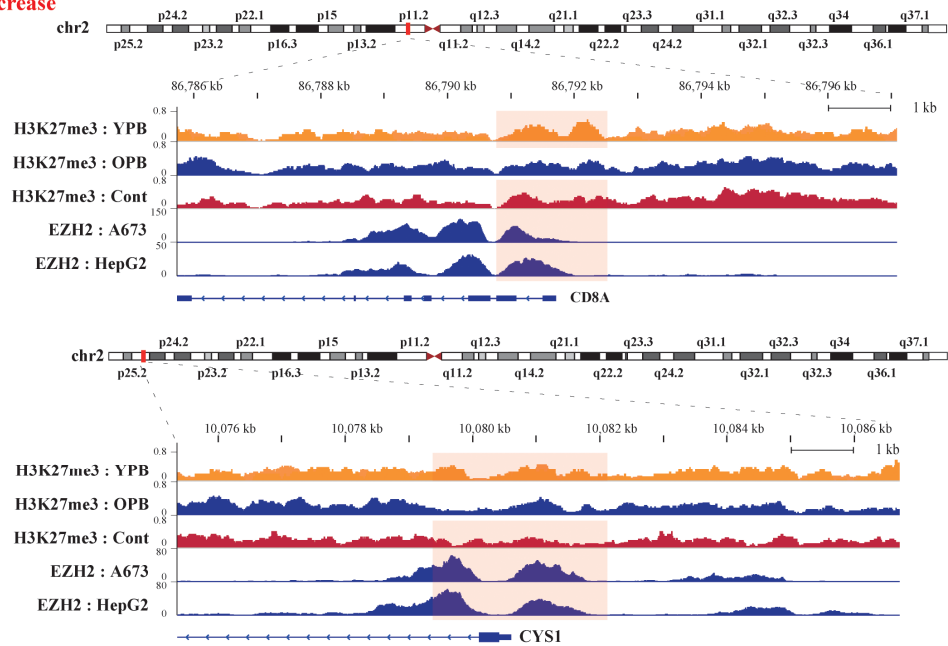


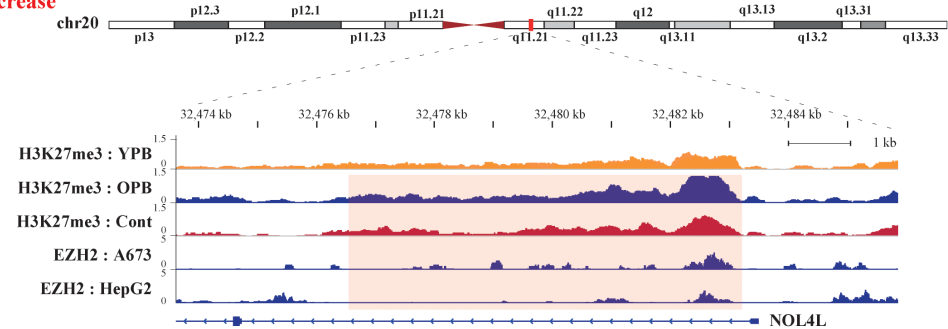
Supplementary Figure 5.

