Table S1a: *B.septemdierum* individuals used in this study*

individual ID	cruise No.	dive No.	date	vent site	Lat./Long.	depth (m)	shell length (mm)	experiment
A1	NT10-08	HPD1126	14-May-10	Myojin	32°6.234′N / 139°52.152′E	1,228	110-120	symbiont genome sequencing, PCR for ISH probe template, qPCR
A2	NT10-08	HPD1126	14-May-10	Myojin	32°6.234′N / 139°52.152′E	1,228		qPCR
A3	NT10-08	HPD1126	14-May-10	Myojin	32°6.234′N / 139°52.152′E	1,228		qPCR
A4	NT10-08	HPD1127	15-May-10	Myojin	32°6.210′N / 139°52.056′E	1,249		qPCR
A5	NT11-09	HPD1286	18-Jun-11	Suiyo	28°34.285′N / 140°38.668′E	1,386		qPCR
A6	NT11-09	HPD1286	18-Jun-11	Suiyo	28°34.285′N / 140°38.668′E	1,386		qPCR
A7	NT11-09	HPD1288	21-Jun-11	Myojin	32°06.287′N / 139°52.193′E	1,278		FISH, RT-PCR
A8	NT11-09	HPD1288	21-Jun-11	Myojin	32°06.287′N / 139°52.193′E	1,278		FISH, RT-PCR
A9	NT11-09	HPD1288	21-Jun-11	Myojin	32°06.287′N / 139°52.193′E	1,278		FISH, RT-PCR
A10	NT11-09	HPD1284	16-Jun-11	Myojin	32°6.278′N / 139°52.081′E	1,303		WISH, RT-PCR
A11	NT11-09	HPD1284	16-Jun-11	Myojin	32°6.278′N / 139°52.081′E	1,303		WISH, RT-PCR
A12	NT11-09	HPD1284	16-Jun-11	Myojin	32°6.278′N / 139°52.081′E	1,303		RT-PCR
A13	NT11-09	HPD1287	19-Jun-11	Suiyo	28°34.267′N / 140°38.609′E	1,384		RT-PCR
A14	NT11-09	HPD1287	19-Jun-11	Suiyo	28°34.267′N / 140°38.609′E	1,384		RT-PCR
A15	NT11-09	HPD1287	19-Jun-11	Suiyo	28°34.267′N / 140°38.609′E	1,384		RT-PCR
J1	NT07-08	HPD0679	24-May-07	Suiyo	28°34.272′N / 140°38.676′E	1,386	2.8	qPCR
J2	NT07-08	HPD0679	24-May-07	Suiyo	28°34.272′N / 140°38.676′E	1,386	3.1	qPCR
J3	NT07-08	HPD0679	24-May-07	Suiyo	28°34.272′N / 140°38.676′E	1,386	3.3	qPCR
J4	NT07-08	HPD0680	25-May-07	Suiyo	28°34.266′N / 140°38.676′E	1,386	3.1	qPCR
J5	NT07-08	HPD0680	25-May-07	Suiyo	28°34.266′N / 140°38.676′E	1,386	3.5	qPCR
J6	NT07-08	HPD0680	25-May-07	Suiyo	28°34.266′N / 140°38.676′E	1,386	4.9	qPCR

*The minimum information about a genome sequence (MIGS) specification and a MARKer gene Sequence (MIMARKS) of *B.septemdierum* individuals used in this study are shown in Table S1b-j.

Table S1b: The minimum information about a genome sequence (MIGS) specification

http://www.ncbi.nlm.nih.gov/nuccore/CP001978.1			
	INSDC name of field	Units	
Investigation			
submitted to insdc	submitted_to_insdc		TRUE
Investigation type	investigation_type		bacteria
Project name	project_name		Bathymodiolus septemdierum endosymbiont genome sequencing
Environment			
Geographic location (latitude and longitude)	lat_lon		32.1041 N 139.2193 E
depth	depth	meter	-1228
Geographic location (country and/or sea,region)	geo_loc_name		Japan:Izu-Bonin Arc, Myojin knoll
Collection date	collection_date		2010-05-14
Environment (biome)	biome		marine hydrothermal vent
Environment (feature)	feature		aminal-associated habitat
Environment (material)	material		organ
MIGS/MIMS/MIMARKS Extension			
Environmental package	env_package		host-associated
host_common_name	host_common_name		Bathymodiolus septemdierum
host taxid	host_taxid		220392
host body site	host_body_site		gill
host length	host_length	millimeter	110-120
Nucleic Acid Sequence Source			
subspecific genetic lineage	subspecf_gen_lin		cellular organisms; Bacteria; Proteobacteria; Gammaproteobacteria; unclassified Gammaproteobacteria; unclassified Gammaproteobacteria (miscellaneous); gamma proteobacterium intracellular symbiont of Bathymodiolus septemdierum
Number of replicons	num_replicons		1
Reference for biomaterial	ref_biomaterial		None
Observed biotic relationship	biotic_relationship		symbiot
Trophic level	trophic_level		chemolithoautotroph
Relationship to oxygen	rel_to_oxygen		aerobic
Isolation and growth condition	isol_growth_condt		Unknown
sample collection device or method	samp_collect_device		ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	samp_mat_process		Frozen speicimen
Sequencing			
nucleic acid extraction	nucl_acid_ext		**17493812**
Sequencing method	sequencing_meth		pyrosequencing, illumina, pacbio
Assembly	assembly		assembler: Newbler (Parameters: Seed step:12; Seed length: 16; minimum overlap length: 40; minimum overlap identity: 90; Alignment identity score: 2; Alignment difference score: -3); error rate: read error 1.62%; error rate estimation: from Newbler base calling
Finishing stratgegy	finishing_strategy		statuts: complete; coverage:40x; contigs: 1
Relevant electronic resources	url		http://www.ncbi.nlm.nih.gov/genomeprj/PRJDB949

