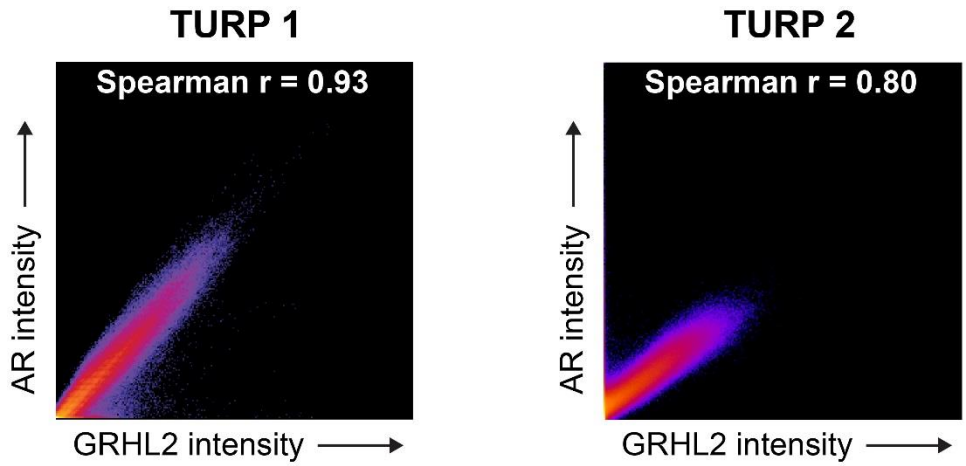
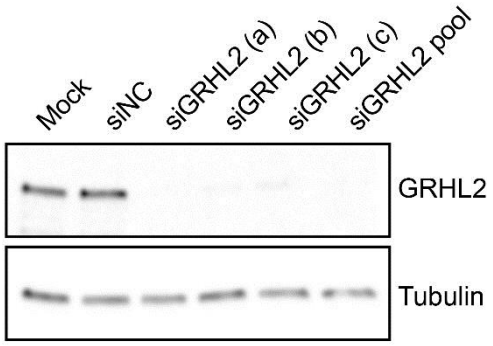
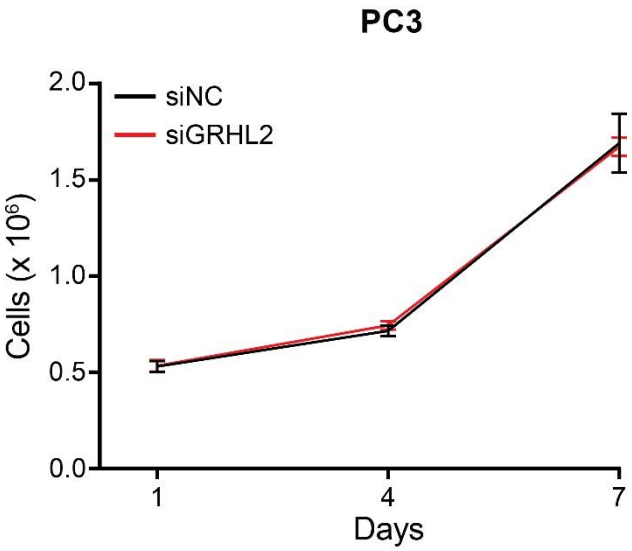
Supplementary Figures and Tables



