Supplementary Material

1 Supplementary Methods

1.1 Aerosol collection

Aerosols – in the form of total suspended particles (TSP) – were sampled in Pico de la Gorra (Canary Islands; 1930 m above sea level; 27º 56'N, 15º 33'W) and onboard the FLUXES I cruise (Mauritanian-Senegalese upwelling; 17-23º N, 18-25º W). TSP concentrations were estimated a few days before and during the FLUXES I cruise by a dust deposition model predictor (provided by AEMET Barcelona Dust Forecast Center). As not enough TSP concentration was predicted to arrive on board, aerosol filter samples from Pico de la Gorra were used for the microcosm experiments.
At Pico de la Gorra, a time-series record of TSP concentration has been recorded from 1 December 1996 to 31 December 1998 (Torres-Padrón et al., 2002) and 1 December 2001 to the present (Gelado-Caballero et al., 2012; unpublished data). Thereby, glass fiber filters (Whatman GF/A) were loaded on high-volume aerosol samplers to obtain a continuous data set of daily gravimetric measurements over each 7-day period. Simultaneous acid-washed cellulose filters (Whatman 41) for chemical composition analysis were collected one day per week. Filters were selected based on TSP concentrations and the forecast presence of African dust intrusions (see Aerosol Classification). In-detail, aerosol samples from Pico de la Gorra were collected on different seasons between July 11th (2014) and March 09th (2017), while FLUXES I filters were sampled from July 15th to 17th (2017).
Trace metals (Al, Co, Fe, Cu, and Mn) and ions (nitrate, phosphate, and silicate) concentrations on Pico de la Gorra aerosol filters have been previously published at Gelado-Caballero et al. (2012), while element and nutrient solubility values at López-García et al. (2017). Trace-metal clean techniques were strictly followed throughout the aerosol collection and manipulation.

1.2 Aerosol classification

The origin and route of the air masses contributing to each dust sample were tracked by calculating 5-day isentropic back trajectories at 6:00 p.m. UTC using the NOAA HYSPLIT model (Stein et al., 2015) and GDAS meteorological dataset. The chosen altitude levels for the interpretation were 200, 750, 1500, 2000, and 2500 m in 6 h steps. According to Gelado-Caballero et al. (2012), three geographic sectors were identified based on source region mineralogy aerosol type: AD (African dust, trajectories over the African continent), MAR (maritime aerosol, trajectories over the Atlantic Ocean), and EUR (European and maritime aerosol, trajectories that cross the European continent and the Atlantic Ocean). Differences between African sectors were not taken into account since chemical variability found in previous studies across the region remains negligible (López-García et al., 2017). As the average of the filters exceeded 300 µg TSP m^{-3}, AD was taken as the main source of dust in the present study.

1.3 Dust stock solution preparation

A dust stock solution was prepared a few hours before the start of each experiment to preserve the concentration of nutrients. Under a laminar flow cabinet, dry deposited material was extracted from a 1/4 Whatman 41 filter piece into 100 mL of aged, low nutrient surface seawater by sonication for 2 x 15 min in an ultrasonic bath. Aerosol extractions were performed on different Whatman 41 filter pieces

and transferred together. At each experiment, the number of filter samples was selected to obtain a dust stock solution of average ~525 mg l^{-1} concentration. The same procedure was performed on identical acid washed blank Whatman 41 filters to assess contamination and/or fertilization effects due to the filter themselves. No particles were detected in this blank solution.

1.4 Particle flux simulation

Dust concentrations used to enrich our bioassays were determined based on a maximum dust deposition of ~5500 µg TSP m^{-3} in the Canary Islands (Gelado-Caballero et al., 2012), an average residence time of 20-days and a 30-m mixed layer depth in the region of study. The maximum dust particle concentration was then estimated in 6336 mg m^{-3}, categorized as intense dust deposition. Our dust additions ranged between 4.2 and 6.7 mg of dust per liter of seawater, thus in agreement with the previously simulated intense event.

1.5 References

Gelado-Caballero, M. D., López-García, P., Prieto, S., Patey, M. D., Collado, C., and Hérnández-Brito, J. J. (2012). Long-term aerosol measurements in Gran Canaria, Canary Islands: Particle concentration, sources and elemental composition. *J. Geophys. Res.* 117, n/a-n/a. doi: 10.1029/2011JD016646.

