A dynamic microbial sulfur cycle in a serpentinizing continental ophiolite

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Supporting Information

Figures

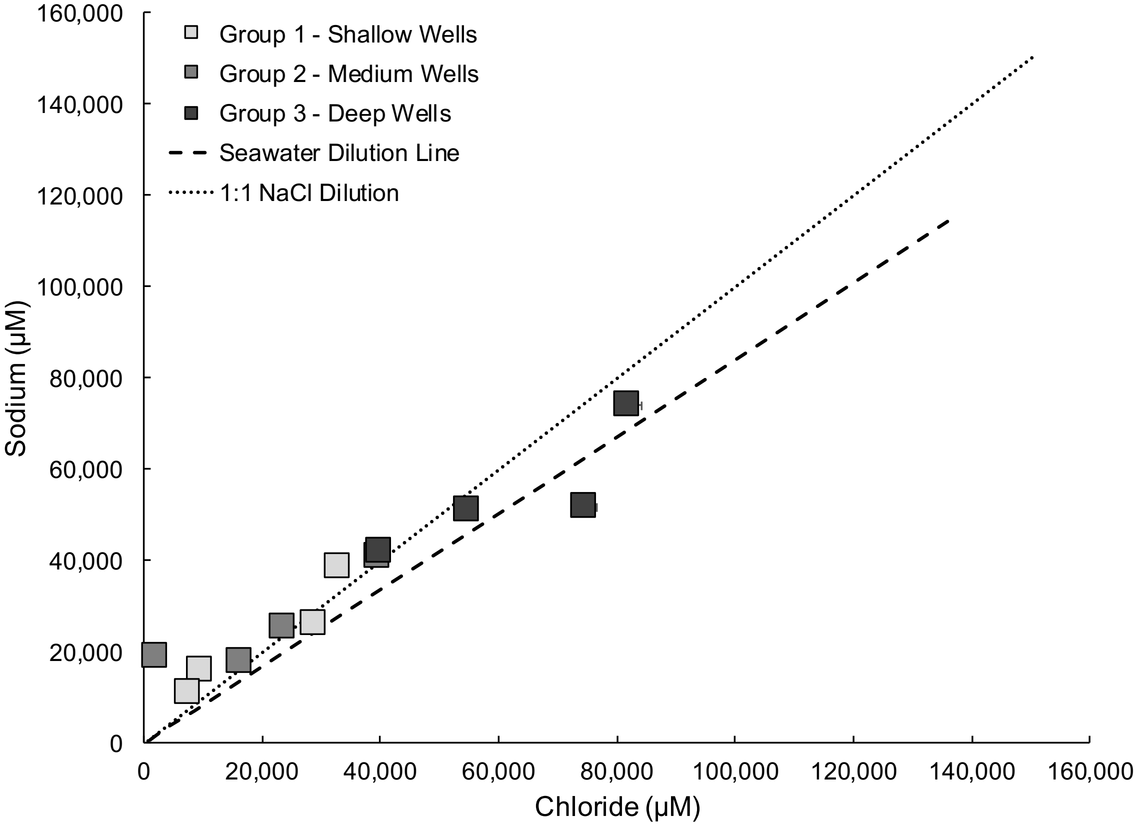

Figure S1 - Fluid salinity for CROMO wells. CROMO monitoring well sodium and chloride values (µM) are compared. Wells are grouped into three clusters based upon their drilled depth. Shallow represents wells drilled to < 15 m (CSW1.4, N08-C, QV1.2, CSW1.2), medium represents wells drilled between 15 and 20 m (CSW1.1, QV1.1, CSW1.3, N08-B), and deep represents wells drilled to depths < 20 m (CSW1.5, QV1.3, N08-A, CSWold).

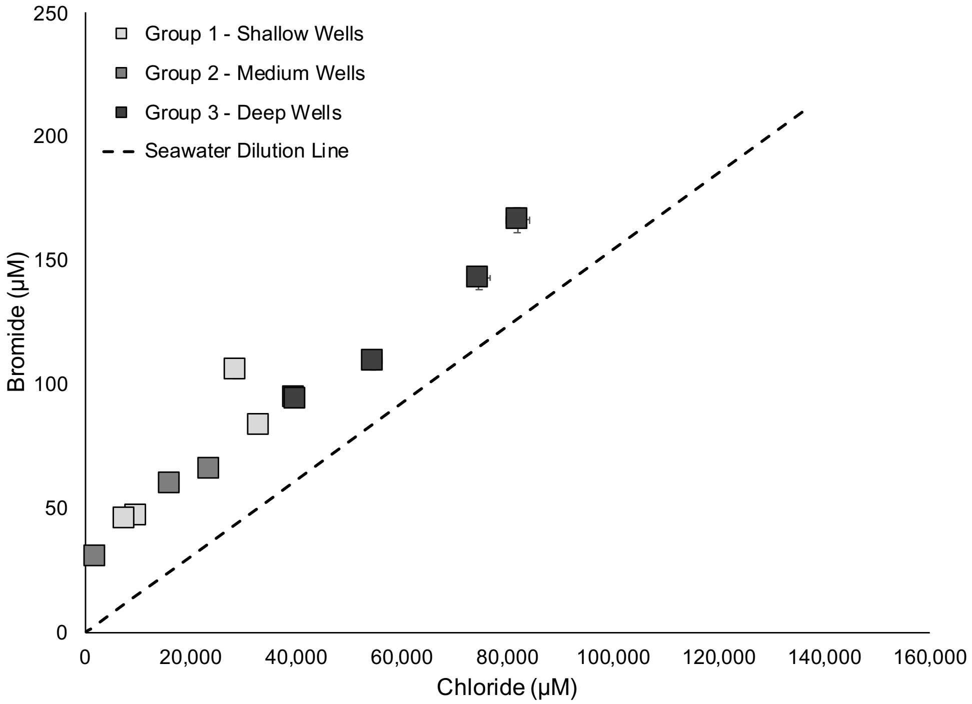

Figure S2 – Br-Cl values for CROMO wells. Measured values for bromide and chloride are plotted here. All values offset the seawater dilution line to slightly higher ratios, as some Cl was likely removed from the fluid at depth, through substitution of Cl for hydroxyl groups in serpentine or precipitated in Cl-bearing minerals such as iowaite.

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Table S1 – CROMO aqueous geochemistry measured for this study.

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Table S1: CROMO July 2014 Aqueous Geochemistry

Well	Well depth (m)	pH	T (℃)	Cond. (μS)	DO (mg/L)	ORP (mV)	Br^-	Cl^-	F^-	NO_2^-	NO_3^-	SO_4^{2-}	HS^-	Ca^{2+}	Na^+	Mg^{2+}	K^+	Mn^{2+}	Fe	Sr	H_2	CO	CH_4	DIC	$HCOO^-$	CH_3COO^-
CSW1.4	8.80	7.75	15.05	1950	2.36	116	46.93	9622.33	13.69	< 1.45	2.58	391.94	1.00	782.73	16082.76	826.37	118.21	<3.14	81.09	3.60	0.29	0.16	3.66	3870.12	1.00	1.00
N08-C	13.70	8.46	15.53	1372	0.42	-153	46.06	7556.82	14.21	< 1.45	13.87	51.22	1.00	487.88	11027.28	176.01	179.17	<3.14	23.98	6.07	0.26	0.04	1.13	674.65	1.00	1.00
QV 1.2	14.90	9.47	17.09	3042	0.40	-143	106.00	28676.00	11.58	< 1.45	< 1.61	32.00	1.00	559.39	26113.34	23.03	156.86	<3.14	52.95	5.13	0.49	0.17	263.77	682.16	1.00	1.00
CSW1.2	19.20	7.76	15.97	4495	0.25	-119	83.60	32994.62	18.95	78.99	< 1.61	191.65	1.00	772.23	38690.27	26.80	287.44	<3.14	14.92	10.34	0.18	0.11	783.87	1238.59	1.00	1.00
CSW1.1	19.50	12.32	16.31	4453	0.43	-297	30.79	1956.11	26.84	< 1.45	< 1.61	266.19	12.88	706.47	18847.22	3.13	1111.17	<3.14	46.01	22.70	0.79	0.18	593.90	192.00	19.00	57.00
QV 1.1	23.00	11.51	17.52	2854	0.28	-234	60.20	16172.67	16.32	< 1.45	< 1.61	257.13	4.76	1978.56	17840.16	3.13	967.73	<3.14	34.78	13.53	0.25	0.12	286.46	45.43	1.00	6.10
CSW1.3	23.20	10.15	15.64	4842	0.16	-205	94.61	39610.63	11.58	< 1.45	< 1.61	151.16	1.00	808.86	40831.81	3.13	307.55	<3.14	17.18	10.55	2.89	0.11	1138.16	254.95	1.00	1.00
N08-B	26.20	10.68	16.12	3132	0.76	-198	65.70	23610.94	15.26	< 1.45	< 1.61	27.69	1.00	1139.10	25520.89	3.13	237.87	<3.14	74.44	17.96	0.09	0.06	303.20	28.04	1.00	1.00
CSW1.5	27.40	9.77	15.80	4792	0.16	-285	94.49	40001.66	14.74	< 1.45	< 1.61	317.41	23.75	926.67	42202.20	3.13	332.29	<3.14	54.90	15.05	0.38	0.16	1075.03	438.78	1.00	1.00
QV 1.3	34.60	9.68	16.60	6507	0.26	-224	142.92	74557.95	17.90	< 1.45	< 1.61	55.69	10.13	1694.40	51677.62	9.15	333.49	<3.14	32.66	45.96	0.17	0.11	1281.63	593.43	1.00	7.90
N08-A	39.60	10.89	16.85	6335	0.09	-250	109.38	54610.27	12.63	< 1.45	< 1.61	40.18	1.14	3194.94	51245.33	3.13	450.21	<3.14	38.88	86.04	0.08	0.07	1268.96	55.77	1.00	1.00
CSW OLD	76.20	9.73	17.43	11529	0.26	-280	166.45	81853.64	15.79	< 1.45	< 1.61	139.29	8.39	1660.11	73939.94	3.13	540.29	<3.14	47.86	38.89	0.15	0.25	1316.97	44.24	1.00	1.00

Anions, cations, and dissolved gases are reported in micromolar concentrations
Gases are reported as concentration dissolved in fluid
T = temperature; Cond = conductivity; DO = dissolved oxygen ; ORP = oxidation reduction potential; DIC = dissolved inorganic carbon
Acetate and Formate values listed were estimated based on data from previous sampling trips

Table S2: Terrestrial Serpentinizing Systems Selected Water Chemistry Parameters

Site Name	Well/ Specific Name	Conductivity (μS/cm)	pH	SO_4^{2-} (μM)	Cl^- (μM)	Na^+ (μM)	References
CROMO, California, USA	CSW 1,1	4453.00	12.32	266.19	1956.11	18847.22	This Work
CROMO, California, USA	CSW 1,2	4495.00	7.76	191.65	32994.62	38690.27	This Work
CROMO, California, USA	CSW 1,3	4842.00	10.15	151.16	39610.63	40831.81	This Work
CROMO, California, USA	CSW 1,4	1950.00	7.75	391.94	9622.33	16082.76	This Work
CROMO, California, USA	CSW 1,5	4792.00	9.77	317.41	40001.66	42202.20	This Work
CROMO, California, USA	CSW OLD	11529.00	9.86	139.29	81853.64	73939.94	This Work
CROMO, California, USA	N-08 A	6335.00	10.89	40.18	54610.27	51245.33	This Work
CROMO, California, USA	N-08 B	3132.00	10.68	27.69	23610.94	25520.89	This Work
CROMO, California, USA	N-08 C	1372.00	8.46	51.22	7556.82	11027.28	This Work
CROMO, California, USA	QV 1,1	2854.00	11.51	257.13	16172.67	17840.16	This Work
CROMO, California, USA	QV 1,2	3042.00	9.47	32.00	28676.00	26113.34	This Work
CROMO, California, USA	QV 1,3	6507.00	9.68	55.69	74557.95	51677.62	This Work
Oman	Yellowstone du pauvre	2700.00	10.10	349.00	21052.00	22086.00	Chavagnac et al., 2013
Oman	Yellowstone du pauvre	2210.00	11.90	15.00	9844.00	10740.00	Chavagnac et al., 2013
Oman	Little Grand Canon	1730.00	11.80	5.00	6091.00	6261.00	Chavagnac et al., 2013
Oman	Little Grand Canon	1690.00	11.70	1.00	5701.00	5939.00	Chavagnac et al., 2013
Oman	Izki les 2 puits	810.00	7.80	71.00	5136.00	7647.00	Chavagnac et al., 2013
Oman	Izki les 2 puits	920.00	11.20	28.00	5464.00	5373.00	Chavagnac et al., 2013
Oman	Le partage du midi	2250.00	11.70	3.00	10301.00	11965.00	Chavagnac et al., 2013
Oman	Lac bleu de Bahla	780.00	10.80	179.00	5215.00	5412.00	Chavagnac et al., 2013
Oman	Rustaq	980.00	8.20	812.00	4007.00	5489.00	Chavagnac et al., 2013
Oman	La poule au pot	1870.00	11.30	45.00	11027.00	10094.00	Chavagnac et al., 2013
Oman	L'ane blanc	1360.00	7.90	2433.00	5327.00	6446.00	Chavagnac et al., 2013
Oman	Two shoes	1480.00	11.60	40.00	4511.00	6581.00	Chavagnac et al., 2013
Oman	Two shoes	1480.00	11.60	41.00	3009.00	6691.00	Chavagnac et al., 2013
Oman	Irma (Yellowstone du pauvre)	2540.00	10.50	44.00	11154.00	18311.00	Chavagnac et al., 2013
Oman	Irma (Yellowstone du pauvre)	2540.00	10.50	46.00	11632.00	18579.00	Chavagnac et al., 2013
Oman	Irma (Yellowstone du pauvre)	2650.00	9.90	48.00	12752.00	20366.00	Chavagnac et al., 2013
Oman	Irma (Yellowstone du pauvre)	2650.00	9.90	48.00	12926.00	20304.00	Chavagnac et al., 2013
New Caledonia	La Coulee 1	n.r.	10.80	7.81	628.57	634.78	Barnes et al., 1978
New Caledonia	La Coulee 2	n.r.	10.70	60.38	465.71	1134.78	Barnes et al., 1978
Liguria, Italy	Fiorino village	n.r.	9.50	12.60	600.00	570.00	Chavagnac et al., 2013
Liguria, Italy	Fiorino village	n.r.	9.50	11.20	600.00	580.00	Chavagnac et al., 2013
Liguria, Italy	Rio Dellecave	n.r.	6.70	31.80	130.00	110.00	Chavagnac et al., 2013
Liguria, Italy	Acquasanta	n.r.	11.70	3.30	450.00	1260.00	Chavagnac et al., 2013
Liguria, Italy	Acquasanta	n.r.	11.70	3.00	450.00	1270.00	Chavagnac et al., 2013
Liguria, Italy	Acquasanta	n.r.	11.70	3.40	450.00	1270.00	Chavagnac et al., 2013
Liguria, Italy	Ponte Arma	n.r.	9.50	32.80	560.00	450.00	Chavagnac et al., 2013
Liguria, Italy	Rio Leone	n.r.	11.30	19.20	650.00	550.00	Chavagnac et al., 2013
Liguria, Italy	Rio Leone	n.r.	11.30	16.70	640.00	550.00	Chavagnac et al., 2013
Liguria, Italy	Rio Leone	n.r.	11.30	7.50	550.00	430.00	Chavagnac et al., 2013
Liguria, Italy	Rio Leone	n.r.	11.30	5.00	550.00	430.00	Chavagnac et al., 2013
Liguria, Italy	Rio Branega	n.r.	11.50	0.60	500.00	1050.00	Chavagnac et al., 2013
Liguria, Italy	Rio Branega	n.r.	11.50	0.50	500.00	1040.00	Chavagnac et al., 2013
Liguria, Italy	Gorzente (lago Lavagnina)	n.r.	11.20	10.50	220.00	280.00	Chavagnac et al., 2013
Liguria, Italy	Gorzente (lago Lavagnina)	n.r.	11.20	10.40	220.00	280.00	Chavagnac et al., 2013
Liguria, Italy	Gorzente (lago Lavagnina)	n.r.	11.50	0.80	220.00	300.00	Chavagnac et al., 2013
Liguria, Italy	Gorzente (lago Lavagnina)	n.r.	11.20	1.20	310.00	410.00	Chavagnac et al., 2013
Liguria, Italy	Gorzente	n.r.	11.60	1.40	420.00	850.00	Chavagnac et al., 2013
Liguria, Italy	Gorzente	n.r.	11.60	1.30	420.00	860.00	Chavagnac et al., 2013
Liguria, Italy	Maddalena (Don Orione)	n.r.	11.10	23.60	420.00	740.00	Chavagnac et al., 2013
Liguria, Italy	Maddalena (Don Orione)	n.r.	11.10	23.80	420.00	740.00	Chavagnac et al., 2013
Genova Province, Italy	V18	n.r.	11.37	42.68	n.r.	n.r.	Cipolli et al., 2004
Genova Province, Italy	BR1	n.r.	11.86	1.46	n.r.	n.r.	Cipolli et al., 2004
Genova Province, Italy	L43	n.r.	11.52	4.58	n.r.	n.r.	Cipolli et al., 2004
Genova Province, Italy	S70	n.r.	11.42	190.51	n.r.	n.r.	Cipolli et al., 2004
Genova Province, Italy	C11	n.r.	10.50	263.38	n.r.	n.r.	Cipolli et al., 2004
Genova Province, Italy	A1	n.r.	11.57	133.25	n.r.	n.r.	Cipolli et al., 2004
Genova Province, Italy	V18	n.r.	11.37	42.68	11700.00	16600.00	Cipolli et al., 2004
Genova Province, Italy	BR1	n.r.	11.86	1.46	21700.00	23700.00	Cipolli et al., 2004
Genova Province, Italy	L43	n.r.	11.52	4.58	18600.00	28300.00	Cipolli et al., 2004
Genova Province, Italy	S70	n.r.	11.42	190.51	23300.00	5500.00	Cipolli et al., 2004
Genova Province, Italy	C11	n.r.	10.50	263.38	23200.00	12800.00	Cipolli et al., 2004
Genova Province, Italy	LER20	n.r.	11.57	133.25	26500.00	12700.00	Cipolli et al., 2004
Genova Province, Italy	BR2	n.r.	11.73	1.04	30500.00	41100.00	Cipolli et al., 2004

