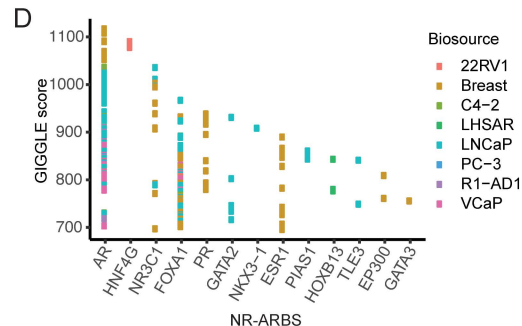
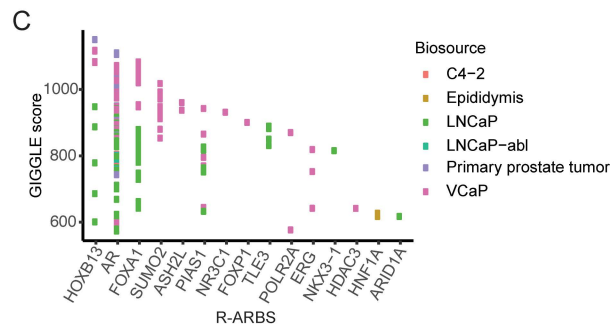
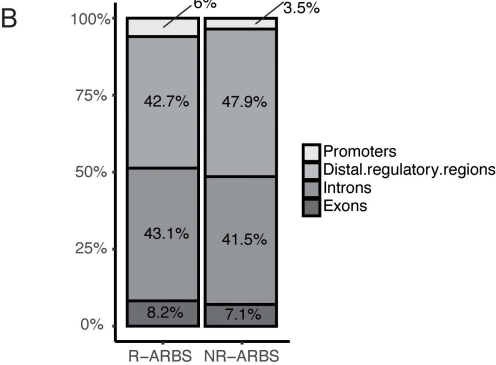
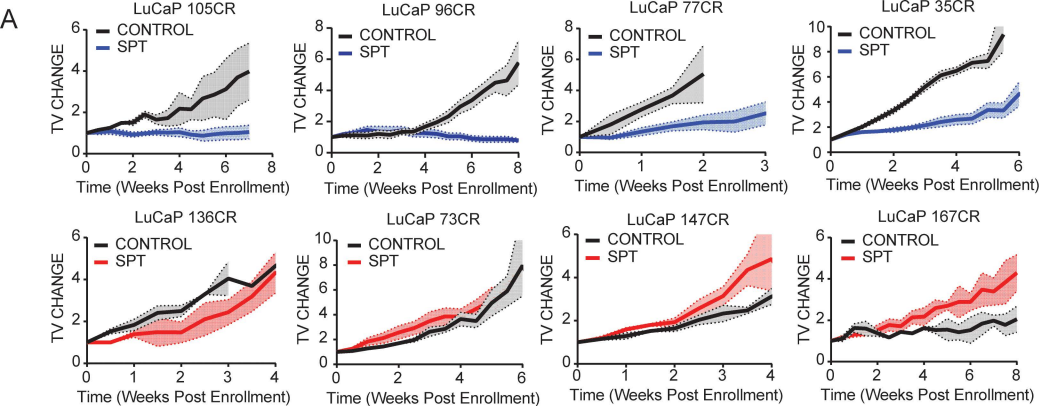


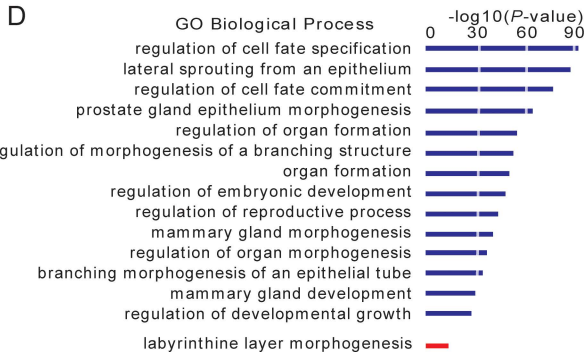
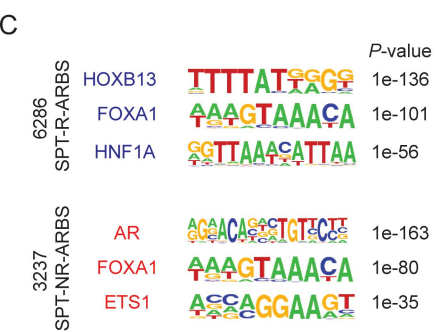
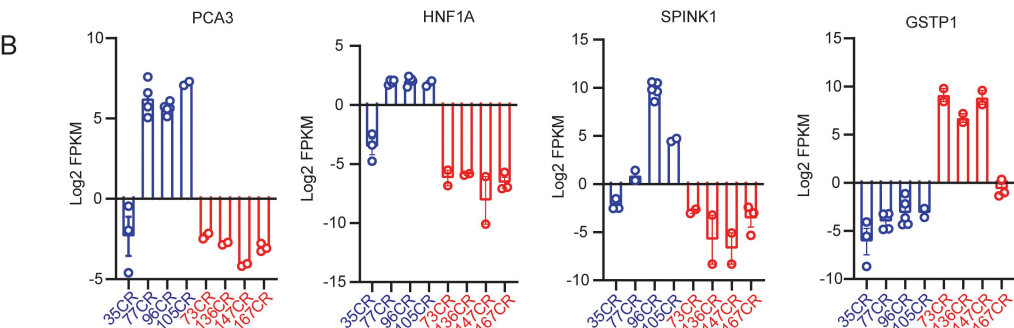
Supplemental Figure 1. (A) LuCaP PDX tumor responses to SPT treatment. (n=3-15 per group (blue: R, top; red: NR, bottom, mean \pm SEM). **(B)** Localization of AR binding sites in R and NR PDX tumors. **(C)** Results illustrating the similarity of publicly available ChIP-Seq datasets ranked by GIGGLE score to R-ARBS and **(D)** in NR-ARBS. The color indicates the biological source of the ChIP-Seq experiments.

