

1 **Supplemental Materials**

2 **Microbial metabolism and adaptations in *Atribacteria*-dominated methane hydrate sediments**

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14 **Running Title:** *Atribacteria* adaptations in methane hydrate ecosystem

15 **Dedication:** To Katrina Edwards

16 **Table S1.** Additional geochemical data for ODP Site 1244 at Hydrate Ridge drilled on IODP Leg 204. Note: data not available (ND) for sample
 17 E5H5 (35.65 mbsf). SMTZ: sulfate-methane transition zone; MRZ: metal reduction zone; GHSZ: gas hydrate stability zone. DNA sequencing
 18 from E19H5 was unsuccessful. TC: total carbon; TN: total nitrogen; TIC: total inorganic carbon; TOC: total organic carbon; C:N carbon:nitrogen.

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Hole	Zone	Depth (mbsf)	%TC	%TN	%TS	%TIC	%TOC	C:N	%CaCO ₃	reactive Fe (%)	reactive Mn (%)
C1H2	SMTZ	1.95/2.25	2.07	0.20	0.42	0.17	1.9	11.05	1.46	0.38	0.002
C1H3	SMTZ	3.45/3.75	1.88	0.14	0.55	0.70	1.2	9.85	5.81	0.45	0.004
F2H4	SMTZ	8.6	1.54	0.17	0.39	0.44	1.1	7.55	3.66	0.57	0.005
F3H4	MRZ	18.1	1.55	0.24	0.64	0.08	1.5	7.14	0.68	0.80	0.004
C3H4	MRZ	20.69	1.22	0.18	0.22	0.08	1.1	7.40	0.65	1.10	0.004
E5H5	MRZ	35.65	NA	NA	NA	NA	NA	NA	NA	NA	NA
E10H5	GHSZ	68.55	1.71	0.22	0.42	0.13	1.6	8.38	1.08	0.51	0.003
E19H5	GHSZ	138.89	1.42	0.20	0.07	0.51	0.9	5.32	4.23	1.41	0.012

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Table S3. Quality evaluation and accession numbers of the 21 metagenome-assembled genomes from IODP Site 1244 generated in this study with >35% completeness and <10% contamination.

Assembly	WGS	BioSample	MAG ID	Taxon	Size (bp)	Contigs	CDS	N50	GC (%)	Completeness (%)	Contamination (%)	Heterogeneity (%)
GCA_009619245	WJOO00000000	SAMN13181020	1244-C1-H3-B20	Dehalococcoidia (Chloroflexi)	1,744,267	338	1772	6,049	52	75	9	0
GCA_009619075	WJOY00000000	SAMN13181030	1244-C3-H4-B3		935,948	47	910	30,310	45	74	3	67
GCA_009619025	WJPC00000000	SAMN13181034	1244-E5-H5-B4		620,966	90	634	7,554	55	49	0	0
GCA_009619235	WJPE00000000	SAMN13181036	1244-E5-H5-B9		1,315,519	215	1385	7,652	53	71	5	75
GCA_009619215	WJPF00000000	SAMN13181037	1244-E10-H5-B3		971,417	200	1038	6,335	56	72	5	29
GCA_009618505	WJOQ00000000	SAMN13181022	1244-F2-H4-B2	Clostridia (Firmicutes)	2,136,034	406	2041	6,910	40	79	4	50
GCA_009619115	WJOR00000000	SAMN13181023	1244-F2-H4-B10		974,022	276	956	3,720	43	39	0	0
GCA_009619015	WJOU00000000	SAMN13181026	1244-F3-H4-B2		2,140,048	47	2077	131,274	34	81	0	0
GCA_009619095	WJOT00000000	SAMN13181025	1244-F3-H4-B3		1,988,642	132	1758	24,484	41	90	5	33
GCA_009618495	WJPA00000000	SAMN13181032	1244-C3-H4-B5		998,110	85	881	18,112	42	57	2	0
GCA_003575245	NMQN00000000	SAMN07342547	1244-E10-H5-B2	Atribacteria	4,055,260	912	4254	5,515	33	69	2	100
GCA_009619225	WJOX00000000	SAMN13181029	1244-C3-H4-B19	Bacteroidetes	3,577,859	750	2889	6,011	38	77	6	14
GCA_009619295	WJOP00000000	SAMN13181021	1244-C1-H3-B22	Calditrichaeota	2,223,554	459	2191	6,605	57	81	10	27
GCA_009619035	WJPB00000000	SAMN13181033	1244-E5-H5-B19	Spirochaeta	1,522,441	390	1452	4,221	47	41	0	0
GCA_009619125	WJON00000000	SAMN13181019	1244-C1-H3-B19	Unclassified bacterium	1,724,327	226	1686	9,503	53	61	2	0
GCA_009619195	WJOZ00000000	SAMN13181031	1244-C3-H4-B23		1,437,950	349	1342	4,977	41	59	1	0
GCA_009618485	WJOM00000000	SAMN13181018	1244-C1-H3-B37		1,464,732	418	1426	3,969	47	50	0	0
GCA_009619155	WJOW00000000	SAMN13181028	1244-C3-H4-B1	Hadesarchaea	1,294,504	20	1460	148,197	50	88	4	17
GCA_009618475	WJOV00000000	SAMN13181027	1244-F3-H4-B6	Methanosarcinales (Euryarchaeota)	1,093,430	165	1299	8,522	43	60	2	0
GCA_009619135	WJPD00000000	SAMN13181035	1244-E5-H5-B17	Unclassified archaeon	1,307,191	249	1467	6,784	58	49	1	0
GCA_009619335	WJOS00000000	SAMN13181024	1244-F2-H4-B13		825,629	212	930	4,508	42	39	1	0

