

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
T3	121	91	92	16	320
T4	153	21	292	25	491
N stage, n					
N0	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					
M0	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	GCAAACTGCCTCCAGATGGAAG	TCAGACTCCTGTAATAAGCCTCC
CST2	CCTACTCCCACCCCTTG TAGT	GCAGCCTTCTCTGTCTTCTCCT
HTR1F	TCTTGTGGCTGTCTGGTGATG	GCAGGTAATGTCAACTCAGCC
IL1RAP	CTGAGGATCTCAAGCGCAGCTA	AGCAGGACTGTGGCTCCAAAAC
NR1D1	CTGCCAGCAATGTCGCTTCAAG	TGGCTGCTCAACTGGTTGTTGG
NTAN1	CATTGTGACGGAACCGACACCA	CTGTGCTCACTGAAGCCTCCAA
OLFML2B	GAACCGAGATGAATAAGCGAGGC	GGACACGGTTTCTTCTGCAGA
TMEM259	TCACTACCGCTTCAATGGGCAG	CTGAAGCAGCATCTCCTGGATG
VTN	TGGCTGTCCTTGTTCTCCAGTG	GTGTGCGAAGATTGACTCGGTAG

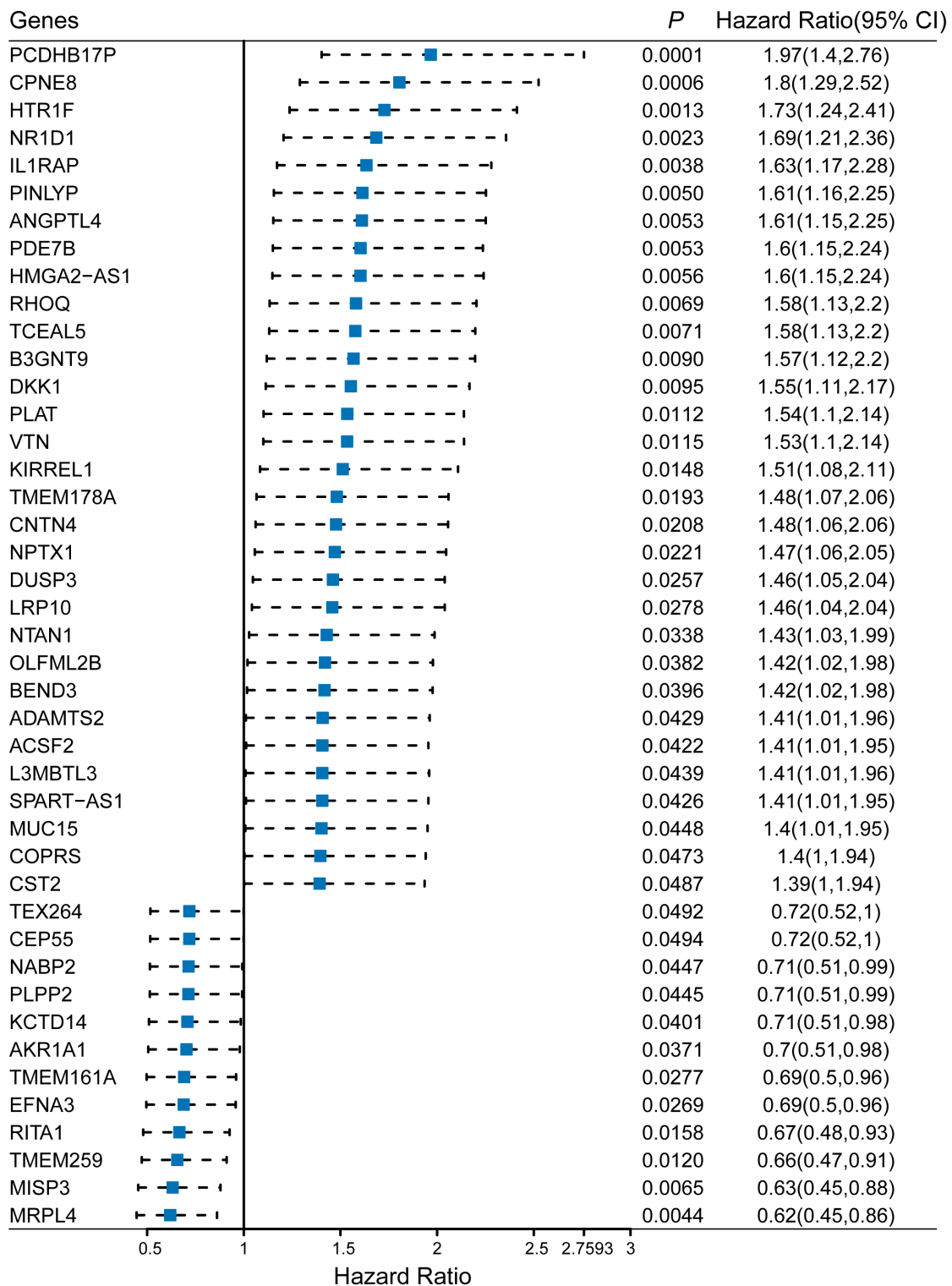


Figure S1 Univariate COX regression in the TCGA-STAD dataset identified 43 genes correlated with OS. TCGA-STAD, The Cancer Genome Atlas Stomach Adenocarcinoma; OS, overall survival; CI, confidence interval.