Table S1c: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *dnaA*)

	Sample name		**A1**	**A2**	**A3**	**A4**	**A5**	**A6**	**A7**	**A8**
	INSDC name of field	**Units**								
Investigation										
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment										
Collection date	**collection_date**		2010-05-10	2010-05-10	2010-05-10	2010-05-10	2011-06-18	2011-06-18	2011-06-21	2011-06-21
Geographic location (latitude and longitude)	**lat_lon**		+32.1039 +139.8692	+32.1039 +139.8692	+32.1039 +139.8692	+32.1035 +139.8676	+28.5714 +140.6445	+28.5714 +140.6445	+32.1048 +139.8699	+32.1048 +139.8699
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension										
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1228	-1228	-1228	-1249	-1386	-1386	-1278	-1278
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source										
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	RNAlater	RNAlater
sequencing										
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*
PCR primers	**pcr_primers**		FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT
PCR conditions	**pcr_cond**		initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

	Sample name		**A9**	**A10**	**A11**	**A12**	**A13**	**A14**	**A15**
	INSDC name of field	**Units**							
Investigation									
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment									
Collection date	**collection_date**		2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension									
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source									
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing									
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*
PCR primers	**pcr_primers**		FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT	FWD:GAAACCTTGAAAGATACTGTGCCAA REV:GGTTTCGATGCCAATTTCAATT
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

	Sample name		**J1**	**J2**	**J3**	**J4**	**J5**	**J6**
	INSDC name of field	**Units**						
Investigation								
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment								
Collection date	**collection_date**		2007-05-24	2007-05-24	2007-05-24	2007-05-25	2007-05-25	2007-05-25
Geographic location (latitude and longitude)	**lat_lon**		+28.5712 +140.6446	+28.5712 +140.6446	+28.5712 +140.6446	+28.5711 +140.6446	+28.5711 +140.6446	+28.5711 +140.6446
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension								
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1386	-1386	-1386	-1386	-1386	-1386
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	2.8	3.1	3.3	3.1	3.5	4.9
nucleic acid sequence source								
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen
sequencing								
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit
Nucleic acid amplification	**nucl_acid_amp**		http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s
Target gene	**target_gene**		*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*	*dnaA*
PCR primers	**pcr_primers**		FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT	FWD:AACCATAATGGCACCCAATACTTC REV:GGTTTCGATGCCAATTTCAATT
PCR conditions	**pcr_cond**		initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1d: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *hupL*)

	Sample name		**A1**	**A2**	**A3**	**A4**	**A5**	**A6**
	INSDC name of field	**Units**						
Investigation								
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment								
Collection date	**collection_date**		2010-05-10	2010-05-10	2010-05-10	2010-05-10	2011-06-18	2011-06-18
Geographic location (latitude and longitude)	**lat_lon**		+32.1039 +139.8692	+32.1039 +139.8692	+32.1039 +139.8692	+32.1035 +139.8676	+28.5714 +140.6445	+28.5714 +140.6445
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension								
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1228	-1228	-1228	-1249	-1386	-1386
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source								
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen
sequencing								
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit
Nucleic acid amplification	**nucl_acid_amp**		http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s
Target gene	**target_gene**		*hupL*	*hupL*	*hupL*	*hupL*	*hupL*	*hupL*
PCR primers	**pcr_primers**		FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA
PCR conditions	**pcr_cond**		initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

	Sample name		**A7**	**A8**	**A9**	**A10**	**A11**	**A12**	**A13**	**A14**	**A15**
	INSDC name of field	**Units**									
Investigation											
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment											
Collection date	**collection_date**		2011-06-21	2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension											
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1278	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source											
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing											
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*hupL*	*hupL*	*hupL*	*hupL*	*hupL*	*hupL*	*hupL*	*hupL*	*hupL*
PCR primers	**pcr_primers**		FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA	FWD:TCCACCTAATGCACATTTAATTCGT REV:TATCTTTGAAATAACCAGGGCTTGA
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

