**Supplementary materials**

**Figure S1. Co-abundance analysis and clustering**. Heatmap reporting the co-presence (red) and co-absence (blue) Pearson correlation between the 15 most abundant bacterial genera. Bacteria have been clustered for co-presence similarity into 5 Co-Abundant Groups (CAG) through Ward linkage, and CAGs have been named after the most abundant genus: "*Gardnerella*-CAG" (yellow), "*Ureaplasma*-CAG" (blue), "*Streptococcus*-CAG" (green), "*Lactobacillus*-CAG" (fuchsia), "*Klebsiella*-CAG" (purple).
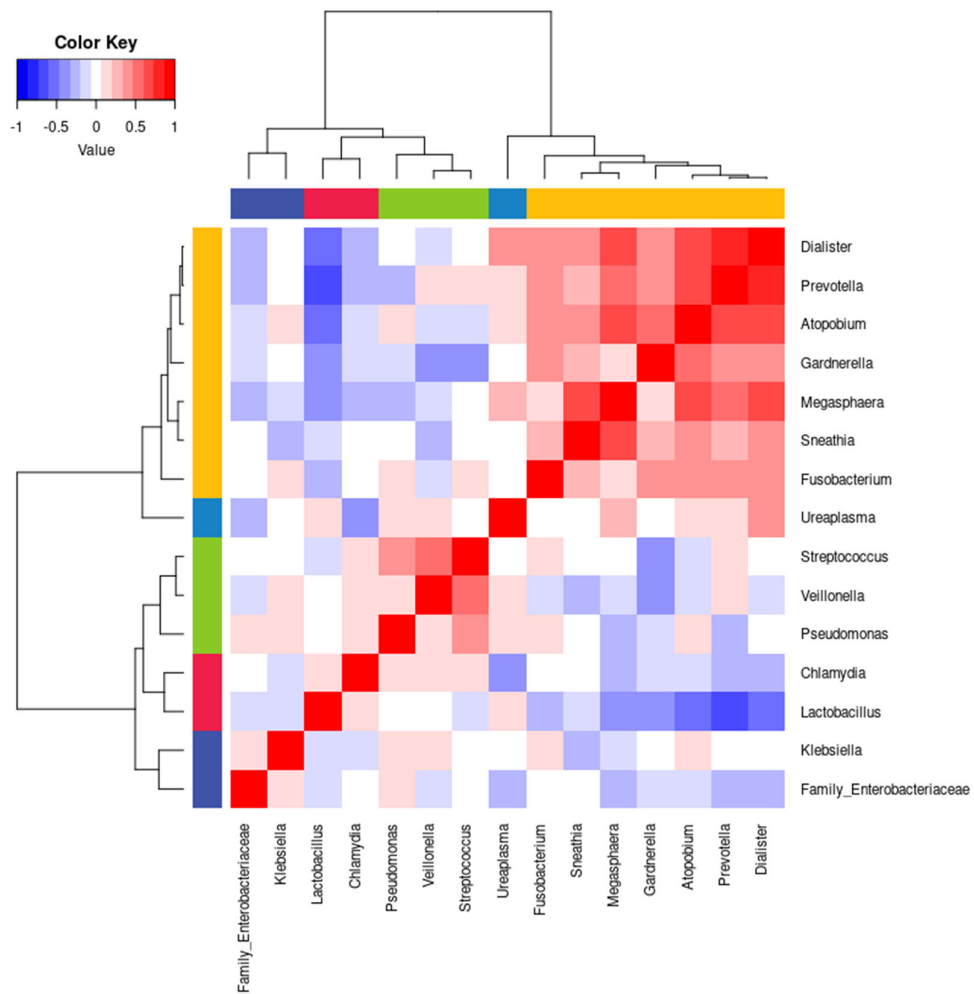
**Table S1. Taxonomic relative abundances at phylum, family, genus levels.** Average relative abundances and standard deviation values are reported for each infection status (not-infected patient, CT-; CT-infected patient, CT+) at the different phylogenetic levels, along with statistical p-values (non-parametric Mann–Whitney U test); p<0.05 were considered significant.