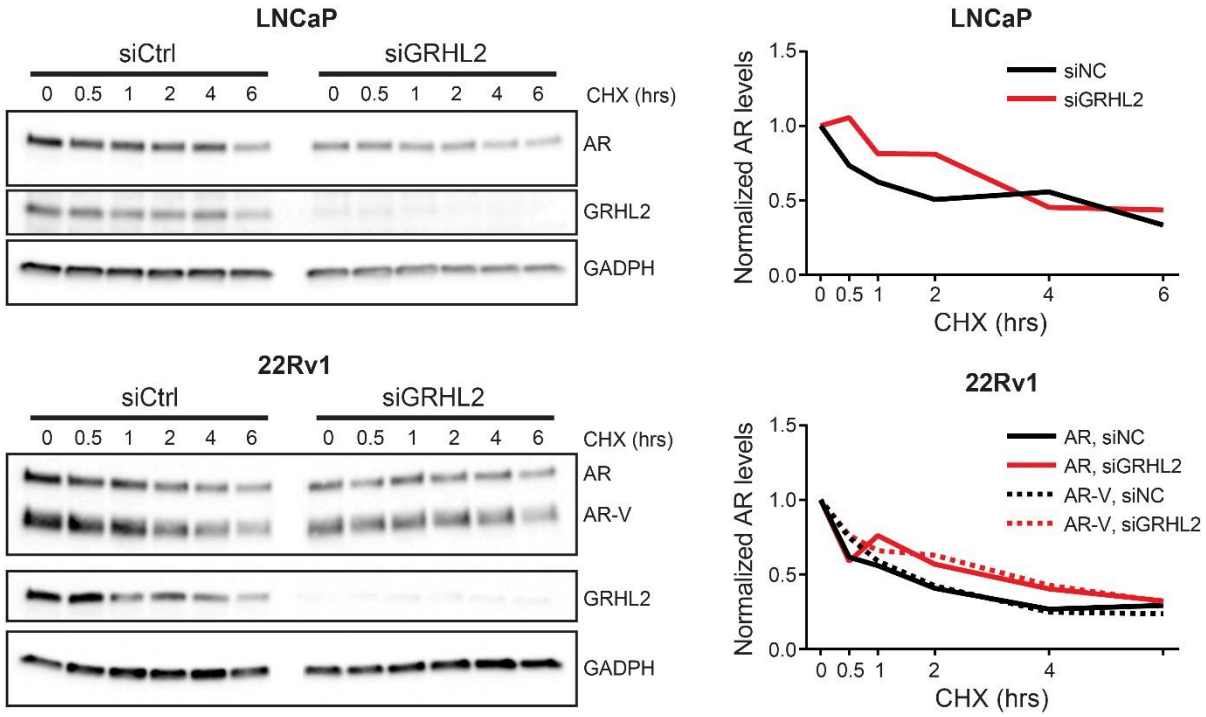
Supplementary Figure 1. Correlation between AR and GRHL2 immunofluorescence staining signals in two representative prostate tumors.



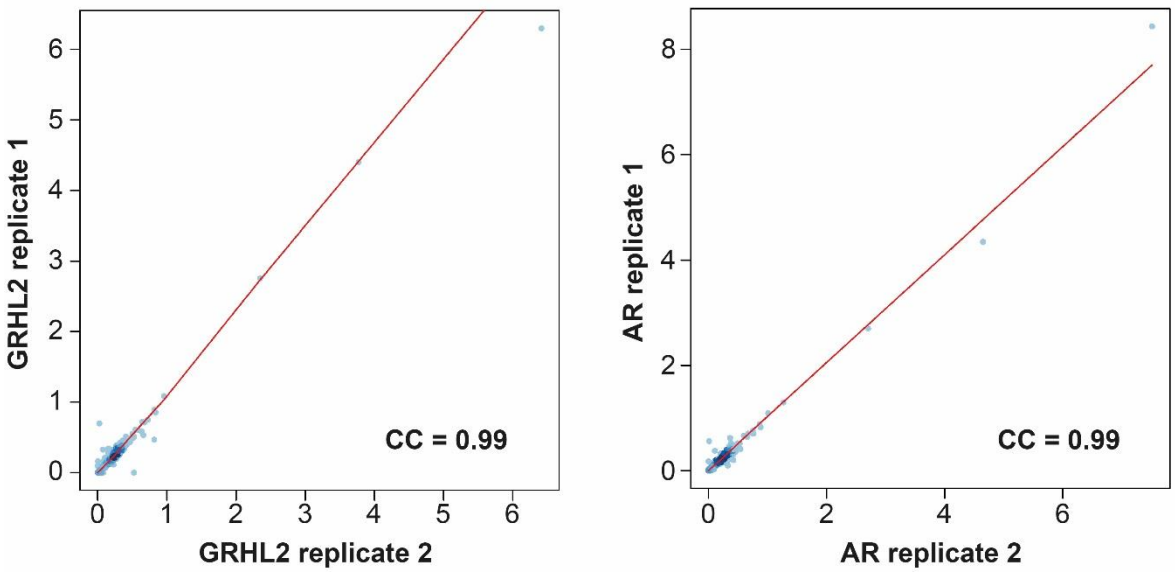
Supplementary Figure 2. Validation of GRHL2 knockdown by siRNA transfection. The siRNAs were obtained from Santa Cruz Biotechnology (Santa Cruz, CA): siGRHL2(a) = sc77606a, siGRHL2(b) = sc77606b and siGRHL2(c) = sc77606c. All siRNAs were used at 20nM; the pool represents 6.66nM of each siRNA. siNC =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



