

Supplementary Tables

Supplementary Table S1 Correlation of DKC1 DNA methylation and gene expression at 21 probes in BRCA

Probe ID	P value	Pearson R value	Promoter Probe
cg15043492	3.2475218200787297e-25	-0.38032257002252956	Yes
cg09055253	1.5539293414418218e-18	-0.3076182233734055	Yes
cg08087512	5.2253128041108885e-21	-0.33439563421910434	Yes
cg13033283	1.8395880942206102e-13	-0.2515996493507603	Yes
cg09411587	4.966767212812491e-20	-0.32380846152598536	Yes
cg19944582	5.8049098687975635e-9	-0.19694009256288553	Yes
cg23712855	3.032183002628016e-16	-0.282660879951007	Yes
cg14350469	5.035003632298603e-10	-0.2106377210115036	Yes
cg17274024	1.6555873533542094e-19	-0.31832447985882345	No
cg01257202	8.828922831869033e-16	-0.2775544404880365	No
cg09049751	1.1185470063292233e-7	0.17931981833450036	No
cg16531342	0.000006026522490192134	0.15295357929783726	No
cg27505756	0.01817943365920727	0.08011009103555952	No
cg03028851	0.0021058743084094098	0.10417416549293944	No
cg13617521	4.322304603603714e-9	0.1986289185160424	No
cg19023236	0.0009464613415447451	0.11195742847484769	No
cg27221747	0.009546019690349005	0.0878789618207002	No
cg14825312	0.0027286255687338844	0.10154135738006013	No
cg22208280	1.5760531235367998e-16	0.28577703489555994	No
cg01112702	0.011615777814286715	0.08557364494095888	No
cg22419482	0.00041138077602523	0.11958512605233133	No

Supplementary Table S2 Analysis of CPTAC-identified phosphorylation sites of DKC via the PhosphoNET database.

Site	Sequence	PMID	Hydropobicity	P-site Similarity Score	Maximum Kinase Specificity	Sum Kinase Specificity Score	Conservation Score
S21	KKKKERKS LPEEDVA	16565220	-2.093	-53.6	549	18,583	23.0
Y419	WKQEYVDY SESAKKE	NA	-1.993	-57.5	509	23,348	36.4
S451	TAKRKRESE SESEDET	16083285	-2.580	-52.2	384	16,711	11.2
S453	KRKRESESE SDETPP	16083285	-2.867	-52.0	297	12,860	12.7
S455	KRESESESD ETPPAA	16083285	-2.067	-52.2	347	14,170	14.2
T458	SESESEDETPP AAPQL	19366988	-1.360	-52.4	291	11,276	12.4
S473	IKKEKSKK KDKKAK	NA	-2.753	-57.8	389	14,554	9.1
S485	KAKAGLES GAEPGDG	18669648	-0.927	-54.4	301	11,220	18.8
S494	AEPGDGDS DTTKKKK	15302935	-2.213	-56.0	374	13,370	26.4
T496	PGDGSDST TKKKKKK	18669648	-2.620	-55.2	229	9,005	26.4
S513	AKEVELVSE	15302935	-0.222	-71.4	302	12,386	23.7

Supplementary Figure Legends

Fig. S1 Structural characteristics of DKC1. (A) Genomic location of human DKC1; (B) Conserved domains of DKC1 in 22 species. (C) The phylogenetic tree of DKC1 in 21 species.

Fig. S2 Expression level of DKC1 in different tissues, cells and plasma according to consensus datasets. (A) RNA tissue specificity of DKC1. (B) Immune cell type specificity of DKC1. (C) RNA single cell type specificity of DKC1. (D) Mass spectrometry-based plasma proteomics of DKC1

Fig. S3 DKC1 expression in different cancers and pathological stages. (A) box plot data for ACC, OV, SARC, TGCT, and UCS in TCGA project including normal tissues of GTEx database as controls. (B) The DKC1 total protein expression level in Clear cell RCC, Glioblastoma multiforme, Pancreatic adenocarcinoma and Hepatocellular carcinoma based on CPTAC database. (C) The main pathological stages of DKC1 expression levels in THCA, UCEC, STAD, CESE, COAD, DLBC, ESCA, HNSC, KIRC, LUAD, LUSC, PAAD, READ, BRCA, UCS, SKMC, BLAC, TGCT and CHOL based on TCGA database. * $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$.

Fig S4. Analysis of DKC1 expression and survival prognosis in Liver cancer, Gastric Cancer, Lung Cancer, Ovarian Cancer and Breast Cancer. (A) The Overall Survival, Progression Free Survival, Relapse Free Survival and Disease-Specific Survival prognosis of DKC1 for Liver Cancer based on Kaplan–Meier plotter database. (B) The First Progression, Overall Survival, and Post Progression Survival prognosis of DKC1 for Gastric Cancer based on Kaplan–Meier plotter database. (C) The First Progression, Overall Survival, and Post Progression Survival prognosis of DKC1 for Lung Cancer based on Kaplan–Meier plotter database. (D) The Overall Survival, Progression Free Survival, and Post Progression Survival prognosis of DKC1 for Ovarian Cancer based on Kaplan–Meier plotter database. (E) The Distant Metastasis Free Survival, Overall Survival, Post Progression Survival and Relapse Free Survival prognosis of DKC1 for Breast Cancer based on Kaplan–Meier plotter database.

Fig S5. DKC1 mutant alterations in BRCA and LUAD based on TCGA. (A) The disease-free survival, disease-specific survival, overall survival, and progression-free survival of DKC1 mutant status in BRCA cases. (B) BRCA samples with DKC1 mutation in TCGA dataset. (C) The disease-free survival, disease-specific survival, overall survival, and progression-free survival of DKC1 mutant status in LUAD cases. (D) LUAD samples with DKC1 mutation in TCGA dataset. (E) Spearman correlation of DKC1 expression data and TMB.

Fig S6. Analysis of DKC1 DNA methylation and survival prognosis (i). (A to K) The relevance of DKC1 DNA methylation and prognosis of BRCA with eight probes

in the non-promoter region of DKC1. (L to N) The DNA methylation level of DKC1 with multiple probes using MEXPRESS tool in the case of READ, CESC and UCEC. The probe ID, Benjamini-Hochberg-adjusted P-value, and Pearson correlation coefficients (R-value) were marked. * P<0.05; ** P<0.01; *** P<0.001.

Fig. S7 Analysis of DKC1 DNA methylation and survival prognosis (ii). (A to E) The DNA methylation level of DKC1 with multiple probes using MEXPRESS tool in the case of LUAD, PRAD, KIRC, LGG and LAML. The probe ID, Benjamini-Hochberg-adjusted P-value, and Pearson correlation coefficients (R-value) were marked. * P<0.05; ** P<0.01; *** P<0.001.

Fig. S8 Protein phosphorylation of DKC1 in different cancers based on the CPTAC dataset. (A) The different expression level of DKC1 in HNSC. (B) The different expression level of DKC1 in HCC. (C) The different expression level of DKC1 in LUAD.

Fig. S9 Analysis of DKC1 expression and immune infiltration in T cell CD8⁺ across all cancer cases in TCGA. (A) The association between DKC1 expression level and infiltration level of T cell CD8⁺ through ten different algorithms. (B) Correlation between DKC1 expression level and infiltration level of T cell CD8⁺ in HNSC, HNSC-HPV-, KIRC, THYM, BRCA, BRCA-Basal, BRCA-LumB, DLBC and UVM with one specific algorithm.

Fig. S10 The association between DKC1 expression level and infiltration level of B cell(A), Mast cell(B), Monocyte(C), Neutrophil(D), NK cell(E), T cell CD4⁺(F), Tregs(G) and Macrophage(H) through different algorithms.

Fig. S11 The KEGG pathway analysis of DKC1.