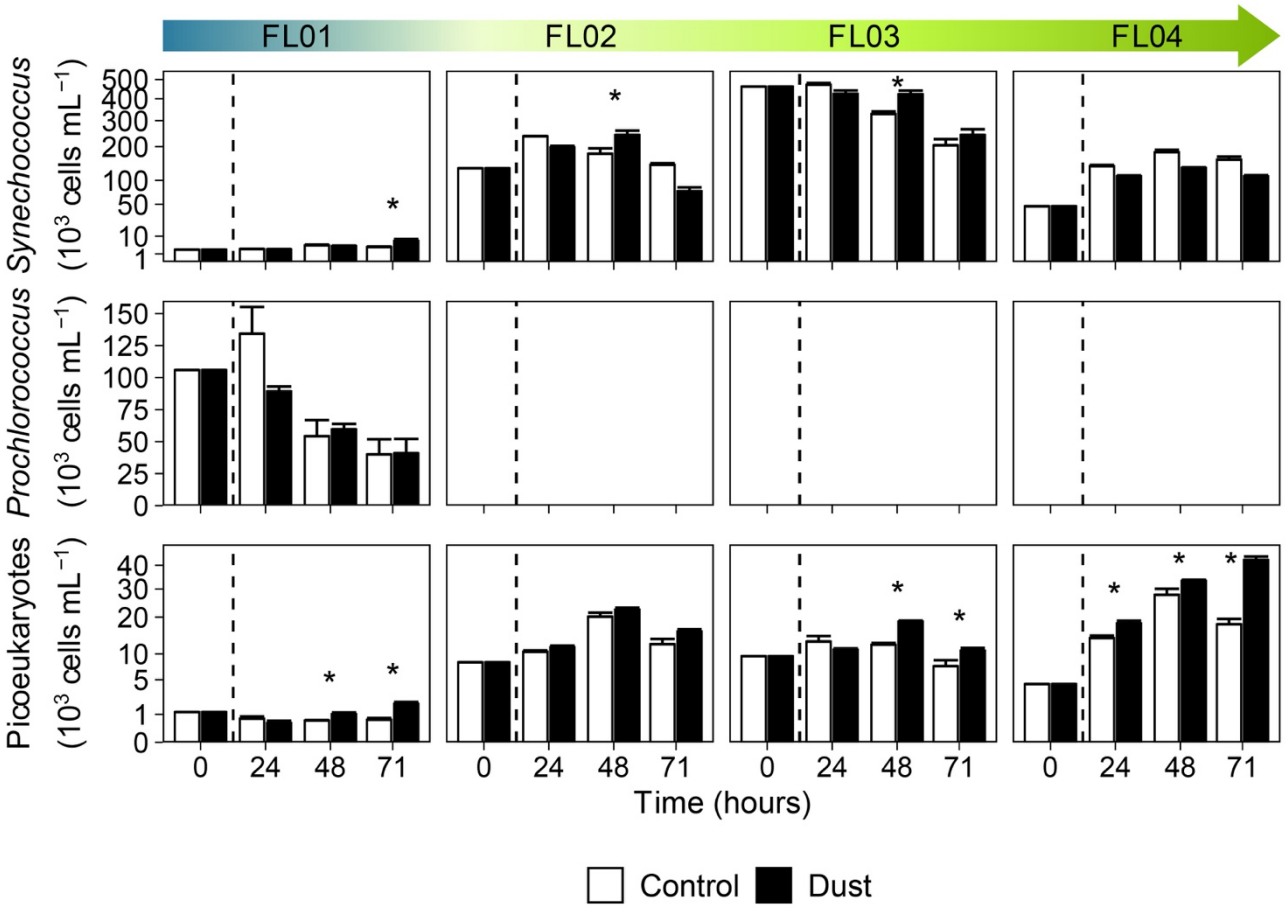
López-García, P., Gelado-Caballero, M. D., Collado-Sánchez, C., and Hernández-Brito, J. J. (2017). Solubility of aerosol trace elements: Sources and deposition fluxes in the Canary Region. *Atmos. Environ.* 148, 167–174. doi: 10.1016/j.atmosenv.2016.10.035.

Stein, A. F., Draxler, R. R., Rolph, G. D., Stunder, B. J. B., Cohen, M. D., and Ngan, F. (2015). Noaa's hysplit atmospheric transport and dispersion modeling system. *Bull. Amer. Meteor. Soc.* 96, 2059–2077. doi: 10.1175/BAMS-D-14-00110.1.

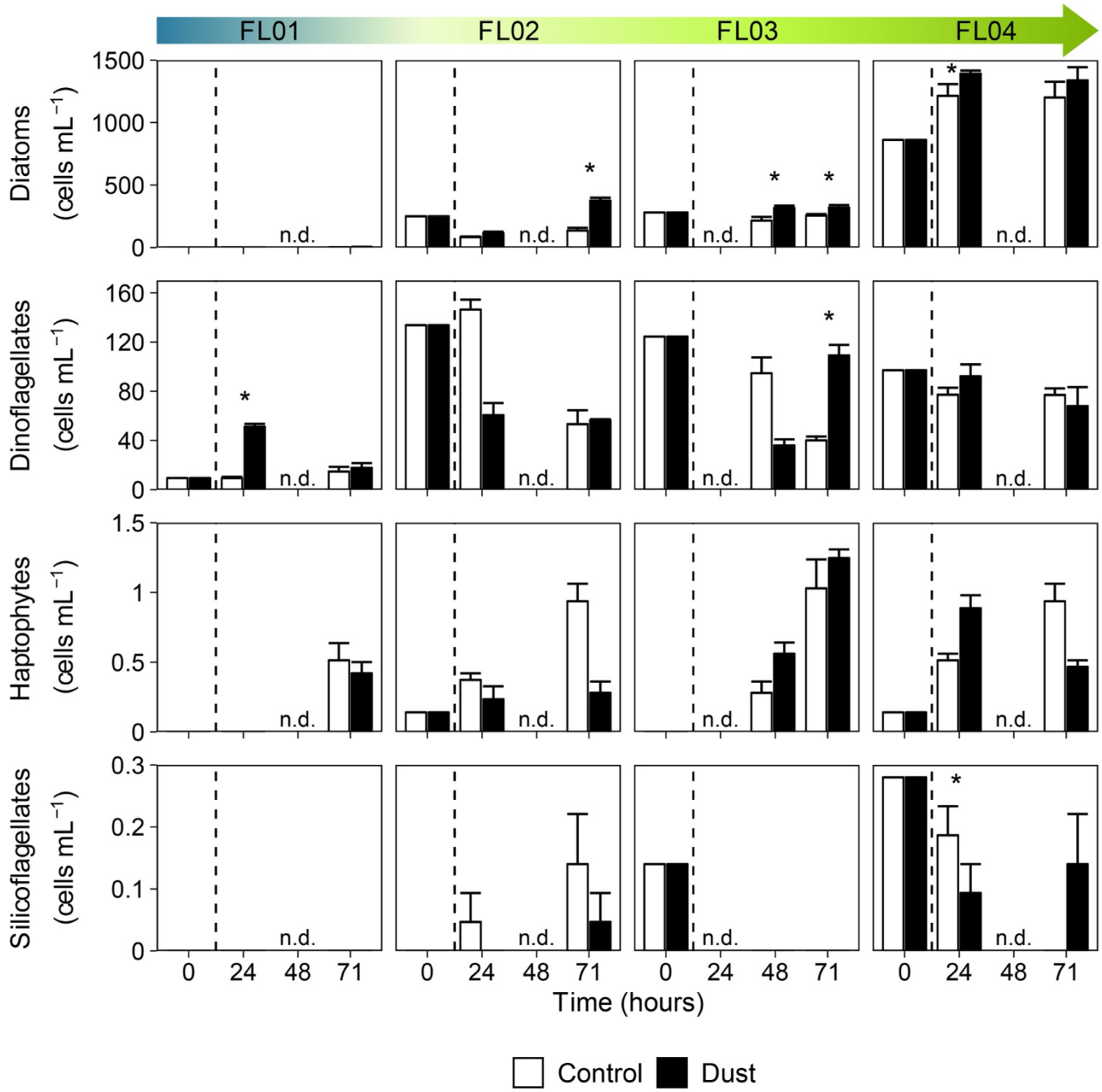
Torres-Padrón, M. E., Gelado-Caballero, M. D., Collado-Sánchez, C., Siruela-Matos, V. F., Cardona-Castellano, P. J., and Hernández-Brito, J. J. (2002). Variability of dust inputs to the CANIGO zone. *Deep Sea Res. Part II Top. Stud. Oceanogr.* 49, 3455–3464. doi: 10.1016/S0967-0645(02)00091-7.

