Figure S1
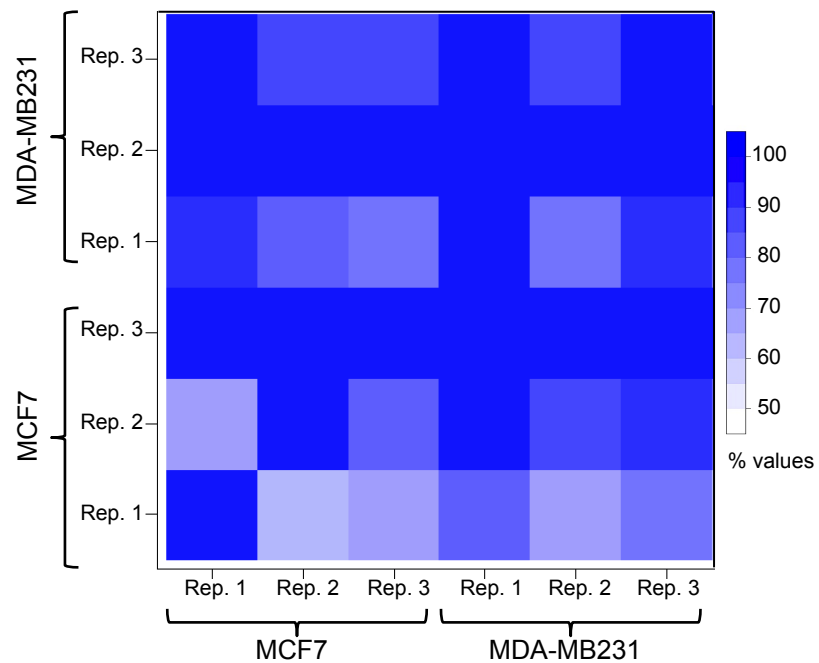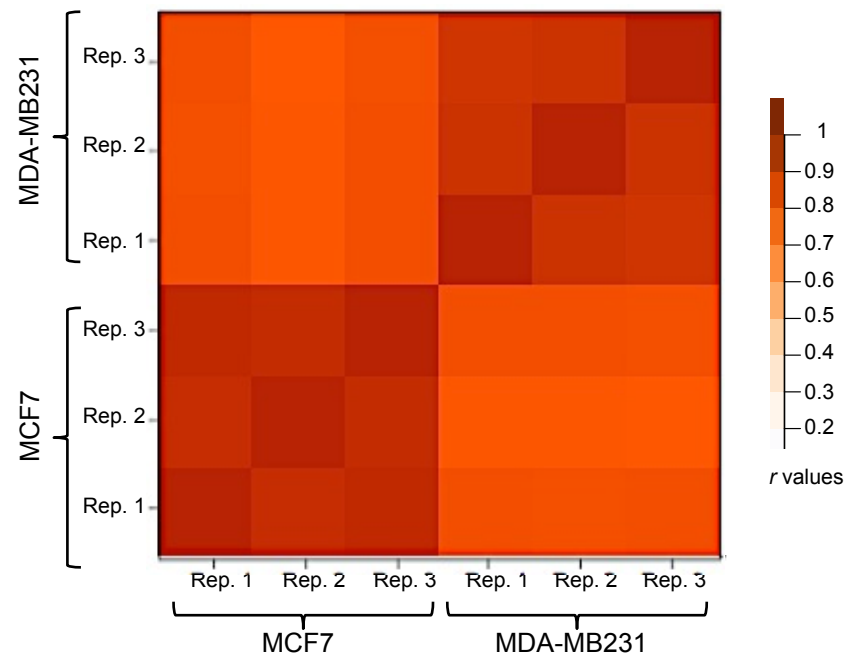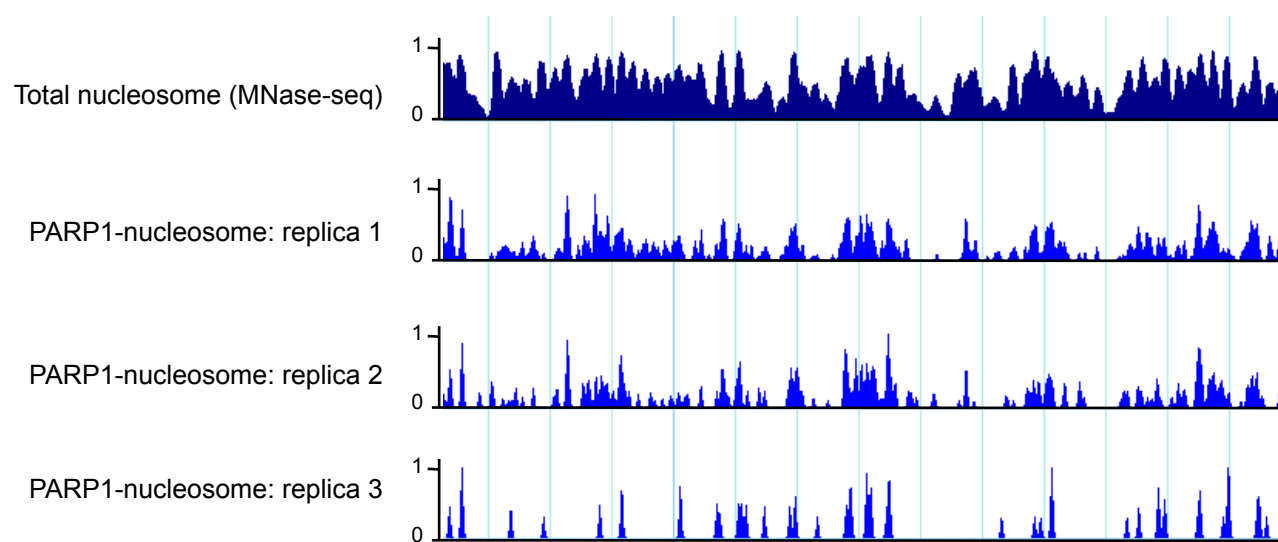
A.

B.

C.

Figure S1: Reproducibility of PARP1-nuc-ChIP-seq data: Using both methods of PARP1 peak calling methods showed high reproducibility with each replicate. A) Peak detection was performed by running model-based analysis of ChIPSeq (MACS) bandwidth of 200 bp, and a P-value threshold of 1×10^{-5}). B) Aligning PARP1-nucleosome reads and mapping the centers of these nucleosomes showed reproducibility with each replicate. C) Wig plots imported into the UCSC browser show reproducibility of the peaks.