

Supplementary material

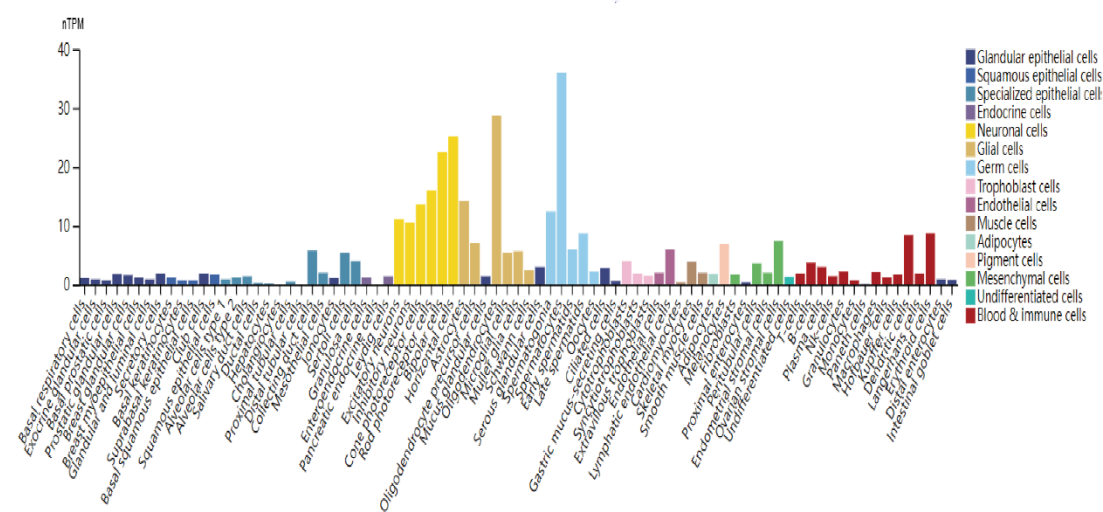
Figures

Figure S1

S1

A

Single cell types



B

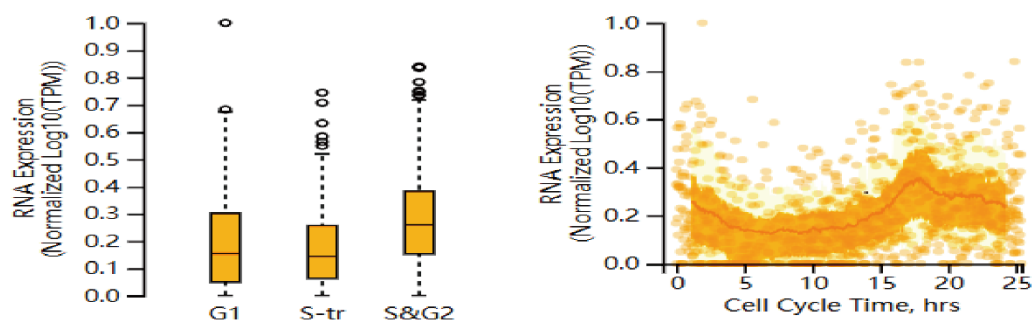
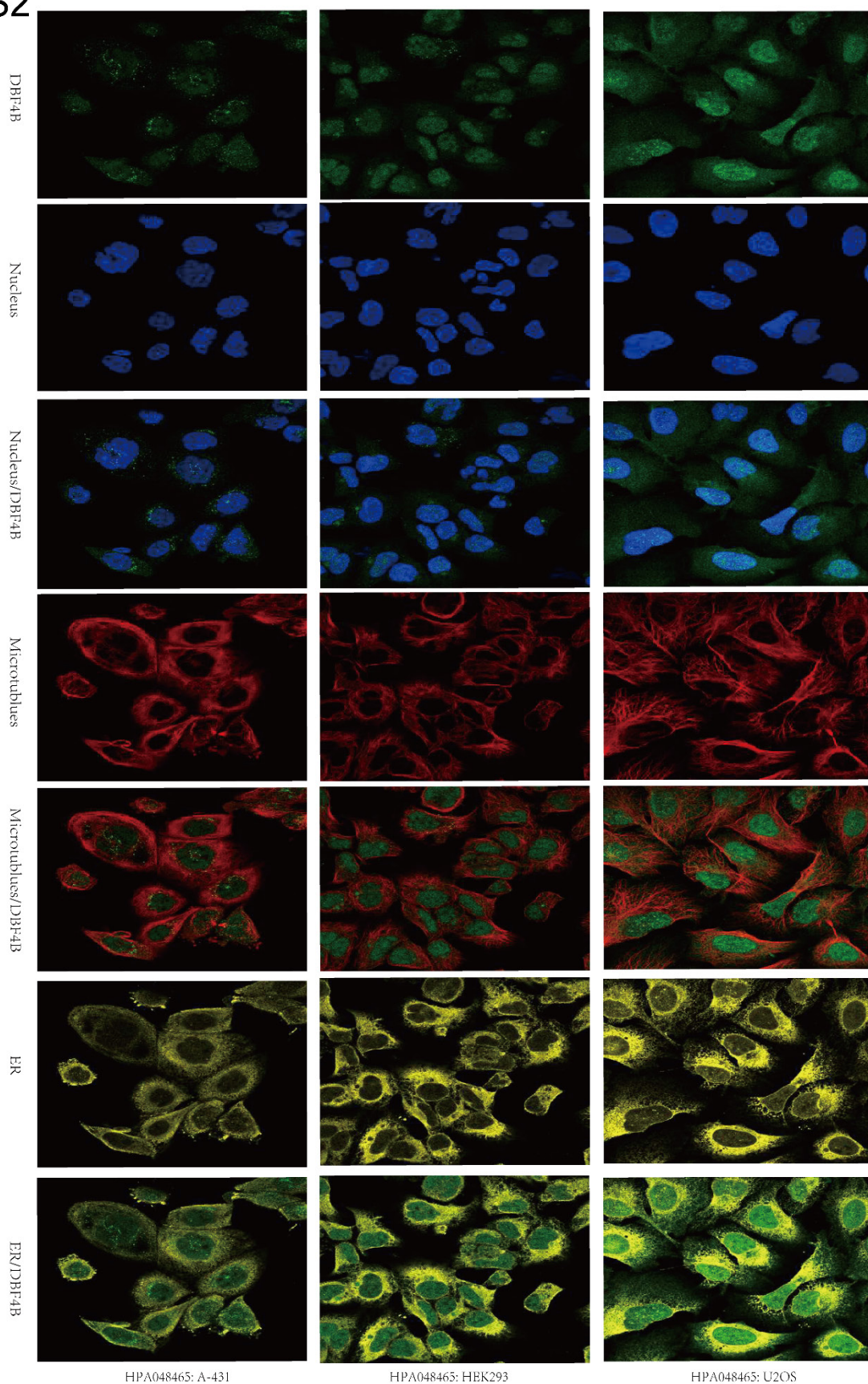


