HOKKAIDO UNIVERSITY

Title	Sulfuriferula multivorans gen. nov., sp nov., isolated from a freshwater lake, reclassification of 'Thiobacillus plumbophilus' as Sulfuriferula plumbophilus sp nov., and description of Sulfuricellaceae fam. nov and Sulfuricellales ord. nov.
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Supplementary material

Sulfuriferula multivorans gen. nov., sp. nov., isolated from a freshwater lake, reclassification of '*Thiobacillus plumbophilus*' as *Sulfuriferula plumbophilus* sp. nov., and description of *Sulfuricellaceae* fam. nov. and *Sulfuricellales* ord. nov.

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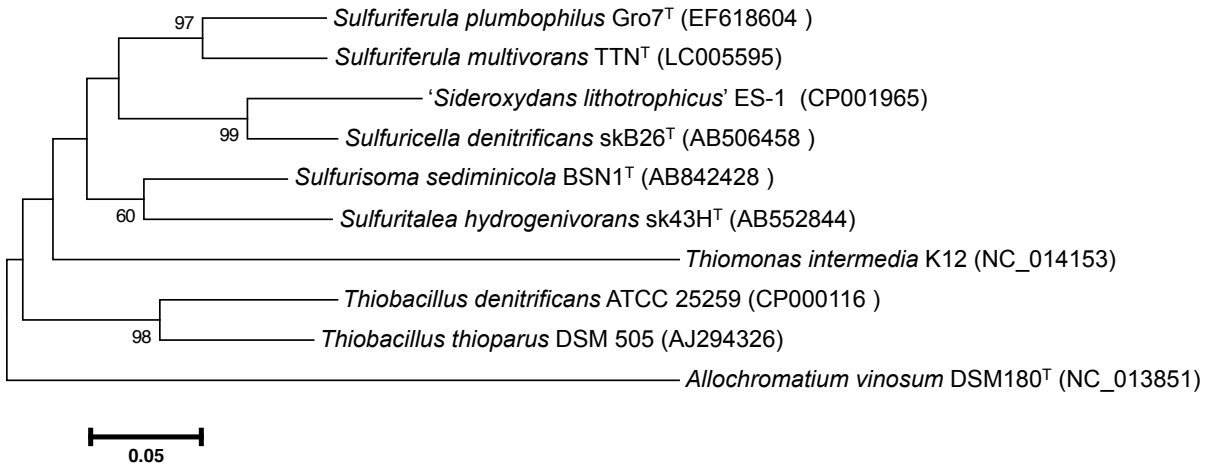


Fig. S1. Phylogenetic position of strain TTN^T within the class *Betaproteobacteria*, based on SoxB amino acid sequences aligned by ClustalW (153 amino acids were used). *Allochromatium vinosum* was used as an outgroup. Tree was constructed by the neighbor-joining method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.02 substitutions per nucleotide position.

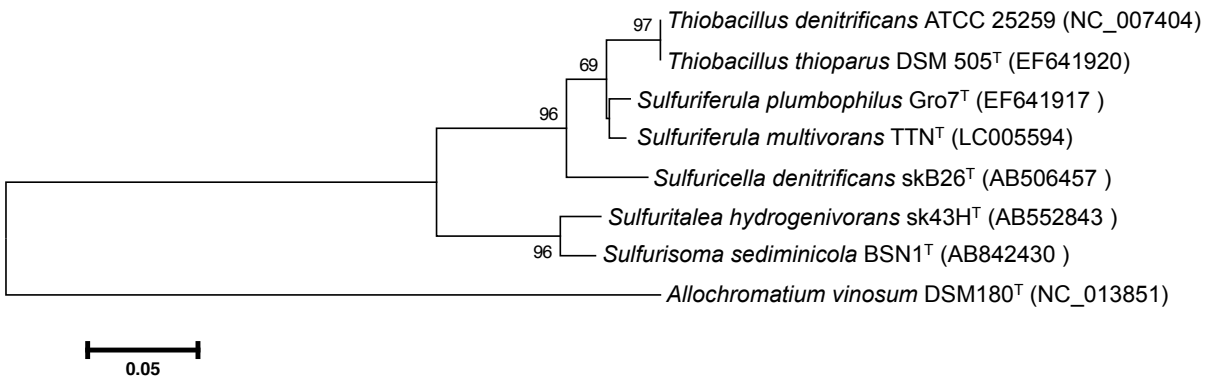


Fig. S2. Phylogenetic position of strain TTN^T within the class *Betaproteobacteria*, based on AprA amino acid sequences aligned by ClustalW (119 amino acids were used). *Allochromatium vinosum* was used as an outgroup. Tree was constructed by the neighbor-joining method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.02 substitutions per nucleotide position.

