

Supplements

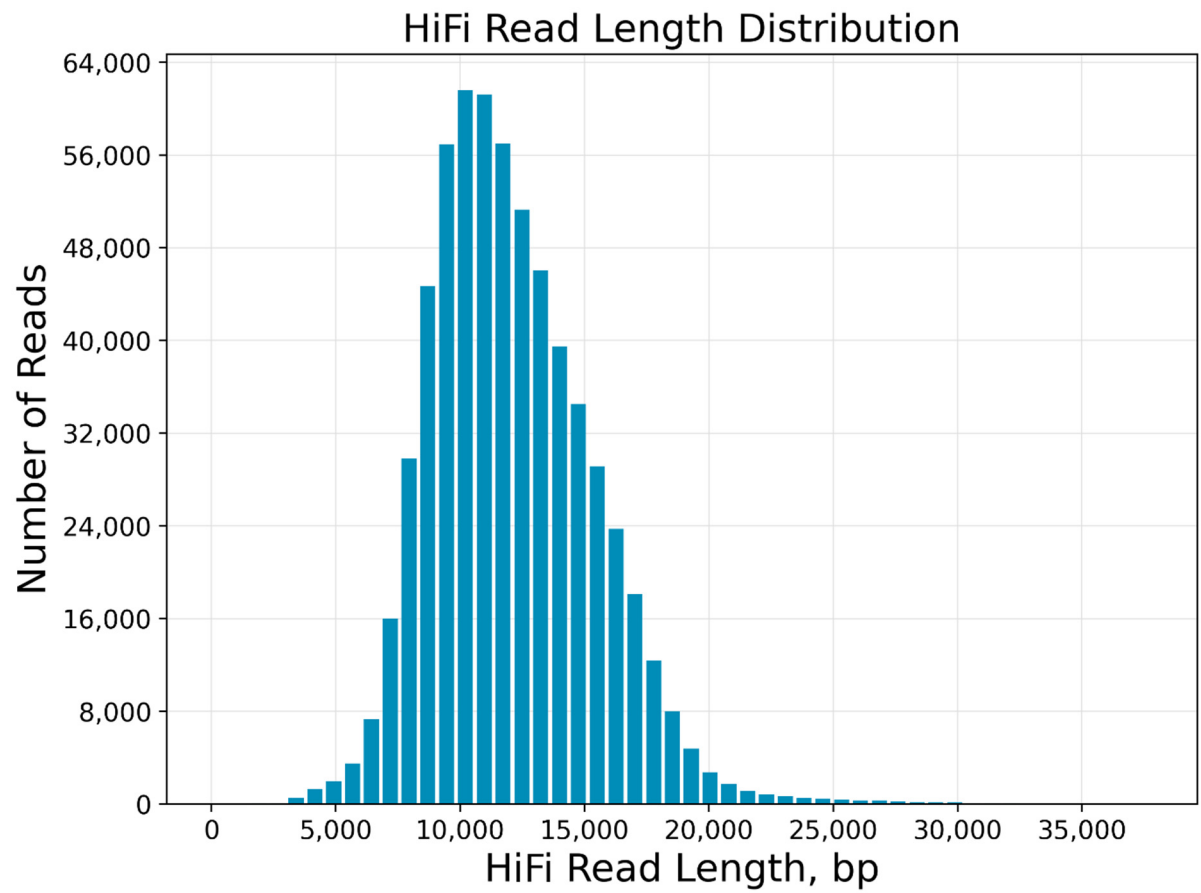


Figure S1. HiFi Read Length Distribution filtered (>Q20) genome sequence data from *D. tertiolecta*

