

Figure S1

A

Data Sources

NIH NATIONAL CANCER INSTITUTE Genomic Data Commons

GEO DataSets

UCSC Xena

CCL Cancer Cell Line Encyclopedia

cellMiner™ Analyze, Integrate, Discover

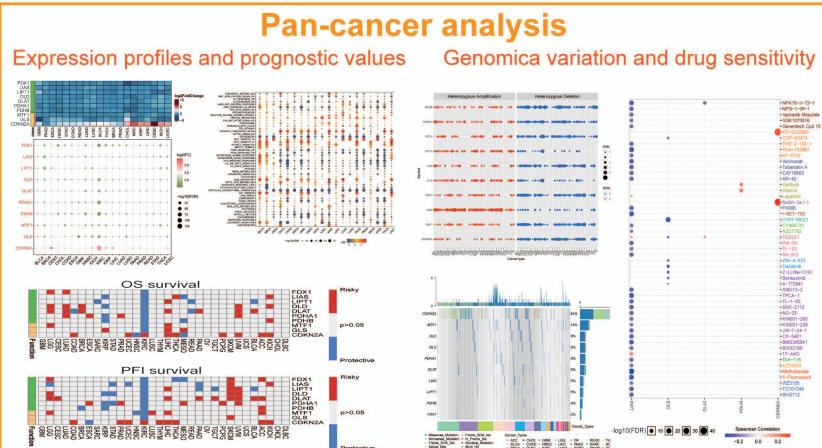
GDSC wellcome sanger institute



TIDE

TIMER

B



C

Two subtypes of ccRCC for copper induced cell death

Risk model construction

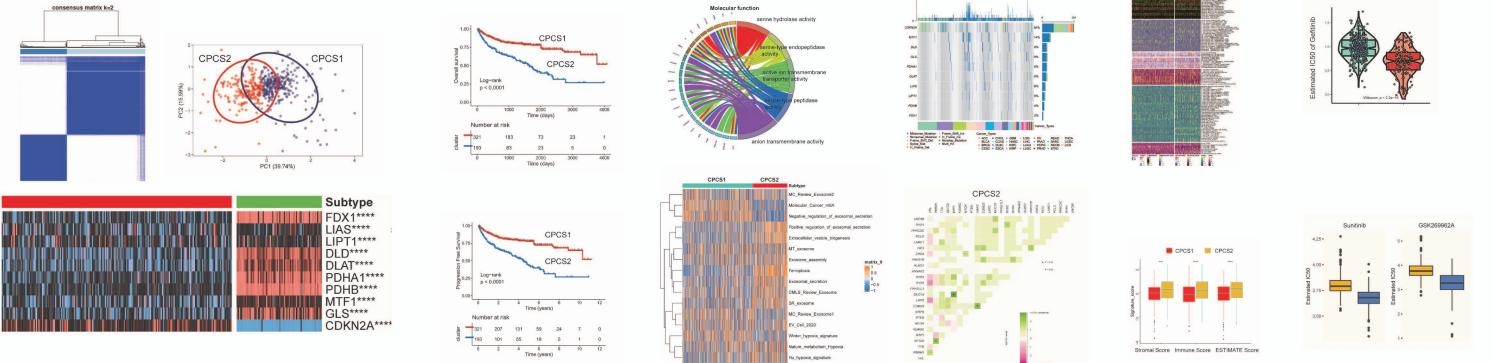
Clinical outcome

Pathway analysis

