

Supplementary Tables and Figures

Table S1: Report on linear model and ANOVA applied to 5-mC data (Adj. $R^2 = 0.2583$; $F_{3,40} = 5.993$; p-value = 0.001795): %5-mC $\sim p\text{CO}_2$ (μatm) + time (days) + $p\text{CO}_2$ * time.

Model Residuals				
<i>Min</i>	<i>1Q</i>	<i>Median</i>	<i>3Q</i>	<i>Max</i>
-0.31964	-0.10896	-0.02583	0.12698	0.31668
Model Coefficients				
<i>Term</i>	<i>Estimate</i>	<i>Std. Error</i>	<i>t value</i>	<i>Pr(> t)</i>
(Intercept)	1.349e+00	1.226e-01	10.996	1.17e-13
Time	-7.881e-02	3.111e-02	-2.533	0.015331
pCO2	-7.817e-04	1.940e-04	-4.029	0.000243
Time:pCO2	1.355e-04	4.872e-05	2.782	0.008204
ANOVA F-stats				
<i>Term</i>	<i>Df</i>	<i>Sum Sq</i>	<i>F value</i>	<i>Pr(>F)</i>
Time	1	0.00000	0.0000	0.999718
pCO2	1	0.26404	10.2382	0.002693
Time:pCO2	2	0.19960	7.7393	0.008204
Residuals	40	1.03160	NA	NA

