Cell Reports, Volume *27*

Supplemental Information

Specific Contributions of Cohesin-SA1 and Cohesin-SA2 to TADs and Polycomb Domains in Embryonic Stem Cells

Ana Cuadrado, Daniel Giménez-Llorente, Aleksandar Kojic, Miriam Rodríguez-Corsino, Yasmina Cuartero, Guillermo Martín-Serrano, Gonzalo Gómez-López, Marc A. Marti-Renom, and Ana Losada

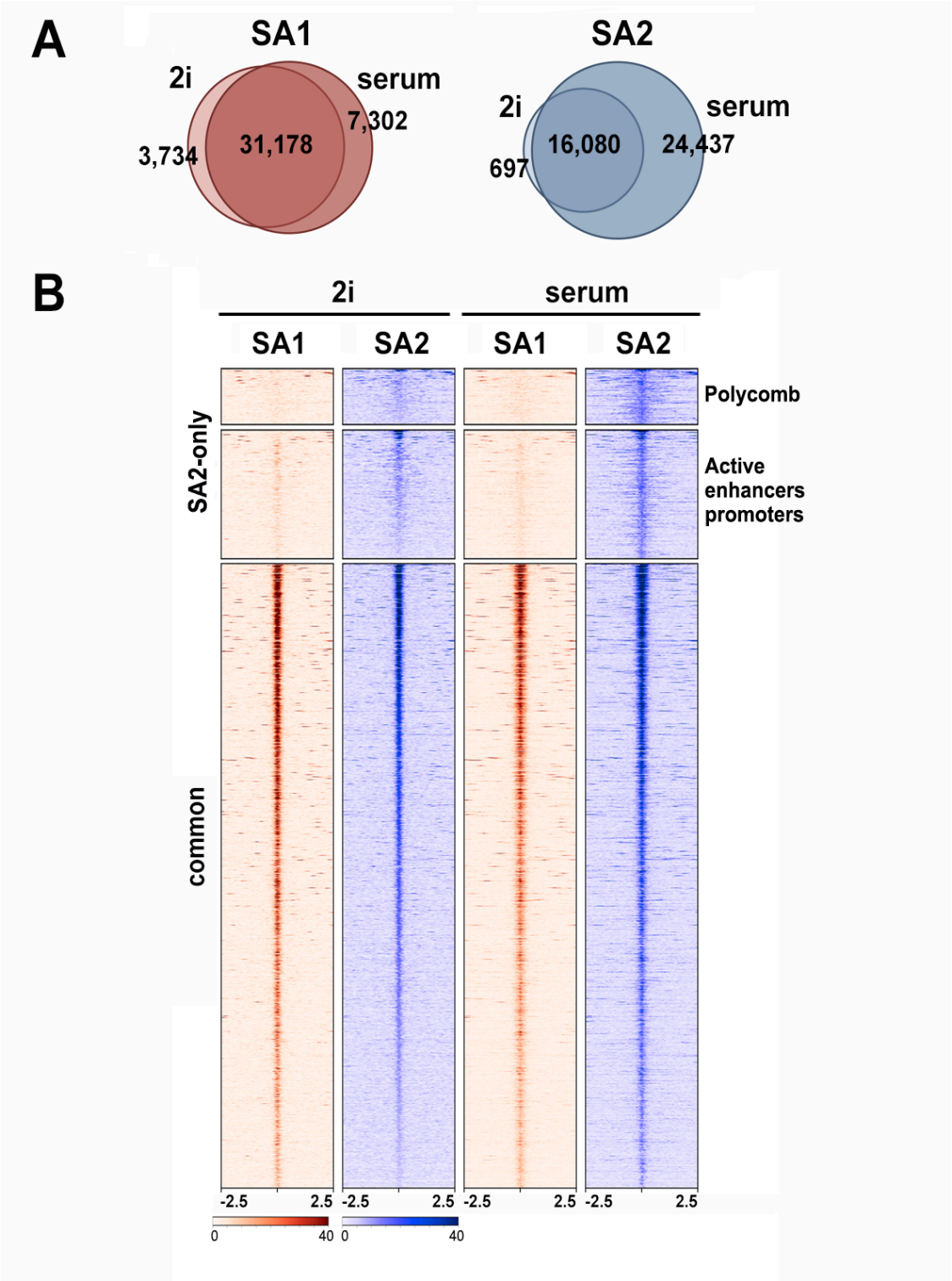

Figure S1 (Related to Figure 2)