Genomic variation

Immune infiltration

Drug sensitivity



D

Construction of risk model and the core role of DLAT

Four genes risk model

TCGA-ccRCC validation

Expression verification

Functional experiments

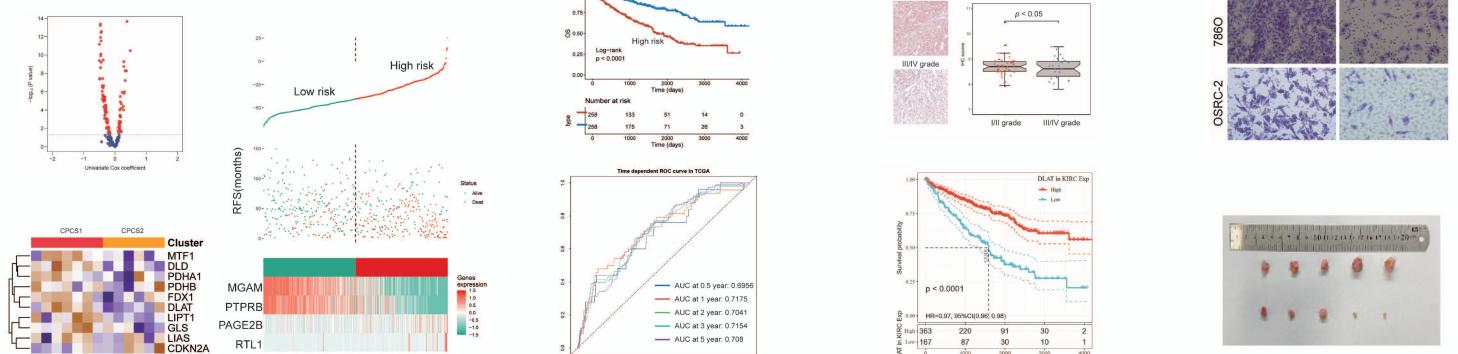
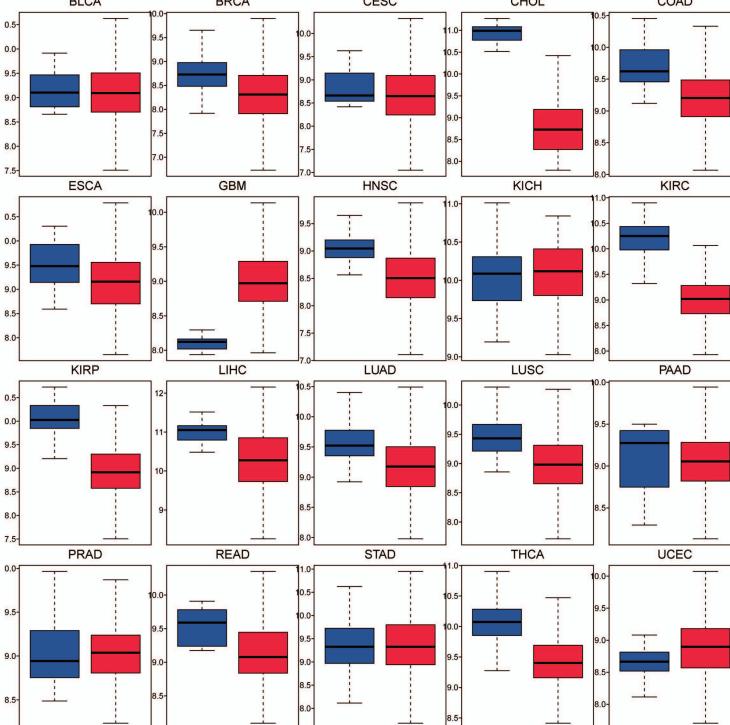
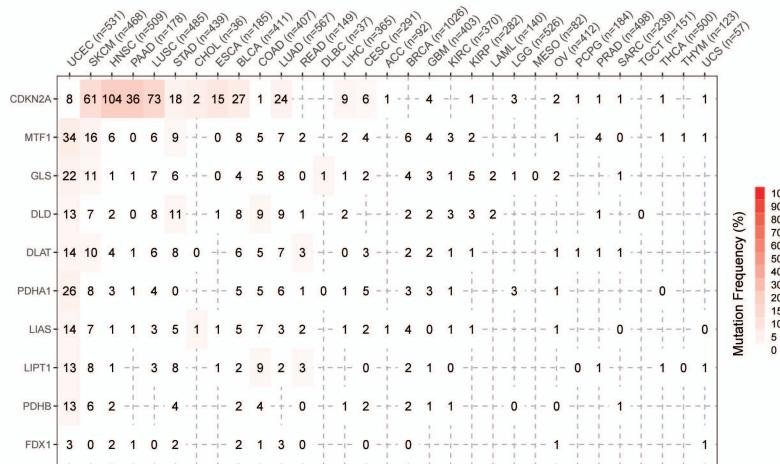


Figure S2

A



B



C

Overall survival difference between hypermethylation and hypomethylation.