	Sample name		**J1**	**J2**	**J3**	**J4**	**J5**	**J6**
	INSDC name of field	**Units**						
Investigation								
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment								
Collection date	**collection_date**		2007-05-24	2007-05-24	2007-05-24	2007-05-25	2007-05-25	2007-05-25
Geographic location (latitude and longitude)	**lat_lon**		+28.5712 +140.6446	+28.5712 +140.6446	+28.5712 +140.6446	+28.5711 +140.6446	+28.5711 +140.6446	+28.5711 +140.6446
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension								
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1386	-1386	-1386	-1386	-1386	-1386
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	2.8	3.1	3.3	3.1	3.5	4.9
nucleic acid sequence source								
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen
sequencing								
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit
Nucleic acid amplification	**nucl_acid_amp**		http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s
Target gene	**target_gene**		*hupL*	*hupL*	*hupL*	*hupL*	*hupL*	*hupL*
PCR primers	**pcr_primers**		FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA	FWD:GCGCTAAGAGTGTAATGGATTATGG REV:ACCGGGAATACTTCGTTCCAA
PCR conditions	**pcr_cond**		initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1e: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *hupS*)

	Sample name		**A7**	**A8**	**A9**	**A10**	**A11**	**A12**	**A13**	**A14**	**A15**
	INSDC name of field	**Units**									
Investigation											
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment											
Collection date	**collection_date**		2011-06-21	2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension											
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1278	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source											
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing											
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*hupS*	*hupS*	*hupS*	*hupS*	*hupS*	*hupS*	*hupS*	*hupS*	*hupS*
PCR primers	**pcr_primers**		FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC	FWD:TGGATTATGATGATACGATTATGGC REV:AAATAATTGCCTTACAGTGTTTCGC
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1f: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *narG*)

	Sample name		A1	A2	A3	A4	A5	A6	A7
	INSDC name of field	Units							
Investigation									
Investigation type	investigation_type		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	project_name		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment									
Collection date	collection_date		2010-05-10	2010-05-10	2010-05-10	2010-05-10	2011-06-18	2011-06-18	2011-06-21
Geographic location (latitude and longitude)	lat_lon		+32.1039 +139.8692	+32.1039 +139.8692	+32.1039 +139.8692	+32.1035 +139.8676	+28.5714 +140.6445	+28.5714 +140.6445	+32.1048 +139.8699
Geographic location (country and/or sea,region)	geo_loc_name		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Myojin Knoll
Environment (biome)	biome		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	feature		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	material		organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension									
Environmental package	env_package		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	elev	meter	-1228	-1228	-1228	-1249	-1386	-1386	-1278
host_common_name	host_common_name		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	host_taxid		220392	220392	220392	220392	220392	220392	220392
host body site	host_body_site		gill	gill	gill	gill	gill	gill	gill
host length	host_length	millimeter	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source									
observed biotic relationship	biotic_relationship		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	trophic_level		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	samp_collect_device		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	samp_mat_process		Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	RNAlater
sequencing									
Nucleic acid extraction	nucl_acid_ext		https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	nucl_acid_amp		http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	target_gene		*narG*	*narG*	*narG*	*narG*	*narG*	*narG*	*narG*
PCR primers	pcr_primers		FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT
PCR conditions	pcr_cond		initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles
sequencing method	seq_meth		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

	Sample name		A8	A9	A10	A11	A12	A13	A14
	INSDC name of field	Units							
Investigation									
Investigation type	investigation_type		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	project_name		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment									
Collection date	collection_date		2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	lat_lon		+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	geo_loc_name		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	biome		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	feature		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	material		organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension									
Environmental package	env_package		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	elev	meter	-1278	-1278	-1303	-1303	-1303	-1384	-1384
host_common_name	host_common_name		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	host_taxid		220392	220392	220392	220392	220392	220392	220392
host body site	host_body_site		gill	gill	gill	gill	gill	gill	gill
host length	host_length	millimeter	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source									
observed biotic relationship	biotic_relationship		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	trophic_level		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	samp_collect_device		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	samp_mat_process		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing									
Nucleic acid extraction	nucl_acid_ext		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	nucl_acid_amp		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	target_gene		*narG*	*narG*	*narG*	*narG*	*narG*	*narG*	*narG*
PCR primers	pcr_primers		FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT
PCR conditions	pcr_cond		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles
sequencing method	seq_meth		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

