

Supplemental Materials

Supplementary Tables

Table S1. BTEX, cycloalkanes, and PAH concentrations in the distal and proximal plume samples, including, when determined, the range of concentrations over the plume intervals.

	Depth (mbsl)	Total alkanes (ug/L)	Cyclohexane (ug/L)	Methylcyclohexane (ug/L)	Benzene (ug/L)	Ethylbenzene (ug/L)	Toluene (ug/L)	Xylenes, Total (ug/L)	PAH (ug/L)
Proximal plume (plume interval range)	1207 1181-1207	292.6 n.d.	49.35 49.35 - 99.90	65.75 65.75 - 121.00	32.15 32.15 - 70.50	10.19 10.19 - 21.70	63.00 63.00 - 135.00	71.25 71.25 - 150.452	9.50 n.d.
Proximal plume (metatranscriptome sample)	1194	238	148.00	154.00	73.60	28.10	158.00	199.00	10.23
Distal plume (plume interval range)	1179 1136-1179	323.8 n.d.	79.20 19.10 - 79.20	86.40 20.90 - 86.40	48.80 15.10 - 48.80	13.90 4.67 - 13.90	106.00 33.80 - 106.00	107.00 30.30 - 107.00	8.10 n.d.

n.d. indicates not determined.

Table S2.16S rRNA gene pyrotag sequence data of percent relative abundance for all observed Bacteria and Archaea.

Taxonomy	Distal plume	Proximal plume	Uncontaminated
Proteobacteria;Oceanospirillales	92.97	80.62	3.98
Proteobacteria;Colwellia	1.39	1.07	1.99
Crenarchaeota;Nitrosopumilus	0.96	3.39	9.62
Proteobacteria;Cycloclasticus	0.92	0.80	21.96
Bacteria;Marine group A	0.65	2.68	4.92
Proteobacteria;Thalassomonas	0.30	0.22	0.41
Proteobacteria;Deltaproteobacteria	0.22	0.96	5.66
Proteobacteria;Gammaproteobacteria	0.22	0.72	2.34
Euryarchaeota;Marine group II	0.21	1.32	4.49
Proteobacteria;Candidatus Pelagibacter	0.16	1.16	5.90
Proteobacteria;Kangiella	0.15	0.30	1.76
Crenarchaeota;Cenarchaeaceae	0.14	0.91	3.24
Proteobacteria;Microbulbifer	0.14	0.12	0.00
Euryarchaeota;Marine group III	0.13	0.71	2.89
Chloroflexi;Chloroflexi-4	0.12	0.38	1.39
Actinobacteria;ZA3409c	0.10	0.26	1.04
Gemmatimonadetes;Gemmatimonadetes (class)	0.08	0.29	1.50
Planctomycetes;Pirellulales	0.06	0.15	1.29
Acidobacteria;Acidobacteriales	0.06	0.19	0.97
Cyanobacteria;Synechococcus	0.06	0.05	0.63
Bacteroidetes;Flavobacteriaceae	0.05	0.11	0.78
Proteobacteria;Candidatus Portiera	0.05	0.10	0.42
Acidobacteria;Acidobacteria	0.05	0.06	0.28
Proteobacteria;Chromatiales	0.05	0.31	2.36
Proteobacteria;Rhodospirillaceae	0.05	0.27	1.25
Bacteroidetes;Flavobacteria	0.04	0.24	0.92
Planctomycetes;Phycisphaerales	0.04	0.11	0.51
Proteobacteria;Sinobacteraceae	0.04	0.08	0.62
Proteobacteria;Nitrospina	0.03	0.32	1.41
Proteobacteria;Methylococcales	0.03	0.02	1.00
Acidobacteria;BPC102	0.03	0.02	0.02
Planctomycetes;Planctomyces	0.03	0.04	0.37
Acidobacteria;BPC102	0.03	0.04	0.39
Bacteroidetes;Sphingobacteriales	0.02	0.07	0.25
Cyanobacteria;Prochlorococcus	0.02	0.07	0.18
Proteobacteria;Coxiellaceae	0.02	0.02	0.23
Proteobacteria;Comamonadaceae	0.02	0.00	0.09
Verrucomicrobia;Puniceicoccaceae	0.02	0.05	0.28
Planctomycetes;OM190	0.01	0.02	0.35
Bacteroidetes;Sediminicola	0.01	0.00	0.00
Planctomycetes;CL500-15	0.01	0.02	0.14
Proteobacteria;Ectothiorhodospiraceae	0.01	0.01	0.00

Table S3.16S rRNA gene metagenome sequence data of percent relative abundance for all observed Bacteria and Archaea.

Taxonomy	Distal plume	Proximal plume	Uncontaminated
Proteobacteria;Oceanospirillales	62.54	60.31	4.67
Proteobacteria;Alteromonadales	9.25	9.09	3.75
Proteobacteria;marine boreal sponge <i>Isops phlegraei</i> Norway:Sula Ridge	5.84	5.47	0.29
Proteobacteria;NB1-j	4.10	4.50	1.04
Proteobacteria;Pseudomonadales	3.92	4.00	0.74
Proteobacteria;Reinekea	2.12	1.66	0.08
Proteobacteria;1097664134132 whole genome shotgun isolate str. KT 71	1.81	1.47	0.10
Proteobacteria;Env Seq	1.51	1.35	1.66
Proteobacteria;Sphingomonadales	1.30	1.26	0.76
Proteobacteria;seawater isolate str. sw-11	1.23	1.15	0.07
Proteobacteria;Aeromonadales	1.21	1.11	0.19
Proteobacteria;Env Seq	1.02	0.95	0.00
Proteobacteria;Boston Harbor surface water isolate str. UMB6E	0.62	0.63	0.08
Proteobacteria;Thiotrichales	0.61	0.55	20.25
Proteobacteria;Env Seq	0.24	0.24	0.00
Proteobacteria;Enterobacteriales	0.20	0.27	0.18
Proteobacteria;Consistiales	0.17	0.85	11.93
Proteobacteria;Methylophaga	0.16	0.14	6.89
Proteobacteria;SAR86	0.15	0.26	0.97
Proteobacteria;Boston Harbor surface water isolate str. UMB3E	0.14	0.21	0.02
Proteobacteria;Vibrionales	0.13	0.19	0.32
Thaumarchaeota;Cenarchaeum	0.12	0.51	4.20
Proteobacteria;HOC28	0.09	0.14	0.00
Proteobacteria;Rhizobiales	0.09	0.09	0.28
Proteobacteria;Pseudomonadaceae	0.08	0.08	0.45
Actinobacteria;Actinomycetales	0.08	0.13	0.50
Proteobacteria;agg47	0.08	0.13	1.64
Proteobacteria;Boston Harbor surface water isolate str. UMB6D	0.06	0.06	0.14
Proteobacteria;Sva0853	0.05	0.29	3.59
Proteobacteria;OM60	0.04	0.05	0.24
Proteobacteria;ZD0417	0.04	0.15	1.29
Proteobacteria;Thiomicrospira	0.04	0.03	0.01
Proteobacteria;Arctic96B-1	0.03	0.03	0.17
Proteobacteria;isolate str. EHK-1	0.03	0.01	1.14
Proteobacteria;ZA2333c	0.03	0.02	0.04
Proteobacteria;SUP05	0.03	0.12	1.76
Proteobacteria;Rhodobacterales	0.03	0.07	0.32
Proteobacteria;BD7-8	0.03	0.01	0.00
Proteobacteria;sulfur-oxidizing symbionts	0.02	0.09	0.26
Proteobacteria;Pasteurellales	0.02	0.01	0.02
Marine_group_A;Env Seq	0.02	0.09	0.73
Proteobacteria;Methylococcales	0.02	0.03	0.99
Proteobacteria;Legionellales	0.02	0.05	0.24
Thermoplasmata_Eury;SB95-72	0.02	0.15	1.45
Firmicutes;Clostridiales	0.02	0.02	0.06
Proteobacteria;Vibrionaceae	0.02	0.01	0.00
Proteobacteria;Chromatiales	0.02	0.01	0.37
Marine_group_A;Env Seq	0.02	0.13	0.85
Chloroflexi;SAR307	0.02	0.06	0.95
Marine_group_A;Env Seq	0.01	0.04	0.35
Proteobacteria;marine str. HTCC2080	0.01	0.02	0.03
Marine_group_A;Env Seq	0.01	0.11	1.62
Actinobacteria;Microthrixineae	0.01	0.10	1.38
Verrucomicrobia;Verruco-3	0.01	0.09	1.12
Proteobacteria;Xanthomonadales	0.01	0.01	0.08
Proteobacteria;Halomonadaceae	0.01	0.01	0.00
Proteobacteria;Env Seq	0.01	0.01	0.44
Proteobacteria;Betaproteobacteria	0.01	0.01	0.31
Bacteroidetes;Flavobacteriales	0.01	0.01	0.35
Proteobacteria;str. NEP2	0.01	0.01	0.04

