Figure S1
Figure S5

The figure shows a series of data plots comparing nucleosome occupancy across various genomic regions. The x-axis represents the distance from the motif in kilobases, and the y-axis depicts nucleosome occupancy in log2 scale. The plots are differentiated by transcript features such as poly A, poly AG, poly G, Sap1, and CTCGCT, each with multiple subplots indicating different genomic locations (proximal, distal). The data points are clustered to illustrate patterns in nucleosome distribution with respect to these motifs.
Figure S6

S. pombe

S. octosporus

S. japonicus

Nucleosome Occupancy (log2) vs. Distance to TSS (kb) for S. pombe, S. octosporus, and S. japonicus.