Figure S2

S2



HPA048465: A-431

HPA048465: HEK293

HPA048465: U2OS

Figure S3

S3

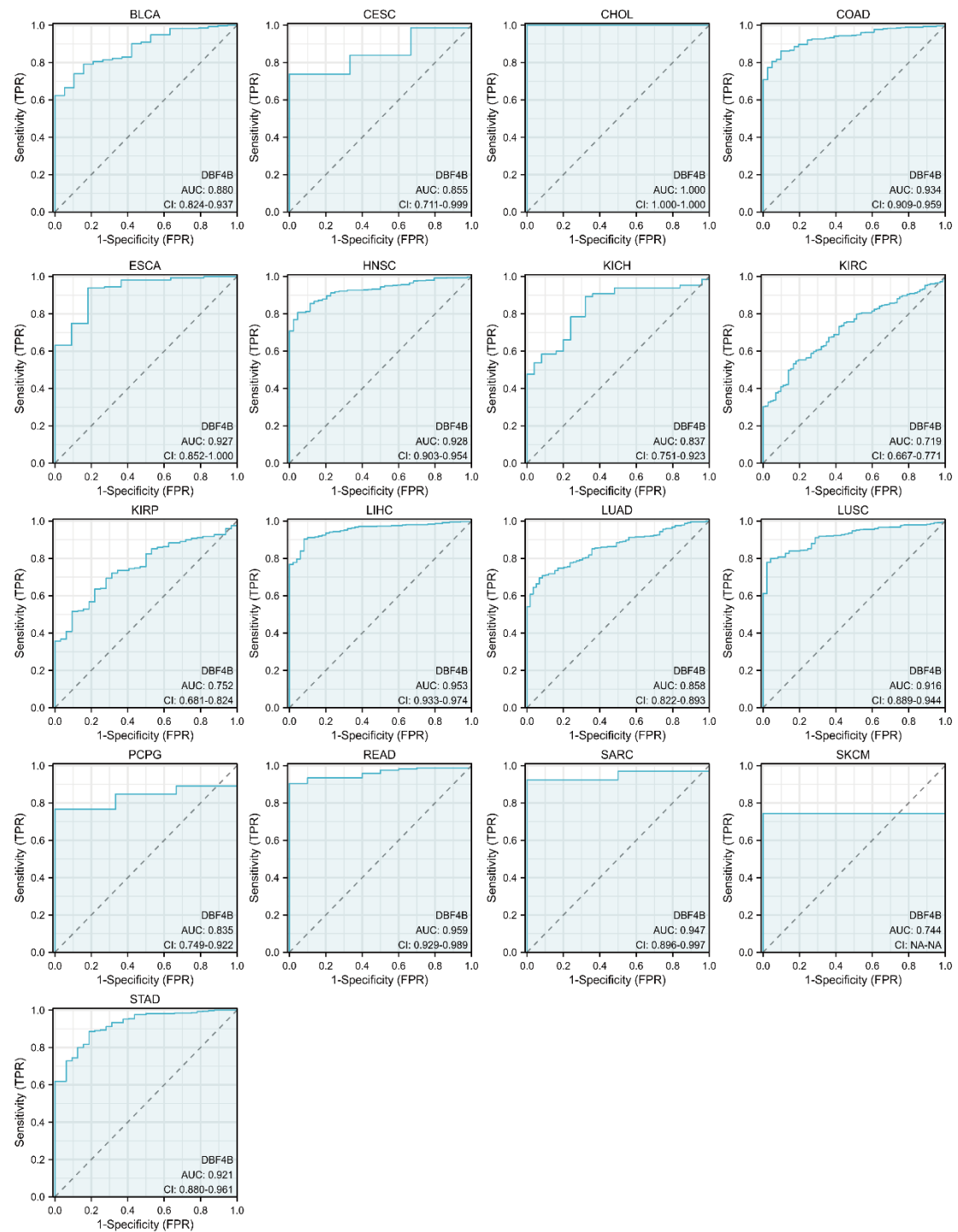


Figure S4

S4

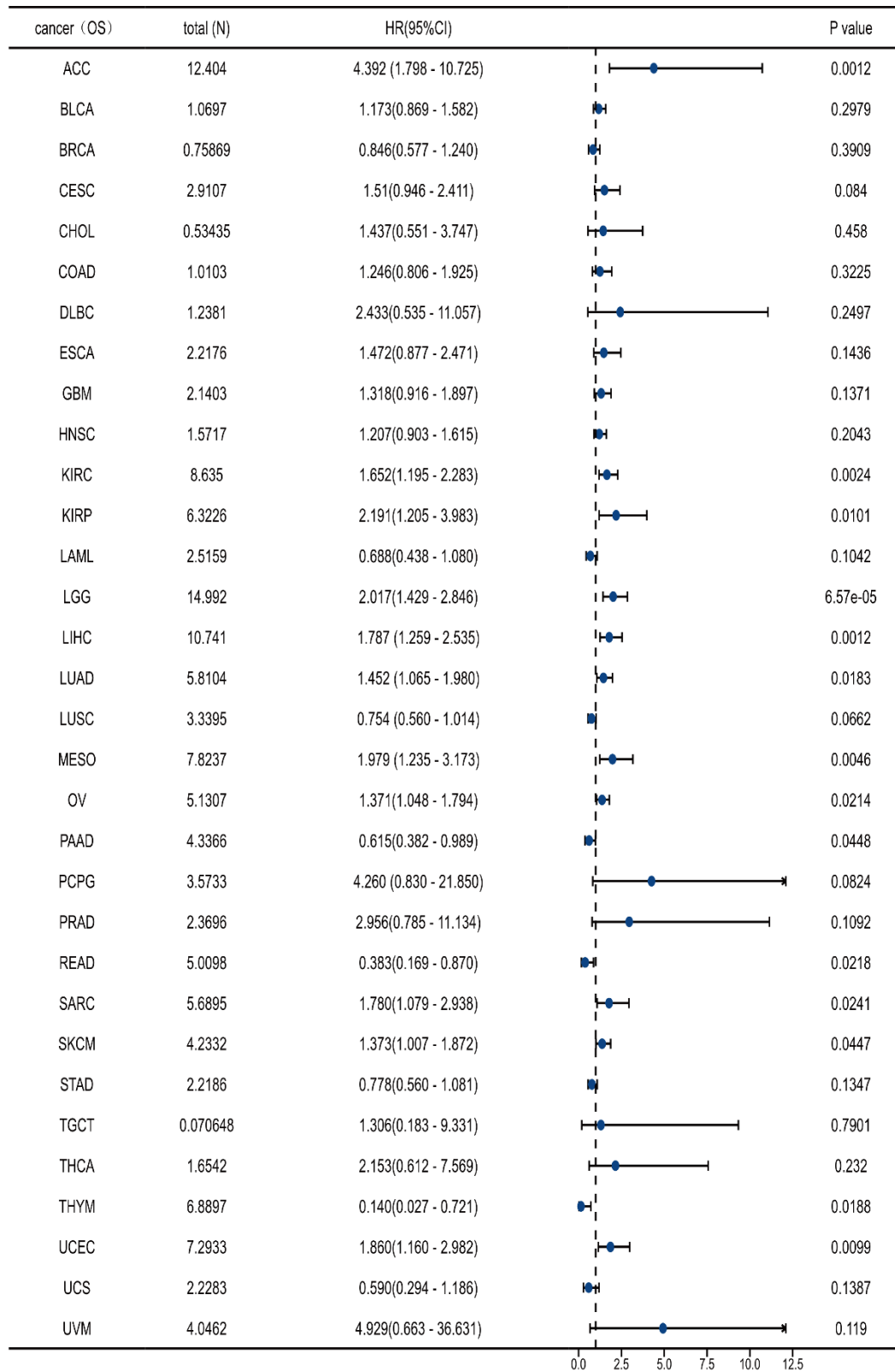


Figure S5
S5

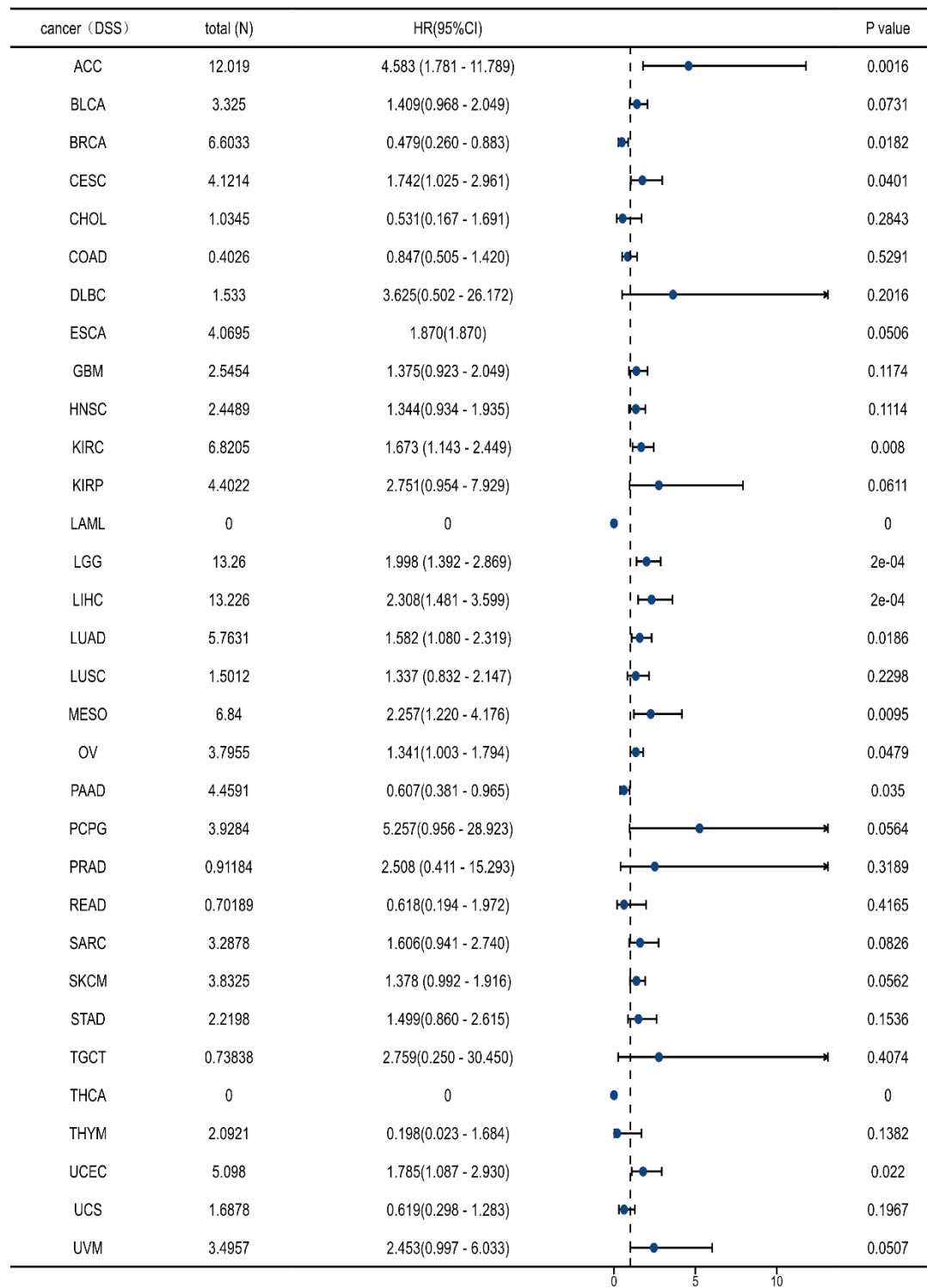


Figure S6
S6

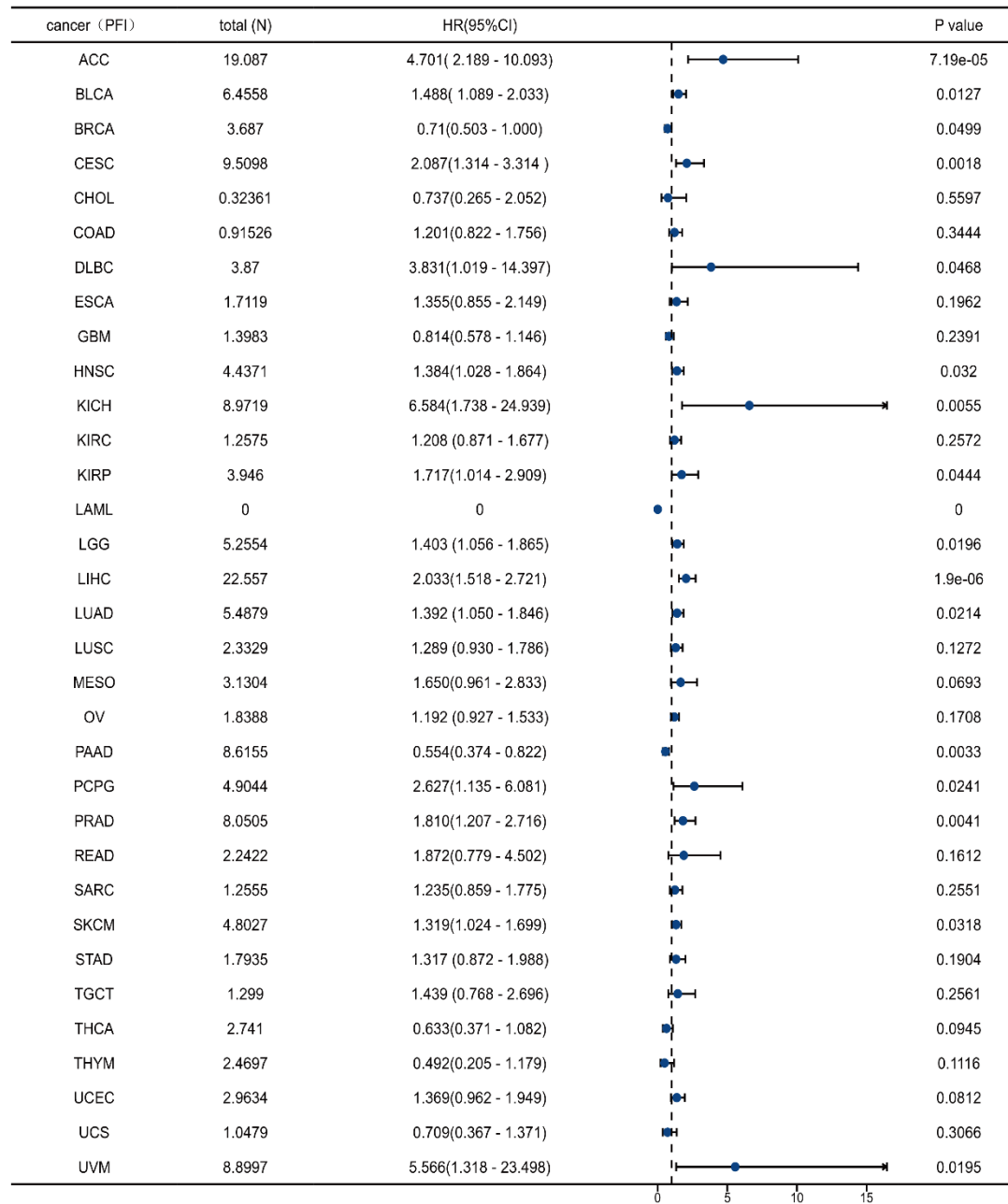


Figure S7

S7

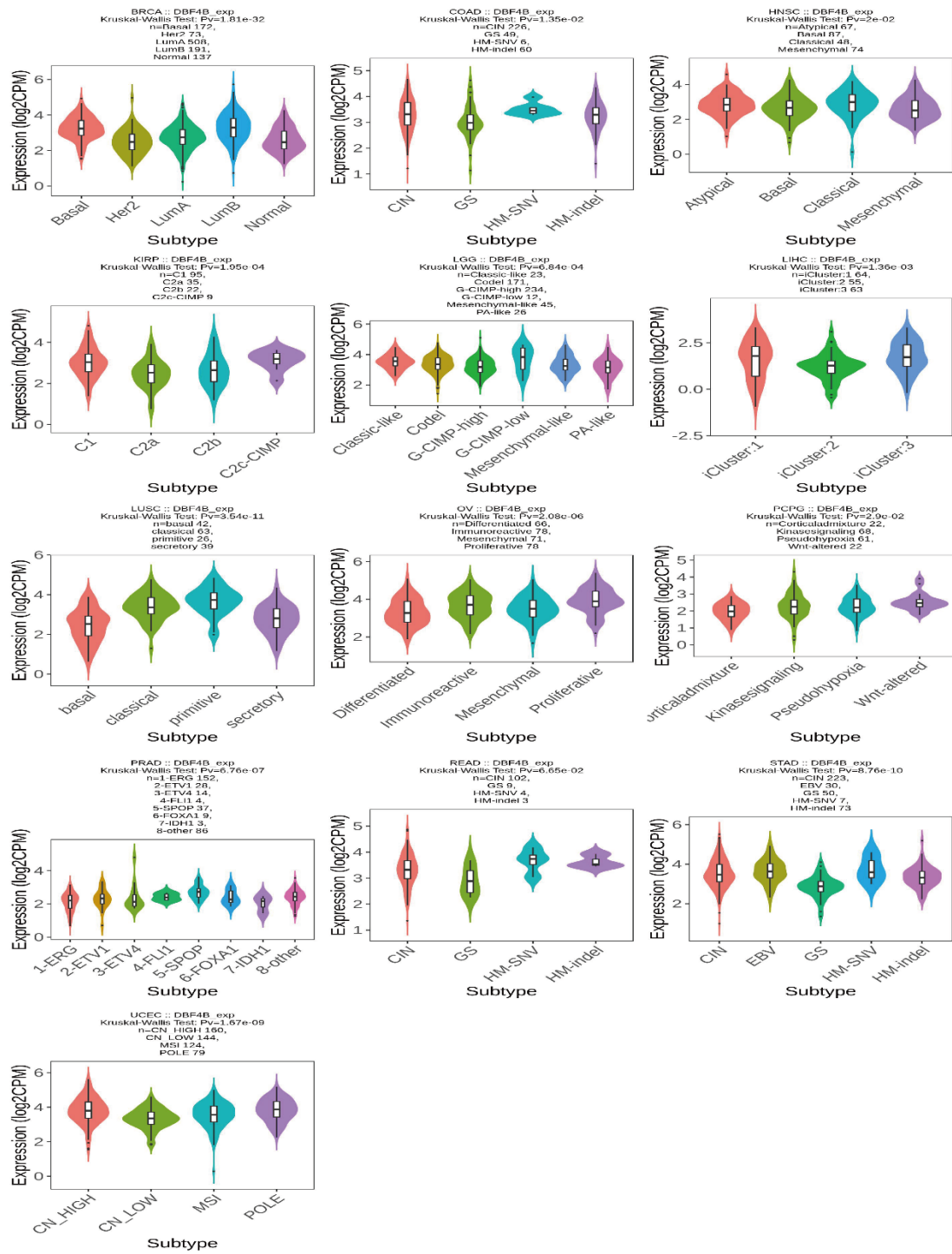


Figure S8
S8

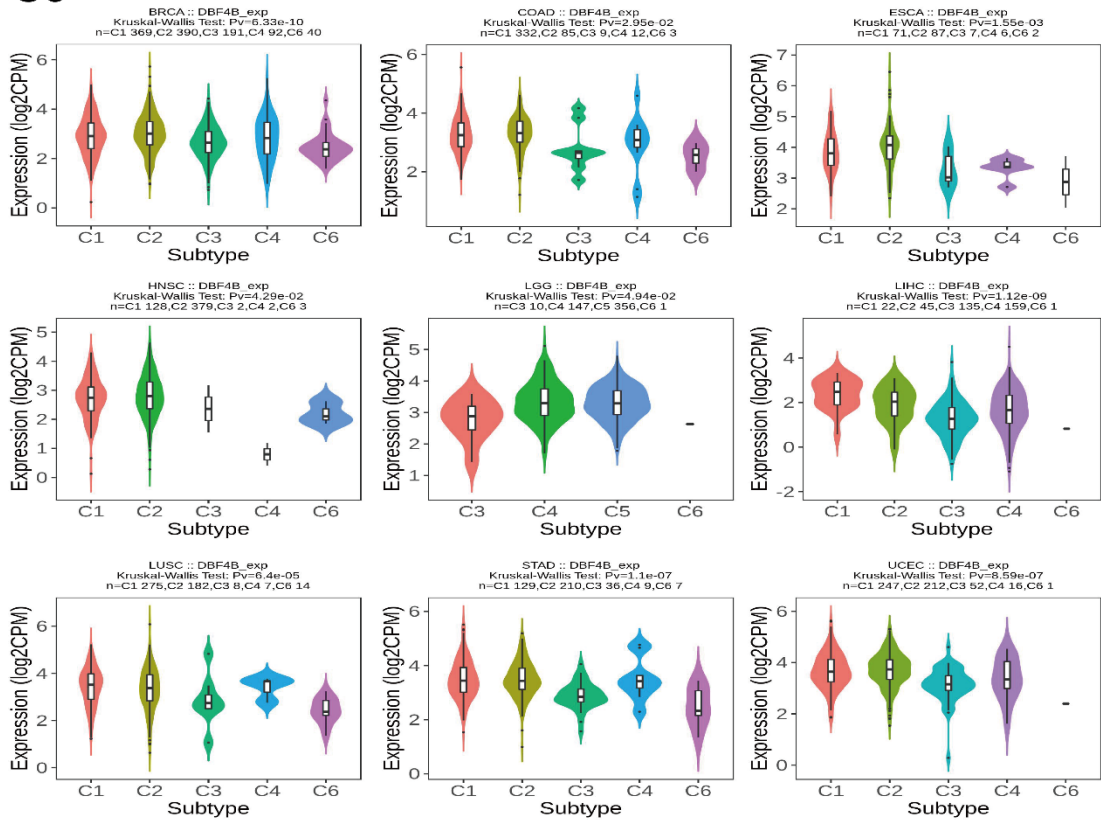


Figure S9

S9

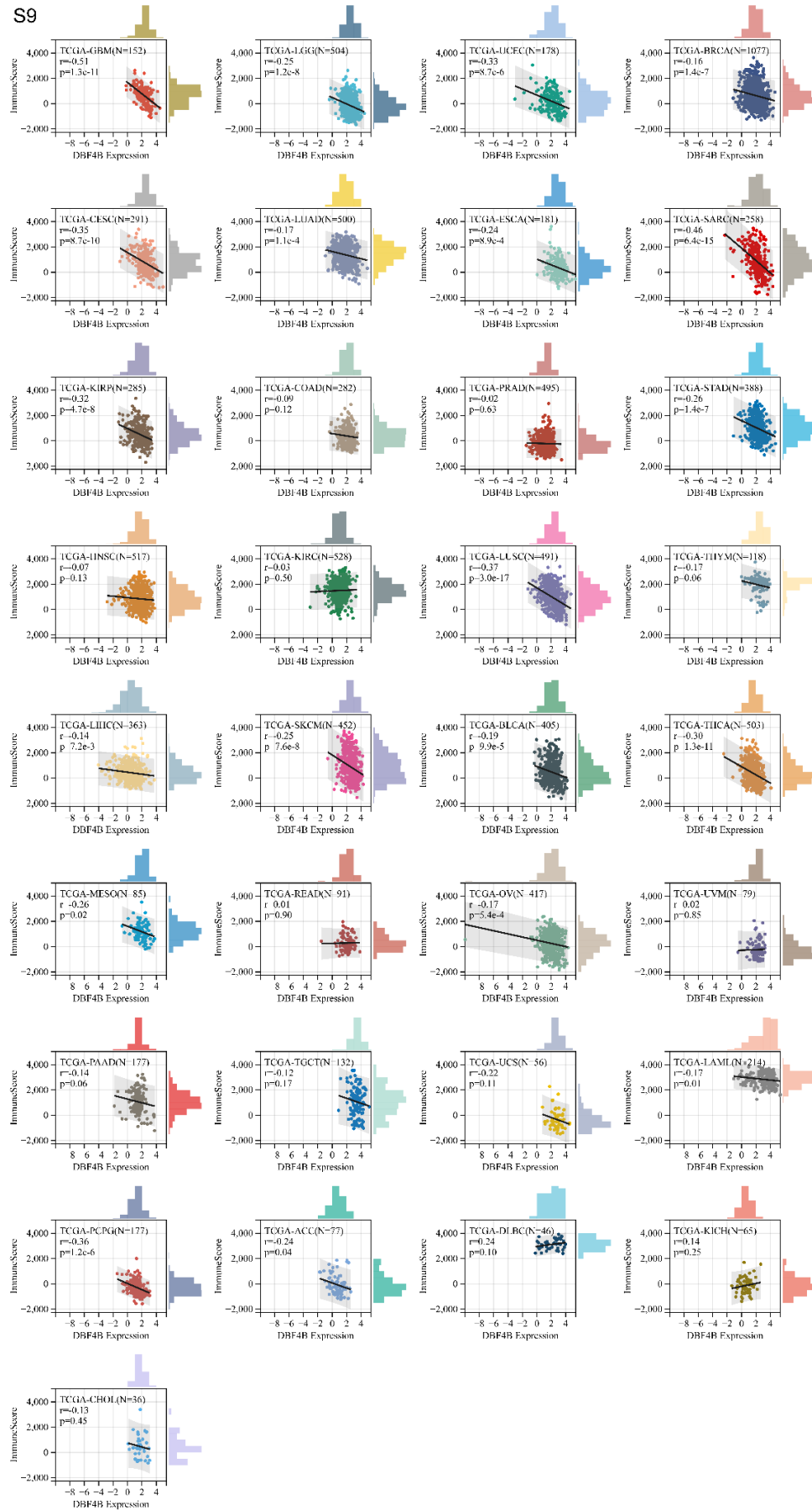


Figure S10

S10

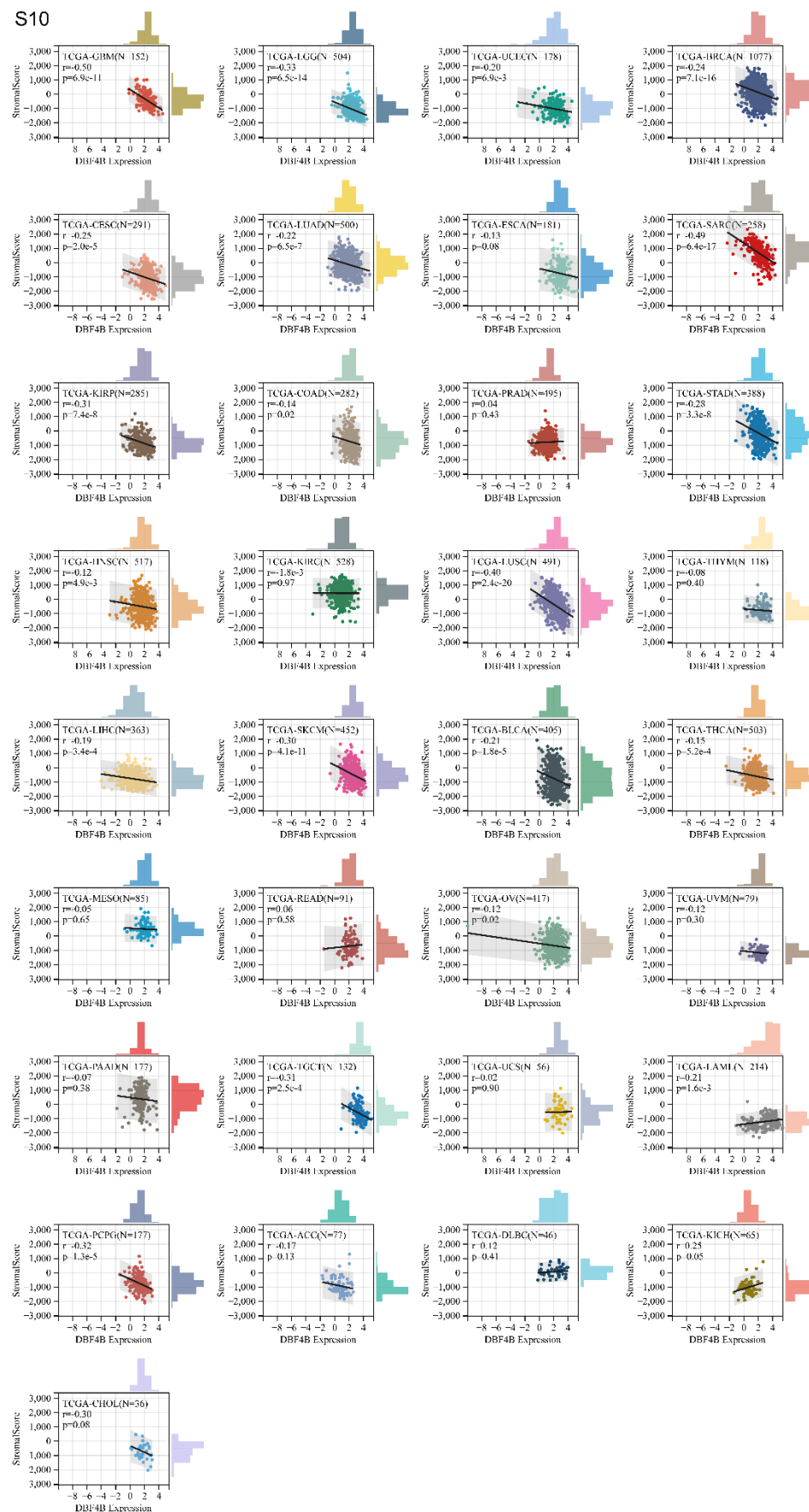


Figure S11

S11

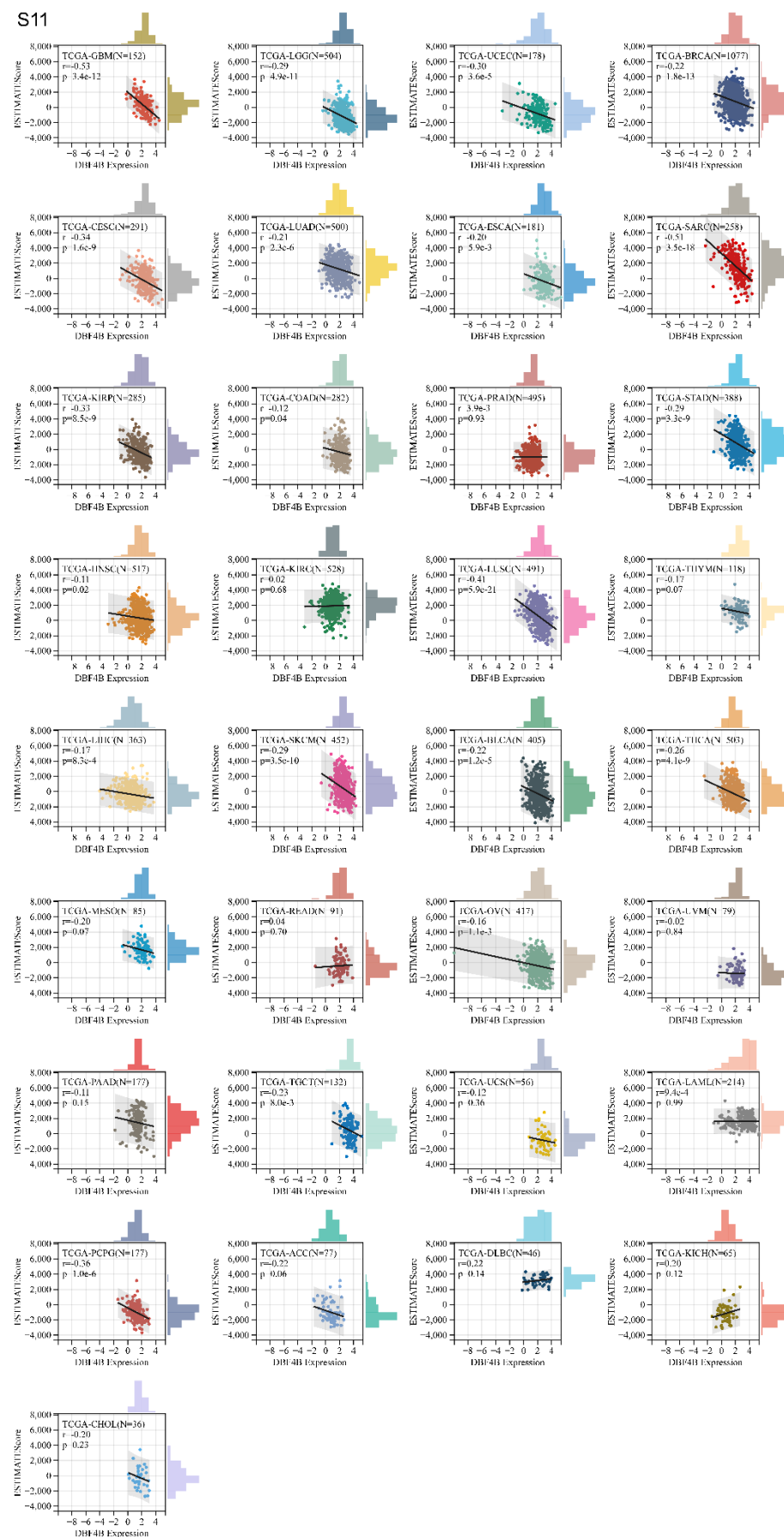


Figure S12

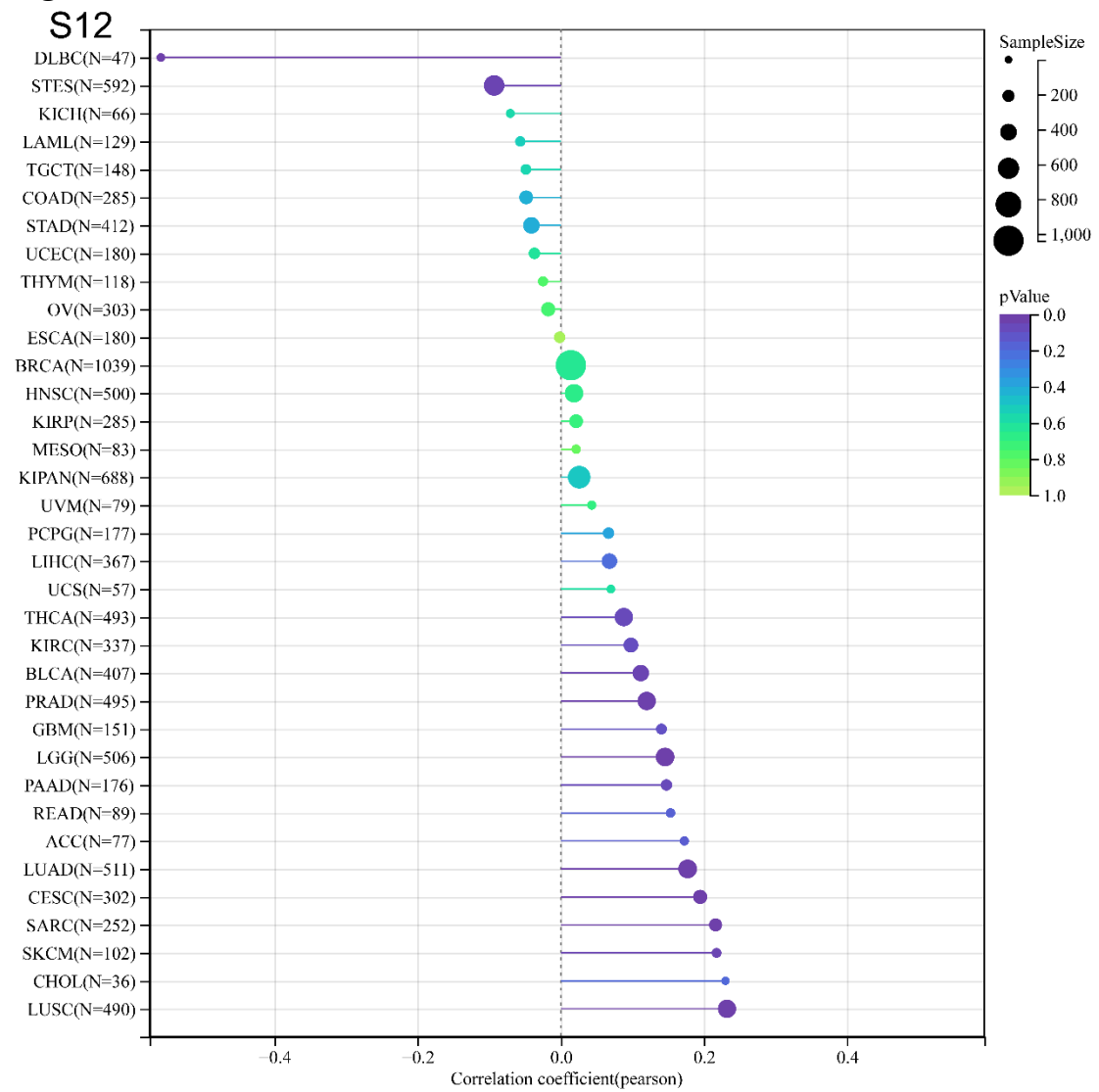


Figure S13
S13

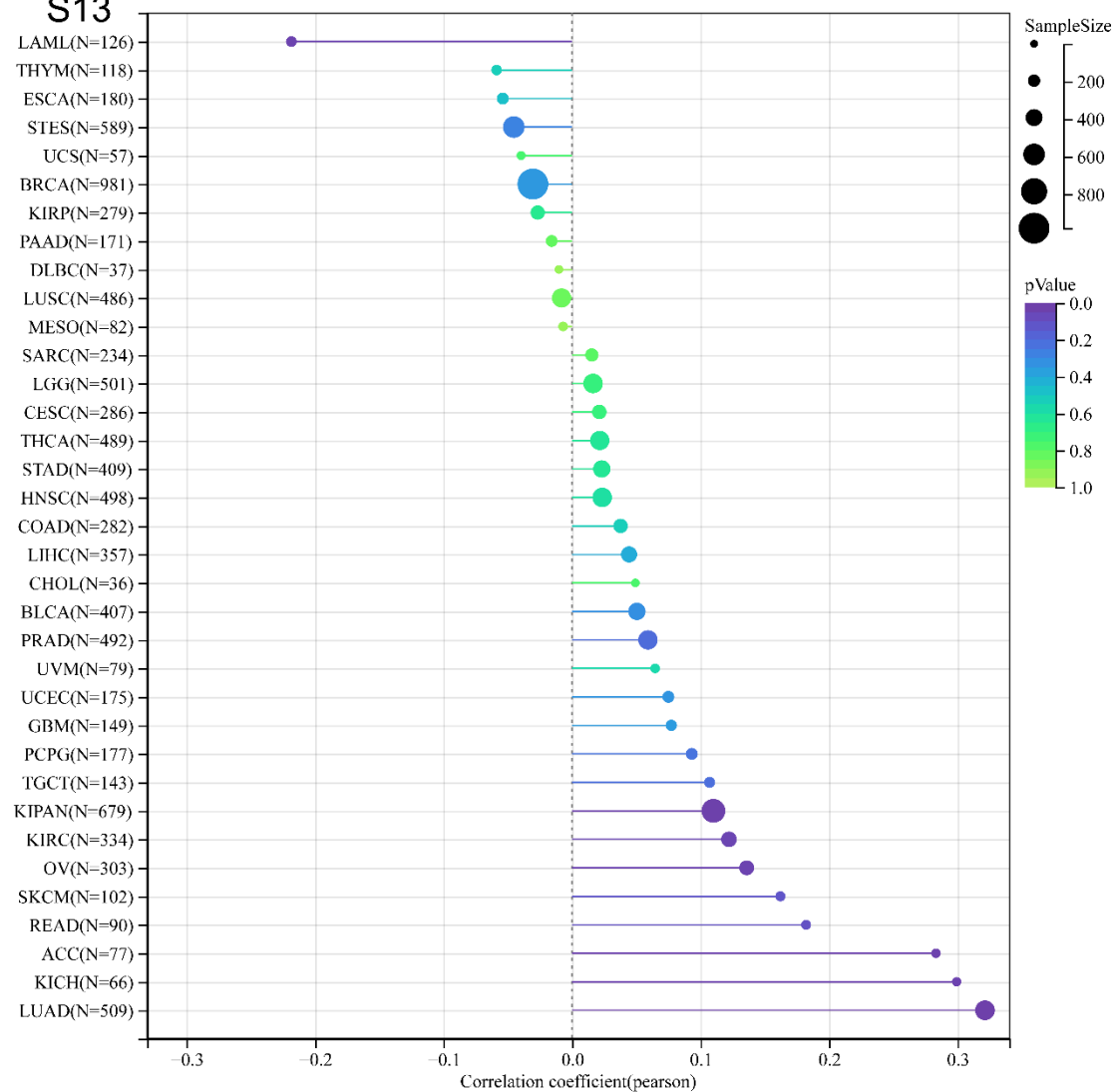


Figure S14

S14

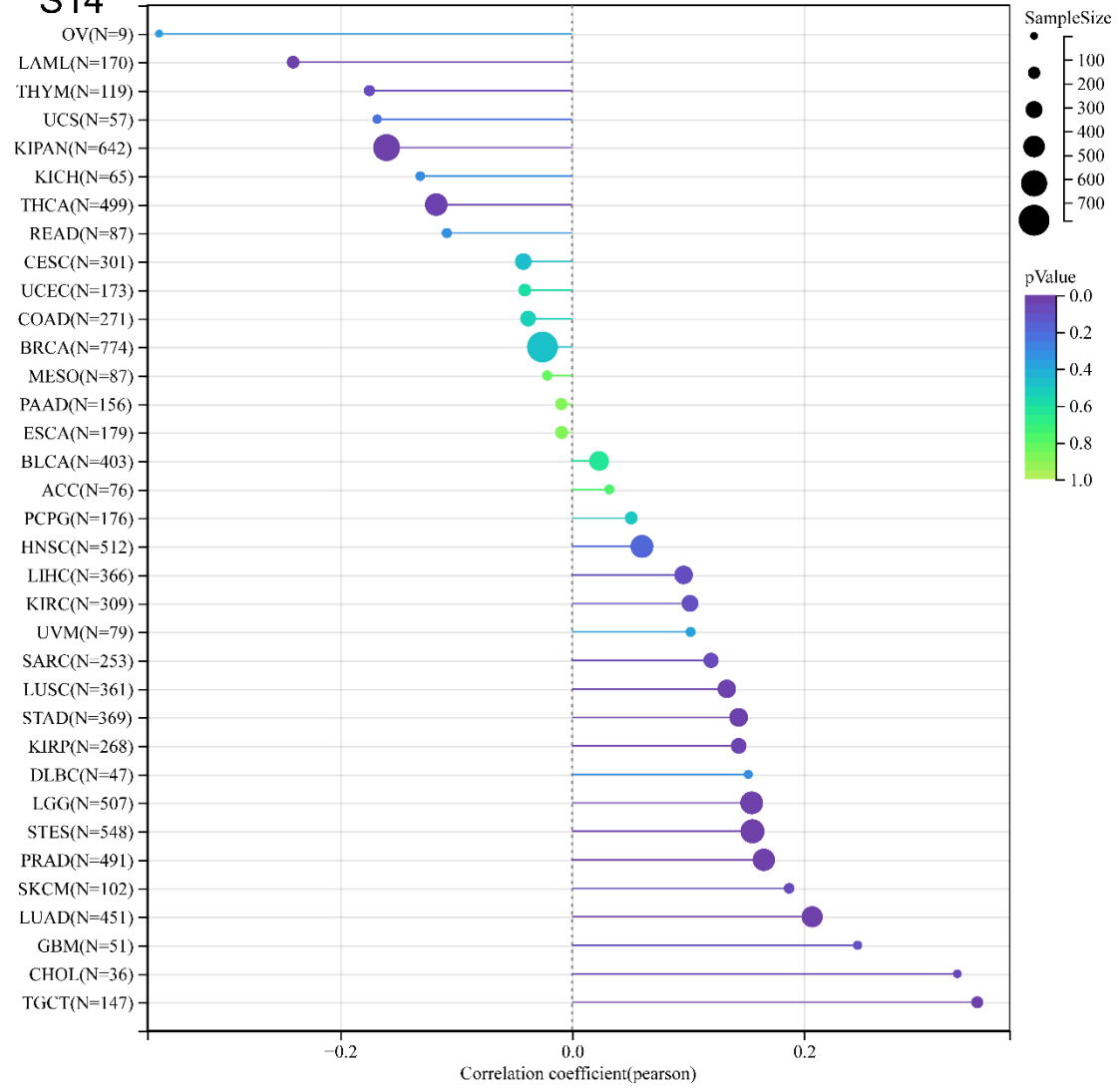


Figure S15

S15

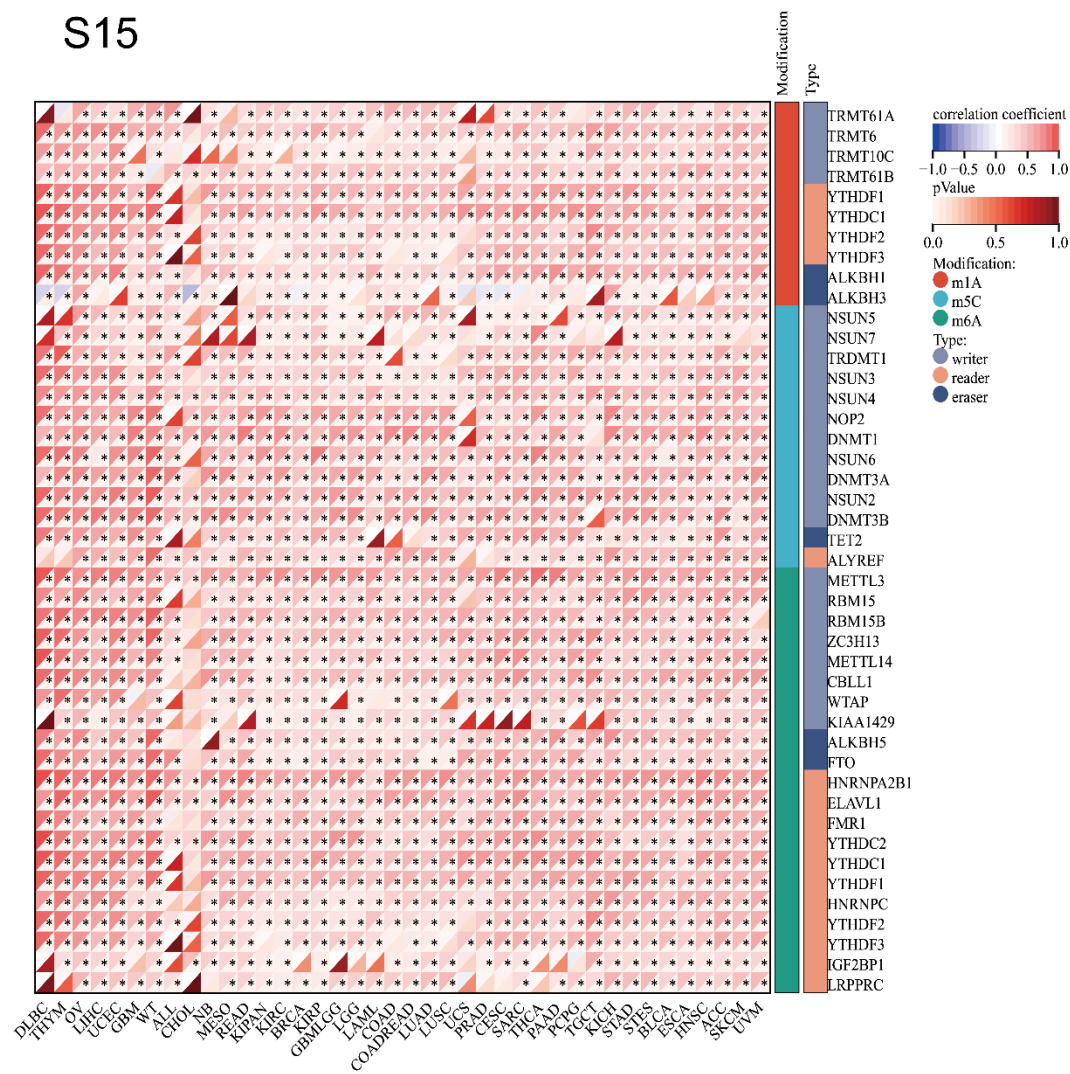


Figure S16

S16

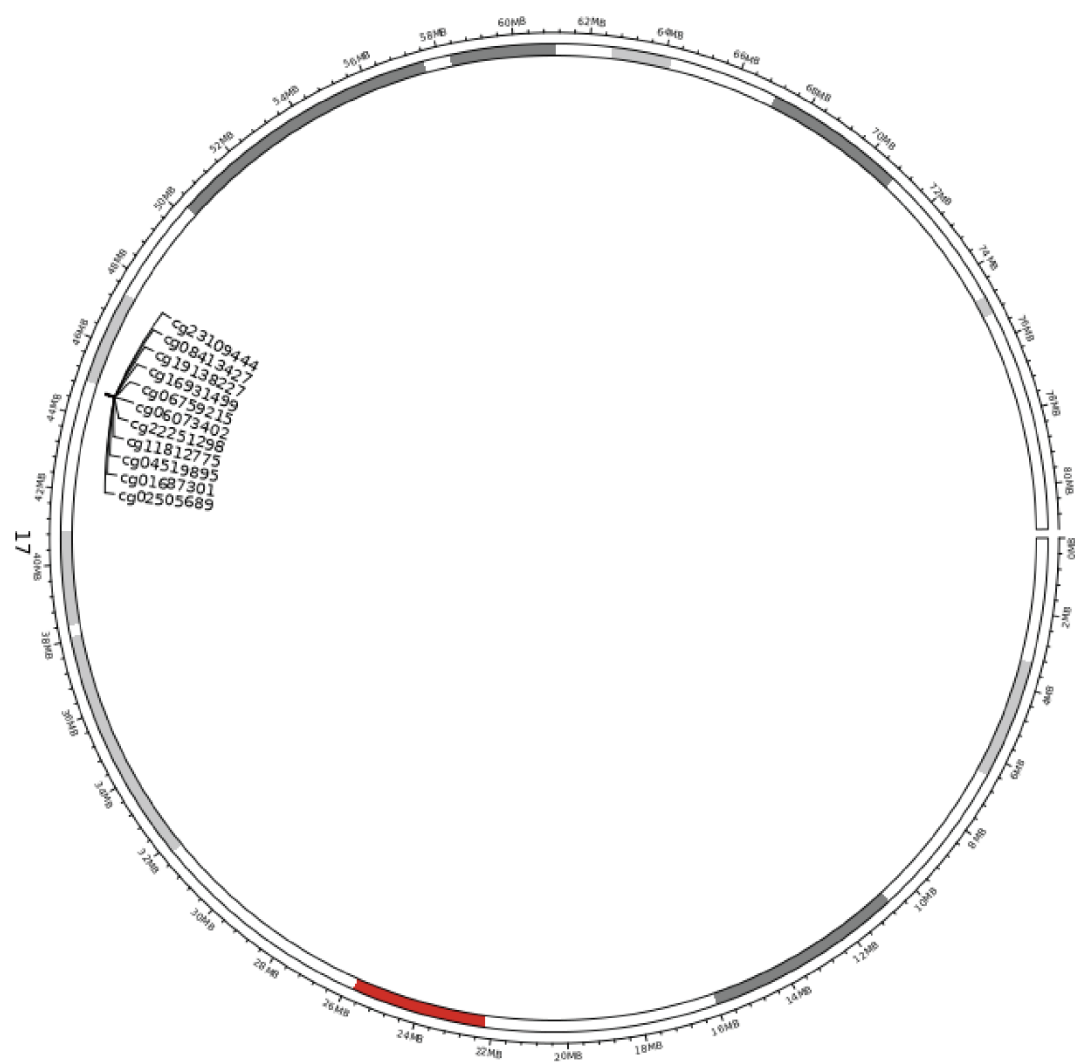


Figure S17

S17

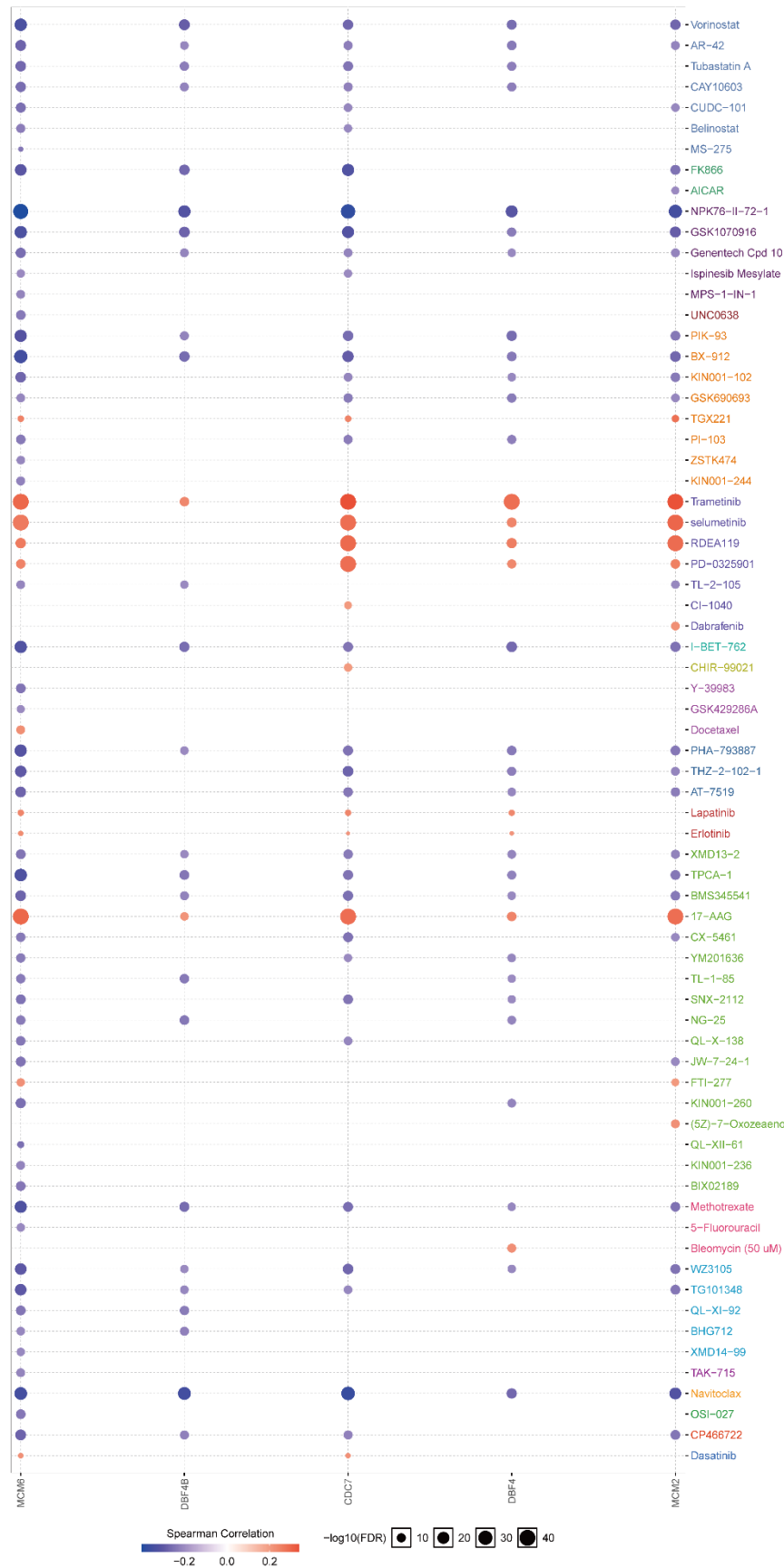


