

Supplementary Figures

Figure S1. AR-repressed genes were identified using publicly available mRNA expression microarray and AR ChIP-seq datasets. All genes were ranked based on p-values calculated by Binding and Expression Target Analysis (BETA). CXCR7 is among top 20 AR-repressed genes.

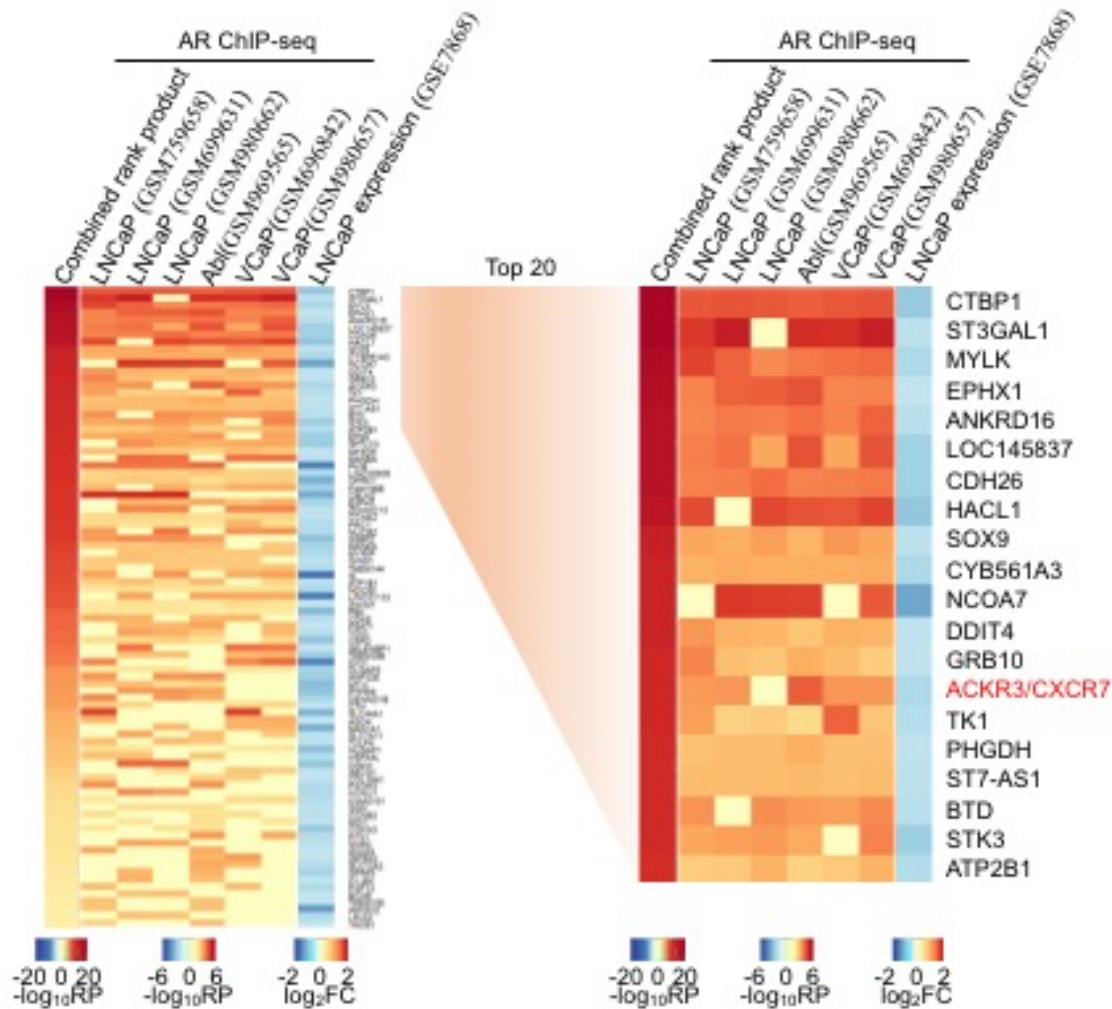


Figure S2. Gene Ontology Biological Processes (GOBP) Analysis

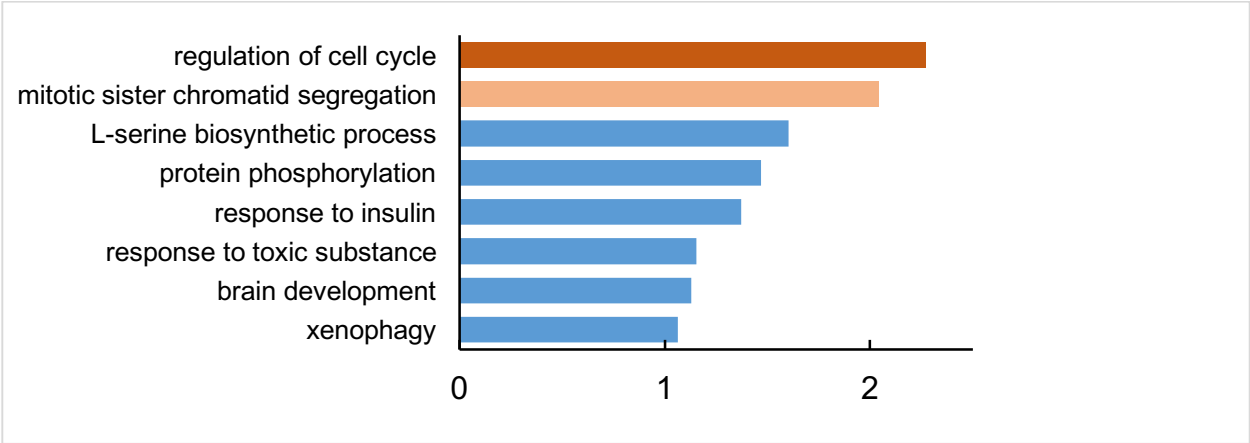


Figure S3. Gene editing efficacy at on-target and potential off-target sites of ARBS-KO C4-2B cell lines. PCR amplicons that span the on-target and potential off-target sites were subjected to sanger sequencing. Top two off-target sites (off1 and off2) of each gRNA were selected using CCToP (see Materials and Methods). A total of 4 off-target sites were analyzed for each ARBS-KO cell line. The gene editing