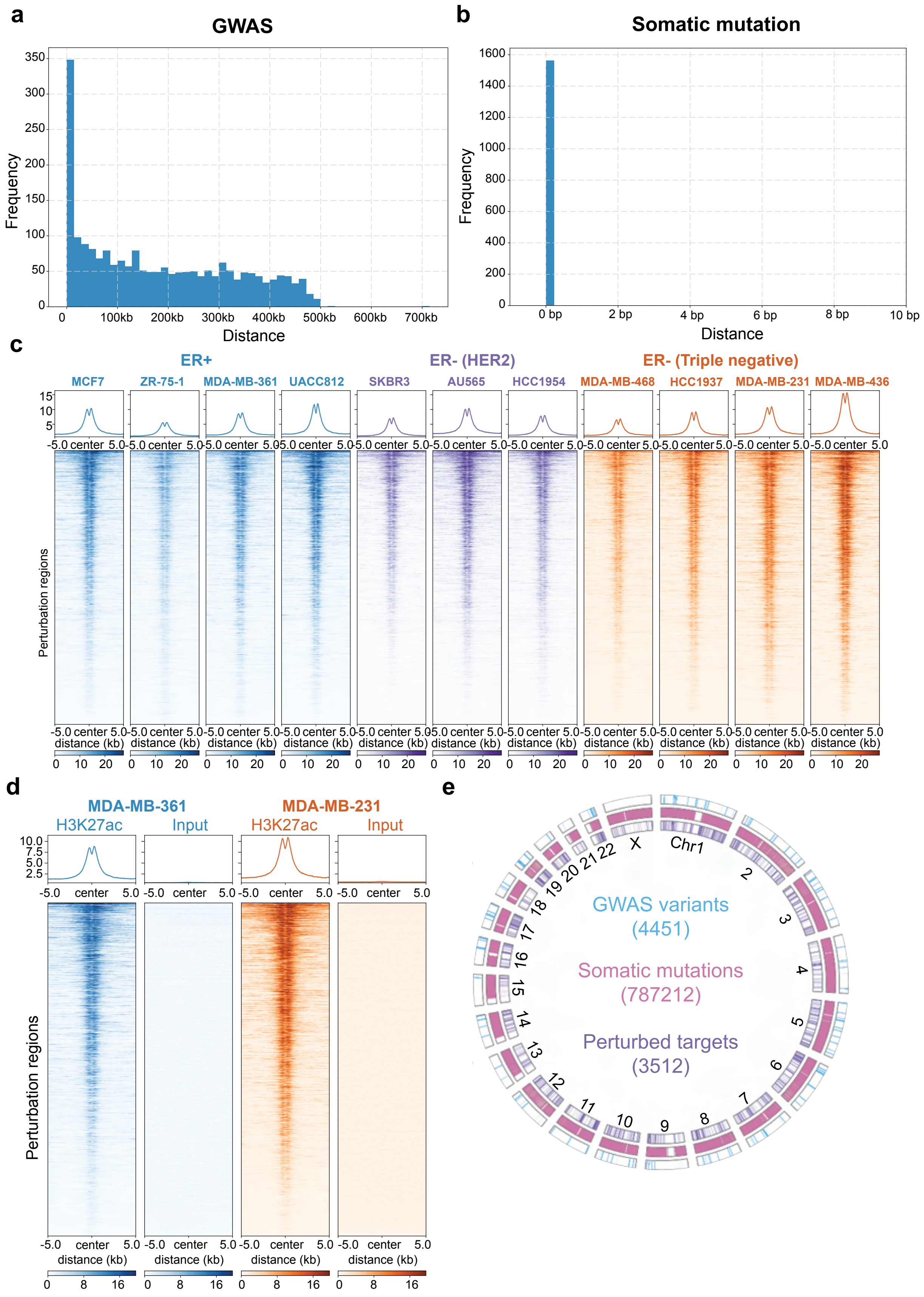
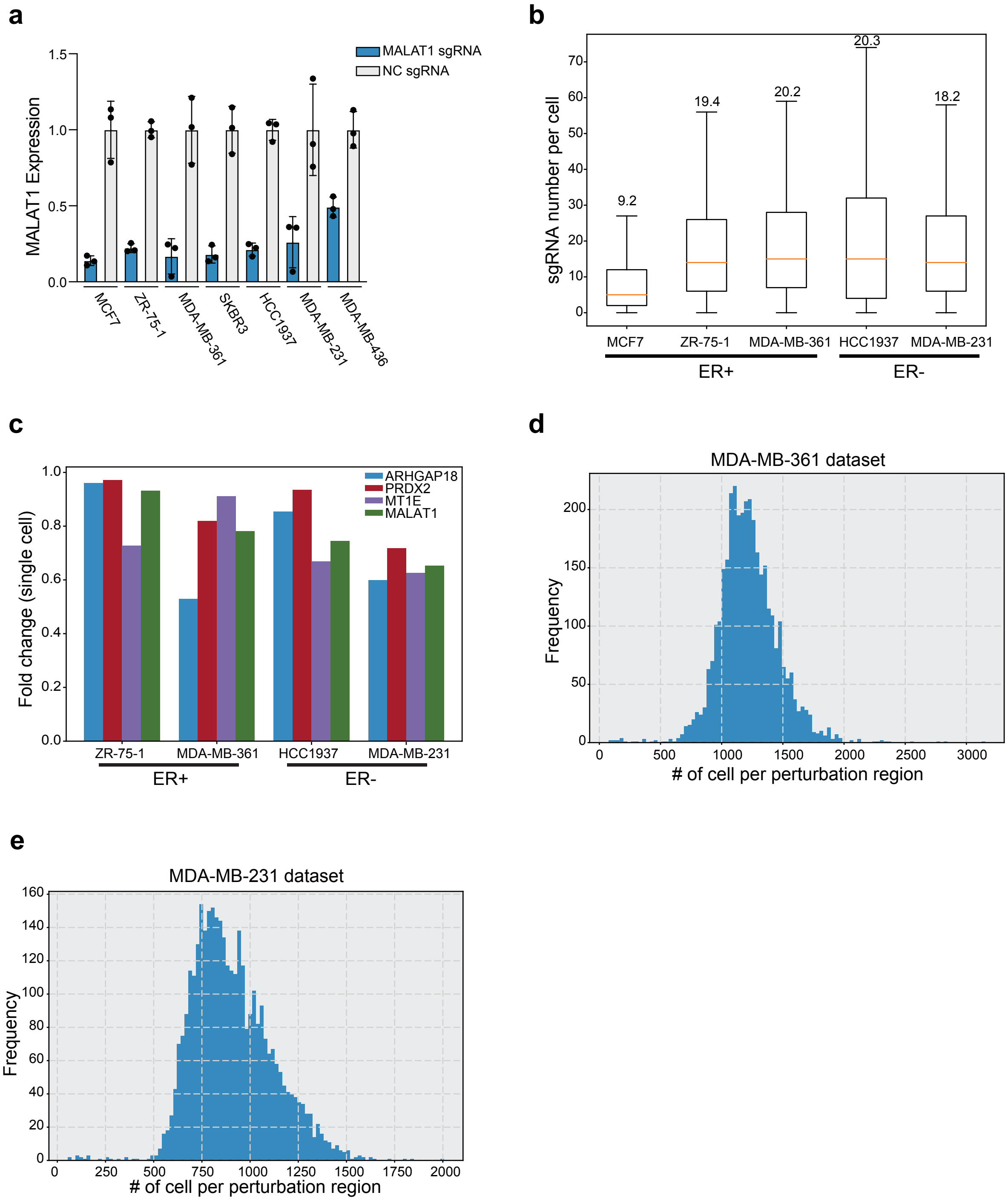
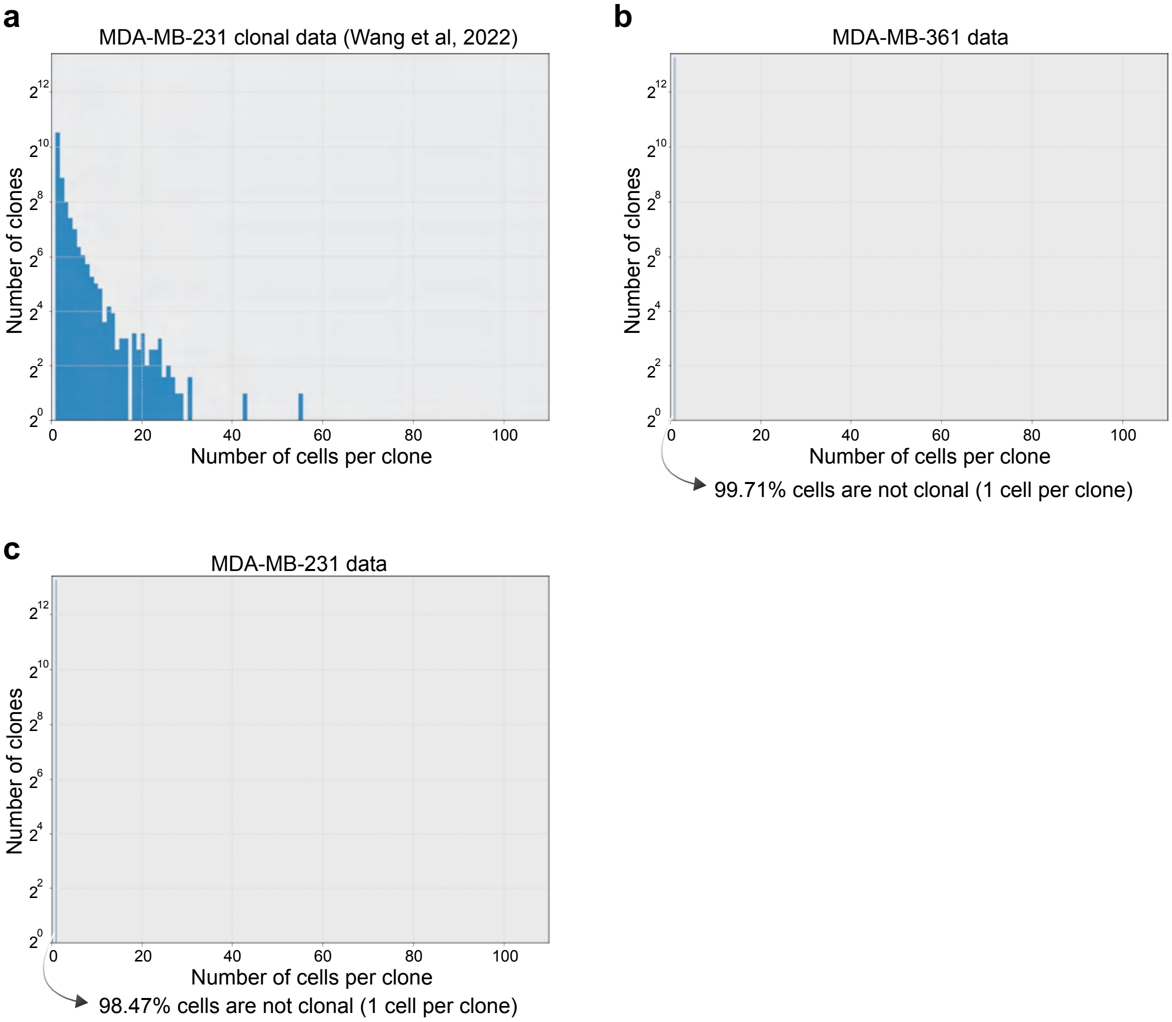
Supplementary Figure 1 - Select