Supplementary Figure 5

a

-E2 21d Rep. (1)

-E2 21d Rep. (2)

b

Positive Controls

IF in T47D −E2

Negative Controls

DF in T47D −E2
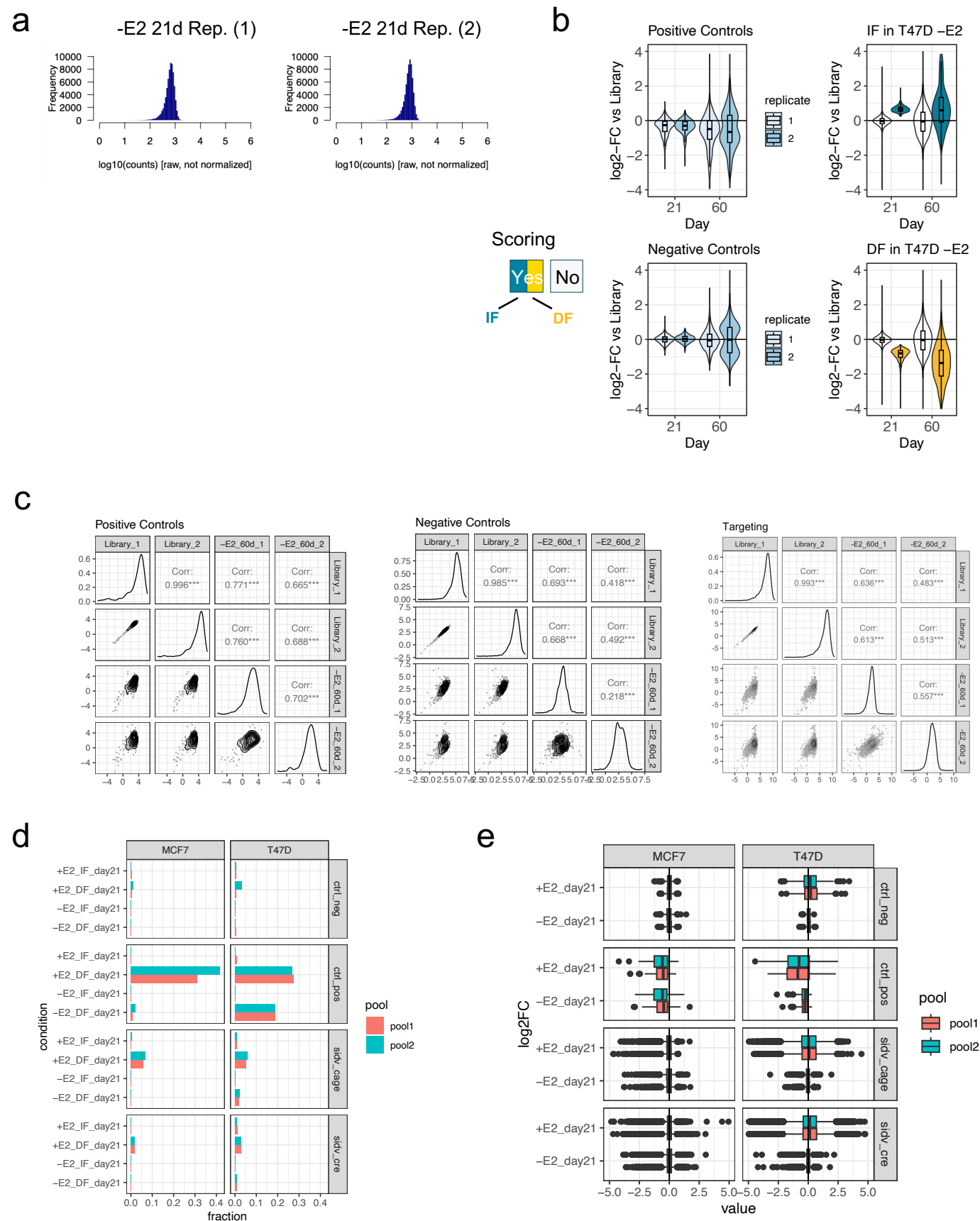
Scoring

c

Positive Controls

Negative Controls

Targeting

d

e

Supplementary Figure 5. Estrogen deprivation in T47D 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 (T47D -E2). (b) Box plots overlaid on violin plots showing the log2-fold-change of positive controls (left panel) and non-targeting sgRNAs (right panel) in two replicates of T47D cells, at 21 days, as compared to the initial library (c) Correlograms (considering either positive controls, non-targeting sgRNAs, or targeting sgRNAs scoring significantly at 21 days post-infection) between the TMM-normalized, log2-transformed counts across replicates (libraries and 60 days post-infection; T47D -E2). Scatterplots of each pair of samples are drawn on the left part of the grid. Pearson correlation is displayed on the right part of the grid (p-value: *** < 0.001; ** < 0.01; * < 0.05; . < 0.10). Distribution of values for each sample is shown on the diagonal. (d) Series of bar plots showing the fraction of sgRNAs significantly increased (IF) or decreased (DF) at 21 days post-infection (either +E2 or –E2). , grouped by sgRNA pool (color-code) and partition (rows; positive controls, non-targeting sgRNAs, and targeting sgRNAs split by CREs and promoters [CAGE]), in either MCF7 or T47D (columns). (e) Series of box plots showing the log2-fold change of all sgRNAs, at 21 days post-infection (either +E2 or –E2), grouped by pool (color-code) and partition (rows; positive controls, non-targeting sgRNAs, and targeting sgRNAs split by CREs and promoters [CAGE]), in either MCF7 or T47D (columns).