

## Supplementary Information:

# The microbiome of coral surface mucus plays a key role in mediating holobiont health and survival upon disturbance

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### PCR protocol

All extracted samples were subjected to PCR using primers U341F (5'- CCT ACG GGR SGC AGC AG -3') and U1053R (5'- CTG ACG RCR GCC ATG C -3') adapted from Wang and Qian (2009) and amplifying a 728-bp fragment of the 16S rRNA gene (including variable regions V3-V6) for both Archaea and Bacteria with expected coverage of ca. 90%, while almost fully excluding Eukaryotes (Klindworth et al., 2012).

Each 25  $\mu$ L PCR reaction consisted of 1x taq buffer, 3 mM MgCl<sub>2</sub>, 2 mM (of each) dNTP, 0.2 mg mL<sup>-1</sup> BSA, 0.25  $\mu$ M of each primer, 0.03U  $\mu$ L<sup>-1</sup> of Taq DNA Polymerase (Fermentas) and 1-2  $\mu$ L of template DNA. Cycling conditions comprised a 4 min initial denaturation step at 95°C, followed by 30 cycles performed at 95°C for 30 s, 65°C for 45 s and 72°C for 1.30 min. A final elongation step at 72°C for 10 min completed each reaction and afterwards products was cooled down to 4°C. PCR products were evaluated via electrophoresis on (1.5%) agarose gels.

### Mucus shedding behavior of poritid corals

Colonies of *Porites astreoides* examined in this study exhibited mucus aging and shedding with an average frequency of  $0.8 \pm 0.3$  times per 30 days. This periodicity does not unequivocally confirm earlier observations by Coffroth (1983 and 1991), who suggested that mucus shedding in *P. astreoides* follows the lunar cycle. However, half of the studied colonies exhibited a conspicuously aged mucus layer during the week before full moon, which is a rather non-random time distribution considering that, on average, each aging event only lasts for one up to three days. Furthermore, negligible variation in measured abiotic parameters during the study period confirms that the mucus aging process of poritid corals is generally decoupled from measurable environmental influences such as temperature and light (Coffroth, 1991) However, stressful conditions, such as increased sedimentation, are proposed to stimulate mucus formation (Bak and Elgershuizen, 1976). Hence, cyclical mucus aging could have been masked by elevated sediment load onto the surface of corals as a result of the high sediment resuspension often associated with shallow depths. Moreover, it is hypothesized that the aggregation of mucus on the surfaces of coral colonies is a consequence of reduced polyp activity and hence, low ciliary current (Coffroth, 1991). Consistent with this hypothesis, we observed polyps to be contracted when colonies were covered with aged mucus sheets, a behavior contrasting with the typical extension of polyps during the day for this coral genus (Abe, 1939, Coffroth, 1991).

Elevated sedimentation rates have been linked to the occurrence of coral diseases (Pollock et al., 2014) as well as to rapid immune responses followed by depletion of the coral's energy storage (Sheridan et al., 2014). Compared to other coral species specialized in removing sediment from their surfaces (see Rogers, 1990), *P. astreoides* and poritiid corals might periodically shut down mucus production and polyp activity to refill depleted energy reserves. This would lead to transformation of mucus aggregates on the coral's surface and their colonization by potentially harmful microbes, which may partially displace the microbiome. Release of mucus sheets would then lead to a new succession and the repeated dominance by a beneficial mucus microbiome. This raises the question of whether the temporal dynamics in the microbiome of corals that exhibit rather continuous mucus release are similar to those of corals with a periodic mucus release. We hypothesize that such corals do not experience such severe shifts in their microbiome composition, but probably need to invest more energy into mucus production by their mucocytes and cleansing activity by their cilia. For *P. astreoides*, however, this cyclic mucus release strategy seems to be well adapted to shallow habitats where resuspension of sediments occurs frequently.

**Table S1.** List of antibiotics used in the disturbance experiment to treat the coral mucus of *Porites astreoides*, including their target spectrum, mode of action and the amount applied (adapted from Polne-Fuller 1991).

<b>Antibiotic</b>	<b>Spectrum</b>	<b>Mode of action</b>	<b>100 ml stock solution (diluted 1:100)</b>
<b>Streptomycin</b>	Gram+/- bacteria	inhibit translation	2083 mg
<b>Kanamycin</b>	Gram+ bacteria	inhibit translation	943 mg
<b>Neomycin</b>	Gram+/- bacteria	inhibit translation	208 mg
<b>Ampicillin</b>	Gram+/- bacteria	inhibit cell wall synthesis	100 mg
<b>Rifampicin</b>	Gram+/- bacteria	inhibits transcription	21 mg
<b>Polymixin-B</b>	Gram- bacteria	inhibit translation	17 mg
<b>Nystatin</b>	Fungi	inactivate membranes containing sterols	7,8 mg
<b>Erythromycin</b>	Gram+/- bacteria	inhibit translation	12 mg
<b>Gentamycin</b>	Gram- bacteria	inhibit translation	4,5 mg

**Table S2.** List of prokaryotic families identified to be solely associated with new or aged mucus of *Porites astreoides* (unique OTUs). Those prokaryotic families were neither present in samples of the opposite mucus stage nor in collected seawater and sediment samples. Letters before taxa names stand for: k=kingdom, p=phylum, c=class, o=order, f=family.

unique OTUs	<b>new mucus</b>	k__Archaea;Other;Other;Other;Other
	k__Archaea;p__Crenarchaeota;c__Thaumarchaeota;o__Cenarchaeales;f__Cenarchaeaceae	
	k__Archaea;p__Euryarchaeota;c__Halobacteria;o__Halobacteriales;f__Halobacteriaceae	
	k__Bacteria;p__Acidobacteria;c__Acidobacteria-6;o__CCU21;f__	
	k__Bacteria;p__Actinobacteria;c__Acidimicrobia;o__Acidimicrobiales;f__OCS155	
	k__Bacteria;p__Actinobacteria;c__Nitriliruptoria;o__Euzebyales;f__Euzebyaceae	
	k__Bacteria;p__Bacteroidetes;c__BME43;o__f__	
	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;Other	
	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__Marinilabiaceae	
	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__SB-1	
	k__Bacteria;p__Bacteroidetes;c__Bacteroidia;o__Bacteroidales;f__[Odoribacteraceae]	
	k__Bacteria;p__Bacteroidetes;c__[Saprosirae];o__[Saprosirales];f__Chitinophagaceae	
	k__Bacteria;p__Chloroflexi;c__Anaerolineae;o__SBR1031;Other	
	k__Bacteria;p__Chloroflexi;c__Dehalococcoidetes;o__Dehalococcoidales;f__Dehalococcoidaceae	
	k__Bacteria;p__Cyanobacteria;c__4C0d-2;o__MLE1-12;f__	
	k__Bacteria;p__Cyanobacteria;c__ML635J-21;o__f__	
	k__Bacteria;p__Cyanobacteria;c__Oscillatoriothycideae;o__Chroococcales;f__Spirulinaceae	
	k__Bacteria;p__Fibrobacteres;c__Fibrobacteria;o__Fibrobacterales;f__Fibrobacteraceae	
	k__Bacteria;p__Fibrobacteres;c__Fibrobacteria;o__Ucp1540;f__	
	k__Bacteria;p__Fibrobacteres;c__TG3;o__TG3-2;f__	
	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;Other	
	k__Bacteria;p__Firmicutes;c__Clostridia;o__Clostridiales;f__Clostridiaceae	
	k__Bacteria;p__GNO2;c__o__f__	
	k__Bacteria;p__OP8;c__OP8_1;o__f__	
	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Kiloniellales;f__Kiloniellaceae	
	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Kordiimonadales;f__Kordiimonadaceae	
	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__	
	k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodobacterales;Other	
	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__MIZ46;f__	
	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;Other	
	k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__O319-6G20	
	k__Bacteria;p__Proteobacteria;c__Epsilonproteobacteria;o__Campylobacterales;f__Campylobacteraceae	
	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Enterobacteriales;f__Enterobacteriaceae	
	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Legionellales;f__Legionellaceae	
	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Alcanivoracaceae	
	k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Oceanospirillales;f__Saccharospirillaceae	
	k__Bacteria;p__Spirochaetes;c__[Brachyspirae];o__[Brachyspirales];f__Brachyspiraceae	
	<b>aged mucus</b>	k__Bacteria;p__Actinobacteria;Other;Other;Other
	k__Bacteria;p__Actinobacteria;c__Actinobacteria;o__Actinomycetales;f__Mycobacteriaceae	
	k__Bacteria;p__Actinobacteria;c__Thermoleophillia;o__Gaiellales;f__AK1AB1_02E	
	k__Bacteria;p__Actinobacteria;c__Thermoleophillia;o__Gaiellales;f__Gaiellaceae	
	k__Bacteria;p__Bacteroidetes;c__Cytophagia;o__Cytophagales;f__Cyclobacteriaceae	
	k__Bacteria;p__Bacteroidetes;c__Flavobacteriia;o__Flavobacteriales;f__NS9	
	k__Bacteria;p__Bacteroidetes;c__Sphingobacteriia;o__Sphingobacteriales;f__	
	k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Nostocales;Other	
k__Bacteria;p__Cyanobacteria;c__Nostocophycideae;o__Stigonematales;f__Rivulariaceae		
k__Bacteria;p__Cyanobacteria;c__Oscillatoriothycideae;o__Chroococcales;f__		
k__Bacteria;p__Fusobacteria;c__Fusobacteriia;o__Fusobacteriales;Other		
k__Bacteria;p__Gemmatimonadetes;c__Gemm-1;o__f__		
k__Bacteria;p__KSB3;c__o__f__		
k__Bacteria;p__OD1;c__ZB2;o__f__		
k__Bacteria;p__PAUC34f;c__o__f__		
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Kordiimonadales;Other		
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhizobiales;f__Bradyrhizobiaceae		
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rhodospirillales;Other		
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Rickettsiales;Other		
k__Bacteria;p__Proteobacteria;c__Alphaproteobacteria;o__Sphingomonadales;Other		
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;Other;Other		
k__Bacteria;p__Proteobacteria;c__Betaproteobacteria;o__Procabacteriales;f__Procabacteriaceae		
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Bdellovibrionales;f__Bdellovibrionaceae		
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Desulfarculales;f__Desulfarculaceae		
k__Bacteria;p__Proteobacteria;c__Deltaproteobacteria;o__Myxococcales;f__Polyangiaceae		
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__HTCC2188;Other		
k__Bacteria;p__Proteobacteria;c__Gammaproteobacteria;o__Thiohalorhabdadales;f__Thiohalorhabdaceae		
k__Bacteria;p__TM6;c__SJA-4;o__S1198;f__		
k__Bacteria;p__Verrucomicrobia;c__Opiritutae;o__f__		
k__Bacteria;p__Verrucomicrobia;c__Opiritutae;o__[Pelagicoccales];f__[Pelagicocaceae]		
k__Bacteria;p__WS3;c__PRR-12;o__wb1_H11;f__		
k__Bacteria;p__[Thermi];c__Deinococci;o__Deinococcales;f__Trueperaceae		

