Table S1 Clinical characteristics of patients from multiple cohorts

| Characteristics | TCGA-STAD (n=353) | GSE62254 (n=300) | GSE84437 (n=433) | Xijing (n=48) | Total (n=1,134) |
|--------------------------|-------------------|------------------|------------------|---------------|-----------------|
| Age, years | | | | | |
| Mean±SD | 65.51±10.62 | 61.94±11.36 | 60.06±11.58 | 58.79±8.62 | 62.19±11.36 |
| Gender | | | | | |
| Female | 125 | 101 | 137 | 13 | 376 |
| Male | 228 | 199 | 296 | 35 | 758 |
| T stage, n | | | | | |
| T1 | 18 | - | 11 | 3 | 32 |
| T2 | 61 | 186 | 38 | 4 | 289 |
| Т3 | 121 | 91 | 92 | 16 | 320 |
| T4 | 153 | 21 | 292 | 25 | 491 |
| N stage, n | | | | | |
| NO | 106 | 38 | 80 | 20 | 244 |
| N1 | 79 | 131 | 188 | 4 | 402 |
| N2 | 75 | 80 | 132 | 10 | 297 |
| N3 | 93 | 51 | 33 | 14 | 191 |
| M stage, n | | | | | |
| MO | 330 | 273 | - | 48 | 651 |
| M1 | 23 | 27 | - | - | 50 |
| TNM stage, n | | | | | |
| I | 46 | 30 | - | 4 | 80 |
| II | 111 | 97 | - | 19 | 227 |
| III | 172 | 96 | - | 25 | 293 |
| IV | 24 | 77 | - | - | 101 |
| Grade, n | | | | | |
| G1 | 9 | - | - | 2 | 11 |
| G2 | 128 | - | - | 33 | 161 |
| G3 | 207 | - | - | 11 | 218 |
| Survival, n | | | | | |
| Alive | 281 | 148 | 224 | 28 | 681 |
| Dead | 72 | 152 | 209 | 20 | 453 |
| Lauren classification, n | | | | | |
| Diffuse | - | 142 | - | - | 142 |
| Intestinal | - | 150 | - | - | 150 |
| Mixed | - | 8 | - | _ | 8 |

TCGA-STAD, The Cancer Genome Atlas Stomach Adenocarcinoma; TNM, Tumor Node Metastasis; SD, standard deviation.

Table S2 Primer sequences of ten prognostic genes

| Primer | Forward sequence | Reverse sequence |
|---------|-------------------------|-------------------------|
| ANGPTL4 | GATGGCTCAGTGGACTTCAACC | TGCTATGCACCTTCTCCAGACC |
| CPNE8 | GCAAAACTGCCTCCAGATGGAAG | TCAGACTCCTGTAATAAGCCTCC |
| CST2 | CCTACTCCCACCCCTTGTAGT | GCAGCCTTCTCTGTCTTCTCCT |
| HTR1F | TCTTGTGGCTGTCCTGGTGATG | GCAGGTAATGTCAACACTCAGCC |
| IL1RAP | CTGAGGATCTCAAGCGCAGCTA | AGCAGGACTGTGGCTCCAAAAC |
| NR1D1 | CTGCCAGCAATGTCGCTTCAAG | TGGCTGCTCAACTGGTTGTTGG |
| NTAN1 | CATTGTGACGGAACCGACACCA | CTGTCGTCACTGAAGCCTCCAA |
| OLFML2B | GAACCGAGATGAATAAGCGAGGC | GGACACGGTTTCTTCCTGCAGA |
| TMEM259 | TCACTACCGCTTCAATGGGCAG | CTGAAGCAGCATCTCCTGGATG |
| VTN | TGGCTGTCCTTGTTCTCCAGTG | GTGTGCGAAGATTGACTCGGTAG |