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Table S4. Matrix of average amino acid identities for the JS-1 Genus-1 MAGs.

	35_14	HGW-1	E44_bin65	MT.SAG.1	UBA7920	E10H5-B2	4572_76
35_14							
HGW-1	78						
E44_bin65	78	74					
MT.SAG.1	76	74	77				
UBA7920	81	79	79	78			
E10H5-B2	77	73	81	76	78		
4572_76	78	76	72	73	80	76	
UBA9311	79	79	77	75	83	80	83

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29 **Table S5. Hun-encoding genes in *Atribacteria* MAG B2 with percent identity to top hits in other MAGs.** Hun genes were also present in other
 30 MAGs from Site 1244 including *Firmicutes* E5B5-B3 (contigs 32 and 225).
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Gene	PFAM	B2 contig E10H5_	B2 gene	<i>Atribacteria</i> bacterium isolate UBA7920	<i>Candidatus Atribacteria</i> bacterium MT.SAG.1	<i>Actinobacteria</i> RBG_13_35_12	<i>Atribacteria</i> JGI 0000014-F07	<i>Atribacteria</i> CG2_30_33_13	<i>Omnitrophica</i> WOR_2 SM23_29	<i>Omnitrophica</i> RBG_13_46_9	<i>Omnitrophica</i> RIFCSPHIGHO2 02_FULL_45_28
<i>hunR</i>	PF02629 (CoA binding), PF06971 (Put DNA-bind N)	C341	RXG63122	N/A	TFB08687 (88%)	OFW53501 (92%)	WP_09059864 (89%)	N/A	N/A	N/A	N/A
<i>hunA</i>	PF17179 (Fer4_22)	C341	RXG63123	HAJ31991 (87%)	TFB08688 (93%)	OFW53497 (91%)	WP_090598643 (89%)	OIP6690 (85%)	KPK38155 (68%)	OGW74721 (62%)	OGW81410 (63%)
<i>hunB</i>	PF00175 (NAD_binding_1), PF00970 (FAD_binding_6), PF10418 (DHODB_Fe-S_bind)	C341	RXG63124	HAJ31992 (94%)	TFB08716 (92%)	OFW53500 (91%)	WP_090598656 (93%)	OIP66908 (89%)	KPK38154 (77%)	OGW74722 (72%)	OGW81411 (69%)
<i>hunC</i>	PF13247 (Fer4_11)	C341	RXG63125	HAJ31993 (94%)	TFB08689 (93%)	OFW53499 (95%)	WP_090598644 (94%)	OIP66907 (91%)	KPK38158 (80%)	OGW74723 (78%)	OGW81412 (68%)
<i>hunD</i>	PF00146 (NADHdh)	C341	RXG63126	HAJ31994 (96%)	TFB08690 (95%)	OFW53496 (93%)	WP_090598646 (95%)	OIP66899 (92%)	KPK38153 (81%)	OGW74724 (79%)	OGW81413 (70%)
