Supplementary Figure 3

a

b

c

d

e
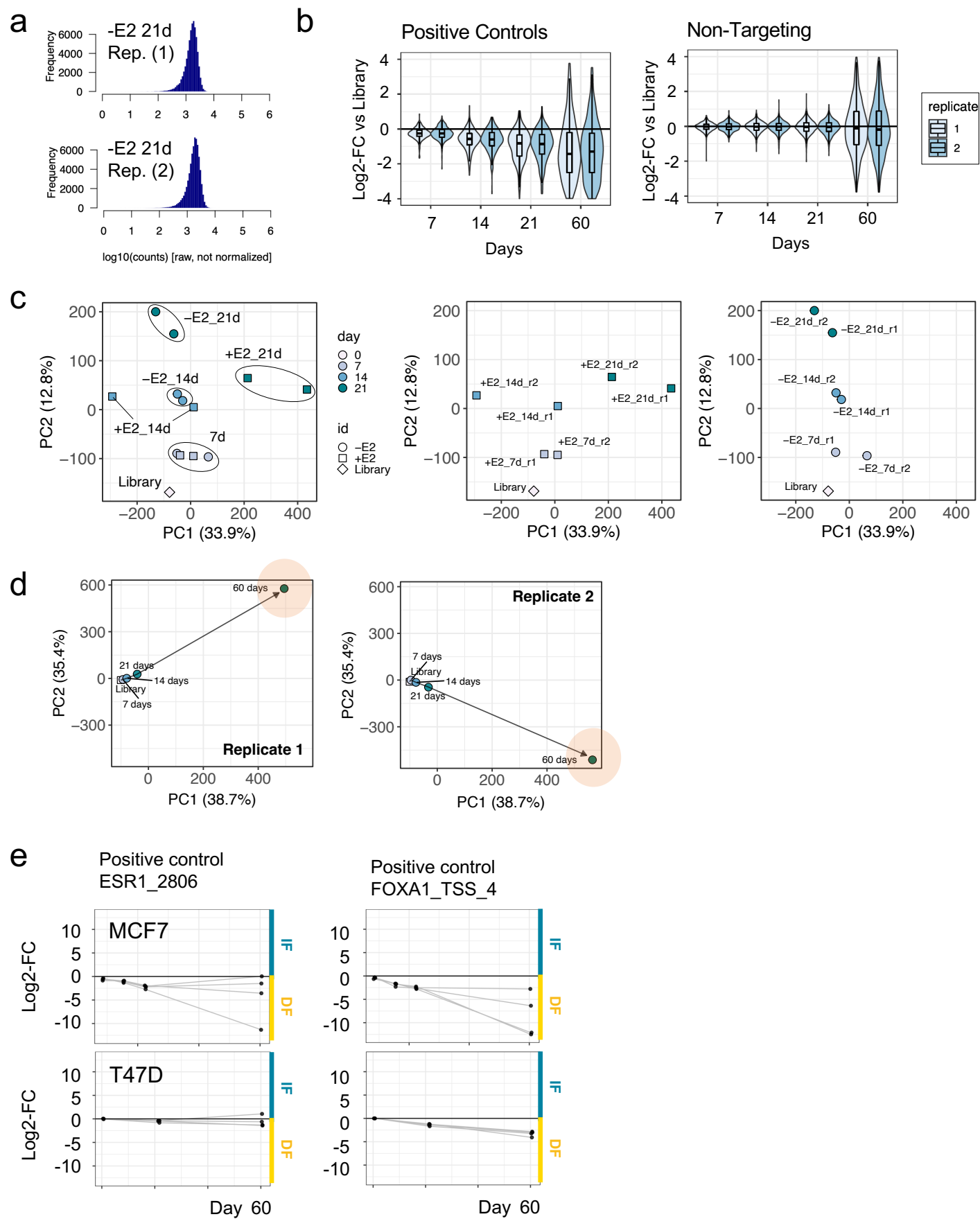
Supplementary Figure 3. Estrogen deprivation in MCF7 cells introduce stochastic selective pressure in long-term CRISPRi screens. (a) Histograms showing the distribution of counts per sgRNAs (log10) for two replicates of sgRNAs in pool 1, at day 21 post-infection (MCF7 -E2). (b) Box plots overlaid to violin plots showing the log2-fold-change of positive controls (left panel) and non-targeting sgRNAs (right panel) in two replicates of –E2 MCF7 cells, at 7, 14, 21 or 60 days post-infection, as compared to the initial library. (c) Principal component analysis (PCA) of all SIDP samples from MCF7 (both +E2 and –E2), except for the two replicates obtained 60 days post-infection. For clarity in the visualization, the analysis was first run on all the samples (left plot), then split by replicate (central and right plots). (d) Same as (a; central and right plot)s but including the two replicates obtained 60 days post-infection. Arrows and orange circles highlight the similarity of the two 60 days replicates on PC1, and divergence on PC2. (e) Longitudinal tracking of individual sgRNAs targeting the CRE of essential genes (ESR1 on the left; FOXA1 on the right), in either MCF7 (top) or T47D cells (bottom), in –E2.