**Table S3.** Statistical output of Repeated Measures ANOVAs (rANOVA) used to test differences in alpha diversity (Shannon index), richness and evenness between the different sampling groups (aged and new mucus of *Porites astreoides*, seawater and sediment).

Alpha diversity	numDF	denDF	F-value	p-value	
(Intercept)	1	15	295.49237	<0.0001	***
Sampling groups	3	3	8.24887	0.0584	.

Richness	numDF	denDF	F-value	p-value	
(Intercept)	1	15	160.86729	<0.0001	***
Sampling groups	3	3	5.96926	0.0882	

Evenness	numDF	denDF	F-value	p-value	
(Intercept)	1	15	399.6659	<0.0001	***
Sampling groups	3	3	7.0190	0.0719	

**Table S4.** Statistical output of a permutation-based analysis (PERMDISP) testing homogeneity of multivariate dispersions between the different sampling groups (aged and new mucus of *Porites astreoides*, seawater and sediment).

	Df	Sum Sq	Mean Sq	F value	N.Perm	Pr(>F)
Sampling groups	3	0.07726	0.025752	1.9974	1000	0.1391
Residuals	26	0.33522	0.012893			

**Table S5.** Statistical output of permutational multivariate analysis of variance (PERMANOVA) testing differences in community composition between the different sampling groups in the natural variability experiment (aged and new mucus of *Porites astreoides*, seawater and sediment).

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Sampling groups	3	4.4156	1.47187	9.8224	0.53125	0.001 ***
Residual	26	3.8961	0.14985		0.46875	
Total	29	8.3117			1	

**Table S6.** Prokaryotic families causing most of the divergence in community composition between aged and new mucus of *Porites astreoides*. Cumulative proportion of percent dissimilarity between habitats was determined by Similarity Percentages (SIMPER) analysis. Letters before taxa names stand for: k=kingdom, p=phylum, c=class, o=order, f=family.

Operational Taxonomic Unit	Cumulative Proportion
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Oceanospirillales.f_Endozoicimonaceae	0.26
k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rickettsiales.f_Pelagibacteraceae	0.32
k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae.o_Verrucomicrobiales.f_Verrucomicrobiaceae	0.37
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Vibrionales.f_Vibrionaceae	0.42
k_Bacteria.p_Proteobacteria.c_Betaproteobacteria.o_Burkholderiales.f_Oxalobacteraceae	0.47
k_Bacteria.Other.Other.Other.Other	0.51
k_Bacteria.p_Bacteroidetes.c_Cytophagia.o_Cytophagales.f_Flammeovirgaceae	0.55
k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.o_Rhodobacterales.f_Rhodobacteraceae	0.59
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_Alteromonadaceae	0.62
k_Bacteria.p_Cyanobacteria.c_Synechococcophycideae.o_Synechococcales.f_Synechococcaceae	0.64
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.f_OM60	0.66
k_Bacteria.p_Bacteroidetes.Other.Other.Other	0.67
k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria.Other.Other	0.69
k_Bacteria.p_Fusobacteria.c_Fusobacteriia.o_Fusobacteriales.f_Fusobacteriaceae	0.69
k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria.o_Alteromonadales.Other	0.71

**Table S7.** Statistical output of Tukey HSD post-hoc analysis reporting pairwise comparisons of prokaryotic cell abundances in coral mucus of *Porites astreoides* throughout the aquaria incubation experiment for antibiotic treated colonies (AB) and the control group (nAB). Treatment codes refer to: reef = initial in situ conditions, 0 h = conditions before antibiotics were added, 24h - 120h = time points (in hours) after first antibiotic inoculation. Adjusted p-values reported (Bonferroni method).

	Estimate	Std. Error	z value	Pr(> z )	
reef nAB - reef AB	-0.361085	0.365383	-0.988	1	
0h AB – reef AB	-0.099027	0.365383	-0.271	1	
0h nAB - reef AB	0.20811	0.383217	0.543	1	
24h AB - reef AB	-1.778666	0.447501	-3.975	0.003172	**
24h nAB - reef AB	0.213043	0.365383	0.583	1	
72h AB - reef AB	-1.43858	0.447501	-3.215	0.058762	.
72h nAB - reef AB	0.478678	0.383217	1.249	1	
120h AB - reef AB	-2.351395	0.447501	-5.255	6.68E-06	***
120h nAB - reef AB	-0.209251	0.447501	-0.468	1	
0h AB - reef nAB	0.262058	0.365383	0.717	1	
0h nAB - reef nAB	0.569195	0.383217	1.485	1	
24h AB - reef nAB	-1.417581	0.447501	-3.168	0.069126	.
24h nAB - reef nAB	0.574128	0.365383	1.571	1	
72h AB - reef nAB	-1.077495	0.447501	-2.408	0.722194	
72h nAB - reef nAB	0.839764	0.383217	2.191	1	
120h AB - reef nAB	-1.99031	0.447501	-4.448	0.000391	***
120h nAB - reef nAB	0.151834	0.447501	0.339	1	
0h nAB - 0h AB	0.307137	0.383217	0.801	1	
24h AB - 0h AB	-1.679639	0.447501	-3.753	0.007851	**
24h nAB - 0h AB	0.31207	0.365383	0.854	1	
72h AB - 0h AB	-1.339554	0.447501	-2.993	0.124146	
72h nAB - 0h AB	0.577705	0.383217	1.508	1	
120h AB - 0h AB	-2.252368	0.447501	-5.033	2.17E-05	***
120h nAB - 0h AB	-0.110225	0.447501	-0.246	1	
24h AB - 0h nAB	-1.986776	0.462177	-4.299	0.000773	***
24h nAB - 0h nAB	0.004933	0.383217	0.013	1	
72h AB - 0h nAB	-1.646691	0.462177	-3.563	0.016505	*
72h nAB - 0h nAB	0.270568	0.400257	0.676	1	
120h AB - 0h nAB	-2.559506	0.462177	-5.538	1.38E-06	***
120h nAB - 0h nAB	-0.417362	0.462177	-0.903	1	
24h nAB - 24h AB	1.991709	0.447501	4.451	0.000385	***
72h AB - 24h AB	0.340085	0.51673	0.658	1	
72h nAB - 24h AB	2.257344	0.462177	4.884	4.67E-05	***
120h AB - 24h AB	-0.572729	0.51673	-1.108	1	
120h nAB - 24h AB	1.569414	0.51673	3.037	0.107452	
72h AB - 24h nAB	-1.651623	0.447501	-3.691	0.010061	*
72h nAB - 24h nAB	0.265636	0.383217	0.693	1	
120h AB - 24h nAB	-2.564438	0.447501	-5.731	4.50E-07	***
120h nAB - 24h nAB	-0.422294	0.447501	-0.944	1	
72h nAB – 72h AB	1.917259	0.462177	4.148	0.001507	**
120h AB - 72h AB	-0.912815	0.51673	-1.767	1	
120h nAB - 72h AB	1.229329	0.51673	2.379	0.781067	
120h AB - 72h nAB	-2.830074	0.462177	-6.123	4.12E-08	***
120h nAB - 72h nAB	-0.68793	0.462177	-1.488	1	
120h nAB - 120h AB	2.142144	0.51673	4.146	0.001525	**

**Table S8.** Statistical output of Tukey HSD post-hoc analysis reporting pairwise comparisons of alpha diversity (based on the Shannon Index) in coral mucus associated prokaryotic communities throughout the disturbance experiment for antibiotic treated colonies (AB) and the control group (nAB) of *Porites astreoides*. Treatment codes refer to: reef = initial in situ conditions, AQ = after aquaria incubation, 1-3 = summary of day 1 to day 3 after reintroduction to the reef, 4-28 = summary of day 4 to day 28 on the reef. Adjusted p-values reported (Bonferroni method).