Table S4. 16S rRNA sequence data from the plume metatranscriptomes of percent relative abundance for all observed Bacteria and Archaea.

Taxonomy	Proximal station metatranscriptome	Distal station metatranscriptome
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales	45.52	68.99
Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales	11.45	8.59
Bacteria; Proteobacteria; Deltaproteobacteria; NB1-j	9.65	1.35
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales	6.48	3.72
Bacteria; Proteobacteria; Gammaproteobacteria; 1097664134132 whole genome shotgun isolate 71KT str. KT 71	3.87	0.38
Bacteria; Proteobacteria; Gammaproteobacteria; SAR86	3.11	1.13
Bacteria; Oxidative ultraviolet C treatment culturable harvested and identified wells groundwater isolate C1groundwater biofilm str. C1	2.65	1.48
Bacteria; symbiont	2.45	2.01
Bacteria; Oceaniserpentilla; Oceaniserpentilla haliotidis	2.41	2.45
Bacteria; Proteobacteria; isolate str. M3-6	1.78	1.05
Bacteria; Proteobacteria; Gammaproteobacteria; deep-sea sediment clone BD1-7	1.46	0.97
Bacteria; Boston Harbor surface water isolate str. UMB8C	1.01	0.62
Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales	0.93	0.48
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales	0.70	0.55
Bacteria; Proteobacteria; Gammaproteobacteria; Boston Harbor surface water isolate str. UMB3E UMB3E	0.50	0.37
Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales	0.39	0.12
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales	0.37	0.21
Bacteria; Proteobacteria; Gammaproteobacteria; Methylophaga	0.31	0.11
Bacteria; Sponge isolate str. Ex6	0.30	0.22
Bacteria; Proteobacteria; Gammaproteobacteria; libraries sediment Kings Bay Svalbard Arctic clone SS1_B_04_41	0.30	0.33
Bacteria; Proteobacteria; Gammaproteobacteria; OM60	0.28	0.43
Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales	0.27	0.14
Bacteria; Proteobacteria; Gammaproteobacteria; deep-sea octacoral clone ctg_NISA145	0.22	0.19
Bacteria; Proteobacteria; Gammaproteobacteria; HOC28	0.20	0.06
Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales	0.19	0.13
Bacteria; Proteobacteria; Gammaproteobacteria; Thiomicrospira	0.17	0.08
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales	0.16	0.11
Bacteria; Proteobacteria; Gammaproteobacteria; sea water isolate sw-11sw-11 str. sw-11	0.16	0.25
Bacteria; Proteobacteria; Gammaproteobacteria; libraries sediment Kings Bay Svalbard Arctic clone SS1_B_06_26	0.14	0.06
Bacteria; Endosymbiont Pogonophora sp. JT-1 clone JTPE-1 Pogonophora	0.14	0.09
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadaceae	0.11	0.14
Bacteria; Proteobacteria; Gammaproteobacteria; Reinekea	0.10	0.43
Bacteria; Proteobacteria; Gammaproteobacteria; agg47	0.10	0.06
Bacteria; Proteobacteria; Gammaproteobacteria; Halomonadaceae	0.10	0.02
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales	0.09	0.22
Bacteria; Proteobacteria; Gammaproteobacteria; sulfur-oxidizing symbionts	0.08	0.12
Bacteria; Proteobacteria; Alphaproteobacteria; Consistiales	0.07	0.03
Bacteria; Proteobacteria; Gammaproteobacteria; BD1-1	0.06	0.02
Bacteria; Proteobacteria; Gammaproteobacteria; marine str. HTCC2080	0.06	0.00
Bacteria; Proteobacteria; Alphaproteobacteria; Bradyrhizobiales	0.05	0.11
Bacteria; Proteobacteria; Gammaproteobacteria; cold seep sediment clone JT58-12	0.04	0.04
Bacteria; Proteobacteria; Gammaproteobacteria; landfill leachate clone GZKB44	0.04	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; BPC036	0.04	0.02
Bacteria; tetracycline and tylosin resistance genes impacted swine effluent holding pit	0.04	0.03
Bacteria; Proteobacteria; Gammaproteobacteria; sulfur_oxidizing_symbionts	0.04	0.03
Bacteria; Proteobacteria; Genetic and functional microbial symbionts new species polychaete worms symbiont Osedax MB4 clone T933_2_H5	0.04	0.03

Table S4. 16S rRNA sequence data from the plume metatranscriptomes of percent relative abundance for all observed Bacteria and Archaea (cont).

