

## *Supplementary Material*

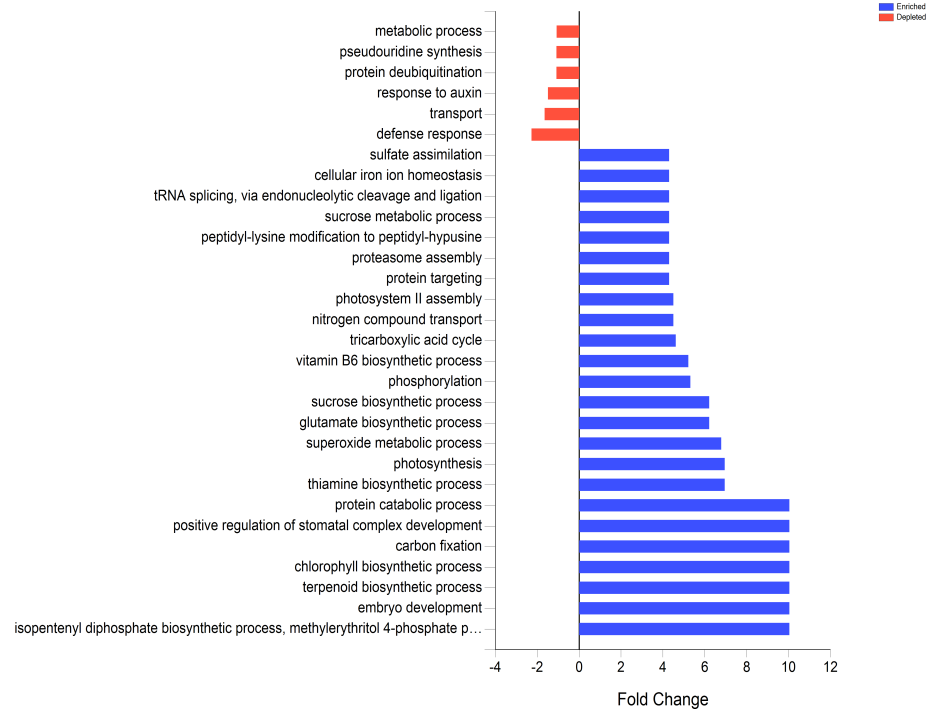
### **Identification of putative transmembrane proteins involved in salinity tolerance in *Chenopodium quinoa* by integrating physiological data, RNAseq and SNP analyses**

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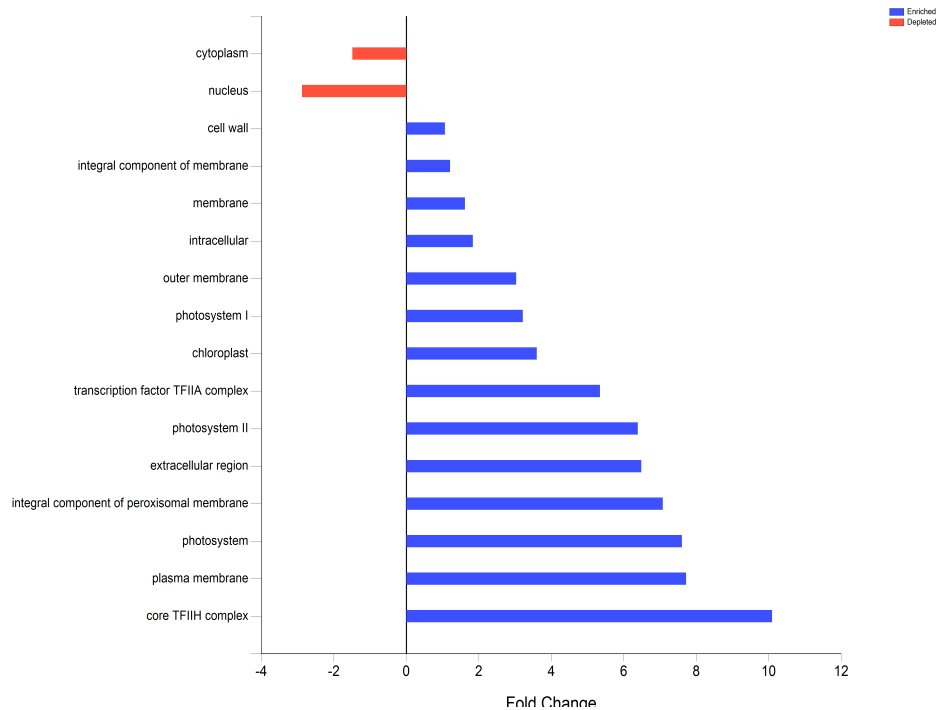
A