<i>hunE</i>	PF01058 (Oxidored_q6)	C341	RXG63127	HAJ31995 (98%)	TFB08691 (92%)	OFW53495 (96%)	WP_090598648 (95%)	OIP66906 (95%)	KPK39520 (90%)	OGW74725 (89%)	OGW81414 (85%)
<i>hunF</i>	PF00329 (Complex1_30kDa)	C341	RXG63128	HAJ31996 (87%)	TFB08692 (91%)	OFW53494 (85%)	WP_090598650 (83%)	OIP66898 (87%)	KPK39524 (73%)	OGW74727 (73%)	OGW81415 (68%)
<i>hunG</i>	PF00346 (Complex1_49kDa), PF00374 (NiFeSe_Hases)	C341	RXG63129	HAJ31997 (95%)	TFB08717 (96%)	OFW53493 (97%)	WP_090598653 (94%)	OIP66897 (94%)	KPK39519 (85%)	OGW74726 (87%)	OGW81416 (78%)
<i>hunH</i>	PF00361 (proton_antipo_M)	C341	RXG63130	HAJ31998 (94%)	TFB08693 (91%)	OFW53492 (88%)	WP_090599466 (88%)	OIP66896 (89%)	N/A	N/A	OGW81417 (77%)
<i>hunI</i>	PF13244 (DUF4040)	C1989	RXG66691	HAJ31999 (92%)	TFB08694 (95%)	OFW53491 (89%)	WP_090599464 (89%)	OIP66895 (80%)	KPK39517 (83%)	OGW74728 (81%)	OGW81418 (72%)
<i>hunJ</i>	PF04039 (MnhB)	C1989	RXG66692	HAJ32000 (97%)	TFB08695 (94%)	OFW53490 (95%)	WP_090599461 (85%)	OIP66894 (88%)	KPK40785 (85%)	OGW74729 (84%)	OGW81419 (80%)
<i>hunK</i>	PF00420 (Oxidored_q2)	C1989	RXG66693	HAJ32001 (96%)	TFB08696 (96%)	OFW53489 (91%)	WP_090599460 (90%)	OIP66893 (90%)	KPK40786 (80%)	N/A	OGW81420 (76%)
<i>hunL</i>	PF00361 (proton_antipo_M), PF00662 (proton_antipo_N)	C1989	RXG66694	HAJ32002 (96%)	TFB08697 (94%)	OFW53498 (87%)	WP_090599470 (82%)	OIP66892 (86%)	N/A	OGW74730 (76%)	OGW81421 (74%)
<i>hunM</i>	PF01899 (MNHE)	C1989	RXG66695	HAJ32003 (95%)	TFB08698 (98%)	OFW53488 (87%)	WP_090599458 (86%)	OIP66891 (86%)	KPK40787 (73%)	OGW74758 (73%)	OGW81422 (65%)
<i>hunN</i>	PF04066 (MrpF_PhaF)	C1989	RXG66696	HAJ32004 (96%)	TFB08699 (97%)	N/A	WP_090599455 (95%)	OIP66905 (91%)	KPK40788 (85%)	OGW74759 (85%)	OGW81430 (70%)
<i>hunO</i>	PF03334 (PhaG_MnhF_YufB)	C5669	RXG63005	HAJ32005 (91%)	TFB08700 (94%)	OFW53487 (91%)	WP_090599453 (88%)	OIP66890 (91%)	KPK40789 (77%)	OGW74731 (74%)	OGW81423 (70%)
<i>hunP</i>	PF12838 (Fer4_7)	C5669	RXG63006	HAJ32006 (89%)	TFB08701 (95%)	N/A	WP_090599451 (91%)	OIP66889 (88%)	KPK40790 (81%)	OGW74732 (76%)	OGW81424 (75%)

