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Supplement of

Organic iron-binding ligands mediate dissolved-particulate exchange in hydrothermal vent plumes along the Mid-Atlantic Ridge

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Introduction

Section S1 briefly describes the methodology used to quantify sulfide concentrations in the supplemental figures S6 and S7. Table S1 reports reference material values quantified through the dilution and seaFAST preconcentration methods. Tables S2–S5 report the dissolved and soluble metal concentrations and Fe speciation measurements for each incubation. Table S6 presents the Fe isotope data from the two large incubations (Rainbow near-field and TAG) and the respective dFe concentrations from that quantification. Figure S1 shows the CTD trace and depth at which each incubation was initiated at the study site. Figures S2-S5 display the size-fractionated manganese and vanadium concentrations within the incubation experiments. Figures S6 and S7 show the H_2S concentrations measured in two incubations at Lucky Strike and Rainbow near-field. Figures S8–S10 display the 16S data from the Rainbow near-field, Lucky Strike, and Rainbow far-field incubations.

S1. *Sulfide concentrations for Lucky Strike and Rainbow near-field*

Sulfide concentrations were measured onboard via stripping voltammetry using a three-electrode set-up (A/AgCl/KCl 3 M reference electrode, carbon auxiliary electrode, and Au/Ag mercury amalgam working 10-25 μm wire electrodes) incorporated into a flow cell. A deposition potential of -0.5 V, selective to sulfide species, was applied under vibrations for 10-300s depending on the initial concentration. Stripping was done in the differential pulse mode (typically 50 mV amplitude, 6 mV step, 100 ms interval, 8 ms pulse time) by scanning the potential from -0.2 to -1.1 V. Quantification of the resulting peak was conducted using a method of standard addition.

		Metal (nM)		
Method		V	Mn	Fe
seaFAST	Blank	0.057	0.002	0.073
	LoD(*n*=6)	0.073	0.002	0.050
	SaFe D2 (*n*=8)	33.96 ± 0.74	0.42 ± 0.05	0.991 ± 0.042
	Consensus	-	0.36 ± 0.05	0.956 ± 0.024
	NASS-7 (*n*=9)	25.42 ± 1.04	13.79 ± 0.52	6.22 ± 0.18
	Consensus	25.52 ± 1.57	13.65 ± 0.38	6.18 ± 0.27
Dilution	Blank	0.81	0.03	0.35
	LoD (*n*=6)	1.13	0.04	0.09
	CASS-6 (*n*=24)	11.68 ± 1.21	38.23 ± 2.44	29.11 ± 4.17
	Consensus	9.8 ± 2.35	40.4 ± 2.18	27.86 ± 2.14

Table S1. Table of blanks, limit of detection (LoD), and reference material values measured using seaFAST-pico preconcentration system and dilution methods and the respective consensus value for each metal. SaFe D2 and NASS-7 were used to evaluate the accuracy of the seaFAST-pico system and CASS-6 was used to evaluate the dilution method.

Rainbow near-field

Treatment	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered
Time (day)	0.1	0.2	0.4	0.6	1.1	2.1	3.3	5.6	7.3
dFe (nM)	361.3 ± 0.5	398.5 ± 22.6	236.3 ± 8.9	226.9 ± 10	415.8 ± 3.1	197.2 ± 21.7	136.6 ± 8.7	241.3 ± 6.1	nda
sFe (nM)	70.9 ± 4.6	§	95.9 ± 4.1	196.8 ± 10.1	29.7 ± 3.8	14.7 ± 1.1	11.7 ± 1.1	nda	5.75 ± 0.36
Colloidal %	80.4 ± 1.3	NA	59.4 ± 4.2	13.3 ± 5.3	92.8 ± 1.3	92.6 ± 11	91.5 ± 6.4	nda	nda
TDFe (nM)	nda	5217 ± 128	5067 ± 170	5125 ± 207	5110 ± 132	4930 ± 377	nda	nda	nda
dMn (nM)	473 ± 9	472 ± 17	481 ± 9	476 ± 8	473 ± 3	482 ± 10	466 ± 16	486 ± 17	nda
sMn (nM)	482 ± 8	475 ± 17	487 ± 12	480 ± 15	484 ± 24	487 ± 5	484 ± 9	nda	496 ± 15
TDMn (nM)	nda	456 ± 13	455 ± 22	458 ± 14	459 ± 14	468 ± 10	nda	nda	nda
dV (nM)	14.69 ± 0.51	14.16 ± 1.84	14.88 ± 0.21	14.91 ± 2.07	13.4 ± 0.8	13.13 ± 0.39	11.12 ± 0.64	11.49 ± 0.4	nda
sV (nM)	14.70 ± 0.01	16.95 ± 2.11	13.75 ± 1.01	14.59 ± 0.63	12.98 ± 0.23	11.53 ± 0.01	13.08 ± 0.17	nda	12.44 ± 1.61
TDV (nM)	nda	29.17 ± 3.64	30.26 ± 2.65	28.97 ± 1.18	28.89 ± 0.92	nda	nda	nda	nda
dL (nM)	*64.4 ± 1.4	*50.6 ± 0.9	*60.0 ± 1.7	*52.0 ± 1.3	*74.1 ± 3.9	*32.8 ± 0.4	*39.4 ± 0.8	*29.2 ± 0.6	*37.2 ± 0.5
$\log K^{cond}_{FedL,Fe'}$	11.82 ± 0.20	11.92 ± 0.16	10.97 ± 0.19	11.74 ± 0.21	10.61 ± 0.34	12.18 ± 0.12	12.12 ± 0.19	12.20 ± 0.18	12.12 ± 0.12
sL (nM)	5.37 ± 0.53	§	2.85 ± 0.98	*14.88 ± 0.89	7.53 ± 0.45	5.23 ± 0.16	4.88 ± 1.19	nda	8.57 ± 0.49
$\log K^{cond}_{FesL,Fe'}$	10.24 ± 0.53	§	10.04 ± 1.57	10.16 ± 0.35	10.80 ± 0.40	11.82 ± 0.28	11.78 ± 0.21	nda	12.10 ± 0.15
Treatment	filtered	filtered	filtered	filtered	filtered	filtered	filtered	filtered	filtered
Time (day)	0.1	0.2	0.4	0.6	1.1	2.1	3.3	5.6	7.3
dFe (nM)	311.5 ± 6.1	252.1 ± 3.5	226.8 ± 10.9	250.9 ± 5.7	105.9 ± 5.7	40.5 ± 9	83.8 ± 3.6	94.7 ± 4.3	nda
sFe (nM)	94.1 ± 5.9	4.68 ± 0.03	62.9 ± 6.2	5.12 ± 0.48	63.3 ± 6.4	4.13 ± 0.09	2.54 ± 0.86	nda	1.91 ± 0.12
Colloidal %	69.8 ± 2.7	98.1 ± 1.4	72.3 ± 5.5	98 ± 2.3	40.2 ± 8.1	89.8 ± 22	97 ± 4.5	nda	nda
TDFe (nM)	nda	363.3 ± 17.3	357.8 ± 8.9	365 ± 19.3	352.4 ± 7.9	340.1 ± 20.3	nda	147.1 ± 8.9	nda
dMn (nM)	494.2 ± 6.7	511.8 ± 8.9	501.1 ± 15.8	506.8 ± 15.4	503.5 ± 11.6	511.5 ± 15.4	501 ± 27	505.6 ± 9.9	nda
sMn (nM)	504 ± 13	495 ± 23	507 ± 28	512 ± 14	510 ± 17	507 ± 19	510 ± 16	nda	515 ± 5
TDMn (nM)	nda	473 ± 15	488 ± 26	486 ± 15	489 ± 18	475 ± 8	nda	491 ± 15	nda
dV (nM)	15.08 ± 1.6	14.12 ± 1.94	15.46 ± 0.41	15.12 ± 0.19	16.43 ± 2.16	14.52 ± 0.97	13.46 ± 0.57	13.82 ± 0.46	nda
sV (nM)	16.14 ± 0.08	14.32 ± 0.15	15.54 ± 0.07	15.52 ± 0.51	15.7 ± 0.51	14.68 ± 0.82	14.72 ± 0.25	nda	15.37 ± 0.04
TDV (nM)	nda	14.87 ± 1.61	15.13 ± 0.66	14.37 ± 1.74	13.98 ± 0.68	13.89 ± 0.46	nda	13.42 ± 0.87	nda
dL (nM)	*45.8 ± 0.8	*47.3 ± 0.5	*52.0 ± 1.3	*45.7 ± 0.7	51.4 ± 1.0	nda	34.7 ± 1.2	28.4 ± 0.4	34.1 ± 0.6
$\log K^{cond}_{FedL,Fe'}$	11.90 ± 0.15	11.98 ± 0.09	11.74 ± 0.21	11.96 ± 0.15	11.84 ± 0.17	nda	11.90 ± 0.28	12.30 ± 0.13	12.22 ± 0.16
sL (nM)	3.57 ± 0.40	1.13 ± 0.16	6.10 ± 0.17	2.98 ± 0.21	6.38 ± 0.21	9.27 ± 0.13	5.64 ± 0.35	nda	6.12 ± 0.11
$\log K^{cond}_{FesL,Fe'}$	10.12 ± 0.55	10.28 ± 0.63	11.58 ± 0.24	11.46 ± 0.56	11.70 ± 0.29	11.69 ± 0.32	12.04 ± 0.14	nda	11.51 ± 0.29