	Sample name		A15	J1	J2	J3	J4	J5	J6
	INSDC name of field	Units							
Investigation									
Investigation type	investigation_type		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	project_name		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment									
Collection date	collection_date		2011-06-19	2007-05-24	2007-05-24	2007-05-24	2007-05-25	2007-05-25	2007-05-25
Geographic location (latitude and longitude)	lat_lon		+28.5711 +140.6435	+28.5712 +140.6446	+28.5712 +140.6446	+28.5712 +140.6446	+28.5711 +140.6446	+28.5711 +140.6446	+28.5711 +140.6446
Geographic location (country and/or sea,region)	geo_loc_name		Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	biome		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	feature		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	material		organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension									
Environmental package	env_package		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	elev	meter	-1384	-1386	-1386	-1386	-1386	-1386	-1386
host_common_name	host_common_name		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	host_taxid		220392	220392	220392	220392	220392	220392	220392
host body site	host_body_site		gill	gill	gill	gill	gill	gill	gill
host length	host_length	millimeter	110-120	2.8	3.1	3.3	3.1	3.5	4.9
nucleic acid sequence source									
observed biotic relationship	biotic_relationship		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	trophic_level		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	samp_collect_device		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	samp_mat_process		RNAlater	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen	Frozen speicimen
sequencing									
Nucleic acid extraction	nucl_acid_ext		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit	https://www.qiagen.com/us/products/catalog/sample-technologies/dna-sample-technologies/genomic-dna/dneasy-blood-and-tissue-kit
Nucleic acid amplification	nucl_acid_amp		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s	http://www.lifetechnologies.com/jp/ja/home/life-science/pcr/real-time-pcr/real-time-pcr-reagents/sybr-green-real-time-master-mixes/power-sybr-green-master-mix.html?gclid=CLDyu56u48QCFY8kvQodVTEAHA&s_kwcid=AL!3652!3!47110095563!b!!g!!power%20sybr%20green%20master%20mix&ef_id=UG1VGwAAFuZQnygc:20150407043135:s
Target gene	target_gene		*narG*	*narG*	*narG*	*narG*	*narG*	*narG*	*narG*
PCR primers	pcr_primers		FWD:GAATTTTCTGATGGACATGGTAAGTT REV:GGACGTGTTCTTGGGTAATTTGTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT	FWD:TGTGGTTGCCTTGCCTATTTT REV:CACTCGTCATCAAACCAAGCTTT
PCR conditions	pcr_cond		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles	initial denaturation:95degC_10min; denaturation:95degC_15sec; annealing and elongation:60degC_1min; 40cycles
sequencing method	seq_meth		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1g: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *narH*)

	Sample name		A7	A8	A9	A10	A11	A12	A13	A14	A15
	INSDC name of field	Units									
Investigation											
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment											
Collection date	**collection_date**		2011-06-21	2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension											
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1278	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source											
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing											
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*narH*	*narH*	*narH*	*narH*	*narH*	*narH*	*narH*	*narH*	*narH*
PCR primers	**pcr_primers**		FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG	FWD:ATTTATGATGTATTTACCACGCCTATG REV:TGATTTTCCAGATTGCCAGTTGTAG
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1h: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *narI*)

	Sample name		A7	A8	A9	A10	A11	A12	A13	A14	A15
	INSDC name of field	Units									
Investigation											
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment											
Collection date	**collection_date**		2011-06-21	2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension											
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1278	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source											
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing											
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*narI*	*narI*	*narI*	*narI*	*narI*	*narI*	*narI*	*narI*	*narI*
PCR primers	**pcr_primers**		FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG	FWD:ACTAAGCAAATAATGGCAATGACTG REV:AAATGTTGTGCTGAATAAGGAATGG
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec;final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1i: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *narJ*)

	Sample name		A7	A8	A9	A10	A11	A12	A13	A14	A15
	INSDC name of field	**Units**									
Investigation											
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment											
Collection date	**collection_date**		2011-06-21	2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension											
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1278	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source											
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing											
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*narJ*	*narJ*	*narJ*	*narJ*	*narJ*	*narJ*	*narJ*	*narJ*	*narJ*
PCR primers	**pcr_primers**		FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT	FWD:GGGCGATACGATTGATATTATTGCT REV:GCTTCTTGCTCTTGCCATAATTCAT
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S1j: Minimum Information about a MARKer gene Sequence of *B.septemdierum* individuals used in this study (for *cbbm*)

