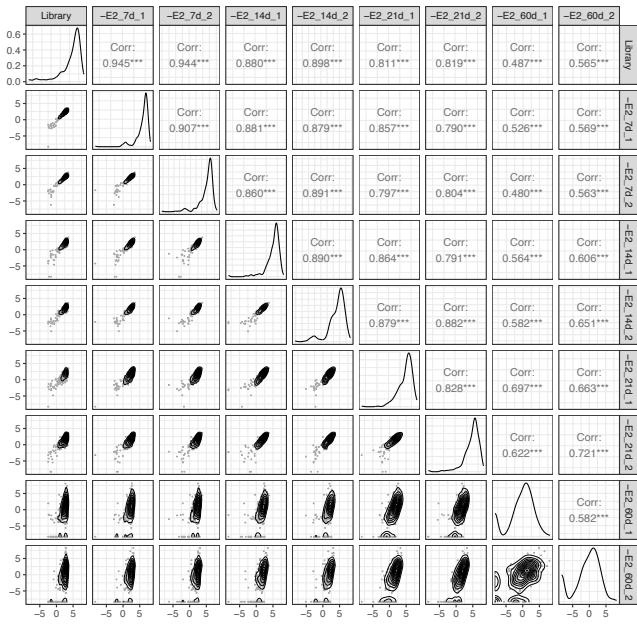
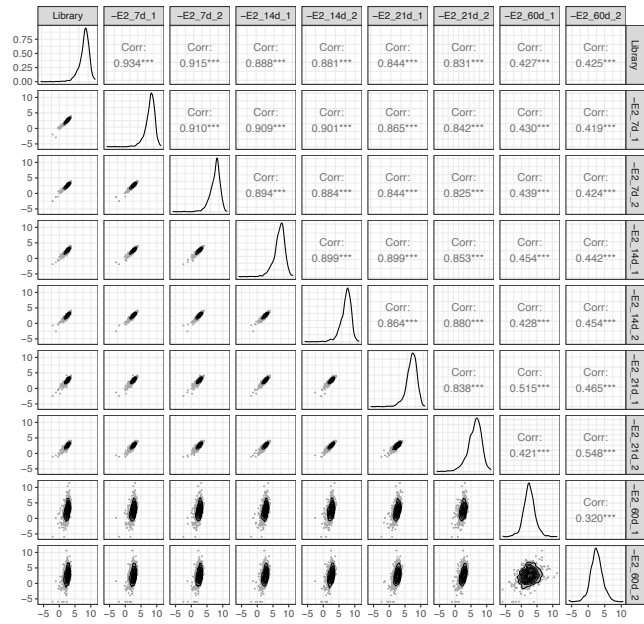


Supplementary Figure 4

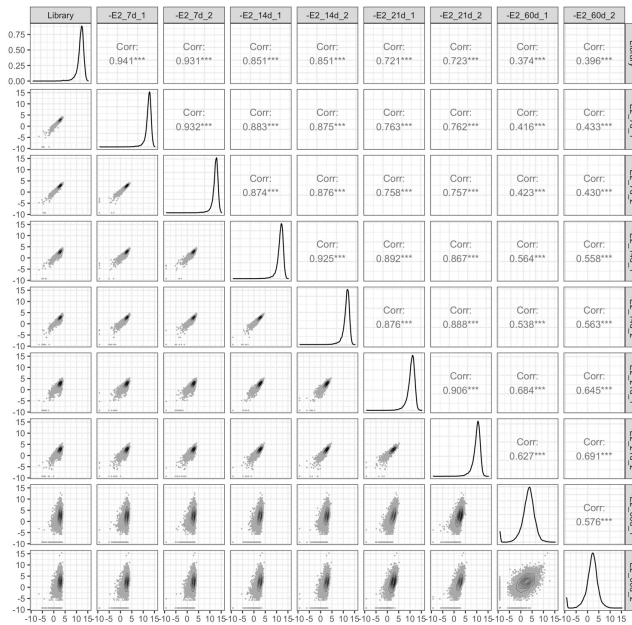
a Positive Controls



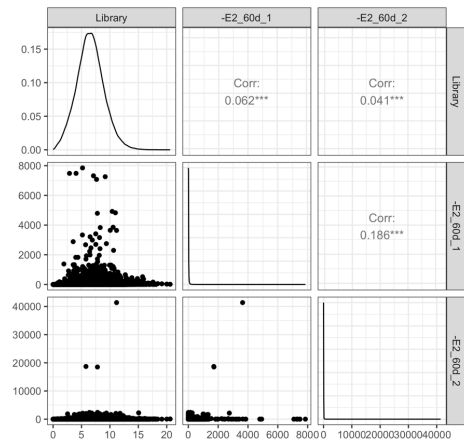
b Non-Targeting



c Targeting (Significant 21 days)



d Targeting (all)



Supplementary Figure 4. Estrogen deprivation in MCF7 cells introduce stochastic selective pressure in long-term CRISPRi screens. (a) Correlograms (considering either positive control sgRNAs) between the TMM-normalized, log₂-transformed counts across replicates (7, 14, 21 and 60 days post-infection; +E2). The initial library is also included. Scatterplots of each pair of samples are drawn on the left part of grid. Pearson correlation is displayed on the right (p-value: *** < 0.001; ** < 0.01; * < 0.05; . < 0.10). Distribution of values for each sample is shown on the diagonal. (b) Same as (a) but for non-targeting sgRNAs. (c) Same as (a) and (b) but for sgRNAs scoring 21 days post-infection. (d) Same as (c) but considering all targeting sgRNAs (scoring and not-scoring). Only the library and the two 60 days post-infection samples are shown. TMM-normalized, but prior to log₂-transformation, were used in this case (to highlight outliers).