

Figure S1. Microscopic observation of diseased seedlings. (A) WH_Hc; (B) YT_Mc; (C) YT_Hc. The area marked by the red box and arrows indicates the diseased or rotten sites.

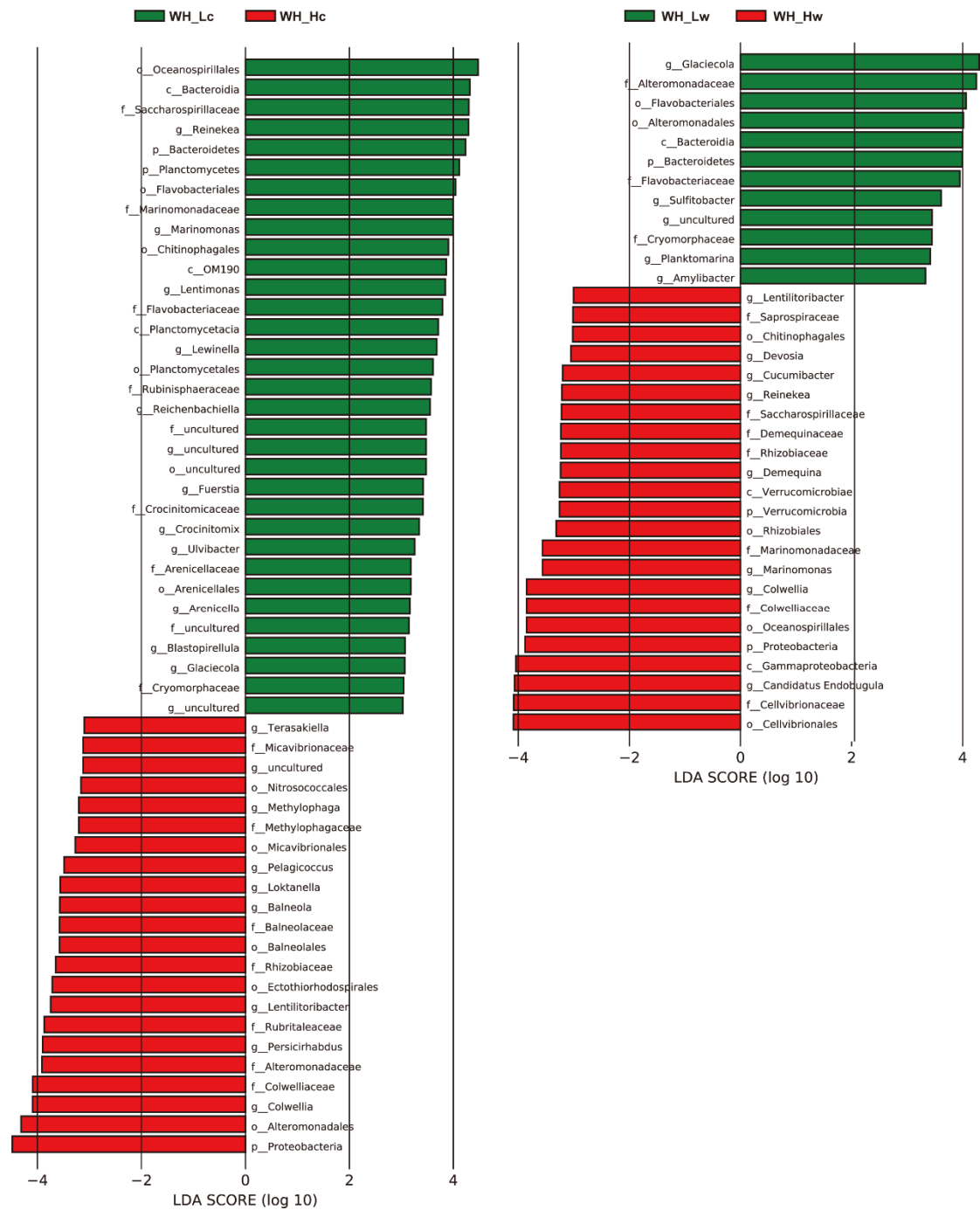


Figure S2. Significant differences in bacterial community composition between L and H tanks in Weihai (WH) determined using LefSe. **(A)** Significantly different taxa between WH_Lc and WH_Hc; **(B)** Significantly different taxa between WH_Lw and WH_Hw.



