



**Figure S5** Determination of threshold for motif analysis. To determine optimal p values to minimize false positive calls and provide reasonable sensitivity, MAST analysis was performed on sequences under peaks with different thresholds for E2F, DREF, FOXJ2 and RAM motifs (A-D). The analysis was repeated five times on sequences of identical A/T composition that had been scrambled. The threshold  $p < 0.0001$  showed the highest fold enrichment, thus further analyses (in Figure 6 B, C and D) were carried out with this value.