(A) Venn diagrams showing overlap between SA1 and SA2 binding sites defined in mESCs growing under 2i and serum conditions. The transition between 2i and serum state involves an important increase in the number of cohesin SA2 positions. (B) Read heat maps showing SA1 and SA2 distribution in mESCs growing under 2i and serum conditions around the cohesin positions defined in Figure 1A.

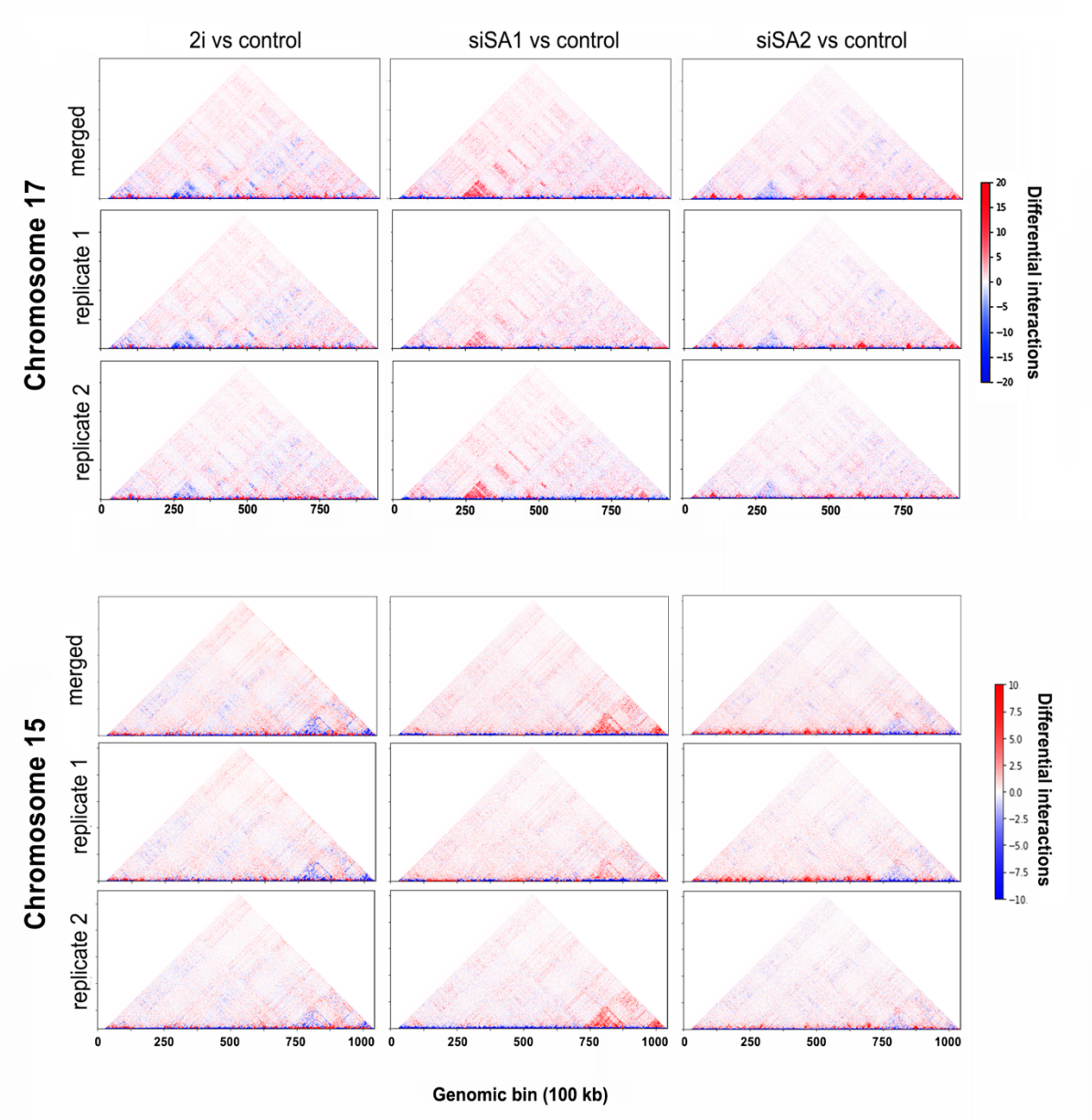

Figure S2 (Related to Figure 3C)

