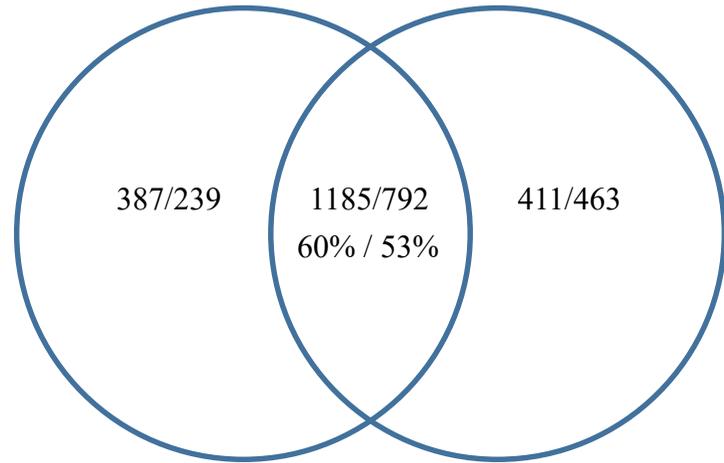


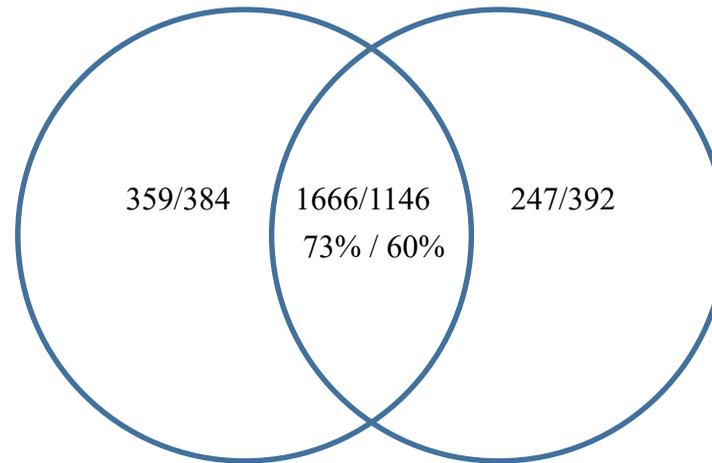
Figure S1 Principal component (PC) analysis of the RNAseq data obtained from stress treated and untreated cultures of *A. nidulans* (A) and *A. wentii* (B) strains. The analysis was carried out using the rlog data generated by the DESeq2 software.

A Sorbitol vs. Untreated (1983/1494)
A. nidulans THS30 (1572/1031) *A. nidulans* Δ *gfdB* (1596/1255)



Sorbitol + NaCl vs. Untreated (1029/882)

B NaCl vs. Untreated (2272/1922)
A. nidulans THS30 (2025/1530) *A. nidulans* Δ *gfdB* (1913/1538)



C *A. nidulans* THS30 (831/687) *A. nidulans* Δ *gfdB* (650/638)