Genova Province, Italy	ERR20	n.r.	11.36	32.06	15400.00	16500.00	Cipolli et al., 2004
Genova Province, Italy	GOR34	n.r.	11.68	1.04	17300.00	18500.00	Cipolli et al., 2004
Genova Province, Italy	GOR34A	n.r.	11.55	5.73	15000.00	18300.00	Cipolli et al., 2004
Genova Province, Italy	LER18A	n.r.	11.38	12.28	18900.00	6800.00	Cipolli et al., 2004
Genova Province, Italy	LER2	n.r.	11.11	39.35	19700.00	10300.00	Cipolli et al., 2004
Genova Province, Italy	LER20	n.r.	11.53	15.93	27900.00	12700.00	Cipolli et al., 2004
Genova Province, Italy	LER2I	n.r.	11.49	11.56	23100.00	9900.00	Cipolli et al., 2004
Genova Province, Italy	ORB101	n.r.	10.59	34.77	14700.00	3900.00	Cipolli et al., 2004
Genova Province, Italy	PIO14	n.r.	10.69	17.49	17200.00	53000.00	Cipolli et al., 2004
Genova Province, Italy	S70	n.r.	11.48	22.28	23900.00	5400.00	Cipolli et al., 2004
Genova Province, Italy	V18	n.r.	11.31	47.89	11200.00	16100.00	Cipolli et al., 2004
Genova Province, Italy	GOR35	n.r.	11.44	1.04	8960.00	6700.00	Cipolli et al., 2004
Genova Province, Italy	L43	n.r.	11.55	4.68	20800.00	27700.00	Cipolli et al., 2004
Genova Province, Italy	BR1	n.r.	11.79	2.08	20800.00	23500.00	Cipolli et al., 2004
Genova Province, Italy	BR3	n.r.	11.72	15.62	17400.00	18400.00	Cipolli et al., 2004
Genova Province, Italy	PIO14	n.r.	10.49	26.23	19600.00	53600.00	Cipolli et al., 2004
Genova Province, Italy	GOR36	n.r.	9.95	30.71	46100.00	84000.00	Cipolli et al., 2004
Genova Province, Italy	V99	n.r.	11.28	212.37	97400.00	68100.00	Cipolli et al., 2004
The Cedars, California, USA	NS1	740.00	11.50	1.00	945.00	945.00	Morrill et al., 2013
The Cedars, California, USA	BS5	870.00	11.60	1.00	1490.00	1980.00	Morrill et al., 2013
The Cedars, California, USA	CREEK	3010.00	8.70	8.00	230.00	60.00	Morrill et al., 2013
The Cedars, California, USA	NS1	740.00	11.50	1.00	970.00	960.00	Suzuki et al., 2013
The Cedars, California, USA	BS5	800.00	11.50	1.00	1450.00	1940.00	Suzuki et al., 2013
Santa Elena, Costa Rica	Camino al inglés	425.00	7.85	26.34	45.14	52.57	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Poza del General	404.00	8.45	23.63	69.14	96.83	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Río Murciélago springs	428.00	7.45	18.22	53.43	74.35	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Casa de Zinc	369.00	8.43	20.92	66.86	76.96	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Río Calera 4	397.00	8.53	18.01	49.43	57.57	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Río Calera 3	401.00	8.24	16.55	48.00	62.17	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Nancite spring	681.00	8.77	30.50	171.71	112.52	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Los Pargos Spring	560.00	7.42	21.03	101.71	92.57	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Casa de Zinc	545.00	8.46	24.05	56.00	70.43	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Río Murciélago	643.00	7.26	14.68	38.00	65.65	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Quebrada Danta	412.00	8.30	21.03	65.14	426.09	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Río Calera	558.00	8.40	15.30	39.71	56.96	Sanchez-Murillo et al., 2014
Santa Elena, Costa Rica	Pozo Aguas Calientes	535.00	7.20	59.75	1181.43	704.78	Sanchez-Murillo et al., 2014
Red Mountain, California, USA	Red Mountain	n.r.	11.78	14.57	914.29	1739.13	Barnes et al., 2015
Zambales, Philippines	Manleluag 1, ML1	315.00	10.90	7.29	514.29	1000.00	Cardace et al., 2015
Zambales, Philippines	Manleluag 2, ML2	337.00	10.80	7.29	534.29	1060.87	Cardace et al., 2015
Zambales, Philippines	Manleluag 3, ML3	307.00	10.80	8.33	485.71	982.61	Cardace et al., 2015
Zambales, Philippines	Bigbiga well, BB1	349.00	9.30	492.40	125.71	4369.57	Cardace et al., 2015
Zambales, Philippines	Poon Bato 1, PB1	505.00	11.30	1.04	685.71	1039.13	Cardace et al., 2015
Zambales, Philippines	Poon Bato 2, PB2 [star pool]	229.00	9.20	1.04	322.86	447.83	Cardace et al., 2015
Zambales, Philippines	Poon Bato 3, PB3	606.00	11.30	0.00	511.43	678.26	Cardace et al., 2015
Zambales, Philippines	San Isidro Spr, SI1	516.00	10.50	40.60	1640.00	3982.61	Cardace et al., 2015
Zambales, Philippines	Mainit Falls, MF1	784.00	9.70	100.98	6534.29	11726.09	Cardace et al., 2015
Zambales, Philippines	Manleluag 2, ML2	388.00	10.80	192.59	485.71	813.04	Cardace et al., 2015
Zambales, Philippines	Manleluag 3, ML3	270.00	10.30	200.92	482.86	860.87	Cardace et al., 2015
Zambales, Philippines	Bigbiga well, BB1	428.00	7.00	485.11	280.00	8691.30	Cardace et al., 2015
Zambales, Philippines	Poon Bato 1, PB1	232.00	9.60	99.94	354.29	834.78	Cardace et al., 2015
Zambales, Philippines	Poon Bato 2, PB2	189.00	8.70	927.55	311.43	643.48	Cardace et al., 2015
Cabeco de Vide, Portugal	Maria Rita (b)	n.r.	8.04	181.14	576.57	1208.70	Marques, et al., 2008
Cabeco de Vide, Portugal	Vale Fabiano (sp)	n.r.	7.37	185.51	314.00	508.70	Marques, et al., 2008
Cabeco de Vide, Portugal	Furo da Camara (b)	n.r.	7.54	150.11	259.43	415.65	Marques, et al., 2008
Turkey	YT-0m	n.r.	11.95	83.28	522.86	499.13	Meyer-Dombard et al., 2015
Turkey	YT-S8.8m	n.r.	9.40	302.94	694.57	532.61	Meyer-Dombard et al., 2015
Leka Ophiolite Complex	gw 1	n.r.	9.56	27.00	414.00	429.00	Okland et al., 2012
Leka Ophiolite Complex	gw 2	n.r.	8.58	38.00	519.00	535.00	Okland et al., 2012
Leka Ophiolite Complex	gw 3	n.r.	8.80	38.00	543.00	545.00	Okland et al., 2012
Leka Ophiolite Complex	sw 1	n.r.	7.90	26.00	433.00	440.00	Okland et al., 2012
Cazadero, California, USA	ultrabasic	n.r.	11.54	4.16	1571.43	2173.91	Barnes et al., 2015
Cyprus Ophiolite	10.00	n.r.	8.50	22.59	200.00	143.04	Neal & Shand 2002
Cyprus Ophiolite	11.00	n.r.	7.90	25.61	228.57	176.52	Neal & Shand 2002
Cyprus Ophiolite	12.00	n.r.	8.60	31.86	257.14	205.65	Neal & Shand 2002
Cyprus Ophiolite	6.00	n.r.	9.10	37.89	257.14	203.48	Neal & Shand 2002
Cyprus Ophiolite	7.00	n.r.	9.80	28.21	228.57	191.30	Neal & Shand 2002
Cyprus Ophiolite	8.00	n.r.	8.40	21.65	228.57	172.17	Neal & Shand 2002
Cyprus Ophiolite	9.00	n.r.	8.40	30.09	257.14	224.35	Neal & Shand 2002

Cyprus Ophiolite	5.00	n.r.	8.70	477.83	1285.71	2260.87	Neal & Shand 2002
Cyprus Ophiolite	13.00	n.r.	9.50	154.07	800.00	521.74	Neal & Shand 2002
Cyprus Ophiolite	1.00	n.r.	9.70	244.64	4857.14	7521.74	Neal & Shand 2002
Cyprus Ophiolite	2.00	n.r.	9.70	229.02	4857.14	7739.13	Neal & Shand 2002
Cyprus Ophiolite	21.00	n.r.	9.50	310.22	4000.00	6347.83	Neal & Shand 2002
Cyprus Ophiolite	15.00	n.r.	9.90	2592.13	3314.29	5956.52	Neal & Shand 2002
Cyprus Ophiolite	14.00	n.r.	9.60	2592.13	3314.29	6173.91	Neal & Shand 2002
Cyprus Ophiolite	17.00	n.r.	9.60	2841.97	3714.29	7521.74	Neal & Shand 2002
Cyprus Ophiolite	3.00	n.r.	11.60	4091.19	12000.00	16739.13	Neal & Shand 2002
Cyprus Ophiolite	4.00	n.r.	11.40	1134.71	12000.00	16739.13	Neal & Shand 2002
Cyprus Ophiolite	19.00	n.r.	11.20	2154.90	5428.57	7086.96	Neal & Shand 2002
Cyprus Ophiolite	18.00	n.r.	9.00	36331.46	222857.14	252173.91	Neal & Shand 2002
Cyprus Ophiolite	16.00	n.r.	9.00	26035.81	3714.29	6782.61	Neal & Shand 2002
Cyprus Ophiolite	20.00	n.r.	9.60	11451.18	11428.57	13130.43	Neal & Shand 2002
seawater	-	56000.00	8.00	28107.43	542857.14	456521.74	Culkin and Cox, 1966
Del Puerto	Adobe Springs Well	n.r.	8.73	166.56	137.14	234.78	Blank et al., 2009
Del Puerto	Del Puerto Creek	n.r.	8.52	104.10	271.43	417.39	Blank et al., 2009
New Caledonia	HP11-BdJ-Ilot1-W1C	n.r.	11.08	100.00	2220.00	2380.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Ilot1-W2	n.r.	10.48	280.00	5470.00	7290.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Ilot1-W3	n.r.	10.01	1240.00	21610.00	26140.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Ilot1-W5	n.r.	11.07	10.00	410.00	1280.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Ilot1-W6	n.r.	10.68	190.00	4020.00	5680.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Ilot1-W1	n.r.	10.87	70.00	1840.00	2980.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil1	n.r.	10.05	3360.00	52670.00	22630.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil2	n.r.	9.13	11850.00	179270.00	197980.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil3	n.r.	8.66	16090.00	241800.00	284150.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil4	n.r.	10.20	2160.00	34520.00	1910.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil5	n.r.	8.30	21450.00	322050.00	392810.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil6	n.r.	11.00	60.00	1440.00	2550.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil7	n.r.	10.92	20.00	660.00	1650.00	Monnin et al., 2014
New Caledonia	HP11-BdJ-Dil8	n.r.	10.88	20.00	760.00	1750.00	Monnin et al., 2014
New Caledonia	HP11-CarKao-W1	n.r.	10.80	bdl	230.00	650.00	Monnin et al., 2014
New Caledonia	HP11-CarKao-W2	n.r.	10.80	bdl	190.00	580.00	Monnin et al., 2014
New Caledonia	HP11-Site11-W1	n.r.	10.64	1540.00	45780.00	40520.00	Monnin et al., 2014
New Caledonia	HP11-Site11-W4	n.r.	9.58	16160.00	327740.00	270850.00	Monnin et al., 2014
New Caledonia	HP11-Site11-W5	n.r.	8.76	22560.00	451960.00	386580.00	Monnin et al., 2014
New Caledonia	HP11-Site11-W10	n.r.	9.06	15790.00	319180.00	263710.00	Monnin et al., 2014
New Caledonia	HP11-Site11-W11	n.r.	9.38	12130.00	248690.00	199400.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W1	n.r.	11.00	380.00	41740.00	40050.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W3	n.r.	8.92	21500.00	432700.00	384520.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W4	n.r.	9.50	11530.00	247310.00	191240.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W5	n.r.	8.85	21790.00	440030.00	385320.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W6	n.r.	9.34	18200.00	371920.00	323690.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W7	n.r.	8.60	22170.00	447210.00	393220.00	Monnin et al., 2014
New Caledonia	HP11-Site12-W8	n.r.	8.15	25890.00	515390.00	475500.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W1	n.r.	9.73	12240.00	252370.00	190960.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W2	n.r.	9.66	12140.00	250440.00	187730.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W3	n.r.	9.67	10170.00	212430.00	154310.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W4	n.r.	9.61	10820.00	225870.00	167610.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W5	n.r.	9.72	12780.00	262810.00	198080.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W6	n.r.	9.61	14590.00	297380.00	235440.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W3Ti	n.r.	9.44	19950.00	400870.00	346460.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W7	n.r.	10.00	14200.00	290680.00	232610.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W8	n.r.	10.13	10640.00	223030.00	163750.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W9	n.r.	9.91	15190.00	309310.00	249170.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W10	n.r.	10.14	7530.00	163850.00	97320.00	Monnin et al., 2014
New Caledonia	HP11-Site7-W11	n.r.	9.96	14250.00	292430.00	228890.00	Monnin et al., 2014
New Caledonia	HP11-Site9-W1	n.r.	10.45	3310.00	81520.00	36670.00	Monnin et al., 2014
New Caledonia	HP11-Site9-W3	n.r.	10.62	1720.00	50580.00	6460.00	Monnin et al., 2014
New Caledonia	HP11-Site9-W4	n.r.	10.46	3820.00	91620.00	44960.00	Monnin et al., 2014
New Caledonia	HP11-Site9-W6	n.r.	9.18	18850.00	380770.00	337760.00	Monnin et al., 2014
New Caledonia	HP11-Site9-W7	n.r.	10.51	4030.00	95840.00	47540.00	Monnin et al., 2014
New Caledonia	La Coulee 1	n.r.	10.80	7.81	628.57	634.78	Barnes et al., 1978
New Caledonia	La Coulee 2	n.r.	10.70	60.38	465.71	1134.78	Barnes et al., 1978
Hakuba Happo	Happo #1	70300.00	10.80	10.00	1770.00	150.00	Suda et al., 2014
Hakuba Happo	Happo #3	48300.00	10.70	10.00	1160.00	130.00	Suda et al., 2014
Lost City Hydrothermal Field	J2-362IGT2	n.r.	10.50	3640.00	541000.00	494000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-362IGT4	n.r.	10.50	3510.00	541000.00	494000.00	Seyfried et al., 2015

Lost City Hydrothermal Field	J2-360IGT2	n.r.	10.40	4120.00	542000.00	491000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-360IGT6	n.r.	10.60	3460.00	541000.00	485000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-360CGTR	n.r.	10.10	5010.00	542000.00	485000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-361IGT5	n.r.	10.50	3990.00	541000.00	495000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-361IGT6	n.r.	10.60	3610.00	543000.00	492000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-361CGTB	n.r.	10.20	6160.00	543000.00	490000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	J2-361CGT-Wu	n.r.	10.50	4240.00	543000.00	493000.00	Seyfried et al., 2015
Lost City Hydrothermal Field	Seawater	n.r.	8.00	28700.00	554000.00	475000.00	Seyfried et al., 2015
Aqua de Ney	Average	35900.00	12.00	2810.74	220771.16	488294.17	Boschetti et al., 2018

Table S3: CROMO sulfur chemistry and YSI probe measurements reported for all wells since establishment

