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Supplementary material

Vertical distribution of major sulfate-reducing bacteria in a eutrophic shallow meromictic lake

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Table S1. Oligonucleotide probes used in this study.

Probe	Specificity	Probe Sequence (5' - 3')	Position	FA (%)**	Probe concentration (fmol μl^{-1})***	Reference
EUB338-I	Most *Bacteria*	GCTGCCTCCCGTAGGAGT	338 - 355	35	28	[1]
EUB338-II	Supplement to EUB338: order *Planctomycetales*	GCAGCCACCCGTAGGTGT	338 - 355	35	28	[2]
EUB338-III	Supplement to EUB338: order *Verrucomicrobiales*	GCTGCCACCCGTAGGTGT	338 - 355	35	28	[2]
NON338	Control probe complementary to EUB338	ACTCCTACGGGAGGCAGC	338 - 355	35	28	[7]
Delta495a	Most *Deltaproteobacteria*	AGTTAGCCGGTGCTTCCT	495 - 512	35	28	[3]
cDelta495a	Competitor for Delta495a	AGTTAGCCGGTGCTTCTT	495 - 512	35	28	[4]
DSS658	Most *Desulfobacteraceae*	TCCACTTCCCTCTCCCAT	658 - 675	50	28	[5]
SEEP1d-468*	Some SEEP SRB-1d bacteria	ACCGTCAGTGCAAGATGG	468 - 485	40	60	This study
SEEP1d-1420*	SEEP-SRB1d group	CAA CTT CTG GTA CAG CCA	1420-1437	40	60	[6]
cSEEP1d-1420*	Competitor for SEEP1d-1420	CAA CTT CTG GTA CAA CCA	1420-1437	40	60	[6]

* Hybridization and washing temperatures were at 35°C.

** Formamide concentrations in the hybridization buffer (v/v).

*** Probe concentration in the hybridization buffer (v/v).

Supplementary figure captions

Fig. S1 Single cells of sulfate-reducing bacteria in Lake Harutori anoxic water column, visualized by CARD-FISH. A. DSS cells (probe DSS658, green). B. SEEP SRB-1d cells (probe SEEP1d-468, green). DAPI signals are in blue. Scale bars = 10 μm

Fig. S2 Partial alignment of the DSS658 probe targeting position and the sequences of *Desulfosarcina-Desulfococcus* specific clone library. Base position is according to *Eschelichia coli*. Identical bases are shown in dots. Sequences in gray-shaded boxes have no mismatch to the probe DSS658.

Fig. S3 A magnified phylogenetic tree based on deduced AprA amino acid sequences of sulfur-oxidizing bacteria retrieved from the water column of Lake Harutori. The tree was constructed based on a distance matrix (119 amino acid positions) by using the neighbor-joining method. Bootstrap value estimation was based on 1000 replicates (only values above 50% are shown). Numbers of sequences obtained in each clone library were indicated in parentheses; 3.0 m, 3.5 m, and 4.0 m in that order. SOP1 and 2 means the different lineages of AprA. The bar represents 5% estimated sequence divergence.

Fig. S4 Alignment of 263 deduced AprA amino acid sequences used in this study. The amino acid sequences were aligned using ClustalW implemented in MEGA5.05 software.

