Supplementary Information

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Supplementary Table 1. Sampling details

ELSC Site/ Vent	Sample	Sample type	Date(DD/MM/ YYYY)	Latitude/Longitude	Depth (m)	Filter size (µm)	No. of reads	Reference
MARINER/ MA3	TN236-J2440-2	Near bottom background	20/06/2009	S 22 10.818293 W 176 36.086423	1915	0.8	x	(Sheik et al., 2014)
	TN236-J2440-6	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1915	0.8	x	(Sheik et al., 2014)
	TN236-J2440-7	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1915	0.8	x	(Sheik et al., 2014)
	TN236-J2440-10	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1910	0.8	x	(Sheik et al., 2014)
	TN236-J2440-11	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1910	0.8	x	(Sheik et al., 2014)
	TN236-J2440-14	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1900	0.8	x	(Sheik et al., 2014)
	TN236-J2440-15	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1900	0.8	x	(Sheik et al., 2014)
	TN236-J2440-18	**Rising Plume**	**20/06/2009**	**S 22 10.818293 W 176 36.086423**	**1890**	**0.8**	**185,135,248**	**THIS STUDY**
	TN236-J2440-19	Rising Plume	20/06/2009	S 22 10.818293 W 176 36.086423	1890	0.8	x	(Sheik et al., 2014)
	TN236-J2440-21	Above plume background	20/06/2009	S 22 10.818293 W 176 36.086423	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2440-24	Blank	20/06/2009	x	x	0.8	x	
ABE/ A1	**TN236-J2449-2**	**Near bottom background**	**04/07/2009**	**S 22 45.677706 W 176 11.369574**	**2155**	**0.8**	**169,488,288**	**THIS STUDY**
	TN236-J2449-4	Rising Plume	04/07/2009	S 22 45.677706 W 176 11.369574	2155	0.8	x	(Sheik et al., 2014)
	TN236-J2449-5	Rising Plume	04/07/2009	S 22 45.677706 W 176 11.369574	2155	0.8	x	(Sheik et al., 2014)
	TN236-J2449-10	Rising Plume	04/07/2009	S 22 45.677706 W 176 11.369574	2150	0.8	x	(Sheik et al., 2014)
	TN236-J2449-14	Rising Plume	04/07/2009	S 22 45.677706 W 176 11.369574	2150	0.8	x	(Sheik et al., 2014)
	TN236-J2449-21	Above plume background	04/07/2009	S 22 45.677706 W 176 11.369574	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2449-24	Blank	04/07/2009	x	x	0.8	x	
ABE/ A1	TN236-J2435-3	Near bottom background	13/06/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
	TN236-J2435-4	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
	TN236-J2435-5	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
	TN236-J2435-8	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2149	0.8	x	(Sheik et al., 2014)
	TN236-J2435-9	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2149	0.8	x	(Sheik et al., 2014)
	TN236-J2435-12	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2129	0.8	x	(Sheik et al., 2014)
	TN236-J2435-13	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2129	0.8	x	(Sheik et al., 2014)
	TN236-J2435-16	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2069	0.8	x	(Sheik et al., 2014)
	TN236-J2435-17	Rising Plume	13/06/2009	S 20 45.672883 W 176 11.434418	2069	0.8	x	(Sheik et al., 2014)
	TN236-J2435-20	Above plume background	13/06/2009	S 20 45.672883 W 176 11.434418	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2435-24	Blank	13/06/2009	x	x	0.8	x	

TAHI MOANA / SP2	TN236-J2450-2	Near bottom background	05/07/2009	S 20 40.894100 W 176 10.940463	2235	0.8	x	(Sheik et al., 2014)
	TN236-J2450-4	Rising Plume	05/07/2009	S 20 40.894100 W 176 10.940463	2235	0.8	x	(Sheik et al., 2014)
	TN236-J2450-5	Rising Plume	05/07/2009	S 20 40.894100 W 176 10.940463	2235	0.8	x	(Sheik et al., 2014)
	TN236-J2450-9	**Rising Plume**	**05/07/2009**	**S 20 40.894100 W 176 10.940463**	**2229**	**0.8**	**186,087,990**	**THIS STUDY**
	TN236-J2450-10	Rising Plume	05/07/2009	S 20 40.894100 W 176 10.940463	2229	0.8	x	(Sheik et al., 2014)
	TN236-J2450-14	Rising Plume	05/07/2009	S 20 40.894100 W 176 10.940463	2229	0.8	x	(Sheik et al., 2014)
	TN236-J2450-20	Above plume background	05/07/2009	S 20 40.894100 W 176 10.940463	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2450-24	Blank	05/07/2009	x	x	0.8	x	
KILO MOANA / KM1	TN236-J2436-2	Near bottom background	15/06/2009	S 20 3.229502 W 176 8.015363	2665	0.8	x	(Sheik et al., 2014)
	TN236-J2436-4	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2665	0.8	x	(Sheik et al., 2014)
	TN236-J2436-5	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2665	0.8	x	(Sheik et al., 2014)
	TN236-J2436-8	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2655	0.8	x	(Sheik et al., 2014)
	TN236-J2436-9	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2655	0.8	x	(Sheik et al., 2014)
	TN236-J2436-12	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2635	0.8	x	(Sheik et al., 2014)
	TN236-J2436-13	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2635	0.8	x	(Sheik et al., 2014)
	TN236-J2436-16	**Rising Plume**	**15/06/2009**	**S 20 3.229502 W 176 8.015363**	**2605**	**0.8**	**174,530,426**	**THIS STUDY**
	TN236-J2436-17	Rising Plume	15/06/2009	S 20 3.229502 W 176 8.015363	2605	0.8	x	(Sheik et al., 2014)
	TN236-J2436-20	Above plume background	15/06/2009	S 20 3.229502 W 176 8.015363	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2436-24	Blank	15/06/2009	x	x	0.8	x	
TUI MALILA / TM1	TN236-J2447-2	Near bottom background	01/07/2009	S 21 59.401181 W 176 34.124651	1929	0.8	x	(Sheik et al., 2014)
	TN236-J2447-4	Rising Plume	01/07/2009	S 21 59.401181 W 176 34.124651	1929	0.8	x	(Sheik et al., 2014)
	TN236-J2447-5	Rising Plume	01/07/2009	S 21 59.401181 W 176 34.124651	1929	0.8	x	(Sheik et al., 2014)
	TN236-J2447-9	Rising Plume	01/07/2009	S 21 59.401181 W 176 34.124651	1919	0.8	x	(Sheik et al., 2014)
	TN236-J2447-10	**Rising Plume**	**01/07/2009**	**S 21 59.401181 W 176 34.124651**	**1919**	**0.8**	**187,067,650**	**THIS STUDY**
	TN236-J2447-14	Rising Plume	01/07/2009	S 21 59.401181 W 176 34.124651	1899	0.8	x	(Sheik et al., 2014)
	TN236-J2447-18	Rising Plume	01/07/2009	S 21 59.401181 W 176 34.124651	1899	0.8	x	(Sheik et al., 2014)
	TN236-J2447-20	Above plume background	01/07/2009	S 21 59.401181 W 176 34.124651	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2447-24	Blank	01/07/2009	x	x	0.8	x	
TUI MALI	TN236-J2442-2	Near bottom background	23/06/2009	S 21 59.274547 W 176 34.060503	1928	0.8	x	(Sheik et al., 2014)
	TN236-J2442-5	Rising Plume	23/06/2009	S 21 59.274547 W 176 34.060503	1928	0.8	x	(Sheik et al., 2014)
	TN236-J2442-9	Above plume background	23/06/2009	S 21 59.274547 W 176 34.060503	~1300	0.8	x	(Sheik et al., 2014)
	TN236-J2442-20	Above plume background	23/06/2009	S 21 59.274547 W 176 34.060503	~1000	0.8	x	(Sheik et al., 2014)

LA/TMS1	TN236-J2442-24	Blank	23/06/2009	x	x	0.8	x	
TAHI MOANA / SP1	TN236-J2445-2	Near bottom background	29/06/2009	S 20 40.927843 W 176 11.001806	2230	0.8	x	(Sheik et al., 2014)
	TN236-J2445-4	Rising Plume	29/06/2009	S 20 40.927843 W 176 11.001806	2230	0.8	x	(Sheik et al., 2014)
	TN236-J2445-10	Rising Plume	29/06/2009	S 20 40.927843 W 176 11.001806	2220	0.8	x	(Sheik et al., 2014)
	TN236-J2445-13	Rising Plume	29/06/2009	S 20 40.927843 W 176 11.001806	2220	0.8	x	(Sheik et al., 2014)
	TN236-J2445-20.2	**Above plume background**	**29/06/2009**	**S 20 40.927843 W 176 11.001806**	**~1300**	**0.2**	**181,482,188**	**THIS STUDY**
	TN236-J2445-20.8	Above plume background	29/06/2009	S 20 40.927843 W 176 11.001806	~1000	0.8	x	(Sheik et al., 2014)
	TN236-J2445-24	Blank	29/06/2009	x	x	0.8	x	
KILO MOANA / KM4	TN235-J2424-7	Rising Plume	22/05/2009	S 20 3.234200 W 176 8.008000	2639	0.8	x	(Sheik et al., 2014)
	TN235-J2424-8	**Rising Plume**	**22/05/2009**	**S 20 3.234200 W 176 8.008000**	**2639**	**0.8**	**118,751,402**	**THIS STUDY**
	TN235-J2424-11	Rising Plume	22/05/2009	S 20 3.234200 W 176 8.008000	2629	0.8	x	(Sheik et al., 2014)
	TN235-J2424-12	Rising Plume	22/05/2009	S 20 3.234200 W 176 8.008000	2629	0.8	x	(Sheik et al., 2014)
	TN235-J2424-16	Rising Plume	22/05/2009	S 20 3.234200 W 176 8.008000	2599	0.8	x	(Sheik et al., 2014)
	TN235-J2424-19	Rising Plume	22/05/2009	S 20 3.234200 W 176 8.008000	2599	0.8	x	(Sheik et al., 2014)
	TN235-J2424-20	**Rising Plume**	**22/05/2009**	**S 20 3.234200 W 176 8.008000**	**2439**	**0.8**	**157,276,514**	**THIS STUDY**
	TN235-J2424-22	Above plume background	22/05/2009	S 20 3.234200 W 176 8.008000	x	0.8	x	(Sheik et al., 2014)
ABE / A1	**TN235-J2426-7**	**Rising Plume**	**25/05/2009**	**S 20 45.672883 W 176 11.434418**	**2159**	**0.8**	**181,094,744**	**THIS STUDY**
	TN235-J2426-12	Rising Plume	25/05/2009	S 20 45.672883 W 176 11.434418	2149	0.8	x	(Sheik et al., 2014)
	TN235-J2426-16	Rising Plume	25/05/2009	S 20 45.672883 W 176 11.434418	2119	0.8	x	(Sheik et al., 2014)
	TN235-J2426-20	**Rising Plume**	**25/05/2009**	**S 20 45.672883 W 176 11.434418**	**1959**	**0.8**	**168,325,584**	**THIS STUDY**
	TN235-J2426-24	Blank	25/05/2009	x	x	0.8	x	
ABE / A1	TN235-J2427-2	Near bottom background	27/05/2009	S 20 45.672883 W 176 11.434418	2155	0.8	x	(Sheik et al., 2014)
	TN235-J2427-7	Rising Plume	27/05/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
	TN235-J2427-8	Rising Plume	27/05/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
	TN235-J2427-19	Rising Plume	27/05/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
	TN235-J2427-20	Rising Plume	27/05/2009	S 20 45.672883 W 176 11.434418	2159	0.8	x	(Sheik et al., 2014)
KILO M	TN236-CTD-KM-IP1	Neutrally buoyant plume	13/06/2009	S 20 3.246489 W 176 8.011308	2305	0.2	x	(Sheik et al., 2014)
	TN236-CTD-KM-IP2	**Neutrally buoyant plume**	**13/06/2009**	**S 20 3.246489 W 176 8.011308**	**2315**	**0.2**	**188,964,668**	**THIS STUDY**

OANA	TN236-CTD-KM-BP1	Below Plume background	13/06/2009	S 20 3.246489 W 176 8.011308	2400	0.2	x	(Sheik et al., 2014)
	TN236-CTD-KM-BP2	Below Plume background	13/06/2009	S 20 3.246489 W 176 8.011308	2350	0.2	x	(Sheik et al., 2014)
TUI MALILA	TN236-CTD-Tui-IP1	Neutrally buoyant plume	20/06/2009	S 21.98790 W 176.56768	1675	0.2	x	(Sheik et al., 2014)
	TN236-CTD-Tui-IP2	Neutrally buoyant plume	20/06/2009	S 21.98790 W 176.56768	1650	0.2	x	(Sheik et al., 2014)
	TN236-CTD-Tui-BP1	Below Plume background	20/06/2009	S 21.98790 W 176.56768	1750	0.2	x	(Sheik et al., 2014)
Tahi Moana/1D	TN236-CTD-TM-IP1	Neutrally buoyant plume	05/07/2009	S 20 40.3905 W 176 10.8435	2050	0.2	x	(Sheik et al., 2014)
MARINER	TN236-CTD-Mar-IP1	Neutrally buoyant plume	19/06/2009	S 20 10.8035165 W 176 36.074496	1740	0.2	x	(Sheik et al., 2014)
	TN236-CTD-Mar-IP2	Neutrally buoyant plume	19/06/2009	S 20 10.8035165 W 176 36.074496	1725	0.2	x	(Sheik et al., 2014)
	TN236-CTD-Mar-BP1	**Below Plume background**	**19/06/2009**	**S 20 10.8035165 W 176 36.074496**	**1785**	**0.2**	**154,673,072**	**THIS STUDY**
	TN236-CTD-Mar-BP2	Below Plume background	19/06/2009	S 20 10.8035165 W 176 36.074496	1780	0.2	x	(Sheik et al., 2014)
	TN236-CTD-Mar-BP1	Above Plume background	19/06/2009	S 20 10.8035165 W 176 36.074496	1680	0.2	x	(Sheik et al., 2014)
	TN236-CTD-Mar-BP2	Above Plume background	19/06/2009	S 20 10.8035165 W 176 36.074496	1600	0.2	x	(Sheik et al., 2014)

Supplementary Table S2. Endmember fluid concentrations for model.

Property	**ABE A1 vent**[a]	**Mariner MA1 vent**[a]	**Kilo Moana KM1 vent**[a]	**Seawater**
T (°C)	309	334	333	2
pH[b]	4.3	2.5	3.6	8
O_2, aqueous	0	0	0	0.15[c]
NH_4^+[d]	0.23	0.23	0.23	0
N_2, aqueous	0.48[e]	0.48[e]	0.48	0.58[e]
NO_3^-	0	0	0	0.035
NO_2^-	0	0	0	0.001
H_2, aqueous[f]	0.20	0.20	0.51	0.0000004
SO_4^{2-}	0	0	0	28
H_2S, aqueous	3.6	6.2	6	0
$\sum CO_2$, aqueous	8	32	8.1	1.8
CH_4, aqueous[f]	0.04	0.04	0.06	0
Cl^-	534	624	581	540
Na^+	430	458	486	464
Ca^{2+}	39	45	35	10.2
Mg^{2+}	0	0	0	52.2
K^+	25	36	17	10.1
SiO_2, aqueous	17	16	19	0.17
Fe	0.27	11.3	2.5	0
Mn^{2+}	0.47	5.94	0.51	0
Cu^+[g]	0.03	0.03	0.03	0
Zn^{2+}[g]	0.07	0.07	0.07	0
Ba^{2+}[g]	0.05	0.05	0.05	0

All concentrations in mmol/kg vent fluid.

(a) Vent chemistry data (Mottl et al., 2011).
(b) *In situ* pH based on 25 °C measurement.
(c) WOCE section P06 background dissolved O2, NO_3^-, and NO_2^- (Talley 2007).
(d) Predicted to exist as NH_3 in vent fluid; , assumed to be due to 17% conversion of seawater dissolved N_2 (Brandes et al., 1998).