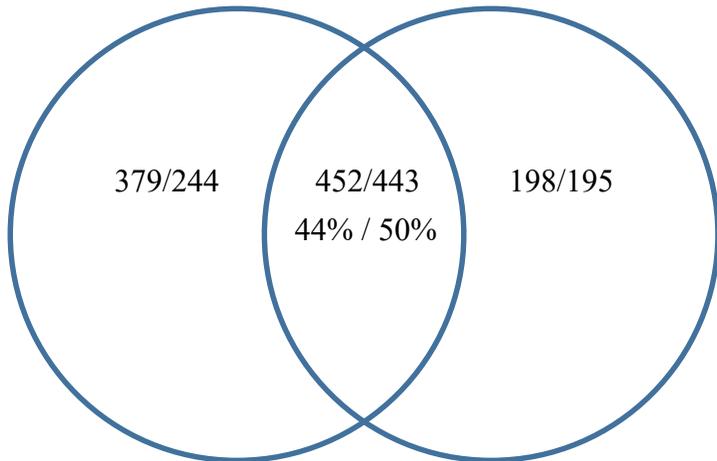
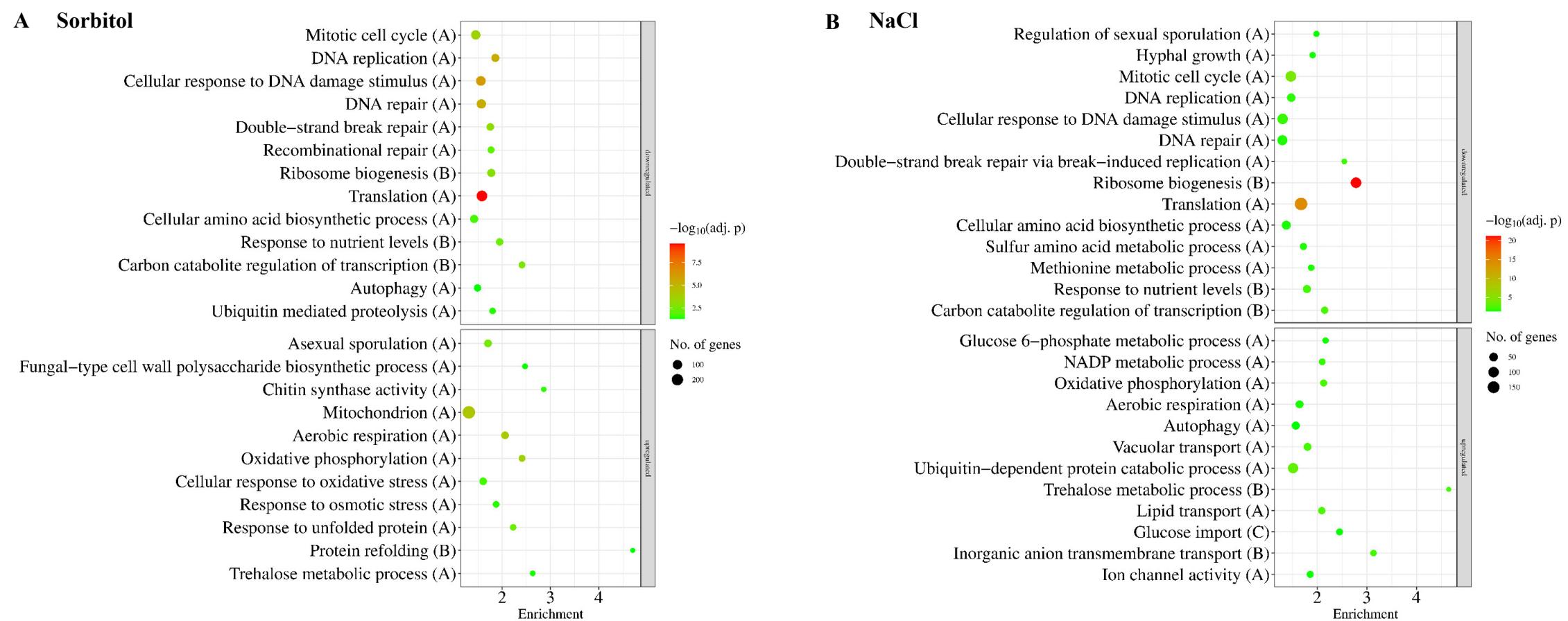


Figure S2 Overlap between the stress responses of the *A. nidulans* THS30 and the Δ *gfdB* strains. Venn-diagrams show the upregulated/downregulated genes observed under sorbitol (A), NaCl (B), and NaCl + sorbitol (C) treatments in the two strain. Percentages presented in the intersections show the number of genes upregulated/downregulated in both strains relative to the number of genes upregulated/downregulated in either of the two strains.



Figures S3A and S3B Gene set enrichment analyses of the effect of sorbitol (A) and NaCl (B) treatments on *A. nidulans* Δ *gfdB*.

Selected significantly enriched (p adjusted < 0.05) GO and KEGG pathway terms are presented. The full list of the enriched terms are available in Table S3. Letters in parentheses indicate the studied gene set: “A”— all DEGs, “B”— DEGs with $|\log_2\text{FC}| > 1$, “C”— DEGs with $|\log_2\text{FC}| > 2$. If a selected term was enriched in more than one gene set, only the set with the strongest criteria is presented.

