

Table S1. Read tracking through the DADA2 pipeline for the V3V4 samples.

V3V4 Sample	input	filtered	denoised	merged	nonchim
Bact674Green (Pohaku)	536524	312116 41.83% reads lost from previous step 41.83% reads lost total	305827 2.01% reads lost from previous step 43.00% reads lost total	287901 5.86% reads lost from previous step 46.34% reads lost total	224147 22.14% reads lost from previous step 58.22% reads lost total
Bact674Blue (Pohaku)	704150	425615 39.56% reads lost from previous step 39.56% reads lost total	418378 1.70% reads lost from previous step 40.58% reads lost total	396312 5.27% reads lost from previous step 43.72% reads lost total	319630 19.35% reads lost from previous step 54.61% reads lost total
Bact677Black (Hiolo South)	671908	352141 47.59% reads lost from previous step 47.59% reads lost total	332288 5.64% reads lost from previous step 50.55% reads lost total	289586 12.85% reads lost from previous step 56.90% reads lost total	226794 21.68% reads lost from previous step 66.25% reads lost total
Bact675Black (Hiolo South)	764345	430823 43.64% reads lost from previous step 43.64% reads lost total	415302 3.60% reads lost from previous step 45.67% reads lost total	381774 8.07% reads lost from previous step 50.05% reads lost total	323532 15.26% reads lost from previous step 57.67% reads lost total
Bact677Green (Hiolo North)	710932	343559 51.67% reads lost from previous step 51.67% reads lost total	326062 5.09% reads lost from previous step 54.14% reads lost total	290176 11.01% reads lost from previous step 59.18% reads lost total	239881 17.33% reads lost from previous step 66.26% reads lost total
Bact677Blue (Hiolo North)	678461	346545 48.92% reads lost from previous step 48.92% reads lost total	327689 5.44% reads lost from previous step 51.70% reads lost total	295553 9.81% reads lost from previous step 56.44% reads lost total	255559 13.53% reads lost from previous step 62.33% reads lost total
Bact676Black (Lohiau)	697317	381310 45.32% reads lost from previous step 45.32% reads lost total	358161 6.07% reads lost from previous step 48.64% reads lost total	315104 12.02% reads lost from previous step 54.81% reads lost total	232219 26.30% reads lost from previous step 66.70% reads lost total
Bact676Green (Lohiau)	523552	237707 54.60% reads lost from previous step 54.60% reads lost total	217428 8.53% reads lost from previous step 58.47% reads lost total	183625 15.55% reads lost from previous step 64.93% reads lost total	130311 29.03% reads lost from previous step 75.11% reads lost total

Table S2. Read tracking through the DADA2 pipeline for the V4V5 samples.

V4V5 Sample	input	filtered	denoised	merged	nonchim
Uni674Green (Pohaku)	631884	354032 43.97% reads lost from previous step 43.97% reads lost total	351996 0.58% reads lost from previous step 44.29% reads lost total	345154 1.94% reads lost from previous step 45.38% reads lost total	316986 8.16% reads lost from previous step 49.83% reads lost total
Uni674Blue (Pohaku)	676630	390580 42.28% reads lost from previous step 42.28% reads lost total	387773 0.72% reads lost from previous step 42.69% reads lost total	378857 2.30% reads lost from previous step 44.01% reads lost total	348909 7.91% reads lost from previous step 48.43% reads lost total
Uni677Black (Hiolo South)	731706	400832 45.22% reads lost from previous step 45.22% reads lost total	390065 2.69% reads lost from previous step 46.69% reads lost total	360354 7.62% reads lost from previous step 50.75% reads lost total	316860 12.07% reads lost from previous step 56.70% reads lost total
Uni675Black (Hiolo South)	713753	387859 45.66% reads lost from previous step 45.66% reads lost total	384187 0.95% reads lost from previous step 46.17% reads lost total	374436 2.54% reads lost from previous step 47.54% reads lost total	365477 2.39% reads lost from previous step 48.80% reads lost total
Uni677Green (Hiolo North)	739724	395620 46.52% reads lost from previous step 46.52% reads lost total	388541 1.80% reads lost from previous step 47.47% reads lost total	369874 4.80% reads lost from previous step 50.0% reads lost total	342737 7.34% reads lost from previous step 53.67% reads lost total
Uni677Blue (Hiolo North)	765667	390372 49.02% reads lost from previous step 49.02% reads lost total	379535 2.78% reads lost from previous step 50.43% reads lost total	354440 6.61% reads lost from previous step 53.71% reads lost total	327206 7.68% reads lost from previous step 57.27% reads lost total
Uni676Black (Lohiau)	684834	359354 47.53% reads lost from previous step 47.53% reads lost total	354785 1.27% reads lost from previous step 48.19% reads lost total	339673 4.26% reads lost from previous step 50.4% reads lost total	320145 4.99% reads lost from previous step 53.25% reads lost total
Uni676Green (Lohiau)	711945	400198 43.79% reads lost from previous step 43.79% reads lost total	392078 2.03% reads lost from previous step 44.93% reads lost total	372252 5.06% reads lost from previous step 47.71% reads lost total	342638 7.96% reads lost from previous step 51.87% reads lost total