Well	Date Sampled	SO_4^{2-} (µM)	HS^- (µM)	pH	Temperature (ºC)	Conductivity (µS/cm)	DO (mg/L)	ORP (mV)
CSW 1.1	March-12	183.64	n.a.	12.38	13.66	4674.00	0.03	-298.90
	June-12	108.27	n.a.	12.30	14.99	5100.00	0.32	-287.90
	August-13	147.08	< 1.0	12.39	16.16	4486.00	0.20	-258.40
	December-13	305.43	n.a.	12.17	14.39	4578.00	0.37	-298.60
	July-14	266.19	12.88	12.32	16.31	4453.00	0.43	-297.00
	August-15	180.46	22.67	11.76	16.71	4206.00	0.17	-243.10
	January-16	340.00	15.49	12.42	14.83	4130.00	0.19	-276.50
	June-16	389.55	3.54	12.06	17.21	3809.00	0.25	-271.60
CSW 1.2	August-13	125.30	< 1.0	9.27	15.62	4174.00	3.55	132.80
	December-13	< 1.56	3.90	8.55	15.38	4278.00	0.30	-55.50
	July-14	191.65	< 1.0	7.76	15.97	4495.00	0.25	-118.50
	June-16	112.43	8.50	8.80	16.90	4627.00	0.41	-97.50
CSW 1.3	August-13	114.90	4.64	10.20	16.51	4708.00	0.14	-246.60
	December-13	135.02	2.64	10.10	15.21	4740.00	0.20	-191.20
	July-14	151.16	< 1.0	10.15	15.64	4842.00	0.16	-204.80
	June-16	174.79	4.20	10.10	18.83	4787.00	0.21	-275.20
CSW 1.4	August-13	222.02	< 1.0	8.04	14.94	1989.00	0.92	336.00
	December-13	393.61	< 1.0	7.64	15.40	1931.00	2.50	500.00
	July-14	391.94	< 1.0	7.75	15.05	1950.00	2.36	116.20
	June-16	429.42	< 1.0	7.87	17.34	1978.00	4.40	203.00
CSW 1.5	August-13	351.39	33.74	9.95	15.91	4643.00	0.27	-216.40
	December-13	433.37	19.81	9.59	15.29	4632.00	0.43	-290.00
	July-14	317.41	23.75	9.77	15.80	4792.00	0.16	-285.20
	August-15	99.99	27.73	9.39	16.15	4755.00	0.19	-211.60
	June-16	358.21	1.41	9.77	15.69	4780.00	0.49	-206.50
CSW OLD	August-13	47.92	34.21	9.82	18.18	10400.00	0.02	-278.00
	December-13	118.88	< 1.0	9.69	17.90	11150.00	0.22	-346.00
	July-14	139.29	8.39	9.73	17.43	11529.00	0.26	-279.90
	August-15	96.14	25.63	9.59	17.24	11110.00	0.55	-213.90
	January-16	46.42	< 1.0	9.87	17.95	11000.00	0.08	-294.90
	June-16	170.21	< 1.0	9.84	18.45	11290.00	1.42	-356.70
N08-A	August-13	n.a.	3.47	10.42	16.41	5917.00	0.19	-161.10
	December-13	32.27	2.61	10.17	15.34	6444.00	0.07	-229.60
	July-14	40.18	1.14	10.89	16.85	6335.00	0.09	-249.50
	June-16	77.14	3.70	10.82	16.32	6040.00	0.27	-216.10
N08-B	August-13	n.a.	< 1.0	10.98	16.03	3070.00	0.31	-74.60
	December-13	27.48	< 1.0	10.55	15.03	4350.00	0.10	-117.90
	July-14	27.69	< 1.0	10.68	16.12	3132.00	0.76	-197.60
	June-16	58.30	< 1.0	10.22	16.87	3047.00	0.15	-78.60
N08-C	August-13	54.53	< 1.0	7.55	14.99	1143.00	0.17	243.90
	December-13	40.70	< 1.0	9.32	15.08	1307.00	0.10	-164.90
	July-14	51.22	< 1.0	8.46	15.53	1372.00	0.42	-153.10
	June-16	77.45	< 1.0	7.25	16.67	1393.00	0.20	39.80
QV 1.1	August-13	< 10.00	11.53	11.64	16.36	2596.00	0.15	-122.70
	December-13	22.17	< 1.0	11.54	15.95	6722.00	0.21	-225.40
	July-14	257.13	4.76	11.51	17.52	2854.00	0.28	-233.50
	August-15	17.49	3.53	11.34	17.69	3075.00	0.19	-139.40
	January-16	< 1.56	< 1.0	11.75	15.90	3274.00	0.19	-218.30
	June-16	76.10	< 1.0	11.41	16.74	3362.00	0.18	-181.00
QV 1.2	August-13	< 10.00	< 1.0	9.07	16.63	2781.00	0.79	-8.50
	December-13	< 1.56	< 1.0	8.99	15.52	4285.00	0.47	-123.00
	July-14	32.00	< 1.0	9.47	17.09	3042.00	0.40	-142.70
	June-16	< 1.56	< 1.0	9.31	16.68	3004.00	0.17	-156.20
QV 1.3	August-13	191.91	4.64	9.63	16.45	6200.00	0.03	-183.40
	December-13	59.96	< 1.0	9.58	16.10	6727.00	0.11	-211.50
	July-14	55.69	10.13	9.68	16.60	6507.00	0.26	-223.60
	June-16	72.25	< 1.0	9.78	16.55	4735.00	0.22	-207.80

n.a. = not analyzed
sulfide detection limit is ~1.0 µM

Table S4 - CROMO OTUs >0.1% Abundance for Statistical Analyses July 2014

Representative Sequence	OTU Number	Sitewide Average Abundance	Taxonomy	Phylum	Class	Order	Family	Genus_Species
HWI-M02808_85_AJHNL_1_1101_20048_2184	OTU83437	13.57%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Burkholderiaceae_unclassified
HWI-M02808_85_AJHNL_1_1103_21100_6722	OTU171116	7.00%	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
HWI-M02808_85_AJHNL_1_1103_27798_17116	OTU1915	4.14%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1101_17918_2017	OTU33777	4.03%	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Trueperaceae	Truepera
HWI-M02808_85_AJHNL_1_1104_8273_4674	OTU90462	3.48%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Hydrogenophaga
HWI-M02808_85_AJHNL_1_1101_17192_2407	OTU136519	2.89%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1109_22908_21284	OTU153801	2.48%	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylomonaceae	Methylomonas
HWI-M02808_85_AJHNL_1_2109_4377_21131	OTU49796	2.43%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1106_5301_8438	OTU26811	1.70%	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelothrix
HWI-M02808_85_AJHNL_1_1104_11682_21160	OTU142042	1.53%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Beijerinckiaceae_unclassified
HWI-M02808_85_AJHNL_1_1109_13355_7771	OTU122688	1.21%	Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	SRB2	SRB2_ge
HWI-M02808_85_AJHNL_1_1101_10693_7658	OTU167481	1.19%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1105_26860_11279	OTU24860	1.14%	Bacteria	Firmicutes	Clostridia	Clostridia_Incertae_Sedis	Unknown_Family	Candidatus_Desulforudis
HWI-M02808_85_AJHNL_1_1103_10683_9335	OTU146119	1.07%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacter
HWI-M02808_85_AJHNL_1_2110_11654_16963	OTU35825	0.96%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Rhodocyclaceae	Rhodocyclaceae_unclassified
HWI-M02808_85_AJHNL_1_1104_20198_4705	OTU130179	0.62%	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Phenylobacterium
HWI-M02808_85_AJHNL_1_2101_12173_12171	OTU22547	0.60%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Methylophilaceae	UBA6140
HWI-M02808_85_AJHNL_1_1108_24510_7557	OTU23329	0.55%	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelothrix
HWI-M02808_85_AJHNL_1_1104_4942_23661	OTU157466	0.55%	Bacteria	Acidobacteria	Blastocatellia_(Subgroup_4)	Blastocatellales	Blastocatellaceae	Blastocatellaceae_uncultured
HWI-M02808_85_AJHNL_1_1103_16857_24687	OTU140311	0.54%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Burkholderiaceae_unclassified
HWI-M02808_85_AJHNL_1_1108_16168_8446	OTU2499	0.53%	Bacteria	Bacteroidetes	Bacteroidia	Sphingobacteriales	Sphingobacteriales_unclassified	Sphingobacteriales_unclassified
HWI-M02808_85_AJHNL_1_1101_16532_7035	OTU140763	0.48%	Bacteria	Chloroflexi	Anaerolineae	Anaerolineales	Anaerolineaceae	Bellilinea
HWI-M02808_85_AJHNL_1_2105_24061_20363	OTU27309	0.48%	Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	SRB2	SRB2_ge
HWI-M02808_85_AJHNL_1_1107_14145_21318	OTU81733	0.48%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiaceae	Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
HWI-M02808_85_AJHNL_1_1107_5134_16942	OTU21542	0.44%	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Porphyrobacter
HWI-M02808_85_AJHNL_1_1112_14170_19757	OTU142009	0.42%	Bacteria	Proteobacteria	Deltaproteobacteria	Syntrophobacterales	Syntrophaceae	Smithella
HWI-M02808_85_AJHNL_1_1112_21164_19133	OTU133065	0.42%	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_uncultured	uncultured_ge
HWI-M02808_85_AJHNL_1_1106_19311_2988	OTU92145	0.41%	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Xanthomonadaceae_uncultured
HWI-M02808_85_AJHNL_1_2110_11524_5121	OTU23922	0.39%	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelothrix
HWI-M02808_85_AJHNL_1_1101_23196_4273	OTU102436	0.38%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Xanthobacteraceae	Bradyrhizobium
HWI-M02808_85_AJHNL_1_1114_20682_21407	OTU128184	0.35%	Bacteria	Firmicutes	Clostridia	Clostridiales	Family_XII	Fusibacter
HWI-M02808_85_AJHNL_1_1107_6126_6665	OTU151977	0.35%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Rhizobiales_Incertae_Sedis	Phreatobacter
HWI-M02808_85_AJHNL_1_1107_23247_21981	OTU62527	0.34%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	Nitrosomonas
HWI-M02808_85_AJHNL_1_1110_17696_7989	OTU167108	0.33%	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	Brevundimonas
HWI-M02808_85_AJHNL_1_1113_15872_17500	OTU145530	0.33%	Bacteria	Nitrospirae	Nitrospira	Nitrospirales	Nitrospiraceae	Nitrospira
HWI-M02808_85_AJHNL_1_1101_4497_8927	OTU75087	0.32%	Bacteria	Firmicutes	Clostridia	Thermoanaerobacterales	SRB2	SRB2_ge
HWI-M02808_85_AJHNL_1_2105_13143_15497	OTU63293	0.32%	Bacteria	Verrucomicrobia	Verrucomicrobiae	Opitutales	Opitutaceae	Lacunisphaera
HWI-M02808_85_AJHNL_1_1101_8018_4755	OTU94893	0.31%	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_4	Clostridiaceae_4_uncultured
HWI-M02808_85_AJHNL_1_2102_13386_18268	OTU55834	0.31%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocystis
HWI-M02808_85_AJHNL_1_2104_9737_12868	OTU28357	0.31%	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prolixibacteraceae	Prolixibacteraceae_uncultured
HWI-M02808_85_AJHNL_1_1106_18337_20397	OTU14737	0.30%	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylomonaceae	Methylomonaceae_unclassified
HWI-M02808_85_AJHNL_1_1104_19259_24357	OTU56632	0.29%	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae	Qipengyuania
HWI-M02808_85_AJHNL_1_1110_2855_18839	OTU184525	0.29%	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
HWI-M02808_85_AJHNL_1_1101_24150_5326	OTU150543	0.28%	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfitispora
HWI-M02808_85_AJHNL_1_1106_10033_4103	OTU145529	0.28%	Bacteria	Firmicutes	Clostridia	Clostridiales	TC1	TC1_ge
HWI-M02808_85_AJHNL_1_2114_4352_18207	OTU139269	0.27%	Bacteria	Bacteroidetes	Ignavibacteria	OPB56	OPB56_fa	OPB56_ge
HWI-M02808_85_AJHNL_1_1101_22499_5481	OTU182127	0.27%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Salinarimonas
HWI-M02808_85_AJHNL_1_1105_18048_6511	OTU28657	0.26%	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_4	Salimesophilobacter
HWI-M02808_85_AJHNL_1_1101_16854_7369	OTU83849	0.25%	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	Bacteroidales_unclassified
HWI-M02808_85_AJHNL_1_1103_25473_23195	OTU17778	0.24%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Betaproteobacteriales_unclassified	Betaproteobacteriales_unclassified
HWI-M02808_85_AJHNL_1_1103_8071_4949	OTU70317	0.24%	Bacteria	Planctomycetes	Planctomycetacia	Pirellulales	Pirellulaceae	Rhodopirellula
HWI-M02808_85_AJHNL_1_1101_9105_4721	OTU85884	0.23%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1101_17949_2457	OTU77385	0.23%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Hydrogenophaga
HWI-M02808_85_AJHNL_1_1108_13218_15855	OTU86472	0.22%	Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Prolixibacteraceae	Prolixibacteraceae_uncultured
HWI-M02808_85_AJHNL_1_1101_8850_3213	OTU107300	0.22%	Bacteria	Proteobacteria	Gammaproteobacteria	Pseudomonadales	Pseudomonadaceae	Pseudomonas
HWI-M02808_85_AJHNL_1_1105_18131_5315	OTU48861	0.22%	Bacteria	Spirochaetes	Spirochaetia	Spirochaetales	Spirochaetaceae	Spirochaetaceae_uncultured
HWI-M02808_85_AJHNL_1_1112_20122_9065	OTU189836	0.21%	Bacteria	Actinobacteria	RBG-16-55-12	RBG-16-55-12_or	RBG-16-55-12_fa	RBG-16-55-12_ge
HWI-M02808_85_AJHNL_1_1101_19096_11828	OTU60509	0.20%	Bacteria	Proteobacteria	Alphaproteobacteria	Acetobacterales	Acetobacteraceae	Roseomonas
HWI-M02808_85_AJHNL_1_1101_20850_21312	OTU6671	0.20%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Betaproteobacteriales_unclassified	Betaproteobacteriales_unclassified
HWI-M02808_85_AJHNL_1_1109_20613_22006	OTU135193	0.20%	Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	Desulfitispora
HWI-M02808_85_AJHNL_1_2110_14519_22333	OTU43135	0.20%	Bacteria	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified	Bacteria_unclassified
HWI-M02808_85_AJHNL_1_2103_26618_18257	OTU27705	0.20%	Bacteria	Planctomycetes	Phycisphaerae	Phycisphaerales	Phycisphaeraceae	Phycisphaeraceae_unclassified

HWI-M02808_85_AJHNL_1_2102_14598_23066	OTU124649	0.19%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1101_20642_3370	OTU8904	0.19%	Bacteria	Firmicutes	Clostridia	Clostridiales	Family_XIV	Family_XIV_uncultured
HWI-M02808_85_AJHNL_1_1101_21249_4130	OTU180109	0.17%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1101_7615_8182	OTU120264	0.17%	Bacteria	Actinobacteria	Nitriliruptoria	Nitriliruptorales	Nitriliruptoraceae	Egicoccus
HWI-M02808_85_AJHNL_1_1105_21800_25660	OTU5365	0.16%	Bacteria	Verrucomicrobia	Verrucomicrobiae	Pedosphaerales	Pedosphaeraceae	Pedosphaeraceae_ge
HWI-M02808_85_AJHNL_1_1101_28097_12743	OTU98303	0.16%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacteraceae_unclassified
HWI-M02808_85_AJHNL_1_1107_22980_6232	OTU123766	0.16%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	Methylocystis
HWI-M02808_85_AJHNL_1_1108_20955_13458	OTU138388	0.15%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Rhodocyclaceae	Denitratisoma
HWI-M02808_85_AJHNL_1_1103_15102_15538	OTU61940	0.15%	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	Rhodobacteraceae_unclassified
HWI-M02808_85_AJHNL_1_1101_21442_4297	OTU29267	0.15%	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiales_unclassified	Clostridiales_unclassified
HWI-M02808_85_AJHNL_1_2111_18984_15162	OTU49101	0.14%	Bacteria	Bacteroidetes	Ignavibacteria	SJA-28	SJA-28_fa	SJA-28_ge
HWI-M02808_85_AJHNL_1_1101_8931_5002	OTU129191	0.13%	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter
HWI-M02808_85_AJHNL_1_1101_7284_6821	OTU85158	0.13%	Bacteria	Chlamydiae	Chlamydiae	Chlamydiales	Simkaniaceae	Simkaniaceae_unclassified
HWI-M02808_85_AJHNL_1_1101_23818_10636	OTU106439	0.13%	Bacteria	Firmicutes	Erysipelotrichia	Erysipelotrichales	Erysipelotrichaceae	Erysipelothrix
HWI-M02808_85_AJHNL_1_1110_18737_15034	OTU4132	0.12%	Bacteria	Acidobacteria	Acidobacteriia	Acidobacteriales	Acidobacteriales_unclassified	Acidobacteriales_unclassified
HWI-M02808_85_AJHNL_1_1101_13289_11050	OTU185606	0.11%	Bacteria	Actinobacteria	Acidimicrobiia	Microtrichales	Microtrichales_uncultured	uncultured_ge
HWI-M02808_85_AJHNL_1_2105_22226_4620	OTU103664	0.11%	Bacteria	Firmicutes	Clostridia	Clostridiales	Clostridiaceae_4	Clostridiaceae_4_unclassified
HWI-M02808_85_AJHNL_1_2113_15368_19109	OTU24139	0.11%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	Burkholderiaceae_unclassified
HWI-M02808_85_AJHNL_1_1113_19158_10121	OTU181493	0.10%	Bacteria	Firmicutes	Clostridia	Clostridiales	Family_XIII	Family_XIII_unclassified
HWI-M02808_85_AJHNL_1_2103_22544_20946	OTU112541	0.10%	Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Nitrosomonadaceae	Nitrosomonas

Table S5: Top Sitewide (≥0.1%) Operational Taxonomic Units vs. Environmental Variables

