

Supplementary Figures and Legends

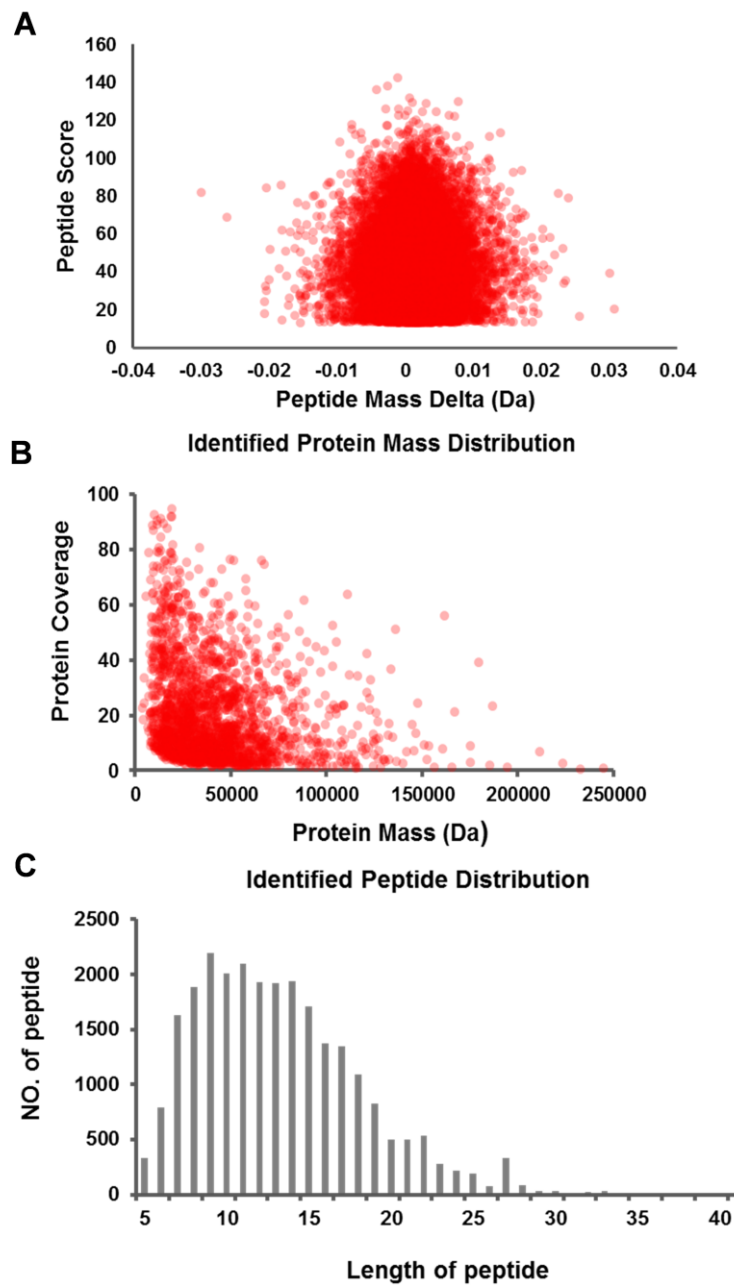


Figure S1. Overview of the proteomic results. (A) Mass errors were determined for all identified peptides. (B) Protein coverage. (C) Identified peptide distribution.

