

**Additional file 5 Mean relative abundance of phylogenetic clusters among Gammaproteobacteria with significant differences between experimental groups.**

Class / Order / Family / Genus / OTU	LH1-LH2	C1-LH2	C1-C2	C1-HG2	HG1-HG2	Test	<i>p</i> *
Proteobacteria / Gammaproteobacteria /	58.6 <sup>yz</sup> ± 3.5	47.8 <sup>yz</sup> ± 6.5	65.0 <sup>y</sup> ± 4.7	54.1 <sup>z</sup> ± 6.3	55.9 <sup>yz</sup> ± 5.7	LEfSe	≤0.001
Gammaproteobacteria / Enterobacteriales / Enterobacteriaceae / <i>Escherichia-Shigella</i> / OTU_1	44.0 <sup>yz</sup> ± 3.5	27.5 <sup>z</sup> ± 6.5	42.1 <sup>y</sup> ± 4.2	43.1 <sup>yz</sup> ± 6.7	39.2 <sup>y</sup> ± 5.2	LEfSe	0.009
Gammaproteobacteria / Enterobacteriales / Enterobacteriaceae / <i>Escherichia-Shigella</i> / OTU_220	0.0133 <sup>yz</sup> ± 0.0051	0.0043 <sup>z</sup> ± 0.0035	0.0227 <sup>y</sup> ± 0.0069	0.0078 <sup>yz</sup> ± 0.0020	0.0165 <sup>yz</sup> ± 0.0048	LEfSe	0.007
Gammaproteobacteria / Enterobacteriales / Enterobacteriaceae / <i>Escherichia-Shigella</i> / OTU_223	0.0039 <sup>z</sup> ± 0.0021	0.0198 <sup>y</sup> ± 0.0082	0.0039 <sup>z</sup> ± 0.0024	0.0181 <sup>y</sup> ± 0.0047	0.0115 <sup>yz</sup> ± 0.0042	KW	0.019
Gammaproteobacteria / Pseudomonadales	10.7 <sup>ab</sup> ± 1.5	9.3 <sup>ab</sup> ± 2.8	17.0 <sup>a</sup> ± 2.3	7.2 <sup>b</sup> ± 1.3	11.0 <sup>ab</sup> ± 2.0	ANOVA	0.021
Gammaproteobacteria / Pseudomonadales / Pseudomonadaceae / <i>Pseudomonas</i>	8.3 <sup>b</sup> ± 1.6	6.9 <sup>b</sup> ± 1.5	16.2 <sup>a</sup> ± 2.3	6.7 <sup>b</sup> ± 1.2	7.2 <sup>b</sup> ± 1.8	ANOVA	≤0.001
Gammaproteobacteria / Pseudomonadales / Pseudomonadaceae / <i>Pseudomonas</i> / OTU_3	6.6 <sup>b</sup> ± 1.3	5.9 <sup>b</sup> ± 1.6	14.7 <sup>a</sup> ± 1.9	6.0 <sup>b</sup> ± 1.1	6.8 <sup>b</sup> ± 1.8	ANOVA	≤0.001
Gammaproteobacteria / Pseudomonadales / Pseudomonadaceae / <i>Pseudomonas</i> / OTU_291	0.0008 <sup>z</sup> ± 0.0008	0.0121 <sup>y</sup> ± 0.0050	0.0016 <sup>z</sup> ± 0.0016	0.0060 <sup>yz</sup> ± 0.0029	0.0036 <sup>yz</sup> ± 0.0020	LEfSe	0.034
Gammaproteobacteria / Pseudomonadales / Moraxellaceae	2.45 <sup>ab</sup> ± 0.64	2.49 <sup>ab</sup> ± 2.14	0.77 <sup>b</sup> ± 0.61	0.55 <sup>b</sup> ± 0.54	3.81 <sup>a</sup> ± 1.08	KW	0.002
Gammaproteobacteria / Pseudomonadales / Moraxellaceae / <i>Acinetobacter</i>	2.21 <sup>y</sup> ± 0.67	2.35 <sup>yz</sup> ± 2.15	0.61 <sup>yz</sup> ± 0.46	0.51 <sup>z</sup> ± 0.50	1.23 <sup>yz</sup> ± 0.58	LEfSe	0.040
Gammaproteobacteria / Pseudomonadales / Moraxellaceae / <i>Alkanindiges</i> / OTU_14	0.144 <sup>ab</sup> ± 0.143	0.139 <sup>ab</sup> ± 0.139	0.002 <sup>ab</sup> ± 0.002	0 <sup>b</sup>	1.526 <sup>a</sup> ± 0.860	KW	0.034
Gammaproteobacteria / Thiotrichales / OTU_5	1.344 <sup>yz</sup> ± 0.904	0.002 <sup>z</sup> ± 0.001	1.787 <sup>y</sup> ± 0.961	0.716 <sup>yz</sup> ± 0.389	3.402 <sup>yz</sup> ± 2.701	LEfSe	0.015
Gammaproteobacteria / E01-9C-26 marine group	0.17 <sup>y</sup> ± 0.13	1.58 <sup>y</sup> ± 0.85	0.80 <sup>yz</sup> ± 0.64	0.24 <sup>yz</sup> ± 0.18	0 <sup>z</sup>	LEfSe	0.024
Gammaproteobacteria / E01-9C-26 marine group / OTU_12	0.12 <sup>yz</sup> ± 0.12	1.51 <sup>y</sup> ± 0.83	0.80 <sup>yz</sup> ± 0.63	0.14 <sup>yz</sup> ± 0.09	0 <sup>z</sup>	LEfSe	0.019
Gammaproteobacteria / E01-9C-26 marine group / OTU_540	0 <sup>z</sup>	0.0060 <sup>y</sup> ± 0.0034	0.0008 <sup>yz</sup> ± 0.0008	0 <sup>z</sup>	0 <sup>z</sup>	KW	0.038
Gammaproteobacteria / Salinisphaerales / Salinisphaeraceae / <i>Salinisphaera</i>	0.538 <sup>yz</sup> ± 0.407	0.060 <sup>yz</sup> ± 0.060	0.324 <sup>y</sup> ± 0.318	0 <sup>z</sup>	0.344 <sup>yz</sup> ± 0.262	LEfSe	0.018
Gammaproteobacteria / Oceanospirillales / SAR86 clade / OTU_67	0.0008 <sup>yz</sup> ± 0.0008	0 <sup>z</sup>	0 <sup>z</sup>	0.420 <sup>y</sup> ± 0.411	0.237 <sup>yz</sup> ± 0.196	KW	0.027
Gammaproteobacteria / Xanthomonadales / JTB255 marine benthic group	0 <sup>b</sup>	0.29 <sup>a</sup> ± 0.17	0 <sup>b</sup>	0 <sup>b</sup>	0 <sup>b</sup>	KW	0.008

The differences were compared between all groups, simultaneously (ANOVA or KW: Kruskal-Wallis test), and between pairs after Linear Discriminant Analysis (LDA) Effective Size (LEfSe) comparisons. The mean percentages with a single superscript a or b on the same line corresponded to the significant differences according to the post-hoc pairwise comparisons (Tukey's and Dunn's methods for ANOVA and KW, respectively). The means with a single superscript y or z on the same line corresponded to significant differences after LEfSe pairwise comparisons (not shown in case of significant difference with ANOVA or KW on the 3 groups); \*in case of LEfSe, only the lowest *p* among the multiple pairwise comparisons was shown.