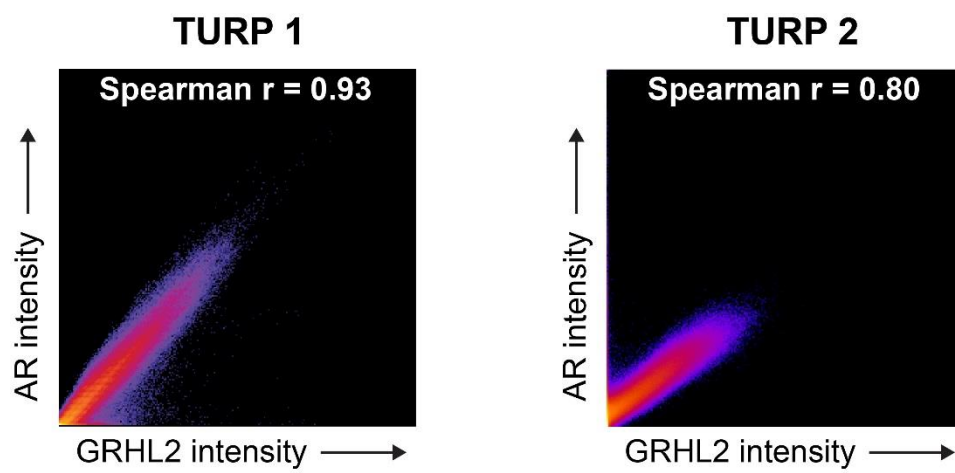
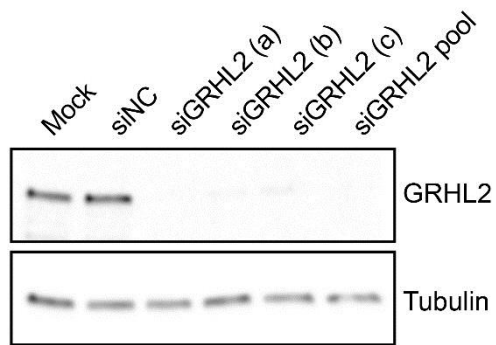