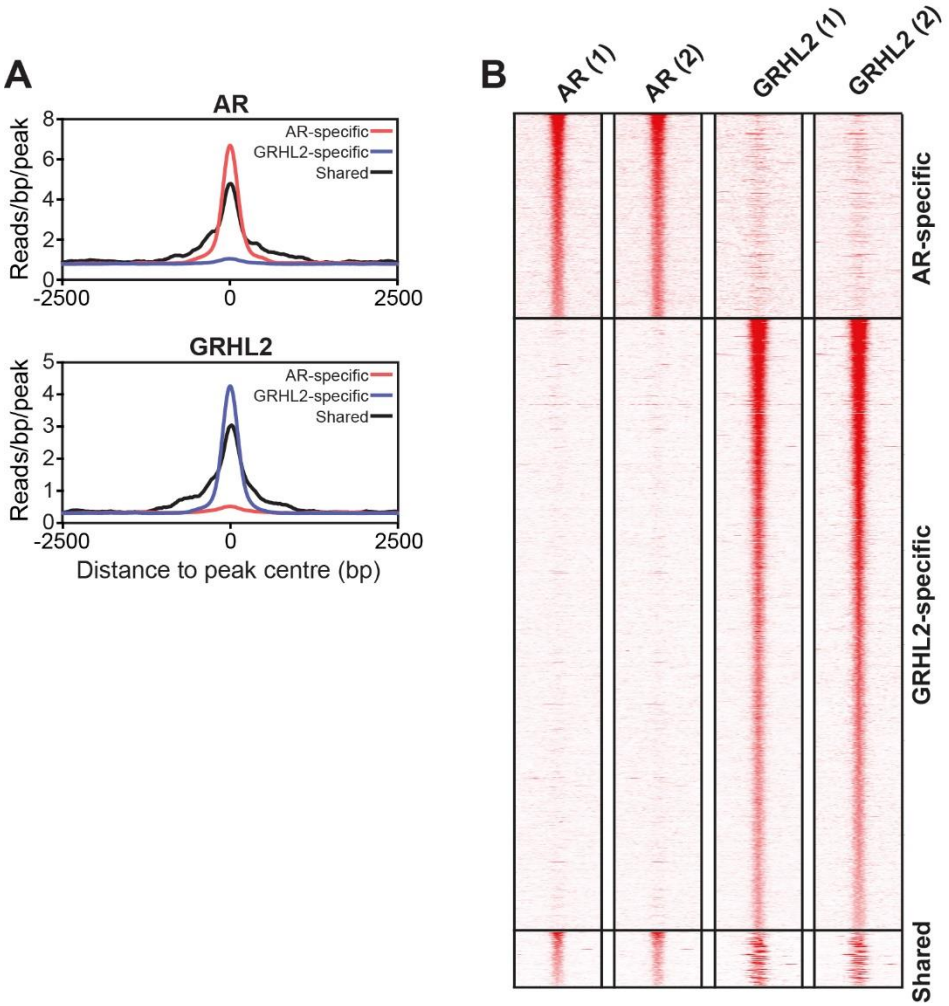
Supplementary Figure 3. Transfection with siGRHL2 does not affect PC3 cell growth, as assessed by Trypan blue assays. Error bars represent ± SD.



