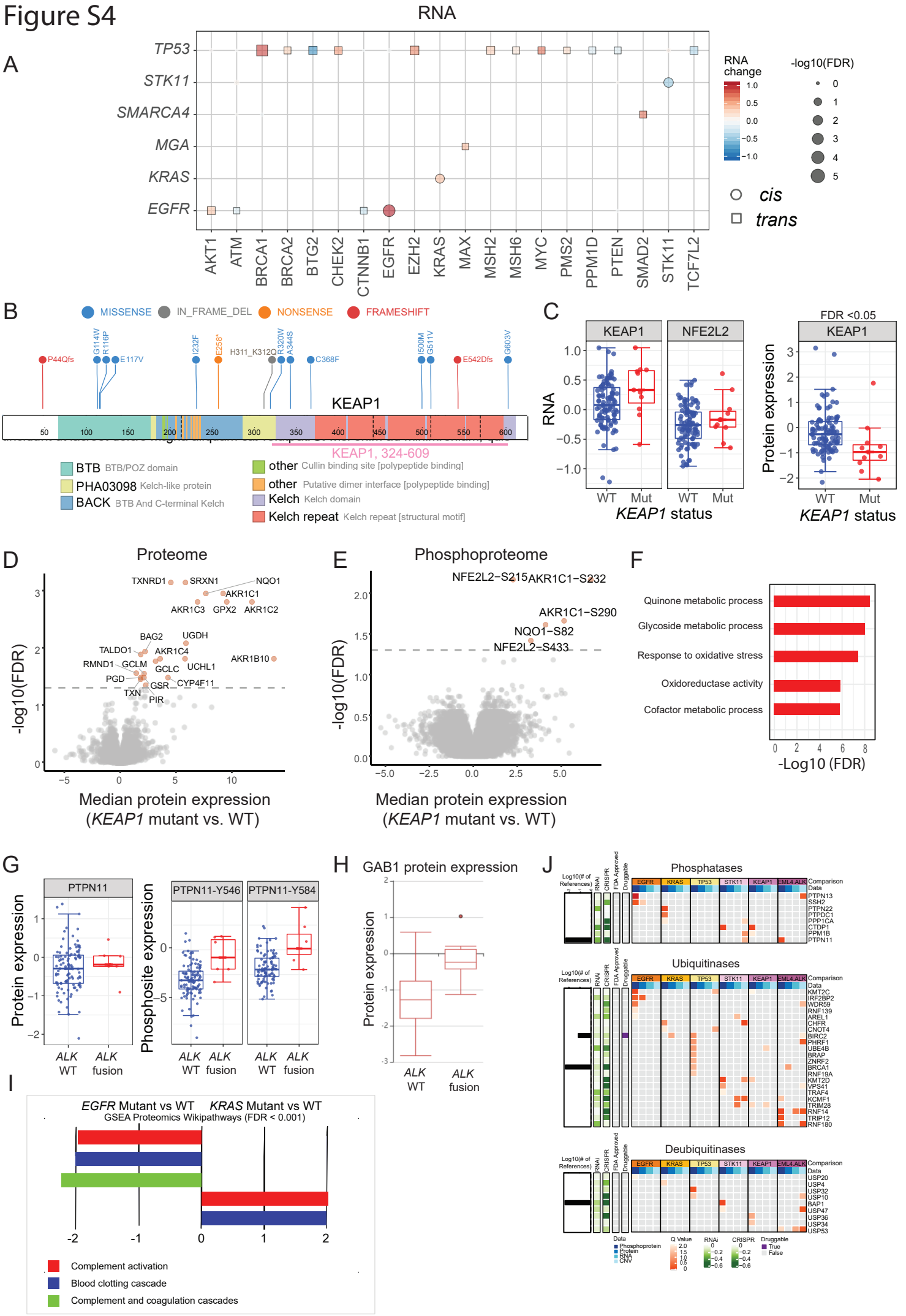
Figure S4


A
RNA
TP53
STK11
SMARCA4
MGA
KRAS
EGFR
AKT1 ATM BRCA1 BRCA2 BTG2 CHEK2 CTNNB1 EGFR EZH2 KRAS MAX MSH2 MSH6 MYC PMS2 PPM1D PTEN SMAD2 STK11 TCF7L2
RNA change
-log10(FDR)
cis
trans
B
MISSENSE IN_FRAME_DEL NONSENSE FRAMESHIFT
KEAP1
KEAP1, 324-609
BTB BTB/POZ domain
PHA03098 Kelch-like protein
BACK BTB And C-terminal Kelch
other Cullin binding site [polypeptide binding]
other Putative dimer interface [polypeptide binding]
Kelch Kelch domain
Kelch repeat Kelch repeat [structural motif]
C
KEAP1
NFE2L2
RNA
WT Mut
KEAP1 status
FDR <0.05
Protein expression
D
Proteome
-log10(FDR)
Median protein expression (KEAP1 mutant vs. WT)
E
Phosphoproteome
NFE2L2−S215
AKR1C1−S232
AKR1C1−S290
NQO1−S82
NFE2L2−S433
F
Quinone metabolic process
Glycoside metabolic process
Response to oxidative stress
Oxidoreductase activity
Cofactor metabolic process
-Log10 (FDR)
G
PTPN11
PTPN11-Y546
PTPN11-Y584
Protein expression
Phosphosite expression
ALK WT ALK fusion
H
GAB1 protein expression
J
Phosphatases
Ubiquitinases
Deubiquitinases
I
EGFR Mutant vs WT
KRAS Mutant vs WT
GSEA Proteomics Wikipathways (FDR < 0.001)
Complement activation
Blood clotting cascade
Complement and coagulation cascades