Adaptations of *Atribacteria* to life in methane hydrates: hot traits for cold life

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Running Title: *Atribacteria* adaptions in methane hydrate ecosystem

Dedication: To Katrina Edwards

Originality-Significance Statement: This work provides insights into the metabolism and adaptations of elusive *Atribacteria* (JS-1 clade) that are ubiquitous and abundant in methane-rich ecosystems. We show that JS-1 (Genus 1) from methane hydrate stability zones contain metabolisms and stress survival strategies similar to hyperthermophilic archaea.

Summary: Gas hydrates harbor gigatons of natural gas, yet their microbiomes remain mysterious. We bioprospected methane hydrate-bearing sediments from under Hydrate Ridge (offshore Oregon, USA, ODP Site 1244) using 16S rRNA gene amplicon, metagenomic, and metaproteomic analysis. *Atribacteria* (JS-1 Genus 1) sequences rose in abundance with increasing sediment depth. We characterized the most complete JS-1 Genus 1 metagenome-assembled genomic bin (B2) from the deepest sample, 69 meters below the seafloor (E10-H5), within the gas hydrate stability zone. B2 harbors functions not previously reported for *Atribacteria*, including a primitive respiratory complex and myriad capabilities to survive extreme conditions (e.g. high salt brines, high pressure, and cold temperatures). Several *Atribacteria* traits, such as a hydrogenase-Na^+/H^+ antiporter supercomplex (Hun) and di-myo-inositol-phosphate (DIP) synthesis, were similar to those from hyperthermophilic archaea. Expressed *Atribacteria* proteins were involved in transport of branched chain amino acids and carboxylic acids. Transporter genes were downstream from a novel helix-turn-helix transcriptional regulator, AtiR, which was not present in *Atribacteria* from other sites. Overall, *Atribacteria* appear to be endowed with unique strategies that may contribute to its dominance in methane-hydrate bearing sediments. Active microbial transport of amino and carboxylic acids in the gas hydrate stability zone may influence gas hydrate stability.

Introduction

Gas hydrates, also known as clathrates, are cages of ice-like water crystals encasing gas molecules such as methane (CH_4). Because hydrates form under high pressure and low temperature, their distribution on Earth is limited to permafrost and continental margins (Hester and Brewer, 2009). These hydrates harbor gigatons of natural gas, which may serve as a potential energy source for the future (Chong et al., 2016). They are also susceptible to dissociation due to rising ocean temperatures, which could release massive methane reservoirs to the atmosphere and exacerbate global warming (Archer et al., 2009; Ruppel and Kessler, 2017).

Despite the global importance of gas hydrates, their microbiomes remain mysterious. Microbial cells are physically associated with hydrates (Lanoil et al., 2001), and the taxonomy of these hydrate-associated microbiomes is distinct from non-hydrate-bearing sites (Inagaki et al., 2006). Because salt ions are excluded during hydrate formation (Ussler III and Paull, 2001; Bohrmann and Torres, 2006), hydrate-associated microbes likely possess adaptations to survive high salinity and low water activity, as well as low temperatures and high pressures (Honkalas et al., 2016). However, knowledge of the genetic basis of such adaptations is incomplete, as genomic data for hydrate communities are sparse and most hydrate microbiomes have been characterized primarily through single-gene taxonomic surveys.

Global 16S rRNA gene surveys show that the JS-1 sub-clade of the uncultivated bacterial candidate phylum *Atribacteria* is the dominant taxon in gas hydrates (Reed et al., 2002; Inagaki et al., 2003; Kormas et al., 2003; Newberry et al., 2004; Webster et al., 2004; Inagaki et al., 2006; Webster et al., 2007; Fry et al., 2008; Kadnikov et al., 2012; Parkes et al., 2014; Chernitsyna et al., 2016) and in other deep sediment ecosystems with abundant methane (Gies et al., 2014; Carr et al., 2015; Hu et al., 2016). The other major *Atribacteria* lineage, OP-9, has only been found in hot springs (Dodsworth et al., 2013; Rinke et al., 2013) and thermal bioreactors (Nobu et al., 2015). Marine *Atribacteria* are dispersed through ejection from submarine mud volcanoes (Hoshino et al., 2017; Ruff et al., 2019), and environmental heterogeneity may select for locally adapted genotypes. Indeed, *Atribacteria* phylogeny is highly diverse, suggesting the potential for wide functional variation and niche specialization.

Genomic evidence for such *Atribacteria* specialization remains limited. To date, near-complete single-cell and metagenomic sequences from hot springs, wastewater, lake sediments, and non-hydrate bearing marine sediments have shown that *Atribacteria* lack respiratory pathways. The high-temperature OP-9 lineage likely ferments sugars (Dodsworth et al., 2013) whereas the low-temperature JS-1 lineage ferments propionate to hydrogen, acetate, and ethanol (Nobu et al., 2016). Both JS-1 and OP-9 lineages possess genes encoding bacterial microcompartment shell proteins that may sequester toxic aldehydes, enabling their condensation

to carbohydrates (Nobu et al., 2016). The available data on *Atribacteria* genomes suggest diversification linked to organic substrate utilization, although a range of other factors, including physical environmental conditions (e.g., temperature and pressure) undoubtedly also play a role.

Here we examined the distribution, phylogeny, and metabolic potential of uncultivated JS-1 *Atribacteria* in cold, salty, and high-pressure sediments beneath Hydrate Ridge, off the coast of Oregon, USA, using a combination of 16S rRNA gene amplicon, metagenomic, and metaproteomic analysis. We found that JS-1 Genus-1 are abundant in the gas hydrate stability zone (GHSZ) and that they harbor numerous strategies for tolerance of osmotic stress, including many biosynthesis pathways for unusual osmolytes similar to those of thermophiles.

Results and Discussion

Geochemical gradients. Sediment core samples spanned four geochemical zones from 0-69 meters below seafloor (mbsf) at the ODP Site 1244C,D,E at Hydrate Ridge, off the coast of Oregon, USA (Fig. S1; Tréhu et al., 2003): near surface (0-2 mbsf), sulfate-methane transition zone (SMTZ; 2-9 mbsf), metal reduction zone (18-36 mbsf), and GHSZ (45-124 mbsf; **Fig. 1**).

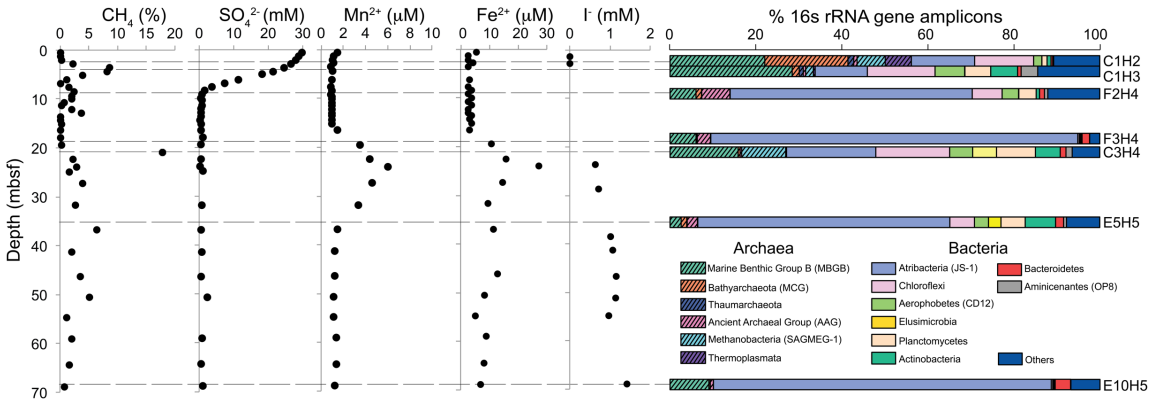


Figure 1. Porewater geochemistry (methane, sulfate, manganese, iron, and iodide) and 16S rRNA gene composition from sediment depth profiles at ODP 204 Site 1244, Hydrate Ridge, offshore Oregon, USA. Hatched and solid bars are archaeal and bacterial 16S rRNA genes, respectively. "Others" category represents bacterial and archaeal phyla with <2% of total sequences.