Figure S3. Significant differences in bacterial community composition between different seedlings in Yantai (YT) determined using LefSe. **(A)** Significantly different taxa between YT_Lc and YT_Mc; **(B)** Significantly different taxa between WH_Lc and WH_Hc.

Table S1. General information for the hatcheries in Weihai (WH) and Yantai (YT), respectively.

	Location	Tank size (length×width×depth)	Tank number	Rope material	Daily water exchange (%)
WH	37.39° N 122.63° E	8 m×2.5 m×0.25 m	200	palm	30~35
YT	37.77° N 120.78° E	8 m×2.5 m×0.25 m	60	vnylon	30~35

Table S2. General statistics for analyzed 16s rRNA gene sequences of all samples.

Sample ID	Raw reads	Merged	Quality filtration ^a	Taxa filtration ^b	Removed Chloroplast	Removed Mitochondria
WH_Lc1	34,884 * 2	29,321	25,449	19,499	5,897	37
WH_Lc2	30,497 * 2	26,259	24,947	15,200	9,663	75
WH_Lc3	35,855 * 2	30,743	27,826	17,334	10,462	25
WH_Lc4	41,524 * 2	35,615	31,911	20,496	11,398	17
WH_Lc5	35,517 * 2	30,261	26,911	18,054	8,825	30
WH_Hc1	30,370 * 2	25,675	23,731	17,204	6,513	12
WH_Hc2	39,886 * 2	33,629	29,768	26,386	3,340	32
WH_Hc3	41,004 * 2	34,959	31,075	25,348	5,679	34
WH_Hc4	50,611 * 2	46,002	32,368	23,533	8,823	5
WH_Hc5	38,337 * 2	32,503	28,489	24,539	3,939	9
WH_Lw1	50,350 * 2	41,461	29,070	28,696	116	5
WH_Lw2	43,593 * 2	36,232	23,324	23,014	113	5
WH_Lw3	46,162 * 2	38,465	24,428	24,042	202	6
WH_Lw4	45,482 * 2	37,836	24,575	24,256	166	6
WH_Lw5	52,752 * 2	43,726	29,781	29,326	236	5
WH_Hw1	49,914 * 2	41,298	28,095	27,717	206	3
WH_Hw2	45,515 * 2	37,725	34,758	34,050	266	23
WH_Hw3	34,997 * 2	28,949	25,207	24,616	293	5
WH_Hw4	44,893 * 2	37,100	23,791	23,520	86	3
WH_Hw5	42,426 * 2	35,265	24,165	23,871	106	3
YT_Lc1	27,172 * 2	23,204	23,069	2,695	20,280	94
YT_Lc2	48,065 * 2	39,099	30,951	9,419	21,407	124
YT_Lc3	40,054 * 2	33,059	30,833	8,142	22,539	151
YT_Lc4	37,221 * 2	31,399	28,129	7,174	20,865	90
YT_Mc1	37,371 * 2	30,597	24,740	10,861	13,773	106
YT_Mc2	21,253 * 2	17,501	17,230	6,163	11,008	59
YT_Mc3	37,560 * 2	32,119	29,880	3,788	26,032	60
YT_Hc1	35,960 * 2	30,513	29,673	6,823	22,740	109
YT_Hc2	48,844 * 2	39,424	34,057	12,751	21,249	55
YT_Hc3	33,044 * 2	27,799	25,847	5,145	20,674	28

^a Indicating the remaining sequences after quality filtration;^b Indicating the remaining sequences after taxa removal.