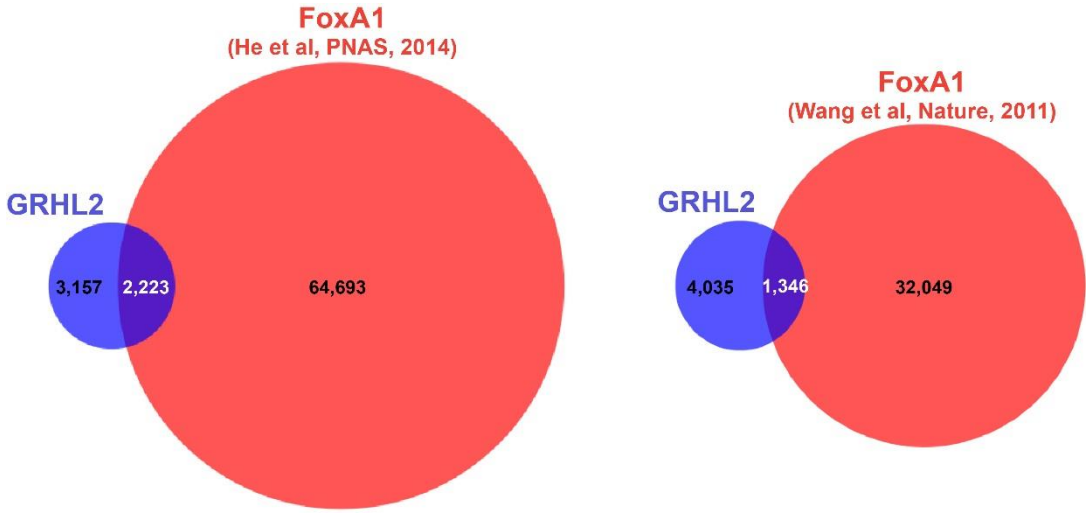
Supplementary Figure 4. Loss of GRHL2 does not affect AR protein stability. Protein stability of AR in LNCaP cells (top) and AR/ARV in 22Rv1 cells (bottom) was determined by treating cells with 25 μM cyclohexamide 48 h after GRHL2 siRNA transfection. AR/ARV protein levels were assessed by Western blotting.



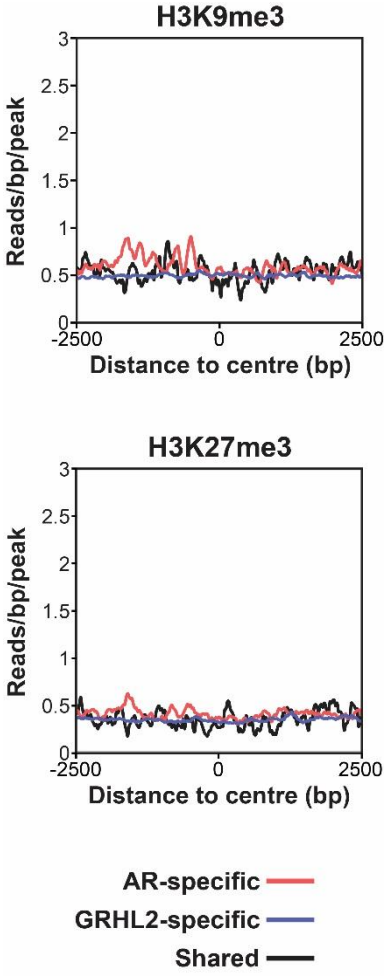
Supplementary Figure 5. Reproducibility of GRHL2 and AR ChIP-seq replicates. Correlation coefficients were calculated using Cistrome (1) with genome-wide wiggle files.