	<b>Estimate</b>	<b>Std. Error</b>	<b>z value</b>	<b>Pr(&gt; z )</b>	
AB_4-28 - AB_1-3	-0.2108	0.21305	-0.989	1	
AQ_AB - AB_1-3	-0.49601	0.2444	-2.029	0.890562	
AQ_nAB - AB_1-3	0.49916	0.25933	1.925	1	
reef - AB_1-3	-0.59303	0.19926	-2.976	0.061289	.
nAB_1-3 - AB_1-3	0.6021	0.19963	3.016	0.053782	.
nAB_4-28 - AB_1-3	0.27557	0.22625	1.218	1	
AQ_AB - AB_4-28	-0.28521	0.27007	-1.056	1	
AQ_nAB - AB_4-28	0.70996	0.28443	2.496	0.263687	
reef - AB_4-28	-0.38223	0.2305	-1.658	1	
nAB_1-3 - AB_4-28	0.81291	0.23131	3.514	0.009255	**
nAB_4-28 - AB_4-28	0.48638	0.25464	1.91	1	
AQ_nAB - AQ_AB	0.99517	0.30846	3.226	0.026342	*
reef - AQ_AB	-0.09702	0.25958	-0.374	1	
nAB_1-3 - AQ_AB	1.09811	0.26029	4.219	0.000516	***
nAB_4-28 - AQ_AB	0.77158	0.28123	2.744	0.127609	
reef - AQ_nAB	-1.09219	0.25958	-4.208	0.000542	***
nAB_1-3 - AQ_nAB	0.10295	0.24452	0.421	1	
nAB_4-28 - AQ_nAB	-0.22358	0.2667	-0.838	1	
nAB_1-3 - reef	1.19513	0.19996	5.977	4.78E-08	***
nAB_4-28 - reef	0.8686	0.22654	3.834	0.002646	**
nAB_4-28 - nAB_1-3	-0.32653	0.20912	-1.561	1	

**Table S9.** Statistical output of Tukey HSD post-hoc analysis reporting pairwise comparisons of richness in coral mucus associated prokaryotic families throughout the disturbance experiment for antibiotic treated colonies (AB) and the control group (nAB) of *Porites astreoides*. Treatment codes refer to: reef = initial in situ conditions, AQ = after aquaria incubation, 1-3 = pooled samples for day 1 to day 3 after reintroduction to the reef, 4-28 = pooled samples for day 4 to day 28 on the reef. Adjusted p-values reported (Bonferroni method).

	<b>Estimate</b>	<b>Std. Error</b>	<b>z value</b>	<b>Pr(&gt; z )</b>	
AB_4-28 - AB_1-3	-22.111	6.233	-3.547	0.008168	**
AQ_AB - AB_1-3	-17.296	7.331	-2.359	0.38453	
AQ_nAB - AB_1-3	17.366	7.903	2.197	0.587697	
reef - AB_1-3	-12.799	5.976	-2.142	0.676471	
nAB_1-3 - AB_1-3	13.81	5.971	2.313	0.435225	
nAB_4-28 - AB_1-3	3.811	6.826	0.558	1	
AQ_AB - AB_4-28	4.815	8.101	0.594	1	
AQ_nAB - AB_4-28	39.477	8.648	4.565	0.000105	***
reef - AB_4-28	9.313	6.915	1.347	1	
nAB_1-3 - AB_4-28	35.921	6.927	5.186	4.52E-06	***
nAB_4-28 - AB_4-28	25.922	7.677	3.377	0.015412	*
AQ_nAB - AQ_AB	34.662	9.463	3.663	0.005239	**
reef - AQ_AB	4.498	7.911	0.569	1	
nAB_1-3 - AQ_AB	31.106	7.922	3.927	0.001808	**
nAB_4-28 - AQ_AB	21.107	8.585	2.459	0.292972	
reef - AQ_nAB	-30.164	7.911	-3.813	0.002885	**
nAB_1-3 - AQ_nAB	-3.556	7.321	-0.486	1	
nAB_4-28 - AQ_nAB	-13.555	8.034	-1.687	1	
nAB_1-3 - reef	26.609	5.982	4.448	0.000182	***
nAB_4-28 - reef	16.609	6.837	2.429	0.317558	
nAB_4-28 - nAB_1-3	-10	6.144	-1.627	1	

**Table S10.** Statistical output of Tukey HSD post-hoc analysis reporting pairwise comparisons of evenness in coral mucus associated prokaryotic families throughout the disturbance experiment for antibiotic treated colonies (AB) and the control group (nAB) of *Porites astreoides*. Treatment codes refer to: reef = initial in situ conditions, AQ = after aquaria incubation, 1-3 = pooled samples for day 1 to day 3 after reintroduction to the reef, 4-28 = pooled samples for day 4 to day 28 on the reef. Adjusted p-values reported (Bonferroni method).

	Estimate	Std. Error	z value	Pr(> z )	
AB_4-28 - AB_1-3	0.0211924	0.0211924	0.503	1	
AQ_AB - AB_1-3	0.074527	0.074527	1.492	1	
AQ_nAB - AB_1-3	0.1322247	0.1322247	2.556	0.29666	
reef - AB_1-3	-0.1228471	-0.1228471	-3.068	0.06036	.
nAB_1-3 - AB_1-3	0.033368	0.033368	0.882	1	
nAB_4-28 - AB_1-3	0.1047823	0.1047823	2.382	0.48222	
AQ_AB - AB_4-28	0.0533346	0.0533346	0.97	1	
AQ_nAB - AB_4-28	0.1110324	0.1110324	1.958	1	
reef - AB_4-28	-0.1440395	-0.1440395	-3.116	0.05141	.
nAB_1-3 - AB_4-28	0.0121756	0.0121756	0.274	1	
nAB_4-28 - AB_4-28	0.08359	0.08359	1.68	1	
AQ_nAB - AQ_AB	0.0576978	0.0576978	0.92	1	
reef - AQ_AB	-0.1973741	-0.1973741	-3.697	0.00612	**
nAB_1-3 - AQ_AB	-0.041159	-0.041159	-0.795	1	
nAB_4-28 - AQ_AB	0.0302554	0.0302554	0.536	1	
reef - AQ_nAB	-0.2550719	-0.2550719	-4.777	4.98E-05	***
nAB_1-3 - AQ_nAB	-0.0988567	-0.0988567	-1.98	1	
nAB_4-28 - AQ_nAB	-0.0274424	-0.0274424	-0.501	1	
nAB_1-3 - reef	0.1562151	0.1562151	3.899	0.0027	**
nAB_4-28 - reef	0.2276295	0.2276295	4.956	2.02E-05	***
nAB_4-28 - nAB_1-3	0.0714143	0.0714143	1.707	1	

**Table S11.** Statistical output of a permutation-based analysis (PERMDISP) testing homogeneity of multivariate dispersions between the different sampling groups in the disturbance experiment of *Porites astreoides*: colonies on the reef, at the end of aquaria incubation (treated vs. control colonies) and after reintroduction (treated vs. control colonies).

	Df	Sum Sq	Mean Sq	F value	N.Perm	Pr(>F)
Sampling groups	4	0.04445	0.0111135	1.2038	1000	0.3163
Residuals	75	0.69238	0.0092317			

**Table S12.** Statistical output of permutational multivariate analysis of variance (PERMANOVA) testing differences in community composition between the different sampling groups in the disturbance experiment of *Porites astreoides*: colonies on the reef, at the end of aquaria incubation (treated vs. control colonies) and after reintroduction (treated vs. control colonies).

	Df	SumsOfSqs	MeanSqs	F.Model	R2	Pr(>F)
Sampling groups	4	5.0762	1.26906	7.151	0.27609	0.001 ***
Residual	75	13.3099	0.17747		0.72391	
Total	79	18.3862			1	



**Table S13.** Prokaryotic families causing most of the divergence in community composition throughout the disturbance experiment of *Porites astreoides*. Cumulative proportion of percent dissimilarity between treatments was determined by Similarity Percentages (SIMPER) analysis. Sections report on prokaryotic families triggering differences between the following sampling groups: (A) antibiotic treated corals after reintroduction to the reef and at initial in situ conditions, (B) antibiotic treated colonies and the control group after reintroduction to the reef and (C) control colonies after reintroduction to the reef and at initial in situ conditions. Letters before taxa names stand for: k=kingdom, p=phylum, c=class, o=order, f=family.

