Supplementary Information for

Community context and pCO_2 remodel the transcriptome of the "helper" bacterium *Alteromonas* in co-culture with picocyanobacteria

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Table S13. Differentially regulated genes in *Alteromonas* EZ55 in response to coculture with *Synechococcus* sp. CC9311 at 800 ppm pCO_2

Table S14. Differentially regulated genes in *Alteromonas* EZ55 in response to coculture with *Synechococcus* sp. WH8102 at 800 ppm pCO_2

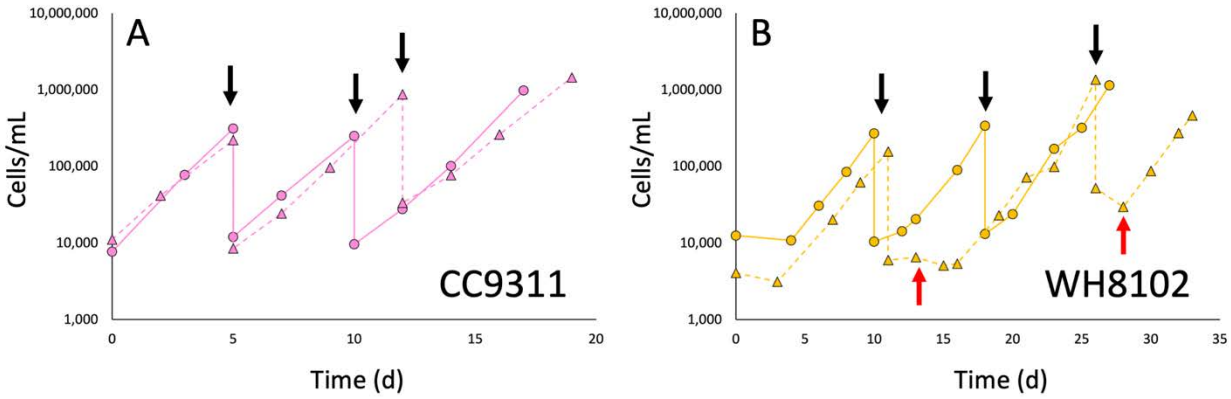


Figure S1. Growth dynamics of *Synechococcus* CC9311 (A) or *Synechococcus* WH8102 (B) under 400 (solid line) or 800 (dashed line) ppm pCO_2 conditions. Each graph shows a representative culture series across three subsequent transfer cycles; cultures were transferred into fresh media by 26-fold dilution whenever they crossed 2.6 x 10^5 cells mL^{-1}. Transfers were performed at the points indicated by black arrows. The red arrows in (B) shows an extended lag period (left arrow) and a moderate cell die-off (right arrow) illustrative of the growth problems experienced by WH8102 at 800 ppm pCO_2.

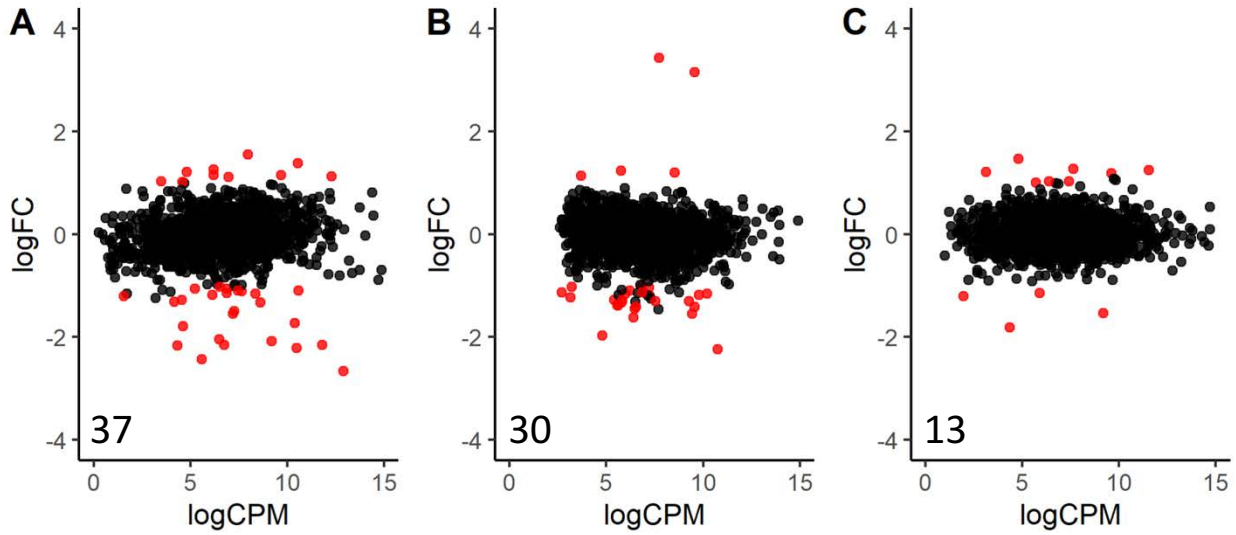


Figure S2. Differential gene transcription in *Prochlorococcus* MIT9312 (A), *Synechococcus* WH8102 (B) and *Synechococcus* CC9311 (C) between growth at 400 and 800 ppm pCO_2. Transcription for each gene is shown on the x-axis as the average abundance in $\log_2$ counts per million (CPM), and the $\log_2$ of the fold change (FC) on the y-axis. Genes which are significantly differentially transcribed ($p < 0.05$ and $|\log_2(FC)| > 1$) are highlighted in red. Values in the bottom left corner of each plot indicate the number of genes significantly differentially regulated in each case.

