**S3 Table: QIIME2 Software Parameters.** Software parameters for QIIME2 used to process and analyse metataxonomic data

| Software Parameter                          | Value       |
|---------------------------------------------|-------------|
| FastQC filtering min gc percentage          | 25          |
| FastQC filtering max gc percentage          | 75          |
| FastQC filtering min average base quality   | 20          |
| DADA2 forward read trim position            | 21          |
| DADA2 reverse read trim position            | 19          |
| DADA2 forward read truncation position      | No truncation|
| DADA2 reverse read truncation position      | No truncation|
| BLAST+ penalty                             | -5          |
| BLAST+ reward                              | 4           |
| BLAST+ gapopen                             | 5           |
| BLAST+ gapextend                           | 5           |