2 Supplementary Figures

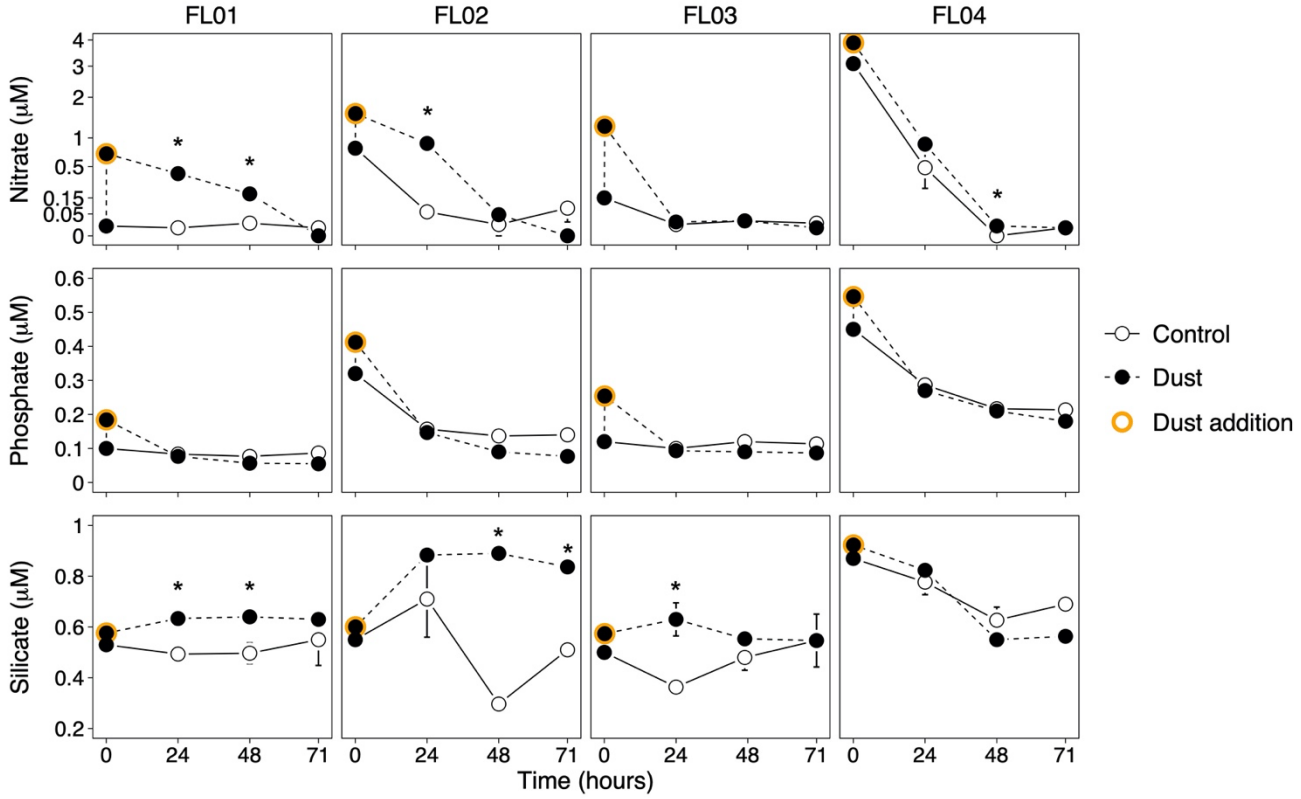
Supplementary Figure 1. Picophytoplankton abundance (cells mL^{-1}) by identified groups: *Synechococcus* and *Prochlorococcus* cyanobacteria, and picoeukaryotes, in the control (white bars) and dust-treated microcosms (black bars). The vertical line indicates the dust addition time. Each data point represents the average and standard deviation of three replicated microcosms. The asterisk denotes where the value of dust triplicates was significantly greater than control ($p < 0.05$, Wilcoxon test). Note that different scales were used.