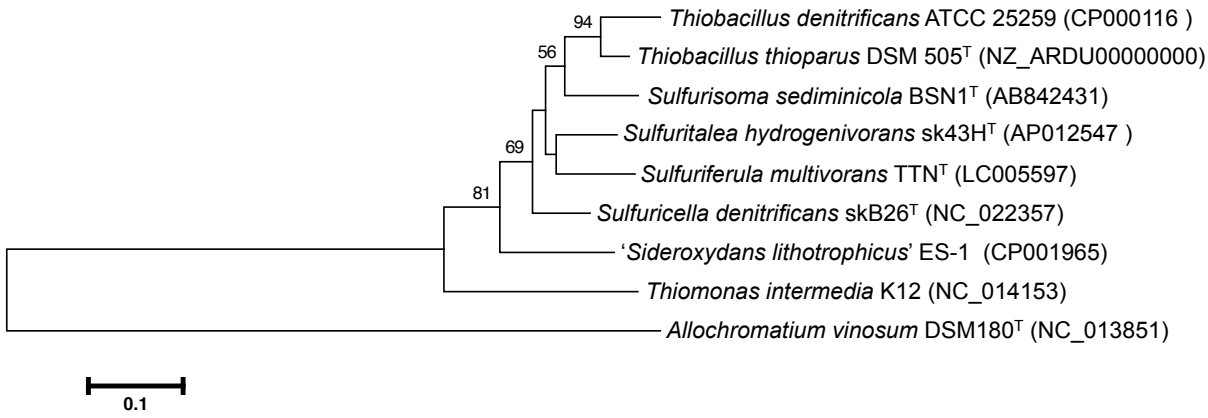


Fig. S3. Phylogenetic position of strain TTN^T within the class *Betaproteobacteria*, based on Sqr amino acid sequences aligned by ClustalW (124 amino acids were used). *Allochromatium vinosum* was used as an outgroup. Tree was constructed by the neighbor-joining method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.02 substitutions per nucleotide position.

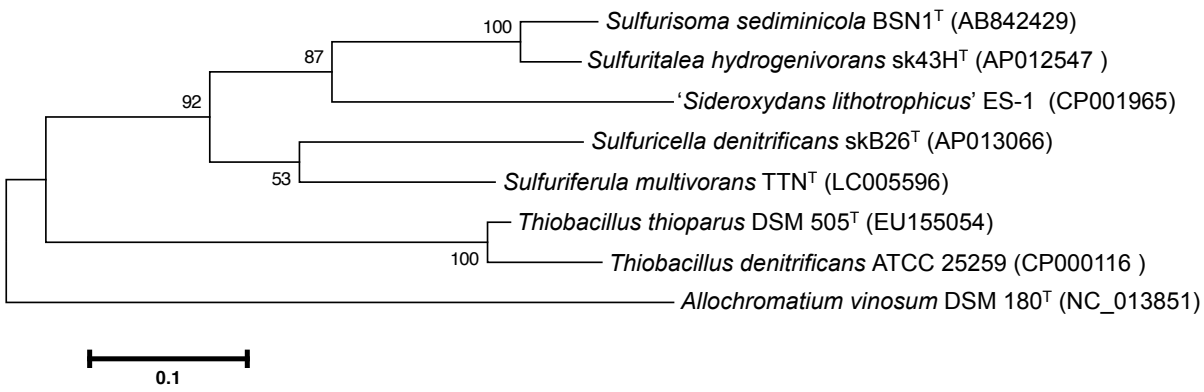


Fig. S4. Phylogenetic position of strain TTN^{T} within the class *Betaproteobacteria*, based on DsrA amino acid sequences aligned by ClustalW (84 amino acids were used). *Allochromatium vinosum* was used as an outgroup. Tree was constructed by the neighbor-joining method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.02 substitutions per nucleotide position.