OTU	Environmental Variable	Correlation	Sign	p-value
OTU83437 Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales; Burkholderiaceae;Burkholderiaceae_unclassified	pH	0.9	+	3.86E-04
OTU33777 Bacteria;Deinococcus-Thermus;Deinococci;Deinococcales;Trueperaceae;Truepera	Ace+C6tate (µM)	0.98	+	6.40E-07
	Formate (µM)	0.995	+	3.43E-09
	Lithium (µM)	0.991	+	2.55E-08
OTU136519 Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;Dethiobacter	pH	0.781	+	7.62E-03
	Potassium (µM)	0.823	+	3.42E-03
OTU49796 Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;Dethiobacter	Specific Conductance (µS)	0.83	+	2.97E-03
	Well Depth (m)	0.916	+	1.97E-04
OTU24860 Bacteria;Firmicutes;Clostridia;Clostridia_Incertae_Sedis;Unknown_Family; Candidatus_Desulforudis	Specific Conductance (µS)	0.825	+	3.29E-03
	Well Depth (m)	0.917	+	1.84E-04
OTU146119 Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Rhodobacter	Dissolved Hydrogen (µM)	0.916	+	1.93E-04
OTU130179 Bacteria;Proteobacteria;Alphaproteobacteria;Caulobacterales;Caulobacteraceae; Phenylobacterium	Bromide (µM)	0.905	+	3.24E-04
	Fluoride (µM)	0.904	+	3.24E-04
OTU157466 Bacteria;Acidobacteria;Blastocatellia_(Subgroup_4);Blastocatellales; Blastocatellaceae;Blastocatellaceae_uncultured	Magnesium (µM)	0.993	+	1.06E-08
	Nitrate (µM)	0.844	+	2.12E-03
OTU2499 Bacteria;Bacteroidetes;Bacteroidia;Sphingobacteriales;Sphingobacteriales_unclassified;Sphingobacteriales_unclassified	Bromide (µM)	0.929	+	1.03E-04
	Fluoride (µM)	0.929	+	1.03E-04
OTU27309 Bacteria;Firmicutes;Clostridia;Thermoanaerobacterales;SRB2;SRB2_ge	Dissolved Oxygen (µM)	0.794	+	6.07E-03
OTU81733 Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Rhizobiaceae; Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium	Bromide (µM)	0.935	+	7.11E-05
	Fluoride (µM)	0.935	+	7.14E-05
OTU21542 Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales; Sphingomonadaceae;Porphyrobacter	Magnesium (µM)	0.993	+	1.30E-08
	Nitrate (µM)	0.841	+	2.32E-03
OTU142009 Bacteria;Proteobacteria;Deltaproteobacteria;Syntrophobacterales;Syntrophaceae; Smithella	Bromide (µM)	0.918	+	1.79E-04
	Fluoride (µM)	0.918	+	1.80E-04
OTU92145 Bacteria;Proteobacteria;Gammaproteobacteria;Xanthomonadales; Xanthomonadaceae;Xanthomonadaceae_uncultured	Magnesium (µM)	0.993	+	9.29E-09
	Nitrate (µM)	0.842	+	2.22E-03
OTU23922 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae; Erysipelothrix	Dissolved Hydrogen (µM)	0.918	+	1.79E-04
OTU102436 Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Xanthobacteraceae; Bradyrhizobium	Dissolved Hydrogen (µM)	0.967	+	4.88E-06
OTU128184 Bacteria;Firmicutes;Clostridia;Clostridiales;Family_XII;Fusibacter	Dissolved Hydrogen (µM)	0.903	+	3.46E-04
OTU62527 Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales; Nitrosomonadaceae;Nitrosomonas	Magnesium (µM)	0.993	+	9.39E-09
	Nitrate (µM)	0.843	+	2.21E-03

OTU145530 Bacteria;Nitrospirae;Nitrospira;Nitrospirales;Nitrospiraceae;Nitrospira	Magnesium (µM)	0.993	+	9.89E-09
	Nitrate (µM)	0.842	+	2.23E-03
OTU63293 Bacteria;Verrucomicrobia;Verrucomicrobiae;Opitutales;Opitutaceae;Lacunisphaera	Magnesium (µM)	0.993	+	9.78E-09
	Nitrate (µM)	0.842	+	2.22E-03
OTU94893 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiaceae_4;Clostridiaceae_4_uncultured	Calcium (µM)	0.823	+	3.41E-03
OTU55834 Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Methylocystis	Dissolved Hydrogen (µM)	0.967	+	4.74E-06
OTU28357 Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Prolixibacteraceae;Prolixibacteraceae_uncultured	Dissolved Hydrogen (µM)	0.943	+	4.22E-05
OTU56632 Bacteria;Proteobacteria;Alphaproteobacteria;Sphingomonadales;Sphingomonadaceae;Qipengyuania	Magnesium (µM)	0.992	+	1.43E-08
	Nitrate (µM)	0.84	+	2.37E-03
OTU184525 Bacteria;Firmicutes;Clostridia;Clostridiales;Clostridiales_unclassified;Clostridiales_unclassified	Bromide (µM)	0.878	+	8.39E-04
	Fluoride (µM)	0.878	+	8.41E-04
OTU150543 Bacteria;Firmicutes;Clostridia;Clostridiales;Peptococcaceae;Desulfitispora	Specific Conductance (µS)	0.825	+	3.29E-03
	Well Depth (m)	0.917	+	1.84E-04
OTU139269 Bacteria;Bacteroidetes;Ignavibacteria;OPB56;OPB56_fa;OPB56_ge	Magnesium (µM)	0.993	+	1.01E-08
	Nitrate (µM)	0.842	+	2.23E-03
OTU182127 Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae;Salinarimonas	Specific Conductance (µS)	0.825	+	3.31E-03
	Well Depth (m)	0.918	+	1.83E-04
OTU83849 Bacteria;Bacteroidetes;Bacteroidia;Bacteroidales;Bacteroidales_unclassified;Bacteroidales_unclassified	Chloride (µM)	0.8	+	5.45E-03
	Specific Conductance (µS)	0.86	+	1.41E-03
	Well Depth (m)	0.793	+	6.16E-03
OTU70317 Bacteria;Planctomycetes;Planctomycetacia;Pirellulales;Pirellulaceae;Rhodopirellula	Magnesium (µM)	0.993	+	9.41E-09
	Nitrate (µM)	0.843	+	2.21E-03
OTU85884 Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;Dethiobacter	Dissolved Oxygen (µM)	0.795	+	6.02E-03
OTU77385 Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Burkholderiaceae;Hydrogenophaga	Specific Conductance (µS)	0.825	+	3.28E-03
	Well Depth (m)	0.918	+	1.82E-04
OTU48861 Bacteria;Spirochaetes;Spirochaetia;Spirochaetales;Spirochaetaceae;Spirochaetaceae_uncultured	Bromide (µM)	0.92	+	1.66E-04
	Fluoride (µM)	0.92	+	1.66E-04
OTU189836 Bacteria;Actinobacteria;RBG-16-55-12;RBG-16-55-12_or;RBG-16-55-12_fa;RBG-16-55-12_ge	Dissolved Oxygen (µM)	0.798	+	5.67E-03
OTU6671 Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales;Betaproteobacteriales_unclassified;Betaproteobacteriales_unclassified	Hydrogen Sulfide (µM)	0.794	+	6.12E-03
OTU43135 Bacteria;Bacteria_unclassified;Bacteria_unclassified;Bacteria_unclassified;Bacteria_unclassified;Bacteria_unclassified	Magnesium (µM)	0.993	+	1.07E-08
	Nitrate (µM)	0.842	+	2.26E-03
OTU27705 Bacteria;Planctomycetes;Phycisphaerae;Phycisphaerales;Phycisphaeraceae;Phycisphaeraceae_unclassified	Magnesium (µM)	0.993	+	1.01E-08
	Nitrate (µM)	0.843	+	2.21E-03

OTU8904 Bacteria;Firmicutes;Clostridia;Clostridiales;Family_XIV;Family_XIV_uncultured	Specific Conductance (µS)	0.785	+	7.16E-03
	Well Depth (m)	0.819	+	3.75E-03
OTU180109 Bacteria;Firmicutes;Clostridia;Clostridiales;Syntrophomonadaceae;Dethiobacter	Specific Conductance (µS)	0.825	+	3.30E-03
	Well Depth (m)	0.917	+	1.85E-04
OTU120264 Bacteria;Actinobacteria;Nitriliruptoria;Nitriliruptorales;Nitriliruptoraceae;Egicoccus	Specific Conductance (µS)	0.826	+	3.26E-03
	Well Depth (m)	0.918	+	1.82E-04
OTU5365 Bacteria;Verrucomicrobia;Verrucomicrobiae;Pedosphaerales;Pedosphaeraceae; Pedosphaeraceae_ge	Magnesium (uM)	0.993	+	9.85E-09
	Nitrate (µM)	0.842	+	2.23E-03
OTU98303 Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Rhodobacteraceae_unclassified	Specific Conductance (µS)	0.825	+	3.29E-03
	Well Depth (m)	0.917	+	1.84E-04
OTU123766 Bacteria;Proteobacteria;Alphaproteobacteria;Rhizobiales;Beijerinckiaceae; Methylocystis	Dissolved Hydrogen (µM)	0.967	+	4.85E-06
OTU138388 Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales; Rhodocyclaceae;Denitratisoma	Magnesium (µM)	0.993	+	9.60E-09
	Nitrate (µM)	0.843	+	2.18E-03
OTU61940 Bacteria;Proteobacteria;Alphaproteobacteria;Rhodobacterales;Rhodobacteraceae; Rhodobacteraceae_unclassified	Calcium (µM)	0.804	+	5.07E-03
OTU49101 Bacteria;Bacteroidetes;Ignavibacteria;SJA-28;SJA-28_fa;SJA-28_ge	Magnesium (uM)	0.993	+	9.56E-09
	Nitrate (µM)	0.842	+	2.22E-03
OTU85158 Bacteria;Chlamydiae;Chlamydiae;Chlamydiales;Simkaniaceae; Simkaniaceae_unclassified	Magnesium (uM)	0.993	+	9.40E-09
	Nitrate (µM)	0.843	+	2.21E-03
OTU106439 Bacteria;Firmicutes;Erysipelotrichia;Erysipelotrichales;Erysipelotrichaceae; Erysipelothrix	Hydrogen Sulfide (µM)	0.791	+	6.42E-03
OTU4132 Bacteria;Acidobacteria;Acidobacteriia;Acidobacteriales; Acidobacteriales_unclassified;Acidobacteriales_unclassified	Magnesium (uM)	0.993	+	9.74E-09
	Nitrate (µM)	0.843	+	2.20E-03
OTU185606 Bacteria;Actinobacteria;Acidimicrobiia;Microtrichales;Microtrichales_uncultured; uncultured_ge	Specific Conductance (µS)	0.825	+	3.30E-03
	Well Depth (m)	0.919	+	1.75E-04
OTU112541 Bacteria;Proteobacteria;Gammaproteobacteria;Betaproteobacteriales; Nitrosomonadaceae;Nitrosomonas	Magnesium (µM)	0.993	+	9.39E-09
	Nitrate (µM)	0.843	+	2.22E-03

OTUs present in >0.1% relative abundance within CROMO wells were used for this analysis. This is not a comprehensive list of OTUs present at CRO

Table S6: Pearson's Correlation Analysis Results: Environmental Variables vs. Environmental Variables

Environmental Variable 1	Environmental Variable 2	Correlation	Sign	*p-value*
Well Depth (m)	Specific Conductance (µS)	0.910	+	2.53E-04
	Sodium (µM)	0.835	+	2.66E-03
pH	Potassium (µM)	0.835	+	2.67E-03
Specific Conductance (µS/cm)	Chloride (µM)	0.852	+	1.77E-03
	Sodium (µM)	0.940	+	5.30E-05
	Dissolved Methane (µM)	0.816	+	3.97E-03
Chloride (µM)	Sodium (µM)	0.956	+	1.51E-05
	Silica (µM)	0.849	+	1.88E-03
	Dissolved Methane (µM)	0.835	+	2.65E-03
Bromide (µM)	Fluoride (µM)	1.00	+	2.96E-27
Nitrate (µM)	Magnesium (µM)	0.873	+	9.66E-04
Lithium (µM)	Acetate (µM)	0.989	+	5.27E-08
	Formate (µM)	0.992	+	1.63E-08
Sodium (µM)	Dissolved Methane (µM)	0.898	+	4.20E-04
Silica (µM)	Dissolved Methane (µM)	0.799	+	5.52E-03
Acetate (µM)	Formate (µM)	0.989	+	5.34E-08

Correlations ($p<0.05$ and $q<0.05$)
Calculated for CROMO wells only

Table S7: Thermodynamic Gibbs free energy calculations for select sulfur reactions using CROMO *in situ* water chemistries

Gibbs energy change (kJ/mol)

	CSW1.1	CSW1.2	CSW1.3	CSW1.4	CSW1.5	CSW OLD	N08-A	N08-B	N08-C	QV 1.1	QV 1.2	QV 1.3
Sulfate Reduction												
$SO_4^{2-} + CH_4 + H^+ \rightarrow HS^- + CO_2 + 2H_2O$	-53.74	-43.10	-48.74	-29.43	-40.41	-46.75	-52.84	-47.54	-28.75	-53.97	-37.96	-37.94
$SO_4^{2-} + CH_3COO^- + 5H^+ \rightarrow HS^- + 2CO_2 + 2H_2O$	-96.13	-58.21	-68.74	-54.54	-58.27	-69.86	-80.22	-76.60	-61.44	-92.56	-57.71	-59.76
$SO_4^{2-} + 4HCOO^- + 5H^+ \rightarrow HS^- + 4CO_2 + 4H_2O$	-151.88	-86.56	-95.31	-77.43	-82.50	-106.12	-118.21	-112.19	-89.01	-129.19	-80.77	-78.43
$SO_4^{2-} + 4H_2 + H^+ \rightarrow HS^- + 4H_2O$	-87.31	-80.35	-92.88	-86.81	-69.59	-61.35	-65.64	-64.97	-80.57	-78.84	-76.11	-60.18
Sulfide Oxidation												
$HS^- + 2O_2 \rightarrow SO_4^{2-} + H^+$	-799.28	-766.45	-778.60	-775.21	-782.28	-783.89	-783.77	-792.72	-772.14	-791.03	-782.62	-786.17
$2HS^- + 2O_2 \rightarrow S_2O_3^{2-} + H_2O$	-743.36	-728.04	-726.65	-738.48	-741.99	-739.45	-724.80	-734.12	-730.72	-736.85	-731.13	-740.19
$HS^- + 0.5O_2 \rightarrow S_{(s)} + H_2O$	-147.79	-165.59	-152.09	-168.39	-161.95	-160.46	-147.80	-151.37	-163.00	-149.35	-157.37	-161.07
$HS^- + NO_3^- \rightarrow S_{(s)} + NO_2^- + H_2O$	-71.01	-98.59	-87.84	-102.82	-86.16	-88.45	-78.64	-71.51	-99.54	-70.67	-91.68	-92.52
$5HS^- + 2NO_3^- + 7H^+ \rightarrow 5S_{(s)} + N_2 + 6H_2O$	-568.25	-728.71	-641.68	-737.52	-672.38	-671.88	-604.57	-595.83	-713.73	-582.40	-669.88	-682.08
$5HS^- + 8NO_3^- + 3H^+ \rightarrow SO_4^{2-} + 4N_2 + 4H_2O$	-3313.56	-3435.30	-3417.86	-3458.26	-3361.81	-3397.69	-3381.14	-3319.41	-3455.58	-3297.73	-3445.11	-3437.64
Thiosulfate Disproportionation												
$S_2O_3^{2-} + H_2O \rightarrow SO_4^{2-} + HS^- + H^+$	-55.92	-38.41	-51.95	-36.73	-40.29	-44.43	-58.97	-58.59	-41.42	-54.18	-51.48	-45.98
$5S_2O_3^{2-} + 4O_2 + H_2O \rightarrow 6SO_4^{2-} + 4S_{(s)} + 2H^+$	-1670.03	-1620.86	-1646.73	-1632.42	-1631.57	-1647.90	-1669.79	-1691.16	-1631.26	-1659.35	-1669.52	-1660.37
Thiosulfate Oxidation												
$5S_2O_3^{2-} + 8NO_3^- + H_2O \rightarrow 10SO_4^{2-} + 4N_2 + 2H^+$	-3593.17	-3627.37	-3677.62	-3641.92	-3563.29	-3619.87	-3675.99	-3612.38	-3662.71	-3568.66	-3702.53	-3667.55
$S_2O_3^{2-} + 2O_2 + H_2O \rightarrow 2SO_4^{2-} + 2H^+$	-855.20	-804.86	-830.56	-811.94	-822.58	-828.32	-842.73	-851.31	-813.56	-845.22	-834.10	-832.15
Thiosulfate Reduction												
$S_2O_3^{2-} + 4HCOO^- + 4H^+ \rightarrow 4CO_2 + 2HS^- + 3H_2O$	-207.95	-125.12	-147.41	-114.31	-122.94	-150.70	-177.33	-170.94	-130.59	-183.52	-132.40	-124.56
$S_2O_3^{2-} + CH_3COO^- + H^+ \rightarrow 2HS^- + 2CO_2 + H_2O$	-151.85	-96.42	-120.49	-91.06	-98.36	-114.09	-138.98	-134.99	-102.66	-146.54	-108.99	-105.53
$S_2O_3^{2-} + CH_4 \rightarrow 2HS^- + H_2O + CO_2$	-109.79	-81.64	-100.81	-66.29	-80.83	-91.31	-111.94	-106.26	-70.31	-108.29	-89.57	-84.04
$S_2O_3^{2-} + 4H_2 \rightarrow 2HS^- + 3H_2O$	-143.23	-118.76	-144.83	-123.54	-109.89	-105.78	-124.60	-123.56	-121.99	-133.03	-127.60	-106.16

