

| Pipeline step | Program | File | Reads | OTUs |
|---|------------------------|--------------------|------------------------|-------------|
| Raw sequence data | | forward reverse | 4,987,876 4,987,876 | |
| 1. Illumina adapter trimming and filtering | Trimmomatic | forward reverse | 1,630,884 1,630,884 | |
| 2. Quality filtering | FastQFS | forward reverse | 1,630,807 1,630,807 | |
| 3. De-multiplexing 4. Barcode and primer trimming 5. Reorient reads 5' – 3' | | 18S <i>cox1</i> | 653,789 3,417 | |
| 6. Similarity clustering | USEARCH v7 | 18S <i>cox1</i> | | 7,734 96 |
| 7. Re-assemble | Geneious® 7.0.4 | 18S <i>cox1</i> | | 1,037 39 |
| 8. Alignment | Geneious® 7.0.4 | 18S <i>cox1</i> | | 851 36 |
| 9. Mapping | USEARCH v7 | 18S <i>cox1</i> | | 826 35 |
| 10. OTU abundance table | Microsoft Excel (2016) | 18S <i>cox1</i> | 536,609 2,638 | 740 31 |