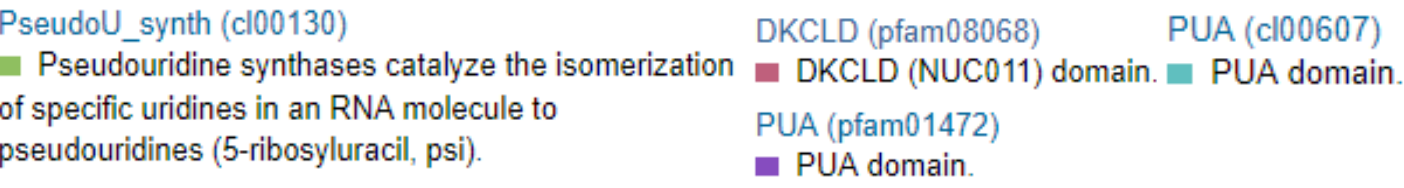
Fig. S12 DKC1 related gene enrichment analysis. (A) GO enrichment analysis of DKC1-binding proteins or DKC1-related genes for keyword “cellular component”. (B) Cnetplot for GO analysis of the first five cellular components were displayed. (C) GO enrichment analysis of DKC1-binding proteins or DKC1-related genes for keyword “biological process”. (D) Cnetplot for GO analysis of the first five biological processes were displayed.

S1

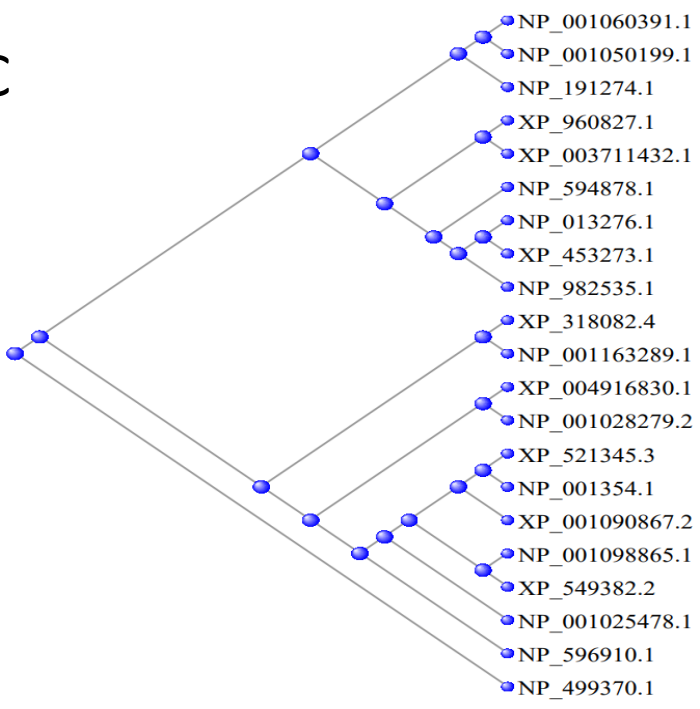
A DKC1(ENSG00000130826) Chromosome X: 154,762,742-154,777,689