Table S3. Representatives of the condensed taxa that significantly correlated with the V3V4 primer set. “ r_{pb} ” refers to the point biserial correlation coefficient.

r_{pb}	p -value	Domain	Phylum	Class	V3V4 Reads
0.845	0.0004	Bacteria	Acetothermia	Acetothermia	5221
0.777	0.0004	Bacteria	Patescibacteria	Microgenomatia	2198
0.735	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	174
0.721	0.0004	Bacteria	Planctomycetota	Planctomycetes	7097
0.705	0.0004	Bacteria	Actinobacteriota	Acidimicrobiia	403
0.698	0.0004	Bacteria	Patescibacteria	ABY1	1931
0.667	0.0004	Bacteria	Patescibacteria	Parcubacteria	1515
0.665	0.0013	Bacteria	Proteobacteria	Alphaproteobacteria	89
0.647	0.0013	Bacteria	Bacteroidota	Unclassified	4220
0.644	0.0259	Bacteria	Myxococcota	Polyangia	181
0.642	0.011	Bacteria	Proteobacteria	Gammaproteobacteria	132
0.62	0.0058	Bacteria	Verrucomicrobiota	Chlamydiae	34
0.619	0.0012	Bacteria	Patescibacteria	ABY1	15791
0.617	0.0064	Bacteria	Proteobacteria	Alphaproteobacteria	915
0.617	0.0209	Bacteria	Acidobacteriota	Unclassified	138
0.616	0.0144	Bacteria	Acidobacteriota	Acidobacteriae	209
0.597	0.0006	Bacteria	Patescibacteria	Parcubacteria	944
0.575	0.0086	Bacteria	Verrucomicrobiota	Verrucomicrobiae	132
0.557	0.0231	Bacteria	Patescibacteria	ABY1	1312
0.547	0.0213	Bacteria	Patescibacteria	Gracilibacteria	1882
0.546	0.0324	Bacteria	Calditrichota	Calditrichia	4349
0.533	0.0355	Bacteria	Patescibacteria	Parcubacteria	213
0.524	0.048	Bacteria	Patescibacteria	Gracilibacteria	180
0.52	0.0013	Bacteria	Patescibacteria	ABY1	729
0.516	0.0017	Bacteria	Proteobacteria	Gammaproteobacteria	110
0.514	0.0008	Bacteria	Patescibacteria	Gracilibacteria	53836
0.514	0.0246	Bacteria	Proteobacteria	Gammaproteobacteria	541
0.512	0.0004	Bacteria	Planctomycetota	Planctomycetes	8660
0.512	0.0004	Bacteria	Patescibacteria	Parcubacteria	269
0.51	0.017	Bacteria	Patescibacteria	ABY1	4854
0.494	0.0159	Bacteria	Proteobacteria	Alphaproteobacteria	313
0.489	0.0004	Bacteria	Desulfobacterota	Desulfuromonadia	4657
0.486	0.0073	Bacteria	Patescibacteria	ABY1	751
0.486	0.0004	Bacteria	Patescibacteria	Parcubacteria	193
0.48	0.0244	Bacteria	Campilobacterota	Campylobacteria	1254
0.472	0.0262	Bacteria	Desulfobacterota	Syntrophobacteria	3707
0.47	0.0004	Bacteria	Actinobacteriota	Acidimicrobiia	1380
0.469	0.0006	Bacteria	Verrucomicrobiota	Chlamydiae	1887
0.469	0.026	Bacteria	Bacteroidota	Bacteroidia	33
0.463	0.0005	Bacteria	Patescibacteria	ABY1	10276
0.463	0.0004	Bacteria	Actinobacteriota	Acidimicrobiia	355
0.454	0.045	Bacteria	Patescibacteria	Microgenomatia	671
0.453	0.0004	Bacteria	Bacteroidota	Bacteroidia	429
0.441	0.0239	Bacteria	Proteobacteria	Gammaproteobacteria	90
0.423	0.0366	Bacteria	Actinobacteriota	Acidimicrobiia	123
0.375	0.0187	Bacteria	Proteobacteria	Gammaproteobacteria	1738
0.375	0.0259	Bacteria	Patescibacteria	Parcubacteria	290
0.334	0.0061	Bacteria	Campilobacterota	Campylobacteria	593
0.32	0.0064	Bacteria	Proteobacteria	Gammaproteobacteria	65
0.264	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	14793

