

Supplementary Material

Impacts on microbial communities in sediments by aquaculture farms

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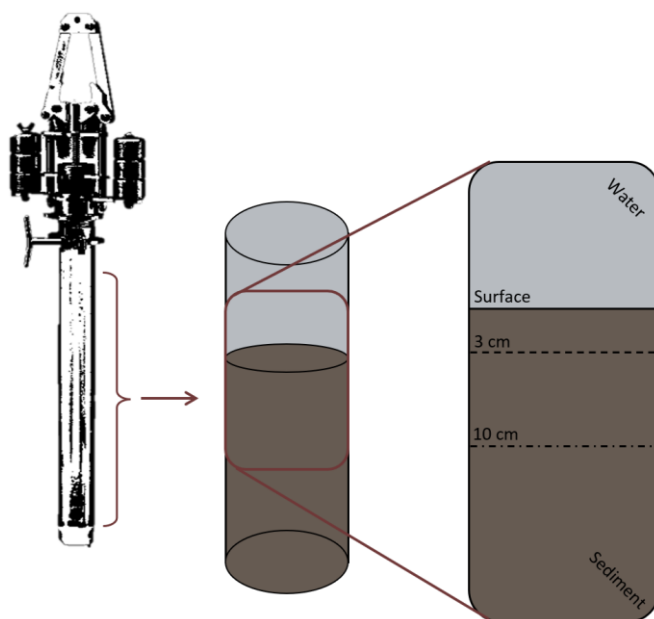
*** Correspondence:**

Bjarta Osberg Johansen

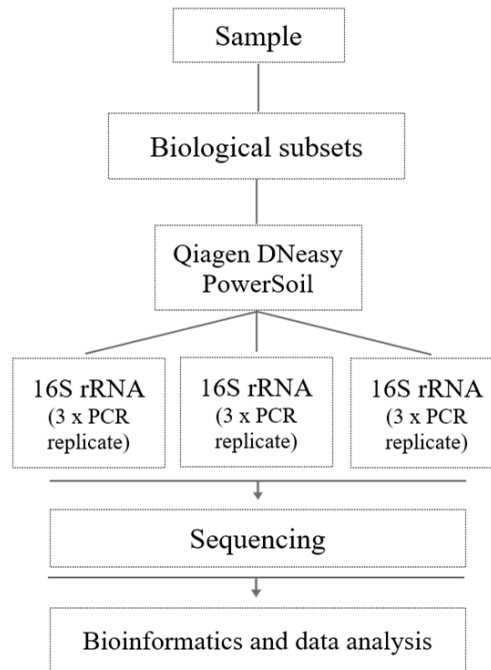
objarta@gmail.com

Anni Djurhuus

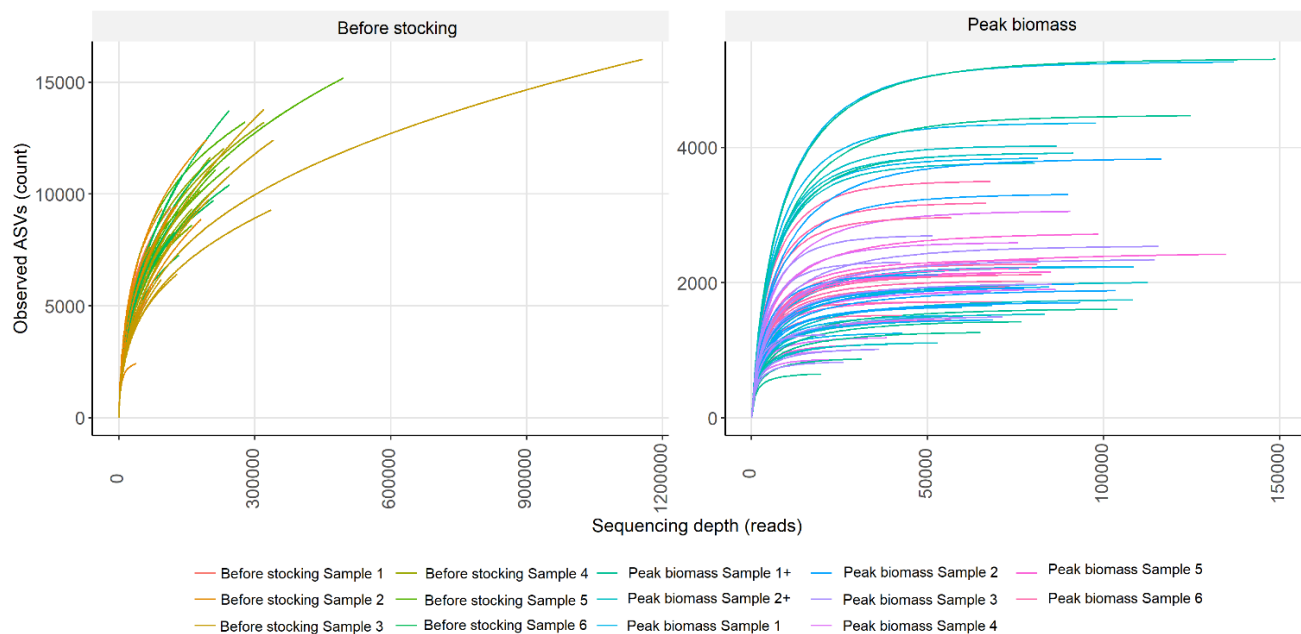
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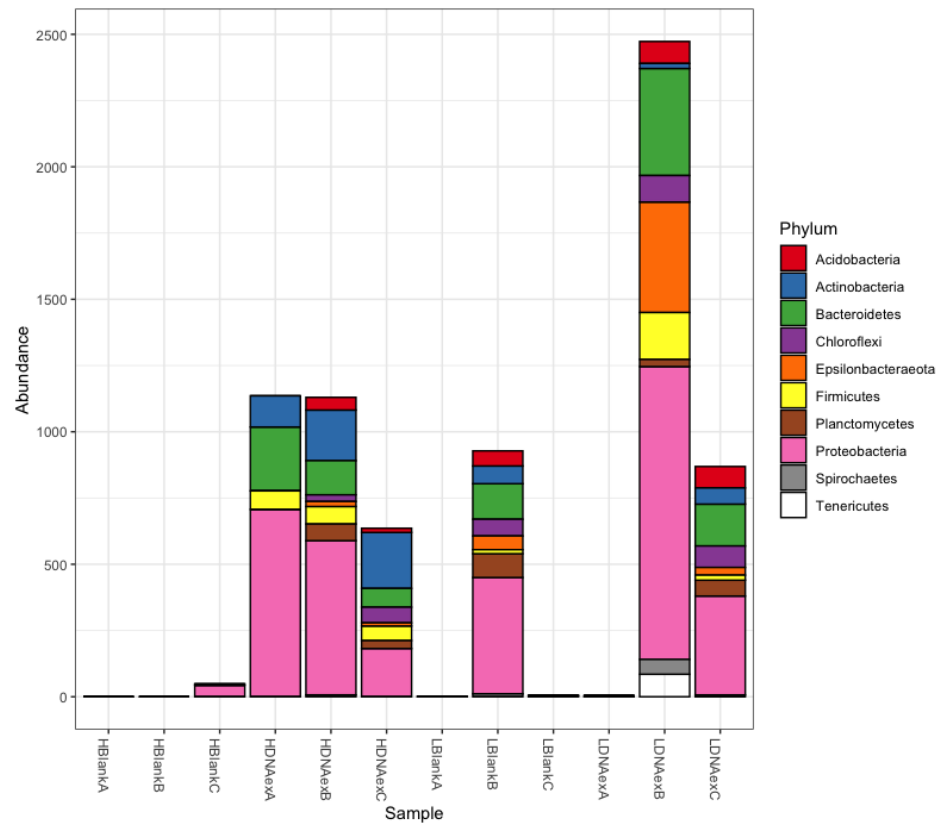
Supplementary file 1: Sketch of the kayak corer used for sampling (to the left) and tube with the selected sediment layers in cm (to the right).



