

Supporting Information

Teytelman et al. 10.1073/pnas.1316064110

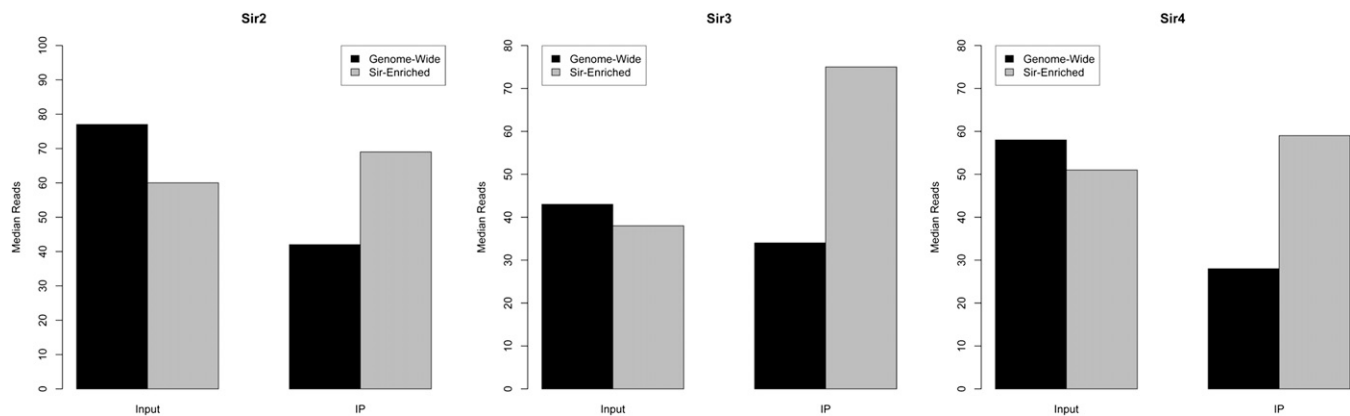


Fig. S1. Enrichment due to high read coverage in the immunoprecipitate. Bar graphs show median number of reads for the input and immunoprecipitate (IP) samples genome-wide (black) and at Sir-enriched loci (gray) for Sir2, Sir3, and Sir4.

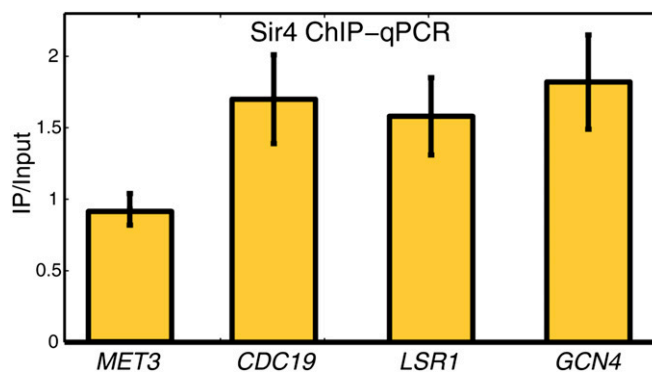


Fig. S2. Confirmation of ChIP enrichment at highly expressed genes by ChIP-qPCR. Sir4 ChIP-qPCR reproduces the ChIP-Seq enrichment at highly expressed *CDC19*, *LSR1*, and *GCN4*. No enrichment is seen at the uninduced *MET3* negative control. The error bars show the SEM values from three biological replicates.