Conserved Domains

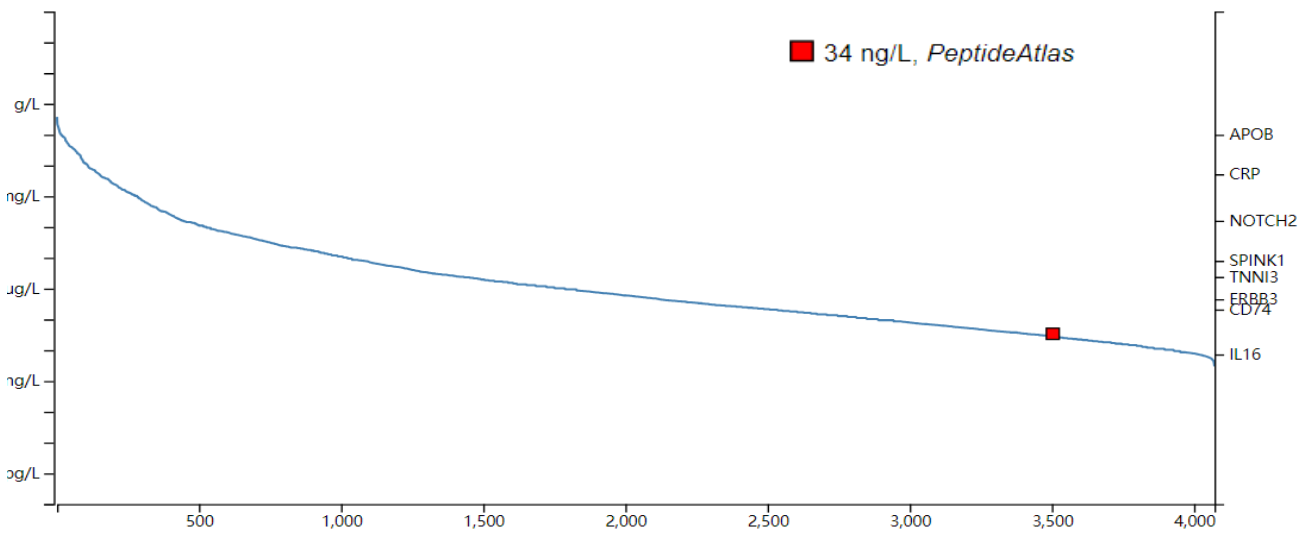


C



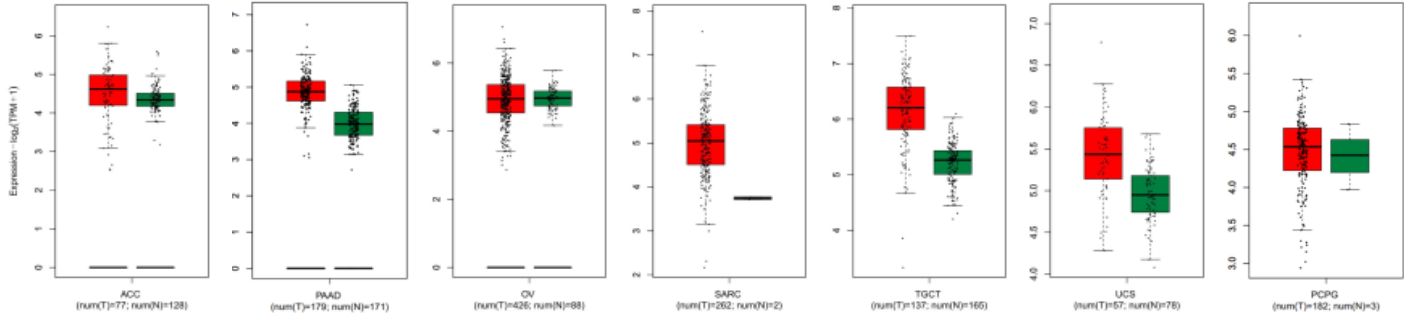
D

Detected in plasma by mass spectrometry

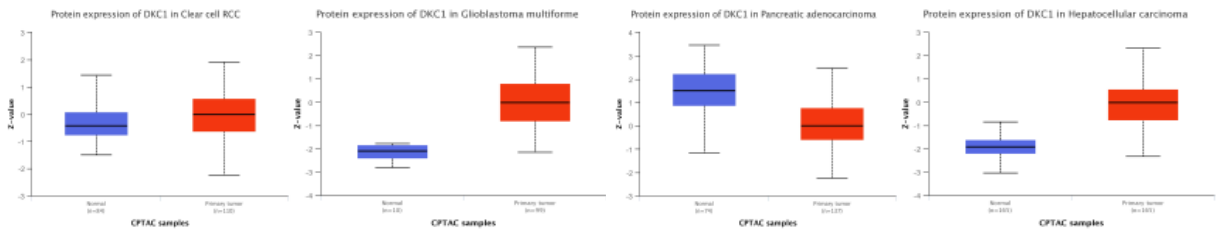


S3

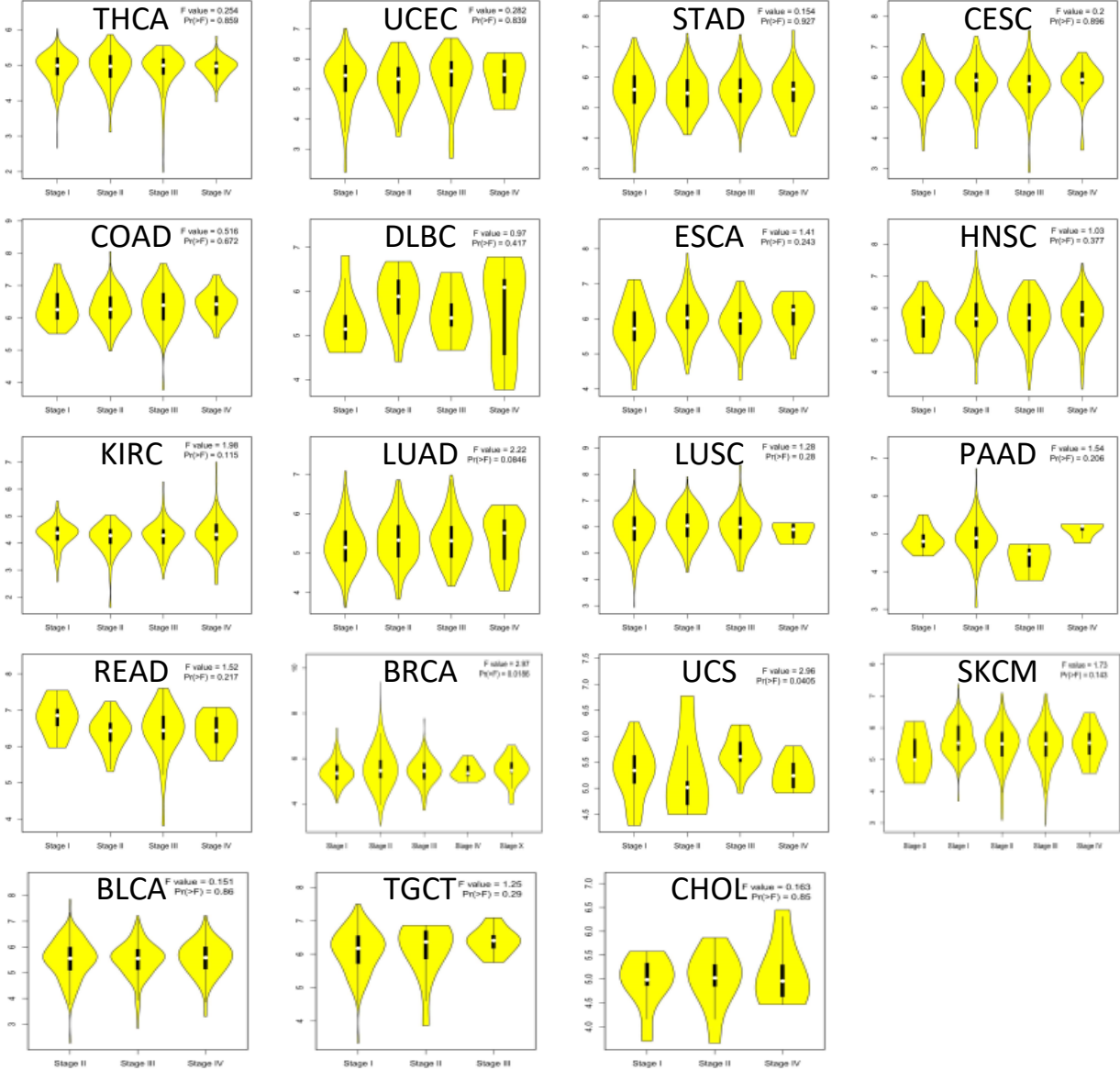
A



B

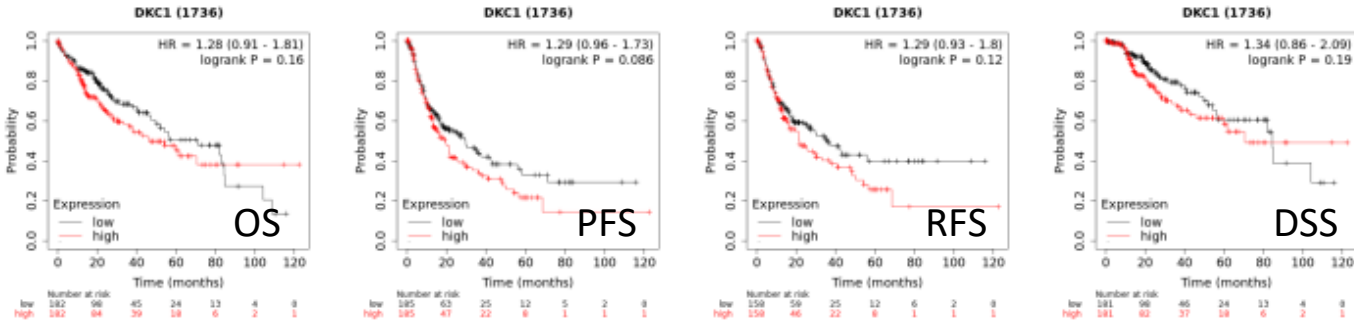


C

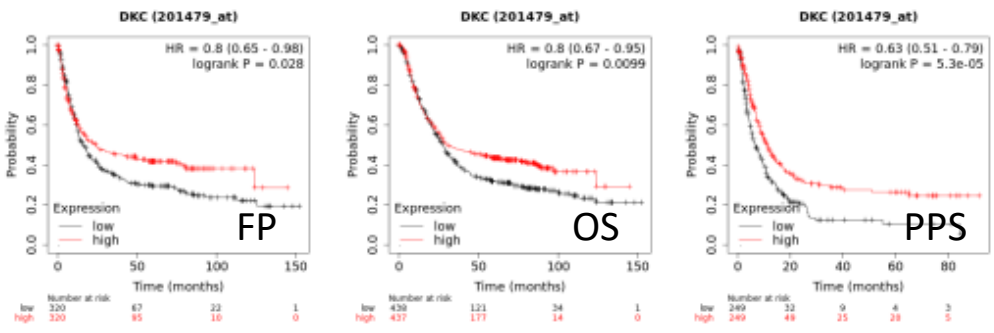


S4

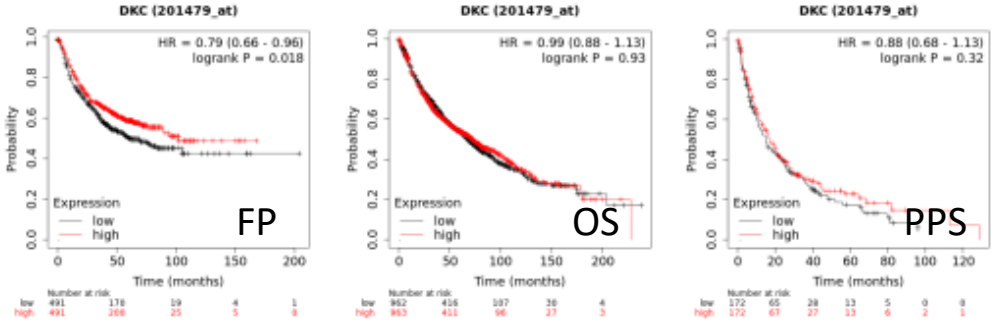
A Liver Cancer



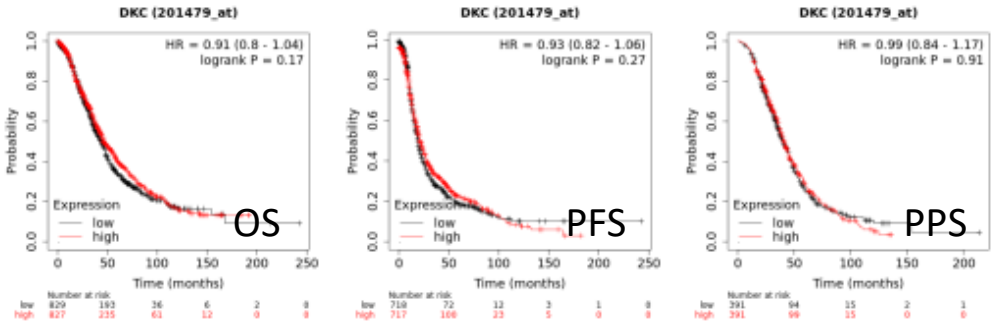
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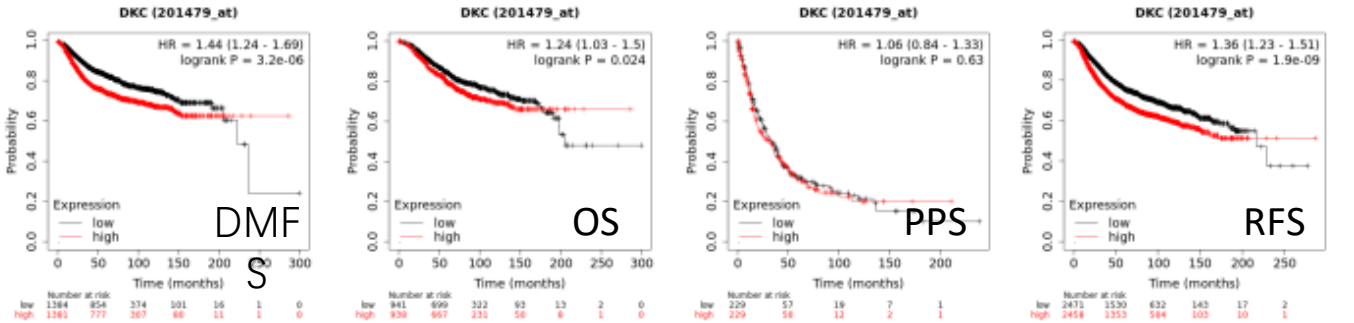
C Lung Cancer