Supplementary file 2: Schematic of sampling and laboratory protocols. Amplification targeted the V4-V5 gene region of the taxonomic group of the 16S rRNA of microorganisms.



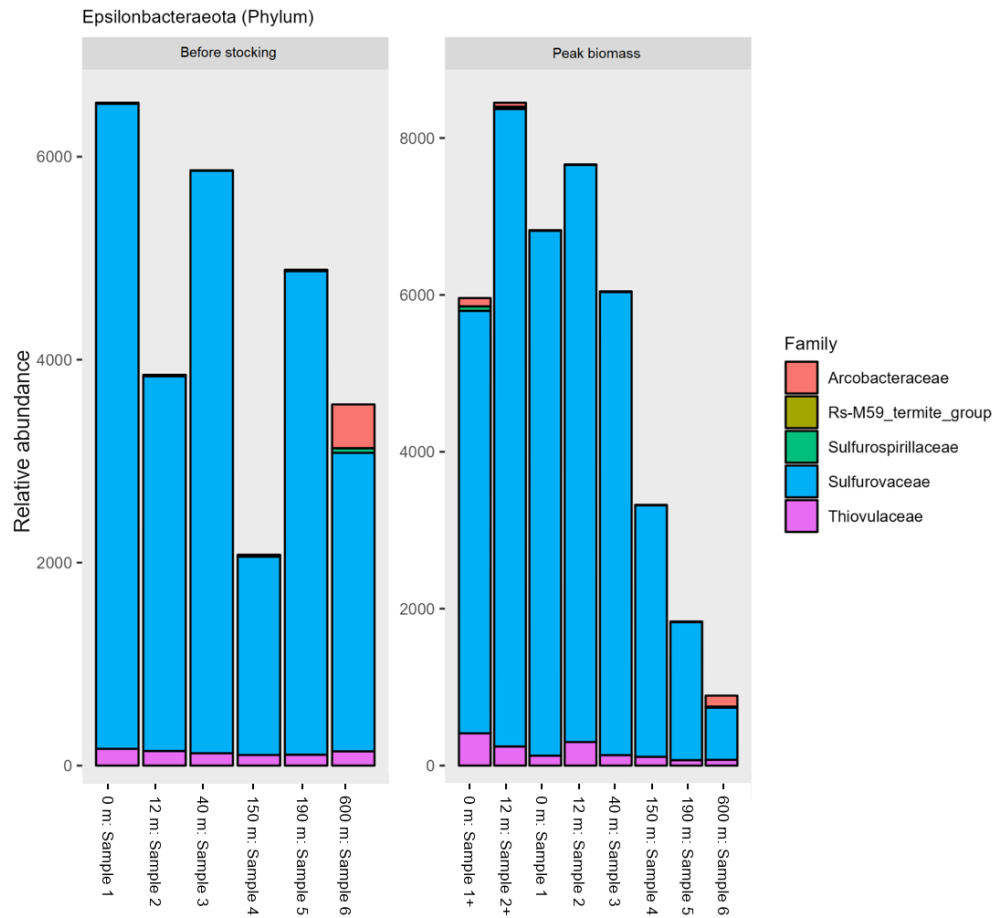
Supplementary file 3: Rarefaction curve of both sampling sets. 'Before stocking' sampling to the left and 'peak biomass' sampling at the right. A 10x difference in scale is between the two sampling sets.



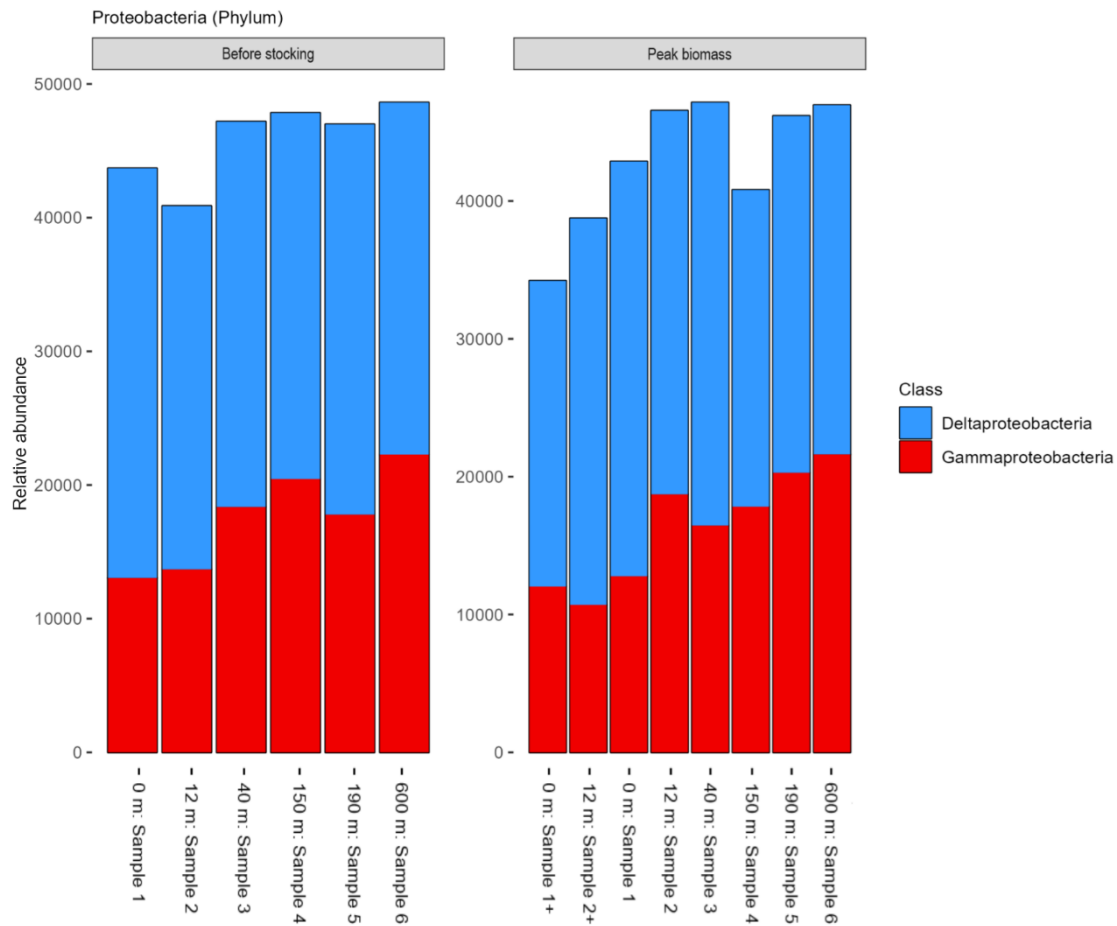
Supplementary file 4: Bar plot depicting sequence abundance in all negative controls (no template controls and DNA extraction negatives).

