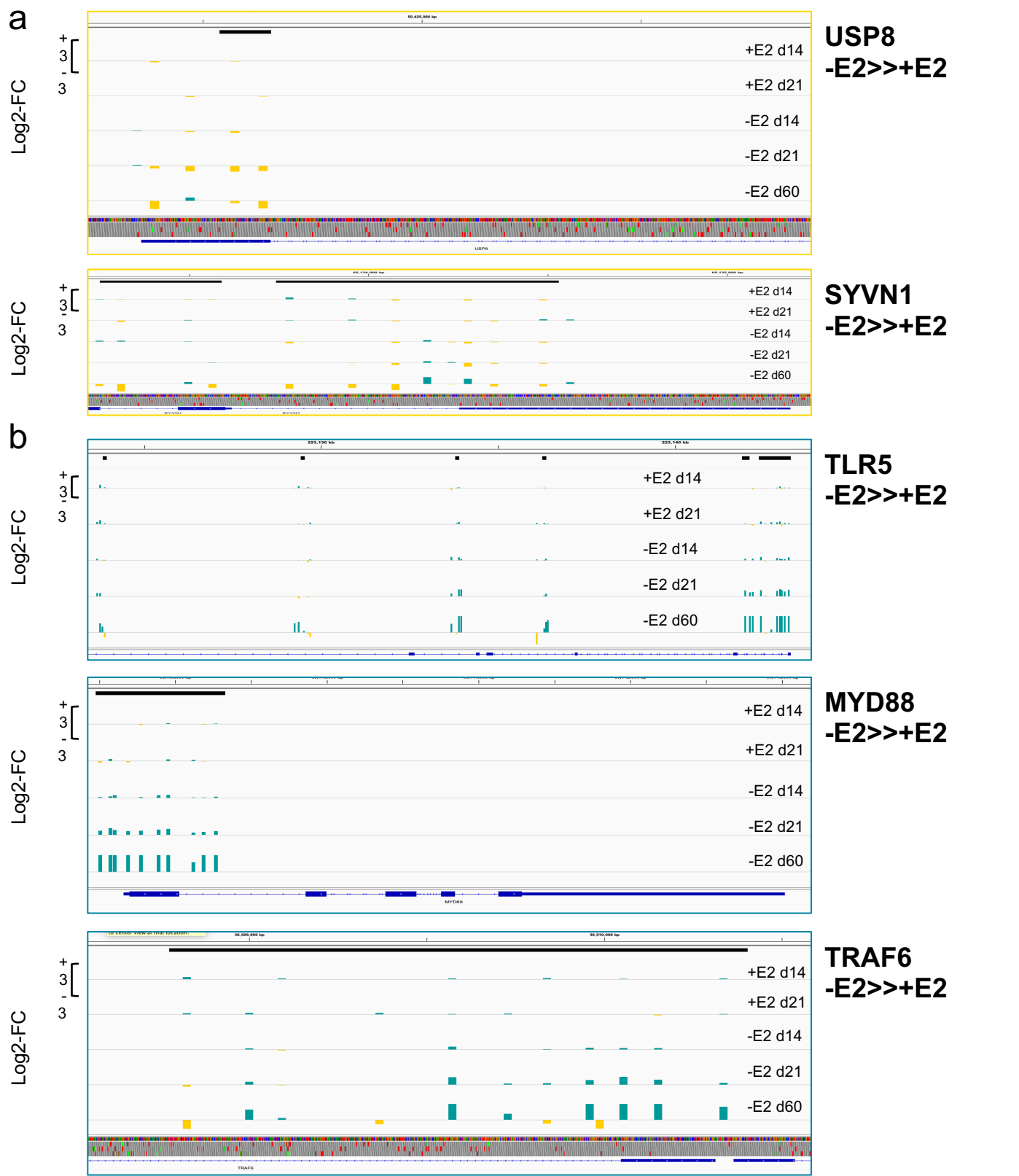
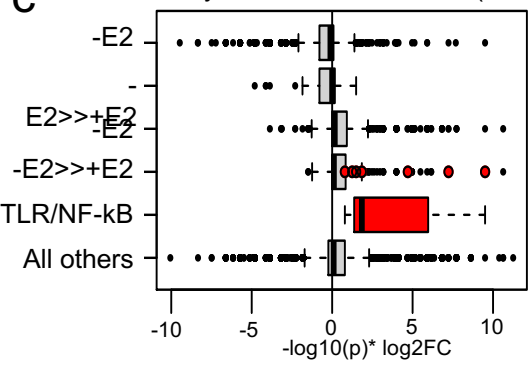


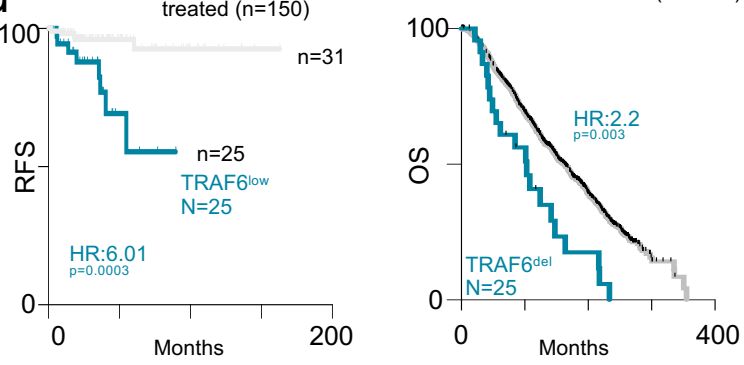
Supplementary Figure 9



c Dormancy Stochastic Entrance (60 days)



d TCGA Database ER+ AI treated (n=150) DNA METABRIC ER+ (n=1506)



Supplementary Figure 9. SIDP identifies regulatory regions with context-dependent activity in MCF7 cells. (a-b) SIDP results at the indicated loci are shown as IGV genome browser screenshots. For each of the indicated condition, the log₂-fold change versus the initial library counts for each sgRNA is indicated, with bars proportional to the effect size, and colour reflecting the sign (blue = increased frequency or IF; yellow = decreased frequency or DF). Note: y-axis for the tracks is only shown for the first one (range is [-3, +3] for all tracks). (c) Box plots showing the distribution of the compounded score ($-\log_{10}$ of the edgeR-estimated p-value times the log₂-FC) for the indicated sets of sgRNAs, at 60 days post-infection. The scoring sgRNAs mapping to the CREs of the genes annotated to TLR/NF- κ B signalling are highlighted in red (as outliers in the distribution of the sgRNAs with a significant increase in frequency in -E2 vs +E2 conditions at 21 days post-infection, and then as separate group). (d) Retrospective patient stratification based on RNA expression of TRAF6. Log-rank p-values calculated with a Mantel-Cox Test.