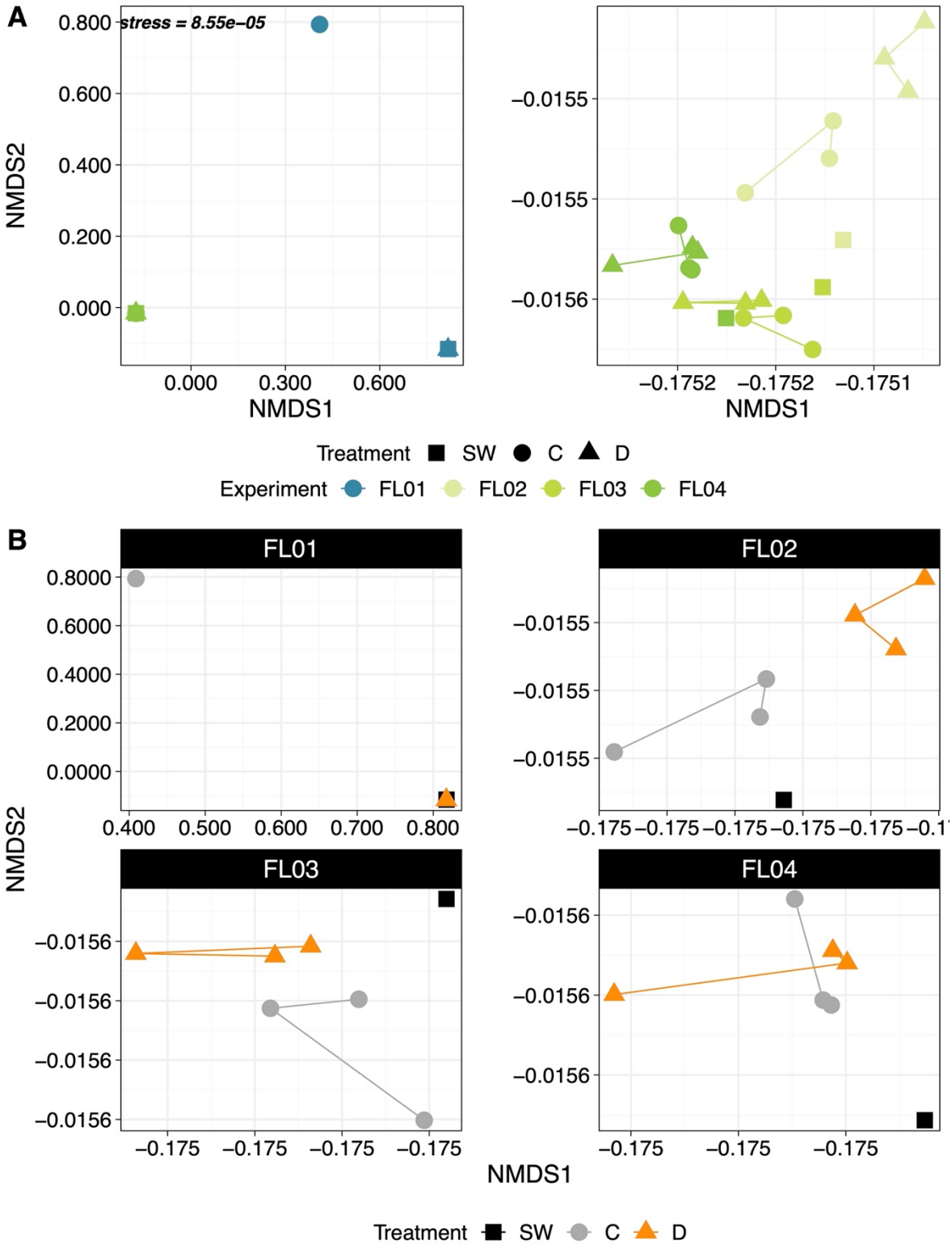
Supplementary Figure 2. Microphytoplankton abundance (cells mL^{-1}) by groups: diatoms, dinoflagellates, haptophytes, and silicoflagellates, in the control (white bars) and dust-treated microcosms (black bars). The vertical line indicates the dust addition time. Each data point represents the average and standard deviation of three replicated microcosms. The asterisk denotes where the value of dust triplicates was significantly greater than control ($p < 0.05$, Wilcoxon test). The abbreviation n.d. (no-data) indicate the absence of data at that time of the experimental incubation. Note that different scales were used.



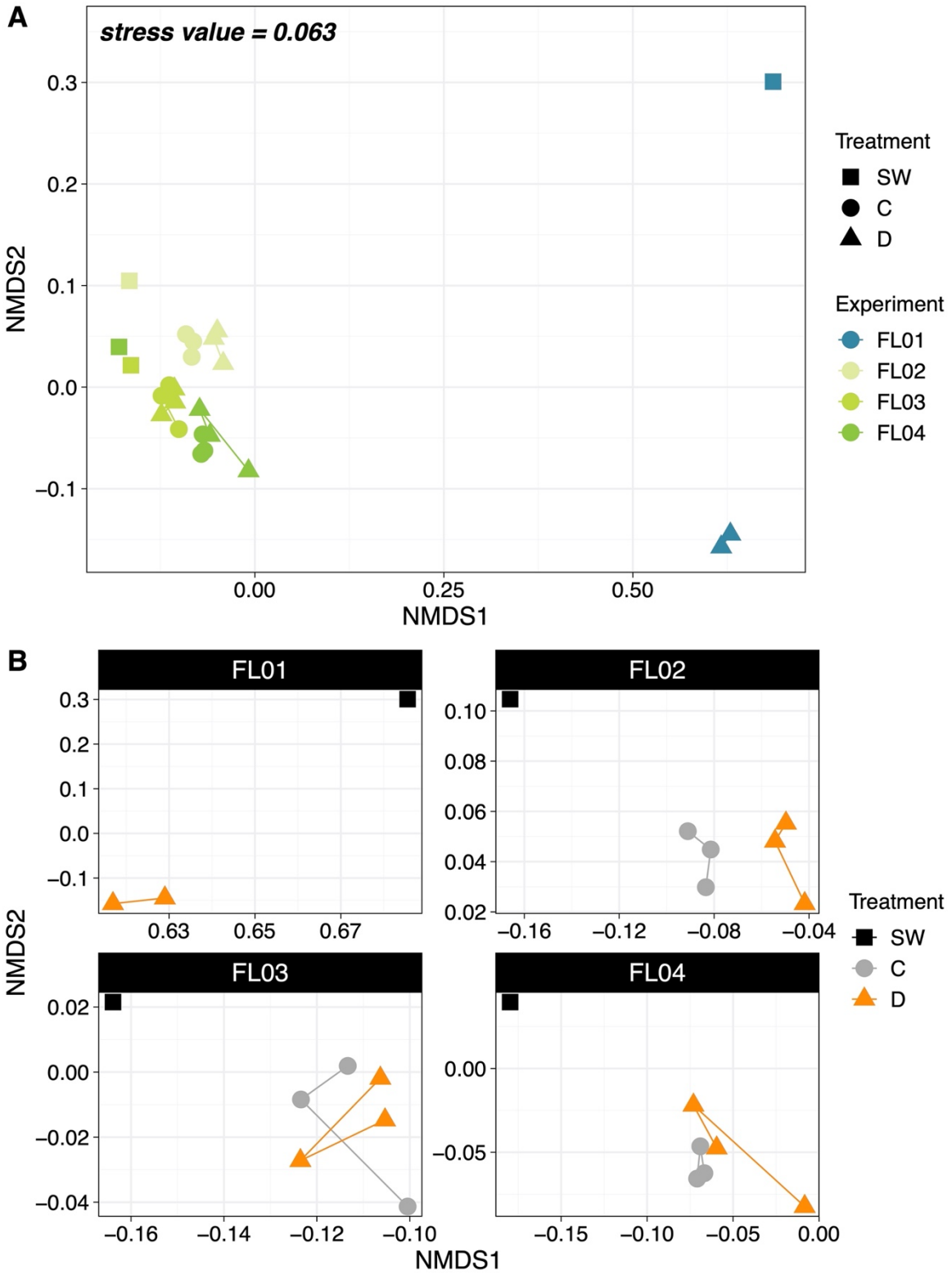
Supplementary Figure 3. Inorganic nutrient concentration (μmol L^{-1}) in the control (white points) and dust-treated microcosms (black points). The orange circle indicates the dust addition time. Each data point represents the average and standard deviation of three replicated microcosms. The asterisk denotes where the value of dust triplicates was significantly greater than control ($p < 0.05$, Wilcoxon test). Note that different scales were used.



