

### Supplementary Figure legends:

**Figure S1.** Landscape of CSC signature in PC patients. **A.** The screening criteria of scRNA in PC samples. **B.** The distribution of six CSC genes in stem cell sub-clusters. **C.** All the risk models were identified in PC via NFM algorithm. **D.** Two categories calculated the risk score of PC using ssGSEA algorithm. **E.** CSC genes are identified in stem genes and subtype genes. **F and G.** The mRNA level of TGIF2 and SOX2 in PC and normal pancreas according to GEPIA database (T: PC; N: pancreas). **H.** Heatmap plot of CSC genes in the expression level of subtypes.

**Figure S2.** The identification and validation of machine learning model. **A** The C-index of each model in four databases based on a machine learning model. **B and C.** The 1-, 3-, and 5-year survival of patient's scores both in E-MTAB and TCGA. **D and E.** The value of CSC model in univariate and multivariate analysis both in E-MTAB and TCGA. **F and G.** The nomogram was established to predict the prognosis, and the overall survival of 1-, 3-, and 5-year was validated via calibration plots and decision curve analysis (DCA) of a nomogram prediction.

**Figure S3.** The enriched pathway in CSC genes. **A-B.** The functional enriched analysis of CSC genes in E-MTAB cohort and TCGA cohort. **C.** The combination of functional pathways in E-MTAB cohort. **D-G.** The survival difference between the high and low-risk groups based on KRAS SIGNALING and EPITHELIAL MESENCHYMAL TRANSITION. **H.** The correlation plot of TGIF2 associated with EMT Key regulator Snail2 (Slug) and EGFR expression in TCGA database.

**Figure S4.** The binding of TGIF2 and SOX2. **A.** The target genes of TGIF2 through Stem genes and TFDB. **B and C.** The EMT signatures of gastric cancer and PC. **D-I.** The correlation between TGIF2 with target genes including MYC, SOX2, TP53, LMNB1, YY1, OTX2. **J.** The Chromatin openness among TGIF2, SOX2 and Smad2 in three represent time including ESC, DE-24h and DE-48h.

**Figure S5.** All the raw images of Western blot in our manuscript. **A.** The Western blot and statistical analysis of Figure 3A. **B-C.** The Western blot and statistical analysis of Figure 3C and Figure 3D respectively. **D-G.** The Western blot and statistical analysis of Figure 4A, Figure 4B, Figure 4D and Figure 4F, respectively. **H.** The Western blot and statistical analysis of Figure 5G. **I.** The Western blot and statistical analysis of Figure 5H. **J.** The Western blot and statistical analysis of Figure 5N.