(e) Seawater dissolved N_2 (Weiss and Craig 1973); vent fluid dissolved N_2 assumed to be 83% of seawater concentration (Brandes et al., 1998).
(f) Dissolved gases (Seewald et al., 2005).
(g) Based on EPR 21° N (Von Damm et al., 1985) for lack of more relevant data.

Supplementary Table 3. Assembly statistics

Velvet+MetaVetvet+Minimus	**IDBA-UD**
Total Sequences: 640793	Total Sequences: 1091773
Total Bases: 841,239,120	Total Bases: 1,511,701,270
Total Bases in sequences greater than 4000: 143,260,994	Total Bases in sequences greater than 4000: 553,583,049
Longest Sequence Length: 818,219	Longest Sequence Length: 830,465
Shortest Sequence Length: 501	Shortest Sequence Length: 91
Mean Length: 1313 bp	Mean Length: 1385 bp
Mean Length after setting the 4000 base limit: 6886 bp	Mean Length after setting the 4000 base limit: 8909 bp
Number of Sequences with Length greater than 4000 bases: 20804	Number of Sequences with Length greater than 4000 bases: 62135
Nucleotide Distribution after setting the 4000 base limit:	Nucleotide Distribution after setting the 4000 base limit:
A : 27.6824 %	A : 28.9150 %
T : 27.6417 %	T : 28.4189 %
G : 22.2372 %	G : 21.2481 %
C : 22.3155 %	C : 21.4015 %
N : 0.1233 %	N : 0.0165 %
	Percentage of reads assembled by site: Kilo Moana: 34.60 % Abe: 33.91 % Mariner: 53.75 % Tahi Moana: 43.96 % Tui Malila: 43.48 %
Sequence Length Range: No. of Contigs	Sequence Length Range: No. of Contigs
1-2000: 554653	1-2000: 909021
2001-4000: 65336	2001-4000: 120617
4001-6000: 13164	4001-6000: 31034
6001-8000: 4049	6001-8000: 12248
8001-10000: 1619	8001-10000: 6256
10001-12000: 713	10001-12000: 3417
12001-14000: 367	12001-14000: 2203
14001-16000: 229	14001-16000: 1565
16001-18000: 144	16001-18000: 1055
18001-20000: 95	18001-20000: 773
20001-22000: 63	20001-22000: 581
22001-24000: 45	22001-24000: 440
24001-26000: 51	24001-26000: 355
26001-28000: 29	26001-28000: 284

28001-30000: 24	28001-30000: 216
30001-32000: 16	30001-32000: 212
32001-34000: 19	32001-34000: 182
34001-36000: 13	34001-36000: 130
36001-38000: 13	36001-38000: 127
38001-40000: 14	38001-40000: 90
40001-42000: 16	40001-42000: 105
42001-44000: 6	42001-44000: 86
44001-46000: 13	44001-46000: 60
46001-48000: 11	46001-48000: 52
48001-50000: 3	48001-50000: 60
50001-52000: 6	50001-52000: 47
52001-54000: 4	52001-54000: 38
54001-56000: 9	54001-56000: 38
56001-58000: 7	56001-58000: 38
58001-60000: 3	58001-60000: 25
60001-62000: 6	60001-62000: 23
62001-64000: 2	62001-64000: 30
64001-66000: 5	64001-66000: 19
66001-68000: 4	66001-68000: 16
68001-70000: 3	68001-70000: 19
70001-72000: 1	70001-72000: 16
72001-74000: 1	72001-74000: 13
74001-76000: 1	74001-76000: 20
76001-78000: 1	76001-78000: 14
78001-80000: 2	78001-80000: 13
80001-82000: 7	80001-82000: 9
82001-84000: 1	82001-84000: 13
88001-90000: 3	84001-86000: 9
90001-92000: 1	86001-88000: 9
92001-94000: 1	88001-90000: 14
96001-98000: 1	90001-92000: 7
98001-100000: 2	92001-94000: 7
100001-1000000: 17	94001-96000: 7
	96001-98000: 5
	98001-100000: 5
	100001-1000000: 150

Supplementary Table 4. Details of identified ORFs

Assembly	Protein coding genes	rRNA genes	tRNA genes	COG clusters	Pfam clusters
KiloMoana	401957	294	4218	4456	13850
Abe	664114	188	8039	4443	14587
Mariner	202932	186	2322	4203	12115
TahiMoana	267200	181	2933	4336	13038
TuiMalila	141590	94	1614	3771	10753

Supplementary Table 5. Details of identified archaeal, bacterial and eukarya bins

Bin name	Organism/Group	No. of Contigs	Total size(bp)	%GC	Estimated no. of genomes	Percent completion of bins
Lau1	Bacteria;Candidate Division TM7	5	909,913	43.52	1	97.2
Lau2	Bacteria;Cyanobacteria/Melainabacteria;MLE1-12	360	4,104,129	49.49	1	34.4
Lau3	Bacteria;Chloroflexi;SAR202 clade	821	6,029,363	56.89	1	90.6
Lau4	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Alteromonas	661	9,888,618	43.86	2	212.5
Lau5	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae;Marinobacter	195	9,438,787	56.12	2	196.9
Lau6	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group II (Group C)	303	7,737,129	44.58	4	381.3
Lau7	Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;JL-ETNP-F27	1335	11,146,757	45.04	5	475.0
Lau8	Eukaryota;Opisthokonta;Metazoa;Mollusca;Bivalvia;Mytiloida;Bathymodiolus tangaroa	9584	54,022,390	33.91	1	21.9
Lau9	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;ZD0405 (ARCTIC96BD-19)	291	2,388,907	39.34	1	68.8
Lau10	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SUP05 Clade	2159	14,020,866	38.01	8	712.5
Lau11	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales;Moraxellaceae;Acinetobacter (LIKELY CONTAMINANT)	696	8,573,787	39.02	2	150.0
Lau12	Bacteria;Chloroflexi;Anaerolineae;Anaerolineales;Anaerolineaceae	111	682,424	42.15	1	15.6
Lau14	Bacteria;Proteobacteria;Alphaproteobacteria;SAR11 clade	4284	30,724,625	30.06	26	2600.0
Lau15	Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas	96	677,211	34.51	1	18.8
Lau16	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SAR86 clade	448	4,266,187	37.37	3	237.5
Lau17	Bacteria; Nitrospinae; Nitrospinia; Nitrospinales; Nitrospinaceae	1713	13,893,733	39.39	6	525.0
Lau19	Archaea;Thaumarchaeota;Marine Group I	2096	15,151,636	33.46	10	918.8
Lau20	Bacteria;Proteobacteria;Deltaproteobacteria;SAR324 clade (Marine Group B)	1435	14,645,818	42.12	8	753.1
Lau21	Bacteria;Poribacteria	1247	19,585,039	44.23	2	171.9
Lau22	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Mesonia	146	2,464,964	34.89	1	31.3
Lau23	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Marixanthomonas	14	3,250,025	40.28	2	118.8
Lau24	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae;Marixanthomonas	131	1,056,646	40.83	1	12.5
Lau26	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales;Rhodospirillaceae;Thalassospira	66	555,626	52.41	1	12.5
Lau27	Bacteria;Cyanobacteria;SHA-109	318	2,573,937	54.10	1	12.5
Lau28	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae	399	3,845,565	45.21	1	21.9
Lau29	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales;Alteromonadaceae	87	556,445	50.32	1	6.3
Lau30	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales	1134	10,534,609	45.25	2	196.9
Lau31	Bacteria;Bacteroidetes;Unclassified	453	4,462,640	38.23	1	100.0
Lau32	Bacteria;Bacteroidetes;Unclassified	78	722,333	40.67	1	0.0
Lau33	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Flavobacteriaceae	59	373,613	40.53	1	6.3
Lau34	Archaea;Euryarchaeota;Halobacteria;Halobacteriales;Deep Sea Hydrothermal Vent Gp 6(DHVEG-6)	293	2,770,233	52.56	1	90.6

Lau35	Bacteria;Planctomycetes;Pla3 lineage	787	6,055,579	57.39	1	84.4
Lau36	Bacteria;Planctomycetes;Pla3 lineage	401	4,733,687	60.40	5	415.6
Lau40	Bacteria;Acidobacteria;Acidobacteria;BPC102	112	728,843	53.76	1	6.3
Lau41	Bacteria; Nitrospinae; Nitrospinia; Nitrospinales; Nitrospinaceae	2066	16,427,353	46.90	5	462.5
Lau42	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;NS9 marine group	274	5,807,840	43.39	3	231.3
Lau44	Bacteria;Nitrospirae	408	4,397,644	52.21	3	234.4
Lau45	Bacteria;Gemmatimonadetes;Gemmatimonadetes;BD2-11 group	378	2,772,136	54.30	1	53.1
Lau46	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Hyphomonadaceae	111	943,398	55.70	1	0.0
Lau47	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;SAR406 clade (Marine Group A)	688	13,711,201	45.88	7	656.3
Lau51	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales; SUP05 Clade	272	3,134,417	36.38	1	6.3
Lau52	Bacteria;Bacteroidetes;Unclassified	106	780,364	42.65	1	9.4
Lau53	Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified	56	323,536	48.99	1	0.0
Lau60	Bacteria;Proteobacteria;Gammaproteobacteria;Order Incertae cedis (Tubeworm symbiont)	823	11,148,002	52.75	5	465.6
Lau62	Bacteria;Proteobacteria;Gammaproteobacteria;E01-9C-26 marine group	1126	16,062,766	52.41	5	200.0
Lau64	Bacteria;Bacteroidetes;Unclassified	758	9,477,688	43.38	2	143.8
Lau65	Unclassified	445	2,679,292	43.14	2	6.3
Lau66	Bacteria;Bacteroidetes;Flavobacteria;Unclassified	491	4,091,476	44.27	1	262.5
Lau92	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group II (Group B)	272	3,084,605	58.48	3	46.9
Lau93	Archaea;Euryarchaeota;Thermoplasmata;Thermoplasmatales;Marine Group II	84	675,085	55.05	1	112.5
Lau94	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae	315	2,328,079	53.02	2	0.0
Lau95	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	37	223,029	49.01	1	87.5
Lau96	Bacteria;Planctomycetes;Planctomycetia;Planctomycetales;Planctomycetaceae	383	3,436,646	48.68	1	18.8
Lau98	Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified	218	1,804,876	52.32	1	0.0
Lau101	Bacteria;Proteobacteria;Unclassified	6	41,648	56.77	1	1328.1
Lau103	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;SAR406 clade (Marine Group A)	4434	43,187,681	41.00	14	178.1
Lau104	Bacteria;Deferribacteres;Deferribacteres;Deferribacterales;SAR406 clade (Marine Group A)	443	3,720,913	38.27	2	0.0
Lau112	Bacteria;Unclassified	20	129,093	45.18	1	218.8
Lau113	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales; Hyd24-01 (OPU3)	312	5,302,821	42.67	3	40.6
Lau114	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	233	2,023,828	51.56	1	0.0
Lau115	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	20	149,321	48.72	1	418.8
Lau117	Bacteria;Unclassified	3	15,852	49.67	1	0.0
Lau118	Bacteria;Proteobacteria;Alphaproteobacteria;Rhodospirillales	492	4,917,635	50.47	2	137.5
Lau122	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales; SUP05 Clade	302	1,876,788	33.89	1	6.3
Lau123	Bacteria;Unclassified	269	1,838,828	55.05	1	37.5
Lau125	Archaea;Euryarchaeota;Unclassified	65	415,496	30.15	1	37.5
Lau126	Bacteria;Unclassified	40	232,436	49.11	1	0.0
Lau127	Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified	32	186,078	44.71	1	3.1
Lau129	Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas	17	96,262	35.98	1	0.0

Lau143	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	6	30,876	34.90	1	0.0
Lau158	Bacteria;Verrucomicrobia;Unclassified	35	308,256	38.65	1	0.0
Lau159	Bacteria;Proteobacteria;Unclassified	9	80,800	42.17	1	0.0
Lau163	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	32	215,013	53.70	1	3.1
Lau164	Bacteria;Verrucomicrobia;Unclassified	10	73,599	56.43	1	0.0
Lau176	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales; Pseudomonadaceae (LIKELY CONTAMINANT)	59	829,333	54.32	1	65.6
Lau177	Bacteria;Proteobacteria;Gammaproteobacteria;Pseudomonadales; Pseudomonadaceae (LIKELY CONTAMINANT)	53	463,345	59.13	1	12.5
Lau178	Bacteria;Proteobacteria;Gammaproteobacteria;Methylococcales	40	237,587	53.25	1	3.1
Lau179	Bacteria;Proteobacteria;Unclassified	8	107,643	39.59	1	0.0
Lau184	Bacteria;Verrucomicrobia;Unclassified	5	23,710	36.52	1	0.0
Lau190	Bacteria;Verrucomicrobia;Arctic97B-4 marine group	417	2,886,548	58.15	2	115.6
Lau197	Bacteria;Proteobacteria;Deltaproteobacteria;Unclassified	2	20,751	44.98	1	0.0
Lau198	Bacteria;Unclassified	4	27,618	46.17	1	0.0
Lau203	Bacteria;Proteobacteria;Unclassified	58	438,706	48.30	1	6.3
Lau208	Bacteria;Verrucomicrobia;Unclassified	6	30,481	38.88	1	0.0
Lau210	Bacteria;Proteobacteria;Betaproteobacteria;Burkholderiales	5	31,669	39.17	1	0.0
Lau227	Bacteria;Aquificae;Aquificae;Aquificales;Aquificaceae	171	1,296,646	48.41	2	181.3
Lau229	Bacteria;Proteobacteria;Epsilonproteobacteria	127	1,142,760	36.98	1	50.0
Lau230	Bacteria;Proteobacteria;Gammaproteobacteria;Salinisphaerales;Salinisphaeraceae;ZD0417 marine group	376	3,589,670	42.05	3	243.8
Lau231	Bacteria;Unclassified	20	190,602	39.64	3	290.6
Lau233	Bacteria;Unclassified	35	210,608	37.71	1	3.1
Lau236	Bacteria;Unclassified	122	879,107	55.12	1	50.0
Lau237	Bacteria;Aquificae;Aquificae;Aquificales;Desulfurobacteriaceae	27	148,555	49.01	1	0.0
Lau248	Bacteria;Proteobacteria;Gammaproteobacteria;Alteromonadales; Alteromonadaceae;Alteromonas	1	4,388	47.47	1	0.0
Lau249	Bacteria;Unclassified	1	63,694	41.61	1	3.1
Lau252	Bacteria;Bacteroidetes;Flavobacteria;Flavobacteriales;Cryomorphaceae;Unclassified	21	120,381	38.76	1	0.0
Lau259	Bacteria;Unclassified	87	501,503	42.49	1	3.1
Lau265	Bacteria;Verrucomicrobia;Unclassified	2	13,130	43.42	1	0.0
Lau269	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	12	84,379	46.85	1	0.0
Lau331	Archaea;Thaumarchaeota;Marine Group I	12	79,139	40.58	1	3.1
Lau371	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	9	45,561	41.34	1	0.0
Lau374	Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified	474	3,950,903	49.99	1	31.3
Lau375	Bacteria;Proteobacteria;Deltaproteobacteria;SAR324 clade (Marine Group B)	551	3,959,011	42.64	2	137.5
Lau376	Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified	598	5,415,484	44.70	2	146.9
Lau377	Bacteria;Poribacteria	328	8,726,215	42.97	3	253.1
Lau378	Bacteria;Proteobacteria;Gammaproteobacteria;Unclassified	139	1,320,110	38.32	2	137.5
Lau379	Bacteria;Unclassified	17	108,542	45.11	1	3.1

*****Numbers higher than 100% in estimates of percent completion of bins indicate the presence of multiple species/strains in a bin that could not be separated.

