.90
No	152	30.30
NA	19	3.80
T Stage		
T1-T2	308	61.40
T3-T4	190	37.80
NA	4	0.80
LNM		
N0	227	45.20

	N1	224	44.60
	NA	51	10.20
Distant metastasis			
	M0	279	55.58
	M1	9	1.79
	MX	212	42.23
	NA	2	0.40
<i>BRAF</i>^{V600E}			
	Mutation	239	47.60
	Wild-type	254	50.60
	NA	9	1.80
<i>RAS</i>			
	<i>KRAS</i> mutation	3	0.59
	<i>NRAS</i> mutation	34	6.78
	<i>HRAS</i> mutation	14	2.79
	Wild-type	442	88.00
	NA	9	1.80
<i>EIF1AX</i>			
	Mutation	6	1.20
	Wild-type	487	97.00
	NA	9	1.80
<i>TERT</i> promoter			
	Mutation	36	7.17
	Wild-type	360	71.71
	NA	106	21.11
<i>TERT</i> exon			
	Mutation	2	0.40
	Wild-type	491	97.80
	NA	9	1.80
<i>ETV6_NTRK3</i>			
	Fusion	5	1.00
	Wild-type	488	97.20
	NA	9	1.80
<i>PAX8_PPARG</i>			
	Fusion	4	0.80
	Wild-type	489	97.40
	NA	9	1.80
<i>CCDC6_RET</i>			
	Fusion	21	4.20
	Wild-type	472	94.0

	NA	9	1.80
BRAF-RAS score			
	BRAF-like	272	54.18
	RAS-like	119	23.71
	NA	111	22.11
TDS			
	Low	196	39.00
	High	195	38.80
	NA	111	22.10

Abbreviations: PTC, papillary thyroid cancer; TCGA, The Cancer Genomics Atlas; SD, standard deviation; NA, not available; HT, Hashimoto's thyroiditis; ETE, extrathyroidal extension; LNM, lymph node metastasis; CNA, copy number alteration; TDS, thyroid differentiation score.

Supplementary Table-S4. Clinicopathological characteristics and genetic alterations of

Variables	GSE76039 (N=37)	
	N	%
Age (years), mean \pm SD (range)	65.51 \pm 13.739 (27-87)	
Gender		
Male	3	8.10
Female	12	32.40
NA	22	59.50
Histology		
PDTC	19	51.40
ATC	18	48.60
T Stage		
T1-T2	2	5.41
T3-T4	27	72.97
NA	8	21.62
LNM		
N0	10	27.00
N1	17	45.90
NA	10	27.00
Distant metastasis		
M0	6	16.20
M1	17	45.90
NA	14	37.80
Overall survival status		
Living	6	16.20
Deceased	29	78.40
NA	2	5.40
Mutation count	7.89 \pm 7.263 (1-34)	
<i>BRAF</i>^{V600E}		
Mutation	13	35.10
Wild-type	24	64.90
<i>RAS</i>		
<i>KRAS</i> mutation	1	2.70
<i>NRAS</i> mutation	8	21.62
<i>HRAS</i> mutation	3	8.11
Wild-type	25	67.57

EIF1AX

DDTC patients in the GSE76039 cohort

	Mutation	5	13.51
	Wild-type	32	86.49
<i>TERT</i> promoter			
	Mutation	20	54.1
	Wild-type	17	45.9
<i>TP53</i>			
	Mutation	16	43.20
	Wild-type	21	56.80
<i>PI3KCA/AKT/mTOR</i>			
	<i>PI3KCA</i> mutation	6	16.21
	<i>AKT</i> mutation	0	0.00
	<i>PTEN</i> mutation	2	5.41
	<i>mTOR</i> mutation	1	2.70
	Wild-type mutation	28	75.68

Abbreviations: DDTC, dedifferentiated thyroid cancer; SD, standard deviation; NA, not available; PDTC, poorly differentiated thyroid cancer; ATC, anaplastic thyroid cancer; LNM, lymph node metastasis.