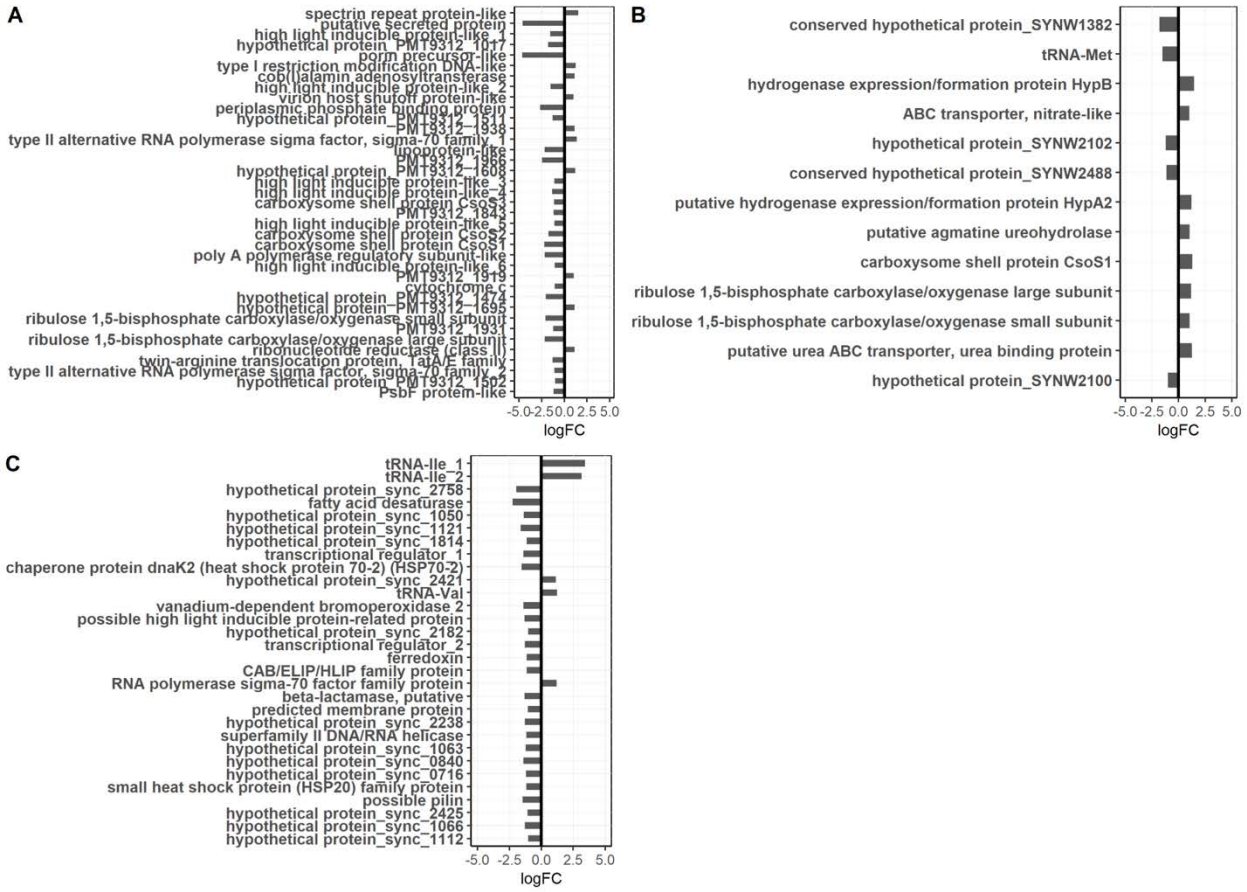


Figure S3. Differentially transcribed individual gene products in *Prochlorococcus* MIT9312 (A), *Synechococcus* WH8102 (B) and *Synechococcus* CC9311 (C) between growth at 400 and 800 ppm pCO_2. Positive or negative transcribed for each gene product is shown on the x-axis as the $\log_2$ of the fold change (FC).

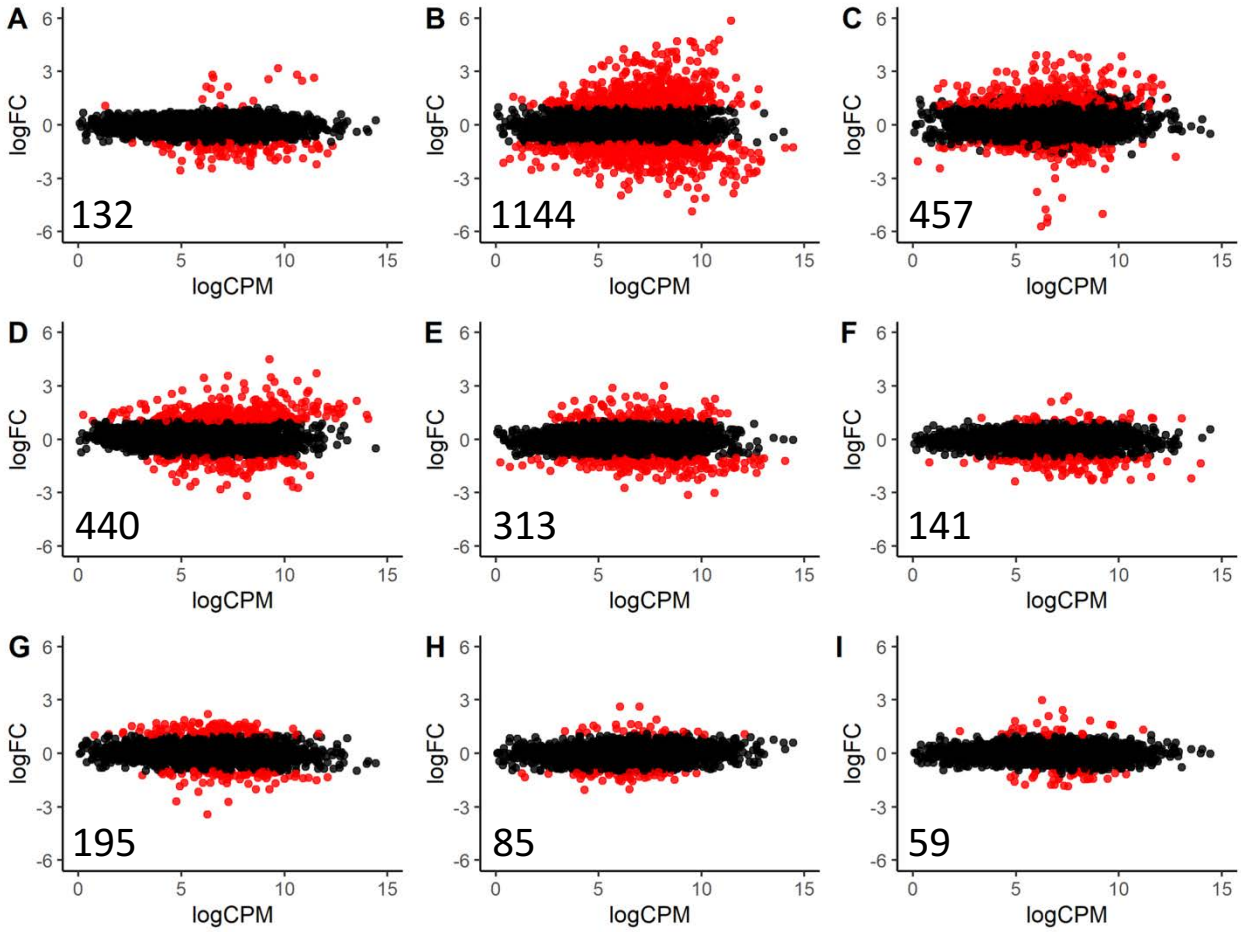


Figure S4. Differential gene transcribed in *Alteromonas* EZ55 under various experimental conditions. Transcription for each gene is shown on the x-axis as the average abundance in $\log_2$ counts per million (CPM) and the $\log_2$ of the fold change (FC) on the y-axis. Genes which are significantly differentially transcribed ($p < 0.05$ and $|\log_2(FC)| > 1$) are highlighted in red. Values in the bottom left corner of each plot indicate the number of genes significantly differentially regulated in each case. (A) General response to 800 ppm pCO2; (B) general response to co-culture with cyanobacteria; (C) genes that are differentially transcribed between pCO_2 conditions in one co-culture context but not the other; (D-F) genes that are differentially transcribed only in coculture with MIT9312, CC9311, or WH8102, respectively, at 400 ppm pCO_2; (G-I) genes that are differentially transcribed only in coculture with MIT9312, CC9311, or WH8102, respectively, at 800 ppm pCO_2.