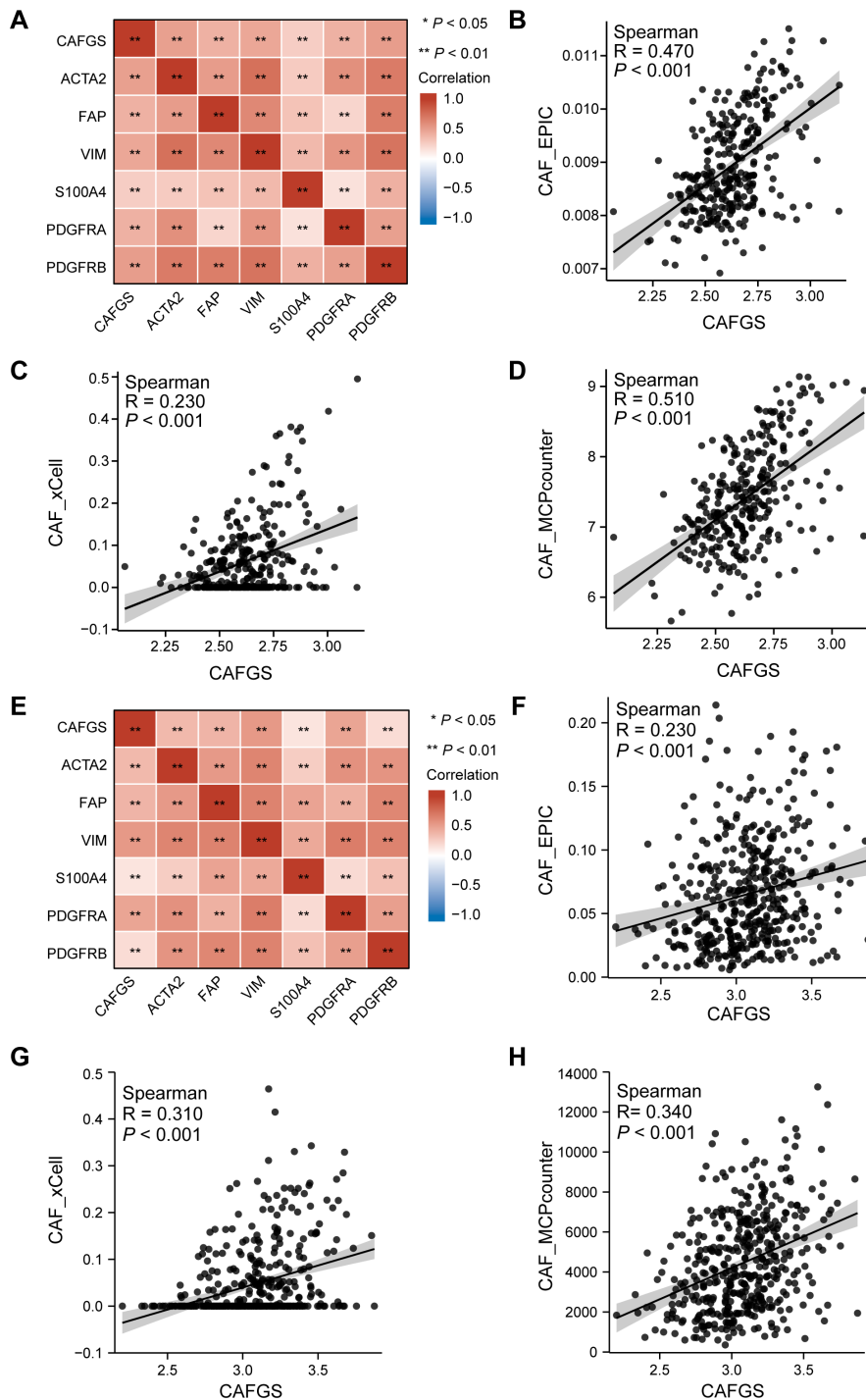


Figure S2 Estimation of CAF infiltration by CAFGS in GSE62254 and GSE84437 validation cohorts, respectively. (A,E) Spearman correlation analysis between CAFGS and classical CAF markers in GSE62254 and GSE84437 validation cohorts, respectively; (B,F) Spearman correlation analysis between CAFGS and CAF 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.