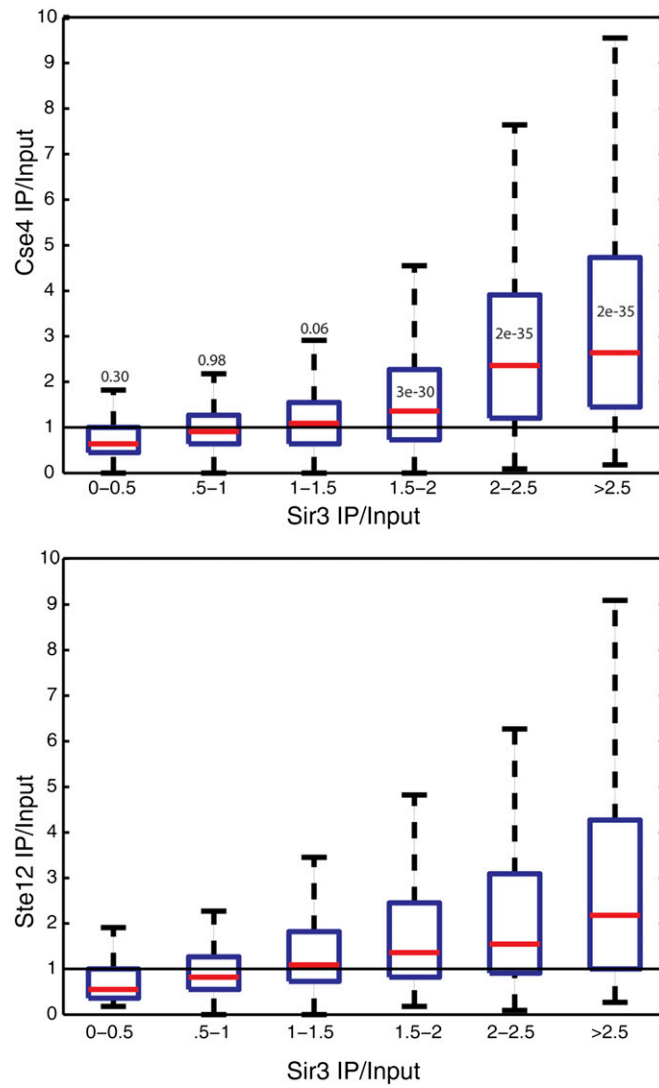


Fig. S3. Sir3 levels correlate with ChIP-Seq signals for Ste12 and Cse4. Boxplots show Cse4 and Ste12 ChIP-Seq levels, as a function of Sir3 enrichment.

