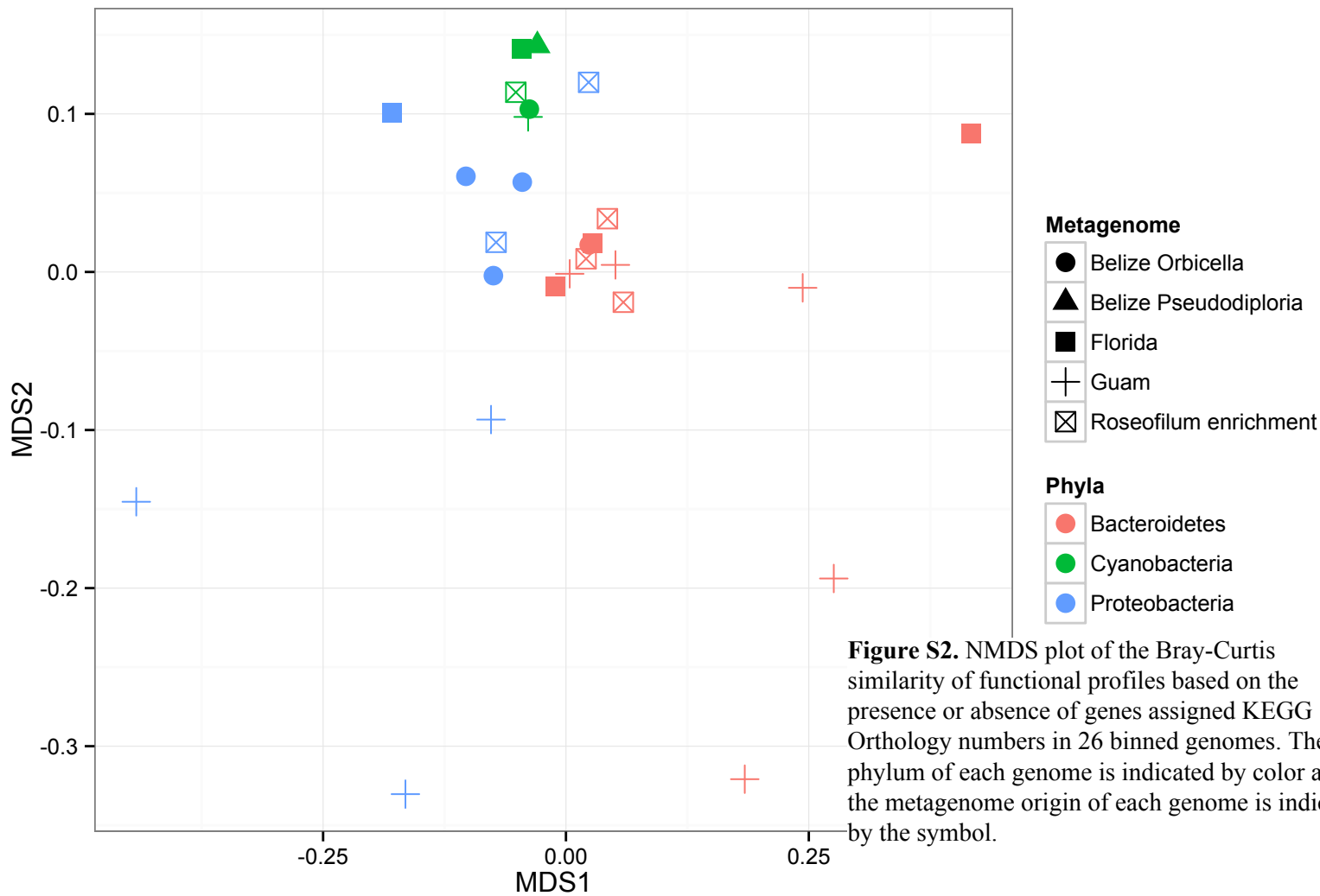


Figure S1. Comparison of A) the coverage (number of sequencing reads mapped to assembled metagenomes) of functional genes assigned to phyla in the non-axenic *Roseofilum* culture and four Black Band Disease mats and B) the relative abundance of 16S amplicon sequences assigned to major bacterial phyla in the same samples.



