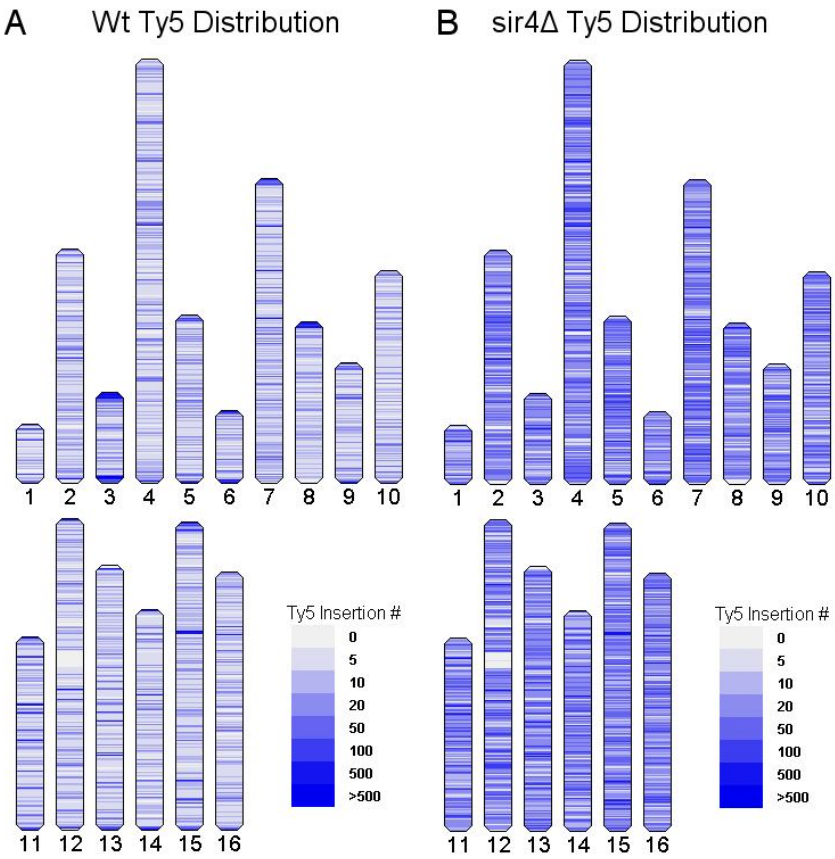
Supplemental Materials

Molecular Biology of the Cell

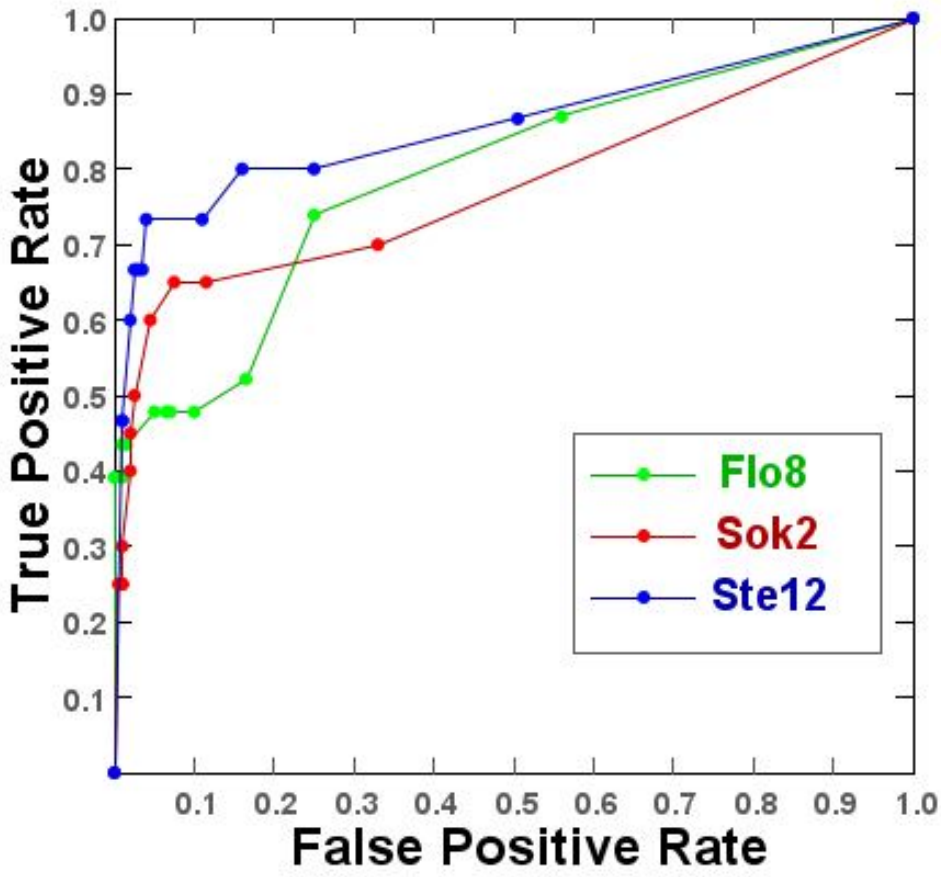
Mayhew et al.