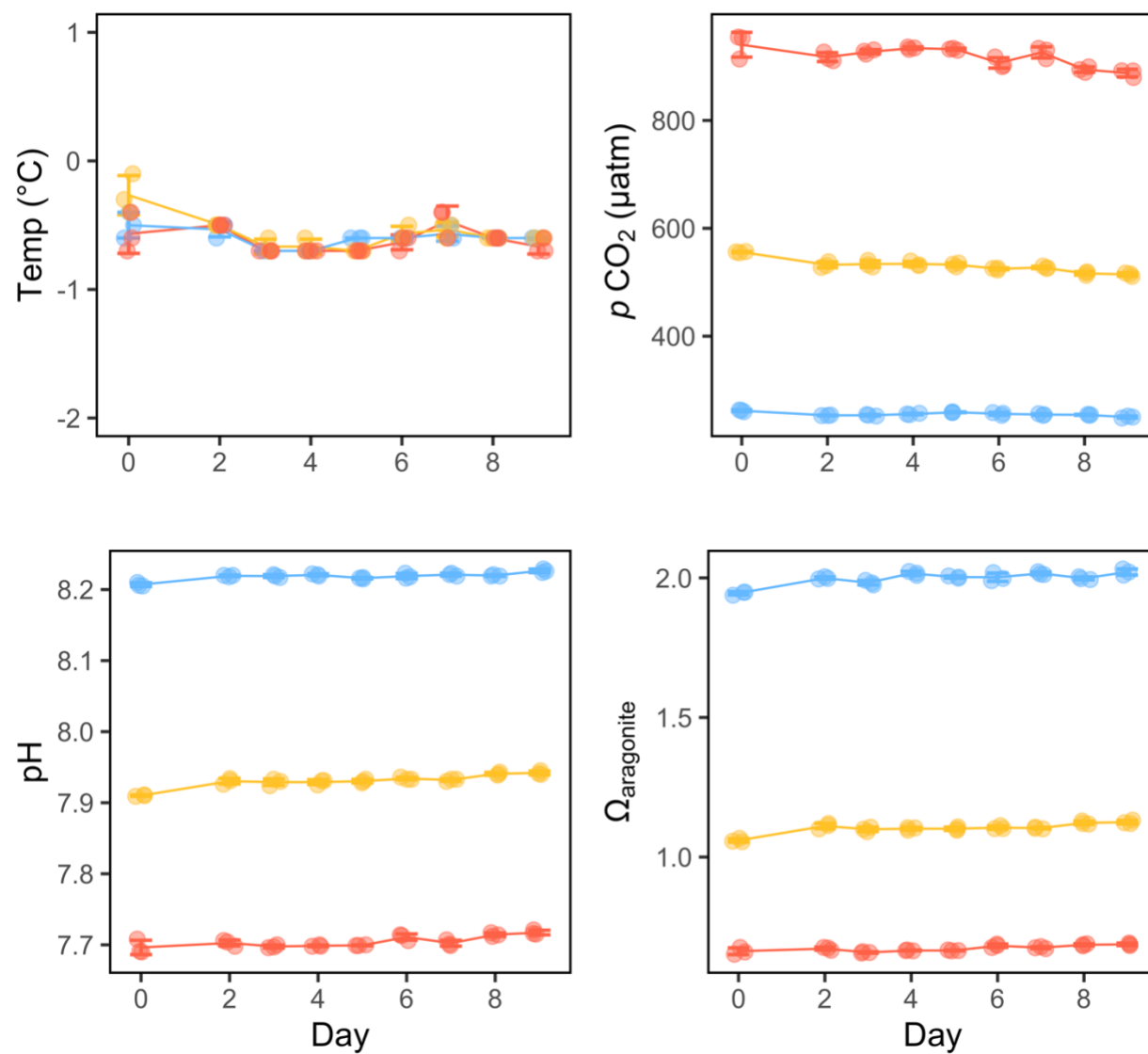


Figure S1: Temperature and seawater chemistry parameters across the duration of the experiment. Mean values for low, intermediate, and high $p\text{CO}_2$ treatments are represented in blue, yellow, and red, respectively. Circles represent replicate cultures and are nudged apart widthwise by 0.15 days. Error bars depict \pm SD.

