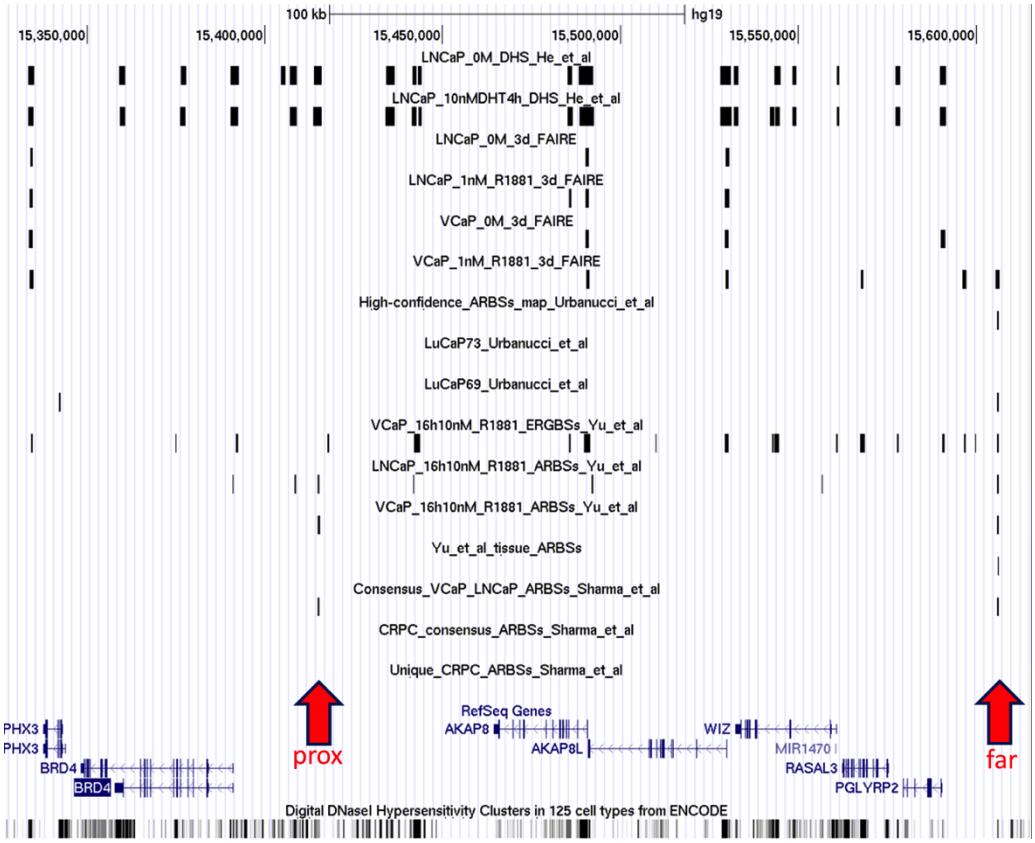
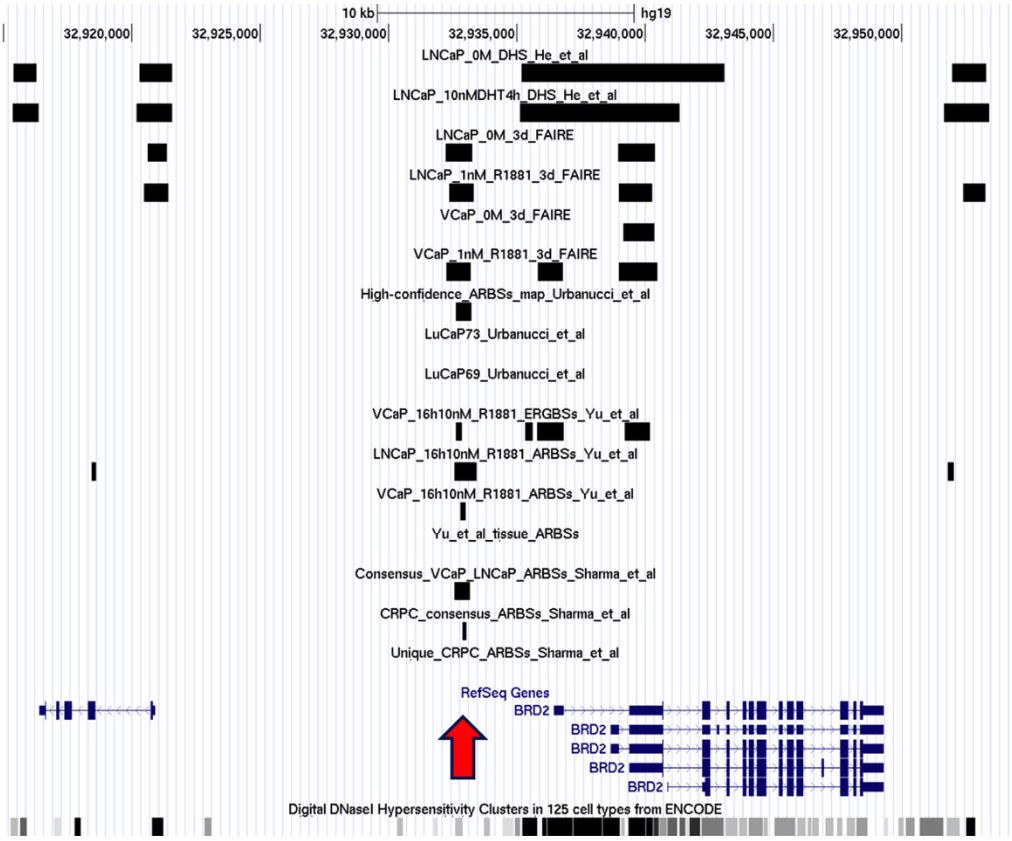
Supplemental Data File 1. Locations of androgen receptor binding sites and FAIRE-seq sites proximal to genes of interest. Relates to main Figure 3.