	Sample name		A7	A8	A9	A10	A11	A12	A13	A14	A15
	INSDC name of field	Units									
Investigation											
Investigation type	**investigation_type**		mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey	mimarks-survey
Project name	**project_name**		Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population	Heterogeneous composition of key metabolic gene clusters in a vent mussel symbiont population
Environment											
Collection date	**collection_date**		2011-06-21	2011-06-21	2011-06-21	2011-06-16	2011-06-16	2011-06-16	2011-06-19	2011-06-19	2011-06-19
Geographic location (latitude and longitude)	**lat_lon**		+32.1048 +139.8699	+32.1048 +139.8699	+32.1048 +139.8699	+32.1046 +139.8680	+32.1046 +139.8680	+32.1046 +139.8680	+28.5711 +140.6435	+28.5711 +140.6435	+28.5711 +140.6435
Geographic location (country and/or sea,region)	**geo_loc_name**		Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Myojin Knoll	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount	Japan:Izu-Bonin Arc:Suiyo Seamount
Environment (biome)	**biome**		marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent	marine hydrothermal vent
Environment (feature)	**feature**		aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat	aminal-associated habitat
Environment (material)	**material**		organ	organ	organ	organ	organ	organ	organ	organ	organ
MIGS/MIMS/MIMARKS Extension											
Environmental package	**env_package**		host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated	host-associated
elevation	**elev**	**meter**	-1278	-1278	-1278	-1303	-1303	-1303	-1384	-1384	-1384
host_common_name	**host_common_name**		Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum	Bathymodiolus septemdierum
host taxid	**host_taxid**		220392	220392	220392	220392	220392	220392	220392	220392	220392
host body site	**host_body_site**		gill	gill	gill	gill	gill	gill	gill	gill	gill
host length	**host_length**	**millimeter**	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120	110-120
nucleic acid sequence source											
observed biotic relationship	**biotic_relationship**		symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont	symbiont
trophic level	**trophic_level**		chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph	chemoautotroph
sample collection device or method	**samp_collect_device**		ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler	ROV (Remotely Operated Vehicle) sucktion sampler
sample material processing	**samp_mat_process**		RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater	RNAlater
sequencing											
Nucleic acid extraction	**nucl_acid_ext**		https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/	https://www.qiagen.com/us/products/catalog/sample-technologies/rna-sample-technologies/total-rna/rneasy-mini-kit/
Nucleic acid amplification	**nucl_acid_amp**		https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/	https://www.qiagen.com/us/products/catalog/assay-technologies/real-time-pcr-and-rt-pcr-reagents/quantitect-reverse-transcription-kit/
Target gene	**target_gene**		*cbbm*	*cbbm*	*cbbm*	*cbbm*	*cbbm*	*cbbm*	*cbbm*	*cbbm*	*cbbm*
PCR primers	**pcr_primers**		FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT	FWD:CCTATACAATGACACCAATGCCT REV:TGCGATCAAACAAACCACAT
PCR conditions	**pcr_cond**		initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles	initial denaturation:94degC_5min;denaturation:94degC_1min;annealing and elongation:60degC_30sec; final elongation:72degC_3min;40 cycles
sequencing method	**seq_meth**		Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger	Sanger

Table S2: qPCR Primers used in this study

Primer set	dnaA-qF, 5′-AACCATAATGGCACCCAATACTTC-3′ dnaA-qR, 5′-GGTTTCGATGCCAATTTCAATT-3′	hupL-qF, 5′-GCGCTAAGAGTGTAATGGATTATGG-3′ hupL-qR, 5′-ACCGGGAATACTTCGTTCCAA-3′	narG-qF, 5′-TGTGGTTGCCTTGCCTATTTT-3′ narG-qR, 5′-CACTCGTCATCAAACCAAGCTTT-3′
Target gene	*dnaA*	*hupL*	*narG*
Amplicon length (bp)	121	115	84
Slope	-3.419	-3.461	-3.547
y-Intercept	14.40	12.77	14.93
Efficiency (%)	96.09	94.50	91.39
R2	1.000	0.999	0.999
Cq of NTC	30.86	32.14	34.37
ΔCq between NTC and minimum sample	13.37	12.31	15.79
Linear dinamic range (Cq)	14.38 to 23.94	12.66 to 22.40	14.93 to 24.76