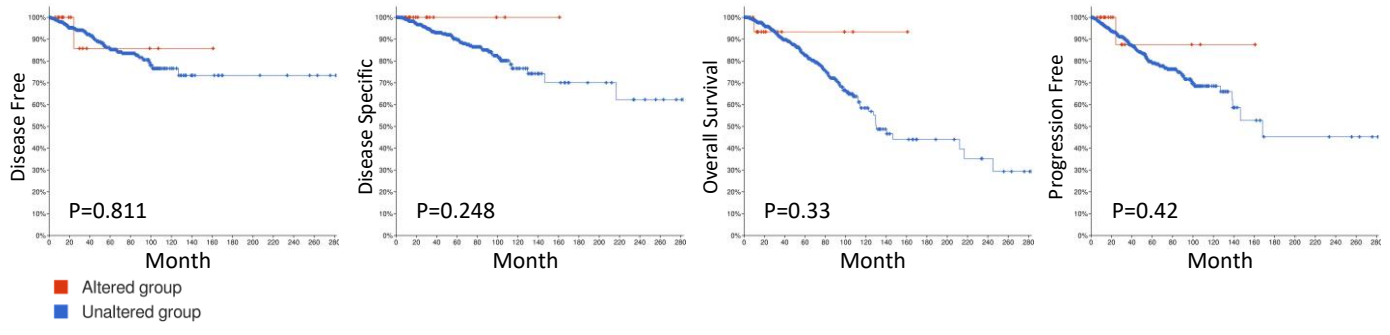
D Ovarian Cancer



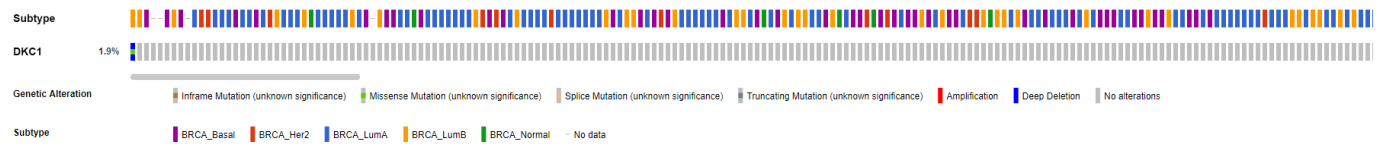
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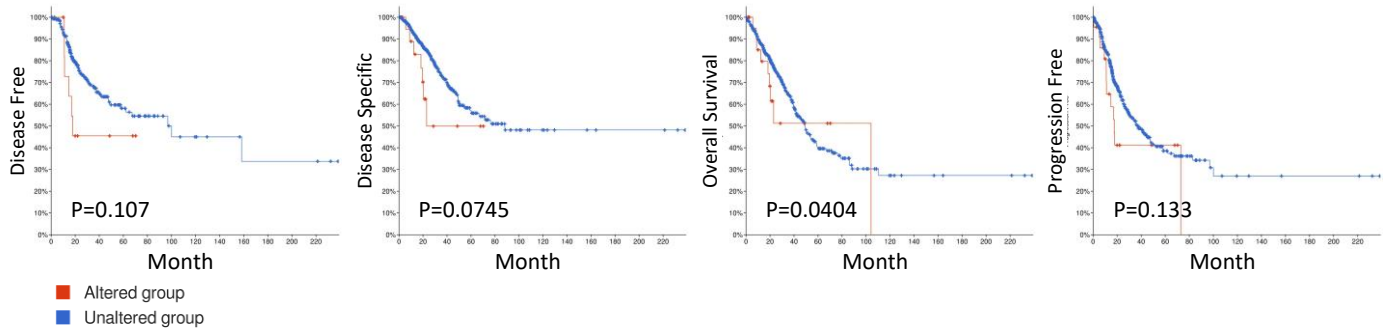
A BRCA



