Table S1 Cox proportional hazard model of RARs and six tumor-infiltrating immune cells in STAD performed using TIMER

Variables	Coefficient	HR	HR 95% CI_l	HR 95% CI_u	P value
B_cell	2.987	19.821	0.278	1412.241	0.17
CD8_T cell	−1.734	0.177	0.011	2.798	0.22
CD4_T cell	−4.462	0.012	0.000	1.098	0.06
Macrophage	5.006	149.360	7.491	2,977.868	0.001*
Neutrophil	−0.183	0.833	0.004	162.588	0.95
Dendritic	1.354	3.873	0.324	46.370	0.29
RARA	0.103	1.109	0.893	1.377	0.35
RARB	0.201	1.223	0.971	1.539	0.09
RARG	−0.104	0.901	0.737	1.101	0.31

*, P<0.05. HR, hazard rate; STAD, stomach adenocarcinoma; RARs, retinoic acid receptors; TIMER, tumor immune estimation resource; 95% CI_u, upper limit of 95% confidence interval; 95% CI_l, lower limit of 95% confidence interval.
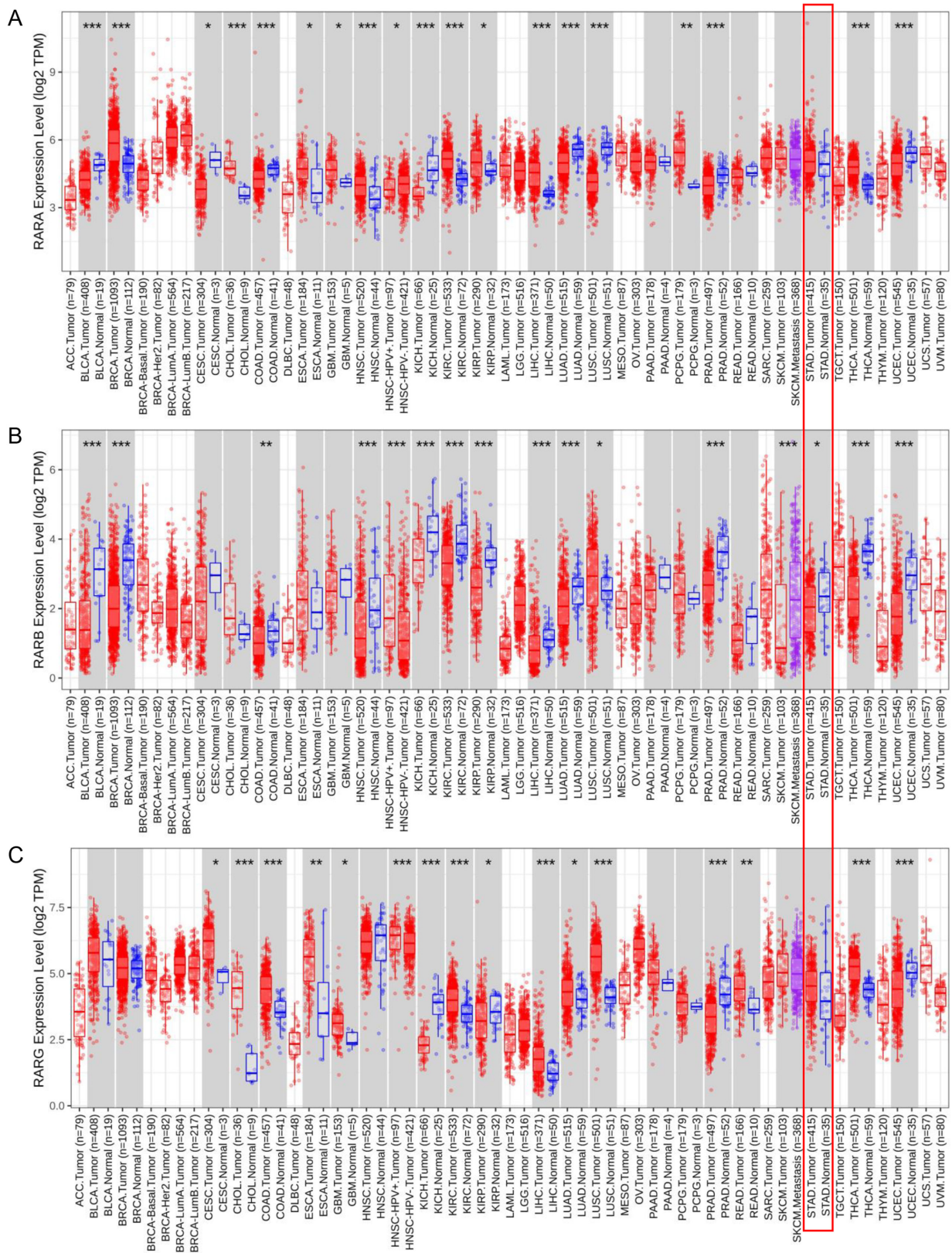
Figure S1 The expression of RARs in different cancers and normal tissues using TIMER database. *, P<0.05; **, P<0.01; ***, P<0.001. ACC, adrenocortical carcinoma; BLCA, bladder urothelial carcinoma; BRCA, breast invasive carcinoma; CESC, cervical squamous cell carcinoma and endocervical adenocarcinoma; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; DLBC, lymphoid neoplasm diffuse large b-cell lymphoma; ESCA, esophageal carcinoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; KIRC, kidney renal clear cell carcinoma; KIRP, kidney renal papillary cell carcinoma; LAML, acute myeloid leukemia; LGG, brain lower grade glioma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MESO, mesothelioma; OV, ovarian serous cystadenocarcinoma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; PRAD, prostate adenocarcinoma; RARs, retinoic acid receptors; READ, rectum adenocarcinoma; SARC, sarcoma; SKCM, skin cutaneous melanoma; STAD, stomach adenocarcinoma; TIMER, tumor immune estimation resource; TGCT, testicular germ cell tumors; THCA, thyroid carcinoma; THYM, thymoma; TPM, transcripts per million; UCEC, Uterine Corpus Endometrial Carcinoma; UCS, uterine carcinosarcoma; UVM, uveal melanoma.
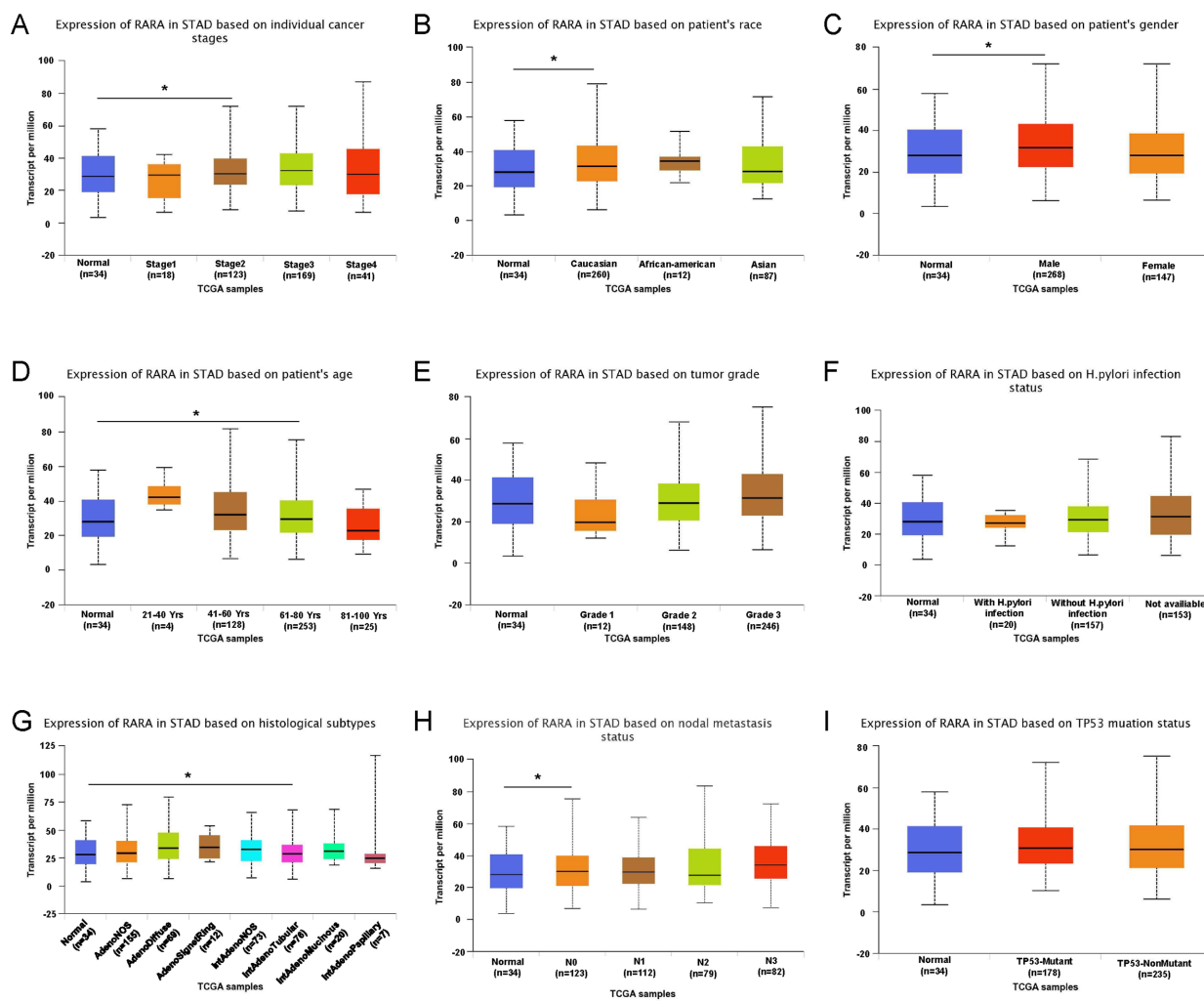
Figure S2 The relationship between mRNA expression levels of RARA and clinicopathological parameters of STAD patients using UALCAN database. *, P<0.05. mRNA, messenger ribonucleic acid; NOS, not otherwise specified; RARA, retinoic acid receptor A; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; UALCAN, University of Alabama at Birmingham cancer data.