efficacy (or mutation frequencies) was determined by TIDE (see Materials and Methods). The off-target sequences were shown on the right with highlighted mismatched in red and core sequences in square brackets.

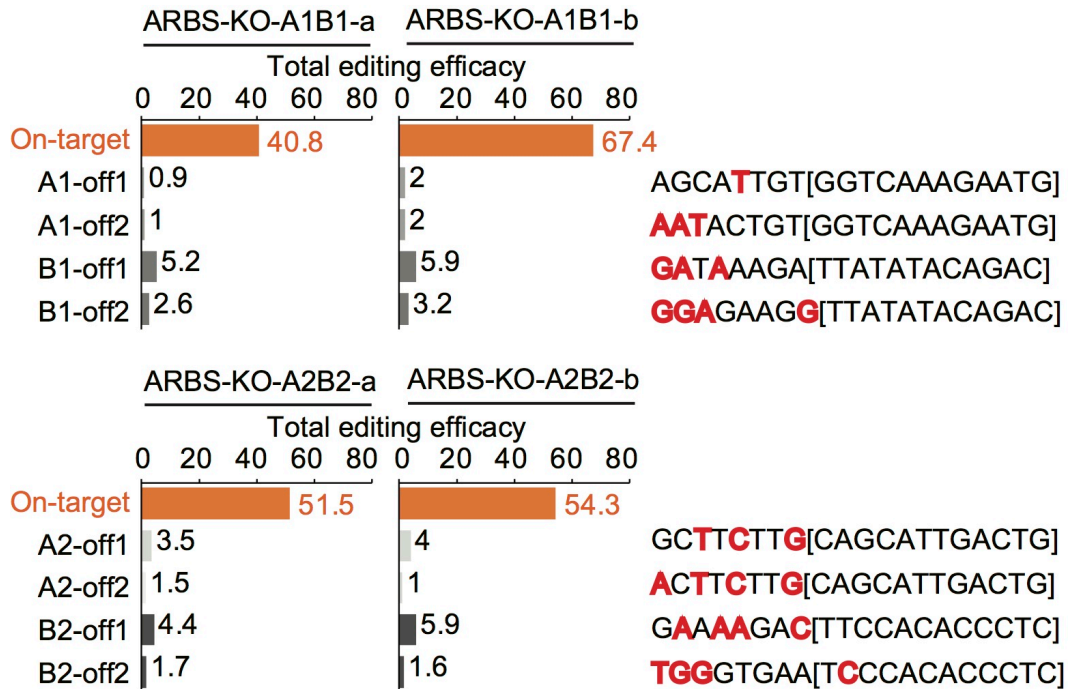


Figure S4. Gene editing efficacy at on-target and potential off-target sites of CXCR7-KO C4-2B cell lines. PCR amplicons that span the on-target and potential off-target sites were subjected to sanger sequencing. Top two off-target sites (off1 and off2) of each gRNA were selected using CCToP (see Materials and Methods). A total of 8 off-target sites were analyzed for each CXCR7-KO cell line. The gene editing efficacy (or mutation frequencies) was determined by TIDE. The off-target sequences were shown on the right with highlighted mismatched in red and core sequences in square brackets.