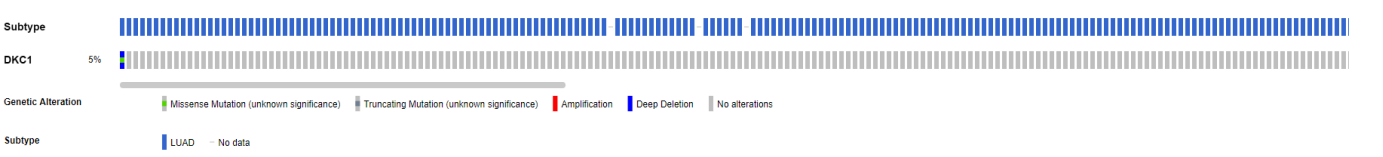
B



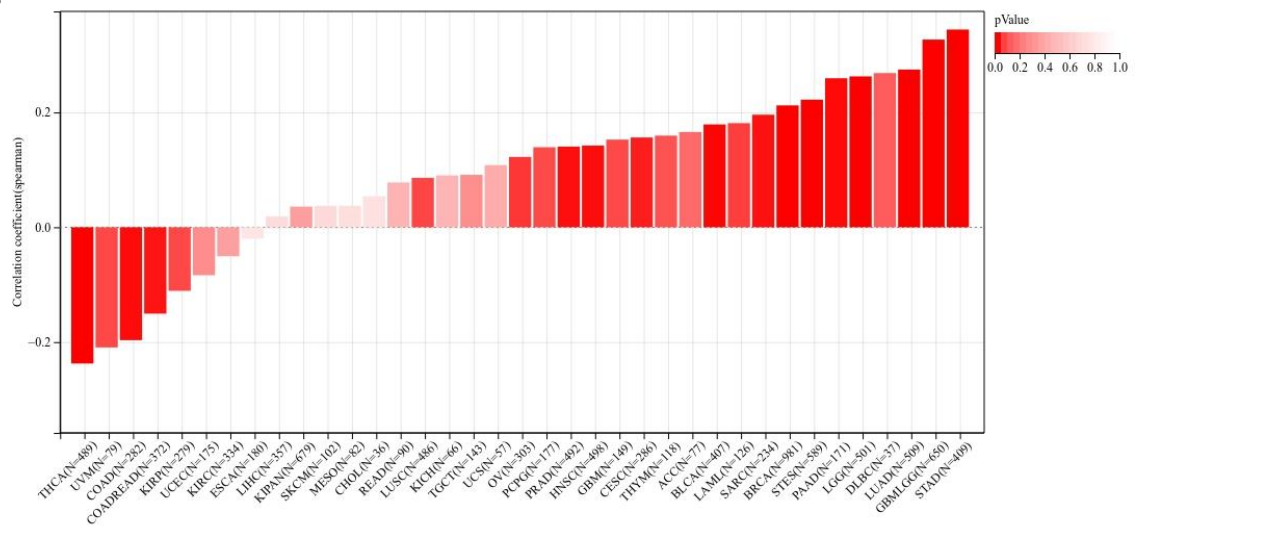
C LUAD



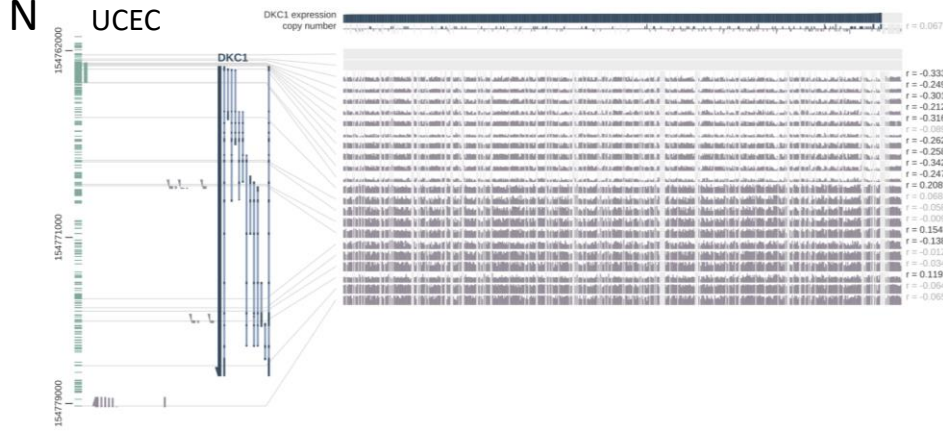
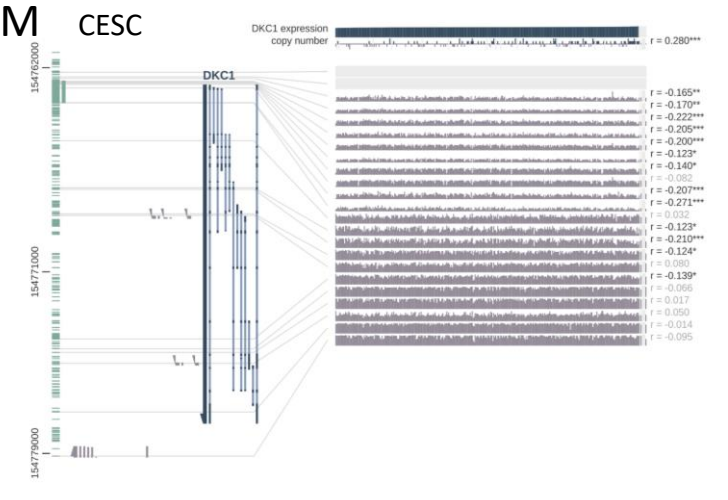
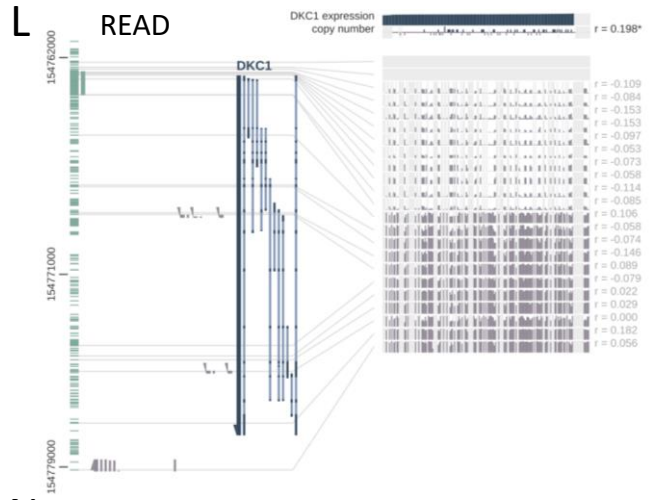
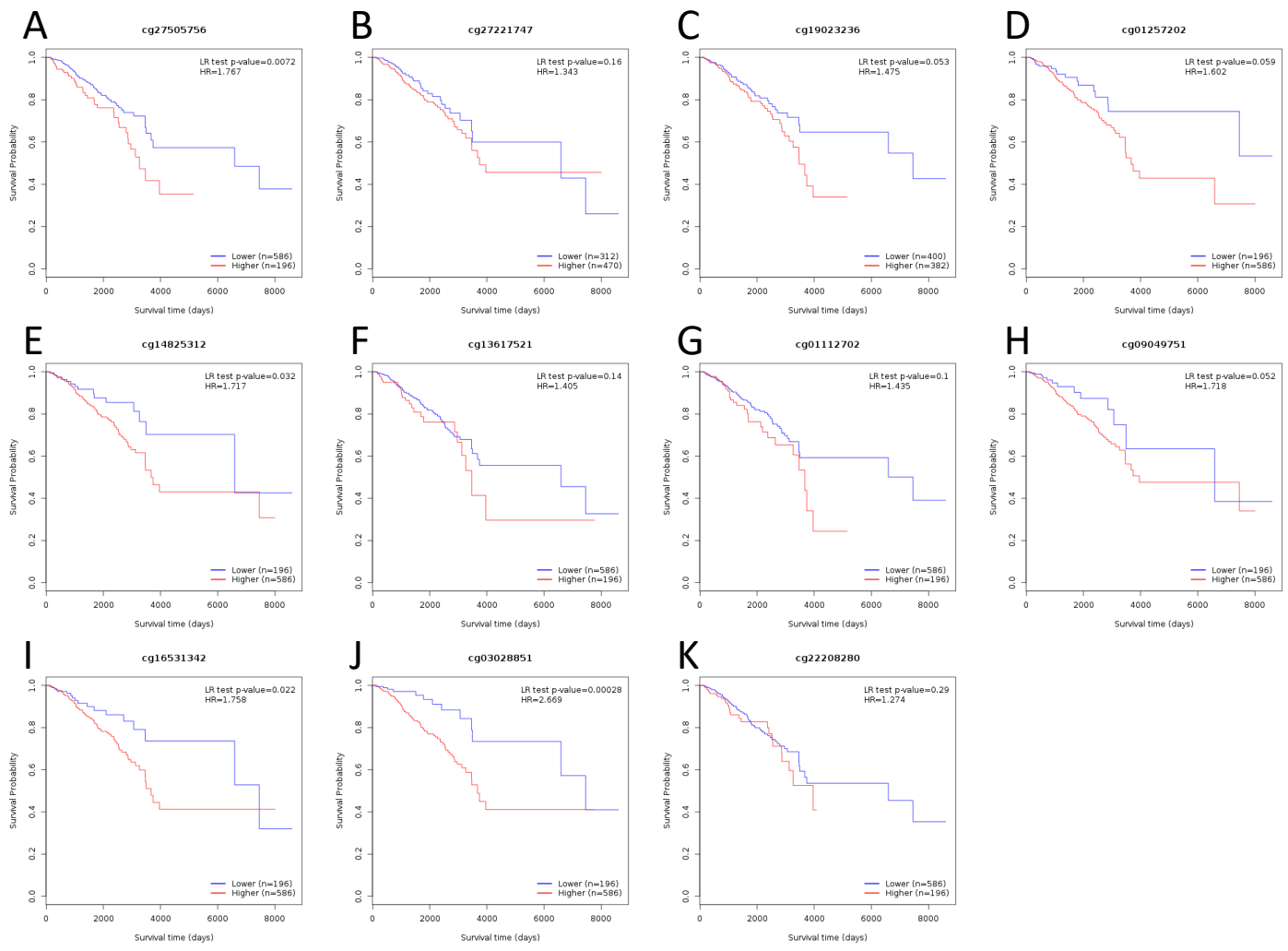
D