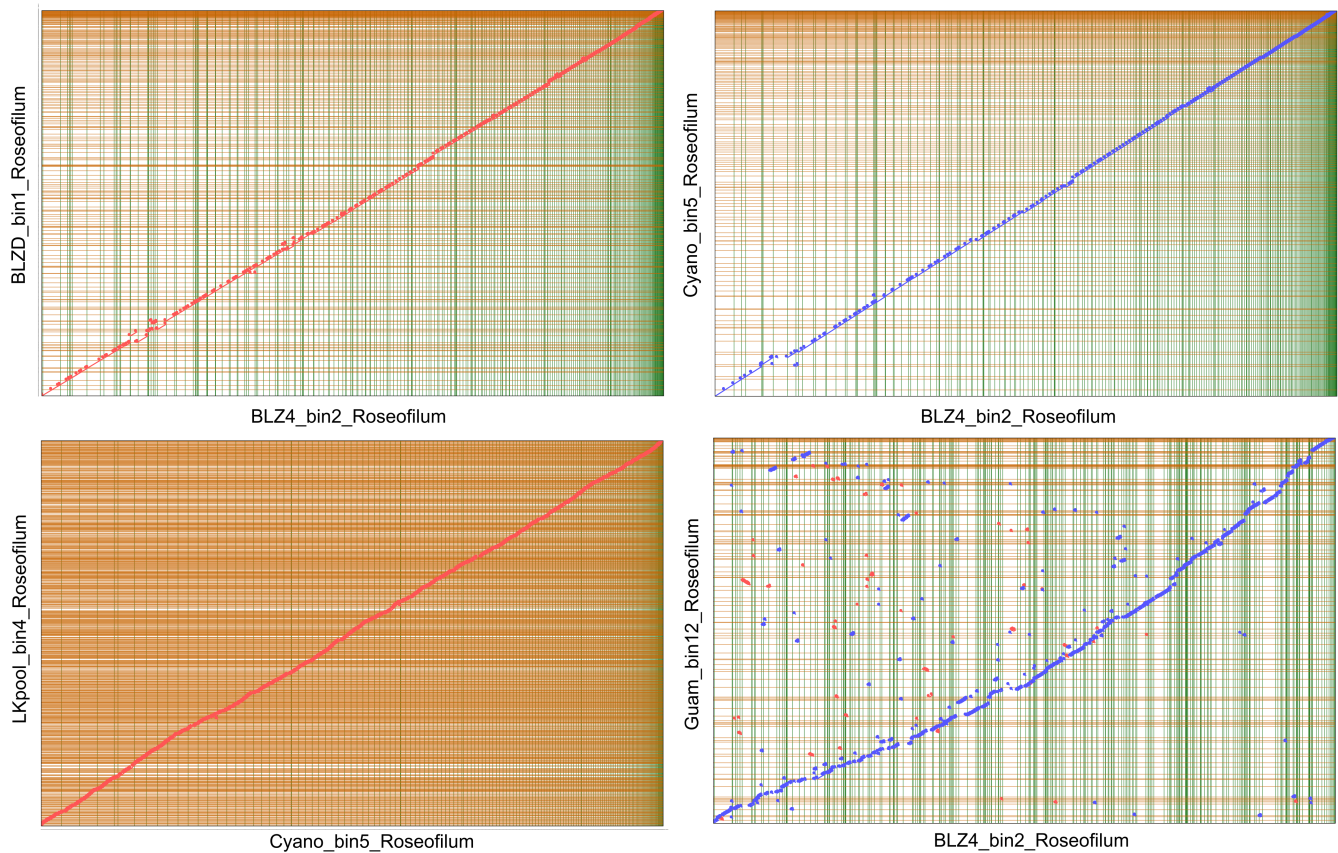


Figure S3. Pairwise dot-plot comparisons of the contigs in *Roseofilum* genomes demonstrates high gene synteny among the four Caribbean-based samples and greater genome rearrangements in the Guam sample.

