

Table S1. Results for tests of normality and homoscedasticity for univariate comparisons of FA biomarkers quantified in pyrosomes that were collected in May 2017 on (N = 17) and off (N = 52) the continental shelf (Distance), across latitude (Latitude, North: N of 44°N, Middle: 43°N – 44°N, South: S of 43°N, N = 35, 11, 23 respectively), and size classes (small = 5 - 10 cm, medium = 11-17cm, and large \geq 18 cm, N = 10, 37, 22 respectively). Biomarkers compared include the ratio of 18:1 9/18:1 7 (potential indicator of relative carnivory), bacterial markers (branched and odd chain FA) as well as 16:1 7 (e.g., diatoms), 18:2 6 (e.g., chlorophytes), 18:4 3 (e.g., prymnesiophytes), and 22:6 3 (e.g., dinoflagellates). *indicates significant differences.

		Normality (Shapiro-Wilk test)		Homoscedasticity (Bartlett test)		
		statistic (W)	p	statistic (K ²)	df	p
Distance	18:1 9/18:1 7	0.96	0.03*	0.06	1	0.80
	Bacteria	0.71	< 0.001*	0.94	1	0.33
	16:1 7	0.99	0.68	0.12	1	0.73
	18:2 6	0.98	0.48	0.15	1	0.70
	18:4 3	0.99	0.61	0.09	1	0.76
	22:6 3	0.98	0.41	0.28	1	0.59
Latitude	18:1 9/18:1 7	0.96	0.03*	5.26	2	0.07
	Bacteria	0.71	< 0.001*	50.25	2	< 0.001*
	16:1 7	0.99	0.68	1.35	2	0.51
	18:2 6	0.98	0.48	1.01	2	0.60
	18:4 3	0.99	0.61	2.22	2	0.33
	22:6 3	0.98	0.41	7.98	2	0.02*
Size	18:1 9/18:1 7	0.96	0.03*	1.73	2	0.42
	Bacteria	0.71	< 0.001*	9.57	2	0.01*
	16:1 7	0.99	0.68	3.35	2	0.19
	18:2 6	0.98	0.48	0.11	2	0.95
	18:4 3	0.99	0.61	0.90	2	0.64
	22:6 3	0.98	0.41	4.84	2	0.09

Table S2. Proportion of fatty acids (FA) (mean \pm SD) identified in pyrosomes collected on May and August 2017 cruises. FA that contributed to $\geq 0.5\%$ are reported. Summary biomarkers include all relevant FA, including those contributing $< 0.5\%$. ¹branched FA, ²saturated FA, ³monounsaturated FA, ⁴polyunsaturated FA, and ⁵long chain PUFA.

FA	Cruise comparisons			
	May mean	May SD	Aug mean	Aug SD
14:0	13.6	1.6	12.5	1.4
i-15:0	0.5	0.1	0.8	0.2
a-15:0	0.3	0.1	0.5	0.1
15:0	3.0	0.7	3.9	0.2
i-16:0	0.6	0.2	0.8	0.1
16:0	31.9	2.0	27.8	1.3
16:1 ⁷	1.4	0.2	1.6	0.2
i-17:0	2.0	0.4	2.5	0.4
17:0	1.4	0.1	1.5	0.1
18:0	2.3	0.3	1.0	1.5
18:1 ⁹	2.2	0.4	2.0	0.4
18:1 ⁷	0.7	0.1	0.7	0.1
18:2 ⁶	2.1	0.2	2.1	0.3
18:3 ³	1.2	0.3	1.4	0.2
19:1	1.7	3.0	0.6	0.2
18:4 ³	3.5	1.2	3.9	0.7
20:0	0.6	0.1	0.5	0.1
20:1 ⁹	0.9	0.2	0.8	0.3
20:2 ⁶	0.1	0.0	0.1	0.0
20:4 ⁶	1.1	0.2	1.4	0.2
20:5 ³	6.2	0.8	6.1	0.6
22:5 ³	0.4	0.0	0.6	0.1
22:6 ³	17.3	1.5	17.0	1.7
-3	29.1	2.0	29.4	2.0
-6	3.5	0.2	3.9	0.5
-3: -6	8.4	0.8	7.6	0.9
BrFA ¹	4.3	0.6	6.0	0.8
SAFA ²	48.6	2.6	42.1	2.8
MUFA ³	7.6	0.7	7.8	0.5
PUFA ⁴	30.3	2.0	31.0	2.1
LCPUFA ⁵	25.4	1.7	25.5	2.3
18:1 ⁹ / 18:1 ⁷	3.2	0.6	2.8	0.6
Bacteria	10.9	2.9	12.6	1.0

Table S3. Proportion of FA (mean \pm SD) identified in pyrosomes collected on the May cruise and grouped associated with collection location. FA that contributed to $\geq 0.5\%$ are reported. Summary biomarkers include all relevant FA, including those contributing $< 0.5\%$. ¹branched FA, ²saturated FA, ³monounsaturated FA, ⁴polyunsaturated FA, and ⁵long chain PUFA.

