

Characterization of the nuclear proteome of *Chlamydomonas* in response to salt stress

Larissa de Oliveira Magalhães^{1,2}, Fabio Nunes de Mello¹, Flavia Vischi Winck^{1,2,*}

¹ Laboratory of Regulatory Systems Biology, Department of Biochemistry, Institute of Chemistry, University of São Paulo (USP), São Paulo, São Paulo, CEP 05508-000, Brazil

² Laboratory of Regulatory Systems Biology, Center for Nuclear Energy in Agriculture, University of São Paulo (USP), Piracicaba, São Paulo, CEP13416-000, Brazil

* Corresponding author: Flavia Vischi Winck

E-mail: winck@cena.usp.br

Address: Center for Nuclear Energy in Agriculture, University of São Paulo (USP), Piracicaba, São Paulo, CEP13416-000, Brazil

Phone: +55.19.982739592

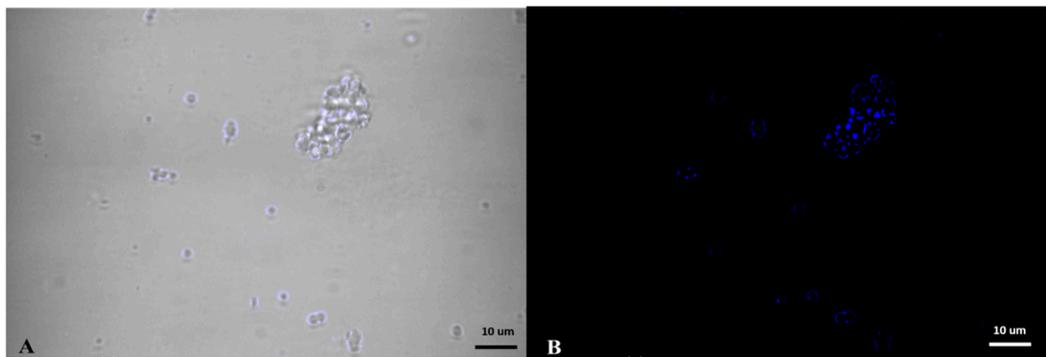


Figure S1. Analysis of the structural integrity of the isolated nucleus of *C. reinhardtii* under 0.1 M NaCl salt stress

A: Isolated *C. reinhardtii* nuclei under a bright-field microscope. **B:** Same isolated nuclei of *C. reinhardtii* stained with 4,6-diamidino-2-phenylindole (DAPI) and analyzed by fluorescence microscope. Blue regions indicate the presence of DNA molecules.

Pearson Correlation

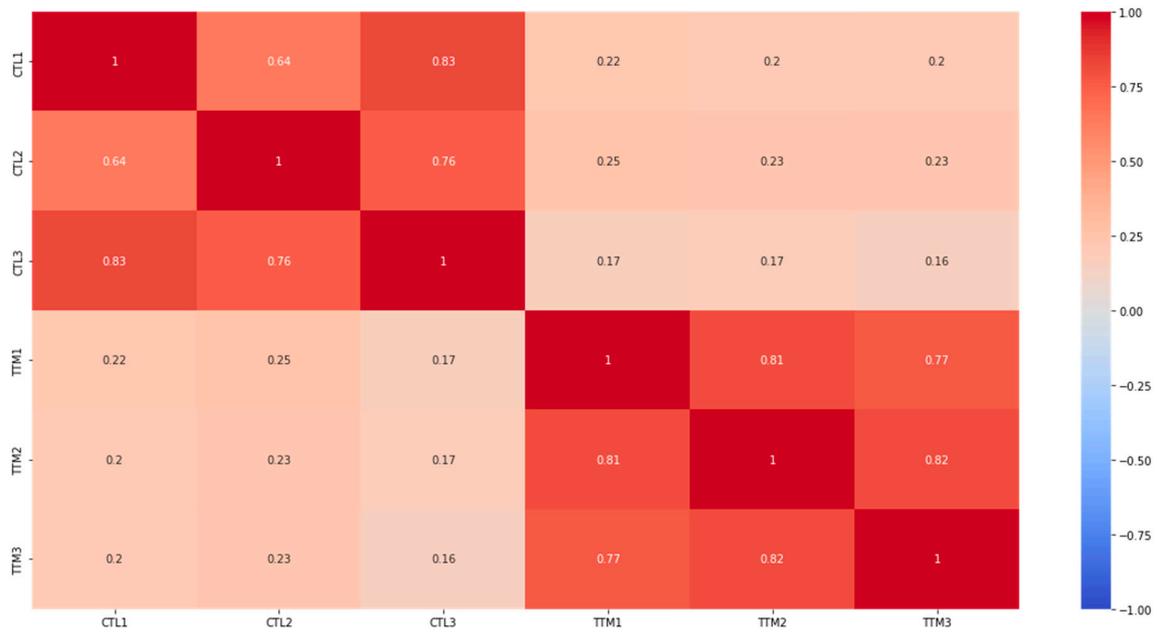


Figure S2. Reproducibility between replicates of proteome datasets

Heatmap with Pearson correlation coefficients (r) for pairwise comparisons of each Control (CTL) and Treatment (TTM) nuclear proteome samples. The numbers inside the square represent the correlation values. Higher r -values are represented as dark red and low correlation between samples are represented as light red.