Supplementary Table-S5. GSEA for the CAF signature score in the GEO cohort

CAF signature score	NES	FDR q-val
Calon CAF score		
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.984771	<0.01
HALLMARK_INFLAMMATORY_RESPONSE	2.8778832	<0.01
HALLMARK_ALLOGRAFT_REJECTION	2.8356714	<0.01
HALLMARK_INTERFERON_GAMMA_RESPONSE	2.8241003	<0.01
HALLMARK_TNFA_SIGNALING_VIA_NFKB	2.7830603	<0.01
HALLMARK_COMPLEMENT	2.5933323	<0.01
HALLMARK_INTERFERON_ALPHA_RESPONSE	2.550976	<0.01
HALLMARK_IL6_JAK_STAT3_SIGNALING	2.5490294	<0.01
HALLMARK_KRAS_SIGNALING_UP	2.4058788	<0.01
HALLMARK_ANGIOGENESIS	2.282798	<0.01
HALLMARK_E2F_TARGETS	2.2827501	<0.01
HALLMARK_APOPTOSIS	2.2228875	<0.01
HALLMARK_COAGULATION	2.2042973	<0.01
HALLMARK_IL2_STAT5_SIGNALING	2.085939	<0.01
HALLMARK_G2M_CHECKPOINT	2.0686011	<0.01
HALLMARK_APICAL_JUNCTION	2.012186	<0.01
HALLMARK_HYPOXIA	1.9844944	<0.01
HALLMARK_UV_RESPONSE_DN	1.873317	1.97E-04
HALLMARK_P53_PATHWAY	1.8237745	3.25E-04
HALLMARK_MITOTIC_SPINDLE	1.8208354	3.08E-04
HALLMARK_MTORC1_SIGNALING	1.7342595	8.92E-04
HALLMARK_UV_RESPONSE_UP	1.6706535	0.002207924
HALLMARK_APICAL_SURFACE	1.5978779	0.004459796
HALLMARK_MYOGENESIS	1.5482724	0.008008626
HALLMARK_XENOBIOTIC_METABOLISM	1.5294921	0.009794958
HALLMARK_TGF_BETA_SIGNALING	1.481768	0.016277058
HALLMARK_ANDROGEN_RESPONSE	1.4658471	0.018546786
HALLMARK_GLYCOLYSIS	1.4636691	0.018320376
HALLMARK_ESTROGEN_RESPONSE_LATE	1.4211131	0.028063923
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	1.3702694	0.045256965
Nurmik CAF score		
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.9978256	<0.01
HALLMARK_ALLOGRAFT_REJECTION	2.7955263	<0.01
HALLMARK_INFLAMMATORY_RESPONSE	2.7465005	<0.01
HALLMARK_INTERFERON_GAMMA_RESPONSE	2.7360613	<0.01
HALLMARK_TNFA_SIGNALING_VIA_NFKB	2.6307452	<0.01
HALLMARK_IL6_JAK_STAT3_SIGNALING	2.5523605	<0.01
HALLMARK_INTERFERON_ALPHA_RESPONSE	2.5047503	<0.01

HALLMARK_COMPLEMENT	2.4488187	<0.01
HALLMARK_E2F_TARGETS	2.3340666	<0.01
HALLMARK_G2M_CHECKPOINT	2.329422	<0.01
HALLMARK_KRAS_SIGNALING_UP	2.2990816	<0.01
HALLMARK_ANGIOGENESIS	2.190217	<0.01
HALLMARK_COAGULATION	2.0774658	<0.01
HALLMARK_MITOTIC_SPINDLE	2.0588603	<0.01
HALLMARK_APICAL_JUNCTION	2.0572546	<0.01
HALLMARK_APOPTOSIS	2.0099964	<0.01
HALLMARK_IL2_STAT5_SIGNALING	1.9991655	<0.01
HALLMARK_HYPOXIA	1.8390589	7.53E-05
HALLMARK_P53_PATHWAY	1.7857056	2.30E-04
HALLMARK_UV_RESPONSE_DN	1.7748599	2.91E-04
HALLMARK_MTORC1_SIGNALING	1.7596632	3.44E-04
HALLMARK_MYOGENESIS	1.6354027	0.002597693
HALLMARK_APICAL_SURFACE	1.5875857	0.004251962
HALLMARK_HEDGEHOG_SIGNALING	1.5705903	0.004820215
HALLMARK_UV_RESPONSE_UP	1.5204134	0.007838684
HALLMARK_GLYCOLYSIS	1.4882275	0.011390877
HALLMARK_NOTCH_SIGNALING	1.4279591	0.021120785
HALLMARK_XENOBIOTIC_METABOLISM	1.4125174	0.023467543
HALLMARK_ANDROGEN_RESPONSE	1.4041364	0.024803555
HALLMARK_TGF_BETA_SIGNALING	1.3994099	0.02497839
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	1.3776578	0.030293263
HALLMARK_CHOLESTEROL_HOMEOSTASIS	1.333473	0.045656573