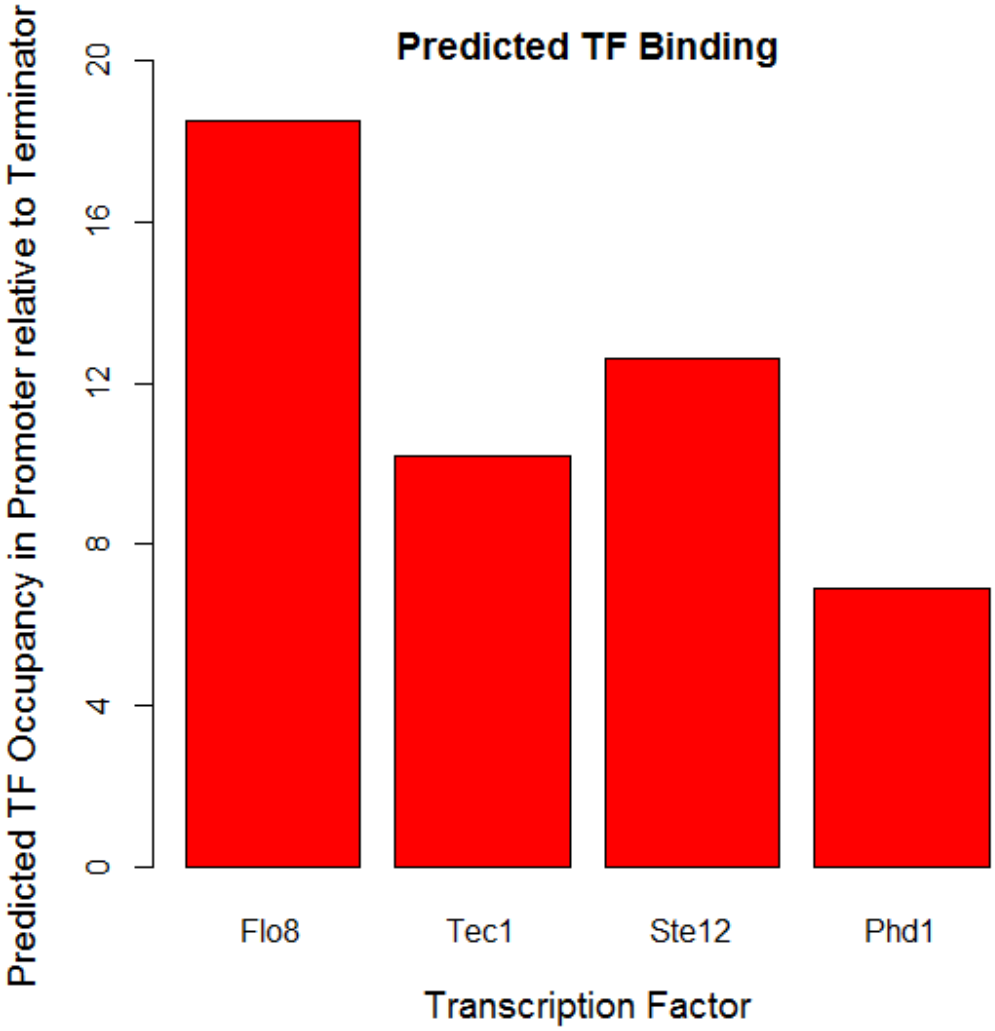
C

	Percentage of genome	Percentage of Ty5 insertions in WT yeast	Percentage of Ty5 insertions in *sir4Δ* yeast
Features			
Nonessential Coding Sequence	0.5775	0.3016	0.3204
Essential Coding Sequence	0.1452	0.0223	0.0199
tRNA Sequence	0.0018	0.0003	0.0007
snRNA Sequence	0.0014	0.0008	0.0021
Centromere Sequence	0.0002	0.0002	0.0000
Intergenic Sequence	0.2740	0.6748	0.6568
Promoters			
Promoters of Nonessential Genes	0.1606	0.2967	0.4049
Promoters of Essential Genes	0.0318	0.0288	0.0568
Not Promoter Sequence	0.8075	0.6745	0.5383