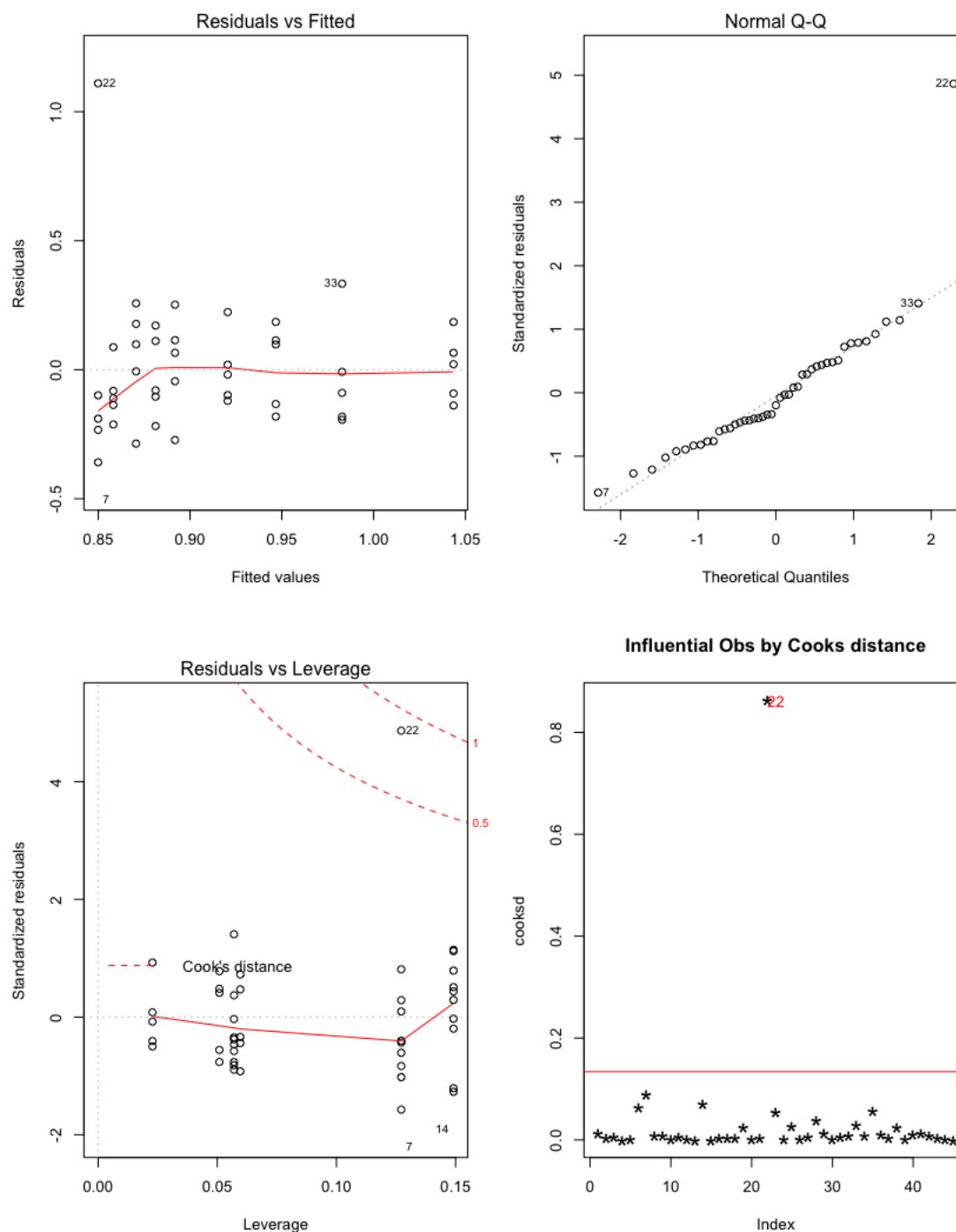


Figure S2: Outlier tests for non-normality (Q-Q plot), high leverage (Cook's distance), and high residual (Residual vs...). Each test included here is derived from a linear model of 5-mC as a function of $p\text{CO}_2$, exposure time, and their interaction. A replicate from the 1 d, 918 $\mu\text{atm } p\text{CO}_2$ treatment group labeled here as replicate '22' tested positively for all three of these metrics representing outlier probability and influence and was thus removed from all analyses including 5-mC data.

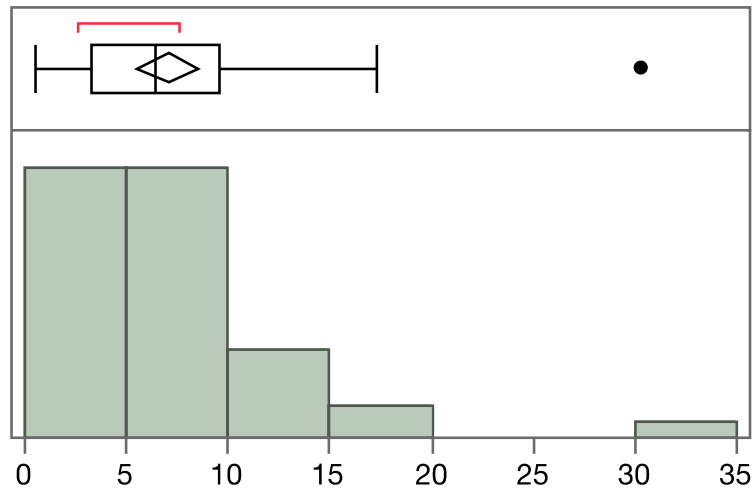


Figure S3: A histogram of CV values derived from OD450 measurements across technical replicates used in 5-mC quantification for 45 samples. A confidence diamond depicts the mean CV and its 95% confidence intervals. A bracket depicts the mode.