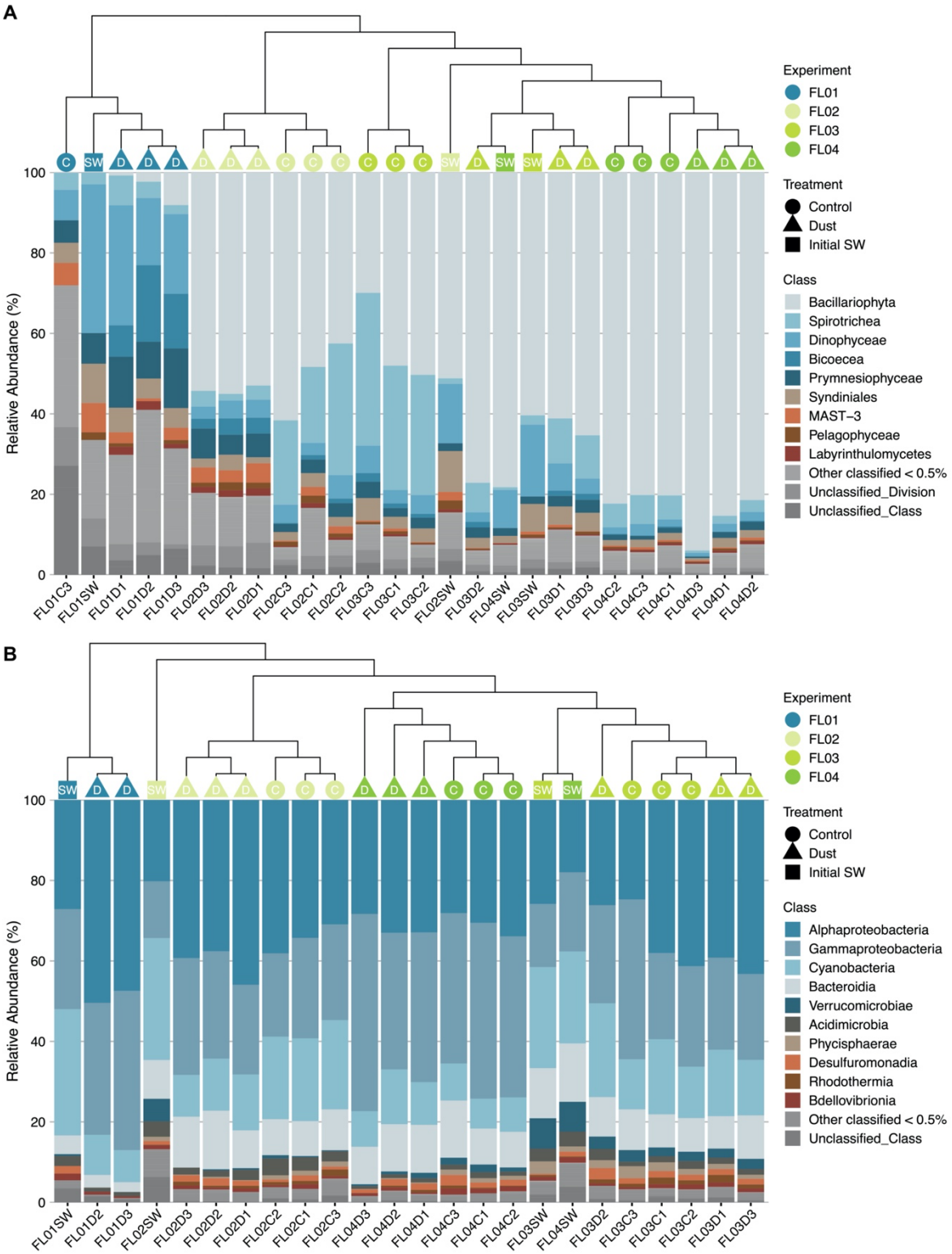
Supplementary Figure 4. NMDS (Non-metric Multidimensional scaling) plots based on Bray-Curtis dissimilarities of eukaryotic diversity samples from FLUXES experiments. Point colors were assigned by (A) experiment and (B) treatment.



