



Figure 4-figure supplement 1. *S. cerevisiae* GapR ChIP-seq.

- (A) Transcriptional profiles of cells with and without GapR-3xFLAG integrated at LEU2. The largest change in expression pattern is at the LEU2 locus.
- (B) Change in gene expression change upon GapR expression in supercoiling-sensitive genes and stress response pathways (see Methods).
- (C) ChIP-seq profiles for GapR-3xFLAG (orange) and untagged GapR (grey) cells grown in glycerol. ChIP-seq profiles for GapR-3xFLAG cells grown in raffinose and in raffinose + α -factor. Cells were grown to OD 0.3-0.5 before addition of 2% galactose for 6 hr followed by fixation and ChIP.
- (D) Correlation between two independent GapR-3xFLAG ChIP-seq experiments in raffinose.
- (E) GapR-3xFLAG ChIP-seq in raffinose versus AT content. Mean enrichment at a given % AT (red dots). Motifs from DREME (below).
- (F) GapR ChIP profiles in raffinose. AT content (top), AT content below the genomic average (64%) is plotted in reverse. Normalized ChIP-seq (middle) of GapR-3xFLAG (orange) or untagged GapR (grey) expressing cells. Transcription (bottom) from the forward (green) and reverse (blue) strands with annotated genes indicated.
- (G) Histogram showing the length of GapR binding events.
- (H) Mean GapR enrichment in glycerol at 5' and 3' ends of long genes at various transcriptional cutoffs. Student's t-test p-value is shown.
- (I) GapR enrichment in glycerol is highest between convergently oriented genes.
- (J) GapR-bound regions in glycerol are more frequently between convergent genes. Pie charts shown as in Fig. 3H.
- (K) GapR enrichment is correlated with expression from upstream gene and uncorrelated with expression of downstream gene.