

Table S1. SIMPER (similarity percentages) results using data from pre-bloom conditions (May 2018) where “Contrast” indicates the two clusters (clusters determined by hierarchical cluster analysis) that are being compared, “Average diss” is the average contribution to overall dissimilarity, “sd” is the standard deviation of contribution, “ratio” is the ratio of average diss to sd, “average” is the average % fatty acid in a given cluster, and “cumsum” is the ordered cumulative contribution. Cumulative contributions >0.70 were not included as per Clarke et al. (1993). The species and fatty acid codes are explained in the footnote.

PRE-BLOOM	summary(may18.sim)					
Contrast:	3_2			Cluster 3	Cluster 2	
				Cm, Eb, Nc, Np	Cm, Eb, Ec, Eh, Nc, Np, Ps, Pse	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
14:0	0.03	0.01	2.09	14.46	2.63	0.12
22:6n-3	0.02	0.01	1.84	10.34	20.43	0.24
SFA	0.02	0.01	1.83	32.34	22.84	0.34
18_22PUFA	0.02	0.01	1.38	16.36	22.76	0.43
18:1n-9	0.02	0.01	1.90	2.51	10.81	0.52
PUFA	0.02	0.01	1.45	36.68	42.69	0.60
MUFA	0.02	0.01	1.53	27.00	31.21	0.67
16:1n-7	0.01	0.01	1.63	6.75	8.27	0.72
Contrast:	3_1			Cluster 3	Cluster 1	
				Cm, Eb, Nc, Np	Eg, Er, Eh, Mp, Pe	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
MUFA	0.06	0.02	2.49	27.00	52.30	0.19
18:1n-9	0.05	0.01	3.74	2.51	21.50	0.33
SFA	0.03	0.02	1.65	32.34	19.01	0.43
PUFA	0.03	0.02	1.51	36.68	25.54	0.51
14:0	0.03	0.01	1.85	14.46	3.47	0.60
20:5n-3	0.02	0.01	2.26	17.14	9.28	0.65
16_20PUFA	0.02	0.01	2.27	17.49	9.67	0.71
Contrast:	2_1			Cluster 2	Cluster 1	
				Cm, Eb, Ec, Eh, Nc, Np, Ps, Pse	Eg, Er, Eh, Mp, Pe	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
MUFA	0.05	0.02	2.33	31.21	52.30	0.17
PUFA	0.04	0.02	2.59	42.69	25.54	0.31
22:6n-3	0.03	0.01	2.19	20.43	9.43	0.40
18_22PUFA	0.03	0.01	2.27	22.76	11.54	0.49
18:1n-9	0.03	0.01	1.71	10.81	21.50	0.57
16_20PUFA	0.02	0.01	2.41	18.40	9.67	0.64
16:0	0.02	0.01	3.13	15.36	11.88	0.71

Copepods: Cm = *Calanus marshallae*, Cp = *Calanus pacificus*, Eg = *Euaugaptilus graciloides*, Eb = *Eucalanus bungii*, Ec = *Eucalanus californicus*, Er = *Euchirella rostrata*, Mp = *Metridia pacifica*, Nc = *Neocalanus cristatus*, Nf = *Neocalanus flemingeri*, Np = *Neocalanus plumchrus*, Pe = *Paraeuchaeta elongata*, Pp = *Pseudhaloptilus pacificus*, Sc = Scaphocalanidae (no species ID); **Chaetognaths:** Eh = *Eukrohnia hamata*, Pse = *Parasagitta elegans*, Peu = *Parasagitta euneritica*, Ps = *Pseudosagitta scrippsae*; **Euphausiids:** Ep = *Euphausia pacifica*, Ti = *Thysanoessa inermis*, Tis = *Thysanoessa inspinasa*, Tl = *Thysanoessa longipes*, Ts = *Thysanoessa spinifera*; **Amphipods:** Hm = *Hyperoche medusarum*, Pa = *Primno abyssalis*, Tp = *Themisto pacifica*. **Fatty acid abbreviations:** SFA = saturated fatty acids, MUFA = monounsaturated fatty acids, PUFA = polyunsaturated fatty acids, OBFA = odd and/or branched fatty acids