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales	0.04	0.03
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionaceae	0.04	0.06
Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales	0.03	0.06
Bacteria; Proteobacteria; Alphaproteobacteria; Pacific arctic surface sediment clone S26-7	0.03	0.03
Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales	0.03	0.02
Bacteria; Firmicutes; Clostridia; Clostridiales	0.03	0.18
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales	0.03	0.01
Bacteria; Actinobacteria; Acidimicrobidae; identification marine actinobacteria sediment isolate YM22-133Acidimicrobidae str. YM22-133	0.02	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; BD7-8	0.02	0.14
Bacteria; Proteobacteria; Gammaproteobacteria; Arctic96B-1	0.02	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; determined library mangrove clone DS095	0.02	0.01
Bacteria; Firmicutes; Bacillales; Bacillaceae	0.02	0.02
Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales	0.02	0.02
Bacteria; Influence starvation ozone and selected isolates on survival southern Jasus edwardsii healthy larval rock lobster	0.02	0.03
Bacteria; Actinobacteria; Acidimicrobidae; EB1017_group	0.02	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; ZA2333c	0.02	0.02
Bacteria; Proteobacteria; Gammaproteobacteria	0.02	0.02
Bacteria; Unexpected symbionts sp. cold seeps eastern Mediterranean: new evolution symbiosis mytilids gill tissue Idas sp clone M2.41	0.02	0.02
Bacteria; Proteobacteria; Gammaproteobacteria; cold seep sediment clone JT75-103	0.02	0.02
Bacteria; Proteobacteria; Gammaproteobacteria; polyphasic description Pocillopora meandrina Palmyra Atoll Calcinus obscurus abdominal flora clone Cobs2TisB5	0.02	0.02
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanimonaceae	0.02	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; SUP05	0.02	0.02
Bacteria; Firmicutes; Mollicutes; Mycoplasmatales	0.01	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; bacterioplankton clone ZA3235c	0.01	0.01
Bacteria; Proteobacteria; Alphaproteobacteria; Andersenella	0.01	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales	0.01	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; Endozoicimonas	0.01	0.11
Bacteria; Proteobacteria; Gammaproteobacteria; deep-sea octacoral clone ctg_CGOF019	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; marine str. HTCC2178	0.01	0.03
Bacteria; Proteobacteria; Gammaproteobacteria; Alkalimonas	0.01	0.00
Bacteria; Proteobacteria; Genetic and functional microbial symbionts new species polychaete worms symbiont Osedax MB3 clone T931_1_B1	0.01	0.00
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales	0.01	0.01
Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; marine sponge clone HOC34	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; Nitrincola	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales	0.01	0.03
Bacteria; Proteobacteria; Gammaproteobacteria; Abundance and microbial life ocean crust seafloor lavas Loi'hi Seamount South Rift X3 clone P7X3b4C08	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; ZD0417	0.01	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; Microbial Adherent Sediment Particles Heavy Metal Contaminated North Sea Surface Sediments marine sediments clone	0.01	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; marine boreal sponge Geodia baretii Norway:Korsfjord	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; isolate str. EHK-1	0.01	0.01
Bacteria; Actinobacteria; Acidimicrobidae; identification marine actinobacteria sand isolate YM16-303Acidimicrobidae str. YM16-303	0.01	0.00
Bacteria; Chloroflexi; Chloroflexi-4; SAR307	0.01	0.00
Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales	0.01	0.02
Bacteria; Proteobacteria; Alphaproteobacteria; Acetobacterales	0.01	0.00
Bacteria; Proteobacteria; Alphaproteobacteria; Brucella_spHJ114	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; Deselenobacterium	0.01	0.00
Bacteria; Proteobacteria; Gammaproteobacteria; Moraxellaceae	0.01	0.01
Bacteria; Proteobacteria; Gammaproteobacteria; Oceanirickettsia	0.01	0.01
Bacteria; Proteobacteria; Deltaproteobacteria; CTD005-82B-02	0.01	0.00
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Bacteria; Isolation and identification hyper-ammonia producing swine storage pits manure	0.01	0.01
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales	0.01	0.00
Bacteria; Proteobacteria; Deltaproteobacteria; Sva0853	0.01	0.00
Other	0.56	0.95

Table S5. Cluster of orthologous groups involved in chemotaxis and nutrient acquisition.

COG	Description	Class	Class description
COG0840	Methyl-accepting chemotaxis protein	NT	Multiple classes
COG0004	Ammonia permease	P	Inorganic ion transport and metabolism
COG3639	ABC-type phosphate/phosphonate transport system, permease component	P	Inorganic ion transport and metabolism
COG0609	ABC-type Fe ³⁺ -siderophore transport system, permease component	P	Inorganic ion transport and metabolism
COG2375	Siderophore-interacting protein	P	Inorganic ion transport and metabolism
COG1918	Fe ²⁺ transport system protein A	P	Inorganic ion transport and metabolism
COG0370	Fe ²⁺ transport system protein B	P	Inorganic ion transport and metabolism
COG0659	Sulfate permease and related transporters (MFS superfamily)	P	Inorganic ion transport and metabolism
COG0053	Predicted Co/Zn/Cd cation transporters	P	Inorganic ion transport and metabolism

Table S6. Complete list of gene categories involved in hydrocarbon degradation from Figure 2. The genes in each gene category represent several genes, thus do not have accession numbers. Gene names in the table are directly from GenBank.

Alcohol dehydrogenase	alcohol dehydrogenase (acceptor) alcohol dehydrogenase (zinc-containing) alcohol dehydrogenase [benzyl] alcohol dehydrogenase GroES domain protein alcohol dehydrogenase zinc-binding domain protein alcohol dehydrogenase zinc-binding domain-containing protein alcohol dehydrogenase zinc-binding type 2 alcohol dehydrogenase, class III, bacterial-like protein alcohol dehydrogenase, zinc-binding alcohol dehydrogenase, NADP-dependent
Aldehyde dehydrogenase	aldehyde dehydrogenase (acceptor) aldehyde dehydrogenase (NAD) aldehyde dehydrogenase 1 aldehyde dehydrogenase A aldehyde dehydrogenase family protein aldehyde dehydrogenase, NADP-dependent
Alkane	alkane 1-monooxygenase alkane hydroxylase alkane hydroxylase A alkane hydroxylase-rubredoxin alkane monooxygenase transmembrane alkane 1-monooxygenase AlkB
Aromatic	aromatic dioxygenase large subunit aromatic ring dioxygenase alpha subunit aromatic ring dioxygenase subunit A aromatic ring hydroxylation dioxygenase A aromatic ring monooxygenase aromatic ring-hydroxylating dioxygenase aromatic-ring hydroxylase aromatic-ring-hydroxylating dioxygenase, alpha subunit aromatic-ring-hydroxylating dioxygenase, alpha subunit-like protein aromatic 1,2-dioxygenase, alpha subunit
Benzene	benzene dioxygenase benzene dioxygenase large subunit benzene monooxygenase oxygenase subunit
Benzoate	benzoate 1,2 dioxygenase alpha subunit benzoate 1,2-dioxygenase alpha subunit / Toluate 1,2-dioxygenase alpha subunit benzoate 1,2-dioxygenase beta subunit benzoate 1,2-dioxygenase hydroxylase component,alpha subunit benzoate 1,2-dioxygenase subunit alpha BenA benzoate 1,2-dioxygenase, large subunit benzoate 1,2-dioxygenase, small subunit benzoate 4-monooxygenase cytochrome P450 benzoate CoA ligase benzoate diol dehydrogenase benzoate dioxygenase alpha subunit benzoate dioxygenase large subunit benzoate dioxygenase, alpha subunit benzoate-CoA ligase benzoate-CoA ligase family benzoate-coenzyme A ligase
Cyclohexanol dehydrogenase	cyclohexanol dehydrogenase

Table S6. Complete list of gene categories involved in hydrocarbon degradation from Figure 2. The genes in each gene category represent several genes, thus do not have accession numbers. Gene names in the table are directly from GenBank.