	BS Sample 1	BS Sample 2	BS Sample 3	BS Sample 4	BS Sample 5	BS Sample 6	PB Sample 1	PB Sample 1+	PB Sample 2	PB Sample 2+	PB Sample 3	PB Sample 4	PB Sample 5
BS Sample 2	0.12547	-	-	-	-	-	-	-	-	-	-	-	-
BS Sample 3	0.01387	0.67107	-	-	-	-	-	-	-	-	-	-	-
BS Sample 4	0.00337	0.56667	0.95236	-	-	-	-	-	-	-	-	-	-
BS Sample 5	0.00066	0.22553	0.56717	0.61858	-	-	-	-	-	-	-	-	-
BS Sample 6	0.03283	0.51854	1.0000	0.95236	0.68064	-	-	-	-	-	-	-	-
PB Sample 1	0.00234	0.00114	0.00013	0.00013	0.00013	0.00066	-	-	-	-	-	-	-
PB Sample 1+	0.00337	0.00114	0.00013	0.00013	0.00013	0.00066	0.42947	-	-	-	-	-	-
PB Sample 2	0.00013	0.00071	0.00013	0.00013	0.00013	0.00021	0.61858	0.42947	-	-	-	-	-
PB Sample 2+	0.00021	0.00114	0.00013	0.00013	0.00013	0.00066	0.52496	0.67746	0.79131	-	-	-	-
PB Sample 3	0.00013	0.00071	0.00013	0.00013	0.00013	0.00013	0.48359	0.91350	0.68064	0.68064	-	-	-
PB Sample 4	0.00021	0.00120	0.00021	0.00021	0.00021	0.00021	0.15341	0.92920	0.26689	0.41950	0.68064	-	-
PB Sample 5	0.00013	0.00042	0.00013	0.00013	0.00013	0.00013	0.68064	0.56717	0.73071	0.91350	0.73071	0.41950	-
PB Sample 6	0.00013	0.00114	0.00013	0.00013	0.00013	0.00013	1.0000	0.42947	0.52496	0.67107	0.40492	0.12547	0.67746

Supplementary file 5: Results of the Wilcoxon rank sum test for the post-hoc analysis. Samples who were significantly different from one another ($p < 0.001$, 0.01 and 0.05) are highlighted in yellow. BS = before stocking. PB = peak biomass.



Supplementary file 6: Relative abundance barplot (>19,000 reads/sample) of the phylum Epsilonbacteraeota. Before stocking (left) and peak biomass (right). X-axis show the distance from the cages and the y-axis show a quantitative display of the relative abundances.



Supplementary file 7: Relative abundance barplot (>19,000 reads/sample) of the phylum of Proteobacteria showing the classes Deltaproteobacteria (blue) and Gammaproteobacteria (red). Before stocking (left) and peak biomass (right). X-axis show the distance from the cages and the y-axis show a quantitative display of the relative abundances.