Table S3: Details of the loci with low mapping depth*, **

Locus name	Type	Locus_tag	Strand	5'of gene	3'of gene	Product	Length (bp)		Ave. depth	
	CDS	BSEPE_0075	+	81,458	82,723	phosphoribosylamine--glycine ligase	1,266		1,185	
	CDS	BSEPE_0076	+	82,944	84,263	conserved hypothetical protein	1,320		2,263	
	CDS	BSEPE_0077	+	84,260	84,823	ribonuclease HII, duplicate gene of BSEPE_0077 and BSEPE_0088	564		1,242	
LDS02 *Locus_N*		DirectRepeat	+	84,326	84,805		480	13,763		716
	CDS	BSEPE_0078	-	84,907	85,389	CBS domain membrane protein	483		489	
	CDS	BSEPE_0079	-	85,409	85,744	tRNA 2-thiouridine synthesizing protein E	336		730	
	CDS	BSEPE_0080	-	85,758	86,213	conserved hypothetical protein	456		927	
	CDS	BSEPE_0081	-	86,219	86,899	nitrate reductase 1, gamma subunit	681		934	
	CDS	BSEPE_0082	-	86,910	87,569	nitrate reductase 1, delta subunit	660		682	
	CDS	BSEPE_0083	-	87,569	89,107	nitrate reductase 1, beta subunit	1,539		557	
	CDS	BSEPE_0084	-	89,104	92,838	nitrate reductase 1, alpha subunit	3,735		666	
	CDS	BSEPE_0085	-	92,890	94,509	MFS transporter, NNP family, nitrate/nitrite transporter	1,620		490	
	CDS	BSEPE_0086	-	94,549	95,826	MFS transporter, NNP family, nitrate/nitrite transporter	1,278		573	
	CDS	BSEPE_0087	+	95,941	97,485	CRP/FNR family transcriptional regulator, transcriptional activator FtrB	1,545		928	
		DirectRepeat	+	97,609	98,088		480			
	CDS	BSEPE_0088	+	97,531	98,103	ribonuclease HII, duplicate gene of BSEPE_0077 and BSEPE_0088	573		1,273	
	CDS	BSEPE_0089	-	98,081	98,806	lipoprotein	726		2,387	
	CDS	BSEPE_0090	-	98,803	99,177	conserved hypothetical protein	375		3,236	
	CDS	BSEPE_0091	+	99,181	100,005	16S rRNA (cytidine1402-2'-O)-methyltransferase	825		1,557	
	CDS	BSEPE_0158	-	168,621	169,445	DNA ligase (ATP)	825		2,498	
LDS03		DirectRepeat	+	169,216	169,225		10	7,186		615
	CDS	BSEPE_0159	-	169,450	169,602	ATP-dependent DNA helicase RecG	153		735	
	CDS	BSEPE_0160	-	169,727	170,959	conserved hypothetical protein	1,233		776	
	CDS	BSEPE_0161	-	170,969	171,811	hypothetical protein	843		760	
	CDS	BSEPE_0162	-	171,812	171,964	hypothetical protein	153		480	
	CDS	BSEPE_0163	-	171,951	172,679	hypothetical protein	729		540	
	CDS	BSEPE_0164	-	172,679	173,248	hypothetical protein	570		639	
	CDS	BSEPE_0165	-	173,281	174,567	hypothetical protein	1,287		441	
	CDS	BSEPE_0166	-	174,583	175,842	hypothetical protein	1,260		583	
	CDS	BSEPE_0167	-	175,835	176,683	conserved hypothetical protein	849		695	
		DirectRepeat	+	176,392	176,401		10			
	CDS	BSEPE_0168	-	176,686	178,089	dihydrolipoamide dehydrogenase	1,404		1,187	
	CDS	BSEPE_0169	-	178,082	179,602	pyruvate dehydrogenase E2 component, dihydrolipoamide acetyltransferase	1,521		1,478	
	CDS	BSEPE_0170	+	179,688	180,599	antibiotic transport system ATP-binding protein	912		2,809	
	CDS	BSEPE_0213	-	214,343	214,816	chorismate--pyruvate lyase	474		2,423	
	CDS	BSEPE_0214	-	214,890	216,953	ATP-dependent DNA helicase RecG	2,064		2,170	
	CDS	BSEPE_0215	-	216,955	217,341	TdcF protein	387		1,674	
	gene	BSEPE_0216	-	217,516	217,743	Pseudogene. C-terminus of hypothetical protein BSEPE_0247	228		3,212	
LDS04 *Locus_H*		DirectRepeat	+	217,501	217,773		273	26,899		560
	CDS	BSEPE_0217	-	218,149	219,171	hydrogenase expression/formation protein HypE	1,023		233	
	CDS	BSEPE_0218	-	219,171	220,301	hydrogenase expression/formation protein HypD	1,131		390	
	CDS	BSEPE_0219	-	220,303	220,578	hydrogenase expression/formation protein HypC2	276		333	
	CDS	BSEPE_0220	-	220,578	221,825	two-component system response regulator HupR	1,248		463	
	CDS	BSEPE_0221	-	222,076	222,966	hydrogenase nickel incorporation protein HypB	891		320	
	CDS	BSEPE_0222	-	222,970	223,293	hydrogenase nickel incorporation protein HypA/HybF	324		262	