Table S1. Summary of sample characteristics for 54 coral surface microbiomes and 1 *Roseofilum* culture used to assess bacterial community structure based on the V6 hypervariable region of 16S rRNA genes.

Sample	Health	Location	Coral Host	Collection Date	Sequences
A46BB	Black Band	Belize ¹	<i>Orbicella annularis</i>	Aug-14	374,772
A50BB	Black Band	Belize	<i>Orbicella faveolata</i>	Aug-14	197,198
BLZ2	Black Band	Belize	<i>Orbicella annularis</i>	Jul-13	126,593
BLZ4*	Black Band	Belize	<i>Orbicella annularis</i>	Jul-13	103,407
BLZ5	Black Band	Belize	<i>Orbicella annularis</i>	Jul-13	85,287
J32BB	Black Band	Belize	<i>Orbicella annularis</i>	Jul-13	232,079
MNC	Black Band	Belize	<i>Orbicella annularis</i>	Aug-14	264,985
BOF	Black Band	Belize	<i>Orbicella faveolata</i>	Aug-14	475,847
DCL	Black Band	Belize	<i>Pseudodiploria clivosa</i>	Aug-14	9,498
BPS	Black Band	Belize	<i>Pseudodiploria strigosa</i>	Aug-14	222,362
DBB	Black Band	Belize	<i>Pseudodiploria strigosa</i>	Aug-14	210,565
A28NC	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	19,215
A33NC	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	86,598
A44NC	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	40,109
F32NC	Healthy Coral	Belize	<i>Orbicella annularis</i>	Feb-13	582,387
M40FT	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	76,764
M47FT	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	95,249
M57FT	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	92,464
M61FTA	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	97,566
M61FTB	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	279,181
M70FT	Healthy Coral	Belize	<i>Orbicella annularis</i>	Aug-14	438,975
A46NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Aug-14	27,814
A50NC	Healthy Tissue	Belize	<i>Orbicella faveolata</i>	Aug-14	184,473
F28NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Feb-13	605,049
F29NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Feb-13	749,884
F33NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Feb-13	300,367
F44NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Feb-13	476,809
F50NC	Healthy Tissue	Belize	<i>Orbicella faveolata</i>	Feb-13	486,621
J32NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Jul-13	6,577
J44HE	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Jul-13	78,016
J44NC	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Jul-13	33,238
MBB	Healthy Tissue	Belize	<i>Orbicella annularis</i>	Aug-14	82,393
DNC	Healthy Tissue	Belize	<i>Pseudodiploria strigosa</i>	Aug-14	218,292
BLZD*	Black Band	Belize	<i>Pseudodiploria strigosa</i>	Feb-13	155,453
FL1	Black Band	Florida	<i>Montastraea cavernosa</i>	May-13	115,256
FL2	Black Band	Florida ²	<i>Montastraea cavernosa</i>	May-13	408,160
FL4	Black Band	Florida	<i>Montastraea cavernosa</i>	May-13	335,680
FL5	Black Band	Florida	<i>Montastraea cavernosa</i>	May-13	57,362
LK1 ⁺	Black Band	Florida	<i>Montastraea cavernosa</i>	Jun-13	244,667
LK2 ⁺	Black Band	Florida	<i>Orbicella faveolata</i>	Jun-13	158,302
LK4 ⁺	Black Band	Florida	<i>Orbicella faveolata</i>	Jun-13	219,775
Cyano*	Enrichment culture	Florida	<i>Montastraea cavernosa</i>	Apr-14	524,581
FLA	Black Band	Florida	<i>Montastraea cavernosa</i>	Apr-14	229,768
FLB	Black Band	Florida	<i>Montastraea cavernosa</i>	Apr-14	152,408
FLC	Black Band	Florida	<i>Montastraea cavernosa</i>	Apr-14	342,213
FLA1	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	159,649
FLA2	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	133,858
FLB1	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	70,947

FLB2	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	185,161
FLB3	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	356,762
FLC1	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	136,954
FLC2	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	357,678
FLC3	Healthy Tissue	Florida	<i>Montastraea cavernosa</i>	Apr-14	127,307
Guam1*	Black Band	Guam ³	<i>Goniopora fruticosa</i>	Jun-14	335,373
Guam2	Black Band	Guam	<i>Goniopora fruticosa</i>	Jun-14	280,831

* Metagenomic sequencing also performed on these samples.

