

S1 Table Misidentified ϵ -proteobacteria sequences based on phylogenetic methods.

Accession #	Environment	Taxonomic affiliation based on BLAST search	
		Phylum (class)	Closest Match (Accession # / % similarity)
AB013265	Nankai Trough sediments	δ -Proteobacteria	Uncultured, clone Hyd89-40 (AJ535251 / 97)
AB015558	Deep-sea sediments	Candidate division TM7	Uncultured clone SBR2004 (AF268997 / 91)
AB030611	Petroleum-contaminated groundwater	Unclassified	Uncultured clone SHA-95 (AJ306788 / 91)
AB030612	Petroleum-contaminated groundwater	Firmicutes (Clostridia)	<i>Acetobacterium wieringae</i> (X96955 / 99)
AB030613	Petroleum-contaminated groundwater	β -Proteobacteria	<i>Rubrivivax gelatinosus</i> (AF487435 / 97)
AB030614	Petroleum-contaminated groundwater	β -Proteobacteria	<i>Rhodofera antarcticus</i> (AY609198 / 98)
AB189341	Cold-seep sediments	Probable chimera	5': strain BD1-5 (ABO15518 / 65.2) 3': clone OPS185 (AF027013 / 66.7)
AF357182	Episymbiotic community of <i>Alvinella pompejana</i>	γ -Proteobacteria	<i>Acinetobacter venetianus</i> (AJ295007 / 99)
AF367482	Deep-sea hydrothermal vent ¹	Unclassified	No clear phylogenetic affiliation ¹
AF367483	Deep-sea hydrothermal vent ¹	Unclassified	No clear phylogenetic affiliation ¹
AF367485	Deep-sea hydrothermal vent ²	Probable chimera	5': clone VC2.1 Bac32 (AF068806 / 70.5) ² 3': strain BD1-5 (AB015518 / 70.4)
AF367487	Deep-sea hydrothermal vent ¹	Unclassified	No clear phylogenetic affiliation ¹
AF367488	Deep-sea hydrothermal vent ¹	Unclassified	No clear phylogenetic affiliation ¹
AF367502	Deep-sea hydrothermal vent	Unclassified	Uncultured clone CH-B4 (AY280399 / 89)
AF445743	Mammoth Hot Springs, Yellowstone NP	Unclassified	Uncultured clone GZKB72 (AJ853566 / 92)
AF449230	Vent worm <i>Riftia pachyptila</i>	Probable chimera	5': clone GCA014 (AF154101 / 82.6) 3': <i>Desulfuromusa kysingii</i> (X79414 / 72.7)
AF529126	Trichloroethene-contaminated site	Probable chimera	5': <i>Geothrix fermentans</i> (U41563 / 79.8) 3': <i>Geobacter akaganeitireducens</i> (U96918 / 86.7)
AY135396	Packed-bed bioreactors	Probable chimera	5': clone VC2.1 Bac4 (AF068786 / 70.1) 3': <i>Campylobacter jejuni</i> (AJ000862 / 76.4)
AY280412	Deep-sea vent chimney ¹	Unclassified	No clear phylogenetic affiliation ¹
AY280413	Deep-sea vent chimney	Probable chimera	5': strain BD1-5 (ABO15518 / 65.2) 3': clone BURTON-48 (AF142866 / 62.9)
AY280425	Deep-sea vent chimney	Probable chimera	5': <i>Thermotoga hypogea</i> (U89768 / 41.7) 3': clone PVB_63 (U15102 / 73.6)

All sequences were assessed for chimera using the RDP (v.8.1) CHIMERA_CHECK program and for taxonomic affiliation using BLAST similarity searches in Genbank.

¹ This group includes sequences from Li et al. (1999) with clone BD1-5, and Corre et al. (2001) 'Group C', with later citation by Dhillion *et al.* (2003).

² These sequences have been previously identified as chimeric.

References:

- Corre, E., Reysenbach, A.L. & Prieur, D. ϵ -Proteobacterial diversity from a deep-sea hydrothermal vent on the Mid-Atlantic Ridge. *FEMS Microbiol. Lett.* **205**, 329–335 (2001).
- Dhillon, A., Teske, A., Dillon, J., Stahl, D.A. & Sogin, M. L. Molecular characterization of sulfate-reducing bacteria in the Guaymas Basin. *Appl. Environ. Microbiol.* **69**, 2765–2772 (2003).
- Huber, T., Faulkner, G. & Hugenholtz, P. Bellerophon: a program to detect chimeric sequences in multiple sequence alignments. *Bioinformatics* **20**, 2317–2319 (2004).
- Li, L., Kato, C. & Horikoshi, K. Microbial diversity in sediments collected from the deepest cold-seep area, the Japan Trench. *Marine Biotechnol.* **1**, 391–400 (1999).