C NaCl + sorbitol

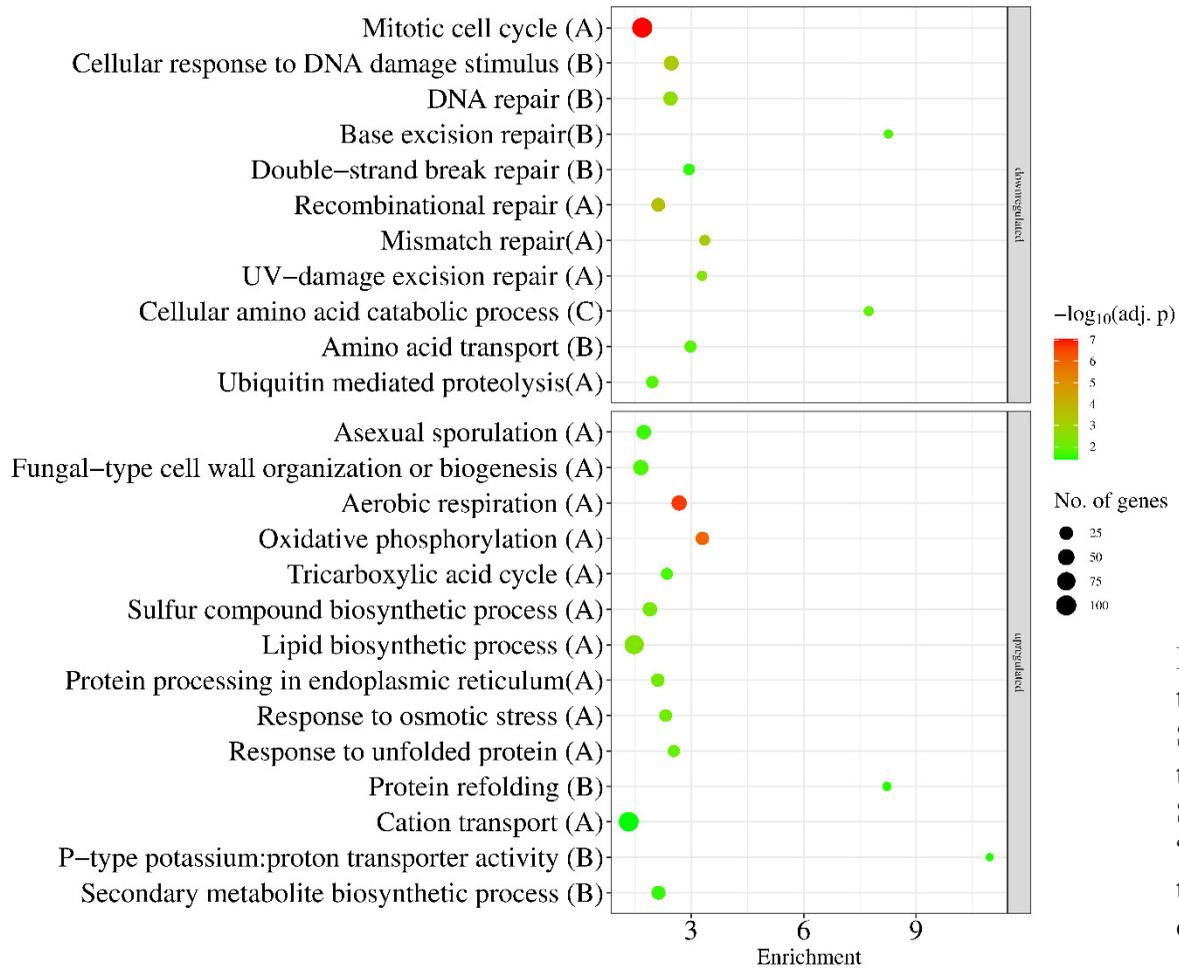


Figure S3C Gene set enrichment analyses of the effect of NaCl + sorbitol (C) treatment on *A. nidulans* $\Delta gfdB$. Selected significantly enriched (p adjusted < 0.05) GO and KEGG pathway terms are presented. The full list of the enriched terms are available in Table S3. Letters in parentheses indicate the studied gene set: “A”— all DEGs, “B”— DEGs with $|\log_2FC| > 1$, “C”— DEGs with $|\log_2FC| > 2$. If a selected term was enriched in more than one gene set, only the set with the strongest criteria is presented.