32 **Table S6. Genes encoded on contigs containing the HTH-XRE transcriptional regulator/antitoxin AtiR in E10H5-B2 *Atribacteria* genomic**
 33 **bin, as shown in Figure 5, and percent identity to homologous genes in other (meta)genomes (excluding Hydrate Ridge hits). Bolded genes**
 34 **were expressed in the metaproteome. *truncated protein; **contain conserved arginine residue for carboxylate transport.**
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Annotation	Gene	Contig	Gene	Top hit (% identity)	Top <i>Atribacteria</i> hit in environmental genome or top hit in non-Hydrate Ridge genome		
HTH-XRE regulator	<i>atiR</i>	E10H5_C107	RXG62479	HDK27529 (69%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C473	RXG64192	HDK27529 (66%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C194	RXG65323	HDK27529 (64%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C1742	RXG64293	HDK27529 (72%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C95	RXG62928*	HDK27529 (65%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C238	RXG62729	HDK27529 (65%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C2	RXG66887	HDK27529 (63%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C2	RXG66902	HDK27529 (65%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C486	RXG66788	HDK27529 (59%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C687	RXG66393	HDK27529 (73%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C103	RXG62795	HDK27529 (66%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C85	RXG66363	HDK27529 (64%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C4712	RXG63519	HDK27529 (67%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C1316	RXG65641	HDK27529 (72%)	<i>Atribacteria</i> HyVt-22		
		E10H5_C5280	RXG63000	HDK27529 (78%)	<i>Atribacteria</i> HyVt-22		
E10H5_C2922	RXG65842	HDK27529 (74%)	<i>Atribacteria</i> HyVt-22				
Tripartite tricarboxylate transporter	<i>tctC</i> <i>tctB</i> <i>tctA</i>	E10H5_C95	RXG62929 RXG62930 RXG62931	WP_066240574 (53%) WP_118245178 (35%) WP_093692001 (54%)	<i>Anaerospromusa subterranea</i> <i>Clostridium</i> AM58-1XD <i>Sporolituus thermophilus</i>		
		<i>tctC</i> <i>tctB</i> <i>tctA</i> <i>sat</i> <i>hyp</i>	E10H5_C107	RXG62483 RXG62484 RXG62485 RXG62486 RXG62487	MBN2395378 (71%) MBN2395379 (53%) MBN2395380 (68%) MBN2395381 (68%) MBN2395382 (61%)	<i>Atribacteria</i> Zod_Metabat.864 <i>Atribacteria</i> Zod_Metabat.864 <i>Atribacteria</i> Zod_Metabat.864 <i>Atribacteria</i> Zod_Metabat.864 <i>Atribacteria</i> Zod_Metabat.864	
	C4-dicarboxylate transporter		<i>dctP</i> <i>dctQ</i> <i>dctM</i>	E10H5_C95	RXG62935** RXG62936 RXG62937	PKL21426 (55%) AEG13811 (34%) PKL21182 (57%)	<i>Spirochaetae</i> HGW-1 <i>Desulfofundulus kuznetsovii</i> DSM 6115 <i>Spirochaetae</i> HGW-4
				<i>dctP</i> <i>dctQ</i> <i>dctM</i>	E10H5_C238	RXG62728 RXG62727 RXG62726	HBV57297 (84%) HBV57298 (74%) HBV57299 (80%)
			<i>dctP</i> <i>dctQ</i> <i>dctM</i>		E10H5_C486	RXG66786** RXG66785 RXG66784	HDK26676 (86%) HDK26675 (69%) HDK26674 (82%)
		<i>dctP</i> <i>dctQ</i> <i>dctM</i>		E10H5_C664	RXG63168 RXG63170 RXG63171	HAI33545 (72%) HAI33544 (73%) HAI33543 (84%)	<i>Atribacteria</i> UBA7920 <i>Atribacteria</i> UBA7920 <i>Atribacteria</i> UBA7920
Glycerol-3-phosphate transporter	<i>ugpB</i> <i>ugpA</i> <i>ugpE</i>	E10H5_C85	RXG66368 RXG66369 RXG66370	KPJ85459 (68%) KPJ85458 (67%) KPJ85457 (71%)	<i>Spirochaetes</i> DG_61 <i>Spirochaetes</i> DG_61 <i>Spirochaetes</i> DG_61		
		<i>ugpB</i>	E10H5_C103	RXG62790	WP_068137292 (47%)	<i>Limnochorda pilosa</i>	