§ represents a sample that was identified as contaminated and have been removed.
* Indicates the sample was diluted for the reverse titration method

Table S2. Dissolved ("d"), soluble ("s"), and total dissolvable ("TD") metal concentrations and speciation measured over the Rainbow near-field incubation study. Each time point of the unfiltered and filtered treatments is presented as the average ± standard deviation determined from replicate measurements or ± average relative standard deviation of all replicates measured. Percent colloidal fractions represent ([dissolved M]-[soluble M])/[dissolved M]) x 100. Ligand concentrations and conditional stability constants are presented with the included error given from the R model or ProMCC titration fitting results. 'nda' indicates 'no data available', no samples were collected or lost.

TAG

Treatment	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered
Time (days)	0.06	0.2	0.3	0.6	1.1	2.1	3.1	5.2	6.1
dFe (nM)	187.8 ± 2.3	179.1 ± 7.8	148.5 ± 11.8	124.8 ± 3	139.1 ± 9.6	72.4 ± 6.8	87.9 ± 9.5	74.9 ± 7.3	61 ± 2.6
sFe (nM)	61.5 ± 8.2	52.9 ± 9.5	46.6 ± 3.7	44.2 ± 6.8	3.84 ± 0.13	18.6 ± 0.3	24.5 ± 3.2	16.7 ± 1.7	14.2 ± 0.7
Colloidal %	67.3 ± 9	70.5 ± 13.1	68.6 ± 7.7	64.6 ± 10	97.2 ± 7.5	74.3 ± 7	72.1 ± 12.2	77.7 ± 10.9	76.8 ± 5
TDFe (nM)	211.1 ± 9.3	nda	nda	nda	nda	nda	nda	nda	174 ± 2.1
dMn (nM)	38.5 ± 1.4	37.7 ± 1.6	40.3 ± 3.9	35.8 ± 2.3	36.1 ± 1.2	35.6 ± 1.6	38 ± 1.6	35.9 ± 2.2	36.5 ± 1.3
sMn (nM)	37.9 ± 0.6	37.7 ± 0.4	37.8 ± 1.6	37.1 ± 2.0	39.5 ± 1.6	37.8 ± 1.1	37.8 ± 1.5	39.6 ± 0.9	37.8 ± 2.5
TDMn (nM)	37.1 ± 1.17	nda	nda	nda	nda	nda	nda	nda	38.03 ± 1.43
dV (nM)	31.2 ± 1.5	32.5 ± 0.2	30.9 ± 2.7	29.2 ± 0.8	32.1 ± 1.1	29.6 ± 0.2	31.6 ± 1	31.7 ± 1.8	30.3 ± 0.6
sV (nM)	29.4 ± 0.6	32.3 ± 1.7	33.6 ± 0.3	29.4 ± 2.3	29.2 ± 2.6	32.6 ± 2.4	31.6 ± 0.2	31.3 ± 1.3	33.2 ± 3.0
TDV (nM)	32.3 ± 1	nda	nda	nda	nda	nda	nda	nda	32.3 ± 2
dL (nM)	nda	nda	*18.4 ± 1.1	*18.6 ± 1.4	*18.0 ± 0.7	13.0 ± 0.7	10.2 ± 0.3	9.3 ± 0.3	6.6 ± 0.4
$\log K^{cond}_{FedL,Fe'}$	nda	nda	10.24 ± 0.36	10.10 ± 0.46	10.21 ± 0.24	11.74 ± 0.55	11.60 ± 0.26	10.37 ± 0.16	11.06 ± 0.46
sL (nM)	nda	8.27 ± 0.76	11.18 ± 0.53	8.64 ± 0.68	4.48 ± 0.27	5.03 ± 0.12	4.17 ± 0.21	6.31 ± 0.28	7.69 ± 0.09
$\log K^{cond}_{FesL,Fe'}$	nda	10.04 ± 0.49	10.59 ± 0.31	10.92 ± 0.59	12.46 ± 0.28	11.82 ± 0.22	11.28 ± 0.35	11.04 ± 0.30	11.43 ± 0.10
Treatment	filtered	filtered	filtered	filtered	filtered	filtered	filtered	filtered	filtered
Time (days)	0.06	0.2	0.3	0.6	1.1	2.1	3.1	5.2	6.1
dFe (nM)	82.4 ± 0.6	74.2 ± 0.4	79.5 ± 7.9	74.7 ± 2.4	68.9 ± 7.6	29.6 ± 3.8	60.1 ± 5.4	34.7 ± 8.6	13.6 ± 3.9
sFe (nM)	19.13 ± 2.33	12.25 ± 0.68	7.41 ± 0.13	6.76 ± 0.18	12.3 ± 1.22	14.25 ± 0.89	10.84 ± 1.23	1.44 ± 0.09	6.27 ± 0.69
Colloidal %	76.8 ± 9.4	83.5 ± 4.7	90.7 ± 9.2	91 ± 3.8	82.1 ± 12.2	51.9 ± 7.5	82 ± 11.9	95.9 ± 24.4	53.8 ± 16.7
TDFe (nM)	86.3 ± 2.7	nda	nda	nda	nda	nda	nda	nda	80.1 ± 9.9
dMn (nM)	31.8 ± 0.3	32 ± 1	31.6 ± 1.4	30.8 ± 2.2	32.1 ± 0.8	31.5 ± 1.5	30.9 ± 1.9	31.5 ± 1.8	30.9 ± 0.6
sMn (nM)	31.8 ± 2.2	30.8 ± 0.9	32.1 ± 1.4	31.0 ± 0.9	31.2 ± 1.7	31.8 ± 0.9	30.4 ± 1.0	32.4 ± 1.6	31.7 ± 2.1
TDMn (nM)	30.37 ± 1.17	nda	nda	nda	nda	nda	nda	nda	30.82 ± 1.26
dV (nM)	34.7 ± 0.6	33.3 ± 1.2	33.1 ± 0.02	34 ± 0.7	30.8 ± 0.2	33.2 ± 0.5	35.3 ± 2.6	34.4 ± 1.5	34.8 ± 0.4
sV (nM)	35.6 ± 0.04	36.0 ± 0.7	34.6 ± 0.1	33.6 ± 0.2	34.1 ± 0.3	35.0 ± 1.1	32.8 ± 0.2	34.9 ± 0.1	36.1 ± 0.9
TDV (nM)	31.9 ± 0.5	nda	nda	nda	nda	nda	nda	nda	31.5 ± 3.4
dL (nM)	5.97 ± 0.25	7.65 ± 1.72	10.81 ± 0.63	9.00 ± 0.84	11.80 ± 0.40	6.95 ± 0.25	9.68 ± 0.15	8.46 ± 0.29	7.03 ± 0.39
$\log K^{cond}_{FedL,Fe'}$	12.56 ± 0.59	10.04 ± 1.18	10.96 ± 0.43	10.22 ± 0.52	10.31 ± 0.20	11.10 ± 0.28	10.48 ± 0.09	10.62 ± 0.22	11.50 ± 0.47
sL (nM)	nda	9.9 ± 0.3	5.0 ± 0.2	7.1 ± 0.3	10.2 ± 0.4	8.8 ± 0.1	6.9 ± 0.2	nda	3.7 ± 0.4
$\log K^{cond}_{FesL,Fe'}$	nda	11.42 ± 0.29	10.7 ± 0.29	12.51 ± 0.31	11.58 ± 0.35	11.39 ± 0.12	11.56 ± 0.23	nda	11.46 ± 0.88