Table S3. Pairwise comparison results based on Bray-Curtis distances for bacterial communities in WH and YT hatcheries, respectively

Communities in WH	R	<i>p</i>-value
WH_Lc vs. WH_Hc	0.44	0.009
WH_Lw vs. WH_Hw	0.471	0.006
WH_Lc vs. WH_Lw	0.936	0.011
WH_Lc vs. WH_Hw	0.912	0.008
WH_Hc vs. WH_Lw	0.907	0.011
WH_Hc vs. WH_Hw	0.878	0.012
Communities in YT	R	<i>p</i>-value
YT_Lc vs. YT_Hc	0.565	0.010
YT_Lc vs. YT_Mc	0.471	0.040
YT_Mc vs. YT_Hc	0.582	0.010

Table S4. Proportions of the top 30 bacterial genera in seedlings and seawater from the WH hatchery

Proportions of the top 30 bacterial genera in seedlings										
Taxonomy	Lc1	Lc2	Lc3	Lc4	Lc5	Hc1	Hc2	Hc3	Hc4	Hc5
Gammaproteobacteria; Cellvibrionales; Cellvibrionaceae; <i>Ca. Endobugula</i>	36.76%	31.60%	43.24%	45.31%	34.55%	29.74%	26.57%	31.10%	57.18%	34.21%
Gammaproteobacteria; Oceanospirillales; Saccharospirillaceae; <i>Reinekea</i>	5.38%	6.89%	5.04%	6.70%	3.97%	1.63%	1.81%	2.10%	1.36%	2.29%
Gammaproteobacteria; Oceanospirillales; Marinomonadaceae; <i>Marinomonas</i>	4.16%	6.10%	4.32%	3.32%	3.67%	3.26%	2.80%	2.06%	1.78%	2.60%
Gammaproteobacteria; Alteromonadales; Colwelliaceae; <i>Colwellia</i>	1.16%	2.34%	2.16%	1.31%	2.31%	4.63%	2.96%	4.37%	4.40%	5.55%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Lentilitoribacter</i>	1.41%	1.61%	1.95%	1.54%	1.11%	2.84%	1.75%	2.58%	2.28%	3.82%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Sulfitobacter</i>	1.01%	1.14%	1.13%	1.19%	1.35%	2.85%	1.28%	1.16%	0.79%	1.62%
Bacteroidetes; Bacteroidia; Chitinophagales; Saprospiraceae; <i>Lewinella</i>	1.34%	1.45%	2.42%	1.51%	1.88%	0.69%	0.97%	1.09%	0.52%	0.69%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Loktanella</i>	0.54%	0.79%	0.75%	0.59%	0.61%	1.51%	1.12%	0.84%	0.80%	2.93%
Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Rubritaleaceae; <i>Persicirhabdus</i>	0.15%	0.03%	0.09%	0.24%	0.24%	1.53%	1.53%	1.97%	0.96%	2.85%
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceicoccaceae; <i>Lentimonas</i>	0.87%	2.34%	1.60%	1.85%	1.14%	0.30%	0.24%	0.45%	0.20%	0.26%