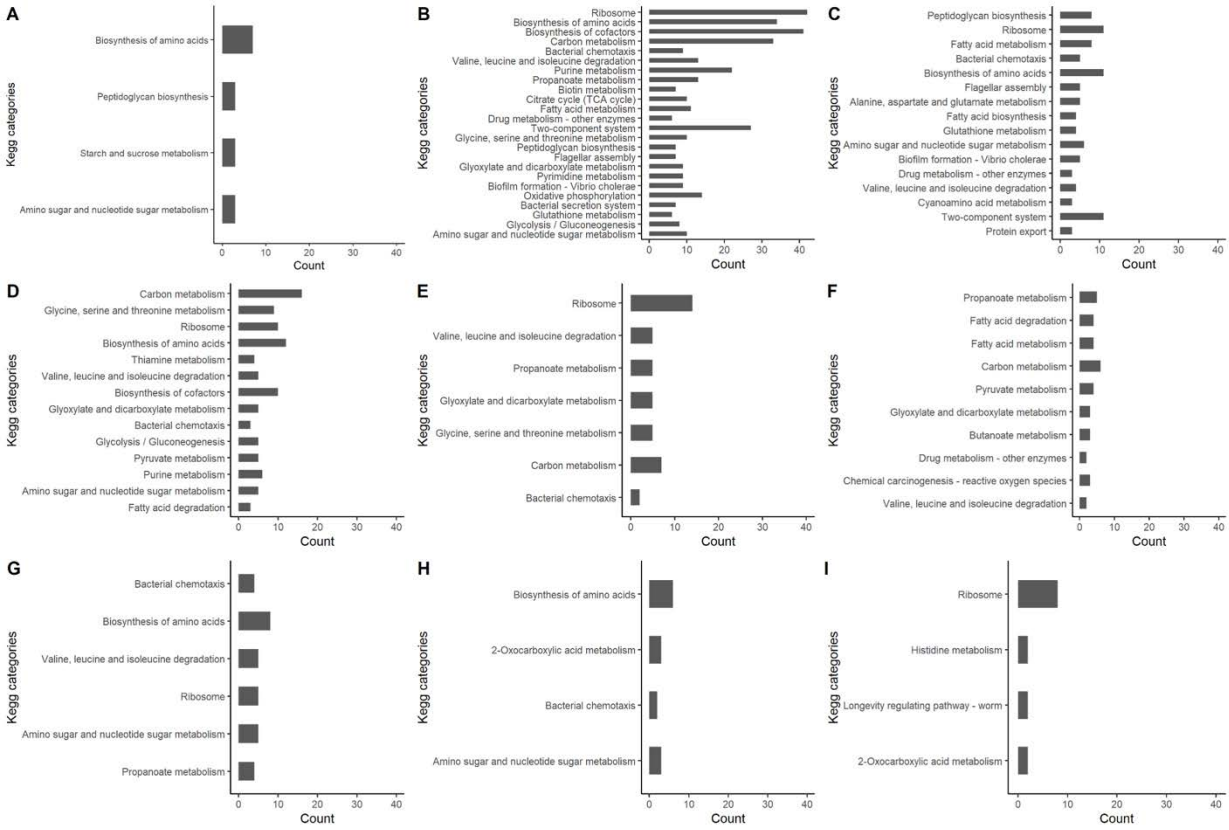


Figure S5. Plots for over-representation analysis (ORA) of significantly-changed KEGG pathways ($p < 0.01$) in *Alteromonas* EZ55 under different experimental conditions. ORA was implemented using hypergeometric tests according to Wu et al., (2021). (A) General response to 800 ppm pCO2; (B) general response to co-culture with cyanobacteria; (C) genes that are differentially transcribed between pCO_2 conditions in one co-culture context but not the other; (D-F) genes that are differentially transcribed only in coculture with MIT9312, CC9311, or WH8102, respectively, at 400 ppm pCO_2; (G-I) genes that are differentially transcribed only in coculture with MIT9312, CC9311, or WH8102, respectively, at 800 ppm pCO_2.