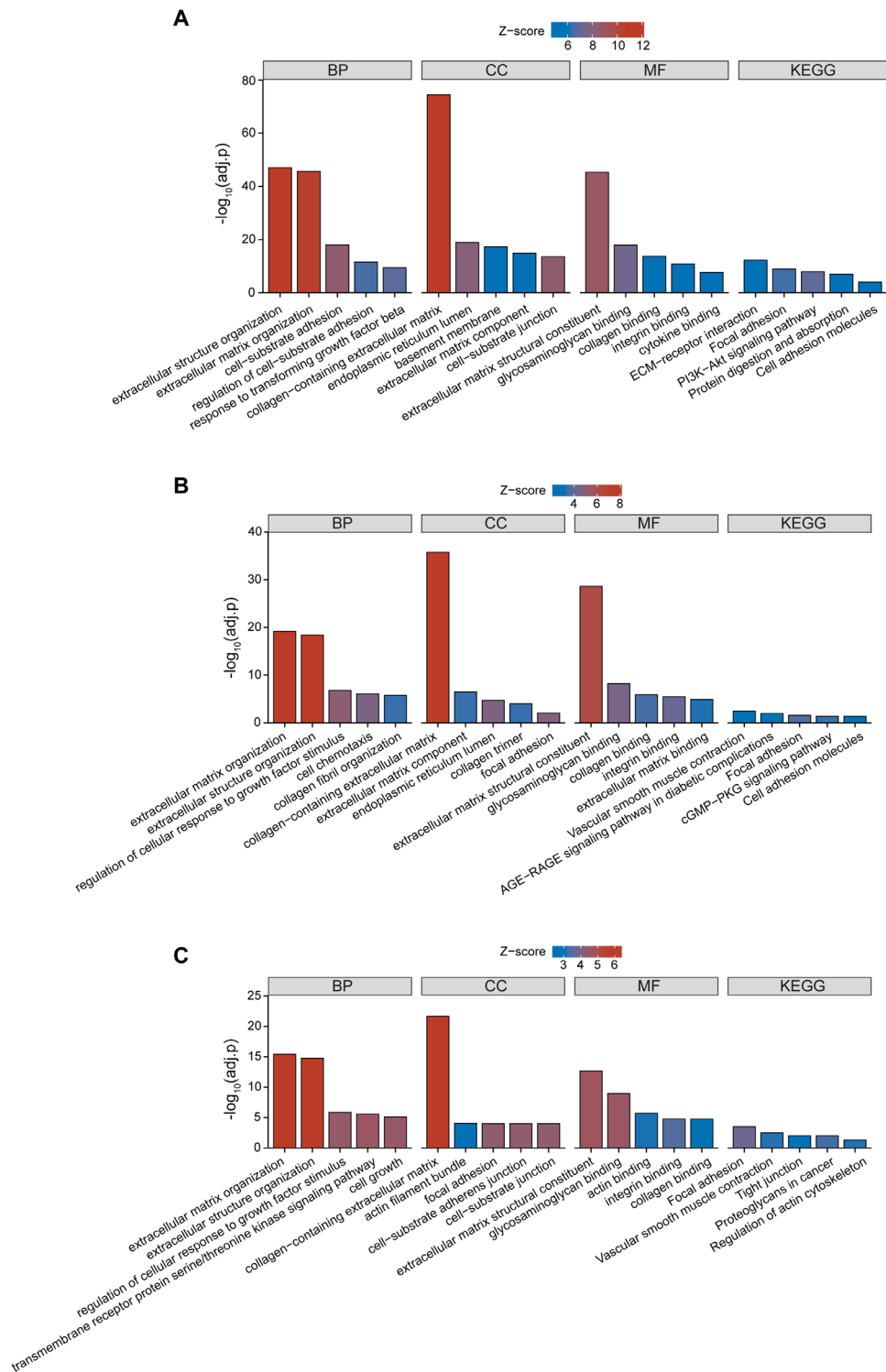


Figure S3 GO/KEGG enrichment analysis for DEGs between low- and high-risk groups in TCGA-STAD (A), GSE62254 (B), and GSE84437 (C) cohorts, respectively. GO, Gene Ontology; BP, Biological Process; MF, Molecular Function; CC, Cellular Component; KEGG, Kyoto Encyclopedia of Genes and Genomes; DEGs, differentially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