Gammaproteobacteria; Oceanospirillales; Pseudohongiellaceae; <i>Pseudohongiella</i>	0.85%	1.12%	0.68%	0.55%	1.26%	0.73%	0.89%	0.93%	0.76%	0.51%
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceicoccaceae; <i>Pelagicoccus</i>	0.37%	0.46%	0.18%	0.41%	0.97%	0.76%	1.60%	1.60%	0.82%	0.79%
Alphaproteobacteria; Rhodospirillales; Thalassospiraceae; <i>Thalassospira</i>	1.57%	0.59%	0.18%	0.31%	0.42%	1.92%	1.44%	0.63%	0.16%	0.59%
Bacteroidetes; Rhodothermia; Balneolales; Balneolaceae; <i>Balneola</i>	0.15%	0.20%	0.16%	0.16%	0.19%	1.27%	1.52%	1.02%	0.20%	0.88%
Alphaproteobacteria; Thalassobaculales; Nisaeaceae; <i>Nisaea</i>	0.66%	0.30%	0.21%	0.42%	0.18%	0.72%	1.06%	0.66%	0.29%	0.53%
Bacteroidetes; Bacteroidia; Cytophagales; Cyclobacteriaceae; <i>Reichenbachiiella</i>	0.36%	1.91%	0.73%	0.48%	0.51%	0.09%	0.26%	0.25%	0.17%	0.18%
Planctomycetes; Planctomycetacia; Planctomycetales; Rubinisphaeraceae; <i>Fuerstia</i>	0.70%	0.81%	0.67%	0.30%	1.22%	0.24%	0.31%	0.22%	0.10%	0.22%
Bacteroidetes; Bacteroidia; Flavobacteriales; Crocinitomicaceae; <i>Crocinitomix</i>	0.24%	0.61%	0.86%	0.86%	0.63%	0.13%	0.21%	0.40%	0.25%	0.20%
Gammaproteobacteria; Nitrosococcales; Methylophagaceae; <i>Methylophaga</i>	0.32%	0.23%	0.15%	0.24%	0.27%	0.75%	0.84%	0.54%	0.29%	0.47%
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae; <i>Magnetospira</i>	0.36%	0.34%	0.17%	0.26%	0.40%	0.60%	0.70%	0.60%	0.19%	0.41%
Lentisphaerae; Lentisphaeria; Lentisphaerales; Lentisphaeraceae; <i>Lentisphaera</i>	0.32%	0.65%	0.63%	0.40%	0.42%	0.24%	0.21%	0.45%	0.14%	0.37%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Hoeflea</i>	0.50%	0.36%	0.31%	0.14%	0.64%	0.41%	0.33%	0.36%	0.34%	0.25%
Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Paraglaeicola</i>	0.13%	0.37%	0.61%	0.29%	0.37%	0.54%	0.27%	0.38%	0.19%	0.44%
Bacteroidetes; Bacteroidia; Cytophagales; Spirosomaceae; <i>Taeseokella</i>	0.33%	0.32%	0.16%	0.11%	0.65%	0.40%	0.69%	0.39%	0.11%	0.34%
Gammaproteobacteria; Oceanospirillales; Saccharospirillaceae; <i>Saccharospirillum</i>	0.50%	0.52%	0.18%	0.19%	0.51%	0.47%	0.26%	0.41%	0.16%	0.20%