### Supplementary Tables legends:

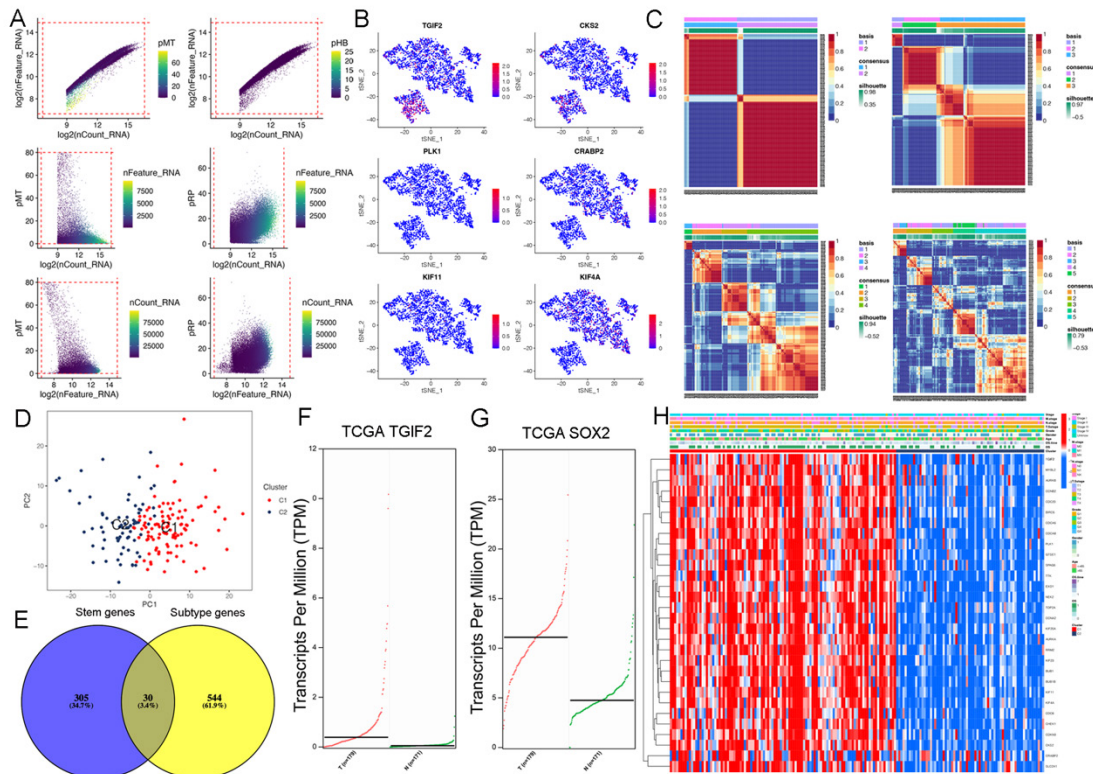
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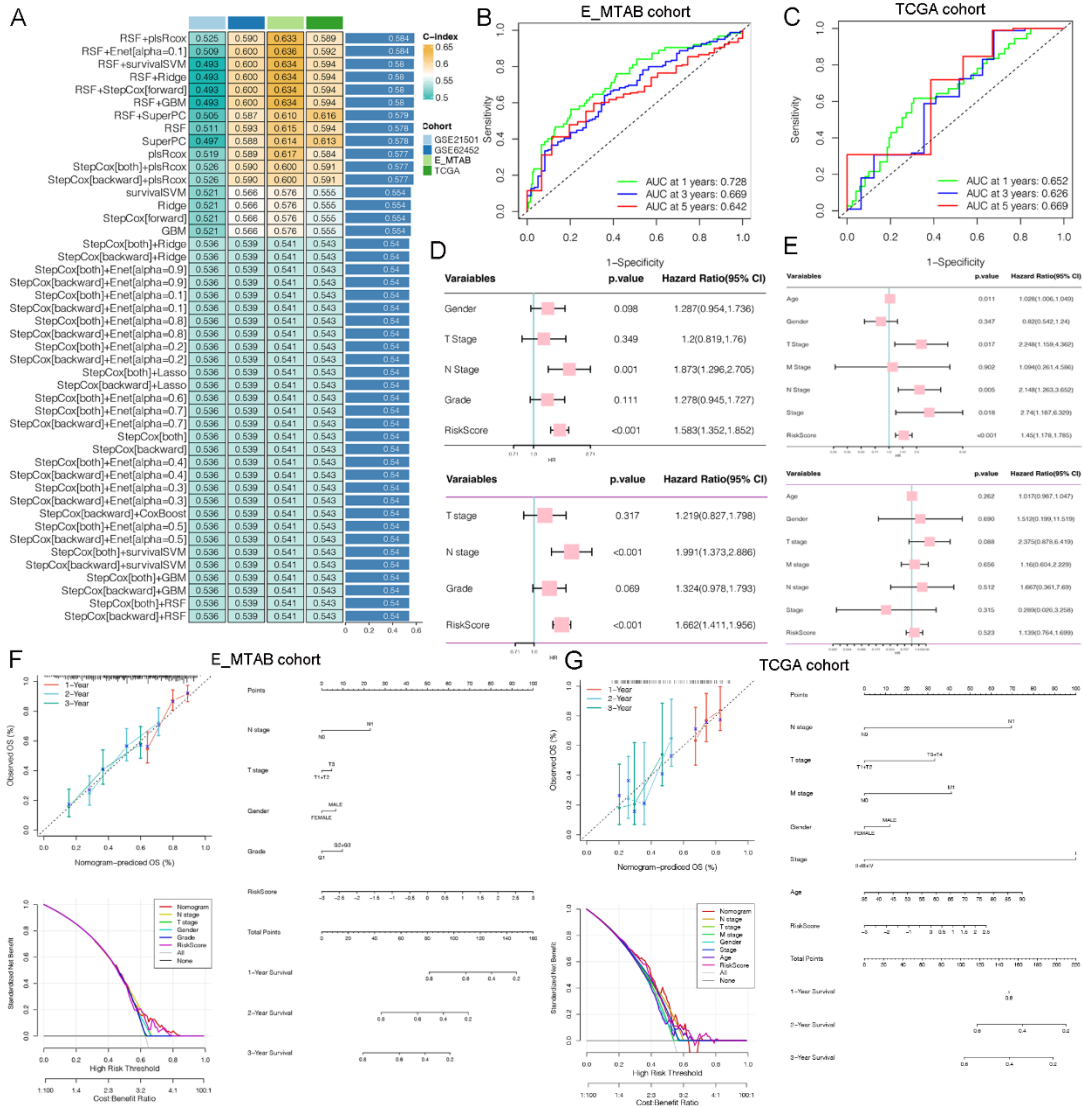
**Table S3.** The clinicopathological significance of in 20 cases in PC