Supplemental Figure 2. (A) Overlap between NARBS and TARBS with R-ARBS (left) and NR-ARBS (right). **(B)** Gene expression (Log₂ FPKM) of PCA3, HNF1A, SPINK1, and GSTP1 in eight PDX model. (blue: R; red: NR, n=2-4 different tumors per each PDX model, mean \pm SEM). **(C)** Significantly enriched motifs in SPT-R-ARBS (blue) and SPT-NR-ARBS (red). **(D)** GREAT analysis characterizing the GO biological processes most significantly associated with genes proximal to the SPT-R-ARBS (upper, blue) and NR-ARBS (lower, red).

Supplemental Figure 3. (A) GSEA analysis of AR-regulated genes by SPT treatment in R (blue) and NR (red) PDX tumors. **(B)** GSEA analyses of SPT effects in each of four R PDX tumors: Hallmark gene sets (top) and Reactome gene sets (bottom) red: up-regulated, blue: down-regulated. **(C)** Venn diagram of overlap between the SPT-Responder signature with Hallmark E2F, Hallmark Androgen Response, and PCa-GI signature. **(D)** Correlation of SPT-Responder

signature and Hallmark E2F (top) and Hallmark Androgen Response (bottom) in SU2C-IDT CRPC cohort (n=266). The Scatter plots show Pearson correlation, the box plots show the groups based on the median of SPT-Responder signature. **(E)** Cutpoint analysis to determine responder and non-responder patients in the discovery SU2C- IDT patient cohort.





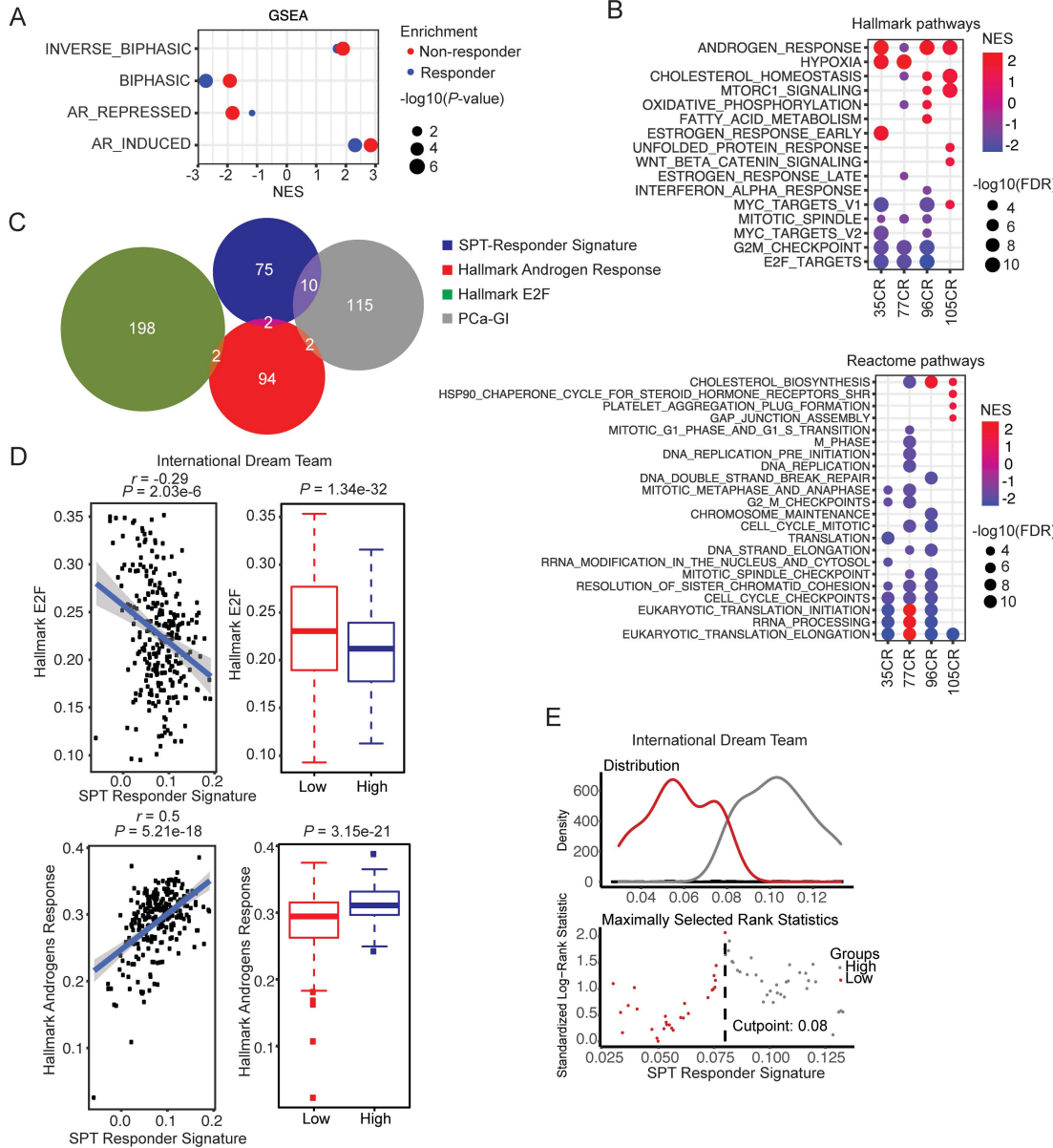


Figure S3