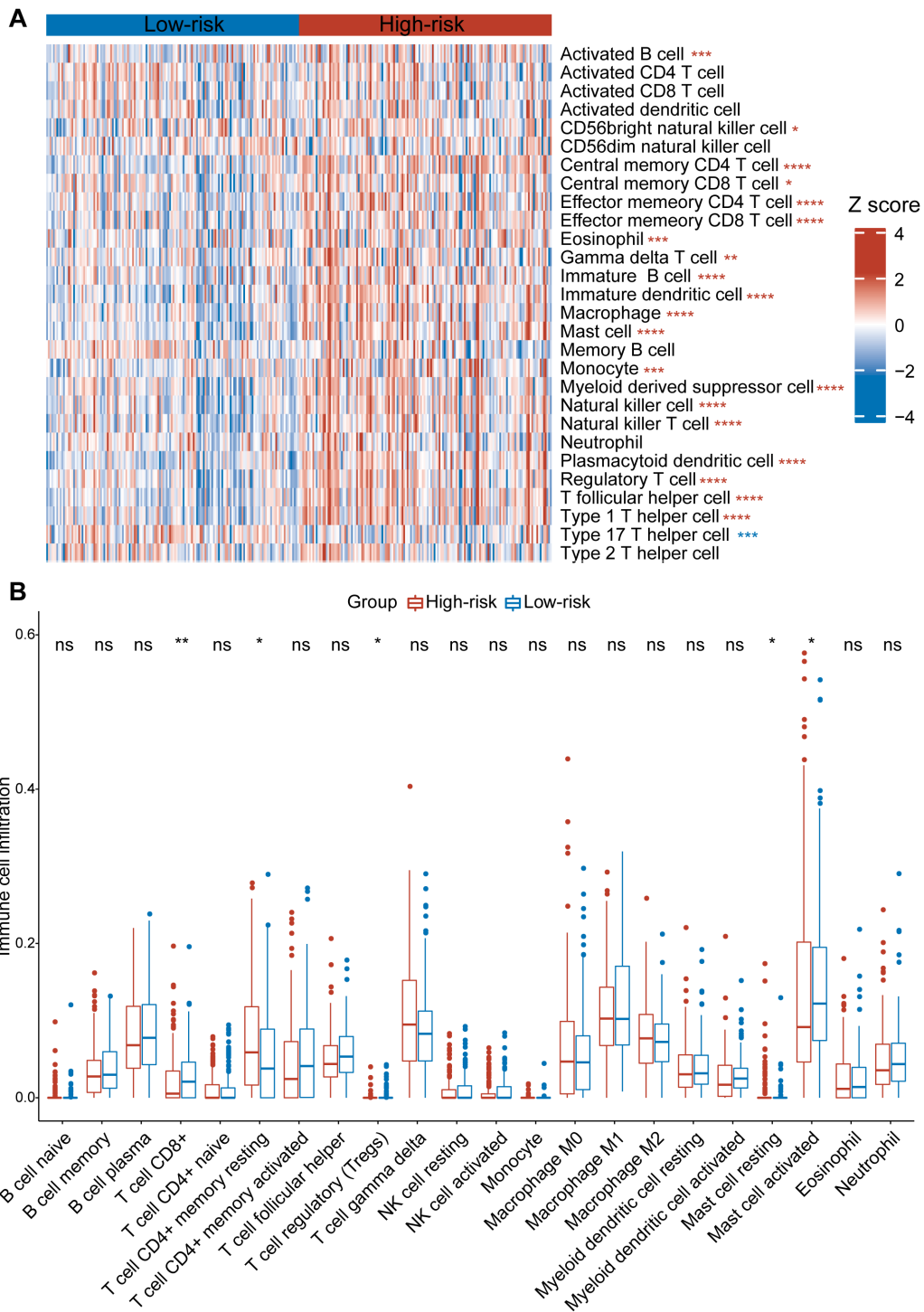


Figure S4 Infiltration of immune cells in the GSE62254 validation cohort between low- and high-risk groups. ns, not statistically significant; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$, red asterisks indicates the corresponding cells are enriched in the high-risk group, while blue asterisks indicates the corresponding cells are enriched in the low-risk group.