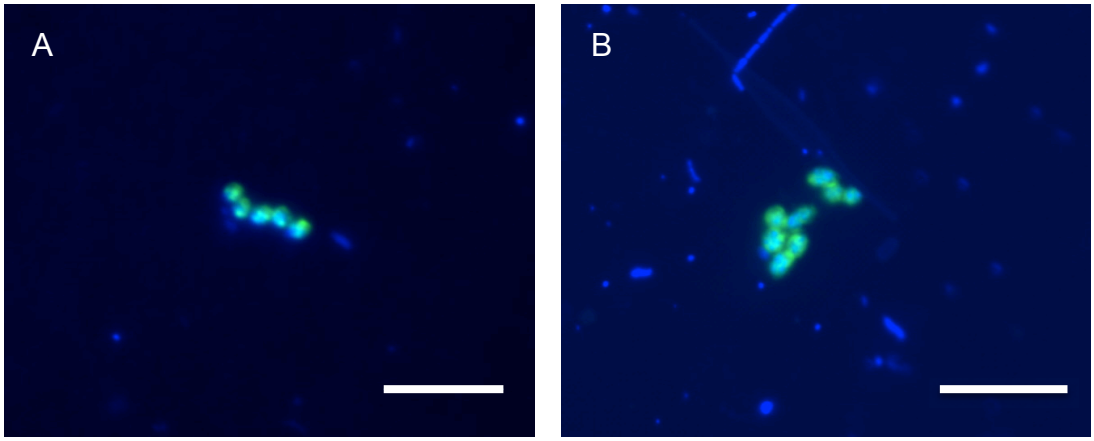
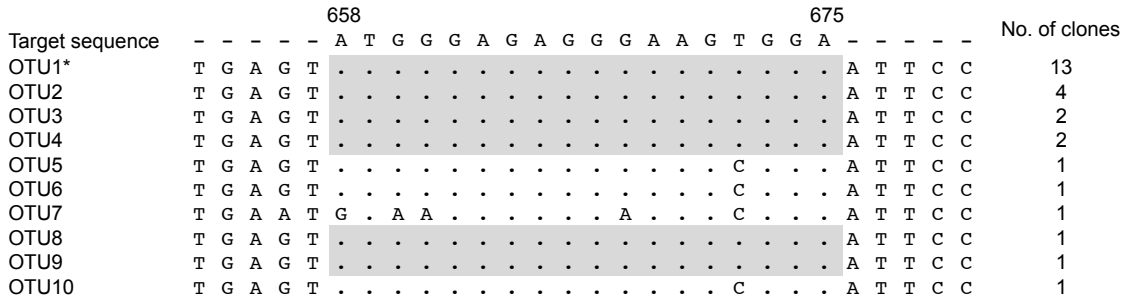


Fig. S1

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*Sequence HADCC-54 (Accession