

**Table S1**

Sample	Mineralogical Group	Paired Reads	% Reads Mapped	# Contigs	N50	Max Length (bp)	# Predicted Proteins	# Known Functions	% Unknown Functions
D12B.1	1	27,028,379	73.27	480,395	1,609	152,799	772,263	221,411	71.33
D12B.2	2	36,398,584	76.72	529,453	1,867	232,657	873,020	265,247	69.62
D67B.1	1	36,944,236	79.68	551,915	1,851	110,939	926,130	274,266	70.39
D67B.2	2	41,065,986	71.34	718,467	1,950	248,332	1,222,333	387,170	68.33
D29.1	1	27,262,857	75.68	431,625	2,162	231,711	723,205	235,225	67.47
D29.2	2	31,153,558	68.34	514,747	1,772	231,545	831,006	271,565	67.32
D33.1	1	31,759,001	78.86	503,866	2,222	222,646	864,854	272,038	68.55
D33.2	2	30,502,979	71.02	556,953	1,880	183,134	930,075	289,647	68.86
D35.1	1	53,706,656	75.09	795,975	2,322	223,962	1,369,835	434,454	68.28
D35.2	3	44,663,651	74.56	768,295	1,461	88,995	1,212,160	325,402	73.16
D35.3	3	54,664,207	70.81	1,046,983	1,281	232,405	1,610,078	369,933	77.02
D56.1	1	35,366,014	77.89	554,687	2,239	231,467	961,743	303,059	68.49
D56.2	3	25,485,574	67.47	497,380	1,467	205,540	775,528	196,824	74.62
D56.3	3	43,499,921	72.23	733,529	1,982	206,649	1,236,617	394,497	68.10
D46.1	1	45,073,753	77.47	802,472	1,481	521,643	1,298,167	357,923	72.43
D46.2	2	32,815,788	65.5	660,420	1,479	162,191	1,060,402	302,249	71.50