Sediment porewater methane concentrations rose from negligible at the seafloor to 8% by volume at 3-5 mbsf, and remained <5% below 5 mbsf, with the exception of one sample at 21 mbsf.

Sulfate rapidly dropped from 28 to <1 mM from 0-9 mbsf and remained <1 mM below 9 mbsf, with the exception of one sample at 50.7 mbsf (2.3 mM sulfate). Outside of the metal reduction zone, dissolved Mn was ~1 μM and dissolved Fe was 3-10 μM. Dissolved Mn and Fe peaked at 6 and 27 μM, respectively, coincident with a single layer of disseminated gas hydrate in the metal reduction zone. Dithionite-extractable Fe and Mn increased slightly from 2 to 21 mbsf (0.4 to 1.1% and 0.002 to 0.005%, respectively; **Table S1**). Iodide concentrations were highest in the GHSZ (1.4 mM), where liquid brines form as a result of methane hydrate formation. Estimated *in situ* salinity ranged from seawater salinity (35 g kg^{-1}) to >100 g kg^{-1} (Milkov et al., 2004). Total organic carbon concentrations in sediment varied between 1-2%. *In situ* temperature ranged from ~4°C at the seafloor to ~6-11°C in the GHSZ.

Phylogenetic diversity. Phylogenetic diversity and species richness in 16S rRNA gene amplicons were highest in the SMTZ and decreased with depth except in the metal reduction zone (**Fig. S2**). The relative abundance of *Atribacteria* (JS-1)-affiliated amplicons increased with depth, from 15% in the near surface to 86% in the GHSZ (**Table S1**). GHSZ sediment (sample E10-H5 from 69 mbsf) contained 230 *Atribacteria* OTUs (89-92% ANI) that spanned a wide diversity of clades within JS-1 Genus 1 (Yarza et al. 2014) **(Fig. 2)**. A single OTU matching GenBank AB804573.1, from an ocean drilling core from offshore Shimokita Peninsula, Japan, comprised 69% of *Atribacteria* 16S rRNA sequences in the GHSZ **(Table S2**). Other *Atribacteria* 16S rRNA sequences also matched marine samples from shallower Hydrate Ridge sediments (Marlow et al., 2014) and methane hydrate sediment off Taiwan (Lin et al., 2014) (**Table S2**). 16S rRNA sequences from amplicons and metagenomes generally showed consistent trends (**Fig. S3**). *Atribacteria* OTU abundance and composition varied significantly with sediment depth (**Fig. S4**).

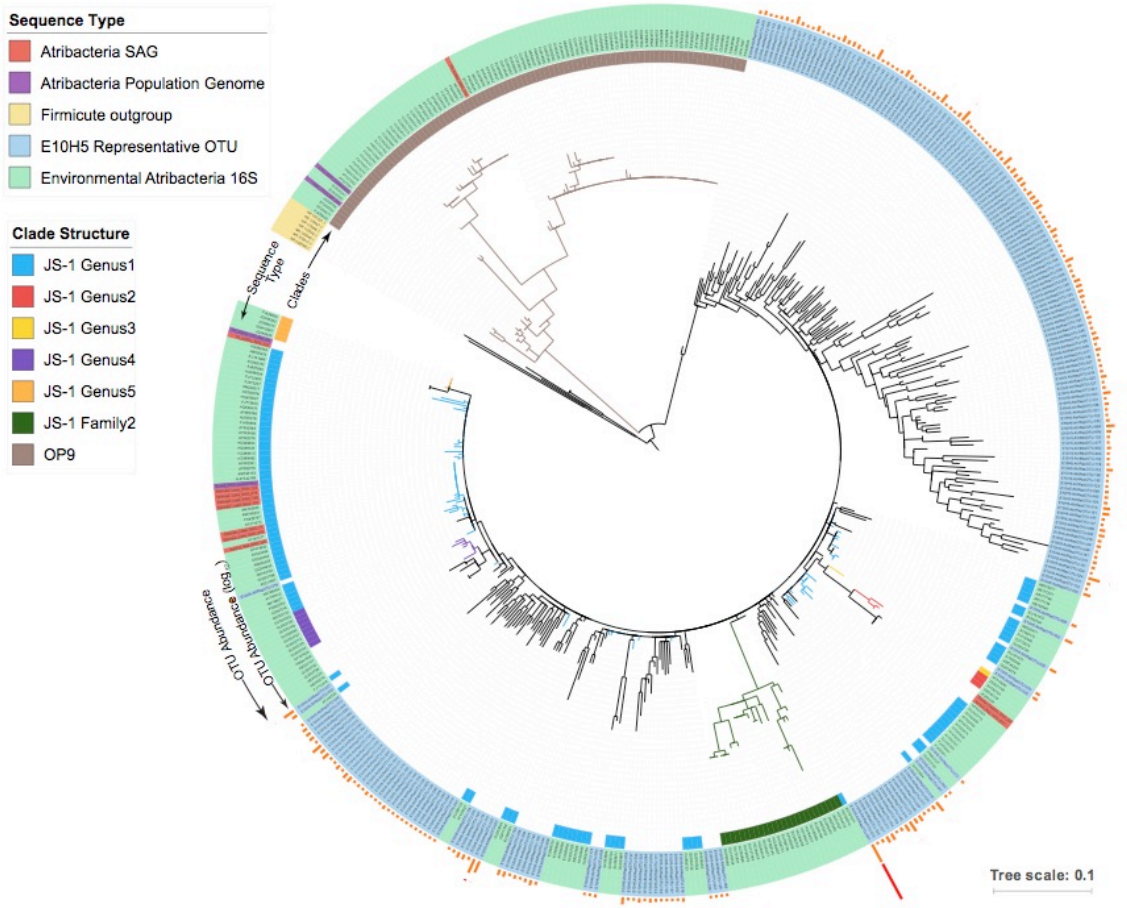
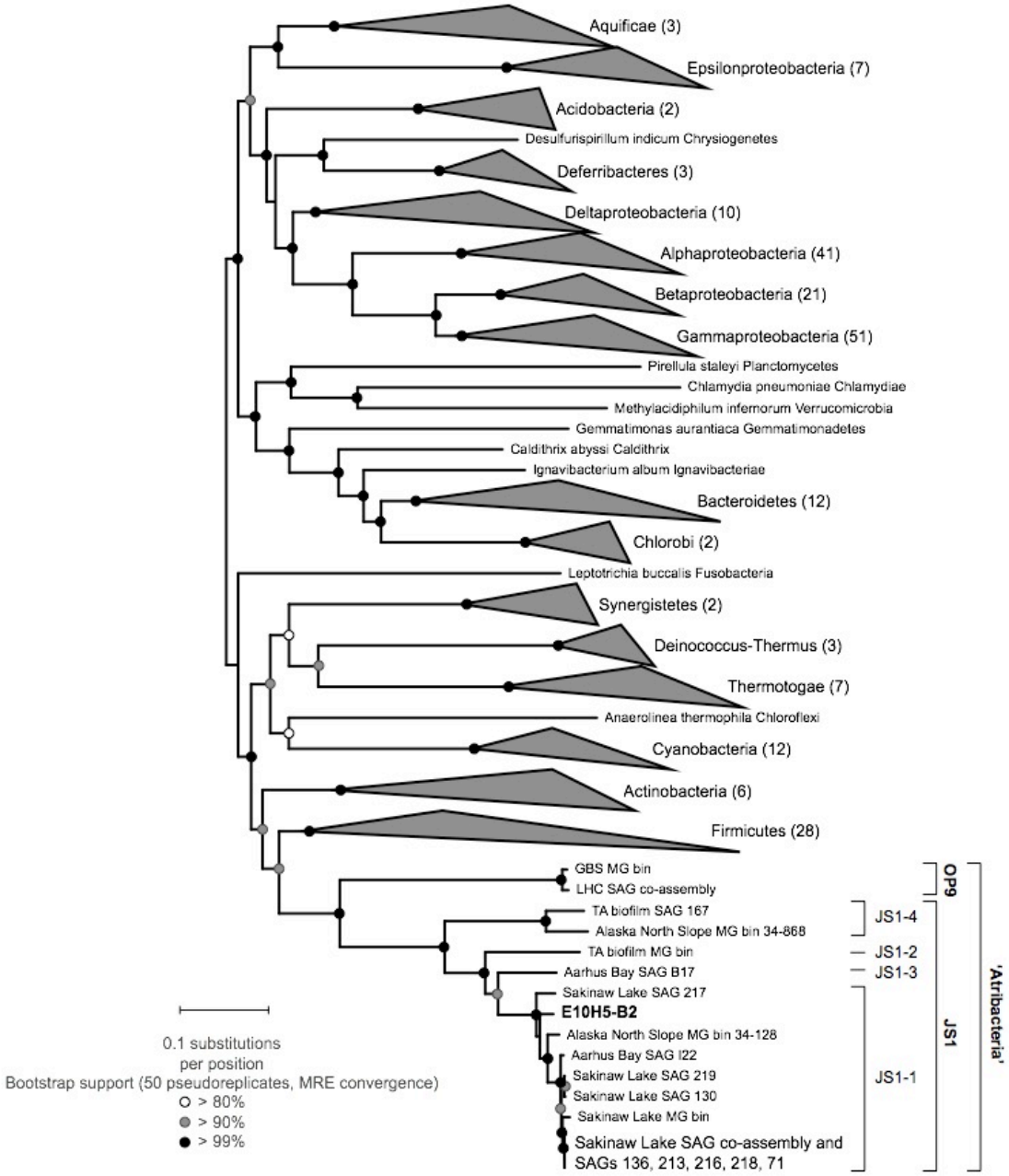