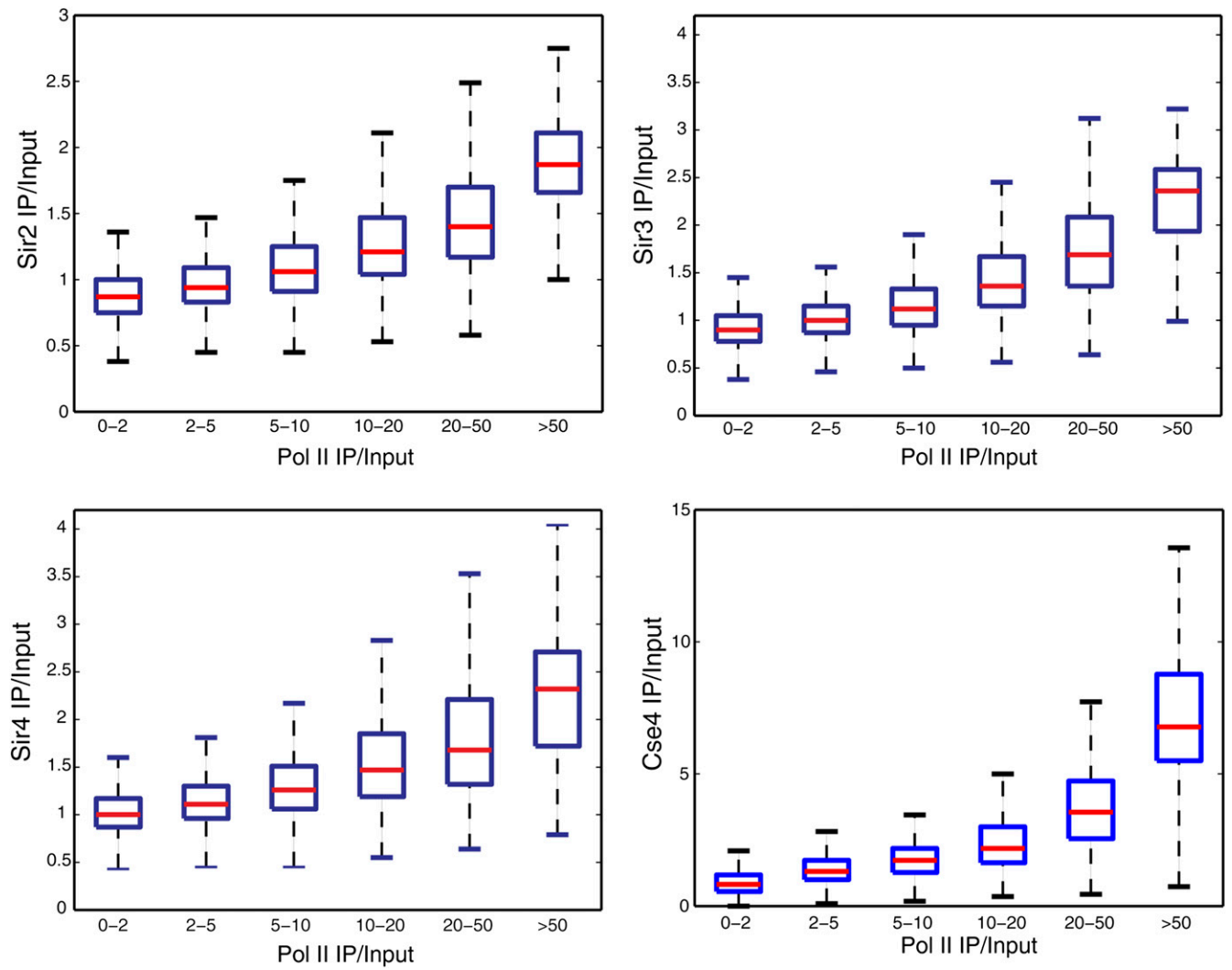


Fig. S4. Pol II levels correlate with ChIP-Seq signals for Sir2, Sir3, Sir4, and Cse4. Boxplots show Sir2, Sir3, Sir4, and Cse4 ChIP-Seq levels, as a function of Pol II enrichment.