	Before stocking						High biomass							
Deltaproteobacteria; Desulfobulbaceae	10.9	9.5	11.9	8.7	9.3	9.2	6.6	8.2	7.8	9.2	8.5	8.9	8.1	7
Deltaproteobacteria; Desulfobacteraceae	6.6	7.2	5.5	5.4	6.5	5.5	6.8	6.7	6.8	6.5	7	7.1	5.3	5
Planctomycetacia; Pirellulaceae	5.9	5.4	8	6.7	5.9	6	2.1	3.9	3.7	5.3	4.3	5.8	6	4.2
Bacteroidia; Flavobacteriaceae	3.1	3.5	5.4	3.9	4	5.5	4.4	3.3	4	4.4	3.5	3.2	5.2	5.8
Thermoanaerobaculia; Thermoanaerobaculaceae	3.9	4	3.8	5.1	4.3	4.8	1.9	3.2	3	4	3.5	4.7	4.8	2.9
Campylobacteria; Sulfurovaceae	4.6	3	4	1.4	3.4	2.1	4.6	5.7	4.5	5.1	4	2.7	1.2	0.4
Gammaproteobacteria; Unknown_Family	1.6	1.6	3.4	3.2	2.4	3.6	0.6	0.8	1.2	2.3	1.6	2.8	2.9	2.2
Gammaproteobacteria; Halieaceae	1.5	2	3.3	3	2.3	2.4	0.7	0.8	1.4	2.4	1.9	2.5	2.7	2.4
Bacteroidia; Bacteroidetes_BD2-2	3.1	2.6	1.8	1.4	2.4	1.5	2	2.8	2.5	2.4	2.2	1.7	1.3	1.2
Anaerolineae; Anaerolineaceae	2	1.9	1.1	2.4	2.1	1.7	1.3	1.6	2.4	1.2	1.8	1.4	1.6	1.8
Acidimicrobia; Illumatobacteraceae	1.3	1.2	2	1.8	1.4	1.4	0.5	0.7	0.9	1.4	1.2	1.6	2.3	2.2
Bacteroidia; Lentimicrobiaceae	2	1.7	1.7	0.8	1.2	0.8	1.2	1.7	1.4	1.5	1.2	1	0.8	0.5
Gammaproteobacteria; Thiomicrospiraceae	1.1	1.2	1.2	1	1.6	1.3	1.2	0.9	1.1	1.7	1.4	2.1	1	0.4
Spirochaetia; Spirochaetaceae	0.9	0.8	0.2	0.3	0.6	0.4	7.2	2.6	0.8	0.8	0.7	0.6	0.5	0.6
Gammaproteobacteria; Sedimenticolaceae	0.8	0.8	1.2	1.1	1.2	1.4	0.7	1.2	0.9	1.6	1.2	1.8	1.2	0.4
Gammaproteobacteria; Spongiibacteraceae	0.9	1.6	1.4	1.3	1	1.2	0.3	0.3	0.9	1	1.2	1.2	1	1.1
Kiritimatiellae; Kiritimatiellaceae	1	1	0.7	0.6	0.7	0.8	1	1.4	1.2	1.4	1.1	1	1.2	1
Bacteroidia; Cyclobacteriaceae	0.5	0.7	0.9	1.1	1	1	0.2	0.3	0.6	0.8	0.7	0.9	1.3	1
Anaerolineae; Caldilineaceae	0.9	0.8	1.1	0.8	0.9	0.8	0.4	0.8	0.7	0.8	0.7	0.8	0.8	0.5
Bacteroidia; Prolixibacteraceae	1.2	1.4	0.8	0.3	0.6	0.4	1.5	1.1	0.7	0.8	0.6	0.4	0.3	0.9
Gammaproteobacteria; Thiotrichaceae	0.5	0.6	0.3	0.8	0.8	1.4	0.5	0.5	0.6	0.9	0.7	1.2	0.9	0.7
Deltaproteobacteria; Sandaracinaceae	0.6	0.6	0.9	1	0.7	1	0.3	0.3	0.6	0.7	0.7	0.9	1.1	0.8
Gammaproteobacteria; Ectothiorhodospiraceae	0.6	0.5	0.7	0.9	0.7	0.8	0.5	0.4	0.7	0.9	0.9	1.1	0.9	0.6
Deltaproteobacteria; Desulfarculaceae	0.6	0.7	0.4	0.6	0.7	0.5	0.5	0.7	0.8	0.5	0.6	0.7	0.5	0.5
Bacteroidia; Marinifilaceae	0.1	0.1	0.1	0	0.1	0.3	4.6	1.9	0.1	0.2	0.1	0.2	0.2	0.3
Deltaproteobacteria; Syntrophobacteraceae	0.6	0.6	0.2	0.6	0.4	0.3	0.3	0.6	1	0.5	1	0.4	0.4	0.6
Thermoleophilia; 67-14	0.5	0.5	0.5	0.7	0.4	0.5	0.3	0.3	0.6	0.5	0.6	0.6	0.6	0.7
Verrucomicrobiae; Rubritaleaceae	0.3	0.3	0.6	0.5	0.4	0.5	0.2	0.3	0.5	0.7	0.6	0.5	0.9	0.7
Alphaproteobacteria; Rhodobacteraceae	0.5	0.5	0.7	0.7	0.5	0.8	0.2	0.2	0.2	0.4	0.3	0.4	0.8	0.7
Gammaproteobacteria; Psychromonadaceae	0.1	0.1	0	0.1	0.1	0.9	2.4	1.2	0.1	0.2	0.3	0.2	0.3	0.9
Alphaproteobacteria; Methyloiligellaceae	0.5	0.5	0.5	0.6	0.4	0.5	0.2	0.3	0.6	0.4	0.7	0.4	0.5	0.5
Acidimicrobia; Microtrichaceae	0.5	0.5	0.5	0.6	0.5	0.5	0.2	0.2	0.4	0.4	0.4	0.5	0.6	0.7
Phycisphaerae; SG8-4	0.3	0.3	0.1	0.3	0.3	0.3	0.8	0.6	0.9	0.4	0.7	0.3	0.2	0.6
Calditrichia; Calditrichaceae	0.4	0.4	0.1	0.3	0.4	0.5	0.5	0.5	0.6	0.3	0.6	0.4	0.4	0.6
Gammaproteobacteria; Chromatiaceae	0.3	0.3	0.4	0.4	0.5	0.5	0.3	0.2	0.3	0.5	0.5	0.8	0.5	0.2
Bacteroidia; Crocinomicaceae	0.2	0.3	0.6	0.5	0.3	0.6	0.1	0.1	0.3	0.4	0.4	0.3	0.6	0.4
Alphaproteobacteria; Hyphomicrobiaceae	0.3	0.4	0.3	0.4	0.3	0.3	0.2	0.4	0.6	0.3	0.6	0.3	0.3	0.4
Latescibacteria; Latescibacteraceae	0.4	0.4	0.1	0.4	0.4	0.3	0.3	0.5	0.4	0.3	0.3	0.4	0.3	0.4
Gammaproteobacteria; Colwelliaceae	0	0.1	0	0	0	0.3	0	0	0	0.2	0.2	0.2	0.5	3.1
Verrucomicrobiae; DEV007	0.3	0.3	0.6	0.5	0.4	0.5	0.1	0.1	0.1	0.2	0.2	0.3	0.4	0.3
Bacteroidia; Marinilabiliaceae	0.4	0.3	0.1	0.2	0.3	0.2	0.7	0.5	0.2	0.3	0.2	0.2	0.2	0.3
Deltaproteobacteria; Sva1033	0.2	0.2	0.4	0.4	0.3	0.4	0.1	0.1	0.1	0.3	0.2	0.3	0.5	0.4
Gammaproteobacteria; Thiohalorhabdaceae	0.3	0.3	0.2	0.4	0.4	0.4	0.1	0.1	0.1	0.1	0.1	0.1	0.3	0.5
Clostridia; Lachnospiraceae	0.1	0.1	0	0.1	0.1	0.3	1.4	0.6	0.1	0.1	0.1	0.1	0.1	0.2
Bacteroidia; Cryomorphaceae	0.1	0.2	0.2	0.3	0.2	0.3	0	0	0.2	0.2	0.2	0.1	0.4	0.5
	Sample 1-	Sample 2-	Sample 3-	Sample 4-	Sample 5-	Sample 6-	Sample 1+	Sample 2+	Sample 1-	Sample 2-	Sample 3-	Sample 4-	Sample 5-	Sample 6-

Supplementary file 8: Top 45 family ranked heatmap (and showing their classes). Separated by samplings events (before stocking and peak biomass). Values and color represent the % read abundance, where red = high abundance and white = low abundance.