	<i>ugdA</i> <i>ugdE</i>		RXG62789 RXG62788	WP_082726097 (46%) WP_068137283 (46%)	<i>Limnochorda pilosa</i> <i>Limnochorda pilosa</i>
Branched chain amino acid transporters	<i>livH</i> <i>livM</i> <i>livG</i> <i>livF</i> <i>livK</i>	E10H5_C2	RXG66901 RXG66900 RXG66899 RXG66898 RXG66897	PKP61938 (90%) PKP61939 (85%) PKP61948 (85%) PKP61940 (80%) PKP61941 (89%)	<i>Atribacteria</i> HGW-1 <i>Atribacteria</i> HGW-1 <i>Atribacteria</i> HGW-1 <i>Atribacteria</i> HGW-1 <i>Atribacteria</i> HGW-1
	<i>livH</i> <i>livM</i> <i>livG</i> <i>livF</i>	E10H5_C238	RXG62732 RXG62736 RXG62731 RXG62730	RLE68614 (60%) RLE68615 (55%) RLE68616 (57%) RLE68617 (56%)	<i>Thermoprotei</i> archaeon <i>Thermoprotei</i> archaeon <i>Thermoprotei</i> archaeon <i>Thermoprotei</i> archaeon
	<i>livK</i> <i>livH</i> <i>livM</i> <i>livG</i> <i>livF</i>	E10H5_C687	RXG66394 RXG66395 RXG66396 RXG66397 RXG66398	OQY40502 (43%) OQY40503 (41%) OQY40504 (42%) OGP70799 (50%) OQY40505 (55%)	<i>Atribacteria</i> 4572_76 <i>Atribacteria</i> 4572_76 <i>Atribacteria</i> 4572_76 <i>Deltaproteobacteria</i> RBG_16_50_11 <i>Atribacteria</i> 4572_76
	<i>livH</i> <i>livM</i>	E10H5_C8009	30420 30421	OQY40503 (95%) OQY40504 (93%)	<i>Atribacteria</i> 4572_76 <i>Atribacteria</i> 4572_76
	Purine transporter	<i>bmpA</i>	E10H5_C473	RXG64193 RXG64197 RXG64194 RXG64195	PKP58720 (94%) PKP60518 (88%) PKP60517 (94%) PKP60516 (96%)
M20 (zinc peptidase, amidohydrolase)		E10H5_C194	RXG65322 RXG65321 RXG65329	WP_034420537 (72%) WP_034420536 (73%) WP_034420535 (75%)	<i>Clostridiales</i> DRI-13 <i>Clostridiales</i> DRI-13 <i>Clostridiales</i> DRI-13
Sulfur-related (and neighboring)	<i>sat</i>	E10H5_C107	RXG62486 RXG62487	HDK26586 (85%) HDK26585 (67%)	<i>Atribacteria</i> HyVt-22 <i>Atribacteria</i> HyVt-22
Other genes	<i>gabT</i> C69 RTX RTX/Ig	E10H5_C4712 E10H5_C2795 E10H5_C1316 E10H5_C2922	RXG63518 RXG64595 RXG65639 RXG65844	PKP55816 (87%) WP_093794159 (43%) OGD35967 (42%) OGD35967 (43%)	<i>Atribacteria</i> HGW-1 <i>Sporomusa acidovorans</i> <i>Atribacteria</i> RBG_16_35_8 <i>Atribacteria</i> RBG_16_35_8

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Table S7. Putative toxin-antitoxin systems in *Atribacteria* E10H5-B2, and percent identity to homologous genes in other genomes.