⁺ Florida samples pooled for metagenomic sequencing.

¹ Carrie Bow Cay, Belize: 16.797 N, 88.084 W

² Looe Key Reef, Florida, USA: 24.548 N, 81.406 W

³ Luminao Reef Flat, Guam: 13.464 N, 144.644 E

Table S2. Characteristics of metagenomes from Black Band Disease mats and cultured *Roseofilum reptotaenium*.

Metagenome locus tag	Cyano	LKpool	BLZ4	BLZD	Guam
IMG Genome ID	3300003272	3300003311	3300003317	3300003641	3300003309
Collection location	Looe Key Reef, Florida	Looe Key Reef, Florida	Carrie Bow Cay, Belize	Carrie Bow Cay, Belize	Luminao Reef Flat, Guam
Collection date	April 2014	June 2013	July 2013	Feb 2013	June 2014
Coral host	<i>Roseofilum</i> culture, isolated from <i>Montastraea cavernosa</i>	pooled: <i>Montastraea cavernosa</i> and <i>Orbicella faveolata</i>	<i>Orbicella annularis</i>	<i>Pseudodiploria strigosa</i>	<i>Goniopora fruticosa</i>
Read pairs	34,974,648	32,180,161	34,193,363	16,853,081	44,199,247
SRA Accession	SRX1017628	SRX1017632	SRX894068	SRX894049	SRX1017629
Scaffolds	62,162	186,345	524,359	56,139	151,976
Total length of contigs (bp)	117,262,816	124,960,495	279,467,519	34,028,000	113,479,370
Protein coding genes	145,980	238,319	612,757	69,548	207,250
Proportion of reads mapped to assembled scaffolds	92%	61%	72%	41%	71%
Estimated sequencing coverage	90%	85%	87%	99%	84%
Estimated number of genomes in metagenome	19 - 22	14 - 17	6 - 19	2 - 4	7 - 24
Binned genomes	6	5	5	1	9

Table S3. Phylogenetic distribution of genes in metagenome assemblies from Black Band Disease mats and cultured *Roseofilum reptotaenium*.

