Article title: Effects of light qualities on the growth and porphyra-334 (a mycosporine-like amino acid) biosynthesis capacity of *Effrenium voratum*

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Table S1. Biological significances of the parameters involved in the JIP-test (Strasser et al. 2004)

Parameter	Biological significance
F_V/F_M	Maximum quantum yield of primary photochemistry (at t = 0)
Mo	Approximated initial slope (ms^{-1}) of the fluorescence transient V = f (t)
Sm	Normalized total complementary area above the O-J-I-P transient (reflecting multiple-turnover Q_A reduction events)
ABS/RC	Absorption flux per RC
TR_0/RC	Trapped energy flux per RC (at t = 0)
ET_0/RC	Electron transport flux per RC (at t = 0)
DI_0/RC	Dissipated energy flux per RC (at t = 0)

Table S2. Biological significances of the parameters involved in the modulated chlorophyll fluorescence and RLC measurements (Ralph and Gademann 2005)

Parameter	Biological significance
ETR	Electron transport rate
Fm	Maximum fluorescence yield in the dark-adapted state
Fm’	Maximum fluorescence yield in the light-adapted state
NPQ	Non-photochemical quenching
PAR	Photosynthetic active radiation
P_{max}	Namely $rETR_{max}$ (maximum relative electron transport rate)
α	Photosynthetic rate in light-limited region of RLC
β	Photoinhibition
I_k	Semi-light saturation point

Table S3. *E. voratum* genes involved in the qRT-PCR analysis and their primers

Gene	Gene ID	Forward primer (5' to 3')	Reverse primer (3' to 5')
COX	OP004348.1	TGGACTTTATATCCACCATTATCCAC	AAGACTTCCAAGAAGAGAAATAGATGAC
DHQS	EVORT383_LOCUS16934	TCGTTGCCGCCTTCTTCTTG	GCTCGCCGTGACAAATGGAAT
OMT	EVOR1521_LOCUS26624	ATATTGCCCGATGCCTACGAG	CTATGGCTGCTGTGGCTTTGT
NRPS	EVOC421_LOCUS32180	GGATTTGGACCCGTCAGTGTTT	AGACCGGAAGGCTATGAAGCAG