A



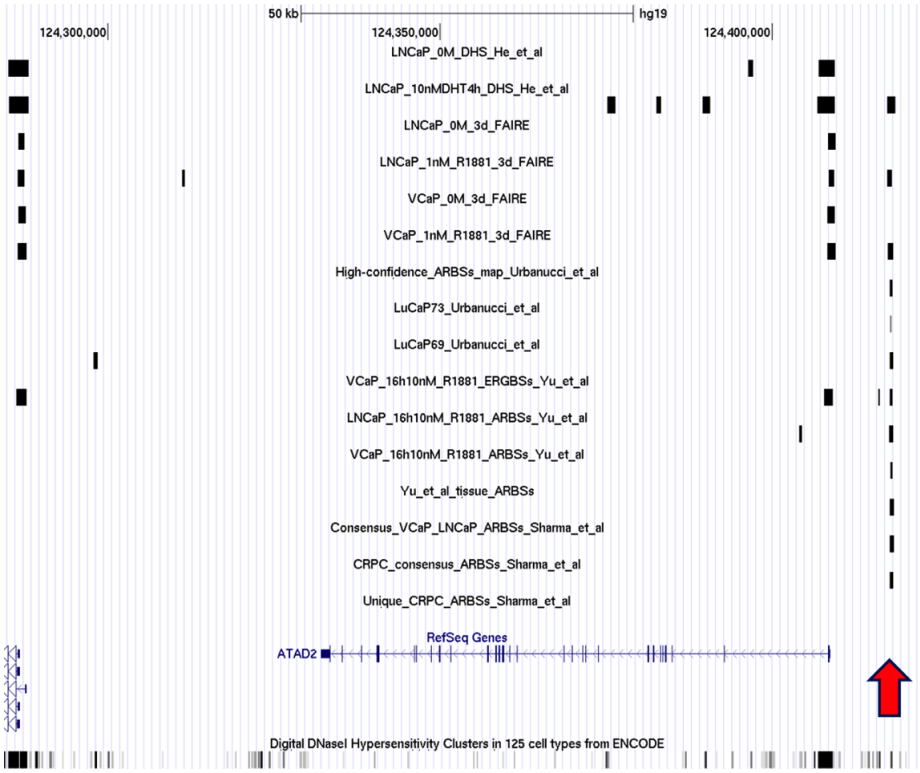
Supplemental Data File Continued

B



Supplemental Data File Continued

C



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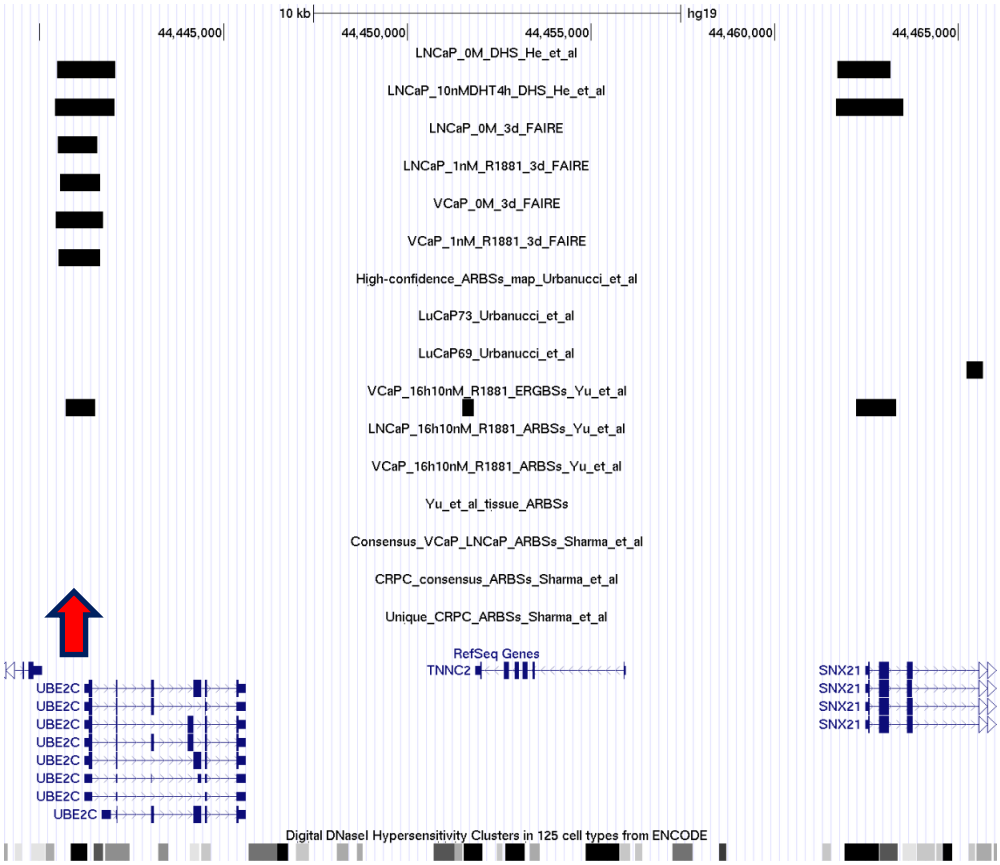
D