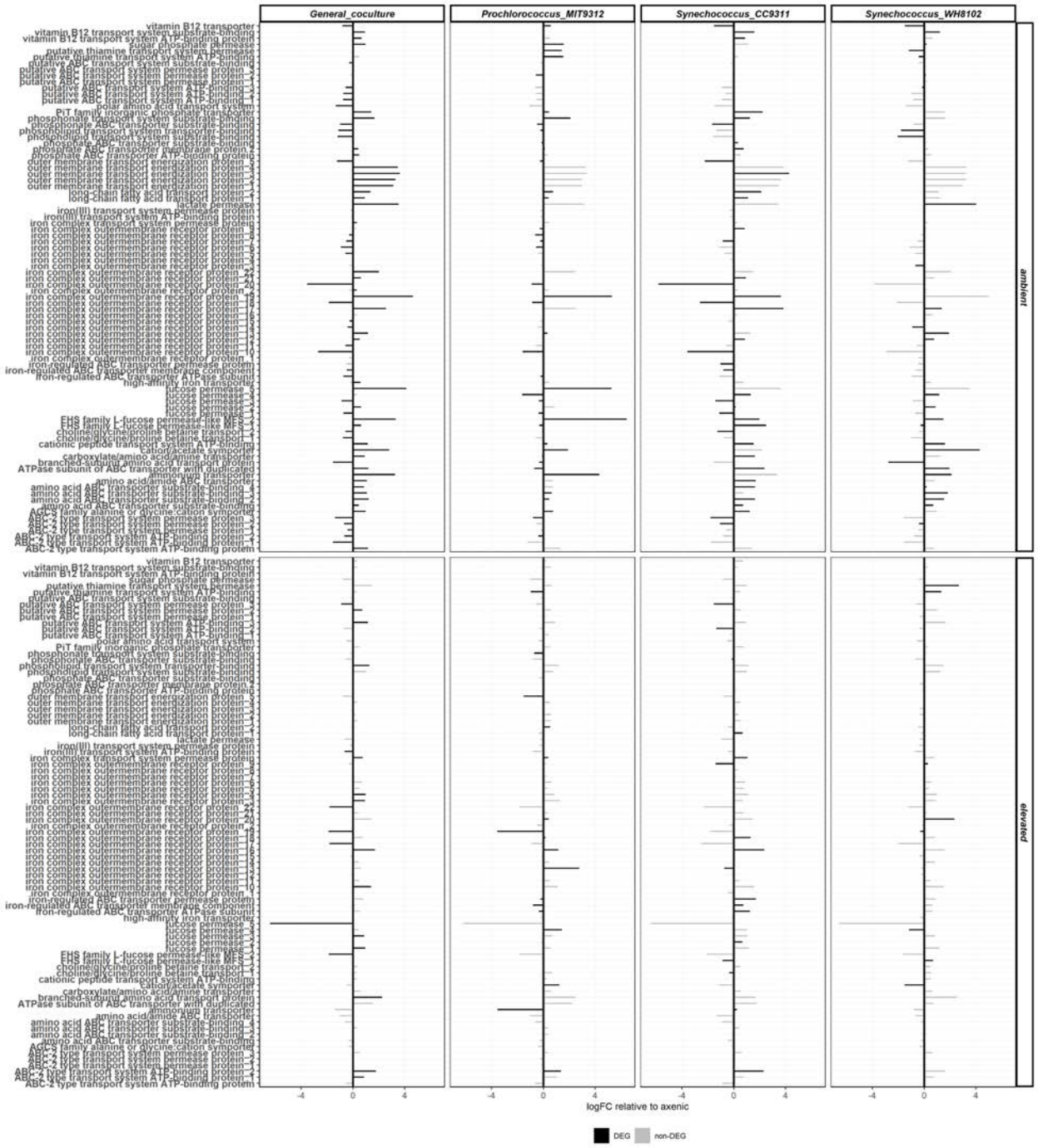


Figure S6. Transporter-related genes in EZ55 representing the general response to co-culture (column 1), and co-culture with specific cyanobacteria (columns 2-4) at 400 or 800 ppm pCO_2, relative to axenic conditions at the same pCO_2. Log_2 fold change (logFC) is plotted relative to axenic EZ55 under the same pCO_2 condition. DEG products are highlighted in black. Black bars in column 1 indicate the average co-culture response is significantly different from the axenic response at the same pCO_2; black bars in columns 2-4 indicate significant difference between the specific cyanobacterial response and the general coculture response shown in column 1.

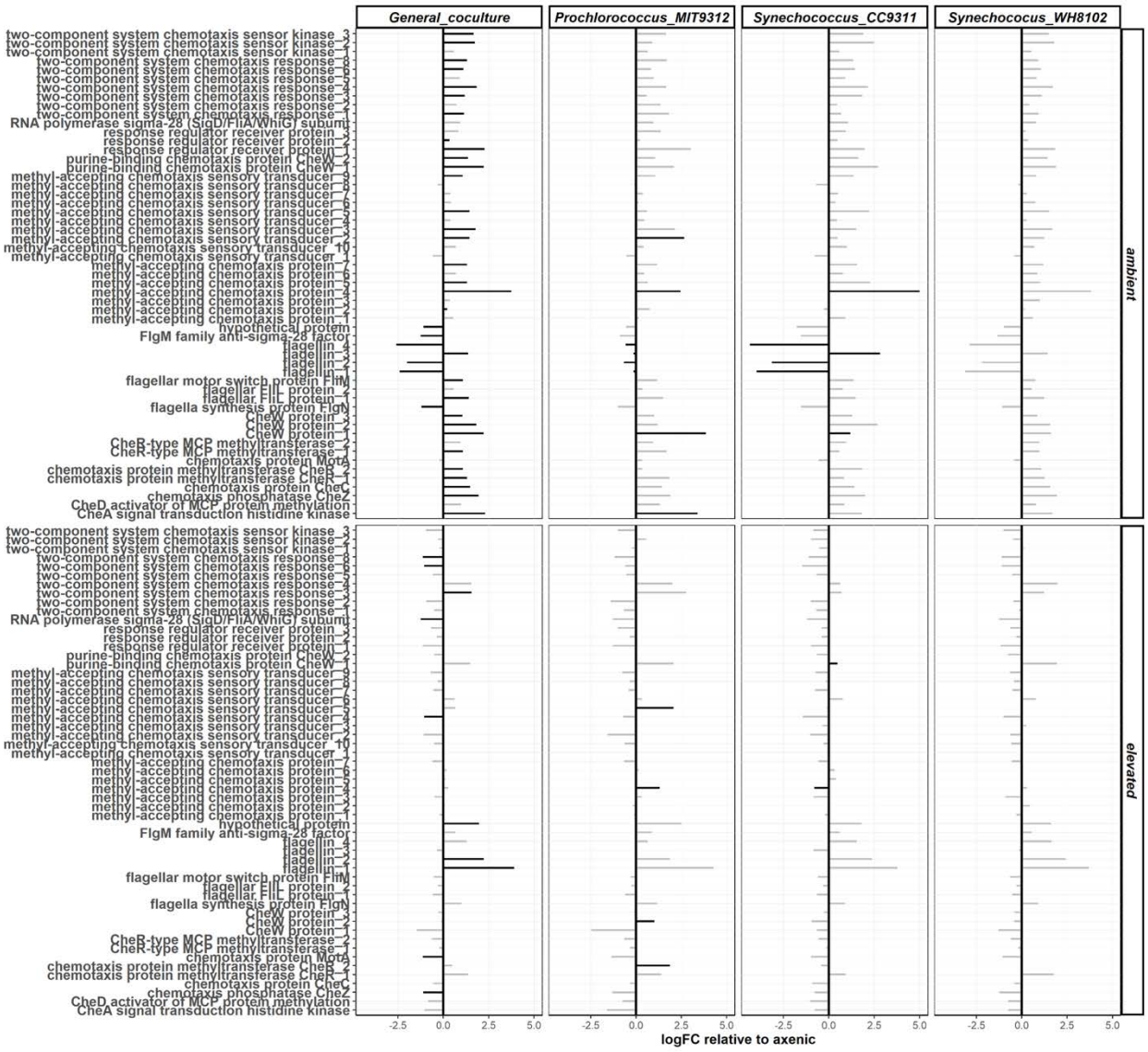


Figure S7. Summary plot of chemotaxis and two-component sensory system gene products in *Alteromonas* EZ55 representing the general response to co-culture (column 1), and co-culture with specific cyanobacteria (columns 2-4) at either 400 or 800 ppm pCO_2, relative to transcription under axenic conditions at the same pCO_2. Log_2 fold change (logFC) is plotted on the x-axis relative to axenic *Alteromonas* under the same pCO_2 condition. Differentially transcribed gene products ($p < 0.05$ and $logFC > 1$) are highlighted in black. Black bars in column 1 indicate the average co-culture response is significantly different from the axenic response at the same pCO_2; black bars in columns 2-4 indicate significant difference between the specific cyanobacterial response and the general coculture response shown in column 1.