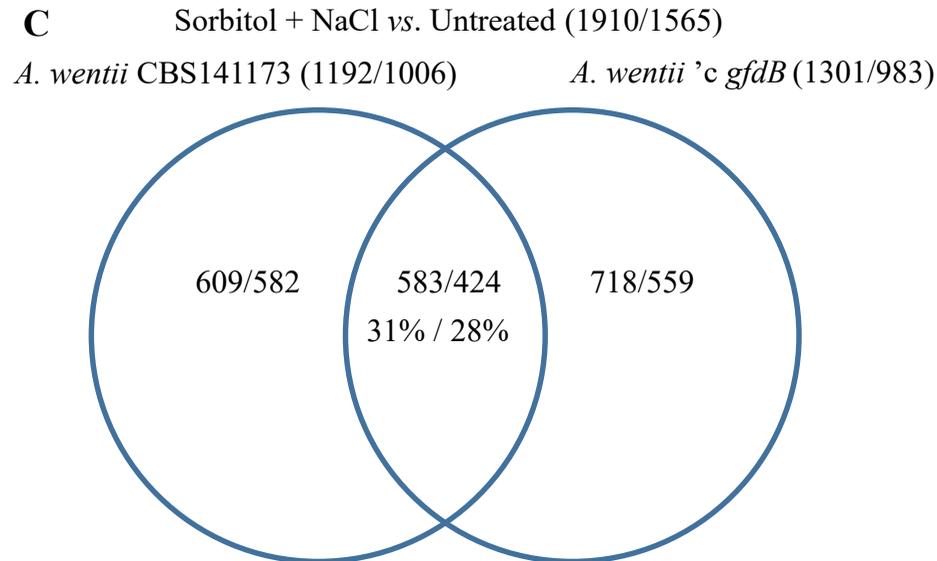
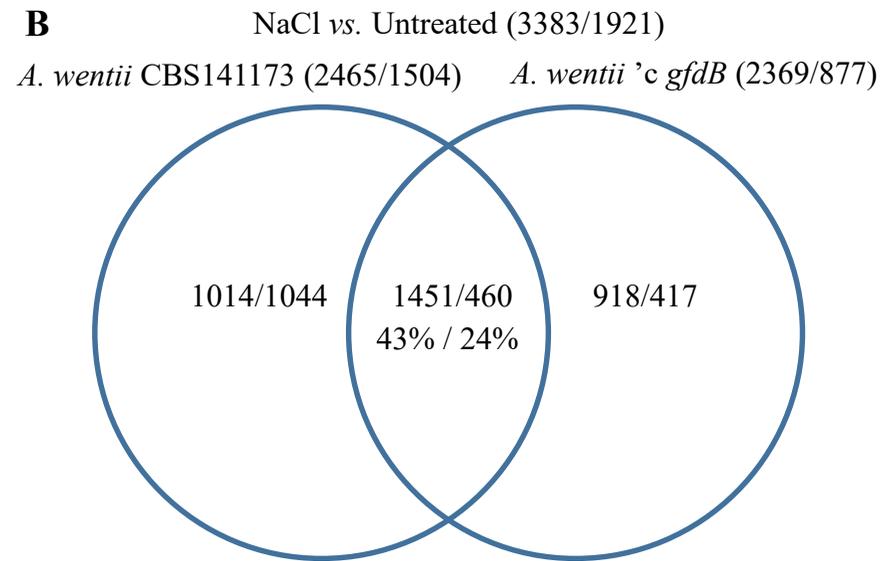