Table S2

BinSanity Bin Id	GTDB-Tk Classify Results	Bin ID	Completeness	Contamination	Strain Heterogeneity
BinSanityLC-kmean-bin_57-bin_0-refined_5	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__g__s__	Halobacteriales.1	92	5.46	35.29
BinSanityLC-kmean-bin_45-bin_0-refined_15	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__g__s__	Halobacteriales.2	62	6.07	40.74
BinSanityLC-kmean-bin_57-bin_0-refined_8	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__g__s__	Halobacteriales.3	47	0	0
BinSanityLC-kmean-bin_35-bin_0-refined_4	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloarculaceae; g__s__	Haloarculaceae.1	90	13.91	15.79
BinSanityLC-kmean-bin_36-bin_0-refined_3	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloarculaceae; g__s__	Haloarculaceae.2	71	11.17	13.95
BinSanityLC-kmean-bin_44-bin_0-refined_5	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloarculaceae; g__s__	Haloarculaceae.3	67	6.81	25
BinSanityLC-kmean-bin_61-bin_0-refined_12	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloarculaceae; g__Halovenus; s__	Halovenus	67	8.27	46.43
BinSanityLC-kmean-bin_53-bin_0-refined_1	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloarculaceae; g__QS-1-69-70; s__	Haloarculaceae.4	87	3.97	18.18
BinSanityLC-kmean-bin_18-bin_0-refined_0	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloarculaceae; g__SW-9-67-25; s__	Haloarculaceae.5	90	5.48	52.38
BinSanityLC-kmean-bin_53-bin_0-refined_2	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloferacaceae; g__s__	Haloferacaceae.1	80	2.31	60
BinSanityLC-kmean-bin_45-bin_0-refined_6	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloferacaceae; g__s__	Haloferacaceae.2	49	0.38	0
BinSanityLC-kmean-bin_45-bin_0-refined_10	d__Archaea; p__Halobacterota; c__Halobacteria; o__Halobacteriales; f__Haloferacaceae; g__s__	Haloferacaceae.3	48	1.2	0
BinSanityLC-kmean-bin_14-bin_0-refined_8	d__Archaea; p__Halobacterota; c__Methanosarcinia; o__Methanosarcinales; f__Methanosarcinaceae; g__Methanohalobium; s__	Methanohalobium	99	0.65	0
BinSanityLC-kmean-bin_57-bin_0-refined_3	d__Archaea; p__Nanohaloarchaeota; c__Nanosalinia; o__Nanosalinales; f__g__s__	Nanosalinales	56	0.93	0
BinSanityLC-kmean-bin_14-bin_0-refined_6	d__Archaea; p__Thermoplasmatota; c__o__f__g__s__	Thermoplasmatota.1	52	1.6	0
BinSanityLC-kmean-bin_14-bin_0-refined_12	d__Archaea; p__Thermoplasmatota; c__SW-10-69-26; o__f__g__s__	Thermoplasmatota.2	57	0.8	0
BinSanityLC-kmean-bin_44-bin_0-refined_1	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__UBA12077; g__s__	Bacteroidales	76	8.46	48
BinSanityLC-kmean-bin_57-bin_0-refined_4	d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__PHOS-HE28; g__s__	Flavobacteriales	58	5.25	88.24
BinSanityLC-kmean-bin_85-bin_0	d__Bacteria; p__Bacteroidota; c__Rhodothermia; o__Rhodothermales; f__Salinibacteraceae; g__Salinivenerus; s__	Salinivenerus	96	4.55	15.79
BinSanityLC-kmean-bin_28-bin_0-refined_2	d__Bacteria; p__Bipolaricaulota; c__Bipolaricaulia; o__RBG-16-55-9; f__RBG-16-55-9; g__s__	Bipolaricaulia	83	11.76	100
BinSanityLC-kmean-bin_24-bin_0-refined_1	d__Bacteria; p__Cyanobacteria; c__Cyanobacteriia; o__Cyanobacteriales; f__Rubridibacteraceae; g__Halotheca; s__	Halotheca	87	2.9	83.33
BinSanityLC-kmean-bin_44-bin_0-refined_9	d__Bacteria; p__Firmicutes; c__Halanaerobiia; o__Halanaerobiales; f__g__s__	Halanaerobiales	64	3.02	0
BinSanityLC-kmean-bin_13-bin_0-refined_3	d__Bacteria; p__Myxococcota; c__Bradymonadia; o__Bradymonadales; f__Bradymonadaceae; g__s__	Bradymonadaceae	53	1.94	0
BinSanityLC-kmean-bin_24-bin_0-refined_5	d__Bacteria; p__Patescibacteria; c__Paceibacteria; o__SW-4-49-11; f__SW-4-49-11; g__SW-4-49-11; s__	Paceibacteria	80	2.59	100
BinSanityLC-kmean-bin_73-bin_0-refined_4	d__Bacteria; p__Proteobacteria; c__Alphaproteobacteria; o__UBA6615; f__g__s__	Alphaproteobacteria	47	1.3	100
BinSanityLC-kmean-bin_55-bin_0-refined_6	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiohalorhabdadales; f__Thiohalorhabdaceae; g__Thiohalorhabdus; s__	Thiohalorhabdaceae.1	80	0.89	0
BinSanityLC-kmean-bin_92-bin_0-refined_3	d__Bacteria; p__Proteobacteria; c__Gammaproteobacteria; o__Thiohalorhabdadales; f__Thiohalorhabdaceae; g__Thiohalorhabdus; s__	Thiohalorhabdaceae.2	59	3.41	66.67
BinSanityLC-kmean-bin_92-bin_0-refined_6	d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Pedosphaerales; f__AV2; g__s__	Pedosphaerales	74	3.38	0

\*Completeness, Contamination, and Strain Heterogeneity Determined by CheckM

[illegible]

