Table 2. Summary of the error rates and number of observed OTUs for each region.

Region	Error rate following (%)			Reads remaining (%)	Average no. of OTUs[a]				
	Basic	Predicted	Precluster		Mock[b]	Mock[c]	Soil	Mouse	Human
V4	0.77	0.35	0.158	62.58	33.4	48.9	629.4	212.6	116.9
V1-V3	0.56	0.27	0.068	67.01	20.5	27.7	726.0	107.3	106.4
V3-V5	0.74	0.22	0.035	63.15	21.1	31.2	NA	112.3	83.8
V1-V5	0.57	0.21	0.019	59.29	19.8	27.2	694.4	65.9	84.9
V1-V6	0.60	0.21	0.031	59.90	20.0	46.5	693.0	75.8	89.4
V1-V9	0.68	0.21	0.027	51.33	19.5	40.4	NA	102.5	117.3

[a] The number of OTUs is based on rarefaction of each sample to 1,000 sequences per sample; cells labeled ND reflect samples that did not have at least 1,000 sequences.

[b] Number of OTUs in the mock community when all chimeras were removed; in the absence of chimeras and sequencing errors, there should be 19 OTUs for all three regions.

[c] Number of OTUs in the mock community when chimeras were removed using UCHIME.