Figure S1  The DNA sequence recognized by Mit1 is similar to that recognized by Wor1. (A) Motif recognized by Mit1 developed using the lowest 50 scoring binding sites. Binding site determination and motif analysis performed using MochiView v1.45. (B) Motif recognized by Mit1 developed using all 74 binding sites. (C) A comparison of the motif from (A) to the motif from (B), the motifs match with an E-value of 0 (as determined by MochiView v1.45, using an approach based on that presented in Gupta et al. 2007 [Gupta et al. 2007]). (D) A comparison of the motif from (A) to the previously published Wor1 motif (Lohe et al. 2010), the motifs match with an E-value of 0.0033. (E) ROC Enrichment plot for the Mit1 motif from (A), the fraction of the experimental set (24 Mit1 binding sites not used to make the motif) bound is plotted on the x-axis (“True Positive”). The bound fraction of a control set of 500bp regions randomly selected from promoters not bound by Mit1 is plotted on the y-axis (“False Positive”). Plots were made using MochiView v1.45 using an approach similar to that previously reported (Lohe et al. 2010). (F) ROC Enrichment plot for the Mit1 motif from (A), using the entire Mit1 binding set (74 sites) for the experimental set.