Operational Taxonomic Unit	Cumulative proportion
<b>(A)</b> k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Endozoicimonaceae	0.18
k_Bacteria.Other.Other.Other.Other	0.27
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodobacterales.f__Rhodobacteraceae	0.34
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Oceanospirillaceae	0.42
k_Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Verrucomicrobiaceae	0.48
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Pelagibacteraceae	0.54
k_Bacteria.p__Bacteroidetes.c__Cytophagia.o__Cytophagales.f__Flammeovirgaceae	0.59
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae	0.63
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Alteromonadaceae	0.67
k_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	0.69
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Colwelliaceae	0.71
<b>(B)</b> k_Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Verrucomicrobiaceae	0.17
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodobacterales.f__Rhodobacteraceae	0.25
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Pelagibacteraceae	0.31
k_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	0.36
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae	0.41
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Endozoicimonaceae	0.45
k_Bacteria.p__Bacteroidetes.c__Cytophagia.o__Cytophagales.f__Flammeovirgaceae	0.49
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Alteromonadaceae	0.53
k_Bacteria.p__Cyanobacteria.c__Synechococcophycideae.o__Synechococcales.f__Synechococcaceae	0.57
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Colwelliaceae	0.59
k_Bacteria.p__Bacteroidetes.c__Cytophagia.o__Cytophagales.f__Amoebophilaceae.	0.61
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.Other.Other	0.63
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Thiotrichales.f__Piscirickettsiaceae	0.64
k_Bacteria.p__Verrucomicrobia.c__Opitutae.o__Puniceococcales.f__Puniceococcaceae	0.66
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__OM60	0.67
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.Other.Other	0.68
k_Bacteria.p__Bacteroidetes.c__Flavobacteriia.o__Flavobacteriales.f__Flavobacteriaceae	0.69
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Pseudoalteromonadaceae	0.70
<b>(C)</b> k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__Endozoicimonaceae	0.19
k_Bacteria.Other.Other.Other.Other	0.29
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Pelagibacteraceae	0.36
k_Bacteria.p__Bacteroidetes.c__Cytophagia.o__Cytophagales.f__Flammeovirgaceae	0.42
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Alteromonadaceae	0.47
k_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Oxalobacteraceae	0.51
k_Bacteria.p__Verrucomicrobia.c__Verrucomicrobiae.o__Verrucomicrobiales.f__Verrucomicrobiaceae	0.55
k_Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rhodobacterales.f__Rhodobacteraceae	0.58
k_Bacteria.p__Cyanobacteria.c__Synechococcophycideae.o__Synechococcales.f__Synechococcaceae	0.61
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Vibrionales.f__Vibrionaceae	0.64
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.Other.Other	0.66
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Alteromonadales.f__Colwelliaceae	0.67
k_Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Thiotrichales.f__Piscirickettsiaceae	0.69
k_Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__Burkholderiales.f__Comamonadaceae	0.70

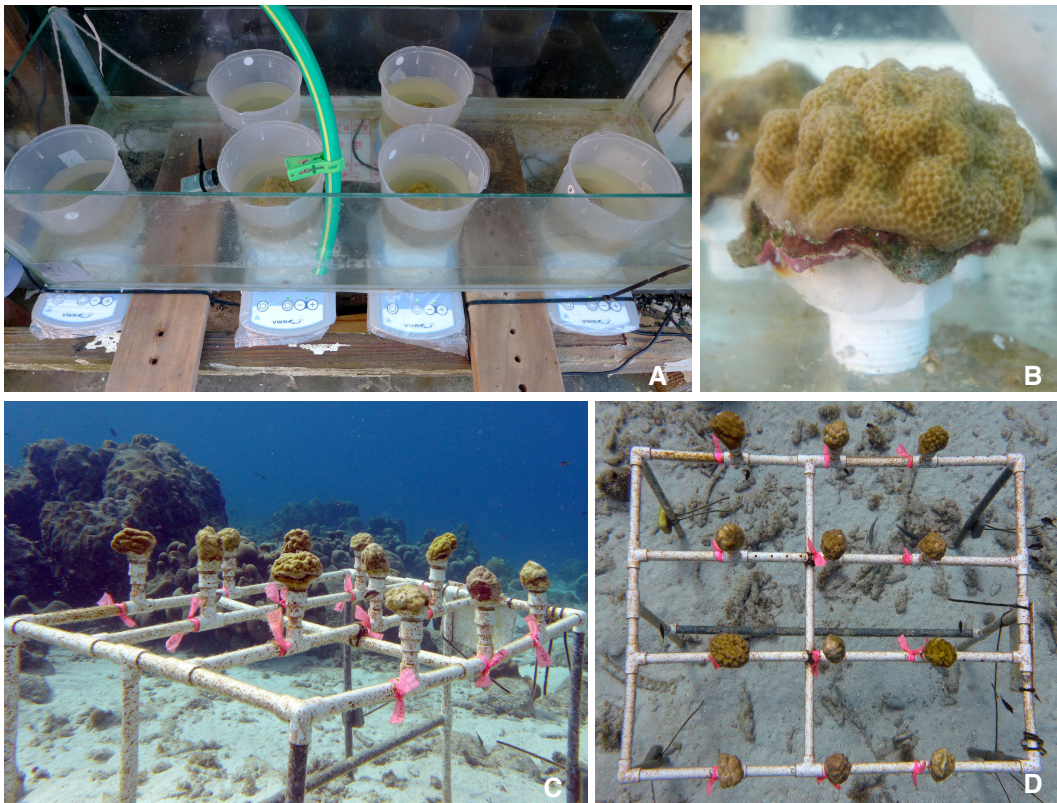
**Table S14.** Indicator prokaryotic families significantly associated with aged and new mucus of *Porites astreoides*, seawater and sediment habitats, based on the Indicator Species Analysis (IndVal). Specificity (A) refers to the probability that the surveyed OTU (family) belongs to the target sampling group given the fact that this specific OTU is present. Fidelity (B), however, describes the probability of detecting the OTU in all samples of the sampling group. Letters before taxa names stand for: k=kingdom, p=phylum, c=class, o=order, f=family.

Habitat	Operational Taxonomic Unit	A	B	stat	p-value		
aged mucus	k_Bacteria.p_Fusobacteria.c_Fusobacteriia. o_Fusobacteriales.f_Fusobacteriaceae	0.8871	0.8333	0.86	0.02797	*	
	k_Bacteria.p_Verrucomicrobia.c_Verrucomicrobiae. o_Verrucomicrobiales.f_Verrucomicrobiaceae	0.725	1	0.851	0.002	**	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Alteromonadales.f__	0.7061	1	0.84	0.004	**	
	k_Bacteria.p_Bacteroidetes.c_Cytophagia. o_Cytophagales.f_Amoebophilaceae.	0.8199	0.8333	0.827	0.005	**	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Alteromonadales.f_Alteromonadaceae	0.6539	1	0.809	0.00599	**	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Vibrionales.f_Vibrionaceae	0.6513	1	0.807	0.02797	*	
	k_Bacteria.p_Bacteroidetes.c_Cytophagia. o_Cytophagales.Other	0.7773	0.8333	0.805	0.004	**	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Alteromonadales.Other	0.7471	0.8333	0.789	0.02298	*	
	k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria. o_Kiloniellales.f__	0.7322	0.8333	0.781	0.00999	**	
	k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria. o_Rhizobiales.f_Phyllobacteriaceae	0.5517	1	0.743	0.02298	*	
	k_Bacteria.p_Bacteroidetes.c_Cytophagia.o_Cytophag ales. f_Flammeovirgaceae	0.5457	1	0.739	0.03596	*	
	k_Bacteria.p_Cyanobacteria.c_Synechococcophycideae. o_Pseudanabaenales.f_Pseudanabaenaceae	0.6383	0.8333	0.729	0.02198	*	
	k_Bacteria.p_Cyanobacteria.Other.Other.Other	0.5274	1	0.726	0.02298	*	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_HOC36.f__	0.7772	0.6667	0.72	0.01598	*	
	k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria. o_Rhodobacterales.f_Rhodobacteraceae	0.4949	1	0.704	0.03297	*	
	k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria. o_Bdellovibrionales.f_Bacteriovoracaceae	0.5908	0.8333	0.702	0.02797	*	
	k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria. o_Rhizobiales.f_Hyphomicrobiaceae	0.5847	0.8333	0.698	0.03297	*	
	k_Bacteria.p_Gemmatimonadetes.c_Gemm.4.o__f__	0.9233	0.5	0.679	0.01199	*	
	k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria. o_Rhodobacterales.f_Hyphomonadaceae	0.9011	0.5	0.671	0.03596	*	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Oceanospirillales.f_Oleiphilaceae	0.8838	0.5	0.665	0.02997	*	
	new mucus	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Oceanospirillales.f_Endozoicimonaceae	0.9091	0.9286	0.919	0.000999	***
		k_Bacteria.p_Proteobacteria.c_Betaproteobacteria. o_Burkholderiales.f_Oxalobacteraceae	0.6739	1	0.821	0.010989	*
		k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Pseudomonadales.f_Pseudomonadaceae	0.9897	0.8333	0.908	0.002997	**
seawater	k_Bacteria.p_Cyanobacteria.c_Synechococcophycideae. o_Synechococcales.f_Synechococcaceae	0.809	1	0.899	0.000999	***	
	k_Bacteria.p_Proteobacteria.c_Deltaproteobacteria. o_Sva0853.f__	0.9183	0.8333	0.875	0.000999	***	
	k_Bacteria.p_SAR406.c_AB16.o_Arctic96B.7. f_A714017	0.8713	0.8333	0.852	0.015984	*	
	k_Bacteria.p_Proteobacteria.c_Gammaproteobacteria. o_Oceanospirillales.f_Halomonadaceae	0.7086	1	0.842	0.000999	***	
	k_Bacteria.p_Proteobacteria.c_Alphaproteobacteria. o__f__	0.6743	1	0.821	0.001998	**	

