**Supporting Information S2**

*R. mucilaginosa* in community metatranscriptomes

*Rothia* was detected in 3/5 metatranscriptomes (Supplementary Figure D1). Even though *R. mucilaginosa* was present in high abundance in the CF1 samples, the number of metatranscriptomic sequences in these samples was too small for significant detection. Metatranscriptome was not generated for the CF1E sample. On the other hand, CF4C, the only time point from patient CF4 containing *R. mucilaginosa* (~20% in the microbiome), had 120 *R. mucilaginosa* hits to mRNAs (1.6% of microbial transcripts) and 15 hits to rRNAs (0.2% of microbial transcripts) in its metatranscriptome. The transcripts were scattered randomly across the genome (Supplementary Figure D2) starting from position 148,000 (no coverage was detected before this position).

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sample | Total number of sequences | Total number of non-rRNA reads | Total number of microbial transcripts | Total  *R. mucilaginosa* hits (rRNA) | Total  *R. mucilaginosa* hits (non-rRNA) |
| CF1D | 1,991 | 1,900 | 283 | 4 | 0 |
| CF1F | 25,238 | 7,971 | 312 | 3 | 2 |
| CF4A | 68,414 | 59,394 | 1,030 | 0 | 0 |
| CF4B | 32,737 | 32,446 | 471 | 0 | 0 |
| CF4C | 36,172 | 34,411 | 7,442 | 15 | 120 |

\* No metatranscriptome was generated from CF1E



SI Fig. D1: The prevalence of *R. mucilaginosa* in the corresponding community transcriptomes.

CF4C_MtMR_rothiacov.pdf

SI Fig. D2: Coverage of 120 CF4C metatranscriptomic mRNA reads on the reference genome *R. mucilaginosa* DY-18 starting from position 148,000 bp.