* Indicates the sample was diluted for the reverse titration method

Table S3. Dissolved ("d"), soluble ("s"), and total dissolvable ("TD") metal concentrations and speciation measured over the TAG near-field incubation study. Each time point of the unfiltered and filtered treatments is presented as the average ± standard deviation determined from replicate measurements or ± average relative standard deviation of all replicates measured. Percent colloidal fractions represent ([dissolved M]-[soluble M])/ [dissolved M]) x 100. Ligand concentrations and conditional stability constants are presented with the included error given from the R model or ProMCC titration fitting results. 'nda' indicates 'no data available', no samples were collected.

Lucky Strike

Treatment	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered
Time (days)	0.06	1.1	1.8	2.7	6.8	14.8	22.0
dFe (nM)	15.1 ± 1.17	16.71 ± 1.29	12.66 ± 0.98	12.45 ± 0.96	10.43 ± 0.81	12.91 ± 1.00	18.25 ± 1.41
sFe (nM)	4.42 ± 0.05	2.00 ± 0.54	1.69 ± 0.11	2.72 ± 1.86	4.13 ± 0.32	2.78 ± 0.11	4.55 ± 0.32
Colloidal %	70.8 ± 7.7	88.1 ± 8.4	86.7 ± 7.8	78.1 ± 16.9	60.4 ± 8.3	78.5 ± 7.8	75.1 ± 7.9
TDFe (nM)	18.6 ± 1.4	nda	nda	nda	22.5 ± 1.8	19 ± 1.5	20.5 ± 1.6
dMn (nM)	10.37 ± 0.4	10.71 ± 0.41	10.39 ± 0.4	10.62 ± 0.41	10.36 ± 0.4	9.88 ± 0.38	10.93 ± 1.46
sMn (nM)	10.51 ± 0.30	10.83 ± 0.52	10.98 ± 0.71	10.71 ± 0.59	11.52 ± 0.45	10.49 ± 0.33	10.99 ± 0.69
TDMn (nM)	10.51 ± 0.41	nda	nda	nda	10.17 ± 0.39	9.27 ± 0.36	11.16 ± 0.43
dV (nM)	31.6 ± 1.4	32.4 ± 1.4	30.2 ± 1.3	31.9 ± 1.4	30.6 ± 1.3	32.9 ± 1.4	31.5 ± 1
sV (nM)	30.9 ± 0.8	34.3 ± 2.2	32.4 ± 2.5	32.5 ± 1.8	35.6 ± 1.6	32.7 ± 0.5	33.4 ± 3.2
TDV (nM)	32.9 ± 1.4	nda	33.3 ± 1.5	nda	31.5 ± 0.2	29.6 ± 1.3	32.7 ± 1.4
dL (nM)	5.40 ± 0.12	4.89 ± 0.27	4.91 ± 0.03	5.63 ± 0.13	6.26 ± 0.12	7.75 ± 0.26	7.08 ± 0.19
$\log K^{cond}_{FedL,Fe'}$	11.66 ± 0.19	11.04 ± 0.39	11.02 ± 0.38	11.70 ± 0.17	11.60 ± 0.16	11.56 ± 0.26	11.56 ± 0.23
sL (nM)	6.00 ± 0.60	3.10 ± 0.20	2.68 ± 0.20	4.30 ± 0.32	6.52 ± 1.11	3.99 ± 0.13	4.74 ± 0.24
$\log K^{cond}_{FesL,Fe'}$	12.19 ± 0.31	12.11 ± 0.11	12.11 ± 0.18	12.12 ± 0.21	11.42 ± 0.31	11.91 ± 0.08	12.80 ± 0.38

Table S4. Dissolved ("d"), soluble ("s"), and total dissolvable ("TD") metal concentrations and speciation measured over the Lucky Strike incubation. Each time point of the unfiltered treatments is presented as the average ± standard deviation determined from replicate measurements or the average relative standard deviation of all replicates measured. Percent colloidal fractions represent ([dissolved M]-[soluble M])/ [dissolved M]) x 100. Ligand concentrations and conditional stability constants are presented with the included error given from the R model or ProMCC titration fitting results. 'nda' indicates 'no data available', no samples were collected.