430316	dmgD_ynf	2-hydroxy-4-methyl-2-oxobutanoate semialdehyde hydrolase	Hydrocarbon Degratation	2.76624186	0.272967201	0.875100002	0.590989816	0.000205647	0.542811789	0.038630056	2.313260334	2.801629262	2.835738274	0.044388926	3.274872235	0.744604685	0.446274821	0.68184137	0.709384652
430317	dhac_ynf_ynfB	2-hydroxy-4-methyl-2-oxobutanoate 2-oxopropionyl dehydrogenase	Hydrocarbon Degratation	0.360128221	0.232937955	2.509044495	0.339353423	0	0.379477913	0.13652107	15.05740568	2.84692961	20.37123326	56.3475783	70.16239336	184.3121374	10.46576505	0.962362495	0.97330645
430322	dhfrB_dhfr	acetylcholine hydrolase 3-carbon thioester, acetylcholine diacylhydrazide	Hydrocarbon Degratation	0	0	0	2.01243609	0.00017584	0	0	0	0	0	0	0	0	0	0	0
431311	dhc	anthranilate 1,2-disoxygenase reductase component	Hydrocarbon Degratation	0	0	0	0.285237637	0	0	0	0	0	0	0	0	0	0	0	0
434578	dhbA_dhbA_dhbB	naphthalene 1,2-disoxygenase ferredoxin component	Hydrocarbon Degratation	0	0.114489078	0	0	0	0.183866149	0	0	0.011211808	0.74532787	0	0	0	0	0	0
434581	dhbA_dhbA_dhbB	naphthalene 1,2-disoxygenase ferredoxin reductase component	Hydrocarbon Degratation	0.05939440	0.087546817	0	0	0	0.087283018	0	0	0.59668967	0	0.877126509	0	0	0	0	0
434584	dhbD	2-hydroxy-3-methyl-2-oxobutanoate hydrolase	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
434585	dhbD	trans-4-hydroxy-2-oxobutanoate hydrolase	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431727	dhc	3-oxoadipate semialdehyde 4-carboxy-2-oxopentanoate decarboxylase	Hydrocarbon Degratation	0	0.03015508	0.972380007	0.717311316	0	0.679137389	0.181850485	0	0.709244909	0	0.153177247	0.72987265	0	0.337163237	0	0
431750	dhbA_dhbA2_dhbB	hydroxy 1,3-disoxygenase subunit beta	Hydrocarbon Degratation	0	0	0.202125387	0	0	0	0	0	0	0	0	0	0	0	0	0
431756	dhc	2-hydroxy-5-oxo-6-(4'-oxophenyl)-2,4-thiazole hydrolase	Hydrocarbon Degratation	0	0.406879908	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431761	dhcD_thuA_thuB	toluene monooxygenase system protein A	Hydrocarbon Degratation	0	0	0	0	0	0	0	0.045446832	0	0	0	0	0	0	0	0
431762	dhcD_thuA_thuB	toluene monooxygenase system protein B	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431763	dhcD_thuA_thuB	toluene monooxygenase system protein D	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431764	dhcD_thuA_thuB	toluene monooxygenase system protein E	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431246	dhcD_dhcF_thuA5	phenyltoluene 2-monooxygenase (PAHs) P450	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0.212648701	0.021950596	0	0.142360595	0	0.048601515
431248	dhcA2_dhcA2_thuA4	hydroxymethylphenylmethane dicarboxylate subunit beta	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0.212648701	0	0.345437748	0	0	0
431249	dhcA2_thuA	cis-1,2-dihydrobenzene 1,2-diol/dihydrobenzene chlorohydrate dehydrogenase	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431087	dhbA_dhbA3_dhbF	hydroxy 2,3-disoxygenase ferredoxin component	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431248	dhcA	anthranilate 1,2-disoxygenase ferredoxin component	Hydrocarbon Degratation	0	0.179334913	0	0	0	0	0	0	0.11452369	0	0	0.257502919	0	0.177592639	0	0
431249	dhcA	anthranilate 1,2-disoxygenase ferredoxin reductase component	Hydrocarbon Degratation	0	2.542317287	0	0	0	0	0	0	0.670088867	0	0	0	0	0	0	0
431364	dhcA_ynf_ynfB	2-oxopent-4-enal:nicotinamide 2-oxopent-4-enal hydrolase	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0.057205981	0	0	0	0	0	0	0
431385	dhbA	6-hydroxy-2-oxocyclohexanone dehydrogenase subunit alpha	Hydrocarbon Degratation	0	0	0	0	0	0	0.338495203	0	0	0	0	0	0	0	0	0
431385	dhbB	6-hydroxy-2-oxocyclohexanone dehydrogenase subunit beta	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431387	dhbA	6-hydroxy-2-oxocyclohexanone dehydrogenase subunit gamma	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431515	dhbB	benzoyl-CoA reductase subunit BdhB	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431516	dhbC	benzoyl-CoA reductase subunit BdhC	Hydrocarbon Degratation	0	0	0	0.142490012	0	0	0	0.0432107723	0	0	0	0	0	0	0	2.781166452
431811	dhbA	nicotinic dehydrogenase subunit A	Hydrocarbon Degratation	0	0	0	0	0	0	0	0.0421594231	0	0	0	0	0	0	0	0
431812	dhbB	nicotinic dehydrogenase subunit B	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0.701420319	0	0	0	0	0
431820	dhbC	nicotinic dehydrogenase subunit C	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
431555	dhc	4-methylumbelliferone oxidase (methylamine-forming)	Hydrocarbon Degratation	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
430170	dhcA1	nicotinic dehydrogenase	Hydrocarbon Degratation	2.058145354	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

\*Values represent transcripts per million (TPM)