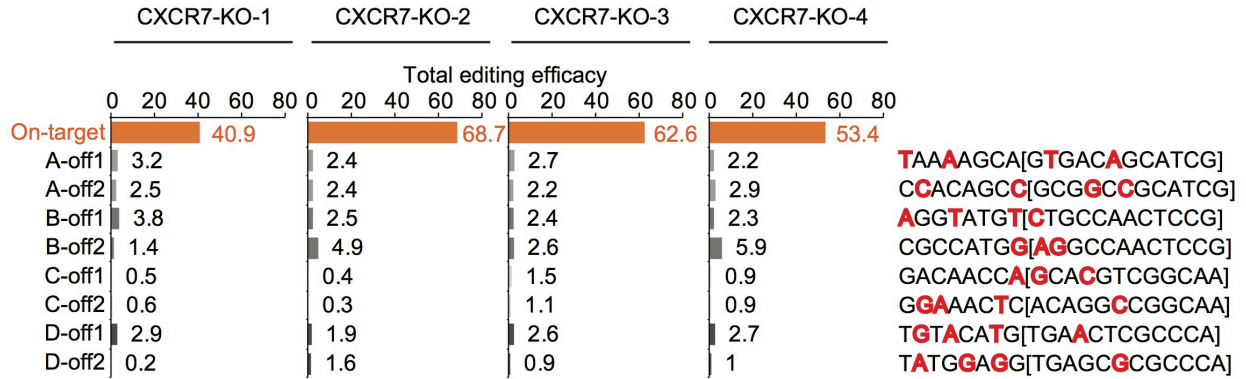


Figure S5. Images of transwell migration assays in HCT116 and C4-2B cells after treatment with AMD1300 or vehicle.

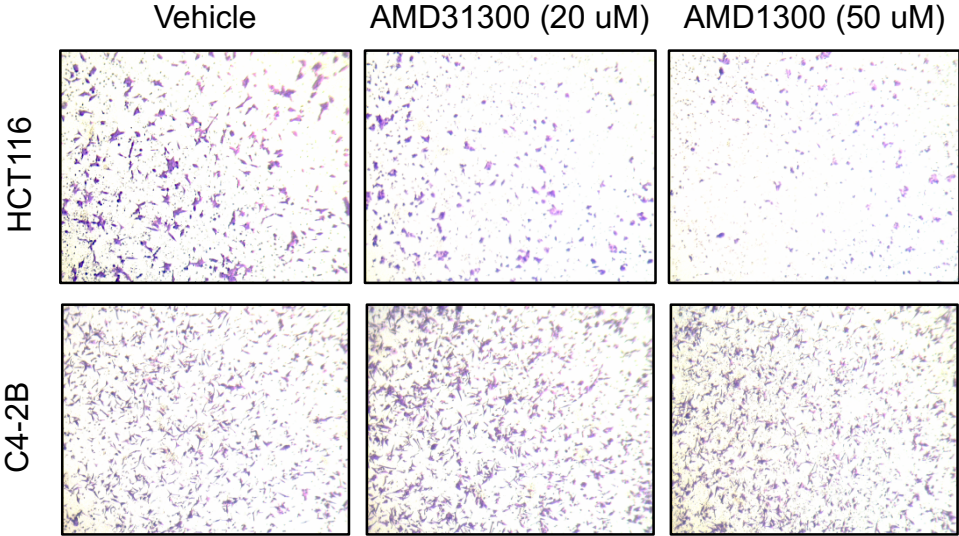
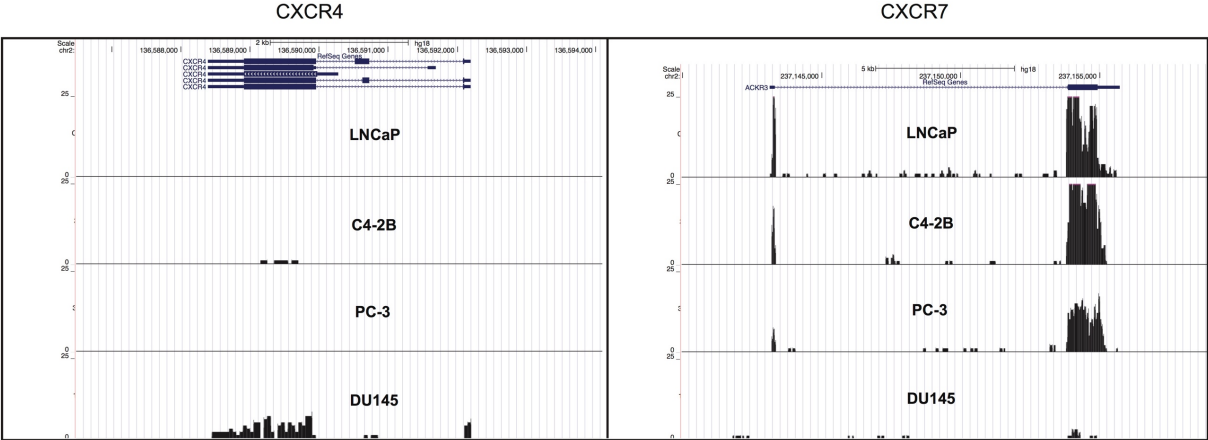


