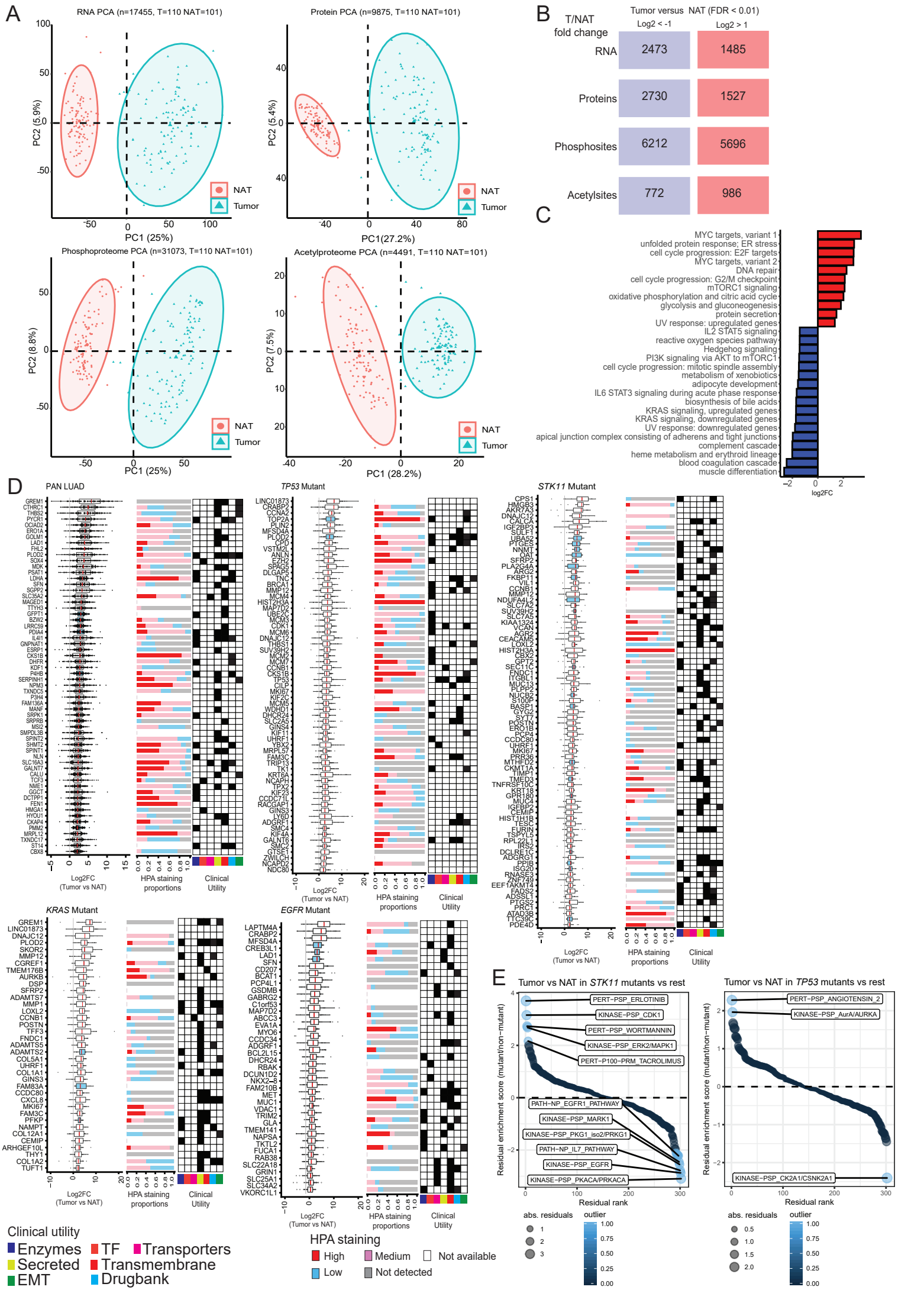
Figure S7


A
RNA PCA (n=17455, T=110 NAT=101)
Protein PCA (n=9875, T=110 NAT=101)
Phosphoproteome PCA (n=31073, T=110 NAT=101)
Acetylproteome PCA (n=4491, T=110 NAT=101)
PC1 (25%)
PC2 (5.9%)
PC1(27.2%)
PC2 (5.4%)
PC2 (8.8%)
PC1 (28.2%)
PC2 (7.5%)
NAT
Tumor
B
T/NAT fold change
Tumor versus NAT (FDR < 0.01)
Log2 < -1
Log2 > 1
RNA 2473 1485
Proteins 2730 1527
Phosphosites 6212 5696
Acetylsites 772 986
C
MYC targets, variant 1
unfolded protein response; ER stress
cell cycle progression: E2F targets
MYC targets, variant 2
DNA repair
cell cycle progression: G2/M checkpoint
mTORC1 signaling
oxidative phosphorylation and citric acid cycle
glycolysis and gluconeogenesis
protein secretion
UV response: upregulated genes
IL2 STAT5 signaling
reactive oxygen species pathway
Hedgehog signaling
PI3K signaling via AKT to mTORC1
cell cycle progression: mitotic spindle assembly
metabolism of xenobiotics
adipocyte development
IL6 STAT3 signaling during acute phase response
biosynthesis of bile acids
KRAS signaling, upregulated genes
KRAS signaling, downregulated genes
UV response: downregulated genes
apical junction complex consisting of adherens and tight junctions
complement cascade
heme metabolism and erythroid lineage
blood coagulation cascade
muscle differentiation
log2FC
D
PAN LUAD
TP53 Mutant
STK11 Mutant
KRAS Mutant
EGFR Mutant
Log2FC (Tumor vs NAT)
HPA staining proportions
Clinical Utility
E
Tumor vs NAT in STK11 mutants vs rest
Tumor vs NAT in TP53 mutants vs rest
Residual enrichment score (mutant/non−mutant)
Residual rank
PERT−PSP_ERLOTINIB
KINASE−PSP_CDK1
PERT−PSP_WORTMANNIN
KINASE−PSP_ERK2/MAPK1
PERT−P100−PRM_TACROLIMUS
PATH−NP_EGFR1_PATHWAY
KINASE−PSP_MARK1
KINASE−PSP_PKG1_iso2/PRKG1
PATH−NP_IL7_PATHWAY
KINASE−PSP_EGFR
KINASE−PSP_PKACA/PRKACA
PERT−PSP_ANGIOTENSIN_2
KINASE−PSP_AurA/AURKA
KINASE−PSP_CK2A1/CSNK2A1
abs. residuals
outlier
Clinical utility
Enzymes
TF
Transporters
Secreted
Transmembrane
EMT
Drugbank
HPA staining
High
Medium
Not available
Low
Not detected