



Figure 5-figure supplement 1. GapR ChIP compared to nucleosome occupancy and chromatin accessibility.

(A) Comparison of transcription in raffinose with and without α -factor treatment.

(B) GapR enrichment at *YGP1* in raffinose without (orange) or with (green) α -factor arrest before GapR induction (top). Transcription of the forward (green) and reverse (blue) strands in raffinose without (2nd panel) or with (3rd panel) α -factor arrest with annotated genes indicated.

(C) α -factor dependent GapR enrichment at 5' and 3' ends for induced vs repressed genes. Student's t-test p-value is reported.

(D) GapR enrichment in raffinose (orange) compared to nucleosome occupancy measured by MNase-seq (light grey) and chromatin accessibility measured by DNase-seq (dark grey) at the yeast mating loci, HML and HMR. Transcription from the forward (green) and reverse (blue) strands with annotated genes indicated (bottom).

(E) GapR binding compared to nucleosome occupancy and DNase-seq at a locus on chromosome IV as in (D).

(F) Heatmap showing MNase-seq at the 500 highest GapR enriched regions.

(G) Heatmap showing GapR enrichment in raffinose at the 500 most DNAse-accessible regions.

(H) Boxplot showing the %AT of GapR-enriched and DNase I sensitive sites showing mean, interquartile range, and outliers.

(I) GapR enrichment in raffinose (orange) compared with psoralen tiling array (blue, plotted in reverse). Psoralen peaks above threshold (+1.5) were called as 'negative supercoils' ($-\sigma$, red), and peaks below threshold (-1.5) were called as 'positive supercoils' ($+\sigma$, green). Transcription from the forward (green) and reverse (blue) strands with annotated genes indicated (bottom).

(J) Correlation between genomic psoralen enrichment (bTMP IP/input) and GapR-3xFLAG ChIP-seq calculated for every 100 bp.