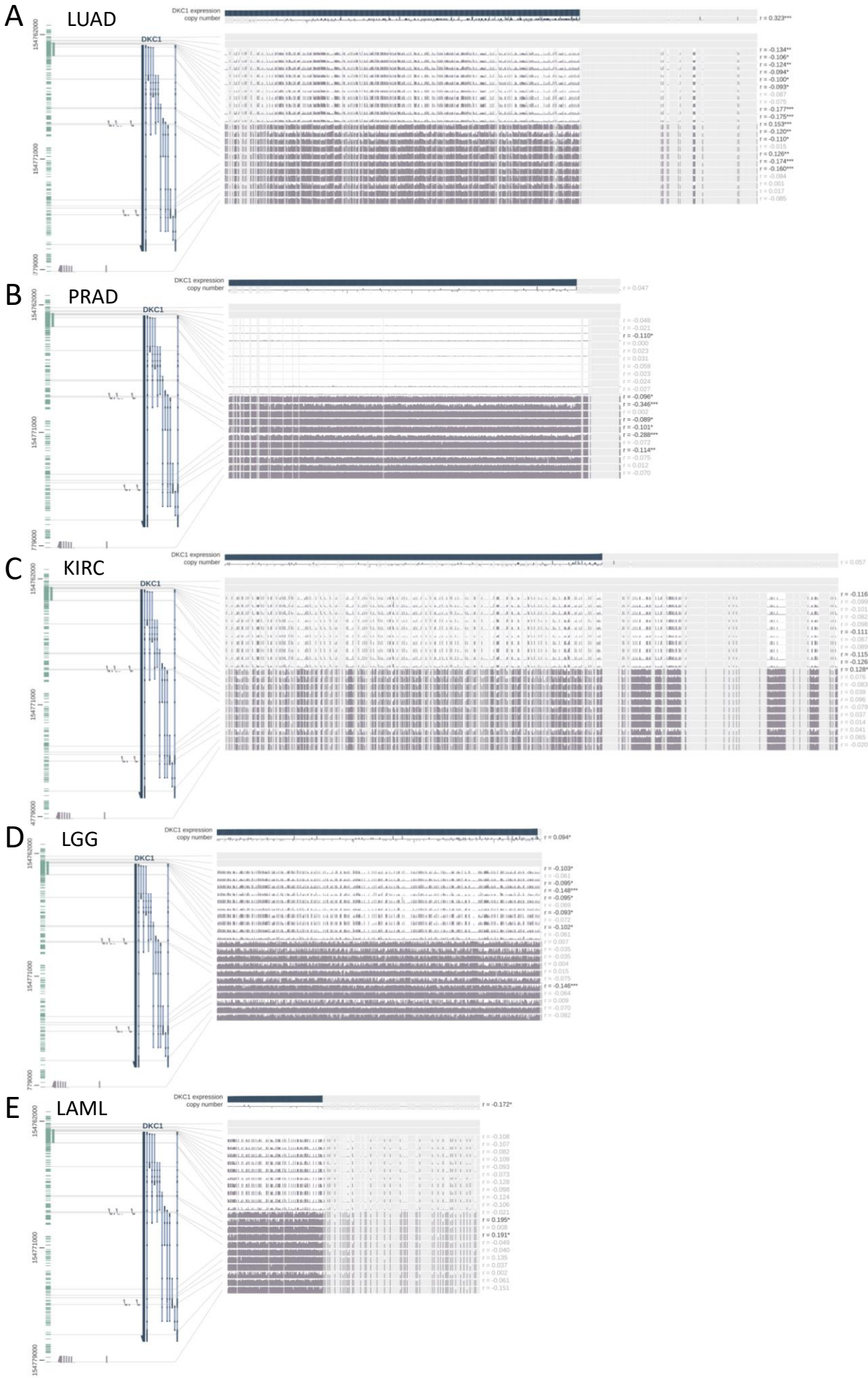


E



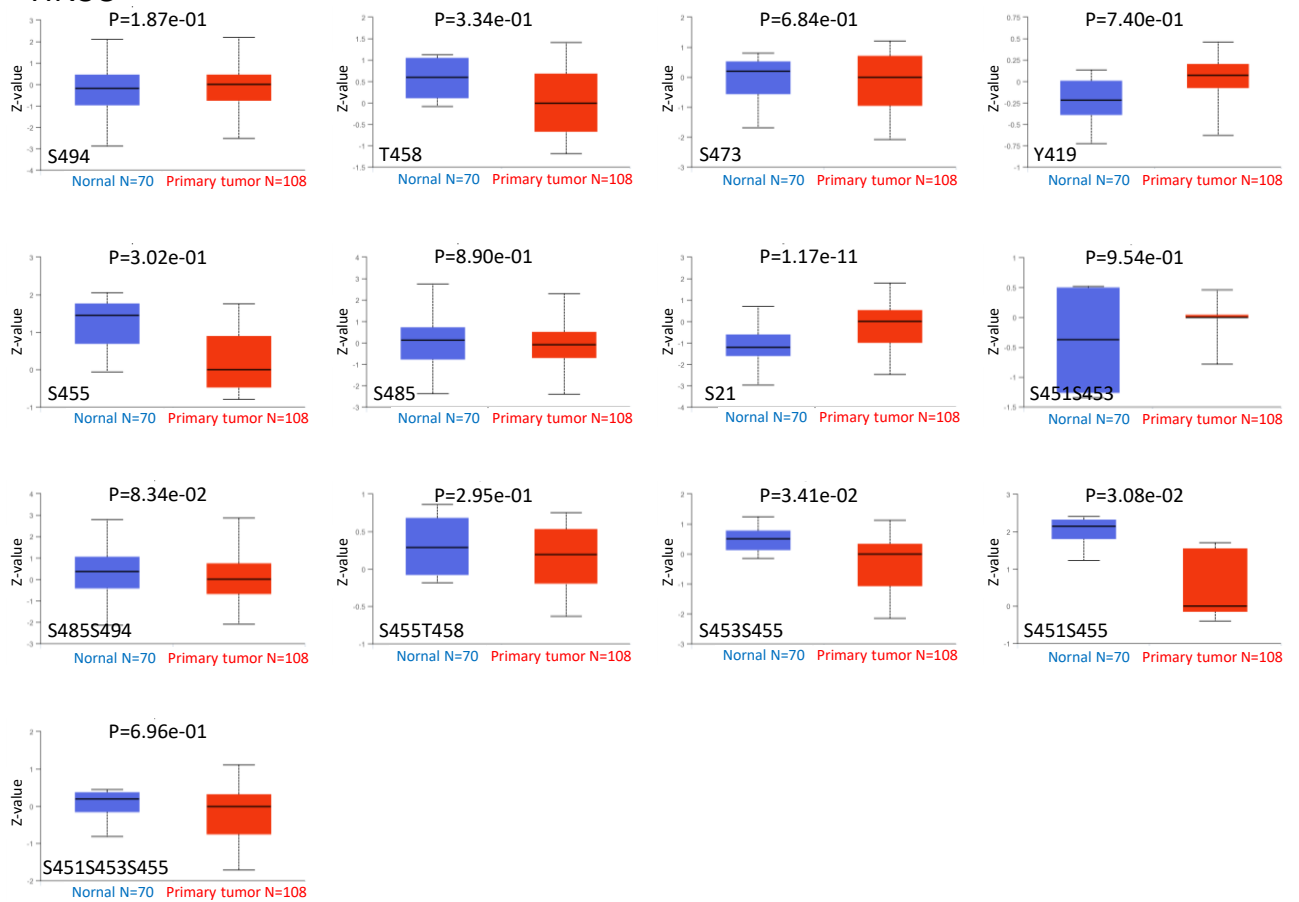
S6





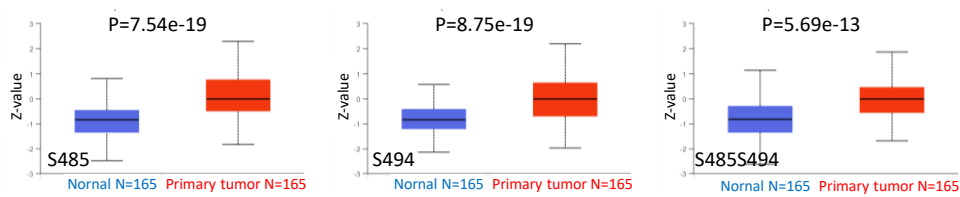
A

HNSC



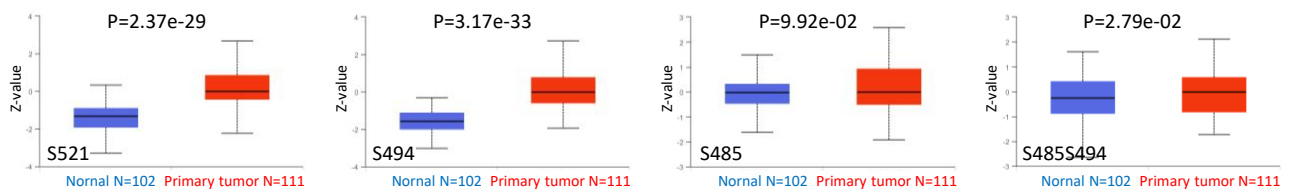
B

HCC

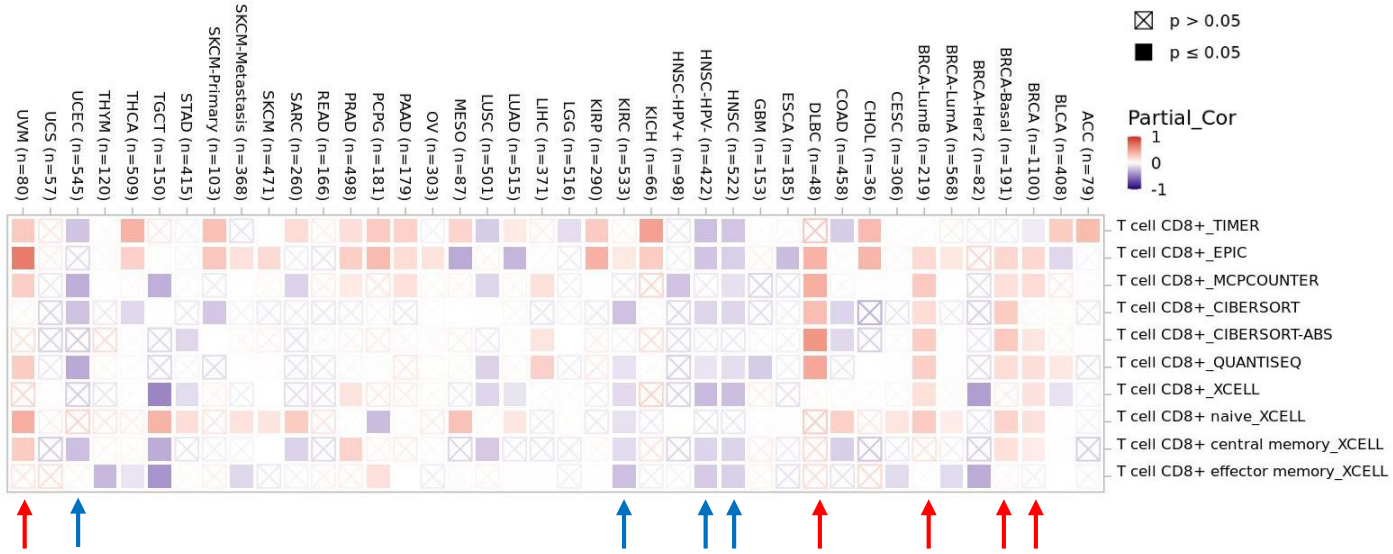