Supplementary Table 6. Details of bins of putative extrachromosomal elements

Bin name	**Organism/Group**	**% of unclassified/viral genes**	**No. of Contigs**	**Total size(bp)**	**%GC**	**No. of genomes**
Lau13	Unclassified/Putative Phage	89.43%	97	906,225	32.81	4
Lau37	Unclassified/Putative Phage	97.17%	24	267,668	39.56	5
Lau38	Unclassified/Putative Phage	97.06%	11	110,943	42.79	4
Lau39	Unclassified/Putative Phage	94.01%	10	218,585	35.75	4
Lau43	Unclassified/Putative Phage	40.91%	161	1,268,671	52.21	5
Lau49	Unclassified/Putative Phage	46.42%	64	665,092	56.63	2
Lau50	Unclassified/Putative Phage	79.11%	39	415,853	35.45	3
Lau54	Unclassified/Putative Phage	90.81%	67	498,303	42.19	4
Lau55	Unclassified/Putative Phage	90.75%	136	958,976	39.62	5
Lau56	Unclassified/Putative Phage	50.00%	2	19,029	52.07	2
Lau57	Unclassified/Putative Phage	98.81%	14	99,492	38.82	3
Lau58	Unclassified/Putative Phage	96.97%	6	40,910	36.58	3
Lau59	Unclassified/Putative Phage	97.87%	13	60,899	53.25	4
Lau61	Unclassified/Putative Phage	95.06%	7	34,875	54.40	3
Lau63	Unclassified/Putative Phage	95.48%	12	65,347	56.15	5
Lau67	Unclassified/Putative Phage	60.00%	12	84,271	45.64	3
Lau68	Unclassified/Putative Phage	86.11%	14	118,281	38.27	4
Lau69	Unclassified/Putative Phage	100.00%	9	55,064	51.12	3
Lau70	Unclassified/Putative Phage	82.86%	4	20,305	53.31	1
Lau72	Unclassified/Putative Phage	100.00%	5	33,263	47.71	3
Lau73	Unclassified/Putative Phage	96.97%	8	51,647	45.93	4
Lau74	Unclassified/Putative Phage	44.44%	6	48,078	41.64	3
Lau75	Unclassified/Putative Phage	86.67%	5	39,146	42.64	3
Lau76	Unclassified/Putative Phage	100.00%	6	42,252	43.52	3
Lau77	Viruses;dsdna viruses (no rna stage);Caudovirales;Myoviridae;T4-like viruses	81.39%	56	823,098	36.81	3
Lau78	Unclassified/Putative Phage	97.02%	12	153,339	45.94	3
Lau79	Unclassified/Putative Phage	100.00%	2	13,172	48.39	1
Lau80	Unclassified/Putative Phage	90.22%	5	54,015	43.61	3
Lau81	Unclassified/Putative Phage	97.59%	14	111,548	46.40	3
Lau82	Unclassified/Putative Phage	100.00%	2	16,979	44.13	2
Lau83	Unclassified/Putative Phage	88.89%	2	19,354	41.04	1
Lau84	Unclassified/Putative Phage	89.83%	9	65,626	42.48	3
Lau85	Viruses;dsdna viruses (no rna stage);Caudovirales;Myoviridae;T4-like viruses	80.85%	59	633,699	36.06	4
Lau86	Unclassified/Putative Phage	70.59%	3	25,238	50.03	3
Lau88	Unclassified/Putative Phage	100.00%	4	31,494	47.11	3
Lau89	Unclassified/Putative Phage	57.23%	12	101,643	46.65	5

Lau90	Unclassified/Putative Phage	34.78%	5	52,667	39.61	2
Lau91	Unclassified/Putative Phage	98.08%	8	60,391	45.55	2
Lau99	Unclassified/Putative Phage	50.00%	5	39,180	47.24	4
Lau100	Unclassified/Putative Phage	98.46%	4	26,653	53.86	3
Lau102	Unclassified/Putative Phage	98.00%	5	156,492	40.85	1
Lau105	Unclassified/Putative Phage	36.84%	9	44,553	30.42	1
Lau106	Unclassified/Putative Phage	25.00%	5	30,862	46.02	3
Lau107	Unclassified/Putative Phage	28.57%	6	28,868	43.20	4
Lau108	Unclassified/Putative Phage	74.07%	11	53,957	38.68	5
Lau109	Unclassified/Putative Phage	100.00%	3	15,772	44.46	2
Lau110	Unclassified/Putative Phage	100.00%	11	86,118	40.52	4
Lau111	Unclassified/Putative Phage	58.33%	11	62,590	42.52	4
Lau120	Unclassified/Putative Phage	88.82%	37	181,802	41.69	2
Lau121	Unclassified/Putative Phage	94.51%	33	163,604	32.91	2
Lau128	Unclassified/Putative Phage	100.00%	15	112,930	56.04	4
Lau130	Unclassified/Putative Phage	85.00%	6	68,113	38.82	3
Lau131	Unclassified/Putative Phage	100.00%	5	36,407	49.18	4
Lau132	Unclassified/Putative Phage	100.00%	7	69,732	53.05	4
Lau133	Unclassified/Putative Phage	100.00%	28	202,724	43.26	3
Lau134	Unclassified/Putative Phage	75.00%	6	34,286	52.18	2
Lau135	Unclassified/Putative Phage	99.15%	19	145,920	43.13	2
Lau136	Unclassified/Putative Phage	93.02%	3	15,424	38.21	1
Lau137	Unclassified/Putative Phage	100.00%	3	13,926	39.18	3
Lau138	Unclassified/Putative Phage	100.00%	2	17,122	44.65	2
Lau139	Unclassified/Putative Phage	82.35%	3	105,599	39.92	3
Lau140	Unclassified/Putative Phage	81.31%	6	65,699	34.84	5
Lau141	Unclassified/Putative Phage	94.74%	20	184,765	36.07	4
Lau142	Unclassified/Putative Phage	95.65%	8	112,031	36.07	4
Lau144	Unclassified/Putative Phage	100.00%	1	4,266	37.79	2
Lau146	Unclassified/Putative Phage	100.00%	4	19,412	48.00	2
Lau147	Unclassified/Putative Phage	57.14%	5	39,643	36.57	3
Lau148	Unclassified/Putative Phage	88.66%	4	39,428	33.40	2
Lau149	Unclassified/Putative Phage	91.40%	12	65,985	37.13	4
Lau150	Unclassified/Putative Phage	97.67%	13	79,549	38.88	3
Lau151	Unclassified/Putative Phage	96.67%	12	116,964	37.17	5
Lau152	Unclassified/Putative Phage	94.12%	12	126,665	41.22	4
Lau153	Unclassified/Putative Phage	97.50%	6	42,312	44.05	3
Lau155	Unclassified/Putative Phage	97.14%	12	67,627	35.44	2
Lau156	Unclassified/Putative Phage	100.00%	4	20,347	35.88	2
Lau160	Unclassified/Putative Phage	64.29%	4	21,657	49.05	2
Lau161	Unclassified/Putative Phage	100.00%	4	24,106	49.63	4

Lau162	Unclassified/Putative Phage	87.65%	6	46,857	51.60	3
Lau166	Unclassified/Putative Phage	91.65%	35	334,702	34.60	4
Lau167	Unclassified/Putative Phage	92.68%	13	81,121	33.29	4
Lau168	Unclassified/Putative Phage	83.33%	10	84,748	34.57	4
Lau169	Unclassified/Putative Phage	60.00%	4	20,769	37.97	4
Lau170	Unclassified/Putative Phage	53.57%	11	54,924	51.80	5
Lau171	Unclassified/Putative Phage	100.00%	12	80,772	45.14	4
Lau172	Unclassified/Putative Phage	84.45%	9	56,636	51.54	1
Lau173	Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;Halomonadaceae	9.47%	25	155,489	53.94	2
Lau174	Unclassified/Putative Phage	100.00%	5	27,495	47.92	4
Lau175	Unclassified/Putative Phage	85.71%	3	16,053	48.28	2
Lau180	Unclassified/Putative Phage	80.91%	21	216,322	41.30	4
Lau181	Unclassified/Putative Phage	96.55%	5	37,947	41.55	3
Lau182	Unclassified/Putative Phage	94.12%	7	54,907	41.26	4
Lau183	Unclassified/Putative Phage	93.02%	4	57,524	44.51	3
Lau185	Unclassified/Putative Phage	100.00%	6	53,218	42.61	4
Lau186	Unclassified/Putative Phage	54.84%	5	28,437	40.04	5
Lau187	Unclassified/Putative Phage	78.95%	6	32,069	31.03	3
Lau189	Unclassified/Putative Phage	80.69%	56	372,832	25.42	3
Lau192	Unclassified/Putative Phage	99.38%	17	75,955	39.47	4
Lau193	Unclassified/Putative Phage	100.00%	5	24,097	39.59	3
Lau194	Unclassified/Putative Phage	97.96%	7	37,358	39.98	4
Lau195	Unclassified/Putative Phage	81.82%	4	20,184	40.08	3
Lau196	Unclassified/Putative Phage	59.38%	9	44,088	55.73	2
Lau199	Unclassified/Putative Phage	100.00%	5	21,049	45.54	3
Lau200	Unclassified/Putative Phage	100.00%	4	18,435	53.26	3
Lau201	Unclassified/Putative Phage	69.23%	6	58,028	45.03	4
Lau204	Unclassified/Putative Phage	93.33%	7	58,332	60.77	2
Lau205	Unclassified/Putative Phage	100.00%	7	38,521	45.72	3
Lau206	Unclassified/Putative Phage	100.00%	7	41,711	41.51	4
Lau207	Unclassified/Putative Phage	66.67%	5	23,211	40.40	4
Lau209	Unclassified/Putative Phage	66.67%	7	48,035	37.52	4
Lau211	Unclassified/Putative Phage	80.00%	5	26,792	41.41	3
Lau212	Unclassified/Putative Phage	100.00%	4	17,419	40.21	3
Lau213	Unclassified/Putative Phage	100.00%	6	30,420	41.41	3
Lau214	Unclassified/Putative Phage	54.55%	8	40,092	40.06	3
Lau215	Unclassified/Putative Phage	100.00%	6	40,915	40.67	4
Lau216	Unclassified/Putative Phage	100.00%	6	54,858	40.21	3
Lau217	Unclassified/Putative Phage	95.83%	8	62,603	50.88	2
Lau218	Viruses;dsdna viruses (no rna stage);Caudovirales;Podoviridae	73.33%	6	83,236	34.56	3
Lau219	Unclassified/Putative Phage	100.00%	4	19,816	49.43	2

Lau220	Viruses;dsdna viruses (no rna stage);Unclassified	84.91%	32	224,624	41.57	3
Lau221	Unclassified/Putative Phage	66.67%	5	42,040	41.44	3
Lau222	Unclassified/Putative Phage	53.85%	7	54,480	44.04	3
Lau223	Unclassified/Putative Phage	95.00%	5	36,732	43.19	5
Lau224	Unclassified/Putative Phage	73.08%	5	42,140	41.32	3
Lau225	Unclassified/Putative Phage	75.00%	8	60,916	41.35	3
Lau226	Unclassified/Putative Phage	73.17%	4	25,815	43.64	4
Lau228	Unclassified/Putative Phage	64.71%	77	377,454	14.39	3
Lau232	Unclassified/Putative Phage	95.06%	12	65,147	42.50	2
Lau234	Unclassified/Putative Phage	92.50%	16	81,867	19.86	2
Lau235	Unclassified/Putative Phage	85.00%	5	59,588	38.57	3
Lau238	Unclassified/Putative Phage	57.14%	5	31,516	60.58	2
Lau241	Unclassified/Putative Phage	96.43%	6	178,448	41.08	3
Lau242	Unclassified/Putative Phage	98.89%	7	48,694	39.89	3
Lau243	Unclassified/Putative Phage	85.00%	6	34,056	36.57	3
Lau244	Unclassified/Putative Phage	100.00%	3	14,339	43.59	2
Lau245	Unclassified/Putative Phage	71.43%	5	23,944	41.81	5
Lau246	Unclassified/Putative Phage	33.33%	3	39,701	44.89	2
Lau247	Unclassified/Putative Phage	92.86%	10	101,421	51.21	3
Lau254	Unclassified/Putative Phage	76.92%	3	40,485	53.90	2
Lau256	Unclassified/Putative Phage	86.67%	7	50,225	55.35	4
Lau257	Unclassified/Putative Phage	73.68%	11	64,635	49.12	5
Lau260	Unclassified/Putative Phage	50.00%	7	71,726	42.90	5
Lau263	Unclassified/Putative Phage	60.87%	5	24,660	39.09	4
Lau264	Unclassified/Putative Phage	71.43%	6	38,540	40.67	5
Lau267	Unclassified/Putative Phage	75.00%	4	18,746	42.52	3
Lau271	Unclassified/Putative Phage	75.00%	4	28,995	54.83	4
Lau272	Unclassified/Putative Phage	45.83%	26	181,661	53.94	4
Lau273	Unclassified/Putative Phage	40.00%	12	82,859	50.73	3
Lau274	Unclassified/Putative Phage	69.70%	8	71,390	50.94	3
Lau278	Unclassified/Putative Phage	100.00%	4	45,859	50.80	4
Lau279	Unclassified/Putative Phage	93.75%	13	118,039	39.94	3
Lau280	Unclassified/Putative Phage	87.81%	8	54,984	40.97	3
Lau281	Unclassified/Putative Phage	100.00%	2	27,017	35.45	4
Lau282	Unclassified/Putative Phage	78.13%	10	134,212	39.02	4
Lau283	Unclassified/Putative Phage	94.12%	4	26,173	41.54	3
Lau284	Unclassified/Putative Phage	70.83%	6	41,525	41.05	3
Lau285	Unclassified/Putative Phage	86.11%	5	30,187	38.96	3
Lau286	Unclassified/Putative Phage	87.50%	6	36,609	46.08	5
Lau287	Unclassified/Putative Phage	90.91%	7	54,240	41.81	3
Lau288	Unclassified/Putative Phage	75.00%	9	72,763	38.78	5

Lau289	Viruses;dsdna viruses (no rna stage);Caudovirales;Myoviridae;T4-like viruses	91.43%	8	110,857	33.29	5
Lau291	Unclassified/Putative Phage	100.00%	5	32,046	37.11	3
Lau292	Unclassified/Putative Phage	88.89%	7	33,690	39.75	4
Lau293	Unclassified/Putative Phage	83.78%	6	32,332	42.88	2
Lau294	Unclassified/Putative Phage	61.49%	12	102,283	37.90	3
Lau295	Unclassified/Putative Phage	80.00%	5	26,793	39.95	3
Lau296	Unclassified/Putative Phage	100.00%	11	96,278	39.39	4
Lau297	Unclassified/Putative Phage	70.31%	9	62,434	36.25	4
Lau298	Unclassified/Putative Phage	90.24%	5	60,744	36.53	3
Lau300	Unclassified/Putative Phage	95.65%	8	51,386	50.20	4
Lau302	Unclassified/Putative Phage	100.00%	3	14,841	52.10	2
Lau303	Unclassified/Putative Phage	53.33%	5	28,013	43.12	5
Lau304	Unclassified/Putative Phage	50.00%	7	48,782	39.82	5
Lau308	Unclassified/Putative Phage	77.78%	5	25,088	47.84	2
Lau309	Unclassified/Putative Phage	72.73%	6	29,853	42.90	3
Lau311	Unclassified/Putative Phage	99.02%	7	47,886	26.40	3
Lau312	Unclassified/Putative Phage	100.00%	2	12,628	51.04	1
Lau313	Unclassified/Putative Phage	92.86%	4	21,420	35.84	3
Lau314	Unclassified/Putative Phage	100.00%	5	42,723	39.31	3
Lau315	Unclassified/Putative Phage	76.00%	3	26,353	38.61	3
Lau316	Unclassified/Putative Phage	87.50%	7	64,627	39.33	4
Lau317	Unclassified/Putative Phage	70.00%	2	10,969	39.77	2
Lau318	Unclassified/Putative Phage	94.60%	7	39,582	35.83	4
Lau319	Unclassified/Putative Phage	78.95%	5	49,849	40.50	2
Lau320	Unclassified/Putative Phage	80.00%	2	10,834	37.40	1
Lau325	Unclassified/Putative Phage	84.93%	12	81,164	35.11	3
Lau326	Unclassified/Putative Phage	83.33%	5	62,189	36.82	4
Lau327	Unclassified/Putative Phage	72.73%	6	31,947	37.85	4
Lau328	Unclassified/Putative Phage	47.06%	6	36,298	51.14	1
Lau329	Unclassified/Putative Phage	75.00%	2	8,463	37.70	1
Lau330	Unclassified/Putative Phage	76.19%	6	27,500	31.59	4
Lau333	Unclassified/Putative Phage	70.00%	2	10,879	48.00	1
Lau334	Unclassified/Putative Phage	100.00%	4	24,216	49.68	3
Lau336	Unclassified/Putative Phage	100.00%	6	61,907	49.63	4
Lau337	Unclassified/Putative Phage	100.00%	4	23,743	46.45	4
Lau338	Unclassified/Putative Phage	60.00%	3	15,394	39.14	3
Lau340	Unclassified/Putative Phage	96.55%	5	23,862	53.97	2
Lau342	Unclassified/Putative Phage	56.25%	50	308,246	44.44	5
Lau343	Unclassified/Putative Phage	80.00%	7	49,298	47.13	2
Lau344	Unclassified/Putative Phage	83.33%	2	14,406	40.77	2
Lau345	Unclassified/Putative Phage	100.00%	8	68,376	52.23	4