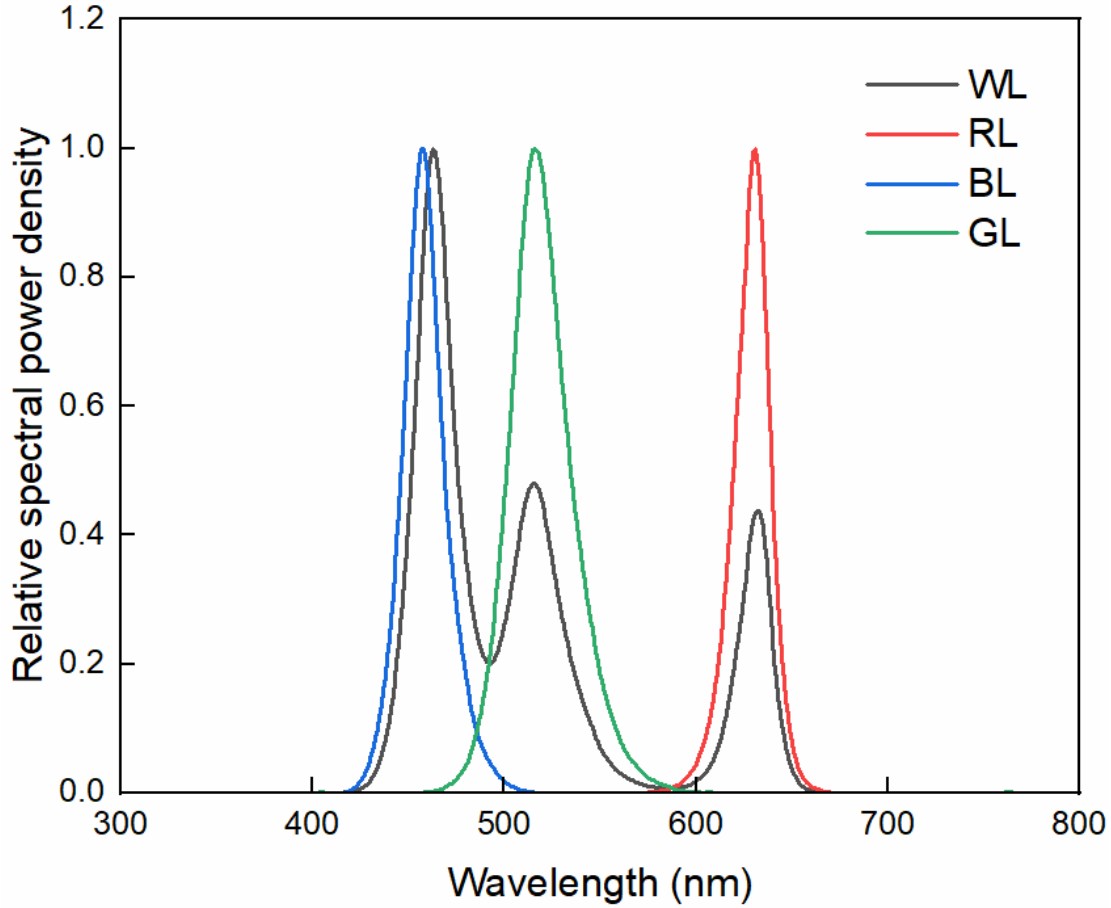
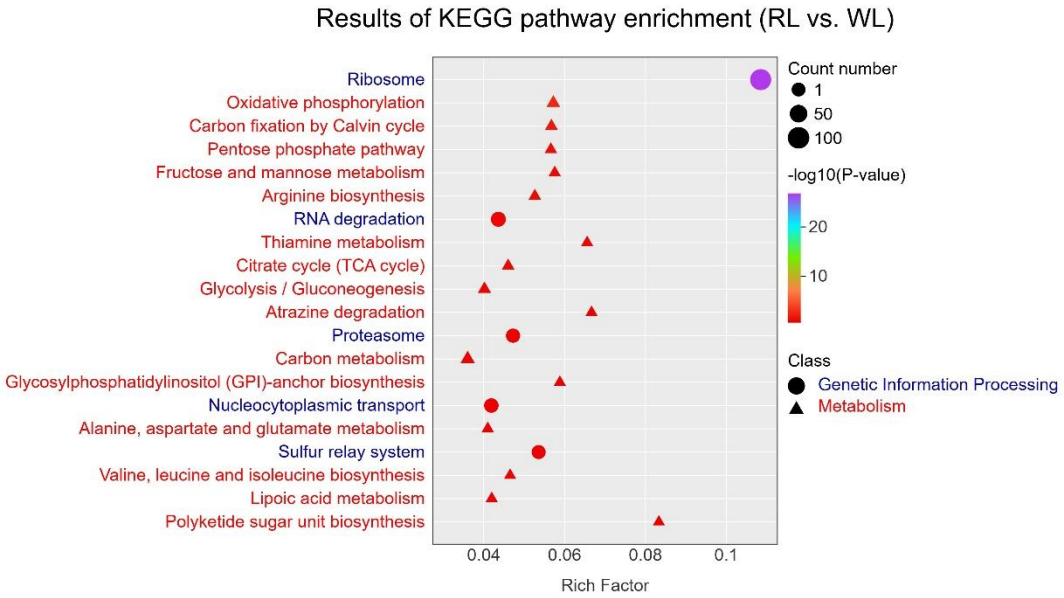
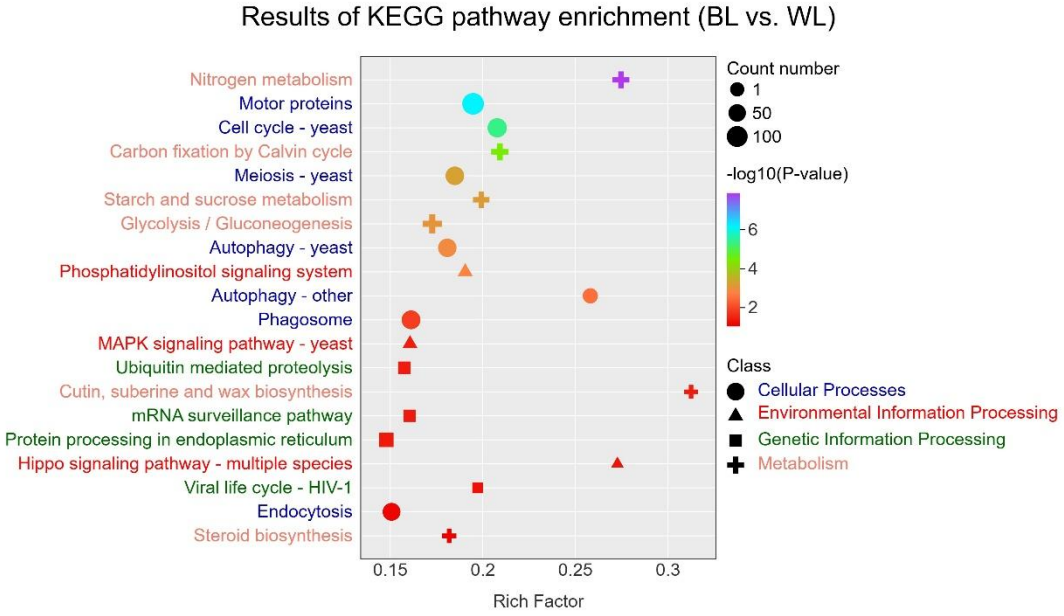