Volumetric Gibbs energy availability (mJ/L)

	CSW 1.1	CSW 1.2	CSW 1.3	CSW 1.4	CSW 1.5	CSW OLD	N08-A	N08-B	N08-C	QV 1.1	QV 1.2	QV 1.3
Sulfate Reduction												
$SO_4^{2-} + CH_4 + H^+ \rightarrow HS^- + CO_2 + 2H_2O$	14304.41	8259.80	7366.95	107.73	12825.81	6511.73	2123.28	1316.38	32.49	13878.55	1214.63	2112.68
$SO_4^{2-} + CH_3COO^- + 5H^+ \rightarrow HS^- + 2CO_2 + 2H_2O$	54794.05	58.21	68.74	54.54	58.27	69.86	80.22	76.60	61.44	564.64	57.71	472.09
$SO_4^{2-} + 4HCOO^- + 5H^+ \rightarrow HS^- + 4CO_2 + 4H_2O$	721.44	21.64	23.83	19.36	20.62	26.53	29.55	28.05	22.25	32.30	20.19	19.61
$SO_4^{2-} + 4H_2 + H^+ \rightarrow HS^- + 4H_2O$	17.24	3.62	67.11	6.29	6.61	2.30	1.31	1.46	5.24	4.93	9.32	2.56
Sulfide Oxidation												
$HS^- + 2O_2 \rightarrow SO_4^{2-} + H^+$	10742.27	76.64	77.86	77.52	1955.71	3186.51	893.49	79.27	77.21	3460.77	78.26	3195.79
$2HS^- + 2O_2 \rightarrow S_2O_3^{2-} + H_2O$	4794.64	36.40	36.33	36.92	1854.97	3005.88	413.14	36.71	36.54	1753.70	36.56	3008.88
$HS^- + 0.5O_2 \rightarrow S_{(s)} + H_2O$	1903.51	16.56	15.21	16.84	1619.55	2692.55	168.49	15.14	16.30	710.90	15.74	1631.69
$HS^- + NO_3^- \rightarrow S_{(s)} + NO_2^- + H_2O$	113.61	9.86	8.78	10.28	138.72	142.40	89.65	7.15	9.95	113.79	9.17	148.95
$5HS^- + 2NO_3^- + 7H^+ \rightarrow 5S_{(s)} + N_2 + 6H_2O$	457.44	14.57	12.83	14.75	541.27	540.86	137.84	11.92	14.27	468.83	13.40	549.07
$5HS^- + 8NO_3^- + 3H^+ \rightarrow SO_4^{2-} + 4N_2 + 4H_2O$	662.71	68.71	68.36	69.17	672.36	683.79	680.45	66.39	69.11	663.67	68.90	691.83
Thiosulfate Disproportionation												
$S_2O_3^{2-} + H_2O \rightarrow SO_4^{2-} + HS^- + H^+$	55.92	38.41	51.95	36.73	40.29	44.43	58.97	58.59	41.42	54.18	51.48	45.98
$5S_2O_3^{2-} + 4O_2 + H_2O \rightarrow 6SO_4^{2-} + 4S_{(s)} + 2H^+$	334.01	324.17	329.35	326.48	326.31	329.58	333.96	338.23	326.25	331.87	333.90	332.07
Thiosulfate Oxidation												
$5S_2O_3^{2-} + 8NO_3^- + H_2O \rightarrow 10SO_4^{2-} + 4N_2 + 2H^+$	718.63	725.47	735.52	728.38	712.66	723.97	735.20	722.48	732.54	713.73	740.51	733.51
$S_2O_3^{2-} + 2O_2 + H_2O \rightarrow 2SO_4^{2-} + 2H^+$	855.20	804.86	830.56	811.94	822.58	828.32	842.73	851.31	813.56	845.22	834.10	832.15
Thiosulfate Reduction												
$S_2O_3^{2-} + 4HCOO^- + 4H^+ \rightarrow 4CO_2 + 2HS^- + 3H_2O$	207.95	31.28	36.85	28.58	30.73	37.68	44.33	42.73	32.65	45.88	33.10	31.14
$S_2O_3^{2-} + CH_3COO^- + H^+ \rightarrow 2HS^- + 2CO_2 + H_2O$	151.85	96.42	120.49	91.06	98.36	114.09	138.98	134.99	102.66	146.54	108.99	105.53
$S_2O_3^{2-} + CH_4 \rightarrow 2HS^- + H_2O + CO_2$	109.79	81.64	100.81	66.29	80.83	91.31	111.94	106.26	70.31	108.29	89.57	84.04
$S_2O_3^{2-} + 4H_2 \rightarrow 2HS^- + 3H_2O$	28.29	5.34	104.64	8.96	10.44	3.97	2.49	2.78	7.93	8.31	15.63	4.51

Calculated log(activities)	CSW 1.1	CSW 1.2	CSW 1.3	CSW 1.4	CSW 1.5	CSW OLD	N08-A	N08-B	N08-C	QV 1.1	QV 1.2	QV 1.3
aCH_4	-3.23	-3.11	-2.94	-5.40	-2.97	-2.88	-2.90	-3.52	-6.00	-3.54	-3.58	-2.89
aSO_4^{2-}	-3.86	-4.09	-4.20	-3.71	-3.89	-4.34	-4.85	-4.88	-3.94	-3.92	-4.81	-4.68
aH^+	-12.30	-7.80	-10.20	-7.80	-9.80	-9.70	-10.89	-10.68	-8.46	-11.51	-9.47	-9.68
aHS^-	-4.96	-6.16	-6.08	-6.14	-4.71	-5.18	-6.05	-6.07	-6.07	-5.39	-6.07	-5.09
aCO_2	-11.90	-4.40	-7.84	-3.88	-7.03	-7.96	-9.90	-9.37	-5.32	-11.10	-6.43	-6.80
aO_2	-4.89	-5.10	-5.30	-4.13	-5.30	-5.10	-5.52	-4.62	-4.89	-5.05	-4.89	-5.10
aNO_3^-	-6.58	-4.93	-4.54	-4.19	-6.61	-5.83	-5.53	-7.00	-4.19	-7.00	-4.59	-5.21
aNO_2^-	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00
aN_2	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00
$aS_2O_3^{2-}$	-6.25	-6.32	-6.32	-6.22	-6.33	-6.41	-6.37	-6.28	-6.20	-6.26	-6.28	-6.36
aH_2	-5.06	-6.74	-5.53	-6.54	-6.41	-6.81	-6.41	-6.49	-6.58	-5.73	-6.31	-6.76
aFormate	-4.79	-6.08	-6.08	-6.06	-6.08	-6.08	-6.08	-6.08	-6.08	-6.08	-6.08	-6.08
aAcetate	-4.31	-6.08	-6.08	-6.06	-6.08	-6.08	-6.08	-6.08	-6.08	-5.30	-6.08	-5.19

Thiosulfate concentrations are estimated at 1 μM for calculations shown here.
CSW1.2 measured nitrite value is an outlier, and is not reflected in the table of calculated activities.This is replaced with a hypothetical activity of 10^-8

Table S8: Thermodynamic Gibbs free energy calculations for select thiosulfate reactions using a range of thiosulfate values

		Gibbs energy change (kJ/mol)												Volumetric Gibbs energy availability (mJ/L)											
		CSW 1.1	CSW 1.2	CSW 1.3	CSW 1.4	CSW 1.5	CSW OLD	N08-A	N08-B	N08-C	QV 1.1	QV 1.2	QV 1.3	CSW 1.1	CSW 1.2	CSW 1.3	CSW 1.4	CSW 1.5	CSW OLD	N08-A	N08-B	N08-C	QV 1.1	QV 1.2	QV 1.3
Thiosulfate Disproportionation	[S2O3]																								
$S_2O_3^{2-} + H_2O \rightarrow SO_4^{2-} + HS^- + H^+$	1 nM	-39.21	-21.70	-35.24	-20.01	-23.58	-27.72	-42.25	-41.88	-24.71	-37.47	-34.77	-29.26	0.04	0.02	0.04	0.02	0.02	0.03	0.04	0.04	0.02	0.04	0.03	0.03
	1 µM	-55.92	-38.41	-51.95	-36.73	-40.29	-44.43	-58.97	-58.59	-41.42	-54.18	-51.48	-45.98	55.92	38.41	51.95	36.73	40.29	44.43	58.97	58.59	41.42	54.18	51.48	45.98
	1 mM	-72.64	-55.13	-68.67	-53.45	-57.01	-61.15	-75.68	-75.31	-58.14	-70.90	-68.20	-62.70	72636.38	55126.66	68666.18	53445.79	57008.94	61148.92	75682.78	75307.90	58139.14	70899.63	68198.41	62695.45
$5S_2O_3^{2-} + 4O_2 + H_2O \rightarrow 6SO_4^{2-} + 4S_{(s)} + 2H^+$	1 nM	-1586.46	-1537.28	-1563.15	-1548.85	-1547.99	-1564.33	-1586.21	-1607.59	-1547.68	-1575.77	-1585.94	-1576.79	0.32	0.31	0.31	0.31	0.31	0.31	0.32	0.32	0.31	0.32	0.32	0.32
	1 µM	-1670.03	-1620.86	-1646.73	-1632.42	-1631.57	-1647.90	-1669.79	-1691.16	-1631.26	-1659.35	-1669.52	-1660.37	334.01	324.17	329.35	326.48	326.31	329.58	333.96	338.23	326.25	331.87	333.90	332.07
	1 mM	-1753.61	-1704.43	-1730.31	-1716.00	-1715.15	-1731.48	-1753.37	-1774.74	-1714.83	-1742.93	-1753.10	-1743.95	5892.13	3327.91	2162.88	31638.78	2143.93	3519.23	1231.74	10537.53	5628.94	3812.66	5478.42	3544.58
Thiosulfate Oxidation																									
$5S_2O_3^{2-} + 8NO_3^- + H_2O \rightarrow 10SO_4^{2-} + 4N_2 + 2H^+$	1 nM	-3509.59	-3543.79	-3594.05	-3558.34	-3479.71	-3536.29	-3592.41	-3528.80	-3579.13	-3485.09	-3618.95	-3583.97	0.70	0.71	0.72	0.71	0.70	0.71	0.72	0.71	0.72	0.70	0.72	0.72
	1 µM	-3593.17	-3627.37	-3677.62	-3641.92	-3563.29	-3619.87	-3675.99	-3612.38	-3662.71	-3568.66	-3702.53	-3667.55	718.63	725.47	735.52	728.38	712.66	723.97	735.20	722.48	732.54	713.73	740.51	733.51
	1 mM	-3676.75	-3710.94	-3761.20	-3725.50	-3646.86	-3703.45	-3759.57	-3695.96	-3746.29	-3652.24	-3786.11	-3751.13	739.95	746.83	756.94	1201.47	733.93	745.32	756.61	743.81	6495.13	735.01	761.95	754.91
$S_2O_3^{2-} + 2O_2 + H_2O \rightarrow 2SO_4^{2-} + 2H^+$	1 nM	-838.48	-788.14	-813.84	-795.22	-805.86	-811.61	-826.02	-834.59	-796.85	-828.50	-817.38	-815.44	0.84	0.79	0.81	0.80	0.81	0.81	0.83	0.83	0.80	0.83	0.82	0.82
	1 µM	-855.20	-804.86	-830.56	-811.94	-822.58	-828.32	-842.73	-851.31	-813.56	-845.22	-834.10	-832.15	855.20	804.86	830.56	811.94	822.58	828.32	842.73	851.31	813.56	845.22	834.10	832.15
	1 mM	-871.91	-821.58	-847.27	-828.65	-839.29	-845.04	-859.45	-868.02	-830.28	-861.93	-850.81	-848.87	5859.25	3212.36	2118.18	30556.64	2098.23	3435.08	1207.53	10307.78	5450.79	3770.96	5317.59	3450.65
Thiosulfate Reduction																									
$S_2O_3^{2-} + 4HCOO^- + 4H^+ \rightarrow 4CO_2 + 2HS^- + 3H_2O$	1 nM	-191.24	-108.41	-130.70	-97.60	-106.22	-133.99	-160.61	-154.22	-113.87	-166.81	-115.69	-107.84	0.19	0.11	0.13	0.10	0.11	0.13	0.16	0.15	0.11	0.17	0.12	0.11
	1 µM	-207.95	-125.12	-147.41	-114.31	-122.94	-150.70	-177.33	-170.94	-130.59	-183.52	-132.40	-124.56	207.95	31.28	36.85	28.58	30.73	37.68	44.33	42.73	32.65	45.88	33.10	31.14
	1 mM	-224.67	-141.84	-164.13	-131.03	-139.65	-167.42	-194.04	-187.65	-147.30	-200.24	-149.12	-141.27	1067.17	35.46	41.03	32.76	34.91	41.85	48.51	46.91	36.83	50.06	37.28	35.32
$S_2O_3^{2-} + CH_3COO^- + H^+ \rightarrow 2HS^- + 2CO_2 + H_2O$	1 nM	-135.13	-79.70	-103.77	-74.35	-81.64	-97.37	-122.27	-118.27	-85.95	-129.83	-92.27	-88.82	0.14	0.08	0.10	0.07	0.08	0.10	0.12	0.12	0.09	0.13	0.09	0.09
	1 µM	-151.85	-96.42	-120.49	-91.06	-98.36	-114.09	-138.98	-134.99	-102.66	-146.54	-108.99	-105.53	151.85	96.42	120.49	91.06	98.36	114.09	138.98	134.99	102.66	146.54	108.99	105.53
	1 mM	-168.56	-113.13	-137.20	-107.78	-115.07	-130.80	-155.70	-151.70	-119.38	-163.26	-125.70	-122.25	9608.06	113.13	137.20	107.78	115.07	130.80	155.70	151.70	119.38	995.88	125.70	965.78
$S_2O_3^{2-} + CH_4 \rightarrow 2HS^- + H_2O + CO_2$	1 nM	-93.07	-64.92	-84.10	-49.58	-64.11	-74.59	-95.22	-89.54	-53.59	-91.57	-72.85	-67.33	0.09	0.06	0.08	0.05	0.06	0.07	0.10	0.09	0.05	0.09	0.07	0.07
	1 µM	-109.79	-81.64	-100.81	-66.29	-80.83	-91.31	-111.94	-106.26	-70.31	-108.29	-89.57	-84.04	109.79	81.64	100.81	66.29	80.83	91.31	111.94	106.26	70.31	108.29	89.57	84.04
	1 mM	-126.50	-98.35	-117.53	-83.01	-97.54	-108.03	-128.65	-122.97	-87.02	-125.00	-106.28	-100.76	75128.81	77095.05	117529.06	303.81	97543.45	108025.14	128653.87	37285.87	98.33	35807.86	28034.11	100758.74
$S_2O_3^{2-} + 4H_2 \rightarrow 2HS^- + 3H_2O$	1 nM	-126.52	-102.04	-128.12	-106.83	-93.17	-89.07	-107.89	-106.85	-105.28	-116.31	-110.88	-89.44	0.13	0.10	0.13	0.11	0.09	0.09	0.11	0.11	0.11	0.12	0.11	0.09
	1 µM	-143.23	-118.76	-144.83	-123.54	-109.89	-105.78	-124.60	-123.56	-121.99	-133.03	-127.60	-106.16	28.29	5.34	104.64	8.96	10.44	3.97	2.49	2.78	7.93	8.31	15.63	4.51
	1 mM	-159.95	-135.47	-161.55	-140.26	-126.60	-122.50	-141.32	-140.28	-138.71	-149.74	-144.31	-122.87	31.59	6.10	116.72	10.17	12.03	4.59	2.83	3.16	9.02	9.36	17.68	5.22

Calculated Activities	CSW 1.1	CSW 1.2	CSW 1.3	CSW 1.4	CSW 1.5	CSW OLD	N08-A	N08-B	N08-C	QV 1.1	QV 1.2	QV 1.3
aCH_4	-3.23	-3.11	-2.94	-5.40	-2.97	-2.88	-2.90	-3.52	-6.00	-3.54	-3.58	-2.89
aSO_4^{2-}	-3.86	-4.09	-4.20	-3.71	-3.89	-4.34	-4.85	-4.88	-3.94	-3.92	-4.81	-4.68
aH^+	-12.30	-7.80	-10.20	-7.80	-9.80	-9.70	-10.89	-10.68	-8.46	-11.51	-9.47	-9.68
aHS^-	-4.96	-6.16	-6.08	-6.14	-4.71	-5.18	-6.05	-6.07	-6.07	-5.39	-6.07	-5.09
aCO_2	-11.90	-4.40	-7.84	-3.88	-7.03	-7.96	-9.90	-9.37	-5.32	-11.10	-6.43	-6.80
aO_2	-4.89	-5.10	-5.30	-4.13	-5.30	-5.10	-5.52	-4.62	-4.89	-5.05	-4.89	-5.10
aNO_3^-	-6.58	-4.93	-4.54	-4.19	-6.61	-5.83	-5.53	-7.00	-4.19	-7.00	-4.59	-5.21
aNO_2^-	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00	-6.00
aN_2	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00	-3.00
$aS_2O_3^{2-}$	-6.25	-6.32	-6.32	-6.22	-6.33	-6.41	-6.37	-6.28	-6.20	-6.26	-6.28	-6.36
aH_2	-5.06	-6.74	-5.53	-6.54	-6.41	-6.81	-6.41	-6.49	-6.58	-5.73	-6.31	-6.76
$aHCOO^-$	-4.79	-6.08	-6.08	-6.06	-6.08	-6.08	-6.08	-6.08	-6.08	-6.08	-6.08	-6.08
aCH_3COO^-	-4.31	-6.08	-6.08	-6.06	-6.08	-6.08	-6.08	-6.08	-6.08	-5.30	-6.08	-5.19