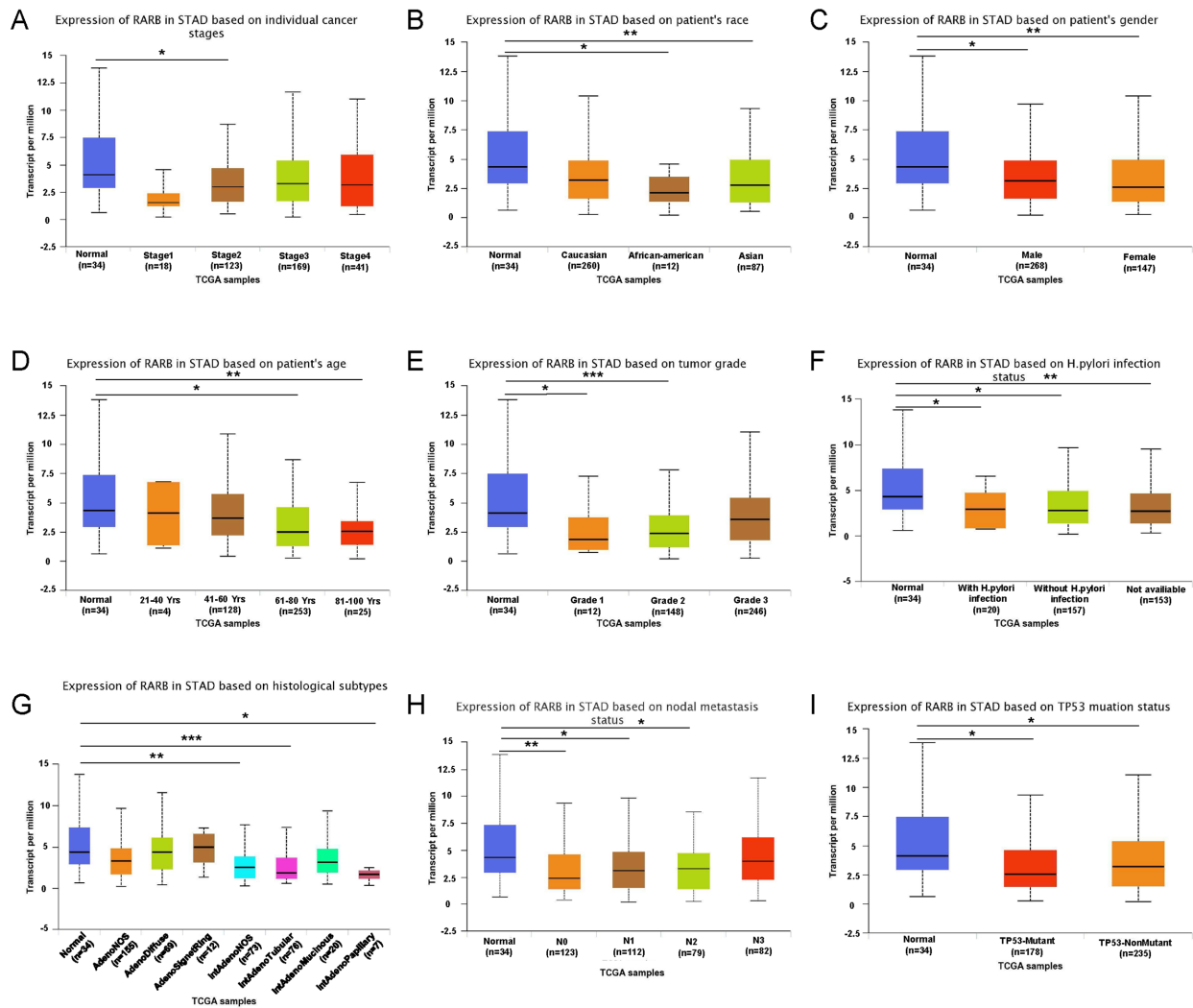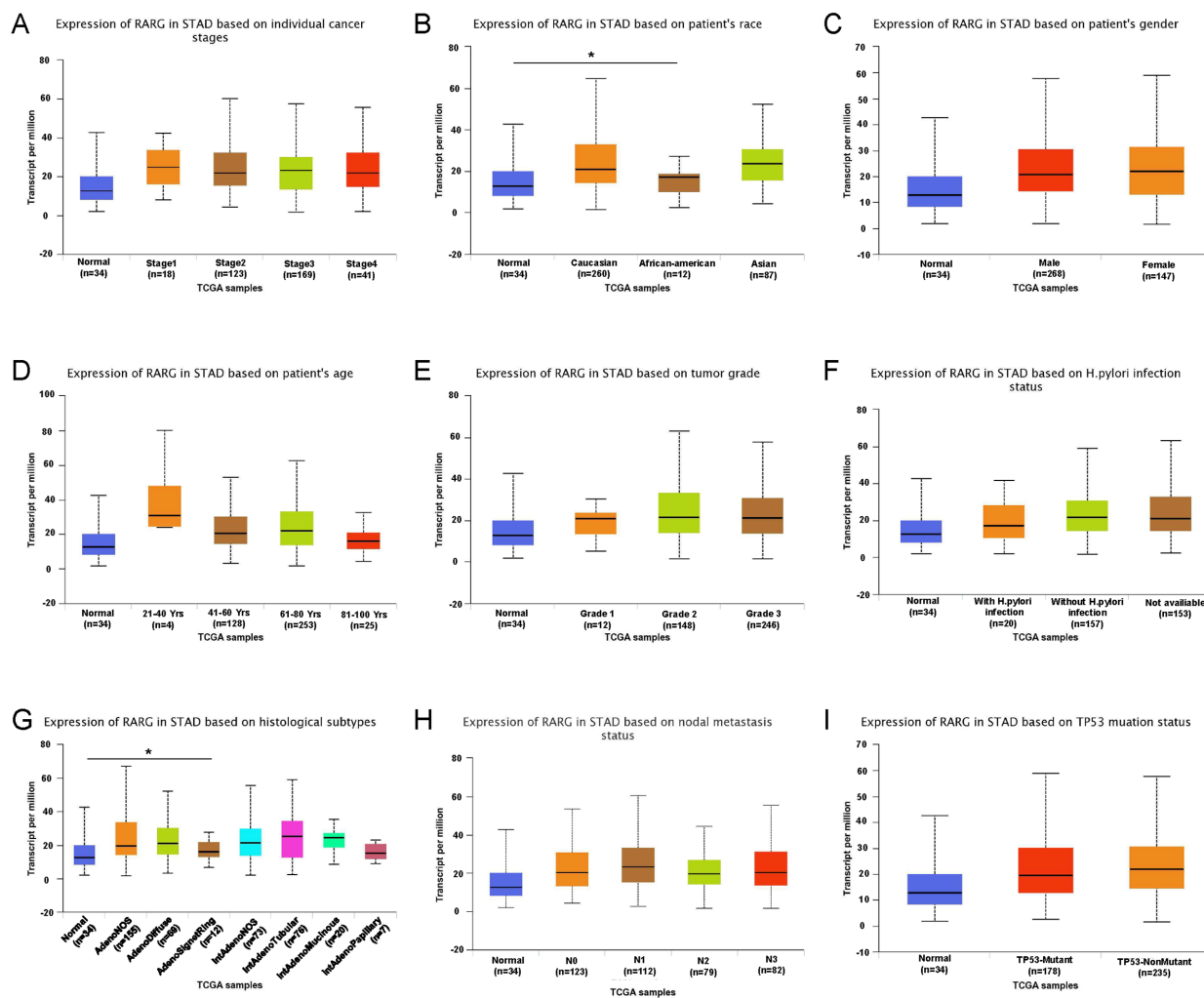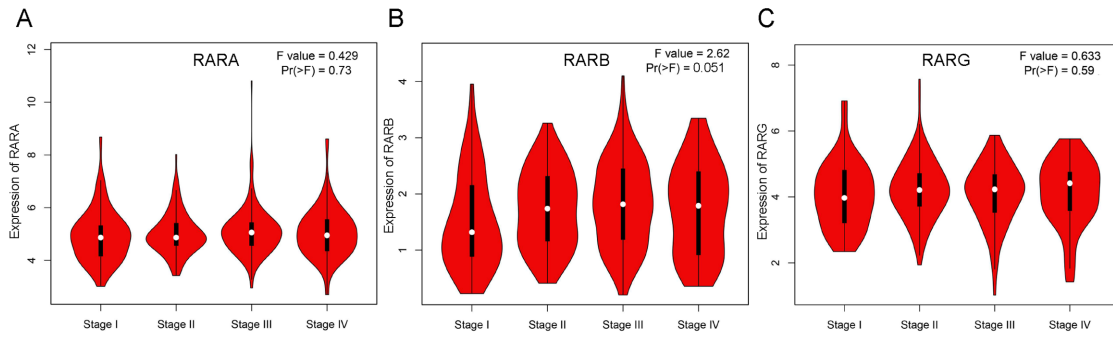
Figure S3 (A-I) The relationship between mRNA expression levels of RARB and clinicopathological parameters of STAD patients using UALCAN database. *, P<0.05; **, P<0.01; ***, P<0.001. mRNA, messenger ribonucleic acid; NOS, not otherwise specified; RARB, retinoic acid receptor B; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; UALCAN, University of Alabama at Birmingham cancer data.