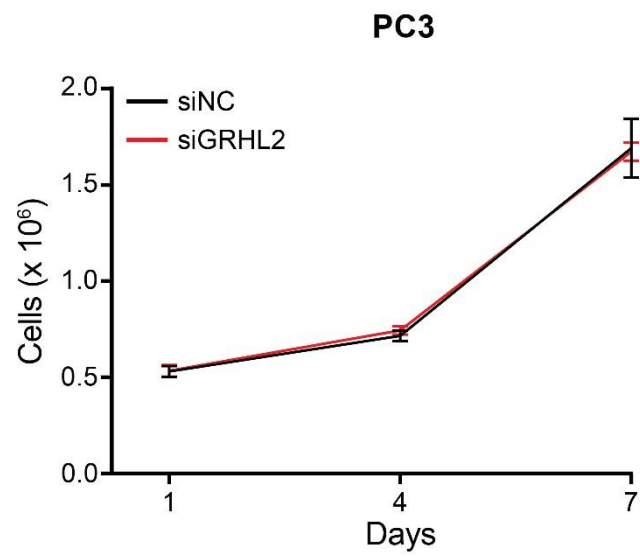
## Supplementary Figures



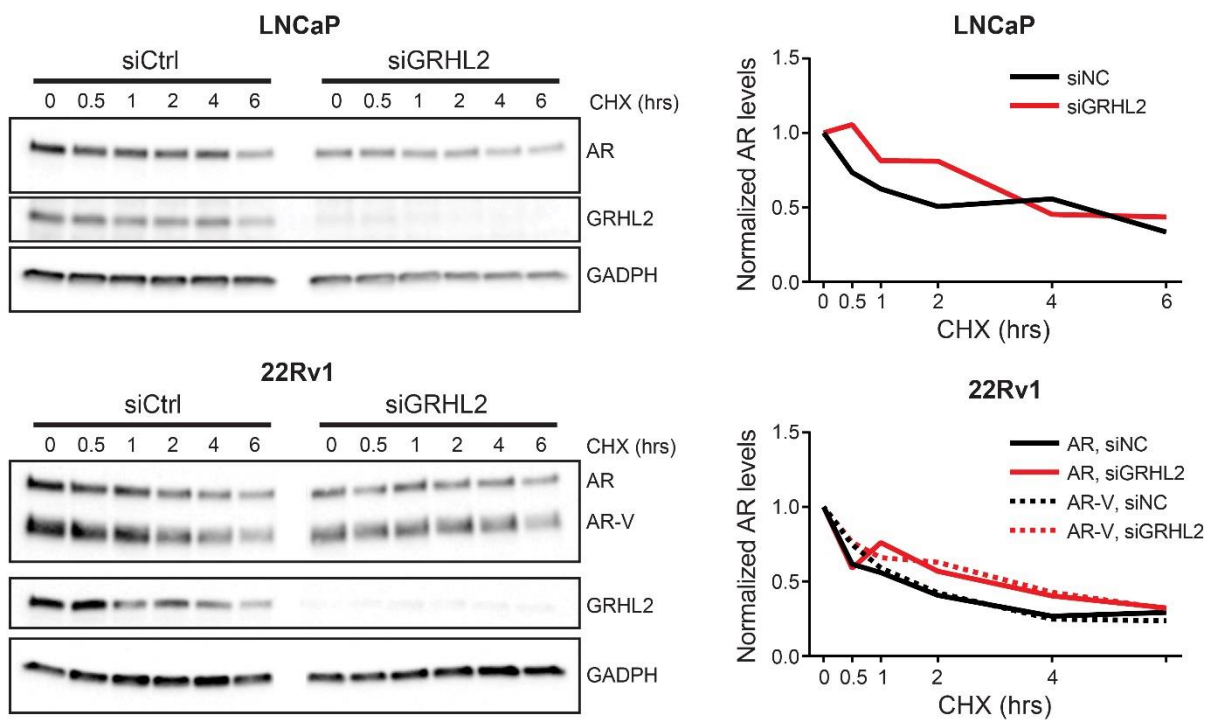
**Supplementary Figure 1.** Correlation between AR and GRHL2 immunofluorescence staining signals in two representative prostate tumors.



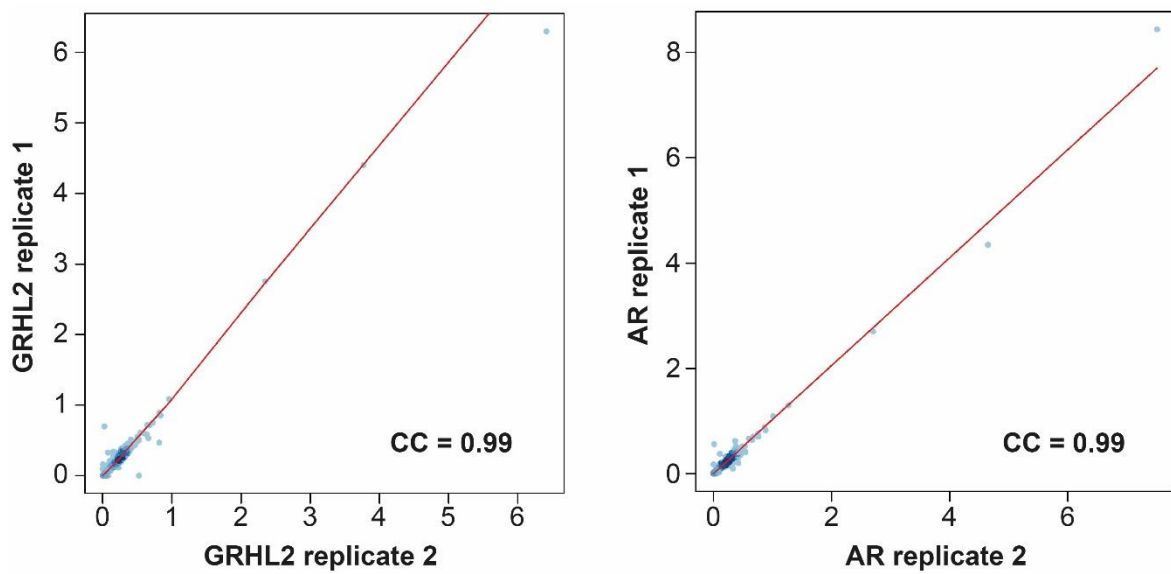
**Supplementary Figure 2.** Validation of GRHL2 knockdown by siRNA transfection. The siRNAs were obtained from Santa Cruz Biotechnology (Santa Cruz, CA): siGRHL2(a) = sc77606a, siGRHL2(b) = sc77606b and siGRHL2(c) = sc77606c. All siRNAs were used at 20nM; the pool represents 6.66nM of each siRNA. siNC = negative control siRNA.