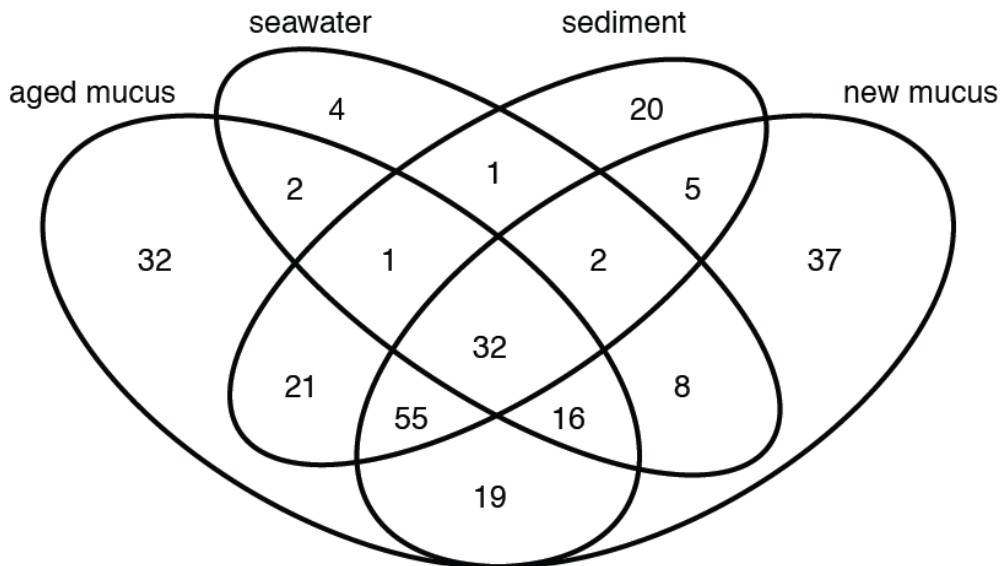
	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__Pelagibacteraceae	0.6458	1	0.804	0.000999	***
	k__Bacteria.p__Proteobacteria.c__Betaproteobacteria.o__MWH.UniP1.f__	0.9069	0.6667	0.778	0.036963	*
	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__	0.5553	1	0.745	0.021978	*
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Legionellales.f__Coxiellaceae	0.7944	0.6667	0.728	0.025974	*
	k__Bacteria.p__Proteobacteria.c__Alphaproteobacteria.o__Rickettsiales.f__AEGEAN_112	0.5288	0.8333	0.664	0.040959	*
<b>sediment</b>	k__Bacteria.p__Cyanobacteria.c__Oscillatoriothycidaeae.o__Chroococcales.f__Xenococcaceae	0.9629	1	0.981	0.000999	***
	k__Bacteria.p__Bacteroidetes.c__Rhodothermi..o__Rhodothermales.f__Rhodothermaceae	0.9295	1	0.964	0.000999	***
	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfobacterales.f__Desulfobacteraceae	0.9062	1	0.952	0.000999	***
	k__Bacteria.p__Actinobacteria.c__Acidimicrobiia.o__Acidimicrobiales.f__koll13	0.8768	1	0.936	0.000999	***
	k__Bacteria.p__Acidobacteria.c__Sva0725.o__Sva0725.f__	0.8656	1	0.93	0.000999	***
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__HTCC2188.f__HTCC2089	0.7979	1	0.893	0.001998	**
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Thiotrichales.f__Piscirickettsiaceae	0.7893	1	0.888	0.000999	***
	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.Other.Other	0.782	1	0.884	0.000999	***
	k__Bacteria.p__Cyanobacteria.c__Oscillatoriothycidaeae.o__Chroococcales.f__Cyanobacteriaceae	0.7752	1	0.88	0.001998	**
	k__Bacteria.p__Bacteroidetes.c__Bacteroidia.o__Bacteroidales.f__	0.7338	1	0.857	0.002997	**
	k__Bacteria.p__Actinobacteria.c__Acidimicrobiia.o__Acidimicrobiales.f__C111	0.7229	1	0.85	0.003996	**
	k__Bacteria.p__Gemmatimonadetes.c__Gemm.2.o__f__	0.7108	1	0.843	0.002997	**
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Oceanospirillales.f__	0.6896	1	0.83	0.002997	**
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Chromatiales.f__	0.6854	1	0.828	0.010989	*
	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Myxococcales.f__	0.6737	1	0.821	0.003996	**
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__f__	0.6656	1	0.816	0.008991	**
	k__Bacteria.p__Spirochaetes.c__Spirochaetes.o__Spirochaetales.f__Spirochaetaceae	0.8207	0.75	0.785	0.011988	*
	k__Bacteria.p__Acidobacteria.c__RB25.o__f__	0.8176	0.75	0.783	0.005994	**
	k__Bacteria.p__Chloroflexi.c__Anaerolineae.o__Caldilineales.f__Caldilineaceae	0.753	0.75	0.752	0.004995	**
	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__Desulfobacterales.f__Desulfobulbaceae	0.5445	1	0.738	0.020979	*
	k__Bacteria.p__Proteobacteria.c__Deltaproteobacteria.o__NB1.j.f__NB1.i	0.6981	0.75	0.724	0.020979	*
	k__Bacteria.p__Cyanobacteria.c__Oscillatoriothycidaeae.o__Chroococcales.Other	0.5194	1	0.721	0.023976	*
	k__Bacteria.p__Proteobacteria.c__Gammaproteobacteria.o__Chromatiales.Other	0.668	0.75	0.708	0.017982	*
	k__Archaea.p__Euryarchaeota.c__Thermoplasmata.o__E2.	1	0.5	0.707	0.012987	*



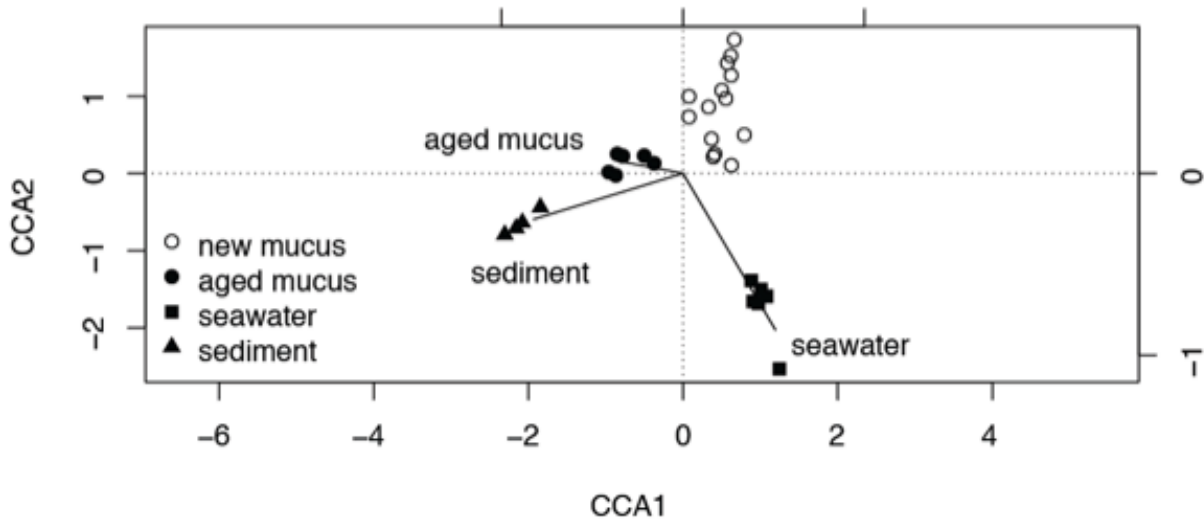
**Figure S1.** In situ impression of the surface mucus layer of *Porites astreoides* showing an overview (top) and a close-up (bottom) of the same colony at two different time points, with new mucus (left panels) and with a conspicuous, aged mucus sheet (right panels).