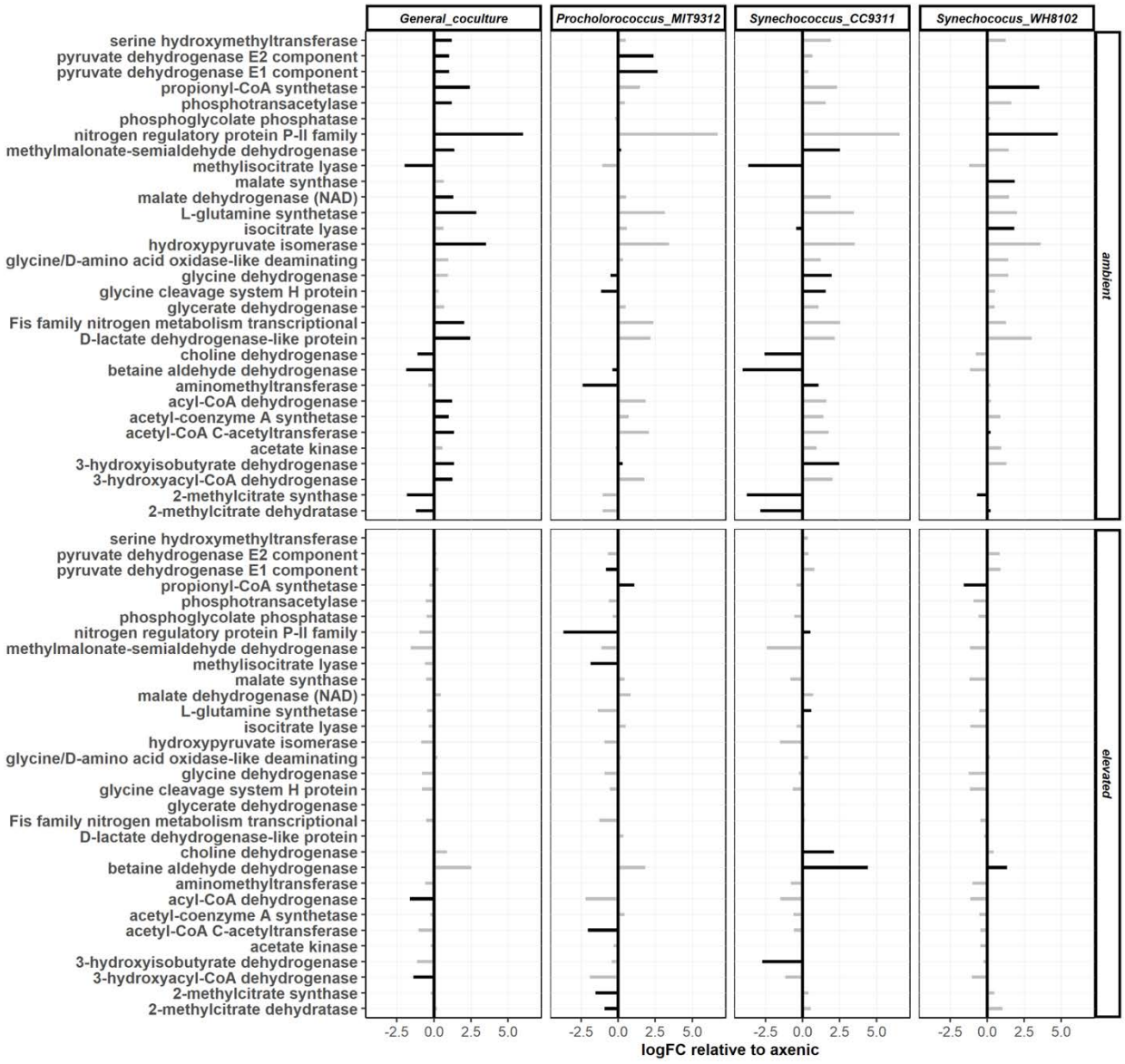


Figure S8. Summary plot of metabolism-related gene products in *Alteromonas* EZ55 representing the general response to co-culture (column 1), and co-culture with specific cyanobacteria (columns 2-4) at either 400 or 800 ppm pCO_2, relative to transcription under axenic conditions at the same pCO_2. Log_2 fold change (logFC) is plotted on the x-axis relative to axenic *Alteromonas* under the same pCO_2 condition. Differentially transcribed gene products ($p < 0.05$ and logFC > 1) are highlighted in black. Black bars in column 1 indicate the average co-culture response is significantly different from the axenic response at the same pCO_2; black bars in columns 2-4 indicate significant difference between the specific cyanobacterial response and the general coculture response shown in column 1.