Lau351	Unclassified/Putative Phage	90.91%	5	44,898	44.73	3
Lau352	Unclassified/Putative Phage	100.00%	6	30,618	43.92	3
Lau353	Unclassified/Putative Phage	86.57%	13	119,349	38.58	5
Lau354	Unclassified/Putative Phage	100.00%	5	24,439	35.79	4
Lau355	Unclassified/Putative Phage	75.00%	3	22,836	41.19	2
Lau356	Unclassified/Putative Phage	60.61%	5	37,042	39.92	4
Lau357	Unclassified/Putative Phage	78.38%	7	53,981	40.40	4
Lau358	Unclassified/Putative Phage	91.31%	2	75,100	37.02	2
Lau359	Unclassified/Putative Phage	100.00%	5	31,939	36.89	5
Lau360	Unclassified/Putative Phage	98.31%	7	43,475	36.74	2
Lau367	Unclassified/Putative Phage	90.48%	4	47,563	37.62	3
Lau368	Unclassified/Putative Phage	100.00%	5	34,212	47.17	4
Lau370	Unclassified/Putative Phage	57.14%	8	54,650	40.97	4
Lau372	Unclassified/Putative Phage	100.00%	12	94,976	39.46	4
Lau373	Unclassified/Putative Phage	100.00%	4	59,850	34.21	3
Lau380	Unclassified/Putative Phage	76.00%	2	12,760	36.18	2
Lau381	Unclassified/Putative Phage	100.00%	4	97,482	35.03	4
Lau382	Unclassified/Putative Phage	100.00%	3	16,557	39.47	3
Lau383	Unclassified/Putative Phage	100.00%	2	11,382	51.88	2
Lau384	Unclassified/Putative Phage	100.00%	2	22,564	36.23	2
Lau385	Unclassified/Putative Phage	100.00%	4	28,322	48.67	4
Lau386	Unclassified/Putative Phage	89.47%	1	31,483	34.93	1
Lau387	Unclassified/Putative Phage	42.86%	2	8,740	48.64	2
Lau388	Unclassified/Putative Phage	75.00%	4	23,139	32.52	3
Lau389	Unclassified/Putative Phage	100.00%	3	13,064	37.83	2

Supplementary Table 7. Conserved LSU proteins identified in bacterial and archaeal bins

Bin name	Large subunit ribosomal proteins										
	COG0080	COG0081	COG0087	COG0091	COG0093	COG0094	COG0097	COG0102	COG0197	COG0200	COG0256
	L11	L1	L3	L22	L14	L5	L6P/L9E	L13	L16/L10E	L15	L18
Lau1	1	1	1	1	1	1	1	1	1	1	1
Lau2	0	0	0	0	0	0	0	1	0	0	0
Lau3	0	0	0	0	1	1	1	1	0	1	1
Lau4	3	3	2	2	2	2	2	1	2	2	2
Lau5	2	2	1	1	1	1	2	2	1	2	2
Lau6	3	3	2	3	3	3	2	4	4	2	2
Lau7	1	1	2	2	2	2	1	9	2	0	1
Lau9	0	0	0	0	0	0	0	1	0	0	0
Lau10	3	4	4	4	5	5	5	4	5	5	5
Lau11	1	1	1	1	1	1	1	3	1	1	1
Lau12	0	0	0	0	0	0	0	0	0	0	0
Lau14	10	9	23	26	27	33	33	19	18	23	21
Lau15	0	0	0	0	0	0	0	0	0	0	0
Lau16	1	1	1	1	2	2	2	3	1	2	2
Lau17	1	1	1	1	1	2	3	5	1	3	3
Lau19	10	11	3	2	2	2	1	8	7	5	6
Lau20	7	8	4	7	7	8	8	5	7	8	8
Lau21	0	0	1	0	0	0	0	3	0	1	1
Lau22	0	0	0	0	0	0	0	0	0	0	0
Lau23	1	1	1	1	1	1	1	1	1	1	1
Lau24	0	0	0	0	0	0	0	0	0	0	0
Lau26	0	0	0	0	0	0	0	0	0	0	0
Lau27	0	0	0	0	0	0	0	0	0	0	0
Lau28	0	0	0	0	0	0	0	0	0	0	0
Lau29	0	0	0	0	0	0	0	0	0	0	0
Lau30	0	0	1	0	0	0	2	3	0	1	1

Lau31	0	0	1	0	0	1	1	1	0	1	1
Lau32	0	0	0	0	0	0	0	0	0	0	0
Lau33	0	0	0	0	0	0	0	0	0	0	0
Lau34	0	0	0	0	0	0	0	0	0	0	0
Lau35	0	0	0	0	0	0	0	1	0	0	0
Lau36	6	7	4	4	5	5	5	0	5	5	5
Lau40	0	0	0	0	0	0	0	0	0	0	0
Lau41	0	0	3	3	2	2	1	5	2	1	1
Lau42	2	2	2	1	1	1	1	3	1	1	2
Lau44	2	2	0	0	2	3	3	3	1	3	3
Lau45	0	0	0	0	0	0	0	0	0	0	0
Lau46	0	0	0	0	0	0	0	0	0	0	0
Lau47	5	5	7	7	7	5	4	7	7	4	4
Lau51	0	0	0	0	0	0	0	0	0	0	0
Lau52	0	0	0	0	0	0	0	0	0	0	0
Lau53	0	0	0	0	0	0	0	0	0	0	0
Lau60	2	2	3	3	4	4	3	1	4	4	3
Lau62	4	4	4	4	4	4	4	4	4	4	3
Lau64	1	1	1	1	1	1	1	2	1	1	1
Lau65	0	3	1	0	0	0	0	5	1	0	0
Lau66	0	0	0	0	0	0	0	0	0	0	0
Lau92	2	2	1	1	1	1	1	1	2	1	1
Lau93	0	0	0	0	0	0	1	0	0	2	2
Lau94	1	1	1	0	1	1	1	1	0	1	1
Lau95	0	0	0	0	0	0	0	0	0	0	0
Lau96	0	0	0	0	1	1	1	1	0	1	1
Lau98	0	0	0	0	0	0	0	0	0	0	0
Lau101	0	0	0	0	0	0	0	0	0	0	0
Lau103	5	5	3	3	6	6	8	14	5	9	8
Lau104	0	0	0	1	2	2	1	3	1	1	1

Lau112	0	0	0	0	0	0	0	0	0	0	0
Lau113	0	1	2	1	2	2	2	2	1	2	2
Lau114	0	0	0	0	0	0	0	1	0	0	0
Lau115	0	0	0	0	0	0	0	0	0	0	0
Lau117	0	0	0	0	0	0	0	0	0	0	0
Lau118	0	0	1	0	0	0	0	2	0	1	0
Lau122	0	0	0	0	0	0	0	0	0	0	0
Lau123	0	0	0	0	0	0	0	1	0	0	0
Lau125	1	1	0	0	0	0	0	0	0	0	0
Lau126	0	0	0	0	0	0	0	0	0	0	0
Lau127	0	0	0	0	0	0	0	0	0	0	0
Lau129	0	0	0	0	0	0	0	0	0	0	0
Lau143	0	0	0	0	0	0	0	0	0	0	0
Lau158	0	0	0	0	0	0	0	0	0	0	0
Lau159	0	0	0	0	0	0	0	0	0	0	0
Lau163	0	0	0	0	0	0	0	0	0	0	0
Lau164	0	0	0	0	0	0	0	0	0	0	0
Lau176	1	1	0	1	1	1	1	1	1	1	1
Lau177	0	0	0	0	0	0	0	1	0	0	0
Lau178	0	0	0	0	0	0	0	0	0	0	0
Lau179	0	0	0	0	0	0	0	0	0	0	0
Lau184	0	0	0	0	0	0	0	0	0	0	0
Lau190	0	0	4	1	2	2	2	0	2	2	2
Lau197	0	0	0	0	0	0	0	0	0	0	0
Lau198	0	0	0	0	0	0	0	0	0	0	0
Lau203	0	0	0	0	0	0	0	0	0	0	0
Lau208	0	0	0	0	0	0	0	0	0	0	0
Lau210	0	0	0	0	0	0	0	0	0	0	0
Lau227	2	2	2	2	2	2	2	2	2	1	2
Lau229	0	0	1	0	0	0	0	1	0	0	0

Lau230	3	3	2	2	2	2	2	1	2	2	2
Lau231	5	5	4	4	4	5	4	0	4	4	4
Lau233	0	0	0	0	0	0	0	0	0	0	0
Lau236	1	1	1	0	0	0	0	0	0	1	1
Lau237	0	0	0	0	0	0	0	0	0	0	0
Lau248	0	0	0	0	0	0	0	0	0	0	0
Lau249	0	0	0	0	0	0	0	0	0	0	0
Lau252	0	0	0	0	0	0	0	0	0	0	0
Lau259	0	0	0	0	0	0	0	0	0	0	0
Lau265	0	0	0	0	0	0	0	0	0	0	0
Lau269	0	0	0	0	0	0	0	0	0	0	0
Lau331	0	0	0	0	0	0	0	0	0	0	0
Lau371	0	0	0	0	0	0	0	0	0	0	0
Lau374	0	0	0	0	0	0	0	0	0	0	0
Lau375	1	1	1	1	1	1	1	0	1	1	1
Lau376	0	0	3	0	0	0	1	2	0	3	2
Lau377	3	3	3	3	3	3	3	1	3	2	2
Lau378	0	0	0	0	0	0	1	3	0	1	1
Lau379	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table 8. Conserved SSU ribosomal proteins in bacterial and archaeal bins

Bin name	Small subunit ribosomal proteins											
	COG 0048	COG 0049	COG 0052	COG 0092	COG 0096	COG 0098	COG 0099	COG 0100	COG 0103	COG 0184	COG 0186	COG 0522
	S12	S7	S2	S3	S8	S5	S13	S11	S9	S15P/ S13E	S17	S4
Lau1	1	1	1	1	1	1	1	1	1	1	1	1
Lau2	0	0	2	0	0	0	0	0	1	0	0	1
Lau3	0	0	3	0	1	1	1	0	1	2	0	1
Lau4	1	1	2	2	2	2	2	2	1	2	3	2
Lau5	1	1	2	1	1	2	2	2	2	2	1	2
Lau6	4	4	4	3	2	2	4	4	4	4	3	4
Lau7	7	8	4	2	1	1	0	0	8	3	2	6
Lau8	0	0	0	0	0	0	0	1	0	0	0	0
Lau9	1	1	0	0	0	0	0	0	1	0	0	0
Lau10	7	5	3	4	5	5	4	4	4	4	5	3
Lau11	1	1	1	1	1	1	1	1	1	4	1	1
Lau12	0	0	0	0	0	0	0	0	0	0	0	0
Lau14	13	15	20	27	34	22	27	25	17	14	27	22
Lau15	0	0	0	0	0	0	0	0	0	0	0	0
Lau16	1	1	1	1	2	2	2	2	3	1	2	2
Lau17	1	1	8	1	2	3	10	10	6	4	1	10
Lau19	12	11	6	2	2	5	8	10	8	10	2	8
Lau20	4	6	8	7	8	8	7	6	2	5	7	5
Lau21	0	0	1	0	0	1	1	1	3	0	0	3
Lau22	1	1	0	0	0	0	0	0	0	0	0	0
Lau23	1	1	1	1	1	1	1	1	1	1	1	1
Lau24	0	0	0	0	0	0	0	0	0	0	0	0
Lau26	0	0	0	0	0	0	0	0	0	0	0	0
Lau27	0	0	0	0	0	0	0	0	0	0	0	0
Lau28	0	0	0	0	0	0	0	0	0	0	0	0

Lau29	0	0	0	0	0	0	0	0	0	0	0	0
Lau30	0	0	2	0	0	1	2	2	3	1	0	4
Lau31	1	1	0	0	1	1	1	1	1	1	0	1
Lau32	0	0	0	0	0	0	0	0	0	0	0	0
Lau33	0	0	0	0	0	0	0	0	0	0	0	0
Lau34	2	2	1	0	0	0	1	1	0	3	0	1
Lau35	0	0	0	0	0	0	0	0	1	3	0	0
Lau36	4	4	4	5	5	5	4	4	0	2	5	4
Lau40	0	0	0	0	0	0	0	0	0	0	0	0
Lau41	3	4	10	2	1	1	1	1	6	8	2	1
Lau42	3	3	3	1	1	1	1	1	3	3	1	1
Lau44	0	0	1	0	3	3	3	2	3	4	1	2
Lau45	0	0	0	0	0	0	0	0	0	0	0	0
Lau46	0	0	0	0	0	0	0	0	0	0	0	0
Lau47	7	7	7	7	4	4	4	4	7	1	7	4
Lau51	0	0	0	0	0	0	0	0	0	0	0	0
Lau52	0	0	0	0	0	0	0	0	0	0	0	0
Lau53	0	0	0	0	0	0	0	0	0	0	0	0
Lau60	6	6	5	4	4	4	4	4	1	3	4	4
Lau62	0	5	6	4	4	4	4	4	4	4	4	4
Lau64	1	1	2	1	1	1	1	1	2	2	1	1
Lau65	0	0	0	0	0	0	2	1	5	1	0	2
Lau66	0	0	0	0	0	0	0	0	0	0	0	0
Lau92	8	9	1	1	1	1	2	2	1	1	1	2
Lau93	1	1	0	0	1	2	0	0	0	0	0	0
Lau94	1	1	1	0	1	1	1	1	1	0	1	1
Lau95	0	0	0	0	0	0	0	0	0	0	0	0
Lau96	0	0	0	0	1	1	1	0	1	0	0	2
Lau98	0	0	0	0	0	0	0	0	0	0	0	0
Lau101	0	0	0	0	0	0	0	0	0	0	0	0

Lau103	3	3	16	4	8	9	8	7	15	10	6	6
Lau104	0	0	3	1	1	1	2	2	3	0	2	2
Lau112	0	0	0	0	0	0	0	0	0	0	0	0
Lau113	0	0	2	1	2	2	2	2	2	0	2	2
Lau114	0	0	0	0	0	0	0	0	0	0	0	0
Lau115	0	0	0	0	0	0	0	0	0	0	0	0
Lau117	0	0	0	0	0	0	0	0	0	0	0	0
Lau118	1	1	0	0	0	0	2	2	3	0	0	3
Lau122	0	0	0	0	0	0	0	0	0	0	0	0
Lau123	0	0	0	0	0	0	0	0	1	0	0	1
Lau125	0	0	0	0	0	0	0	0	0	0	0	0
Lau126	0	0	0	0	0	0	0	0	0	0	0	0
Lau127	0	0	0	0	0	0	0	0	0	0	0	0
Lau129	0	0	0	0	0	0	0	0	0	0	0	0
Lau143	0	0	0	0	0	0	0	0	0	0	0	0
Lau158	0	0	0	0	0	0	0	0	0	0	0	0
Lau159	0	0	0	0	0	0	0	0	0	0	0	0
Lau163	0	0	0	0	0	0	0	0	0	0	0	0
Lau164	0	0	0	0	0	0	0	0	0	0	0	0
Lau176	0	0	0	1	1	1	1	1	1	0	1	1
Lau177	0	0	1	0	0	0	0	0	1	0	0	0
Lau178	0	0	0	0	0	0	0	0	0	0	0	0
Lau179	0	0	0	0	0	0	0	0	0	0	0	0
Lau184	0	0	0	0	0	0	0	0	0	0	0	0
Lau190	3	4	0	2	2	2	1	0	0	0	2	0
Lau197	0	0	0	0	0	0	0	0	0	0	0	0
Lau198	0	0	0	0	0	0	0	0	0	0	0	0
Lau203	0	0	0	0	0	0	0	0	0	0	0	0
Lau208	0	0	0	0	0	0	0	0	0	0	0	0
Lau210	0	0	0	0	0	0	0	0	0	0	0	0