Bacteroidetes; Bacteroidia; Cytophagales; Cyclobacteriaceae; <i>Marinoscillum</i>	0.25%	0.23%	0.22%	0.20%	0.33%	0.34%	0.51%	0.54%	0.37%	0.31%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Ulvibacter</i>	0.38%	0.52%	0.65%	0.46%	0.38%	0.11%	0.11%	0.24%	0.08%	0.13%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Oricola</i>	0.17%	0.18%	0.17%	0.16%	0.39%	0.30%	0.41%	0.28%	0.28%	0.21%
Planctomycetes; Planctomycetacia; Pirellulales; Pirellulaceae; <i>Blastopirellula</i>	0.34%	0.33%	0.48%	0.13%	0.54%	0.19%	0.17%	0.11%	0.03%	0.15%
Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Glaciecola</i>	0.43%	0.41%	0.39%	0.32%	0.27%	0.13%	0.15%	0.19%	0.10%	0.08%

Proportions of the top 30 bacterial genera in seawater

Taxonomy	Lw1	Lw2	Lw3	Lw4	Lw5	Hw1	Hw2	Hw3	Hw4	Hw5
Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Glaciecola</i>	27.56%	28.47%	28.69%	27.59%	27.75%	25.44%	21.01%	22.05%	26.35%	25.39%
Gammaproteobacteria; Cellvibrionales; Cellvibrionaceae; <i>Ca. Endobugula</i>	9.66%	8.72%	9.73%	9.33%	9.55%	11.50%	12.68%	12.69%	10.88%	10.93%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Sulfitobacter</i>	6.85%	7.03%	6.54%	6.77%	6.73%	6.70%	4.95%	5.70%	6.27%	6.19%
Gammaproteobacteria; Oceanospirillales; Marinomonadaceae; <i>Marinomonas</i>	3.13%	3.68%	3.74%	3.39%	3.70%	4.33%	4.08%	5.43%	3.72%	3.97%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Planktomarina</i>	3.52%	3.13%	3.13%	3.25%	3.21%	3.21%	2.26%	2.53%	2.82%	2.78%
Gammaproteobacteria; Alteromonadales; Colwelliaceae; <i>Colwellia</i>	2.13%	2.18%	2.50%	2.10%	2.13%	3.55%	4.34%	3.89%	2.97%	3.25%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Amylibacter</i>	2.44%	2.66%	2.47%	2.56%	2.47%	2.14%	1.91%	2.08%	2.35%	2.10%
Gammaproteobacteria; Oceanospirillales; Pseudohongiellaceae; <i>Pseudohongiella</i>	1.47%	1.39%	1.51%	1.32%	1.41%	1.59%	2.38%	1.78%	1.40%	1.45%
Verrucomicrobia; Verrucomicrobiae; Verrucomicrobiales; Rubritaleaceae; <i>Persicirhabdus</i>	1.21%	0.93%	1.06%	1.24%	1.08%	1.31%	0.99%	1.11%	1.49%	1.58%
Alphaproteobacteria; SAR11 clade; Clade I; Clade Ia	0.76%	0.71%	0.76%	0.59%	0.64%	0.38%	1.71%	1.34%	0.71%	0.70%
Gammaproteobacteria; Oceanospirillales; Saccharospirillaceae; <i>Reinekea</i>	0.51%	0.46%	0.67%	0.66%	0.59%	0.72%	1.24%	1.07%	0.76%	0.73%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Ulvibacter</i>	0.46%	0.33%	0.34%	0.40%	0.43%	0.39%	1.22%	1.01%	0.45%	0.38%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Lentilitoribacter</i>	0.51%	0.37%	0.40%	0.38%	0.49%	0.63%	0.60%	0.61%	0.63%	0.59%
Bacteroidetes; Bacteroidia; Chitinophagales; Saprospiraceae; <i>Lewinella</i>	0.32%	0.32%	0.27%	0.27%	0.21%	0.41%	0.56%	0.58%	0.30%	0.29%
Actinobacteria; Acidimicrobiia; Actinomarinales; Actinomarinaceae; <i>Ca. Actinomarina</i>	0.38%	0.28%	0.32%	0.32%	0.32%	0.24%	0.43%	0.52%	0.33%	0.22%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; NS5 marine group	0.18%	0.15%	0.16%	0.16%	0.16%	0.16%	0.29%	0.32%	0.18%	0.23%
Verrucomicrobia; Verrucomicrobiae; Opitutales; Puniceicoccaceae; <i>Lentimonas</i>	0.18%	0.11%	0.15%	0.20%	0.14%	0.18%	0.25%	0.25%	0.16%	0.22%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Loktanella</i>	0.15%	0.13%	0.12%	0.11%	0.11%	0.22%	0.16%	0.22%	0.17%	0.30%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Flavicella</i>	0.14%	0.15%	0.13%	0.11%	0.15%	0.11%	0.23%	0.12%	0.17%	0.22%
Gammaproteobacteria; Cellvibrionales; Porticoccaceae; SAR92 clade	0.14%	0.17%	0.12%	0.13%	0.15%	0.13%	0.23%	0.21%	0.11%	0.13%
Planctomycetes; Planctomycetacia; Planctomycetales; Rubinisphaeraceae; <i>Fuerstia</i>	0.18%	0.13%	0.11%	0.21%	0.11%	0.10%	0.10%	0.14%	0.12%	0.15%