Cyclohexanone	cyclohexanone 1,2-monooxygenase cyclohexanone monooxygenase cyclohexanone monooxygenase 1 cyclohexanone monooxygenase 2
Ethylbenzene	ethylbenzene dehydrogenase, beta subunit ethylbenzene dioxygenase alpha subunit ethylbenzene dioxygenase large subunit
Fatty Acid	fatty acid oxidation complex alpha subunit fatty acid oxidation complex alpha subunit [includes: enoyl-co hydratase (ec 4.2.1.17); 3-hydroxyacyl-coa dehydrogenas (ec 1.1.1.35); 3-hydroxybutyryl-coa epimerase (ec 5.1.2.3)] fatty oxidation complex fatty oxidation complex alpha subunit fatty oxidation complex alpha subunit [includes: enoyl-CoA hydratase; 3-hydroxyacyl-CoA dehydrogenase and 3-hydroxybutyryl-CoA epimerase] fatty oxidation complex, alpha subunit FadB fatty oxidation complex, alpha subunit FadJ fatty acid oxidation complex subunit alpha, multifunctional fatty acid desaturase
PAH	PAH dioxygenase iron sulfur protein large subunit PAH dioxygenase large subunit PAH ring-hydroxylating dioxygenase alpha subunit
Particulate methane monooxygenase	particulate methane monooxygenase A subunit particulate methane monooxygenase alpha subunit particulate methane monooxygenase protein A particulate methane monooxygenase subunit particulate methane monooxygenase subunit A particulate methane monooxygenase-like particulate methane monooxygenase beta (PmoA) subunit particulate methane oxygenase particulate Methane Oxygenase A PmoA
Ring cleavage/hydroxylating	extradiol ring-cleavage dioxygenase, class III enzyme, subunit B intradiol ring-cleavage dioxygenase intradiol ring-cleavage dioxygenase:Catechol dioxygenase, N-terminal large subunit of ring-hydroxylating dioxygenase ring hydroxylating alpha subunit ring hydroxylating alpha subunit (catalytic domain) protein ring hydroxylating dioxygenase alpha subunit ring hydroxylating dioxygenase alpha subunit (catalytic domain) ring hydroxylating dioxygenase subunit ring hydroxylating dioxygenase, alpha subunit:Rieske ring hydroxylating dioxygenase, alpha subunit:Rieske (2Fe-2S) region ring hydroxylating dioxygenase, alpha subunit/Rieske (2Fe-2S) protein ring hydroxylating dioxygenase, Rieske (2Fe-2S) protein ring-hydroxylating dioxygenase ring-hydroxylating dioxygenase alpha subunit ring-hydroxylating dioxygenase large subunit ring-hydroxylating dioxygenase large terminal subunit
Toluene	toluene 4-monooxygenase protein A toluene 4-monooxygenase protein E toluene dioxygenase toluene dioxygenase small subunit toluene o-xylene monooxygenase component toluene-3-monooxygenase oxygenase subunit 1 toluene-3-monooxygenase oxygenase subunit 2 toluene-4-monooxygenase system protein A toluene/benzoate dioxygenase alpha subunit toluene/biphenyl Rieske non-heme iron oxygenase alpha subunit toluene 1,2-dioxygenase alpha subunit

Figures

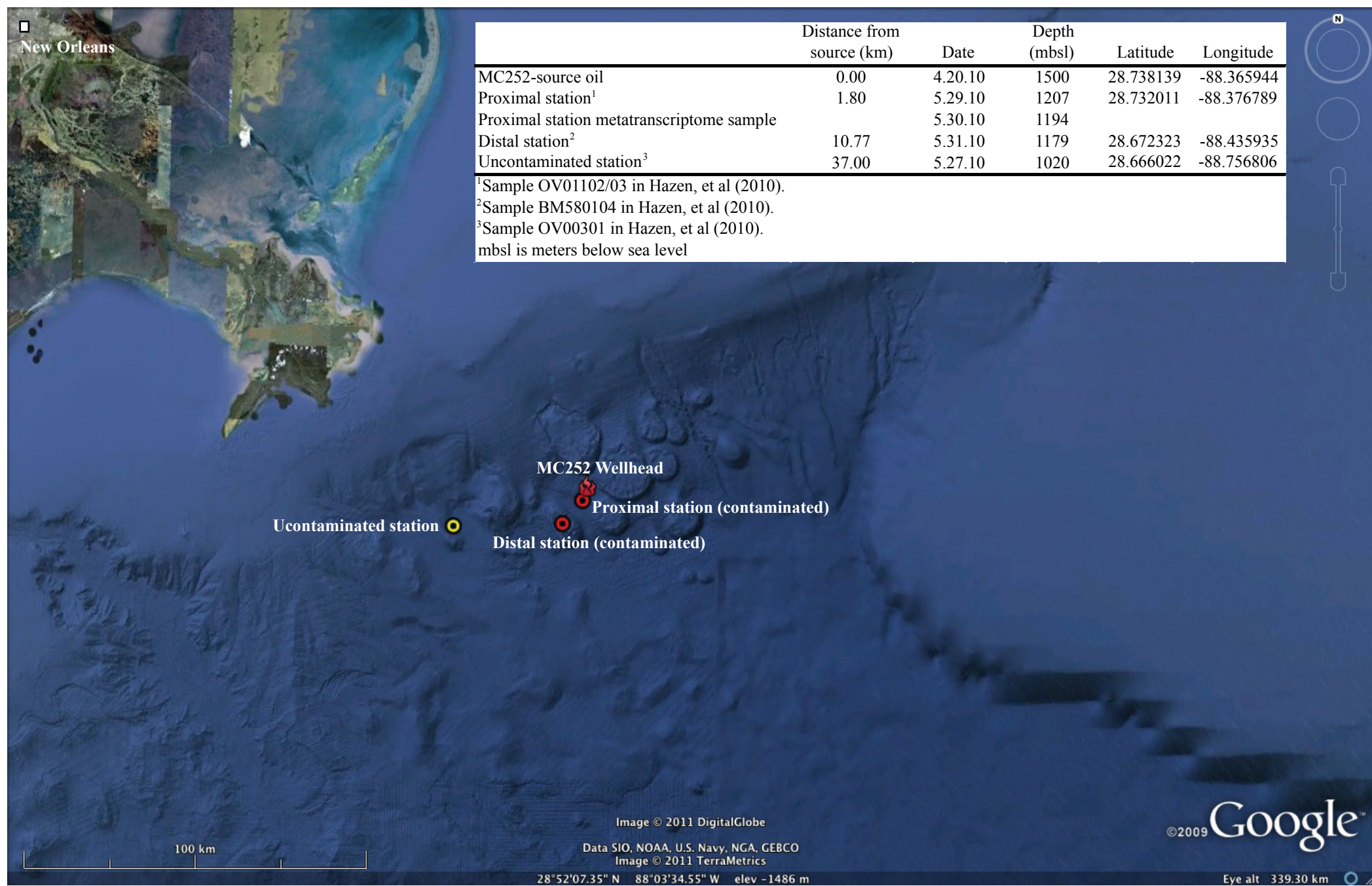


Figure S1. Map of sampling sites and MC252 Deepwater Horizon oil spill site.