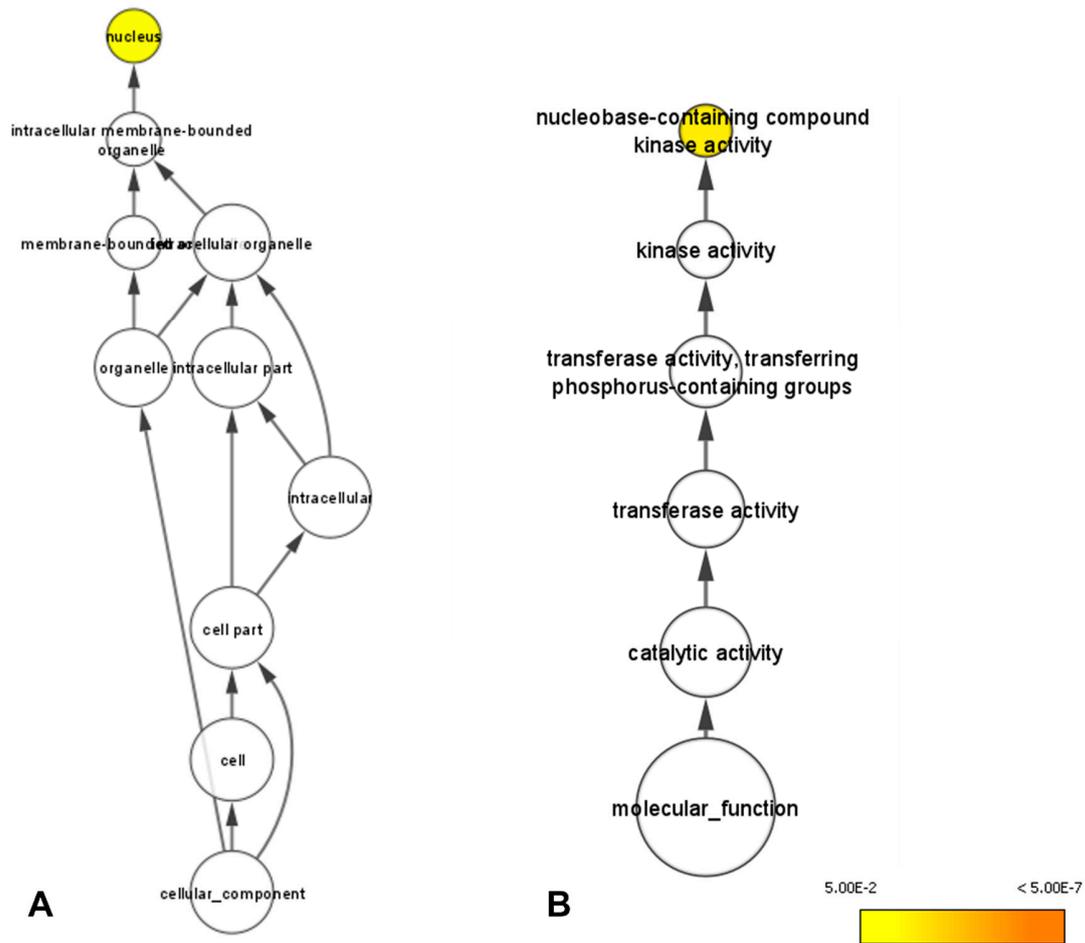
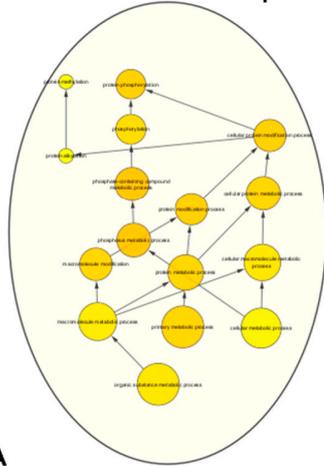


Figure S3. Functional classification of overrepresented Gene Ontology (GO) annotation terms in the dataset of differentially expressed (DEs) nuclear proteins under salt stress (0.1 M NaCl) according to BiNGO (Cytoscape software) tool

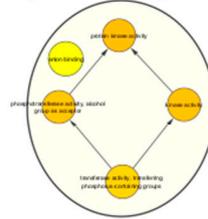
A. Illustration of DEs GO enrichment category of Cellular Component (CC). **B:** Illustration of DEs GO enrichment category of Molecular Function (MF). The color gradient of distribution networks is the enrichment scale (*orange* stands for the highest significance of enrichment and *yellow* the minimum significance of enrichment above the cutoff (FDR corrected = 0.05) and node size represents the GO hierarchy. The threshold of hypergeometric distribution of the functional annotation was set as p-value < 0.05).

process metabolic protein



A

activity transferring kinase



B

atpase hydrogen exporting

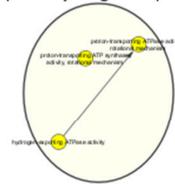


Figure S4. Functional classification of overrepresented Gene Ontology (GO) terms in the dataset of putative targets of Cre17.g702650.t1.1 according to BiNGO (Cytoscape software) tool

A. Network illustration of the enriched GO annotation categories of Biological Process (BP) for the putative targets of Cre17.g702650.t1.1 (HMG) Transcription factor. **B.** Network illustration of the enriched GO annotation categories of Cellular Component (CC) of putative targets of Cre17.g702650.t1.1(HMG). The color gradient of distribution networks is the enrichment scale (*orange* stands for the highest significance of enrichment and *yellow* the minimum significance of enrichment above the cutoff (FDR corrected = 0.05) and node size represents the GO hierarchy. The threshold of hypergeometric distribution of the functional annotation was set as p-value < 0.05).