Figure S18

S18

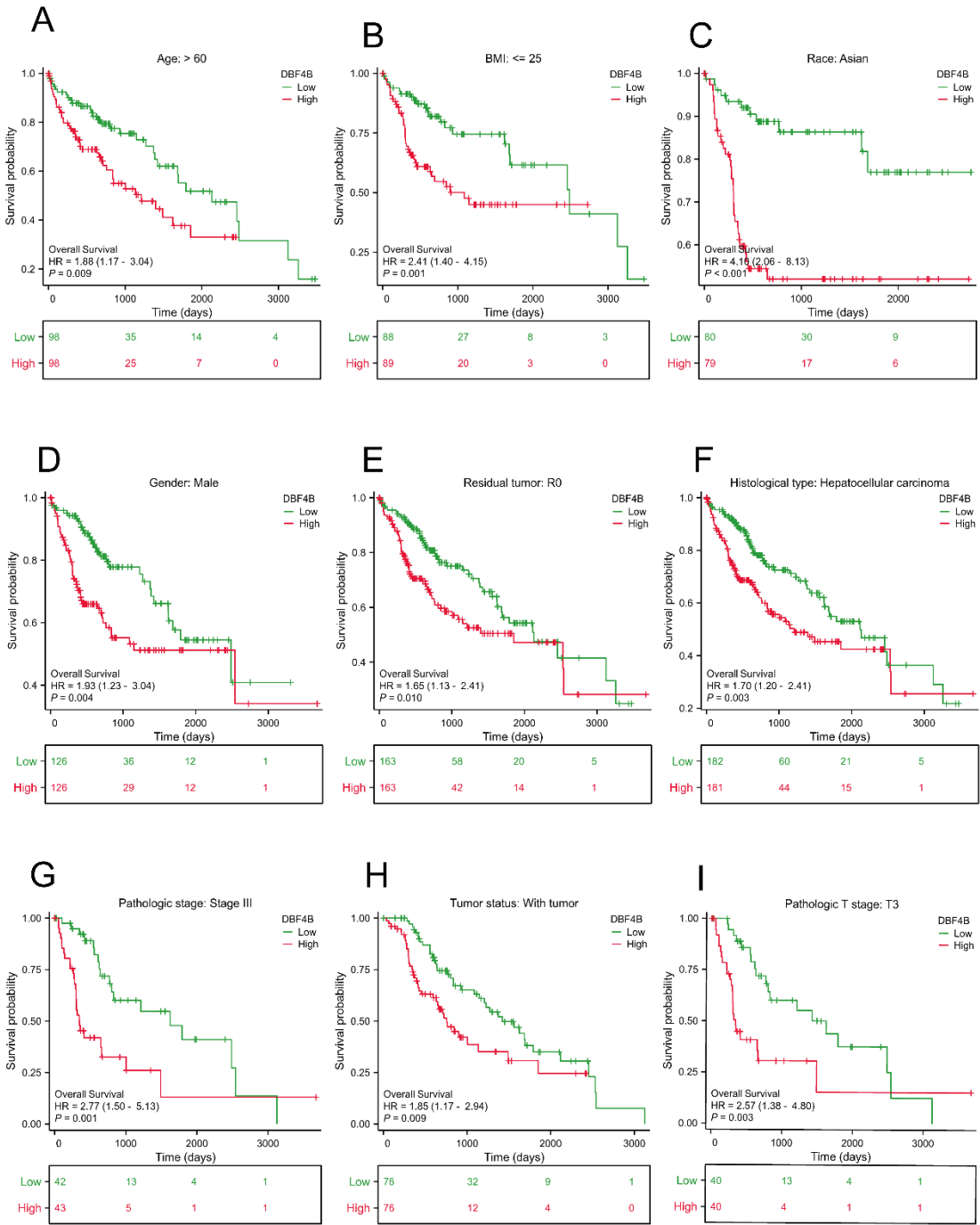


Figure S19

S19

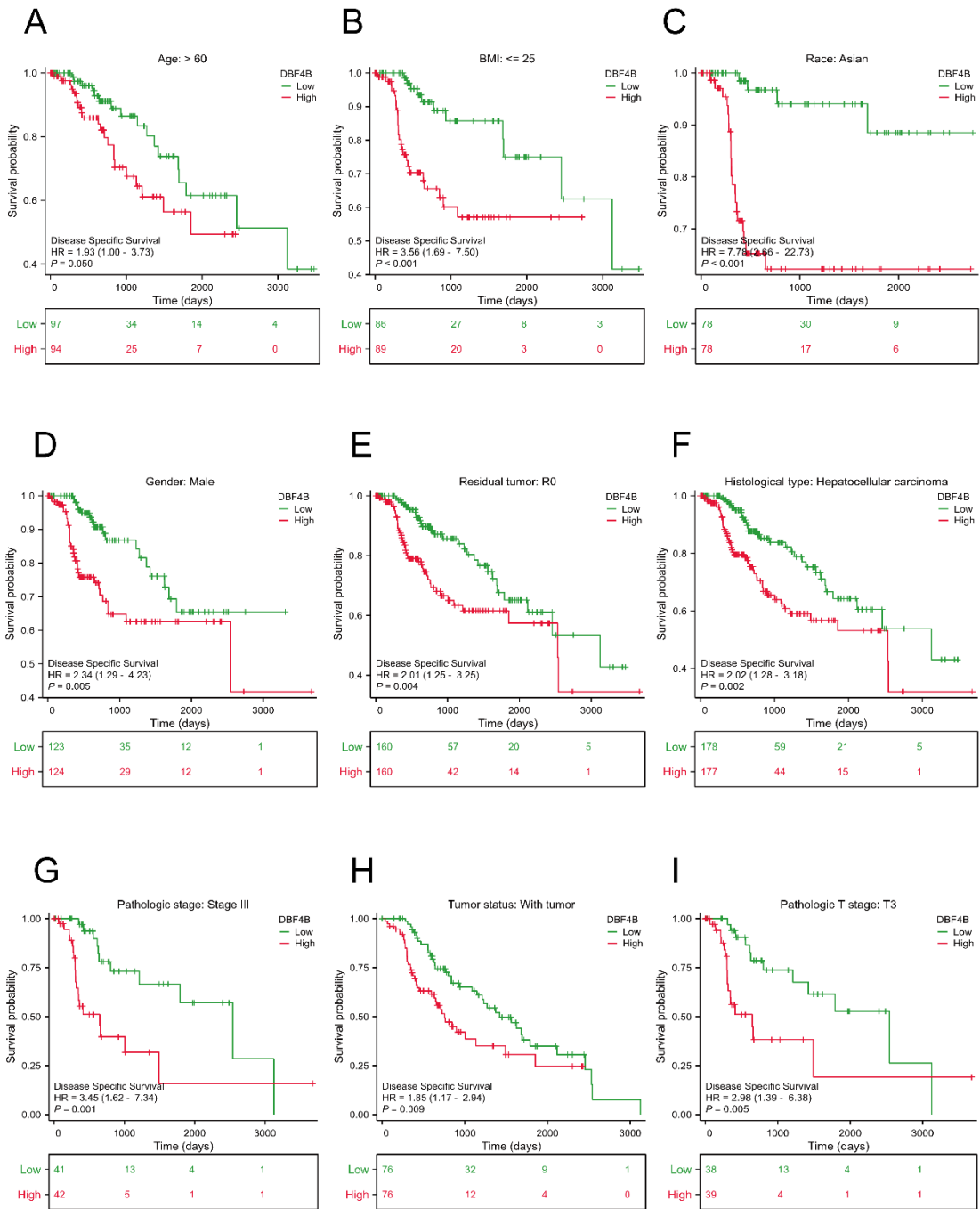


Figure S20

S20

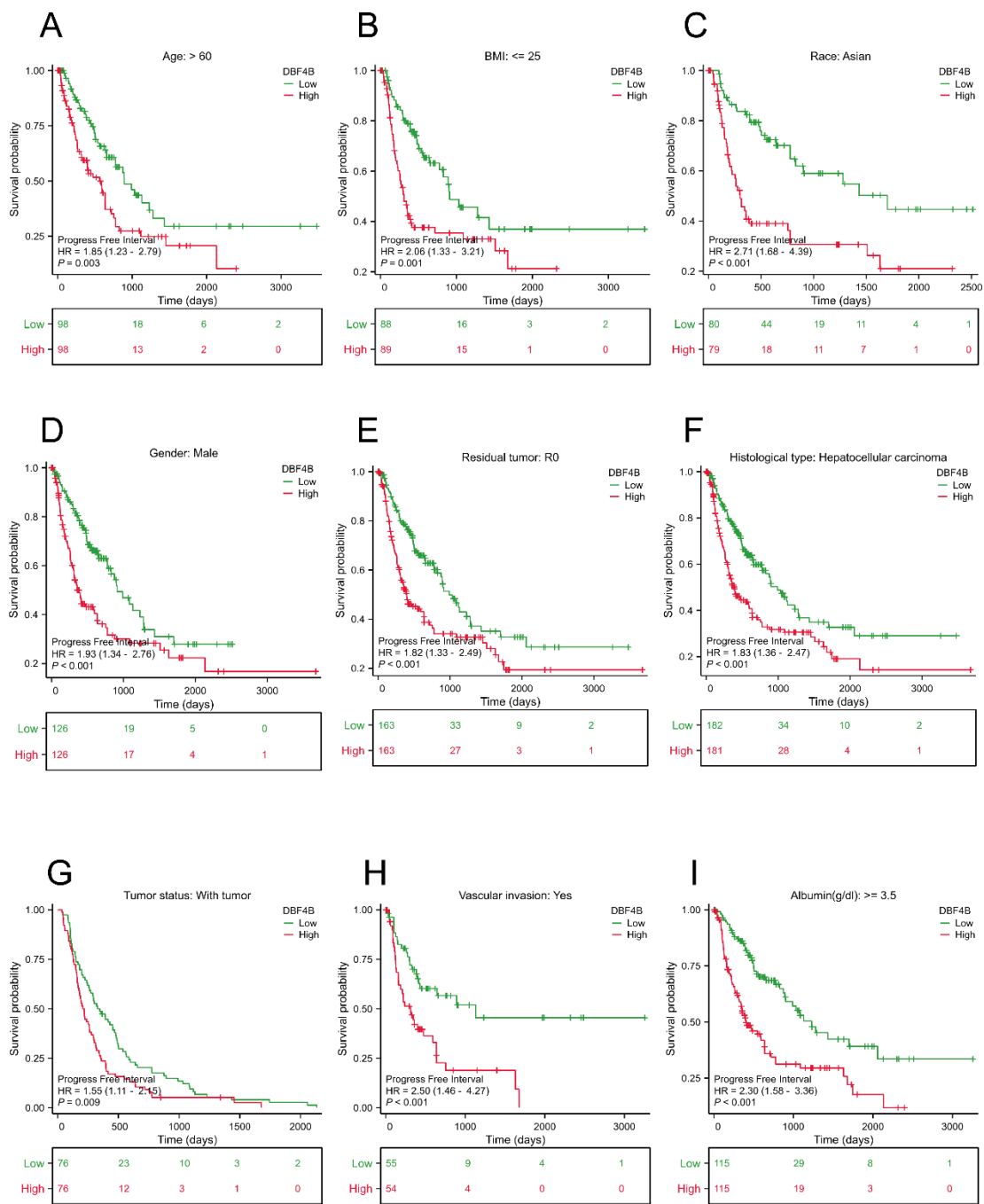


Figure S21
S21

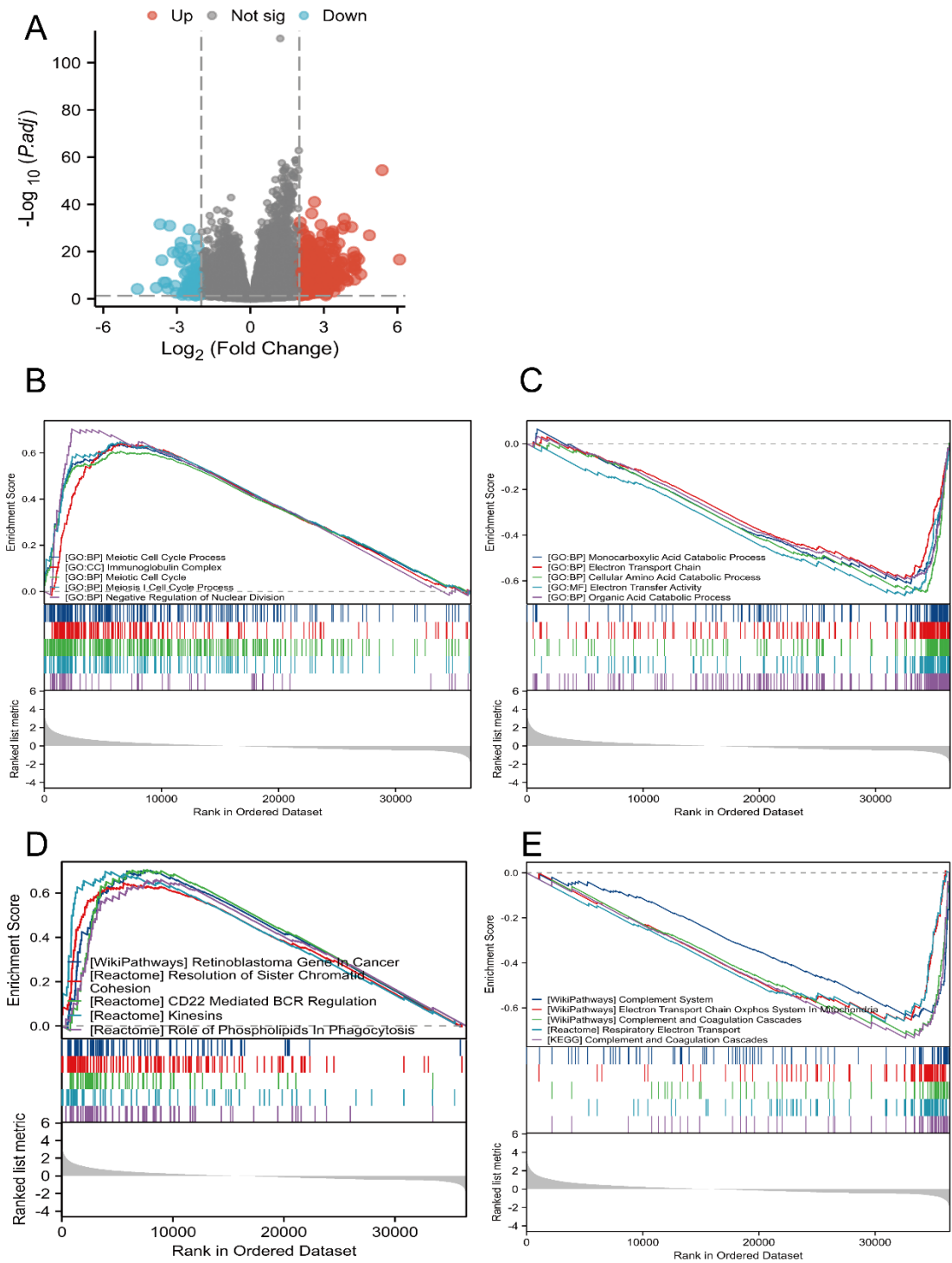


Figure legends

FigureS1.

DBF4B expression from HPA database. (A) DBF4B expression in normal cell lines from the HPA database. (B) Plots of single-cell RNA-sequencing data from the Fucci U-2 cell line showing the correlation between DBF4B RNA expression and cell cycle progression.

FigureS2.

Immunofluorescence staining of the subcellular localization of DBF4B in HPA database.

FigureS3.

Diagnostic value of DBF4B in pan-cancer using AUC of ROC curves response based on TCGA data

FigureS4.

Forest plot of OS associations in pan cancer.

FigureS5.

Forest plot of DSS associations in pan cancer.

FigureS6.

Forest plot of PFI associations in pan cancer.

FigureS7.