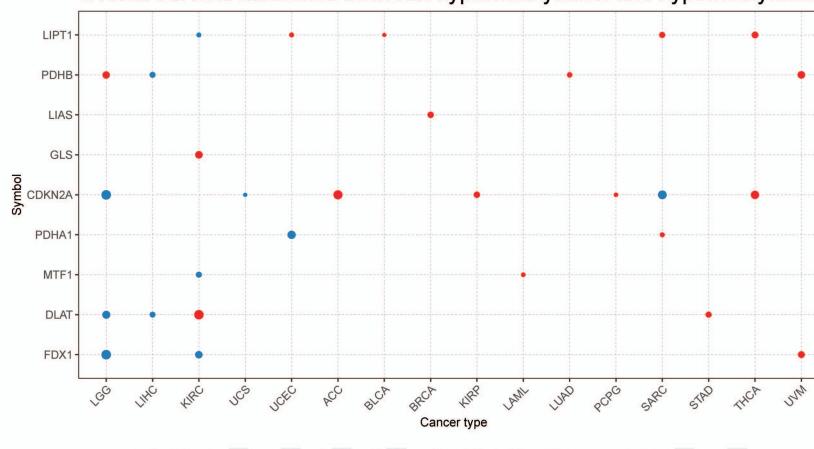


Figure S3

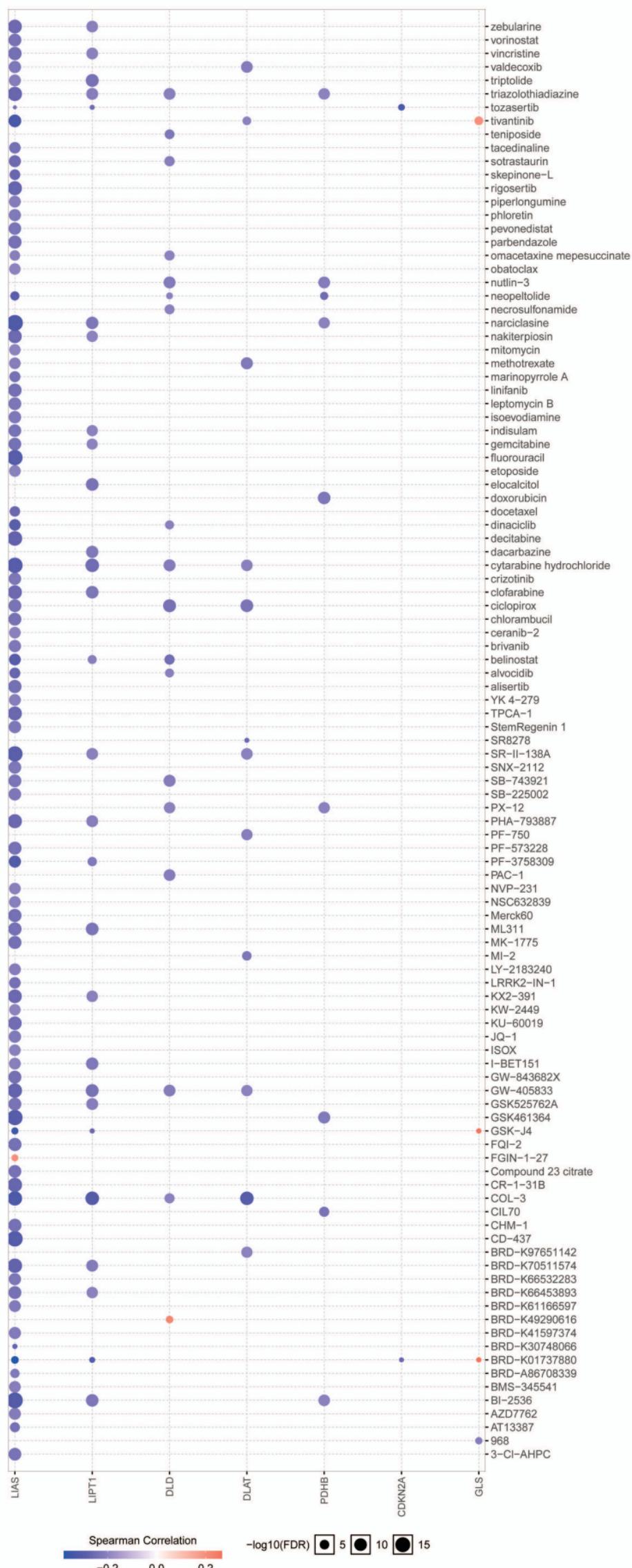
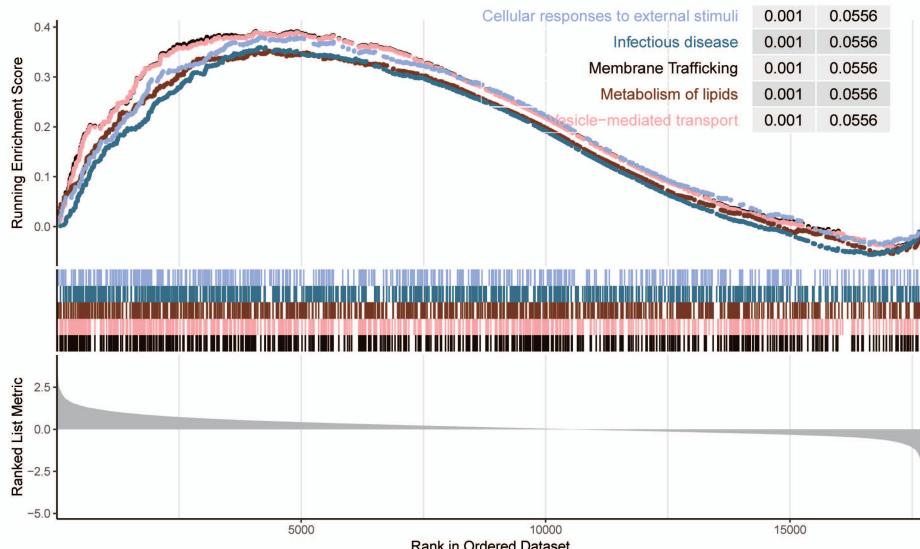
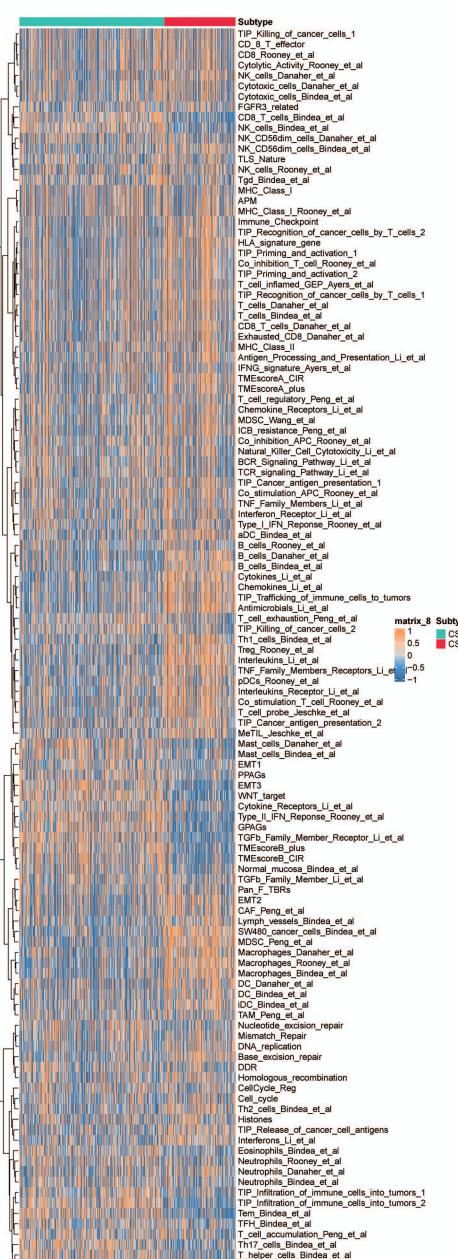