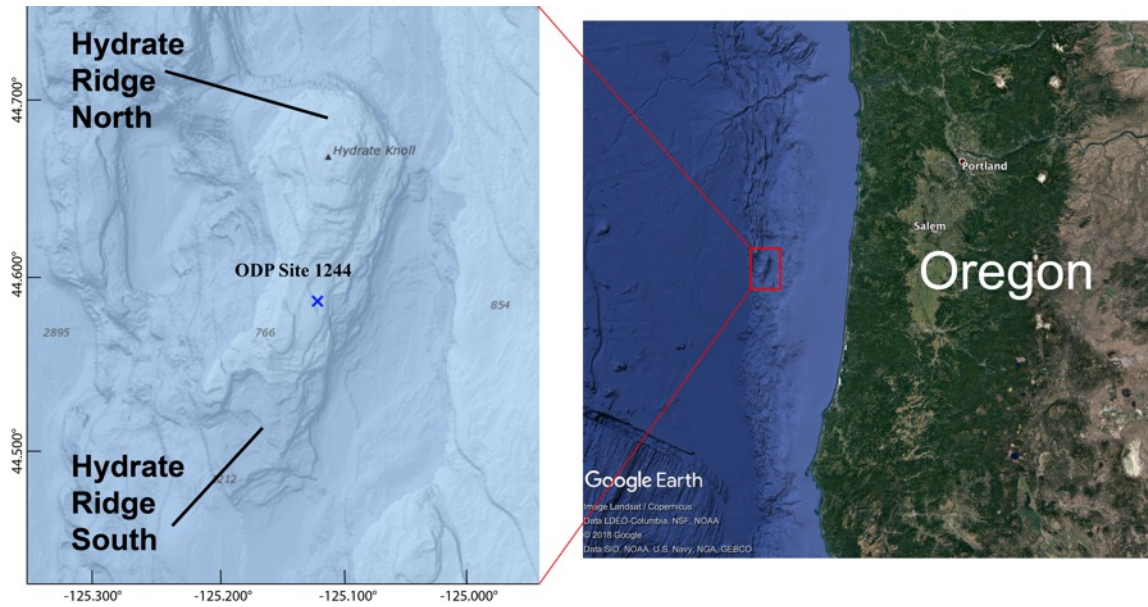
Annotation	Gene	Contig	Gene	Top hit (% identity)	Top hit	
Antitoxin	MazE-like	E10H5_C26	RXG62841	PIU28774 (82%)	<i>Actinobacteria</i> CG08_land_8_20_14_0_20_35_9	39
Toxin	MazF-like		RXG62840	PIU28775 (88%)	<i>Actinobacteria</i> CG08_land_8_20_14_0_20_35_9	40
Antitoxin	NikR-like	E10H5_C33	RXG63986	PIU25819 (95%)	<i>Atribacteria</i> CG08_land_8_20_14_0_20_33_29	41
Toxin	MazF-like		RXG63985	PIU25820 (83%)	<i>Atribacteria</i> CG08_land_8_20_14_0_20_33_29	42
Antitoxin	MazE-like	E10H5_C68	RXG64905	PKP54844 (89%)	<i>Atribacteria</i> HGW-1	44
Toxin	MazF-like		RXG64906	PKP54843 (84%)	<i>Atribacteria</i> HGW-1	45
Antitoxin	VapC-like	E10H5_C81	RXG64104	PKP54729 (90%)	<i>Atribacteria</i> HGW-1	46
Toxin	MazE-like		RXG64105	PKP54728 (81%)	<i>Atribacteria</i> HGW-1	47
Antitoxin	MazE-like	E10H5_C81	RXG64330	PIY33044 (92%)	<i>Atribacteria</i> CG_4_10_14_3_um_filter_34_134	48
Toxin	MazF-like		RXG64331	PIY33045 (92%)	<i>Atribacteria</i> CG_4_10_14_3_um_filter_34_134	49
Antitoxin	MazE-like	E10H5_C184	RXG64099	OQY39409 (97%)	<i>Atribacteria</i> 4572_76	50
Toxin	MazF-like		RXG64098	OQY39408 (98%)	<i>Atribacteria</i> 4572_76	51
Antitoxin	MazE-like	E10H5_C1146	RXG64860	WP_090599534 (91%)	<i>Atribacteria</i> JGI 0000014-F07	52
Toxin	MazF-like		RXG64859	WP_090599536 (89%)	<i>Atribacteria</i> JGI 0000014-F07	53
Antitoxin	MazE-like	E10H5_C1351	RXG65145	PKP54770 (94%)	<i>Atribacteria</i> HGW-1	54
Toxin	MazF-like		RXG65146	PKP54769 (89%)	<i>Atribacteria</i> HGW-1	55
Antitoxin	MazE-like	E10H5_C5010	RXG67035	WP_078128337 (59%)	<i>Leptospira alexanderi</i>	
Toxin	MazF-like		RXG67036	WP_010577027 (74%)	<i>Leptospira alexanderi</i>	

56 **Table S8. Glycosyltransferase contigs in E10-H5-B2 *Atribacteria* genomic bin, and percent identity to homologous genes in other genomes.**

