

Supplement 2

Note: Tables S1, S2 & S4 are contained within Supplement 1.

Table S3: Summary statistics for morphometric measurements. ANOVA and post-hoc results.

Table 3a: Welch's ANOVA results for morphometric data

Measurement	d.f. ¹	Welch's <i>F</i>	p-value
Prosome length	4, 35.57	6.96	0.00302
Prosome width	4, 35.82	2.15	0.095
Oil sac volume	4, 35.01	0.54	0.54
Fractional fullness	4, 34.605	5.43	0.0017

¹ Sample sizes (in parentheses) for each station: 47(36), 66(111), 82(79), 102(73), 113(79).

Table S3b: Statistically significant post-hoc comparisons between pairs of stations via Games-Howell test on morphometric data

Measurement	Contrast station pair ¹	t	d.f.	p-value
Length	66 - 47	4.46	56.09	<0.001
	102 - 66	4.34	79.89	<0.001
Fullness	66 - 47	4.46	51.09	<0.01
	82 - 47	3.78	19.75	0.009

¹ Station position from south to north: 47, 66, 82, 102; see also Figs. 1, 2 and 4.

Table S5: Summary statistics for gene expression in field-collected copepods. ANOVA and post-hoc results.

Table 5a: Welch's ANOVA results for gene expression

Gene	n	d.f. ¹	Welch's <i>F</i>	p-value
ELOV	10	3, 16.39	19.64	<0.001
FABP	10	3, 18.40	30.60	<0.001
GPATa	10	3, 19.29	1.46	0.26
GPATb	10	3, 19.12	3.26	0.044
PEPCK	6-7	3, 11.19	1.19	0.36
PDKa	6-7	3, 11.20	0.30	0.83
Lipase	6-7	3, 11.29	0.78	0.53

¹ Sample sizes (in parentheses) for each station: 47(36), 66(111), 82(79), 102(73), 113(79).

Table S5b: Statistically significant post-hoc comparisons between pairs of stations via Games-Howell test on gene expression

Gene	Contrast station pair	t	d.f.	p-value
ELOV	66 - 47	7.06	10.95	<0.001
	102 - 66	4.00	9.66	0.012
FABP	66 - 47	3.96	10.67	0.01
	102 - 66	9.55	16.84	<0.001
	102 - 82	3.70	10.89	0.016
GPATb	102 - 66	2.98	14.94	0.042

¹ Station position from south to north: 47, 66, 82, 102; see also Figs. 1, 2 and 4.

Table S6: Summary statistics for feeding experiments. Sample sizes, ANOVA and post-hoc results

Table S6a: Sample size per group

Genes	Field	Short Fed	Short Starved	Long Fed	Long Starved
ELOV, FABP, GPATa, & GPATb	20	6	8	11	13
PEPCK, PDKa & Lipase	12	4	5	8	5

Table S6b: Welch's ANOVA results

Gene	d.f.	Welch's <i>F</i>	p-value
ELOV	4, 22.85	19.77	<0.01
FABP	4, 22.95	13.35	<0.01
GPATa	4, 19.57	0.55	0.70
GPATb	4, 21.19	21.67	<0.01
PEPCK	4, 11.24	7.73	<0.01
PDKa	4, 11.82	1.58	0.24
Lipase	4, 11.90	0.80	0.55

Table S6c: Statistically significant post-hoc comparisons via Games-Howell test

Gene	Contrast	t	d.f.	p-value
ELOV	Field - Long Fed	4.77	19.4	<0.01
	Field - Long Starved	7.32	26.9	<0.01
	Short Fed - Long Fed	4.88	13.4	<0.01
	Short Fed - Long Starved	7.92	16.8	<0.01
	Short Starved - Long Starved	4.12	15.8	<0.01
FABP	Field - Short Fed	6.24	23.74	<0.01
	Field - Short Starved	3.60	10.56	0.03
	Field - Long Fed	5.48	23.71	<0.01
	Field - Long Starved	7.03	29.13	<0.01
	Short Fed - Long Fed	3.92	14.51	0.01
GPATb	Field - Short Starved	5.44	25.02	<0.01
	Field - Long Fed	6.94	18.00	<0.01
	Field - Long Starved	8.60	25.41	<0.01
	Short Fed - Long Starved	4.86	13.33	<0.01
	Short Starved - Long Fed	3.56	13.92	0.02
PEPCK	Short Starved - Long Starved	4.82	18.05	<0.01
	Field - Long Fed	3.64	17.84	0.01
	Field - Long Starved	4.72	13.61	<0.01
	Short Fed - Long Starved	4.56	8.72	0.03