Figure S4

A



B



C

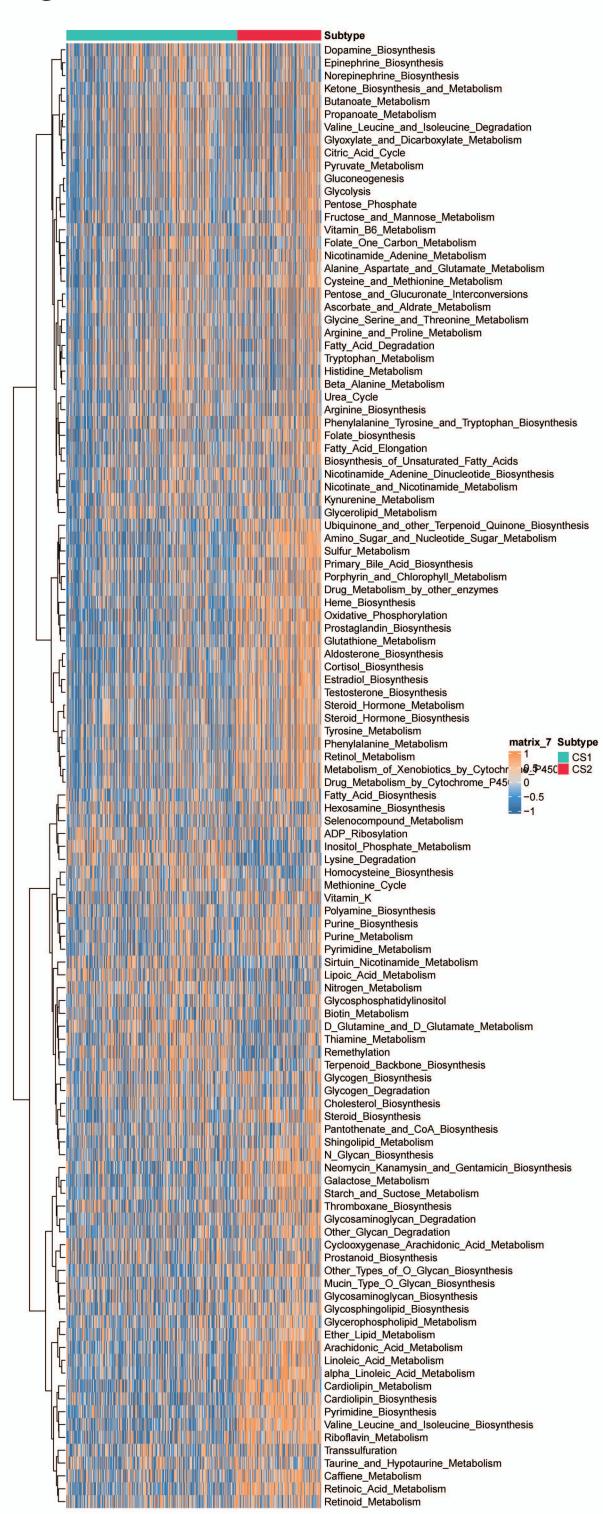