**Table S4**

<b>Bin ID</b>	<b>Operon Order on Contigs</b>	<b>Form</b>
Halobacteriales.2	coxSL, coxLM	Infer form II
Halobacteriales.3	none	form II or mis-annotated
Haloarculaceae.1	coxLM	form II
Haloarculaceae.2	coxGSL, coxMS, coxLM	Infer both
Haloarculaceae.5	coxSLM, coxMSL, coxGMSL	form I, form II
Halanerobiales	coxMS, coxMSMS, coxMS, coxMS	Infer form I missing coxL

**Table S5**

Query	Reference	ANI Estimate	Matches	Total
PCN9.gz_assembly	Haloferacaceae.3	75.5033	51	981
Haloferacaceae.2	Haloarculaceae.1	75.5864	54	416
Haloarculaceae.4	Halovenus	75.5912	76	678
WSH3.gz_assembly	Haloferacaceae.2	75.6237	81	1077
Haloferacaceae.2	WSH3.gz_assembly	75.6309	59	416
WSH3.gz_assembly	Haloferacaceae.3	75.6391	51	1077
Haloarculaceae.3	Haloferacaceae.1	75.6425	52	604
Haloferacaceae.1	Haloarculaceae.3	75.6458	54	713
Halovenus	WSA2.gz_assembly	75.6842	58	605
Haloferacaceae.3	Haloarculaceae.4	75.6976	57	347
Haloarculaceae.4	Haloferacaceae.3	75.7592	57	678
Haloarculaceae.1	Haloferacaceae.1	75.7632	92	953
Halovenus	Haloarculaceae.2	75.7656	56	605
Haloarculaceae.2	Halobacteriales.2	75.7952	66	663
Halobacteriales.2	Haloarculaceae.2	75.8023	68	686
Haloarculaceae.2	Halovenus	75.8058	61	663
Halobacteriales.2	Haloarculaceae.1	75.8343	65	686
WSA2.gz_assembly	Haloarculaceae.3	75.8417	118	1248
Haloarculaceae.3	WSA2.gz_assembly	75.8542	121	604
Haloarculaceae.1	Halobacteriales.2	75.8638	64	953
WSA2.gz_assembly	Halovenus	75.8747	67	1248
Haloarculaceae.5	Halobacteriales.2	75.8963	77	824
Halovenus	Haloarculaceae.4	75.9099	64	605
Haloferacaceae.3	WSA2.gz_assembly	75.9147	84	347
WSA2.gz_assembly	Haloferacaceae.3	75.9204	93	1248
PCN9.gz_assembly	Halovenus	75.9496	75	981
Halobacteriales.2	Haloarculaceae.5	75.9543	87	686
WSA2.gz_assembly	Halobacteriales.2	75.9709	104	1248
Haloferacaceae.2	Haloarculaceae.5	75.9789	57	416
Haloarculaceae.1	Haloferacaceae.2	75.9804	54	953
Halobacteriales.2	Haloferacaceae.1	75.9858	60	686
PCN9.gz_assembly	Halobacteriales.2	75.996	70	981
Haloferacaceae.2	Haloarculaceae.4	76.0114	57	416
Halobacteriales.2	Haloarculaceae.4	76.0409	81	686

Haloferacaceae.1	Halobacteriales.2	76.0496	53	713
Haloarculaceae.4	Halobacteriales.2	76.0591	70	678
Halobacteriales.2	PCN9.gz_assembly	76.067	58	686
Halobacteriales.2	WSA2.gz_assembly	76.0745	101	686
Haloarculaceae.4	Haloferacaceae.2	76.1068	60	678
Haloarculaceae.3	Haloarculaceae.4	76.1343	124	604
PCN9.gz_assembly	Haloarculaceae.3	76.1655	107	981
PCN9.gz_assembly	Haloarculaceae.2	76.2202	157	981
Haloarculaceae.2	Haloferacaceae.1	76.2264	100	663
Haloarculaceae.5	Haloferacaceae.2	76.2338	55	824
Haloarculaceae.2	PCN9.gz_assembly	76.2443	159	663
Haloferacaceae.1	Haloarculaceae.1	76.2665	95	713
WSH3.gz_assembly	Halobacteriales.2	76.2729	94	1077
Haloferacaceae.1	Haloarculaceae.2	76.2759	94	713
PCN9.gz_assembly	Haloferacaceae.1	76.276	164	981
Halovenus	PCN9.gz_assembly	76.3011	66	605
Haloarculaceae.3	PCN9.gz_assembly	76.3024	103	604
Haloarculaceae.4	Haloarculaceae.3	76.3097	119	678
PCN9.gz_assembly	Haloferacaceae.2	76.3385	78	981
Haloarculaceae.2	WSA2.gz_assembly	76.3494	195	663
Halovenus	Haloarculaceae.5	76.3631	89	605
Halobacteriales.2	WSH3.gz_assembly	76.3671	83	686
Haloarculaceae.5	Halovenus	76.3789	92	824
WSA2.gz_assembly	Haloarculaceae.2	76.4137	209	1248
Haloarculaceae.5	Haloferacaceae.1	76.4297	99	824
Haloferacaceae.2	PCN9.gz_assembly	76.4777	61	416
Haloferacaceae.1	PCN9.gz_assembly	76.5038	147	713
PCN9.gz_assembly	Haloarculaceae.1	76.5093	226	981
Halovenus	Haloarculaceae.1	76.5207	76	605
Haloferacaceae.1	Haloarculaceae.5	76.5286	91	713
Haloferacaceae.1	WSH3.gz_assembly	76.5404	121	713
WSH3.gz_assembly	Haloferacaceae.1	76.5728	136	1077
WSH3.gz_assembly	Haloarculaceae.2	76.5878	217	1077
Haloarculaceae.3	Haloarculaceae.2	76.6097	124	604
Haloarculaceae.2	Haloarculaceae.3	76.6156	108	663
Haloferacaceae.1	Haloarculaceae.4	76.623	182	713