perturbation regions based on variants.



Supplementary Figure 2 - (ER+) MDA-MB-361 and (ER-) MDA-MB-231 were selected by testing different subtypes of breast cancer cell lines.



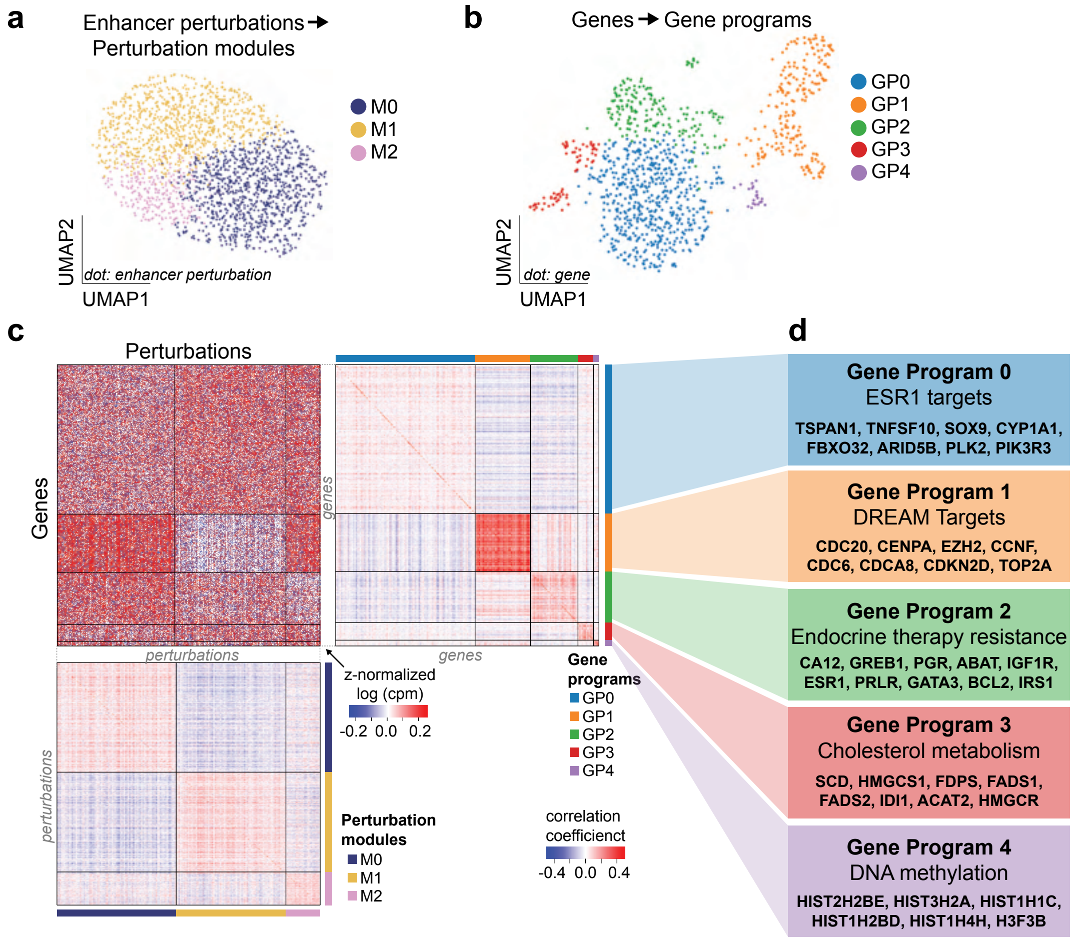
Supplementary Figure 3 - Clonality does not affect the quality of this study.