Rainbow far-field

Treatment	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered	unfiltered
Time (days)	0.05	0.6	1.0	2.94	6.8	13.6	19.0
dFe (nM)	3.42 ± 0.26	3.04 ± 0.23	2.96 ± 0.23	5.85 ± 0.45	8.52 ± 0.65	6.78 ± 0.52	7.1 ± 0.54
sFe (nM)	0.88 ± 0.04	§	1.37 ± 0.04	1.21 ± 0.04	1.52 ± 0.01	7.95 ± 0.53	5.53 ± 0.04
Colloidal %	74.4 ± 6.5	nda	53.6 ± 4.4	79.3 ± 6.5	82.1 ± 6.3	-17.3 ± -1.8	22.1 ± 1.7
TDFe (nM)	30.1 ± 2.3	nda	25.5 ± 1.9	28.9 ± 2.2	nda	nda	17.7 ± 2.6
dMn (nM)	2.53 ± 0.1	2.58 ± 0.1	2.37 ± 0.09	2.48 ± 0.1	2.44 ± 0.09	2.36 ± 0.09	2.47 ± 0.1
sMn (nM)	2.45 ± 0.02	2.51 ± 0.06	2.52 ± 0.09	2.54 ± 0.13	2.38 ± 0.13	2.51 ± 0.08	2.45 ± 0.15
TDMn (nM)	2.46 ± 0.1	nda	2.21 ± 0.09	1.62 ± 0.06	nda	nda	2.28 ± 0.39
dV (nM)	36.3 ± 1.6	36.6 ± 1.6	34.3 ± 1.5	34.5 ± 1.5	35 ± 1.5	33.7 ± 1.5	35.2 ± 1.5
sV (nM)	33.1 ±1.9	34.1 ± 0.5	34.5 ± 0.7	33.1 ± 0.4	32.8 ± 2.0	34.0 ± 0.1	32.9 ± 0.1
TDV (nM)	33 ± 1.4	nda	31.2 ± 1.4	31.2 ± 1.4	nda	nda	32.5 ± 3.2
dL (nM)	1.55 ± 0.12	1.88 ± 0.07	2.90 ± 0.11	5.56 ± 0.22	5.41 ± 0.17	5.66 ± 0.09	5.11 ± 0.09
$\log K^{cond}_{FeL,Fe'}$	10.52 ± 0.38	11.54 ± 0.27	10.81 ± 0.21	11.54 ± 0.33	11.72 ± 0.27	11.58 ± 0.14	11.72 ± 0.16
sL (nM)	bd	§	1.64 ± 0.31	2.49 ± 0.37	2.09 ± 0.14	3.09 ± 0.12	2.74 ± 0.09
$\log K^{cond}_{FeL,Fe'}$	bd	§	11.99 ± 0.18	11.82 ± 0.24	12.59 ± 0.28	11.14 ± 0.24	11.26 ± 0.22

§ represents a sample that was identified as contaminated from the TDFe phase and has been removed.

Table S5. Dissolved ("d"), soluble ("s"), and total dissolvable ("TD") metal concentrations and speciation measured over the Rainbow far-field incubation study. Each time point of the unfiltered treatments is presented as the average ± standard deviation from replicate measurements or ± average relative standard deviation of all replicates measured. Percent colloidal fractions represent ([dissolved M]-[soluble M])/ [dissolved M]) x 100. Ligand concentrations and conditional stability constants are presented with the included error given from the R model or ProMCC titration fitting results. 'nda' indicates 'no data available', no samples were collected. 'bd' indicates sample appeared saturated in the forward titration CLE-AdCSV method and below detection limits of the reverse titration method.

Sample description	Time (days)	δ^{56}dFe (‰)	2SD (‰)	dFe (nM)
TAG				
Filtered	0.2	-1.43	0.03	75.2
Filtered	1.1	-1.34	0.09	84.2
Filtered	5.2	-1.35	0.05	21
Unfiltered	0.2	0.58	0.03	149.6
Unfiltered	1.1	0.09	0.02	162.3
Unfiltered	5.2	3.57	0.01	73.5
Rainbow near-field				
Filtered	0.1	-7.34	0.03	280.4
Filtered	0.6	-7.45	0.02	206
Filtered	5.6	-7.14	NA	47
Unfiltered	0.1	0.76	0.04	345.6
Unfiltered	0.6	-0.16	0.03	202.9
Unfiltered	5.6	1.17	NA	175

Table S6. Dissolved Fe (dFe) isotope measurements for selected samples from the TAG and Rainbow near-field incubations. Presented are three timepoints for each treatment (filtered and unfiltered) for the TAG and Rainbow incubations displaying the ^{56}dFe and the dFe concentration quantified from the sample's measurement. NA = not available; here 2SD is the uncertainty on two or three MC-ICP-MS measurements of the same sample.