Lau227	2	2	1	2	2	2	0	0	2	1	2	0
Lau229	1	1	0	0	0	0	0	0	1	0	0	0
Lau230	3	3	3	2	2	2	2	2	1	0	2	2
Lau231	6	6	0	4	4	4	3	3	0	0	4	3
Lau233	0	0	0	0	0	0	0	0	0	0	0	0
Lau236	1	1	0	0	0	1	1	1	0	0	0	1
Lau237	0	0	0	0	0	0	0	0	0	0	0	0
Lau248	0	0	0	0	0	0	0	0	0	0	0	0
Lau249	0	0	0	0	0	0	0	0	0	0	0	0
Lau252	0	0	0	0	0	0	0	0	0	0	0	0
Lau259	0	0	0	0	0	0	0	0	0	0	0	0
Lau265	0	0	0	0	0	0	0	0	0	0	0	0
Lau269	0	0	0	0	0	0	0	0	0	0	0	0
Lau331	0	0	0	0	0	0	0	0	0	0	0	0
Lau371	0	0	0	0	0	0	0	0	0	0	0	0
Lau374	1	1	0	0	0	0	0	0	0	0	0	0
Lau375	7	6	0	1	1	1	0	0	0	0	1	0
Lau376	0	0	0	0	1	2	3	3	2	4	0	3
Lau377	3	3	3	3	3	2	2	2	1	4	3	1
Lau378	0	0	1	0	1	1	1	2	3	3	0	2
Lau379	0	0	0	0	0	0	0	0	0	0	0	0

Supplementary Table 9. Other conserved genes in identified bacterial and archaeal bins

Bin name	tRNA synthetases									RNA polymerase subunits			
	COG0016	COG 0018	COG 0060	COG 0124	COG 0143	COG 0172	COG 0201	COG 0495	COG 0525	COG0202	COG0085	COG 0012	COG 0533
	Phenylalanyl-tRNA synthethase alpha subunit	Arginyl-tRNA synthetase	Isoleucyl-tRNA synthetase	Histidyl-tRNA synthetase	Methionyl-tRNA synthetase	Seryl-tRNA synthetase	Preprotein translocase subunit SecY	Leucyl-tRNA synthetase	Valyl-tRNA synthetase	DNA-directed RNA polymerase, alpha subunit/40 kD subunit	DNA-directed RNA polymerase, beta subunit/140 kD subunit	Predicted GTPase	Metal-dependent protease
Lau1	0	1	1	1	1	1	1	1	1	1	1	1	1
Lau2	1	1	1	0	0	0	1	0	1	0	0	1	0
Lau3	0	1	2	0	0	2	1	4	2	1	0	0	0
Lau4	1	1	2	2	1	2	2	2	2	2	3	2	1
Lau5	2	2	2	2	2	2	2	2	3	2	2	2	2
Lau6	4	4	2	4	4	4	2	4	4	5	4	4	4
Lau7	1	12	6	12	5	11	0	14	4	9	1	5	7
Lau8	0	0	0	0	0	3	0	0	1	0	0	0	0
Lau9	0	1	1	1	1	2	0	3	3	0	0	5	1
Lau10	9	12	13	10	9	13	4	16	8	6	16	7	3
Lau11	2	3	1	1	1	2	1	2	1	1	1	2	2
Lau12	1	0	0	0	0	1	0	0	1	0	0	1	1
Lau14	18	20	36	14	12	27	27	21	35	24	25	33	35
Lau15	0	0	0	2	0	1	1	0	1	0	0	0	1
Lau16	1	3	4	2	4	3	3	2	6	2	1	2	5
Lau17	6	8	4	7	8	12	10	7	8	10	1	3	5
Lau19	3	10	17	13	17	14	11	11	4	6	14	24	9
Lau20	6	9	9	9	5	6	8	1	7	5	10	7	9
Lau21	4	2	4	0	4	1	1	8	4	2	5	3	1
Lau22	1	1	1	1	1	1	0	1	1	0	0	0	0
Lau23	1	1	2	1	1	1	1	1	2	1	1	1	1
Lau24	0	1	0	0	1	1	0	1	0	0	0	0	0

Lau26	0	0	0	0	0	0	2	0	1	0	0	0	1
Lau27	1	1	0	0	0	0	0	0	2	0	0	0	0
Lau28	0	0	0	0	0	1	0	2	1	0	0	1	2
Lau29	0	0	0	0	1	0	0	1	0	0	0	0	0
Lau30	3	5	3	3	6	5	2	0	4	2	2	4	1
Lau31	1	2	2	2	0	2	1	2	2	0	0	1	2
Lau32	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau33	0	2	0	0	0	0	0	0	0	0	0	0	0
Lau34	1	2	1	0	3	0	0	2	2	1	1	3	2
Lau35	2	0	4	3	2	3	0	3	2	1	0	2	0
Lau36	0	2	3	3	2	1	5	2	2	7	9	0	0
Lau40	0	0	0	0	0	0	0	0	0	0	0	2	0
Lau41	8	7	6	11	4	4	2	15	8	6	4	9	4
Lau42	3	3	4	3	3	3	1	3	4	1	1	3	3
Lau44	3	1	4	0	1	3	3	2	4	3	3	2	2
Lau45	1	3	0	3	2	3	0	0	2	0	0	0	3
Lau46	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau47	7	5	9	6	7	7	4	9	7	4	5	7	8
Lau51	0	0	0	0	0	0	1	1	0	0	0	0	0
Lau52	0	0	0	0	1	2	0	0	0	0	0	0	0
Lau53	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau60	5	0	6	3	2	5	4	6	7	3	5	4	2
Lau62	5	5	4	5	5	6	4	4	5	4	5	4	3
Lau64	4	2	3	4	4	2	1	3	5	2	1	3	3
Lau65	3	0	4	2	3	1	0	2	3	0	4	1	2
Lau66	0	0	0	0	0	0	0	0	0	0	0	0	2
Lau92	1	1	0	0	9	2	2	2	8	2	4	1	8
Lau93	0	0	0	0	1	0	2	1	0	0	0	0	1
Lau94	1	1	1	1	0	1	1	1	0	4	1	3	2
Lau95	0	0	0	0	0	0	0	0	0	0	0	0	0

Lau96	1	0	0	4	1	2	1	2	2	1	0	2	0
Lau98	0	0	1	2	1	0	0	0	1	0	0	0	1
Lau101	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau103	16	31	30	29	22	16	9	19	24	10	7	27	18
Lau104	3	3	2	2	1	4	3	0	2	3	0	5	0
Lau112	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau113	2	2	1	3	3	4	2	4	4	2	2	3	4
Lau114	1	1	0	1	2	2	0	3	1	0	0	0	1
Lau115	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau117	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau118	4	3	1	5	0	4	1	1	2	3	0	3	1
Lau122	0	0	0	0	0	0	0	0	0	0	2	0	0
Lau123	0	2	0	1	0	0	0	2	2	1	0	1	0
Lau125	0	0	1	2	2	3	0	0	1	0	1	0	0
Lau126	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau127	0	0	0	0	0	0	0	0	1	0	0	0	0
Lau129	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau143	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau158	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau159	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau163	0	0	1	0	0	0	0	0	0	0	0	0	0
Lau164	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau176	1	0	0	0	0	0	1	0	0	1	0	0	0
Lau177	0	0	0	0	1	0	0	0	0	0	0	0	0
Lau178	0	0	0	0	0	0	0	0	0	0	0	1	0
Lau179	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau184	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau190	0	0	0	0	0	0	1	0	1	0	1	1	0
Lau197	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau198	0	0	0	0	0	0	0	0	0	0	0	0	0

Lau203	0	1	0	0	1	0	0	0	0	0	0	0	0
Lau208	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau210	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau227	1	0	2	2	2	1	4	3	3	1	2	0	0
Lau229	1	1	1	3	1	1	0	1	1	0	0	0	1
Lau230	0	4	6	4	3	0	2	0	3	1	3	5	0
Lau231	0	0	0	0	0	0	4	0	0	3	6	0	0
Lau233	0	0	0	0	0	0	0	1	0	0	0	0	0
Lau236	0	1	1	0	0	0	1	1	0	1	0	0	0
Lau237	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau248	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau249	0	1	0	0	0	0	0	0	0	0	0	0	0
Lau252	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau259	1	0	0	0	0	0	0	0	0	0	0	0	0
Lau265	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau269	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau331	0	0	1	0	0	0	0	0	0	0	0	0	0
Lau371	0	0	0	0	0	0	0	0	0	0	0	0	0
Lau374	0	0	0	3	1	0	0	0	1	1	2	0	0
Lau375	0	0	4	1	0	0	0	0	0	0	5	0	7
Lau376	3	0	0	0	2	3	3	1	1	2	3	0	0
Lau377	0	2	4	3	0	3	2	2	0	2	0	1	3
Lau378	3	0	0	0	0	7	1	4	3	2	0	0	4
Lau379	0	0	0	0	0	0	0	0	1	0	0	0	0

Supplementary Table S10. List of identified soxZ genes and their amino acid identities to best hits in Genbank.

Scaffold	Bin	IMG Gene ID	Gene Size (bp)	% Id	NCBI Database Best Hit
Abe_scaffold_36	Lau113	Abe_1000003728	311	63	Methylobacter tundripaludum (WP_006893629)
Abe_scaffold_515	Lau51	Abe_1000051623	302	65	Uncultured SUP05 bacterium (EEZ80661)
Abe_scaffold_9180	Lau20	Abe_100091814	353	90	SAR324 cluster bacterium SCGC AAA001-C10 (WP_010512894)
Abe_scaffold_17538	Lau20	Abe_100175394	326	84	Deltaproteobacteria bacterium SCGC AAA003-F15 (WP_029734853)
Abe_scaffold_17577	Lau10	Abe_100175783	302	56	Uncultured SUP05 bacterium (EEZ80661)
Kilo_Moana_scaffold_51	Lau113	KiloMoana_1000005230	311	63	Methylobacter tundripaludum (WP_006893629)
Kilo_Moana_scaffold_91	Lau60	KiloMoana_1000009231	311	51	Thiobacillus denitrificans (WP_011311077)
Kilo_Moana_scaffold_256	Lau60	KiloMoana_1000025739	311	65	uncultured hydrothermal vent organism (ACZ28666)
Kilo_Moana_scaffold_987	Lau376	KiloMoana_1000098810	338	91	SAR324 cluster bacterium SCGC AAA001-C10 (WP_010512894)
Kilo_Moana_scaffold_1856	Lau20	KiloMoana_1000185715	326	84	Deltaproteobacteria bacterium SCGC AAA003-F15 (WP_029734853)
Kilo_Moana_scaffold_2824	Lau10	KiloMoana_100028252	302	90	Uncultured SUP05 bacterium (EEZ80661)
Kilo_Moana_scaffold_3404	Lau10	KiloMoana_100034055	302	86	Uncultured SUP05 bacterium (EEZ80661)
Kilo_Moana_scaffold_5970	Lau374	KiloMoana_100059715	353	69	SAR324 cluster bacterium SCGC AAA001-C10 (WP_010512894)
Kilo_Moana_scaffold_13444	Lau3	KiloMoana_100134454	314	46	Azospirillum brasilense (EZQ04064)
Mariner_scaffold_1440	Lau20	Mariner_10014416	353	90	SAR324 cluster bacterium SCGC AAA001-C10 (WP_010512894)
Mariner_scaffold_4902	Lau10	Mariner_10049034	305	51	Uncultured SUP05 bacterium (EEZ80661)
Mariner_scaffold_5573	Lau10	Mariner_10055744	302	56	Uncultured SUP05 bacterium (EEZ80661)
Tahi_Moana_scaffold_736	Lau113	TahiMoana_100073715	311	63	Methylobacter tundripaludum (WP_006893629)
Tahi_Moana_scaffold_1020	Lau51	TahiMoana_10010213	302	65	Uncultured SUP05 bacterium (EEZ80661)
Tahi_Moana_scaffold_2867	Lau20	TahiMoana_10028686	341	87	SAR324 cluster bacterium SCGC AAA001-C10 (WP_010512894)
Tahi_Moana_scaffold_6096	Lau10	TahiMoana_10060975	302	86	Uncultured SUP05 bacterium (EEZ80661)
Tahi_Moana_scaffold_8493	Lau10	TahiMoana_10084944	302	56	Uncultured SUP05 bacterium (EEZ80661)
Tui_Malila_scaffold_128	#N/A	TuiMalila_10001299	302	94	Uncultured SUP05 bacterium (EEZ80661)
Tui_Malila_scaffold_216	Lau20	TuiMalila_10002171	338	91	SAR324 cluster bacterium SCGC AAA001-C10 (WP_010512894)
Tui_Malila_scaffold_476	Lau20	TuiMalila_10004772	326	84	Deltaproteobacteria bacterium SCGC AAA003-F15 (WP_029734853)
Tui_Malila_scaffold_1447	Lau10	TuiMalila_100144811	305	51	Uncultured SUP05 bacterium (EEZ80661)
Tui_Malila_scaffold_3360	Lau15	TuiMalila_10033616	311	63	Sulfurimonas autotrophica (WP_013327894)
Tui_Malila_scaffold_3455	Lau10	TuiMalila_10034565	302	90	Uncultured SUP05 bacterium (EEZ80661)

Supplementary Table S11. Comparison of identified nxrB genes to *Nitrospirae* and *Nitrospinae*.

