



Figure S6

Figure S6 . Proteasome inhibition affects accessibility of transcriptionally active ER regions.

A) Non-genic DOCR transcription is responsive to E2 treatment. Heatmaps showing GRO-seq signal at nongenic TSSs that overlap GAIN (left) and LOST DOCRs (right) in cells treated with vehicle (veh) and estradiol (E2). **B)** MG132 and E2 repress transcription of SUMO1P1 SE region. Graph showing RNA-seq expression (read counts) of the DOCR regions that overlap with the SUMO1P1 SE. **Bottom:** Graph showing RNA expression from the SE region, x-axis shows the primer sets used qPCR analysis. Right: Graph showing RNA expression of selected regions within SE in cells treated with MG132 and E2. Primer genomic coordinates (P) are indicated **C)** Tracks showing chromatin state and transcription features of TFF1 and ZNF217, representative genes induced and repressed by E2. Graphs show RNA expression TFF1 and ZNF217. RNA expression normalized to 5S rRNA.