Figure S4 The relationship between mRNA expression levels of RARG and clinicopathological parameters of STAD patients using UALCAN database. *, P<0.05. mRNA, messenger ribonucleic acid; NOS, not otherwise specified; RARG, retinoic acid receptor G; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; UALCAN, University of Alabama at Birmingham cancer data.

Figure S5 The association between RARs and clinical stage of STAD patients from GEPIA database. GEPIA, gene expression profiling interactive analysis; RARs, retinoic acid receptors; STAD, stomach adenocarcinoma.

Figure S6 The effect of immune cell infiltration on the association between RARs mRNA expressions and STAD prognosis using Kaplan-Meier plotter database. CI, confidence interval; HR, hazard ratio; mRNA, messenger ribonucleic acid; RARs, retinoic acid receptors; STAD, stomach adenocarcinoma.
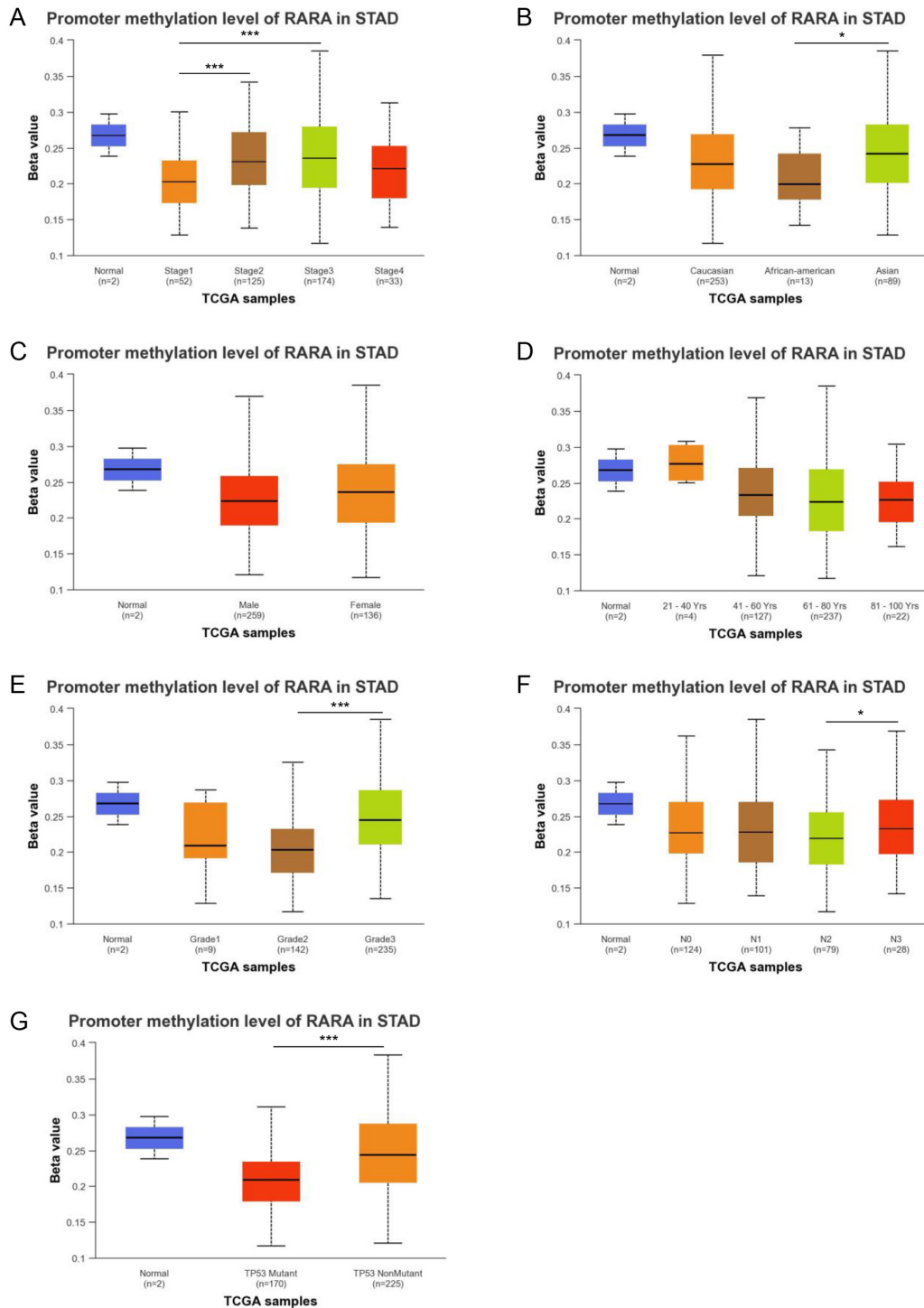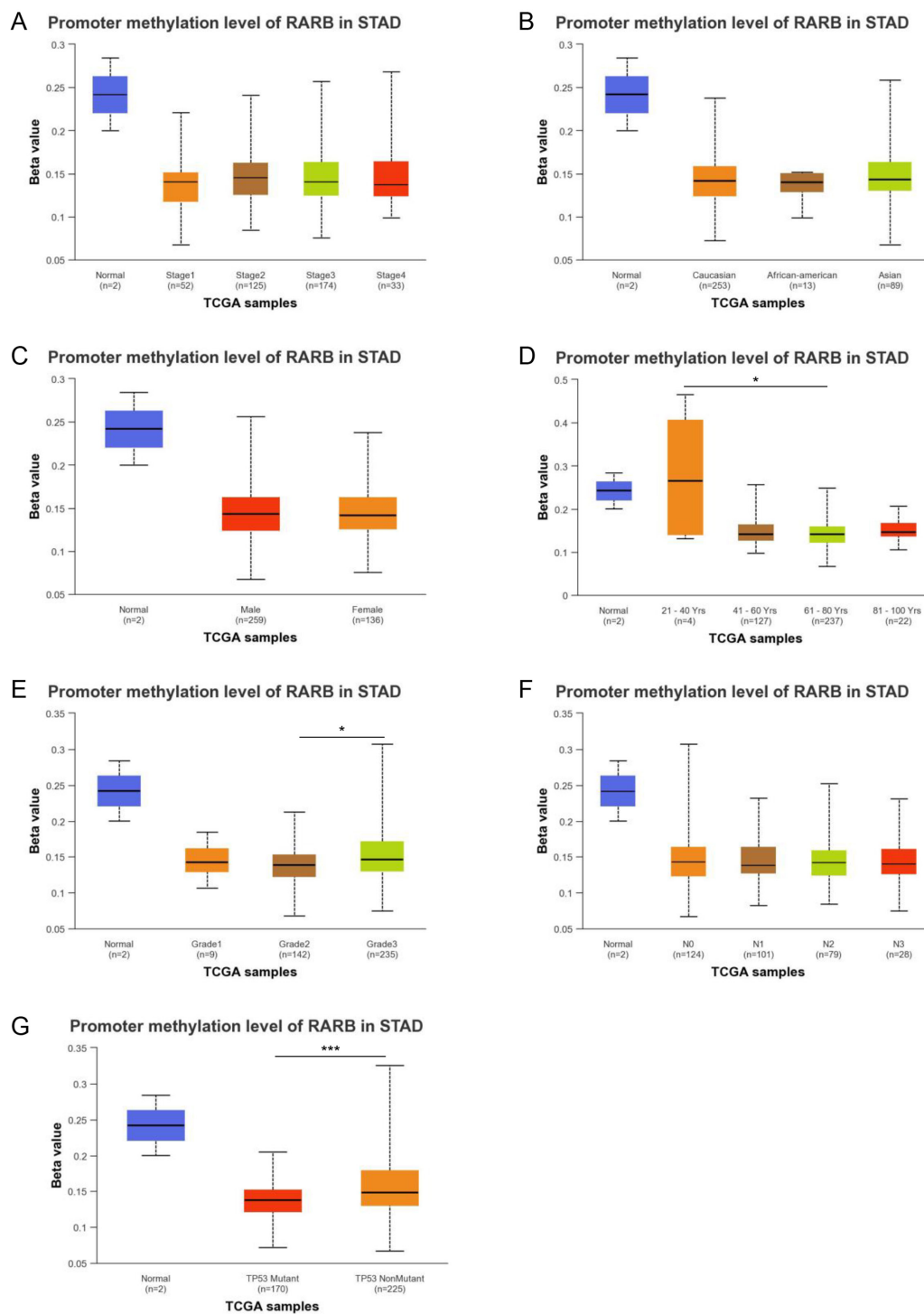
Figure S7 The relationship between methylation status of RARA and clinicopathological parameters of STAD patients using UALCAN database. *, P<0.05; ***, P<0.001. RARA, retinoic acid receptor A; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; UALCAN, University of Alabama at Birmingham cancer data.
