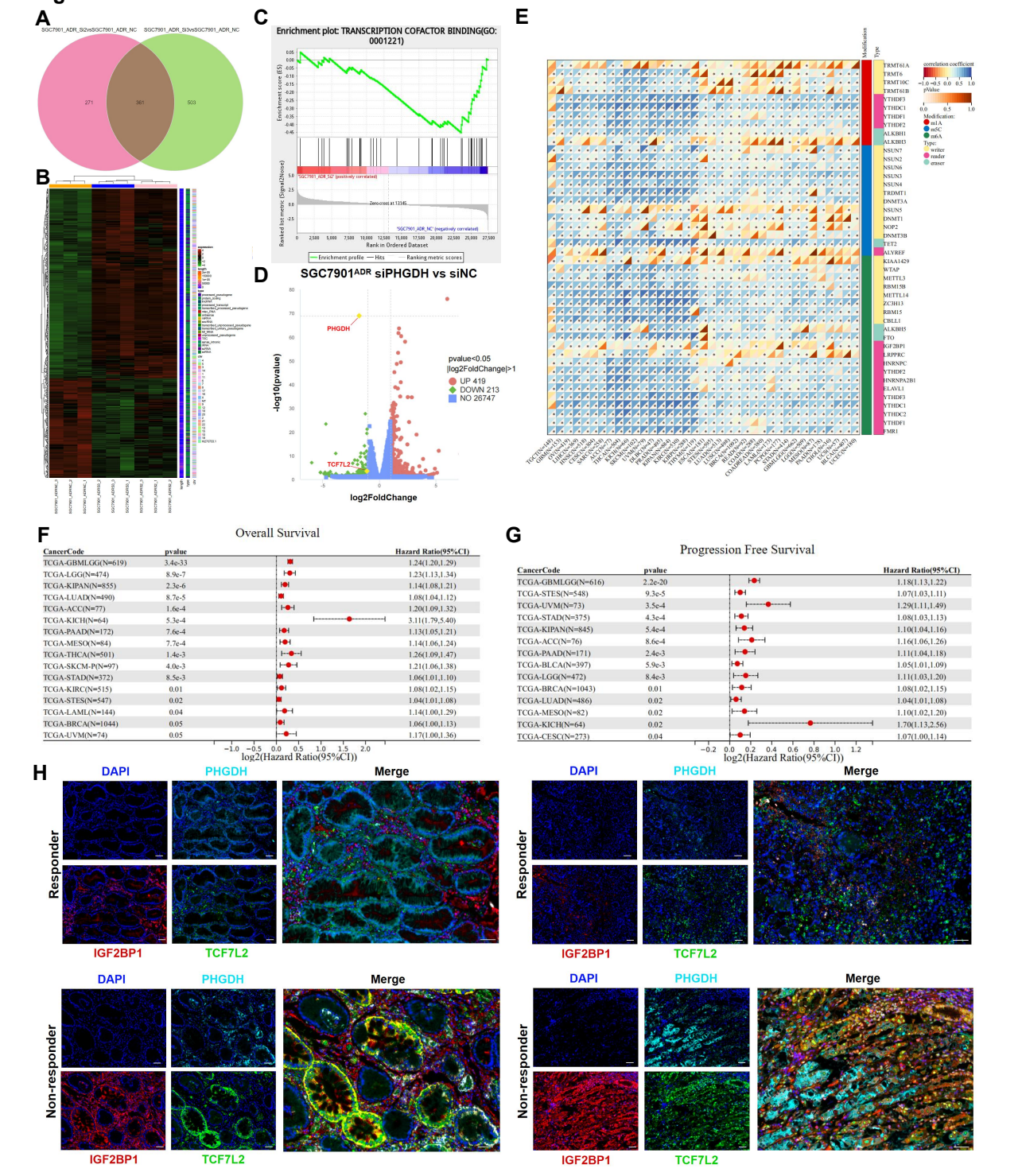
Fig. S3


A
SGC7901_ADR_Si2vsSGC7901_ADR_NC
SGC7901_ADR_Si3vsSGC7901_ADR_NC
271
361
503
B
C
Enrichment plot: TRANSCRIPTION COFACTOR BINDING(GO: 0001221)
Enrichment score (ES)
Ranked list metric (Signal2Noise)
Zero cross at 13145
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores
D
SGC7901ADR siPHGDH vs siNC
PHGDH
TCF7L2
pvalue<0.05
|log2FoldChange|>1
UP 419
DOWN 213
NO 26747
-log10(pvalue)
log2FoldChange
E
Modification
Type
correlation coefficient
pvalue
Modification:
m1A
m5C
m6A
Type:
writer
reader
eraser
F
Overall Survival
CancerCode
pvalue
Hazard Ratio(95%CI)
TCGA-GBMLGG(N=619) 3.4e-33 1.24(1.20,1.29)
TCGA-LGG(N=474) 8.9e-7 1.23(1.13,1.34)
TCGA-KIPAN(N=855) 2.3e-6 1.14(1.08,1.21)
TCGA-LUAD(N=490) 8.7e-5 1.08(1.04,1.12)
TCGA-ACC(N=77) 1.6e-4 1.20(1.09,1.32)
TCGA-KICH(N=64) 5.3e-4 3.11(1.79,5.40)
TCGA-PAAD(N=172) 7.6e-4 1.13(1.05,1.21)
TCGA-MESO(N=84) 7.7e-4 1.14(1.06,1.24)
TCGA-THCA(N=501) 1.4e-3 1.26(1.09,1.47)
TCGA-SKCM-P(N=97) 4.0e-3 1.21(1.06,1.38)
TCGA-STAD(N=372) 8.5e-3 1.06(1.01,1.10)
TCGA-KIRC(N=515) 0.01 1.08(1.02,1.15)
TCGA-STES(N=547) 0.02 1.04(1.01,1.08)
TCGA-LAML(N=144) 0.04 1.14(1.00,1.29)
TCGA-BRCA(N=1044) 0.05 1.06(1.00,1.13)
TCGA-UVM(N=74) 0.05 1.17(1.00,1.36)
log2(Hazard Ratio(95%CI))
G
Progression Free Survival
CancerCode
pvalue
Hazard Ratio(95%CI)
TCGA-GBMLGG(N=616) 2.2e-20 1.18(1.13,1.22)
TCGA-STES(N=548) 9.3e-5 1.07(1.03,1.11)
TCGA-UVM(N=73) 3.5e-4 1.29(1.11,1.49)
TCGA-STAD(N=375) 4.3e-4 1.08(1.03,1.13)
TCGA-KIPAN(N=845) 5.4e-4 1.10(1.04,1.16)
TCGA-ACC(N=76) 8.6e-4 1.16(1.06,1.26)
TCGA-PAAD(N=171) 2.4e-3 1.11(1.04,1.18)
TCGA-BLCA(N=397) 5.9e-3 1.05(1.01,1.09)
TCGA-LGG(N=472) 8.4e-3 1.11(1.03,1.20)
TCGA-BRCA(N=1043) 0.01 1.08(1.02,1.15)
TCGA-LUAD(N=486) 0.02 1.04(1.01,1.08)
TCGA-MESO(N=82) 0.02 1.10(1.02,1.20)
TCGA-KICH(N=64) 0.02 1.70(1.13,2.56)
TCGA-CESC(N=273) 0.04 1.07(1.00,1.14)
log2(Hazard Ratio(95%CI))
H
DAPI
PHGDH
Merge
Responder
Non-responder
IGF2BP1
TCF7L2