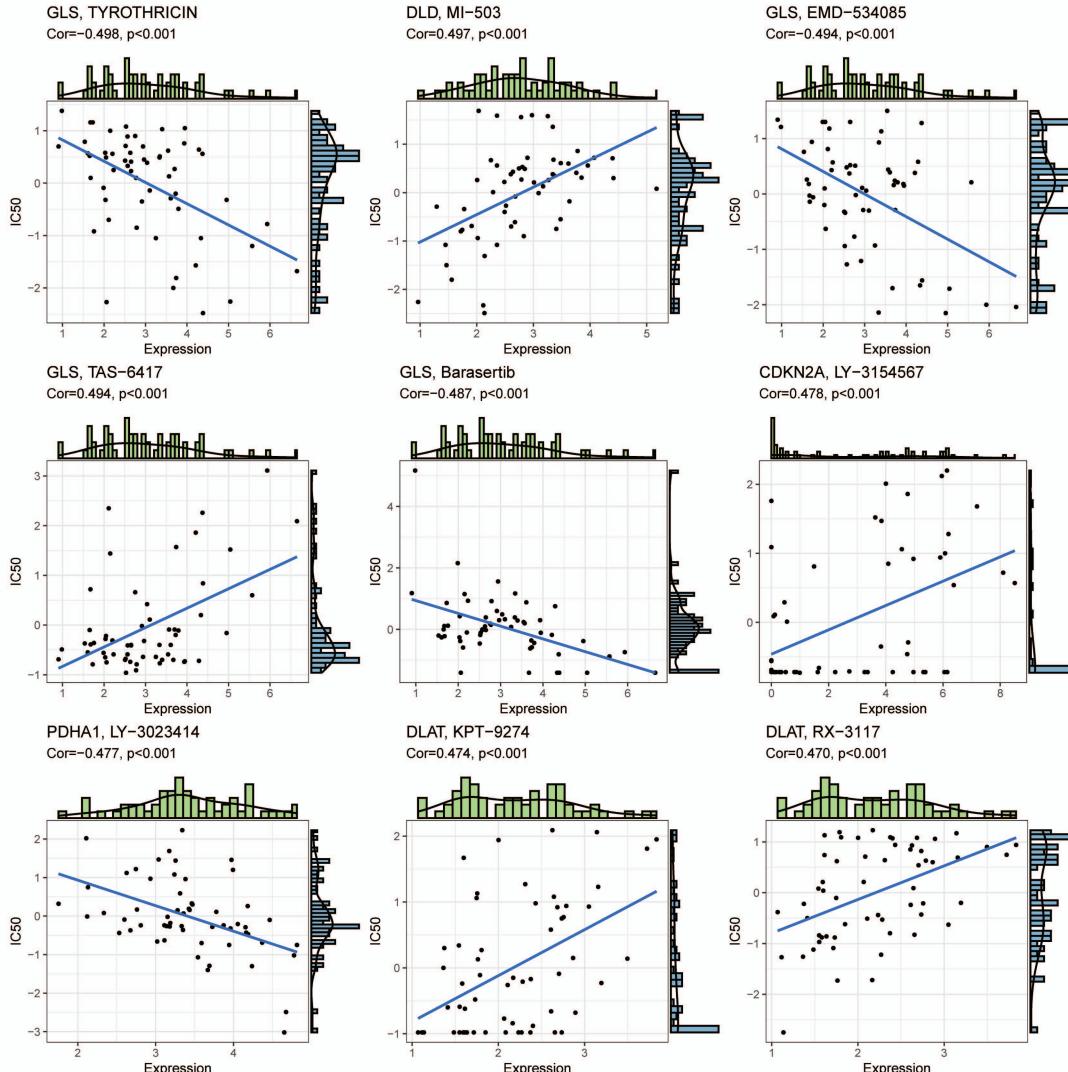
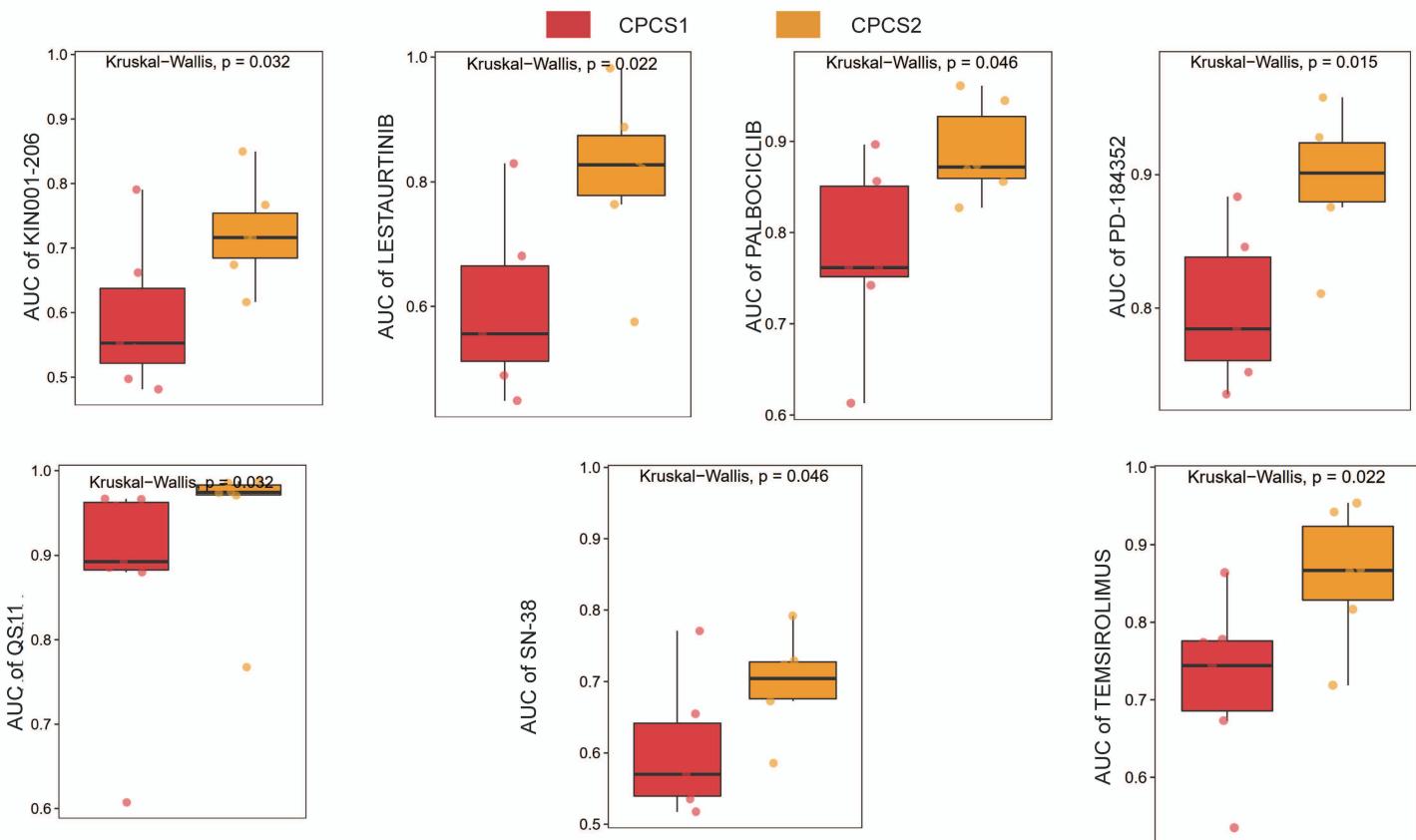
Figure S5**B**