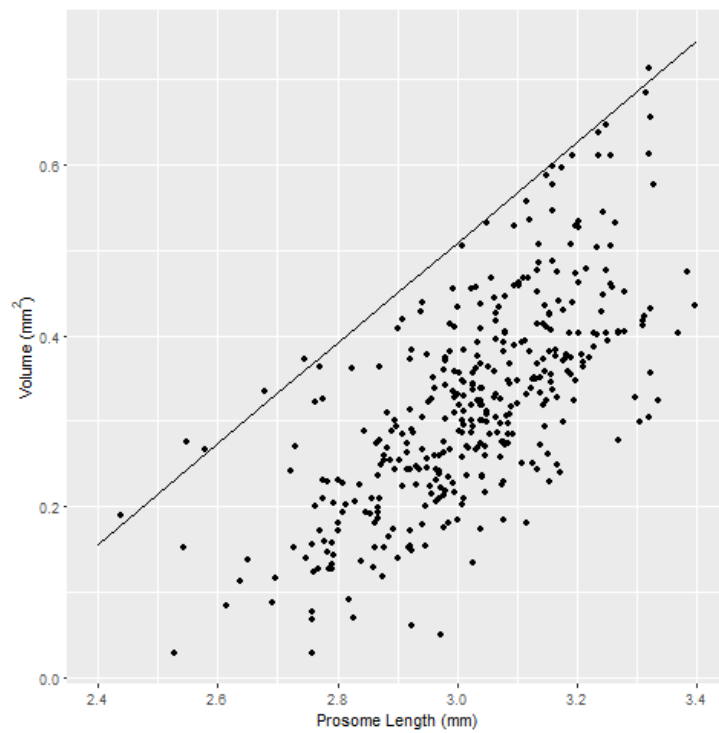
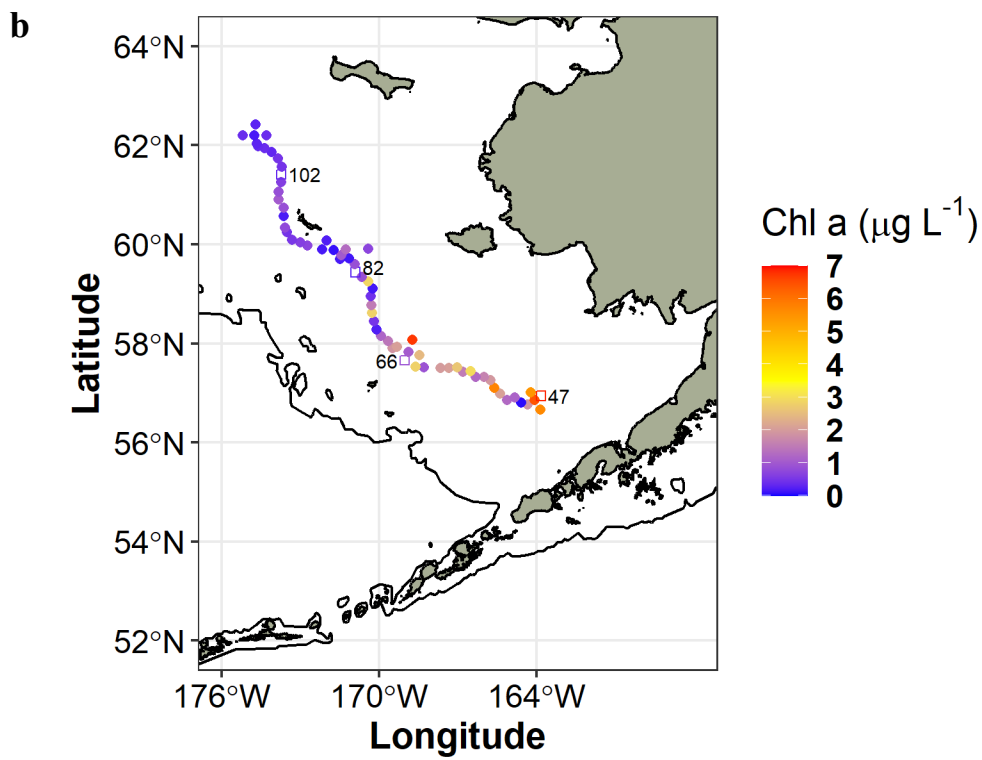
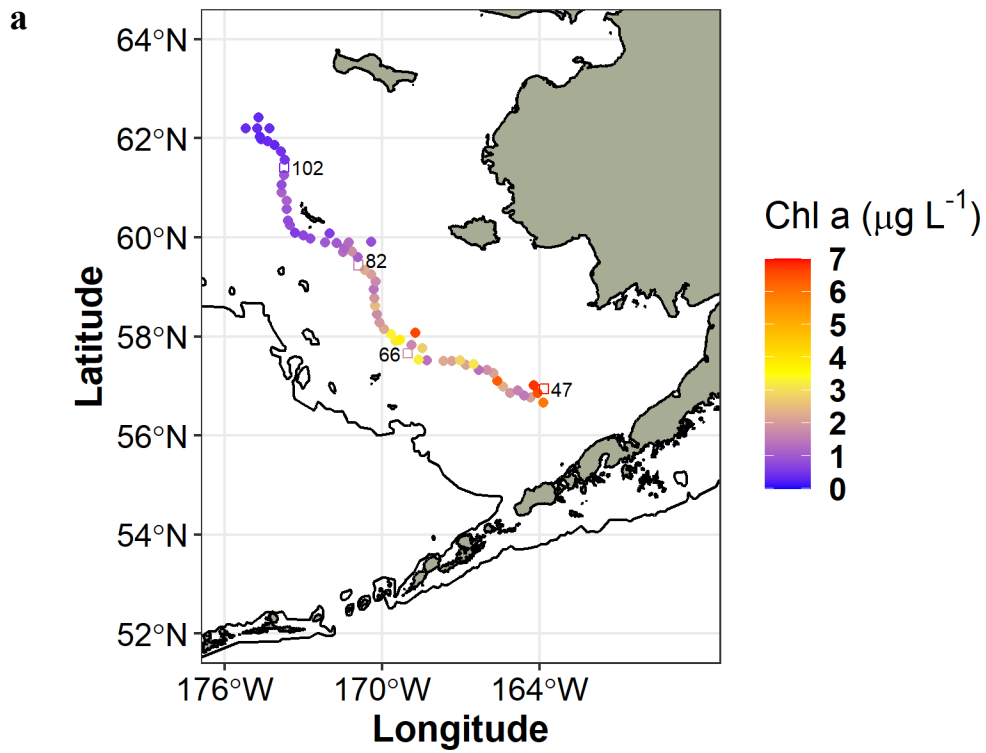