Annotation	Contig	Gene	Top hit (% identity)	Top hit
Glycosyltransferase 2	E10H5_C38	N/A	OFW63513 (72%)	<i>Actinobacteria</i> RBG_19FT_COMBO_36_27
Glycosyltransferase 1		RXG64781	OFW63514 (72%)	<i>Actinobacteria</i> RBG_19FT_COMBO_36_27
Glycosyltransferase 2		RXG64782	OGD31966 (66%)	<i>Atribacteria</i> RBG_16_35_8
Glycosyltransferase 2		RXG64783	WP_104083790 (34%)	<i>Cryobacterium</i> Y11
Glycosyltransferase 2		RXG64791	GBC98638 (43%)	Bacterium HR17
NAD-dependent epimerase/dehydratase		RXG64792	OFW55242 (82%)	<i>Actinobacteria</i> RBG_13_35_12
NDP-sugar synthase		RXG64793	OFW55241 (82%)	<i>Actinobacteria</i> RBG_13_35_12
GDP-mannose 4,6-dehydratase		RXG64794	OFW55240 (88%)	<i>Actinobacteria</i> RBG_13_35_12
Glycosyltransferase 1	E10H5_C81	RXG64335	WP_093394743 (45%)	<i>Thermodesulforhabdus norvegica</i>
Glycosyltransferase 1		RXG64336	WP_093394743 (53%)	<i>Thermodesulforhabdus norvegica</i>
Glycosyltransferase 1		RXG64337	OGI06781 (40%)	<i>Melainabacteria</i> RIFCSPLOWO2_12_FULL_35_11
Glycosyltransferase 1		RXG64338	SPE32180 (46%)	<i>Solibacteres</i> SbA2
O-antigen ligase		RXG64339	OGD19921 (30%)	<i>Aminicenantes</i> RBG_13_64_14
Glycosyltransferase 1		RXG64340	OGD19922 (55%)	<i>Aminicenantes</i> RBG_13_64_14
Polysaccharide (de)acetylase	E10H5_C230	RXG63410	WP_019599125 (28%)	<i>Rhodonellum</i> spp.
Exopolysaccharide polyprenyl glycosylphosphotransferase		RXG63411	PKP61696 (88%)	<i>Atribacteria</i> HGW-1
Sugar epimerase		RXG63412	PKP61697 (77%)	<i>Atribacteria</i> HGW-1
Glycosyltransferase 1 (Cap1E-like)		RXG63413	WP_071120025 (57%)	<i>Romboutsia timonensis</i>
UDP-N-acetylglucosamine 4-epimerase		RXG63414	WP_036938033 (71%)	<i>Pseudobacteroides celluloso</i> lvens
Vi polysaccharide biosynthesis protein		RXG63415	WP_071120026 (68%)	<i>Romboutsia timonensis</i>
Phospholipid carrier-dependent glycosyltransferase		RXG63416	WP_036935155 (48%)	<i>Pseudobacteroides celluloso</i> lvens
Glycosyltransferase		RXG63417	PJE73714 (51%)	Terrybacteria CG10_big_fil_rev_8_21_14_0_10_41_10
Phospholipid carrier-dependent glycosyltransferase		RXG63418	WP_036935155 (43%)	<i>Pseudobacteroides celluloso</i> lvens
Glycosyltransferase 1		E10H5_C3323	RXG63206	PKP61698 (81%)
GDP-fucose synthetase	RXG63207		PKP61699 (85%)	<i>Atribacteria</i> HGW-1
GDP-mannose 4,6-dehydratase	(2,613-2,990)		PKP61700 (82%)	<i>Atribacteria</i> HGW-1
UDP-glucose 6-dehydrogenase (Ugd)	E10H5_C266	RXG63573	PKP61722 (77%)	<i>Atribacteria</i> HGW-1
NAD-dependent epimerase/dehydratase		RXG63566	PKP59007 (93%)	<i>Atribacteria</i> HGW-1
Aminotransferase		RXG63567	PKP59008 (93%)	<i>Atribacteria</i> HGW-1
Formyltransferase (non-ribosomal peptide synthetase-like)		RXG63568	PKP59009 (90%)	<i>Atribacteria</i> HGW-1
Acetyltransferase		RXG63569	PKP59010 (87%)	<i>Atribacteria</i> HGW-1
Deacetylase		RXG63570	RME50047 (61%)	<i>Deltaproteobacteria</i> bacterium
7-keto-8-aminopelargonate synthetase	E10H5_C306	RXG65589	OGD15025 (91%)	<i>Atribacteria</i> RBG_19FT_COMBO_35_14
UDP-glucose 4-epimerase		RXG65590	OGD15024 (84%)	<i>Atribacteria</i> RBG_19FT_COMBO_35_14
UDP-glucose 4-epimerase	E10H5_C441	RXG65590	OGD15024 (87%)	<i>Atribacteria</i> RBG_19FT_COMBO_35_14
Radical SAM P-methyltransferase	E10H5_C558	RXG63508	OGD16377 (81%)	<i>Atribacteria</i> RBG_19FT_COMBO_35_14
Glycosyltransferase 1	E10H5_C1163	RXG62499	WP_090599978 (92%)	<i>Atribacteria</i> JGI_0000014-F07
Glycosyltransferase 1 (Cap1E-like)	E10H5_C3994	RXG63236	WP_071605078 (53%)	<i>Anaeroarcus burkinensis</i>
Exopolysaccharide polyprenyl glycosylphosphotransferase		RXG63237	PKP62045 (76%)	<i>Atribacteria</i> HGW-1
Acetyltransferase		RXG63239	PKP62044 (84%)	<i>Atribacteria</i> HGW-1
Polysaccharide biosynthesis protein		RXG63238	PKP62043 (87%)	<i>Atribacteria</i> HGW-1