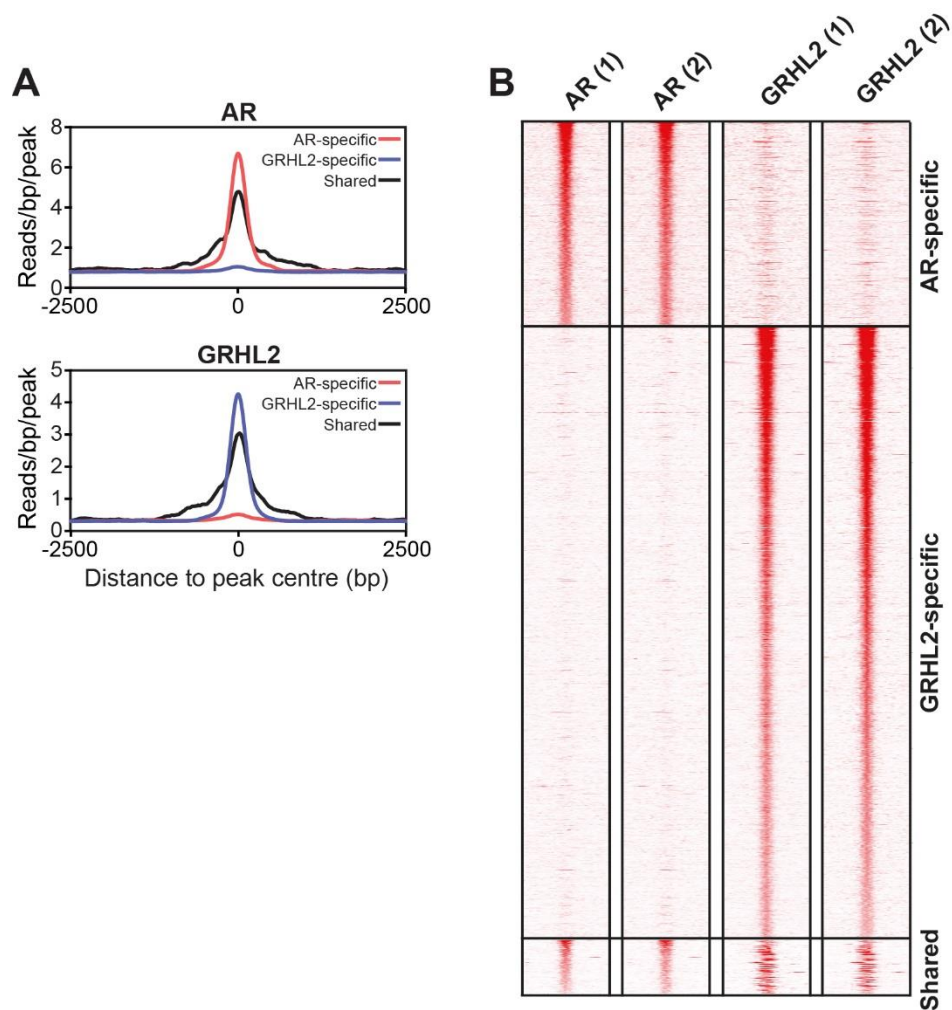
**Supplementary Figure 3.** Transfection with siGRHL2 does not affect PC3 cell growth, as assessed by Trypan blue assays. Error bars represent  $\pm$  SD.