| Genes | | | Р | Hazard Ratio(95% CI |
|--------------|---|----------------------------------|--------|---------------------|
| PCDHB17P | | F | 0.0001 | 1.97(1.4,2.76) |
| CPNE8 | | ⊢−−− − −−−−− | 0.0006 | 1.8(1.29,2.52) |
| HTR1F | | F4 | 0.0013 | 1.73(1.24,2.41) |
| NR1D1 | | ► <mark>-</mark> 1 | 0.0023 | 1.69(1.21,2.36) |
| IL1RAP | | ⊢−−− | 0.0038 | 1.63(1.17,2.28) |
| PINLYP | | F | 0.0050 | 1.61(1.16,2.25) |
| ANGPTL4 | | F | 0.0053 | 1.61(1.15,2.25) |
| PDE7B | | ⊬∎4 | 0.0053 | 1.6(1.15,2.24) |
| HMGA2-AS1 | | ⊬┫4 | 0.0056 | 1.6(1.15,2.24) |
| RHOQ | | ► ■ + | 0.0069 | 1.58(1.13,2.2) |
| TCEAL5 | | ⊢−−−∎−−−−+ | 0.0071 | 1.58(1.13,2.2) |
| B3GNT9 | | ▶∎4 | 0.0090 | 1.57(1.12,2.2) |
| DKK1 | | F - I | 0.0095 | 1.55(1.11,2.17) |
| PLAT | | F B 1 | 0.0112 | 1.54(1.1,2.14) |
| VTN | | F B 1 | 0.0115 | 1.53(1.1,2.14) |
| KIRREL1 | | F - 1 | 0.0148 | 1.51(1.08,2.11) |
| TMEM178A | | ► = | 0.0193 | 1.48(1.07,2.06) |
| CNTN4 | | ► - | 0.0208 | 1.48(1.06.2.06) |
| NPTX1 | | ► - | 0.0221 | 1.47(1.06.2.05) |
| DUSP3 | | ► - | 0.0257 | 1.46(1.05.2.04) |
| LRP10 | | ► - | 0.0278 | 1.46(1.04.2.04) |
| NTAN1 | | ⊨ – – – <mark>–</mark> – – – 4 | 0.0338 | 1.43(1.03,1.99) |
| OLFML2B | | ⊢ – – – <mark>–</mark> − – – – 4 | 0.0382 | 1.42(1.02,1.98) |
| BEND3 | | ⊢ – – – <mark>–</mark> − – – – 4 | 0.0396 | 1.42(1.02.1.98) |
| ADAMTS2 | | | 0.0429 | 1.41(1.01,1.96) |
| ACSF2 | | | 0.0422 | 1.41(1.01,1.95) |
| L3MBTL3 | | | 0.0439 | 1.41(1.01,1.96) |
| SPART-AS1 | | | 0.0426 | 1.41(1.01,1.95) |
| MUC15 | | | 0.0448 | 1.4(1.01,1.95) |
| COPRS | | | 0.0473 | 1.4(1,1.94) |
| CST2 | | | 0.0487 | 1.39(1,1.94) |
| TEX264 ► · | | | 0.0492 | 0.72(0.52,1) |
| CEP55 ⊢· | | | 0.0494 | 0.72(0.52,1) |
| NABP2 - | | | 0.0447 | 0.71(0.51,0.99) |
| PLPP2 - | | | 0.0445 | 0.71(0.51,0.99) |
| KCTD14 - | | | 0.0401 | 0.71(0.51,0.98) |
| AKR1A1 - | | | 0.0371 | 0.7(0.51,0.98) |
| TMEM161A ⊢ - | | | 0.0277 | 0.69(0.5,0.96) |
| EFNA3 | | | 0.0269 | 0.69(0.5.0.96) |
| RITA1 - | | | 0.0158 | 0.67(0.48.0.93) |
| TMEM259 ⊢ – | | | 0.0120 | 0.66(0.47.0.91) |
| MISP3 F- | + | | 0.0065 | 0.63(0.45.0.88) |
| MRPL4 - | 1 | | 0.0044 | 0.62(0.45.0.86) |
| | | | | 0.02(0.10,0.00) |
| 0.5 | | Hazard Ratio | 5 5 | |

Figure S1 Univariate COX regression in the TCGA-STAD dataset identified 43 genes correlated with OS. TCGA-STAD, The Cancer Genome Atlas Stomach Adenocarcinoma; OS, overall survival; CI, confidence interval.



Figure S2 Estimation of CAF infiltration by CAFGS in GSE62254 and GSE84437 validation cohorts, respectively. (A,E) Spearman correlation analysis between CAFGS and classical CAF markers in GSE62254 and GSE84437 validation cohorts, respectively; (B,F) Spearman correlation analysis between CAFGS and CAF infiltration was estimated by EPIC in GSE62254 and GSE84437 validation cohorts, respectively; (C,G) Spearman correlation analysis between CAFGS and CAF infiltration was estimated by xCell in GSE62254 and GSE84437 validation cohorts, respectively; (D,H) Spearman correlation analysis between CAFGS and CAF infiltration was estimated by MCPcounter in GSE62254 and GSE84437 validation cohorts, respectively. CAF, cancer-associated fibroblast; CAFGS, CAF gene signature.



Figure S3 GO/KEGG enrichment analysis for DEGs between low- and high-risk groups in TCGA-STAD (A), GSE62254 (B), and GSE84437 (C) cohorts, respectively. GO, Gene Ontology; BP, Biological Process; MF, Molecular Function; CC, Cellular Component; KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially expressed genes; TCGA-STAD, The Cancer Genome Atlas Stomach Adenocarcinoma.



Figure S4 Infiltration of immune cells in the GSE62254 validation cohort between low- and high-risk groups. ns, not statistically significant; *, P<0.05; **, P<0.01; ****, P<0.001; red asterisks indicates the corresponding cells are enriched in the high-risk group, while blue asterisks indicates the corresponding cells are enriched in the low-risk group.



Figure S5 Immune cell infiltration between the high-risk group and low-risk group in the GSE84437 validation cohort. ns, not statistically significant; *, P<0.05; **, P<0.01; ****, P<0.001; red asterisks indicates the corresponding cells are enriched in the high-risk group, while blue asterisks indicates the corresponding cells are enriched in the low-risk group.



Figure S6 Estimation of immune infiltration by TIMER and ESTIMATE. (A) Three datasets were analyzed for correlations between CAFGS score and major immune cells; (B-E) tumor purity, stromal, immune, and ESTIMATE scores of two groups in the TCGA-STAD dataset; (F-I) tumor purity, stromal, immune, and ESTIMATE scores of two groups in the GSE62254 dataset; (J-M) tumor purity, stromal, immune, and ESTIMATE scores of two groups in the GSE84437 dataset. TCGA-STAD, The Cancer Genome Atlas Stomach Adenocarcinoma; CAFGS, cancer-associated fibroblast gene signature.



Figure S7 Construction of nomograms in the GSE62254 validation cohort. (A) Univariate and multivariate COX regression; (B) CAFGS nomogram; (C) clinicopathological nomogram. CAFGS, cancer-associated fibroblast gene signature; CI, confidence interval.