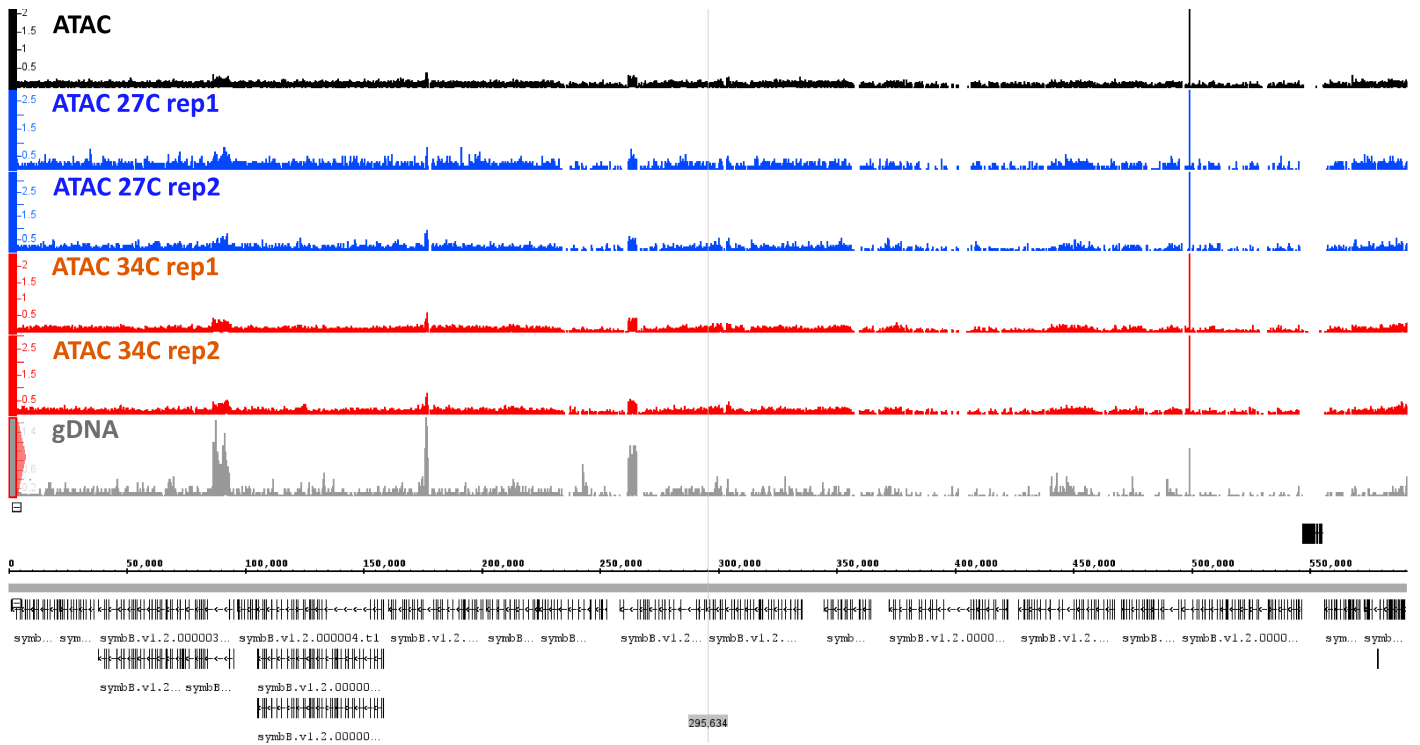
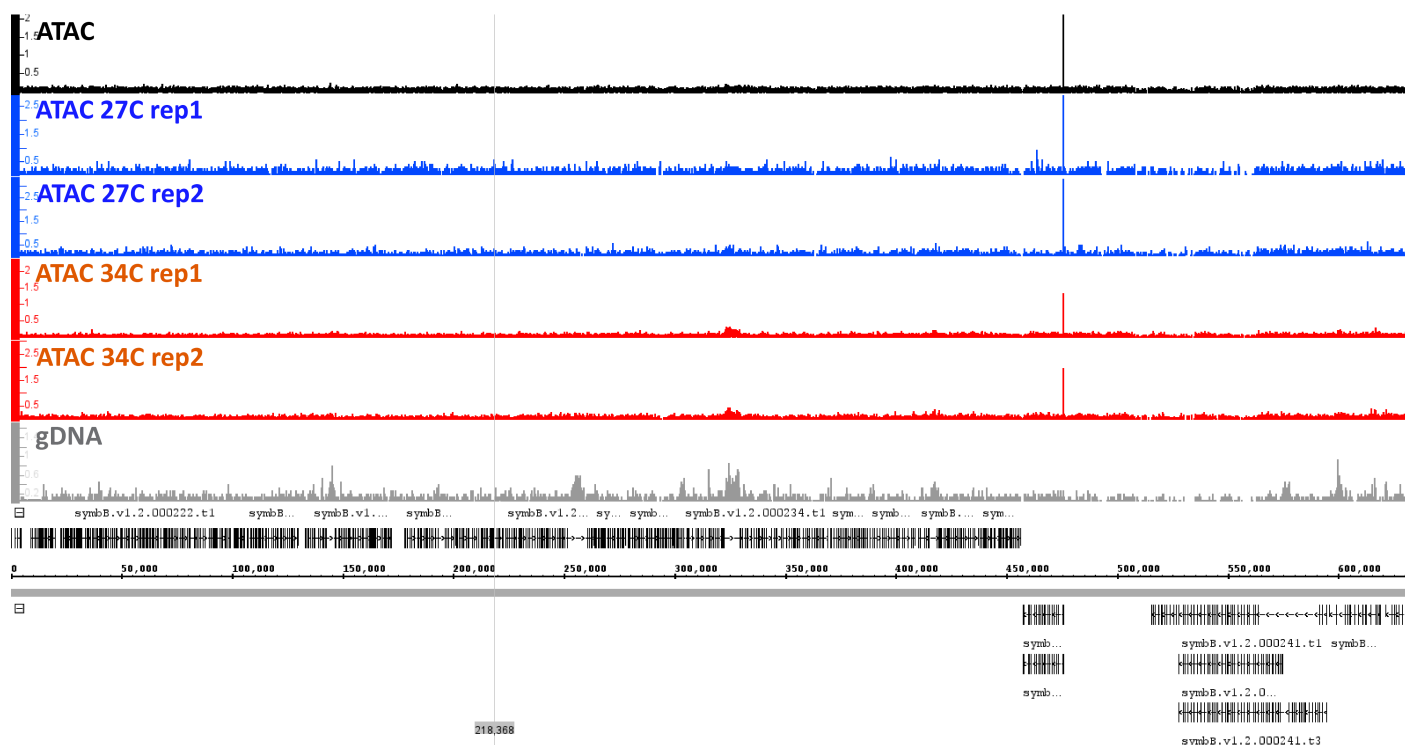


Supplementary Materials

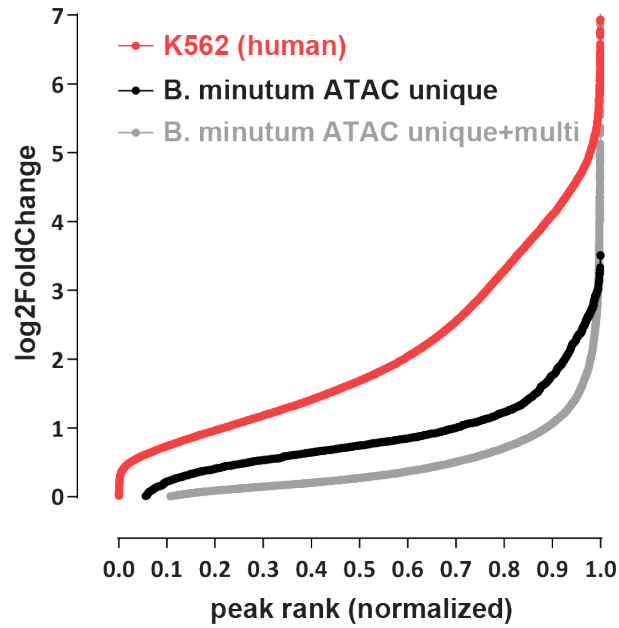