Figure S6. Genome browser view of RNA-seq at CXCR4 and CXCR7 loci from LNCaP, C4-2B, PC-3, and DU145 cells. The data is downloaded from GSE25183.



Prensner et al. Nat Biotechnol. 2011 Jul 31;29(8):742-9

Figure S7. C4-2B cells were co-cultured with mouse bone marrow stroma ST2 cells (1:1 ratio) in RPMI 1640 with 10% charcoal stripped fetal bovine serum. Cell culture supernatants were collected 48 hours after DHT (10 nM) or vehicle treatment and centrifuged at 12k rpm for 10 min at 4°C. Protein levels of 56 cytokines, chemokines, and growth factors were measured using Bio-plex magnetic beads-based assays (Bio-Rad).

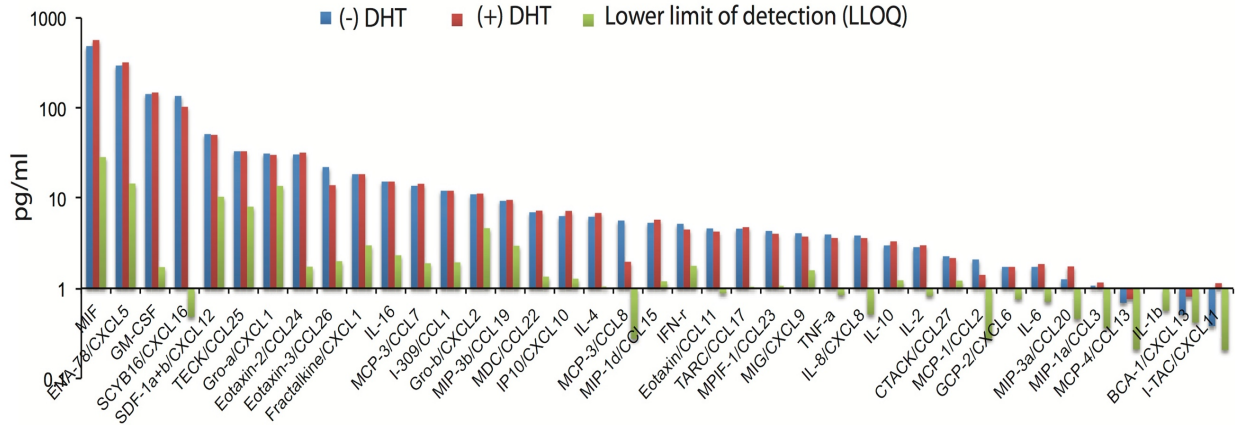


Figure S8. C4-2B cells (1×10^5 cells/well in a 6-well plate) and mouse bone marrow stroma ST2 cells (1×10^5 cells/well in a 6-well plate) were culture independently or co-cultured in RPMI 1640 with 10% fetal bovine serum. The full media were replaced with serum-free RPMI 1640 24 hours before supernatant collection. Cell culture supernatants were collected and centrifuged at 12k rpm for 10 min at 4°C. MIF protein levels were measured using human-specific (R & D Systems) and mouse-specific (Abcam) MIF ELISA kit. * $P < 0.05$.