Table S9: Bacterial Species Present in >1% Relative Abundance in CSWold

Domain	Phylum	Class	Order	Family	Genus_Species	Average Counts	Percent Abundance (%)
Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	*Dethiobacter*	13852.83	22.74
Bacteria	Firmicutes	Clostridia	Clostridia_Incertae_Sedis	Unknown_Family	*Candidatus_Desulforudis*	6813.67	11.19
Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	*Dethiobacter*	6654.83	10.93
Bacteria	Firmicutes	Clostridia	Clostridiales	Peptococcaceae	*Desulfitispora*	1687.17	2.77
Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Beijerinckiaceae	*Salinarimonas*	1679.50	2.76
Bacteria	Proteobacteria	Gammaproteobacteria	Betaproteobacteriales	Burkholderiaceae	*Hydrogenophaga*	1377.67	2.26
Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	*Dethiobacter*	1021.50	1.68
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	*Rhodobacteraceae_unclassified*	958.17	1.57
Bacteria	Actinobacteria	Nitriliruptoria	Nitriliruptorales	Nitriliruptoraceae	*Egicoccus*	949.83	1.56
Bacteria	Bacteroidetes	Bacteroidia	Bacteroidales	Bacteroidales_unclassified	*Bacteroidales_unclassified*	904.17	1.48
Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae	*Brevundimonas*	894.83	1.47
Bacteria	Firmicutes	Clostridia	Clostridiales	Family_XIV	*Family_XIV_uncultured*	782.00	1.28
Bacteria	Actinobacteria	Acidimicrobiia	Microtrichales	Microtrichales_uncultured	*uncultured_ge*	667.83	1.10
Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	*Rhodobacter*	636.00	1.04

Classified using Silva v.132

Table S10: KEGG Accessions and Genes, Transcripts Associated with MetaCyc Sulfur Metabolic Pathways (Reported as FPKM)

	Metabolic Pathway	Gene	KEGG ID	LIG	LCY 3862	LCY H08	QV1.1	QV1.1 mt	QV1.2	QV12 mt	N08-B	N08B mt	CSWold	CSWold mt
Sulfate Reduction	dissimilatory sulfate reduction I (to sulfide)	*sat*	K00956	13.80	10.17	6.75	65.06	7.03	176.51	120.99	121.06	10.27	35.76	0.83
	dissimilatory sulfate reduction I (to sulfide)	*sat*	K00957	24.48	35.55	247.90	145.56	6.19	224.29	576.35	241.63	84.02	90.17	2.72
	dissimilatory sulfate reduction I (to sulfide)	*sat*	K00958	57.30	95.74	64.40	0.38	0.00	0.59	29.74	18.60	15.10	72.96	2043.18
	dissimilatory sulfate reduction I (to sulfide)	*aprA*	K00394	32.63	4.63	11.92	65.87	0.65	0.34	35.91	9.85	80.79	10.05	5970.80
	dissimilatory sulfate reduction I (to sulfide)	*aprB*	K00395	68.48	14.66	17.57	21.79	0.00	1.20	65.43	7.53	5.40	6.57	7228.29
	dissimilatory sulfate reduction I (to sulfide)	*dsrA*	K11180	66.98	12.13	9.53	139.56	224.49	1.17	127.06	23.53	47.04	19.81	49.68
	dissimilatory sulfate reduction I (to sulfide)	*dsrB*	K11181	59.15	9.71	45.96	98.72	111.89	0.69	25.46	8.15	29.67	3.94	22.94
Thiosulfate Disproportionation	thiosulfate disproportionation IV (rhodanese)	*sseA*	K01011	27.29	66.16	63.06	20.06	0.00	130.71	55.29	86.52	188.53	102.00	71.23
	thiosulfate disproportionation IV (rhodanese)	*glpE*	K02439	-	14.57	81.70	0.26	0.00	86.86	0.00	0.64	0.00	1.21	0.00
	thiosulfate disproportionation III (quinone)	*phsA*	K08352	57.30	0.42	0.00	5.45	73.79	1.23	1.64	21.83	30.84	14.43	0.71
	thiosulfate disproportionation III (quinone)	*phsB*	K08354	5.61	-	-	0.00	0.00	2.76	7.15	0.36	0.00	0.00	0.00
Sulfide Oxidation	sulfide oxidation I (sulfide-quinone reductase)	*sqr*	K17218	54.75	467.294	1281.73	193.54	31.97	217.98	395.21	140.38	61.92	109.28	10.61
	sulfide oxidation II (sulfide dehydrogenase)	*fccB*	K17229	-	277.898	701.805	0.13	0.00	1.38	3.67	0.26	0.00	0.27	0.00
	sulfide oxidation II (sulfide dehydrogenase)	*fccA*	K17230	-	0.00	23.3227	0.00	0.00	0.13	0.00	0.00	0.00	0.27	0.00
Thiosulfate Oxidation	Thiosulfate Oxidation I	*tsdA*	K19713	-	-	-	0.08	0.00	10.14	3.47	0.77	0.00	0.18	0.00
	Thiosulfate Oxidation II	*doxA*	K16936	-	-	-	-	-	-	-	-	-	-	-
	Thiosulfate Oxidation II	*doxD*	K16937	3.91	-	-	0.00	0.00	23.24	0.00	7.97	36.37	4.22	2.84
	Thiosulfate Oxidation III	*soxA*	K17222	45.13	350.286	278.92	0.50	0.00	147.64	121.86	41.87	123.76	76.44	1.93
	Thiosulfate Oxidation III	*soxX*	K17223	62.11	150.015	167.72	0.27	0.00	133.91	122.76	18.46	21.49	35.31	0.00
	Thiosulfate Oxidation III	*soxB*	K17224	3.42	954.826	710.79	0.29	0.00	158.38	56.98	13.51	59.26	16.62	0.23
	Thiosulfate Oxidation III	*soxC*	K17225	8.20	162.12	520.28	0.25	0.00	150.21	117.05	16.33	12.40	25.78	0.92
	Thiosulfate Oxidation III	*soxY*	K17226	118.89	529.582	454.28	109.93	321.47	119.55	558.46	218.55	1276.78	55.38	2.23
	Thiosulfate Oxidation III	*soxZ*	K17227	119.17	157.039	189.48	105.84	314.48	188.64	489.35	265.02	1143.75	83.26	4.31
	Thiosulfate Oxidation III	*CYC*	K08378	-	-	-	-	-	-	-	-	-	-	-
Reference Gene	recombination protein	*recA*	K03553	173.41	415.3	4702.84	375.11	467.32	280.89	241.47	175.83	166.13	206.83	326.19

mt = metatranscript
LCY = Lost City; LIG = Liguria
(-) = no sequences were observed meeting the given criteria
KEGG = Kyoto Encyclopedia of Genes and Genomes
Metagenomes from Aug 12; Metatranscriptomes from Aug. 2013.
Abundances reported as metagenome fragments per kilobase of predicted protein sequence per million mapped reads
CSWOLD mt from dec of 2013

Table S11 : All quantified metagenome and metatranscriptome abundances in CROMO waters for select sulfur pathways through time (reported as FPKM)

	Gene	KEGG ID	CSW1.1 November-11	CSW1.1 August-12	CSW1.3 August-12	CSW1.4 March-12	CSW old August-11	CSW old mt December-13	QV1.1 March-12	QV1.1 June-12	QV1.1 August-12	QV1.1 December-12	QV1.1 mt March-13	QV1.1 mt August-13	QV1.2 August-12	QV1.2 mt August-13	QV1.2 mt December-13	N08-A April-11	N08-A July-11	N08-A August-11	N08-A August-12	N08-B April-11	N08-B July-11	N08-B August-12	N08-B mt March-13	N08-B mt August-13	N08-B mt December-13	N08-C August-12
Sulfate Reduction																												
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*sat*	K00956	107.12	206.83	111.13	46.54	35.76	**0.83**	81.51	86.93	65.06	88.25	**1.81**	**7.03**	176.51	**120.99**	**270.78**	174.50	203.25	236.15	197.40	174.82	78.68	121.06	**43.11**	**10.27**	**39.64**	7.96
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*sat*	K00957	328.79	375.85	213.73	197.23	90.17	**2.72**	176.31	196.39	145.56	174.37	**4.41**	**6.19**	224.29	**576.35**	**629.20**	403.18	420.16	455.92	444.99	515.14	280.91	241.63	**110.69**	**84.02**	**109.75**	111.34
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*sat*	K00958	0.00	0.75	2.66	1.86	72.96	**2043.18**	0.00	0.36	0.38	0.15	**0.00**	**0.00**	0.59	**29.74**	**439.54**	31.71	24.18	21.07	30.47	29.54	7.24	18.60	**43.99**	**15.10**	**43.27**	84.26
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*aprA*	K00394	0.18	0.37	3.03	0.77	10.05	**5970.80**	74.69	89.71	65.87	97.57	**0.00**	**0.65**	0.34	**35.91**	**1018.52**	17.71	19.12	17.53	25.51	19.61	3.47	9.85	**27.36**	**80.79**	**47.03**	0.05
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*aprB*	K00395	0.00	0.00	3.68	22.79	6.57	**7228.29**	31.67	27.89	21.79	30.39	**0.00**	**0.00**	1.20	**65.43**	**1064.03**	17.20	18.41	13.90	34.02	17.96	29.75	7.53	**19.69**	**5.40**	**61.68**	0.00
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*dsrA*	K11180	0.51	0.71	6.98	6.65	19.81	**49.68**	158.45	235.96	139.56	256.59	**1.65**	**224.49**	1.17	**127.06**	**557.94**	127.11	132.99	161.71	209.17	160.81	29.43	23.53	**98.20**	**47.04**	**703.53**	0.08
Sulfate reduction I (dissimilatory, to hydrogen sulfide)	*dsrB*	K11181	0.16	0.82	5.58	1.03	3.94	**22.94**	108.29	160.01	98.72	173.96	**5.54**	**111.89**	0.69	**25.46**	**331.55**	9.89	12.94	10.37	20.06	13.45	3.27	8.15	**30.48**	**29.67**	**24.81**	0.00
Thiosulfate Disproportionation																												
thiosulfate disproportionation IV (rhodanese)	*sseA*	K01011	10.80	75.41	206.36	132.32	102.00	**71.23**	19.28	13.03	20.06	5.72	**354.76**	**0.00**	130.71	**55.29**	**71.30**	121.12	143.70	105.62	143.26	97.77	181.66	86.52	**284.59**	**188.53**	**21.42**	366.21
thiosulfate disproportionation IV (rhodanese)	*glpE*	K02439	0.00	0.00	2.47	0.00	1.21	**0.00**	0.00	0.00	0.26	0.00	**0.00**	**0.00**	86.86	**0.00**	**0.00**	0.00	0.00	0.00	0.00	1.62	1.24	0.64	**0.00**	**0.00**	**0.72**	3.68
thiosulfate disproportionation III (quinone)	*phsA*	K08352	79.01	1.79	7.77	29.11	14.43	**0.71**	6.29	8.75	5.45	9.26	**76.05**	**73.79**	1.23	**1.64**	**13.78**	96.08	102.69	71.31	104.70	28.77	41.69	21.83	**17.57**	**30.84**	**197.91**	0.09
thiosulfate disproportionation III (quinone)	*phsB*	K08354	0.00	0.00	0.00	8.53	0.00	**0.00**	0.00	0.00	0.00	0.00	**0.00**	**0.00**	2.76	**7.15**	**6.05**	0.19	0.00	0.00	0.00	0.00	10.20	0.36	**0.00**	**0.00**	**0.00**	0.00
Sulfide Oxidation																												
sulfide oxidation I (sulfide-quinone reductase)	*sqr*	K17218	129.75	123.53	98.08	143.94	109.28	**10.61**	205.01	228.28	193.54	216.60	**28.24**	**31.97**	217.98	**395.21**	**461.06**	420.29	414.81	408.64	413.50	551.63	254.71	140.38	**439.82**	**61.92**	**439.54**	141.19
sulfide oxidation II (sulfide dehydrogenase)	*fccA*	K17230	0.00	0.00	0.00	7.21	0.27	**0.00**	0.15	0.00	0.00	0.00	**0.00**	**0.00**	0.13	**0.00**	**0.37**	2.28	1.56	3.16	13.47	0.16	9.82	0.00	**0.00**	**0.00**	**0.00**	0.00
sulfide oxidation II (sulfide dehydrogenase)	*fccB*	K17229	0.00	0.14	0.06	25.52	0.27	**0.00**	0.00	0.07	0.13	0.08	**0.00**	**0.00**	1.38	**3.67**	**8.05**	3.04	1.85	2.49	13.58	1.40	30.78	0.26	**0.00**	**0.00**	**0.00**	0.08
Thiosulfate Oxidation																												
Thiosulfate Oxidation I	*tsdA*	K19713	0.34	0.00	10.41	65.88	0.18	**0.00**	0.00	0.00	0.08	0.00	**0.00**	**0.00**	10.14	**3.47**	**5.32**	0.15	0.23	0.20	0.13	0.22	76.73	0.77	**6.08**	**0.00**	**0.53**	21.47
Thiosulfate Oxidation II	*doxA*	K16936	0.00	0.00	0.00	0.00	0.00	**0.00**	0.00	0.00	0.00	0.00	**0.00**	**0.00**	0.00	**0.00**	**0.00**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**	**0.00**	**0.00**	0.00
Thiosulfate Oxidation II	*doxD*	K16937	0.00	0.00	0.00	1.71	4.22	**2.84**	0.00	0.00	0.00	0.00	**0.00**	**0.00**	23.24	**0.00**	**0.60**	6.67	3.12	1.20	5.18	18.22	3.93	7.97	**82.45**	**36.37**	**5.39**	90.81
Thiosulfate Oxidation III	*soxA*	K17222	1.15	0.63	65.72	119.72	76.44	**1.93**	0.25	0.18	0.50	0.20	**0.00**	**0.00**	147.64	**121.86**	**261.55**	271.79	287.00	340.16	389.40	326.88	175.15	41.87	**177.16**	**123.76**	**56.71**	2.39
Thiosulfate Oxidation III	*soxX*	K17223	1.00	1.25	69.45	82.98	35.31	**0.00**	0.60	0.00	0.27	0.00	**0.00**	**0.00**	133.91	**122.76**	**259.20**	143.68	131.93	133.49	166.91	226.10	120.36	18.46	**52.60**	**21.49**	**16.25**	5.27
Thiosulfate Oxidation III	*soxB*	K17224	0.19	0.50	62.42	101.22	16.62	**0.23**	0.35	0.11	0.29	0.12	**0.00**	**0.00**	158.38	**56.98**	**82.42**	49.43	52.86	52.21	85.63	55.22	130.21	13.51	**96.16**	**59.26**	**56.42**	0.11
Thiosulfate Oxidation III	*soxC*	K17225	0.37	0.13	62.24	89.36	25.78	**0.92**	0.07	0.00	0.25	0.00	**0.00**	**0.00**	150.21	**117.05**	**359.16**	20.21	15.95	8.92	19.28	17.09	114.83	16.33	**96.09**	**12.40**	**3.83**	6.37
Thiosulfate Oxidation III	*soxY*	K17226	411.71	321.15	152.90	175.48	55.38	**2.23**	129.85	123.30	109.93	112.74	**56.83**	**321.47**	119.55	**558.46**	**653.53**	271.94	290.05	322.61	347.35	297.40	245.52	218.55	**1307.53**	**1276.78**	**1500.90**	20.64
Thiosulfate Oxidation III	*soxZ*	K17227	422.93	388.66	118.96	115.94	83.26	**4.31**	149.96	125.45	105.84	122.05	**129.20**	**314.48**	188.64	**489.35**	**763.61**	375.67	425.19	481.19	474.50	475.26	196.59	265.02	**1913.85**	**1143.75**	**940.05**	35.46
Thiosulfate Oxidation III	*CYC*	K08378	0.00	0.00	0.00	0.00	0.00	**0.00**	0.00	0.00	0.00	0.00	**0.00**	**0.00**	0.00	**0.00**	**0.00**	0.00	0.00	0.00	0.00	0.00	0.00	0.00	**0.00**	**0.00**	**0.00**	0.00
Reference Gene																												
recombination protein	*recA*	K03553	72.01	180.47	319.41	263.30	206.83	**326.19**	319.48	345.45	375.11	337.18	**467.32**	**260.13**	280.89	**241.47**	**189.85**	195.07	192.91	168.94	213.55	187.39	353.38	175.83	**166.13**	**416.78**	**135.05**	1000.28

mt = metatranscript
KEGG = Kyoto Encyclopedia of Genes and Genomes
CSW = Core Shed Well
QV = Quarry Valley Well
- Previously owned by Homestake Mining Company

Table S12: Log$_2$ Fold Change for CROMO Metatranscriptomic Data Associated with MetaCyc Sulfur Metabolic Pathways (reported as FPKM)

