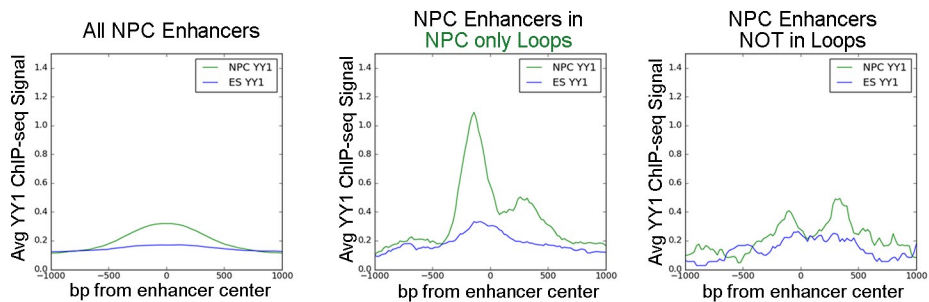
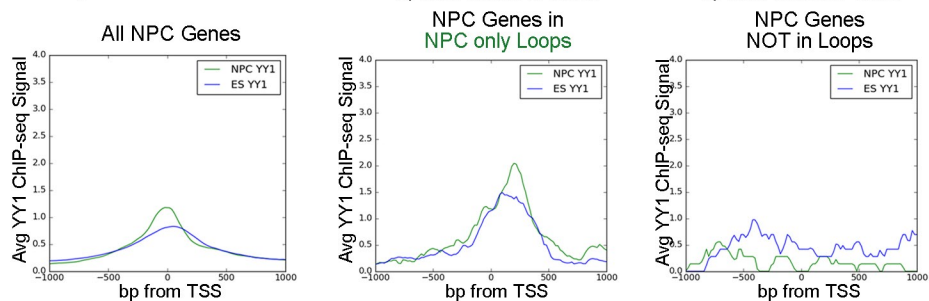


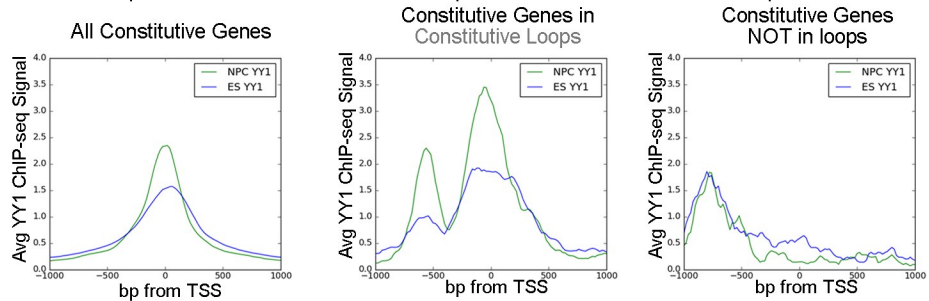
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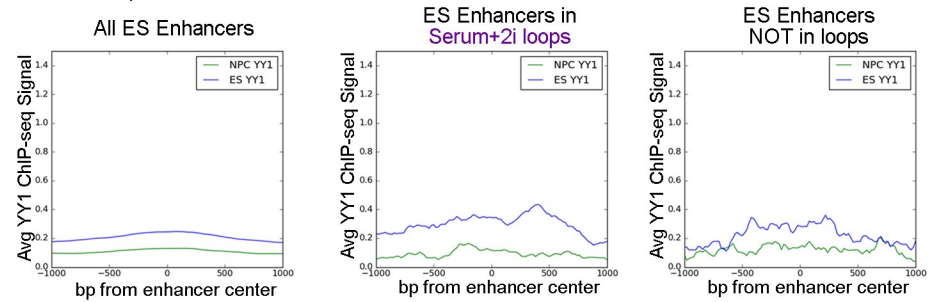
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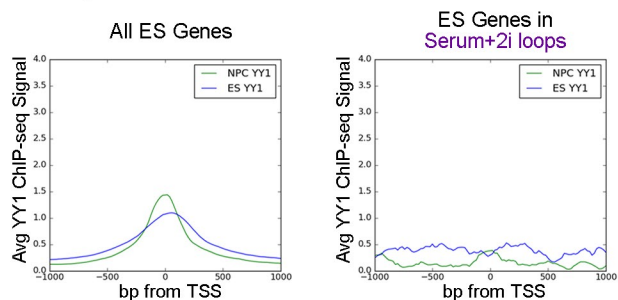
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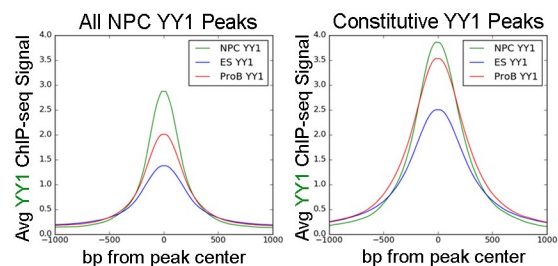