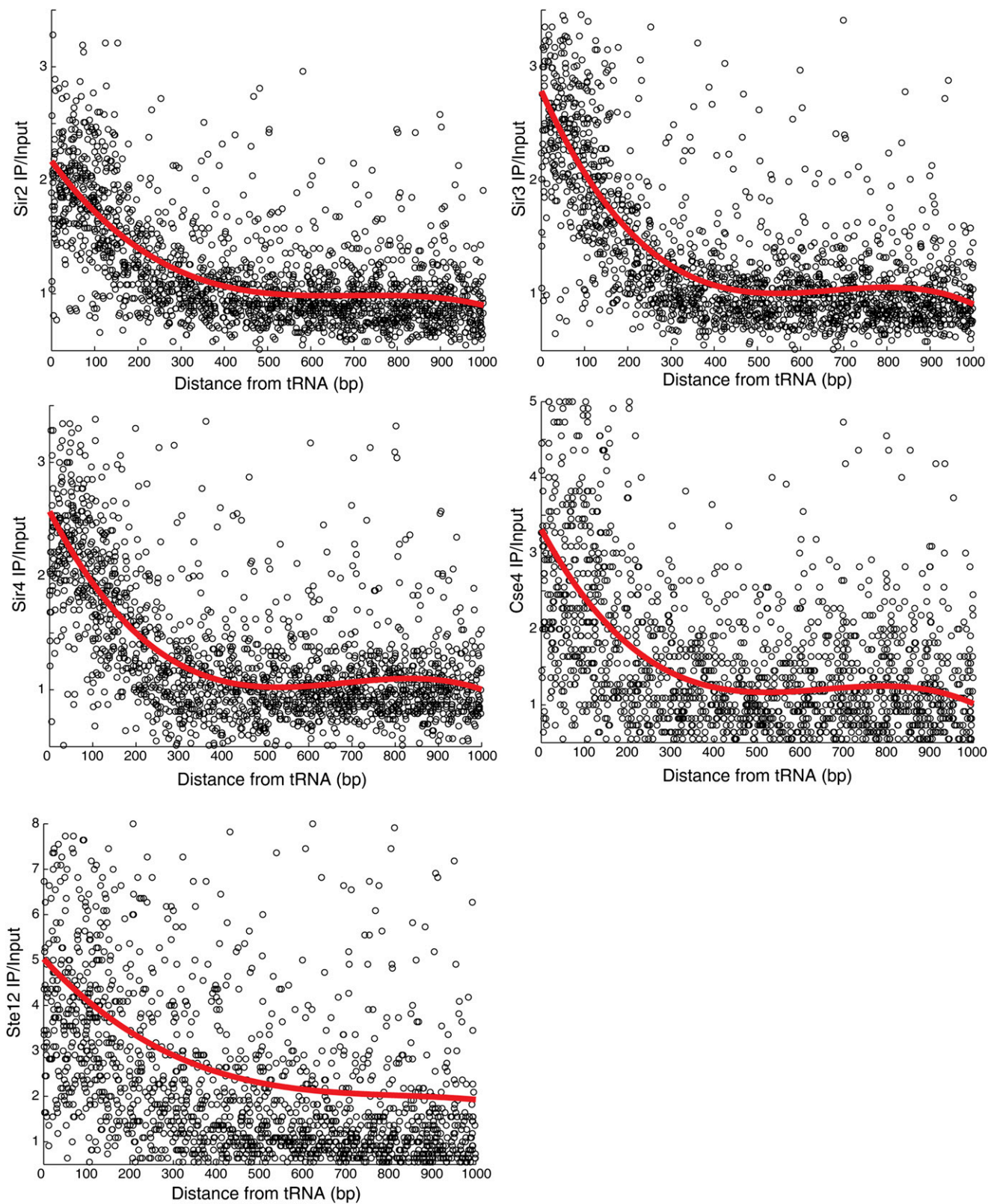


Fig. S5. tRNA proximity correlates with ChIP-Seq signals for Sir2, Sir3, Sir4, Cse4, and Ste12. Sir2, Sir3, Sir4, Cse4, and Ste12 ChIP-Seq levels are shown as a function of the distance from *S. cerevisiae* annotated tRNAs. The red curve is a polynomial fit to the scatterplot.

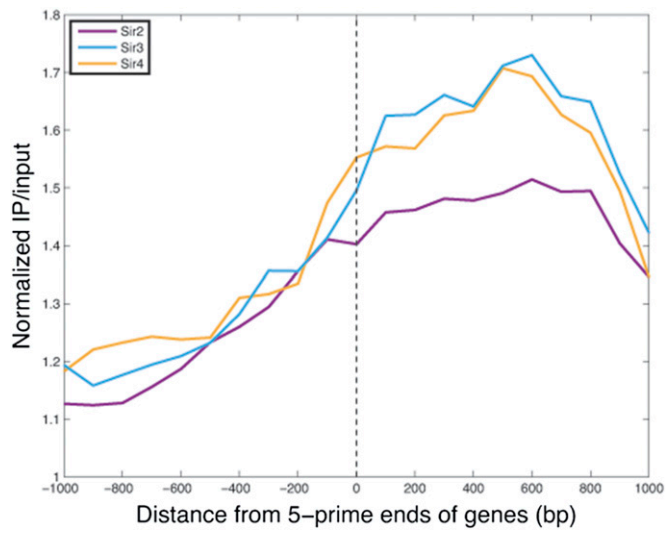


Fig. 56. Sir proteins are enriched across the entire ORF. Sir2, Sir3, and Sir4 ChIP-Seq levels are shown as a function of the distance from the 5' starts of the 200 most highly expressed genes in the *Saccharomyces cerevisiae* genome.

