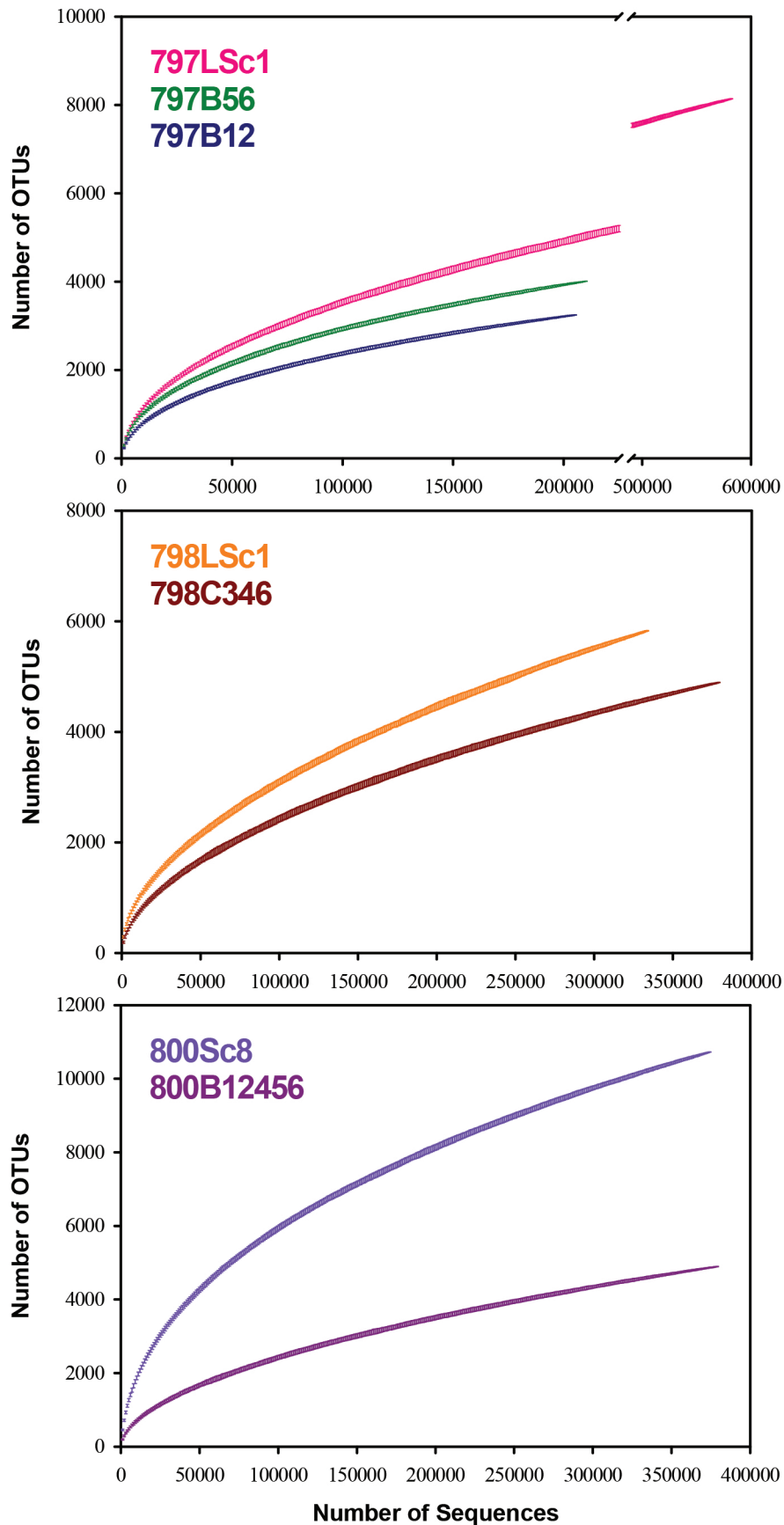
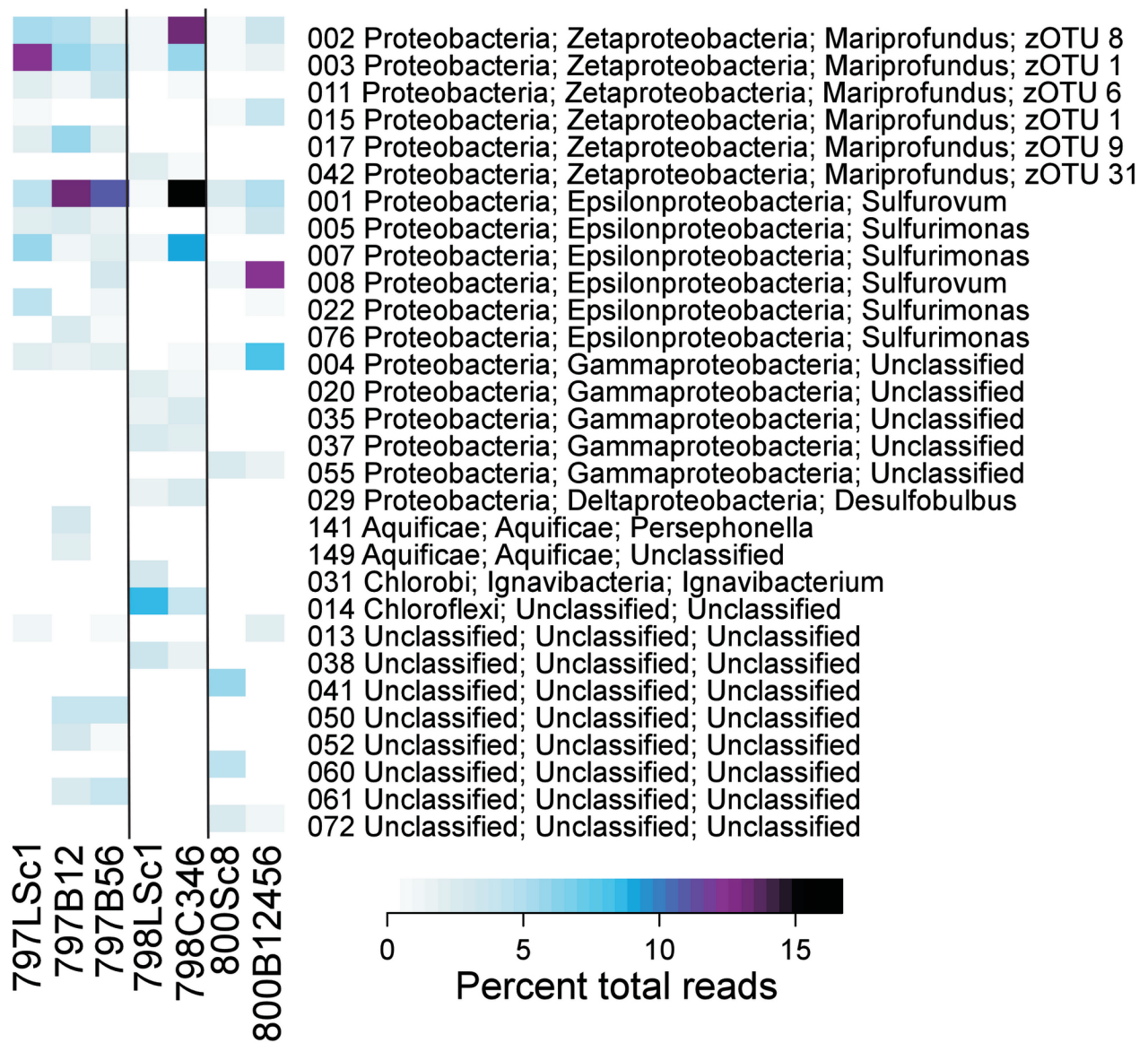


Supplemental Table 1. Top BLAST hits of the abundant unclassified Gammaproteobacteria to the nucleotide collection (nr/nt) and SSU ribosomal RNA databases.