Table S4. Representatives of the condensed taxa that significantly correlated with the V4V5 primer set. “ r_{pb} ” refers to the point biserial correlation coefficient.

r_{pb}	p-value	Domain	Phylum	Class	V4V5 Reads
0.839	0.0004	Bacteria	Planctomycetota	028H05-P-BN-P5	65
0.815	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	178
0.759	0.0008	Bacteria	Chloroflexi	Anaerolineae	2096
0.756	0.0004	Archaea	Crenarchaeota	Nitrososphaeria	12947
0.743	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	638
0.726	0.0004	Archaea	Crenarchaeota	Nitrososphaeria	5372
0.708	0.0037	Bacteria	PAUC34f	Unclassified	511
0.696	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	441
0.691	0.0006	Bacteria	Proteobacteria	Gammaproteobacteria	1050
0.683	0.0004	Bacteria	Planctomycetota	Phycisphaerae	4590
0.683	0.0058	Bacteria	Proteobacteria	Unclassified	8055
0.677	0.0004	Bacteria	Proteobacteria	Alphaproteobacteria	125
0.668	0.0037	Bacteria	Bacteroidota	Bacteroidia	196
0.65	0.0004	Bacteria	Acidobacteriota	Vicinamibacteria	153
0.643	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	174
0.64	0.0099	Bacteria	Desulfobacterota	Desulfuromonadia	7181
0.636	0.0011	Bacteria	Gemmatimonadota	BD2-11	658
0.633	0.007	Bacteria	Proteobacteria	Gammaproteobacteria	153
0.63	0.001	Bacteria	Bacteroidota	Kryptonia	9136
0.622	0.0129	Bacteria	Gemmatimonadota	Unclassified	57
0.615	0.0066	Bacteria	Proteobacteria	Gammaproteobacteria	78
0.613	0.0014	Bacteria	AncK6	Unclassified	409
0.591	0.0014	Bacteria	Verrucomicrobiota	Lentisphaeria	86
0.59	0.0004	Bacteria	Verrucomicrobiota	Omnitrophia	173
0.584	0.0005	Archaea	Nanoarchaeota	Nanoarchaeia	2566
0.575	0.0121	Bacteria	Bacteroidota	Ignavibacteria	38647
0.571	0.0004	Bacteria	Hydrogenedentes	Hydrogenedentia	175
0.569	0.001	Bacteria	Proteobacteria	Gammaproteobacteria	774
0.566	0.0004	Bacteria	Proteobacteria	Alphaproteobacteria	14900
0.564	0.0211	Bacteria	Bacteroidota	Bacteroidia	583
0.563	0.0022	Bacteria	Verrucomicrobiota	Lentisphaeria	361
0.561	0.0004	Bacteria	Proteobacteria	Alphaproteobacteria	1053
0.553	0.0256	Bacteria	Desulfobacterota	Desulfuromonadia	47
0.553	0.026	Bacteria	Proteobacteria	Alphaproteobacteria	120