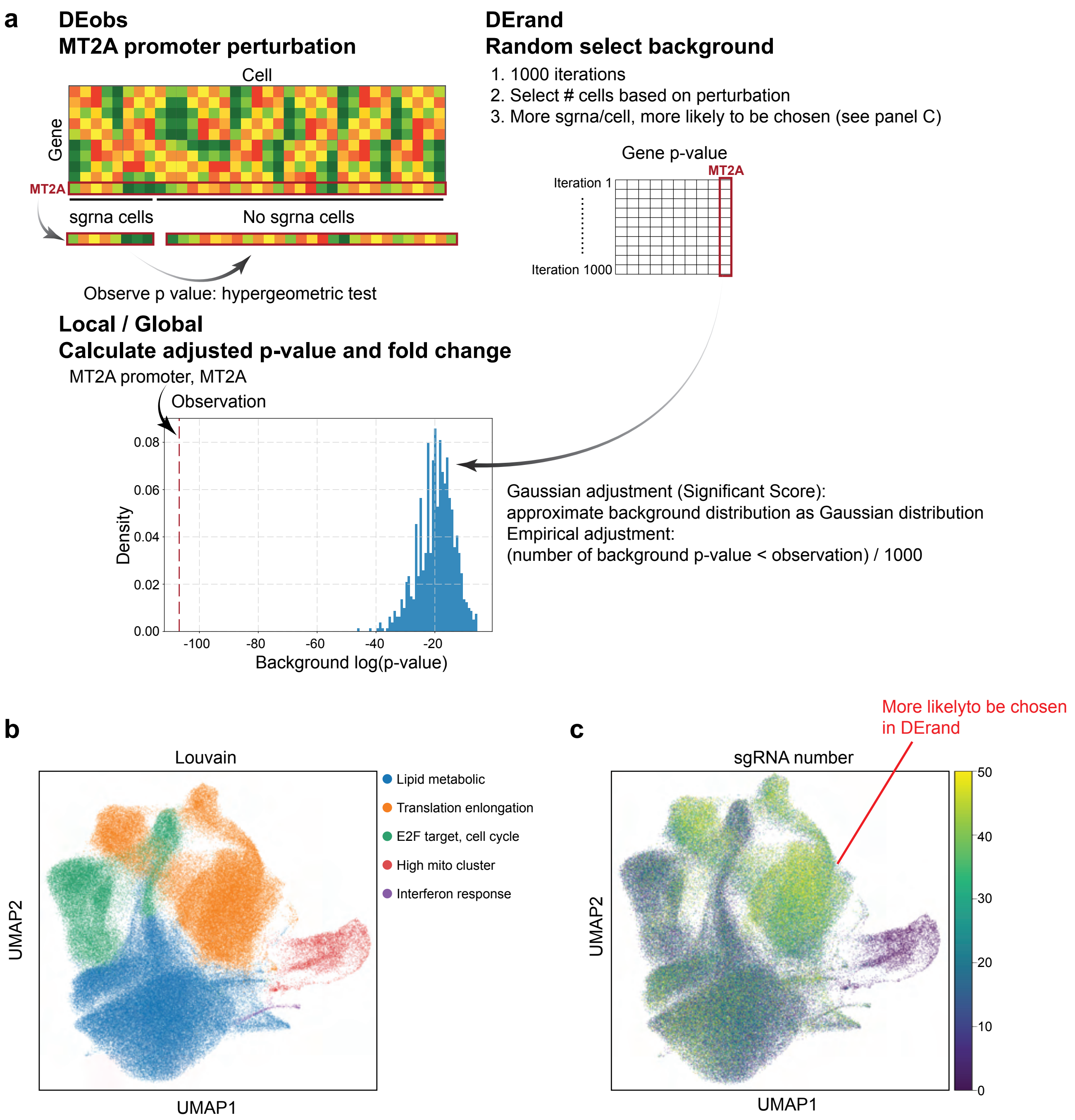
99.71% cells are not clonal (1 cell per clone)

98.47% cells are not clonal (1 cell per clone)

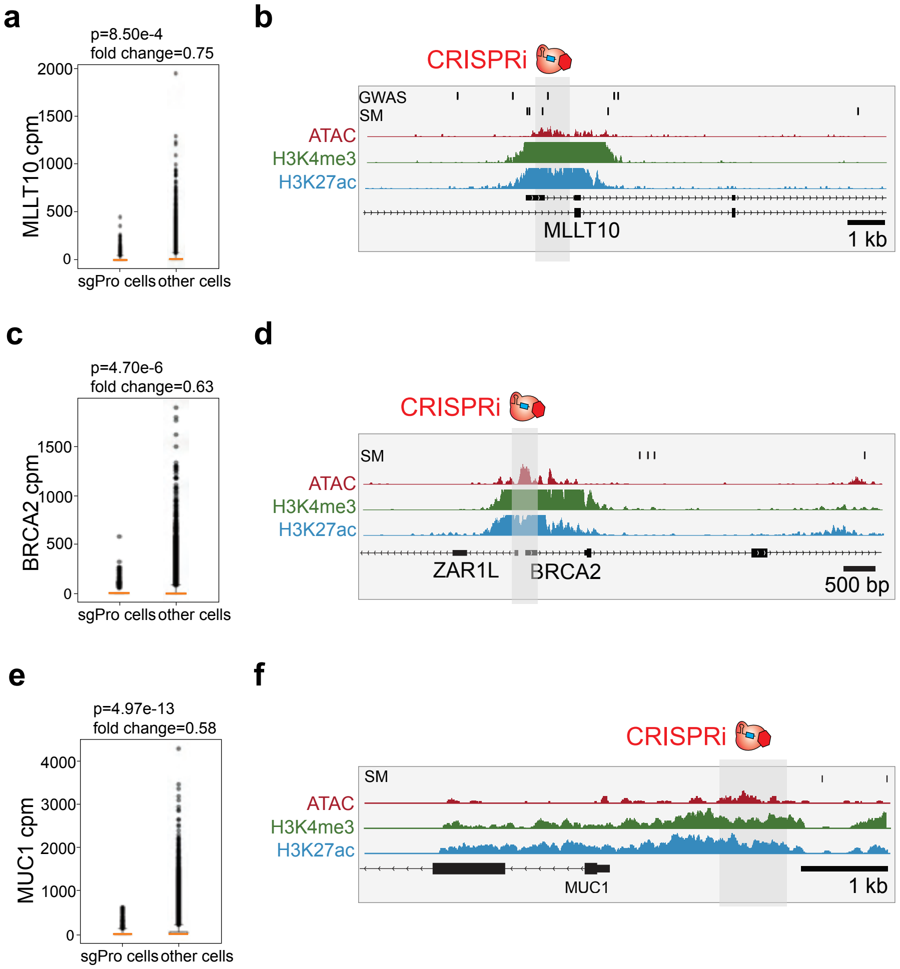