Gammaproteobacteria; Betaproteobacteriales; Methylophilaceae; OM43 clade	0.10%	0.12%	0.07%	0.09%	0.09%	0.06%	0.26%	0.18%	0.10%	0.13%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Pseudahrensia</i>	0.13%	0.09%	0.07%	0.11%	0.12%	0.09%	0.14%	0.15%	0.12%	0.17%
Gammaproteobacteria; Alteromonadales; Pseudoalteromonadaceae; <i>Pseudoalteromonas</i>	0.08%	0.09%	0.07%	0.08%	0.09%	0.12%	0.19%	0.17%	0.11%	0.10%
Gammaproteobacteria; Nitrosococcales; Methylophagaceae; <i>Methylophaga</i>	0.09%	0.07%	0.08%	0.06%	0.09%	0.12%	0.23%	0.13%	0.08%	0.14%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Hoeflea</i>	0.10%	0.09%	0.08%	0.11%	0.09%	0.12%	0.14%	0.11%	0.07%	0.12%
Bacteroidetes; Rhodothermia; Balneolales; Balneolaceae; <i>Balneola</i>	0.06%	0.09%	0.05%	0.09%	0.09%	0.08%	0.14%	0.11%	0.11%	0.08%
Cyanobacteria; Oxyphotobacteria; Synechococcales; Cyanobiaceae; <i>Synechococcus</i> CC9902	0.09%	0.07%	0.07%	0.12%	0.07%	0.05%	0.10%	0.07%	0.07%	0.10%
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae; <i>Magnetospira</i>	0.08%	0.04%	0.07%	0.07%	0.06%	0.06%	0.14%	0.12%	0.06%	0.07%
Gammaproteobacteria; Betaproteobacteriales; Methylophilaceae; <i>Methylotenera</i>	0.06%	0.07%	0.07%	0.04%	0.02%	0.06%	0.15%	0.13%	0.05%	0.13%

Table S5. Proportions of the top 30 bacterial genera in seedlings from the YT hatchery