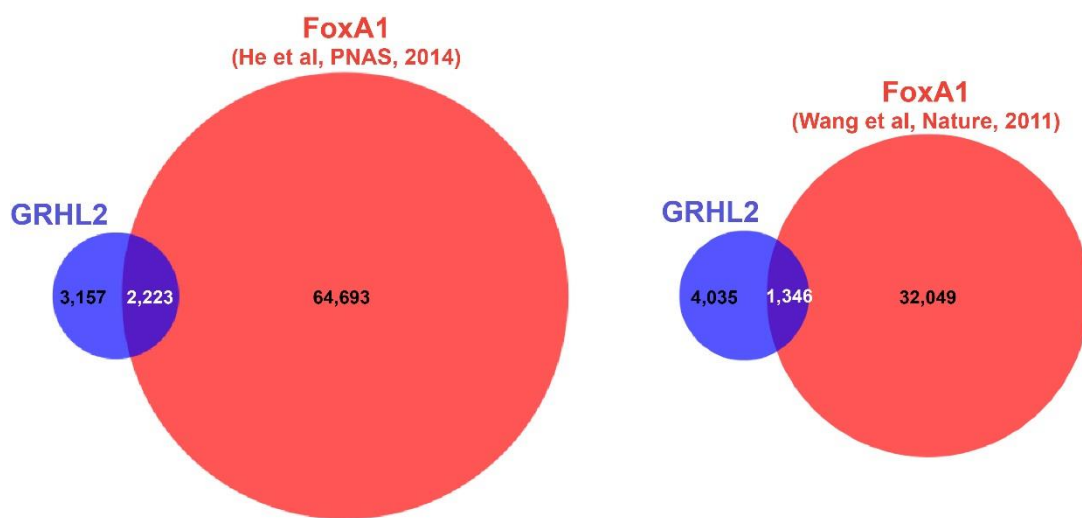
**Supplementary Figure 4.** Loss of GRHL2 does not affect AR protein stability. Protein stability of AR in LNCaP cells (top) and AR/ARV in 22Rv1 cells (bottom) was determined by treating cells with 25  $\mu$ M cyclohexamide 48 h after GRHL2 siRNA transfection. AR/ARV protein levels were assessed by Western blotting.



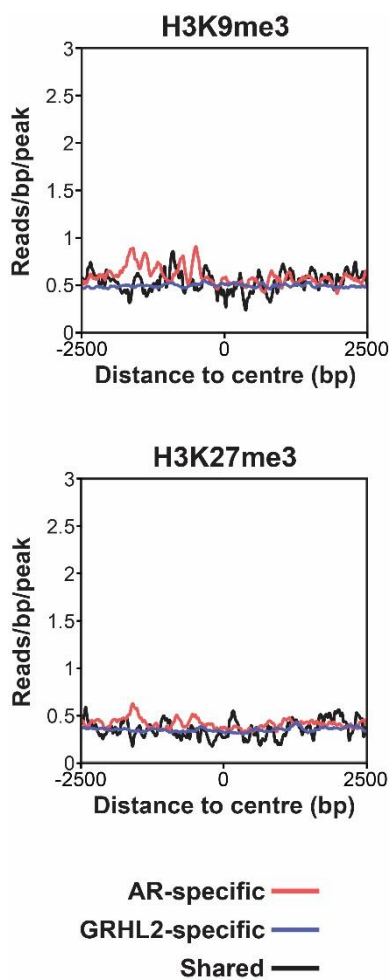
**Supplementary Figure 5.** Reproducibility of GRHL2 and AR ChIP-seq replicates. Correlation coefficients were calculated using Cistrome (1) with genome-wide wiggle files.



**Supplementary Figure 6.** Comparison of AR and GRHL2 binding intensity (from ChIP-seq data) at factor-specific and shared sites. **(A)** Graphs showing read density for AR ChIP-seq (top) and GRHL2 ChIP-seq (bottom) factor-specific and shared sites. Read density around the sites was measured using HOMER (2). **(B)** Heatmaps showing binding signal intensity of AR and GRHL2 at factor-specific and shared sites. The heatmaps were generated using Cistrome (1).