Domain	Phylum	Cyano	Cyano	Guam	Guam	LKpool	LKpool	BLZ4	BLZ4	BLZD	BLZD
		3300003272	3300003272	3300003309	3300003309	3300003311	3300003311	3300003317	3300003317	3300003641	3300003641
		Gene Count	%	Gene Count	%	Gene Count	%	Gene Count	%	Gene Count	%
Bacteria	Bacteroidetes	20329	13.93	25494	12.3	30784	12.92	17397	2.84	5904	8.49
Bacteria	Proteobacteria	18877	12.93	25163	12.14	15006	6.3	29159	4.76	3920	5.64
Bacteria	Cyanobacteria	4460	3.06	3679	1.78	4119	1.73	5939	0.97	2778	3.99
Bacteria	Firmicutes	3086	2.11	3922	1.89	9370	3.93	11437	1.87	1858	2.67
Bacteria	Actinobacteria	2174	1.49	762	0.37	1056	0.44	3356	0.55	408	0.59
Bacteria	Cloacimonetes	60	0.04	124	0.06	106	0.04	199	0.03	371	0.53
Bacteria	Verrucomicrobia	1927	1.32	277	0.13	390	0.16	1206	0.2	189	0.27
Archaea	Euryarchaeota	612	0.42	427	0.21	553	0.23	2254	0.37	166	0.24
Bacteria	Spirochaetes	433	0.3	484	0.23	766	0.32	1368	0.22	155	0.22
Bacteria	Lentisphaerae	306	0.21	26	0.01	625	0.26	617	0.1	143	0.21
Bacteria	Planctomycetes	12015	8.23	255	0.12	418	0.18	862	0.14	140	0.2
Bacteria	Fusobacteria	66	0.05	145	0.07	294	0.12	474	0.08	72	0.1
Bacteria	Chloroflexi	2136	1.46	141	0.07	160	0.07	474	0.08	68	0.1
Bacteria	Chlorobi	148	0.1	180	0.09	187	0.08	233	0.04	53	0.08
Bacteria	Acidobacteria	474	0.32	110	0.05	119	0.05	323	0.05	39	0.06
Bacteria	Ignavibacteriae	106	0.07	839	0.4	153	0.06	156	0.03	39	0.06
Bacteria	Thermotogae	50	0.03	39	0.02	85	0.04	237	0.04	34	0.05
Bacteria	Aquificae	70	0.05	54	0.03	79	0.03	308	0.05	26	0.04
Bacteria	Deinococcus-Thermus	389	0.27	85	0.04	73	0.03	247	0.04	31	0.04
Bacteria	Aminicenantes	112	0.08	105	0.05	89	0.04	113	0.02	26	0.04
Archaea	Crenarchaeota	69	0.05	48	0.02	57	0.02	564	0.09	19	0.03
Bacteria	Chlamydiae	65	0.04	42	0.02	37	0.02	241	0.04	19	0.03
Bacteria	Synergistetes	43	0.03	40	0.02	66	0.03	99	0.02	24	0.03
Bacteria	Marinimicrobia	56	0.04	57	0.03	85	0.04	125	0.02	18	0.03
Bacteria	Caldithrixae	62	0.04	100	0.05	80	0.03	134	0.02	21	0.03
Bacteria	Tenericutes	38	0.03	53	0.03	61	0.03	539	0.09	14	0.02
Bacteria	Deferribacteres	39	0.03	43	0.02	74	0.03	163	0.03	15	0.02
Bacteria	Atribacteria	29	0.02	46	0.02	79	0.03	53	0.01	11	0.02
Bacteria	Latescibacteria	88	0.06	47	0.02	78	0.03	79	0.01	16	0.02
Bacteria	unclassified	29	0.02	46	0.02	46	0.02	56	0.01	11	0.02
Bacteria	Parcubacteria	9	0.01	11	0.01	16	0.01	102	0.02	10	0.01
Bacteria	Thermodesulfobacteria	31	0.02	14	0.01	27	0.01	94	0.02	4	0.01
Bacteria	Nitrospirae	43	0.03	21	0.01	27	0.01	51	0.01	6	0.01
Bacteria	Hydrogenedentes	33	0.02	9	0	21	0.01	36	0.01	4	0.01
Bacteria	Fibrobacteres	25	0.02	21	0.01	39	0.02	39	0.01	8	0.01
Bacteria	Gemmatimonadetes	93	0.06	19	0.01	20	0.01	64	0.01	8	0.01
Bacteria	BRC1	73	0.05	12	0.01	27	0.01	34	0.01	8	0.01
Bacteria	Poribacteria	48	0.03	9	0	15	0.01	34	0.01	9	0.01
Bacteria	Aerophobetes	33	0.02	17	0.01	18	0.01	22	0	8	0.01
Bacteria	Armatimonadetes	69	0.05	10	0	10	0	22	0	4	0.01
Archaea	Thaumarchaeota	11	0.01	10	0	10	0	106	0.02	2	0
Bacteria	Gracilibacteria	4	0	24	0.01	12	0.01	119	0.02	0	0
Archaea	Aigarchaeota	6	0	11	0.01	3	0	40	0.01	0	0
Bacteria	Microgenomates	4	0	1	0	2	0	47	0.01	0	0
Bacteria	Chrysiogenetes	18	0.01	9	0	9	0	33	0.01	1	0
Bacteria	Dictyoglomi	15	0.01	8	0	14	0.01	50	0.01	0	0
Archaea	Candidatus Korarchaeota	7	0	4	0	5	0	58	0.01	2	0
Bacteria	Nitrospirinae	39	0.03	9	0	25	0.01	39	0.01	3	0
Bacteria	Calescamantes	7	0	2	0	4	0	22	0	0	0
Bacteria	Fervidibacteria	27	0.02	5	0	6	0	16	0	1	0
Bacteria	Omnitrophica	34	0.02	8	0	11	0	24	0	2	0
Archaea	Diapherotrites	5	0	4	0	4	0	21	0	0	0
Bacteria	Caldiserica	4	0	1	0	5	0	22	0	0	0
Bacteria	Candidatus Saccharibacteria	4	0	0	0	4	0	28	0	0	0
Bacteria	Elusimicrobia	3	0	2	0	8	0	5	0	1	0
Bacteria	Acetothermia	4	0	4	0	7	0	2	0	1	0
Bacteria	EM3	2	0	0	0	0	0	1	0	0	0
Bacteria	PER	1	0	4	0	3	0	30	0	2	0
Bacteria	WS1	6	0	2	0	1	0	3	0	2	0