Correlations between DBF4B expression and molecular subtypes across TCGA cancers. CIN, chromosomal instability; GS, genomically stable; POLE, Polymerase ϵ ; EBV, Epstein-Barr virus. C1: wound healing, C2: IFN-gamma dominant, C3: inflammatory, C4: lymphocyte depleted, C5: immunologically quiet, and C6: TGF- β dominant.

FigureS8.

Correlations between DBF4B expression and immune subtypes across TCGA cancers. CIN, chromosomal instability; GS, genomically stable; POLE, Polymerase ϵ ; EBV, Epstein-Barr virus. C1: wound healing, C2: IFN-gamma dominant, C3: inflammatory, C4: lymphocyte depleted, C5: immunologically quiet, and C6: TGF- β dominant.

FigureS9.

Scatter plot of correlation between DBF4B expression and immune score.

FigureS10.

Scatterplot of correlation between DBF4B expression and stromal score.

FigureS11.

Scatterplot of correlation between DBF4B expression and estimated score.

FigureS12.

The correlation of DBF4B expression with TMB.

FigureS13.

The correlation of DBF4B expression with MSI.

FigureS14.

The correlation of DBF4B expression with DNAss.

FigureS15.

The correlation between DBF4B expression and m1A, m5C, m6A regulatory genes.

*: $p < 0.05$.

FigureS16.

Chromosomal distribution of the methylation probes associated with DBF4B.

FigureS17.

Association of GSCALite-based expression of DBF4B and related genes with drug sensitivity.

FigureS18.

Associations between DBF4B expression and the OS in different clinical subgroups of LIHC. (A) Age > 60 ; (B) BMI ≤ 25 ; (C) Race: Asian; (D) Gender: male; (E) Residual tumor: R0; (F) Histological type: Hepatocellular carcinoma; (G) Pathological stage: Stage III; (H) Tumor state: With tumor; (I) Pathological T stage: T3.

FigureS19.

Associations between DBF4B expression and the DSS in different clinical subgroups of LIHC. (A) Age > 60 ; (B) BMI ≤ 25 ; (C) Race: Asian; (D) Gender: male; (E) Residual