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**Diversity and activity of sulfate-reducing prokaryotes in Kamchatka hot springs.**

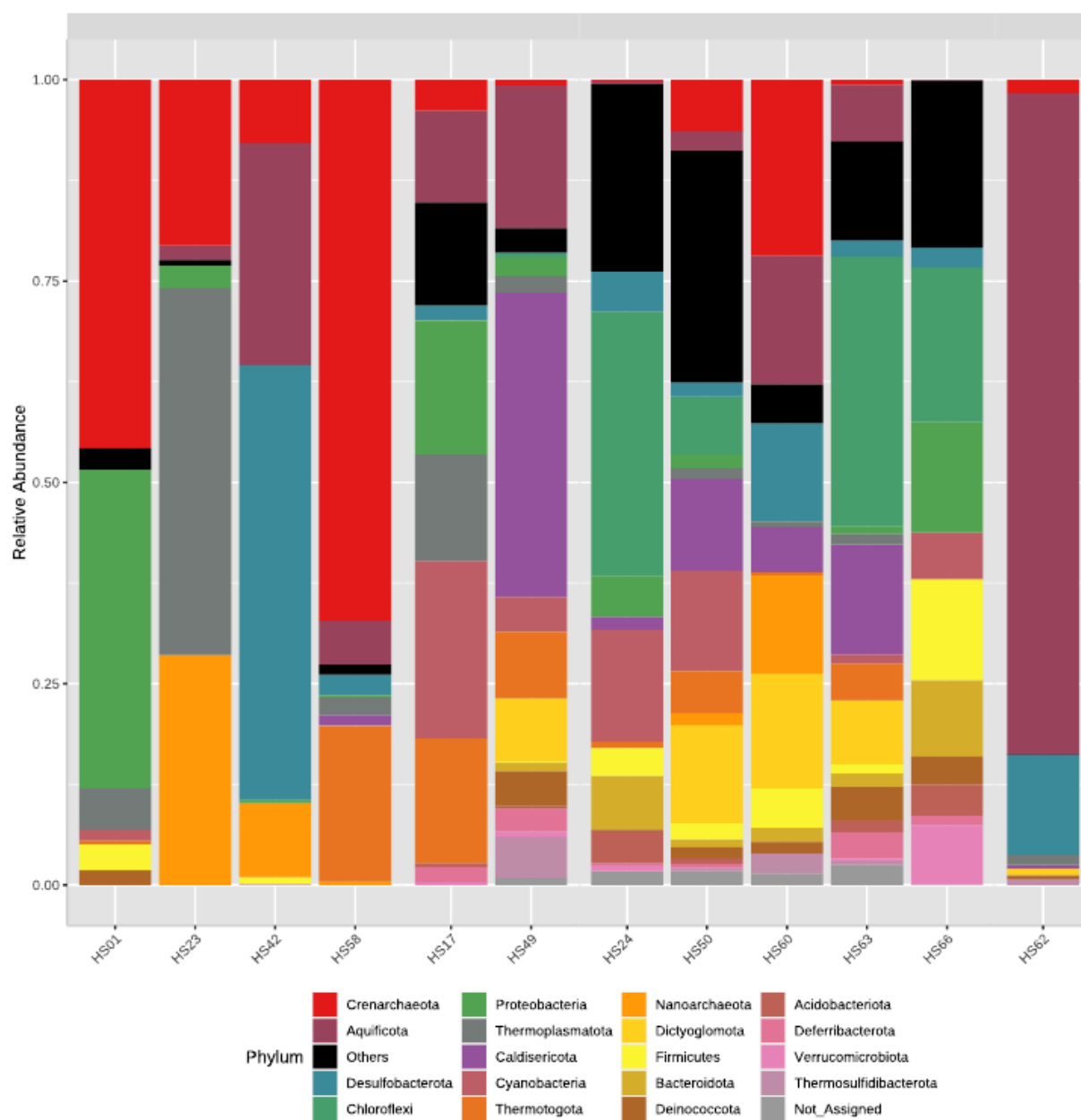
**Supplementary Materials**

**Figure S1** Phylogeny of *dsrB* amplicons (on next page). Tree was constructed using PhyML 3.0 [103], Smart Model Selection v1.8.1 [104], Approximate Likelihood-Ratio Test for Branches [105] and previously published database [33]. Bootstrap values are shown at the nodes. Bar, 0.10 changes per position.

