







**Supplementary Figure 6. SIDP results are consistent across ER+ BC cell lines.** (a) Series of bar plots showing the number of sgRNAs, loci with one or more significant sgRNAs, loci with two or more significant sgRNAs, and the corresponding unique, nearby genes, that show significantly higher counts (FDR <= 0.05 and fold-change larger then 1.5) in either MCF7 or T47D cells (21 days post-infection), in the indicated condition (+E2, -E2). Y-axis is in log10 scale. (b) Bubble plot highlighting the enrichment of distinct biological functions, when considering sets of genes near CREs showing context-specific responses to perturbation. (c) Heat maps showing the relative pattern of counts across conditions and replicates, for the significant sgRNAs at loci showing two or more significant and consistent sgRNAs (as highlighted in (a)). TMM-normalized counts were transformed as z-scores (by sgRNA). (d) Box plots overlaid on violin plots showing the distribution of distances to the nearest gene-TSS, for the indicated groups of loci.