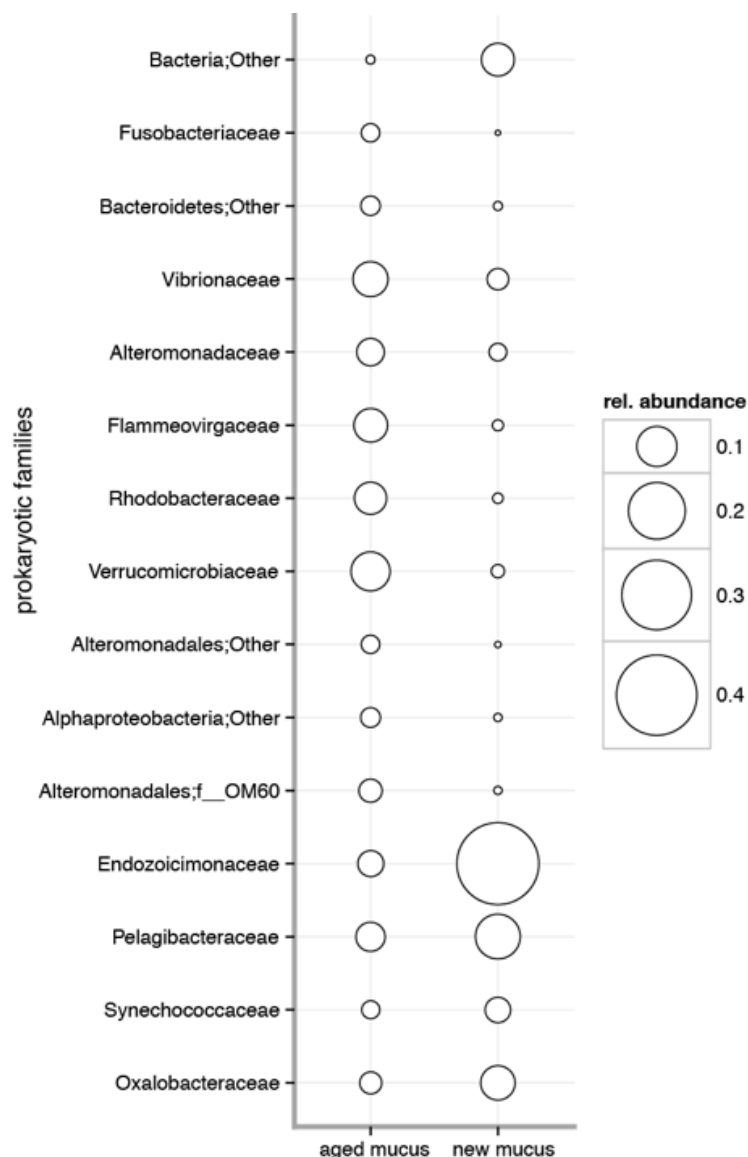
**Figure S2.** Experimental setup for the disturbance experiment of *Porites astreoides* mucus microbiome. Pictures were taken in the aquaria (A,B) and underwater at the sampling site (C,D). Colonies of *P. astreoides* were incubated in transparent plastic beakers with a mix of antibiotics and seawater (A). Colonies were mounted on PVC screw caps (B) that were used to fix antibiotic treated and control colonies to a rack at 5 m depth (C,D).



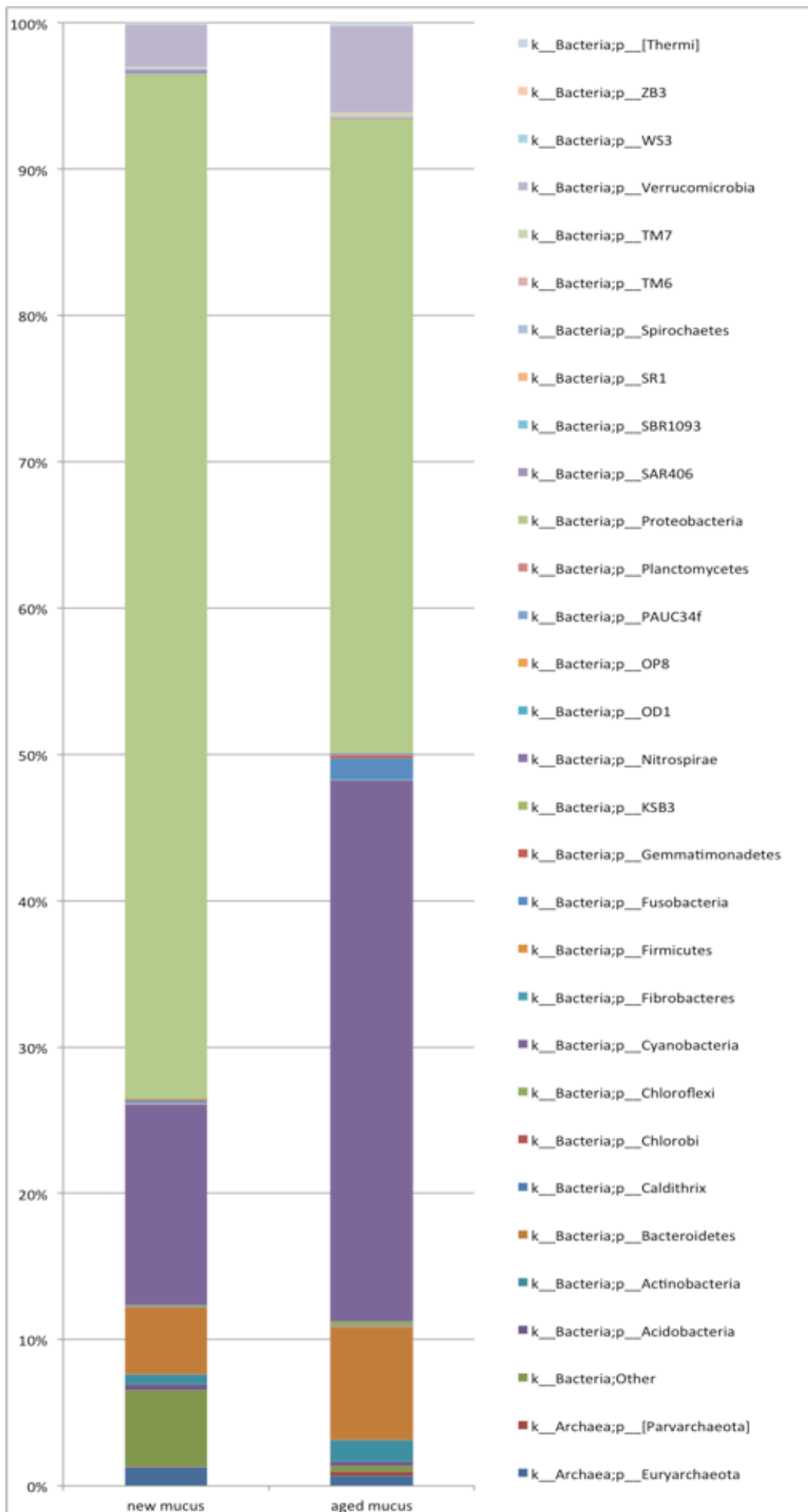
**Figure S3.** Venn diagram displaying absolute numbers of unique, shared, and ubiquitous prokaryotic families in aged and new mucus of *Porites astreoides*, in seawater and sediment samples.



**Figure S4.** Canonical Correspondence Analysis (CCA) showing separation of prokaryotic communities regarding their habitat (new and aged mucus of *Porites astreoides*, seawater and sediment). The first and second axes of the ordination explain 47% and 34%, respectively, of the observed variation in prokaryotic community structure among habitats.

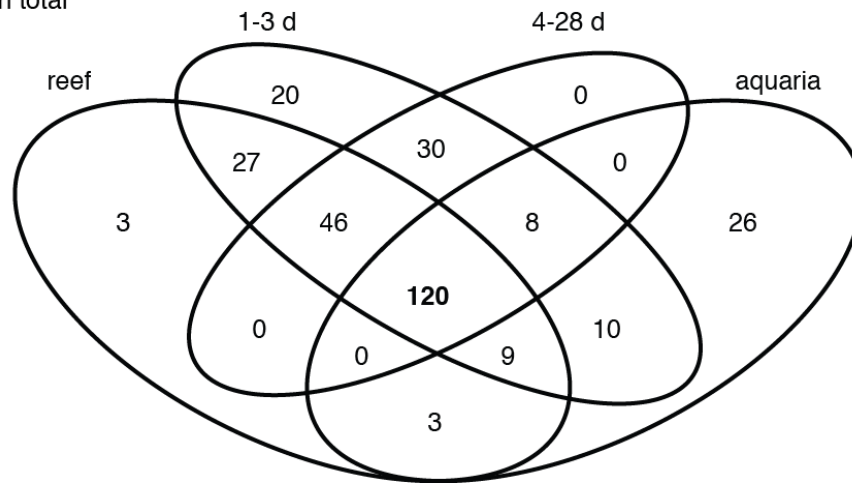


**Figure S5.** Relative abundance of prokaryotic families explaining 70% of community dissimilarity (as determined by Similarity Percentages analysis) between aged and new mucus of *Porites astreoides*.