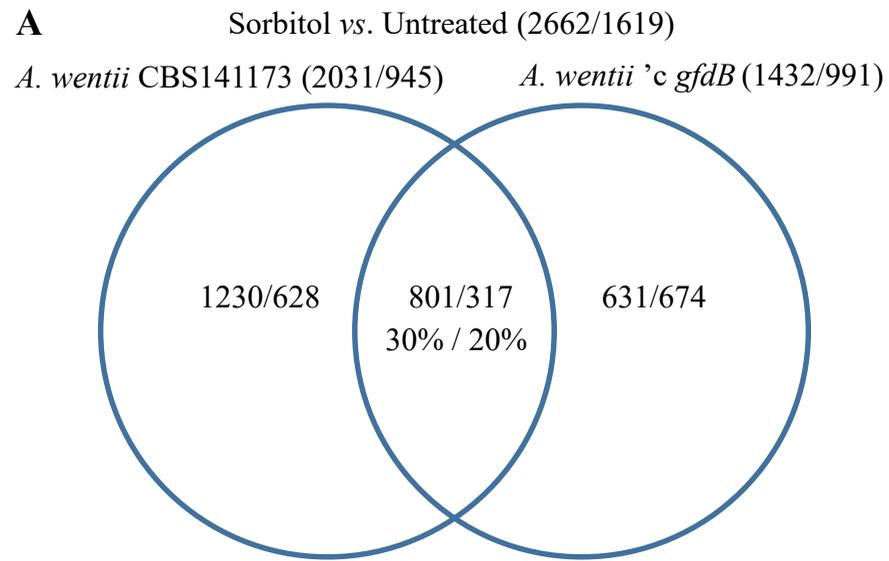
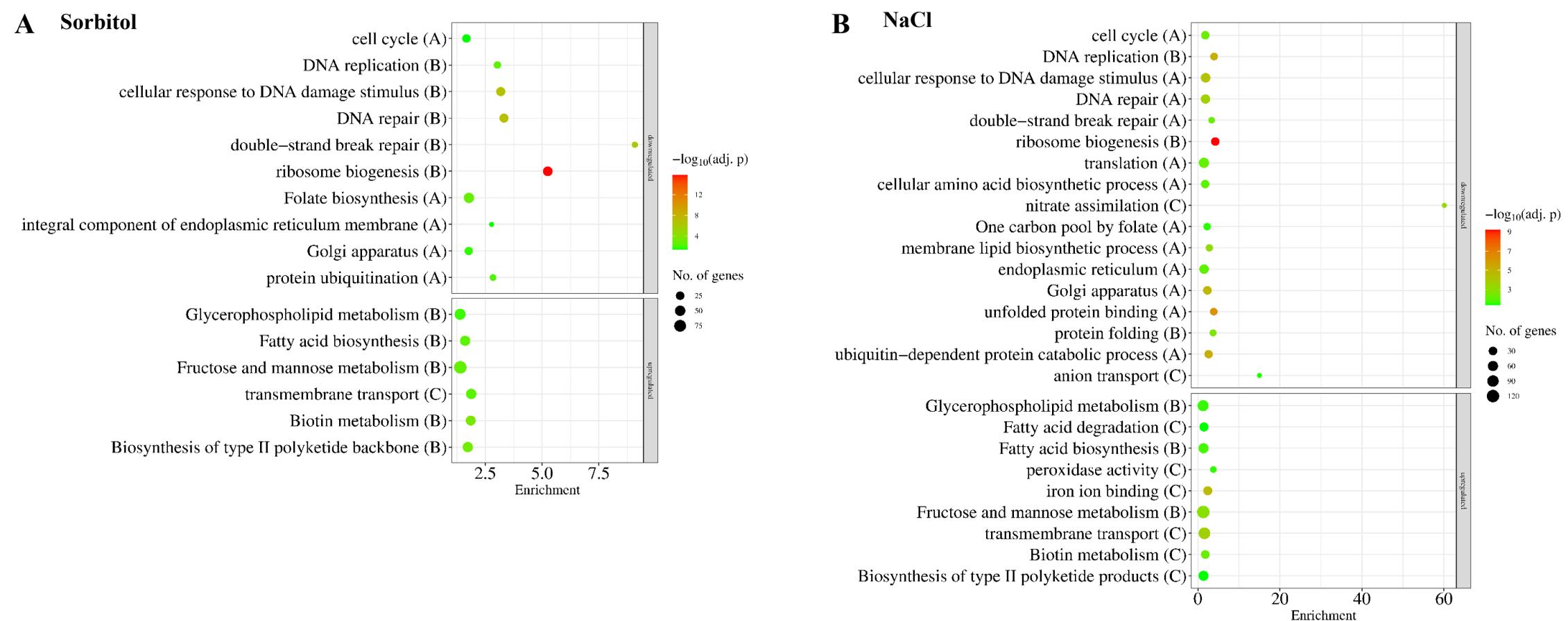


