**Table S1.** Overview of samples and read counts for 16S rRNA (V3-V4) and *tuf* gene sequencing.

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Nares** | **Groin** | **Operation site** |
| **Patients sampled *before* and *after* arthroplasty** | **79** | **61** | **37** |
| **16S (V3-V4) Gene Sequencing Data** |  |  |  |
| Average raw sequencing read counts | 18,015 | 17,376 | 10,076 |
| Average read counts after *decontam()* | 14,171 | 13,127 | 3,429 |
| Patients with >2,000 reads in *before* samples | 65 (82%)1 | 54 (89%)1 | 13 (35%)1 |
| Patients with >2,000 reads in *after* samples | 65 (82%)1 | 42 (69%)1 | 7 (19%)1 |
| Patients with >2,000 reads for both time points | 59 (75%)1 | 39 (64%)1 | 4 (11%)1 |
| Average read count in samples used for analysis | 17,127 | 17,887 | 10,678 |
| ***Tuf* Gene Sequencing Data** |  |  |  |
| Average raw sequencing read counts | 38,653 | 31,334 | 20,805 |
| Average reads mapped to the *tuf* gene database | 38,416 | 30,820 | 20,328 |
| Patients with >2,000 reads in *before* samples | 71 (90%)1 | 58 (95%)1 | 32 (87%)1 |
| Patients with >2,000 reads in *after* samples | 72 (91%)1 | 47 (77%)1 | 23 (62%)1 |
| Patients with >2,000 reads for both time points | 65 (82%)1 | 41 (67%)1 | 20 (54%)1 |
| Average read count in samples used for analysis | 42,107 | 35,029 | 27,114 |

1 Percentages indicate communities remaining for each sampling site after filtering samples with <2000 read counts.