Table S2. SIMPER (similarity percentages) results using data from mid-bloom conditions (May-June 2019) where “Contrast” indicates the two clusters (clusters determined by hierarchical cluster analysis) that are being compared, “Average diss” is the average contribution to overall dissimilarity, “sd” is the standard deviation of contribution, “ratio” is the ratio of average diss to sd, “average” is the average % fatty acid in a given cluster, and “cumsum” is the ordered cumulative contribution. Cumulative contributions >0.70 were not included as per Clarke et al. (1993). See Table S1 for a description of the species and fatty acid codes.

MID-BLOOM	summary(mayjune19.sim)					
Contrast:	3_2			Cluster 3	Cluster 2	
				Cm, Nc, Np	Cm, Eh, Peu, Ps, Pse	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
16_20PUFA	0.03	0.01	2.49	31.91	17.38	0.13
20:5n-3	0.03	0.01	2.31	26.80	15.21	0.24
22:6n-3	0.02	0.01	2.75	8.14	18.87	0.34
PUFA	0.02	0.01	1.52	47.88	40.12	0.42
SFA	0.02	0.01	1.23	25.89	29.52	0.49
18_22PUFA	0.02	0.01	1.82	14.74	22.38	0.56
14:0	0.02	0.01	2.10	10.54	3.24	0.63
16:0	0.02	0.01	1.68	10.30	17.19	0.70
MUFA	0.02	0.01	1.62	23.18	24.92	0.76
Contrast:	3_1			Cluster 3	Cluster 1	
				Cm, Nc, Np	Eh, Pe	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
18:1n-9	0.06	0.01	3.80	1.81	26.26	0.18
MUFA	0.05	0.01	3.07	23.18	43.19	0.32
16_20PUFA	0.03	0.02	2.01	31.91	18.32	0.43
PUFA	0.03	0.01	2.18	47.88	36.12	0.52
20:5n-3	0.03	0.01	2.10	26.80	15.62	0.62
14:0	0.02	0.01	2.94	10.54	1.13	0.68
SFA	0.02	0.01	1.42	25.89	17.17	0.75
Contrast:	2_1			Cluster 2	Cluster 1	
				Cm, Eh, Peu, Ps, Pse	Eh, Pe	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
MUFA	0.04	0.02	2.31	24.92	43.19	0.16
18:1n-9	0.04	0.02	2.20	8.30	26.26	0.32
SFA	0.03	0.02	1.57	29.52	17.17	0.43
16:0	0.03	0.01	2.45	17.19	5.50	0.53
22:6n-3	0.02	0.01	1.66	18.87	12.11	0.59
PUFA	0.01	0.01	1.64	40.12	36.12	0.64
OBFA	0.01	0.01	2.00	3.02	8.85	0.70
18_22PUFA	0.01	0.01	1.30	22.38	17.25	0.74

Table S3. SIMPER (similarity percentages) results using data from post-bloom conditions (September 2018) where “Contrast” indicates the two clusters (clusters determined by hierarchical cluster analysis) that are being compared, “Average diss” is the average contribution to overall dissimilarity, “sd” is the standard deviation of contribution, “ratio” is the ratio of average diss to sd, “average” is the average % fatty acid in a given cluster, and “cumsum” is the ordered cumulative contribution. Cumulative contributions >0.70 were not included as per Clarke et al. (1993). See Table S1 for a description of the species and fatty acid codes.