Biological process



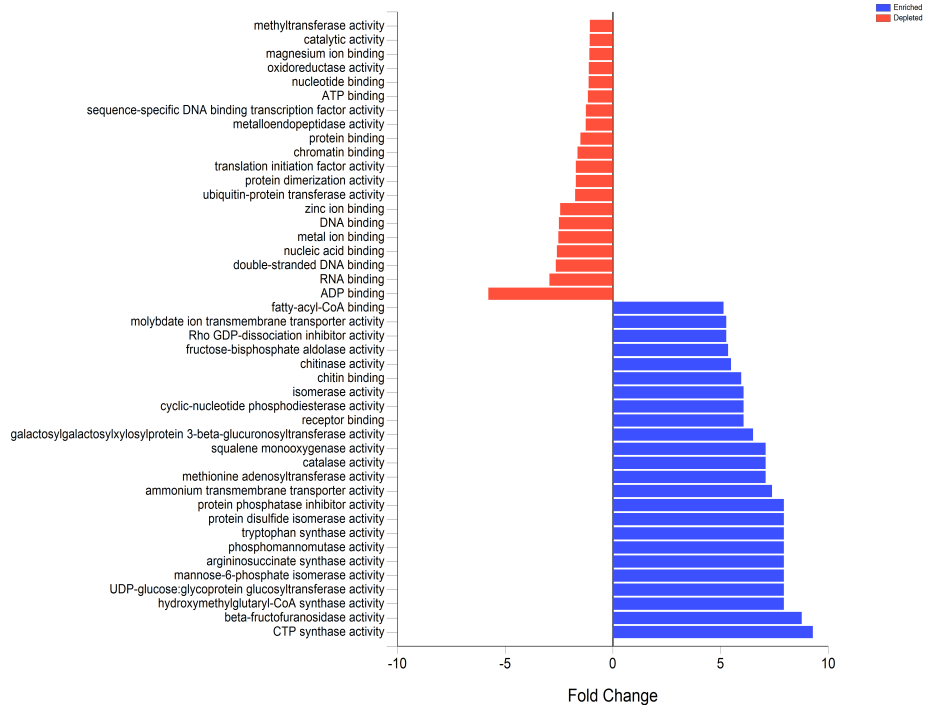
B

Cellular component

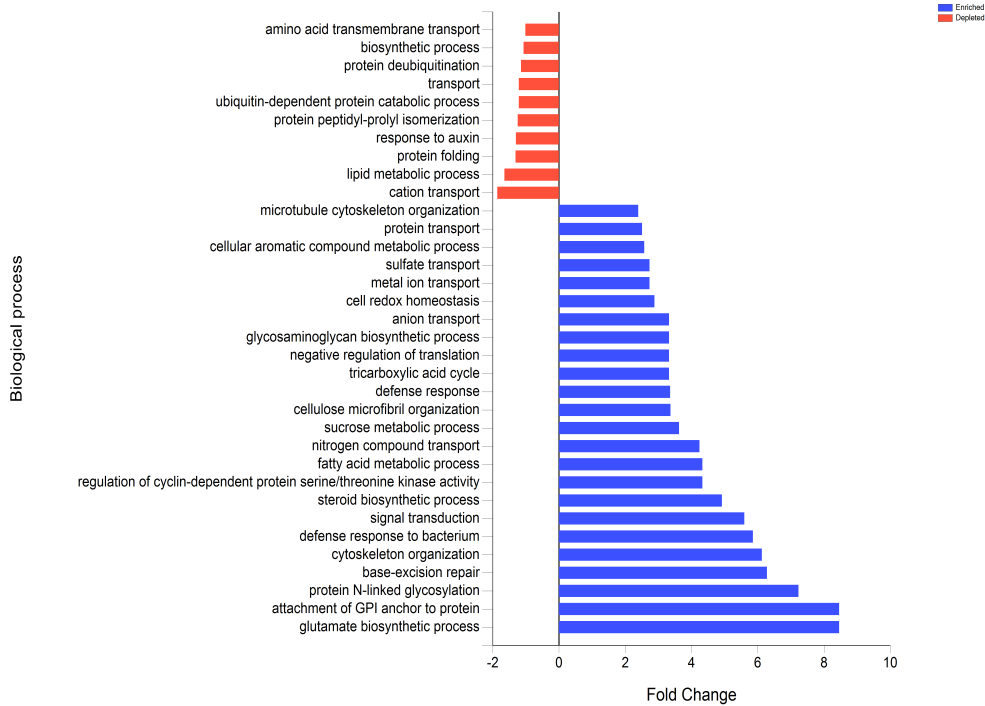


C

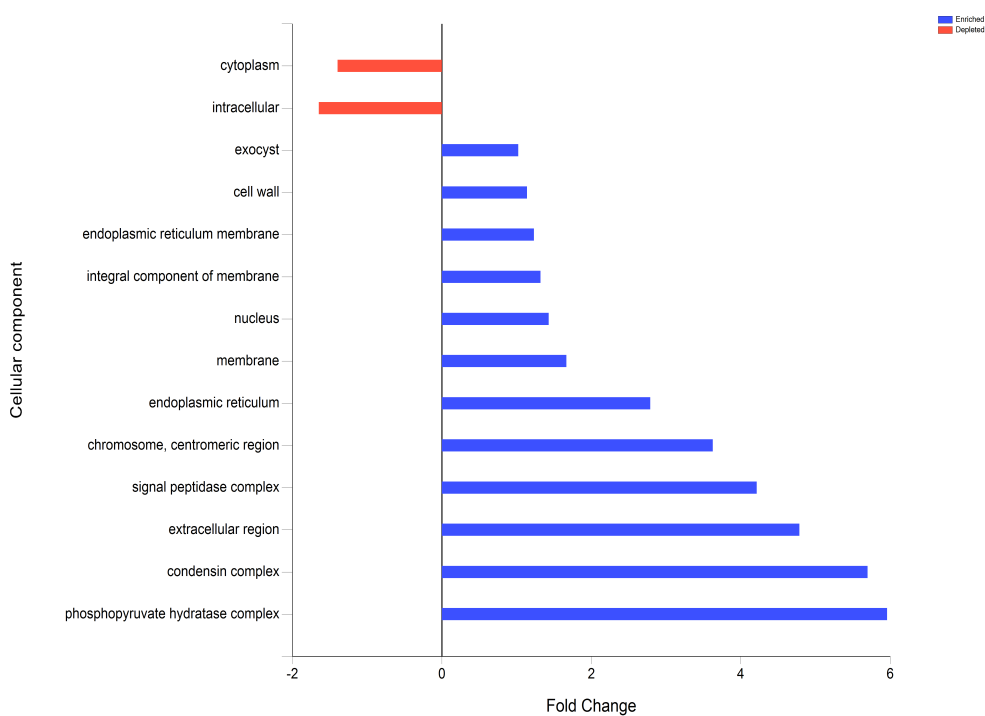