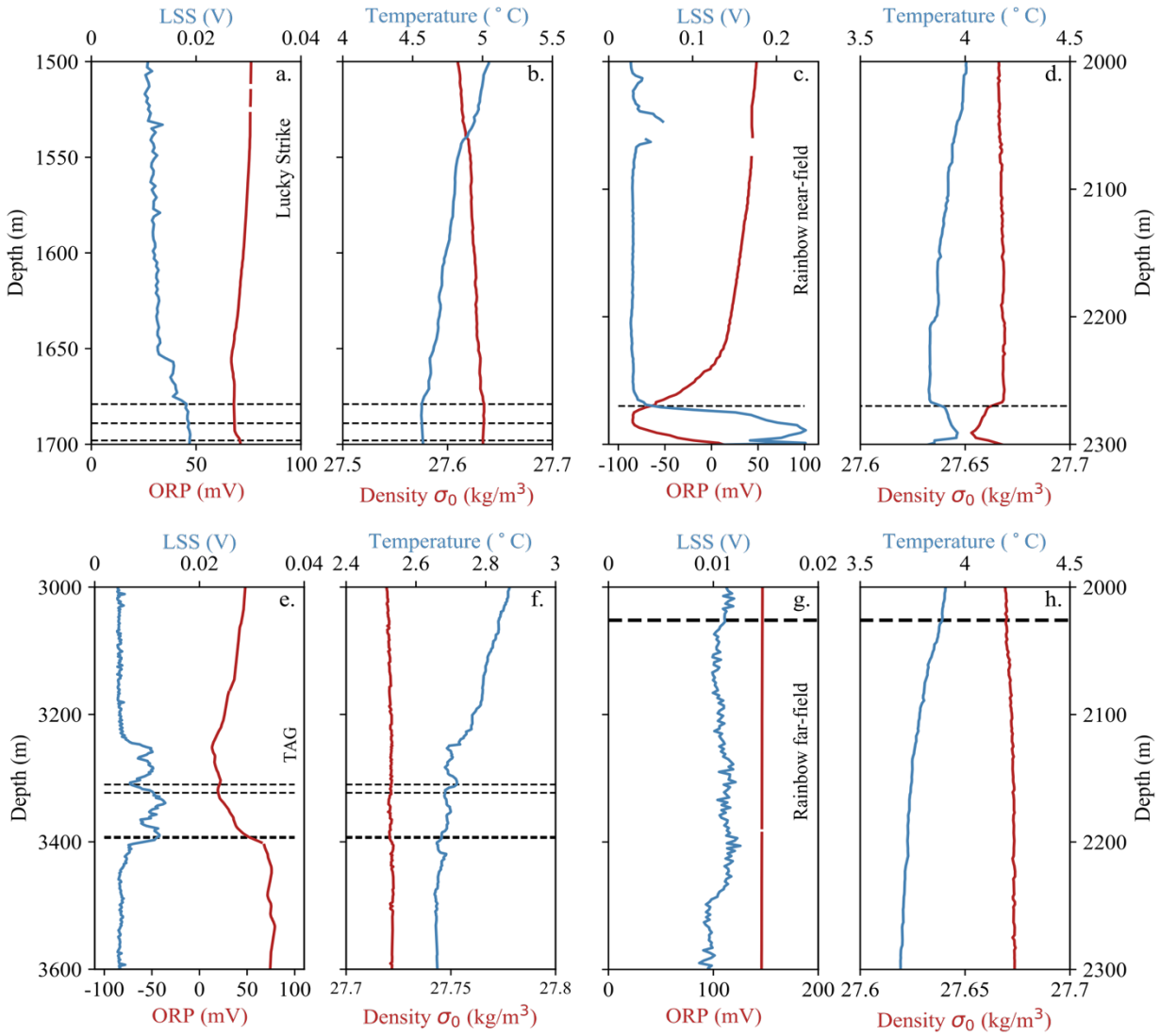

Figure S1. Hydrothermal vent system overview of the incubations CTD profiles that initiated each incubation. Plotted the CTD profiles for each of the four hydrothermal incubations, Lucky Strike (a, b), Rainbow near-field (c, d), TAG (e, f), and Rainbow far-field (g, h). Each profile displays the light scatter sensor (LSS) data, a proxy for particles, the oxidation-reduction potential (ORP) sensor data, a proxy for reduced chemical species, the temperature data, and potential density (σ_0) of each cast where water was collected. Dashed lines indicate the depth(s) that bottles were closed and used as the starting point of each incubation

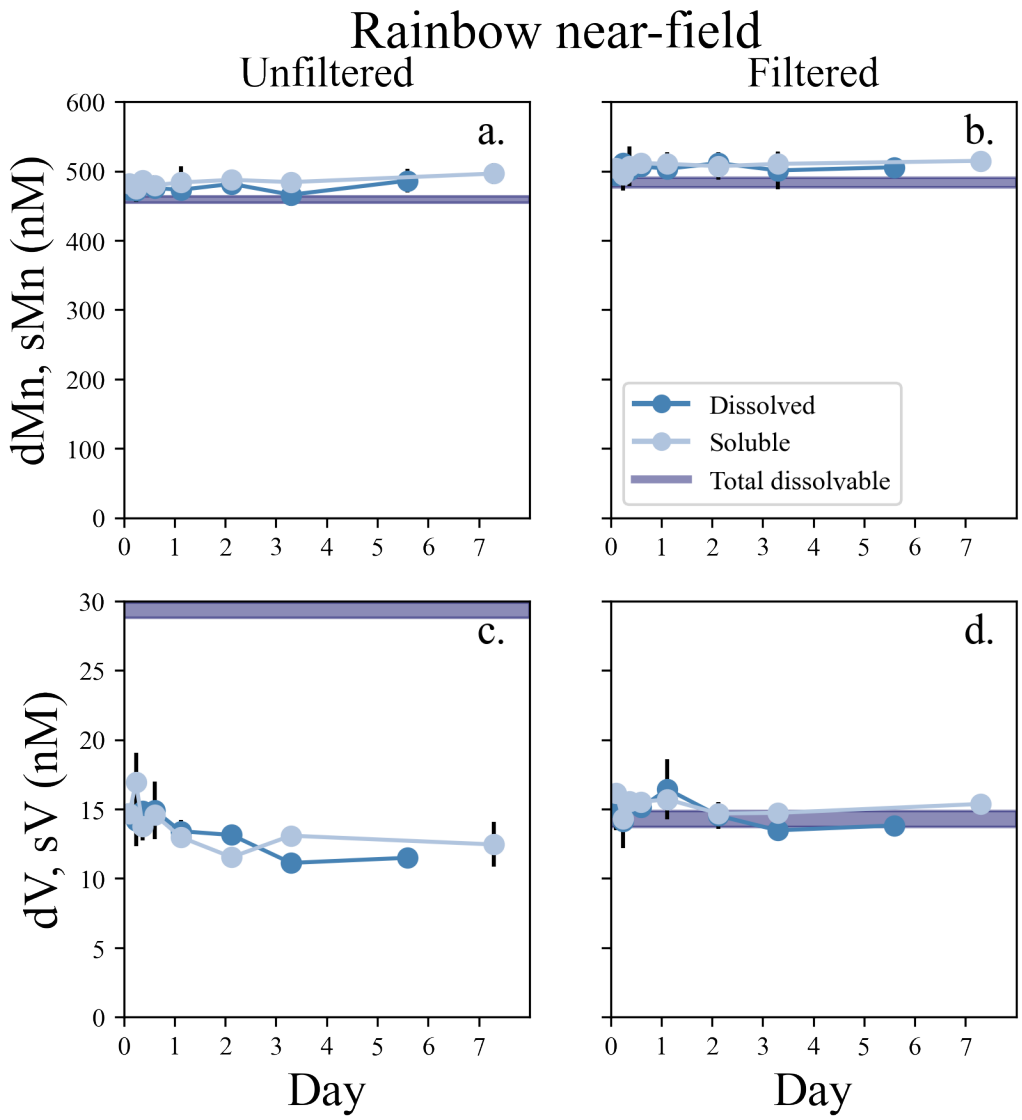

Figure S2. Dissolved, soluble, and total dissolvable manganese (Mn) and vanadium (V) concentrations in the Rainbow buoyant plume incubation. Presented are the soluble (<0.02 µm) fraction (light blue circles) and dissolved (<0.2 µm) fraction (dark blue circles) concentrations for Mn (a, b) and V (c, d) in the unfiltered and filtered treatments. The blue band represents the average ± the standard deviation of all total dissolvable (unfiltered, acidified) from every sample taken in the incubation (*n*=5).

