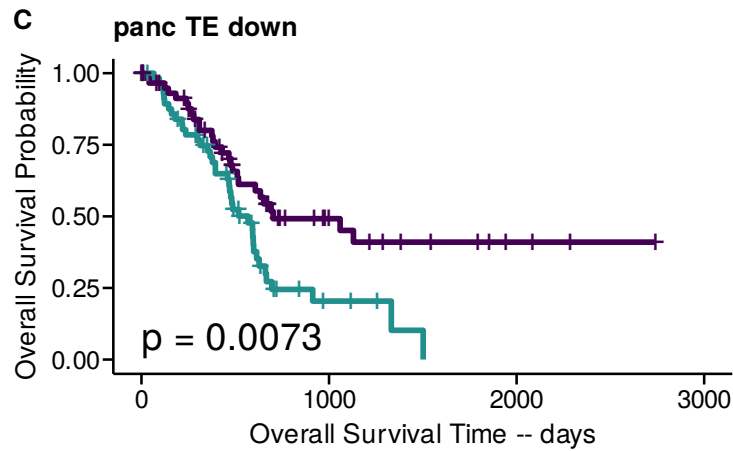


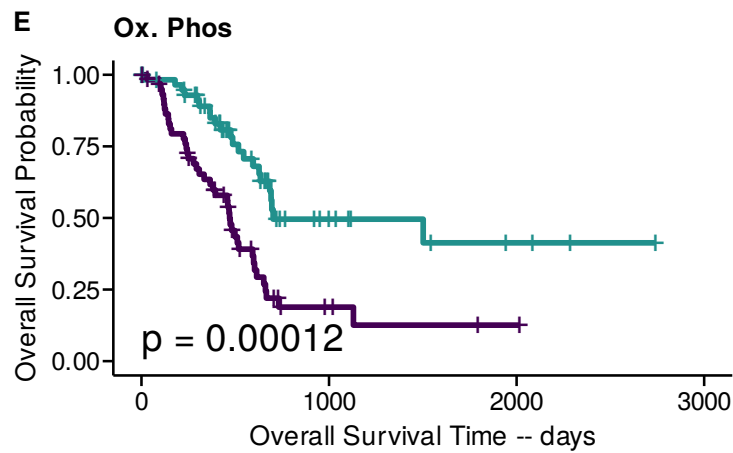
**B**

gene	baseMean	log2FoldChange	padj
FABP4	106.54128	2.1034740	0.0001776200
ERG	31.83506	1.9271951	0.0007709475
PSMA4	57.69876	1.5442380	0.0013074177
VIM	157.51316	0.9644253	0.0014370321
PRDX1	41.73367	1.3592749	0.0021591363
TOMM22	20.95705	1.4777595	0.0023310662
GDI2	62.64346	1.2257128	0.0024882770
ATP5F1C	58.37683	1.1040535	0.0028969289
LDHA	149.01895	1.3690875	0.0034140621
EIF4A1	38.81587	1.3476925	0.0035775090



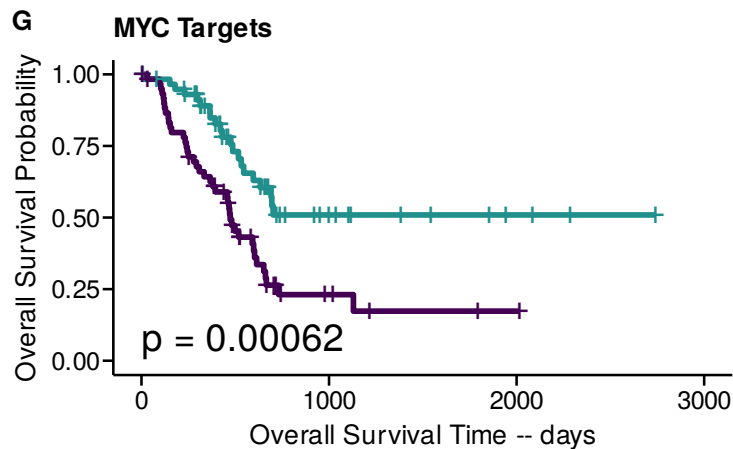
**D**

gene	baseMean	log2FoldChange	padj
tRNA-Leu-TTA(m)	4223.19250	-8.012879	3.453306e-09
LTR12D	68.29436	-2.597167	5.840136e-05
MER11B	119.27491	-2.410952	2.488277e-03
LSU-rRNA_Hsa	1322.39275	-1.582830	4.942226e-03
Ricksha_c	145.45955	-2.606646	7.889564e-03
LTR12C	192.26249	-1.602142	1.403354e-02
MLT2A2	41.21840	-1.446672	3.123549e-02
MLT1J2	26.52759	-1.397311	3.420151e-02



**F**

gene	baseMean	log2FoldChange	padj
TOMM22	20.95705	1.4777595	0.002331066
ATP5F1C	58.37683	1.1040535	0.002896929
LDHA	149.01895	1.3690875	0.003414062
SLC25A3	96.36592	0.7688971	0.012898831
ATP5PB	97.40330	0.8377167	0.013462613
ACAA2	24.03469	0.9882870	0.021725984
MDH1	33.22993	0.7525787	0.029464365
UQCRCFS1	39.94807	0.8495154	0.038581319



**H**

gene	baseMean	log2FoldChange	padj
PSMA4	57.69876	1.5442380	0.001307418
LDHA	149.01895	1.3690875	0.003414062
EIF4A1	38.81587	1.3476925	0.003577509
PSMA6	113.83012	1.0497443	0.011548304
SLC25A3	96.36592	0.7688971	0.012898831
COPS5	23.64079	0.9856271	0.029752217
PTGES3	43.46210	0.8993616	0.035691074
CNBP	136.51636	0.7536330	0.047257620