Haloarculaceae.1	PCN9.gz_assembly	76.6728	220	953
PCN9.gz_assembly	WSH3.gz_assembly	76.688	189	981
Haloarculaceae.4	Haloferacaceae.1	76.6991	166	678
Haloarculaceae.1	WSA2.gz_assembly	76.7738	235	953
Haloarculaceae.2	WSH3.gz_assembly	76.7878	201	663
WSA2.gz_assembly	Haloarculaceae.1	76.8051	263	1248
Haloarculaceae.1	Haloarculaceae.3	76.8539	153	953
WSA2.gz_assembly	Haloarculaceae.5	76.8577	265	1248
WSH3.gz_assembly	PCN9.gz_assembly	76.8622	178	1077
Haloarculaceae.1	Halovenus	76.8764	81	953
PCN9.gz_assembly	Haloarculaceae.5	76.9259	233	981
Haloarculaceae.3	Haloarculaceae.1	76.9321	154	604
PCN9.gz_assembly	Haloarculaceae.4	76.9435	259	981
Haloferacaceae.2	WSA2.gz_assembly	76.9708	128	416
Haloferacaceae.1	Haloferacaceae.3	76.9895	96	713
Haloarculaceae.4	PCN9.gz_assembly	76.9934	249	678
Haloarculaceae.2	Haloarculaceae.4	77.0054	206	663
WSA2.gz_assembly	WSH3.gz_assembly	77.0281	287	1248
Haloarculaceae.5	WSA2.gz_assembly	77.0404	254	824
Haloarculaceae.4	Haloarculaceae.2	77.0858	218	678
WSA2.gz_assembly	Haloferacaceae.2	77.0998	144	1248
WSH3.gz_assembly	WSA2.gz_assembly	77.1226	281	1077
Haloarculaceae.4	Haloarculaceae.1	77.151	233	678
WSH3.gz_assembly	Haloarculaceae.4	77.1535	256	1077
Haloarculaceae.1	Haloarculaceae.4	77.2056	233	953
Haloarculaceae.4	WSH3.gz_assembly	77.2218	234	678
Haloferacaceae.3	Haloferacaceae.1	77.2904	98	347
WSH3.gz_assembly	Haloarculaceae.3	77.3682	184	1077
Haloarculaceae.1	Haloarculaceae.2	77.374	175	953
WSA2.gz_assembly	Haloferacaceae.1	77.3798	299	1248
Haloarculaceae.2	Haloarculaceae.1	77.4171	173	663
Haloarculaceae.5	PCN9.gz_assembly	77.4383	202	824
Haloarculaceae.3	WSH3.gz_assembly	77.4672	175	604
Haloferacaceae.1	WSA2.gz_assembly	77.4823	282	713
Haloarculaceae.5	Haloarculaceae.3	77.5149	163	824
WSA2.gz_assembly	Haloarculaceae.4	77.5401	334	1248