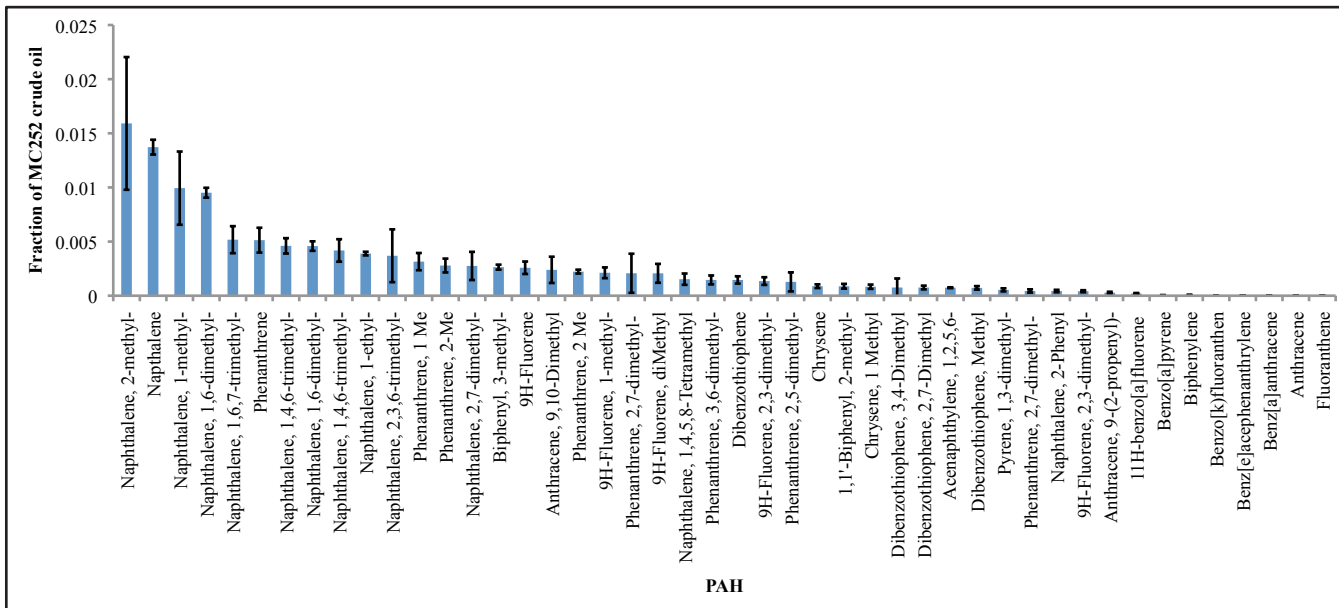
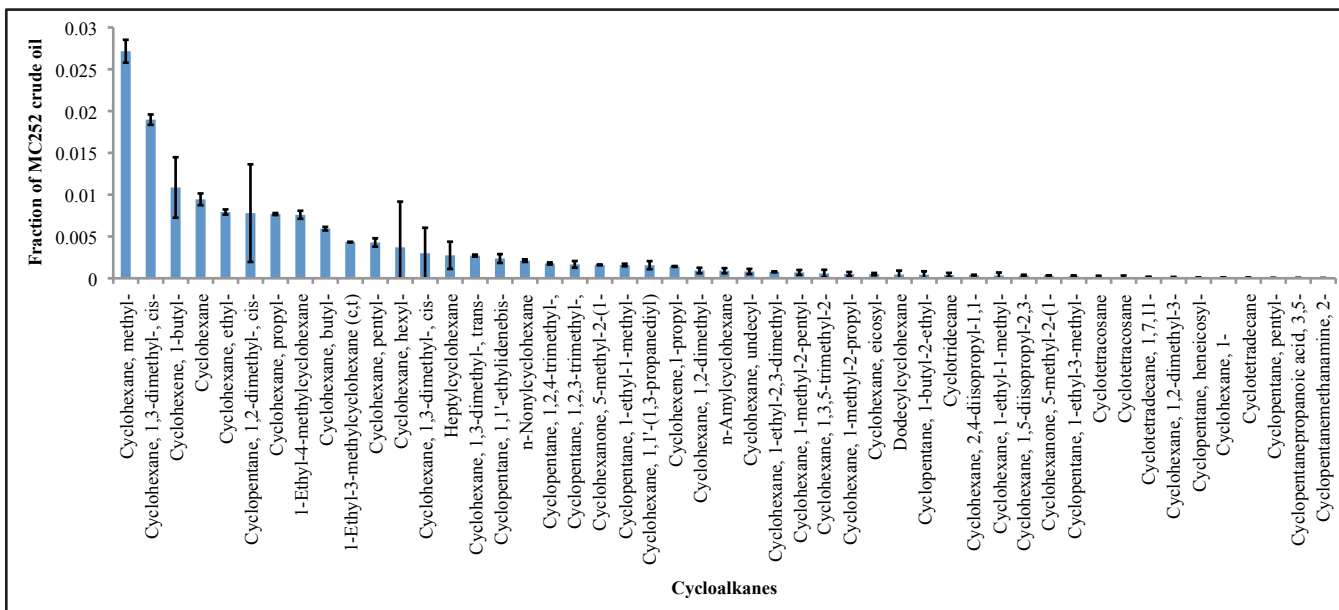
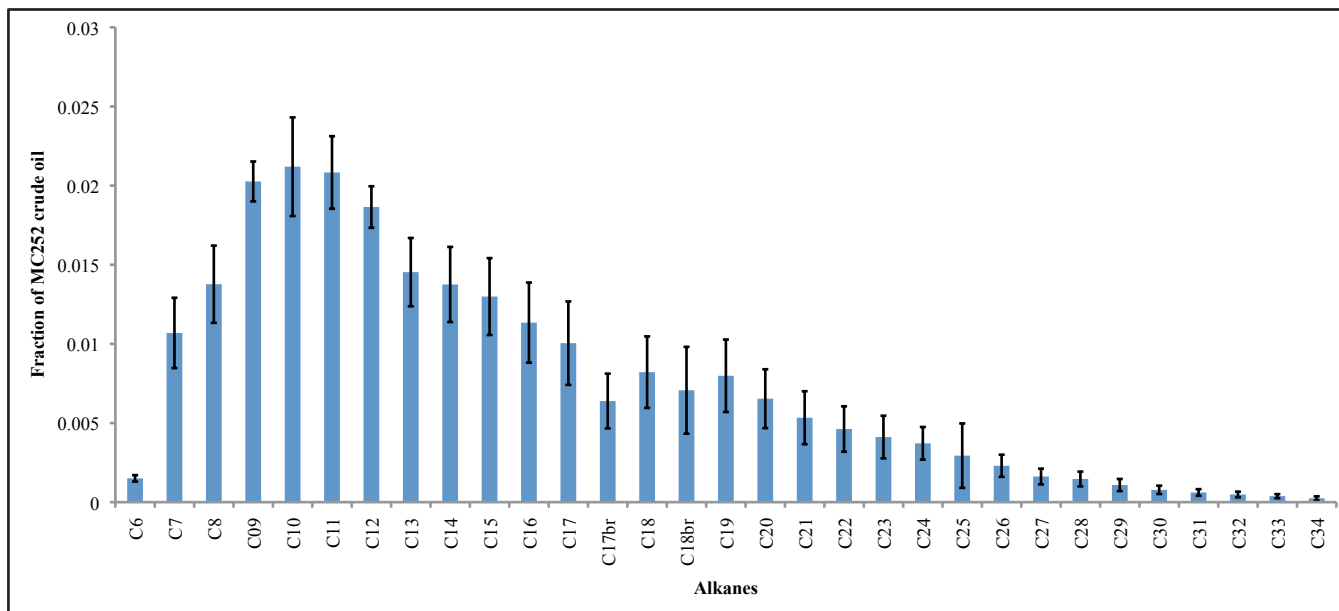


