



Figure.S15: AR-ERG loops are better predictor of DHT regulated genes in VCaP cell compared to other interaction models. (a) Graph showing the respective fold enrichment of the number of up/down-regulated genes defined by RNA-seq data associated with six categories based AR/ERG cobound status and whether the binding sites associate with either AR loops and ERG loops 6hrs (6hrs vs 0hrs) after DHT stimulation. The fold enrichment is calculated with reference to the total number of up/down-regulated genes with expression increase/decrease more than 2 folds . (b) Similar to (a), but compare the RNA-seq derived expression between 24hrs and 6 hrs after DHT stimulation. (c) Fold enrichment is calculated based on GRO-seq data between 2hrs and 0 hrs after DHT stimulation, and we observed similar result as (a).