Haloarculaceae.4	WSA2.gz_assembly	77.5402	325	678
WSH3.gz_assembly	Haloarculaceae.1	77.6034	272	1077
WSH3.gz_assembly	Haloarculaceae.5	77.654	273	1077
Haloarculaceae.4	Haloarculaceae.5	77.6572	243	678
Haloarculaceae.5	Haloarculaceae.4	77.6658	245	824
Haloarculaceae.3	Haloarculaceae.5	77.6723	164	604
Haloarculaceae.1	WSH3.gz_assembly	77.7218	250	953
PCN9.gz_assembly	WSA2.gz_assembly	77.7903	357	981
Haloferacaceae.1	Haloferacaceae.2	77.7996	147	713
Haloferacaceae.2	Haloferacaceae.1	77.8223	144	416
Haloarculaceae.5	WSH3.gz_assembly	77.9163	272	824
WSA2.gz_assembly	PCN9.gz_assembly	77.93	348	1248
Haloarculaceae.1	Haloarculaceae.5	78.4522	267	953
Haloarculaceae.5	Haloarculaceae.1	78.6182	271	824
Halovenus	WSH3.gz_assembly	79.7953	340	605
WSH3.gz_assembly	Halovenus	79.933	331	1077
Halovenus	Haloarculaceae.3	81.4079	105	605
Haloarculaceae.3	Halovenus	81.5705	111	604
Haloarculaceae.5	Haloarculaceae.2	85.8727	359	824
Haloarculaceae.2	Haloarculaceae.5	85.9246	370	663

Table S6

Gene ID	Gene	Best BLAST Hit	Acession #	% ID	E-value
<b>12B.1 Metagenome</b>					
c_000000339582_1	<i>nifD</i>	<i>Chloroflexaceae bacterium</i> (stromatolite metagenome)	NJN65560.1	56.36	1.00E-138
c_000000029304_3	<i>nifD</i>	<i>Chloroflexaceae bacterium</i> (stromatolite metagenome)	NJN65560.1	57.2	3.00E-100
c_000000286385_1	<i>nifD</i>	<i>Chloroflexaceae bacterium</i> (stromatolite metagenome)	NJN65560.1	55.86	2.00E-129
c_000000146019_1	<i>nifH</i>	<i>Halorhodospira halochloris</i>	BAU57913.1	84.11	5.00E-89
c_000000150855_1	<i>nifH</i>	<i>Roseiflexus sp. RS-1</i>	WP_011955961.1	75.68	3.00E-99
c_000000412048_2	<i>nifH</i>	<i>Roseiflexus castenholzii</i>	WP_012122497.1	70.09	4.00E-44
c_000000419371_3	<i>nifH</i>	<i>Roseiflexus sp. RS-1</i>	WP_011955961.1	72.69	2.00E-142
c_000000029304_2	<i>nifK</i>	archaeon BMS3Bbin16	GBE57063.1	54.3	0
c_000000266741_1	<i>nifK</i>	archaeon BMS3Abin16	GBE18617.1	56.92	8.00E-50
c_000000348638_1	<i>nifK</i>	archaeon BMS3Abin16	GBE18617.1	54.92	1.00E-40
c_000000476483_1	<i>nifK</i>	archaeon BMS3Bbin16	GBE57063.1	56.07	2.00E-32
<b>67B.1 Metagenome</b>					
c_000000142325_1	<i>nifD</i>	<i>Rhodovibrio salinarum</i>	WP_027289759.1	90.7	1.00E-47
<b>12B.2 Metagenome</b>					
c_000000324579_1	<i>nifD</i>	<i>Rhodovibrio salinarum</i>	WP_027289759.1	84.58	0.00E+00
c_000000324579_2	<i>nifH</i>	<i>Rhodoplanes serenus</i>	WP_155481001.1	81.82	1.00E-16
c_000000210854_1	<i>nifH</i>	<i>Rhodovibrio salinarum</i>	WP_027289758.1	90.87	1.00E-154
c_000000219157_1	<i>nifK</i>	<i>Rhodovibrio salinarum</i>	WP_027289760.1	83.64	7.00E-134
<b>33.2 Metagenome</b>					
c_000000151043_1	<i>nifD</i>	<i>Deltaproteobacteria bacterium</i> (wastewater metagenome)	NCC26223.1	78	3.00E-143
c_000000156957_1	<i>nifD</i>	<i>Desulfovibrio brasiliensis</i>	WP_054649226.1	78.31	4.00E-38
c_000000055755_1	<i>nifH</i>	<i>Desulfobulbus sp. Tol-SR</i>	KGO35492.1	88.89	3.00E-49
c_000000074817_2	<i>nifH</i>	<i>Deltaproteobacteria bacterium</i> (wastewater metagenome)	NCC25938.1	82.78	2.00E-170
c_000000066890_1	<i>nifK</i>	<i>Desulfovibrio gilchinskyi</i>	WP_085099001.1	78.9	1.00E-59
c_000000105010_1	<i>nifK</i>	<i>Desulfocurvus vexinensis</i>	WP_028586618.1	82.76	2.00E-49
<b>35.2 Metagenome</b>					
c_000000163780_1	<i>nifD</i>	Candidatus <i>Electrothrix aarhusiensis</i> ( <i>Desulfbulbaceae</i> )	RWX47654.1	71.17	9.00E-85
c_000000144626_1	<i>nifD</i>	<i>Rhodovibrio salinarum</i>	WP_027289759.1	83.33	2.00E-96
c_000000242108_1	<i>nifK</i>	<i>Halorhodospira halophila</i>	WP_011813089.1	76.42	2.00E-53