Molecular function



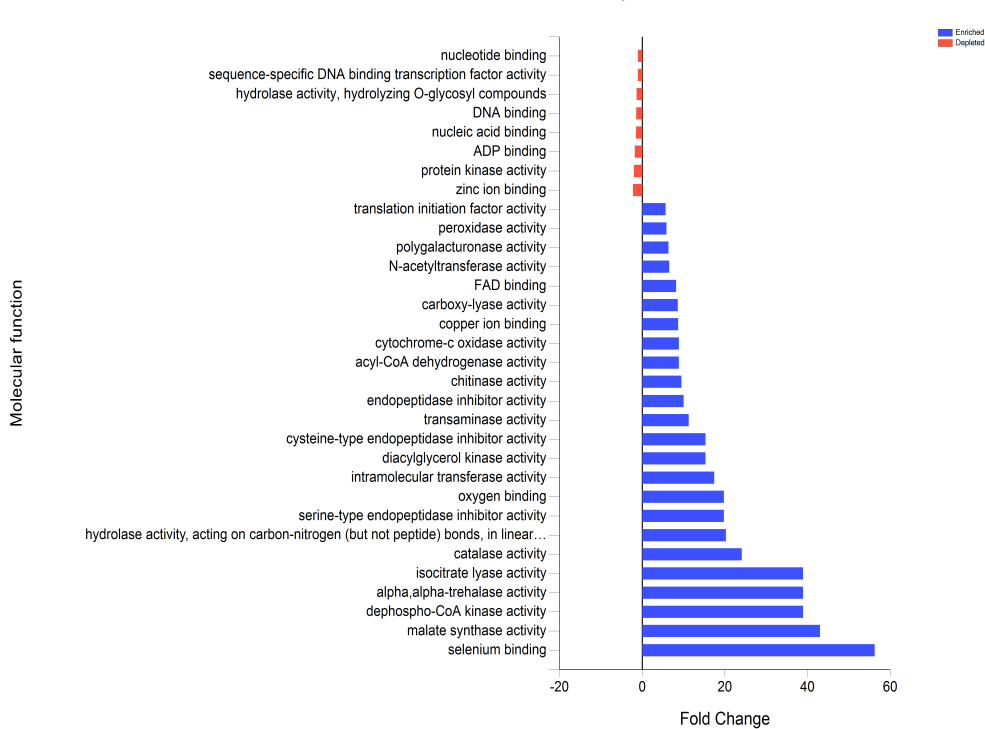
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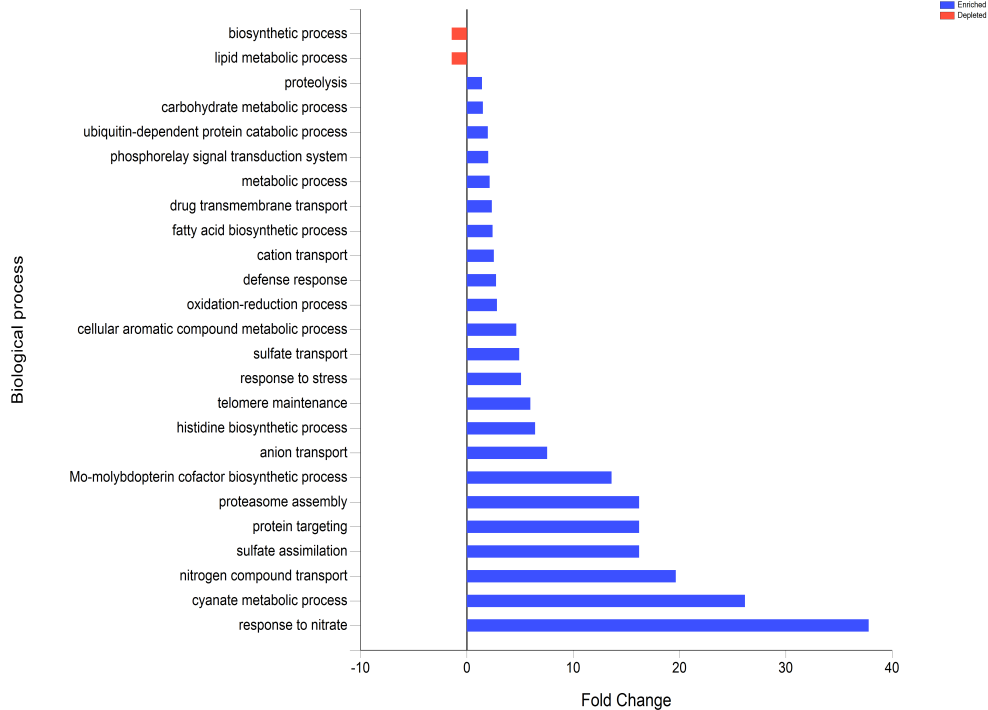
