

File Name: Supplementary Data 1

Description: Genes with significant (adjusted $p < 0.05$) differences in copy amplification frequency between KRAS wildtype versus mutant tumors in the PanGen discovery cohort of unresectable PDAC. P values are based on two-tailed Fisher's exact tests and adjusted p values were subjected to Benjamini-Hochberg multiple test correction.

File Name: Supplementary Data 2

Description: Genes differentially expressed (adjusted $p < 0.05$) in KRAS wildtype versus mutant tumors in the PanGen cohort of unresectable PDAC. P values based on two-tailed Wald tests, and adjusted p values were subjected to Benjamini-Hochberg multiple test correction.

File Name: Supplementary Data 3

Description: Genes conservatively differentially expressed (adjusted $p < 0.005$, absolute $\log_2$ fold change > 2.5) in KRAS wildtype versus mutant tumors in the PanGen cohort of unresectable PDAC. P values based on two-tailed Wald tests, and adjusted p values were subjected to Benjamini-Hochberg multiple test correction.

File Name: Supplementary Data 4

Description: Genes sets enriched among genes up-regulated (adjusted $p < 0.005$, $\log_2$ fold change > 2.5) in KRAS wildtype versus mutant tumors in the PanGen cohort of unresectable PDAC. P values based on one-tailed hypergeometric tests, and adjusted p values were subjected to Benjamini-Hochberg multiple test correction.

File Name: Supplementary Data 5

Description: Genes sets enriched among genes down-regulated (adjusted $p < 0.005$, $\log_2$ fold change < -2.5) in KRAS wildtype versus mutant tumors in the PanGen cohort of unresectable PDAC. P values based on one-tailed hypergeometric tests, and adjusted p values were subjected to Benjamini-Hochberg multiple test correction.

File Name: Supplementary Data 6

Description: Proteins with unadjusted $p < 0.01$ from results of differential protein analysis (KRAS wildtype versus mutant) in the PanGen cohort of unresectable PDAC. P values based on two-tailed loess regression, and adjusted p values were subjected to Benjamini-Hochberg multiple test correction.

File Name: Supplementary Data 7

Description: Normalized protein expression values for PROX1 and VTCN1 across the PanGen cohort of mPDAC (n=46). Values represent protein relative abundance levels on a log2 scale.