Supplementary Figure 4 - Perturbation modules and gene programs of MDA-MB-361 GWAS dataset.



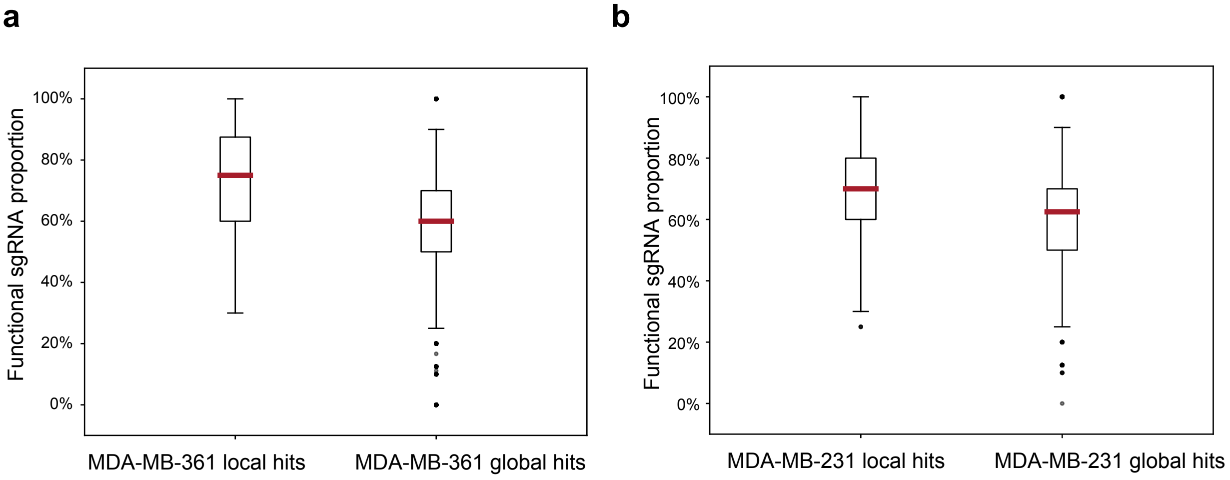
Supplementary Figure 5 - Overview of pySpade and MDA-MB-361 single cell clustering.



