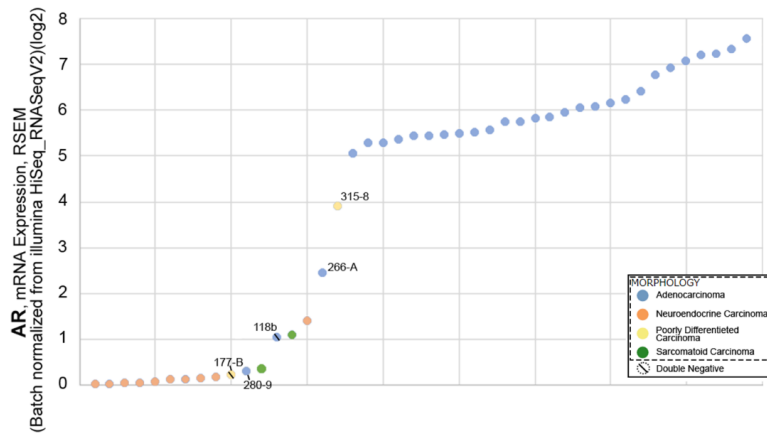


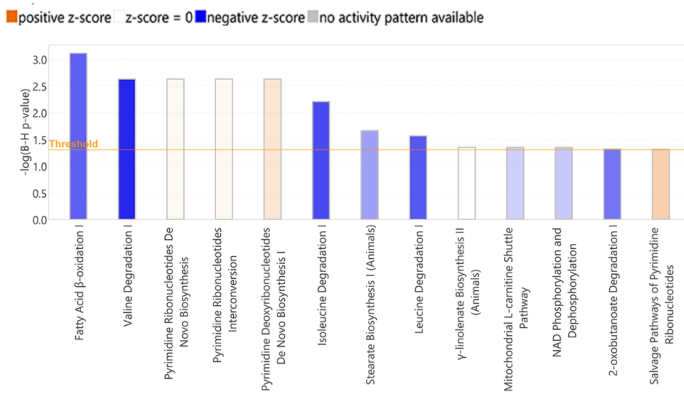
Figure S6

A



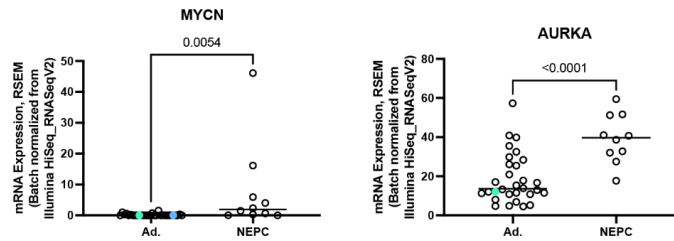
B

MDA PCa PDX



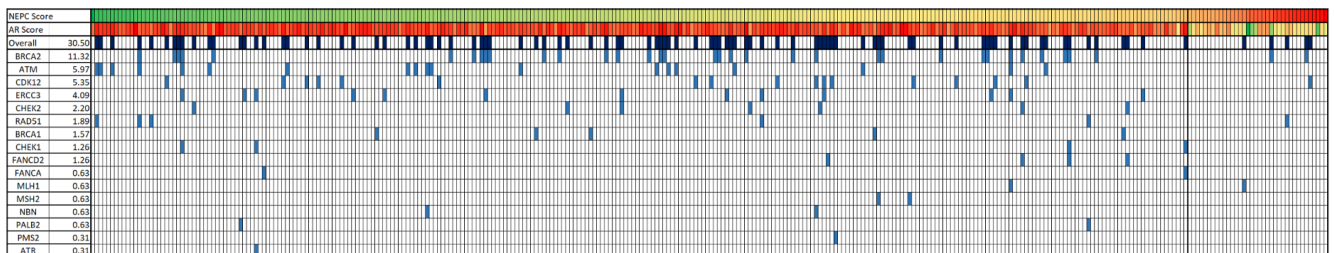
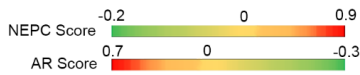
C

MDA PCa PDX



D

SU2C



**Fig S6. Comparison between adenocarcinoma and neuroendocrine carcinoma. A.** Scatter plot of AR mRNA expression levels on MDA PCa PDX arranged by ascending order. **B.** Bar chart showing significant “metabolic pathways” identified from Ingenuity Pathway Analysis (IPA) based on differential expressed genes (NEPC/Ad). The orange and blue-colored bars indicate predicted pathway activation ( $z\text{-score} \geq 2$ ) or inhibition ( $z\text{-score} \leq -2$ ). For gray bars, no activity prediction can currently be made. White bars indicate pathways with  $z\text{-scores}$  at or very close to 0; or those that are ineligible for analysis because there are fewer than four molecules in the dataset associated with the pathway ( $z\text{-score} = \text{NaN}$ ). **C.** mRNA expression of *AURKA* and *MYCN* in Ad and NEPC in MDA PCa PDX. Green dots: driver mutation; light blue dots: deep deletion **D.** Genomic status of main DDR genes in Ad and NEPC human PCa SU2C dataset samples ranked **D.** Genomic status of main DDR genes in Ad and NEPC human PCa SU2C dataset samples ranked based on NEPC and AR score. Colored rectangles indicate presence of driver genomic alterations.