POST-BLOOM	summary(sept18.sim)					
Contrast:	1_2			Cluster 1	Cluster 2	
				Pe, Pp, Sc	Eh, Er, Ps, Pse	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
MUFA	0.09	0.03	3.00	69.31	33.51	0.20
18:1n-9	0.05	0.02	3.19	35.37	13.10	0.33
PUFA	0.05	0.02	1.98	19.17	37.98	0.44
SFA	0.05	0.01	4.55	6.93	25.74	0.54
18_22PUFA	0.03254	0.02	1.84	10.49	23.41	0.62
16:0	0.03	0.01	3.09	4.24	16.72	0.69
22:6n-3	0.03	0.01	1.92	8.65	19.94	0.76
Contrast:	1_3			Cluster 1	Cluster 3	
				Pe, Pp, Sc	Ec, Eb	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
MUFA	0.10	0.03	3.51	69.31	28.25	0.21
18:1n-9	0.07	0.01	6.38	35.37	6.05	0.35
SFA	0.07	0.01	7.61	6.93	34.91	0.49
16:0	0.05	0.01	5.43	4.24	24.42	0.59
16_20PUFA	0.04	0.01	4.06	5.74	22.31	0.67
20:5n-3	0.04	0.01	3.66	5.53	20.94	0.75
Contrast:	1_4			Cluster 1	Cluster 4	
				Pe, Pp, Sc	Cm, Cp, Nc, Nf, Np	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
MUFA	0.10	0.03	2.97	69.31	31.13	0.20
18:1n-9	0.08	0.01	7.00	35.37	2.13	0.38
SFA	0.06	0.02	2.67	6.93	31.54	0.50
PUFA	0.04	0.02	1.74	19.17	33.91	0.59
14:0	0.04	0.02	1.93	1.05	15.78	0.67
16:1n-7	0.03	0.02	1.59	14.49	4.43	0.72
Contrast:	2_3			Cluster 2	Cluster 3	
				Eh, Er, Ps, Pse	Ec, Eb	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
18_22PUFA	0.03	0.01	2.27	23.41	9.69	0.12

22:6n-3	0.03	0.01	2.56	19.94	7.44	0.23
SFA	0.02	0.01	2.44	25.74	34.91	0.32
16_20PUFA	0.02	0.01	1.82	13.32	22.31	0.40
20:5n-3	0.02	0.01	1.70	12.77	20.94	0.47
16:1n-7	0.02	0.01	1.53	6.56	14.31	0.54
16:0	0.02	0.01	1.99	16.72	24.42	0.61
18:1n-9	0.02	0.01	1.45	13.10	6.05	0.68
PUFA	0.02	0.01	1.56	37.98	33.50	0.74
Contrast:	2_4			Cluster 2	Cluster 4	
				Eh, Er, Ps, Pse	Cm, Cp, Nc, Nf, Np	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
14:0	0.03	0.02	1.69	3.26	15.78	0.12
18:1n-9	0.03	0.01	1.82	13.10	2.13	0.23
22:6n-3	0.02	0.01	2.08	19.94	9.42	0.33
SFA	0.02	0.02	1.12	25.74	31.54	0.41
PUFA	0.02	0.01	1.45	37.98	33.91	0.48
18_22PUFA	0.02	0.01	1.39	23.41	17.80	0.55
MUFA	0.02	0.01	1.33	33.51	31.13	0.62
18:4n-3	0.01	0.01	1.80	3.05	7.42	0.67
16:0	0.01	0.01	1.72	16.72	11.99	0.72
Contrast:	3_4			Cluster 3	Cluster 4	
				Ec, Eb	Cm, Cp, Nc, Nf, Np	
Fatty acid	Average diss.	sd	ratio	average	average	cumsum
16:0	0.03	0.01	3.46	24.42	11.99	0.12
16:1n-7	0.02	0.01	1.89	14.31	4.43	0.21
16_20PUFA	0.02	0.01	2.15	22.31	12.97	0.30
14:0	0.02	0.02	1.21	6.51	15.78	0.39
SFA	0.02	0.01	2.06	34.91	31.54	0.47
20:5n-3	0.02	0.01	2.02	20.94	12.43	0.56
18_22PUFA	0.02	0.01	1.73	9.69	17.80	0.64
MUFA	0.02	0.01	1.70	28.25	31.13	0.70