Fig. S1 Spectra of different light qualities

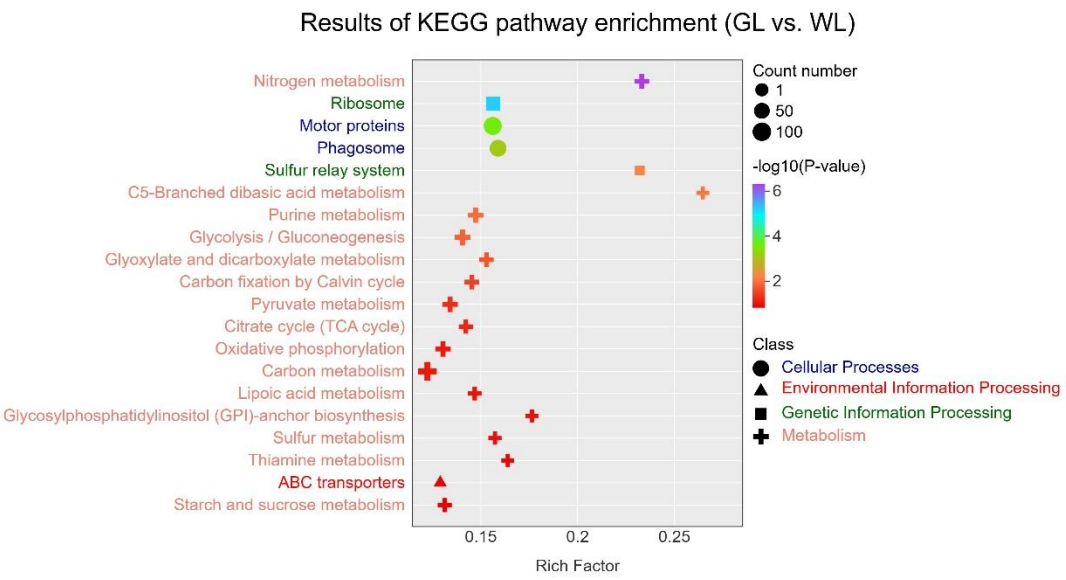
A


Results of KEGG pathway enrichment (RL vs. WL)
Ribosome
Oxidative phosphorylation
Carbon fixation by Calvin cycle
Pentose phosphate pathway
Fructose and mannose metabolism
Arginine biosynthesis
RNA degradation
Thiamine metabolism
Citrate cycle (TCA cycle)
Glycolysis / Gluconeogenesis
Atrazine degradation
Proteasome
Carbon metabolism
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
Nucleocytoplasmic transport
Alanine, aspartate and glutamate metabolism
Sulfur relay system
Valine, leucine and isoleucine biosynthesis
Lipoic acid metabolism
Polyketide sugar unit biosynthesis
0.04
0.06
0.08
0.1
Rich Factor
Count number
1
50
100
-log10(P-value)
20
10
Class
Genetic Information Processing
Metabolism

