

Additional File

Spotting disease disrupts the microbiome of infected sea urchins

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Table S1. Relative abundance of phyla on the global surface microbiome samples¹

Phylum	D1S	D2S	D3S	D4S	H1S	H2S	H3S	H4S	fSW²
Verrucomicrobiota	2.51 ³	5.53	13.19	7.33	35.49	16.62	4.83	4.14	13.31
Planctomycetota	1.13	0.97	5.37	4.62	7.92	10.98	1.71	2.36	24.68
Bacteroidota	53.32	42.19	5.37	61.12	10.69	10.39	0.47	2.51	2.40
Proteobacteria	42.66	33.89	75.75	26.37	43.69	60.53	92.72	90.41	58.63
Patescibacteria	0.38	15.35	0.00	0.25	0.78	1.19	0.23	0.18	0.13
Actinobacteriota	0.00	0.00	0.24	0.12	0.00	0.00	0.00	0.03	0.15
Firmicutes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria	0.00	0.97	0.08	0.18	0.11	0.15	0.00	0.03	0.70
Campylobacterota	0.00	1.11	0.00	0.00	0.17	0.00	0.04	0.12	0.00
Cyanobacteria	0.00	0.00	0.00	0.00	1.16	0.15	0.00	0.21	0.00

¹Abbreviations are: D, diseased animals 1-4; H, healthy animals 1-4; S; Surface, global surface microbiome samples. See also Table 1 in the main paper.

²Average of the taxa identified by filtering two sea water samples, fSW1 and fSW2.

³Percent relative abundance per sample.

Table S2. Genera with an average relative abundance > 0.1% shown as the relative abundance per sample for the global surface microbiome samples

Species	D1S ¹	D2S	D3S	D4S	H1S	H2S	H3S	H4S	fSW ¹
<i>Psychromonas</i>	4.77 ²	5.39	41.86	16.02	26.52	33.38	53.99	86.80	11.44
HOC36	29.86	4.15	6.08	3.14	7.09	2.67	2.06	0.98	42.76
<i>Colwellia</i>	1.51	9.41	22.20	5.98	8.53	23.15	34.60	1.96	2.66
Bacteroidia	1.51	4.29	3.48	59.77	10.30	9.94	0.47	2.51	1.83
Pir4 lineage	0.88	0.97	5.29	4.62	3.93	6.38	1.71	1.62	23.67
<i>Cyclobacteriaceae</i>	19.45	26.42	0.39	0.00	0.00	0.00	0.00	0.00	0.00
BD2-3	0.50	0.83	1.42	5.48	23.98	5.34	0.23	1.59	1.53
<i>Cryomorphaceae</i>	24.72	5.81	1.26	0.00	0.39	0.30	0.00	0.00	0.57
<i>Methylacidiphilaceae</i>	1.76	3.32	0.63	0.18	1.77	3.12	1.79	0.52	4.59
JGI 0000069-P22	0.38	15.35	0.00	0.25	0.78	1.19	0.23	0.18	0.13
<i>Rubritalea</i>	0.25	0.69	3.55	0.55	0.83	2.67	1.28	0.92	2.91
<i>Persicirhabdus</i>	0.00	0.00	6.08	0.31	1.22	1.63	1.25	0.55	2.52
MSBL3	0.00	0.69	1.26	0.37	7.36	3.56	0.19	0.55	0.57
<i>Lutibacter</i>	7.65	5.67	0.24	0.00	0.00	0.00	0.00	0.00	0.00
vadinHA49	0.25	0.00	0.00	0.00	3.99	4.60	0.00	0.74	1.00
<i>Cellvibrionaceae</i>	3.64	5.67	1.18	0.00	0.39	0.00	0.00	0.00	0.00
<i>Pseudoalteromonas</i>	0.00	0.00	2.92	0.06	0.50	0.74	1.60	0.31	0.22
Gammaproteobacteria	1.13	0.28	0.32	0.12	0.33	0.30	0.23	0.12	1.55
<i>Pseudoteredinibacter</i>	0.88	4.01	0.47	0.00	0.00	0.00	0.00	0.00	0.00
<i>Pseudophaeobacter</i>	0.63	2.77	0.32	0.00	0.06	0.00	0.00	0.00	0.00
<i>Chlamydiaceae</i>	0.00	0.00	0.24	0.43	0.33	0.30	0.08	0.00	1.19
Bacteria ³	0.00	0.97	0.08	0.18	0.11	0.15	0.00	0.03	0.70
Candidatus <i>Photodesmus</i>	0.13	0.41	0.00	0.80	0.06	0.15	0.00	0.03	0.00
Gastranaerophilales	0.00	0.00	0.00	0.00	1.16	0.15	0.00	0.21	0.00
Bacteroidales	0.00	0.00	0.00	1.36	0.00	0.15	0.00	0.00	0.00
<i>Rhodobacteraceae</i>	0.13	1.24	0.00	0.00	0.00	0.00	0.04	0.03	0.00
<i>Halarcobacter</i>	0.00	1.11	0.00	0.00	0.17	0.00	0.04	0.12	0.00
<i>Vibrio</i>	0.00	0.55	0.16	0.25	0.00	0.00	0.08	0.00	0.00

