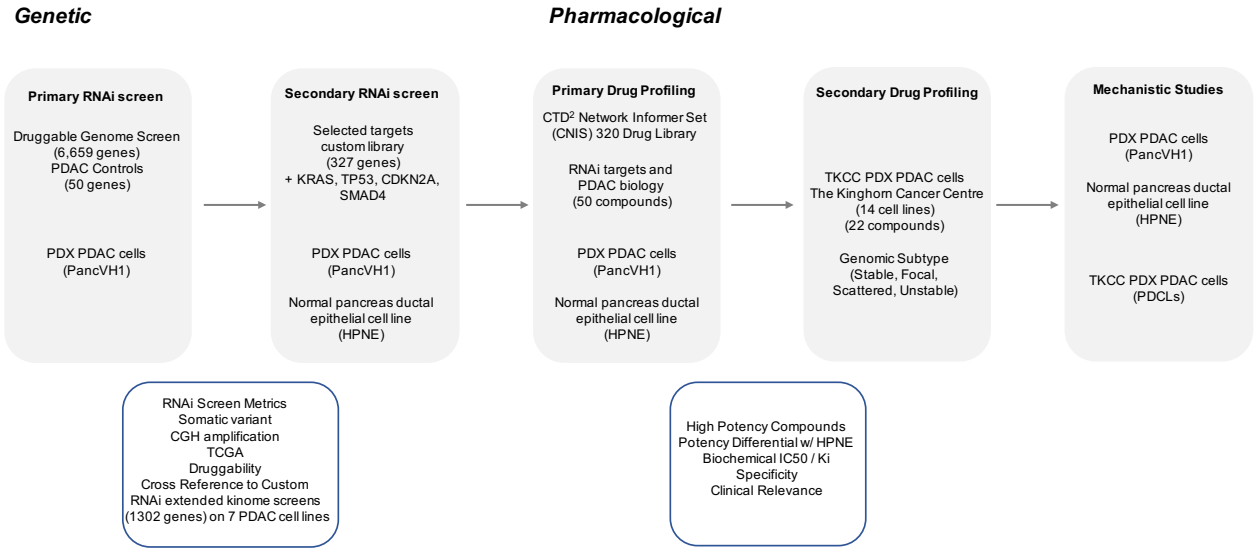
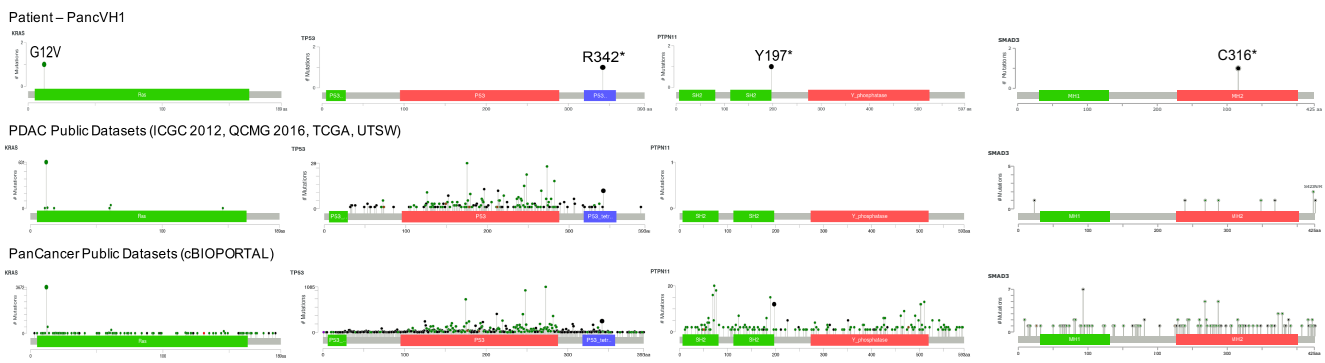
A



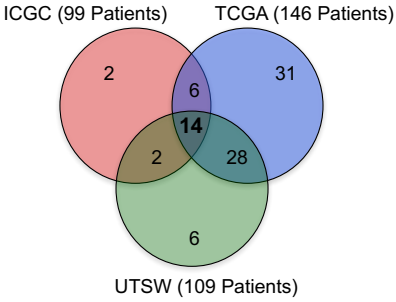
B



C

Variant Type	Number of Variants	Percentage
Missense and Nonsense	117	26.9
Coding Synonymous	48	11
Intronic	182	41.8
Intergenic	63	14.5
5' and 3' UTRs	19	4.4
Indels (CCDS)	9	2.1
Total	438	100

D



Gene	ICGC (%)	TCGA (%)	UTSW (%)
KRAS	95	84	92
TP53	33	68	50
MUC16	5	11	16
RYR1	1	8	2
RYR2	2	6	5
FN1	1	4	2
CSMD1	5	3	6
MUC4	2	3	6
MYO7B	1	2	2
DOPEY1	1	1	1
EML5	1	1	2
KLHL5	1	1	1
NTRK3	1	1	2
RNF145	1	1	1

Figure S1. Extended Data. A. Schematic overview of functional genetic and pharmacological profiling performed in this study; blue outline boxes list criteria utilized to select targets and drugs for secondary screening efforts. **B**. cBioportal mutation mapper of driver mutations in PancVH1 whole exome sequencing (WES) results. **C**. WES variant type and prevalence. **D**. WES gene level shared variants in public datasets ICGC, TCGA, UTSW in cBioPortal.