Figure S1: Prosome length and oil sac volume measurements for 378 field-collected copepods. The line was manually fitted to separate the top 1.5% of measurements and represents the size-dependent apparent maximum oil storage capacity (approach modeled after Miller et al. 2000): Max volume (mm³) = [Prosome length (mm) * 0.588] - 1.255



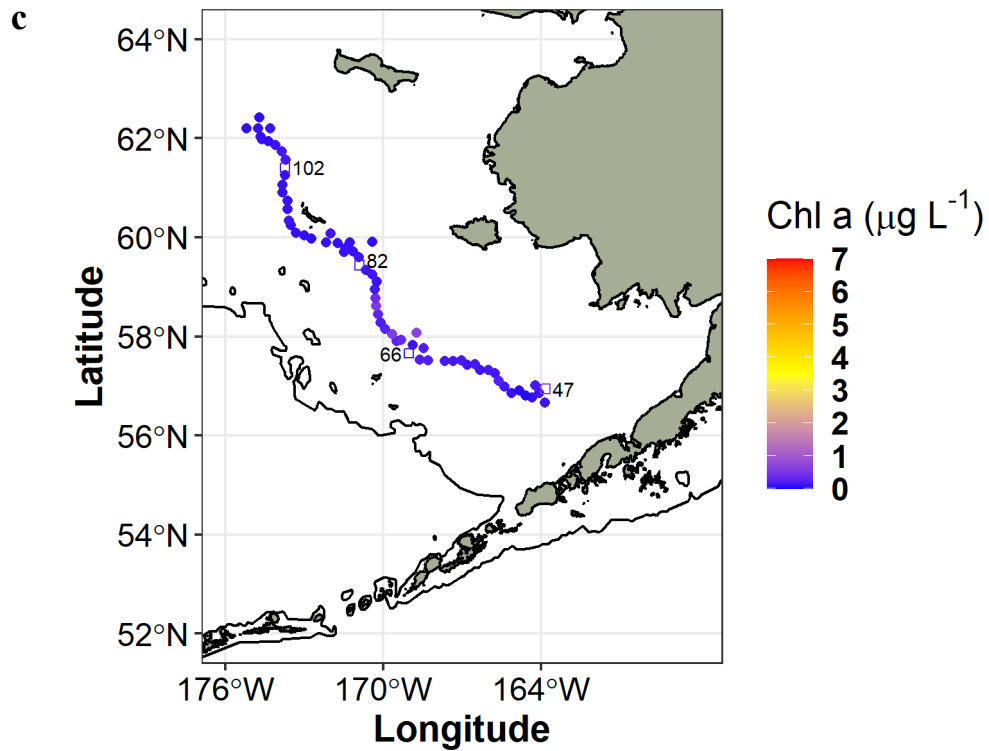


Figure S2: Chl a for each station in September - October 2015 at depths of 0 m (a), 30 m (b) and 50 m (c). The cruise track follows the 70m isobath of the eastern Bering Sea shelf, west of the Alaskan mainland. The solid black line is the 200 m isobath, indicating the shelf edge. Numbers and open square symbols indicate focal stations for molecular studies of *Calanus glacialis*.