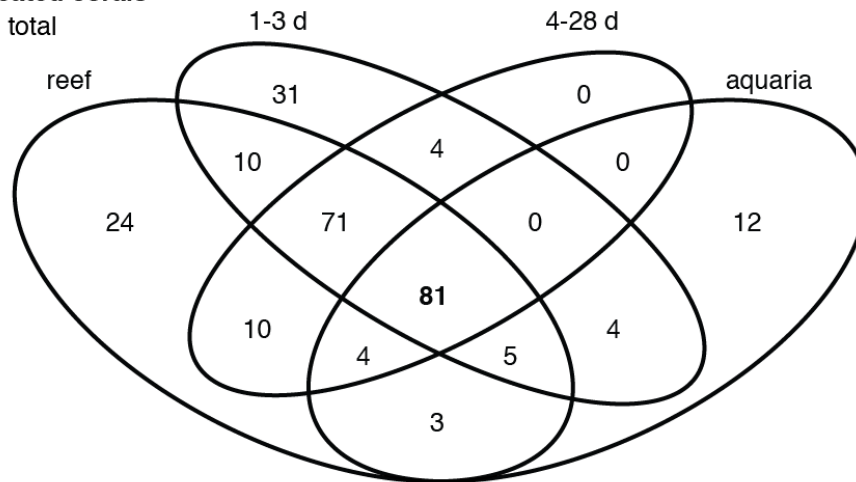


**Figure S6.** Relative abundance of phyla associated with new and aged mucus of *Porites astreoides*. Letters before taxa names stand for: k=kingdom, p=phylum.

a) **control group**  
304 OTUs in total

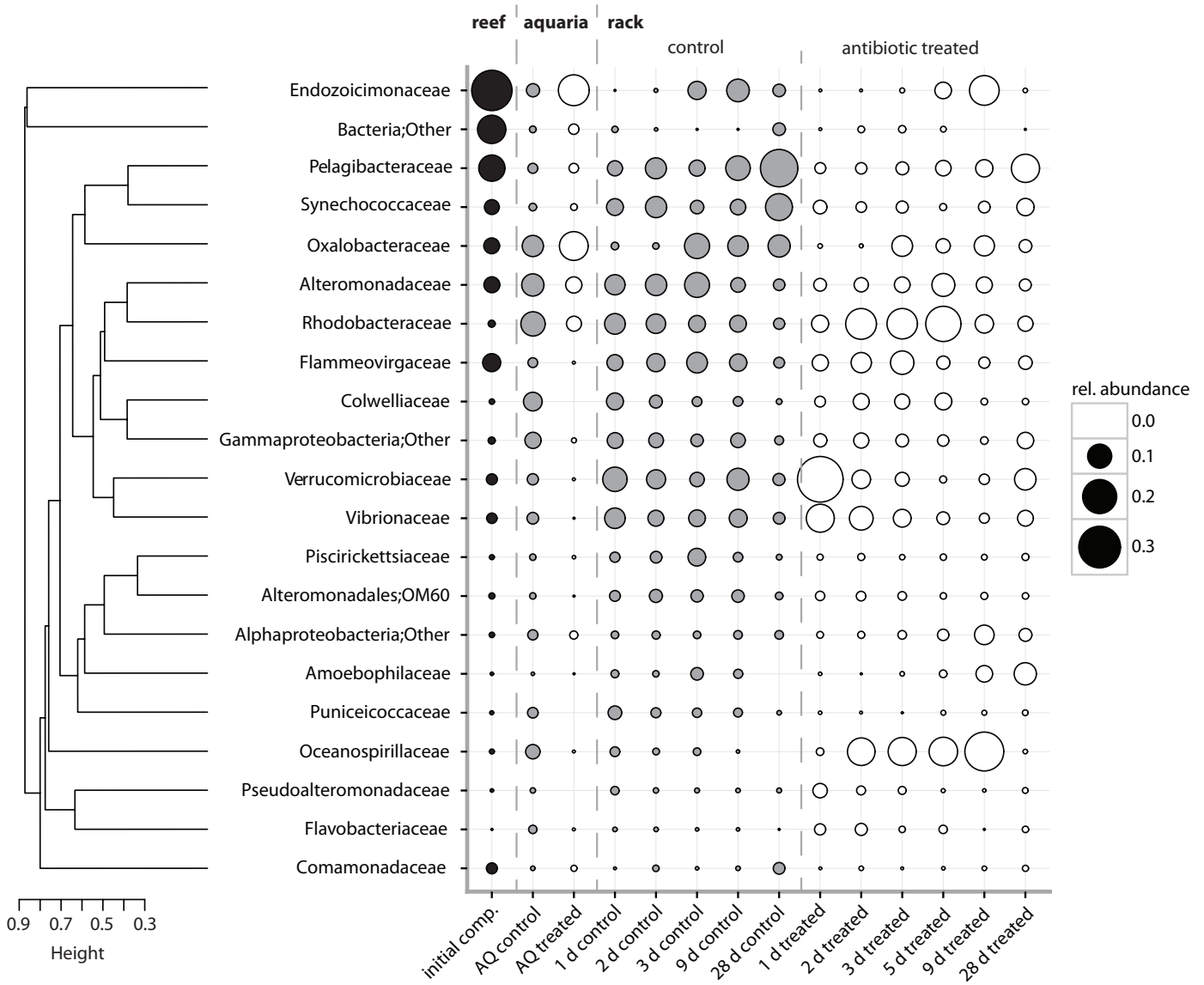


b) **antibiotic treated corals**  
359 OTUs in total

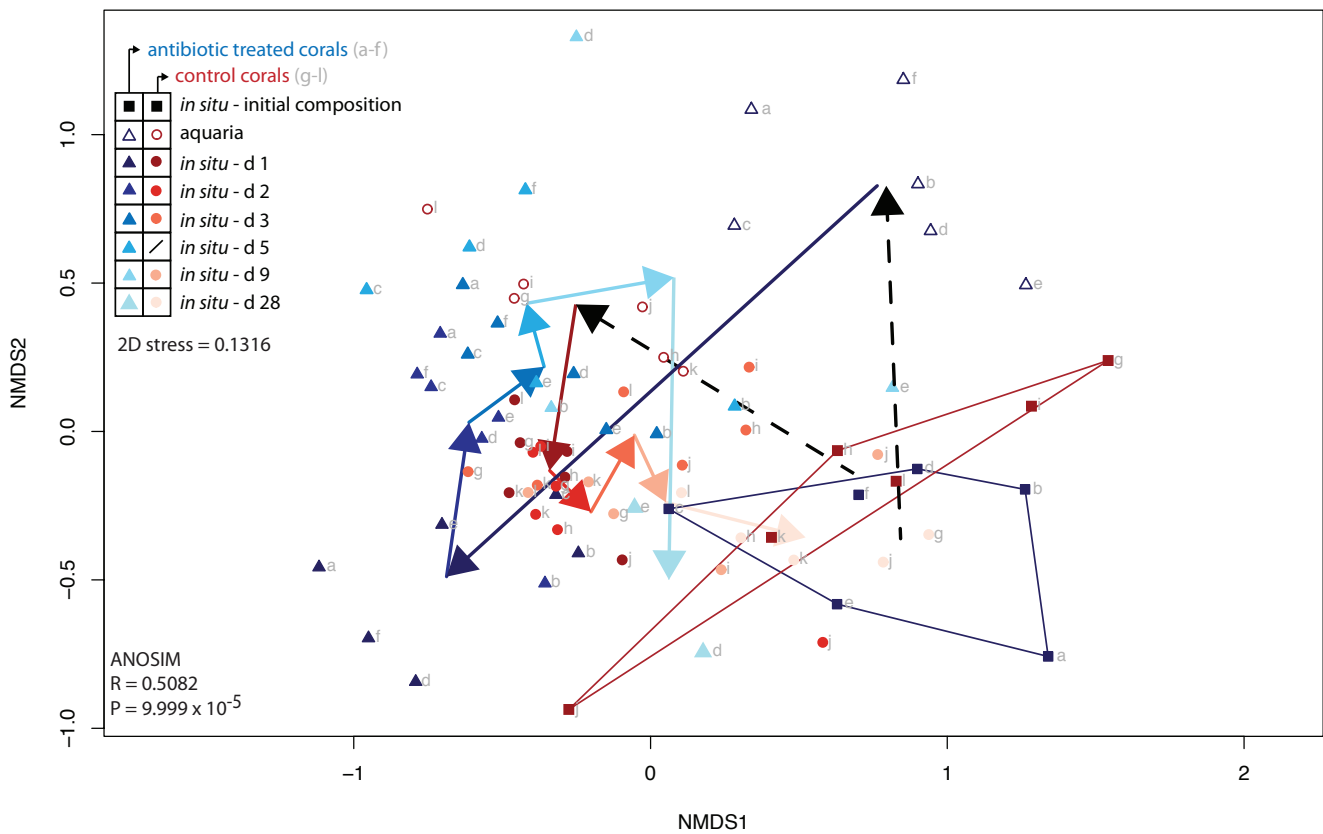


**Figure S7.** Venn diagram displaying absolute numbers of unique, shared, and ubiquitous prokaryotic families (OTUs) for antibiotic treated colonies a) and the control group b) throughout the disturbance experiment of *Porites astreoides*. Treatment codes refer to: reef = initial in situ conditions, aquaria = at the end of aquaria incubation, 1-3d and 4-28d concatenate samples collected on the first 3 consecutive days and between day 4 to day 28, respectively, after the reintroduction to the reef.