	Well depth (m)			19.20	23.00		26.20		76.20	
	Metabolic Pathway	**Gene**	**KEGG ID**	**QV1.2 mt**	**QV1.1 mt**	**Log$_2$ Fold Change (QV1.2/QV1.1)**	**N08-B mt**	**Log$_2$ Fold Change (QV1.2/N08-B)**	**CSWold mt**	**Log$_2$ Fold Change (QV1.2/CSWold)**
Sulfate Reduction	dissimilatory sulfate reduction I (to sulfide)	*sat*	K00956	120.99	7.03	**-4.10**	10.27	**-3.56**	0.83	**-7.19**
	dissimilatory sulfate reduction I (to sulfide)	*sat*	K00957	576.35	6.19	**-6.54**	84.02	**-2.78**	2.72	**-7.73**
	dissimilatory sulfate reduction I (to sulfide)	*sat*	K00958	29.74	0.00	**-18.18**	15.10	**-0.98**	2043.18	**6.10**
	dissimilatory sulfate reduction I (to sulfide)	*aprA*	K00394	35.91	0.65	**-5.79**	80.79	**1.17**	5970.80	**7.38**
	dissimilatory sulfate reduction I (to sulfide)	*aprB*	K00395	65.43	0.00		5.40	**-3.60**	7228.29	**6.79**
	dissimilatory sulfate reduction I (to sulfide)	*dsrA*	K11180	127.06	224.49	**0.82**	47.04	**-1.43**	49.68	**-1.35**
	dissimilatory sulfate reduction I (to sulfide)	*dsrB*	K11181	25.46	111.89	**2.14**	29.67	**0.22**	22.94	**-0.15**
Thiosulfate Disproportionation	thiosulfate disproportionation IV (rhodanese)	*sseA*	K01011	55.29	0.00		188.53	**1.77**	71.23	**0.37**
	thiosulfate disproportionation IV (rhodanese)	*glpE*	K02439	0.00	0.00		0.00		0.00	
	thiosulfate disproportionation III (quinone)	*phsA*	K08352	1.64	73.79	**5.49**	30.84	**4.23**	0.71	**-1.22**
	thiosulfate disproportionation III (quinone)	*phsB*	K08354	7.15	0.00		0.00		0.00	
Sulfide Oxidation	sulfide oxidation I (sulfide-quinone reductase)	*sqr*	K17218	395.21	31.97	**-3.63**	61.92	**-2.67**	10.61	**-5.22**
	sulfide oxidation II (sulfide dehydrogenase)	*fccB*	K17229	3.67	0.00		0.00		0.00	
	sulfide oxidation II (sulfide dehydrogenase)	*fccA*	K17230	0.00	0.00		0.00		0.00	
Thiosulfate Oxidation	Thiosulfate Oxidation I	*tsdA*	K19713	3.47	0.00		0.00		0.00	
	Thiosulfate Oxidation II	*doxA*	K16936	-	-					
	Thiosulfate Oxidation II	*doxD*	K16937	0.00	0.00		36.37		2.84	
	Thiosulfate Oxidation III	*soxA*	K17222	121.86	0.00		123.76	**0.02**	1.93	**-5.98**
	Thiosulfate Oxidation III	*soxX*	K17223	122.76	0.00		21.49	**-2.51**	0.00	
	Thiosulfate Oxidation III	*soxB*	K17224	56.98	0.00		59.26	**0.06**	0.23	**-7.95**
	Thiosulfate Oxidation III	*soxC*	K17225	117.05	0.00		12.40	**-3.24**	0.92	**-6.99**
	Thiosulfate Oxidation III	*soxY*	K17226	558.46	321.47	**-0.80**	1276.78	**1.19**	2.23	**-7.97**
	Thiosulfate Oxidation III	*soxZ*	K17227	489.35	314.48	**-0.64**	1143.75	**1.22**	4.31	**-6.83**
	Thiosulfate Oxidation III	*CYC*	K08378	-	-		-		-	

mt = metatranscript
LCY = Lost City Hydrothermal Field; LIG = Liguria
(-) = no sequences were observed meeting the given criteria
KEGG = Kyoto Encyclopedia of Genes and Genomes
Metagenomes from Aug 12; Metatranscriptomes from Aug. 2013.
CSWold mt from Dec of 2013
Abundances reported as metagenome fragments per kilobase of predicted protein sequence per million mapped reads (FPKM)
Log2 Fold Changes are calculated for the shallowest well, QV1.2, compared to all CROMO wells with available metatranscriptomic data.
Log2 Fold Changes cannot be calculated for wells reporting 0.00 for metatranscriptomic data. These spaces are left blank.

Table S13 - PhyloPythiaS+ Assigned Taxonomy for each Contig Encoding a Sulfur Gene and Calculated Abundance of each Contig in each Metagenome and Metatranscriptome

																	PhyloPythiaS+ Taxonomic Assignment						
Gene	**KEGG ID**	**Contig**	**PROKKA**	**CSW1.1**	**QV1.1**	**CSW1.3**	**QV1.2**	**N08-A**	**N08-B**	**N08-C**	**CSWold**	**CSW1.4**	**QV1.1 mt**	**CSWold mt**	**N08-B mt**	**QV1.2 mt**	**Domain**	**Phylum**	**Class**	**Order**	**Family**	**Genus**	**Genus, Species**
aprA	K00394	c_000000997749	PROKKA_681849	0.00	0.00	0.00	0.00	0.00	0.00	0.00	69.82	1.04	0.00	10384.23	0.00	42.48	Bacteria	Proteobacteria	Deltaproteobacteria				
aprAB	K00394, K00395	c_000000283170	PROKKA_200060	0.00	0.00	0.00	0.00	0.00	0.00	0.00	145.54	0.00	0.00	487114.56	0.00	0.00	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae		
aprAB	K00394, K00395	c_000000848240	PROKKA_569718, PROKKA_569719	0.00	0.00	0.00	2.57	2.22	70.53	0.00	27.90	0.00	0.00	4033.03	2821.95	2090.42	Bacteria	Firmicutes	Clostridia	Clostridiales			
aprAB	K00394, K00395	c_000000000009	PROKKA_01633, PROKKA_01634	57.78	24241.81	1137.75	59.40	243.88	98.03	15.19	205.54	72.88	5438.98	32.15	56.76	82.56	Bacteria						
aprAB	K00394, K00395	c_000000423537	PROKKA_285558, PROKKA_285557	36.51	18.61	13.55	60.36	23.18	22.81	7.87	13.31	75.38	2.04	0.42	7.42	7.77	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
aprAB	K00394, K00395	c_000000706742	PROKKA_463859, PROKKA_463860	4.54	4.37	5.73	11.66	21.70	5.89	31.82	2.29	24.58	0.00	301.48	0.00	12.48	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
aprB	K00395	c_000000337380	PROKKA_256459	0.00	0.00	0.00	0.00	0.00	0.00	0.00	42.12	0.00	0.00	16553.58	0.00	0.00							
dsrA	K11180	c_000000631759	PROKKA_436008	64.30	7.74	13.56	30.02	86732.15	4792.45	0.00	7907.83	215.43	0.00	0.00	11766.11	17213.37	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Azoarcus	
dsrA	K11180	c_000000491049	PROKKA_344146	33.69	16.21	14.21	30.46	67908.42	9546.10	28.35	8183.20	106.85	0.00	0.00	8793.94	23854.45	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
dsrAB	K11180, K11181	c_000000000103	PROKKA_06634, PROKKA_06633	22.98	12.08	12.78	20.62	3.13	14.03	7.06	6.01	56.41	0.00	0.00	2.95	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
dsrAB	K11180, K11181	c_000000284787	PROKKA_210993, PROKKA_210994	0.00	0.00	0.00	0.00	0.00	24.71	0.00	9.61	3.56	0.00	0.00	0.00	401.05	Bacteria	Proteobacteria					
dsrAB	K11180, K11181	c_000000285367	PROKKA_213123, PROKKA_213122	0.00	0.00	0.00	2.82	0.00	58.76	0.00	36.50	2.26	0.00	4743.09	1980.40	2596.92	Bacteria	Proteobacteria	Deltaproteobacteria				
dsrAB	K11180, K11181	c_000000774717	PROKKA_539297, PROKKA_539296	83.04	24355.88	1137.08	73.39	206.18	88.78	19.68	191.18	81.19	6924.59	684.59	62.67	103.89	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae		
sat	K00957	c_000000398317	PROKKA_270118	28.82	14.10	10833.90	7.23	10.64	17.61	16.21	10.34	26.12	0.00	4.59	0.00	1.48	Bacteria	Proteobacteria	Burkholderiales	Comamonadaceae	Acidovorax		
sat	K00956	c_000000977096	PROKKA_638597	84526.58	19876.01	11205.54	72.78	49003.63	50882.12	57.91	6675.43	153.67	9740.85	0.00	10862.14	16924.84	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales		Rubrivivax	Rubrivivax gelatinosus
sat	K00956	c_000001130468	PROKKA_733719	54531.37	288.35	224.00	2.70	18.46	29068.37	1.62	3.64	0.54	980.42	0.00	0.00	0.93	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Acidovorax sp. KKS102
sat	K00956	c_000000706657	PROKKA_458240	266.54	46.89	0.91	1.01	822.41	543.77	3.89	123.25	2.61	0.00	1.56	1455.56	13515.27	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	Methylomonas methanica
sat	K00956	c_000000844528	PROKKA_551519	11.47	6.15	3.43	11.39	0.93	5.93	36.45	0.00	2.60	0.00	79.45	0.00	0.64	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
sat	K00956, K00957	c_000000991007	PROKKA_668415, PROKKA_668414	14921.21	4163.72	2365.59	18.99	15539.69	8876.58	16.98	2228.88	76.28	2538.42	4.56	980.61	2958.11	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
sat	K00956, K00957	c_000000706934	PROKKA_471525, PROKKA_471524	20.52	15.59	16.84	21.72	6.00	23.58	21.07	0.78	0.36	0.00	2.67	0.00	0.09	Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylovorus	
sat	K00956, K00957	c_000000988584	PROKKA_647411,PROKKA_647412	79.20	9142.45	17068.56	6.29	8.43	45.63	5.46	2.79	42.66	2354.78	0.00	0.00	30.35	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter	Dethiobacter alkaliphilus
sat	K00956, K00957	c_000000283369	PROKKA_202629, PROKKA_202628	433.91	8466.31	11.35	9.29	9066.61	359.80	3.94	361.66	27.97	1356.55	1.11	240.51	0.00	Bacteria	Firmicutes	Clostridia	Clostridiales			
sat	K00956, K00957	c_000001130590	PROKKA_738185,PROKKA_738184	7.82	8.77	13.27	8426.91	1.34	4.59	0.93	0.47	817.90	0.00	0.00	0.00	581.92	Bacteria	Bacteroidetes	Cytophagia	Cytophagales	Cyclobacteriaceae	Belliella	Belliella baltica
sat	K00957	c_000000918750	PROKKA_628355	125814.64	38594.52	18683.03	99.12	108815.23	74943.16	34.18	12715.45	414.81	1085.08	0.00	15617.41	2041.07	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
sat	K00957	c_000000706203	PROKKA_451323	8.09	0.00	1811.77	797.88	6.46	136.22	210.66	0.00	3.02	0.00	113.62	311.45	46465.63	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylocystis	Methylocystis sp. SC2
sat	K00957	c_000000423398	PROKKA_283984	0.00	0.00	327.65	1.36	0.00	0.00	0.00	1.60	1.19	33.54	0.00	0.00	34644.73	Bacteria	Proteobacteria	Alphaproteobacteria				
sat	K00957	c_000000289758	PROKKA_223010	0.00	11.84	2449.62	2755.79	29.48	0.00	13.80	43.41	174.15	0.00	0.00	0.00	2076.87	Bacteria	Proteobacteria	Gammaproteobacteria				
sat	K00957	c_000000493173	PROKKA_344723	0.00	0.00	241.42	3525.73	16.07	0.00	180.56	15.22	25865.78	0.00	0.00	511.00	44.29	Bacteria	Proteobacteria	Gammaproteobacteria	Xanthomonadales	Xanthomonadaceae	Pseudoxanthomonas	Pseudoxanthomonas suwonensis
sat	K00957	c_000000564124	PROKKA_367597	9.15	5.75	3.30	3.32	16.94	3.63	20972.95	0.36	0.00	0.00	0.00	0.00	0.00	Bacteria						
sat	K00957	c_000000486621	PROKKA_342957	0.00	0.00	18.37	4.07	0.00	0.00	2.44	0.00	10342.90	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales			
sat	K00957	c_000000707125	PROKKA_477682	0.00	0.77	9.41	484.47	0.00	0.00	0.00	3.22	7795.69	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria					
sat	K00958	c_000000997109	PROKKA_680919	0.00	0.00	0.00	0.00	0.00	56.90	0.00	44.28	0.00	0.00	13589.05	4758.88	4230.45	Bacteria	Proteobacteria	Deltaproteobacteria				
sat	K00958	c_000000564734	PROKKA_379015	0.00	0.00	0.00	0.00	0.00	0.00	0.00	102.82	0.00	0.00	91198.10	0.00	0.00	Bacteria						
sat	K00958	c_000000283222	PROKKA_200850	21.37	10.66	12.23	79.51	0.61	12.36	11.57	13.09	91.58	0.00	0.00	0.00	1.97	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sat	K00958	c_000000988663	PROKKA_651441	20.77	10.98	6.69	11.09	4.56	10.38	6.40	4.31	41.02	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sat	K00958	c_000000995678	PROKKA_678588	0.00	0.00	0.00	0.00	0.00	0.00	0.00	12469.00	0.00	0.00	203.96	0.00	0.00	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales			
sat	K00958	c_000000706642	PROKKA_457811	9.35	2.71	0.00	1.76	10.52	7.89	11341.59	0.00	0.00	0.00	0.00	0.00	0.00	Archaea	Thaumarchaeota		Nitrosopumilales	Nitrosopumilaceae		
sat	K00958	c_000000853757	PROKKA_588190	0.00	0.00	0.00	0.00	0.00	0.00	0.00	9.24	0.00	0.00	10183.02	0.00	21.09	Bacteria	Proteobacteria	Deltaproteobacteria				
sat, aprA	K00958, K00394	c_000000988818	,PROKKA_654936	19.19	13.12	12.75	19.06	2.56	12.44	5.40	3.64	85.97	0.00	2.91	0.00	0.58	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sat, aprAB	K00958, K00394, K00395	c_000000848590	PROKKA_572459, PROKKA_572457, PROKKA_572458	0.00	0.00	0.00	0.00	0.00	58.23	0.00	5.66	35.64	0.00	0.00	0.00	300.05	Bacteria	Proteobacteria	Deltaproteobacteria				
sat, sseA	K01011, K00956, K00957	c_000001130721	PROKKA_742611, PROKKA_742612	48.12	28.05	158.09	39949.88	13.37	38.06	63.15	1.89	15.71	0.00	1.25	0.00	2152.07	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
dsrAB, soxA	K11180, K11181, K17222, K17224	c_000000563866	PROKKA_357998, PROKKA_357997, PROKKA_358010, PROKKA_358009	3.41	4.93	4.32	3.19	702.07	119.29	32.33	90.34	31.21	0.00	76.92	44.12	167.93	Bacteria	Proteobacteria	Betaproteobacteria				
phsA	K08352	c_000000706397	PROKKA_453193	0.00	0.00	0.00	2.40	4114.25	742.20	8.65	427.61	23.91	0.00	0.00	2652.94	0.00	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Trueperaceae	Truepera	Truepera radiovictrix
phsA	K08352	c_000000712386	PROKKA_499875	19.15	5804.73	4.04	0.00	434.45	43.43	0.00	71.38	21.47	73203.83	0.00	246.68	6.49	Bacteria	Proteobacteria	Gammaproteobacteria				
phsA	K08352	c_000000002143	PROKKA_21962	182.72	831.40	1574.87	0.00	808.11	123.31	0.00	156.50	7.46	37888.28	114.24	800.17	22.45	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae	Dethiobacter	Dethiobacter alkaliphilus
sseA	K01011	c_000000988440	PROKKA_641444	2.30	1.11	0.97	1.61	606.80	313.25	3.87	81.83	0.86	27.97	2.12	4738.30	34224.89	Bacteria	Proteobacteria	Gammaproteobacteria	Methylococcales	Methylococcaceae	Methylomonas	Methylomonas methanica
sseA	K01011	c_000000988355	PROKKA_640577	0.00	0.00	0.00	924.97	0.00	0.00	7.39	0.00	3.59	0.00	6.37	0.00	11236.07	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Thauera	
sseA	K01011	c_000000670881	PROKKA_444268	0.00	0.00	29.41	2981.63	0.00	0.00	0.00	21.05	23826.74	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria					
sseA	K01011	c_000000563829	PROKKA_357637	4.41	3.30	76.06	3380.51	1.82	2.86	32.02	26.35	19868.45	0.00	2.09	0.00	2.12	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae		
sseA	K01011	c_000000007983	PROKKA_34705	17790.20	6391.00	22.17	18.11	379.74	9555.44	2.70	127.75	48.58	5806.54	0.00	22453.38	167.66	Bacteria	Proteobacteria	Deltaproteobacteria	Myxococcales			
sseA	K01011	c_000000423185	PROKKA_279770	81.89	17.23	21352.15	1.15	25.51	54.84	1.49	1.34	1.98	0.00	0.00	0.00	3.95	Bacteria	Firmicutes					
sseA	K01011	c_000000706442	PROKKA_453740	3.58	5.15	2.26	5.01	15.72	4.64	20849.28	1.80	0.00	0.00	1.71	0.00	0.00	Archaea	Thaumarchaeota		Nitrosopumilales	Nitrosopumilaceae		
sseA	K01011	c_000000847966	PROKKA_566017	3.60	5.20	6.06	20.11	0.00	4.67	4.04	4.50	37.63	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sseA	K01011	c_000000989118	PROKKA_658739, PROKKA_658742	11.30	3.59	2.64	3.28	24.10	7.61	19601.26	0.40	0.00	0.00	0.37	0.00	0.00	Archaea	Thaumarchaeota		Nitrosopumilales	Nitrosopumilaceae		
sseA	K01011	c_000000848504	PROKKA_571919	18.38	12.64	6.65	7.36	14.69	11.91	19365.54	0.00	0.00	0.00	0.00	0.00	0.00	Archaea	Thaumarchaeota		Nitrosopumilales	Nitrosopumilaceae		
sseA	K01011	c_000000072116	PROKKA_71817	22.66	21.81	0.00	0.00	18.11	14.68	17752.16	0.00	0.00	0.00	0.00	0.00	0.00	Archaea	Thaumarchaeota		Nitrosopumilales	Nitrosopumilaceae		
sseA	K01011	c_000000425171	PROKKA_294931	0.00	5.30	3.10	3.43	4058.11	541.06	8.24	369.30	16.47	0.00	0.00	839.09	0.00	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Trueperaceae	Truepera	Truepera radiovictrix
sseA	K01011	c_000000140882	PROKKA_85902	0.00	0.00	0.00	0.00	0.00	0.00	0.00	15840.65	2.54	0.00	233.62	0.00	0.00	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales			
sseA	K01011	c_000001130348	PROKKA_731945	0.00	0.00	7.41	0.00	1.75	0.00	0.00	5.53	11442.87	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Alphaproteobacteria				
sseA	K01011	c_000000995730	PROKKA_678688	18.84	4.58	4.01	5.55	0.00	12.21	26.69	0.00	3.56	0.00	117.75	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
sseA	K01011	c_000000988651	PROKKA_651012	38.32	10.91	10766.41	10.43	7.82	21.79	20.86	20.32	37.17	0.00	5.77	185.50	7.90	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
sseA	K01011	c_000000002451	PROKKA_22964	4.90	0.00	0.00	0.00	0.00	9.19	10378.67	0.00	0.00	0.00	0.00	0.00	0.00	Archaea	Thaumarchaeota		Nitrosopumilales	Nitrosopumilaceae	Nitrosopumilus	Nitrosopumilus maritimus
sseA	K01011	c_000000282673	PROKKA_181404	23.74	14.48	9807.09	21.81	12.44	15.40	55.90	91.22	107.40	0.00	7.30	130.64	9.76	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Acidovorax sp. KKS102
sseA	K01011	c_000000000140	PROKKA_07756	0.00	0.00	5.51	416.76	0.73	0.00	0.51	3.44	7049.61	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales			
sseA	K01011	c_000000328761	PROKKA_253260	0.00	3.03	0.00	11.76	0.00	0.00	7.06	0.00	0.00	0.00	12.01	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria				
sqr	K17218	c_000000448349	PROKKA_325676	73055.51	16991.27	1174.83	78.17	6809.68	38999.13	23.56	719.20	86.27	5221.91	0.00	0.00	3522.51	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales			
sqr	K17218	c_000000581008	PROKKA_410729	0.00	0.00	0.00	0.00	0.00	0.00	0.00	13433.39	0.00	0.00	218.76	0.00	0.00	Bacteria	Actinobacteria	Actinobacteria	Actinomycetales	Nocardioidaceae		
sqr	K17218	c_000000140824	PROKKA_84930	65032.49	19877.86	10954.38	142.00	94048.06	42273.69	36.48	10542.71	305.12	3247.87	0.00	4368.36	5662.39	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
sqr	K17218	c_000000459937	PROKKA_332553	12009.32	27219.13	2388.33	90.36	78010.96	10452.47	32.71	7869.74	271.75	1684.04	4.66	2377.53	17985.21	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
sqr	K17218	c_000000000017	PROKKA_02758	60.43	24400.52	1128.18	63.06	155.95	79.74	21.98	207.90	79.64	8105.34	72.77	231.47	149.80	Bacteria	Firmicutes	Clostridia	Clostridiales	Syntrophomonadaceae		
sqr	K17218	c_000000706490	PROKKA_454450	0.00	3.58	51.03	3078.38	0.00	0.00	1.04	27.23	27054.57	0.00	0.00	0.00	2.00	Bacteria	Proteobacteria					
sqr	K17218	c_000000988639	PROKKA_650605	29.87	9.66	15.09	25.01	5.17	20.57	19.83	0.24	0.35	0.00	7.15	0.00	0.68	Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylovorus	
sqr	K17218	c_000000285577	PROKKA_213762	16.66	0.00	986.35	1118.55	8.88	168.61	227.23	11.20	8.30	154.26	121.94	0.00	23397.80	Bacteria	Proteobacteria	Alphaproteobacteria	Rhizobiales	Methylocystaceae	Methylocystis	Methylocystis sp. SC2
sqr	K17218	c_000000461334	PROKKA_333348	0.00	0.00	2123.69	1523.21	0.00	0.00	0.00	15.40	17.06	0.00	0.00	0.00	1425.64	Bacteria	Proteobacteria	Alphaproteobacteria	Caulobacterales	Caulobacteraceae		

