



Figure S2. Extended Data. A. MISSION Sigma Druggable Genome RNAi Library. B. Druggable Genome RNAi Screen results displayed as percent viability (n=3 per data point, mean of three technical replicates (pooled siRNAs with 3 independent siRNAs per target) vs. whole library index (6659 genes) with hits and selection criteria depicted. C. Breakdown of Druggable Genome RNAi metrics criteria utilized for selection of targets. D. PDAC cell lines (JHU) RNAi Extended Kinome Screens mean gene target rank differentials (298 gene targets including KRAS) with HPNE cells utilized for hit selection; top differential gene target: CFLAR.