			Amino Acid % ID to	
IMG Gene ID	**Scaffold**	**Bin**	**Candidatus *Nitrospira defluvii***	***Nitrospina* sp. AB-629-B18**
Abe_100221103	Abe_scaffold_22109	#N/A	68.5	99.8
Abe_100311344	Abe_scaffold_31133	#N/A	68.4	98.2
KiloMoana_100103282	Kilo_Moana_scaffold_10327	#N/A	68.5	99.8
KiloMoana_100138161	Kilo_Moana_scaffold_13815	#N/A	69	98
KiloMoana_100171201	Kilo_Moana_scaffold_17119	#N/A	69.6	98
KiloMoana_100633711	Kilo_Moana_scaffold_63370	#N/A	69.5	98.2
Mariner_10103292	Mariner_scaffold_10328	#N/A	68.8	97.9
Mariner_10301911	Mariner_scaffold_30190	#N/A	68.5	99.8
Mariner_10468281	Mariner_scaffold_46827	#N/A	70.5	98.3
TahiMoana_10143943	Tahi_Moana_scaffold_14393	#N/A	70.1	98
TahiMoana_10155273	Tahi_Moana_scaffold_15526	#N/A	65.5	98
TahiMoana_10220734	Tahi_Moana_scaffold_22072	#N/A	63.4	98.1
TahiMoana_10614511	Tahi_Moana_scaffold_61450	#N/A	70.7	98.2
TuiMalila_10045731	Tui_Malila_scaffold_4572	Lau41	70	98

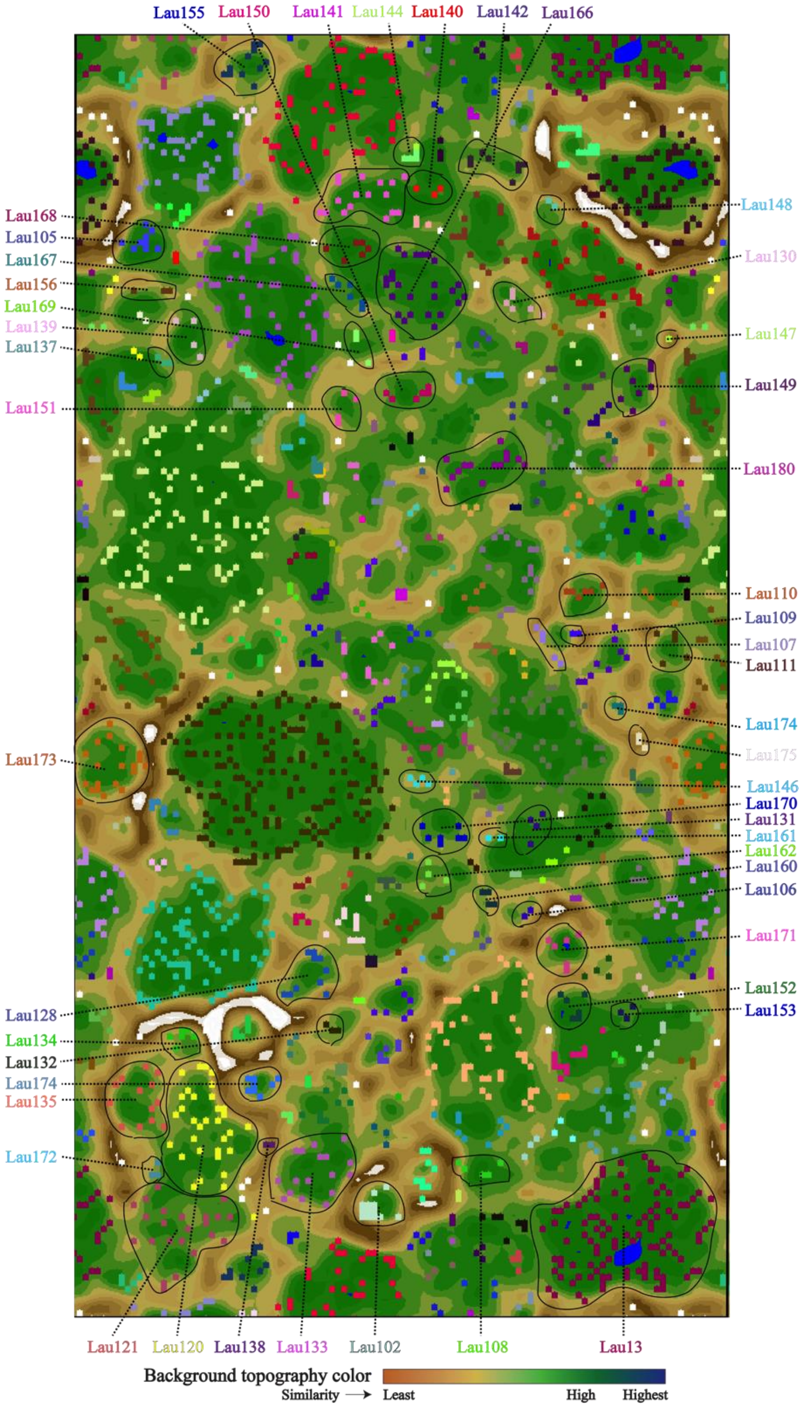
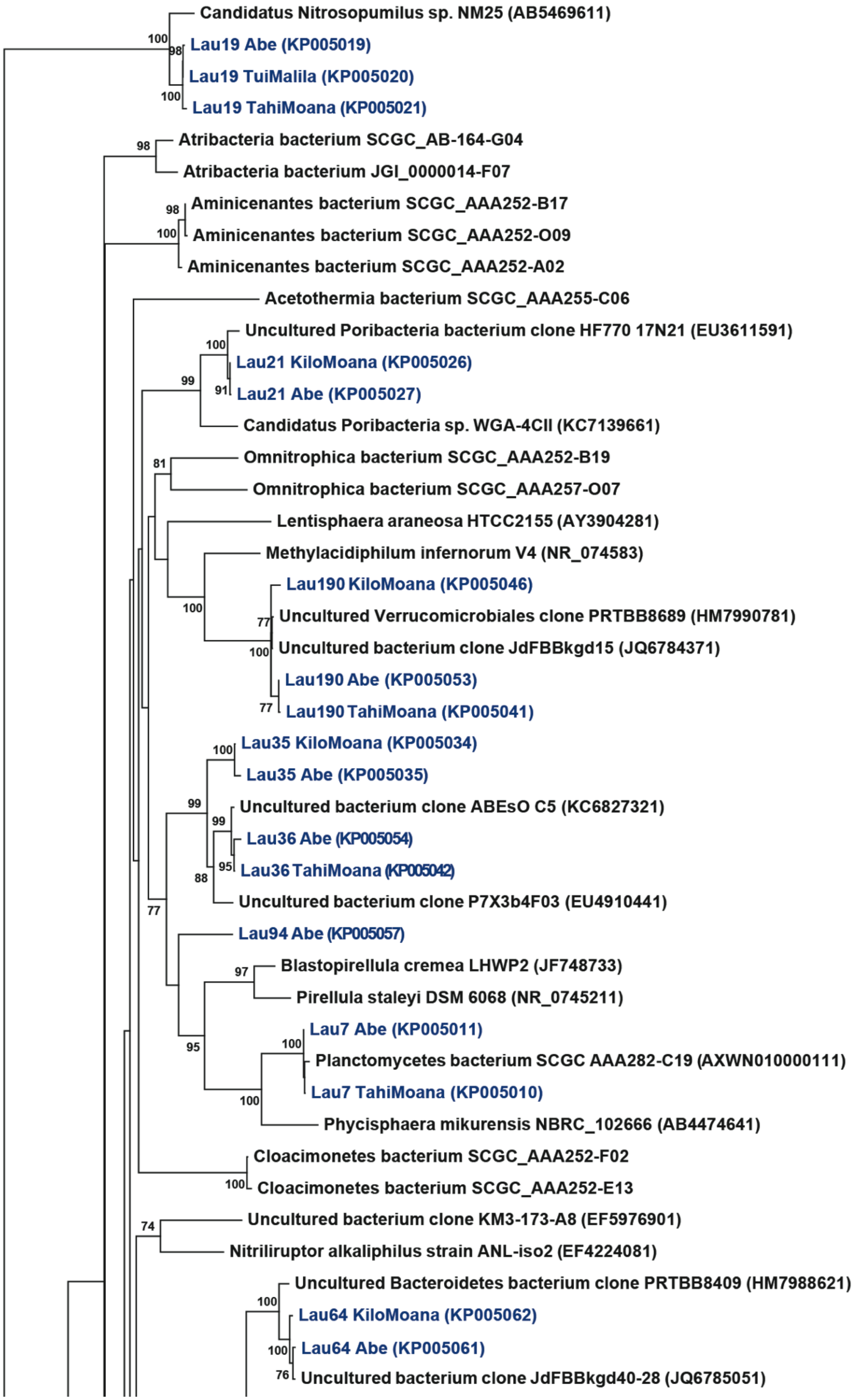
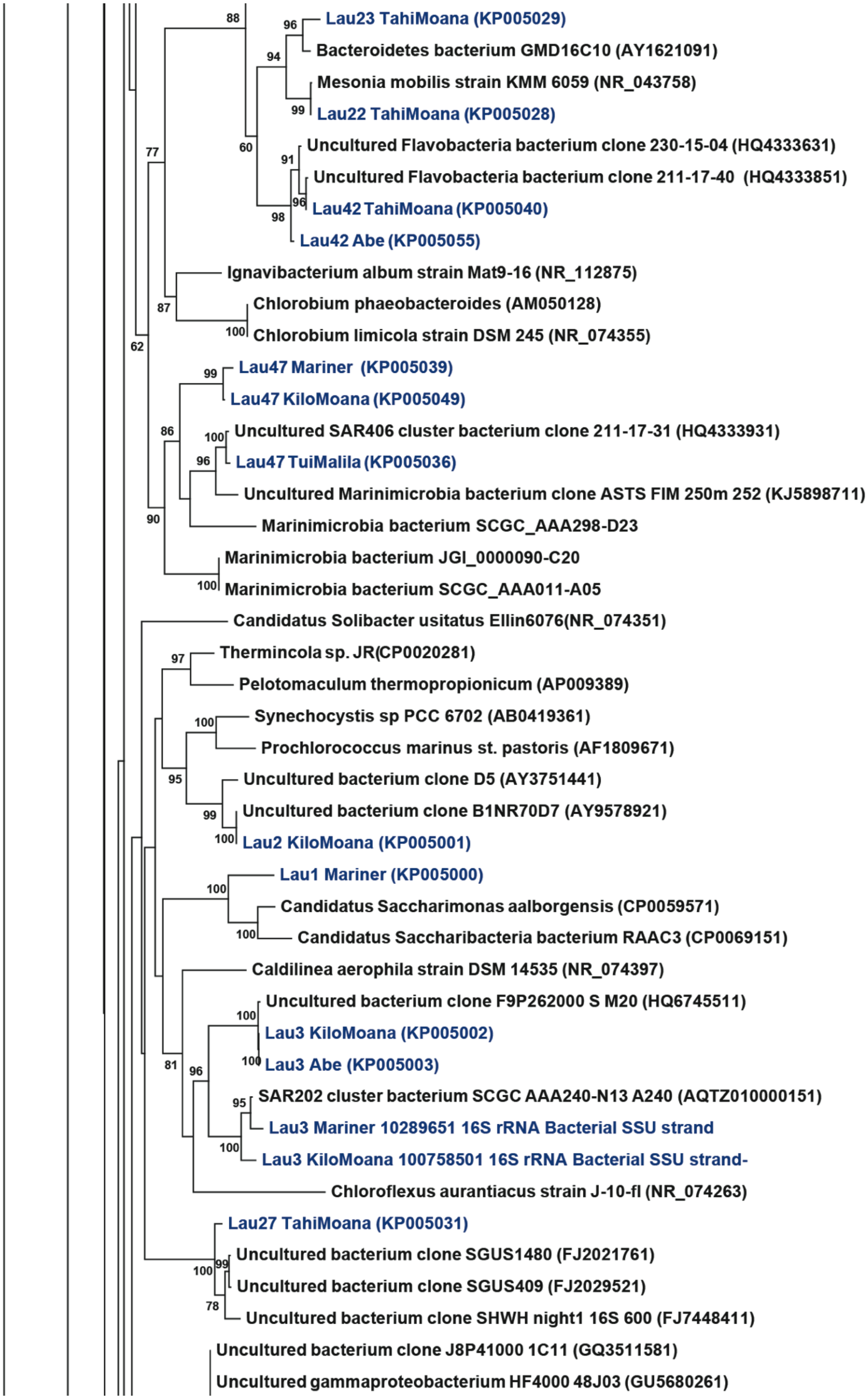


Fig. S1 Assignment of assembled contigs from ELSC to specific bins containing extrachromosomal elements using ESOM implemented with tetranucleotide frequencies. Each point on the map represents a contig (>4 kb) or contig fragment generated *in silico* (4-8 kb). All identified bins are indicated by black lines and uniquely color coded as indicated. The ESOM map displayed is tiled and torroidal (i.e., continuous from top to bottom and left to right). Only top 40 bins are shown.


Candidatus Nitrosopumilus sp. NM25 (AB5469611)
100
98
Lau19 Abe (KP005019)
Lau19 TuiMalila (KP005020)
100
Lau19 TahiMoana (KP005021)
98
Atribacteria bacterium SCGC_AB-164-G04
Atribacteria bacterium JGI_0000014-F07
98
Aminicenantes bacterium SCGC_AAA252-B17
100
Aminicenantes bacterium SCGC_AAA252-O09
Aminicenantes bacterium SCGC_AAA252-A02
Acetothermia bacterium SCGC_AAA255-C06
Uncultured Poribacteria bacterium clone HF770 17N21 (EU3611591)
100
Lau21 KiloMoana (KP005026)
99
91
Lau21 Abe (KP005027)
Candidatus Poribacteria sp. WGA-4CII (KC7139661)
81
Omnitrophica bacterium SCGC_AAA252-B19
Omnitrophica bacterium SCGC_AAA257-O07
Lentisphaera araneosa HTCC2155 (AY3904281)
Methylacidiphilum infernorum V4 (NR_074583)
Lau190 KiloMoana (KP005046)
100
77
Uncultured Verrucomicrobiales clone PRTBB8689 (HM7990781)
100
Uncultured bacterium clone JdFBBkgd15 (JQ6784371)
Lau190 Abe (KP005053)
77
Lau190 TahiMoana (KP005041)
100
Lau35 KiloMoana (KP005034)
Lau35 Abe (KP005035)
99
Uncultured bacterium clone ABEsO C5 (KC6827321)
99
Lau36 Abe (KP005054)
95
Lau36 TahiMoana (KP005042)
88
Uncultured bacterium clone P7X3b4F03 (EU4910441)
77
Lau94 Abe (KP005057)
97
Blastopirellula cremea LHWP2 (JF748733)
Pirellula staleyi DSM 6068 (NR_0745211)
Lau7 Abe (KP005011)
100
95
Planctomycetes bacterium SCGC AAA282-C19 (AXWN010000111)
Lau7 TahiMoana (KP005010)
100
Phycisphaera mikurensis NBRC_102666 (AB4474641)
Cloacimonetes bacterium SCGC_AAA252-F02
100
Cloacimonetes bacterium SCGC_AAA252-E13
74
Uncultured bacterium clone KM3-173-A8 (EF5976901)
Nitriliruptor alkaliphilus strain ANL-iso2 (EF4224081)
Uncultured Bacteroidetes bacterium clone PRTBB8409 (HM7988621)
100
Lau64 KiloMoana (KP005062)
100
Lau64 Abe (KP005061)
76
Uncultured bacterium clone JdFBBkgd40-28 (JQ6785051)


88
96
Lau23 TahiMoana (KP005029)
Bacteroidetes bacterium GMD16C10 (AY1621091)
94
Mesonia mobilis strain KMM 6059 (NR_043758)
99
Lau22 TahiMoana (KP005028)
60
77
Uncultured Flavobacteria bacterium clone 230-15-04 (HQ4333631)
91
Uncultured Flavobacteria bacterium clone 211-17-40 (HQ4333851)
96
Lau42 TahiMoana (KP005040)
98
Lau42 Abe (KP005055)
Ignavibacterium album strain Mat9-16 (NR_112875)
87
Chlorobium phaeobacteroides (AM050128)
100
Chlorobium limicola strain DSM 245 (NR_074355)
62
99
Lau47 Mariner (KP005039)
Lau47 KiloMoana (KP005049)
86
100
Uncultured SAR406 cluster bacterium clone 211-17-31 (HQ4333931)
96
Lau47 TuiMalila (KP005036)
Uncultured Marinimicrobia bacterium clone ASTS FIM 250m 252 (KJ5898711)
90
Marinimicrobia bacterium SCGC_AAA298-D23
Marinimicrobia bacterium JGI_0000090-C20
100
Marinimicrobia bacterium SCGC_AAA011-A05
Candidatus Solibacter usitatus Ellin6076(NR_074351)
97
Thermincola sp. JR(CP0020281)
Pelotomaculum thermopropionicum (AP009389)
100
Synechocystis sp PCC 6702 (AB0419361)
Prochlorococcus marinus st. pastoris (AF1809671)
95
Uncultured bacterium clone D5 (AY3751441)
99
Uncultured bacterium clone B1NR70D7 (AY9578921)
100
Lau2 KiloMoana (KP005001)
100
Lau1 Mariner (KP005000)
Candidatus Saccharimonas aalborgensis (CP0059571)
100
Candidatus Saccharibacteria bacterium RAAC3 (CP0069151)
Caldilinea aerophila strain DSM 14535 (NR_074397)
100
Uncultured bacterium clone F9P262000 S M20 (HQ6745511)
Lau3 KiloMoana (KP005002)
81
96
100
Lau3 Abe (KP005003)
95
SAR202 cluster bacterium SCGC AAA240-N13 A240 (AQTZ010000151)
Lau3 Mariner 10289651 16S rRNA Bacterial SSU strand
100
Lau3 KiloMoana 100758501 16S rRNA Bacterial SSU strand-
Chloroflexus aurantiacus strain J-10-fl (NR_074263)
Lau27 TahiMoana (KP005031)
99
Uncultured bacterium clone SGUS1480 (FJ2021761)
100
Uncultured bacterium clone SGUS409 (FJ2029521)
78
Uncultured bacterium clone SHWH night1 16S 600 (FJ7448411)
Uncultured bacterium clone J8P41000 1C11 (GQ3511581)
Uncultured gammaproteobacterium HF4000 48J03 (GU5680261)