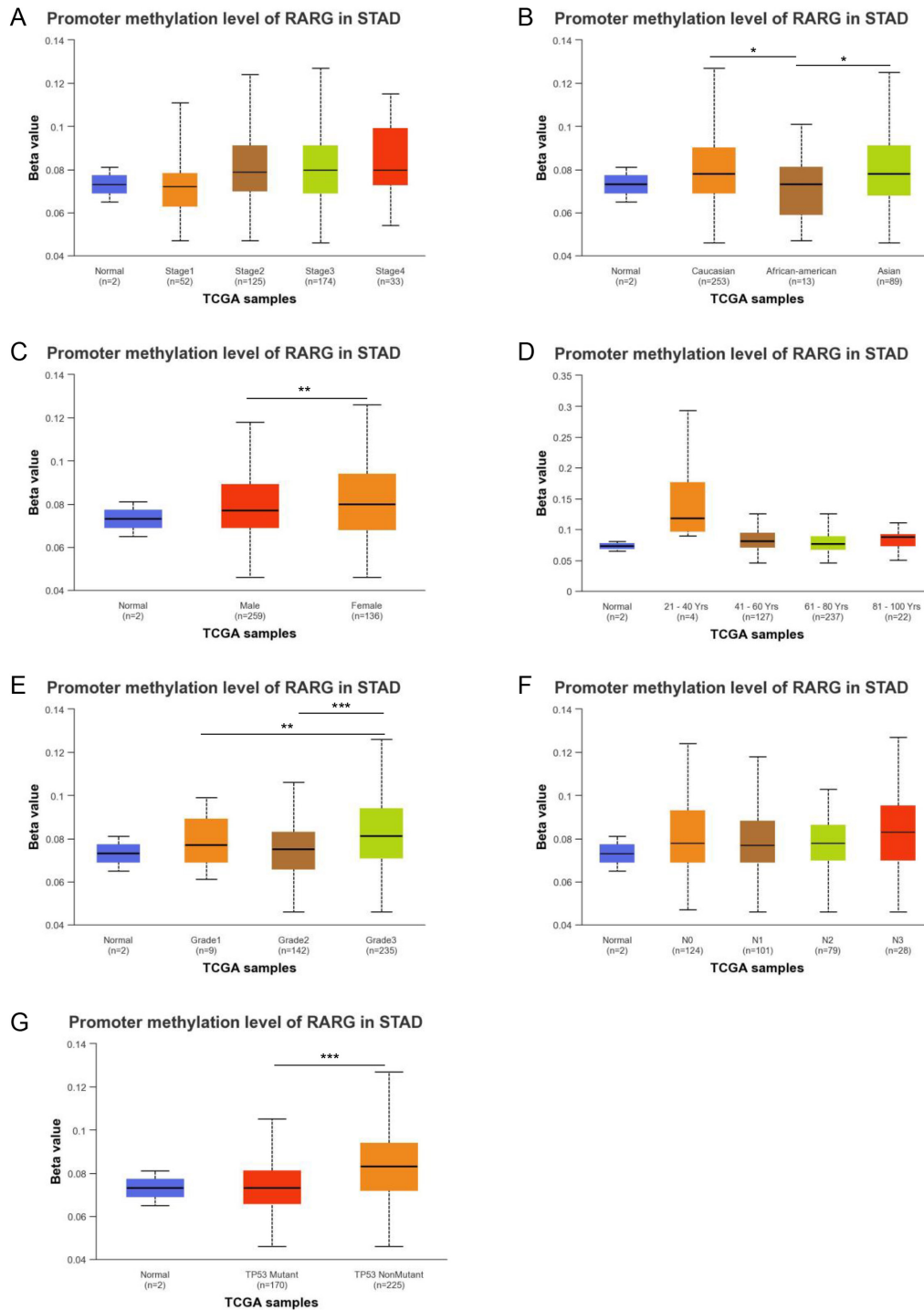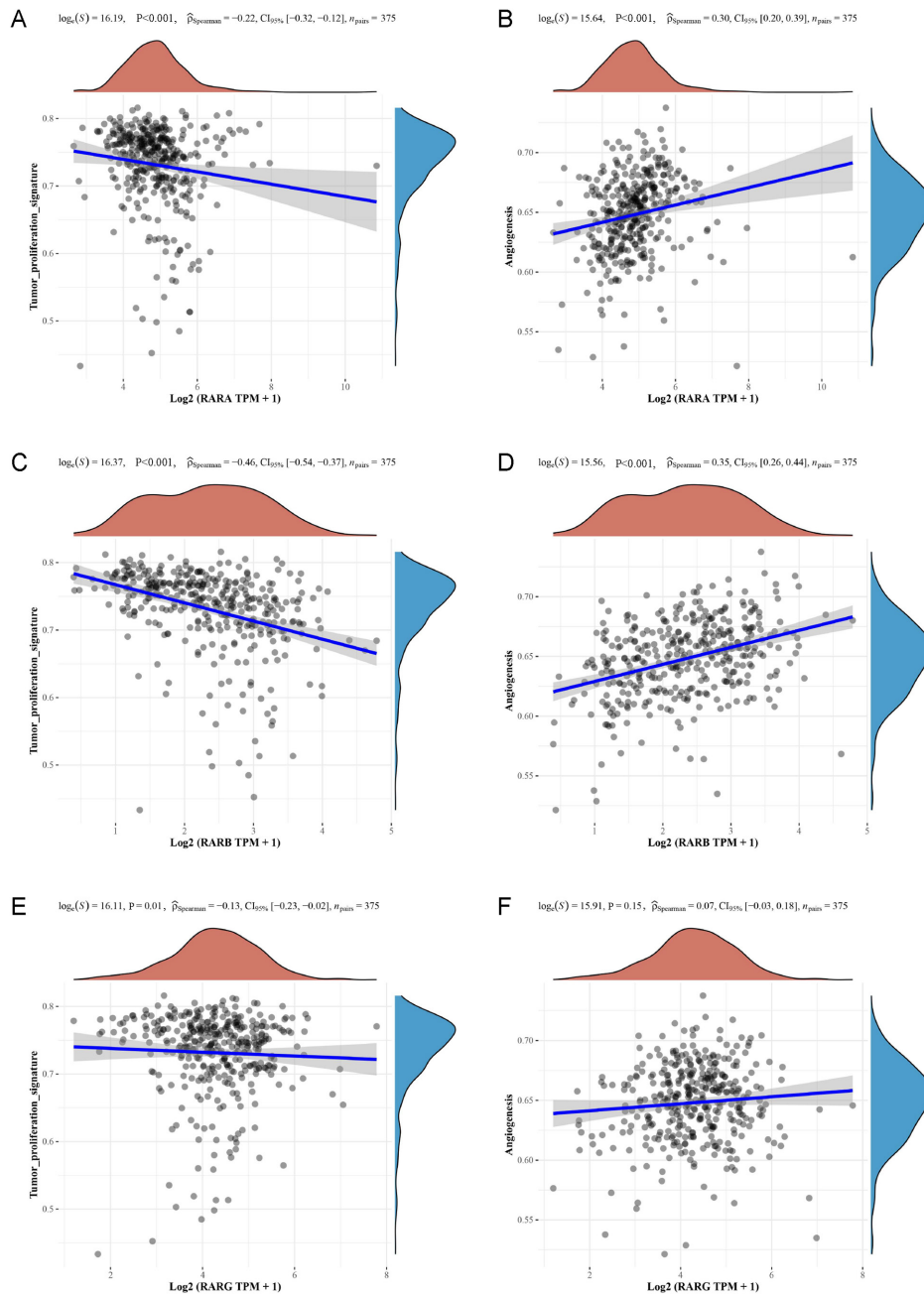
Figure S8 The relationship between methylation status of RARB and clinicopathological parameters of STAD patients using UALCAN database. *, P<0.05; ***, P<0.001. RARB, retinoic acid receptor B; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; UALCAN, University of Alabama at Birmingham cancer data.