Figure 2: Phylogenetic reconstruction of *Atribacteria* 16S rRNA gene sequences from sample E10-H5 (69 mbsf). The tree includes the 230 *Atribacteria* OTUs with two or more sequences as well as reference sequences from environmental clones, SAGs, and MAGs, with *Firmicutes* as the outgroup. Reconstruction was performed in RAxML with 275 positions spanning the V3-V4 region of the 16S rRNA gene using a GAMMA model of rate heterogeneity, a GTR model of substitution, and 500 bootstraps followed by a thorough Maximum Likelihood search. The relative abundances of recovered amplicons from diverse lineages/OTUs is shown in the outermost circle. Additional information on the most abundant JS-1 OTUs from E10-H5 is provided in **Table S2**.

JS-1 Genus-1 partial genome. To gain insight into the function of JS-1 *Atribacteria* in the GHSZ, we analyzed a 4-Mbp metagenome-assembled genome (MAG) from sample E10-H5 (**Table S3**). This MAG, hereafter designated "B2", was chosen for its relatively high completeness (69%) and low contamination (2%). B2 lacked a 16S rRNA gene, but contained a *rpoB* gene with 94% similarity to *Atribacteria* bacterium 34_128 from an oil reservoir (Hu et al., 2016). B2 had 35% GC content, similar to other *Atribacteria* (Carr et al., 2015). Phylogenetic placement based on 69 concatenated single-copy genes confirmed that B2 belonged to JS1-Genus

140 1 and was most closely related to JS1-Genus 1 genomes from a sediment-hosted aquifer at Rifle,
141 Colorado (RBG_COMBO_35; Anantharaman et al., 2016), cold CO_2-rich fluids at Crystal
142 Geyser, Utah (CG2_30_33_13; Probst et al., 2017), and hydrothermal vent sediments at Guaymas
143 Basin, Gulf of California (4572_76; Dombrowski et al., 2017) (**Fig. 3**).



144
145 **Figure 3**: **Maximum likelihood phylogeny for B2 with 220 representative and 20 previously**
146 **found *Atribacteria* SAGs and population genomes using multiple (minimum 6, maximum**
147 **69) core single copy genes.** Tree made in RAxML with GAMMA model, 1000 rapid bootstraps,
148 MRE convergence bootstop (50 replicates) followed by a thorough ML search.
149

150 Despite the relatively cool *in situ* temperature of the E10-H5 sediment (7-8°C
151 (ShipboardScientificParty, 2003)), the most closely related genomes from cultured isolates were
152 thermophilic gram-positive Firmicutes: halophilic *Halothermothrix orenii* spp. (Mavromatis et
153 al., 2009) and metal-respiring *Therminocola potens* strain JR (Byrne and Nicholas, 1986). Below
154 we highlight features of the B2 genome and proteome potentially relevant to life in the unique
155 environment of methane clathrates, with particular focus on a putative respiratory complex and
156 genes involved in stress response and environmental homeostasis.
157
158 **Predicted respiratory function of the Hun supercomplex.** B2 contained genes for a putative
159 operon encoding a 16-subunit respiratory complex, hereafter designated Hun. The *hun* operon
160 was also present in two other MAGs from ODP Site 1244 (*Planctomycetes* C1H3-B36 and
161 *Firmicutes* E5H5-B3) and in *Atribacteria, Actinobacteria*, and *Omnitrophica* MAGs from other
162 deep subsurface ecosystems (Rinke et al., 2013; Baker et al., 2015; Anantharaman et al., 2016;
163 Probst et al., 2017) (**Table S4**). The gene arrangement and predicted function of the putative Hun
164 complex are similar to those of an ancient Mrp-Mbh-type membrane-bound [NiFe] hydrogenase-
165 Na^+/H^+ antiporter respiratory complex in hyperthermophilic archaea (Yu et al., 2018), which is
166 thought to be the ancestor of Complex I, also known as NADH:ubiquinone oxidoreductase (Nuo)
167 (Friedrich and Scheide, 2000; Moparthi and Hägerhäll, 2011; Schut et al., 2013). Complex I's
168 modules likely had separate origins: the ubiquinone-reducing subunits NuoBCD ("Q-module")
169 evolved from an ancient membrane-bound [NiFe] hydrogenase, while its proton-pumping
170 subunits NuoLMN ("P module") evolved from an ancient Na^+/H^+ antiporter (Mathiesen and
171 Hägerhäll, 2002; Moparthi et al., 2014; Spero et al., 2015).
172 *Atribacteria hun* genes likely encode a complex of four protein modules that couple H^+
173 and Na^+ translocation to H_2 production, similar to Mrp-Mbh-type complexes in hyperthermophilic
174 archaea **(Fig. 4**). Based on the similarity of HunAB to anaerobic sulfite reductase (Asr) subunits
175 A and B, which transfer electrons from ferredoxin to the active site in AsrC (missing in the *hun*