	CDS	BSEPE_0223	-	223,307	224,476	hydrogenase expression/formation protein HupK	1,170		415	
	CDS	BSEPE_0224	-	224,476	225,009	hydrogenase expression/formation protein HupJ	534		494	
	CDS	BSEPE_0225	-	225,018	225,245	rubredoxin HupI	228		421	
	CDS	BSEPE_0226	-	225,242	226,120	hydrogenase-1 operon protein HyaF	879		528	
	CDS	BSEPE_0227	-	226,137	226,544	hydrogenase-1 operon protein HyaE	408		346	
	CDS	BSEPE_0228	-	226,549	226,857	hydrogenase expression/formation protein HypC	309		250	
	CDS	BSEPE_0229	-	226,858	227,553	hydrogenase 1 maturation protease HyaD	696		399	
	CDS	BSEPE_0230	-	227,626	228,357	Ni/Fe-hydrogenase 1 B-type cytochrome subunit HyaC	732		410	
	CDS	BSEPE_0231	-	228,384	228,653	conserved hypothetical protein	270		712	
	CDS	BSEPE_0232	-	228,664	230,478	hydrogenase large subunit HupL	1,815		402	
	CDS	BSEPE_0233	-	230,482	231,588	hydrogenase small subunit HupS	1,107		296	
	CDS	BSEPE_0234	+	231,809	232,936	RNA polymerase sigma-54 factor RpoN	1,128		586	
	gene	BSEPE_0235	-	232,928	233,041	Pseudogene. C-terminus of transhydrogenase subunit beta	114		543	
	gene	BSEPE_0236	-	233,248	234,184	Pseudogene. conserved hypothetical protein	937		494	
	CDS	BSEPE_0237	-	234,278	235,675	NAD(P) transhydrogenase subunit beta	1,398		453	
	CDS	BSEPE_0238	-	235,684	237,249	NAD(P) transhydrogenase subunit alpha	1,566		351	
	CDS	BSEPE_0239	-	237,311	237,841	inorganic pyrophosphatase	531		326	
	gene	BSEPE_0240	-	237,860	238,093	Pseudogene. N-terminus of carbonic anhydrase	234		234	
	CDS	BSEPE_0241	-	238,071	238,814	conserved hypothetical protein	744		372	
	gene	BSEPE_0242	-	238,814	238,984	Pseudogene. N-terminus of rhodanese domain protein	171		615	
	CDS	BSEPE_0243	-	239,142	239,780	D-sedoheptulose 7-phosphate isomerase	639		376	
	CDS	BSEPE_0244	-	239,770	242,136	hydrogenase maturation protein HypF	2,367		398	
	CDS	BSEPE_0245	-	242,093	242,401	conserved hypothetical protein	309		423	
	CDS	BSEPE_0246	-	242,696	243,973	IS256 family transposase	1,278		***N.C.	
		DirectRepeat	+	244,127	244,399		273			
	CDS	BSEPE_0247	-	244,142	244,912	conserved hypothetical protein	771		2,459	
		BSEPE_0248	-	244,918	245,247	hypothetical protein	330		2,086	
		BSEPE_0249	-	245,244	246,113	succinyl-CoA synthetase alpha subunit	870		1,017	
	CDS	BSEPE_0452	-	436,410	437,447	erythronate-4-phosphate dehydrogenase	1,038		1,737	
	CDS	BSEPE_0453	-	437,461	438,123	uracil-DNA glycosylase	663		1,873	
	CDS	BSEPE_0454	-	438,105	438,605	thioredoxin	501		1,806	
LDS05		DirectRepeat	+	438,622	438,698		77	7,640		608
	gene	BSEPE_0455	+	438,760	439,809	Pseudogene. IS256 family transposase	1,050		930	
	CDS	BSEPE_0456	+	439,862	440,041	transposase	180		802	
	gene	BSEPE_0457	+	440,121	440,270	Pseudogene. N-terminus of integrase	150		515	
	CDS	BSEPE_0458	+	440,476	440,970	hypothetical protein	495		467	
	CDS	BSEPE_0459	+	440,981	441,274	conserved hypothetical protein	294		503	
	CDS	BSEPE_0460	+	441,403	442,176	conserved hypothetical protein	774		564	
	CDS	BSEPE_0461	+	442,160	445,753	DEAD/DEAH box helicase	3,594		441	
		DirectRepeat	+	446,185	446,261		77			
	CDS	BSEPE_0462	+	446,166	446,825	thiopurine S-methyltransferase	660		1,830	
	CDS	BSEPE_0463	+	446,829	447,149	cold shock protein	321		1,413	
	CDS	BSEPE_0482	+	459,558	461,189	acetolactate synthase I/II/III large subunit	1,632		2,101	
	CDS	BSEPE_0483	+	461,199	462,575	aldehyde dehydrogenase	1,377		1,398	
LDS06	CDS	BSEPE_0484	+	462,758	462,895	conserved hypothetical protein	138	2,416	658	676
	CDS	BSEPE_0485	+	463,194	463,550	hypothetical protein	357		115	
	CDS	BSEPE_0486	+	463,687	464,091	conserved hypothetical protein	405		843	
	CDS	BSEPE_0487	+	464,111	464,626	conserved hypothetical protein	516		949	