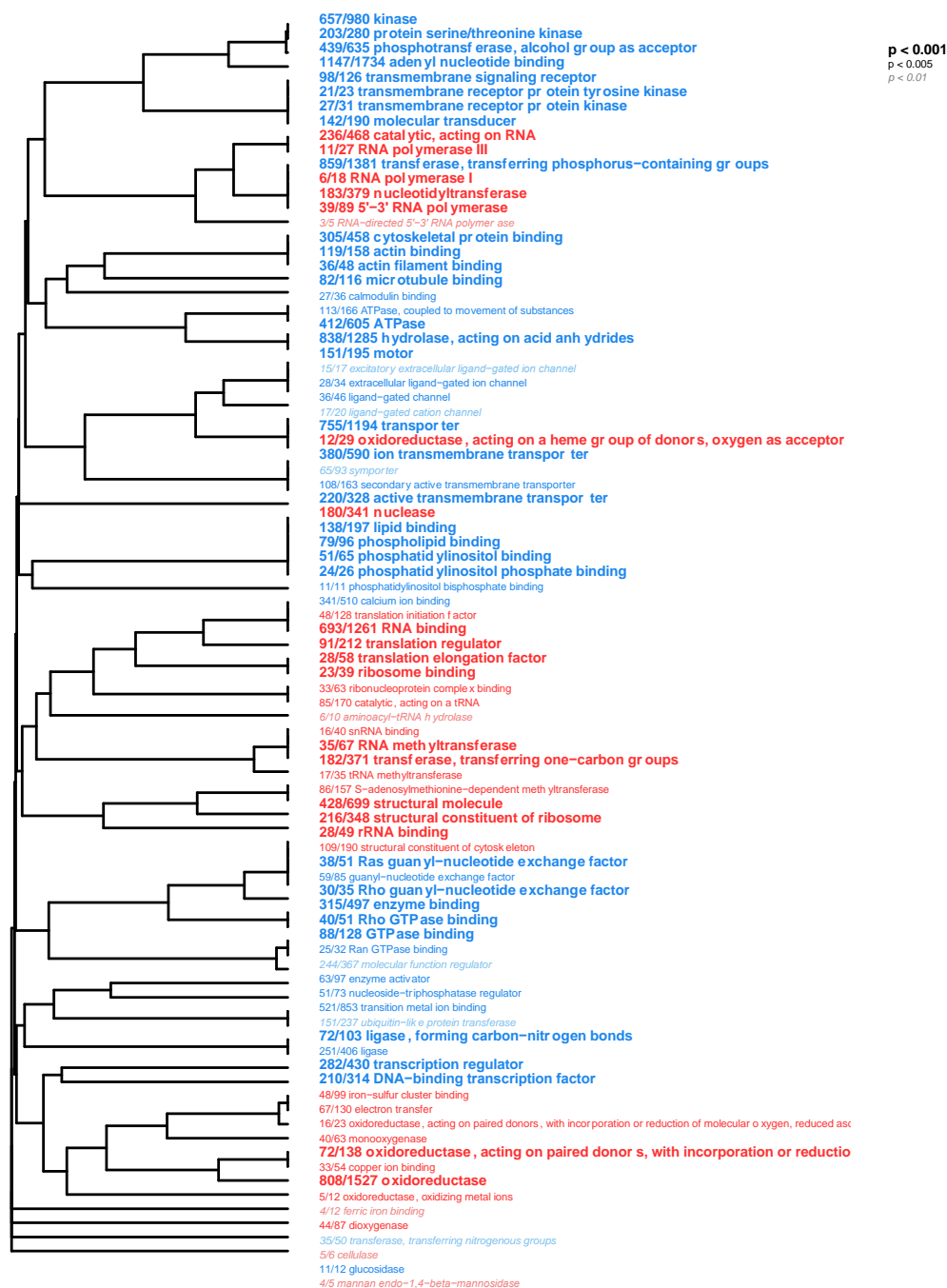


Figure S4: GO terms enriched among up- (red) and downregulated (blue) genes expressed under 918 μatm $p\text{CO}_2$ relative to 255 μatm after 0.5 days. GO terms are clustered according to shared genes. Text size depicts significance.