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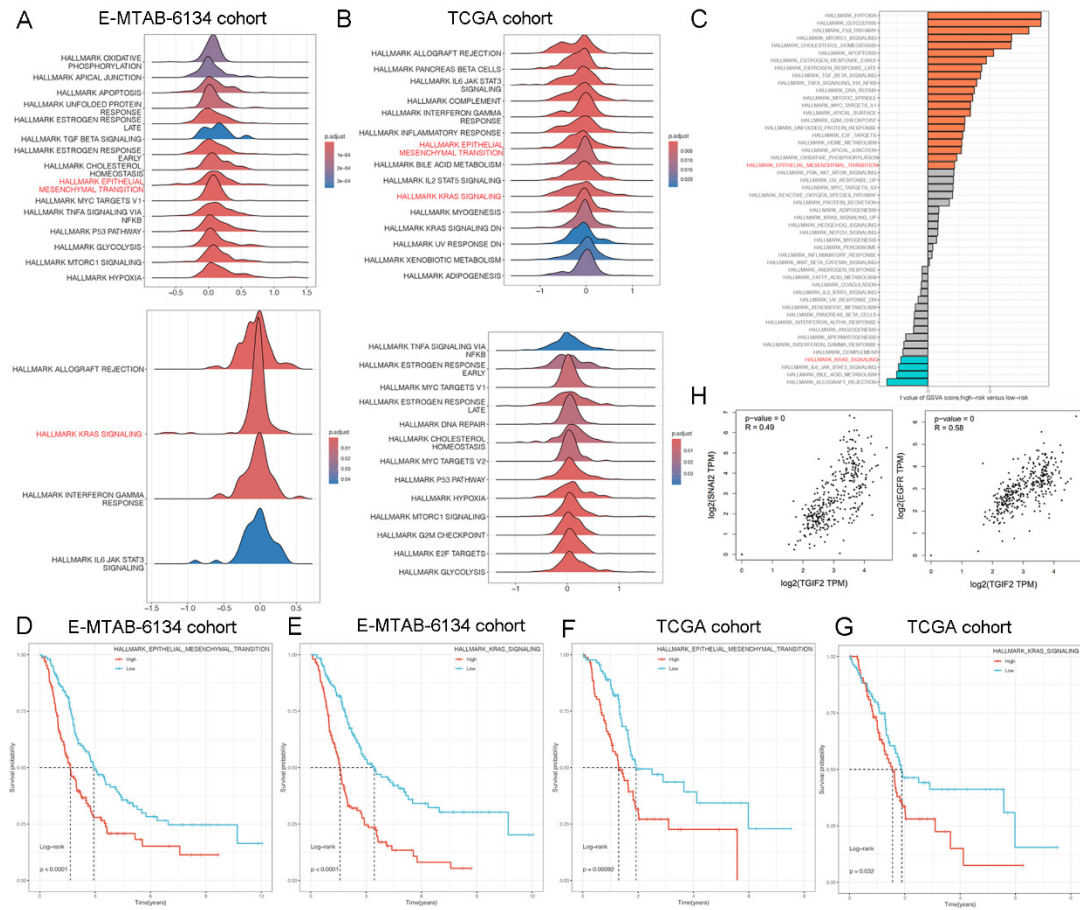
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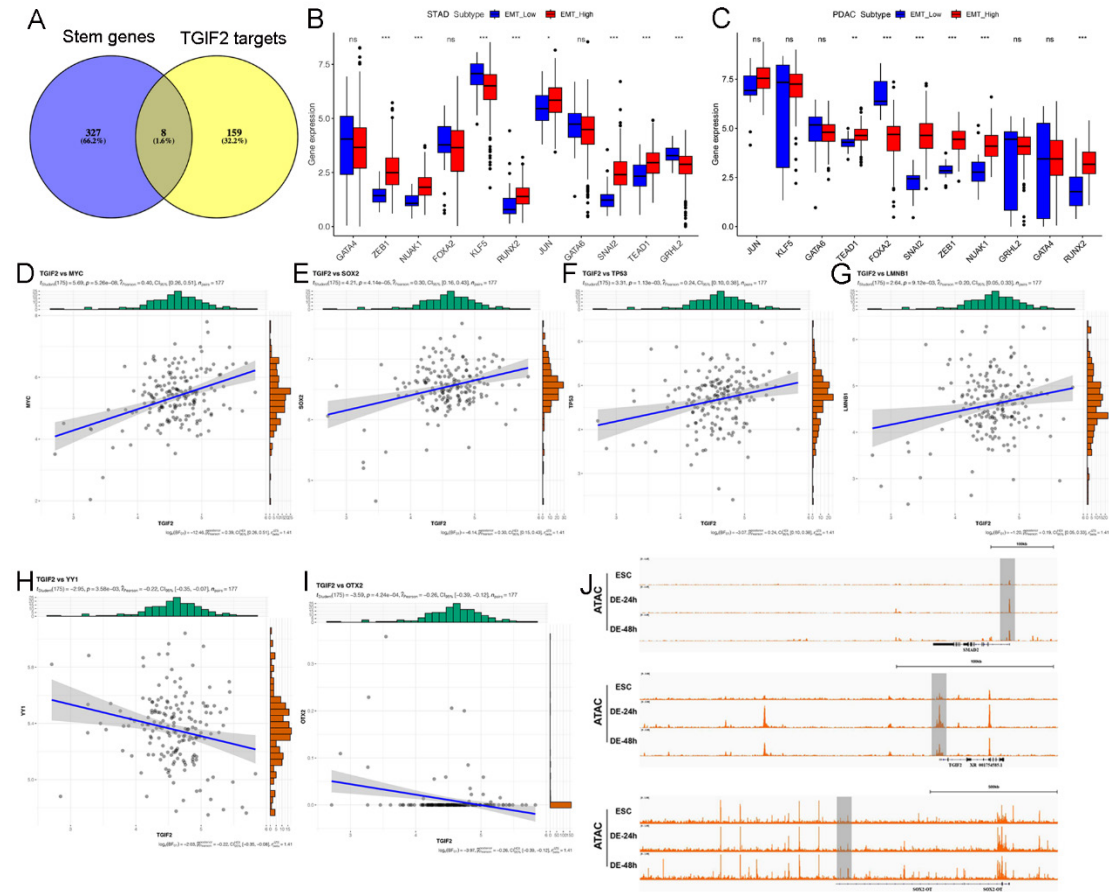