Glycosyltransferase 4 Cyclic nucleotide-binding domain- containing protein	E10H5_C4124	RXG64087 RXG64088	PKP55791 (95%) PKP55792 (93%)	<i>Atribacteria</i> HGW-1 <i>Atribacteria</i> HGW-1
NAD-dependent epimerase/dehydratase Glycosyltransferase 4	E10H5_C4631	RXG66927 RXG66928	PKP58948 (97%) PKP58071 (83%)	<i>Atribacteria</i> HGW-1 <i>Atribacteria</i> HGW-1
Bacillithiol biosynthesis deacetylase Glycosyltransferase 2	E10H5_C4676	RXG65226 RXG65225	OGD13744 (93%) OGW00676 (55%)	<i>Atribacteria</i> RBG_19FT_COMBO_35_14 <i>Nitrospinae</i> RIFCSPLOWO2_01_FULL_39_10

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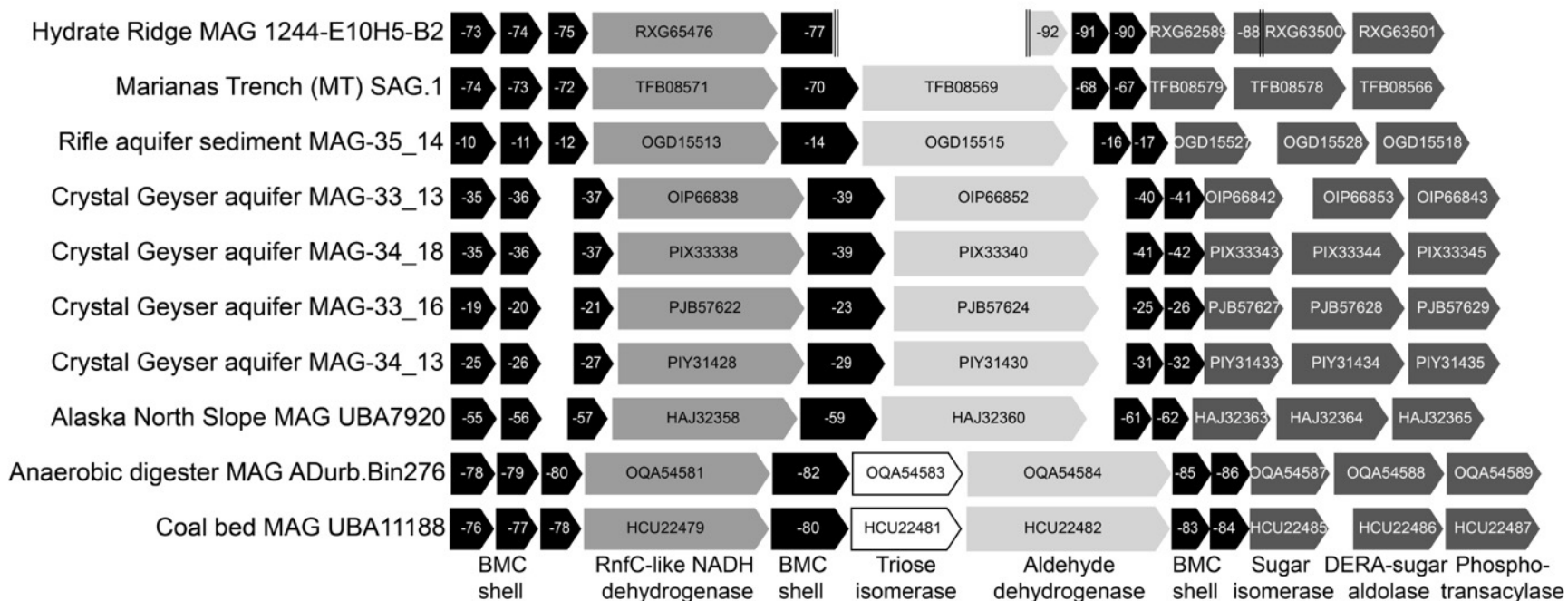
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60 **Figure S1.** Map of Site ODP 1244 ($44^{\circ}35.1784'N$; $125^{\circ}7.1902'W$) on Hydrate Ridge, drilled on IODP Leg 204. The site is located 80 km west of
 61 Oregon, in the accretionary complex of the Cascadia subduction zone, on the eastern flank of Hydrate Ridge, ~3 km northeast of the southern summit.

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67 **Figure S2.** Bacterial microcompartment (BMC) gene loci from *Atribacteria* (JS-1) MAGs and SAGs in UniProt. Each gene is labeled with its NCBI
68 accession. Short genes are labeled with the last two digits of the NCBI accession (see neighboring genes for remainder of accession). The BMC loci
69 from Hydrate Ridge MAG 1244-E10H5-B2 is distributed over three short contigs with some genes truncated (indicated by double vertical lines).