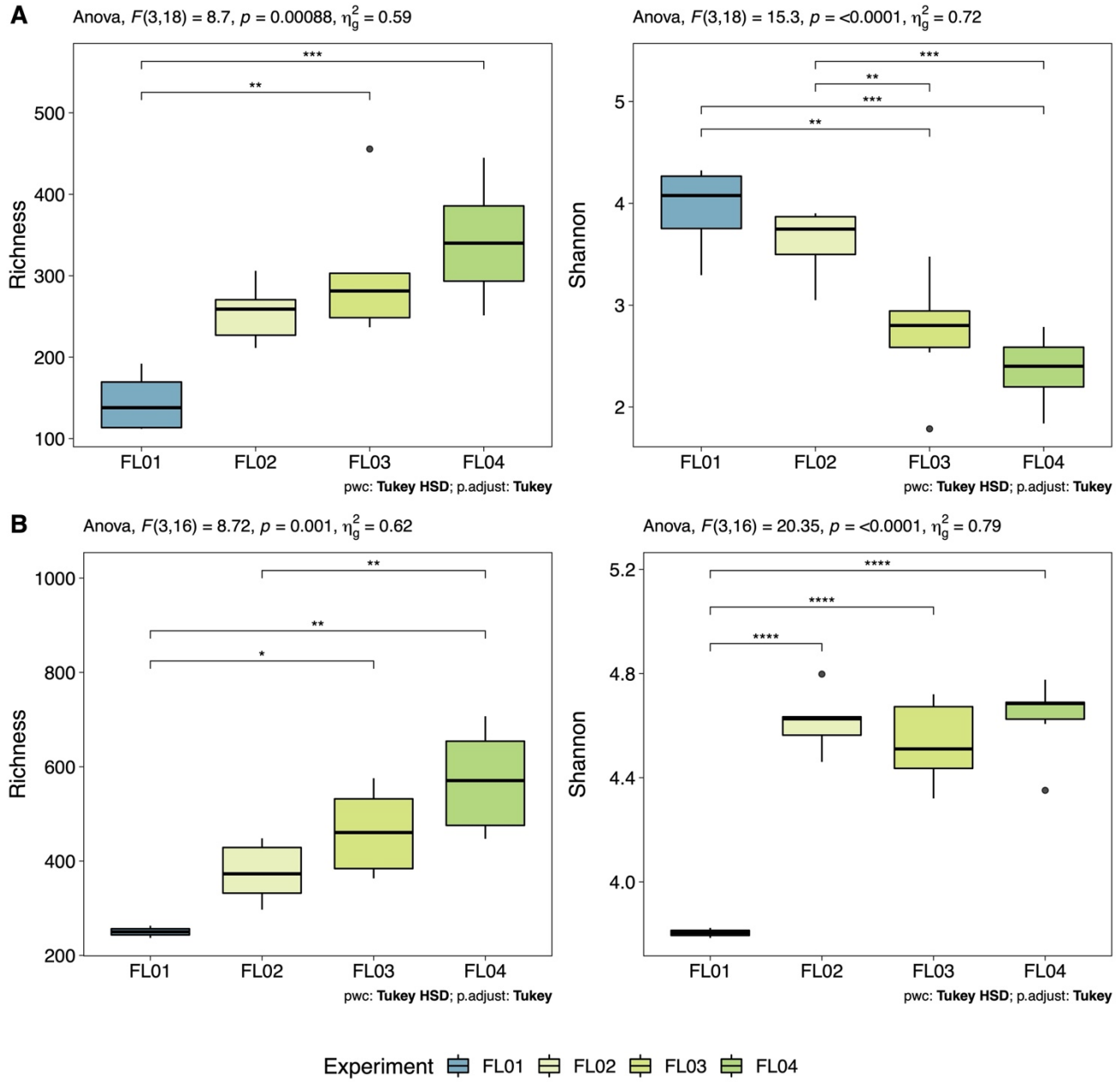
Supplementary Figure 5. NMDS (Non-metric Multidimensional scaling) plots based on Bray-Curtis dissimilarities of prokaryotic diversity samples from FLUXES experiments. Point colors were assigned by (A) experiment and (B) treatment.



Supplementary Figure 6. Hierarchical clustering and relative abundance of class-classified (A) eukaryotes and (B) prokaryotes. Groups are ordered by decreasing median relative abundances. Histograms colours were assigned for all phyla detected with a relative abundance ≥ 0.5%. Data represent the initial time (SW) of the incubations, and control (C) and dust-treated (D) triplicate microcosms at the end of the experiments.



Supplementary Figure 7. One-way ANOVA and post-hoc Tukey HSD test comparing (A) eukaryotic and (B) prokaryotic Chao1 richness and Shannon diversity estimates across the four experiments. Data correspond to the end of the experiments. Significance level of 0.05 (*), 0.01 (**), 0.001 (***) and 0.0001 (****).



3 Supplementary Tables

Supplementary Table 1. Results from Wilcoxon Signed-Rank test on inorganic nutrients, phytoplankton size-groups and bacteria abundance and production differences between control and dust-treated microcosms for each experiment. The abbreviation n.d. (no-data) indicate the absence of data at that time of the experimental incubation. Significance level of 0.05 (*), 0.005 (**) and 0.001 (***).