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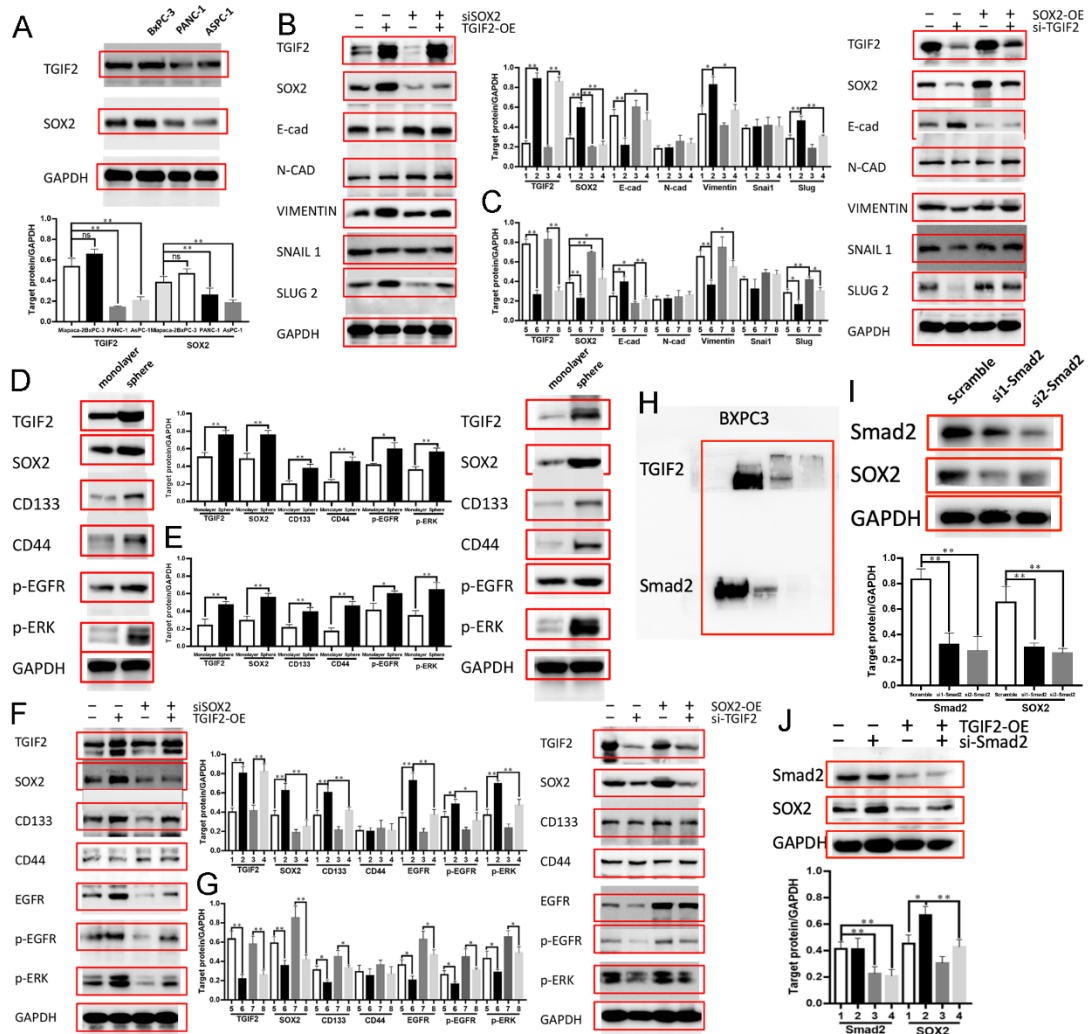
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**Table S1.** Primers used in this study