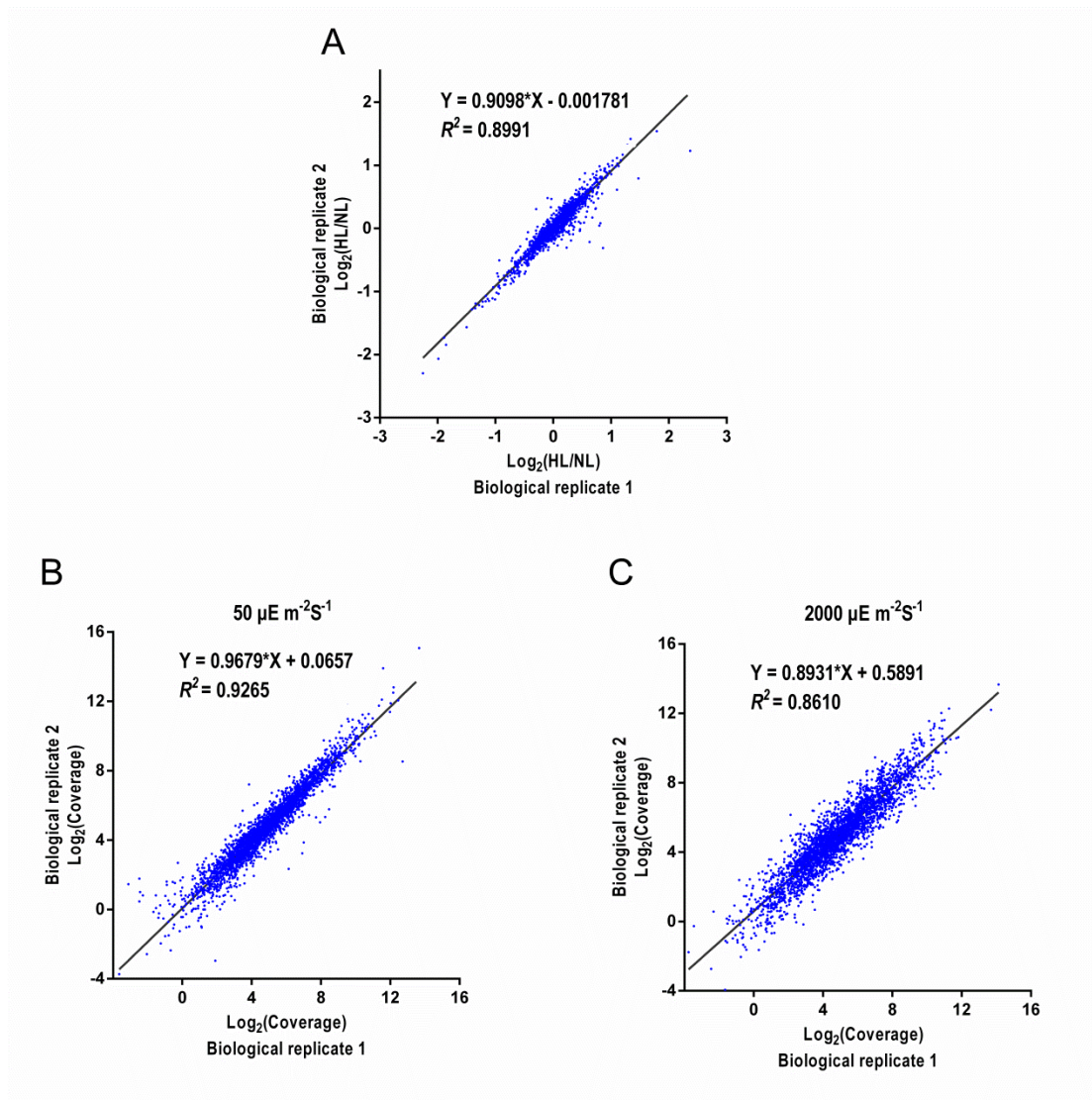


Figure S2. Repeatability of the quantitative proteomic and transcriptomic data. (A) Scatterplot of the relationship of the protein ratios (HL/NL) in both biological replicates. (B) Scatterplot of the relationship of the gene coverage in both biological replicates under NL (B) and HL (C) conditions. All data were log₂-transformed.