Table S5. Genes associated with nitrogen and sulfur cycling in Black Band Disease metagenome-assembled genomes.

IMG gene_oid	IMG Locus Tag	Gene Product Name	IMG Genome ID	Genome Name
2628137143	Ga0079951_10908	cyanophycin synthetase	2627853583	Cyano_bin9_Gammaproteobacteria Ga0079951
2628137144	Ga0079951_10909	cyanophycin synthetase	2627853583	Cyano_bin9_Gammaproteobacteria Ga0079951
2628137703	Ga0079951_11613	cyanophycinase	2627853583	Cyano_bin9_Gammaproteobacteria Ga0079951
2628137704	Ga0079951_11614	cyanophycin synthetase	2627853583	Cyano_bin9_Gammaproteobacteria Ga0079951
2628068922	Ga0079929_112012	cyanophycin synthetase	2627853561	Roseofilum sp. BLZ4_bin2 Ga0079929
2628067756	Ga0079929_10588	cyanophycinase	2627853561	Roseofilum sp. BLZ4_bin2 Ga0079929
2628068923	Ga0079929_112013	cyanophycinase	2627853561	Roseofilum sp. BLZ4_bin2 Ga0079929
2628072855	Ga0079930_105840	cyanophycin synthetase	2627853562	Roseofilum sp. BLZD_bin1 Ga0079930
2628072856	Ga0079930_105841	cyanophycinase	2627853562	Roseofilum sp. BLZD_bin1 Ga0079930
2628072760	Ga0079930_105511	cyanophycinase	2627853562	Roseofilum sp. BLZD_bin1 Ga0079930
2628058810	Ga0079927_105340	cyanophycin synthetase	2627853559	Roseofilum sp. Cyano_bin5 Ga0079927
2628059528	Ga0079927_10888	cyanophycinase	2627853559	Roseofilum sp. Cyano_bin5 Ga0079927
2628058811	Ga0079927_105341	cyanophycinase	2627853559	Roseofilum sp. Cyano_bin5 Ga0079927
2628062588	Ga0079928_102436	cyanophycin synthetase	2627853560	Roseofilum sp. Guam_bin12 Ga0079928
2628062589	Ga0079928_102437	cyanophycinase	2627853560	Roseofilum sp. Guam_bin12 Ga0079928
2628062244	Ga0079928_101985	cyanophycinase	2627853560	Roseofilum sp. Guam_bin12 Ga0079928
2628077039	Ga0079931_13262	cyanophycinase	2627853563	Roseofilum sp. LKpool_bin4 Ga0079931
2628062393	Ga0079928_102162	Mo-nitrogenase MoFe protein subunit NifK	2627853560	Roseofilum sp. Guam_bin12 Ga0079928
2628060320	Ga0079927_117712	Mo-nitrogenase MoFe protein subunit NifK	2627853559	Roseofilum sp. Cyano_bin5 Ga0079927
2628129200	Ga0079949_100635	Mo-nitrogenase iron protein subunit NifH	2627853581	Alteromonadales bin3 BLZ4 Ga0079949
2628075613	Ga0079931_10724	Mo-nitrogenase MoFe protein subunit NifK	2627853563	Roseofilum sp. LKpool_bin4 Ga0079931
2628071631	Ga0079930_102629	Mo-nitrogenase iron protein subunit NifH	2627853562	Roseofilum sp. BLZD_bin1 Ga0079930
2628062394	Ga0079928_102163	nitrogenase molybdenum-iron protein alpha chain	2627853560	Roseofilum sp. Guam_bin12 Ga0079928
2628071635	Ga0079930_102633	Mo-nitrogenase MoFe protein subunit NifK	2627853562	Roseofilum sp. BLZD_bin1 Ga0079930
2628071634	Ga0079930_102632	nitrogenase molybdenum-iron protein alpha chain	2627853562	Roseofilum sp. BLZD_bin1 Ga0079930