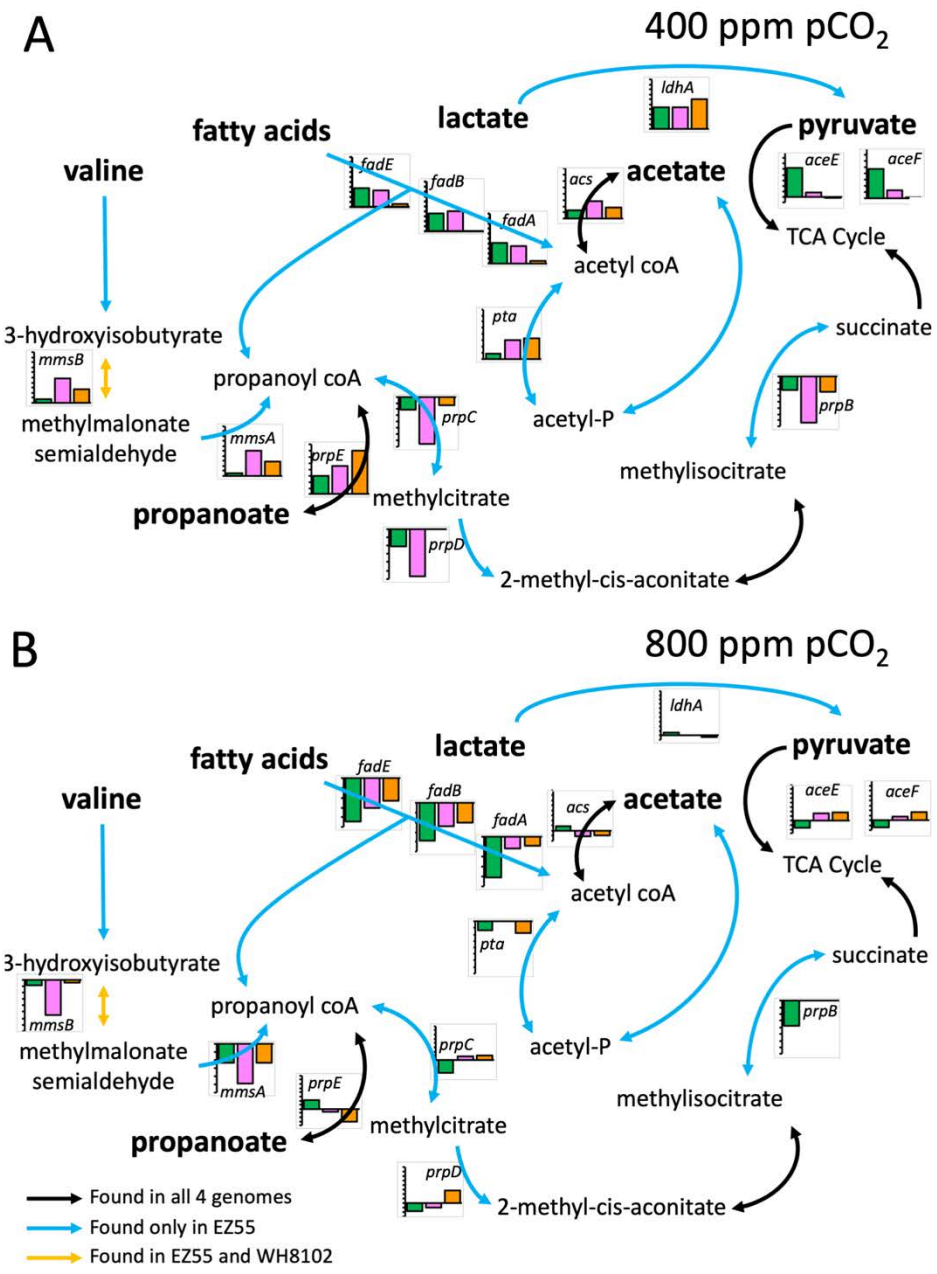
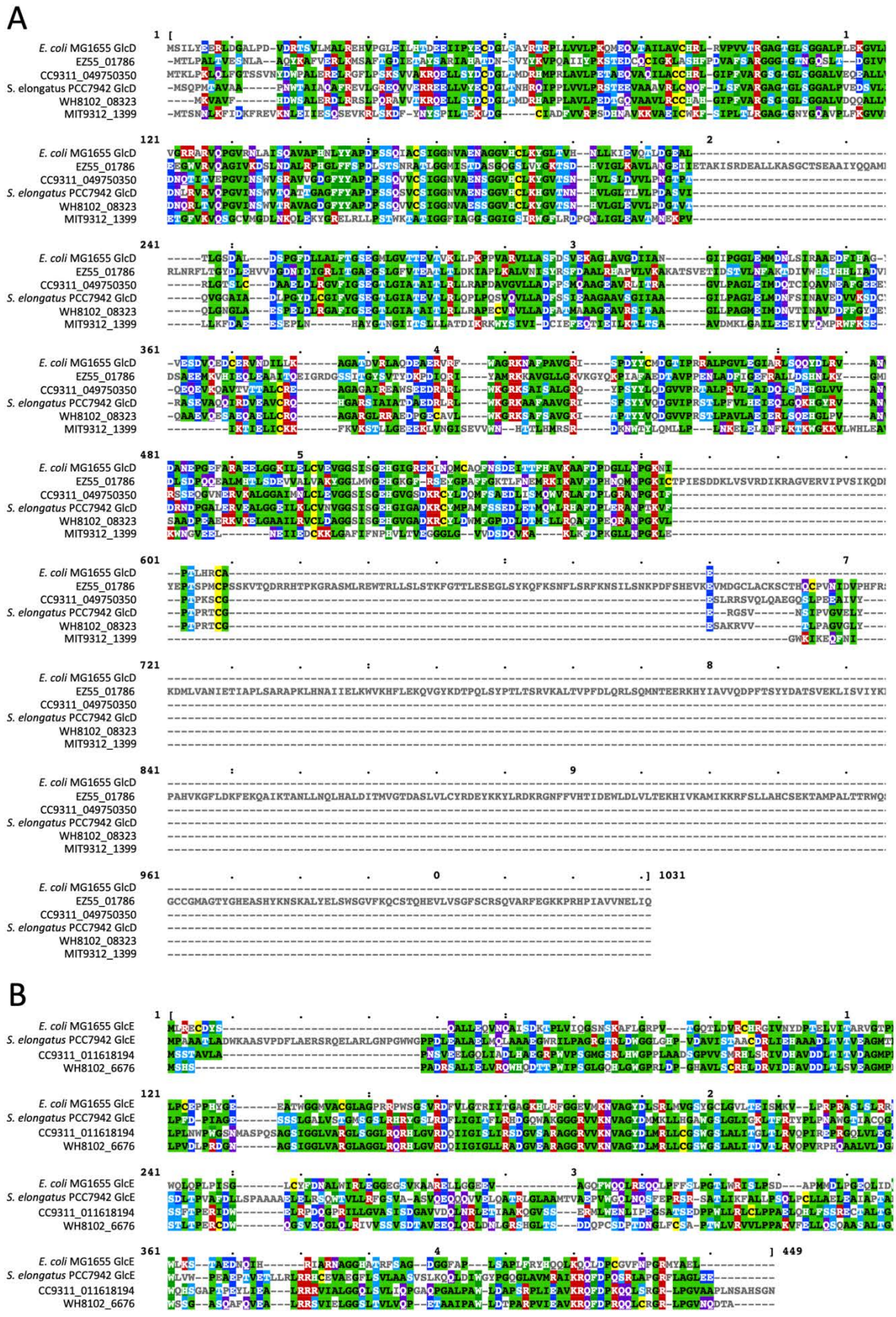
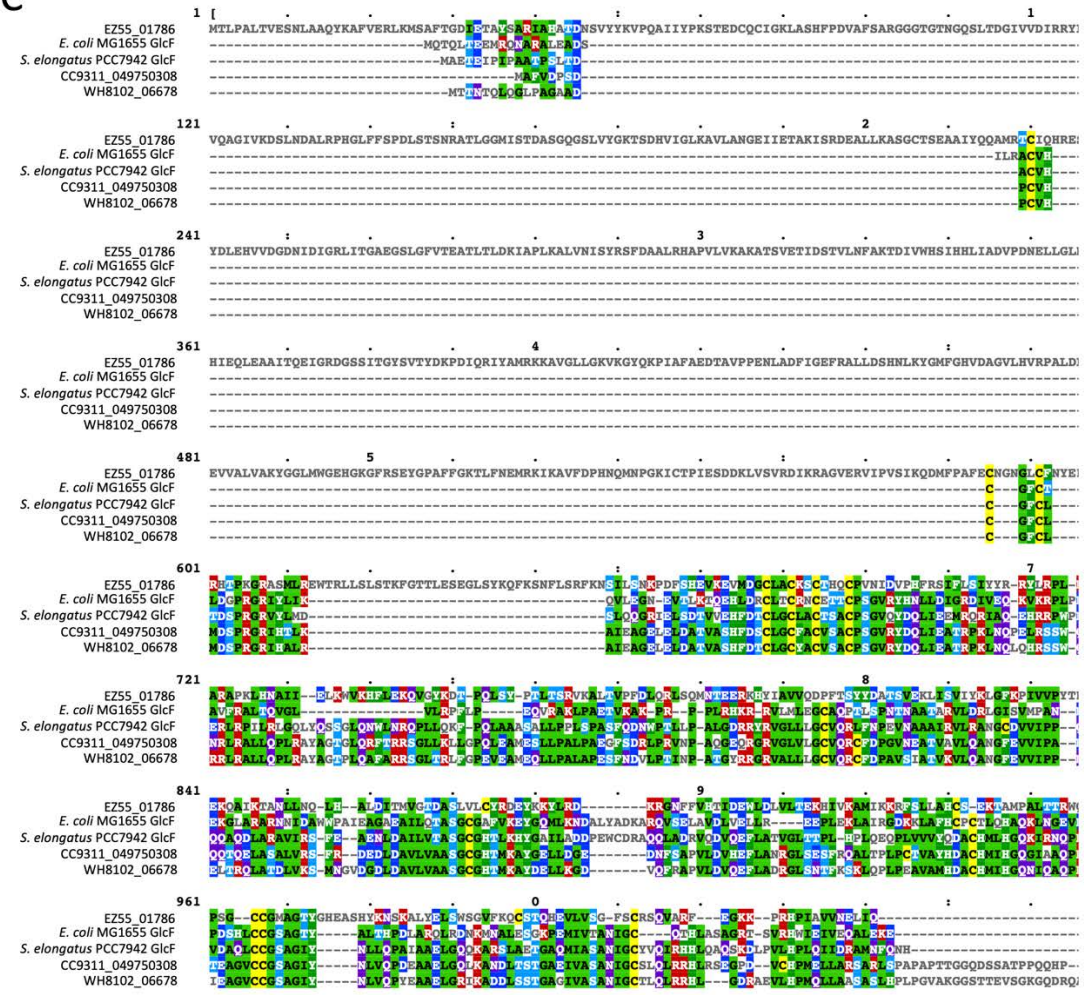