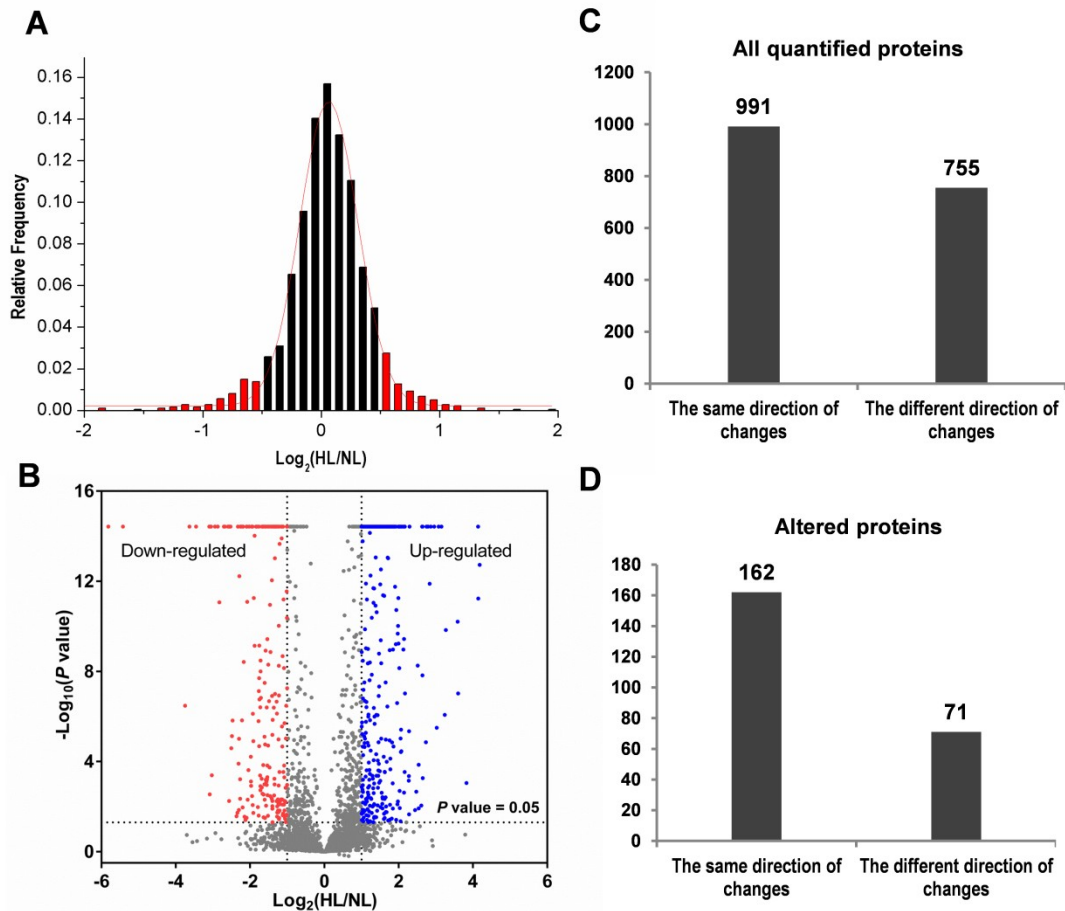


Figure S3. Analysis of the proteome and transcriptome data. (A) Histogram showing the frequency distribution of the log_2 fold changes of the quantified proteins. Proteins with a log_2 fold change ≥ 0.485 (ratio=1.400) or ≤ -0.485 (ratio= 0.714) are shown as red bars. Fold change denotes the HL/NL ratio. (B) Volcano plot showing P value ($-\log_{10}$) versus gene ratio in high-light treated cells (\log_2) of all 526 genes fulfilling strict quantitation criteria (blue, 311 up-regulated transcripts; red, 215 down-regulated transcripts; $P < 0.05$). (C) Bar graph show the number of quantitated proteins which have the same or different direction of changes with the corresponding transcripts. (D) Bar graph show the number of DEPs which have the same or different direction of changes with the corresponding transcripts.

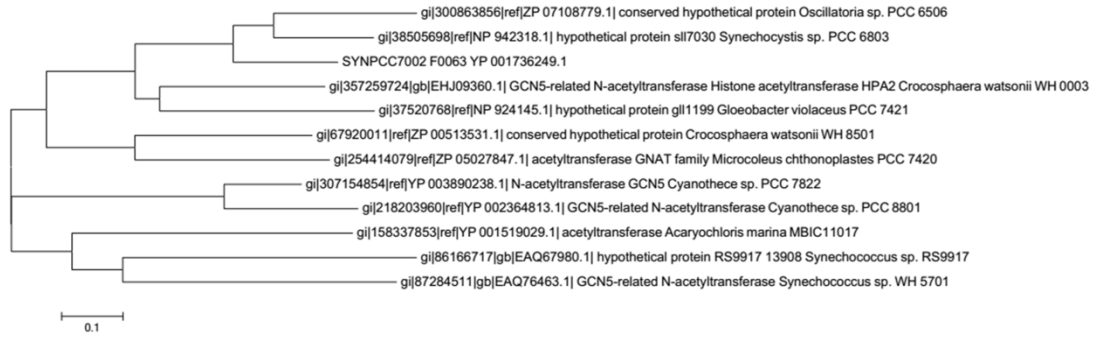


Figure S4. Phylogenetic analysis of F0063 gene of 12 cyanobacteria strains.