No. AB894641) in OTU1 has a single terminal mismatch to the probe DSS658.

Fig. S2

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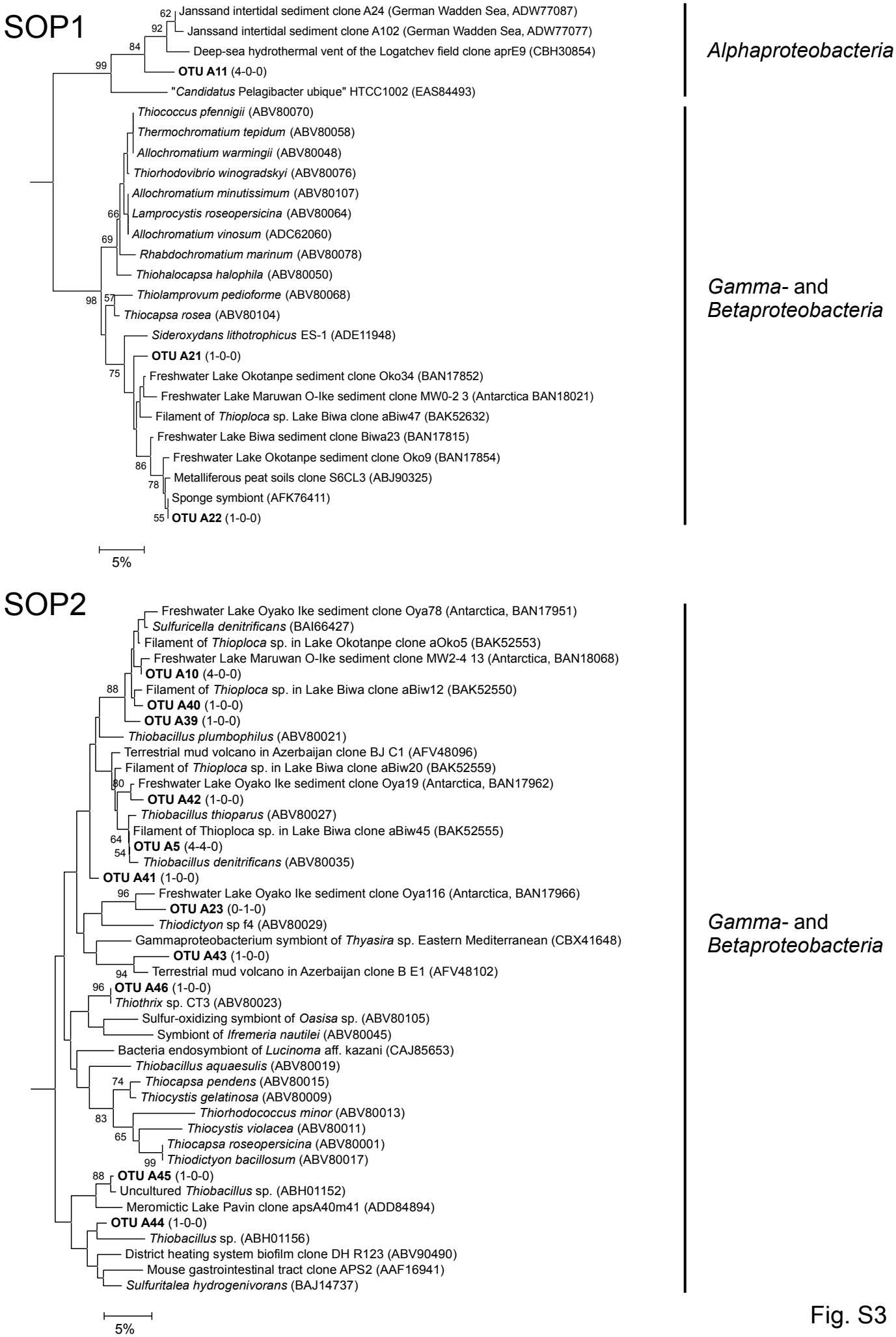