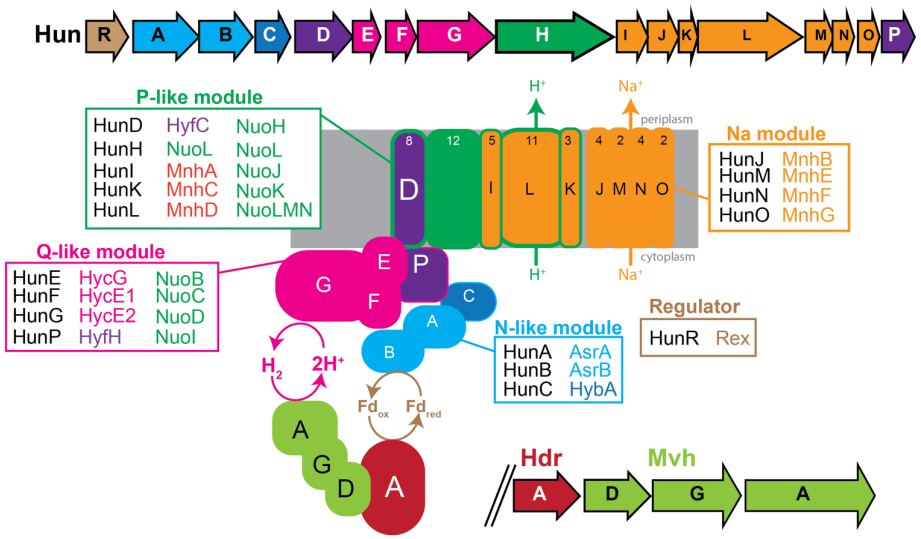
176 operon), we inferred that N module-like subunits HunABC likely accept electrons from

177 ferredoxin and pass them through iron-sulfur clusters to Q-module-like subunit HunEFGP.

178 Instead of accepting electrons from NADPH and passing them to ubiquinone as in Complex I,

179 HunABC likely accepts electrons from ferredoxin and passes them to $2H^+$ for reduction to H_2 at

180 HunEFGP's Ni-Fe active site **(Table 1; Fig. 4)**.



181

182 **Figure 4: Predicted structure and function of a multi-subunit respiratory complex,**
183 **hereafter "Hun", found in B2 and other deep subsurface genomes.** *Top:* conserved gene
184 cluster arrangement, with each color representing a different predicted protein. *Below:* predicted
185 cellular locations and functions based on homologs of the genes of the same colors encoded by
186 the putative *hun* operon, and predicted regeneration of substrates by the heterodisulfide reductase
187 (HdrA)-methyl viologen hydrogenase (MvhAGD) complex. Predicted functions of *hun* genes are
188 based on Mrp-Mbh complexes in thermophilic archaea (Schut et al., 2013; Yu et al., 2018). See
189 **Table S4** for accession numbers.
190

191 P-module-like subunits HunDHILK are predicted to be proton-pumping transmembrane proteins

192 and Na-module-like subunits HunIJKLMNO are homologs of the Na^+/H^+ antiporter

193 MnhABCDEFGH in Mrp-Mbh-type complexes. The presence of F0F1-type and V-type ATPases

194 suggest that H^+ and Na^+ ions pumped outward by HunIJKLMNO are pumped back in to make

195 ATP. Electrons from H_2 could be transferred back to ferredoxin by the activity of the

196 heterodisulfide reductase (HdrA)-methyl viologen hydrogenase (MvhAGD) complex (**Fig. 4**). A

197 redox-sensing transcriptional repressor gene (*hunR*) immediately upstream of the *hun* operon

198 suggests that the hydrogenase may not be used strictly for energy conservation, but could also be
199 for balancing reducing equivalent by disposing of extra electrons (McLaughlin et al., 2010).
200
201 **Osmotic stress survival.** Any life that can persist in brine pockets within methane hydrate must
202 contend with high salinity (up to ~3x that of seawater) and low water potential. B2 contained
203 numerous genes for the "salt out" survival strategy, in which osmotic pressure is maintained by
204 exporting cations (Wood, 2015). B2's cation export systems included efflux systems,
205 mechanosensitive ion channels, and Na^+-H^+ antiporters (**Table 1**).
206 A second salt survival strategy is import and/or biosynthesis of osmolytes, most often
207 polar, water-soluble, and uncharged organic compounds and/or extracellular polymers. For
208 example, glycine betaine is abundant in saline fluids from deep sediment basins (Daly et al.,
209 2016). B2 contained genes for transport of trehalose and biosynthesis of the common osmolytes
210 glutamine, glutamate, and poly-gamma-glutamate, all of which had homologs in other
211 *Atribacteria* MAGs (**Table 1**). B2 also encoded genes for glycine betaine and dihydroxyacetone
212 biosynthesis without homologs in other *Atribacteria*. Surprisingly, B2 also encoded biosynthetic
213 genes (myo-inositol-1 phosphate synthase (MIPS)/bifunctional IPC transferase and DIPP
214 synthase (IPCT-DIPPS)) for the unusual solute di-myo-inositol-phosphate (DIP) made by
215 hyperthermophiles (Santos and Da Costa, 2002). The MIPS gene had closest similarity to
216 halophilic and psychrophilic *Euryarchaeota*, without homologs in other *Atribacteria*. The IPCT-
217 DIPPS gene was also present in *Atribacteria* HGW-1 from subsurface Japan (Hernsdorf et al.,
218 2017) and *Atribacteria* 4572_76 from Guaymas Basin (Dombrowski et al., 2017).
219 Immediately upstream from B2's MIPS/IPCT-DIPPS genes was an acyl carrier protein
220 (*acpP*) gene, commonly involved in fatty acid and polyketide biosynthesis. Sixteen additional
221 *acpP* copies were present in B2, often flanked by transposon scars, suggestive of recent
222 horizontal gene transfer (**Table S5)**. Other *Atribacteria* MAGs had only 1-2 copies of *acpP*,
223 usually near fatty acid biosynthesis genes.

224 **Table 1. Putative osmotic stress-related genes in B2.** *Atribacteria* homologs all had >80%
225 AAI. AAI to other taxa (56-76%) are provided. *indicates multiple copies.