Figure S2. MC252 crude oil constituents >C5 determined by direct on-column GC/MS analysis. Bars indicate average (n = 3) fraction of each constituent in source oil.

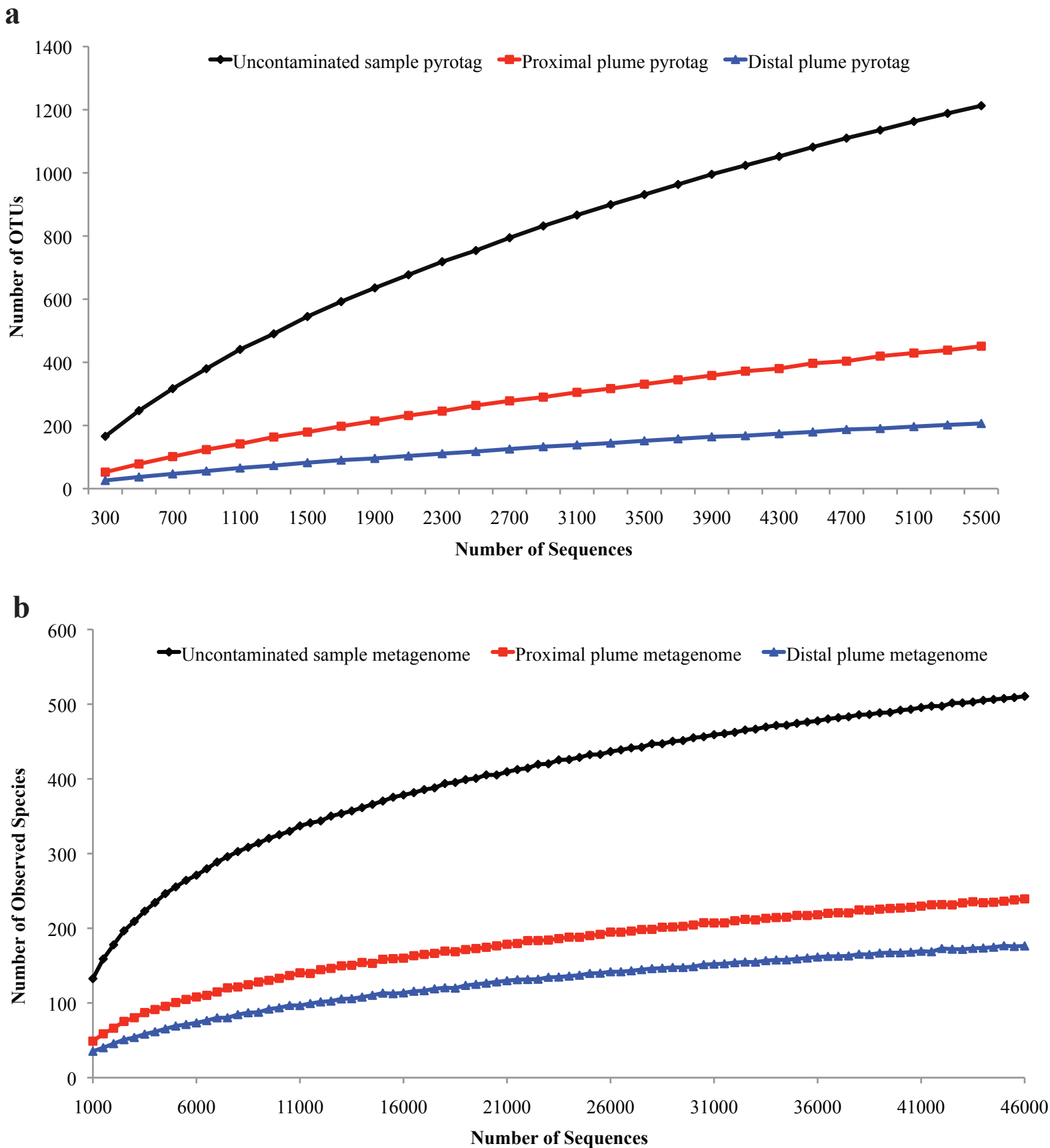


Figure S3. Rarefaction curves for 16S rRNA genes from the proximal and distal plume stations and from the uncontaminated sample collected from plume depth. Data was rarefied prior to analysis. A) Rarefaction curve of pyrotag data. B) Rarefaction curve of metagenome data.

