

Lohbeck et al. - Gene expression changes in the coccolithophore *Emiliana huxleyi* after 500 generations of selection to ocean acidification

Supplementary Table S2: Multivariate analyses of variance on $-\Delta\text{CT}$ data from ambient, medium and high CO₂ adapted *Emiliana huxleyi* populations. Results from 2x2 factorial multivariate analyses of variance (MANOVA, repeated measures model) using all 10 candidate genes are given. We assessed **a)** ambient and medium CO₂ and **b)** ambient and high CO₂ responses in the physiological and the adaptive treatment comparisons.

a)

Effect	Numerator df	Denominator df	Adjusted <i>F</i>	<i>P</i>
Among subjects				
intercept	1	16	396.54	<0.0001
evolution environment	1	16	0.6229	0.4415
assay environment	1	16	4.881	0.0421
evolution * assay environment	1	16	0.1147	0.7393
Within subjects				
gene	9	8	4398.7	<0.0001
evolution environment * gene	9	8	2.8388	0.0783
assay environment * gene	9	8	3.090	0.0634
evolution environment * assay environment * gene	9	8	9.4948	0.0021

b)

Effect	Numerator df	Denominator df	Adjusted <i>F</i>	<i>P</i>
Among subjects				
intercept	1	16	1063	<0.0001
evolution environment	1	16	0.9603	0.3417
assay environment	1	16	50.25	<0.0001
evolution * assay environment	1	16	4.689	0.0458
Within subjects				
gene	9	8	7008.8	<0.0001
evolution environment * gene	9	8	2.265	0.1318
assay environment * gene	9	8	16.577	0.0003
evolution environment * assay environment * gene	9	8	2.098	0.1551