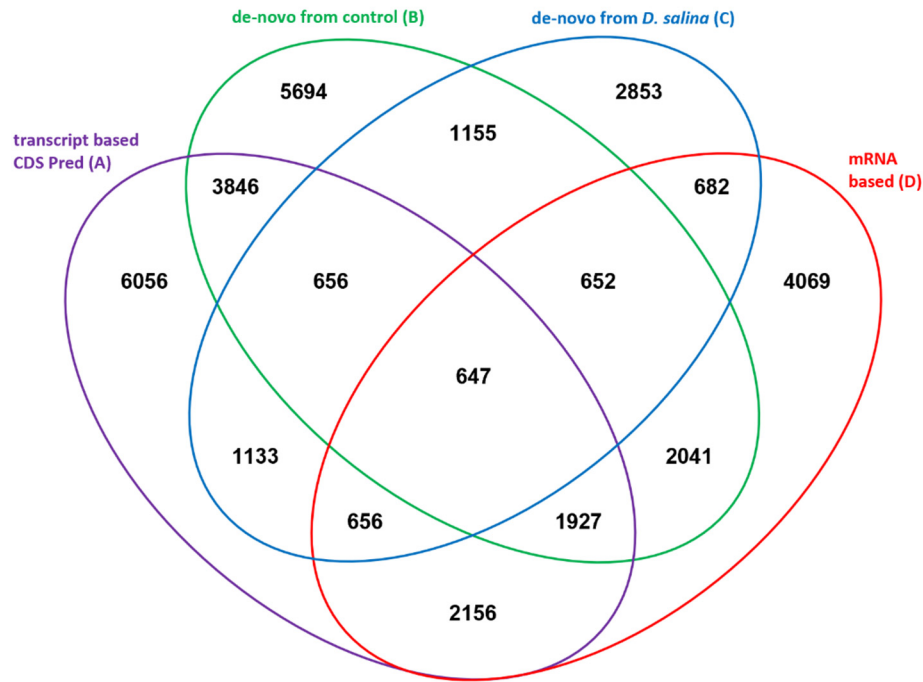


Figure S2. Venn diagram of identical predicted genes from *D. tertiolecta* after removing redundant protein coding sequences that have been identified in all proteomics data sets using PEAKS with SPIDER. A: set of all *de-novo* predicted genes from 2 M NaCl for 30 min and 4 h treated cells and the control without NaCl using Augustus-BRAKER. B: *de-novo* predicted genes using the predicted Augustus-BRAKER training set from the 0 M NaCl sample. C: *de-novo* predicted genes using the available Augustus training set for *Dunaliella salina*. D: predicted open reading frames from assembled mRNA data from all transcripts (2 M NaCl for 30 min and 4 h treated cells and the control without NaCl).

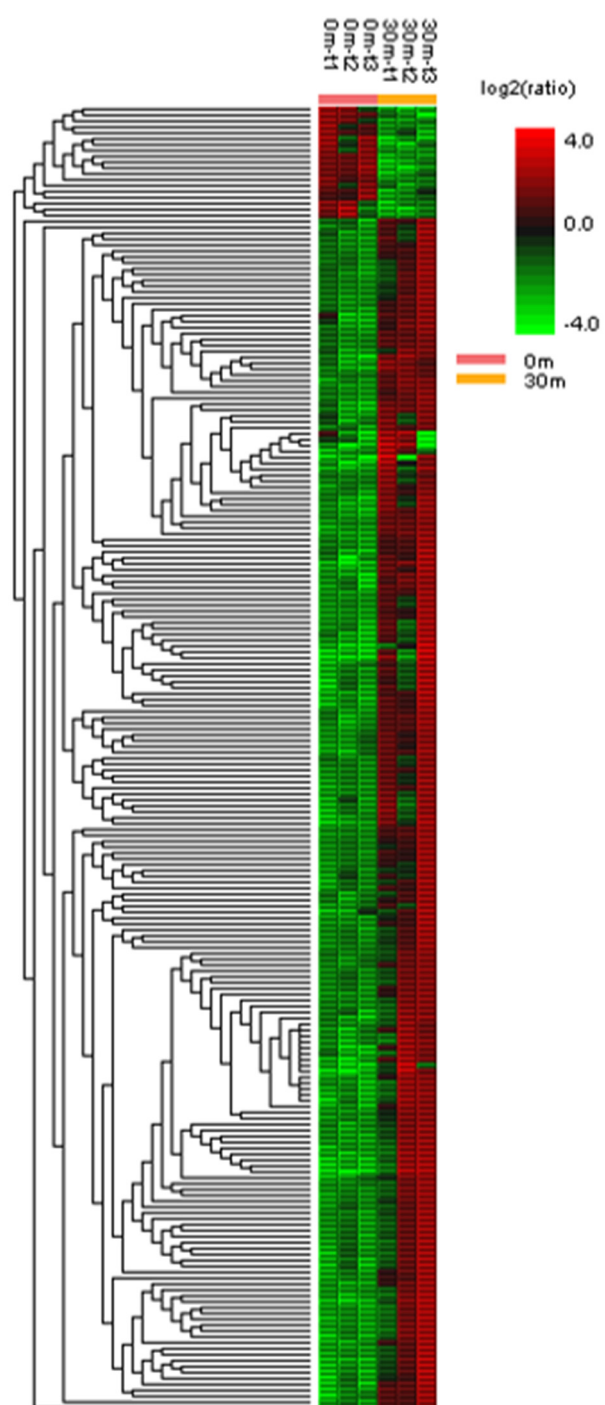


Figure S3. Heatmap of up- or down-regulated proteins after 30 min of salt stress.