63
Lau230 Mariner (KP005037)
Uncultured bacterium clone Prespill-800m-021 (JX8790191)
100
Lau230 KiloMoana (KP005044)
Lau230 TahiMoana (KP005043)
Uncultured bacterium clone F9P122000 S F04 (HQ6738391)
89
Lau4 TahiMoana (KP005006)
100
Alteromonas macleodii ATCC 27126 (CP0038411)
94
Lau4 Mariner (KP005007)
Nitrosomonas europaea ATCC 19718 (NR_074774)
Uncultured gamma proteobacterium clone KM3-174-C5 (EF5976911)
100
Lau62 Mariner (KP005038)
Lau62 Abe (KP005052)
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Uncultured bacterium clone F9P262000 S L06 (HQ6745241)
99
Methylomonas methanica MC09 (NR_074627)
Methylobacter sp. XLMV4 (KC9639661)
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Uncultured bacterium clone JdFBBkgd38 1 (JQ6784541)
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Lau113 KiloMoana (KP005051)
100
Uncultured bacterium clone CTD17 1470m 65F (KC5228481)
100
Lau116 KiloMoana (KP005047)
100
Lau116 Abe (KP005058)
61
Uncultured bacterium clone V1F15b (FJ9057001)
Uncultured bacterium clone KiMba2A6 (KC6828351)
Bacterial symbiont of Spinaxinus sp. CR-2013 (HG0080451|)
Myrtea tanimbarensis gill endosymbiont (FN8695331)
99
Gloverina rectangularis gill endosymbiont (FN8695451)
Lamellibrachia anaximandri endosymbiont clone Tw1_134 (KC8327291)
91
Guaymas Basin Metagenome SUP05 GB-1 (AJXC01001769)
98
Lau 10 TuiMalila (KP005012)
99
Bathymodiolus azoricus endosymbiont clone aMG-5-159 (AM0839711)
Uncultured bacterium clone SHZZ401 (HQ1628521)
64
100
Uncultured bacterium clone A723009 (AY9078221)
Uncultured SAR86 cluster bacterium clone IMS3D37 (JN2330561)
Uncultured gamma proteobacterium HF4000_19M20 (GU4748911)
100
Lau16 KiloMoana (KP005015)
83
Uncultured SAR86 cluster bacterium clone C139300047 (JX5284361)
100
Lau16 Mariner (KP005016)
64
Lau16 Abe (KP005017)
94
Marinobacter algicola DG893 (NR_042807)
Lau5 Mariner (KP005008)
100
Lau5 TahiMoana (KP005009)
Lau20 TahiMoana (KP005022)
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Lau20 Mariner (KP005025)
Lau20 TuiMalila (KP005024)
69
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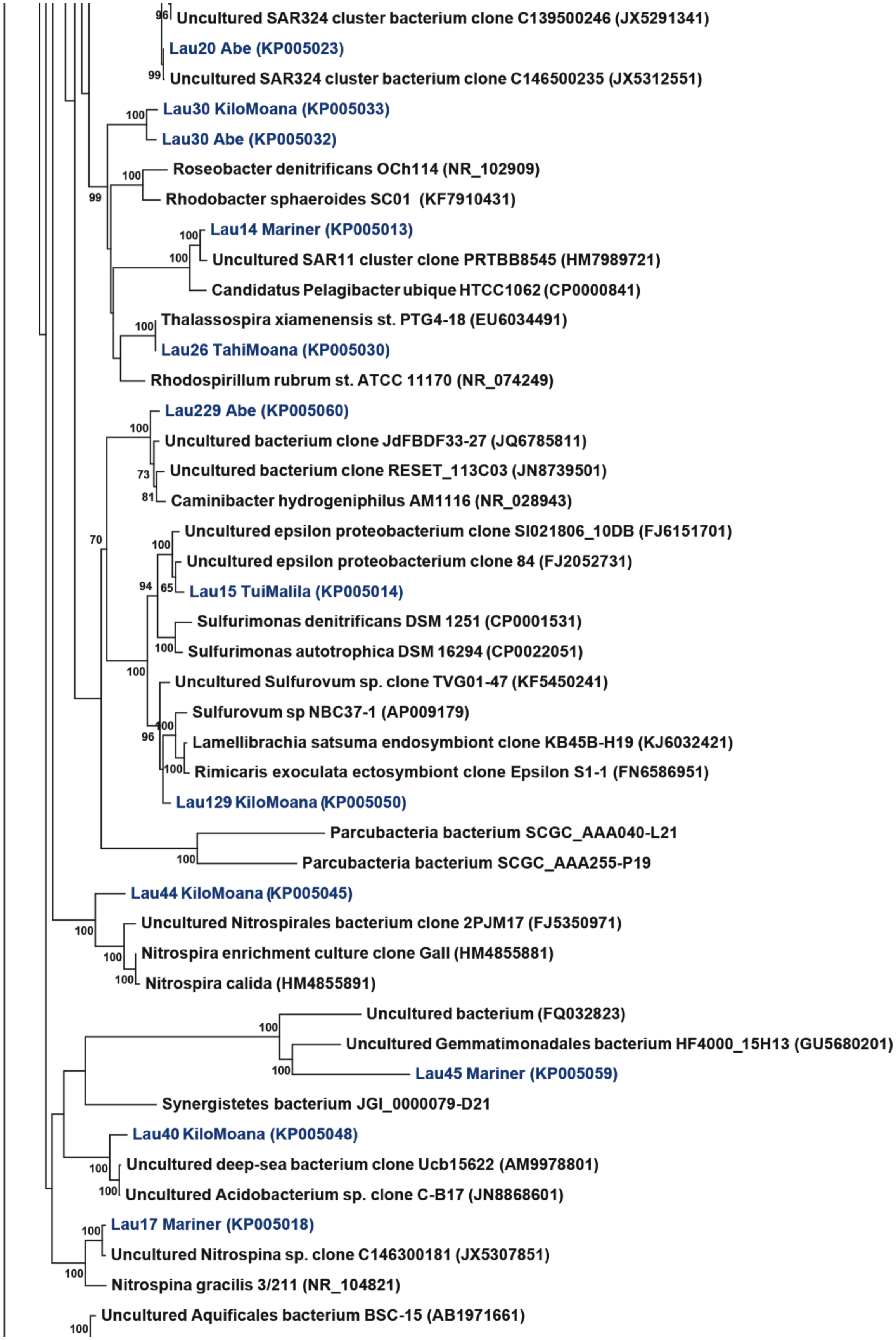
Uncultured SAR324 cluster bacterium clone GBSar324 (JX4064331)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Lau30 KiloMoana (KP005033)
Lau30 Abe (KP005032)
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Roseobacter denitrificans OCh114 (NR_102909)
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Rhodobacter sphaeroides SC01 (KF7910431)
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Lau14 Mariner (KP005013)
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Candidatus Pelagibacter ubique HTCC1062 (CP0000841)
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Thalassospira xiamenensis st. PTG4-18 (EU6034491)
Lau26 TahiMoana (KP005030)
Rhodospirillum rubrum st. ATCC 11170 (NR_074249)
Lau229 Abe (KP005060)
100
Uncultured bacterium clone JdFBDF33-27 (JQ6785811)
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Uncultured bacterium clone RESET_113C03 (JN8739501)
81
Caminibacter hydrogeniphilus AM1116 (NR_028943)
Uncultured epsilon proteobacterium clone SI021806_10DB (FJ6151701)
70
100
Uncultured epsilon proteobacterium clone 84 (FJ2052731)
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65
Lau15 TuiMalila (KP005014)
Sulfurimonas denitrificans DSM 1251 (CP0001531)
100
Sulfurimonas autotrophica DSM 16294 (CP0022051)
100
Uncultured Sulfurovum sp. clone TVG01-47 (KF5450241)
Sulfurovum sp NBC37-1 (AP009179)
100
96
Lamellibrachia satsuma endosymbiont clone KB45B-H19 (KJ6032421)
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Rimicaris exoculata ectosymbiont clone Epsilon S1-1 (FN6586951)
Lau129 KiloMoana (KP005050)
Parcubacteria bacterium SCGC_AAA040-L21
100
Parcubacteria bacterium SCGC_AAA255-P19
Lau44 KiloMoana (KP005045)
Uncultured Nitrospirales bacterium clone 2PJM17 (FJ5350971)
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100
Nitrospira enrichment culture clone GaII (HM4855881)
100
Nitrospira calida (HM4855891)
Uncultured bacterium (FQ032823)
100
Uncultured Gemmatimonadales bacterium HF4000_15H13 (GU5680201)
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Lau45 Mariner (KP005059)
Synergistetes bacterium JGI_0000079-D21
Lau40 KiloMoana (KP005048)
100
Uncultured deep-sea bacterium clone Ucb15622 (AM9978801)
100
Uncultured Acidobacterium sp. clone C-B17 (JN8868601)
100
Lau17 Mariner (KP005018)
Uncultured Nitrospina sp. clone C146300181 (JX5307851)
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Nitrospina gracilis 3/211 (NR_104821)
Uncultured Aquificales bacterium BSC-15 (AB1971661)
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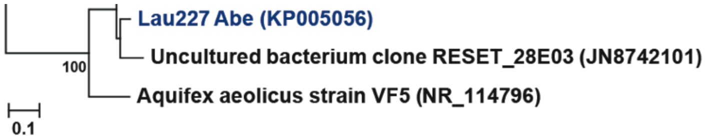

Fig S2. Phylogenetic tree of SSU rRNA genes in identified bins inferred by maximum likelihood. All sequences from ELSC are colored blue.

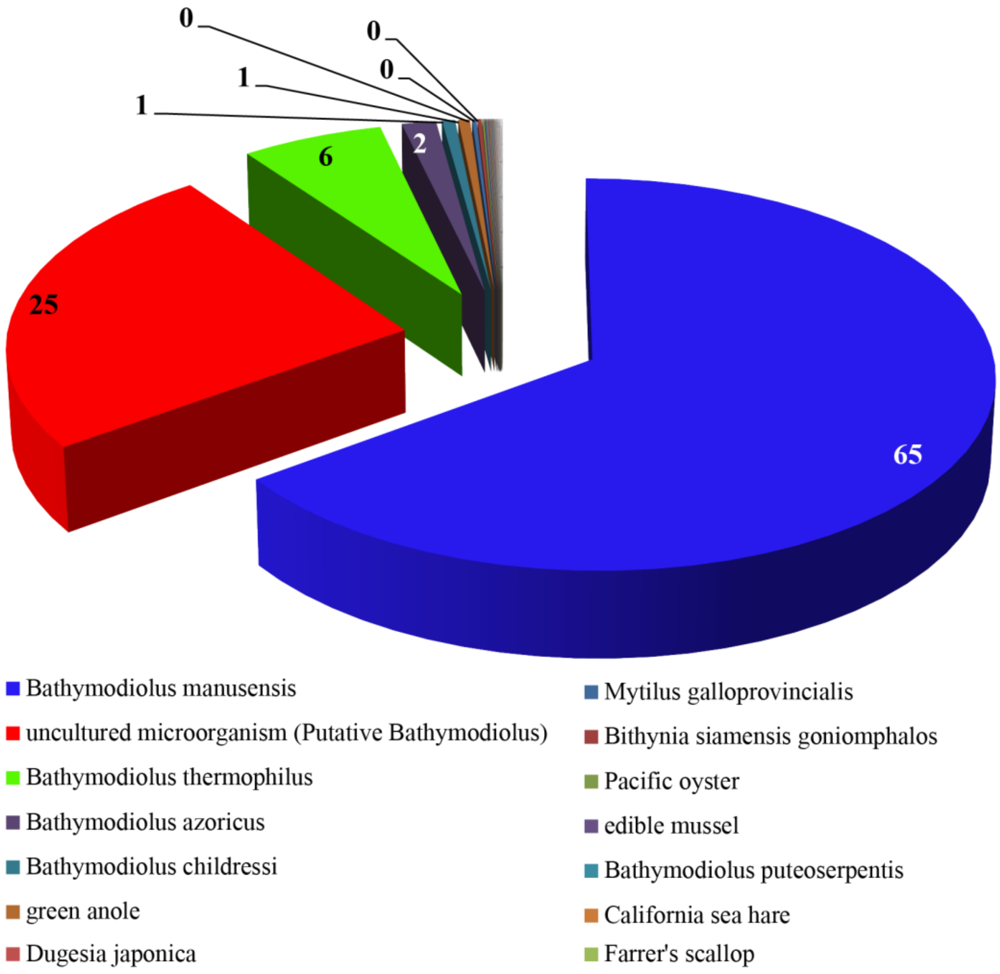

Fig. S3 Identification of eukaryotic bin “Lau8”. Pie-chart indicates the distribution of blastn hits of all identified ORFs in bin “Lau8” to organisms in NCBI-nt as indicated in the legend. Inset number indicates the percentage (%) of hits.

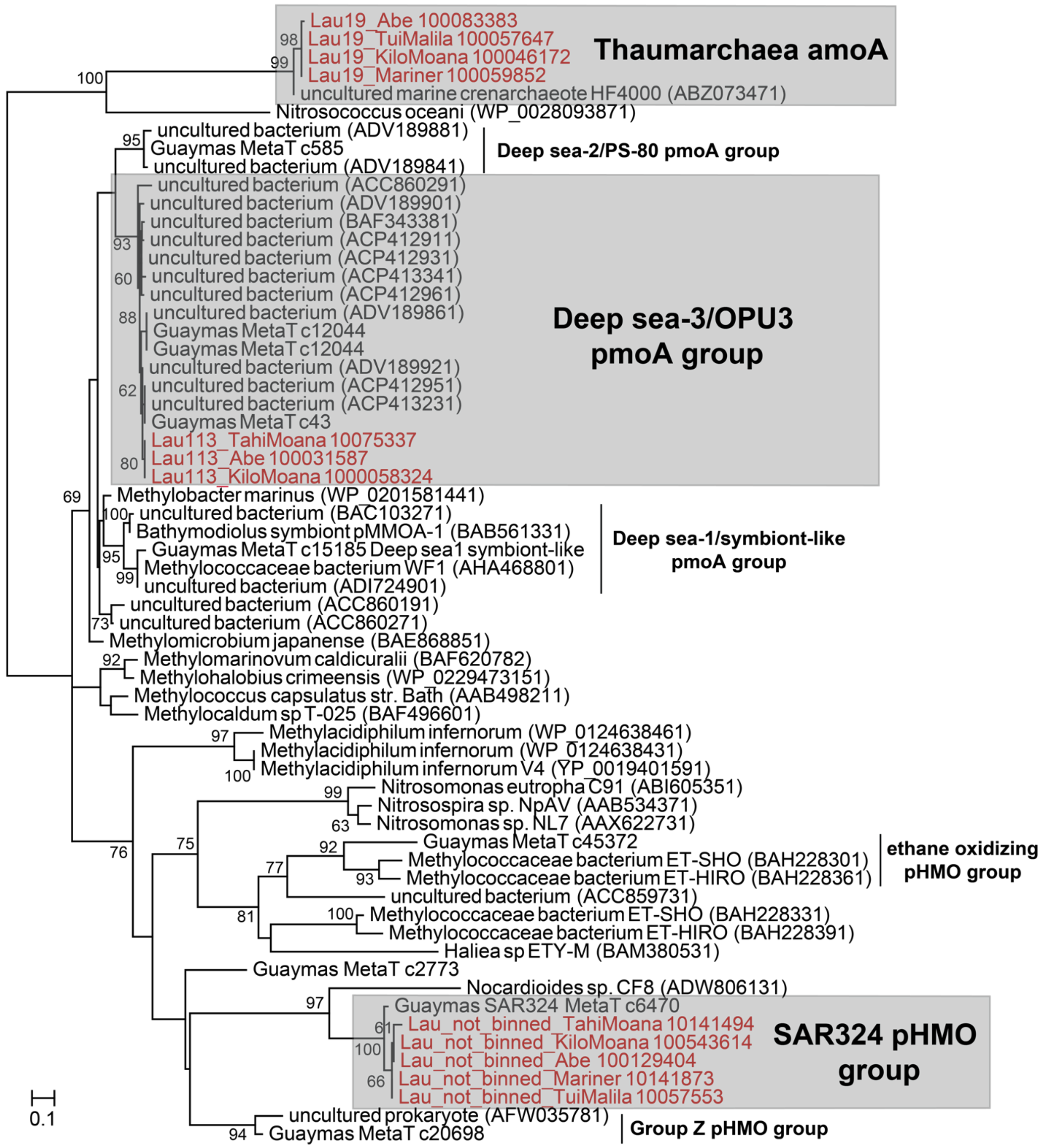

Fig S4. Phylogeny of pHMO subunit A inferred with maximum likelihood. Bootstrap values >60 are shown. Sequences in red are from ELSC. Grey boxes indicate phylogenetic clusters of ELSC sequences.

