



Fig. S9. Comparison of genome-wide signal between MDA-MB-231 replicates. (A) Correlation of mean FAIRE signal in 300 bp windows across the genome in pairwise comparisons between replicates. Canonical chromosomes (chr1-22, chrX, chrY) colored black, non-canonical chromosomes (alternative haplotypes, unplaced/unlocalized contigs) colored purple. (B) Mean normalized FAIRE signal in each replicate 1.2 kb from the center of the union set of peaks called. Log₂FoldChange between mean FAIRE signal 50 bp around summit and mean FAIRE signal at 50 bp flanking peak end shown. (C) Distribution of mean FAIRE signal in each replicate at non-canonical genome wide bins (replicate 1, orange; replicate 2, brown; replicate 3, gold). (D) Distribution of mean FAIRE signal in each replicate at union set of peaks called (replicate 1, orange; replicate 2, brown; replicate 3, gold). (E) Range of mean FAIRE signal in each replicate at union set of peaks called. FAIRE signal in replicate 3 significantly greater than replicate 1 and 2, marked by asterisk.