Annotation	Gene	Accession	Top hit	Top hit
Na^+/H^+ antiporter	*mrpEFGB*	RXG65834.1-RXG65838.1	OQY40657.1-OQY40661.1	*Atribacteria* 4572_76
Na^+ efflux	*natB*	RXG65900.1	OGD31203.1	*Atribacteria* RBG....
Threonine efflux	*rhtB*	RXG66248.1	OGD15641.1	*Atribacteria* RBG....
Na^+ channel	DUF554	RXG63559.1	KUK55705.1	*Atribacteria* 34_128
Mechanosensitive ion channel	*mscS*	RXG63036.1	KUK56353.1	
Trehalose transporter	*sugAB*	RXG66833.1-RXG66834.1	KUK55397.1 KUK55398.1	
Glutamine synthetase	*glnA*	RXG65164.1	KUK55578.1	
K^+ transport	*trkAH**	RXG63511.1 RXG63512.1	PKP56013.1 PKP56012.1	*Atribacteria* HGW-1
Aromatic aa exporter	*yddG**	RXG63201.1	PKP55084.1	
Glutamate synthase	*gltD*	RXG66270.1	PKP56573.1	
Proline racemase	*prdF*	RXG63210.1	PKP58887.1	
Poly-gamma glutamate synthase	*pgsCBW*	RXG66317.1-RXG66319.1	PKP60458.1-PKP60460.1	
Glycerol uptake	*glpF*	RXG65629.1	OHV10031.1 (61%)	*Kushneria* YCWA18
Betaine-aldehyde dehydrogenase	*betB*	RXG62957.1	KUJ28189.1 (56%)	*Catabacter hongkongensis*
Dihydroxy-acetone kinase	*dhaKLM*	RXG65626.1-RXG65628.1	RLC64130.1- (67%) RLC64131.1 (61%)	*Chloroflexi* bacterium
DIPP synthesis pathway	MIPS/IPCT-DIPPS*	RXG66889.1 RXG66888.1	AAU82306.1 (76%) PKP58414.1	Archaeon GZfos13E1 *Atribacteria* HGW-1

226

227 Like other *Atribacteria*, B2 contained genes encoding a sugar phosphate-utilizing class of
228 proteinaceous bacterial microcompartments that neighbored sugar isomerases, RnfC NADH
229 dehydrogenase and an oxidoreductase (Axen et al., 2014; Nobu et al., 2016) (**Table S6**). Further
230 exploration of sugar-related genes revealed that B2 and other *Atribacteria* encode the non-
231 mevalonate pathway for isoprenoid biosynthesis (*ispDEFGH*), exopolysaccharide synthesis
232 proteins, numerous glycosyltransferases for transferring UDP- and GDP-linked sugars to a variety
233 of substrates, and several proteins related to N-linked glycosylation (**Table S7**). The capacity for
234 glycosylation may be another adaptation for survival of salt stress (Kho and Meredith, 2018).
235

236 **Expression of lipopolysaccharide and transport-related proteins.** Metaproteomic analysis
237 identified six expressed peptides affiliated with B2, all associated with assembly or transport
238 (**Table 2**). One was an outer member lipopolysaccharide assembly protein (LptD), also known as

239 Imp/OstA (increased membrane permeability/organic solvent tolerance (Braun and Silhavy,
240 2002). Another was a capsular polysaccharide biosynthesis protein (YveK). The other expressed
241 peptides were predicted to be transporters of purines (BmpA), branched chain amino acids (LivH,
242 LivM), and C4-dicarboxylates (DctQ). All *liv* genes on the operon with the expressed *livH* had
243 homologs in other *Atribacteria* genomes (**Table S8**) with the exception of *livG*, which encodes a
244 protein related to the lipopolysaccharide export system ATP-binding protein LptB that may serve
245 a specific purpose in methane-hydrate *Atribacteria*. Upstream of *liv* genes we found a *ykkC-yxkD*
246 riboswitch implicated in detoxification and efflux control (Barrick et al., 2004), suggesting that
247 branched chain amino acids may be involved in environmental stress response, as seen in other
248 microbes (Liu et al., 2005).

249 **Table 2. Metaproteomic peptide hits for B2.**

Peptide	Protein	Contig	Gene	Top hit (% identity)	Top hit
EYKPKEDWKMNFSS SYNLNTK	LptD	C10125	33494	OQY39007.1 (90%)	*Atribacteria* 4572_76
GIIILIFLIAVITAVLV SYFVLSPTP	YveK	C456	RXG64813.1	PKP59499.1 (74%)	*Atribacteria* HGW-1
CSNLIIKALLVVLVL SLGITLGIAKAP	BmpA	C473	RXG64193.1	PKP58720.1 (94%)	*Atribacteria* HGW-1
KPFRKSPGLIILLSTV AVGFIIR	LivH	C8009	30420	OQY40503.1 (94%)	*Atribacteria* 4572_76
LIFLLLLAVAVVVPF LLGLLILRF	LivM	C2171	15004	RKY02958.1 (46%)	*Spirochaetes* bacterium
NKINLIFSILIIIFLIVL TYEGIILVKVGLNA	DctQ	C95	RXG62936.1	AEG13811.1 (34%)	*Desulfofundulus kuznetsovii*

250

251 In addition to numerous transporters for branched chain amino acids, B2 encoded abundant
252 TRAP (tripartite ATP-independent periplasmic) transporters of dicarboxylic (DctPQM) and
253 tricarboxylic (TctCBA) acids (**Table S7; Fig. 5**). TRAP transporters use an electrochemical
254 gradient (H^+ or Na^+) and a substrate-binding protein to transport solutes across the membrane
255 (Fischer et al., 2010). A conserved arginine residue in the DctP substrate-binding protein confers
256 specificity for carboxylate groups (Lecher et al., 2009; Fischer et al., 2015).