Surface layer

	Core						Peak							
	Core						Peak							
Deltaproteobacteria; Desulfobulbaceae	2.2	1.6	1.9	9	0.2	9.5	6.6	9.7	10.7	9.4	9.6	9.6	7.4	5.2
Bacteroidia; Flavobacteriaceae	5.6	5.6	5.4	6.8	7.2	7.4	4.1	5.6	7	8.8	5.8	6.1	10.2	2.5
Planctomycetia; Planellulaceae	6.4	4.8	8.3	6.8	6.1	5.6	1.3	2.6	5	5.5	4.1	5.9	4.9	2.2
Deltaproteobacteria; Desulfobulbaceae	3.8	6.4	5.4	4.1	4.7	4.5	3.7	4.7	4.9	5.4	5.8	5.9	3.4	1.6
Campylobacteriia; Sulfurovaceae	8.1	3.9	4.7	1.9	4.4	1.8	5.7	7.3	6.5	5.8	3.8	3.7	1.5	0.3
Gammaproteobacteria; Halieaceae	2.5	3.3	3.8	4.6	3.9	3.4	0.6	0.8	3.2	3.3	3.5	2.9	4	4.6
Gammaproteobacteria; Unknown_Family	2.2	2.1	3.3	4.3	3.6	4.4	0.3	0.6	2	2.8	2.1	3.3	3.2	2.1
Thermoanaerobactilia; Thermoanaerobactulaceae	2.5	1.9	3.3	3.8	3.2	3.7	0.8	1.4	2.3	3	2.5	3.4	2.7	0.3
Bacteroidia; Bacteroidetes_BD2-2	3.7	3	1.7	1.3	2.6	1.3	2.3	3.4	4	2.8	2.9	2.2	1.5	
Kiritimallaei; Kiritimallaeaceae	1.4	1.3	0.7	0.8	1	1.3	1	3.4	2.8	2.5	2.2	2.3	2.6	1.9
Gammaproteobacteria; Thiomicrospiraceae	1.8	1.9	1.4	1	2.5	1.5	1	1.5	2.5	3.2	3.2	2.3	1.4	0.4
Gammaproteobacteria; Spongibacteriaceae	1.6	3.1	1.3	1.8	1.4	1.6	0.3	0.4	2.1	1.5	2.3	1.7	1.6	1.8
Bacteroidia; Lentimicrobiaceae	2.6	2.3	1.5	1	1.3	0.8	1.4	2.4	2.8	2	1.8	1.6	0.9	0.6
Acidimicrobia; Illumatobacteriaceae	1.7	1.5	2	2.2	1.8	1.6	0.2	0.5	1.3	1.4	1.5	1.4	2.8	1.8
Spirochaetia; Spirochaetaceae	0.9	0.8	0.3	0.3	0.4	0.3	10	8.3	1.1	1	1	0.8	0.8	0.6
Bacteroidia; Prolixibacteriaceae	2	2	0.8	0.5	0.7	0.4	1.6	2.3	1.4	1.1	1.1	0.8	0.5	1
Bacteroidia; Cyctobacteriaceae	0.7	1.2	0.9	1.7	1.3	1.2	0.2	0.2	1.2	1.2	1.3	1.2	2.3	1.3
Gammaproteobacteria; Sedimenticolaceae	1.1	0.9	1.3	1.1	1.3	1.6	0.5	0.8	1.4	1.7	1.4	1.9	1.1	0.2
Gammaproteobacteria; Psychromonadaceae	0.1	0.2	0	0.1	0.1	1.4	7.2	3.5	0.2	0.4	0.7	0.5	0.8	2.5
Bacteroidia; Marinifilaceae	0.1	0.1	0	0.1	0.1	0.4	7.5	5.3	0.2	0.3	0.3	0.4	0.5	0.5
Gammaproteobacteria; Colwelliaceae	0.1	0.1	0	0.1	0.1	0.4	0.1	0.1	0.5	0.7	0.6	1.4	9	
Verrucomicrobiae; Rubritellaceae	0.6	0.5	0.6	0.8	0.7	0.7	0.4	0.7	1	1.4	0.9	1.3	1.2	1.1
Alphaproteobacteria; Rhodobacteriaceae	1	0.9	0.7	1.2	1	1.2	0.2	0.2	0.4	0.6	0.5	0.6	1.7	1.2
Gammaproteobacteria; Ectothiorhodospiraceae	0.4	0.6	0.7	0.8	0.8	0.8	0.1	0.3	1	1	1.2	1.2	0.8	0.3
Anaerolineae; Caldilineaceae	0.9	0.9	1	0.6	0.7	0.8	0.3	0.5	0.9	0.7	0.8	0.8	0.7	0.3
Bacteroidia; Crocinitomacaceae	0.5	0.6	0.6	0.9	0.7	0.8	0.1	0.1	0.7	0.5	0.7	0.6	1.2	0.7
Deltaproteobacteria; Sandaracinaceae	0.4	0.6	0.9	1	0.7	1	0.1	0.1	0.5	0.5	0.7	0.8	0.3	0.3
Anaerolineae; Anaerolineaceae	0.6	0.5	1	1.2	0.8	0.7	0.3	0.3	0.7	0.5	0.4	0.6	0.4	1
Bacteroidia; Cryomorphaceae	0.3	0.5	0.3	0.8	0.5	0.5	0.2	0.1	0.5	0.4	0.4	0.4	1.2	1.5
Gammaproteobacteria; Thiotrichaceae	0.3	0.6	0.3	0.5	0.6	1.3	0.2	0.2	0.4	0.6	0.5	0.7	0.8	0.6
Gammaproteobacteria; Chromatiaceae	0.4	0.5	0.5	0.4	0.5	0.6	0.1	0.3	0.6	0.7	1	0.8	0.6	0
Bacteroidia; Saprospiraceae	0.3	0.6	0	0.4	0.3	0.4	0.1	0.1	0.6	0.3	0.7	0.3	0.7	0.7
Verrucomicrobiae; DEV007	0.5	0.4	0.6	0.7	0.6	0.6	0	0.1	0.2	0.3	0.2	0.3	0.5	0.2
Deltaproteobacteria; Sva1033	0.2	0.3	0.4	0.4	0.4	0.5	0	0.1	0.2	0.4	0.3	0.5	0.7	0.6
Mollicutes; Izimiplasmataceae	0.1	0.2	0	0	0.1	0.1	1.3	1.6	0.2	0.3	0.3	0.2	0.2	0.6
Bacteroidia; Marinifilabaceae	0.3	0.3	0	0.1	0.2	0.1	0.7	0.8	0.4	0.3	0.4	0.2	0.5	0.5
Gammaproteobacteria; Thiohalorhabdaceae	0.3	0.5	0.2	0.7	0.5	0.5	0	0	0.1	0.1	0.1	0.1	0.5	0.7
Deltaproteobacteria; Desulfurulaceae	0.4	0.5	0.4	0.4	0.5	0.4	0.2	0.2	0.3	0.2	0.3	0.3	0.2	0.1
Acidimicrobia; Microthricaceae	0.4	0.4	0.5	0.5	0.4	0.5	0	0	0.2	0.2	0.3	0.3	0.2	0.2
Clostridia; Lachnospiraceae	0.1	0	0	0.1	0.1	0.3	1.8	1.6	0	0	0.1	0.1	0.1	0.5
Deltaproteobacteria; Desulfurimonadaceae	0.2	0.3	0.3	0.2	0.3	0.1	0.2	0.2	0.4	0.5	0.6	0.3	0.3	0.3
Deltaproteobacteria; Bacteriovoraceae	0.3	0.6	0	0.3	0.3	0.2	0.2	0.1	0.2	0.1	0.3	0.1	0.4	0.7
Ignitavibacteria; Melioribacteriaceae	0.4	0.5	0.3	0.1	0.4	0.2	0.2	0.4	0.3	0.2	0.3	0.1	0.1	0
Thermoleophilii; 67-14	0.2	0.1	0.5	0.4	0.2	0.3	0	0	0.2	0.2	0.2	0.3	0.2	0.3
Clostridia; Desulfuillatellaceae	0.1	0.1	0	0	0	0.1	1.3	1.5	0.2	0.1	0.1	0.1	0.1	0.1
Alphaproteobacteria; Methylophilgellaceae	0.2	0.2	0.5	0.4	0.3	0.3	0	0	0.2	0.2	0.2	0.3	0.3	0.2
Gammaproteobacteria; Arenicellaceae	0.3	0.3	0.2	0.3	0.2	0.2	0	0	0.2	0.3	0.4	0.2	0.3	0.3
Cloacimonadia; MSLB1	0.2	0.3	0	0	0	0.1	1.1	1.2	0.2	0.1	0.1	0.1	0.1	0
Clostridia; Ruminococcaceae	0.2	0.3	0	0.1	0.1	0.1	0.5	1	0.2	0.2	0.2	0.1	0.1	0.1
Campylobacteriia; Thiouulaceae	0.2	0.2	0.1	0.1	0.1	0.1	0.8	0.4	0.2	0.3	0.2	0.2	0.1	0.1
Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 7	Sample 8	Sample 9	Sample 10	Sample 11	Sample 12	Sample 13	Sample 14	Sample 15