Figure S9 (A-G) The relationship between methylation status of RARG and clinicopathological parameters of STAD patients using UALCAN database. *, P<0.05; **, P<0.01; ***, P<0.001. RARG, retinoic acid receptor G; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; UALCAN, University of Alabama at Birmingham cancer data.
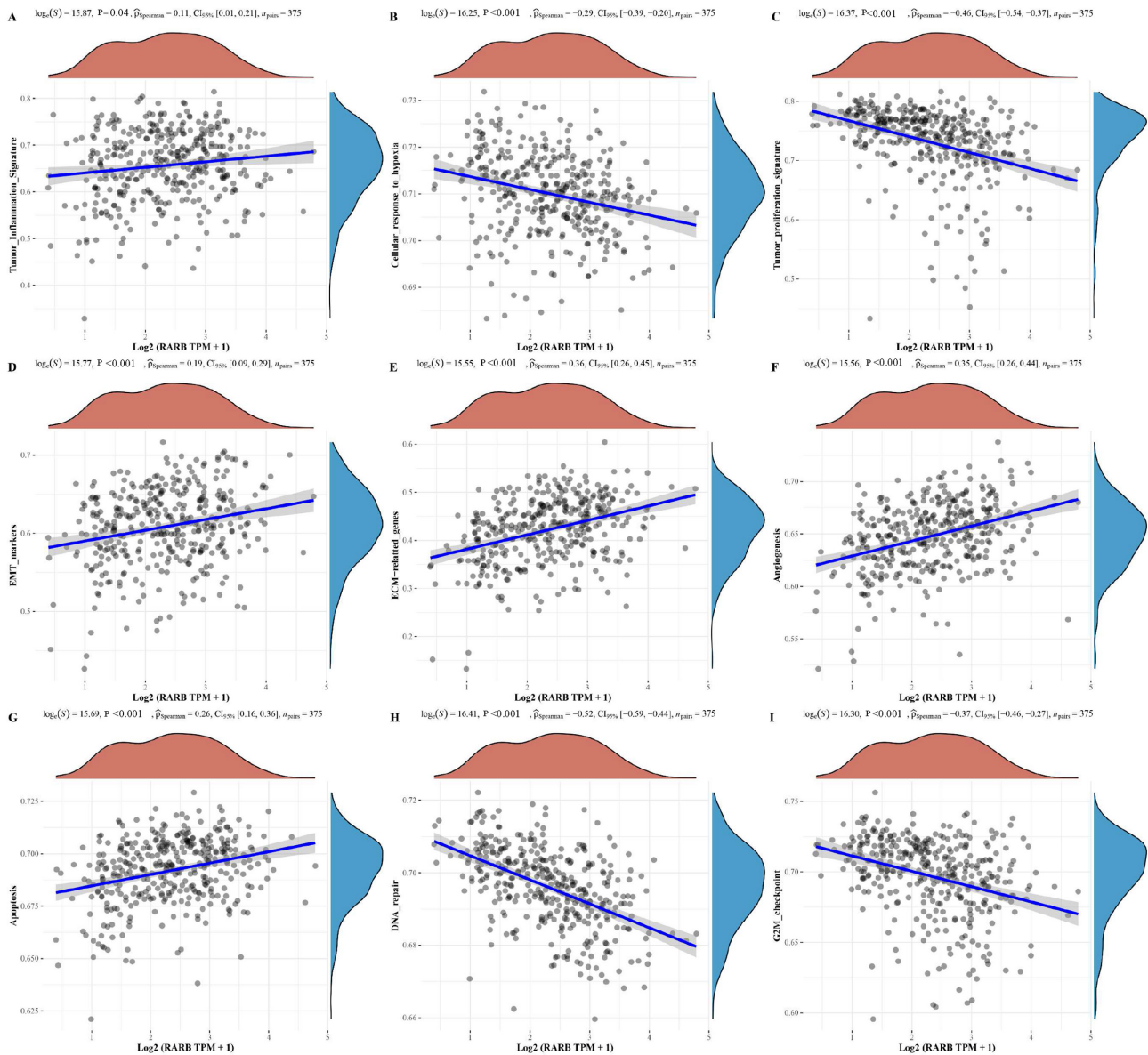
Figure S10 The correlations between RARA and STAD related signaling pathways using TCGA database. CI, confidence interval; RARA, retinoic acid receptor A; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; TPM, transcripts per million.