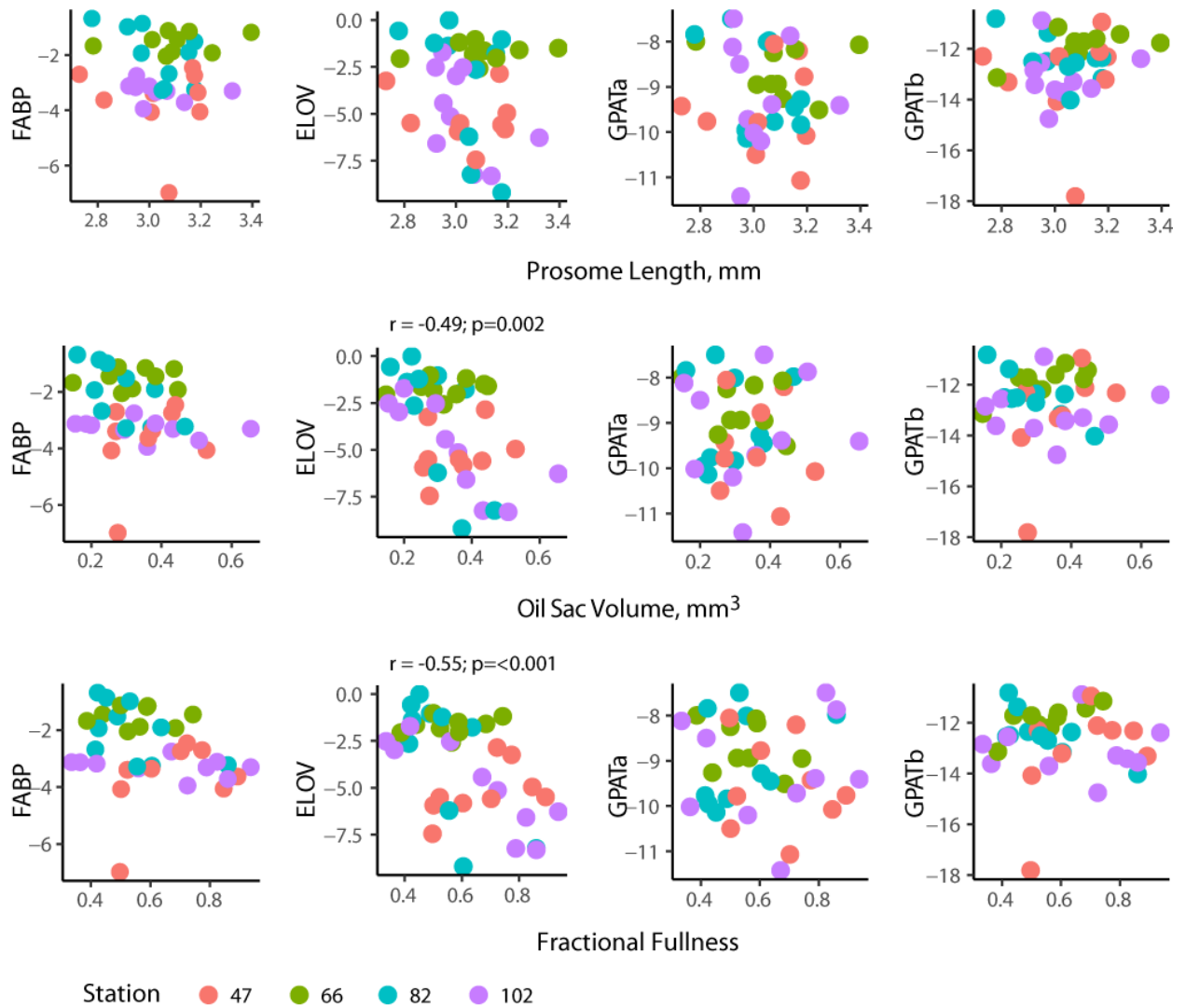


Figure S3: Expression of lipid storage genes versus morphometric parameters. Gene expression values (arbitrary fluorescence units) have been \log_2 -transformed and normalized to expression of a reference gene (EF1a, see also Materials and Methods). ELOV was negatively correlated with oil sac volume and fractional fullness; other relationships were not statistically significant.