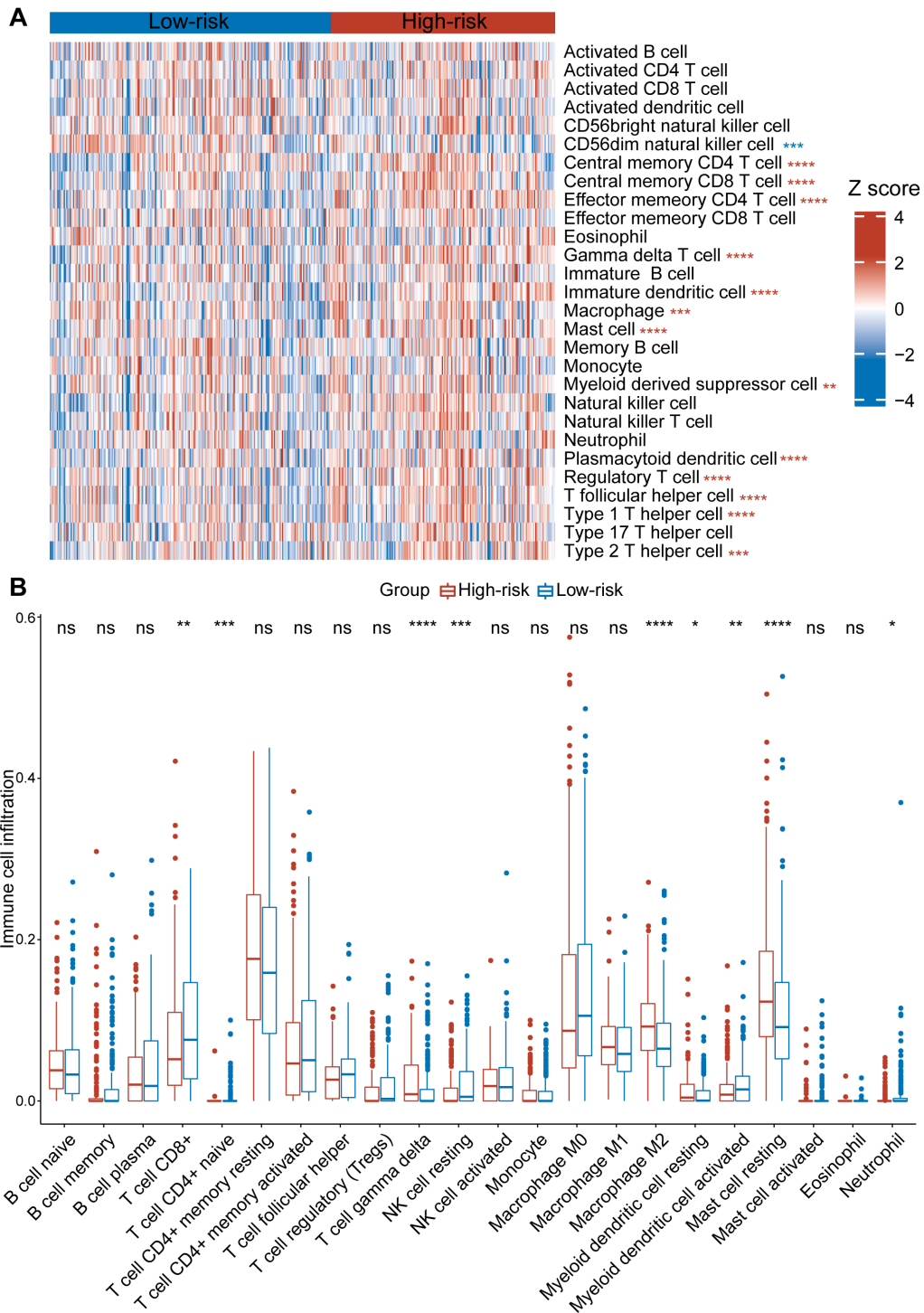


Figure S5 Immune cell infiltration between the high-risk group and low-risk group in the GSE84437 validation cohort. ns, not statistically significant; *, $P < 0.05$; **, $P < 0.01$; ***, $P < 0.001$; ****, $P < 0.0001$, red asterisks indicates the corresponding cells are enriched in the high-risk group, while blue asterisks indicates the corresponding cells are enriched in the low-risk group.