Table S7

Gene ID	Gene Name	Best BLAST Hit	Accession #	% ID	E-value
<b>12B.2 Metagenome</b>					
c_00000000782_2	dsrA	uncultured Desulfohalobiaceae bacterium (MgCl <sub>2</sub> -containing environments)	ABD38984.1	87.805	2.23E-20
c_00000000782_1	dsrB	Desulfovermiculus halophilus	WP_027370030.1	81.05	0
c_000000307376_1	dsrB	Desulfovermiculus halophilus	WP_027370031.1	79.487	1.72E-113
<b>67B.2 Metagenome</b>					
c_000000052251_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	95.489	4.30E-89
c_000000096034_1	dsrA	Betaproteobacteria bacterium (groundwater environment)	MBI3042764.1	61.224	8.99E-34
c_000000263801_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	91.71	3.68E-128
c_000000328055_1	dsrA	Desulfovermiculus halophilus	WP_027370030.1	84.516	5.50E-80
c_000000431746_4	dsrA	uncultured Desulfohalobiaceae bacterium (MgCl <sub>2</sub> -containing environments)	ABD38987.1	98	1.04E-25
c_000000552184_1	dsrA	Desulfovermiculus halophilus	WP_027370030.1	83.133	4.03E-144
c_000000263801_2	dsrB	Desulfovermiculus halophilus	WP_027370031.1	82.544	0
c_000000423115_1	dsrB	Gammaproteobacteria bacterium HGW-Gammaproteobacteria-1 (groundwater metagenome)	PKM45266.1	78.431	4.51E-55
c_000000431746_3	dsrB	Desulfovermiculus halophilus	WP_027370031.1	84.557	0
c_000000652016_2	dsrB	Candidatus Reidiella endopervernicosa	WP_078483318.1	74.638	5.54E-71
<b>29.2 Metagenome</b>					
c_000000349271_2	dsrA	Desulfovermiculus halophilus	WP_027370030.1	81.507	0
c_000000158655_1	dsrB	Desulfovermiculus halophilus	WP_027370031.1	78.824	6.07E-42
c_000000349271_1	dsrB	Desulfovermiculus halophilus	WP_027370031.1	83.578	0
<b>33.2 Metagenome</b>					
c_000000095341_6	dsrA	Desulfovermiculus halophilus	WP_027370030.1	81.735	0
c_000000115348_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	98.013	1.01E-103
c_000000154383_1	dsrA	Desulfovermiculus halophilus	WP_027370030.1	84.131	0
c_000000440998_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	94.841	7.52E-179
c_000000470085_1	dsrA	Desulfovermiculus halophilus	WP_027370030.1	83.784	2.90E-75
c_000000095341_7	dsrB	Desulfovermiculus halophilus	WP_027370031.1	82.544	0
c_000000099172_1	dsrB	Desulfovibrionales bacterium (anaerobic digester metagenome)	NLW80111.1	84.706	1.53E-50
c_000000115348_2	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45533.1	94.924	2.14E-142
c_000000138427_1	dsrB	Desulfovermiculus halophilus	WP_027370031.1	83.465	2.03E-73
c_000000182614_1	dsrB	Desulfovermiculus halophilus	WP_027370031.1	84.255	1.03E-150
<b>35.1 Metagenome</b>					
c_000000234629_1	dsrA	Halorhodospira halophila	WP_201171943.1	90.323	0
c_000000667957_1	dsrA	Thiobacillus denitrificans	WP_011311881.1	70.27	1.11E-29
c_000000698539_6	dsrA	Desulfovermiculus halophilus	WP_027370030.1	81.735	0
c_000000698539_5	dsrB	Desulfovermiculus halophilus	WP_027370031.1	82.045	0
<b>35.2 Metagenome</b>					
c_000000146673_4	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	93.214	0
c_000000196400_16	dsrA	Desulfovermiculus halophilus	WP_027370030.1	81.34	1.94E-113
c_000000146673_3	dsrB	Desulfovermiculus halophilus	WP_027370031.1	82.294	0
c_000000507418_1	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45525.1	94.624	1.53E-129
<b>35.3 Metagenome</b>					
c_000000154008_1	dsrA	Desulfovermiculus halophilus	WP_027370030.1	82.609	3.86E-146
c_000000154017_1	dsrA	Desulfovermiculus halophilus	WP_027370030.1	86.611	7.69E-144