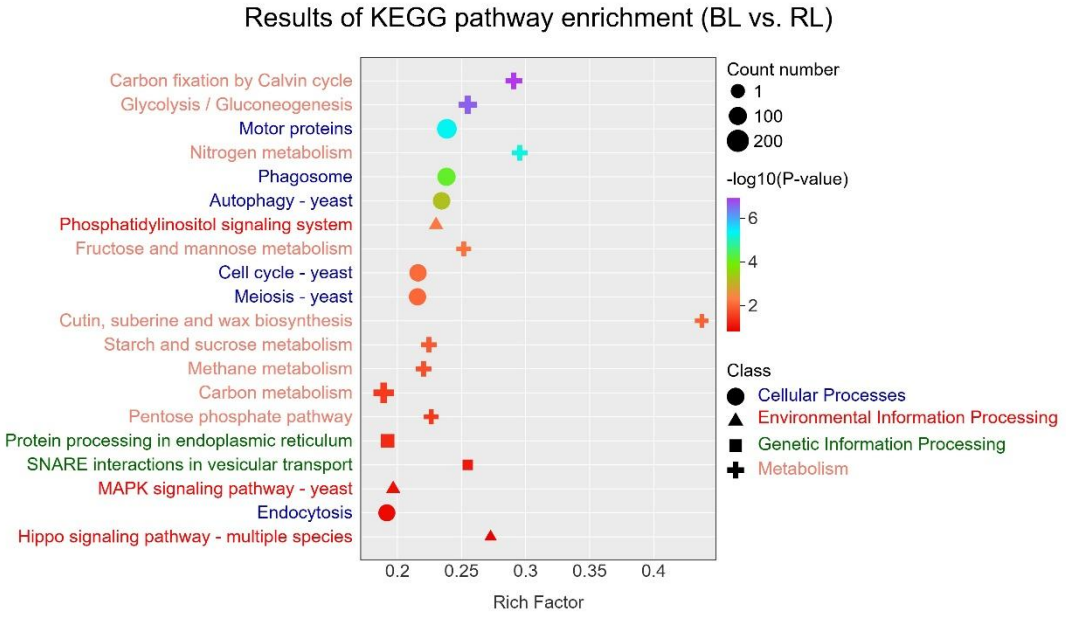
B


Results of KEGG pathway enrichment (BL vs. WL)
Nitrogen metabolism
Motor proteins
Cell cycle - yeast
Carbon fixation by Calvin cycle
Meiosis - yeast
Starch and sucrose metabolism
Glycolysis / Gluconeogenesis
Autophagy - yeast
Phosphatidylinositol signaling system
Autophagy - other
Phagosome
MAPK signaling pathway - yeast
Ubiquitin mediated proteolysis
Cutin, suberine and wax biosynthesis
mRNA surveillance pathway
Protein processing in endoplasmic reticulum
Hippo signaling pathway - multiple species
Viral life cycle - HIV-1
Endocytosis
Steroid biosynthesis
0.15
0.2
0.25
0.3
Rich Factor
Count number
1
50
100
-log10(P-value)
6
4
2
Class
Cellular Processes
Environmental Information Processing
Genetic Information Processing
Metabolism

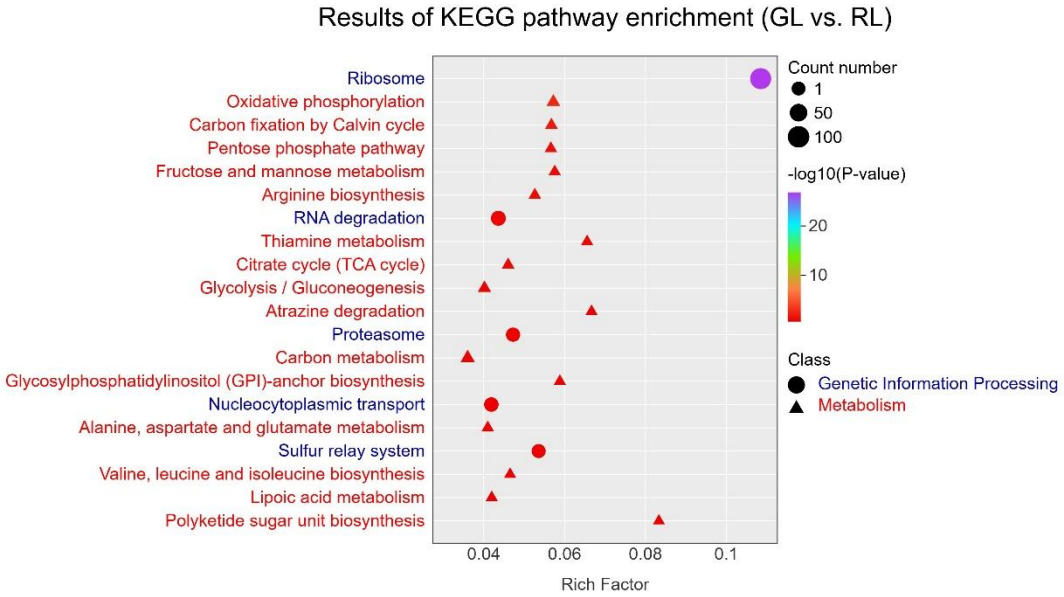
C


Results of KEGG pathway enrichment (GL vs. WL)
Nitrogen metabolism
Ribosome
Motor proteins
Phagosome
Sulfur relay system
C5-Branched dibasic acid metabolism
Purine metabolism
Glycolysis / Gluconeogenesis
Glyoxylate and dicarboxylate metabolism
Carbon fixation by Calvin cycle
Pyruvate metabolism
Citrate cycle (TCA cycle)
Oxidative phosphorylation
Carbon metabolism
Lipoic acid metabolism
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis
Sulfur metabolism
Thiamine metabolism
ABC transporters
Starch and sucrose metabolism
0.15
0.2
0.25
Rich Factor
Count number
1
50
100
-log10(P-value)
6
4
2
Class
Cellular Processes
Environmental Information Processing
Genetic Information Processing
Metabolism