Wu CAF score

HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	3.321382	<0.01
HALLMARK_E2F_TARGETS	3.0996614	<0.01
HALLMARK_TNFA_SIGNALING_VIA_NFKB	3.0554311	<0.01
HALLMARK_G2M_CHECKPOINT	3.03104	<0.01
HALLMARK_ALLOGRAFT_REJECTION	2.9594667	<0.01
HALLMARK_INFLAMMATORY_RESPONSE	2.9281523	<0.01
HALLMARK_INTERFERON_GAMMA_RESPONSE	2.8667862	<0.01
HALLMARK_INTERFERON_ALPHA_RESPONSE	2.6953769	<0.01
HALLMARK_MITOTIC_SPINDLE	2.6799238	<0.01
HALLMARK_IL6_JAK_STAT3_SIGNALING	2.6483963	<0.01
HALLMARK_COMPLEMENT	2.6245914	<0.01
HALLMARK_KRAS_SIGNALING_UP	2.532551	<0.01
HALLMARK_MTORC1_SIGNALING	2.4995513	<0.01
HALLMARK_MYC_TARGETS_V1	2.4988406	<0.01
HALLMARK_APOPTOSIS	2.4183846	<0.01
HALLMARK_ANGIOGENESIS	2.3088732	<0.01

HALLMARK_IL2_STAT5_SIGNALING	2.2797976	<0.01
HALLMARK_P53_PATHWAY	2.2401302	<0.01
HALLMARK_UV_RESPONSE_DN	2.237269	<0.01
HALLMARK_HYPOXIA	2.2043593	<0.01
HALLMARK_MYC_TARGETS_V2	2.180035	<0.01
HALLMARK_UNFOLDED_PROTEIN_RESPONSE	2.1749065	<0.01
HALLMARK_APICAL_JUNCTION	2.1643062	<0.01
HALLMARK_UV_RESPONSE_UP	2.1026237	<0.01
HALLMARK_GLYCOLYSIS	2.0964649	<0.01
HALLMARK_TGF_BETA_SIGNALING	2.0267172	5.16E-05
HALLMARK_COAGULATION	1.963178	1.55E-04
HALLMARK_DNA_REPAIR	1.8629909	3.11E-04
HALLMARK_CHOLESTEROL_HOMEOSTASIS	1.8585715	3.00E-04
HALLMARK_WNT_BETA_CATENIN_SIGNALING	1.7513405	9.13E-04
HALLMARK_ANDROGEN_RESPONSE	1.745254	9.78E-04
HALLMARK_ESTROGEN_RESPONSE_LATE	1.731877	0.001194931
HALLMARK_APICAL_SURFACE	1.7276926	0.001253671
HALLMARK_NOTCH_SIGNALING	1.572162	0.005994814
HALLMARK_PI3K_AKT_MTOR_SIGNALING	1.5655571	0.006077498
HALLMARK_ESTROGEN_RESPONSE_EARLY	1.5317363	0.008013841
HALLMARK_MYOGENESIS	1.4694945	0.014644829
HALLMARK_HEDGEHOG_SIGNALING	1.4131165	0.025254091
HALLMARK_XENOBIOTIC_METABOLISM	1.4090146	0.025649486
HALLMARK_PROTEIN_SECRETION	1.3775179	0.034286644