	CDS	BSEPE_0488	+	464,628	465,050	conserved hypothetical protein	423		907	
	gene	BSEPE_0489	-	465,075	465,173	Pseudogene. C-terminus of lipid A export ATP-binding/permease	99		926	
	CDS	BSEPE_0490	-	465,664	467,400	lipid A export ATP-binding/permease		1,737		1,854
	CDS	BSEPE_0491	+	467,472	469,112	CTP synthase		1,641		2,210
	CDS	BSEPE_0544	-	516,857	517,987	rod shape determining protein RodA		1,131		1,563
	CDS	BSEPE_0545	-	517,984	518,361	conserved hypothetical protein		378		2,538
LDS07	CDS	BSEPE_0546	-	518,596	523,320	hypothetical protein	4,725	7,701	478	573
	CDS	BSEPE_0547	-	523,323	523,946	conserved hypothetical protein	624		566	
	CDS	BSEPE_0548	+	524,067	524,252	XRE family transcriptional regulator	186		724	
	gene	BSEPE_0549	+	524,385	525,129	Pseudogene. IS256 family transposase	327		886	
	CDS	BSEPE_0550	+	525,358	526,296	conserved hypothetical protein	939		755	
	CDS	BSEPE_0551	+	526,455	526,901	conserved hypothetical protein		447		1,590
	CDS	BSEPE_0552	+	526,898	528,268	glutamyl-tRNA synthetase		1,371		1,679
	CDS	BSEPE_0779	+	741,180	741,770	putative toluene tolerance protein		591		2,841
	CDS	BSEPE_0780	+	741,794	742,093	ArsR family transcriptional regulator		300		1,370
LDS11		DirectRepeat	+	742,142	742,189		48	10,451		385
	tRNA	BSEPE_t22	+	742,110	742,186	tRNA-Arg	77		743	
	CDS	BSEPE_0781	+	742,327	742,830	hypothetical protein	504		505	
	CDS	BSEPE_0782	-	742,844	743,581	hypothetical protein	738		375	
	CDS	BSEPE_0783	-	743,568	744,998	type I restriction enzyme, S subunit	1,431		210	
	CDS	BSEPE_0784	-	745,028	747,013	type I restriction enzyme, M subunit	1,986		320	
	CDS	BSEPE_0785	-	747,173	748,231	Fic family protein	1,059		443	
	CDS	BSEPE_0786	-	748,329	749,774	conserved hypothetical protein	1,446		366	
	CDS	BSEPE_0787	-	749,929	750,162	conserved hypothetical protein	234		322	
	CDS	BSEPE_0788	-	750,386	751,234	hypothetical protein	849		569	
	CDS	BSEPE_0789	-	751,237	752,388	integrase	1,152		452	
		DirectRepeat	+	752,548	752,592		45			
	CDS	BSEPE_0790	+	752,602	753,369	phosphatidylglycerol:prolipoprotein diacylglycerol transferase		768		1,495
	CDS	BSEPE_0791	+	753,369	754,223	thymidylate synthase		855		1,709
	CDS	BSEPE_0792	+	754,238	754,567	phosphonoacetate hydrolase		330		1,972
	CDS	BSEPE_0857	+	813,535	814,374	conserved hypothetical protein		840		936
	CDS	BSEPE_0858	-	814,662	815,261	transposase		600		2,395
	CDS	BSEPE_0859	+	815,407	815,739	hypothetical protein		333		1,001
LDS12	CDS	BSEPE_0860	-	816,221	817,615	DNA (cytosine-5-)-methyltransferase	1,395	2,401	712	667
	CDS	BSEPE_0861	-	817,599	818,621	type II site-specific deoxyribonuclease	1,023		610	
	CDS	BSEPE_0862	-	819,015	820,889	NAD+ synthase (glutamine-hydrolysing)		1,875		1,353
	CDS	BSEPE_0863	+	821,188	822,195	general L-amino acid transport system substrate-binding protein		1,008		1,616
	CDS	BSEPE_1030	+	994,662	995,672	IS4 family transposase		1,011		N.C.
LDS14	CDS	BSEPE_1031	+	995,971	999,078	filamentous hemagglutinin		3,108		742
	CDS	BSEPE_1032	+	999,075	999,344	hypothetical protein		270		1,637
	CDS	BSEPE_1404	+	1,353,164	1,354,441	IS256 family transposase		1,278		N.C.
LDS19	CDS	BSEPE_1405	+	1,354,854	1,357,313	DNA (cytosine-5-)-methyltransferase	2,460	3,576	471	468
	CDS	BSEPE_1406	+	1,357,315	1,358,529	conserved hypothetical protein	1,215		493	
	CDS	BSEPE_1407	-	1,358,858	1,359,145	XRE family transcriptional regulator		288		3,286
	gene	BSEPE_1408	-	1,359,170	1,359,316	Pseudogene. C-terminus of addiction module toxin, RelE/StbE family		147		2,748
	CDS	BSEPE_1419	+	1,365,193	1,365,678	hypothetical protein		486		2,299
LDS20	CDS	BSEPE_1420	+	1,365,700	1,371,624	hypothetical protein		5,925		1,067
	CDS	BSEPE_1421	-	1,371,632	1,372,975	magnesium chelatase family protein		1,344		1,327

*Loci occupying longer than 2,000 bp with average mapping depth lower than 1,000 are listed (grey, except for *Locus_N* in blue and *Locus_H* in orange).

**Genomic heterogeneities of these loci were confirmed by PacBio sequencing (see Figure S4)

***N.C., nonspecific count in the mapped reads due to multi-copies of the gene in the BSEPE genome.