0.55	0.0229	Bacteria	Bacteroidota	Bacteroidia	366
0.547	0.0264	Bacteria	Proteobacteria	Zetaproteobacteria	990865
0.54	0.0326	Bacteria	Nitrospirota	BMS9AB35	28284
0.538	0.0329	Bacteria	Planctomycetota	BD7-11	3262
0.536	0.0238	Bacteria	Proteobacteria	Gammaproteobacteria	19
0.532	0.0235	Bacteria	Bacteroidota	Bacteroidia	25
0.53	0.0309	Bacteria	Bdellovibrionota	Bdellovibrionia	3130
0.526	0.0407	Bacteria	Nitrospinota	Nitrospina	7061
0.522	0.0259	Bacteria	Myxococcota	Myxococcia	94
0.522	0.0067	Bacteria	Proteobacteria	Gammaproteobacteria	116
0.52	0.001	Archaea	Asgardarchaeota	Heimdallarchaeia	166
0.519	0.0273	Archaea	Asgardarchaeota	Lokiarchaeia	90
0.515	0.0433	Bacteria	Chloroflexi	Chloroflexia	476
0.515	0.0413	Bacteria	Unclassified	Unclassified	102035
0.509	0.001	Bacteria	Chloroflexi	Chloroflexia	1049
0.5	0.0007	Bacteria	Deinococcota	Deinococci	3676
0.495	0.0019	Bacteria	Verrucomicrobiota	Verrucomicrobiae	247
0.49	0.0045	Bacteria	Desulfobacterota	Unclassified	11101
0.486	0.0016	Bacteria	Proteobacteria	Alphaproteobacteria	19849
0.481	0.006	Bacteria	Proteobacteria	Alphaproteobacteria	547
0.479	0.006	Bacteria	Bacteroidota	Bacteroidia	381
0.478	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	1245
0.476	0.0273	Bacteria	Chloroflexi	Anaerolineae	126
0.471	0.0023	Bacteria	Bacteroidota	Ignavibacteria	3042
0.464	0.0251	Bacteria	Acidobacteriota	Thermoanaerobaculia	738
0.462	0.001	Bacteria	Desulfobacterota	Desulfarculia	172
0.462	0.0239	Bacteria	Spirochaetota	Leptospirae	1861
0.46	0.0015	Bacteria	Bacteroidota	Bacteroidia	148
0.454	0.0273	Bacteria	Chloroflexi	Dehalococcoidia	6015
0.454	0.0372	Bacteria	Marinimicrobia	Unclassified	130
0.451	0.0206	Bacteria	Planctomycetota	Planctomycetes	183
0.449	0.006	Bacteria	Spirochaetota	Spirochaetia	1587
0.433	0.0453	Bacteria	Proteobacteria	Gammaproteobacteria	79
0.424	0.023	Bacteria	Actinobacteriota	Coriobacteriia	209
0.409	0.0045	Bacteria	Dependentiae	Babeliae	189
0.39	0.0004	Bacteria	Bacteroidota	Bacteroidia	11087
0.382	0.0134	Bacteria	Planctomycetota	Planctomycetes	437
0.325	0.0461	Archaea	Halobacterota	Unclassified	1570
0.269	0.0004	Bacteria	Proteobacteria	Gammaproteobacteria	7319

