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

Larissa de Oliveira Magalhães1,2, Fabio Nunes de Mello1, Flavia Vischi Winck1,2,\*

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](about:blank)

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

Phone: +55.19.982739592

Interface gráfica do usuário, Aplicativo

Descrição gerada automaticamente

**Fig 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.

Gráfico

Descrição gerada automaticamente

**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.

Forma

Descrição gerada automaticamente com confiança baixa

**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).

Diagrama

Descrição gerada automaticamente

**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).