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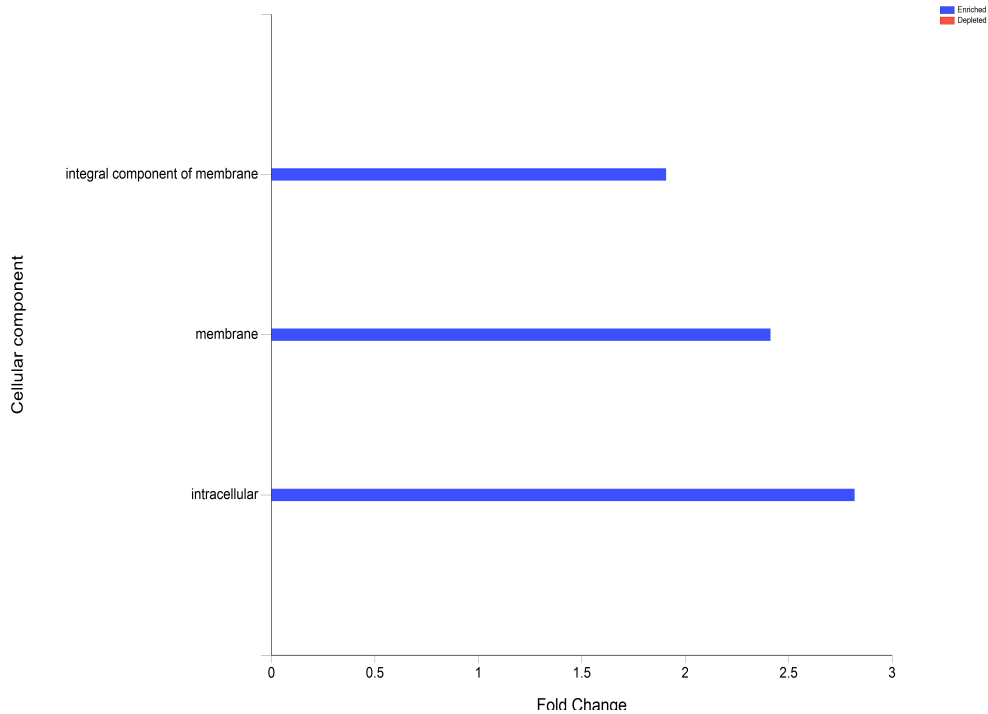
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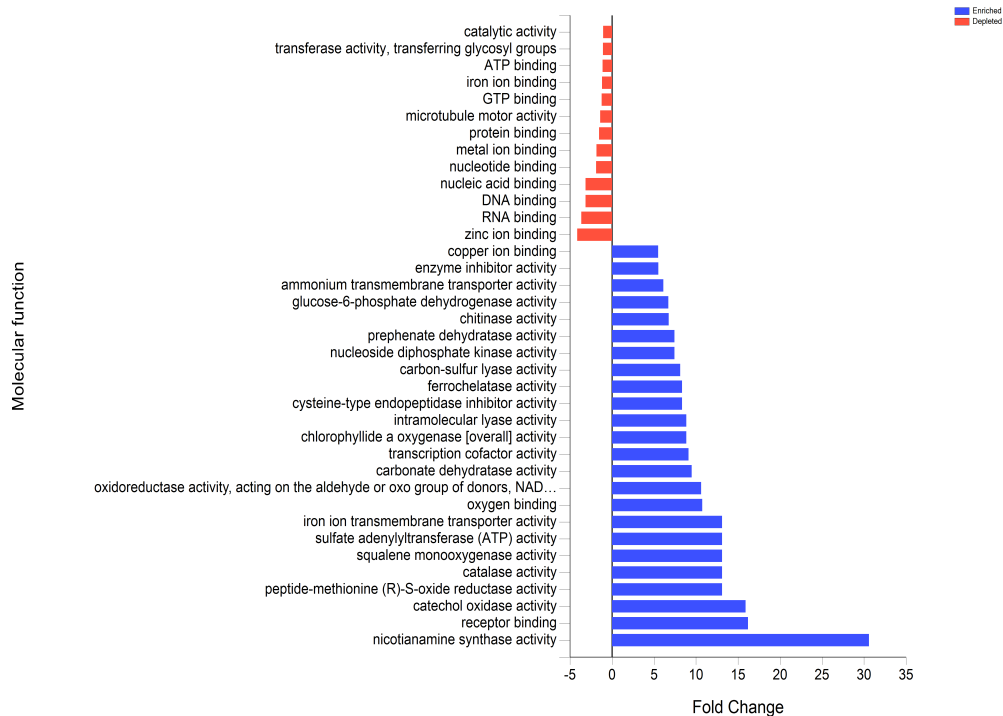