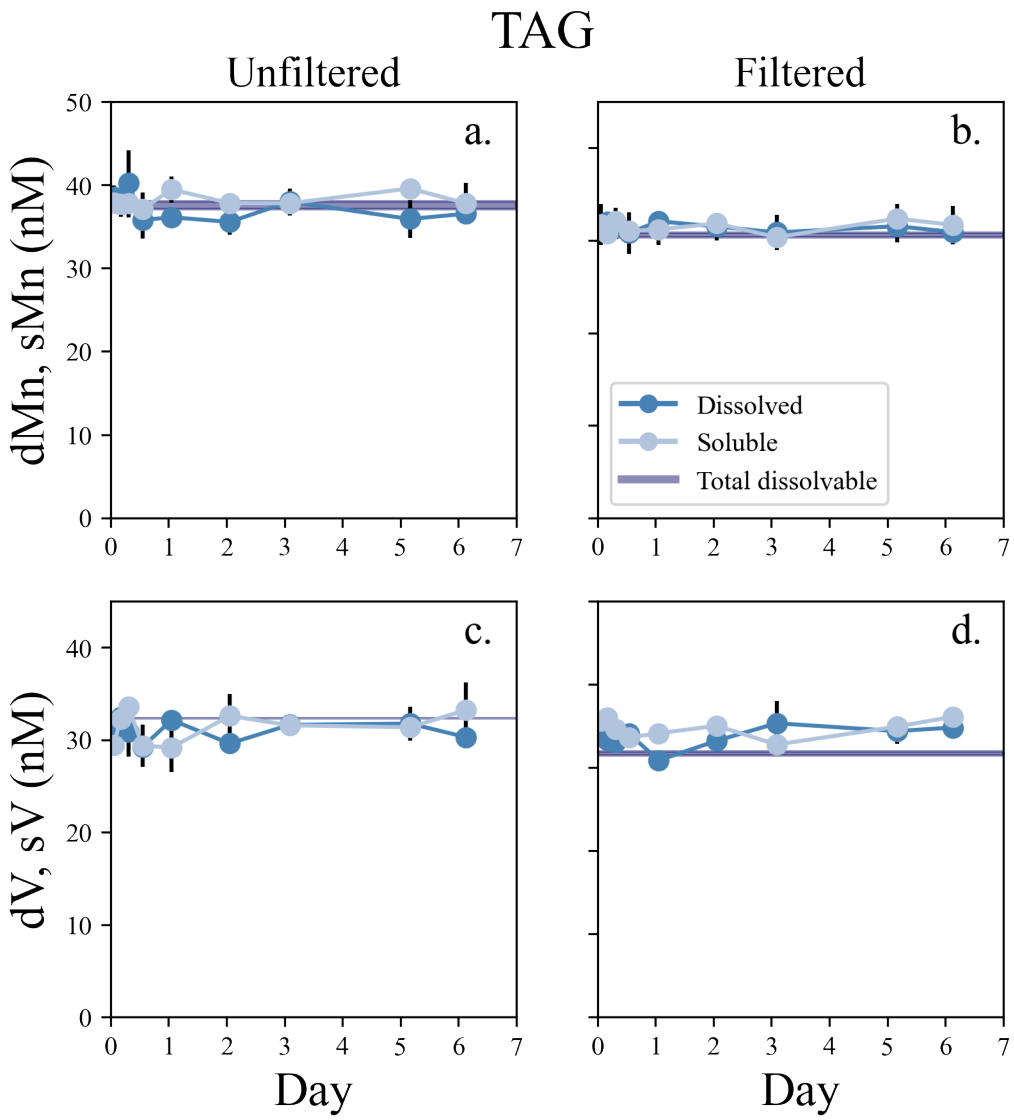

Figure S3. Dissolved, soluble, and total dissolvable manganese (Mn) and vanadium (V) concentrations in the TAG neutrally buoyant plume incubation. Presented are the soluble (<0.02 µm) fraction (light blue circles) and dissolved (<0.2 µm) fraction (dark blue circles) concentrations for Mn (a, b) and V (c, d) in the unfiltered and filtered treatments. The blue band represents the average ± the standard deviation of all total dissolvable (unfiltered, acidified) from every sample taken in the incubation (*n*=2).

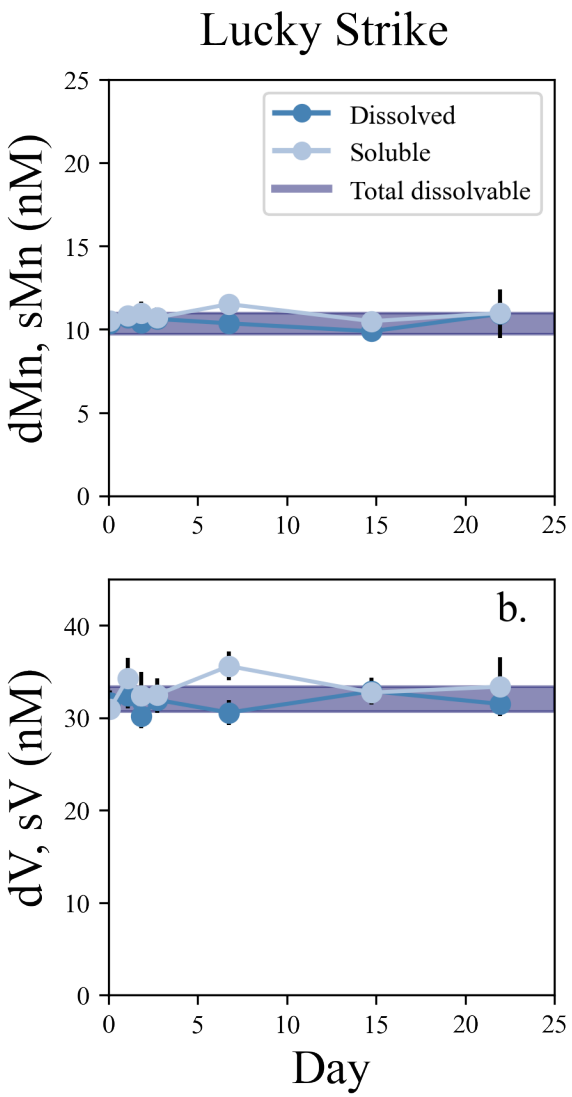

Figure S4. Dissolved, soluble, and total dissolvable manganese (Mn) and vanadium (V) concentrations in the Lucky Strike neutrally buoyant plume incubation. Presented are the soluble (<0.02 µm) fraction (light circles) and dissolved (<0.2 µm) fraction (dark blue circles) concentrations for Mn (a) and V (b) in the unfiltered and filtered treatments. The blue band represents the average ± the standard deviation of all total dissolvable (unfiltered, acidified) from every sample taken in the incubation (*n*=4).

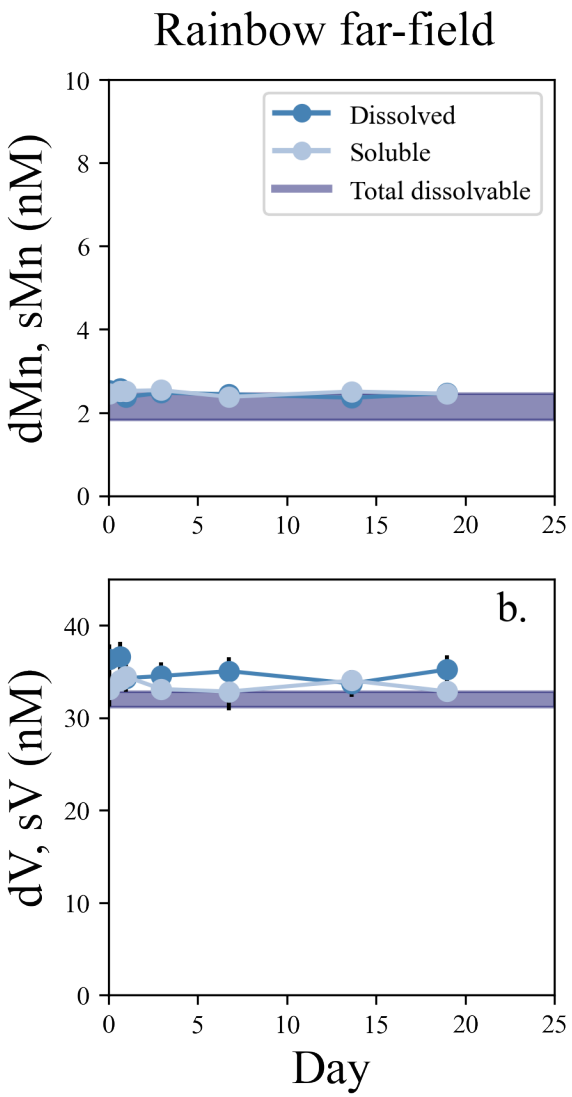

Figure S5. Dissolved, soluble, and total dissolvable manganese (Mn) and vanadium (V) concentrations in the Rainbow neutrally buoyant plume incubation. Presented are the soluble (<0.02 μm) fraction (light circles) and dissolved (<0.2 μm) fraction (dark blue circles) concentrations for Mn (a) and V (b) in the unfiltered and filtered treatments. The blue band represents the average ± the standard deviation of all total dissolvable (unfiltered, acidified) from every sample taken in the incubation (*n*=4).