OTU	nucleotide collection (nr/nt) database				SSU ribosomal RNA database					
	Top hit identification	% identity	E-value	Bit score	Type strain	Type strain metabolism	Top hit identification	% identity	E-value	Bit score
004	gb FJ497398	98.8	0	756	<i>Spongibacter marinus</i> strain DSM 17750	Heterotrophic	NR_118015	92.3	3.71E-171	599
009	gb FJ640816	96.9	0	710	<i>Thioalkalipira microaerophila</i> strain ALEN 1	Sulfur-oxidizing	NR_025239	89.4	2.95E-152	536
020	gb KT460324	99.5	0	725	<i>Thiohalobacter thiocyanaticus</i> strain HRh1	Sulfur-oxidizing	NR_116699	94.2	6.16E-174	608
030	dbj AB831349	99.3	0	765	<i>Sedimenticola thiotaurini</i> strain SIP-G1	Sulfur-oxidizing	NR_136790	90.8	3.76E-161	566
035	emb LN589523	96.9	0	712	<i>Thiopfundum lithotrophicum</i> strain 106	Sulfur-oxidizing	NR_112829	90.6	6.29E-159	558
037	gb KR920926	97.4	0	721	<i>Thiopfundum lithotrophicum</i> strain 106	Sulfur-oxidizing	NR_112829	92.4	7.97E-173	604
043	gb JN977144	99.8	0	774	<i>Wenzhouxiangella marina</i> strain Ma-11	Heterotrophic	NR_136878	93.4	1.70E-179	627
046	gb KM042683	100.0	0	782	<i>Halochromatium salexigens</i> strain 6310	Mixotrophic	NR_036810	89.4	3.81E-151	532
048	emb LN589563	99.1	0	760	<i>Bacterioplanes sanyensis</i> strain GYP-2	Heterotrophic	NR_126264	92.0	1.72E-169	593
049	gb FJ497359	100.0	0	782	<i>Marinicella litoralis</i> strain KMM 3900	Heterotrophic	NR_112913	90.1	1.36E-155	547
055	dbj AB831336	99.5	0	771	<i>Pseudomonas endophytica</i> strain BSTT44	Heterotrophic	NR_136473	91.0	2.25E-163	573
080	gb GU197441	97.6	0	726	<i>Sedimenticola thiotaurini</i> strain SIP-G1	Sulfur-oxidizing	NR_136790	91.5	3.73E-166	582
085	gb KM018594	98.1	0	737	<i>Sedimenticola thiotaurini</i> strain SIP-G1	Sulfur-oxidizing	NR_136790	91.3	1.74E-164	577
114	gb FJ535296	96.7	0	704	<i>Rheinheimera tuosuensis</i> strain TS-T4	Heterotrophic	NR_133840	89.2	1.77E-149	527
121	emb LN589480	99.5	0	771	<i>Thiohalophilus thiocyanatoxydans</i> strain HRhD 2	Sulfur-oxidizing	NR_043875	90.8	1.35E-160	564
153	gb AY883934	99.3	0	765	<i>Thiopfundum lithotrophicum</i> strain 106	Sulfur-oxidizing	NR_112829	89.1	1.77E-149	527
161	gb FJ497623	92.7	0	610	<i>Thiohalomonas denitrificans</i> strain HLD 2	Sulfur-oxidizing	NR_044097	88.4	6.43E-144	508
230	emb LN589561	97.4	0	721	<i>Thiohalophilus thiocyanatoxydans</i> strain HRhD 2	Sulfur-oxidizing	NR_043875	90.2	1.36E-155	547



Supplemental Figure 1. Rarefaction curves for OTUs at 97% sequence similarity with 95% confidence intervals for three locations where scoop and biomat samples were taken of the same microbial mats. Sample 797LSc1 corresponds with 797B12 and 797B56 at Snap-Snap Vent, Urashima; 798LSc1 corresponds with 798C346 at Yellow Cone Vent, NW Eifuku; 800Sc8 corresponds with 800B12456 at Olde Iron Slides, NW Rota-1.



Supplemental Figure 2. Heatmap comparing bacterial OTU abundance at three different locations between scoop and biomat samples taken from the same microbial mats. OTUs with a maximum abundance > 2% in at least one of these seven samples are included with OTU number, phylum, class, and genus classifications. For Zetaproteobacteria, zOTU classification is also listed. Sample 797LSc1 corresponds with 797B12 and 797B56 at Snap-Snap Vent, Urashima; 798LSc1 corresponds with 798C346 at Yellow Cone Vent, NW Eifuku; 800Sc8 corresponds with 800B12456 at Olde Iron Slides, NW Rota-1. Black lines separate the three locations.