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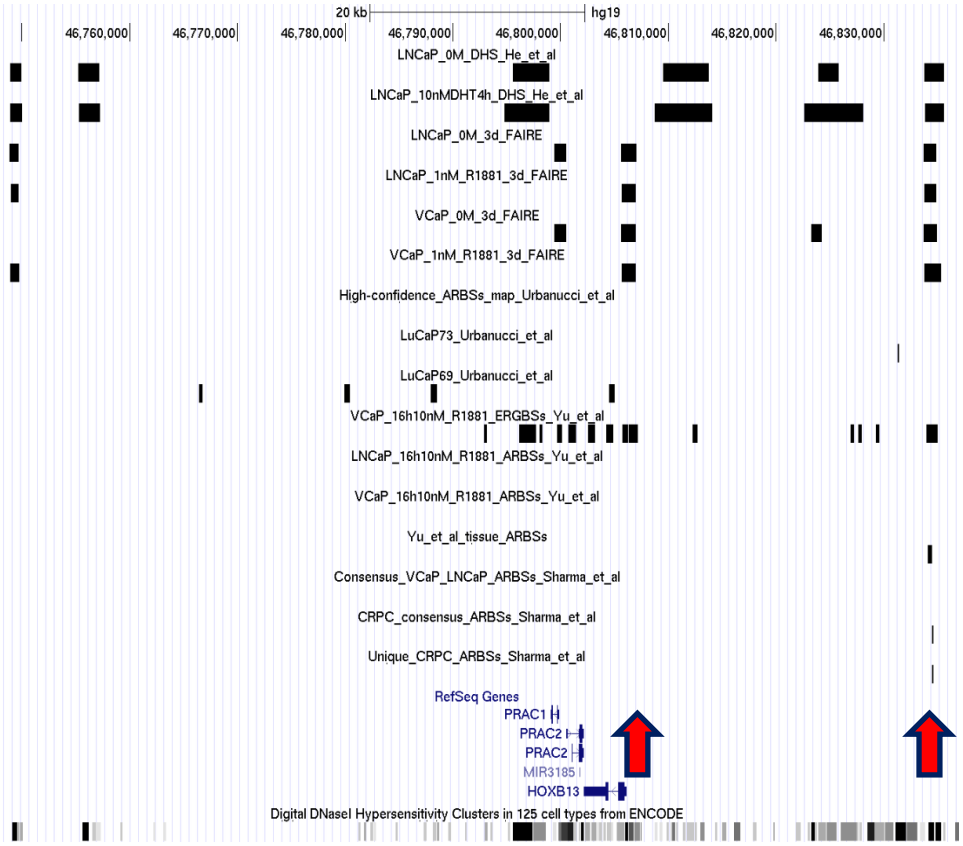
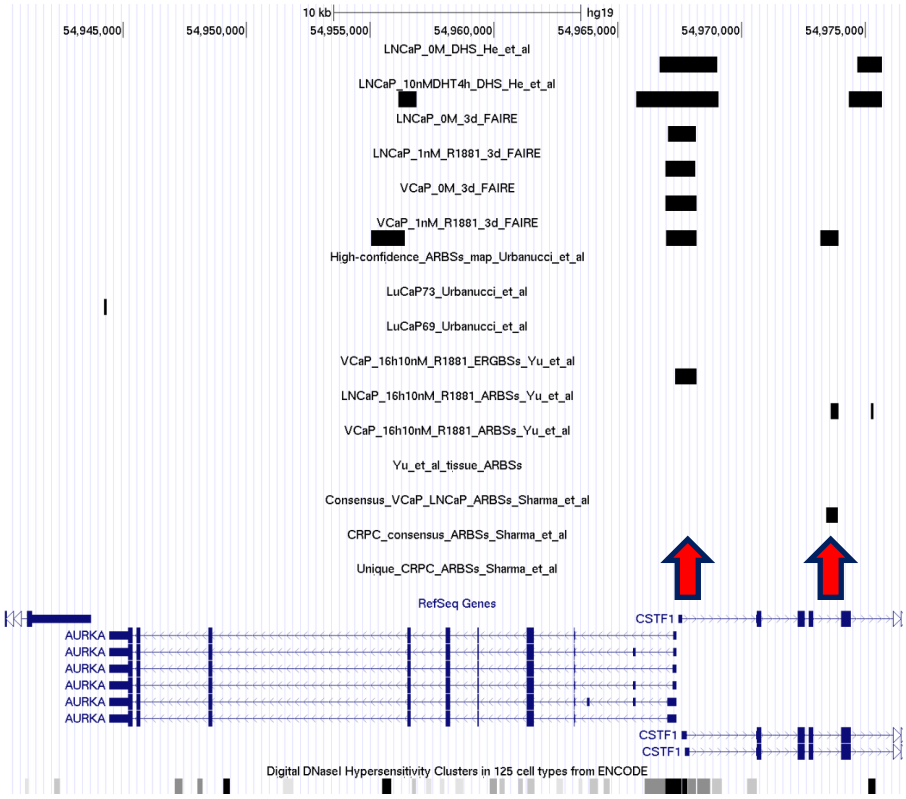
E