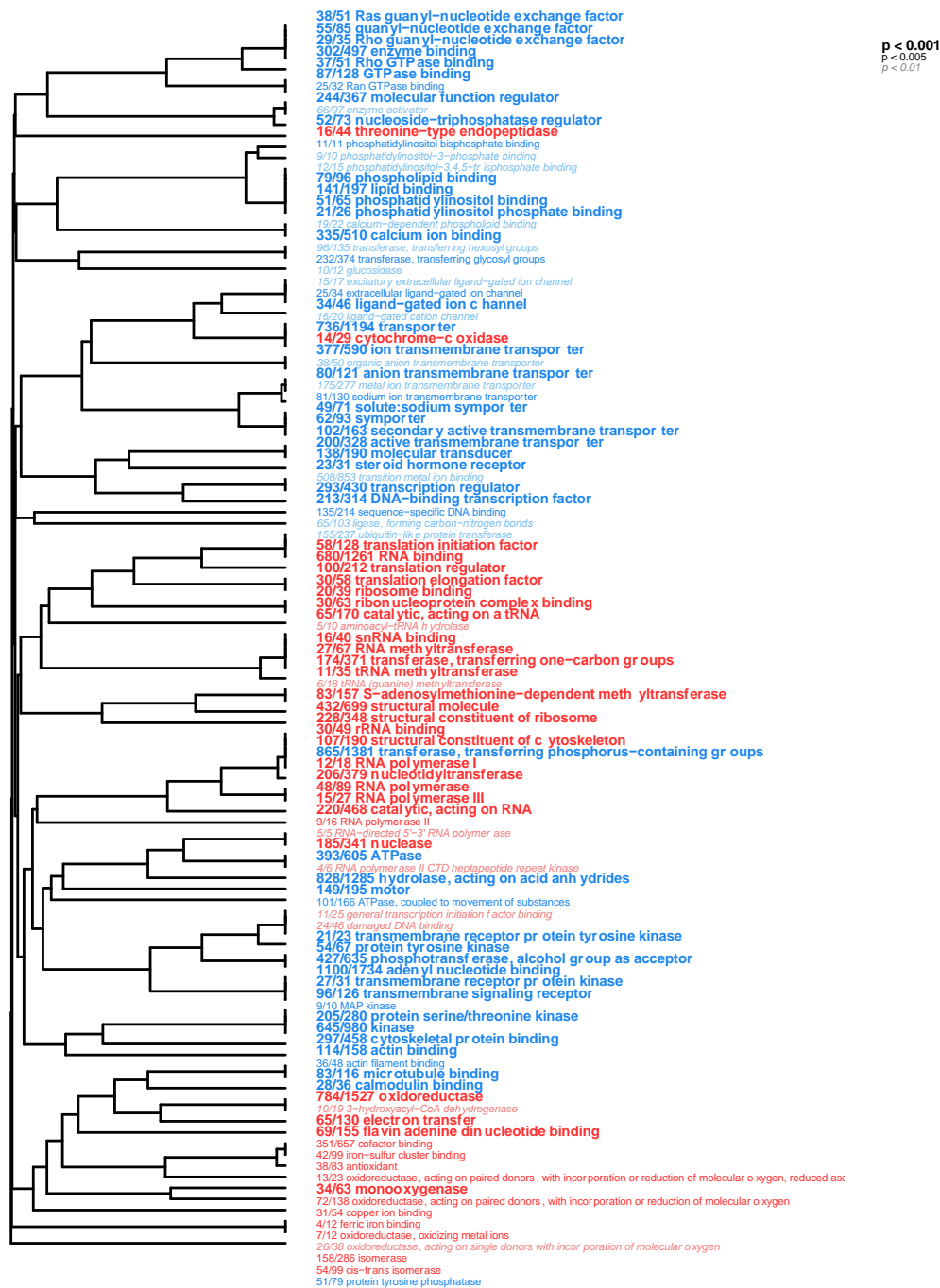


Figure S5: GO terms enriched among up- (red) and downregulated (blue) genes expressed under 918 μatm $p\text{CO}_2$ relative to 255 μatm after 7 days. GO terms are clustered according to shared genes. Text size depicts significance.