| Taxonomy | | | Average (SD) | | | |
| Phylum | Family | Genus | CT- | CT+ | *p* | significance |
|---|---|---|---|---|---|---|
| Firmicutes | | | 77.17 (19.93) | 66.43 (26.36) | 0.205 | |
| | *Lactobacillaceae* | | 66.52 (28.28) | 62.3 (28.92) | 0.693 | |
| | | *Lactobacillus* | 66.52 (28.28) | 62.3 (28.92) | 0.693 | |
| | *Veillonellaceae* | | 5.08 (13.3) | 1.36 (2.57) | 0.369 | |
| | | *Veillonella* | 3.09 (13.15) | 0.03 (0.03) | 0.449 | |
| | | *Dialister* | 1.53 (3.37) | 0.51 (0.73) | 0.329 | |
| | | *Megasphaera* | 0.42 (1.63) | 0.82 (1.89) | 0.536 | |
| Actinobacteriota | | | 7.96 (9.99) | 10.92 (17.64) | 0.547 | |
| | *Bifidobacteriaceae* | | 6.83 (9.57) | 9.98 (17.12) | 0.507 | |
| | | *Gardnerella* | 6.38 (9.79) | 9.94 (17.12) | 0.457 | |
| | | *Bifidobacterium* | 0.37 (1.17) | 0.01 (0.02) | 0.310 | |
| | *Atopobiaceae* | | 0.47 (1.02) | 0.68 (1.59) | 0.659 | |
| | | *Atopobium* | 0.47 (1.02) | 0.68 (1.59) | 0.658 | |
| | | *Corynebacterium* | 0.30 (0.59) | 0.11 (0.23) | 0.313 | |
| Proteobacteria | | | 7.13 (10.4) | 12.41 (18.85) | 0.312 | |
| | *Pseudomonadaceae* | | 4.05 (6.14) | 5.98 (7.87) | 0.451 | |
| | | *Pseudomonas* | 4.05 (6.14) | 5.98 (7.87) | 0.451 | |
| | *Enterobacteriaceae* | | 2.2 (9.15) | 6.02 (19.25) | 0.449 | |
| | | *Uncl. Enterobacteriaceae* | 2.00 (9.18) | 0.14 (0.42) | 0.508 | |
| | | *Klebsiella* | 0.02 (0.08) | 5.81 (19.28) | 0.172 | |
| Bacteroidetes | | | 6.29 (10.21) | 6.07 (12.40) | 0.957 | |
| | *Prevotellaceae* | | 5.74 (9.39) | 5.59 (11.34) | 0.967 | |
| | | *Prevotella* | 5.58 (9.15) | 5.58 (11.33) | 1 | |
| | *Streptococcaceae* | | 0.61 (1.34) | 0.35 (0.51) | 0.534 | |
| | | *Streptococcus* | 0.61 (1.34) | 0.35 (0.51) | 0.534 | |
| | *Porphyromonadaceae* | | 0.34 (1.18) | 0.42 (1.04) | 0.858 | |
| | | *Porphyromonas* | 0.34 (1.18) | 0.42 (1.04) | 0.852 | |
| | | *Chlamydia* | 0.01 (0.03) | 2.13 (5.10) | 0.063 | |
| Fusobacteriota | | | 1.22 (4.88) | 1.92 (4.00) | 0.682 | |
| | *Leptotrichiaceae* | | 0.72 (3.04) | 1.64 (4.07) | 0.472 | |
| | *Fusobacteriaceae* | | 0.50 (1.84) | 0.28 (0.54) | 0.707 | |
| | | *Sneathia* | 0.72 (3.04) | 1.64 (4.07) | 0.472 | |
| | | *Fusobacterium* | 0.5 (1.84) | 0.28 (0.54) | 0.707 | |

Other phyla

| | | | | |
|---|---|---|---|---|
| *Mycoplasmataceae* | 3.24 (3.60) | 0.37 (0.53) | 0.014 | * |
| *Ureaplasma* | 3.11 (3.44) | 0.34 (0.53) | 0.013 | * |