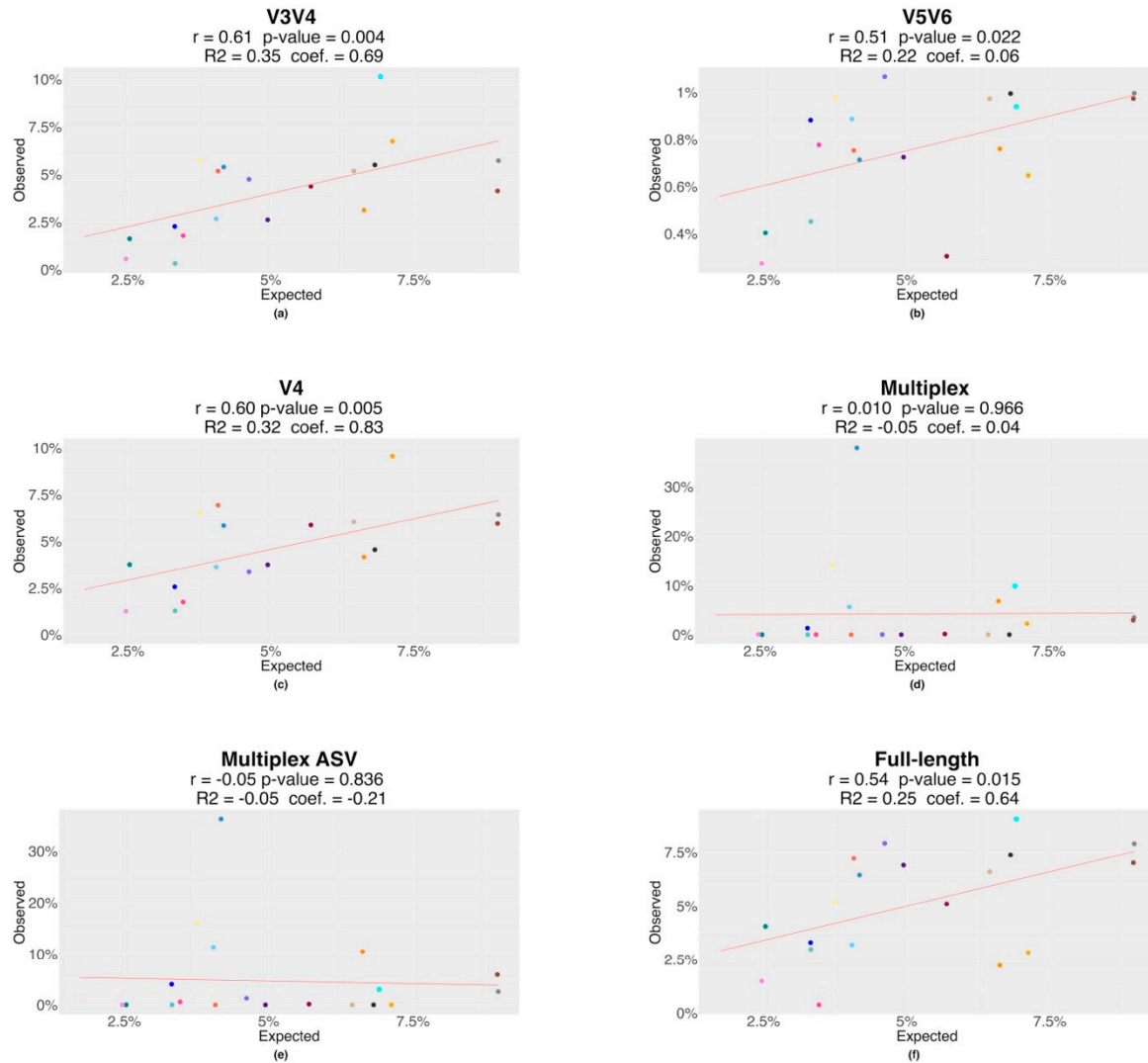


Supplementary Figure S1: Correlation between the expected and observed relative abundances (%) of reads mapping on 16S rRNA genes of the mock species. (a) Correlation for the V3V4 region; (b) correlation for the V5V6 region; (c) correlation for the V4 region; (d) correlation for the multiplex approach; (e) correlation for preliminary ASVs of the multiplex approach; (f) correlation for the full-length approach. For each method, the adjusted R², linear model coefficient (coef.), Pearson correlation coefficient (r) and p-value are shown.



Species

- | | |
|---------------------------------------|-------------------------------------|
| • <i>Acinetobacter baumannii</i> | • <i>Lactobacillus gasseri</i> |
| • <i>Bacillus pacificus</i> | • <i>Neisseria meningitidis</i> |
| • <i>Bacteroides vulgatus</i> | • <i>Porphyromonas gingivalis</i> |
| • <i>Bifidobacterium adolescentis</i> | • <i>Pseudomonas aeruginosa</i> |
| • <i>Clostridium beijerinckii</i> | • <i>Rhodobacter sphaeroides</i> |
| • <i>Cutibacterium acnes</i> | • <i>Schaalia odontolytica</i> |
| • <i>Deinococcus radiodurans</i> | • <i>Staphylococcus aureus</i> |
| • <i>Enterococcus faecalis</i> | • <i>Staphylococcus epidermidis</i> |
| • <i>Escherichia coli</i> | • <i>Streptococcus agalactiae</i> |
| • <i>Helicobacter pylori</i> | • <i>Streptococcus mutans</i> |