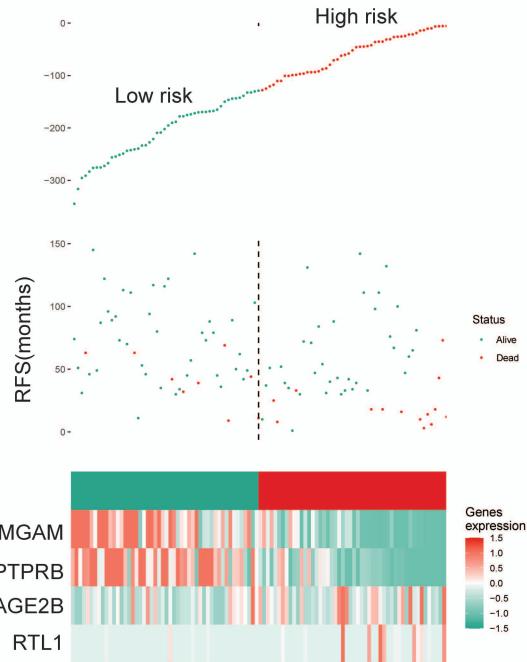
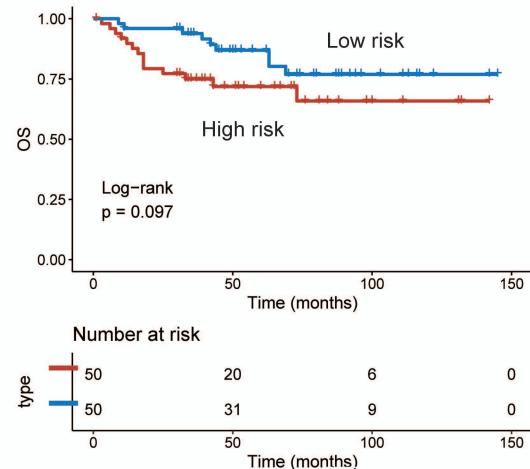
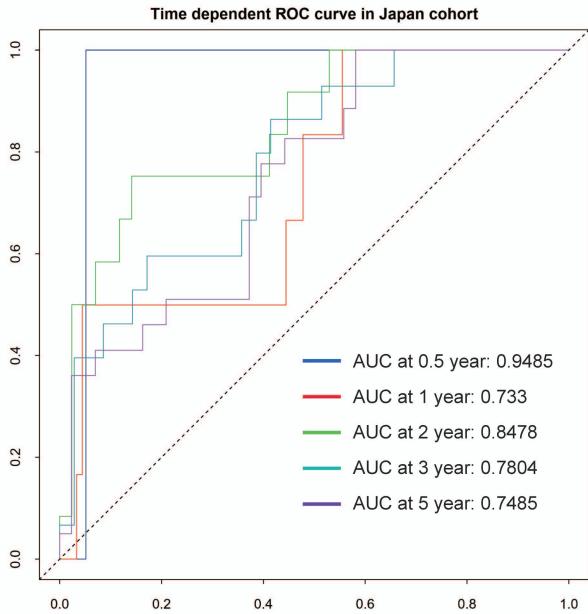
Figure S6**A****B****C**