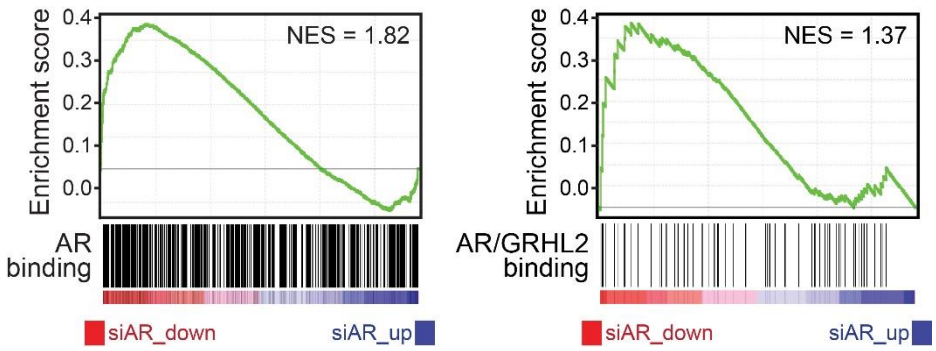
Supplementary Figure 6. Comparison of AR and GRHL2 binding intensity (from ChIP-seq data) at factor-specific and shared sites. **(A)** Graphs showing read density for AR ChIP-seq (top) and GRHL2 ChIP-seq (bottom) factor-specific and shared sites. Read density around the sites was measured using HOMER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



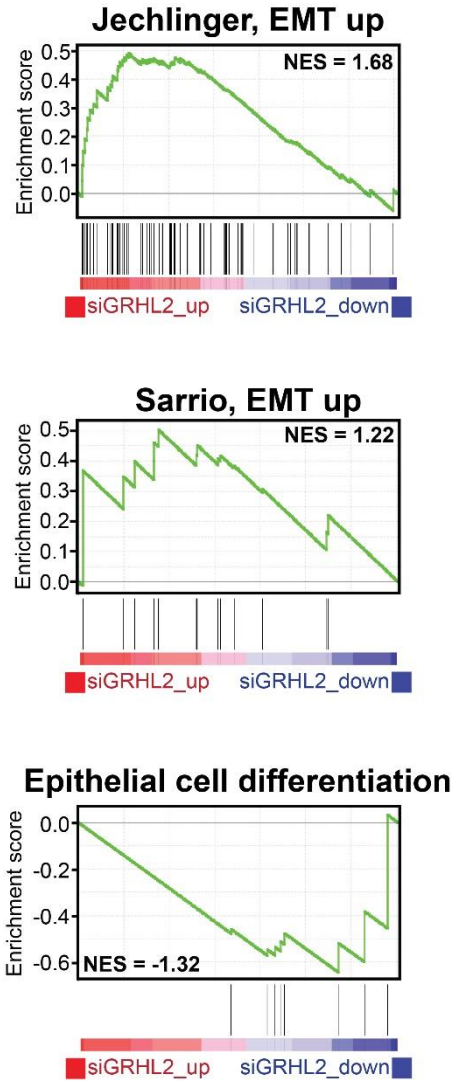
Supplementary Figure 7. Overlap between the GRHL2 LNCaP cistrome and published FoxA1 LNCaP cistromes (3,4).