D


Results of KEGG pathway enrichment (BL vs. RL)
Carbon fixation by Calvin cycle
Glycolysis / Gluconeogenesis
Motor proteins
Nitrogen metabolism
Phagosome
Autophagy - yeast
Phosphatidylinositol signaling system
Fructose and mannose metabolism
Cell cycle - yeast
Meiosis - yeast
Cutin, suberine and wax biosynthesis
Starch and sucrose metabolism
Methane metabolism
Carbon metabolism
Pentose phosphate pathway
Protein processing in endoplasmic reticulum
SNARE interactions in vesicular transport
MAPK signaling pathway - yeast
Endocytosis
Hippo signaling pathway - multiple species
0.2
0.25
0.3
0.35
0.4
Rich Factor
Count number
1
100
200
-log10(P-value)
6
4
2
Class
Cellular Processes
Environmental Information Processing
Genetic Information Processing
Metabolism

E



F

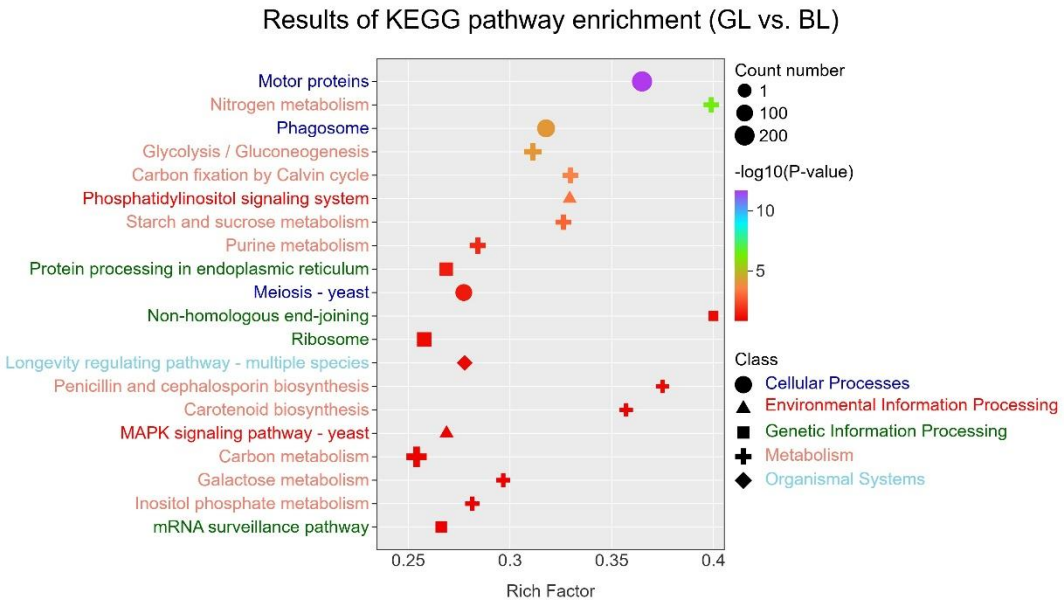
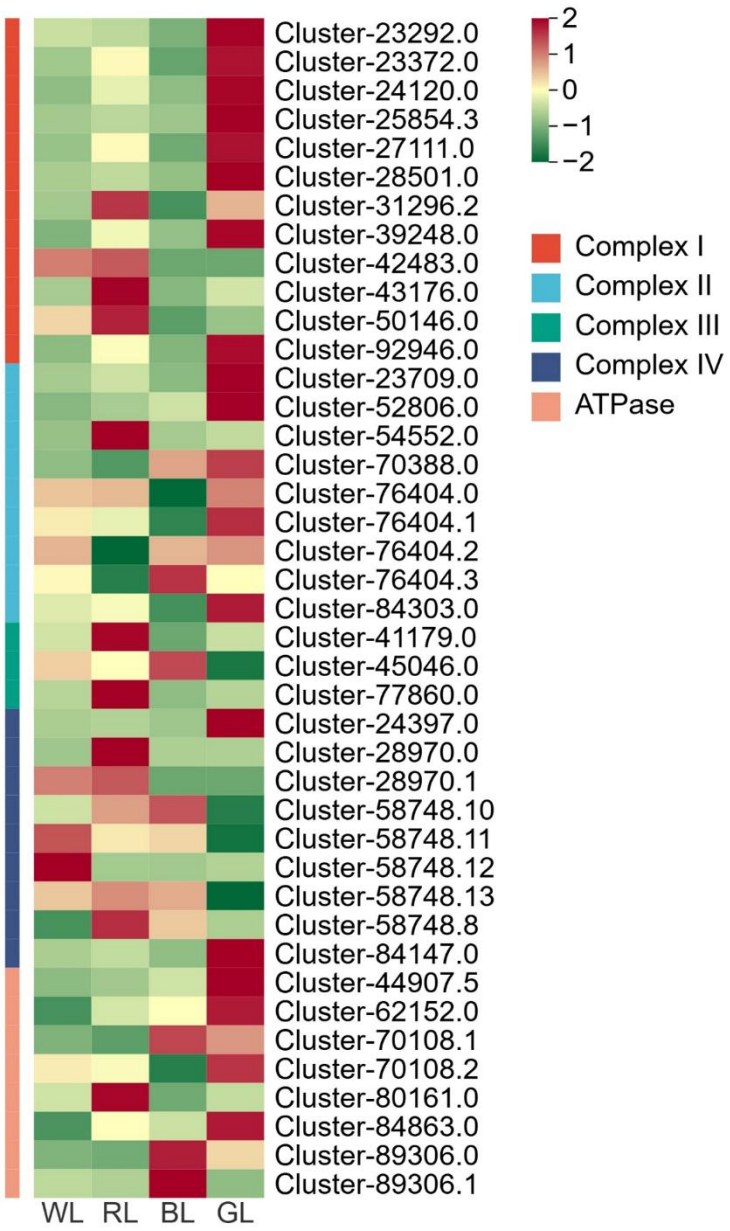