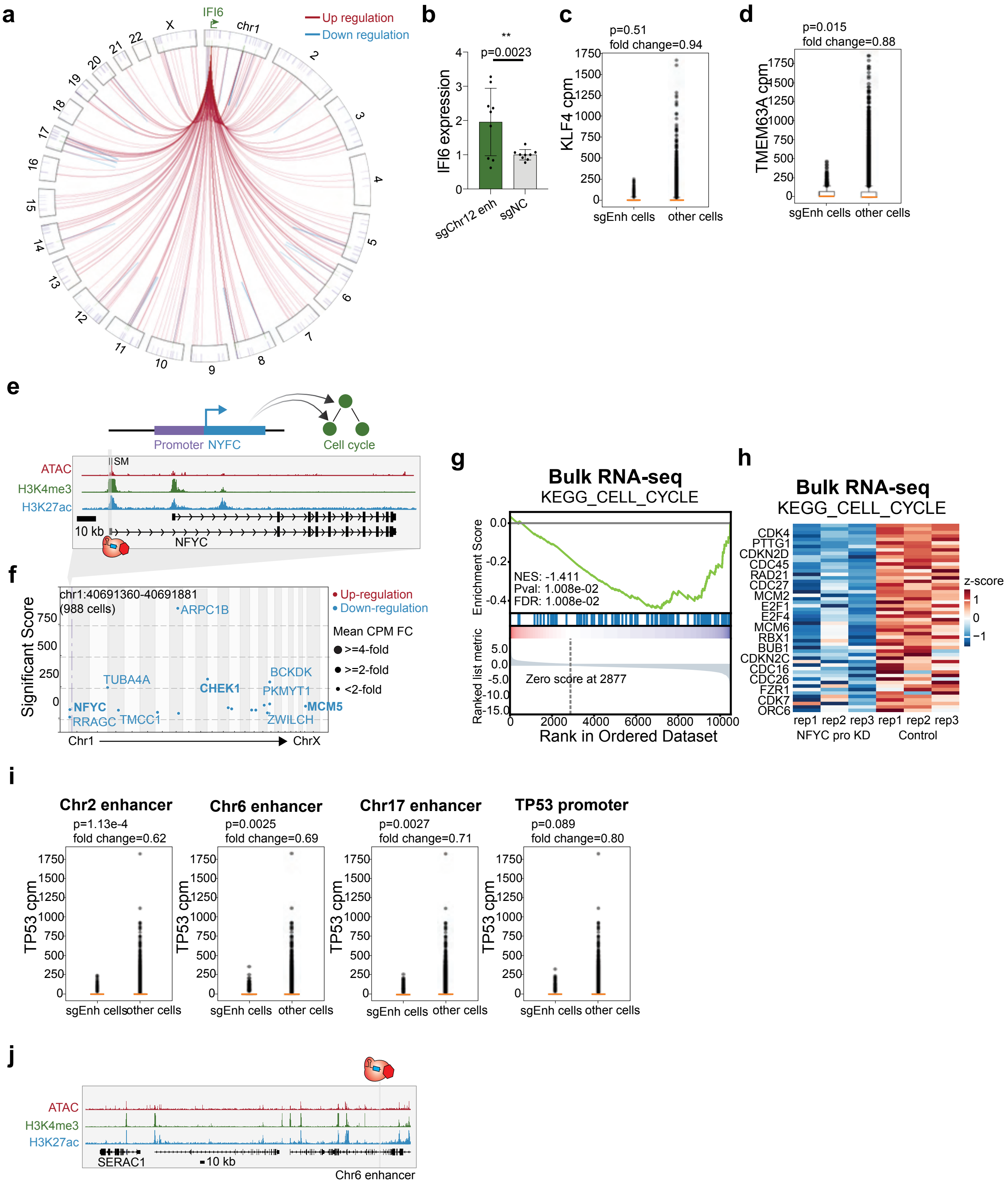
Supplementary Figure 6 - Perturb-seq identifies non-coding regulatory elements that regulate cancer genes.



