

*The following supplement accompanies the article*

## **Contrasting macrobenthic activities differentially affect nematode density and diversity in a shallow subtidal marine sediment**

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Table S1. Results from PERMANOVA analysis for differences in nematode density among procedural controls (field, reconstruction and experimental controls) and depth based on a Euclidean resemblance matrix. P-values obtained by permutation

	Treatment			Slice			Treatment _ Slice		
	MS	Pseudo-F	p	MS	Pseudo-F	p	MS	Pseudo-F	p
Nematode density	485.18	2.71	0.14	4521.00	25.46	<0.001	1468.50	8.27	<0.001

Table S2. Results from PERMANOVA analysis for differences in multivariate community structure among procedural controls treatments and depth, based on a Bray-Curtis resemblance matrix (df = 2, 7 and 14 respectively), with p-values obtained by permutation. Where the Treatment \_ Slice interaction is significant, pairwise tests of factor Treatment within Treatment \_ Slice were performed, from which the significantly different slices among treatments are indicated with p-values drawn from Monte-Carlo samplings (p (MC)). C: control; FC: field control

	Treatment			Slice			Treatment _ Slice		
	MS	Pseudo-F	p	MS	Pseudo-F	p	MS	Pseudo-F	p
Raw data	13420	3.85	0.003	5936.4	2.95	<0.001	3235.6	1.61	<0.001
Standardised, square root-transformed data	11619	3.77	0.004	4564.3	2.60	<0.001	2275.8	1.30	0.031

Slice (cm)	Pairwise tests on raw data			Pairwise tests on standardised, square root-transformed data			
	Groups	t	p (MC)	Slice (cm)	Groups	t	p (MC)
0-1	C, FC	2.16	0.028	6-7	C, FC	1.86	0.043
2-3	C, FC	1.91	0.039				

Table S3. Results from PERMANOVA analysis pairwise tests of factor Treatment within Treatment \_ Slice for differences in the univariate measures sediment median grain size, %silt, water content, chl *a* and its degradation products phaeophytin *a* and phaeophytin *a*-like pigment among experimental treatments and depth, based on a normalised Euclidean resemblance matrix. The significantly different slices among treatments are indicated with p-values drawn from Monte-Carlo samplings (p (MC))

Water content pairwise tests				Chl <i>a</i> pairwise tests			
Slice (cm)	Groups	<i>t</i>	p (MC)	Slice (cm)	Groups	<i>t</i>	p (MC)
0-0.5	<i>Abra, Lanice</i>	2.93	0.042	0-0.5	<i>Abra, control</i>	6.89	0.003
2-3	<i>Abra, control</i>	3.46	0.028		<i>Abra, Lanice</i>	4.26	0.014
	<i>control, Lanice</i>	3.19	0.033		<i>Abra, Nephtys</i>	8.23	0.001
4-5	<i>Abra, Lanice</i>	3.19	0.034	0.5-1	<i>Abra, control</i>	5.21	0.008
5-6	<i>Abra, Lanice</i>	5.21	0.007		<i>Abra, Lanice</i>	4.76	0.010
6-7	<i>Abra, control</i>	4.18	0.013		<i>Abra, Nephtys</i>	7.58	0.002
Phaeophytin <i>a</i> pairwise tests				1-1.5	<i>Abra, control</i>	3.04	0.041
Slice (cm)	Groups	<i>t</i>	p(MC)		<i>Abra, Nephtys</i>	4.82	0.008
0-0.5	<i>Abra, control</i>	2.84	0.048	4-5	<i>Abra, Lanice</i>	3.95	0.016
	<i>Abra, Nephtys</i>	2.92	0.042				
3-4	<i>control, Lanice</i>	4.96	0.008				
4-5	<i>Abra, Lanice</i>	5.65	0.005				
	<i>Lanice, Nephtys</i>	1.22	0.050				
6-7	<i>Abra, control</i>	3.37	0.028				

Table S4. Result of 1-way ANOVA on total nematode density, species richness (S), evenness (J') and Hill's diversity indices  $N_1$  and  $N_\infty$  in experimental treatments (experimental control, *Abra alba*, *Lanice conchilega*, *Nephtys hombergii*) (df = 3, 8 respectively). ns: not significant

	MS	<i>F</i>	p
Density	11334	4.096	0.049
S	7.19	0.33	ns
J'	0.00	3.68	ns
$N_1$	7.32	4.70	0.036
$N_\infty$	1.28	5.77	0.021

Table S5. Results from PERMANOVA pairwise tests of factor Treatment within Treatment \_ Slice for differences in nematode density (N), species richness (S) and Hill's diversity index  $N_1$  among experimental treatments and depth based on a Euclidean resemblance matrix. The significantly different slices among treatments are indicated with p-values drawn from Monte-Carlo samplings (p (MC))