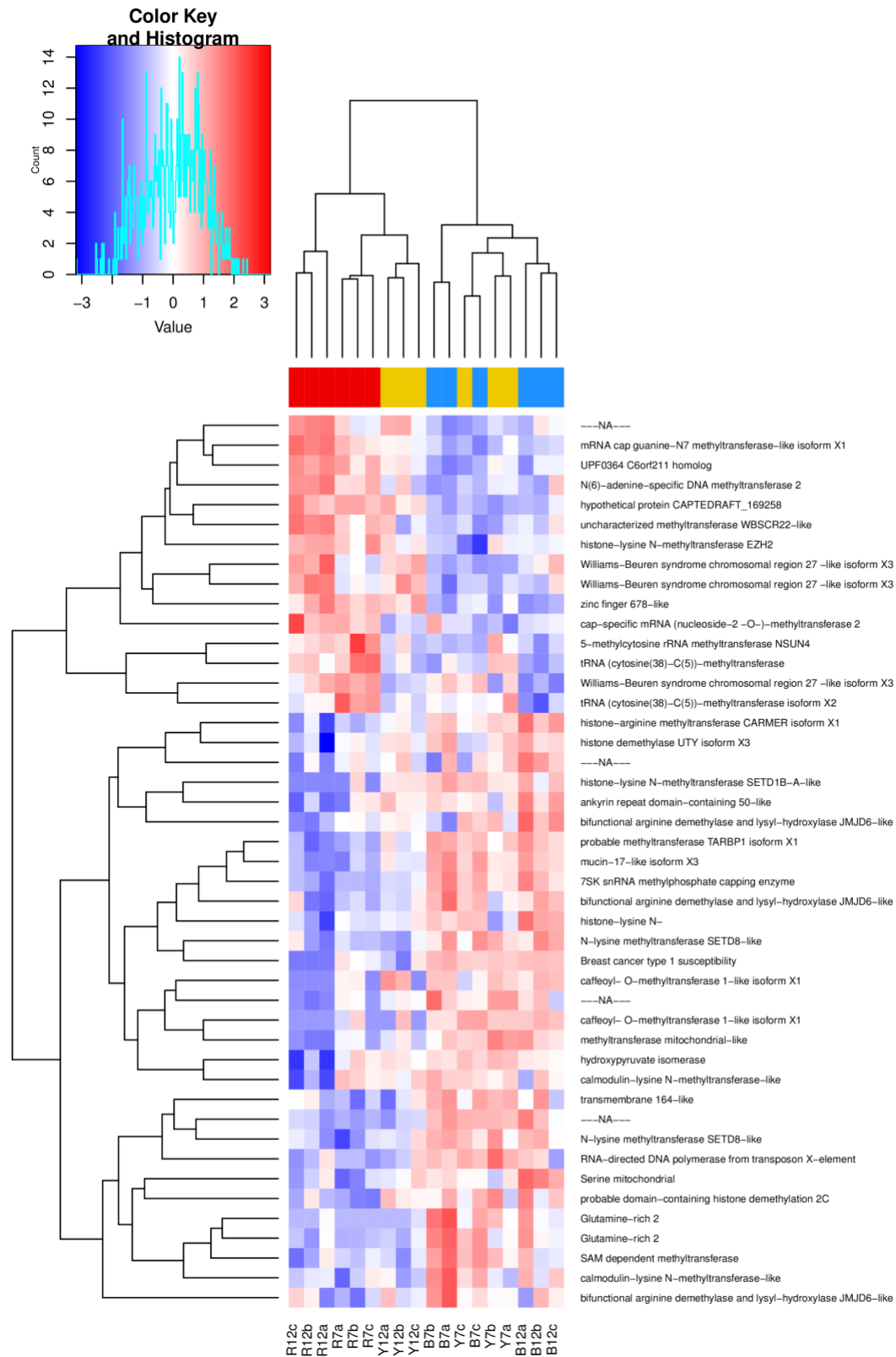


Figure S6: Two-way clustering and heat mapping of methyltransferase genes that were differentially expressed under 918 μatm $p\text{CO}_2$ relative to 255 μatm after either 0.5 days or 7 days. Heat maps depict Z-scores derived from log-transformed CPM read counts.

