

Table S3 The average error rates of the raw sequences reported by sequencing machine, QC sequences passing different quality control methods, the final qualified sequences for OTU delineation, and the qualified sequences pre-clustered with up to 1 difference per 100 bp.

	reported by machine	UPARSE	mothur	moira	S+BH+P	qualified	pre.cluster
run1	2.51%	0.19%	0.22%	0.20%	0.18%	0.07%	0.03%
run2	2.09%	0.47%	0.51%	0.49%	0.48%	0.13%	0.04%
run3	3.91%	0.46%	0.52%	0.50%	0.56%	0.17%	0.06%