tumor: R0; (F) Histological type: Hepatocellular carcinoma; (G) Pathological stage: Stage III; (H) Tumor state: With tumor; (I) Pathological T stage: T3.

FigureS20.

Associations between DBF4B expression and the PFI in different clinical subgroups of LIHC. (A) Age > 60 ; (B) BMI ≤ 25 ; (C) Race: Asian; (D) Gender: male; (E) Residual tumor: R0; (F) Histological type: Hepatocellular carcinoma; (G) Tumor state: With tumor; (H) Vascular invasion: Yes; (I) Albumin(g/dl): ≥ 3.5 .

FigureS21.

Analysis of differentially expressed genes and functional enrichment of DBF4B in LIHC. (A) Volcano plot of DEGs, with up-regulated genes in red and down-regulated genes in blue. (B) GO annotates five classes of pathways positively associated with high levels of DBF4B expression. (C) GO annotates five classes of pathways negatively associated with high levels of DBF4B expression. (D) KEGG analysis of five pathways positively associated with DBF4B expression. (E) KEGG analysis of five pathways negatively associated with DBF4B expression.

Table S1

The clinical parameters of 30 patients

Pati ents	Gen der	A g e	Cance r type	CN LC	BC LC	Child pugh	AFP (n g/ml)	Vasc ular Tumo r thro mbus	M V I	Smoking history	Alcohol history	H B V	hypert ension	diab etes	Hea rt dis eas e	His tor y of sur ger y	Othe r Dise ases
1	mal e	54	HCC	IA	A	A	68.37	0	M0	1	1	1	0	0	0	0	0
2	fem ale	66	HCC	IB	B	A	59.37	0	M0	0	0	1	0	0	0	0	0
3	mal e	66	HCC	IB	B	A	195.35	1	M0	1	0	1	0	0	0	0	0
4	mal e	72	HCC	IB	B	A	67.89	0	M0	1	1	1	0	0	0	0	0
5	mal e	51	HCC	IA	A	A	197.59	1	M0	1	1	1	0	0	0	1	0
6	fem ale	70	HCC	IA	A	A	65.38	0	M0	0	0	1	0	0	0	0	0
7	mal e	44	HCC	IB	B	A	59.49	0	M1	1	1	1	0	0	0	1	0
8	mal e	48	HCC	IA	A	A	65.36	1	M0	1	1	1	0	0	0	0	0
9	mal e	59	HCC	IA	A	A	59.59	0	M0	1	1	1	0	0	0	1	0
10	mal e	71	HCC	II B	B	A	65.34	0	M0	0	0	1	1	1	0	0	1
11	mal e	39	HCC	IA	A	A	46.56	0	M0	0	0	1	0	0	0	0	0