¹See Table S1 for definitions of abbreviations and Table 1 in the main paper.

²Percent relative abundance per sample.

³Bacteria denotes taxa that could not be assigned to a phylum.

Table S3. Significantly differentially abundant taxa as identified by LEfSe for diseased and healthy global surface microbiome samples

Taxa	Enriched group	LDA score ¹	<i>p</i> value	<i>p</i> adjusted
Gastranaerophilales	Healthy	3.54322854	0.0472209	0.0472209
Enterobacterales	Healthy	3.18015404	0.03839358	0.03839358
Cyclobacteriaceae	Diseased	5.09216384	0.0472209	0.0472209
<i>Lutibacter</i>	Diseased	4.57012195	0.0472209	0.0472209
<i>Pseudoteredinibacter</i>	Diseased	4.16907426	0.0472209	0.0472209

¹The linear discriminant analysis (LDA) threshold was set to 2.

Table S4. Relative abundance of phyla for the LBW and LS samples

Phylum	D1 LBW ¹	D2a LBW	D2b LBW	D3 LBW	D1 LS	D2a LS	D2b LS	D3 LS	D4 LS	sSW ¹	fSW ¹
Verrucomicrobiota	0.01 ²	0.00	0.04	0.00	0.24	0.88	0.00	0.00	2.71	0.00	13.31
Planctomycetota	0.01	0.00	0.22	0.00	0.00	4.05	0.00	0.22	0.81	0.00	24.68
Bacteroidota	78.42	17.25	91.17	28.03	79.86	53.63	69.61	92.30	6.50	0.00	2.40
Proteobacteria	21.36	80.77	7.88	68.17	19.62	40.66	25.43	7.48	88.89	76.99	58.63
Patascibacteria	0.07	0.44	0.69	0.71	0.24	0.41	4.24	0.00	0.00	0.00	0.13
Actinobacteriota	0.03	0.00	0.00	0.24	0.00	0.05	0.00	0.00	1.08	23.01	0.15
Firmicutes	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Bacteria ³	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.70
Campylobacterota	0.10	1.54	0.00	2.85	0.05	0.31	0.72	0.00	0.00	0.00	0.00
Cyanobacteria	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

¹Definitions of sample name abbreviations can be found in Table 1 in the main paper and Table S1.

²Percent relative abundance per sample.

³Bacteria denotes taxa that could not be assigned to a phylum.

