**Supplemental Table S1** Analysis workflow and QIIME parameter settings used in this study.

|  |  |
| --- | --- |
| Command | Options |
| gunzip | -c Sample\_S##\_L001\_R#\_001.fastq.gz > Sample.fastq |
| sed | -e “s/ #:N/\_#\_N /g” Sample .fastq > conv.fastq |
| fastx\_barcode\_splitter.pl | --bol --exact --bcfile [primer\_f/r\_list] --prefix[split\_prefix\_f /r] |
| fastqExtracter.pl | [seqid\_list\_bothmatch\_f/r] > [both\_primer\_match\_fastq\_f/r] |
| fastx\_trimmer | -i [both\_primer\_match\_fastq\_f/r] -o [primer\_trim\_fastq\_f/r]-f 20 -l 250 |
| sickle | pe -f [primer\_trim\_fastq\_f] -r [primer\_trim\_fastq\_r]-t sanger -o [quality\_trim\_fastq\_f] -p [quality\_trim\_fastq\_f]-s [quality\_trim\_fastq\_fr] -q 20 -l 130 |
| flash | [quality\_trim\_fastq\_f] [quality\_trim\_fastq\_r] -f 250 -r 230-m 20 -o merged.fastq |
| fastq\_to\_fasta | -i [merged.fastq, reandlen=246-260] -o [converted\_fasta] -n |
| usearch | -uchime\_ref [converted\_fasta] -db [GG13-8\_97\_otus.udb]-strand plus -chimeras chimera.fasta |
| filter\_fasta.py | -n -f chimera.fasta -s [chimera\_ID\_list] -o final.fasta |
| cat | \*.fasta (all samples) > input.fas |
| pick\_de\_novo\_otus.py | -i input.fas -o otus |
| biom | summarize-table -i otus/otu\_table.biom -o otus/summary |
| summarize\_taxa\_through\_plots.py | -i otus/otu\_table.biom -o Taxa\_summary -m map.txt -s-c Description |
| biom | convert -i otus/otu\_table.biom -o otu\_table.txt-table -type=”OTU table” -to-tsv -header-key taxonomy |

QIIME version 1.9.0 (http://qiime.org/1.9.0/) was used in this study.

These commands (from gunzip to filter\_fasta.py) were used for each MiSeq run file.