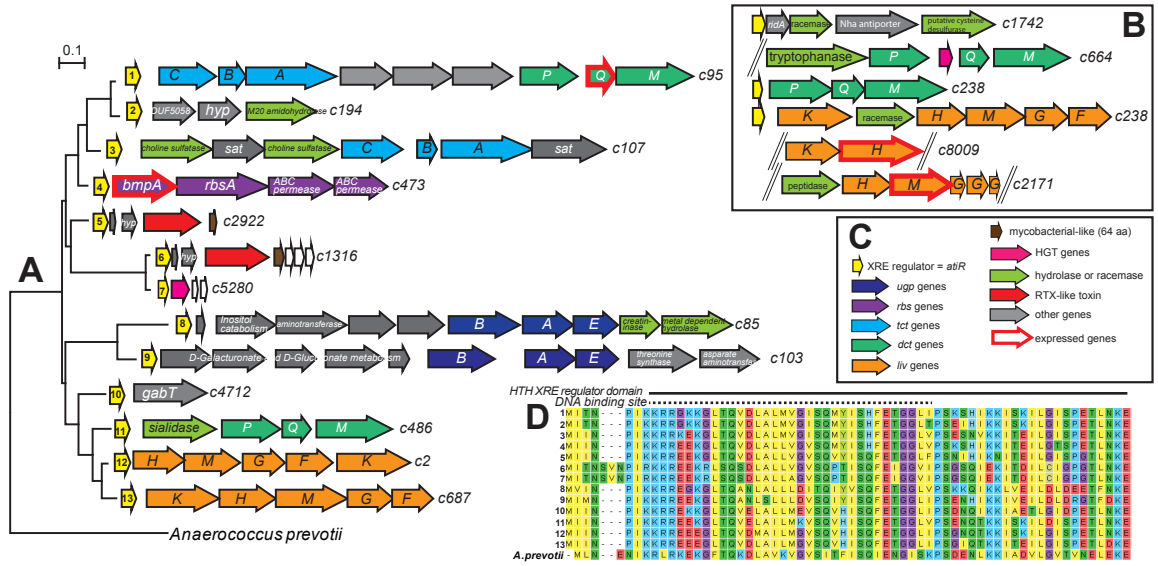


Figure 5: Phylogeny of HTH-XRE regulators/antitoxins (yellow), hereafter "AtiR", from B2 and synteny of downstream genes. Genes highlighted in thick red lines were expressed in the metaproteome. **A)** AtiR maximum likelihood phylogeny based on contigs (labeled on the right) from E10-H5 B2, with *Anaerococcus prevotii* as the outgroup. **B)** Additional putative operons from B2 likely regulated by *atiR*, which is truncated partially or completely on these contigs. **C)** Legend for panels A and B; **D)** AtiR amino acid alignment for the 13 AtiR sequences from *Atribacteria* E10-H5-B2 shown in panel A. Abbreviations: *bmpA*: basic membrane protein A; *dctPQM*: C4-dicarboxylate transporter; *gabT*: 4-aminobutyrate aminotransferase; *livHMGF*: branched chain amino acid transporter; *rbs*: ribose transporter; *sat:* sulfate adenylyltransferase; *tctCBA*: tricarboxylate transporter; *ugpBAE*: sn-glycerol-3-phosphate transporter. See **Table S7** for accession numbers and % identity to closest gene hits in other genomes.

A novel regulator. Three out of six of the expressed transporter proteins were encoded by genes located downstream from a novel gene predicted to encode a helix-turn-helix xenobiotic response element transcriptional regulator, which we named "AtiR" (**Table S8; Fig. 5**). AtiR was not found in *Atribacteria* MAGs (the top BLAST hit was the skin firmicute *Anaerococcus prevotii* (41-49% AAI)), suggesting that it may serve a specific purpose in methane-hydrate *Atribacteria*. Genes downstream of *atiR* were dominated by transporters for organic solutes (*tct, dct, ugp*), branched chain amino acids (*liv*), hydrolases (choline sulfatase, sialidase, tryptophanase, cysteine desulfurase), peptidases, and racemases (**Table S8; Fig. 5**). In two instances, genes encoding RTX-toxin repeats were located on *atiR* contigs (**Table S8)**. B2 also contained numerous MazEF toxin-antitoxin systems (**Table S9**), which trigger programmed cell death in response to stress (Engelberg-Kulka et al., 2005). *Atribacteria* may use AtiR to regulate cellular degradation of

281 peptides and proteins to amino acids, either for nutrients acquisition or for survival under
282 environmental stress (Bergkessel et al., 2016).
283
284 **Adaptations to life in methane hydrates.** The GHSZ in deep subsurface sediments is dominated
285 by *Atribacteria* that appear to contain unique adaptations for survival in an extreme system with
286 high salinity, high pressure, low water activity, and low temperatures. Our analysis of the B2
287 *Atribacteria* MAG from the GHSZ (69 mbsf at Hydrate Ridge, offshore Oregon, *in situ* sediment
288 temperature ~6-11°C) revealed multiple survival strategies with similarity to hyperthermophiles.
289 In B2, these "hot traits in cold life" included genes for an ancient respiratory system (Hun) and an
290 unusual osmolyte (DIP). Other probable environmental stress adaptations include glycosylation,
291 membrane modifications, and a novel regulatory mechanism (AtiR) for transport of carboxylic
292 acids and branched chain amino acids.
293 Our findings suggest that *Atribacteria* may actively modulate the composition and
294 concentration of organic compounds in methane hydrate sediments. Active cellular transport of
295 organics would change environmental concentrations, which in turn could influence hydrate
296 stability. The hydrophobicity of branched chain amino acids has been shown to influence hydrate
297 stability; less hydrophobic amino acids like glycine and alanine inhibit hydrate formation by
298 disrupting the hydrogen bond network, while more hydrophobic amino acids, such as leucine,
299 valine and isoleucine, promote hydrate growth by strengthening the local water structure (Sa et
300 al., 2013; Liu et al., 2015; Veluswamy et al., 2017). Gas hydrate growth is also promoted by
301 anionic surfactants (Kumar et al., 2015), which include carboxylic acids. Thus, we surmise that
302 bacterial transport of organic compounds may influence hydrate stability. Our results motivate
303 future studies of methane stability that account for the influence of microbial processes, in
304 particular those of abundant *Atribacteria*.
305

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Experimental Procedures

Sample collection. Sediments were cored at ODP site 1244 (44°35.1784´N; 125°7.1902´W; 895 m water depth; **Fig. S1**) on the eastern flank of Hydrate Ridge ~3 km northeast of the southern summit on ODP Leg 204 in 2002 (Tréhu et al., 2003) and stored at -80°C at the ODP Gulf Coast Repository.

Geochemistry. Data for dissolved methane, sulfate, manganese, iron, and iodide in sediment porewaters were obtained from (Tréhu et al., 2003). Reactive iron and manganese were extracted from frozen sediments using the citrate-dithionite method (Roy et al., 2013) and measured by inductively coupled plasma optical emission spectrometer (Agilent Technologies 700 Series). Total carbon, total nitrogen and total sulfur were determined by CNS analyzer (Perkin Elmer 2400). Total inorganic carbon was measured by CO_2 coulometer (CM5130) with a CM5130 acidification module. Geochemical metadata are given in **Table S1** and archived in **BCO-DMO project 626690**.

DNA extraction. DNA was extracted, in duplicate, from 8-20 g of sediment from the following depths in meters below seafloor (mbsf): 1.95-2.25 (C1-H2); 3.45-3.75 (C1-H3); 8.60 (F2-H4); 18.10 (F3-H4); 20.69 (C3-H4); 35.65 (E5-H5); 68.55 (E10-H5); 138.89 (core E19-H5) using a MO-BIO PowerSoil total RNA Isolation Kit with the DNA Elution Accessory Kit, following the manufacturer protocol without beads. Approximately 2 grams of sediments were used per extraction, and DNA pellets from the two replicates from each depth were pooled together. DNA concentrations were measured using a Qubit 2.0 fluorometer with dsDNA High Sensitivity reagents (Invitrogen, Grand Island, NY, USA). DNA yields ranged from 4-15 ng per gram of sediments. Core E19-H5 (139 mbsf) yielded only 2 ng DNA per gram of sediment and yielded unreliable data due to contamination with sequences from the enzymes used in the library preparations. Therefore, this core segment was excluded from further analysis.

16S rRNA gene amplicon sequencing. Microbial community composition was assessed by Illumina sequencing of the V3-V4 region of the 16S rRNA gene. The V3-V4 region was PCR-amplified using primers F515 and R806 (Caporaso et al., 2011), each appended with barcodes and Illumina-specific adapters according to (Kozich et al., 2013). Reactions consisted of 1-2 µL DNA template (2 ng), 5 µL of 10x Taq Mutant reaction buffer, 0.4 µL of Klentaq LA Taq Polymerase (DNA Polymerase Technology, St. Louis, MO, USA), 2 µL of 10 mM dNTP mix (Sigma Aldrich, St. Louis, MO, USA), 2 µL of reverse and forward primers (total concentration 0.4 µM), and the remainder DNA-free water to 50 µL (Ambion, Grand Island, NY, USA). PCR conditions were an initial 5-min denaturation at 94ºC, followed by 35 cycles of denaturation at 94ºC (40 sec), primer annealing at 55ºC (40 sec), and primer extension at 68ºC (30 sec). Amplicon libraries were purified using a QIAquick PCR Purification Kit (Qiagen, Germantown, MD, USA), quantified by Qubit (Life Technologies), and pooled in equimolar concentration. Amplicons were sequenced on an Illumina MiSeq across two different runs using the V2 500-cycle kit with 5% PhiX to increase read diversity. 16S rRNA sequences were deposited into NCBI SAMN04214977-04214990 (**PRJNA295201**).