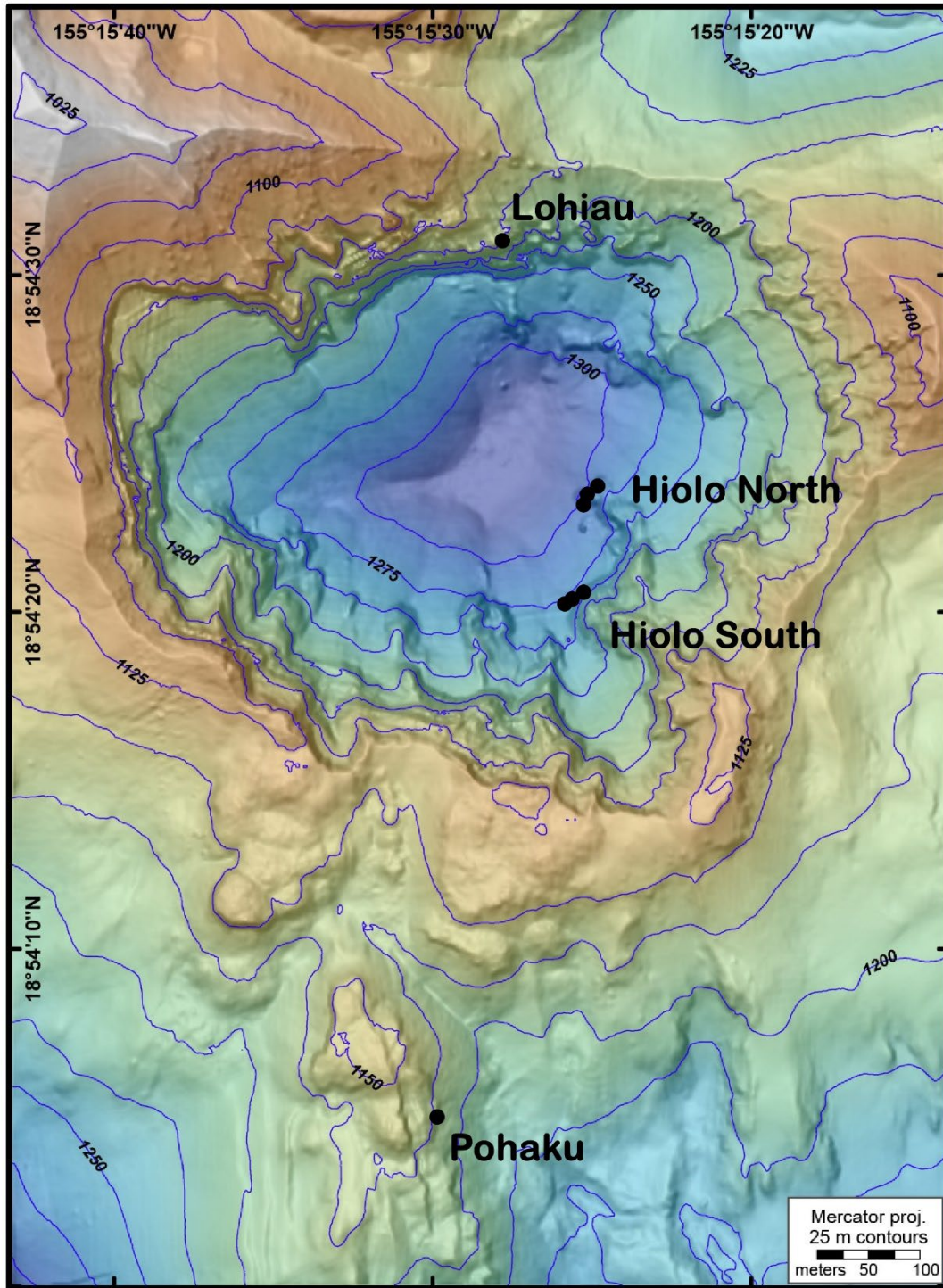


Fig. S1. Bathymetric map (high resolution at <2 m) of sampling sites in and near Pele's Pit caldera on the summit of Kama'ehuakanaloa Seamount, Hawai'i. Precise marker locations include Pohaku (Marker 57), Lohiau (Marker 2), Hiolo North (Markers 36, 39 and 31), and Hiolo South (Markers 34, 38 and Ku'kulu). Courtesy of Susan Merle, NOAA EOI/OSU.