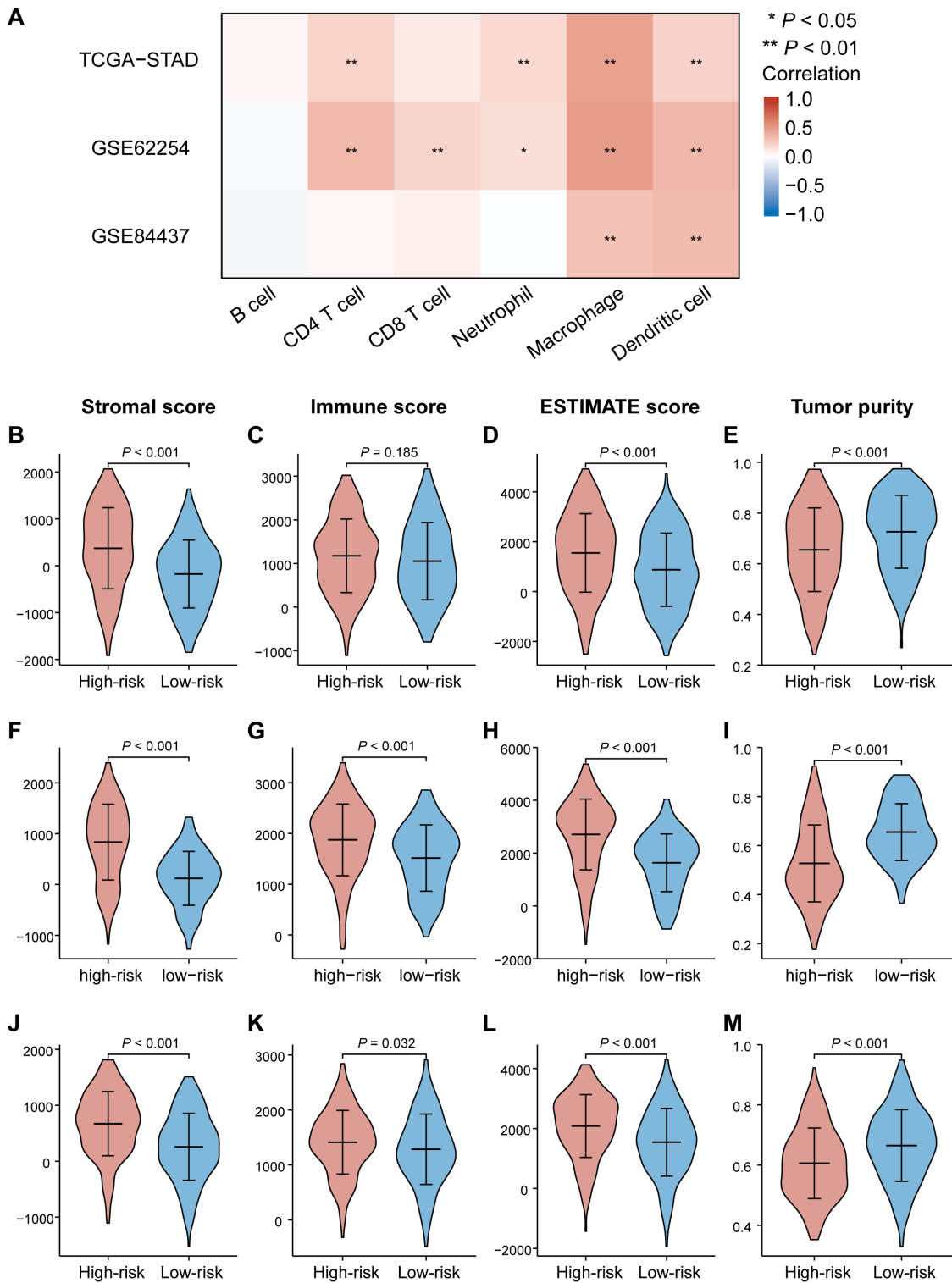


Figure S6 Estimation of immune infiltration by TIMER and ESTIMATE. (A) Three datasets were analyzed for correlations between CAFGS score and major immune cells; (B-E) tumor purity, stromal, immune, and ESTIMATE scores of two groups in the TCGA-STAD dataset; (F-I) tumor purity, stromal, immune, and ESTIMATE 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.