3 cm depth layer

	Before stocking						Peak domain											
Deltaproteobacteria; Desulfobulbaceae	3	2	2	1	2	0	8	7	9	1	5	0	6	2	9	0	8	9
Planctomycetia; Planellulaceae	5	8	5	6	8	3	7	6	5	5	6	1	6	7	4	3	7	8
Deltaproteobacteria; Desulfobacteraceae	8	3	7	5	6	5	4	7	4	9	6	5	8	4	8	1	6	7
Campylobacteria; Sulfohalobaceae	5	6	5	8	3	9	1	8	5	7	2	9	4	3	1	9	0	6
Bacteroidia; Flavobacteriaceae	3	3	4	8	4	9	4	1	8	4	7	7	3	9	4	6	2	6
Thermoanaerobactia; Thermoanaerobactaceae	2	9	2	8	4	4	6	3	2	3	1	5	5	5	4	9	5	1
Gammaproteobacteria; Unknown_Family	1	4	1	6	3	5	3	8	2	3	5	0	5	1	4	2	8	2
Bacteroidia; Bacteroidetes_BD2-2	4	2	3	9	1	7	1	5	3	3	1	2	1	3	9	2	1	5
Gammaproteobacteria; Haaliaceae	1	1	1	6	3	2	9	2	2	4	9	0	1	4	0	2	3	9
Acidimicrobia; Illumatobacteriaceae	1	1	1	2	2	1	2	1	4	1	6	0	3	1	4	1	2	4
Bacteroidia; Lentimicrobiaceae	3	1	3	1	2	1	1	9	1	1	7	2	3	1	6	1	7	9
Gammaproteobacteria; Sedimentibacteriaceae	0	7	0	8	1	1	3	1	5	1	4	0	7	2	4	1	1	9
Spirochaeta; Spirochaetaceae	1	2	1	0	2	0	3	0	3	0	2	1	1	3	0	4	0	5
Anaerolineae; Anaerolineaceae	1	5	1	2	1	3	1	5	1	3	1	0	3	1	2	9	0	7
Gammaproteobacteria; Thiomicrospiraceae	1	3	1	6	0	7	1	6	2	1	5	1	8	1	0	7	1	0
Anaerolineae; Caldilineaceae	1	5	1	3	1	2	1	2	1	2	0	9	0	5	1	8	1	1
Gammaproteobacteria; Spongiibacteraceae	0	9	1	2	1	3	1	4	1	2	1	4	0	5	0	4	0	6
Bacteroidia; Prolixobacteriaceae	1	6	2	2	0	7	1	5	1	0	5	2	6	0	9	0	7	0
Kiritimatiellae; Kiritimatiellaceae	1	3	1	5	0	7	0	6	0	9	0	8	1	7	0	6	0	5
Bacteroidia; Cyclobacteriaceae	0	4	0	6	0	8	1	2	1	1	1	0	1	0	5	0	4	0
Deltaproteobacteria; Sandaracinaceae	0	4	0	4	1	1	1	0	5	0	9	0	1	0	2	0	7	0
Bacteroidia; Marinifilaceae	0	1	0	1	0	1	0	1	0	1	0	7	2	0	2	0	1	0
Gammaproteobacteria; Ecotiorhodospiraceae	0	3	0	3	0	7	0	9	0	6	0	7	0	2	0	3	0	6
Verrucomicrobiae; Rubritellaceae	0	4	0	4	0	6	0	6	0	4	0	6	0	2	0	3	0	6
Gammaproteobacteria; Thiotrichaceae	0	2	0	2	0	2	0	7	0	9	1	3	0	2	0	3	0	3
Acidimicrobia; Microthricaceae	0	3	0	6	0	5	0	3	0	4	0	0	2	0	2	0	7	0
Thermoplasma; 67-14	0	2	0	2	0	6	0	5	0	2	0	3	0	1	0	2	0	9
Alphaproteobacteria; Rhodobacteraceae	0	3	0	4	0	7	0	5	0	4	1	0	2	0	3	0	2	0
Deltaproteobacteria; Desulfurcalaceae	0	6	0	5	0	4	0	4	0	5	0	4	0	2	0	5	0	3
Verrucomicrobiae; DEV007	0	3	0	3	0	6	0	6	0	3	0	5	0	1	0	2	0	2
Alphaproteobacteria; Methylophilaceae	0	2	0	2	0	5	0	4	0	2	0	3	0	1	0	1	0	7
Bacteroidia; Crocinomitaceae	0	2	0	2	0	6	0	5	0	3	0	7	0	1	0	1	0	5
Gammaproteobacteria; Chromatiaceae	0	2	0	2	0	3	0	5	0	4	0	5	0	3	0	2	0	3
Deltaproteobacteria; Sva1033	0	3	0	2	0	5	0	5	0	4	0	4	0	1	0	1	0	1
Bacteroidia; Mainilabiaceae	0	7	0	5	0	1	0	2	0	5	0	3	1	0	3	0	1	0
Cloacimonadia; MSLB1	1	1	0	9	0	0	0	0	5	0	1	0	1	3	0	2	0	1
Clostridia; Defluviitaleaceae	0	4	0	2	0	0	0	1	0	1	0	2	2	0	1	0	1	0
Clostridia; Ruminococcaceae	0	7	0	6	0	0	2	0	4	0	1	0	6	0	2	0	4	0
Clostridia; Lachnospiraceae	0	1	0	1	0	1	0	1	0	5	2	5	0	1	0	1	0	1
Ignavibacteria; Melioribacteriaceae	0	3	0	5	0	2	0	1	0	3	0	2	0	2	0	7	0	1
Alphaproteobacteria; Hyphomicrobiaceae	0	1	0	1	0	4	0	3	0	2	0	0	1	0	1	0	6	2
Latescibacteria; Latescibacteraceae	0	3	0	2	0	1	0	3	0	3	0	2	0	1	0	4	0	2
Gammaproteobacteria; Thiohalorhabdaceae	0	2	0	2	0	3	0	3	0	3	0	0	1	0	1	0	1	0
Calditricha; Caldithrichaceae	0	2	0	2	0	0	2	0	4	0	3	0	1	0	1	0	3	0
Deltaproteobacteria; Desulfurimonadaceae	0	4	0	3	0	2	0	3	0	4	0	1	0	1	0	1	0	3
Gammaproteobacteria; Psychromonadaceae	0	0	0	1	0	0	0	0	1	1	3	0	0	0	1	0	0	1
Deltaproteobacteria; Syntrophobacteraceae	0	0	0	3	0	2	0	1	0	1	0	0	0	8	0	2	0	2
Bacteroidia; Saprospiraceae	0	4	0	3	0	1	0	1	0	3	0	3	0	1	0	1	0	1
Moduliflexia; Moduliflexaceae	0	1	0	1	0	2	0	2	0	1	0	1	0	1	0	2	0	2
Bacteroidia; Bacteroidaceae	0	0	0	0	0	0	0	0	0	0	2	1	0	0	0	0	0	0
Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	Sample 1	Sample 2	Sample 3	Sample 4	Sample 5	Sample 6	