Matrices showing differential interactions in chromosome 17 (top) and chromosome 15 (bottom) when comparing mESCs growing in 2i, SA1 depleted or SA2 depleted cells growing in serum to mock depleted cells (control) also growing in serum. Independent matrices for each of two biological replicates as well as the merge are shown.

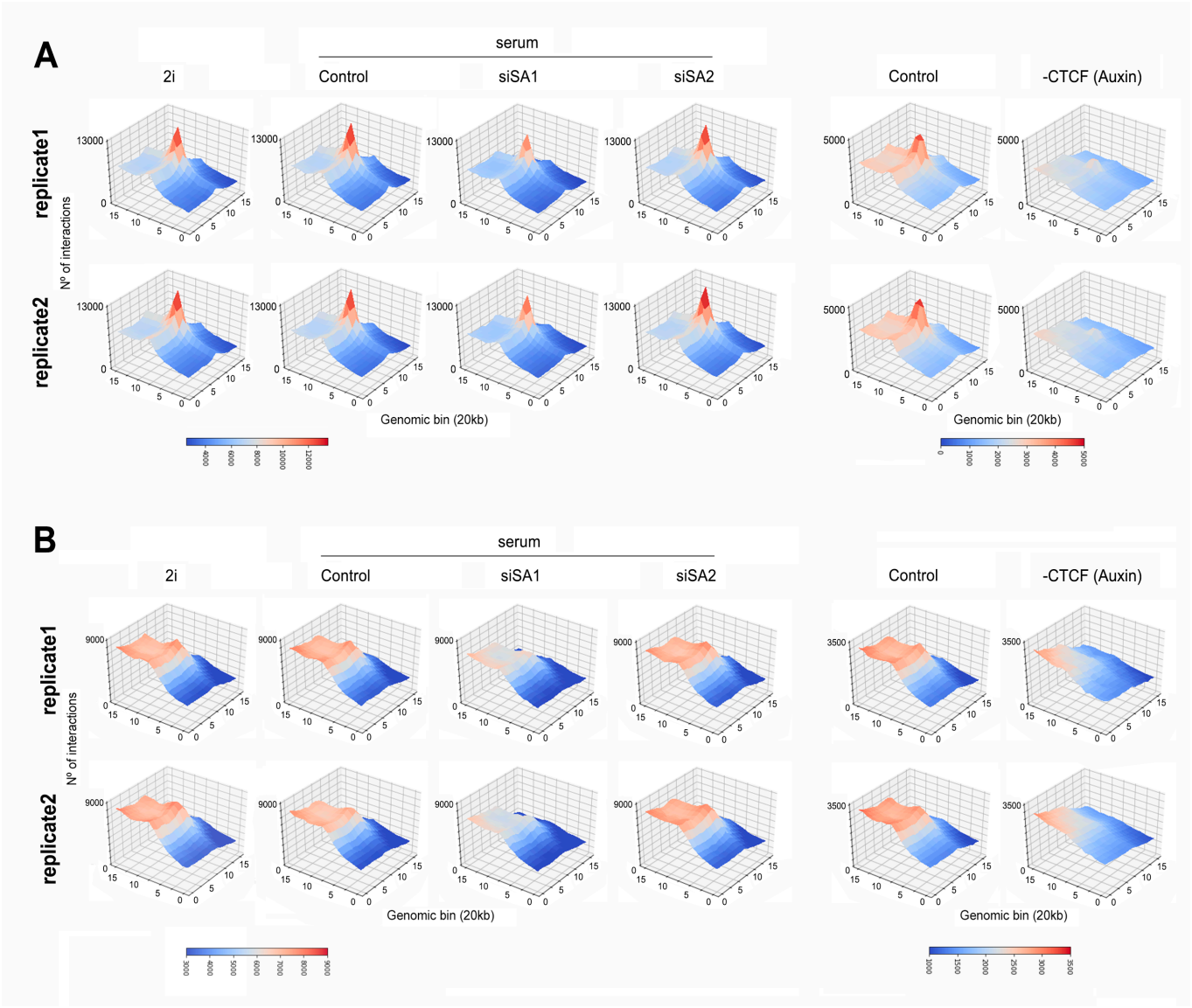

Figure S3 (Related to Figure 3D,E)