Slice (cm)	N			Slice (cm)	S (whole core, cm scale)		
	Groups	<i>t</i>	p (MC)		Groups	<i>t</i>	p (MC)
0-0.5	<i>Abra, Nephtys</i>	4.16	0.014	1-2	Control, <i>Lanice</i>	2.82	0.044
0.5-1	<i>Abra, control</i>	4.80	0.012	2-3	<i>Abra, Control</i>	3.90	0.016
	<i>Abra, Lanice</i>	2.98	0.041		Control, <i>Lanice</i>	2.85	0.044
	<i>Abra, Nephtys</i>	3.15	0.034	4-5	<i>Abra, Lanice</i>	4.22	0.015
1-1.5	<i>Abra, control</i>	5.12	0.006		Control, <i>Lanice</i>	7.07	0.002
	control, <i>Lanice</i>	3.19	0.031	5-6	Control, <i>Lanice</i>	3.18	0.032
2-3	<i>Abra, control</i>	5.75	0.004	6-7	<i>Abra, Lanice</i>	5.37	0.007
	control, <i>Nephtys</i>	3.32	0.030		Control, <i>Lanice</i>	3.21	0.034
3-4	<i>Abra, control</i>	4.25	0.015		<i>Lanice, Nephtys</i>	5.37	0.006
	control, <i>Nephtys</i>	6.61	0.003	7-8	Control, <i>Nephtys</i>	4.22	0.013
4-5	control, <i>Lanice</i>	3.55	0.020	S (upper 2 cm, 0.5 cm scale)			
6-7	<i>Abra, control</i>	4.16	0.013	0.5-1	<i>Abra, Nephtys</i>	3.71	0.021
	<i>Abra, Lanice</i>	6.26	0.003	1-1.5	<i>Abra, control</i>	2.89	0.046
	control, <i>Lanice</i>	4.73	0.008		Control, <i>Lanice</i>	3.36	0.029
	control, <i>Nephtys</i>	5.33	0.006	1.5-2	Control, <i>Lanice</i>	2.80	0.049
	<i>Lanice, Nephtys</i>	6.60	0.003		Control, <i>Nephtys</i>	3.05	0.039
N <sub>1</sub> (whole core, cm scale)				N <sub>1</sub> (upper 2 cm, 0.5 cm scale)			
0-1	<i>Abra, Lanice</i>	5.19	0.007	0-0.5	<i>Abra, Lanice</i>	2.18	0.029
2-3	<i>Abra, Control</i>	3.55	0.024		<i>Abra, Nephtys</i>	3.21	0.017
	<i>Abra, Nephtys</i>	2.91	0.041		Control, <i>Nephtys</i>	3.00	0.038
	Control, <i>Lanice</i>	3.09	0.039	1-1.5	Control, <i>Lanice</i>	3.12	0.034
4-5	<i>Abra, Control</i>	4.00	0.016				
	<i>Abra, Lanice</i>	2.90	0.045				
	Control, <i>Lanice</i>	3.74	0.022				
6-7	<i>Abra, Lanice</i>	2.97	0.037				
	<i>Lanice, Nephtys</i>	4.09	0.016				
7-8	Control, <i>Nephtys</i>	3.97	0.017				

Table S6. Results from PERMANOVA analysis for differences in multivariate community structure among experimental treatments and depth, based on a Bray-Curtis resemblance matrix, both for raw and standardised square root-transformed data (df = 3, 7 and 21 in whole core (cm scale) analysis and df = 3, 3 and 9 in upper 2 cm (0.5 cm scale) analysis). P-values obtained by permutation. ns: not significant

	Treatment			Slice			Treatment _ Slice		
	MS	Pseudo-F	p	MS	Pseudo-F	p	MS	Pseudo-F	p
raw data (whole core)	7523.4	2.96	0.002	9565.9	5.54	<0.001	2688.1	1.56	<0.001
standardised, square root-transformed data (whole core)	4515.5	2.24	0.011	6153.7	4.04	<0.001	2176.9	1.43	0.002
raw data (upper 2 cm)	3310.5	1.75	ns	9740.1	6.89	<0.001	2209.8	1.56	0.004
standardised, square root-transformed data (upper 2 cm)	2280.7	1.36	ns	6315.3	4.73	<0.001	1423.9	1.07	ns

Table S7. Results from SIMPER analyses (50% cut-off). Average (raw) abundance of species most contributing to the dissimilarity (diss) between treatments in the analysis on the whole core (cm scale) and on the upper 2 cm (0.5 cm scale)

Whole core (cm scale)			
3–4 cm	Average abundance		Dissimilarity between treatments Contribution (%)
	<i>Abra</i>	control	Control and <i>Abra</i> (diss: 83.20)
<i>Sabatieria punctata</i>	7.67	1.39	30.71
<i>Spirinia</i> spp.	3.67	0.00	18.09
<i>Richtersia inaequalis</i>	0.00	1.33	6.83
Upper 2 cm (0.5 cm scale)			
0.5–1 cm	Average abundance		Contribution (%)
	<i>Abra</i>	<i>Nephtys</i>	<i>Abra</i> and <i>Nephtys</i> (diss: 62.84)
<i>Richtersia inaequalis</i>	34.67	9.33	29.53
<i>Dichromadora cucullata</i>	9.33	2.67	7.89
<i>Sabatieria celtica</i>	4.44	7.11	6.21
<i>Sabatieria punctata</i>	4.00	5.56	5.29
<i>Microlaimus conothesis</i>	7.33	5.33	4.84