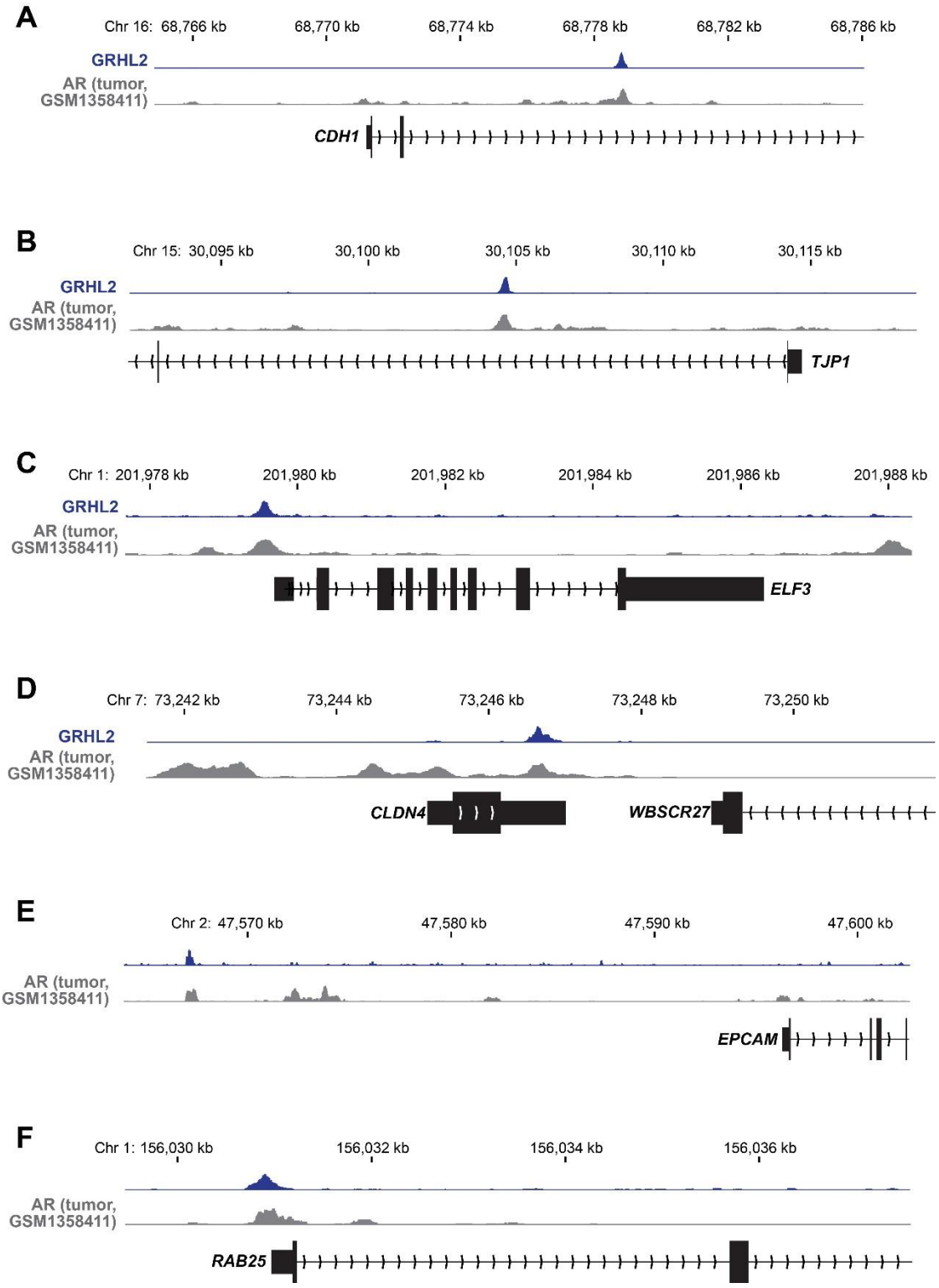
Supplementary Figure 8. Distribution of normalized sequence tag density for H3K9me3 and H3K27me3.



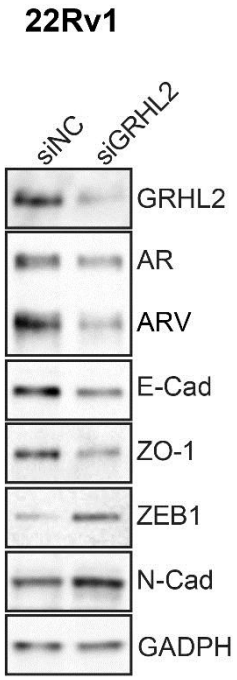
Supplementary Figure 9. Shared AR/GRHL2 (right) and AR-specific (left) binding events are associated with AR-upregulated genes, as determined by gene set enrichment analysis (5). The AR-responsive gene signature was kindly provided by He and colleagues (3).



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 siGHRL2 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).



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.

References for Supplementary Data

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