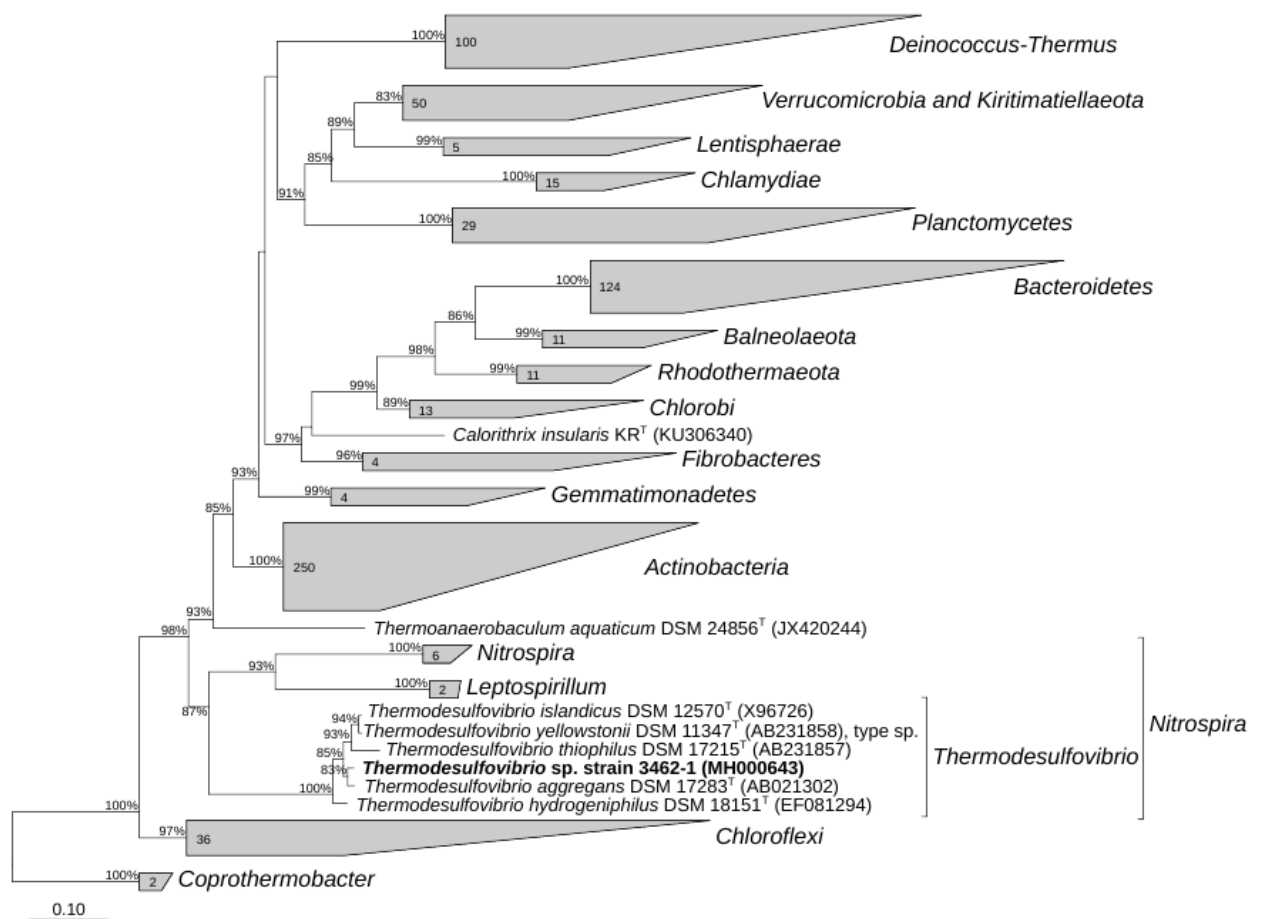








**Figure S2** Relative abundance of phylums of prokaryotes in the studied microbial communities.



**Figure S3** A 16S rRNA gene sequence-based maximum-likelihood phylogenetic tree, showing the position of strain 3462-1.

## References

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