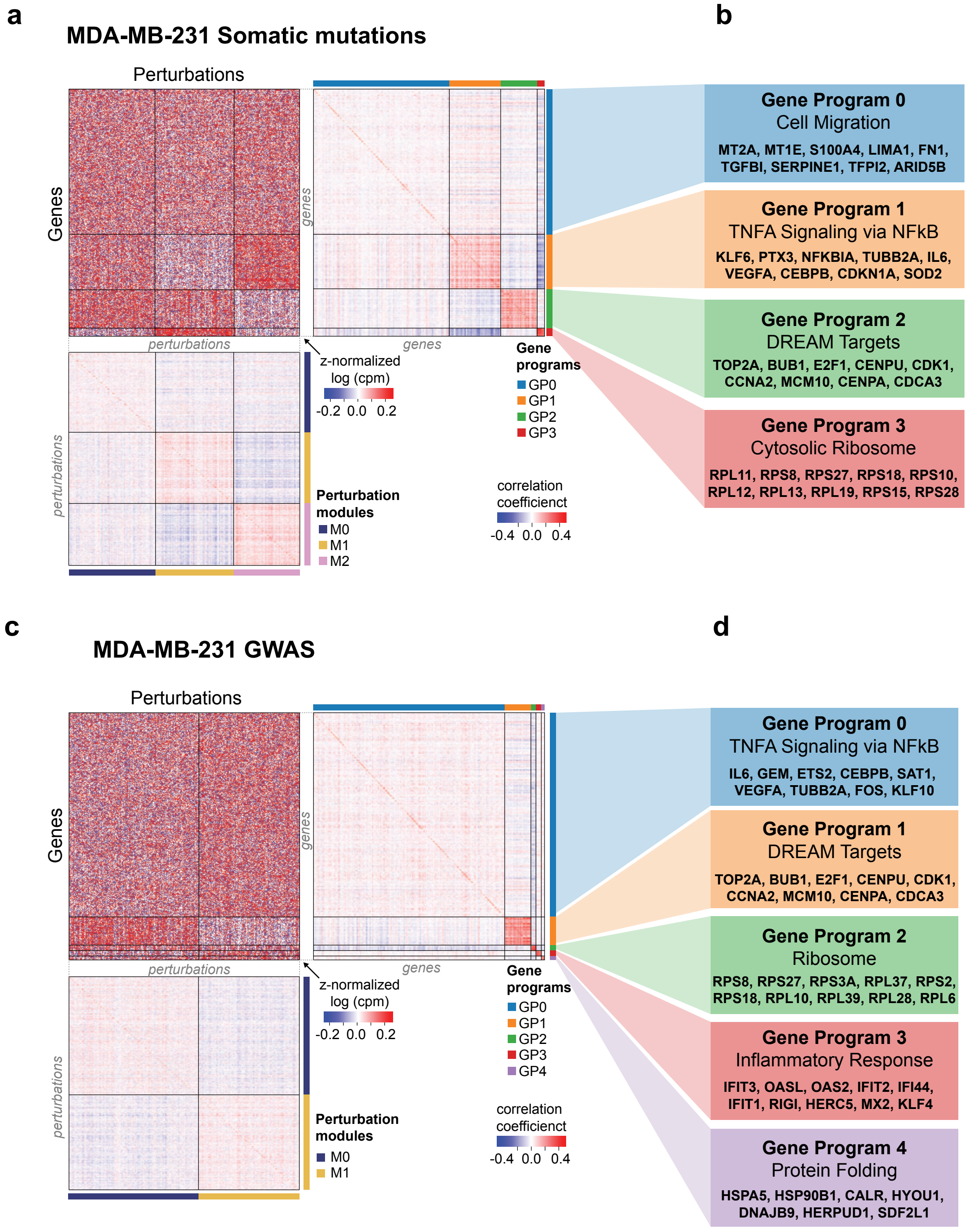
Supplementary Figure 7 - sgRNAs targeting the same region are functionally consistent with each other.



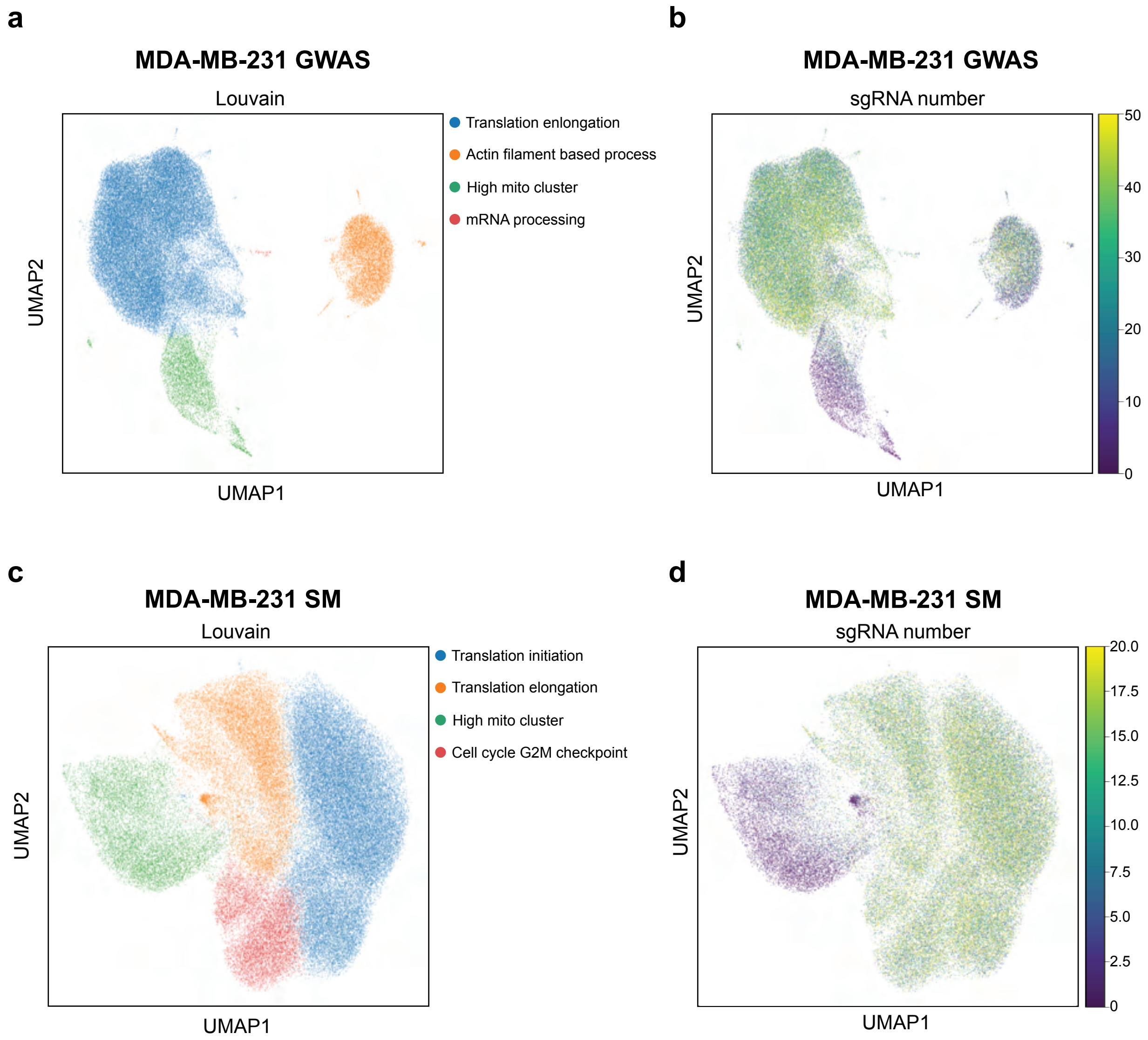
Supplementary Figure 8 - Single cell data of enhancer indirect hits.



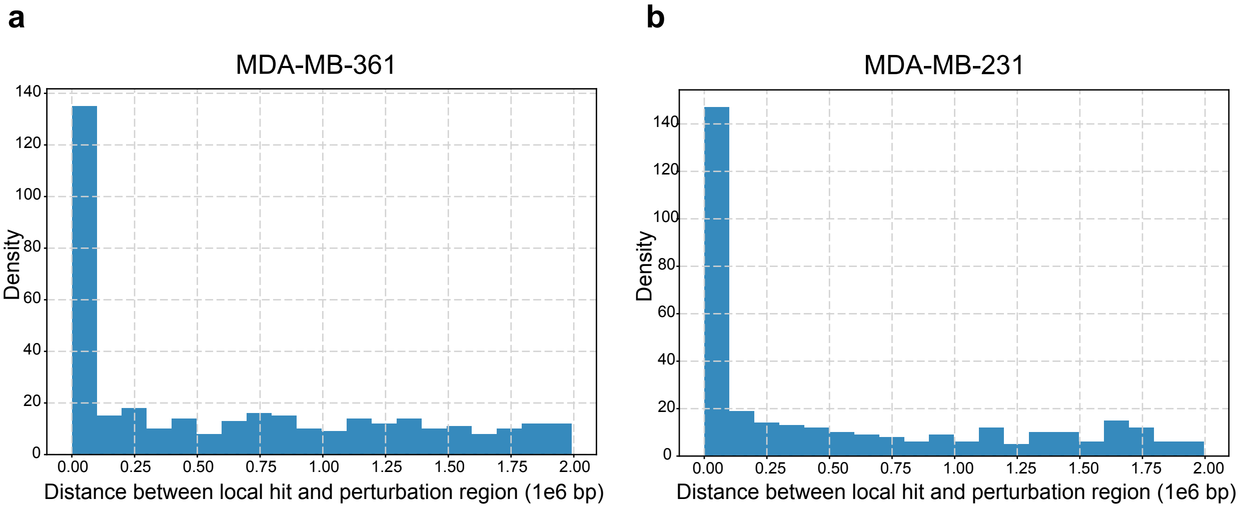
Supplementary Figure 9 - Perturbation modules and gene programs of MDA-MB-231 screens.



Supplementary Figure 10 - MDA-MB-231 single cell clustering.



Supplementary Figure 11 - Local hit comparison in ER+ and ER- cells.



Supplementary Figure 12 - Comparison between empirical adjustment and bootstrapping adjustment.