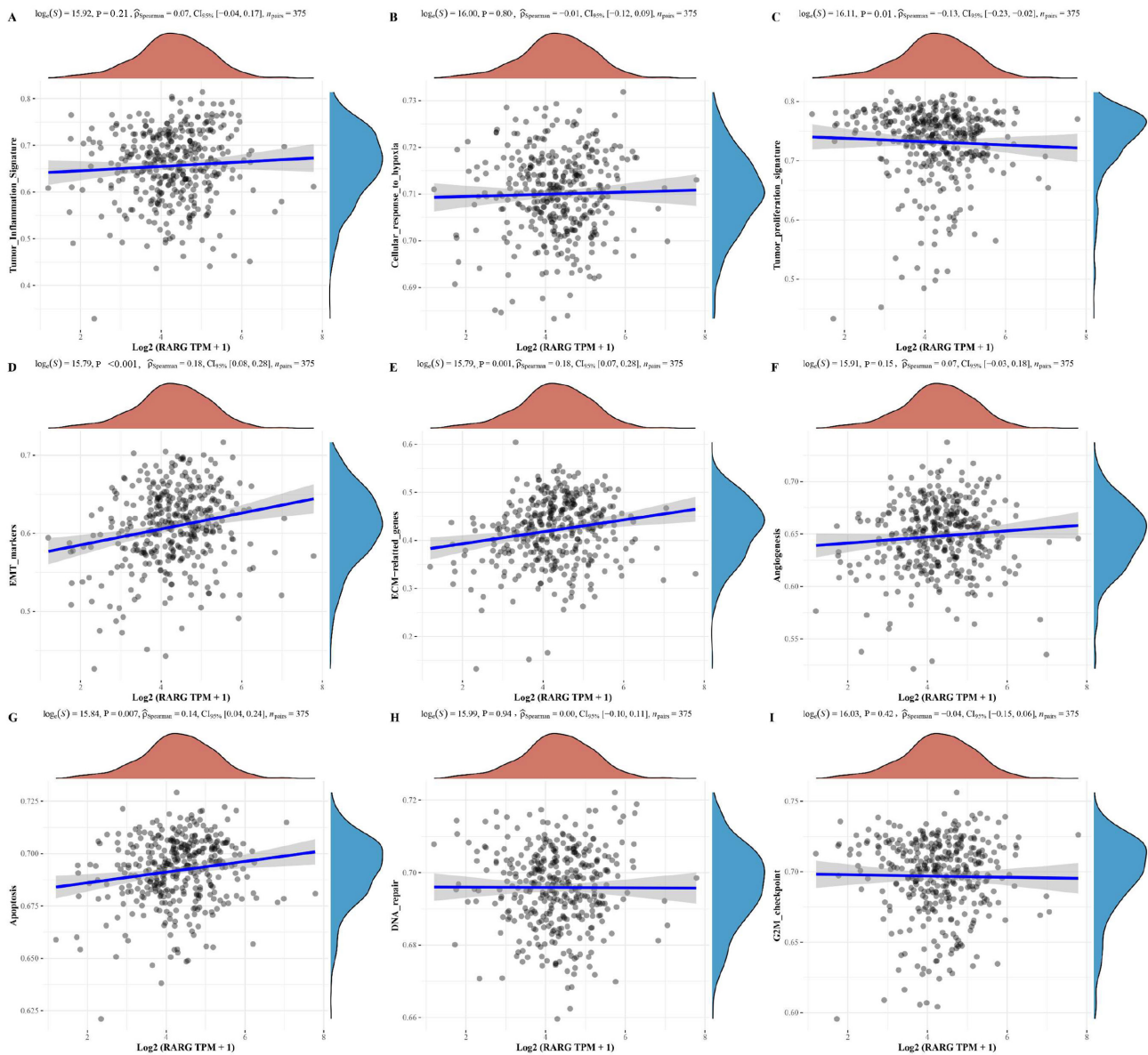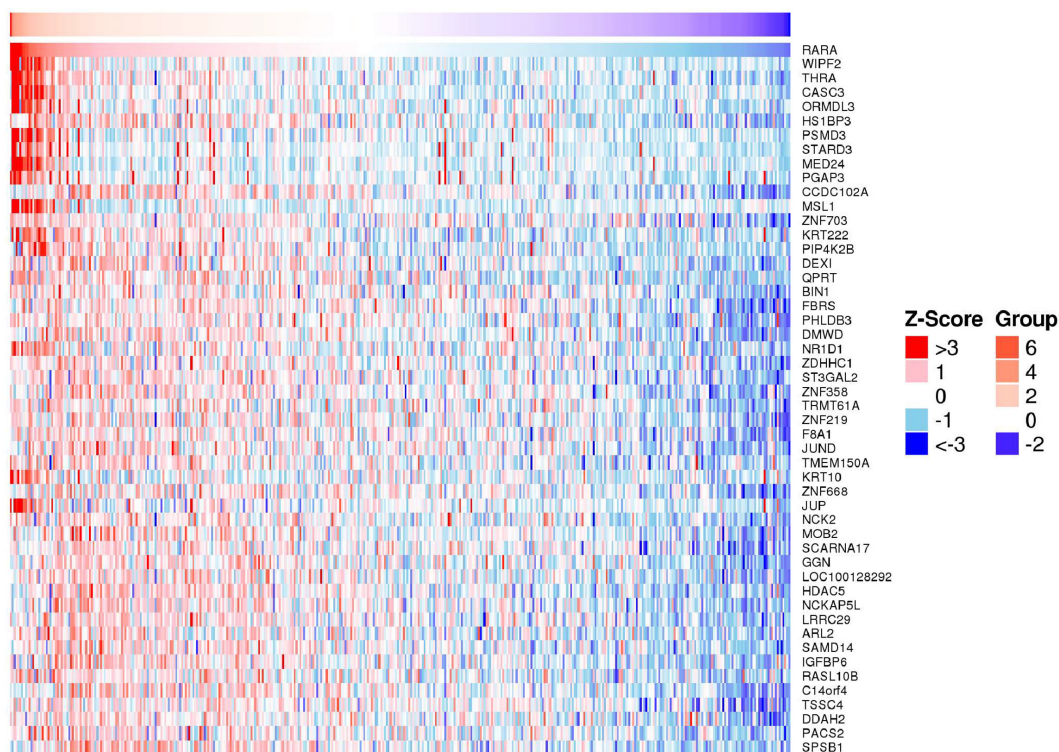
Figure S11 The correlations between RARB and STAD related signaling pathways using TCGA database. CI, confidence interval; ECM, extracellular matrix; EMT, epithelial-mesenchymal transition; RARB, retinoic acid receptor B; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; TPM, transcripts per million.

Figure S12 The correlations between RARG and STAD related signaling pathways using TCGA database. CI, confidence interval; ECM, extracellular matrix; EMT, epithelial-mesenchymal transition; RARG, retinoic acid receptor G; STAD, stomach adenocarcinoma; TCGA, The Cancer Genome Atlas; TPM, transcripts per million.