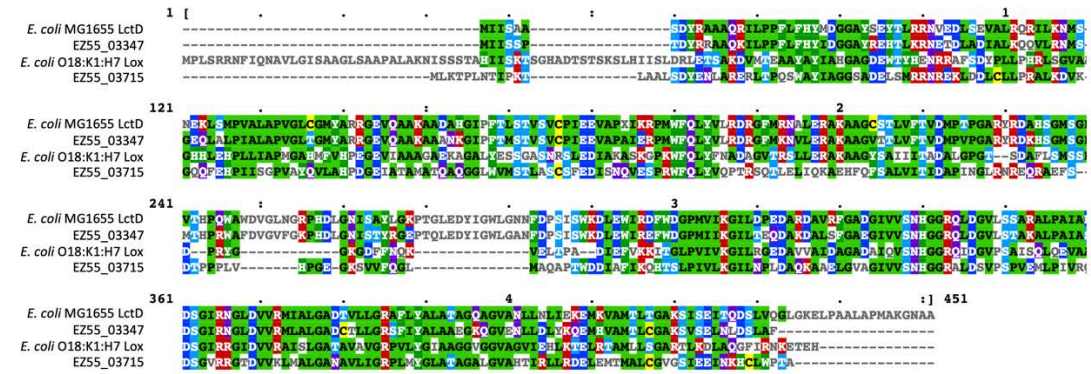
Figure S9. Reconstruction of metabolic pathways involving genes not directly involved in the recovery of photorespiratory byproducts that were significantly differentially regulated in *Alteromonas* EZ55 between axenic and co-culture conditions at 400 (A) or 800 (B) ppm pCO_2. Small inset graphs indicate the log fold change of transcription, relative to axenic culture, in co-culture with MIT9312 (green bars), CC9311 (pink bars), or WH8102 (orange bars). Gene names correspond to the related genes in *E. coli*. Only genes that are differently transcribed between axenic and co-culture in at least one condition are shown. Metabolites in bold print are hypothesized to be phytoplankton exudates used by EZ55 under certain conditions. Arrow colors indicate which of the four genomes are capable of performing the indicated reaction based on annotated gene functions; see inset legend in panel (B) for explanation.


A
E. coli MG1655 GlcD
EZ55_01786
CC9311_049750350
S. elongatus PCC7942 GlcD
WH8102_08323
MIT9312_1399
B
E. coli MG1655 GlcE
S. elongatus PCC7942 GlcE
CC9311_011618194
WH8102_6676

C


EZ55_01786
E. coli MG1655 GlcF
S. elongatus PCC7942 GlcF
CC9311_049750308
WH8102_06678

D


E. coli MG1655 LctD
EZ55_03347
E. coli O18:K1:H7 Lox
EZ55_03715

E

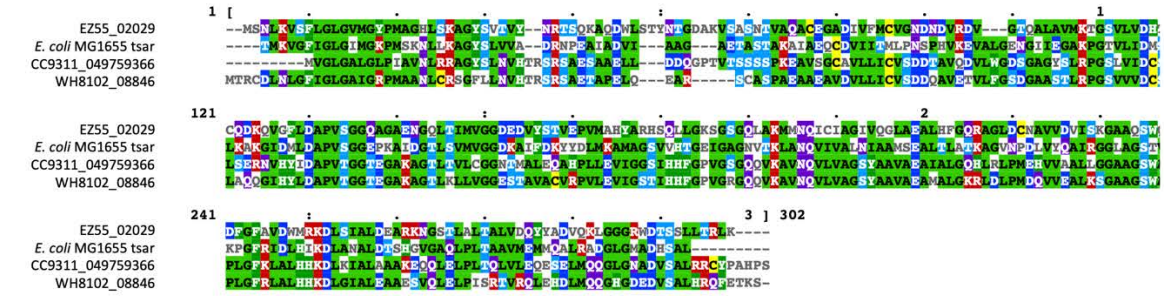


Figure S10. Alignment of hypothesized missing genes in the glycolate utilization pathways of the four strains in this study. Colored residues represent 70% consensus at the level of amino acid equivalence class. A-C) Candidates for the three subunits of bacterial glycolate dehydrogenase, GlcD, GlcE, and GlcF, respectively. For GlcD and GlcF, the putative *Alteromonas macleodii* EZ55 GlcDF fusion protein is included to show its homology with both enzymes. D) Putative lactate/glycolate oxidases. E) Putative tartronate semialdehyde reductases.