Taxonomy	Lc1	Lc2	Lc3	Mc1	Mc2	Mc3	Hc1	Hc2	Hc3
Gammaproteobacteria; Oceanospirillales; Marinomonadaceae; <i>Marinomonas</i>	0.00%	0.04%	0.00%	30.14%	15.41%	1.95%	2.54%	26.31%	29.21%
Gammaproteobacteria; Alteromonadales; Colwelliaceae; <i>Thalassotalea</i>	10.13%	9.80%	5.02%	5.63%	3.88%	12.67%	13.85%	5.71%	3.60%
Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Glaciecola</i>	3.66%	6.87%	6.06%	8.09%	11.05%	5.04%	3.43%	0.76%	1.48%
Gammaproteobacteria; Alteromonadales; Pseudoalteromonadaceae; <i>Algicola</i>	0.00%	0.00%	0.01%	4.18%	3.15%	1.45%	2.56%	31.23%	22.97%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Maribacter</i>	3.35%	3.87%	3.74%	2.65%	4.15%	7.13%	4.62%	1.23%	2.74%
Alphaproteobacteria; Rhodospirillales; Magnetospiraceae; <i>Magnetospira</i>	4.00%	2.08%	3.05%	4.11%	3.93%	6.97%	6.43%	1.57%	2.06%
Gammaproteobacteria; Alteromonadales; Pseudoalteromonadaceae; <i>Psychrosphaera</i>	0.01%	0.01%	0.00%	13.60%	13.52%	1.03%	0.79%	0.21%	0.27%
Alphaproteobacteria; Sneathiellales; Sneathiellaceae; <i>Sneathiella</i>	0.28%	0.32%	0.59%	1.57%	2.58%	3.62%	3.84%	1.20%	2.04%
Alphaproteobacteria; Parvibaculales; Parvibaculaceae; Mf105b01	0.34%	0.42%	0.92%	1.71%	2.82%	1.72%	1.88%	0.54%	0.52%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Polaribacter</i>	1.20%	1.38%	2.01%	0.29%	0.70%	1.35%	1.36%	0.29%	0.80%
Alphaproteobacteria; Thalassobaculales; Nisaeaceae; <i>Nisaea</i>	1.15%	0.90%	1.20%	1.07%	0.89%	2.03%	2.05%	0.52%	0.82%
Alphaproteobacteria; Rhodospirillales; Terasakiellaceae; <i>Terasakiella</i>	0.00%	0.00%	0.00%	0.06%	0.03%	0.08%	0.26%	5.40%	9.33%
Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; <i>Sulfitobacter</i>	1.39%	1.08%	1.60%	0.71%	1.22%	1.21%	1.29%	0.84%	1.21%
Planctomycetes; Phycisphaerae; Phycisphaerales; Phycisphaeraceae; SM1A02	0.47%	0.16%	0.22%	0.30%	0.65%	0.66%	1.26%	0.18%	0.37%
Alphaproteobacteria; Kordiimonadales; Kordiimonadaceae; <i>Kordiimonas</i>	1.04%	0.96%	1.94%	0.38%	0.84%	1.21%	1.11%	0.20%	0.14%
Alphaproteobacteria; Rhizobiales; Rhizobiaceae; <i>Lentilitoribacter</i>	1.04%	1.62%	1.49%	0.87%	1.35%	1.03%	1.06%	0.33%	0.52%
Actinobacteria; Acidimicrobiia; Microtrichales; Ilumatobacteraceae; <i>Ilumatobacter</i>	3.64%	1.30%	2.61%	0.24%	0.15%	0.82%	0.31%	0.48%	0.29%
Gammaproteobacteria; Oceanospirillales; Oleiphilaceae; <i>Oleiphilus</i>	0.47%	0.26%	0.39%	2.05%	1.25%	1.27%	1.54%	0.60%	0.54%
Alphaproteobacteria; Caulobacterales; Hyphomonadaceae; <i>Maricaulis</i>	0.37%	0.65%	0.46%	0.66%	0.13%	0.77%	2.07%	0.35%	0.25%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Kordia</i>	0.12%	0.66%	0.14%	0.44%	1.02%	1.37%	0.53%	0.06%	0.02%
Actinobacteria; Actinobacteria; Corynebacteriales; Nocardiaceae; <i>Rhodococcus</i>	1.16%	0.79%	0.74%	0.32%	0.16%	0.48%	0.29%	0.42%	0.29%
Gammaproteobacteria; Oceanospirillales; Saccharospirillaceae; <i>Saccharospirillum</i>	1.06%	1.25%	1.03%	0.10%	0.05%	1.08%	0.69%	0.70%	0.64%
Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Dokdonia</i>	0.14%	2.51%	0.49%	0.04%	0.89%	0.13%	0.19%	0.02%	0.00%
Gammaproteobacteria; Alteromonadales; Colwelliaceae; <i>Colwellia</i>	0.15%	0.22%	0.20%	1.32%	1.27%	0.26%	0.51%	0.29%	0.66%
Bacteroidetes; Bacteroidia; Cytophagales; Cyclobacteriaceae; <i>Fabibacter</i>	0.25%	1.44%	0.82%	0.04%	0.11%	0.63%	0.45%	0.45%	0.10%
Gammaproteobacteria; Cellvibrionales; Halieaceae; <i>Halioglobus</i>	0.24%	0.28%	0.56%	0.07%	0.23%	0.45%	0.60%	0.45%	0.33%
Gammaproteobacteria; Alteromonadales; Alteromonadaceae; <i>Paraglaciecola</i>	0.27%	0.55%	0.45%	0.17%	0.16%	0.48%	0.28%	0.36%	0.49%

Bacteroidetes; Bacteroidia; Flavobacteriales; Flavobacteriaceae; <i>Winogradskyella</i>	0.15%	0.20%	0.08%	0.11%	0.00%	0.16%	0.06%	0.02%	0.08%
Gammaproteobacteria; Betaproteobacteriales; Methylophilaceae; <i>Methylothera</i>	0.29%	0.37%	0.28%	0.19%	0.06%	0.58%	0.43%	0.13%	0.27%
Bacteroidetes; Bacteroidia; Flavobacteriales; Crocinitomicaceae; <i>Crocinitomix</i>	0.76%	0.29%	0.22%	0.02%	0.10%	0.40%	0.37%	0.20%	0.06%