10 cm depth layer

		Before stocking					High biomass								
1	Deltaproteobacteria; Desulfobacteraceae	7.8	7.6	5.7	6.8	7.4	7.1	6.7	6.7	6.8	8.1	6.9	6.9	5.4	
2	Deltaproteobacteria; Desulfobulbaceae	6.4	6.2	12.8	6	7	8	5.3	5.4	1.8	7.2	3.9	6.9	6	5.9
3	Thermoanaerobaculum; Thermoanaerobaculaceae	5.3	6.9	3.9	6.7	7	6.6	6.9	3.6	2.8	1.4	3	4.7	6.5	2.9
4	Planctomycetia; Planctomycetaceae	5.4	5.8	7.4	5.7	6.2	6.3	2.5	2.1	1.7	3.5	2.4	3.9	5.2	3.2
5	Anaerolineae; Anaerolineaceae	3.9	3.9	1	4.6	4.2	3.5	3	3.5	3.6	2.6	3.4	2.9	3.6	3.3
6	Bacteroidia; Bacteroidetes; B2D-2	1.3	1.2	1.2	1.2	1.4	1.8	1.6	1	1	1.1	1.4	1.4	1.1	1.5
7	Deltaproteobacteria; Syntrophobacteraceae	1.7	1.7	0.2	1.3	1.2	0.6	0.7	1.7	0.1	1	2.6	1	1	1.7
8	Gammaproteobacteria; Unknown_Family	1.2	1.1	3.4	1.6	1.3	2.9	0.8	0.3	0.2	1.2	0.2	1.5	1.4	0.8
9	Gammaproteobacteria; Thiotrichaceae	1.2	0.8	0.4	1.1	1.1	1.6	1	0.9	1	1.7	1.2	2.2	1.6	1.3
10	Bacteroidia; Flavobacteriaceae	0.5	0.6	5.8	0.7	0.4	1.3	1.2	0.4	0.3	1.8	0.2	1.3	0.6	1.2
11	Gammaproteobacteria; Halaeaceae	0.9	1.1	3.1	1.7	1.5	1.4	0.7	0.2	0.1	1.5	0.3	1.7	1.6	0.6
12	Deltaproteobacteria; Desulfurcalaceae	0.9	0.9	0.4	0.5	0.9	1	0.8	1.1	1.5	1.7	1.4	1.2	0.8	1.2
13	Phycisphaerae; SG8-4	0.7	0.7	0.1	0.5	0.7	0.3	1.9	1.8	2.4	1	1.8	0.7	0.5	1.7
14	Calditrichia; Calditrichaceae	0.9	0.8	0.1	0.6	0.7	0.8	1.1	1.4	1.3	0.7	1.4	0.8	0.8	1.4
15	Acidimicrobia; Ilumatobacteriaceae	1.1	1.1	1.8	1.2	1.1	1.1	0.7	0.2	0.1	0.8	0.4	1	1.6	0.7
16	Campylobacteria; Sulfurovaceae	0.2	0.2	0.3	0.5	0.4	0.1	1.5	1.3	0.4	0.2	2.2	0.1	1.3	0.3
17	Thermoleptothrix; 67-114	1.2	1.2	0.3	1.1	0.9	1	0.6	0.8	0.6	0.7	1.1	0.8	1.1	0.6
18	Gammaproteobacteria; Ectothiorhodospiraceae	1.1	0.7	0.6	1	0.8	0.9	1	0.6	0.4	1	0.8	1.3	1	0.6
19	Deltaproteobacteria; Sandaracinaceae	0.9	0.7	0.8	0.8	0.8	0.6	0.3	0.6	0.5	0.7	0.7	0.9	1.3	0.5
20	Alphaproteobacteria; Methylotigellaceae	0.9	1	0.4	0.9	0.6	0.9	0.5	0.7	0.9	0.6	1.5	0.5	0.9	0.6
21	Gammaproteobacteria; Sedimenticolaceae	0.7	0.7	1.3	0.9	0.8	1.2	0.8	0.3	0.2	1.2	0.4	1.5	1	0.5
22	Latescibacteria; Latescibacteriaceae	0.8	0.8	0.1	0.7	0.9	0.5	0.8	0.9	0.9	0.7	0.8	0.7	0.7	0.9
23	Alphaproteobacteria; Hyphomicrobiaceae	0.8	0.8	0.3	0.7	0.6	0.5	0.5	1	1.1	0.5	1.3	0.4	0.6	0.5
24	Gammaproteobacteria; Thiomicrospiraceae	0.3	0.3	1.5	0.5	0.3	1	1.1	0.2	0.1	1.8	0.1	1.6	0.4	0.4
25	Spirochaetia; Spirochaetaceae	0.5	0.6	0.3	0.4	0.5	0.3	1.1	0.7	0.9	0.7	0.7	0.5	0.4	0.9
26	Acidimicrobia; Microtrichaceae	0.7	0.8	0.5	0.8	0.7	0.6	0.4	0.4	0.2	0.5	0.5	0.5	0.6	0.2
27	Anaerolineae; Caldilineaceae	0.4	0.5	1.2	0.7	0.7	0.8	0.3	0.2	0.1	0.5	0.2	0.5	0.9	0.4
28	Bacteroidia; Lentimicrobiaceae	0.3	0.3	1.6	0.3	0.4	0.6	0.6	0.3	0.2	0.8	0.2	0.6	0.3	0.4
29	Bacteroidia; Cyclobacteriaceae	0.4	0.4	1	0.4	0.4	0.8	0.2	0.2	0.2	0.5	0.2	0.4	0.6	0.6
30	Gammaproteobacteria; Spongibacteriaceae	0.3	0.3	1.4	0.6	0.4	0.6	0.2	0	0.1	0.6	0.1	0.6	0.5	0.3
31	Gammaproteobacteria; Chromatiales	0.4	0.3	0.3	0.4	0.5	0.5	0.4	0.2	0.1	0.6	0.2	0.8	0.6	0.3
32	Kiritimatiellae; Kiritimatiellaceae	0.4	0.3	0.7	0.2	0.3	0.3	0.3	0.3	0.1	1	0.1	0.4	0.3	0.5
33	Gammaproteobacteria; Thioalkalipiraceae	0.4	0.2	0	0.2	0.2	0.1	0.3	0.6	0.5	0.3	0.6	0.3	0.2	0.6