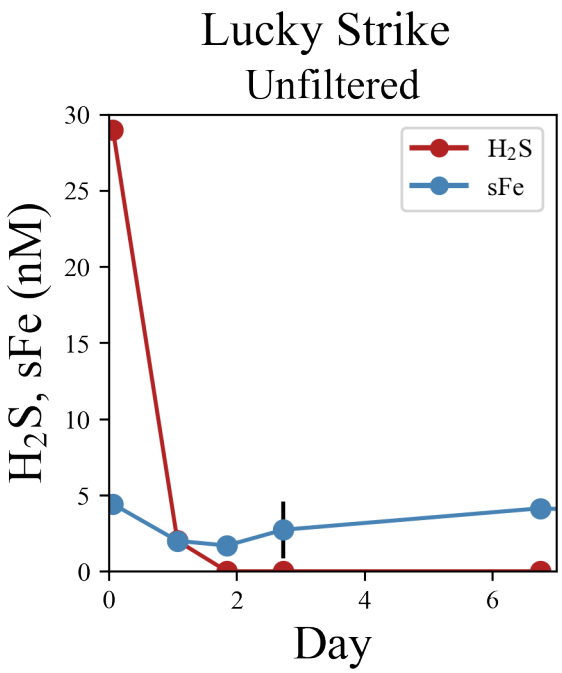

Figure S6. Hydrogen sulfide concentrations in the Lucky Strike incubation. Presented are the dissolved (<0.2 μm) sulfide concentrations (blue circles) plotted with the soluble (<0.02 μm) Fe concentrations (red circles) for the unfiltered treatment.

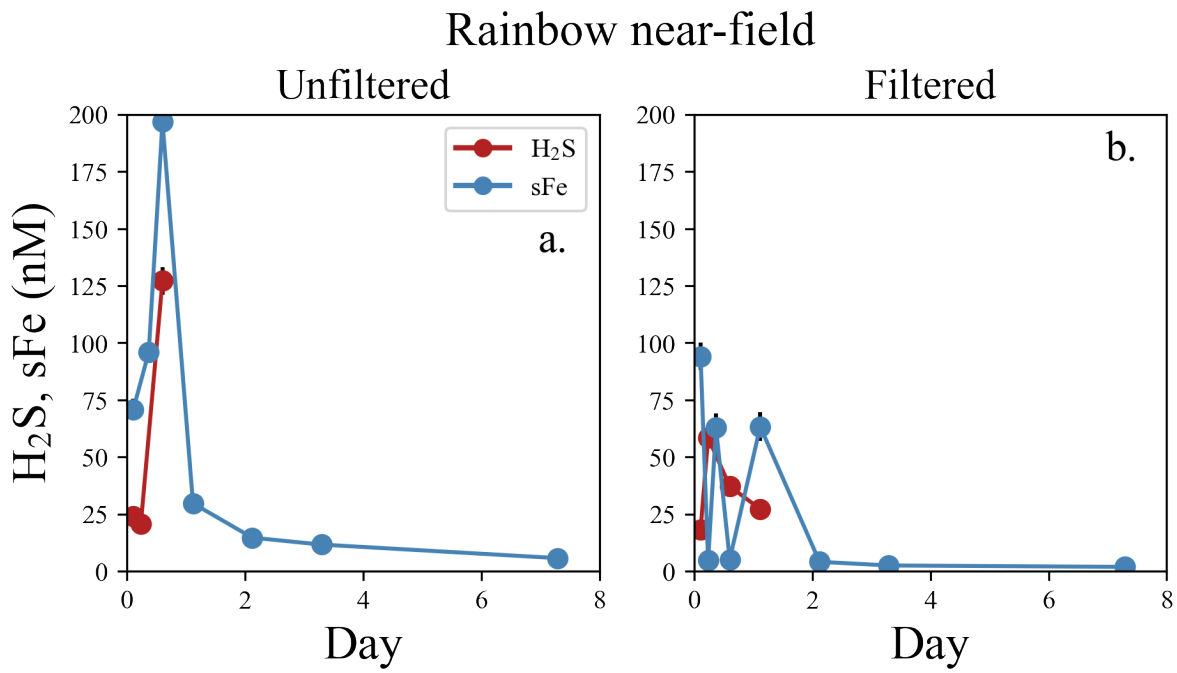

Figure S7. Hydrogen sulfide concentrations in the Rainbow near-field incubation. Presented are the dissolved (<0.2 µm) hydrogen sulfide concentrations (blue circles) plotted with the soluble (<0.02 µm) Fe concentrations (red circles) for the unfiltered (left) and filtered (right) treatments.

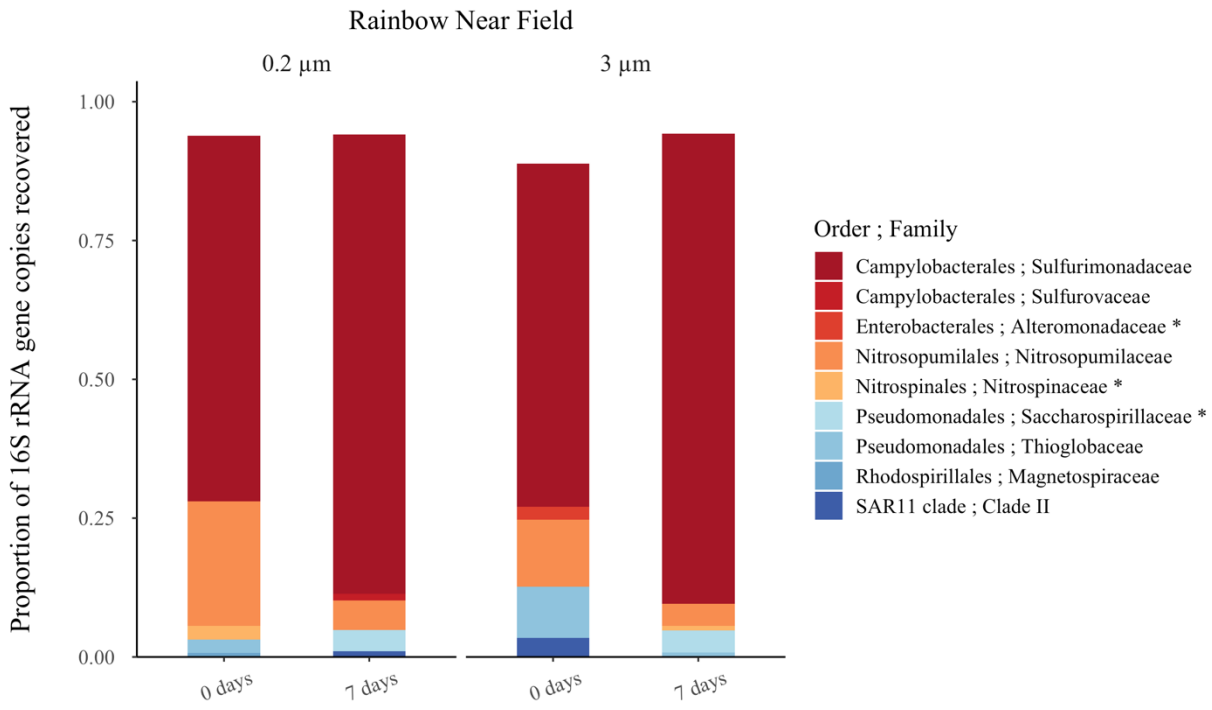

Figure S8. Rainbow near-field incubation microbial community composition. The relative abundance of the top 5 families from each sample as determined by 16S rRNA gene amplicon sequencing, were used for the stacked bar charts displays their relative abundance at day 0 and day 7 of the incubation for both the 0.2 µm and 3 µm filter fractions. *Indicates families that have members capable of producing siderophores.