Fig. S3

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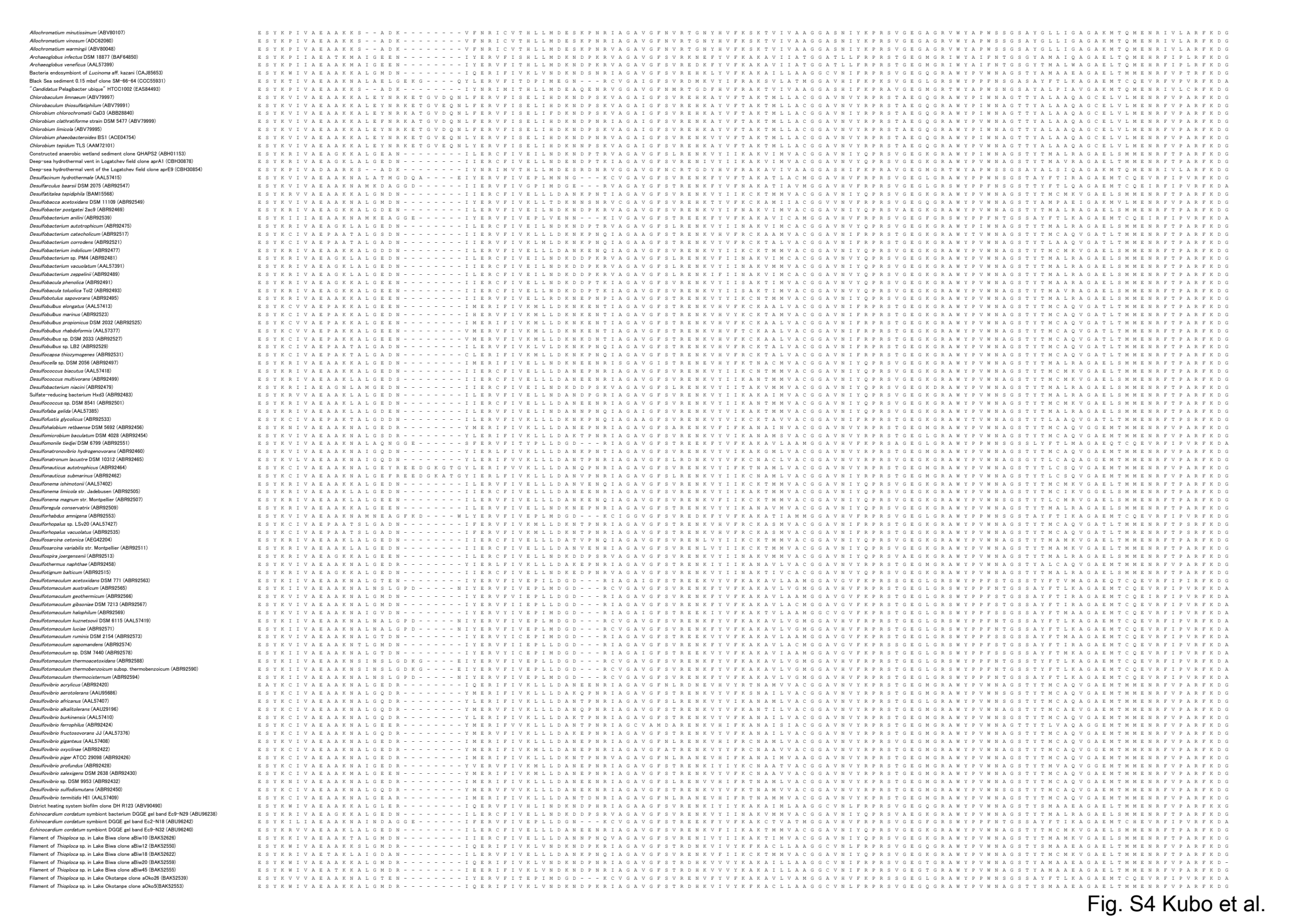