Supplementary Figures



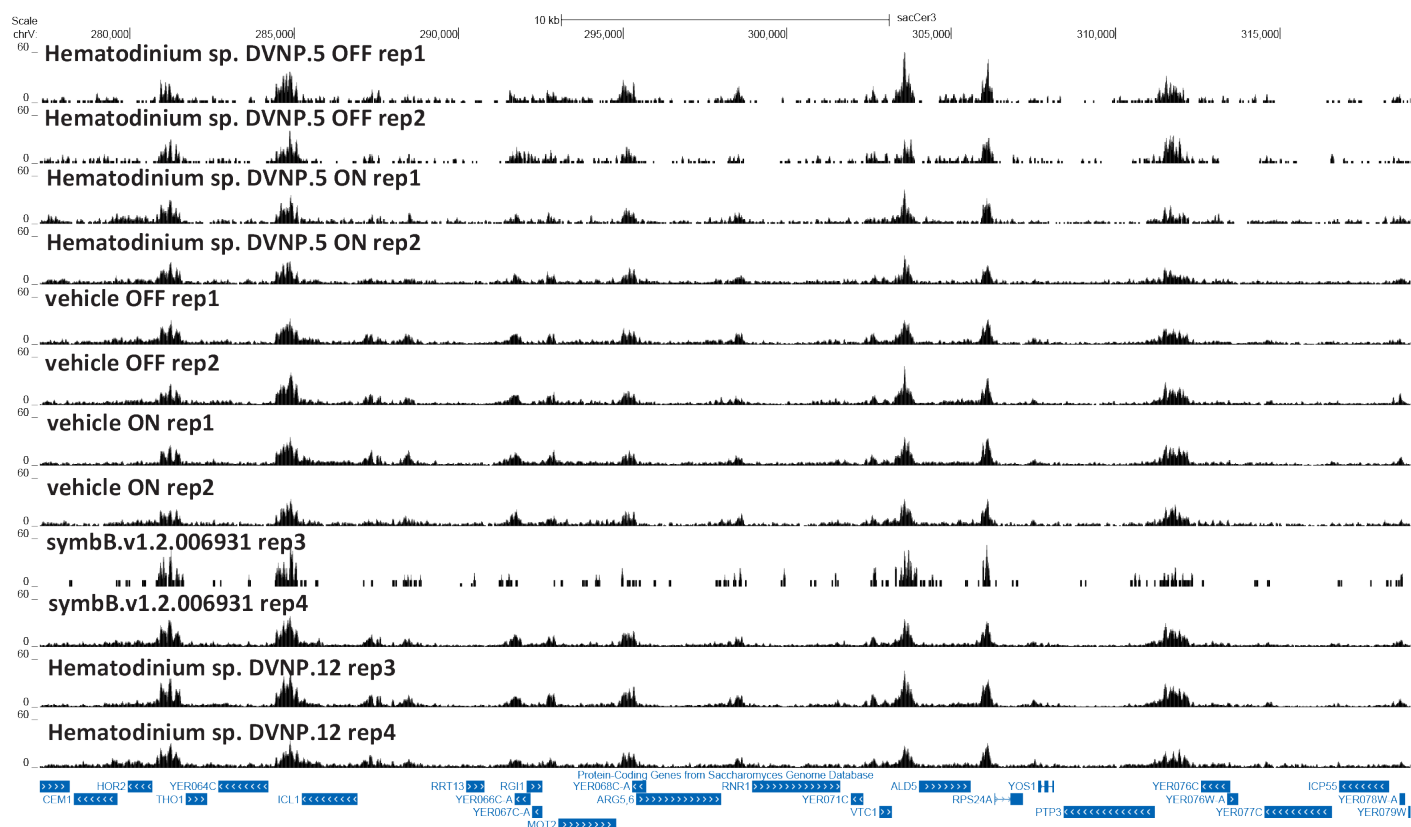
Supplementary Figure 1: Representative genome browser view of ATAC-seq and gDNA control signal in the *B. minutum* genome. Note the presence of collapsed repeats visible in the gDNA track.