A Positively correlated significant genes of RARA
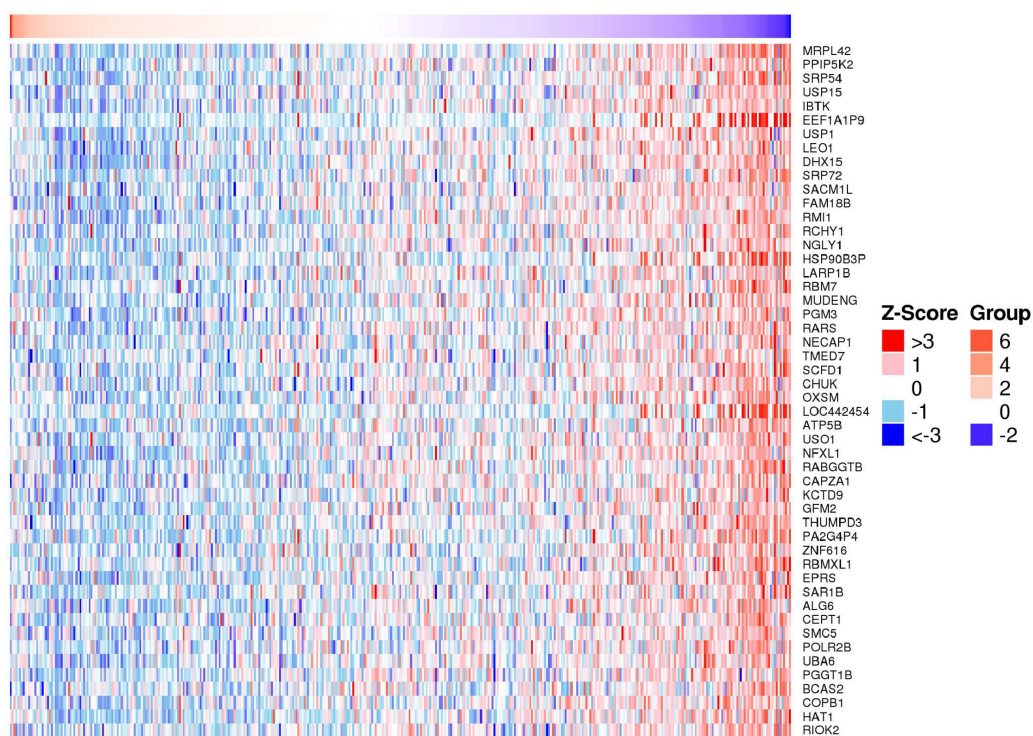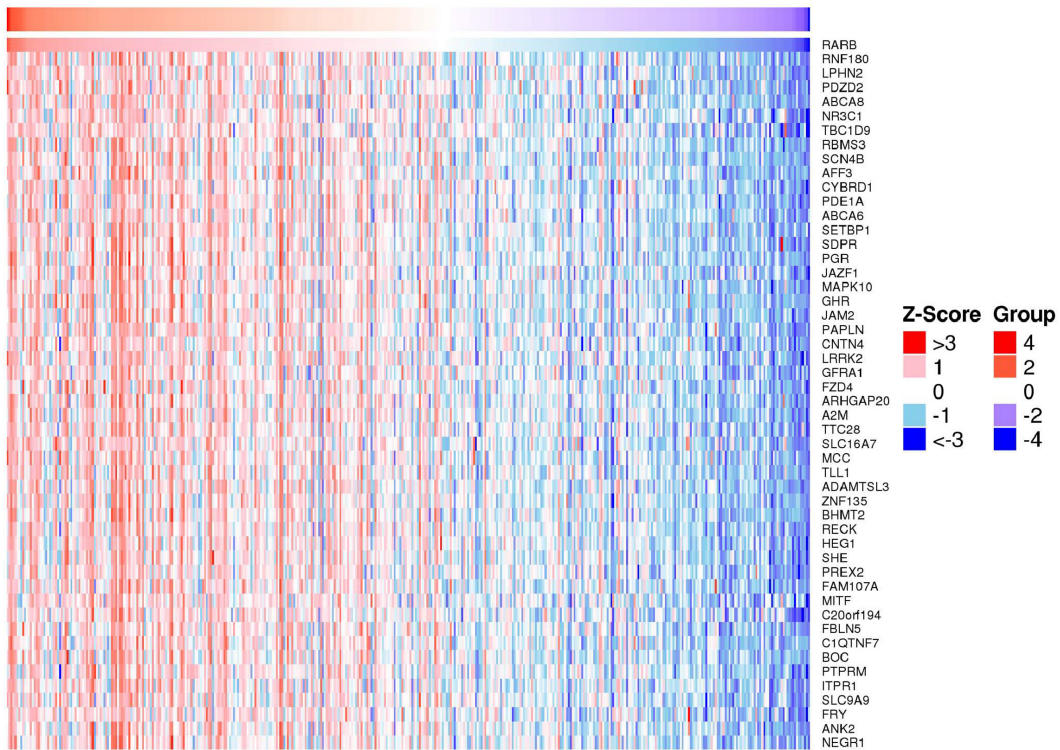

B Negatively correlated significant genes of RARA

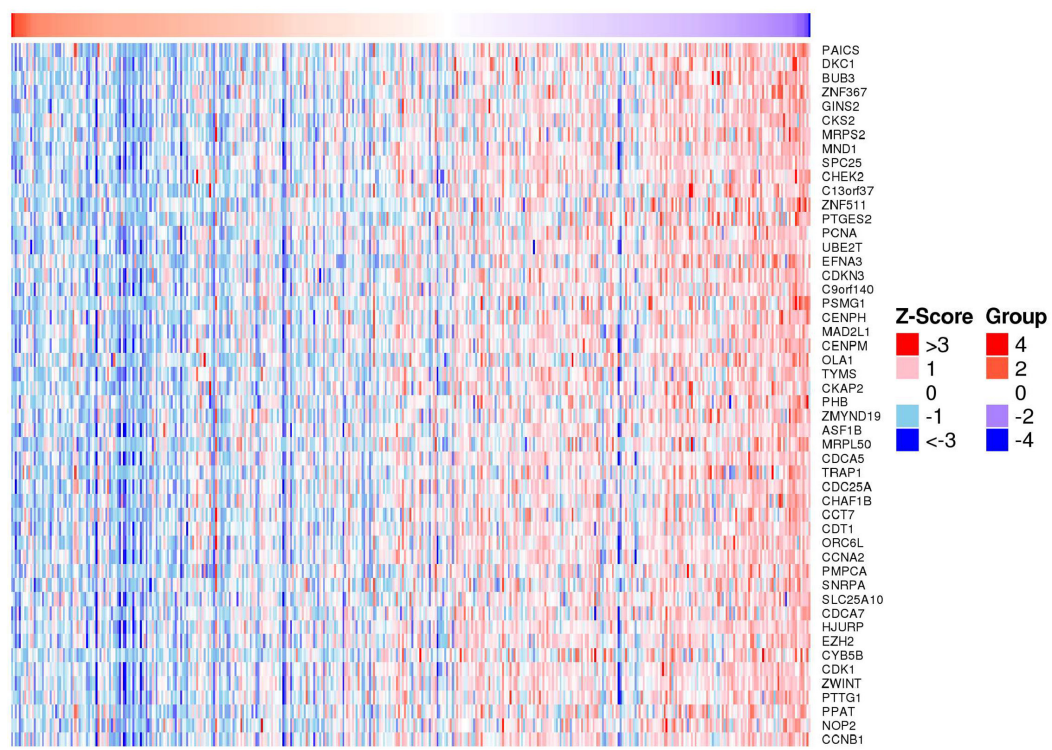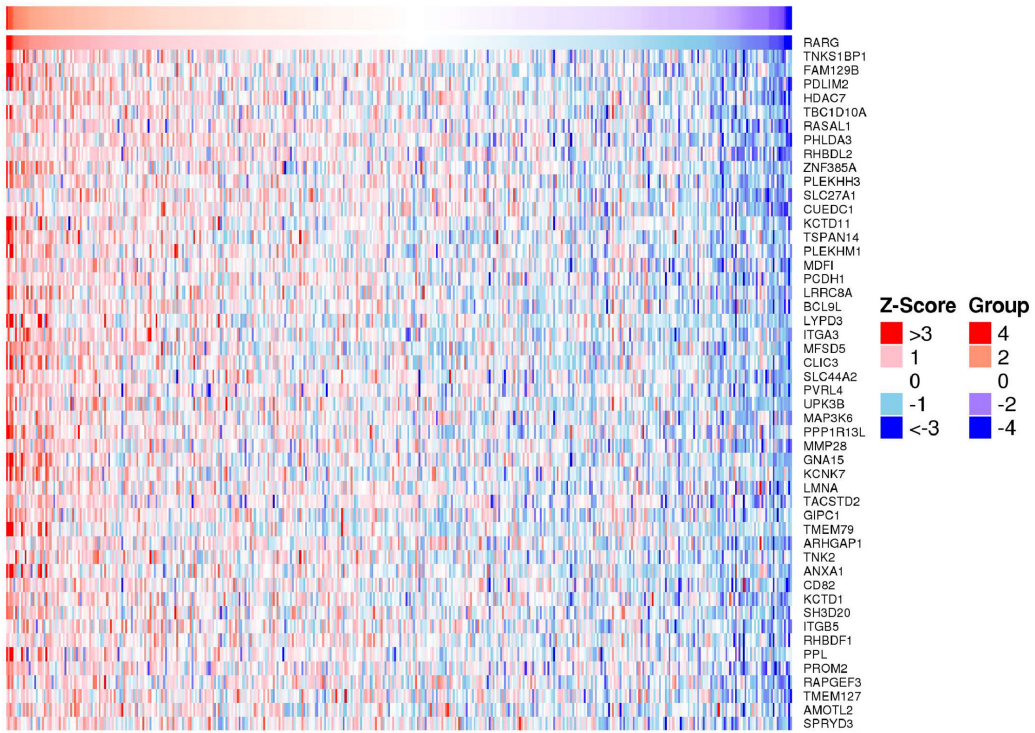**Figure S13** The top 50 positively (A) and negatively (B) related genes of RARA using LinkedOmics. RARA, retinoic acid receptor A.

Figure S14 The top 50 positively (A) and negatively (B) related genes of RARB using LinkedOmics. RARB, retinoic acid receptor B.
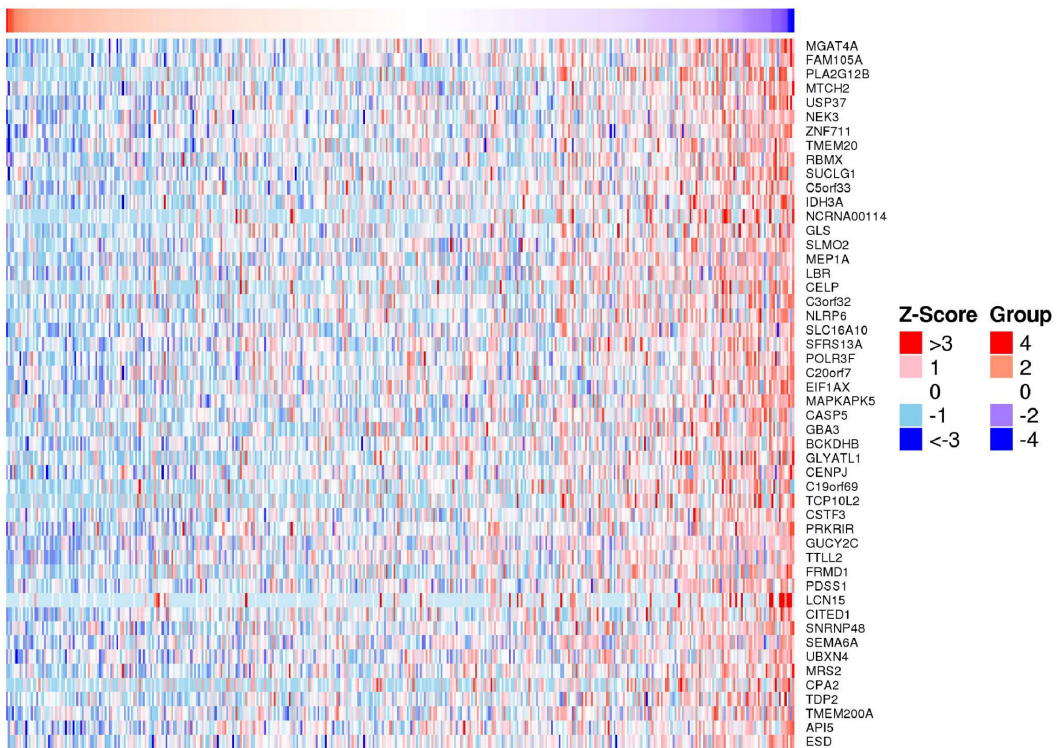
Figure S15 The top 50 positively (A) and negatively (B) related genes of RARG using LinkedOmics. RARG, retinoic acid receptor G.