Supplementary Table-S6. GSEA for the CAF signature score in the TCGA cohort

CAF signature score	NES	FDR q-val
Calon CAF score		
HALLMARK_ALLOGRAFT_REJECTION	1.9949901	<0.01
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	1.9652183	<0.01
HALLMARK_INFLAMMATORY_RESPONSE	1.9548606	<0.01
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.8912655	<0.01
HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.8712671	<0.01
HALLMARK_KRAS_SIGNALING_UP	1.7765495	<0.01
HALLMARK_INTERFERON_ALPHA_RESPONSE	1.7631664	<0.01
HALLMARK_IL6_JAK_STAT3_SIGNALING	1.7263116	<0.01
HALLMARK_IL2_STAT5_SIGNALING	1.7116135	1.04E-04
HALLMARK_COMPLEMENT	1.6481407	2.76E-04
HALLMARK_ANGIOGENESIS	1.6337253	3.34E-04
HALLMARK_G2M_CHECKPOINT	1.6095858	6.11E-04
HALLMARK_COAGULATION	1.6020452	6.36E-04
HALLMARK_APOPTOSIS	1.5881389	9.83E-04
HALLMARK_APICAL_JUNCTION	1.5324992	0.002879546
HALLMARK_E2F_TARGETS	1.5167933	0.003674479
HALLMARK_MITOTIC_SPINDLE	1.4248508	0.014652742
HALLMARK_KRAS_SIGNALING_DN	1.4203945	0.014855285
HALLMARK_ESTROGEN_RESPONSE_LATE	1.392818	0.02118957
HALLMARK_APICAL_SURFACE	1.385867	0.02183633
HALLMARK_P53_PATHWAY	1.3751973	0.024297427
HALLMARK_UV_RESPONSE_DN	1.3635736	0.027068948
Nurmik CAF score		
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	1.8438131	<0.01
HALLMARK_ALLOGRAFT_REJECTION	1.8338305	<0.01
HALLMARK_INFLAMMATORY_RESPONSE	1.8278651	<0.01
HALLMARK_INTERFERON_GAMMA_RESPONSE	1.7155617	<0.01
HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.7122353	<0.01
HALLMARK_KRAS_SIGNALING_UP	1.673658	1.57E-04
HALLMARK_IL6_JAK_STAT3_SIGNALING	1.6381247	4.03E-04
HALLMARK_ANGIOGENESIS	1.6353917	3.53E-04
HALLMARK_INTERFERON_ALPHA_RESPONSE	1.6126686	5.29E-04
HALLMARK_IL2_STAT5_SIGNALING	1.6074618	4.76E-04
HALLMARK_COAGULATION	1.5755605	6.92E-04
HALLMARK_COMPLEMENT	1.5641097	7.96E-04
HALLMARK_APOPTOSIS	1.5123887	0.001828536
HALLMARK_APICAL_JUNCTION	1.4698442	0.004953782
HALLMARK_UV_RESPONSE_DN	1.4264145	0.010394453
HALLMARK_KRAS_SIGNALING_DN	1.3959996	0.016334955

HALLMARK_ESTROGEN_RESPONSE_LATE	1.378591	0.018609487
HALLMARK_APICAL_SURFACE	1.3678466	0.021008836
HALLMARK_G2M_CHECKPOINT	1.3607527	0.022146618
HALLMARK_P53_PATHWAY	1.317818	0.040031724
HALLMARK_MYOGENESIS	1.3066779	0.044095755
HALLMARK_MITOTIC_SPINDLE	1.3008221	0.04559826
HALLMARK_E2F_TARGETS	1.3002547	0.04378004
Wu CAF score		
HALLMARK_ALLOGRAFT_REJECTION	2.2163436	<0.01
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	2.084185	<0.01
HALLMARK_INFLAMMATORY_RESPONSE	2.068243	<0.01
HALLMARK_INTERFERON_GAMMA_RESPONSE	2.030704	<0.01
HALLMARK_TNFA_SIGNALING_VIA_NFKB	1.9751998	<0.01
HALLMARK_INTERFERON_ALPHA_RESPONSE	1.9425185	<0.01
HALLMARK_KRAS_SIGNALING_UP	1.8719102	<0.01
HALLMARK_IL6_JAK_STAT3_SIGNALING	1.8241647	1.17E-04
HALLMARK_COAGULATION	1.788996	2.08E-04
HALLMARK_COMPLEMENT	1.7858615	1.87E-04
HALLMARK_IL2_STAT5_SIGNALING	1.7838882	1.70E-04
HALLMARK_ANGIOGENESIS	1.7750955	2.36E-04
HALLMARK_APOPTOSIS	1.6812643	5.67E-04
HALLMARK_APICAL_JUNCTION	1.5608996	0.003880591
HALLMARK_P53_PATHWAY	1.4813607	0.012458951
HALLMARK_ESTROGEN_RESPONSE_LATE	1.4709675	0.01371656
HALLMARK_KRAS_SIGNALING_DN	1.440713	0.019081507
HALLMARK_E2F_TARGETS	1.4317158	0.020748567
HALLMARK_G2M_CHECKPOINT	1.4215562	0.022300782

Supplementary Table-S7. Overlapped signaling pathways of GSEA analyses in both GEO and TCGA

Biological signaling pathways

HALLMARK_ALLOGRAFT_REJECTION
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
HALLMARK_INFLAMMATORY_RESPONSE
HALLMARK_INTERFERON_GAMMA_RESPONSE
HALLMARK_TNFA_SIGNALING_VIA_NFKB
HALLMARK_KRAS_SIGNALING_UP
HALLMARK_INTERFERON_ALPHA_RESPONSE
HALLMARK_IL6_JAK_STAT3_SIGNALING
HALLMARK_IL2_STAT5_SIGNALING
HALLMARK_COMPLEMENT
HALLMARK_ANGIOGENESIS
HALLMARK_G2M_CHECKPOINT
HALLMARK_COAGULATION
HALLMARK_APOPTOSIS
HALLMARK_APICAL_JUNCTION
HALLMARK_E2F_TARGETS
HALLMARK_P53_PATHWAY