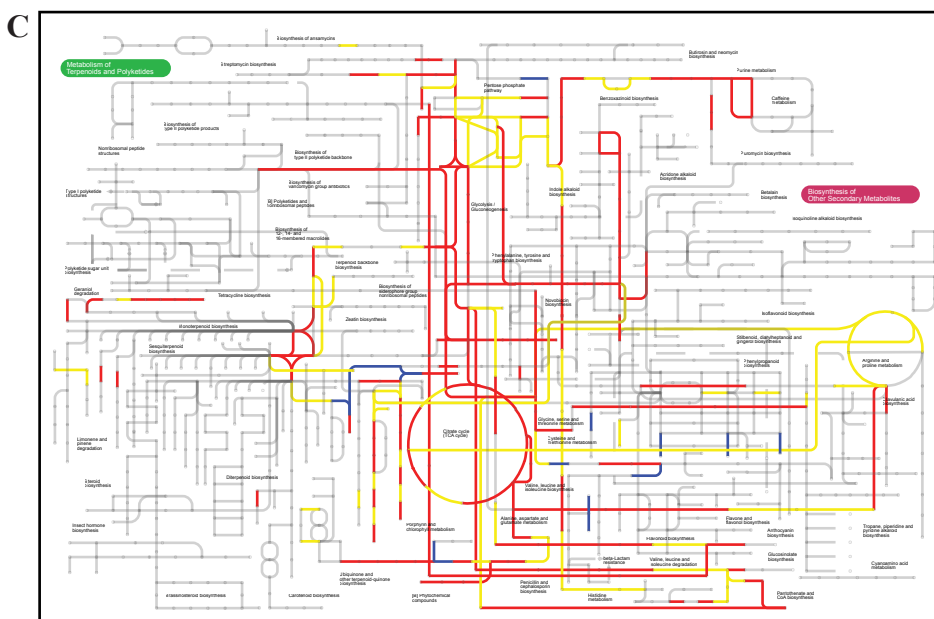
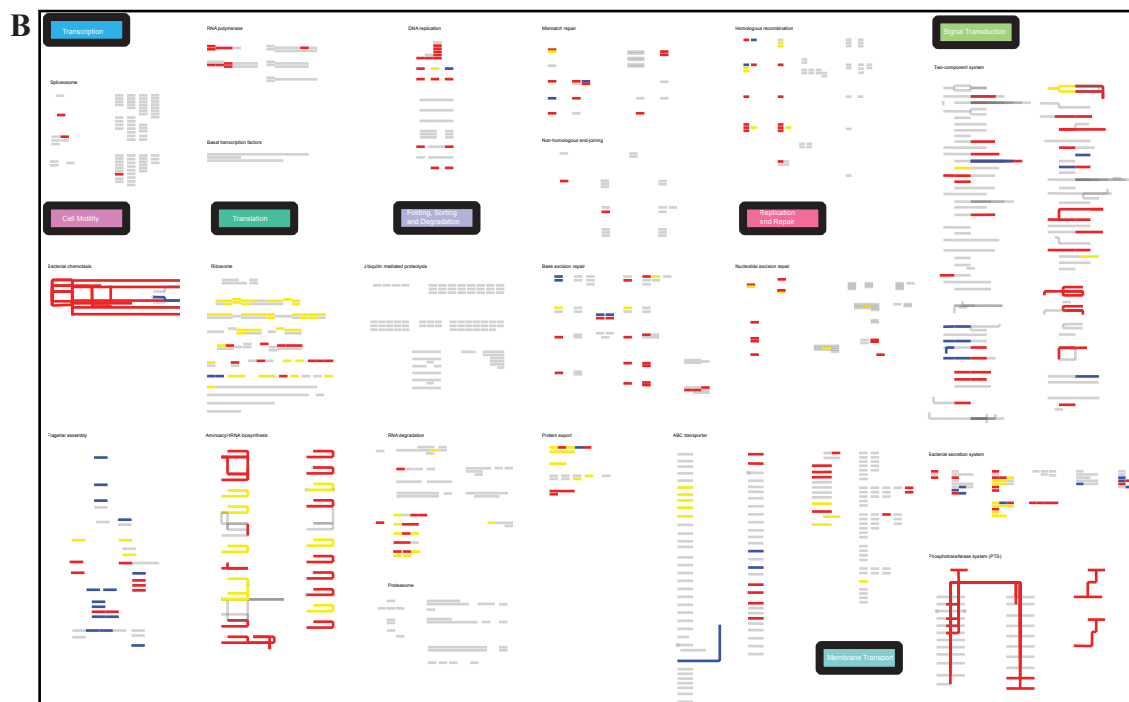
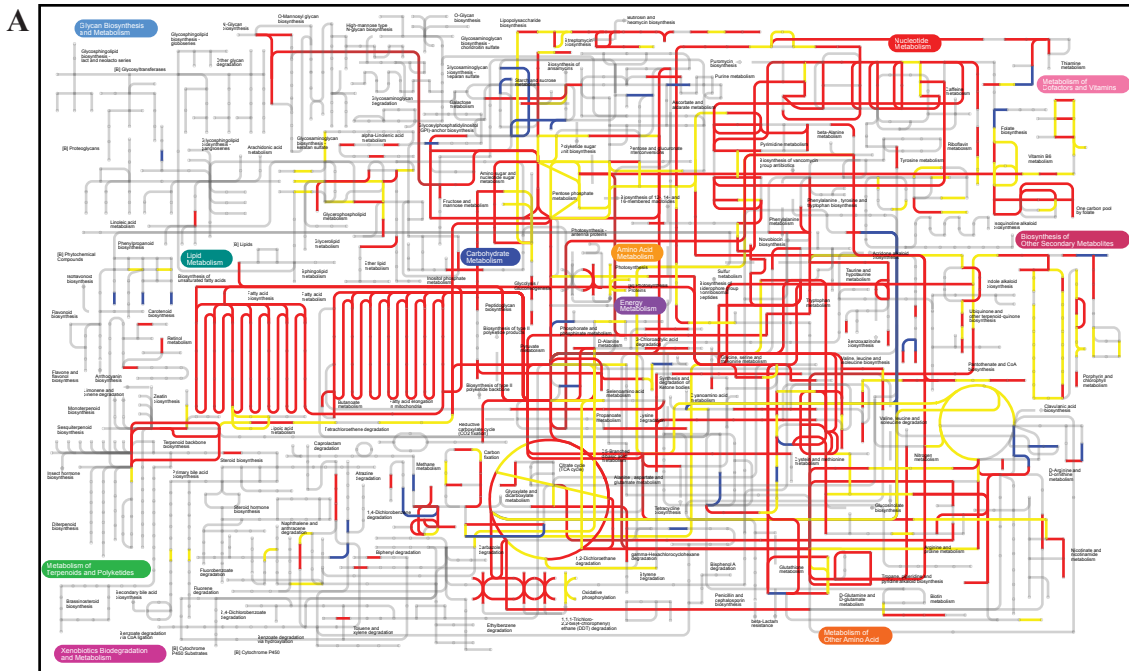


Figure S4. Mapped COG data from the *Oceanospirillales* draft genome and the metatranscriptome. Panel A shows metabolic pathways; panel B shows regulatory pathways; panel C shows the pathways for biosynthesis of secondary metabolites. Red indicates that an element was present in the draft genome and expressed; blue indicates that an element was present in the draft genome only; yellow indicates that an element was present in the metatranscriptome only.