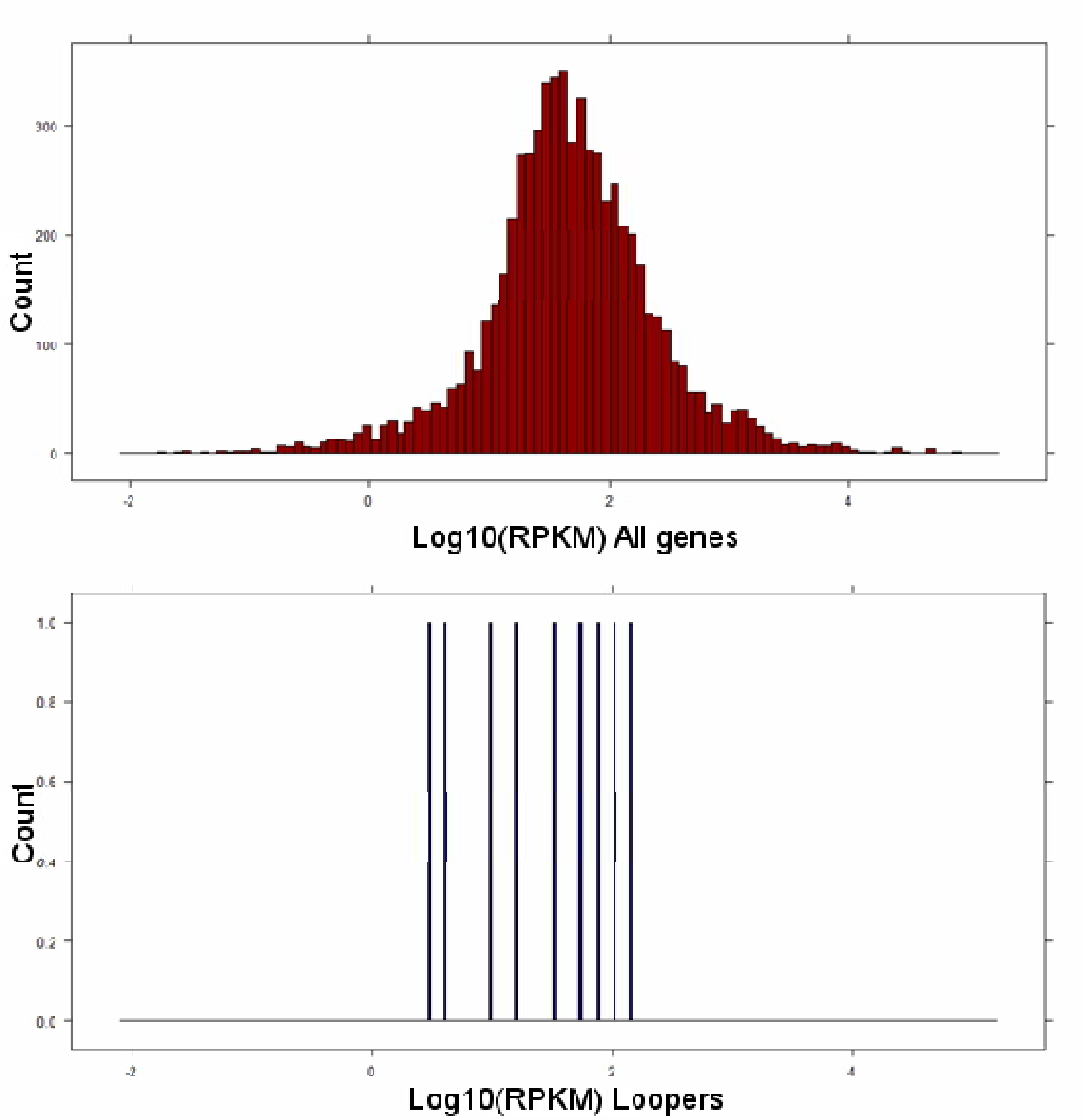
Supplemental Figure 1. Background distribution of Ty5 in the absence of TF-Sir4 expression. (A) In Wt cells the distribution of insertions is biased towards the telomeres and HML on chr III. (B) In *sir4Δ* mutant cells the distribution is more uniform across chromosomes. (C) Insertions into the coding sequence of essential genes are strongly selected against in both yeast strains; however, insertions into their promoters are not.



Supplemental Figure 2. Accuracy of 3 TFs from the Calling Card multiplex compared to those 3TFs tested in Σ1278b background in diploid pseudohyphal growth conditions by ChIP-chip (Borneman et al. 2006) and a list of 250 negative targets generated from the same dataset. AUCs for Flo8, Sok2, and Ste12 were 0.79, 0.78, and 0.86 respectively.



Supplemental Figure 3. TFs which serve as activators of *FLO11* expression are all more likely to be bound in the promoter of *FLO11* relative to its terminator given the DNA sequence and the known PWSM for each TF.



Supplemental Figure 4. Genes with looping events are not enriched for the most highly expressed genes. The expression of all 9 of the "looping" genes were at levels below the average of all genes.