16S rRNA gene amplicon analysis. Sequences were trimmed using Trim Galore (criteria: length >100 bp length, Phred score >25), and paired reads were merged using FLASH (Magoč & Salzberg, 2011) with the criteria of a minimum length of 250 bp per input read, minimum length of 300 bp for merged fragments, and maximum fragment standard deviation of 30 bp. Merged reads were imported into QIIME1 (Caporaso et al., 2010) and chimeric sequences were detected by searches using 'identity_chimeric_seqs' and then removed. Sequences sharing 97% nucleotide similarity were clustered into operational taxonomic units (OTUs) using 'pick_open_reference_otus' with taxonomy assigned to OTUs by comparison to the greengenes

370 database (DeSantis et al., 2006). The datasets were rarefied to a uniform depth of 14,391
371 sequences, and the rarefied OTU table was used for all downstream analyses. A core set of
372 QIIME diversity analyses was performed using 'core_diversity_analyses'. The phylogenetic
373 diversity (PD) metric (Faith, 1992) was used to quantify alpha diversity across samples.
374
375 ***Atribacteria* OTU phylogenetic analysis.** We generated a reference alignment of *Atribacteria*
376 full length 16S rRNA sequences to use as a scaffold for mapping OTU sequences generated in
377 this study. The reference alignment included *Atribacteria* 16S rRNA gene sequences from
378 environmental clones (from Nobu et al. (2016), Carr et al. (2015) and Yarza et al. (2014)) and
379 published SAGs and MAGs available in Prokka at the time of analysis (spring 2018), as well as 8
380 sequences from *Firmicutes* bacteria for use as an outgroup. The sequences were aligned in
381 MAFFT with the linsi option, alignment reordering, and reverse complement matching enabled.
382 We then extracted representative sequences from 230 OTU clusters identified as *Atribacteria* OP-
383 9 and JS-1 in the E10-H5 amplicon dataset; OTUs represented by only a single sequence were
384 excluded. These sequences were recruited to the reference alignment via MAFFT using
385 previously described parameters, without modifying base pair positions in the reference
386 alignment. The alignment was manually inspected and trimmed to include only the V3-V4 region
387 spanned by the *Atribacteria* OTU sequences, resulting in a final alignment with 275 bases.
388 This alignment was used for phylogeny reconstruction in RAxML with a GTR model of
389 base substitution and GAMMA model of rate heterogeneity, and 500 rapid bootstraps followed by
390 a thorough ML search. The resulting phylogenetic tree was edited for viewing in iTOL. The
391 relative abundance of each OTU (from which a representative sequence was extracted) was
392 mapped onto the resulting phylogeny and shown as a proportion of total sequences in the
393 amplicon dataset.
394 Pairwise distances between all *Atribacteria* sequences in the alignment were calculated
395 using the p-distance method in MEGA7 and summarized in R as: min 0.0, 1st quartile 0.5, median
396 0.09, mean 0.11, 3rd quartile 0.18 and max 0.27. Pairwise distances between only the OTUs
397 generated in this study were summarized in R as: min 0.004, 1st quartile 0.056, median 0.075,
398 mean 0.076, 3rd quartile 0.095 and max 0.194.
399
400 ***Atribacteria* community structure.** OTU abundance from the rarified *Atribacteria* OTU table
401 (previously generated during diversity analysis) was used for NMDS analysis after square root
402 transformation and calculation of Bray-Curtis dissimilarity metrics, all processed via the
403 metaMDS function from Vegan package in R. After examination of the Shepard plot for scatter
404 around the regression line, the NMDS plot was created showing individual OTUs and the
405 midpoint for whole communities. A hierarchical clustering dendrogram was generated using
406 Bray-Curtis dissimilarities.
407
408 **Multiple displacement amplification, library preparation, and sequencing**. Genomic DNA
409 was amplified using a REPLI-g Single Cell Kit (Qiagen, Germantown, MD, USA) using UV-
410 treated sterile plasticware and reverse transcription-PCR grade water (Ambion, Grand Island, NY,
411 USA). Quantitative PCR showed that the negative control began amplifying after 5 hr of
412 incubation at 30°C, and therefore, the 30°C incubation step was shortened to 5 hr using a Bio-Rad
413 C1000 Touch thermal cycler (Bio-Rad, Hercules, CA, USA). DNA concentrations were measured
414 by Qubit. Two micrograms of MDA-amplified DNA were used to generate genome libraries
415 using a TruSeq DNA PCR-Free Kit following the manufacturer's protocol (Illumina, San Diego,
416 CA, USA). The resulting libraries were sequenced using a Rapid-Run on an Illumina HiSeq 2500
417 to obtain 100 bp paired-end reads. Sequencing statistics are provided in **Table S3**. Metagenomic
418 sequences were deposited into NCBI SAMN07256342-07256348 (**PRJNA390944**).
419
420 **Metagenome assembly, binning, and annotation.** Demultiplexed Illumina reads were mapped
421 to known adapters using Bowtie2 in local mode to remove any reads with adapter contamination.