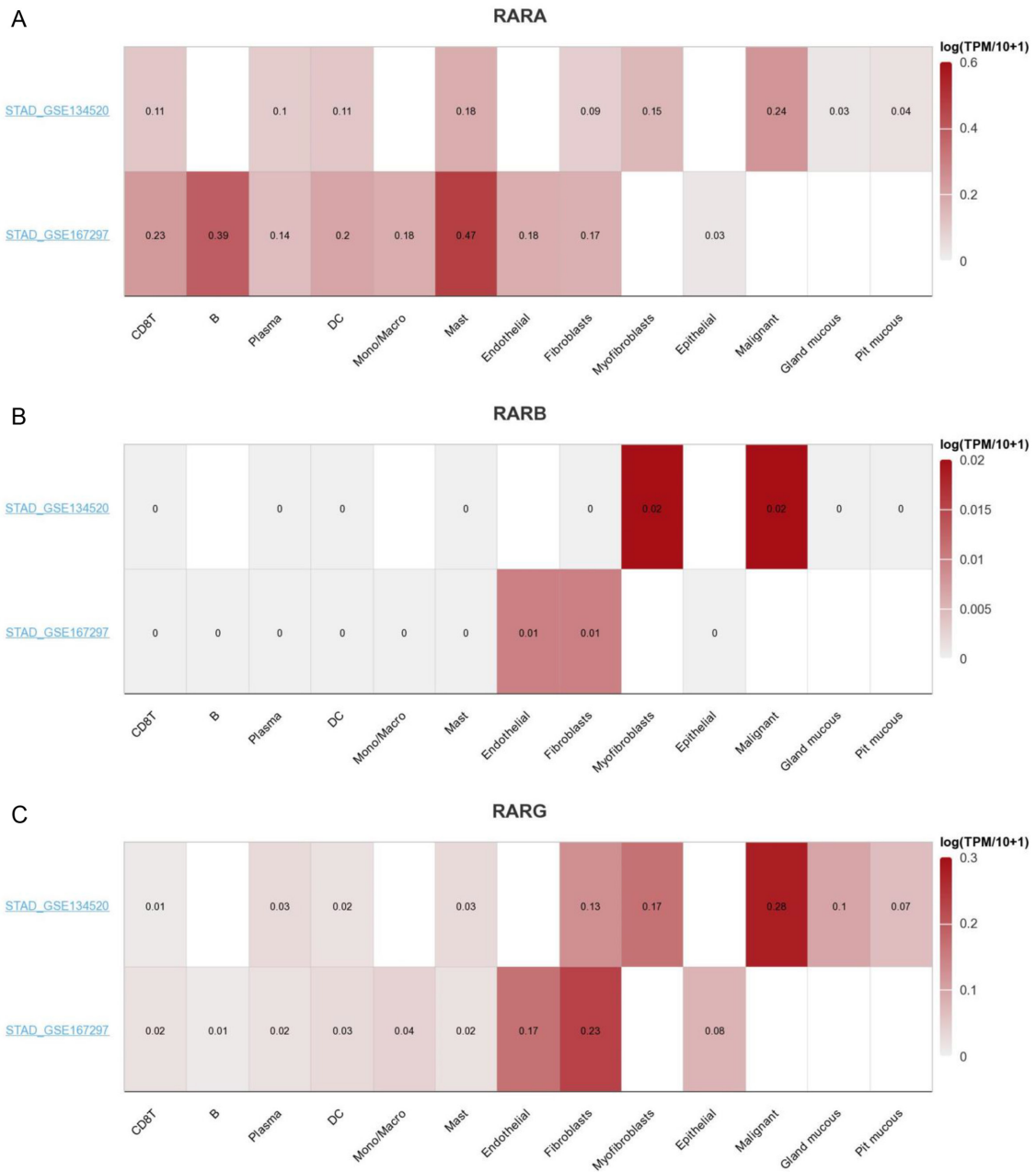
Figure S16 The RARs expression at the single-cell level from TISCH database. RARs, retinoic acid receptors; STAD, stomach adenocarcinoma; TISCH, tumor immune single-cell hub; TPM, transcripts per million.
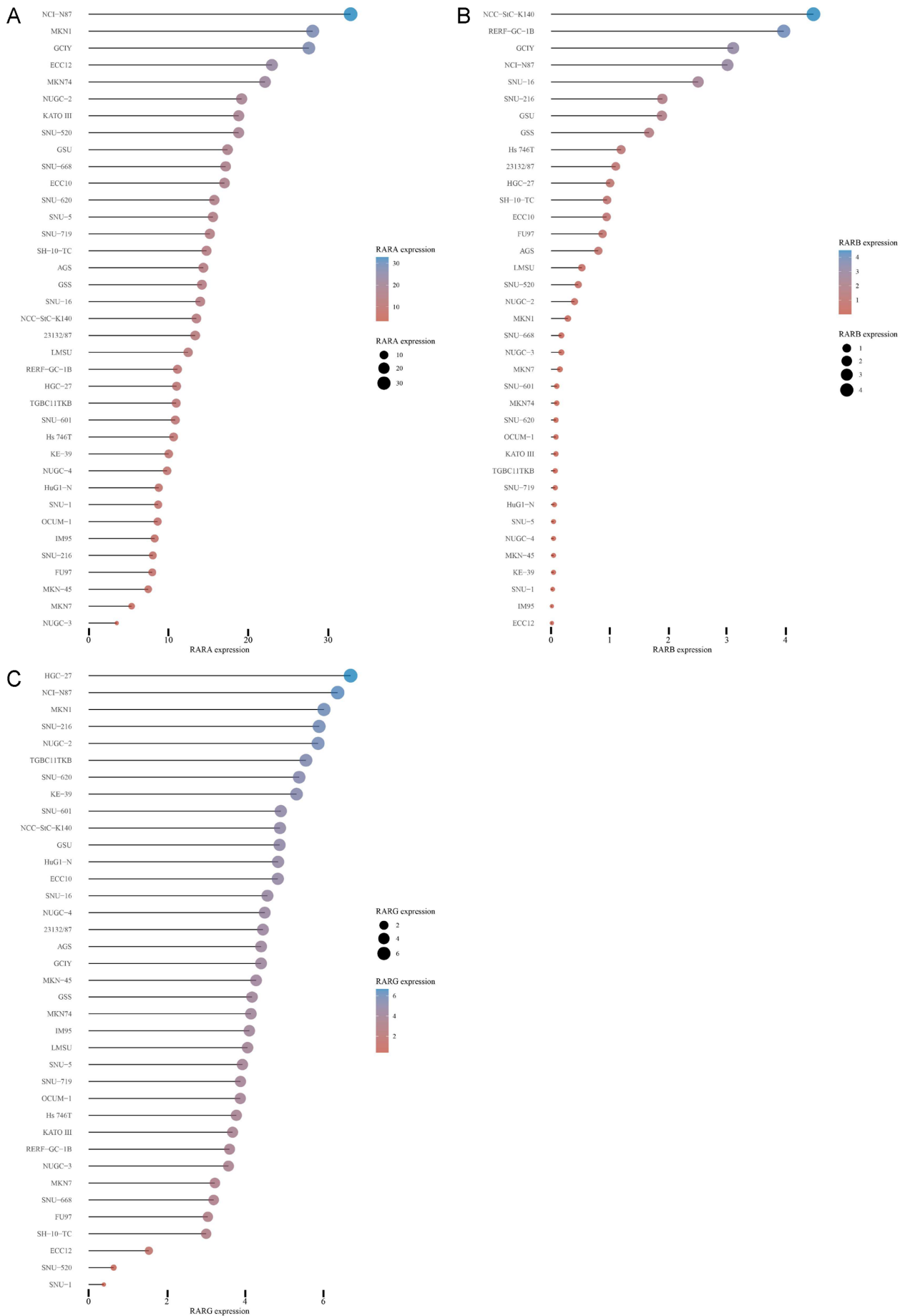
Figure S17 Differential expressions of RARs in STAD cell lines using CCLE dataset. RARA (A), RARB (B) and RARG (C) expressions in different STAD cell lines. CCLE, cancer cell line encyclopedia; RARs, retinoic acid receptors; STAD, stomach adenocarcinoma.