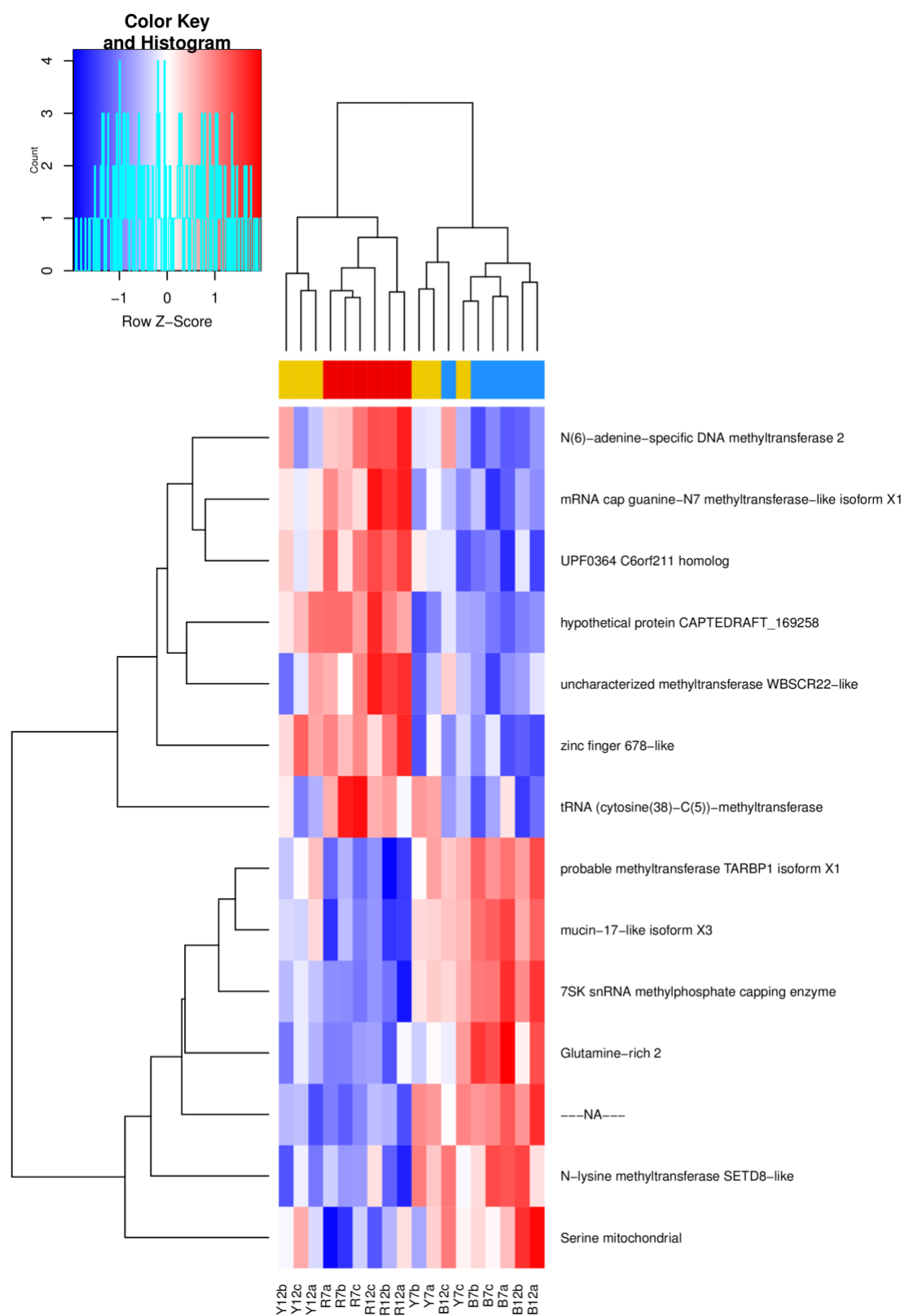


Figure S7: Two-way clustering and heat mapping of methyltransferase genes differentially expressed under 918 μatm $p\text{CO}_2$ relative to 255 μatm after both 0.5 and 7 days. Heat maps depict Z-scores derived from log-transformed CPM read counts.