422 Demultiplexed Illumina read pairs were quality trimmed with Trim Galore (Babraham
423 Bioinformatics) using a base Phred33 score threshold of Q25 and a minimum length cutoff of 80
424 bp. Paired-end reads were then assembled into contigs using SPAdes assembler with --meta
425 option for assembling metagenomes, iterating over a range of k-mer values
426 (21,27,33,37,43,47,51,55,61,65,71,75,81,85,91,95). Assemblies were assessed with reports
427 generated with QUAST. Features on contigs were predicted through the Prokka pipeline with
428 RNAmmer for rRNA, Aragorn for tRNA, Infernal and Rfam for other non-coding RNA and
429 Prodigal for protein coding genes. Metagenomic 16S rRNA sequences were analyzed by
430 BLASTN analysis against the Greengenes reference database. Matches with a bit score above 50
431 and reads matching multiple reference genes with the highest bit score were retained for
432 comparison with 16S rRNA amplicons (**Fig. S3).** Annotation of protein-coding genes was
433 performed as follows: 1) BLASTP search against the default set of core genomes, followed by
434 HMM search against a set of default core HMM profiles available in Prokka, 2) use of the
435 BLAST Descriptor Annotator algorithm in BLAST2GO, which conducts BLAST against the
436 NCBI nr database, 3) KEGG orthology assignment using GhostKoala and 4) InterProScan
437 analysis, which involves cross-reference HMM searches across multiple databases to find Pfam
438 families with close homology.
439 Metagenome contigs were partitioned through MetaBAT (Kang et al., 2015) into
440 metagenome-assembled genomes (MAGs) using tetranucleotide frequency and sequencing depth.
441 Sequencing depth was estimated by mapping reads on to assembled contigs using Bowtie2 and
442 Samtools. Completeness, contamination and strain level heterogeneity were assessed using single
443 copy marker genes in CheckM (Parks et al., 2015). Gene features and their functional annotations
444 for genome bins were extracted from the metagenome for the contigs that belong to the bins.
445 Initial taxonomic affiliation for bins was inferred via the least common ancestor (LCA) algorithm
446 in MEGAN6 and by the top BLAST matches to the marker gene *rpoB*. The B2 MAG was
447 deposited into Genbank as "Candidatus *Atribacteria* bacterium 1244-E10-H5-B2"
448 (SAMN07342547; **NMQN00000000.1**).
449
450 **Phylogeny reconstruction for MAGS.** Coding sequences from whole genomes were
451 downloaded from the NCBI representative genomes collection using NCBI e-utilities, comprising
452 405 genomes in total, spanning all bacterial lineages. Only one candidate per genus with more
453 than 1000 genes and maximum isolate information available was selected for this purpose.
454 Sequence duplication (100% identity, unlikely to be biological duplication) within genomes was
455 removed using CD-HIT. Available reference *Atribacteria* genomes, 24 in total, as either single-
456 cell amplified genomes (SAGs) or MAGs, were downloaded and annotated using the Prokka
457 pipeline. A list of 139 core single copy genes (CSCG) as HMM profiles was obtained from Rinke
458 et al. (2013). B2 and representative reference *Atribacteria* genomes were then scanned for the
459 presence of these HMM profiles using HMMer with the recommended score threshold for each
460 profile as provided in Rinke et al. (2013). In a series of manual subsampling steps, 69 CSCG
461 clusters were selected in 220 representative genomes and 20 *Atribacteria* genomes where 1) 69
462 clusters were present in only a single copy, 2) all 69 clusters were present in 220 representative
463 genomes and 3) the minimum number of clusters present in any *Atribacteria* genome was 6. All
464 69 CSCG clusters were aligned individually using the L-INS-i mode in MAFFT. Alignments
465 were then concatenated using a custom script Aln.cat.rb from the Enveomics collection (link)
466 with invariable sites removed. Phylogeny reconstruction was performed in RAxML using a
467 GAMMA model of rate heterogeneity, iterating over all models of protein substitution to choose
468 the one with best log likelihood. The analysis was performed with 1000 rapid bootstraps with the
469 MRE convergence bootstrap criterion (50 bootstrap replicates performed), followed by a
470 thorough ML search. The resulting phylogenetic tree was modified for optimal viewing in iTOL
471 with a full view including all lineages and a pruned view confirming placement of MAG B2 in
472 the *Atribacteria* phylogeny. *Atribacteria* taxonomic classifications were based on Yarza et al.
473 (2014). To examine gene orthology between B2 and other reference *Atribacteria*, 23 reference

Atribacteria (MAGs and SAGs) genomes were annotated using Prokka. The predicted genes were analyzed by BLAST best hit (BBH) clustering for orthologous group identification through Proteinortho5. In B2, 55% of genes (2333/4254) lacked orthologs in other *Atribacteria* genomes.

Metaproteomic sample preparation, mass spectrometry, and data analyses. Proteins from E10-H5 were extracted from a 10 g of frozen sediment using a protocol adapted from Nicora et al. (2013). Briefly, 2.5 mL of desorption buffer (0.5 M NaCl, 0.1 M glycerol, 0.2% SDS, 6 M urea, 1 mM EDTA, 100 mM ammonium bicarbonate) and 2 mL of a pH-buffered amino acid solution (containing equimolar histidine, lysine, and arginine, all 83 g 1 L^{-1} in ultra-pure water, pH 7.0) was added to the sample on ice. The goal of the pH-buffered amino acid solution is to fill the electronegative mineral sites in the sample with positively charged amino acids to reduce absorption of proteins to the particles. Samples were vortexed 4x, alternating 5 minutes vortexing and 5 min ice. The sediment slurry was then sonicated with Bronson probe sonicator (4 x 30 s) to lyse cells and heated at 95ºC for 5 min. The sediment was pelleted by centrifugation (10,000 x g, 30 min, 4ºC), and the supernatant was collected and stored on ice. The sediment pellet was washed 2 more times with 3 mL desorption buffer and supernatants were combined. In order to remove the SDS prior to protein digestion and mass spectrometry analysis, the filter aided sample preparation (FASP) method was used (Ostasiewicz et al., 2010). Millipore Amicon 10 kDa filter units were used and cleaned following manufacturer's directions. Samples were loaded on top of filters (~9 mL) and centrifuged (3000 rpm, 90 min, 4ºC). In order to remove all SDS, proteins retained on the filter were rinsed 3 times by adding 5 mL of 8 M urea in 50 mM ammonium bicarbonate and repeating the prior centrifugation step. Iodoacetamide (3 mL, 15 mM) was added to samples, incubated in the dark at room temperature for 30 minutes, and then centrifuged (3000 rpm, 90 min, 4ºC). Proteins were then rinsed two times with 10 mL of 100 mM ammonium bicarbonate and centrifuged to remove liquid (3000 rpm, 90 min, 4ºC). To digest protein on the filter, 0.5 µg of trypsin (modified, sequencing grade, Promega) was added to the filter, topped with 2.5 mL of 25 mM ammonium bicarbonate, vortexed, and incubated 12 hr at room temperature. Filtrate was collected by centrifugation (3000 rpm, 90 min, 4ºC), and SpeedVaced to near dryness at 4ºC. Peptides were then resuspended in 50 µL of 2% acetonitrile and 0.1% formic acid and desalted using Nest Group C18 Proto centrifugal macro columns following manufacturer's instructions. Each 10 µL sample was separated on a NanoAquity UPLC with a 60 min gradient (2-35% acetonitrile) and analyzed on a Thermo Scientific Orbitrap Fusion Tribrid Mass Spectrometer operated in top20 data dependent acquisition mode.

A protein database for identifying the collected fragmentation spectra was generated from *Atribacteria* MAGs (C1H2_C3H4ab_E10H5_contam.fasta).These databases were concatenated with 50 common contaminants, yielding a protein database of 10,325 proteins. To assign spectra to peptide sequences, correlative database searches were completed using Comet v. 2015.01 rev. 2 (Eng et al., 2013; Eng et al., 2015). Comet parameters included: trypsin enzyme specificity, semi-digested, allowance of 1 missed cleavage, 10 ppm mass tolerance, cysteine modification of 57 Da (resulting from the iodoacetamide) and modifications on methionine of 15.999 Da (oxidation). Minimum protein and peptide thresholds were set at $P > 0.95$ on Protein and Peptide Prophet (Nesvizhskii et al., 2003). Protein inferences from the whole-cell lysates were accepted by ProteinProphet if the thresholds noted above were passed, two or more peptides were identified, and at least one terminus was tryptic (Keller et al., 2002; Nesvizhskii et al., 2003; Pedrioli, 2010). For each peptide discussed in the manuscript, manual inspection of the spectral identification was completed. The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE partner repository (Vizcaíno et al., 2015) with the dataset identifier **PXD01247** (https://www.ebi.ac.uk/pride/archive/ Login: reviewer08969@ebi.ac.uk Password: BP2V3yGA).

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