Figure S4 Overlap between the stress responses of the *A. wentii* CBS141173 and the 'c *gfdB* strains. Venn-diagrams show the upregulated/downregulated genes observed under sorbitol (A), NaCl (B), and NaCl + sorbitol (C) treatments in the two strain. Percentages presented in the intersections show the number of genes upregulated/downregulated in both strains relative to the number of genes upregulated/downregulated in either of the two strains.



Figures S5A and S5B Gene set enrichment analyses of the effect of sorbitol (A) and NaCl (B) treatments on *A. wentii* 'c *gfdB*.

Selected significantly enriched (p adjusted < 0.05) GO and KEGG pathway terms are presented. The full list of the enriched terms are available in Table S3. Letters in parentheses indicate the studied gene set: “A”— all DEGs, “B”— DEGs with $|\log_2\text{FC}| > 1$, “C”— DEGs with $|\log_2\text{FC}| > 2$. If a selected term was enriched in more than one gene set, only the set with the strongest criteria is presented.

C NaCl + sorbitol

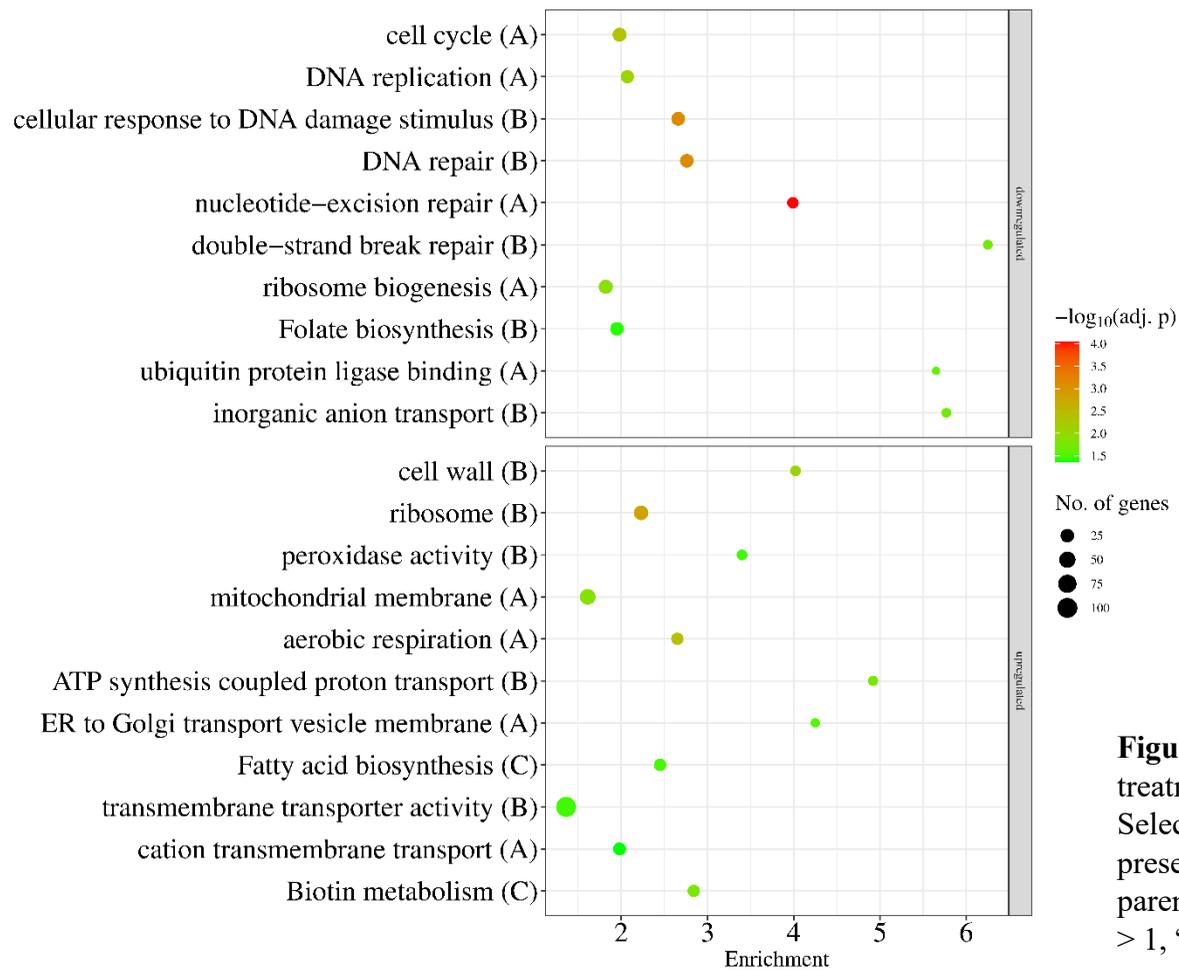


Figure S5C Gene set enrichment analyses of the effect of NaCl + sorbitol (C) treatment on *A. wentii* 'c *gfdB*.

Selected significantly enriched (p adjusted < 0.05) GO and KEGG pathway terms are presented. The full list of the enriched terms are available in Table S3. Letters in parentheses indicate the studied gene set: “A”— all DEGs, “B”— DEGs with $|\log_2\text{FC}| > 1$, “C”— DEGs with $|\log_2\text{FC}| > 2$. If a selected term was enriched in more than one gene set, only the set with the strongest criteria is presented.