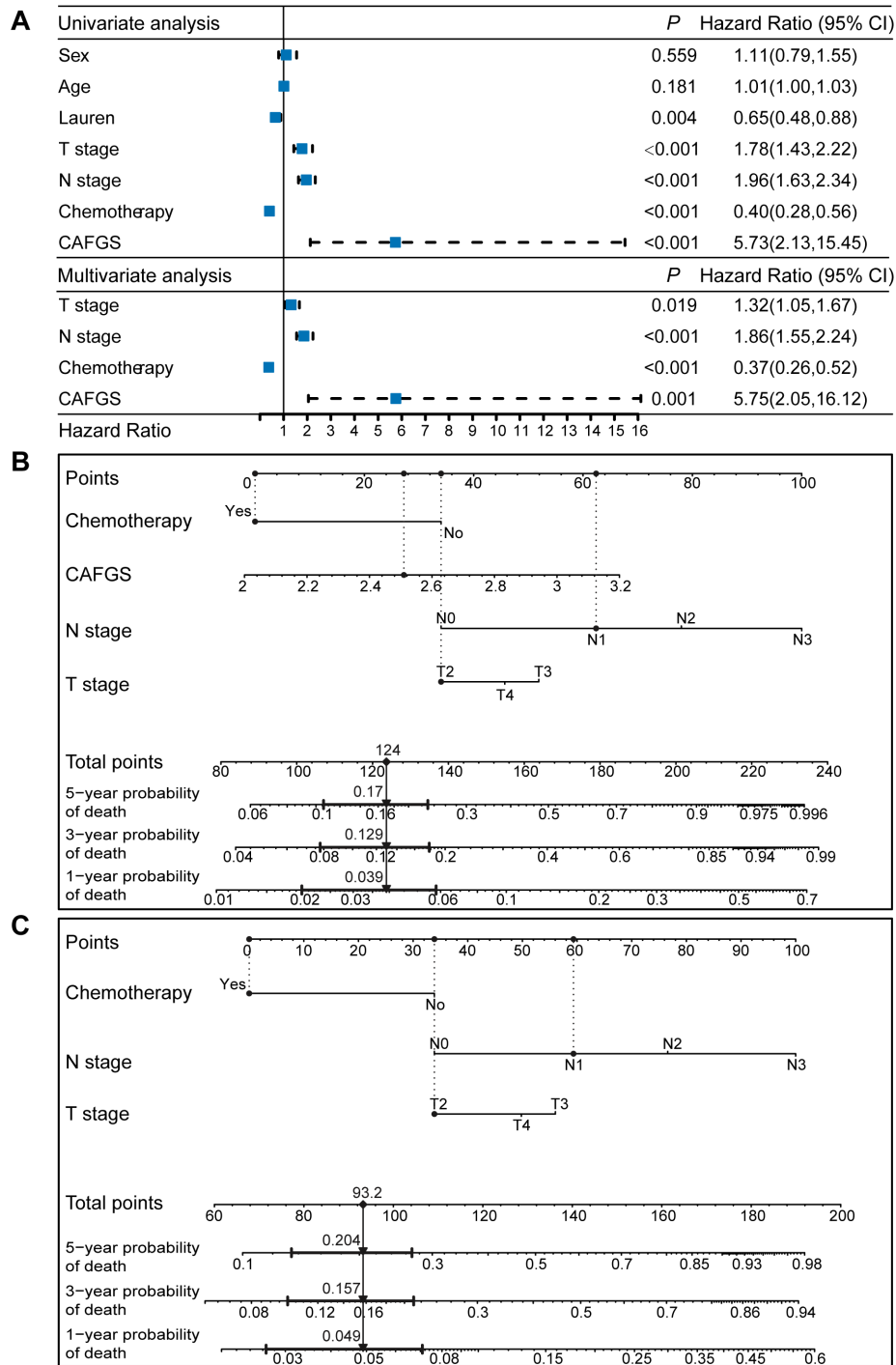


Figure S7 Construction of nomograms in the GSE62254 validation cohort. (A) Univariate and multivariate COX regression; (B) CAFGS nomogram; (C) clinicopathological nomogram. CAFGS, cancer-associated fibroblast gene signature; CI, confidence interval.