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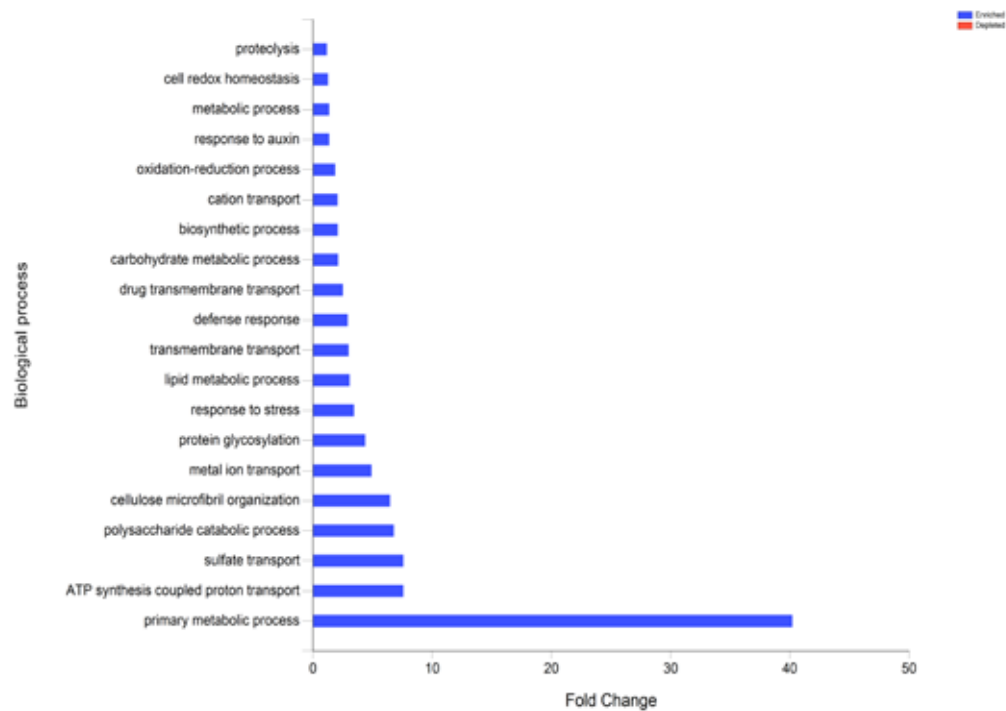
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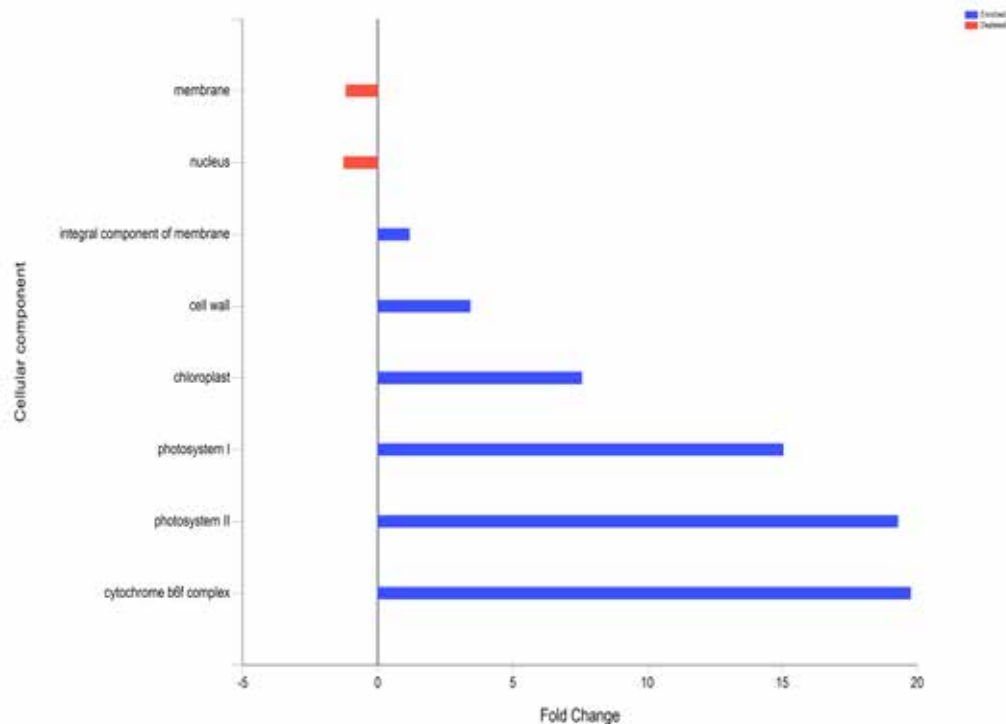
I