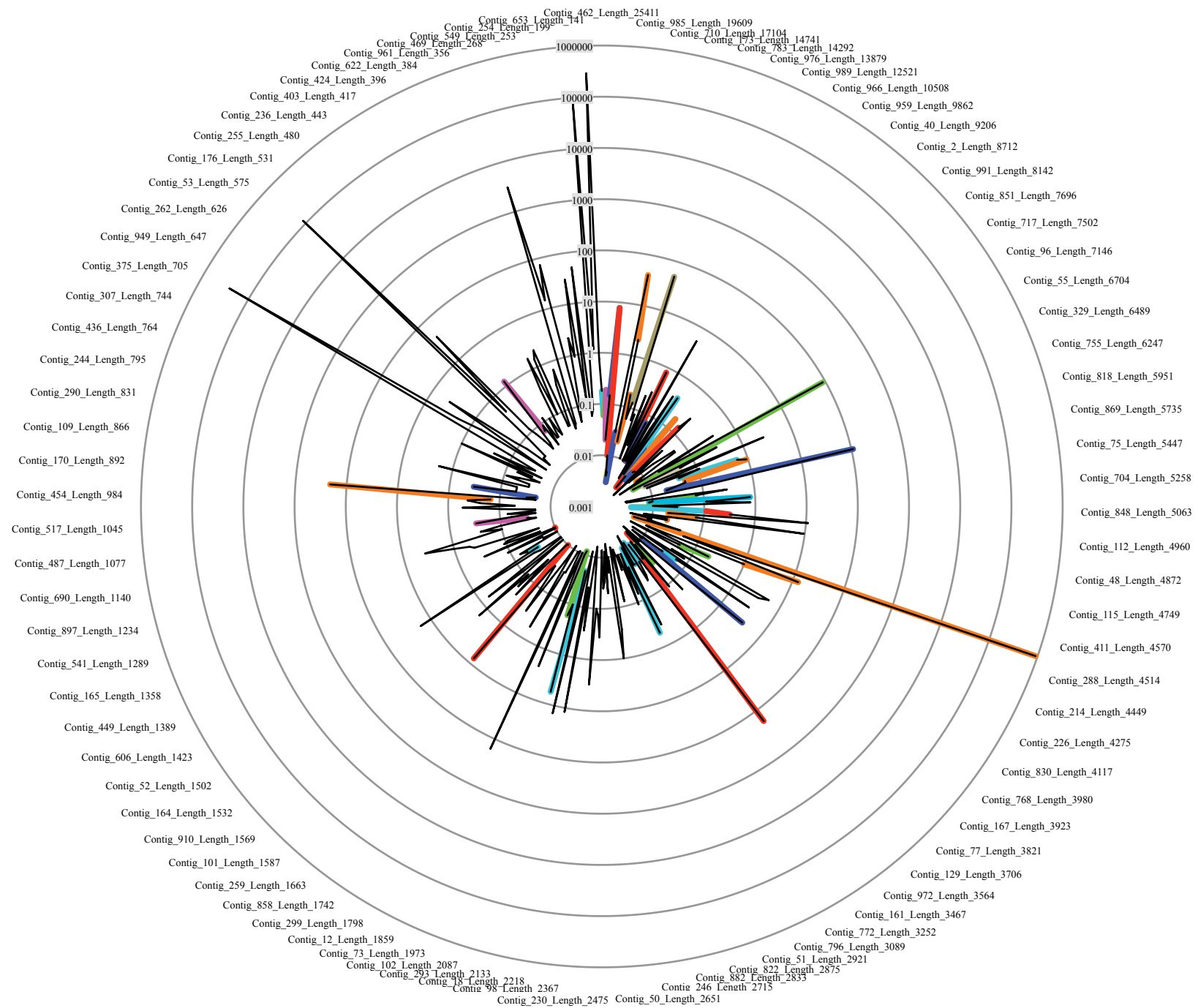


Figure S5. Unassembled paired-end reads (5.1 Gb) from the metatranscriptome were mapped to the *Oceanospirillales* draft genome. A total of 3.0 Gb from the metatranscriptome mapped to the assembled draft genome. The average contig coverage is shown above. Contigs containing COGs coding for methyl-accepting chemotaxis proteins are shown in red. Contigs containing COGs for flagellar processes are shown in green. COGs for pilin are shown in purple. COGs implicated in biofilm formation are shown in dark blue. COGs for nutrient acquisition are shown in light blue. COGs for signal transduction are shown in orange. COGs for plasmid maintenance and stabilization are shown in light brown. Contigs are shown in length order.

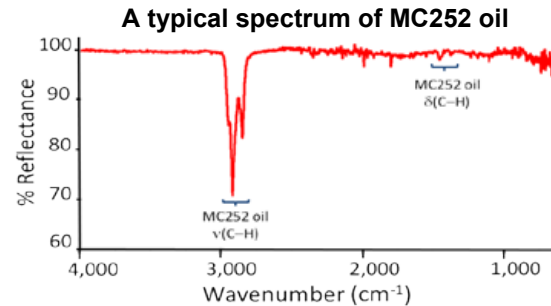
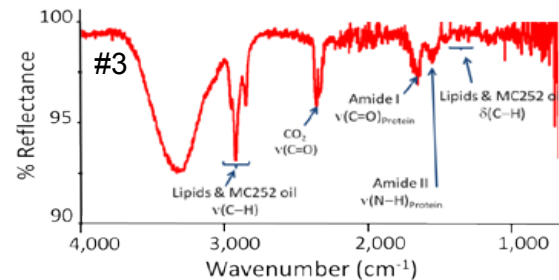
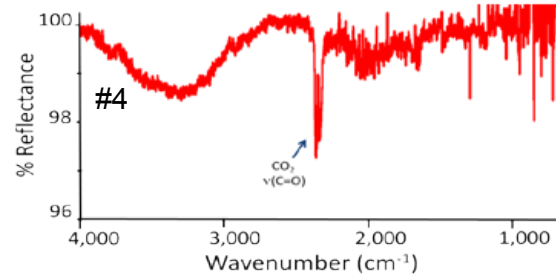
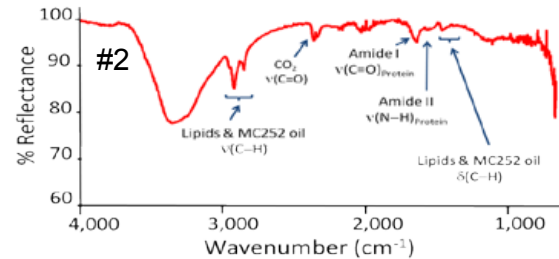
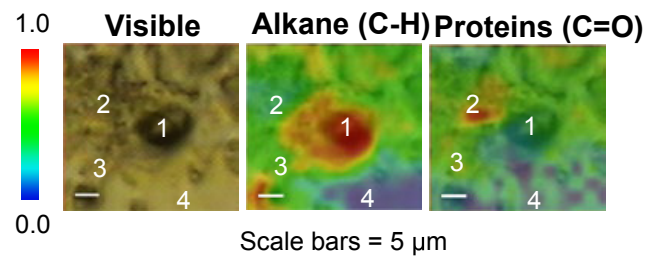
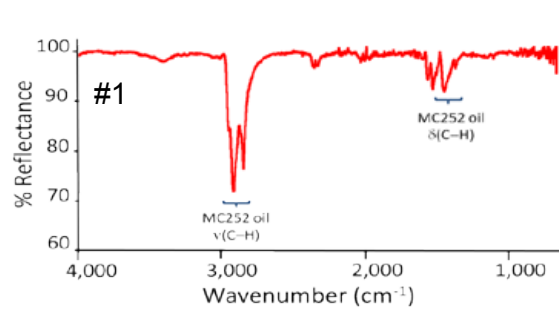


Figure S6. SR-FTIR analysis of proximal plume water. The spot labelled as 1 in the visible and infrared image corresponds to spectrum #1, which is interpreted as MC252 oil. Spot 2 corresponds with spectrum #2, which is interpreted as a cluster of prokaryotic cells. Spot 3 corresponds with spectrum #3, which represents a mixture of prokaryotic cells and MC252 oil. Spot 4 corresponds to spectrum #4, which represents a blank spot.