		Wilcoxon Signed-Rank test (p-value)											
Experiment	**Time**	**Nitrate**	**Phosphate**	**Silicate**	**Chl *a***	**Micro-phytoplankton abundance**	**Nano-phytoplankton abundance**	**Pico-phytoplankton abundance**	**Phytoplankton production (PP_{DOC})**	**Phytoplankton production (PP_{POC})**	**Phytoplankton production (PP_{TOC})**	**Bacterial abundance**	**Bacterial production**
FL01	24	0.04*	0.94	0.04*	0.33	0.04*	0.09	0.98	0.98	0.81	0.98	0.67	0.04*
	48	0.04*	0.99	0.04*	n.d.	n.d.	0.04*	0.33	n.d.	n.d.	n.d.	0.5	n.d.
	71	0.89	0.98	0.39	0.09	0.19	0.04*	0.5	0.27	0.04*	0.27	0.19	0.19
FL02	24	0.04*	0.91	0.33	0.5	0.99	0.99	0.98	0.61	0.81	0.39	0.09	0.33
	48	0.13	0.99	0.03*	n.d.	n.d.	0.19	0.04*	n.d.	n.d.	n.d.	0.5	n.d.
	71	0.99	0.99	0.04*	0.04*	0.04*	0.09	0.98	0.04*	0.67	0.5	0.98	0.09
FL03	24	0.33	0.88	0.04*	n.d.	n.d.	0.04*	0.98	n.d.	n.d.	n.d.	0.09	n.d.
	47	0.68	0.99	0.19	0.04*	0.33	0.04*	0.04*	0.04*	0.04*	0.04*	0.04*	0.33
	71	0.91	0.99	0.5	0.33	0.04*	0.04*	0.19	0.88	0.12	0.12	0.81	0.04*
FL04	24	0.19	0.82	0.33	0.19	0.04*	0.33	0.98	0. 98	0.07	0.07	0.33	0.90
	48	0.02*	0.87	0.94	n.d.	n.d.	0.81	0.98	n.d.	n.d.	n.d.	0.67	n.d.
	71	0.68	0.96	0.99	0.19	0.33	0.09	0.98	0.04*	0.07	0.07	0.5	0.81

Supplementary Table 2. Results from Kruskal-Wallis and *post hoc* Conover tests inorganic nutrients, and phytoplankton and bacterial abundance and production differences between the dust-treated microcosms of all four experiments at 24-hour sampling time. The abbreviation n.d. (no-data) indicate the absence of data at that time of the experimental incubation. Bonferroni adjusted p-values. Significance level of 0.05 (*), 0.005 (**) and 0.001 (***).

	Kruskal-Wallis test (p-value)	**Post hoc Conover test (p-value)**					
	Sampling time	**Experiment pair**					
	24 h	**1 – 2**	**1 – 3**	**2 – 3**	**1 – 4**	**2 – 4**	**3 – 4**
Nitrate	0.02*	0.02*	0.15	0.001**	0.04*	1	0.002**
Phosphate	0.01*	2.97e-05***	0.0036**	0.004**	1.35e-06***	0.0036**	2.97e-05***
Silicate	0.02*	0.0007***	1	0.002**	0.01*	0.14	0.04*
Chl *a*	0.03*	0.01*	n.d.	n.d.	0.0005***	0.01*	n.d.
Micro-phytoplankton abundance	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.	n.d.
Nano-phytoplankton abundance	0.01*	0.02*	2.40e-04***	0.02*	1.22e-05***	2.40e-04***	0.02*
Pico-phytoplankton abundance	0.01*	2.40e-04***	1.22e-05***	0.02*	0.02*	0.02*	2.40e-04***
Phytoplankton production (PP_{DOC})	0.04*	0.02*	n.d.	n.d.	0.002**	0.05	n.d.
Phytoplankton production (PP_{POC})	0.04*	0.02*	n.d.	n.d.	0.002**	0.05	n.d.
Phytoplankton production (PP_{TOC})	0.04*	0.02*	n.d.	n.d.	0.002**	0.05	n.d.
Bacterial abundance	0.01*	0.02*	1.22e-05***	2.40e-04***	2.40e-04***	0.02*	0.02*
Bacterial production	0.04*	0.12	n.d.	n.d.	0.003**	0.04*	n.d.

Supplementary Table 3. Eukaryote and bacteria indicator species ($p < 0.05$ and $stat > 0.75$) for the control microcosms. The parameter *str* indicates the strength of the association between a species and the site-group (seawater used to fill the microcosms, SW; control microcosms, C; dust-treated microcosms, D). The abbreviation *stat* indicates the association value and *p* the degree of statistical significance of the association (p-values are based on 999 permutations). Significance level of 0.05 (*), 0.005 (**) and 0.001 (***).

OTU	**Kingdom**	**Supergroup**	**Division**	**Class**	**Order**	**Family**	**Genus**	**Species**	str_{SW}	str_{C}	str_{D}	***stat***	***p***
ASV_35	Eukaryota	Alveolata	Ciliophora	Spirotrichea	Tintinnida	*Tintinnidae*	Unclassified_Tintinnidae	Unclassified_Tintinnidae	0.161	0.827	0.307	0.83	0.008*
ASV_17	Eukaryota	Alveolata	Ciliophora	Spirotrichea	Choreotrichida	*Strobilidiidae_I*	Unclassified_Strobilidiidae_I	Unclassified_Strobilidiidae_I	0	0.825	0.319	0.82	0.01*
ASV_73	Eukaryota	Alveolata	Ciliophora	Spirotrichea	Choreotrichida	*Strobilidiidae_I*	*Pelagostrobilidium*	*Pelagostrobilidium paraepacrum*	0.084	0.752	0.069	0.75	0.04*
ASV_10	Eukaryota	Alveolata	Ciliophora	Spirotrichea	Tintinnida	*Tintinnidae*	Unclassified_Tintinnidae	Unclassified_Tintinnidae	0.223	0.836	0.341	0.84	0.05*
ASV_47	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Alteromonadaceae*	*Salinimonas*	Unclassified_Salinimonas	0.168	0.798	0.486	0.80	0.001***
ASV_266	Bacteria	-	Bacteroidota	Bacteroidia	Flavobacteriales	*NS7 marine group*	Unclassified_NS7 marine group	Unclassified_NS7 marine group	0.285	0.865	0.155	0.86	0.001***
ASV_88	Bacteria	-	Planctomycetota	Phycisphaerae	Phycisphaerales	*Phycisphaeraceae*	*Urania-1B-19 marine sediment group*	Unclassified_Urania-1B-19 marine sediment group	0.468	0.789	0.198	0.79	0.004**
ASV_3	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Vibrionaceae*	*Vibrio*	*artabrorum/atlanticus/celticus/chagasii/crassostreae/cyclitrophic*	0.04	0.824	0.535	0.82	0.005**