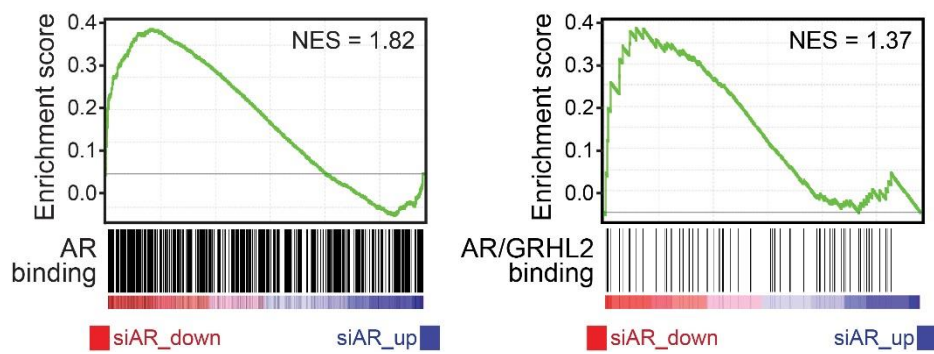


**Supplementary Figure 7.** Overlap between the GRHL2 LNCaP cistrome and published FoxA1 LNCaP cistromes (3,4).

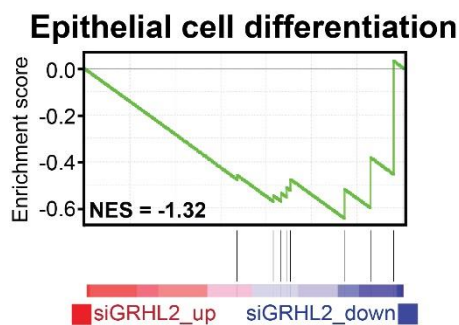
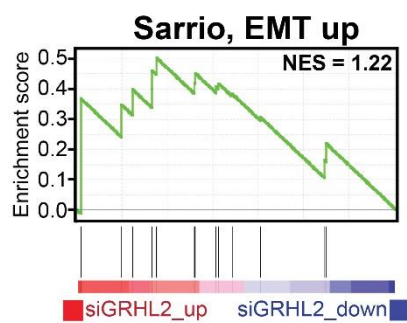
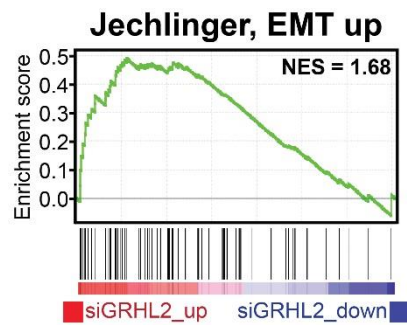