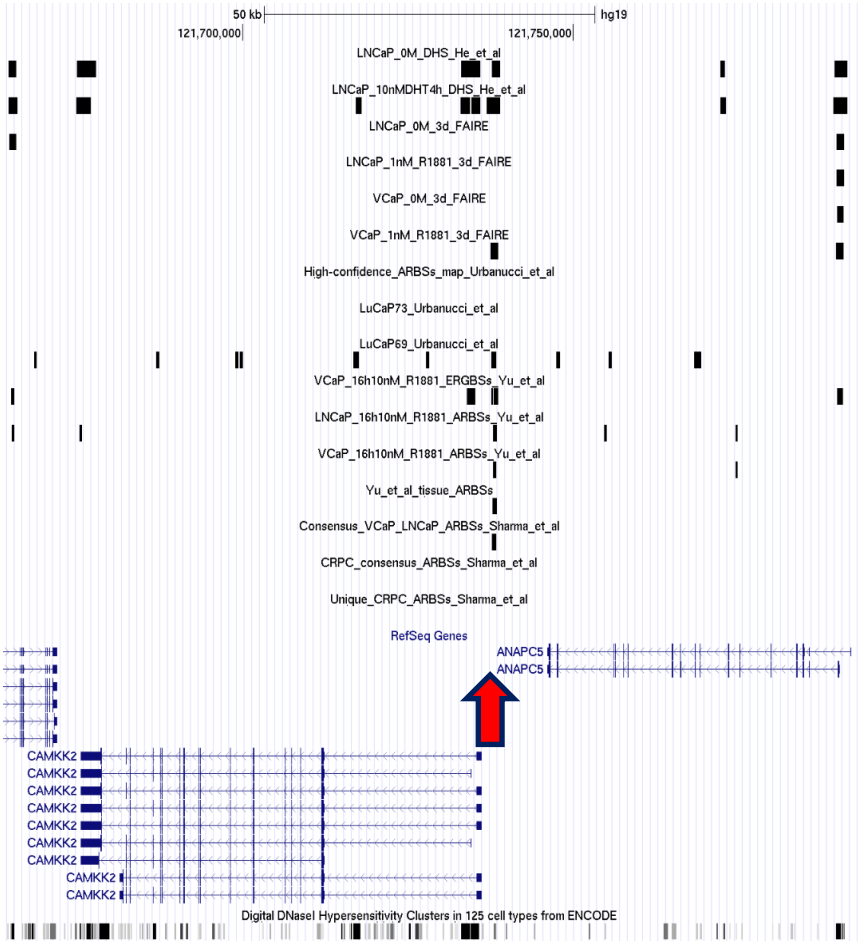
Supplemental Data File Continued

F



Supplemental Data File Continued

G



Supplemental Data File 1. Positions of proximal androgen receptor binding sites and open chromatin/FAIRE-seq sites at specific loci. Androgen receptor binding sites (ARBSs) in proximity of BRD4 (**A**), BRD2 (**B**) and ATAD2 (**C**) genes according to 3 publicly available datasets showing binding of AR in LNCaP and VCAP cells lines as well as in primary tumours (Yu et al., 2010) tissue), CRPC tumour samples (Sharma et al., 2013) CRPC), and LuCaP xenografts (Urbanucci et al., 2012)). Tracks (He et al., 2012) show DNA hypersensitive sites (DHS) in LNCaP treated as indicated, while FAIRE tracks refer to this study. Validated ARBSs by chromatin immunoprecipitation (ChIP)-qPCR analysis (in Figure 2A) are indicated by a red arrow in the respective UCSC panels. PSA mid region is a region in between PSA enhancer and promoter (as previously described(Urbanucci et al., 2011)) and serves as ARBS negative control. LNCaP and VCaP cells were hormone starved for three days and subsequently treated with 1 nM R1881 for 4 hours prior to the ChIP assay with IgG control antibody or androgen receptor (AR) antibody. ARBSs in proximity of UBE2C (**D**), HOXB13 (**E**), AURKA (**F**) and CAMKK2 (**G**) Validated FAIRE-seq sites by FAIRE-qPCR analysis are indicated by a red arrow in the respective UCSC panels.

References

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