A

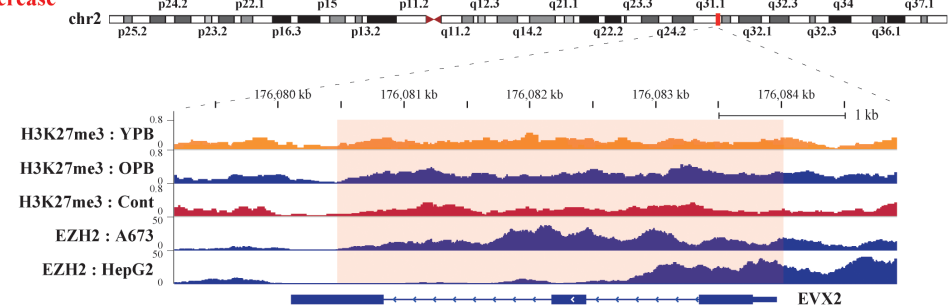
YPB-caused
H3K27me3 increase



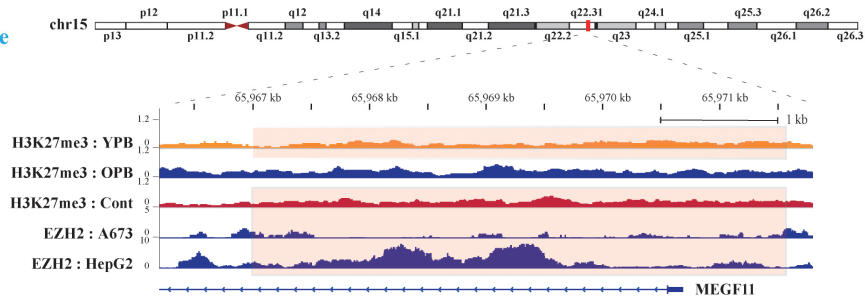
OPB-caused
H3K27me3 increase



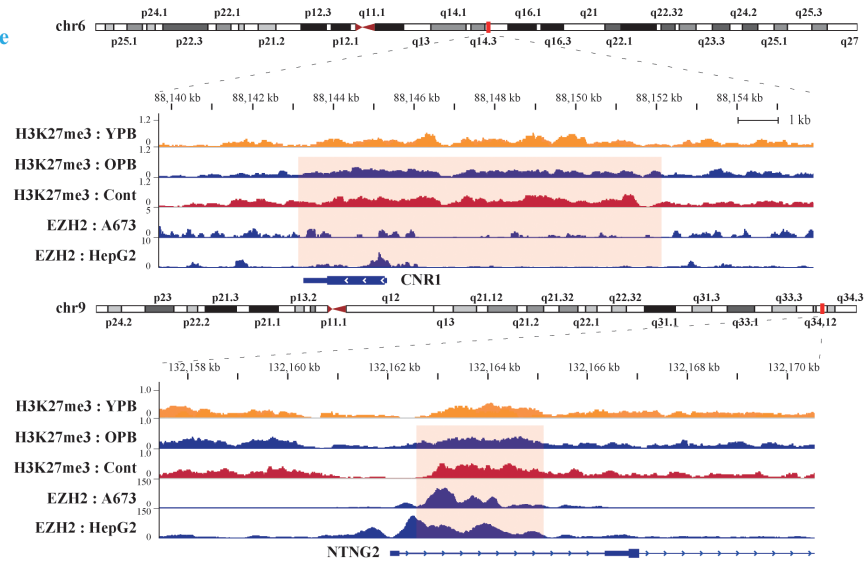
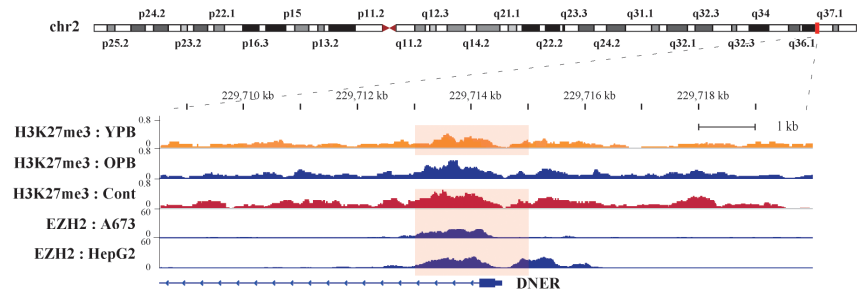
YPB/OPB-caused
H3K27me3 increase



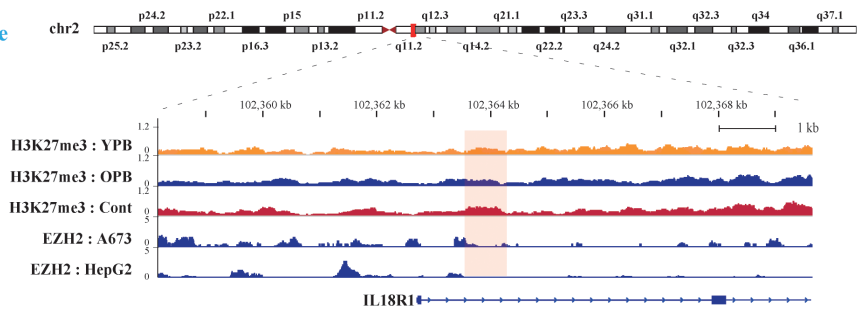
B YPB-caused
H3K27me3 decrease

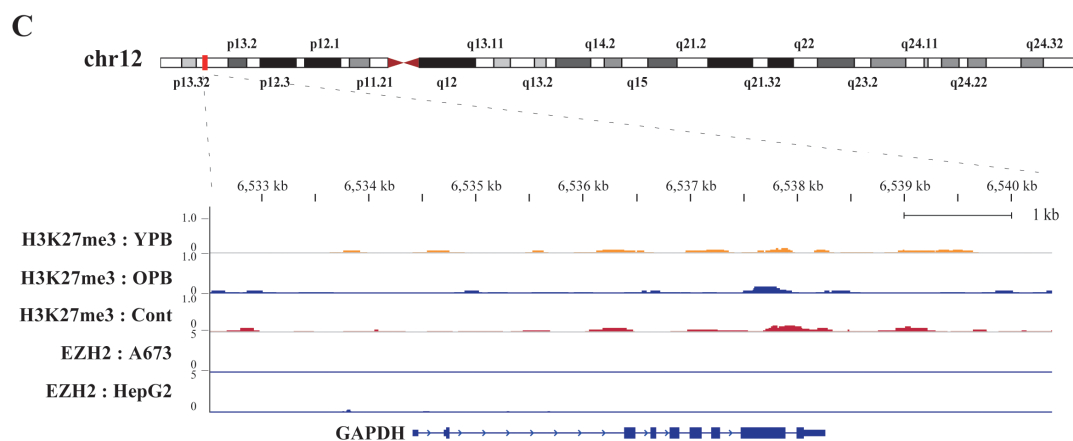


OPB-caused
H3K27me3 decrease



YPB/OPB-caused
H3K27me3 decrease





Supplementary Figure 5. Aligned gene browser tracks between the H3K27me3 ChIP-seq dataset from the YPB/OPB-treated MDA-MB-231 cells and two EZH2 ChIP-seq datasets from other cell lines. Both increased (A) and decreased (B) H3K27me3 signals caused by YPB, OPB or both treatments are presented, together with the EZH2 ChIP-seq signals from the A673 and HepG2 cells (ENCFF521AKL and ENCFF545XSF in the ENCODE database) at the same loci. The regions of the tracks with increased (in A) and decreased (in B) changes are marked with shadows. In C, the gene browser tracks of the GAPDH gene locus are presented.