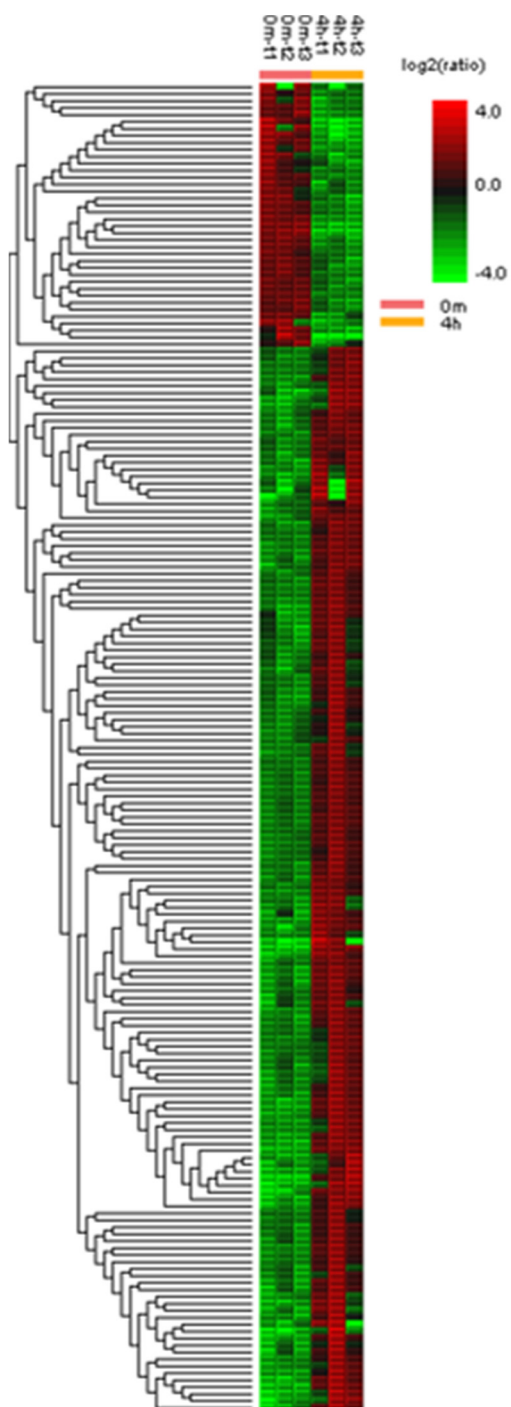


Figure S4. Heatmap of up- or down-regulated proteins after 4 h of salt stress.

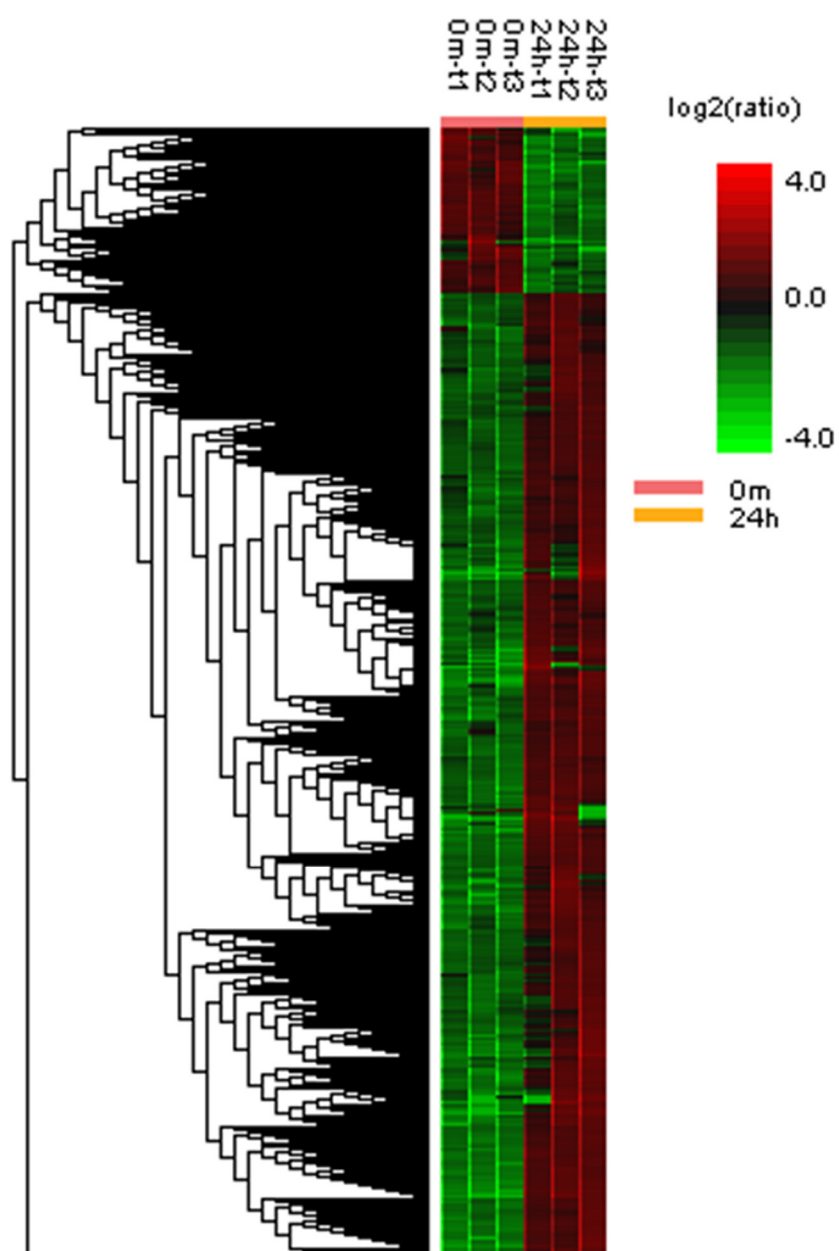


Figure S5. Heatmap of up- or down-regulated proteins after 24 h of salt stress.