Figure S7

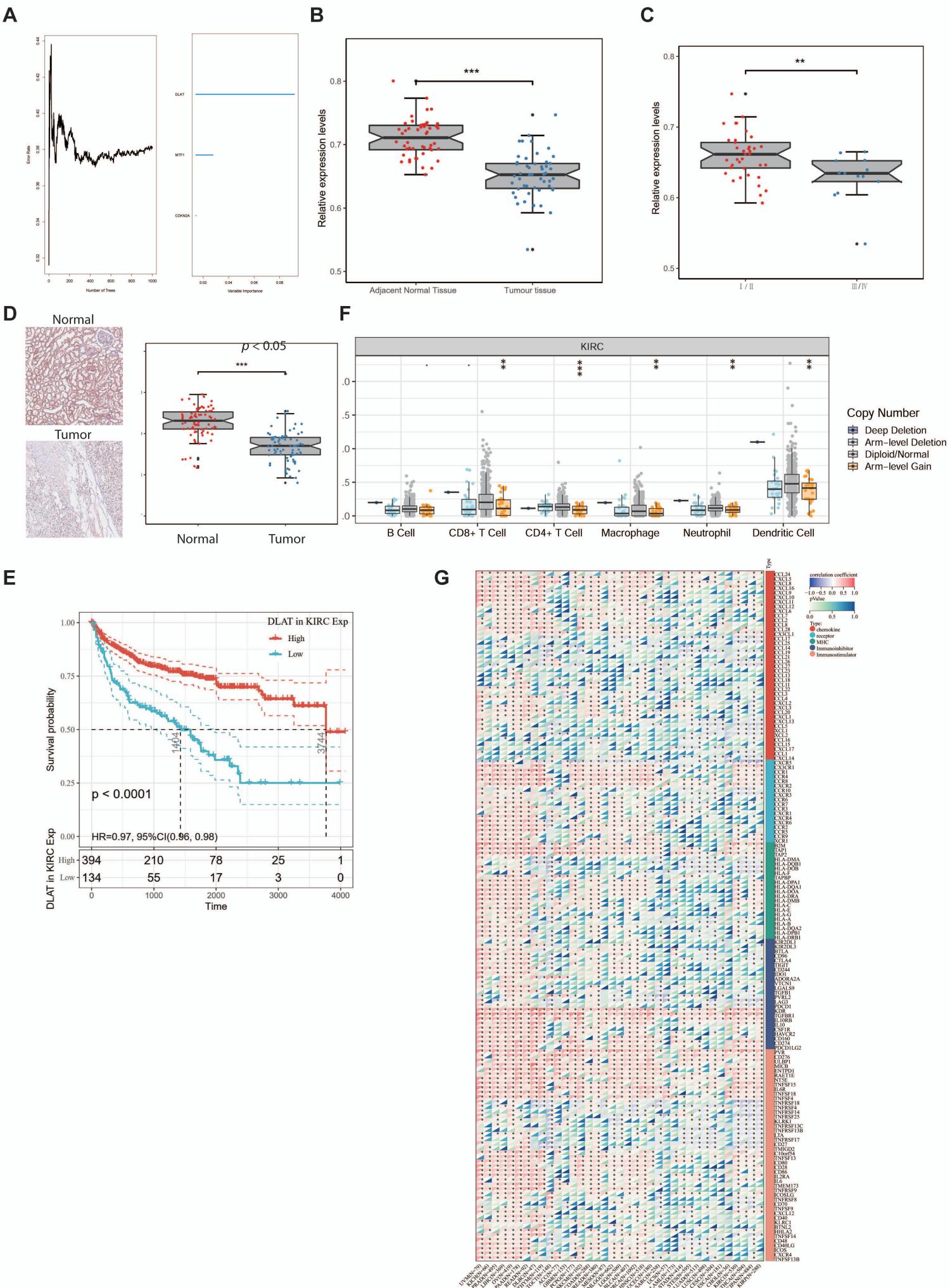
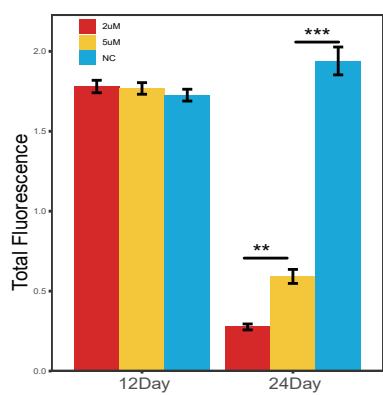
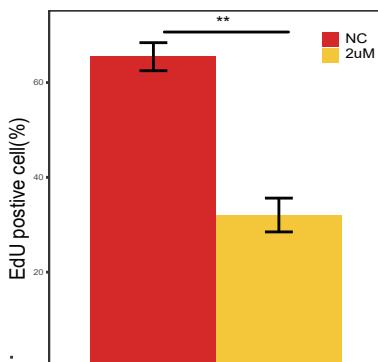


