



Title	Sulfuriferula thiophila sp nov., a chemolithoautotrophic sulfur-oxidizing bacterium, and correction of the name Sulfuriferula plumbophilus Watanabe, Kojima and Fukui 2015 to Sulfuriferula plumbiphila corrig.
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Supplementary material

***Sulfuriferula thiophila* sp. nov., a chemolithoautotrophic sulfur-oxidizing
bacterium**

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Table S1. Cellular fatty acid content (as percentages of the total) of strain mst6^T and strains of closely related species. Strains: 1, strain mst6^T; 2, *Sulfuriferula multivorans* TTN^T; 3, *Sulfurirhabdus autotrophica* BiS0^T; 4, *Sulfuricella denitrificans* skB26^T.

Fatty acid	1	2	3	4
C _{8:0} 3-OH	-	-	-	2.4
C _{9:0}	-	-	0.1	-
C _{9:0} 3-OH	-	-	0.1	-
C _{10:0}	2.9	0.4	0.2	-
C _{10:0} 3-OH	1.4	1.5	5.4	-
C _{11:0}	0.1	-	-	-
C _{12:0}	6.8	5.1	0.5	-
C _{12:0} 2-OH	0.2	0.2	-	-
C _{12:0} 3-OH	1.6	2.7	-	-
C _{13:1} at 12-13	-	-	-	0.1
C _{14:0}	0.4	0.2	1.1	0.4
C _{14:0} ω5c	0.2	-	-	-
C _{15:1} ω8c	-	-	0.1	-
C _{15:1} ω6c	0.4	0.2	0.2	-
C _{16:1} ω5c	-	-	0.6	1.4
C _{16:0}	26.7	33.6	26.4	23.5
C _{16:0} 3-OH	0.2	0.2	0.2	0.3
C _{17:0}	0.3	0.6	0.2	-
C _{17:1} ω8c	-	-	0.3	-
C _{17:1} ω6c	0.2	-	0.4	-
cyclo-C _{17:0}	-	2.9	-	-
C _{18:0}	-	1.1	-	-
C _{18:1} ω9c	-	-	0.3	0.9
Summed features*				
3	55.5	44.7	61.8	62.2
4	-	3.7	-	-
8	3.3	3.8	2.0	8.4
C _{18:1} ω5c	-	-	-	0.1
C _{18:0}	0.3	1.1	0.4	0.4

* Summed features represent groups of two or three fatty acids that could not be separated using the MIDI system. Summed feature 3 comprises C_{16:1}ω7c and/or C_{16:1}ω6c; summed feature 4 comprises C_{16:1}ω7c and/or iso-C₁₅ 2-OH; summed feature 8 comprises C_{18:1}ω7c and/or C_{18:1}ω6c.

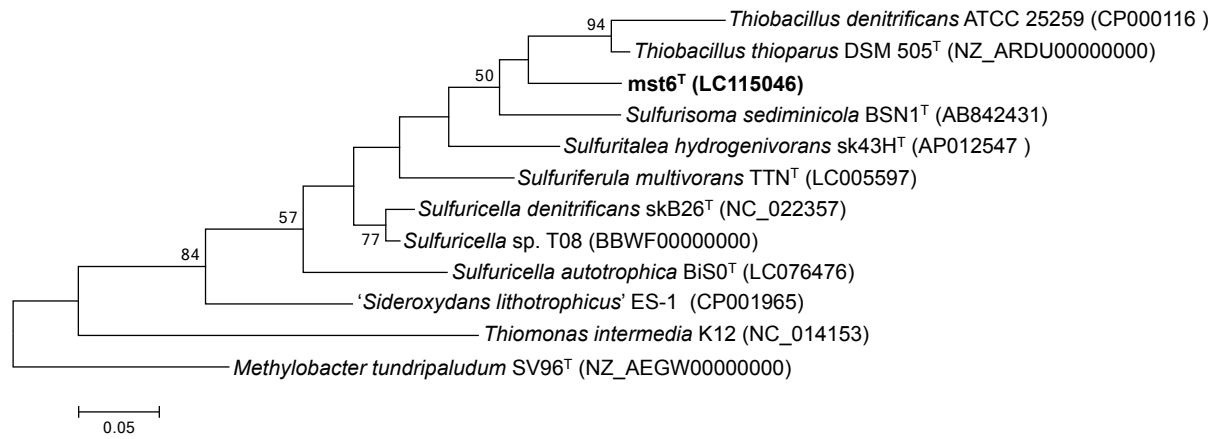


Fig. S1. Phylogenetic position of strain *mst6^T* within the class *Betaproteobacteria*, based on Sqr amino acid sequences aligned by ClustalW (118 amino acids were used). *Methylobacter tundripaludum* was used as an outgroup. Tree was constructed by the maximum likelihood method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.05 substitutions per amino acid position.

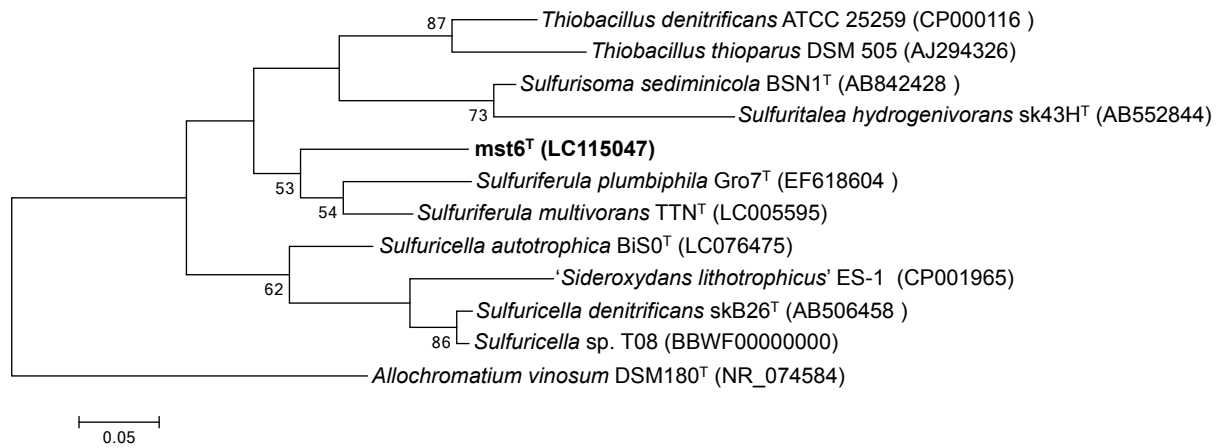


Fig. S2. Phylogenetic position of strain *mst6^T* within the class *Betaproteobacteria*, based on SoxB amino acid sequences aligned by ClustalW (117 amino acids were used). *Allochromatium vinosum* was used as an outgroup. Tree was constructed by the maximum likelihood method with 1000 bootstrap resamplings (bootstrap values > 50% are shown at the nodes). Bar, 0.05 substitutions per amino acid position.