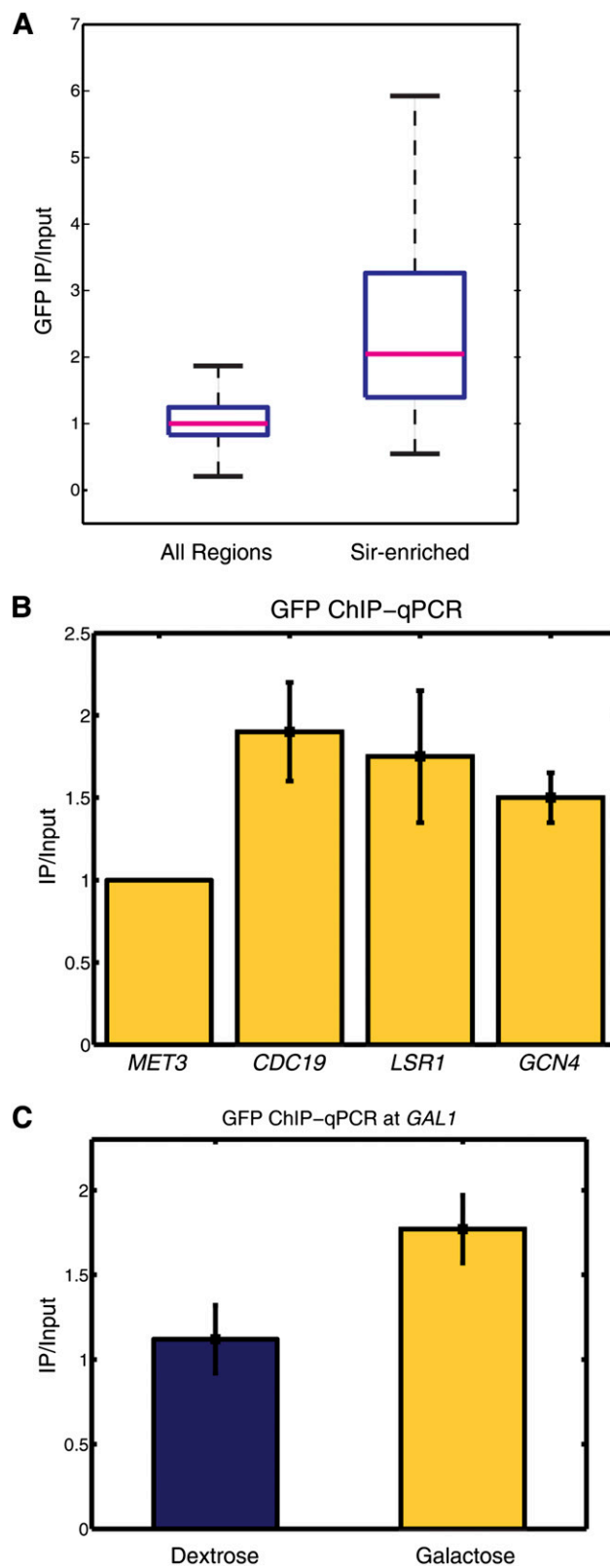


Fig. S7. Confirmation of GFP hyper-ChIPability. (A) Boxplots comparing the GFP ChIP-Seq levels genome-wide versus the 238 Sir-enriched euchromatic loci. Data are from the glucose condition. (B) GFP ChIP-qPCR in glucose reproduces the ChIP-Seq enrichment at highly expressed *CDC19*, *LSR1*, and *GCN4*. All values are shown as relative to the uninduced *MET3* negative control. The error bars show the SEM values from three biological replicates. (C) ChIP-qPCR values, normalized to *SEN1*, of an NLS-tagged GFP protein. Induction-dependent enrichment of the *GAL1* gene is shown; enrichment is seen only in the induced galactose condition. The error bars show the SEM values from three biological replicates.

Other Supporting Information Files

[Table S1 \(DOCX\)](#)

[Table S2 \(DOCX\)](#)

[Table S3 \(DOCX\)](#)