Table S5. Genera with an average relative abundance of > 0.1% in the LBW and LS microbiome samples

Species	D1 LBW ¹	D2a LBW	D2b LBW	D3 LBW	D1LS	D2aLS	D2bLS	D3LS	D4LS	sSW	fSW ²
<i>Cyclobacteriaceae</i>	62.23 ³	13.24	73.55	16.62	41.22	45.97	40.57	66.70	1.11	0.00	0.00
<i>Cryomorphaceae</i>	15.43	3.49	20.83	15.40	25.80	5.92	19.07	20.45	5.57	0.00	0.57
Candidatus <i>Photodesmus</i>	0.39	47.45	1.88	39.65	0.00	0.47	0.16	0.00	0.00	0.00	0.00
HOC36	0.03	0.00	0.05	0.00	0.67	1.77	0.57	1.70	22.28	8.52	42.76
<i>Psychromonas</i>	10.29	7.28	0.09	0.00	0.14	0.21	0.10	0.11	1.39	43.75	11.44
<i>Cellvibrionaceae</i>	0.38	0.19	0.40	0.00	9.19	30.08	7.08	1.93	20.06	22.44	0.00
<i>Vibrio</i>	0.64	24.96	0.99	22.75	0.19	1.77	1.29	0.57	0.00	0.00	0.00
Pir4 lineage	0.01	0.00	0.00	0.00	0.00	0.26	0.00	0.23	0.56	0.00	23.67
<i>Pseudophaeobacter</i>	0.10	0.05	0.00	0.00	3.54	2.08	8.06	0.34	31.48	1.42	0.00
<i>Lutibacter</i>	2.03	0.56	0.32	0.14	12.88	1.82	9.92	6.82	0.00	0.00	0.00
<i>Pseudoteredinibacter</i>	1.81	0.10	0.69	1.09	4.64	1.71	5.53	0.91	10.31	0.00	0.00
<i>Microbacterium</i>	0.03	0.00	0.00	0.27	0.00	0.05	0.00	0.00	1.11	23.01	0.07
<i>Colwellia</i>	6.37	0.41	0.00	0.00	0.86	0.57	0.67	0.00	1.67	0.00	2.66
<i>Methylacidiphilaceae</i>	0.00	0.00	0.00	0.00	0.00	0.16	0.00	0.00	0.00	0.00	4.59
JGI 0000069-P22	0.07	0.44	0.71	0.82	0.24	0.42	4.24	0.00	0.00	0.00	0.13
<i>Halarcobacter</i>	0.11	1.55	0.00	3.27	0.05	0.31	0.72	0.00	0.00	0.00	0.00
<i>Rubritalea</i>	0.01	0.00	0.00	0.00	0.24	0.10	0.00	0.00	1.11	0.00	2.91
<i>Persicirhabdus</i>	0.00	0.00	0.00	0.00	0.00	0.62	0.00	0.00	1.39	0.00	2.52
Gammaproteobacteria	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.11	1.11	0.85	1.55
<i>Rhodobacteraceae</i>	0.00	0.24	0.21	0.00	0.19	1.56	1.86	0.11	0.00	0.00	0.00
<i>Gimesiaceae</i>	0.00	0.00	0.23	0.00	0.00	3.79	0.00	0.00	0.28	0.00	0.00
Bacteroidia	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.00	1.83
BD2-3	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.53
<i>Chlamydiaceae</i>	0.00	0.00	0.04	0.00	0.00	0.00	0.00	0.00	0.28	0.00	1.19
vadinHA49	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.00

¹Definitions of sample name abbreviations can be found in Table 1 in the main paper and Table S1.

²Average of the taxa identified by filtering two sea water samples, fSW1 and fSW2.

³Percent relative abundance per sample.

Table S6. Significantly differentially abundant taxa as identified by LEFSe for the LBW and LS microbiome samples

Taxa	Enriched group	LDA score¹	<i>p</i> value	<i>p</i> adjusted
Cellvibrionaceae	LS ²	5.17687914	0.00255609	0.00255609
<i>Pseudophaeobacter</i>	LS	4.81626803	0.00202884	0.00202884
HOC36	LS	4.70352662	0.00202884	0.00202884
Gammaproteobacteria	LS	3.55714684	0.0145743	0.0145743
<i>Roseobacter</i>	LS	3.27102339	0.0145743	0.0145743
Candidatus <i>Photodesmus</i>	LBW ³	5.19269004	0.01248356	0.01248356

¹The linear discriminant analysis (LDA) threshold was set to 2.

²LS; Lesion surface samples.

³LBW; Lesion body wall samples.