Fig. S4 Kubo et al.

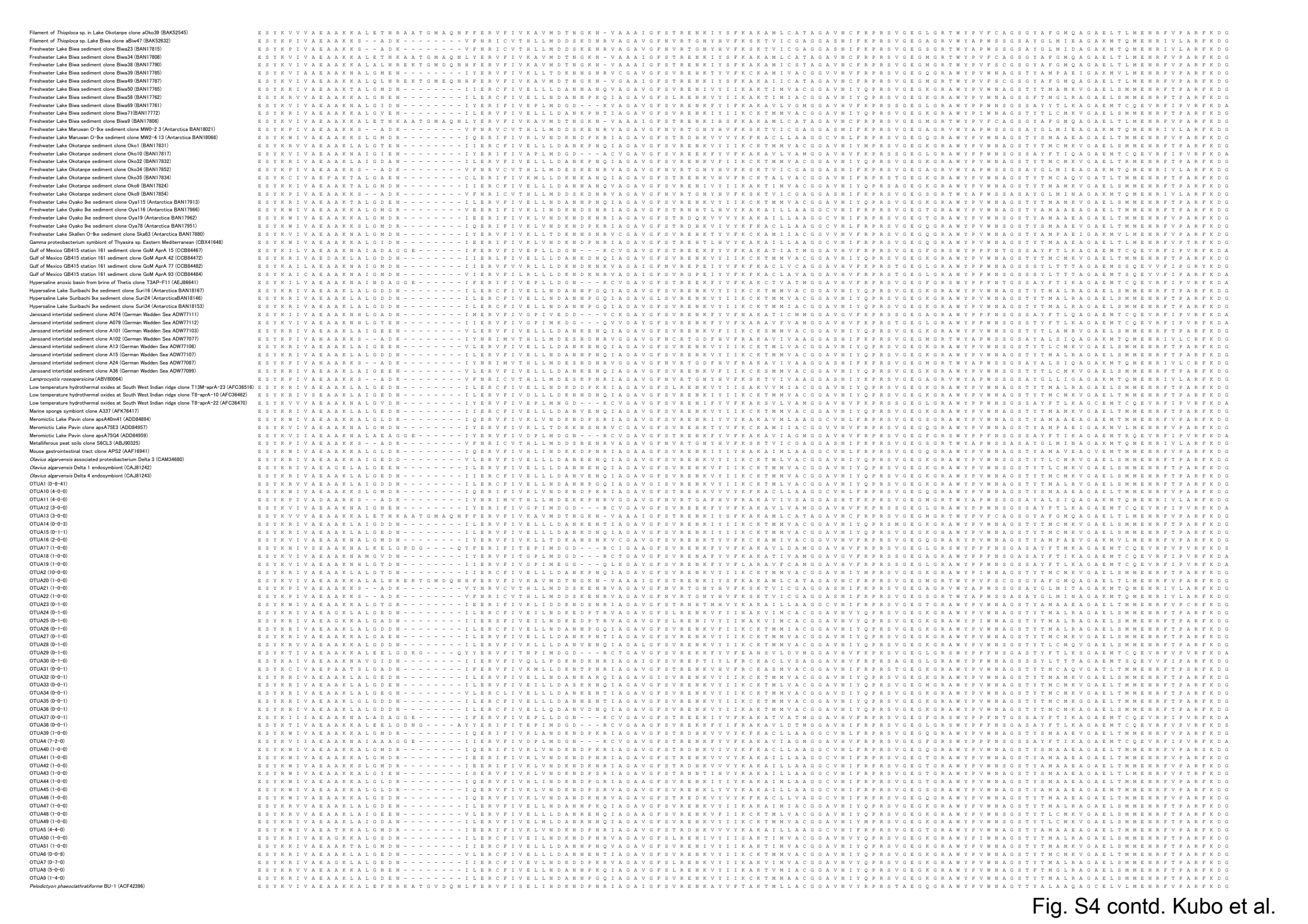


Fig. S4 contd. Kubo et al.

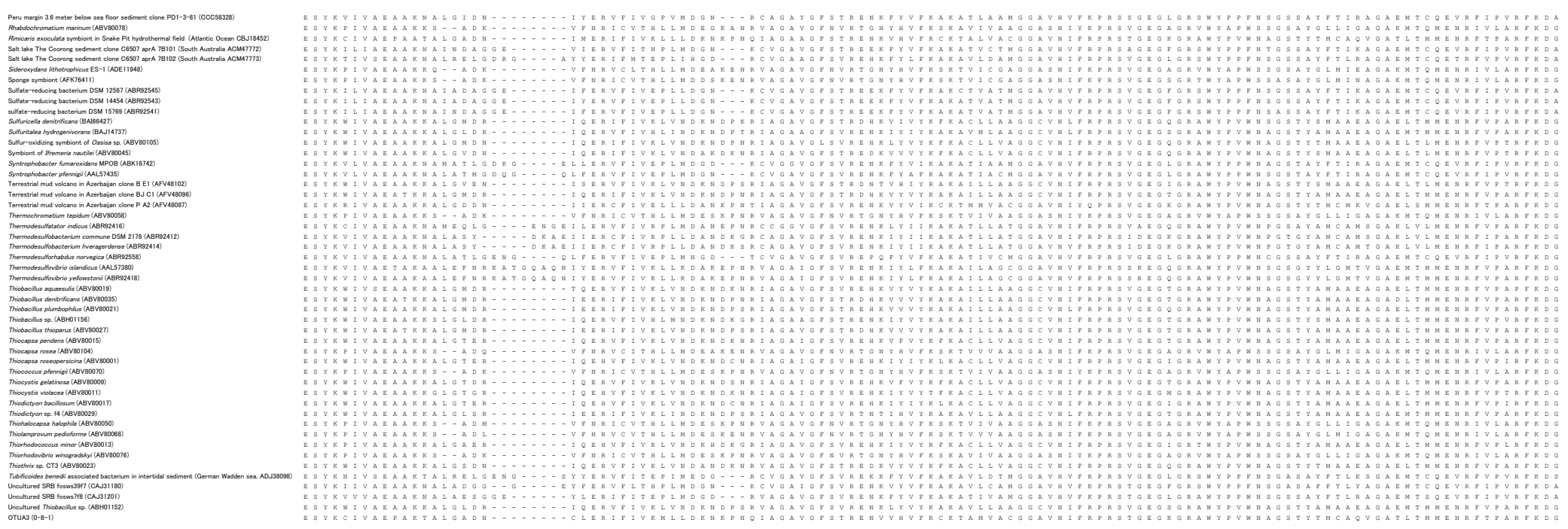


Fig. S4 contd.

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