J

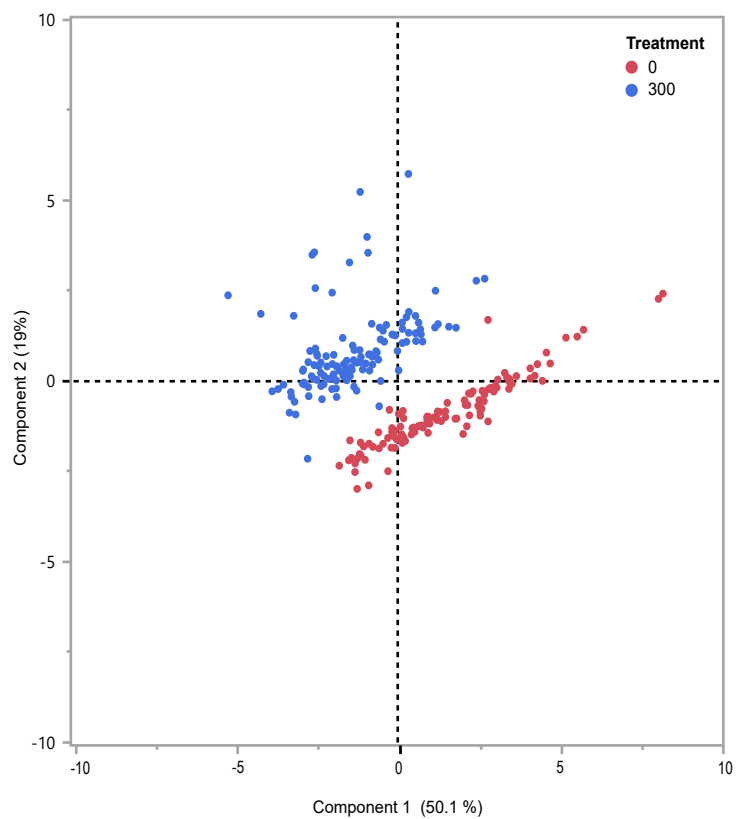


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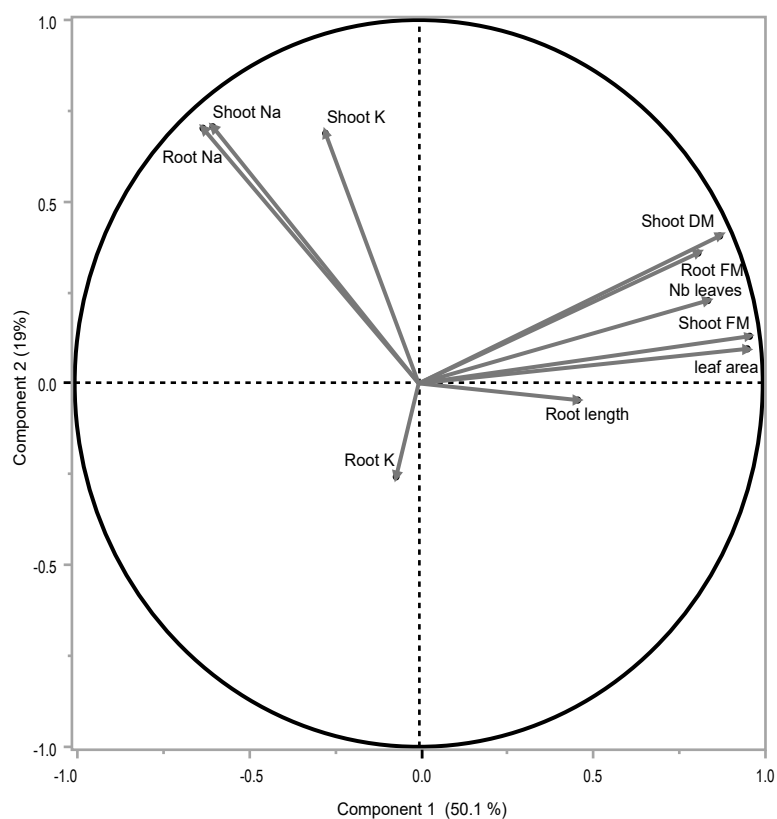


**Supplementary Figure S1:** Fold change of select gene ontology terms of genes differentially expressed in response to salt stress. Three-wk-old hydroponically grown plants were grown under control conditions or treated with 300 mM NaCl for 1 wk. Root and shoot samples were used for RNAseq analysis. Fold change of select biological process (A) and cellular component (B) gene ontology terms of genes upregulated in shoots in response to salt. Fold change of select molecular function (C, F, I), biological process (D, G, J) and cellular component (E, H, K) gene ontology terms of genes downregulated in shoots (C, D, E), upregulated in roots (F, G, H), or downregulated in roots (I, J, K) in response to salt. Blue bars, enriched gene ontology terms; red bars, depleted gene ontology terms.