Figure S8

A

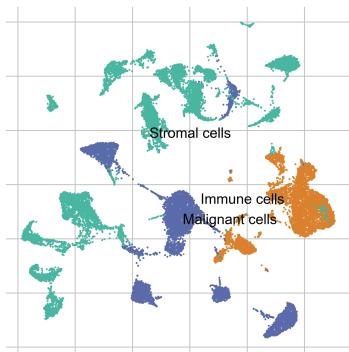


B

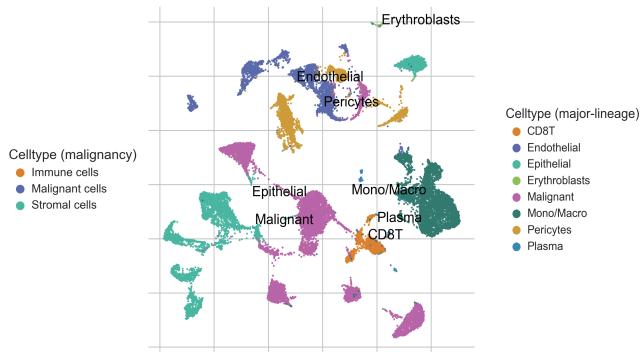


C

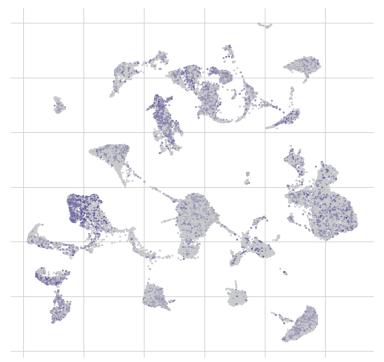
KIRC_GSE159115



KIRC_GSE159115

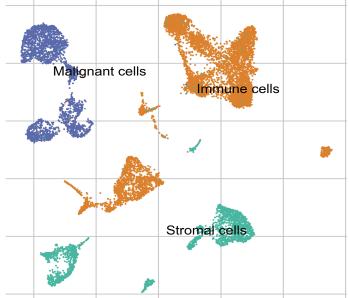


Cuprotosis Score

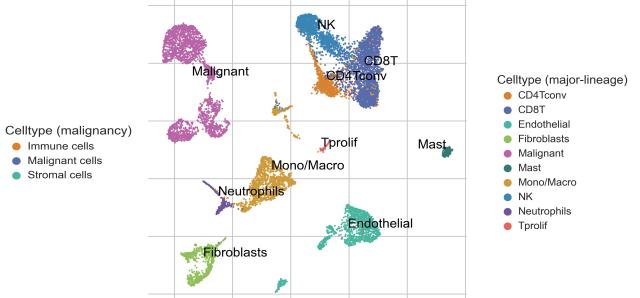


D

KIRC_GSE171306



KIRC_GSE171306



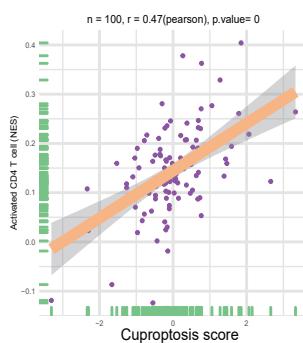
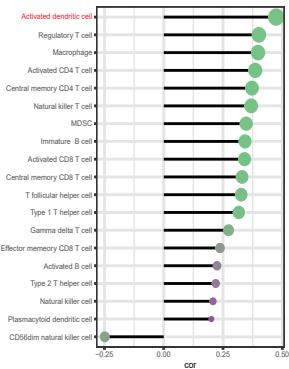
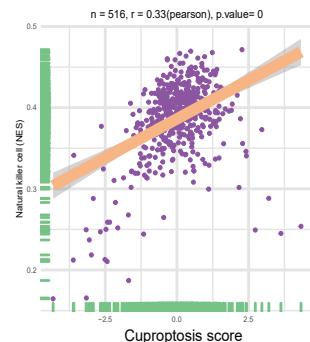
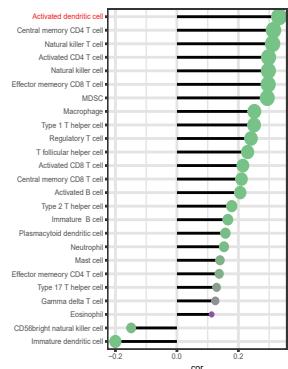
Cuprotosis Score



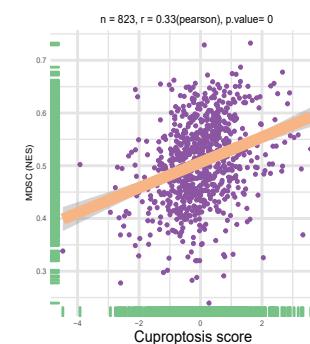
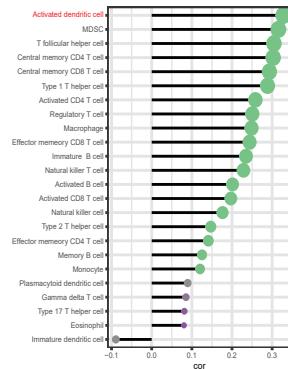
Figure S9

A

TCGA-KIRC cohort JAPAN-KIRC cohort



Cancer cell-KIRC cohort



B

