



Figure 6. Proteome analysis of PLCD leaves. **A.** Principal component analysis (PCA) of protein profiling. Between parentheses, the variance explained by each component (%) is shown. **B.** Summary of differentially accumulated proteins (DAPs). Up- and down-regulated proteins were computed using Perseus software, p -value < 0.05, 0.05% FDR and q -value < 0.05, DAPs were filtered based on $0.5 < FC < 1.5$. Proteins present in one of the samples of the comparisons but absent in the other sample were also computed as (+) and (-) as depicted in Table S10. **C.** Functional classification of DAPs according to MapMan ontology. Proteins are grouped based on the total number of proteins in the comparison (total), up- or down-regulated proteins. The Venn diagram shows the number of DAPs in the comparisons G7N vs. G0 and G7C vs. G0.