								us/gallaeicus/gigantis/harveyi/kanaloae/lentus/pomeroyi/splendidus/tasmaniensis/toranzoniae					
ASV_469	Bacteria	-	Planctomycetota	Phycisphaerae	Phycisphaerales	*Phycisphaeraceae*	*CL500-3*	Unclassified_CL500-3	0.226	0.787	0	0.79	0.009**
ASV_185	Bacteria	-	Proteobacteria	Alphaproteobacteria	Puniceispirillales	*SAR116 clade*	Unclassified_SAR116 clade	Unclassified_SAR116 clade	0.308	0.782	0.403	0.78	0.01*
ASV_258	Bacteria	-	Proteobacteria	Alphaproteobacteria	SAR11 clade	*Clade IV*	Unclassified_Clade IV	Unclassified_Clade IV	0.161	0.783	0.274	0.78	0.02*
ASV_144	Bacteria	-	Proteobacteria	Alphaproteobacteria	Rhizobiales	*Stappiaceae*	*Labrenzia*	*marina*	0	0.762	0.617	0.76	0.02*
ASV_410	Bacteria	-	Bacteroidota	Bacteroidia	Flavobacteriales	*Flavobacteriaceae*	*Aureicoccus*	*marinus*	0	0.771	0.327	0.77	0.03*

Supplementary Table 4. Eukaryote and bacteria indicator species ($p < 0.05$ and $stat > 0.75$) for the dust-treated microcosms. The parameter *str* indicates the strength of the association between a species and the site-group (seawater used to fill the microcosms, SW; control microcosms, C; dust-treated microcosms, D). The abbreviation *stat* indicates the association value and *p* the degree of statistical significance of the association (p-values are based on 999 permutations). Significance level of 0.05 (*), 0.005 (**) and 0.001 (***).

OTU	Kingdom	Supergroup	Division	Class	Order	Family	Genus	Species	str_{SW}	str_{C}	str_{D}	*stat*	*p*
ASV_5	Eukaryota	Stramenopiles	Ochrophyta	Bacillariophyta	Bacillariophyta_X	*Raphid-pennate*	Unclassified_Raphid-pennate	Unclassified_Raphid-pennate	0.231	0.529	0.786	0.79	0.01*
ASV_258	Eukaryota	Hacrobia	Haptophyta	Prymnesiophyceae	Prymnesiales	*Chrysochromulinaceae*	*Chrysochromulina*	*Chrysochromulina_rotalis*	0	0.302	0.798	0.80	0.02*
ASV_57	Eukaryota	Stramenopiles	Sagenista	Labyrinthulomycetes	Labyrinthulomycetes_X	*Labyrinthulomycetes_X_LAB7*	*Labyrinthulomycetes_X_LAB7_X*	*Labyrinthulomycetes_X_LAB7_X sp.*	0.22	0.317	0.821	0.82	0.03*
ASV_118	Eukaryota	Stramenopiles	Unclassified_Stramenopiles	Unclassified_Stramenopiles	Unclassified_Stramenopiles	Unclassified_Stramenopiles	Unclassified_Stramenopiles	Unclassified_Stramenopiles	0	0.07	0.754	0.75	0.04*
ASV_5	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Alteromonadaceae*	*Alteromonas*	*alvinellae/australica/gracilis/litorea/macleodii/marina/mediterranea/simiduii/tagae*	0.163	0.5	0.85	0.85	0.001 ***
ASV_13	Bacteria	-	Proteobacteria	Alphaproteobacteria	Caulobacterales	*Hyphomonadaceae*	*Hyphomonas*	*atlantica/johnsonii*	0	0.18	0.979	0.98	0.001 ***
ASV_109	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Alteromonadaceae*	*Alteromonas*	Unclassified_Alteromonas	0.15	0.573	0.801	0.80	0.005 **
ASV_43	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Alteromonadaceae*	Unclassified_Alteromonadaceae	Unclassified_Alteromonadaceae	0.03	0.531	0.824	0.82	0.01*

ASV_254	Bacteria	-	Proteobacteria	Alphaproteobacteria	Sphingomonadales	*Sphingomonadaceae*	*Erythrobacter*	*citreus*	0	0.146	0.875	0.87	0.01*
ASV_269	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Colwelliaceae*	*Colwellia*	Unclassified_Colwellia	0.232	0.261	0.777	0.78	0.03*
ASV_16	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Alteromonadaceae*	*Alteromonas*	*australica*	0.019	0.627	0.778	0.78	0.03*
ASV_444	Bacteria	-	Proteobacteria	Gammaproteobacteria	Enterobacterales	*Alteromonadaceae*	*Aestuariibacter*	Unclassified_Aestuariibacter	0	0.328	0.766	0.77	0.03*
ASV_76	Bacteria	-	Proteobacteria	Alphaproteobacteria	Rhodobacterales	*Rhodobacteraceae*	*Thalassobius*	Unclassified_Thalassobius	0	0.439	0.801	0.80	0.05*

Supplementary Table 5. Two-way ANOVA test comparing eukaryotic and prokaryotic Chao1 richness and Shannon diversity estimates on the interaction between Treatment and Experiment. Data correspond to the end of the experiments. Significance level of 0.05 (*), 0.005 (**) and 0.001 (***).

Two-way ANOVA at time 71 h											
		Chao1 richness					**Shannon diversity**				
Dataset	**Effect**	**DFn**	**DFd**	**F**	**p**	**ges**	**DFn**	**DFd**	**F**	**p**	**ges**
Eukaryotic	Experiment	3	14	8.778	0.002**	0.653	3	14	24.485	7.85e-06***	0.840
	Treatment	1	14	0.004	0.949	0.0003	1	14	0.019	0.892	0.001
	Experiment:Treatment	3	14	1.588	0.237	0.254	3	14	5.116	0.013*	0.523
Prokaryotic	Experiment	3	13	7.829	0.003**	0.644	3	13	17.296	0.00008***	0.800
	Treatment	1	13	1.059	0.322	0.075	1	13	1.871	0.195	0.126
	Experiment:Treatment	2	13	1.053	0.377	0.139	2	13	0.884	0.436	0.120