c_000000699647_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45524.1	93.798	6.79E-83
c_000000614952_1	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45543.1	85.143	2.36E-110
c_000000743744_3	dsrB	Desulfovermiculus halophilus	WP_027370031.1	83.399	6.52E-160
<b>56.2 Metagenome</b>					
c_000000223435_2	dsrA	Desulfohalobium retbaense	WP_015750705.1	80.899	6.03E-90
c_000000481738_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	90.526	1.36E-55
c_000000296478_1	dsrB	Desulfovibrio sp. (anaerobic digester metagenome)	NMC50171.1	82	5.35E-58
c_000000481738_2	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45535.1	86.512	1.81E-142
<b>56.3 Metagenome</b>					
c_000000266214_1	dsrA	Desulfonatronovibrio magnus	WP_045212625.1	82.639	5.23E-68
c_000000310384_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	90	6.89E-73
c_000000083255_1	dsrB	Candidatus Reidiella endopervernicosa	WP_078483318.1	75	8.36E-34
c_000000129612_1	dsrB	Sulfurifustis variabilis	WP_096457663.1	77.348	2.88E-103
c_000000310384_2	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45533.1	89.706	1.46E-41
<b>46.2 Metagenome</b>					
c_000000109617_1	dsrA	uncultured prokaryote (GSL sediments)	ABD46878.1	94.958	8.99E-78
c_000000109642_9	dsrA	Desulfovermiculus halophilus	WP_027370030.1	81.579	3.78E-154
c_000000123025_2	dsrA	Desulfomicrobium norvegicum	WP_092194128.1	74.576	2.38E-23
c_000000169346_1	dsrA	Gammaproteobacteria bacterium (hydrothermal sediment)	RKZ39678.1	72.678	8.41E-96
c_000000196300_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	97.143	1.23E-94
c_000000206341_1	dsrA	Desulfonatronovibrio magnus	WP_045212625.1	83.333	6.74E-35
c_000000225585_8	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	91.365	0
c_000000388521_2	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	95.652	4.07E-39
c_000000388564_2	dsrA	Desulfovermiculus halophilus	WP_027370030.1	82.877	0
c_000000442685_1	dsrA	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45532.1	99.057	2.05E-70
c_000000483844_2	dsrA	uncultured microorganism (hydrothermal fluid)	AJA06229.1	62.903	2.71E-20
c_000000537023_1	dsrA	Archaeoglobaceae archaeon (Mid-Cayman Rise Vent Fluids)	HID42311.1	68.77	6.00E-168
c_000000544283_1	dsrA	uncultured prokaryote (GSL sediments)	ABD46878.1	93.45	3.67E-161
c_000000544595_1	dsrA	uncultured prokaryote (GSL sediments)	ABD46870.1	93.023	2.23E-81
c_000000655084_1	dsrA	uncultured prokaryote (GSL sediments)	ABD46878.1	91.818	6.03E-69
c_00000069099_1	dsrB	Archaeoglobus sp. (hot spring sediment)	HGQ78171.1	76.033	5.44E-63
c_000000122840_1	dsrB	Betaproteobacteria bacterium (soil metagenome)	HAN56732.1	75.806	3.70E-26
c_000000225585_7	dsrB	Desulfovermiculus halophilus	WP_027370031.1	82.544	0
c_000000276611_1	dsrB	Magnetococcus bacterium (lake sediments)	MBF0613955.1	73.786	2.98E-48
c_000000312408_3	dsrB	Desulfobacteraceae bacterium SEEP-SAG9 (marine sediment)	PQP34394.1	87.273	5.54E-31
c_000000388521_1	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45525.1	94.286	6.10E-96
c_000000388564_1	dsrB	uncultured sulfate-reducing bacterium (Mediterranean solar saltern)	ACM45533.1	95	4.59E-96
c_000000483844_1	dsrB	uncultured microorganism (hydrothermal fluid)	AJA06230.1	61.224	2.29E-64
c_000000539054_3	dsrB	Desulfovermiculus halophilus	WP_027370031.1	86.093	0

c_000000545959_1	<i>dsrB</i>	Desulfovibrio ferrophilus	WP_126380811.1	84.685	6.96E-65
c_000000658443_1	<i>dsrB</i>	Desulfohalophilus alkaliarsenatis	AFJ04155.1	88.462	3.42E-63