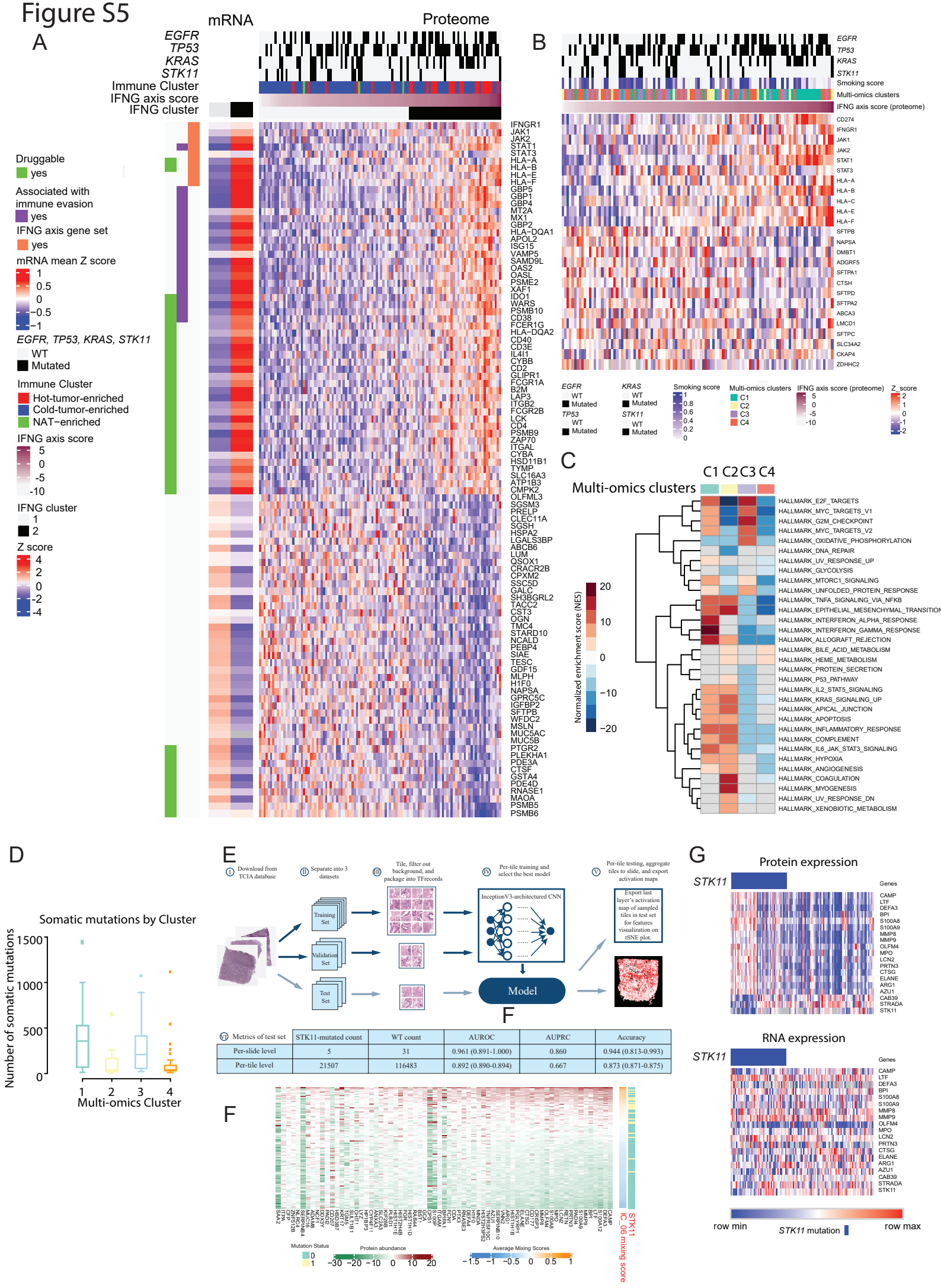
# Figure S5


A
mRNA
Proteome
EGFR
TP53
KRAS
STK11
Immune Cluster
IFNG axis score
IFNG cluster
Druggable
yes
Associated with immune evasion
yes
IFNG axis gene set
yes
mRNA mean Z score
EGFR, TP53, KRAS, STK11
WT
Mutated
Immune Cluster
Hot-tumor-enriched
Cold-tumor-enriched
NAT-enriched
IFNG axis score
IFNG cluster
Z score
B
Smoking score
Multi-omics clusters
IFNG axis score (proteome)
Z_score
C
C1 C2 C3 C4
Multi-omics clusters
Normalized enrichment score (NES)
D
Somatic mutations by Cluster
Number of somatic mutations
Multi-omics Cluster
E
Download from TCIA database
Separate into 3 datasets
Tile, filter out background, and package into TFrecords
Per-tile training and select the best model
Per-tile testing, aggregate tiles to slide, and export activation maps
Training Set
Validation Set
Test Set
InceptionV3-architectured CNN
Model
Export last layer's activation map of sampled tiles in test set for features visualization on tSNE plot.
F
Metrics of test set
STK11-mutated count
WT count
AUROC
AUPRC
Accuracy
Per-slide level
5
31
0.961 (0.891-1.000)
0.860
0.944 (0.813-0.993)
Per-tile level
21507
116483
0.892 (0.890-0.894)
0.667
0.873 (0.871-0.875)
F
Mutation Status
Protein abundance
Average Mixing Scores
STK11 IC_06 mixing score
G
Protein expression
STK11
Genes
RNA expression
STK11
Genes
row min
STK11 mutation
row max