12	male	43	HCC	IA	A	A	2.63	0	M1	1	1	1	0	0	0	0	0
13	male	57	HCC	IA	A	A	78.36	0	M0	1	1	1	0	0	0	1	0
14	female	72	HCC	II B	B	A	123.36	0	M0	1	1	1	0	0	0	0	0
15	male	35	HCC	IA	A	A	65.39	0	M0	1	0	1	0	0	0	0	0
16	female	48	HCC	II B	B	A	477.32	0	M0	0	0	1	0	0	0	1	0
17	male	34	HCC	IA	A	A	68.36	0	M0	1	1	1	0	0	0	0	0
18	male	47	HCC	IA	A	A	135.36	0	M0	1	1	1	0	0	0	0	0
19	female	72	HCC	IA	A	A	89.57	0	M0	0	0	1	0	0	0	0	0
20	male	53	HCC	IA	A	A	75.5	1	M0	0	0	1	0	0	0	0	0
21	female	44	HCC	IA	A	A	2.89	0	M0	0	0	1	0	0	0	0	0
22	male	45	HCC	II B	B	A	89.45	0	M1	0	1	1	0	0	0	1	0
23	male	60	HCC	IA	A	A	45.68	0	M0	1	1	0	1	0	0	1	0
24	female	59	HCC	IA	A	A	84.54	0	M0	0	0	1	0	0	0	0	0
25	female	67	HCC	II B	B	A	356.45	0	M0	0	0	1	0	0	0	0	0
36	male	44	HCC	IA	A	A	56.54	0	M0	1	1	1	0	0	0	0	0
37	female	69	HCC	IA	A	A	86.65	0	M1	0	0	1	0	0	0	0	0
38	female	41	HCC	IA	A	A	68.98	0	M0	0	0	1	0	0	0	0	0
39	male	56	HCC	II B	B	A	59.67	0	M0	1	1	1	0	0	0	0	0
30	male	67	HCC	IA	A	A	167.65	0	M0	1	1	1	0	0	0	0	0