Fig. S2 Results of KEGG pathway enrichment. Rich Factor is proportional to the level of enrichment; the symbol size is proportional to the number of the DEGs enriched on the pathway involved; -log$_{10}$(P-value) is proportional to the significance of enrichment.

A


Cluster-22547.0
Cluster-27710.0
Cluster-29913.1
Cluster-38848.0
Cluster-39713.0
Cluster-49213.0
Cluster-49795.0
Cluster-50414.0
Cluster-55143.0
Cluster-56138.0
Cluster-58195.2
Cluster-61737.0
Cluster-61737.1
Cluster-62808.0
Cluster-70381.0
Cluster-78684.0
Cluster-82689.0
Cluster-84566.1
Cluster-89334.0
Cluster-90185.3
Cluster-91731.0
Cluster-34035.0
Cluster-34143.0
Cluster-38722.0
Cluster-42213.0
Cluster-44886.0
Cluster-50743.0
Cluster-51314.0
Cluster-60039.0
Cluster-72769.0
Cluster-78795.0
Cluster-78795.1
Cluster-78795.5
Cluster-78795.6
Cluster-81886.0
Cluster-82081.0
Cluster-82081.1
Cluster-82081.2
Cluster-82081.3
Cluster-83364.0
Cluster-90807.0
Cluster-90807.1
Cluster-90807.2
Cluster-40605.0
Cluster-46122.0
Cluster-75741.0
Cluster-86578.0
Cluster-23719.0
Cluster-27717.0
Cluster-44907.2
Cluster-44907.3
Cluster-44907.4
Cluster-44907.5
Cluster-46397.0
Cluster-50725.0
Cluster-53726.0
Cluster-64905.0
Cluster-65466.0
Cluster-70108.1
Cluster-70108.2
Cluster-73478.0
Cluster-74766.0
Cluster-74766.1
Cluster-79109.0
Cluster-79980.1
Cluster-80075.0
Cluster-80075.1
Cluster-80075.2
Cluster-80075.5
Cluster-80075.6
Cluster-80161.0
Cluster-83636.3
Cluster-84555.1
Cluster-84555.2
Cluster-84555.3
Cluster-84863.0
Cluster-85544.0
Cluster-85544.1
Cluster-85544.2
Cluster-85544.3
Cluster-85610.0
Cluster-86949.0
Cluster-89306.0
Cluster-89306.1
Cluster-9201.0
Cluster-92711.0
Cluster-92711.2
Cluster-92711.3
Cluster-92711.4
Cluster-92711.5
WL RL BL GL
2
1
0
−1
−2
Photosystem II
Photosystem I
Cytochrome b6/f complex
F-type ATPase