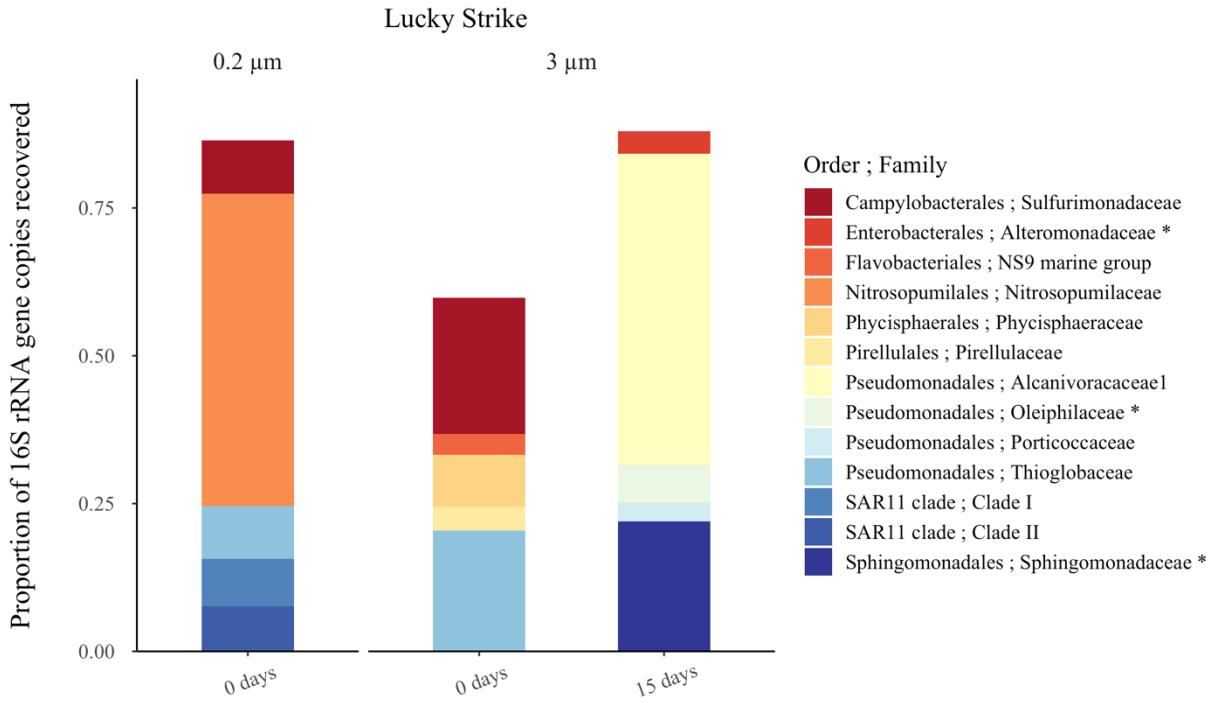

Figure S9. Lucky Strike neutrally buoyant plume microbial community response. Presented are stacked bar charts indicating the relative abundance of the top 5 families in each sample as determined by 16S rRNA gene amplicon sequencing. The chart displays the relative abundance of each family at day 0 and day 15 of the incubation for both 0.2 µm and 3 µm filter fractions measured. No data is available for the 0.2 µm sample on day 15. *Indicates families that have members capable of biosynthesizing siderophores.

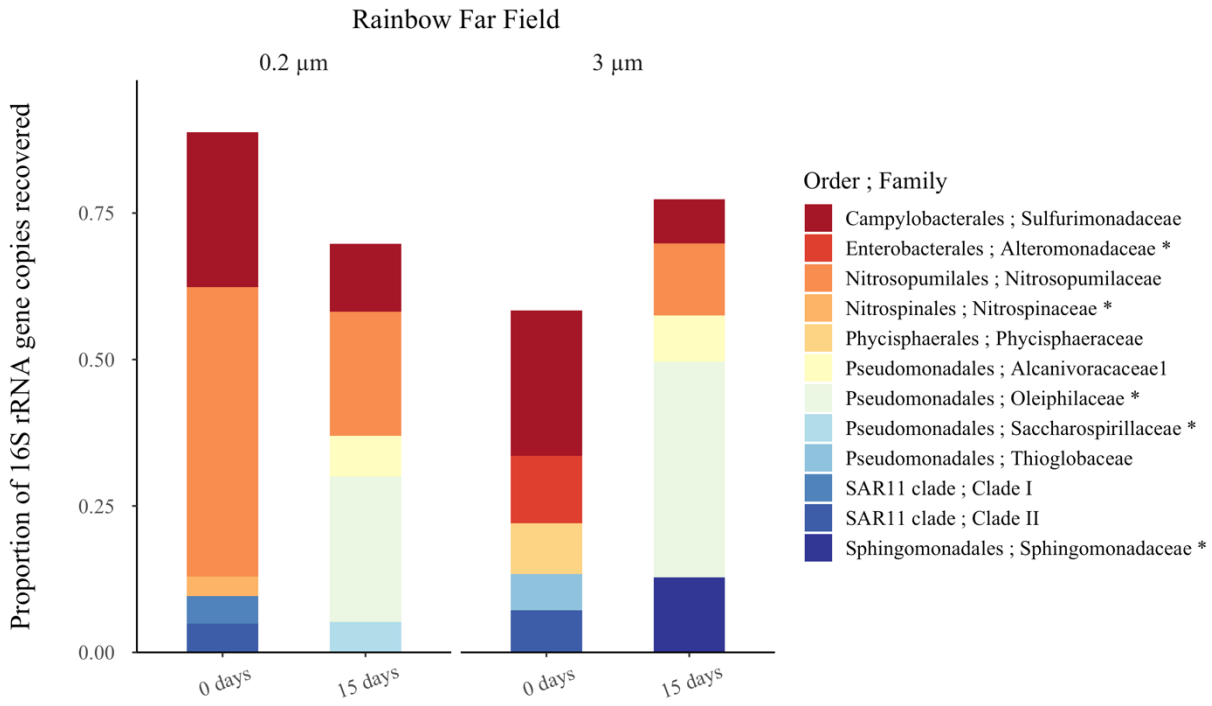

Figure S10. Rainbow neutrally buoyant plume microbial community response. Presented are stacked bar charts indicating the relative abundance of the top 5 families in each sample as determined by 16S rRNA gene amplicon sequencing. The chart displays the relative abundance of each family at day 0 and day 15 of the incubation for both the 0.2 µm and 3 µm filter fractions measured. *Indicates families that have members capable of biosynthesizing siderophores.