<b>Primer name</b>	<b>Sequence (5'-3')</b>
TGIF2-F	CGGACAGTGATCTAGGTGAGGACG
TGIF2-R	GGGAAATGGTAAACTGATTAGGGTCTT
SOX2-F	GCTACAGCATGATGCAGGACCA
SOX2-R	TCTGCGAGCTGGTCATGGAGTT
EGFR-F	AACACCCTGGTCTGGAAGTACG
EGFR-R	TCGTTGGACAGCCTTCAAGACC
Slug-F	ATCTGCGGCAAGGCGTTTTCCA
Slug-R	GAGCCCTCAGATTTGACCTGTC
GAPDH-F	CATGAGAAGTATGACAACAGCCT
GAPDH-R	AGTCCTTCCACGATACCAAAGT
SOX2 promotor-F1 (SOX2: -1428 to -1439)	GTGGATGAGCGGGAGAACAA
SOX2 promotor-R1 (SOX2: -1428 to -1439)	GTCACACCACACGCCTTTTC
SOX2 promotor-F2 (SOX2: -1141 to -1132)	GTGGATGAGCGGGAGAACAA
SOX2 promotor-R2 (SOX2: -1141 to -1132)	GTCACACCACACGCCTTTTC
SOX2 promotor-F3 (SOX2: -196 to -187)	GTGGATGAGCGGGAGAACAA
SOX2 promotor-R3 (SOX2: -196 to -187)	GTCACACCACACGCCTTTTC
EGFR promotor-F1 (EGFR:-485 to-495)	AGAGCCGAGAGATCAGGGTT
EGFR promotor-R1 (EGFR:-485 to-495)	CTTGACACAAACAGCCGTGG
EGFR promotor-F2 (EGFR:-705 to -715)	AAAGGCAGGCTGATCGGAAG
EGFR promotor-R2 (EGFR:-705 to -715)	AGAGAATGTCCGGTGGTTCC
Slug promotor-F (Slug: 667 to 677)	GCAGGCTGATCGGAAGAACT
Slug promotor-R	TGTCCGGTGGTTCCAAATGA