2628124723	Ga0079947_14533	Mo-nitrogenase iron protein subunit NifH	2627853579	Rhodospirillales bin7 BLZ4 Ga0079947
2628060321	Ga0079927_117713	nitrogenase molybdenum-iron protein alpha chain	2627853559	Roseofilum sp. Cyano_bin5 Ga0079927
2628060324	Ga0079927_117716	Mo-nitrogenase iron protein subunit NifH	2627853559	Roseofilum sp. Cyano_bin5 Ga0079927
2628124724	Ga0079947_14534	Nitrogenase component 1 type Oxidoreductase	2627853579	Rhodospirillales bin7 BLZ4 Ga0079947
2628131269	Ga0079949_112512	Mo-nitrogenase MoFe protein subunit NifK	2627853581	Alteromonadales bin3 BLZ4 Ga0079949
2628125228	Ga0079947_16012	Mo-nitrogenase MoFe protein subunit NifK	2627853579	Rhodospirillales bin7 BLZ4 Ga0079947
2628131270	Ga0079949_112513	Mo-nitrogenase MoFe protein subunit NifD precursor	2627853581	Alteromonadales bin3 BLZ4 Ga0079949
2628066997	Ga0079929_10325	nitrogenase molybdenum-iron protein alpha chain	2627853561	Roseofilum sp. BLZ4_bin2 Ga0079929
2628075612	Ga0079931_10723	nitrogenase molybdenum-iron protein alpha chain	2627853563	Roseofilum sp. LKpool_bin4 Ga0079931
2628067000	Ga0079929_10328	Mo-nitrogenase iron protein subunit NifH	2627853561	Roseofilum sp. BLZ4_bin2 Ga0079929
2628062390	Ga0079928_102159	nitrogenase molybdenum-iron protein NifN	2627853560	Roseofilum sp. Guam_bin12 Ga0079928
2628125227	Ga0079947_16011	Nitrogenase component 1 type Oxidoreductase	2627853579	Rhodospirillales bin7 BLZ4 Ga0079947
2628066996	Ga0079929_10324	Mo-nitrogenase MoFe protein subunit NifK	2627853561	Roseofilum sp. BLZ4_bin2 Ga0079929
2628083846	Ga0079933_14002	dissimilatory adenylylsulfate reductase beta subunit	2627853565	Desulfovibrio bin6 BLZ4 Ga0079933
2628080331	Ga0079932_12942	dissimilatory adenylylsulfate reductase beta subunit	2627853564	LKpool_bin5_Desulfovibrio Ga0079932
2628083845	Ga0079933_14001	dissimilatory adenylylsulfate reductase alpha subunit precursor	2627853565	Desulfovibrio bin6 BLZ4 Ga0079933
2628080330	Ga0079932_12941	dissimilatory adenylylsulfate reductase alpha subunit precursor	2627853564	LKpool_bin5_Desulfovibrio Ga0079932