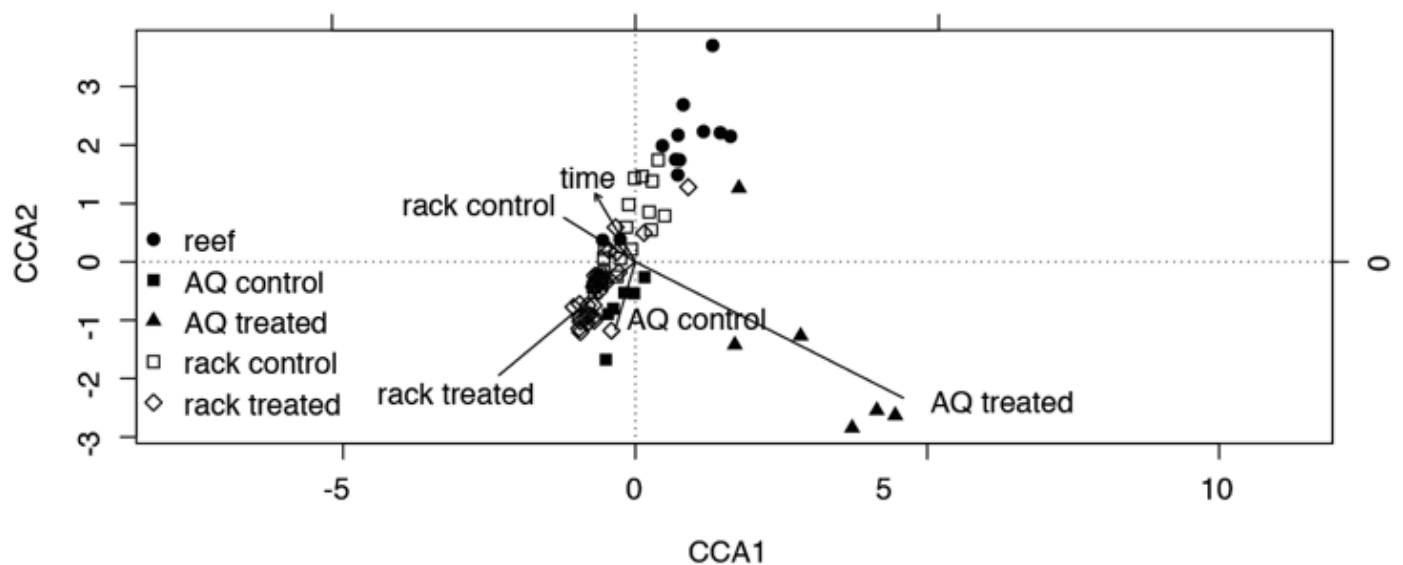




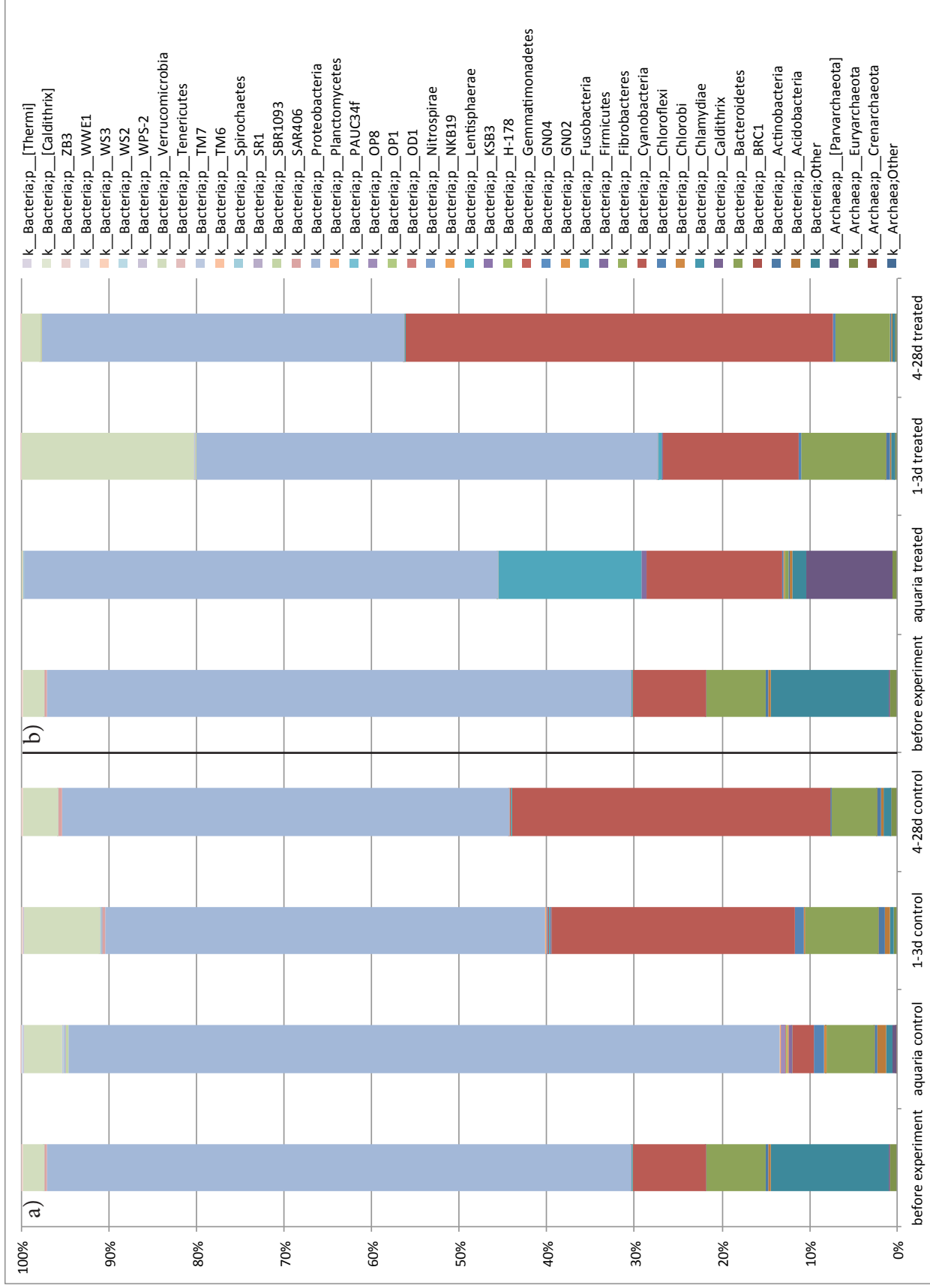
**Figure S8.** Relative abundance of prokaryotic families causing community dissimilarity (as determined by Similarity Percentages analysis) throughout the disturbance experiment of *Porites astreoides*. Prokaryotic families are ordered according to (Bray Curtis) similarity in their distribution among samples. Treatment codes refer to: reef = in situ condition, AQ = at the end of aquaria incubation, rack = day 1 to day 28 after reintroduction to the reef.



**Figure S9.** Prokaryotic mucus re-colonization after antibiotics disturbance: Non-metric multidimensional scaling (nMDS) plot of the Bray-Curtis-based dissimilarity matrix of prokaryotic communities colonizing the mucus of *Porites astreoides* and their shifts after a disturbance event. The successional path, here represented by arrows was reconstructed based on the position of group centroids and follows each group of corals (antibiotic-treated, a-f; control, g-l) at a particular time (indicated by color gradient). The starting point ‘in situ - initial community composition’ represents the original in situ state, followed by the shift in the community composition in the aquaria incubation (dashed arrows) and finally describing the successional path over 28 days observed in the field after the two experimental groups of corals were brought back to the reef (normal arrows). Prokaryotic community structure is given for individual colonies.



**Figure S10.** Canonical Correspondence Analysis (CCA) showing separation of prokaryotic communities associated with coral mucus of *Porites astreoides* throughout the disturbance experiment for antibiotic treated colonies and the control group. Treatment codes refer to: reef = initial in situ condition, AQ = at the end of aquaria incubation, rack = pooled samples for day 1 to day 28 after reintroduction to the reef. The first and second axes of the ordination explain 39% and 28%, respectively, of the observed variation in prokaryotic community structure among treatments.



**Figure S11.** Relative abundance of phyla associated with mucus of a) control colonies and b) antibiotic treated corals throughout the disturbance experiment. Treatment codes refer to: before experiment = initial in situ conditions, aquaria = at the end of aquaria incubation, 1-3d and 4-28d concatenate samples collected on the first 3 consecutive days and between day 4 to day 28, respectively, after the reintroduction to the reef.

