**Additional file 6 Mean relative abundance of phylogenetic clusters among Alpha- and Beta-Proteobacteria with significant differences between experimental groups.**

| Class / Order / Family / *Genus* / OTU | LH1-LH2 | C1-LH2 | C1-C2 | C1-HG2 | HG1-HG2 | Test | *P** |
|---|---|---|---|---|---|---|---|
| Proteobacteria / Alphaproteobacteria / | $32.7^{yz}$ ± 5.4 | $44.6^{y}$ ± 7.5 | $23.1^{z}$ ± 6.2 | $40.1^{yz}$ ± 6.4 | $35.9^{yz}$ ± 6.0 | LEfSe | 0.035 |
| Alphaproteobacteria / Sphingomonadales | $22.8^{yz}$ ± 5.8 | $34.0^{yz}$ ± 7.5 | $17.3^{z}$ ± 5.8 | $37.2^{y}$ ± 6.7 | $29.8^{yz}$ ± 5.7 | LEfSe | 0.024 |
| Alphaproteobacteria / Sphingomonadales / Sphingomonadaceae / *Sphingomonas* / OTU_2 | $21.8^{yz}$ ± 6.0 | $33.8^{yz}$ ± 7.5 | $16.2^{z}$ ± 5.7 | $36.8^{yz}$ ± 6.7 | $28.9^{y}$ ± 5.4 | LEfSe | 0.042 |
| Alphaproteobacteria / Sphingomonadales / Sphingomonadaceae / *Sphingomonas* / OTU_169 | $0.0149^{yz}$ ± 0.0042 | $0.0250^{yz}$ ± 0.0078 | $0.0102^{z}$ ± 0.0040 | $0.0362^{yz}$ ± 0.0131 | $0.0374^{y}$ ± 0.0103 | LEfSe | 0.048 |
| Alphaproteobacteria / Sphingomonadales / Sphingomonadaceae / *Sphingomonas* / OTU_201 | $0.0063^{z}$ ± 0.0020 | $0.0190^{yz}$ ± 0.0051 | $0.0149^{yz}$ ± 0.0067 | $0.0276^{y}$ ± 0.0073 | $0.0381^{yz}$ ± 0.0114 | LEfSe | 0.026 |
| Alphaproteobacteria / Sphingomonadales / Sphingomonadaceae / *Sphingomonas* / OTU_271 | $0.0008^{z}$ ± 0.0008 | $0.0035^{yz}$ ± 0.0014 | $0.0031^{yz}$ ± 0.0021 | $0.0069^{yz}$ ± 0.0042 | $0.0065^{y}$ ± 0.0022 | LEfSe | 0.028 |
| Alphaproteobacteria / Sphingomonadales / Sphingomonadaceae / *Sphingobium* / OTU_31 | $0.643^{yz}$ ± 0.641 | $0^{z}$ | $0.932^{yz}$ ± 0.932 | $0.007^{yz}$ ± 0.007 | $0.028^{y}$ ± 0.026 | LEfSe | 0.0499 |
| Alphaproteobacteria / Rhodospirillales / Rhodospirillaceae | $0^{z}$ | $0.18^{yz}$ ± 0.12 | $0^{z}$ | $0.23^{yz}$ ± 0.23 | $0.31^{y}$ ± 0.22 | LEfSe | 0.040 |
| Betaproteobacteria | $1.36^{yz}$ ± 0.37 | $2.15^{yz}$ ± 1.01 | $3.77^{y}$ ± 1.37 | $1.09^{z}$ ± 0.38 | $2.41^{yz}$ ± 0.85 | LEfSe | 0.049 |
| Betaproteobacteria / Burkholderiales / Comamonadaceae | $0.50^{ab}$ ± 0.29 | $0.08^{b}$ ± 0.05 | $2.31^{a}$ ± 0.87 | $0.16^{b}$ ± 0.15 | $0.78^{ab}$ ± 0.50 | KW | 0.042 |
| Betaproteobacteria / Burkholderiales / Oxalobacteraceae / *Herbaspirillum* / OTU_10 | $0.19^{z}$ ± 0.13 | $0.93^{yz}$ ± 0.77 | $0.78^{y}$ ± 0.35 | $0.22^{yz}$ ± 0.12 | $1.26^{yz}$ ± 0.83 | LEfSe | 0.043 |
| Betaproteobacteria / Burkholderiales / Oxalobacteraceae / *Undibacterium* / OTU_50 | $0.0008^{yz}$ ± 0.0008 | $0^{z}$ | $0.513^{y}$ ± 0.509 | $0.0862^{yz}$ ± 0.0862 | $0.0014^{yz}$ ± 0.0010 | LEfSe | 0.040 |

The differences were compared between all groups, simultaneously (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 (Dunn's method). 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 KW on the 3 groups); *in case of LEfSe , only the lowest *p* among the multiple pairwise comparisons was shown.