FA	Shelf comparisons				Latitude comparisons					
	On mean	On SD	Of mean	Off SD	North mean	North SD	Middle mean	Middle SD	South mean	South SD
14:0	13.3	1.6	13.7	1.6	13.4	1.8	13.3	0.8	14.1	1.4
i-15:0	0.5	0.1	0.4	0.1	0.4	0.1	0.5	0.1	0.5	0.1
a-15:0	0.3	0.1	0.3	0.1	0.3	0.1	0.3	0.1	0.3	0.0
15:0	3.2	0.4	3.0	0.7	2.8	0.8	3.3	0.3	3.3	0.4
i-16:0	0.6	0.2	0.6	0.2	0.6	0.2	0.6	0.2	0.6	0.2
16:0	32.8	2.4	31.6	1.8	31.5	2.6	33.1	1.3	31.9	0.9
16:1 7	1.5	0.2	1.4	0.2	1.4	0.2	1.5	0.1	1.5	0.2
i-17:0	2.1	0.3	2.0	0.4	2.0	0.3	2.2	0.2	2.1	0.5
17:0	1.4	0.1	1.4	0.2	1.4	0.2	1.4	0.1	1.3	0.1
18:0	2.4	0.3	2.3	0.3	2.3	0.3	2.3	0.2	2.4	0.2
18:1 9	2.3	0.3	2.2	0.4	2.3	0.4	2.3	0.4	2.1	0.3
18:1 7	0.8	0.1	0.7	0.1	0.7	0.1	0.8	0.1	0.7	0.1
18:2 6	2.1	0.2	2.1	0.2	2.0	0.2	2.1	0.2	2.2	0.1
18:3 3	1.2	0.3	1.2	0.3	1.0	0.3	1.2	0.2	1.4	0.2
19:1	1.2	2.6	1.9	3.2	2.8	4.0	0.6	0.2	0.5	0.1
18:4 3	3.2	1.2	3.6	1.1	3.2	1.2	3.0	0.9	4.1	0.9
20:0	0.6	0.1	0.6	0.1	0.5	0.1	0.6	0.1	0.6	0.0
20:1 9	1.0	0.2	0.9	0.2	0.9	0.2	1.0	0.1	0.9	0.2
20:2 6	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0	0.1	0.0
20:4 6	1.1	0.2	1.1	0.2	1.1	0.2	1.1	0.2	1.0	0.1
20:5 3	6.2	1.1	6.3	0.7	5.9	0.8	6.4	1.0	6.7	0.6
22:5 3	0.4	0.0	0.4	0.1	0.4	0.1	0.4	0.0	0.4	0.0
22:6 3	17.1	1.3	17.3	1.6	17.8	1.6	17.2	0.7	16.4	1.2
-3	28.4	2.6	29.3	1.7	29.0	2.3	28.5	2.2	29.5	1.3
-6	3.5	0.3	3.5	0.2	3.5	0.3	3.5	0.3	3.5	0.2
-3: -6	8.2	1.0	8.4	0.8	8.4	0.9	8.2	1.1	8.4	0.6
BrFA ¹	4.2	0.6	4.3	0.6	4.1	0.4	4.4	0.5	4.5	0.7
SAFA ²	49.4	2.9	48.4	2.5	48.0	3.3	49.5	1.8	49.2	1.1
MUFA ³	7.8	0.7	7.5	0.7	7.6	0.7	8.0	0.7	7.3	0.7
PUFA ⁴	29.6	2.6	30.5	1.7	30.3	2.3	29.7	2.1	30.6	1.3
LCPUFA ⁵	25.1	2.0	25.5	1.6	25.8	2.0	25.4	1.2	24.8	1.1
18:1 9/ 18:1 7	3.1	0.6	3.3	0.6	3.4	0.6	3.0	0.5	3.0	0.4
Bacteria	10.5	2.5	11.1	3.0	11.8	3.8	10.1	0.6	10.1	1.1