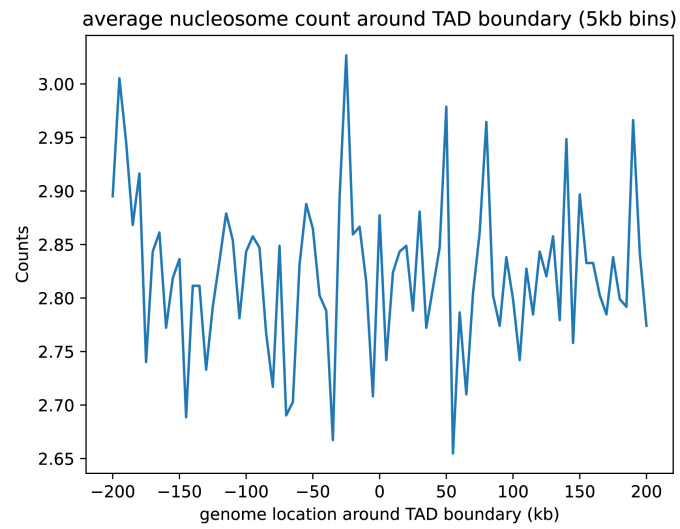
Supplementary Figure 2: Representative genome browser view of ATAC-seq and gDNA control signal in the *B. minutum* genome. Note the presence of collapsed repeats visible in the gDNA track.



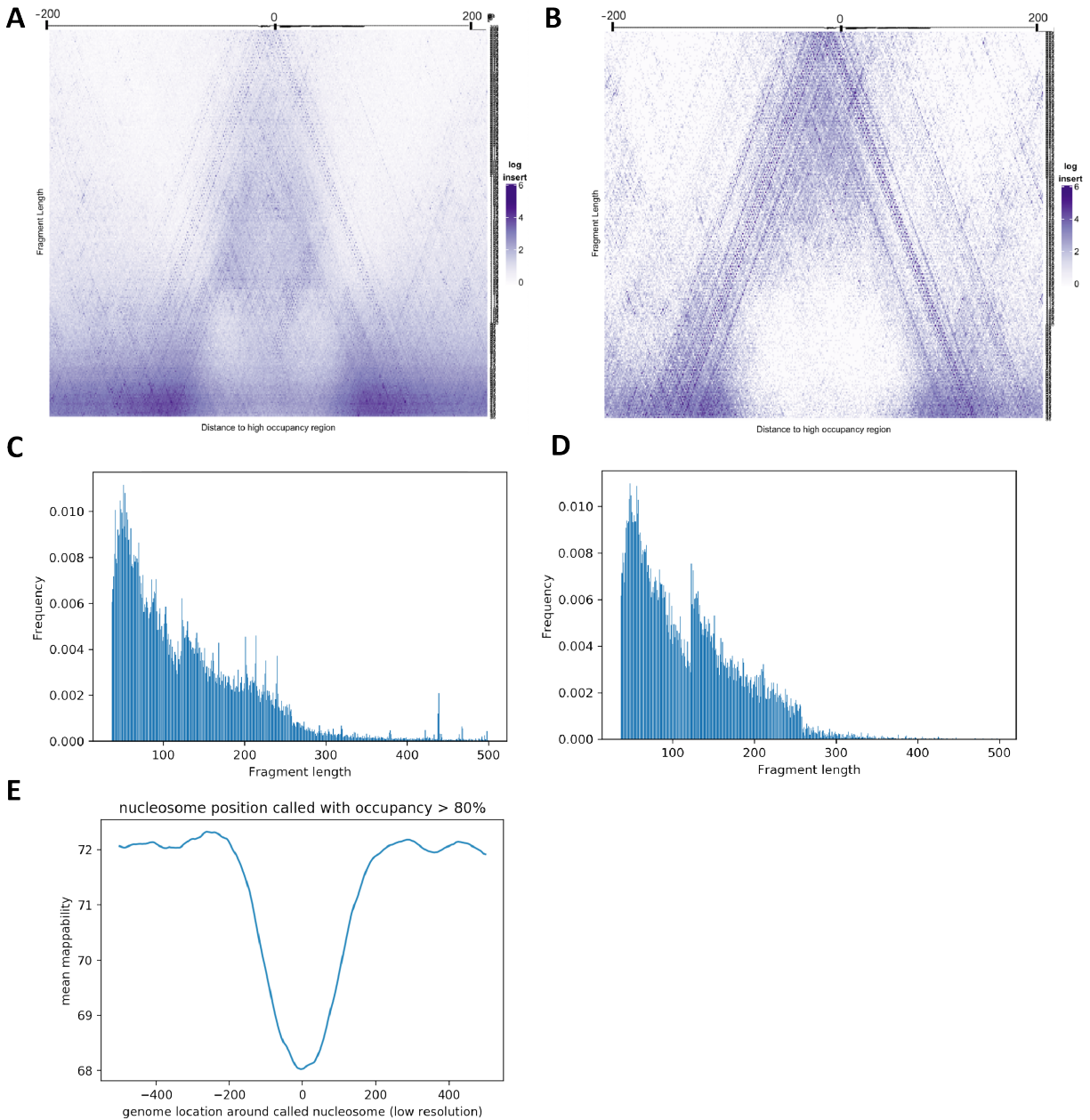
Supplementary Figure 3: Relative degree of ATAC-seq enrichment in *B. minutum* versus a representative mammalian genome sample. Shown is the $\log_2$ (fold change) ratio of ATAC-seq signal versus a negative control for a representative human ATAC-seq sample (K562 cell line from the ENCODE Project Consortium⁵⁸; dataset ID ENCFF512VEZ was used for ATAC and dataset ID ENCFF285UKJ – a whole genome bisulfite sequencing library – as a negative control, over peaks from dataset ID ENCFF695IGF). A separately sequenced gDNA control was generated for the *B. minutum* ATAC.



Supplementary Figure 5: Effects of exogenous expression of dinoflagellate DVNPs on chromatin accessibility in the yeast *S. cerevisiae*. ATAC-seq profiles of *S. cerevisiae* expressing *Hematodinium* sp. DVNP.5 (from Irwin et al. 2018⁵⁹) and a vehicle control, as well as additional replicates for *B. minutum* DVNP symbB.v1.2.006931 and *Hematodinium* sp. DVNP.12 and control samples. “OFF” and “ON” refer to cells in which the expression of *Hematodinium* sp. DVNP.5 is induced or not.



Supplementary Figure 6: Positioned nucleosomes as a whole are not strongly enriched around dinoTAD boundaries.



Supplementary Figure 7: Properties of putative positioned nucleosomes in the *B. minutum* genome. (A) V-plot of low-resolution positioned nucleosomes ($n=30,107$) (B) V-plot of low-resolution positioned nucleosomes with minimum occupancy cutoff of 0.8 ($n=2,166$) (C) Fragment distribution over low-resolution positioned nucleosomes (D) Fragment distribution over high-resolution positioned nucleosomes with minimum occupancy cutoff of 0.8 (E) Average mappability (for reads of length 75 bp) over positioned nucleosomes.