C

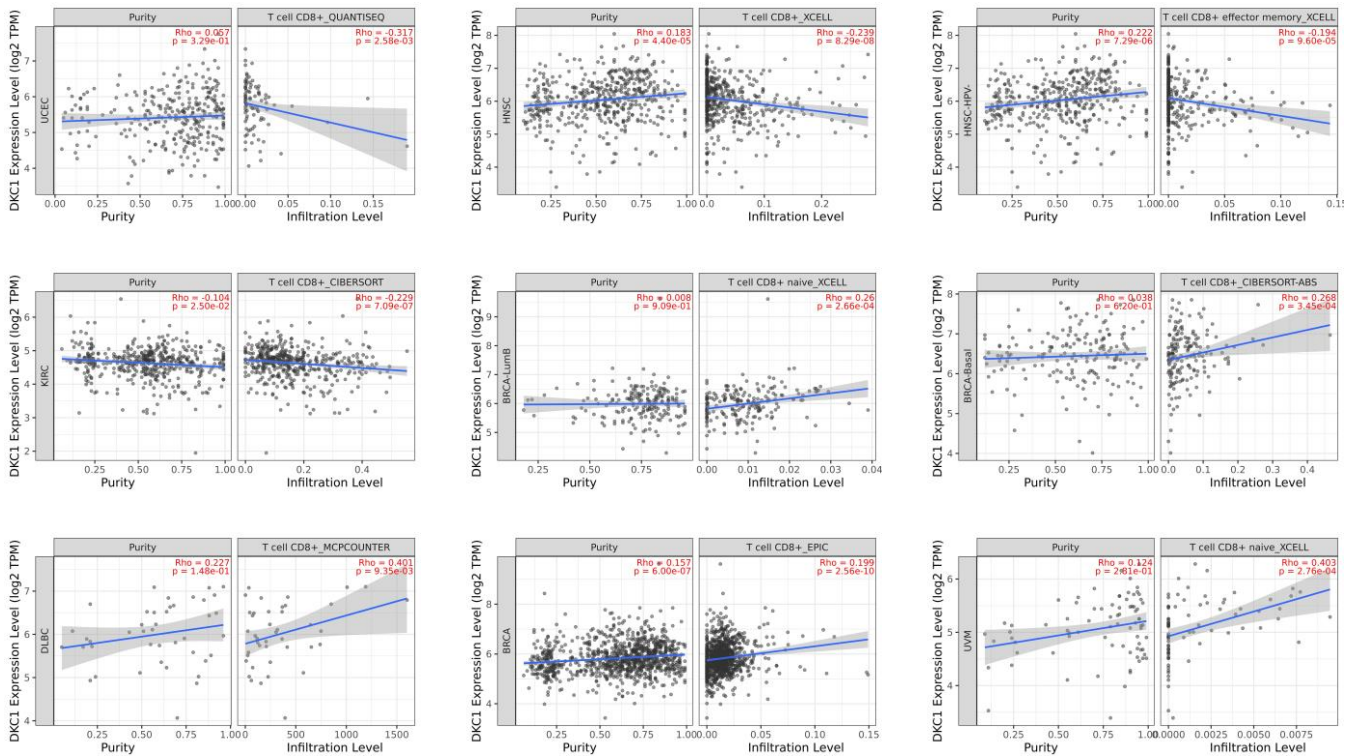
LUAD



A

T cell CD8⁺

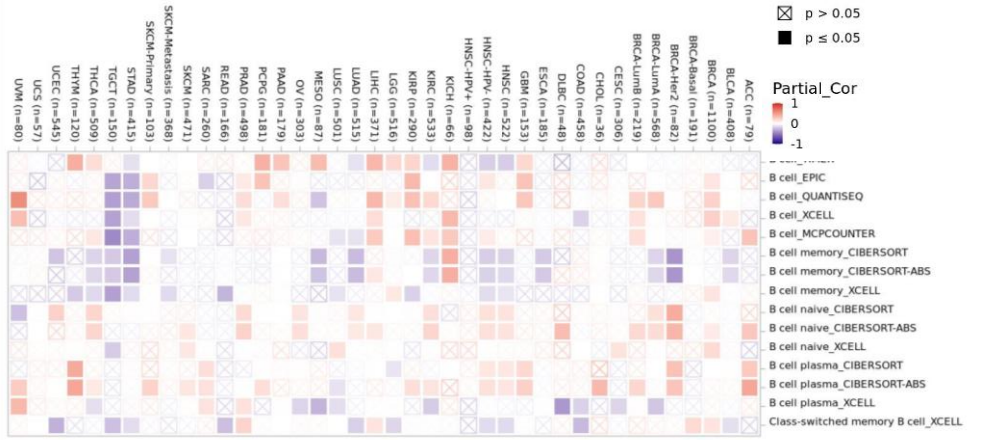
B



S10

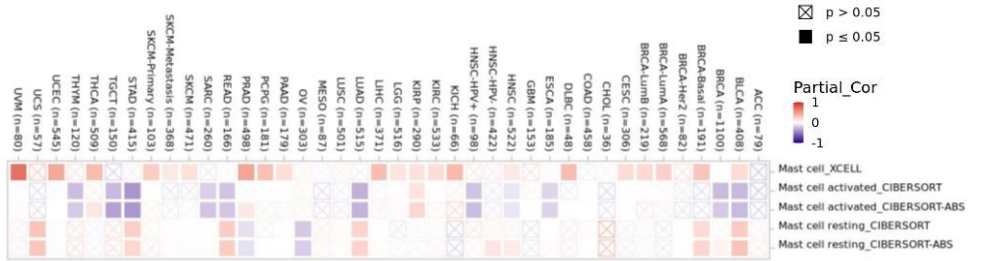
A

B cell



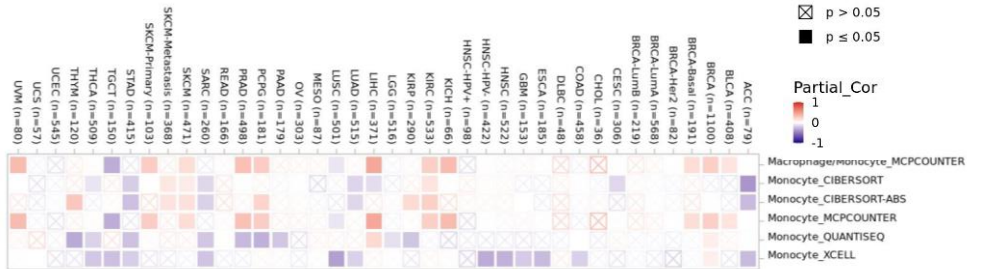
B

Mast cell