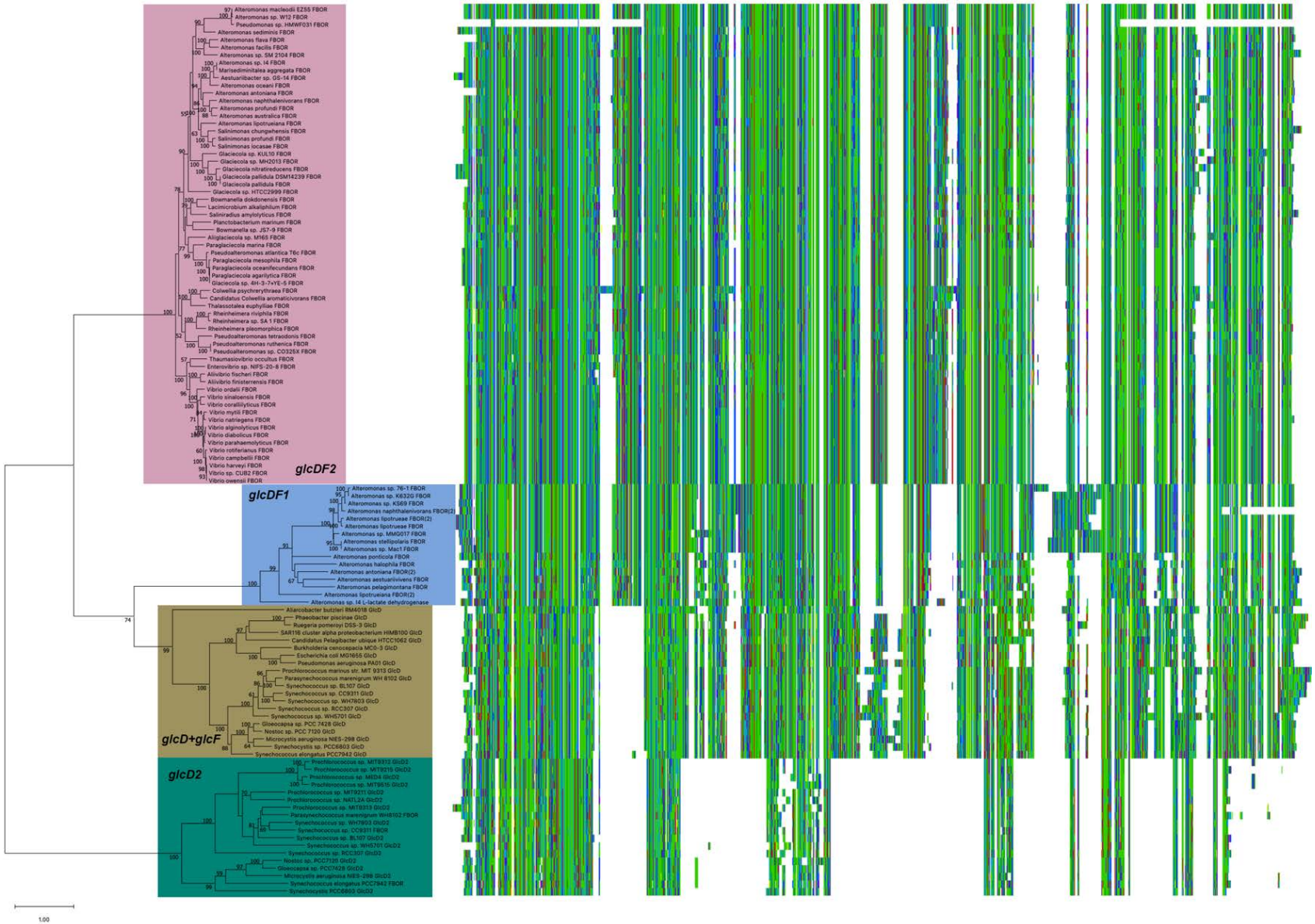

glcDF2
glcDF1
glcD+glcF
glcD2
1.00

Figure S11. Maximum likelihood tree of GlcDF-like proteins. Tree was constructed in MEGA 11 using WAG+G+I+F substitution model. Node values are the percentage support from 100 bootstrap replicates. *Micromonas pusilla* peroxisomal GOX was used as an outgroup to root the tree and was subsequently pruned for easier visualization. Colored patterns to the right of the tree show the protein alignments with mview color coding, indicating the strong conservation between the separate *glcD* and *glcF* genes previously studied and the *glcDF* fusion protein described here. FBOR, FAD-binding oxidoreductase.

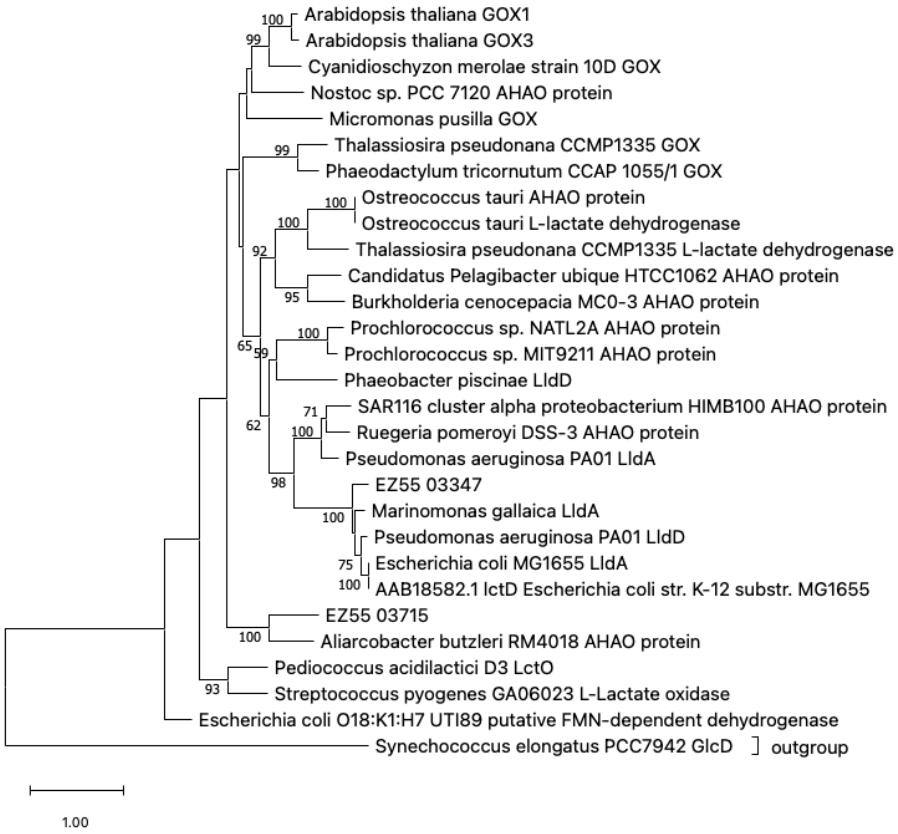


Figure S12. Maximum likelihood tree of LOX/GOX-like proteins. Tree was constructed in MEGA 11 using LG+G substitution model. Node values are the percentage support from 100 bootstrap replicates. *Synechococcus elongatus* glycolate dehydrogenase subunit GlcD was used as an outgroup to root the tree. AHAO, alpha-hydroxy-acid oxidizing