sqr	K17218	c_000000141364	PROKKA_102238, PROKKA_102239	10180.24	3145.86	1258.00	17.01	12908.74	6532.75	6.83	2087.76	67.28	103.21	0.00	481.90	946.26	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
sqr	K17218	c_000000433572	PROKKA_311898	0.00	0.00	0.00	875.77	0.00	0.00	0.00	0.00	11.33	0.00	14.53	0.00	1786.88	Bacteria	Proteobacteria	Gammaproteobacteria				
sqr	K17218	c_000000847661	PROKKA_553400	0.00	0.65	0.00	1.26	4299.42	568.53	2.27	378.73	23.60	0.00	0.00	1793.18	0.00	Bacteria	Deinococcus-Thermus	Deinococci	Deinococcales	Trueperaceae	Truepera	Truepera radiovictrix
sqr	K17218	c_000000564250	PROKKA_372601	0.00	0.00	1.38	0.00	610.70	407.95	4.93	96.32	1.30	5.06	1.64	3993.35	15502.00	Bacteria	Proteobacteria	Gammaproteobacteria				
sqr	K17218	c_000000283007	PROKKA_197001	30.11	11.94	10.99	23.77	4.18	16.12	5.14	8.58	58.19	0.00	0.00	0.00	1.39	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sqr	K17218	c_000000282745	PROKKA_183540	11.32	8.47	6.22	11.56	2.83	6.42	12.26	7.09	62.60	0.00	0.00	0.00	3.05	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sqr	K17218	c_000000283105	PROKKA_198937	9.92	8.30	9.66	13.51	3.47	8.71	5.89	4.06	38.21	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
sqr	K17218	c_000000711408	PROKKA_497537	14.81	4.99	8.68	15.85	0.00	9.60	17.45	0.00	12.72	0.00	63.89	0.00	4.23	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
fccB	K17229	c_000000283845	PROKKA_206080	45.45	10.94	9.59	0.00	8.72	22.09	3.19	0.00	21.23	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
fccB	K17229	c_000000564232	PROKKA_372077, PROKKA_372078	16.32	10.16	9.31	20.10	4.60	11.20	4.31	2.42	42.30	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
fccB	K17229	c_000000141967	PROKKA_107929	0.00	4.05	1.77	421.29	0.00	0.00	0.00	8.08	7458.79	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Alphaproteobacteria	Sphingomonadales	Sphingomonadaceae		
sqr,doxD	K17229, K16937	c_000000847790	PROKKA_558845, PROKKA_558944	10.93	3.56	4.29	4.21	15.54	7.62	17421.41	0.25	0.00	0.00	0.00	0.00	0.00	Bacteria	Actinobacteria	Actinobacteria				
sseA, soxAXBCYZ	K01011, K17222, K17223, K17224, K17225, K17226, K17227	c_000001130720	PROKKA_742322, PROKKA_742400, PROKKA_742399, PROKKA_742398, PROKKA_742404, PROKKA_742402, PROKKA_742401	43.40	27.72	169.50	40932.68	15.68	35.43	71.76	1.51	21.31	0.00	1.54	0.00	4212.05	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Dechloromonas	Dechloromonas aromatica
soxAXBCYZ	K17222, K17223, K17224, K17225, K17226, K17227	c_000000423423	PROKKA_284276, PROKKA_284275, PROKKA_284280, PROKKA_284280, PROKKA_284278, PROKKA_284277	0.00	0.00	5.62	778.79	0.00	0.00	3.74	0.00	7.48	0.00	0.00	0.00	3926.74	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		
soxAXYZ	K17222, K17223, K17226, K17227	c_000000564381	PROKKA_375127, PROKKA_375128, PROKKA_375126, PROKKA_375125	5.38	2.61	4.60	2.55	0.00	3.49	15.30	0.00	0.00	0.00	6.39	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Azoarcus	
soxAX	K17222, K17223	c_000000928519	PROKKA_630679, PROKKA_630680	57502.43	14891.85	7959.52	123.10	79500.31	33741.68	30.68	7575.85	250.54	1298.37	0.00	3563.65	5421.23	Bacteria	Proteobacteria	Gammaproteobacteria				
soxAB	K17222, K17224	c_000000990013	PROKKA_664302, PROKKA_664301	7.28	7.01	12.14	15.29	23.25	11.79	34.66	20.18	36.68	0.00	1.74	0.00	3.93	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	Thiobacillus denitrificans
soxX	K17223	c_000000000343	PROKKA_11141	41.34	9.91	10.91	20.53	2.07	23.47	0.00	13.05	84.90	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Hydrogenophilales	Hydrogenophilaceae	Thiobacillus	
soxXY	K17223, K17226	c_000000423219	PROKKA_280719, PROKKA_280718	0.00	1.31	6.50	471.93	0.00	0.29	3.06	3.88	7214.59	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Alphaproteobacteria	Rhodobacterales			
soxX	K17223	c_000000423595	PROKKA_286197	0.00	9.21	8.08	7.15	0.00	14.69	0.00	1.93	12.87	0.00	0.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae		
soxXBCYZ	K17223, K17224, K17225, K17226, K17227	c_000000706726	PROKKA_462551, PROKKA_462550, PROKKA_462556, PROKKA_462554, PROKKA_462553	86.84	23.56	113.32	3912.23	41.40	50.50	30.75	40.31	31340.39	3.33	1.26	3.45	24.01	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
soxX	K17223, K17224, K17225, K17226, K17227	c_000000988538	PROKKA_644392, PROKKA_644391, PROKKA_644398, PROKKA_644395, PROKKA_644394	103.03	49.64	10491.04	9.73	132.45	65.75	15.78	46.11	26.28	3.70	7.22	66.72	46.57	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Acidovorax sp. KKS102
soxB	K17224	c_000000339213	PROKKA_257126	6929.75	2302.17	1406.22	10.60	61366.05	6093.68	12.73	6671.63	144.21	1157.68	0.00	14012.84	6022.29	Bacteria	Proteobacteria	Gammaproteobacteria				
soxB	K17224	c_000001045896	PROKKA_712449	33876.63	11297.80	9458.50	110.24	75658.12	25400.59	37.85	9232.19	201.70	10613.45	8.09	45045.78	28452.53	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales			
soxYZ	K17226, K17227	c_000000172352	PROKKA_148392, PROKKA_148393	8635.10	2850.19	2092.54	36.09	61874.45	16445.90	4.82	8624.51	102.69	170.98	7.96	61942.65	39979.50	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
soxYZ	K17226, K17227	c_000000423099	PROKKA_275779, PROKKA_275778	24.70	15.86	16.85	20.89	7.52	25.21	16.17	1.23	1.17	0.00	2.00	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylovorus	
soxY	K17226	c_000000440997	PROKKA_319797	10.53	5.07	4.44	9.84	16.83	6.83	5.91	0.00	0.00	0.00	5.05	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales			
soxYZ	K17226, K17227	c_000000563897	PROKKA_358335, PROKKA_358334	0.00	0.00	11.34	465.26	0.00	0.00	1.31	5.89	7495.40	0.00	0.00	0.00	1.73	Bacteria	Proteobacteria					
soxYZ	K17226, K17227	c_000000564326	PROKKA_374123, PROKKA_374124	13683.58	4092.42	2117.62	29.05	14828.92	8426.94	18.10	2194.42	75.37	2194.07	0.00	409.72	1435.20	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
soxY	K17226	c_000000596759	PROKKA_422048	0.00	0.00	0.00	0.00	781.54	636.12	0.00	85.10	12.58	0.00	0.00	114544.35	0.00							
soxYZ	K17226, K17227	c_000000601491	PROKKA_424590, PROKKA_424589	205384.17	56861.67	24071.25	281.21	9431.76	109784.92	35.57	895.19	372.60	73227.38	0.00	0.00	4891.69	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Acidovorax	Acidovorax sp. KKS102
soxYZ	K17226, K17227	c_000000903751	PROKKA_623776, PROKKA_623777	56600.97	18356.68	8188.31	75.52	85444.31	34611.89	52.99	9071.24	314.86	2032.36	0.00	16491.97	9409.28	Bacteria	Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	Polaromonas	
soxY	K17226	c_000000988678	PROKKA_651867	28.31	13.27	17.13	16.75	4.71	22.14	18.31	0.54	0.00	0.00	6.11	0.00	0.15	Bacteria	Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	Methylovorus	
soxYZ	K17226, K17227	c_000000993711	PROKKA_675067, PROKKA_675066	24.39	5.87	6.43	25.62	0.00	15.80	10.26	0.00	20.50	0.00	31.44	0.00	0.00	Bacteria	Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	Thauera	
soxZ	K17227	c_000000026914	PROKKA_53495	0.00	0.00	22.16	78.26	25.19	0.00	70.74	5.30	23.56	0.00	0.00	0.00	8574.64	Bacteria	Proteobacteria	Gammaproteobacteria				

Table S14 - *dsrB* Phylogenetic Tree Data

PROKKA	Contig	Site	# aa	Included in tree
>PROKKA_539303 hydrogensulfite reductase	c_000000774717	CROMO	368	y
>PROKKA_587390 hydrogensulfite reductase	c_000000853312	CROMO	368	y
>PROKKA_06633 sulfite reductase, dissimilatory-type beta subunit	c_000000000103	CROMO	356	y
>PROKKA_135376 dsrA; sulfite reductase, dissimilatory-type, beta subunit	c_000000155579	CROMO	85	n
>PROKKA_192589 sulfite reductase, dissimilatory-type beta subunit	c_000000282889	CROMO	357	y
>PROKKA_196277 sulfite reductase, dissimilatory-type beta subunit	c_000000282982	CROMO	357	y
>PROKKA_210994 dsrB; dissimilatory-type sulfite reductase subuit beta	c_000000284787	CROMO	356	y
>PROKKA_213122 sulfite reductase, dissimilatory-type beta subunit	c_000000285367	CROMO	395	y
>PROKKA_224266 sulfite reductase, dissimilatory-type beta subunit	c_000000290566	CROMO	295	n
>PROKKA_326785 dsrB; dissimilatory sulfite reductase subunit B	c_000000449980	CROMO	122	n
>PROKKA_330124 sulfite reductase, dissimilatory-type beta subunit	c_000000455538	CROMO	357	y
>PROKKA_349922 sulfite reductase, dissimilatory-type beta subunit	c_000000516947	CROMO	82	n
>PROKKA_357997 sulfite reductase, dissimilatory-type beta subunit	c_000000563866	CROMO	358	y
>PROKKA_359048 dsrB; sulfite reductase, dissimilatory-type subunit beta	c_000000563943	CROMO	356	y
>PROKKA_444110 sulfite reductase, dissimilatory-type beta subunit	c_000000669909	CROMO	44	n
>PROKKA_451956 sulfite reductase beta subunit	c_000000706274	CROMO	197	n
>PROKKA_458891 dsrB; dissimilatory sulfite reductase subunit B	c_000000706678	CROMO	354	y
>PROKKA_473929 sulfite reductase, dissimilatory-type beta subunit	c_000000706981	CROMO	392	y
>PROKKA_498108 dissimilatory sulfite reductase beta subunit	c_000000711526	CROMO	357	y
>PROKKA_539296 dissimilatory sulfite reductase beta subunit	c_000000774717	CROMO	352	y
>PROKKA_16556 sulfite reductase, dissimilatory-type beta subunit	contig-42395000000	LCY H08	61	n
>PROKKA_17090 dissimilatory sulfite reductase subunit B	contig-46854000000	LCY H08	55	n
>PROKKA_21790 dsrB; dissimilatory-type sulfite reductase subuit beta	contig-2000003	LIG	356	y
>PROKKA_42088 sulfite reductase, dissimilatory-type beta subunit	contig-14436000005	LIG	382	y
>PROKKA_81017 sulfite reductase, dissimilatory-type beta subunit	contig-6808000011	LIG	353	y

aa = amino acids; cutoff = 352 aa
LCY = Lost City; LIG = Liguria