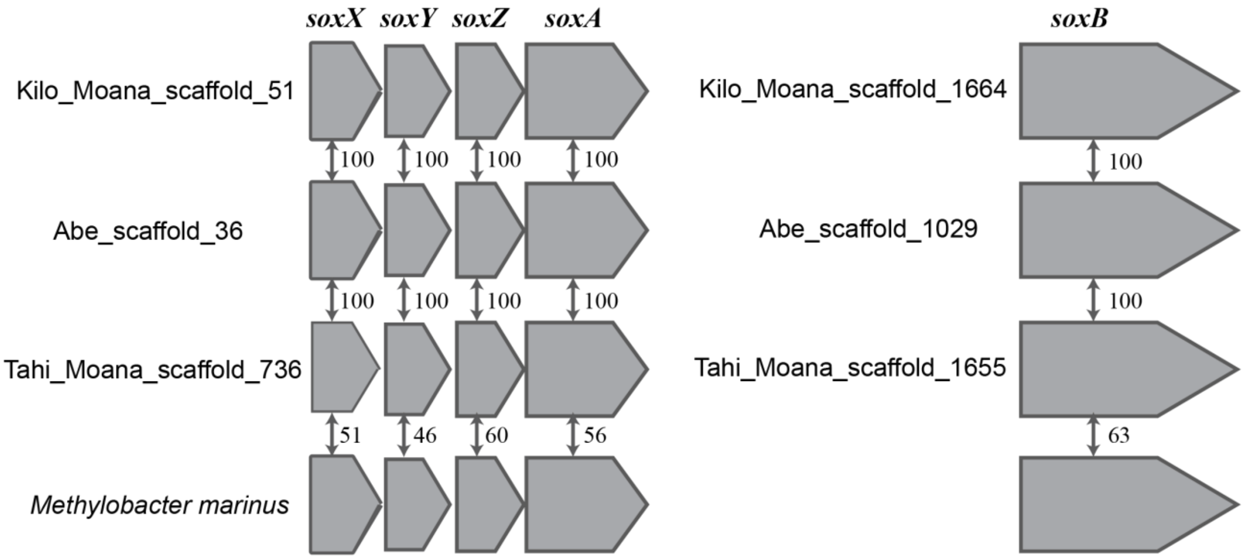

Fig. S5 Organization of sox genes in Lau113 and comparison with closely related sequences from GenBank. Arrows indicate shared genes and percent amino acid identity between predicted proteins.

Bin Name	**Organism/Group**	**CBB**	**R-TCA**	**3HP/4HB**
Lau10	**Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SUP05 Clade**	🟩		
Lau15	**Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas**		🟩	
Lau16	**Bacteria;Proteobacteria;Gammaproteobacteria;Oceanospirillales;SAR86 clade**			
Lau17	**Bacteria; Nitrospinae; Nitrospinia; Nitrospinales; Nitrospinaceae**		🟩	
Lau19	**Archaea;Thaumarchaeota;Marine Group I**			🟩
Lau20	**Bacteria;Proteobacteria;Deltaproteobacteria;SAR324 clade (Marine Group B)**	🟩		
Lau35	**Bacteria;Planctomycetes;Pla3 lineage**	🟩		
Lau41	**Bacteria; Nitrospinae; Nitrospinia; Nitrospinales; Nitrospinaceae**		🟩	
Lau60	**Bacteria;Proteobacteria;Gammaproteobacteria;Order Incertae cedis (Tubeworm symbiont)**	🟩		
Lau125	**Archaea;Euryarchaeota;Unclassified**	🟩		
Lau129	**Bacteria;Proteobacteria;Epsilonproteobacteria;Campylobacterales;Helicobacteraceae;Sulfurimonas**		🟩	
Lau227	**Bacteria;Aquificae;Aquificae;Aquificales;Aquificaceae**		🟩	
Lau229	**Bacteria;Proteobacteria;Epsilonproteobacteria**		🟩	
Lau376	**Bacteria;Proteobacteria;Alphaproteobacteria;Unclassified**	🟩		

Fig S6. Identification of carbon fixation pathways in ELSC bins. Green boxes indicate the presence of the pathways.

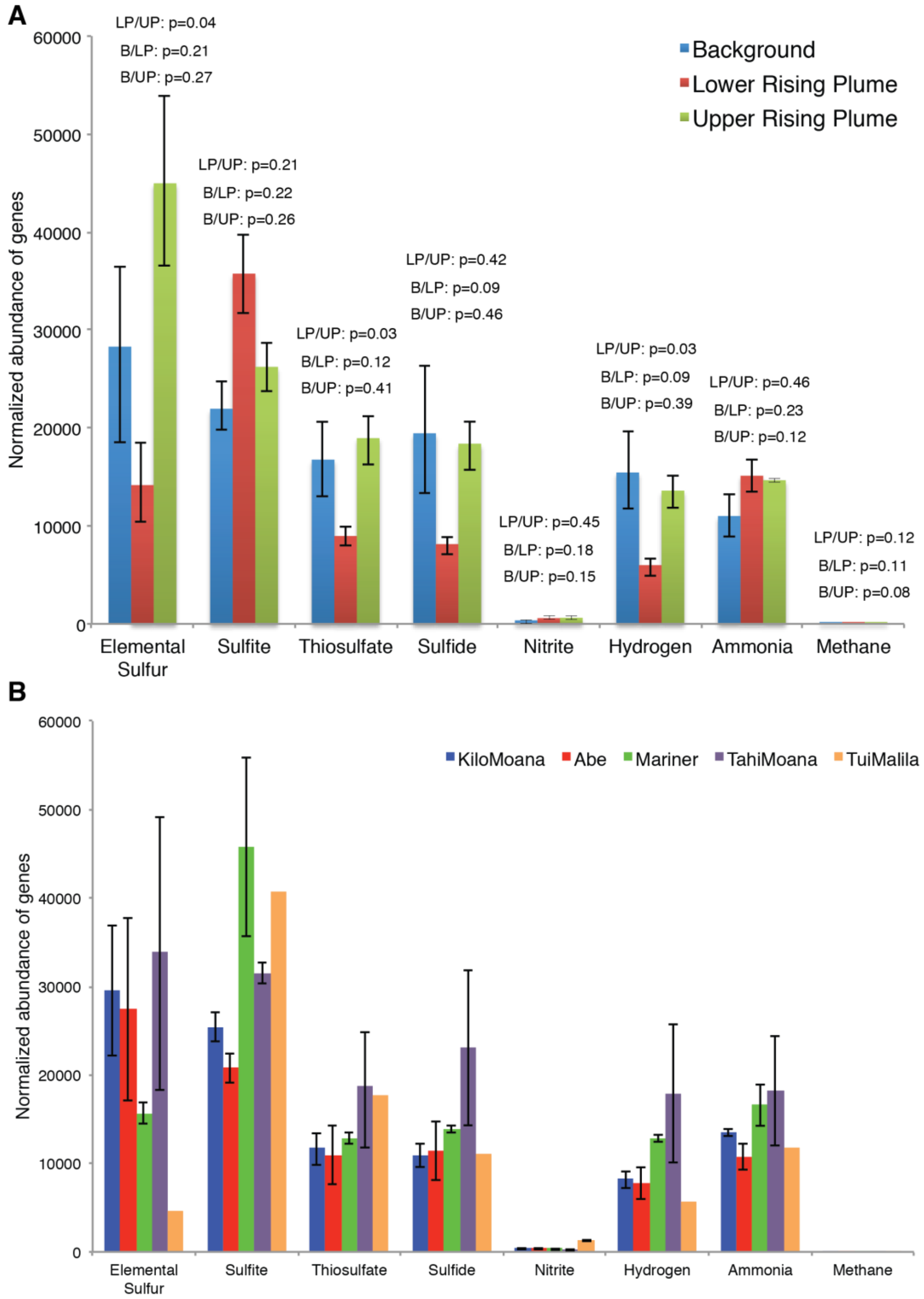

Figure S7. **A:** Normalized abundance of genes associated with electron donors, averaged by sample type. (S_0 – *dsrA*; SO_3^{2-} - *aprA*; $S_2O_3^{2-}$ – *soxZ*; H_2S – *fcc*+*sqr*, H_2–*hupL*, NO_2^-–*nxrB*, NH_3– *amoA*, CH4–*pmoA*). Inset p-values were computed by pairwise Student's t-tests; LP, lower plume, UP; upper plume; B, background. **B:** Normalized abundance of genes associated with electron donors averaged by site. (S_0 – *dsrA*; SO_3^{2-} - *aprA*; $S_2O_3^{2-}$ – *soxZ*; H_2S – *fcc*+*sqr*, H_2–*hupL*, NO2^{-}–*nxrB*, NH_3– *amoA*, CH4–*pmoA*). Error bars represent the standard error of mean.

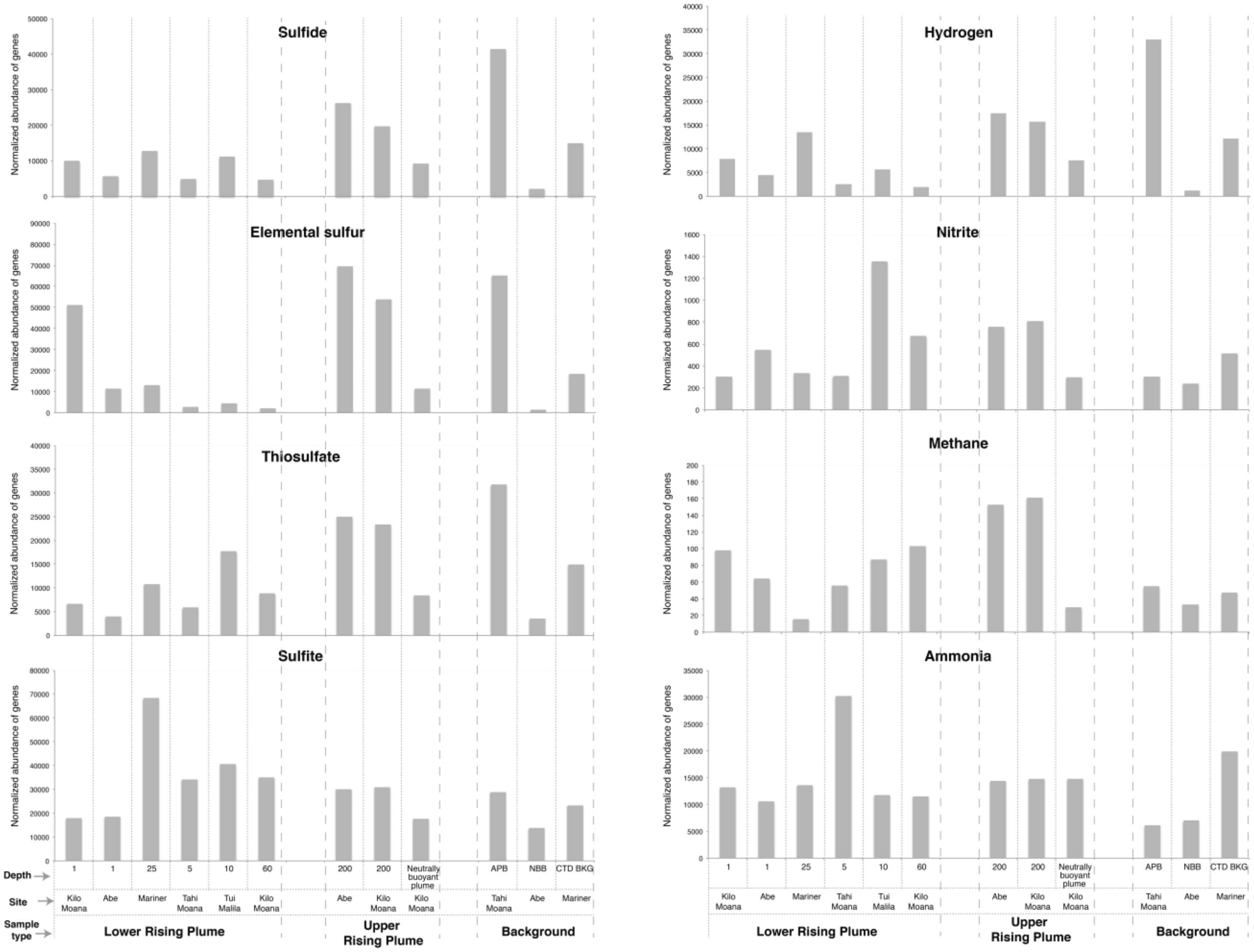

Figure S8. Normalized abundance of genes associated with electron donors, arranged by electron donor and sample type. (S_0 – *dsrA*; SO_3^{2-} - *aprA*; $S_2O_3^{2-}$ – *soxZ*; H_2S – *fcc*+*sqr*, H_2– *hupL*, NO_2^-–*nxrB*, NH_3– *amoA*, CH_4–*pmoA*). Note that the scale is different for each panel.

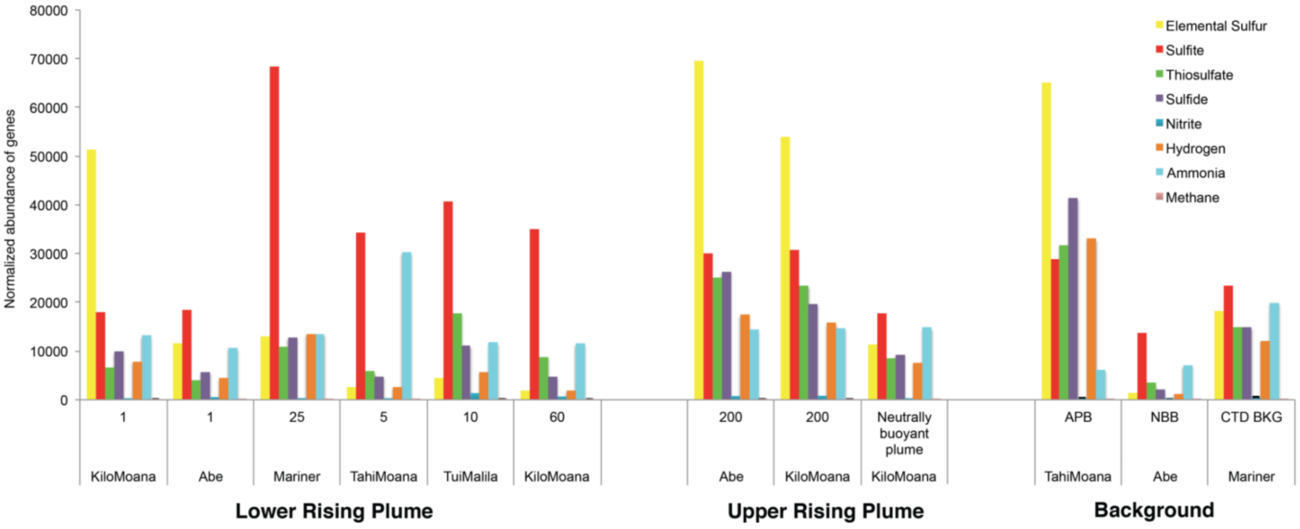

Figure S9. Normalized abundance of genes associated with electron donors, arranged by sample type and site. (S_0 – *dsrA*; SO_3^{2-} - *aprA*; $S_2O_3^{2-}$ – *soxZ*; H_2S – *fcc*+*sqr*, H_2–*hupL*, NO_2^-– *nxrB*, NH_3– *amoA*, CH_4–*pmoA*).

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