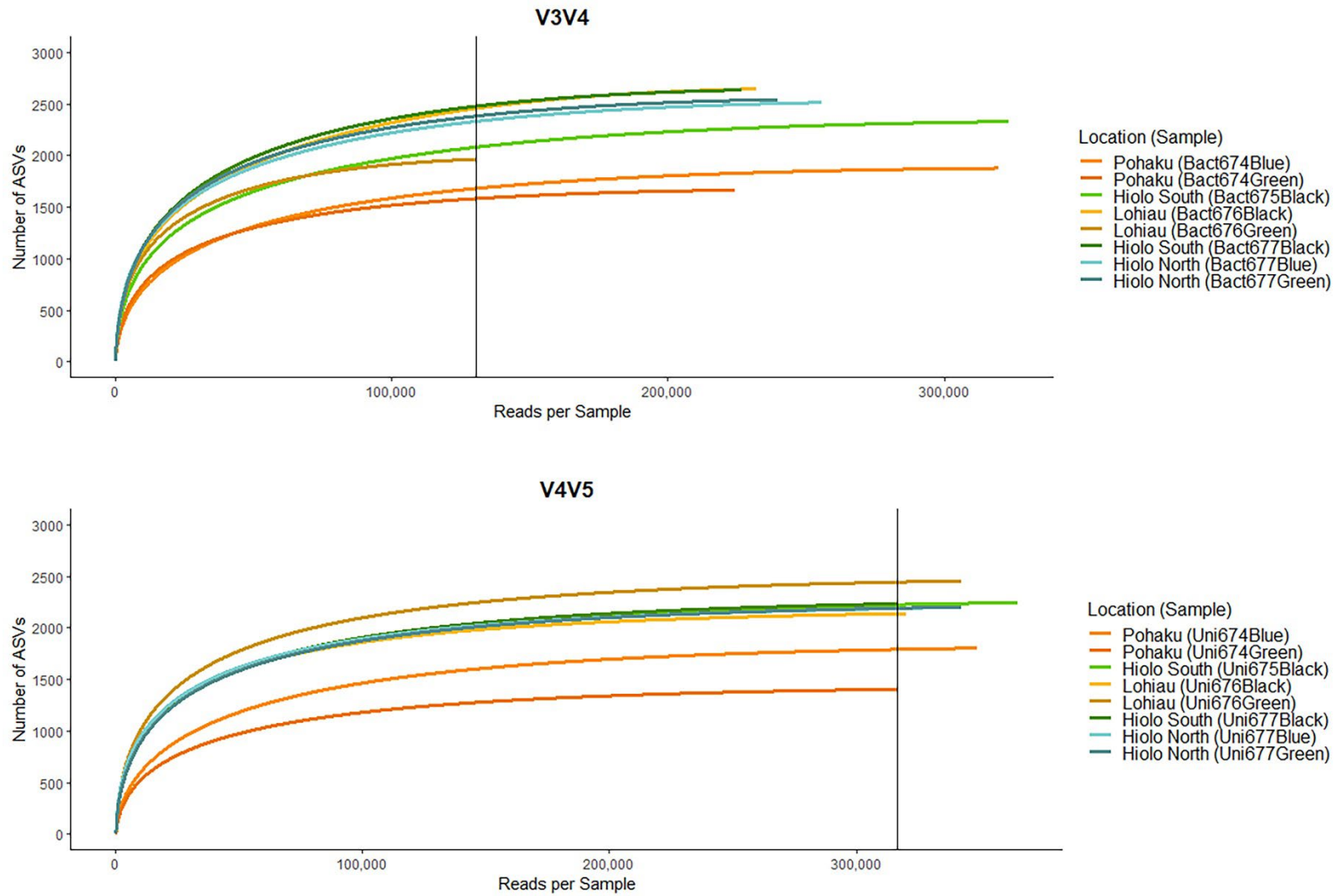


Fig. S2. Rarefaction curves for each microbial mat community, colored by sample location for both primer sets. Vertical lines denote the minimum read depth. NB: The difference in the x-axis scales.