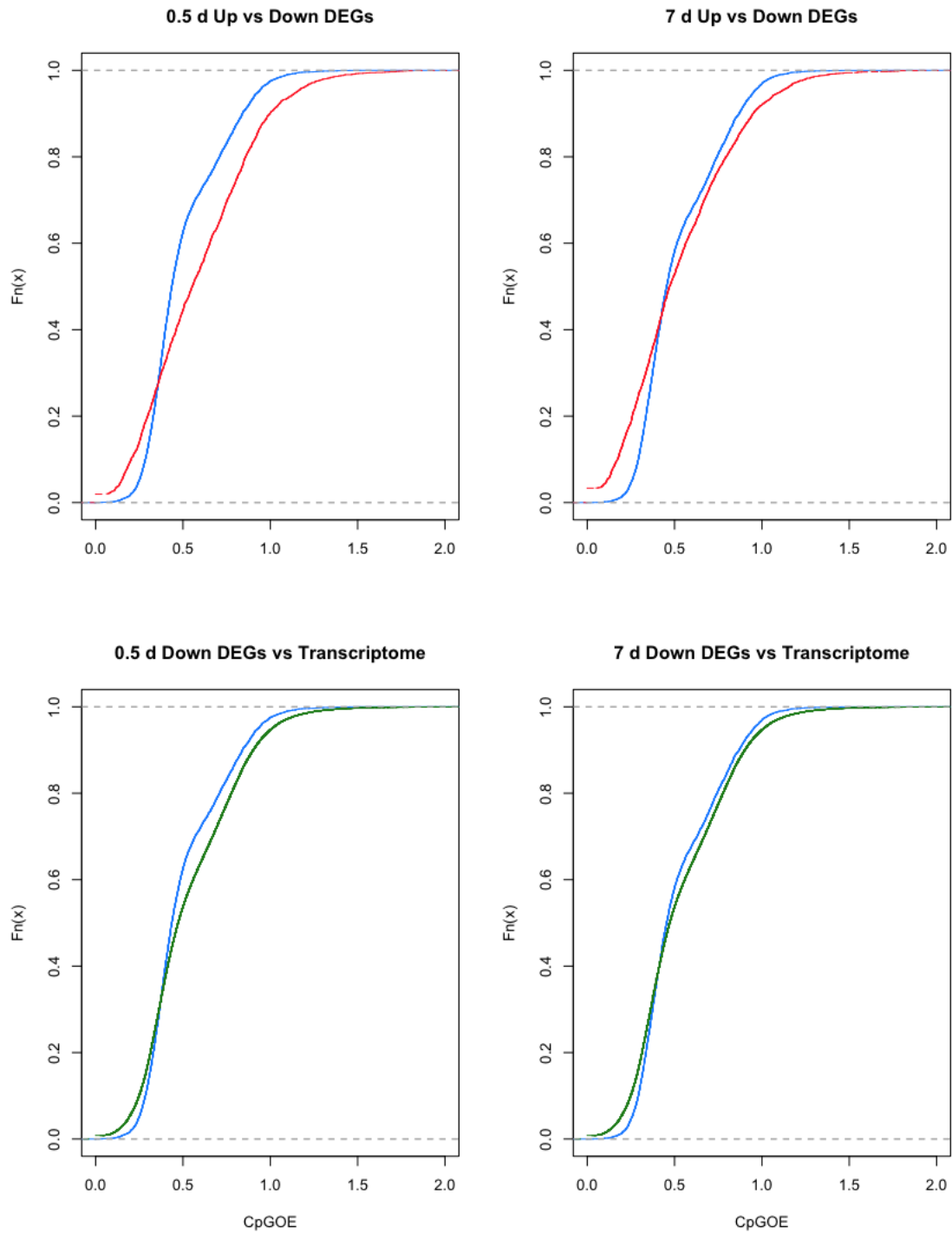


Figure S8: Cumulative distribution functions for transcript CpGOE values plotted for DEGs that were either up- (red) or downregulated (blue) under 918 $\mu\text{atm } p\text{CO}_2$ and across the whole *Limacina helicina antarctica* transcriptome (green).