Figure.S14: EZH2 specially target AR Enhancer hub. (a)The graph shows dierent distribution between EZH2BS associated hub and all EZH2BS. The EZH2 in hub regions signicantly associate with Enhancer regions. (b)ERG motif percentage in ERG-AR-EZH2 co-binding sites, ERG-AR co-binding sites without EZH2 (ERG-AR-noEZH2) and ERG alone binding sites (ERG-noAR-noEZH2). (c) Snapshot representation of (from top to bottom) the ERG looping, AR looping(dened by ChIA-PET), EZH2, HDAC3, HDAC2 and HDAC1 binding sites (dened by ChIRP-seq), transcriptional rate proles before and after DHT (dened by Gro-Seq) Yellow rectangle highlights the transcriptional hub region.