B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Cluster-25854.3
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Cluster-28501.0
Cluster-31296.2
Cluster-39248.0
Cluster-42483.0
Cluster-43176.0
Cluster-50146.0
Cluster-92946.0
Cluster-23709.0
Cluster-52806.0
Cluster-54552.0
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Cluster-76404.2
Cluster-76404.3
Cluster-84303.0
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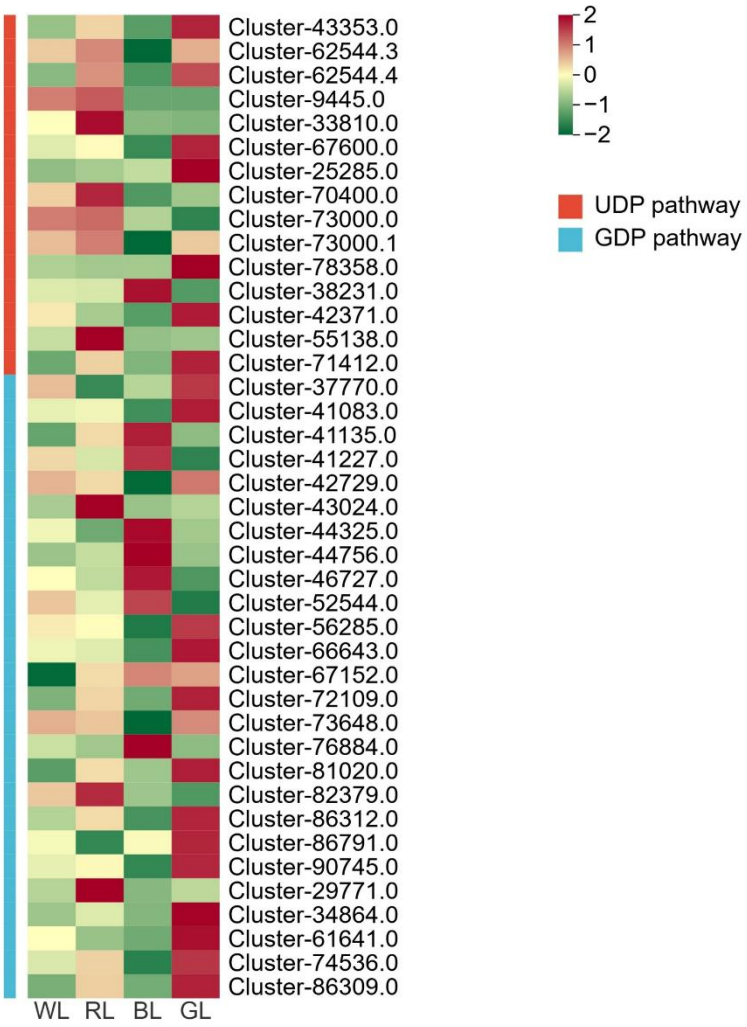
Cluster-77860.0
Cluster-24397.0
Cluster-28970.0
Cluster-28970.1
Cluster-58748.10
Cluster-58748.11
Cluster-58748.12
Cluster-58748.13
Cluster-58748.8
Cluster-84147.0
Cluster-44907.5
Cluster-62152.0
Cluster-70108.1
Cluster-70108.2
Cluster-80161.0
Cluster-84863.0
Cluster-89306.0
Cluster-89306.1
WL
RL
BL
GL
2
1
0
−1
−2
Complex I
Complex II
Complex III
Complex IV
ATPase