(Slug: 667 to 677)

**Table S2.** siRNA sequences for TGIF2 and SOX2

Gene	siRNA sequences
si1-TGIF2	CCAGCAGACUCUGACUCAATT
si2-TGIF2	GCACACUCCCAUCCCUUUUATT
si1-SOX2	GGACAUGAUCAGCAUGUAUTT
si2-SOX2	CCACCUACAGCAUGUCCUATT
Si-Ctrl	UUCUCCGAACGUGUCACGUTT
sh-TGIF2	CAGGACCCATCACTCCCATTA
sh-SOX2	TTCACATGTCCCAGCACTACC
shRNA Control	TCTCGCTTGGGCGAGAGTAAG



**Table S3.** The clinicopathological significance of in 20 cases in PC

Parameters	No. of patients
Cases	20
Age(years)	
≤65	12
>65	8
Gender	
Male	14
Female	6
Tumor size(cm)	
<3	12
≥3	8
Tumor location	
Head	16
Body-tail	4
Differentiation	
Well	9
Moderate to Poor	11
T stage <sup>a</sup>	
T1	13
T2+T3	7
LN metastasis <sup>b</sup>	
N0(negative)	17
N1(positive)	3
UICC stage <sup>a</sup>	
I stage	9
II+III stage	11
Vascular permeation	
Absent	12
Present	8

a. According to 8th TNM stage of AJCC. b. Lymph node

**Table S4.** Common targets of TGIF2 in TFDB 3.0 database.

Target	Position1	Position2
MYC	chr20,36573224,36573541,8.42,-264,pr,dataset-2142	chr20,36574570,36575060,10.3,1082,gb,dataset-2142
SOX2	chr20,36571773,36571869,8.04,-171,pr,dataset-3048	chr20,36571755,36571890,11.7,-173,pr,dataset-3051
TP53	chr20,36573429,36573712,4.94,-59,pr,dataset-3631	chr20,36573429,36573712,4.94,-59,pr,dataset-3631
LMNB1	chr20,36575199,36575676,2.45,1711,gb,dataset-1931	chr20,36565722,36565966,4.68,-776,pr,dataset-1931
YY1	chr20,36573595,36573747,4.62,107,pr,dataset-3761	chr20,36573091,36573470,8.98,-397,pr,dataset-3761
OTX2	chr20,36585545,36585718,4.98,1205,gb,dataset-2384	chr20,36585545,36585718,4.98,1205,gb,dataset-2384
CBX3	chr20,36573062,36573171,2.94,-426,pr,dataset-340	chr20,36574689,36575036,5.31,1201,gb,dataset-340
HDAC1	chr20,36573089,36573819,18.9,-399,pr,dataset-4505	chr20,36573089,36573819,18.9,-399,pr,dataset-4505