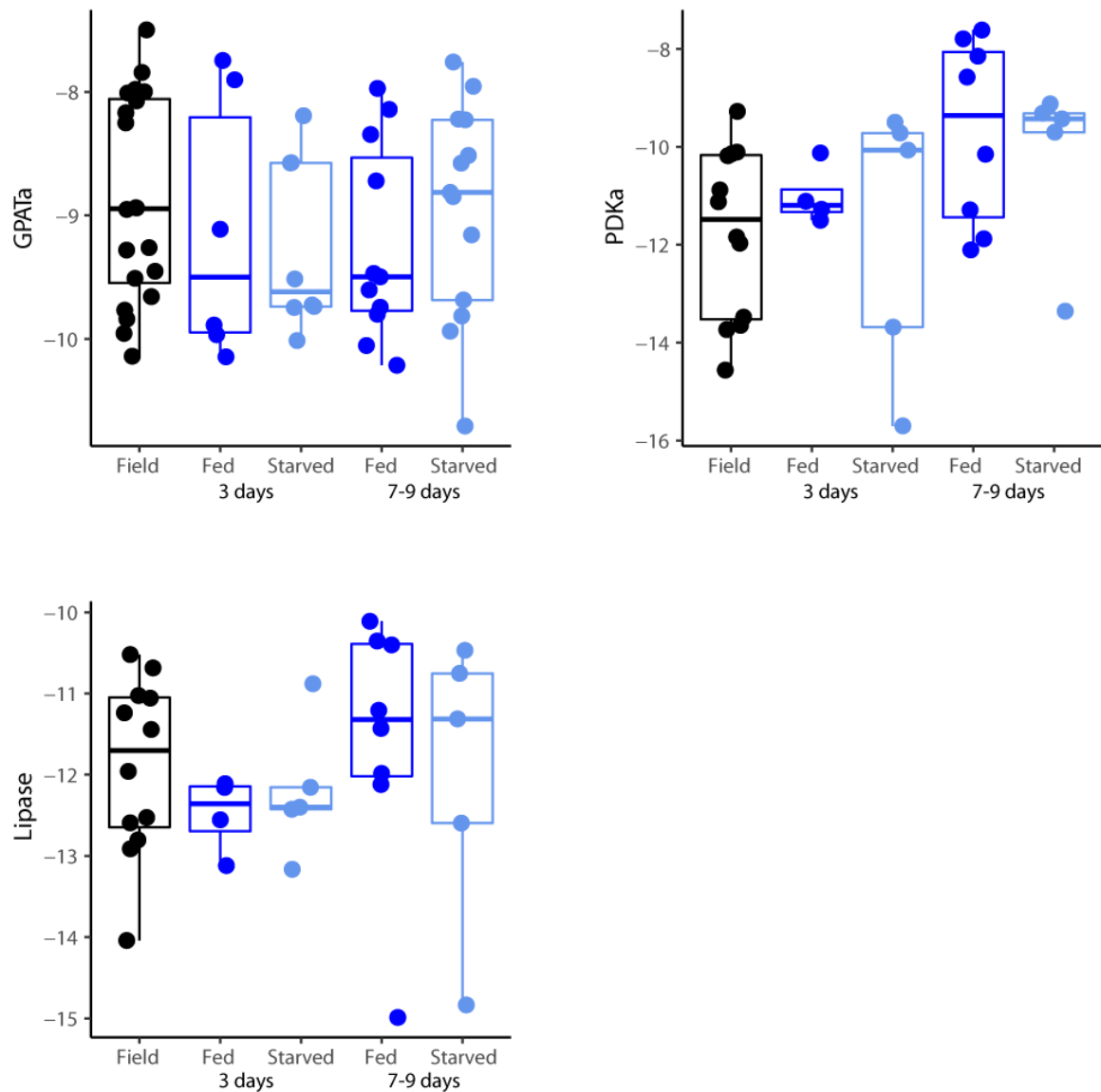


Figure S4: Expression of additional metabolic genes (see also Figure 10) from *C. glacialis* collected from the field, or incubated for varying periods (3 days, 7-9 days) with natural microplankton (fed) or in filtered seawater (starved). Gene expression was log₂-transformed and normalized prior to plotting and analysis (see methods). Boxplots show the first and third quartiles, with a line showing the median; individual measurements are displayed as horizontally jittered points. No groups were significantly different from one another for any of these genes.