**Supplementary Figure 8.** Distribution of normalized sequence tag density for H3K9me3 and H3K27me3.

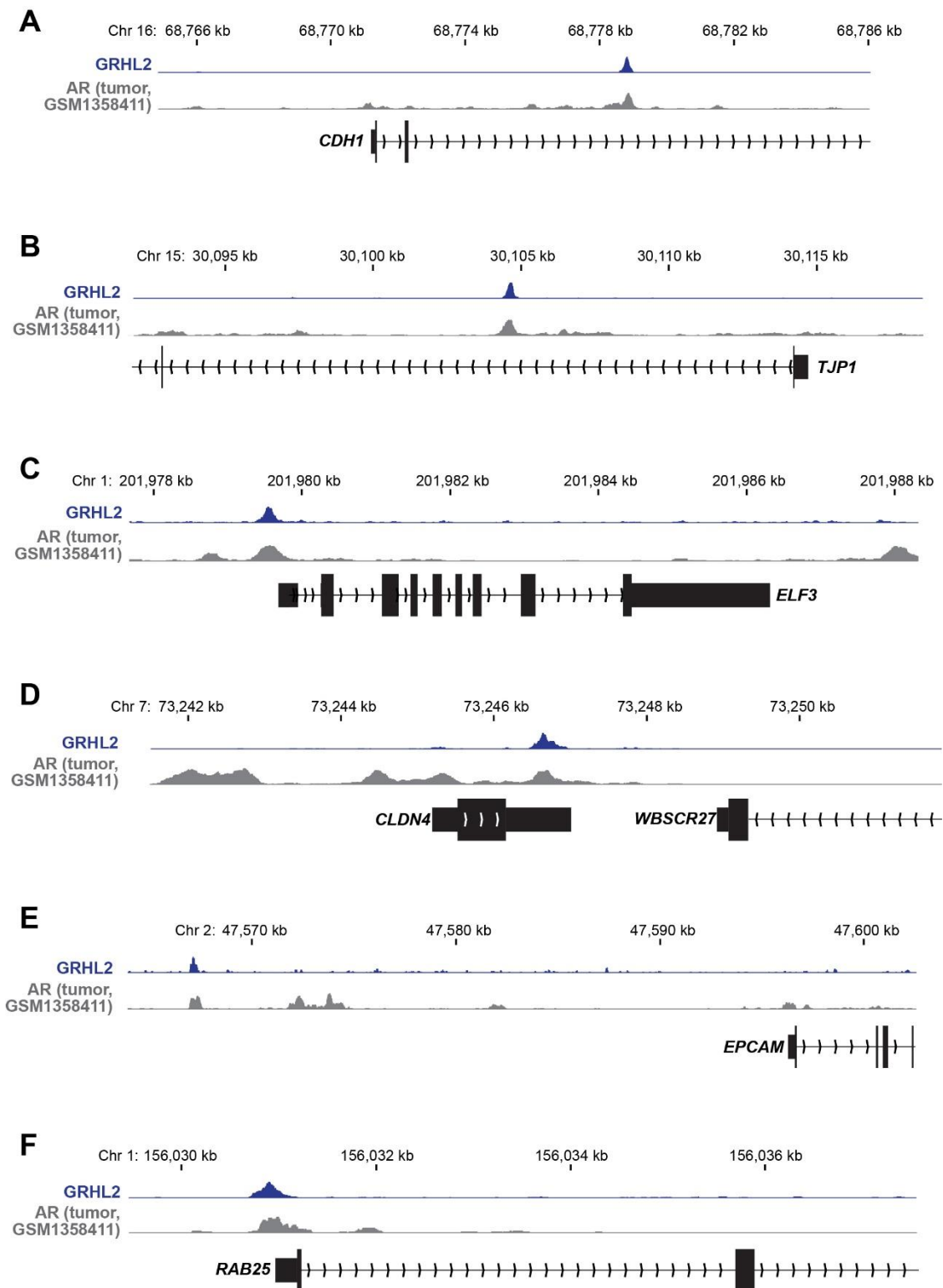




**Supplementary Figure 9.** Shared AR/GRHL2 (right) and AR-specific (left) binding events are associated with AR-upregulated genes, as determined by gene set enrichment analysis (5). The AR-responsive gene signature was kindly provided by He and colleagues (3).

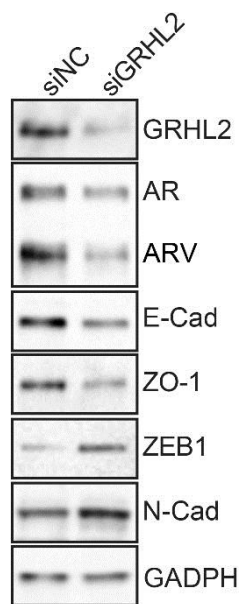


**Supplementary Figure 10.** GSEA reveals that genes upregulated in response to GRHL2 siRNA knockdown (siGRHL2 up) are enriched in epithelial-mesenchymal transition (EMT) gene sets (6,7), and genes downregulated in response to siGRHL2 knockdown (siGRHL2 down) are enriched in the GO “epithelial cell differentiation” gene set.



**Supplementary Figure 11.** GRHL2 and AR binding events proximal to genes that regulate epithelial identity. GRHL2 ChIP-seq data was derived from LNCaP cells (this study). AR ChIP-seq data was derived from a prostate tumor (published data; Pomerantz et al., 2015).

## 22Rv1



**Supplementary Figure 12.** GRHL2 knockdown decreases epithelial marker (E-cad, ZO-1) and increases mesenchymal marker (N-cad, ZEB1) expression at the protein level in 22Rv1 cells. ARV, AR variant; E-cad, E-cadherin; N-cad, N-cadherin; Vim, Vimentin.

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