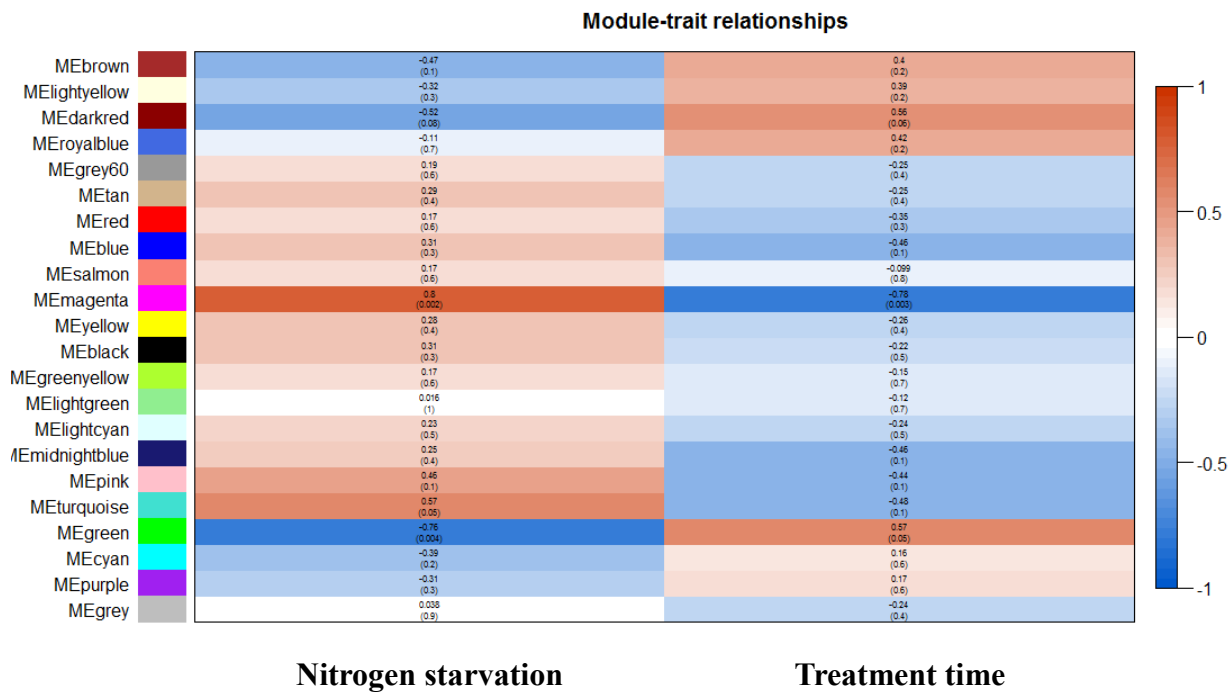


Supplementary Tables available online:

- SUPPLEMENTARY TABLE S1. Primers used for mutant construction in this study.
- SUPPLEMENTARY TABLE S2. Differentially expressed proteins (fold changes) revealed by quantitative iTRAQ proteomic analysis.
- SUPPLEMENTARY TABLE S3. Full lists of genes in the “Hypothetical protein” and “Photosynthesis” modules derived from the WGCNA analysis. N24, N48, N72 indicate the nitrogen starvation times.
- SUPPLEMENTARY TABLE S4. Comparison of mRNA and protein levels of responsive genes under nitrogen starvation.
- SUPPLEMENTARY TABLE S5. Comparison of RNA and protein levels of the genes involved in photosynthesis components in cyanobacteria.

Suppl. Fig. S1 module-trait relationships



SUPPLEMENTARY FIGURE S1. Module-trait relationships based on WGCNA analysis. ME (module) names were listed on the left, and the correlation coefficient to nitrogen starvation was showed on the first column for each module, with the *p*-value appearing at the bottom with a (. For instance, MEgreen (-0.76 (0.004)) represents as the module green, with *r* = -0.76, *p*-value = 0.004.