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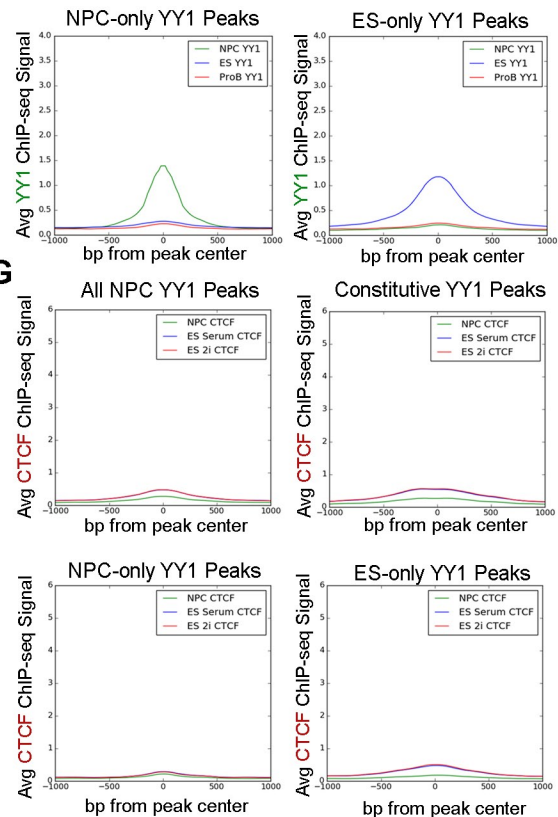


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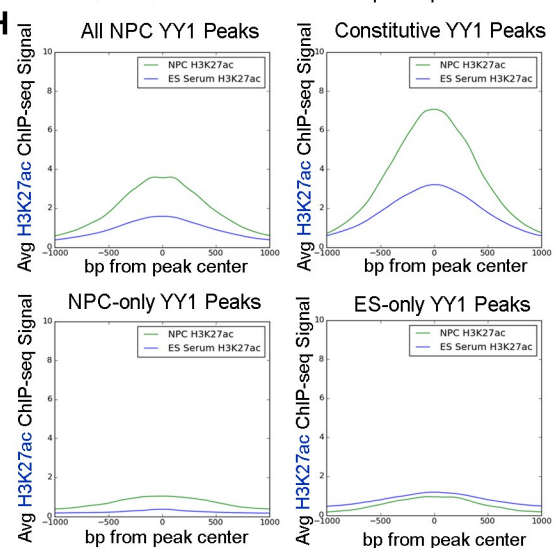
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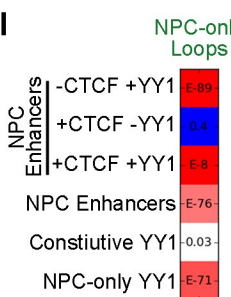
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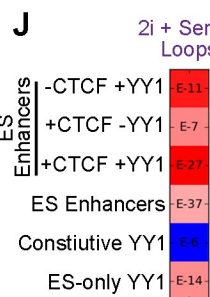
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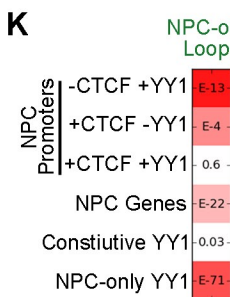
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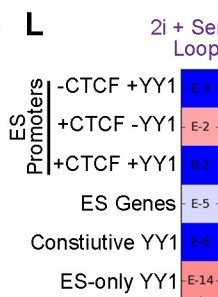
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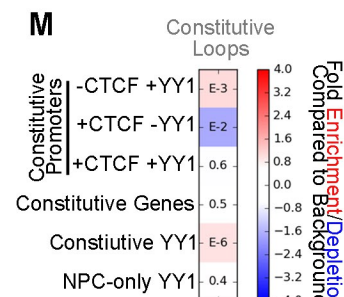
K



L



M



Fold Enrichment/Depletion Compared to Background

Supplemental Figure S12. YY1 is enriched across genomic annotations 'active' in NPCs in looping interactions. (A-E) Pileups of YY1 ChIP-seq signal at (A) NPC enhancers, (B) NPC genes, (C) constitutive genes, (D) ES enhancers, and (E) ES genes for the total set of each annotation (left), the subset of each annotation found at the base of the loops of the relevant class (middle), and the subset of each annotation not involved in any looping interaction (right). **(F)** Pileups of YY1 ChIP-seq signal at (top left) all YY1 peaks called in NPCs, (top right) YY1 peaks present in ES cells, NPCs, and ProB cells, (bottom left) NPC-specific YY1 peaks, and (bottom right) ES-specific YY1 peaks. **(G)** Pileups of CTCF ChIP-seq signal across the same set of YY1 peaks as presented in (F). **(H)** Pileups of H3K27ac ChIP-seq signal across the set of YY1 peaks listed above. **(I-M)** Fold enrichment/depletion of the parsed chromatin regulatory elements from (A-E) in the relevant looping class compared to background interactions. P-values are computed with Fisher's Exact test and listed in each entry.