Table S7. Relative abundance of phyla in the tissue microbiome samples

Phylum	D1 ¹	D2a	D2b	D3	D1	D2	D3	D1	D2	D3	D1	D2	D3	H1	H2	H3	H1	H2	H3
	LBW	LBW	LBW	LBW	BW	BW	BW	CF	CF	CF	CF	CF	CF	BW	BW	BW	CF	CF	CF
Verrucomicrobiota	0.03 ²	0.00	0.04	0.00	0.06	0.25	0.00	0.00	0.00	0.00	1.25	0.01	20.80	12.34	19.87	0.00	37.41	0.00	0.00
Planctomycetota	0.03	0.00	0.20	0.00	0.00	0.42	0.00	0.00	0.19	0.00	0.00	0.00	1.13	0.19	1.47	0.00	4.70	0.00	0.00
Bacteroidota	56.86	14.32	90.93	28.03	2.68	3.30	0.00	4.35	9.49	3.32	0.43	12.51	9.40	3.70	13.91	33.36	3.70	13.91	33.36
Proteobacteria	42.70	82.78	8.16	68.17	96.36	86.28	64.16	21.74	76.28	92.56	70.12	62.08	58.83	5.17	72.61	4.70	5.17	72.61	4.70
Patescibacteria	0.13	0.48	0.67	0.71	0.10	3.02	0.00	0.00	8.81	0.00	0.00	0.00	0.00	0.00	0.00	0.05	0.00	0.00	0.05
Actinobacteriota	0.05	0.00	0.00	0.24	0.10	5.45	1.51	0.00	4.26	2.68	18.97	3.49	16.78	6.35	13.48	19.69	6.35	13.48	19.69
Firmicutes	0.00	0.00	0.00	0.00	0.12	0.00	33.47	73.91	0.10	0.00	10.46	0.00	63.43	0.00	0.00	0.00	63.43	0.00	0.00
Bacteria	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Campylobacterota	0.21	2.41	0.00	2.85	0.59	1.29	0.87	0.00	0.87	0.19	0.00	0.00	0.00	0.01	0.00	0.10	0.01	0.00	0.10
Cyanobacteria	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	2.45	0.00	0.00	0.00	0.00	0.00	0.00

¹Definitions of sample name abbreviations can be found in Table 1 in the main paper and Table S1.

²Percent relative abundance per sample.

Table S8. Genera with an average relative abundance of > 0.1% in the tissue microbiome samples

