**S2 Table**: Sequence metadata: products, raw read #’s, raw Q-scores, read numbers

|  |  |
| --- | --- |
| Parameter |  |
| Raw Sequences | 8,821,880 |
| Trimmed/Filtered Sequences (fastq\_quality\_trimmer –l 250 –t 10) | 6,812,005 |
| Sequences discarded due to “barcode errors” (split\_libraries.py –b 10 –H 7) | 691,595 |
| “Barcode error” sequences discarded because of barcode not used in analysis | 639,657 |
| Sequences discarded due to primer mismatches | 759,327 |
| Reads discarded due to mean quality score <25 | 246,031 |
| Reads discarded due to Homopolymer > 7 (split\_libraries.py –b 10 –H 7) | 36,261 |
| Sequences lengths written into split\_library\_out (min/max/mean) | 229/557/276.2 |
| Sequence Counts written into split\_library\_out (min/max/mean) | 20,549/228,067/112,862.02 |
| Sequences written by split\_libraries.py | 5,078,791 |
| Sequences in OTU table (reference-picked, gg\_13\_5) | 3,738,578 |
| Sequences after 0.1% abundance threshold filter | 3,548,180 |
| Sequences lengths in OTU Table mean(standard deviation) | 79,013 (32614) |
| Sequence counts min/max | 11,477/164,828 |
| Sequences lengths in OTU Table, combined replicates, mean(standard deviation) | 236,545 (56,138) |
| Sequence counts, combined replicates, min/max | 163,680/331,857 |