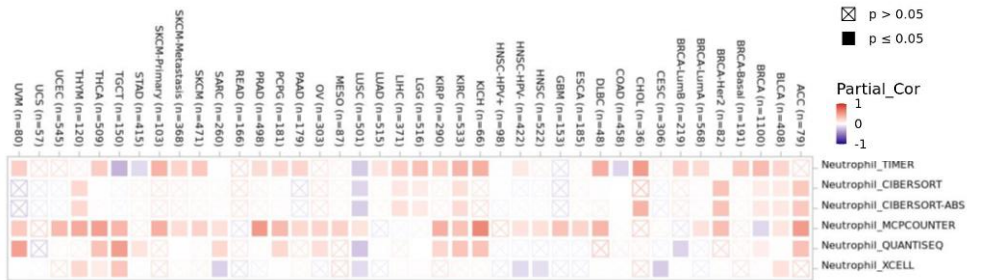
C

Monocyte

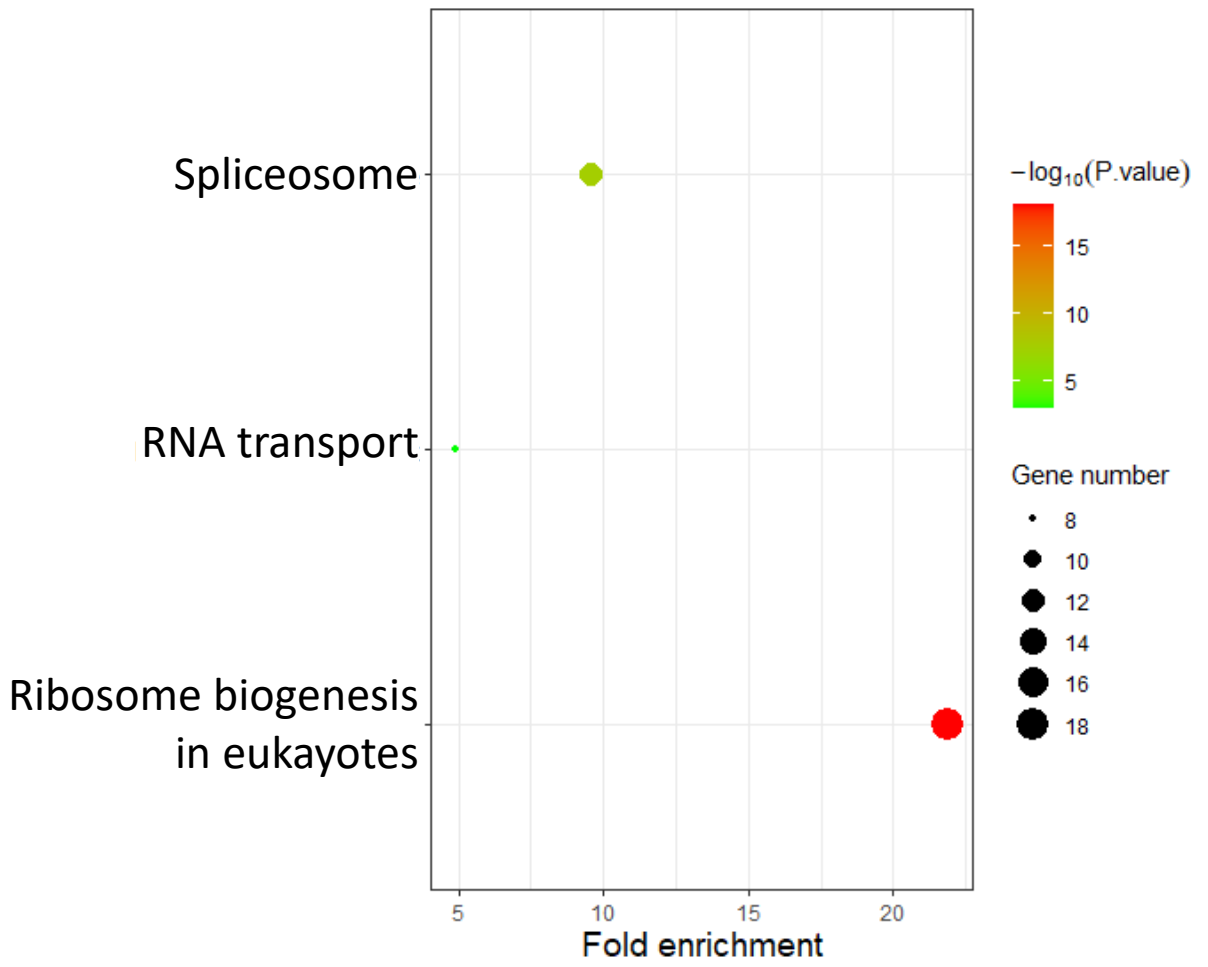


D

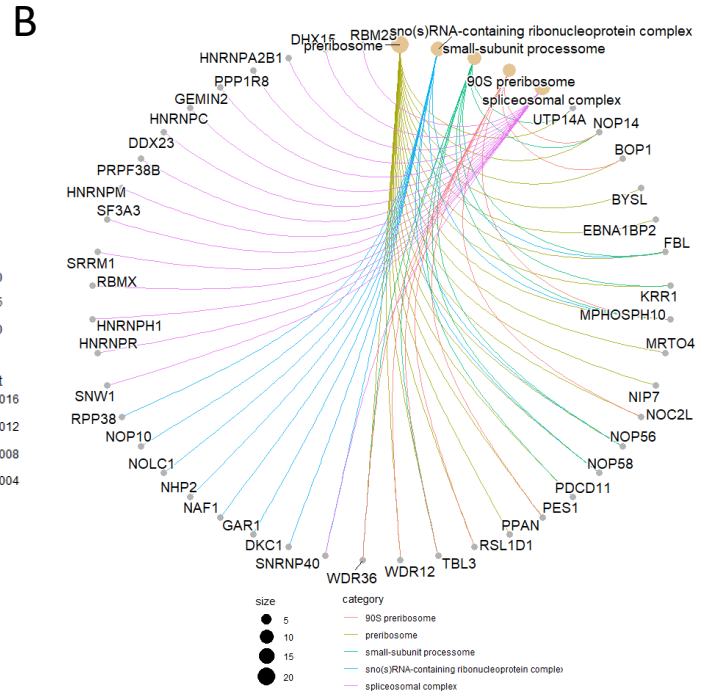
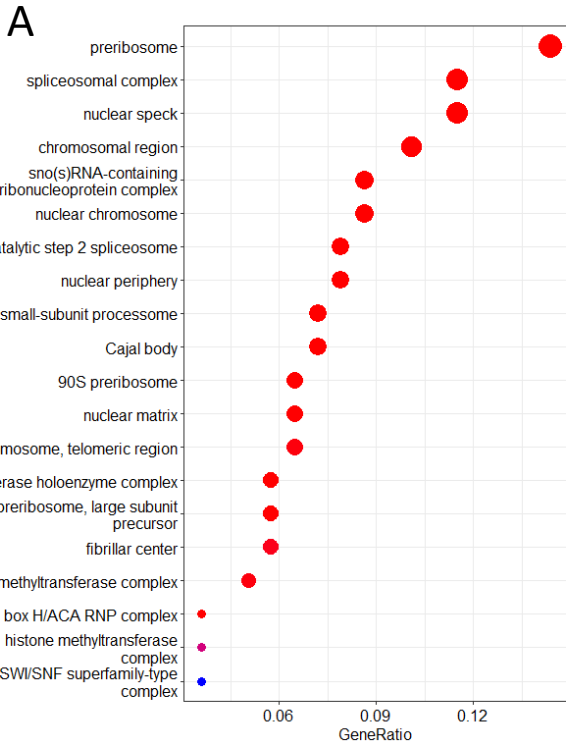
Neutrophil



S11



Cellular component



Biological process