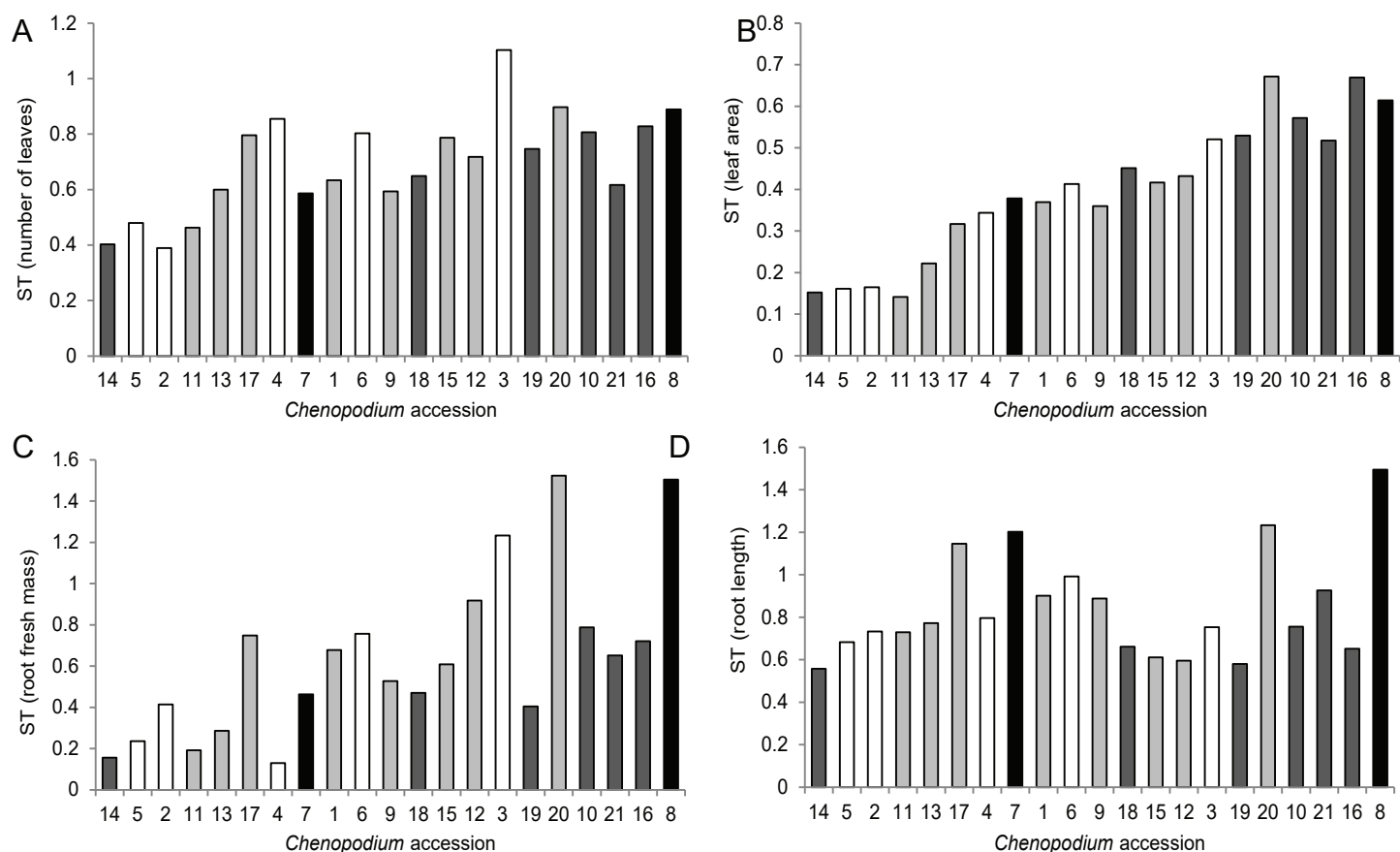
A



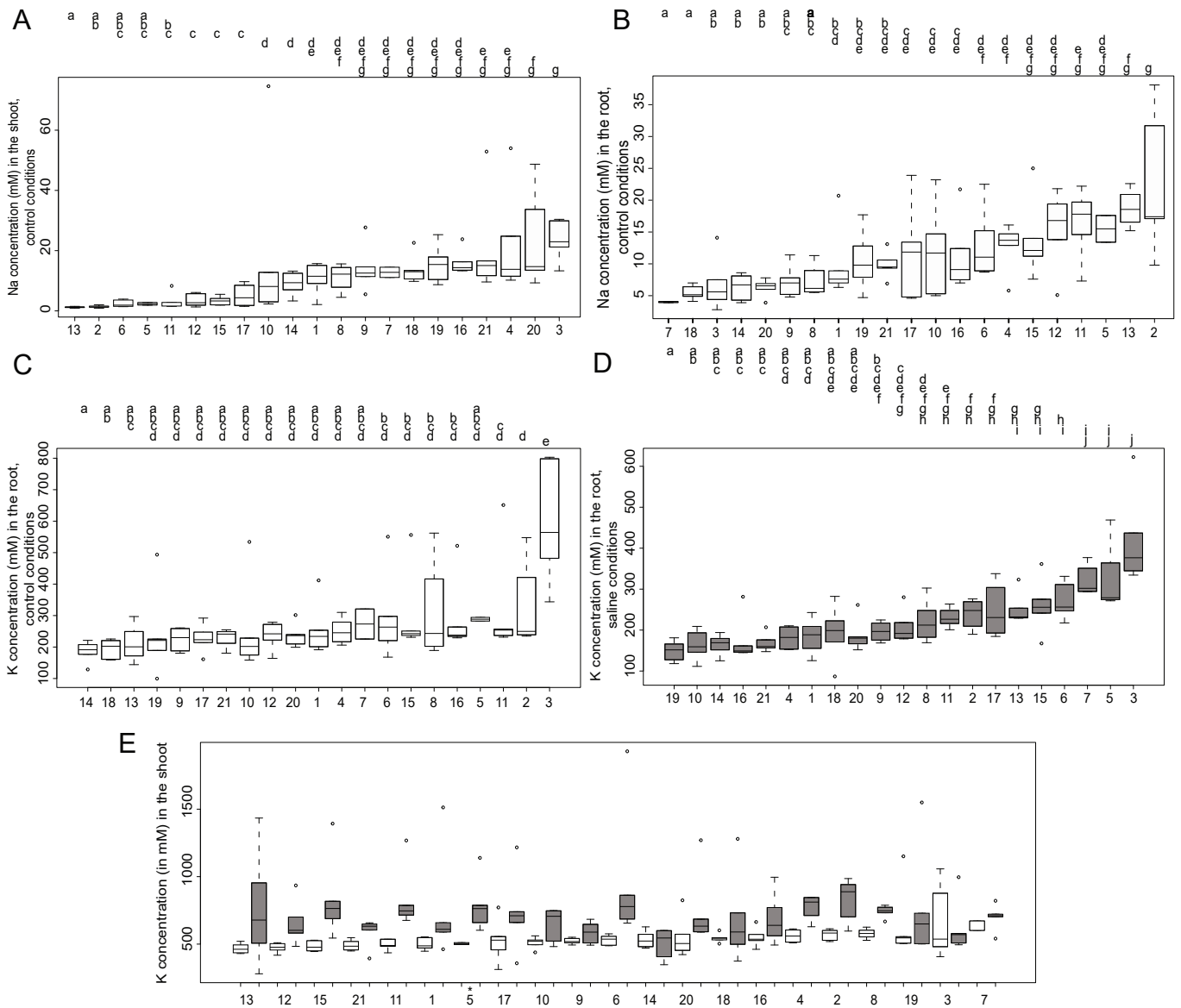
B



**Supplementary Figure S2:** Principal component analysis for traits hypothesized to contribute to salinity tolerance. (A) Scatter plot of PCA analysis with control (red) and salt treated (blue) *Chenopodium* accessions. Plotted points represent the average value for each measured trait for each accession. (B) Arrows indicate PCA analysis for traits indicated. All statistical analyses were performed in JMP.



**Supplementary Figure S3:** Comparison of salt tolerance (ST) of different *Chenopodium* accessions. ST was calculated for (A) number of leaves, (B) leaf area, (C) fresh root mass and (D) root length. ST was calculated as the ratio of the trait during the salinity treatment compared to the control treatment. Accessions are described in Table 1. In short: (1) *C. q.* 0654; (2) *C. b.* PI 568156; (3) *C. b.* BYU 937; (4) *C. b.* PI 666279; (5) *C. b.* Ames 33013; (6) *C. b.* BYU 1314; (7) *C. h.* BYU 1101; (8) *C. h.* BYU 566; (9) *C. q.* CICA-17; (10) *C. q.* G-205-95DK; (11) *C. q.* Ollague; (12) *C. q.* Pasankalla; (13) *C. q.* Real; (14) *C. q.* Regalona; (15) *C. q.* Salcedo INIA; (16) *C. q.* Cherry Vanilla; (17) *C. q.* Ku-2; (18) *C. q.* Chucapaca (19) *C. q.* PI 634921; (20) *C. q.* Kurmi; (21) *C. q.* PI 614868.



**Supplementary Figure S4:** Na and K distribution in salt stressed *Chenopodium* accessions. (A) Na concentration in the shoot and (B) root of control treated *Chenopodium* accessions. (C) K concentration in the root of control and (D) salt treated *Chenopodium* accessions. (E) K concentration in the shoot of control (in light grey) and salt (in dark grey) treated *Chenopodium* accessions; n=6, statistical analyses were performed as described in the methods section. F-statistic for (A), (B), (C) and (D) accession <0.0001, and for (E) accession 0.911 and treatment 0.062; levels not connected by the same letter are significantly different,  $P \leq 0.05$ . (Different layouts were chosen as the result of the fitted model suggesting in (E) no significant differences between accessions and treatment.)