Species	D1			D2			D3			H1			H2			H3		
	LBW ¹	LBW	CF	LBW	LBW	CF	LBW	LBW	CF	LBW	LBW	CF	LBW	LBW	CF	LBW	LBW	CF
<i>Psychromonas</i>	20.57 ²	11.40	0.08	0.00	0.00	0.00	36.17	81.01	1.73	8.55	24.95	6.47	9.09	58.84	3.93	1.87	64.00	4.08
<i>Paenibacillus</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.12	0.00	47.40	20.33	0.00	0.00	72.73	0.11	0.00	50.02	0.00	0.00
<i>Microbacterium</i>	0.05	0.00	0.00	0.27	0.10	0.00	0.10	5.43	4.11	49.21	4.34	23.59	0.00	4.45	16.29	6.17	14.86	19.66
Cyclobacteriaceae	24.51	10.59	73.01	16.62	0.00	0.00	0.65	1.33	0.00	0.00	0.00	0.00	0.00	3.00	0.00	0.00	0.00	0.00
Cryomorphaceae	30.85	3.56	21.30	15.40	0.00	0.00	0.58	0.34	0.00	0.18	9.79	23.94	4.55	0.56	0.00	0.00	0.00	0.00
<i>Colwellia</i>	12.73	0.65	0.00	0.00	0.00	0.00	58.37	0.34	0.00	0.00	0.00	0.00	4.55	0.56	0.00	0.00	0.00	0.49
<i>Candidatus</i>	0.79	40.50	1.98	39.65	1.59	0.00	1.53	1.53	0.22	0.00	0.00	0.00	0.00	3.67	14.89	0.00	0.00	0.05
<i>Photodesmus</i>	1.28	29.59	1.03	22.75	0.14	0.00	0.14	0.57	0.22	0.22	0.00	0.04	0.00	3.34	23.31	0.02	0.00	0.05
<i>Vibrio</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.02	20.16	13.62	0.00	0.00	0.00	19.40	0.00	27.86
BD2-3	0.00	0.00	0.00	0.00	0.00	0.00	2.04	0.00	0.00	1.15	17.63	13.82	0.00	0.00	0.00	3.74	5.71	33.28
Bacteroidia	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	16.23	6.14	0.00	4.55	0.00	0.00	14.00	0.00	0.00
Paenibacillaceae	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.11	0.00	0.00
<i>Bacillus</i>	0.76	0.08	0.37	0.00	0.00	0.00	0.06	0.00	0.00	4.52	11.02	3.56	0.00	1.56	0.28	2.24	0.00	0.00
Cellvibrionaceae	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.59	2.85	0.00	0.00	0.00	0.69	0.00	9.55
MSBL3	0.14	0.49	0.70	0.82	0.10	0.00	0.10	3.06	0.00	0.00	0.00	0.00	0.00	10.12	0.00	0.00	0.00	0.05
JGI 0000069-P22	0.22	2.43	0.00	3.27	0.59	0.00	0.59	1.27	0.00	0.00	0.00	0.00	0.00	1.00	1.40	0.01	0.00	0.10
<i>Halarcobacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.08	0.00	1.19	0.65	1.08	0.00	0.44	3.65	0.25	2.86	0.03
<i>Brevibacterium</i>	0.03	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.27	0.00	0.00	0.00
<i>Rubritalea</i>	0.11	0.00	0.00	0.00	0.00	0.00	0.00	2.21	0.00	0.00	0.00	5.48	0.00	1.22	0.00	0.00	0.00	0.00
Rickettsiaceae	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.62	0.28	0.00	0.00	0.00	1.49	0.00	4.70
vadinHA49	3.62	0.16	0.70	1.09	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	1.45	0.56	0.00	0.00	0.00
<i>Pseudoteredinibacter</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	7.17	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Proteobacteria	4.05	0.24	0.33	0.14	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.78	1.12	0.00	0.00	0.00
<i>Lutibacter</i>	0.00	0.00	0.00	0.00	0.10	0.25	0.00	0.00	0.00	0.00	0.00	0.00	4.55	1.22	0.28	0.00	0.00	0.00
<i>Pseudoaeromonas</i>	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

¹Definitions of sample name abbreviations can be found in Table 1 in the main paper and Table S1.

²Percent relative abundance per sample.

Table S9. Significantly differentially abundance taxa as identified by LEfSe in the tissue microbiome samples

Taxa	Enriched group	LDA score¹	<i>p</i> value	<i>p</i> adjusted
<i>Pseudoalteromonas</i>	DCF ²	3.90070717	0.00255785	0.00255785
<i>Pseudophaeobacter</i>	DCF	3.2835783	0.04218883	0.04218883
<i>Microbacterium</i>	HCF	4.91327528	0.00841746	0.00841746
BD2-3	HCF	4.89332032	0.0094217	0.0094217
Bacteroidia	HCF	4.84050663	0.01834497	0.01834497
vadinHA49	HCF	3.98707961	0.04004801	0.04004801
<i>Brevibacterium</i>	HCF	3.65176359	0.00252176	0.00252176
Cyclobacteriaceae	LBW	5.32451733	0.0006317	0.0006317
Candidatus <i>Photodesmus</i>	LBW	4.83418387	0.01436621	0.01436621
Cryomorphaceae	LBW	4.76870085	0.00726085	0.00726085
<i>Vibrio</i>	LBW	4.57190404	0.0312891	0.0312891
<i>Pseudoteredinibacter</i>	LBW	3.60968065	0.00872441	0.00872441
<i>Lutibacter</i>	LBW	3.55196684	0.00872441	0.00872441

¹The linear discriminant analysis (LDA) threshold was set to 2.

²Definitions of sample name abbreviations can be found in Table 1 in the main paper. For this table, definitions are: D, diseased; H, healthy; CF, coelomic fluid; LBW, lesion body wall.