C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Cluster-73000.0
Cluster-73000.1
Cluster-78358.0
Cluster-38231.0
Cluster-42371.0
Cluster-55138.0
Cluster-71412.0
Cluster-37770.0
Cluster-41083.0
Cluster-41135.0
Cluster-41227.0
Cluster-42729.0
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Cluster-44325.0
Cluster-44756.0
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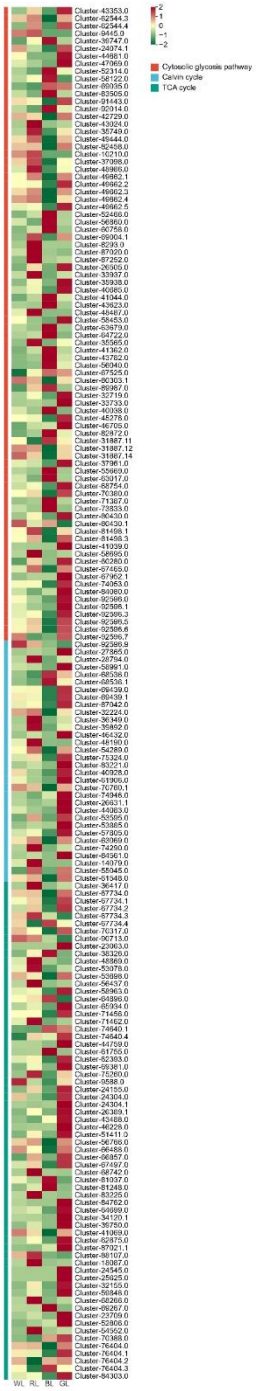
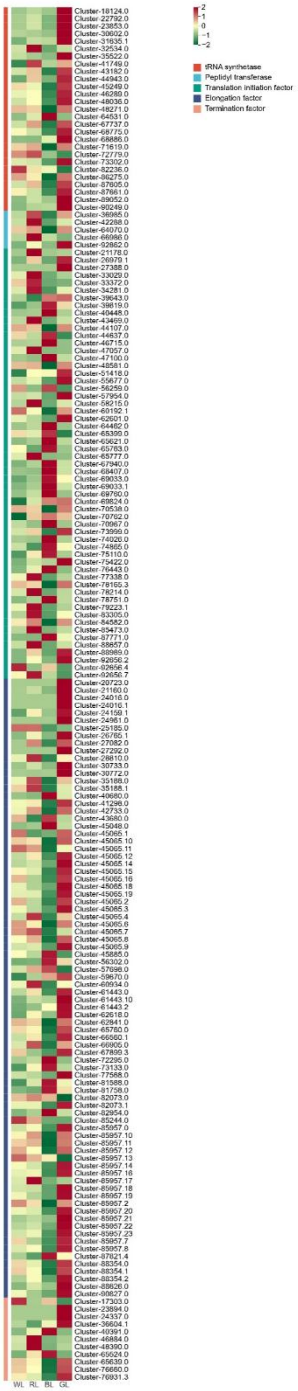
Cluster-66643.0
Cluster-67152.0
Cluster-72109.0
Cluster-73648.0
Cluster-76884.0
Cluster-81020.0
Cluster-82379.0
Cluster-86312.0
Cluster-86791.0
Cluster-90745.0
Cluster-29771.0
Cluster-34864.0
Cluster-61641.0
Cluster-74536.0
Cluster-86309.0
WL RL BL GL
2
1
0
−1
−2
UDP pathway
GDP pathway

D


2
1
0
−1
−2
Cytosolic glycosis pathway
Calvin cycle
TCA cycle
WL
RL
BL
GL

E


2
1
0
−1
−2
tRNA synthetase
Peptidyl transferase
Translation initiation factor
Elongation factor
Termination factor
WL
RL
BL
GL

F

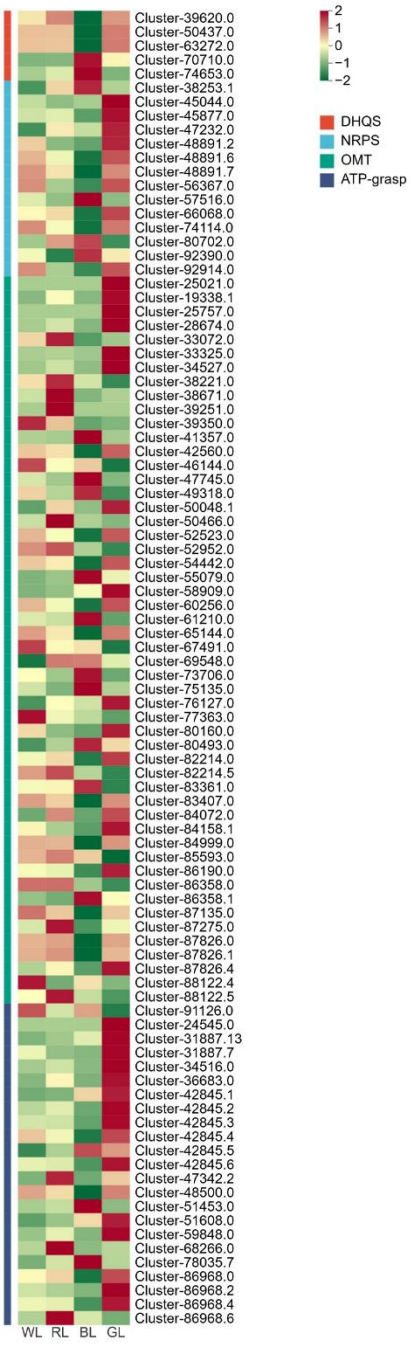


Fig. S3 DEG enrichment in *E. voratum* under different light qualities. A. Heat map of photosynthesis-related DEGs; B. Heat map of respiration-related DEGs; C. Heat map of polysaccharide synthesis-related DEGs; D. Heat map of lipid synthesis-related DEGs; E. Heat map of protein synthesis-related DEGs; F. Heat map of porphyra-334 synthesis-related DEGs