



Figure 2 – Supplementary Figure 1

Figure 2 - Supplementary Figure 1. Correlation of coregulator-dependent androgen-responsiveness of AR target genes

A. Pair-wise pearson correlation of coregulator-dependent androgen-responsiveness of AR target genes

For each pair of coregulators, the correlation was calculated based on the effect of loss of coregulator on androgen-regulation of AR target gene expression, as described in **Supplementary File 7, panel A**.

B. Cistrome analysis on ARBSs found in 4 pairs of AR target gene sets with the strongest Pearson correlation

AR target gene set pairs CTNNB1+NCOA1, PARK7+PKN1, SMARCA4+WDR77 and SMARCC1+KDM1A showed the strongest Pearson correlation of coregulator-dependent androgen-responsiveness, as shown in panel A. For each paired gene set, cistrome analysis was done on ARBSs from the individual AR target gene sets and on combined ARBSs found in both gene sets. The heatmap summarized the clustering of overrepresented TFBSs within and among ARBSs in the AR target gene sets. Blue bar, one overrepresented TFBS.

C. Ingenuity Pathway Analysis on gene signatures that are make up 4 pairs of AR target gene sets with the strongest Pearson correlation

AR target gene set pairs CTNNB1+NCOA1, PARK7+PKN1, SMARCA4+WDR77 and SMARCC1+KDM1A showed the strongest Pearson correlation of coregulator-dependent androgen-responsiveness, as shown in panel A. For each paired gene set, IPA identified the enriched functions annotations that are associated the individual AR target gene sets and the combined gene set. The heatmap summarizes the clustering of enriched functions within and among AR target gene sets. Blue bar, one enriched function term.