Meta-plots of 3D interactions showing contact strength in the cohesin mediated loops defined by Hi-ChIP (A) or in high resolution TADs (B) in two biological replicates analyzed independently. The corresponding plots using the merge of the two replicates are shown in Figure 3 (D) and (E), respectively.

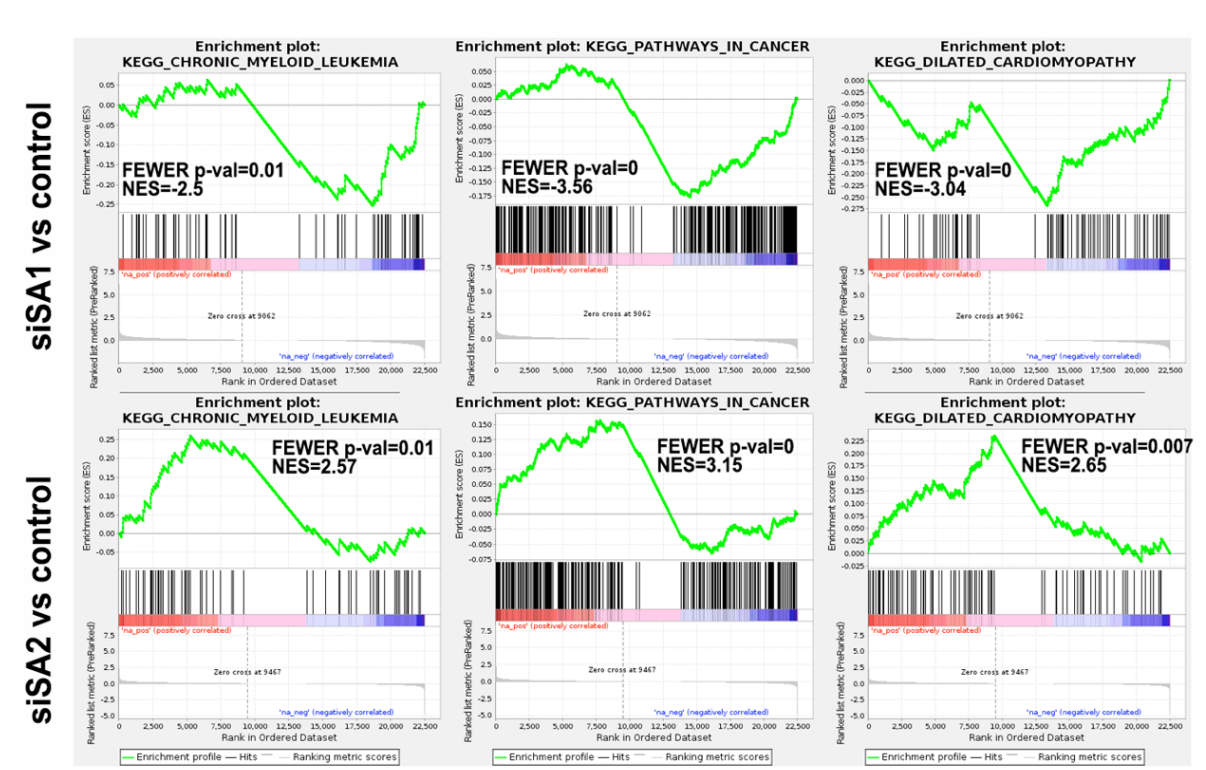

Figure S4 (Related to Figure 6)

Enrichment plots for genes in KEGG pathways that are upregulated in mESCs upon SA2 depletion (NES>0) and downregulated upon SA1 depletion (NES<0). Statistical significant threshold was established by FEWER p-value<0.05.