34	Ignavibacteria; PHOS-HE36	0.4	0.3	0	0.2	0.2	0.3	0.3	0.5	0.4	0.3	0.4	0.3	0.5	0.5
35	Fibrobacteria; TG3	0.2	0.2	0	0.1	0.2	0	0.2	0.5	0.7	0.4	0.4	0.3	0.3	0.5
36	Gammaproteobacteria; Woeseiaceae	0.6	0.4	0.1	0.3	0.4	0.4	0.4	0.2	0.1	0.2	0.2	0.3	0.4	0.2
37	Phycisphaerae; AKAU3564_sediment_group	0.3	0.3	0.1	0.2	0.2	0.1	0.4	0.4	0.5	0.2	0.4	0.2	0.1	0.5
38	Gammaproteobacteria; Nitrosomonadaceae	0.3	0.3	0.1	0.2	0.3	0.2	0.2	0.4	0.4	0.2	0.4	0.2	0.2	0.3
39	Modiflexia; Modiflexiaceae	0.2	0.3	0.1	0.2	0.3	0.3	0.3	0.3	0.2	0.2	0.2	0.3	0.3	0.3
40	Phycisphaerae; Phycisphaeraceae	0.4	0.3	0.1	0.3	0.3	0.2	0.2	0.2	0.3	0.2	0.2	0.2	0.3	0.2
41	Gemmatimonadetes; Gemmatimonadaceae	0.3	0.2	0	0.2	0.3	0.1	0.2	0.2	0.3	0.2	0.4	0.2	0.2	0.3
42	Bacteroidia; Polixibacteriaceae	0.1	0.2	1	0.1	0.1	0.1	0.3	0.1	0.1	0.6	0.1	0.2	0.1	0.3
43	Bacteroidia; Mariniflabellaceae	0.2	0.2	0.1	0.2	0.2	0.2	0.3	0.2	0.2	0.3	0.2	0.2	0.3	0.4
44	Deltaproteobacteria; MiDBa	0.2	0.2	0.3	0.2	0.3	0.2	0.2	0.1	0.1	0.2	0.1	0.2	0.2	0.2
45	Gammaproteobacteria; Thiohalohalobacteriaceae	0.2	0.2	0.2	0.2	0.3	0.3	0.2	0.1	0.1	0.1	0.1	0.2	0.3	0.2
46	Verrucomicrobiae; DEV007	0.1	0.2	0.5	0.3	0.2	0.2	0.1	0.1	0.1	0	0.1	0.2	0.2	0.1
47	Gammaproteobacteria; Arenicellaceae	0.2	0.2	0.1	0.2	0.2	0.1	0.2	0	0	0.3	0	0.3	0.4	0.2
48	Phycisphaerae; 4572-13	0.2	0.2	0.1	0.2	0.1	0.2	0.1	0.1	0.1	0.1	0.1	0.1	0.2	0.2
49	Alphaproteobacteria; Rhodobacteraceae	0.1	0.2	0.6	0.2	0.1	0.1	0.2	0	0	0	0.1	0	0.1	0.1
50	Deltaproteobacteria; Sva1033	0.1	0.1	0.5	0.1	0.1	0.2	0.1	0.1	0	0.2	0.1	0.1	0.2	0.2
Sample 1		Sample 1						Sample 1							
Sample 2		Sample 2						Sample 2							
Sample 3		Sample 3						Sample 3							
Sample 4		Sample 4						Sample 4							
Sample 5		Sample 5						Sample 5							
Sample 6		Sample 6						Sample 6							

Supplementary file 9: Top 50 family ranked heatmap (and showing their classes) in a combined plot (surface layer = left, 3 cm depth layer = middle, 10 cm depth layer = right). Separated by samplings events (before stocking and peak biomass). Values and color represent the % read abundance, where red = high abundance and white = low abundance.

	Before stocking						Peak biomass							
Flavobacteriaceae; Lutimonas -	43.2	41.3	54.2	46.7	45.2	40.1	25.5	40.8	47.9	49.6	48.3	53.2	48.3	28.4
Flavobacteriaceae; Lutibacter -	10.3	11.9	9.8	10.3	7.9	11.6	41.4	29.2	18.7	16.6	14.6	10.9	9.2	20.6
Flavobacteriaceae; Actibacter -	10.8	12.8	17.3	17.6	14.5	17.5	1.8	2.8	7.3	12.2	8.8	19.4	19.2	10.6
Flavobacteriaceae; Arcticiflavibacter -	4.4	3.6	6.1	6.2	5.8	2.1	5.5	4.1	4.6	6.8	2.4	3.6	2.5	1.7
Flavobacteriaceae; Maribacter -	4.3	4.3	1.2	1.6	2.6	1.8	4.4	3.6	3.7	1.9	6.6	2	2.2	2.8
	Sample 1 -	Sample 2 -	Sample 3 -	Sample 4 -	Sample 5 -	Sample 6 -	Sample 1 +	Sample 2 +	Sample 1 -	Sample 2 -	Sample 3 -	Sample 4 -	Sample 5 -	Sample 6 -

Supplementary file 10: Top 5 genus ranked heatmap of the family Flavobacteriaceae. Separated by samplings events (before stocking and peak biomass). Values and color represent the % read abundance, where red = high abundance and white = low abundance.