

Supplementary Material

The globally widespread genus *Sulfurimonas*: versatile energy metabolisms and adaptations to global redox cline

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1. Supplementary Table S1

Supplementary Table S1. List of enzymes for sulfur and hydrogen metabolisms in representative strains within *Epsilonproteobacteria*. The genome sequences were acquired from NCBI databases, and the sequences of PsrAs, SoxBs, SorAs, SQRs and hydrogenases were compared with the non-redundant protein database of NCBI by using BLASTP.

Genus	Habitats	Representative strain	PsrA	SoxB	SorA	SQR					Hydrogenase			Reference
						II	III	IV	V	VI	I	II	IV	
<i>Nautilia</i>	hydrothermal vent	<i>N. profundicola</i>	1	-	-	-	-	-	-	-	2	1	4	(Campbell et al., 2009)
<i>Caminibacter</i>	hydrothermal vent	<i>C. mediatlanticus</i>	1	-	-	-	-	1	-	1	2	1	4	(Giovannelli et al., 2011)
<i>Lebetimonas</i>	hydrothermal vent	<i>L. sp. JH369</i>	1	-	-	-	-	1	-	-	1	1	4	(Meyer and Huber, 2014)
<i>Nitratiruptor</i>	hydrothermal vent	<i>N. sp. SB155-2</i>	1	1	-	1	-	1	-	1	1	1	1	(Nakagawa et al., 2007)
<i>Nitratifractor</i>	hydrothermal vent	<i>N. salsuginis</i>	1	1	-	1	-	1	-	1	1	1	1	(Anderson et al., 2011)
<i>Sulfurovum</i>	hydrothermal vent and marine sediment	<i>S. sp. NBC37-1</i>	1	1	2	4	-	1	-	1	2	1	2	(Nakagawa et al., 2007)

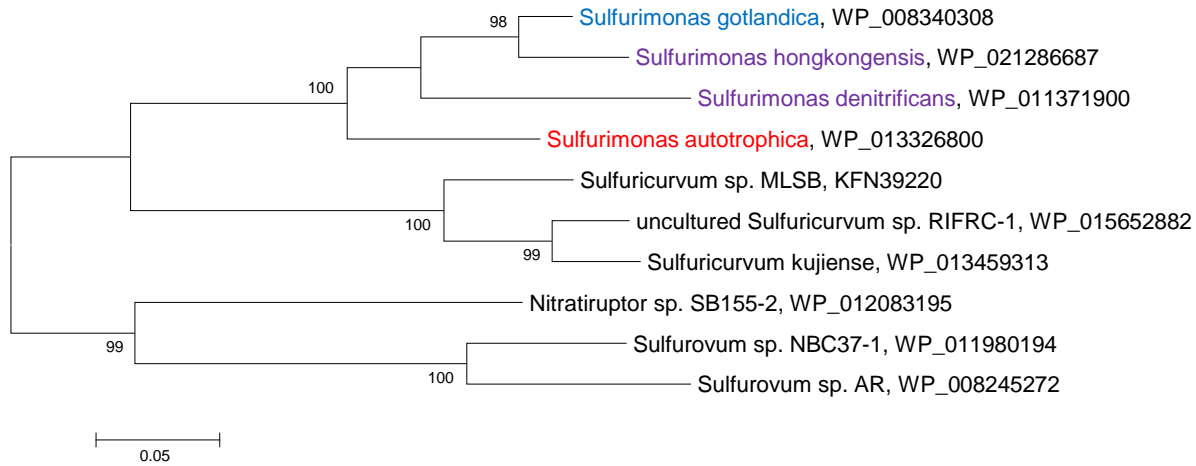
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		<i>S. sp. AR</i>	1	1	1	1	-	1	-	1	2	-	-	(Park et al., 2012)	
<i>Sulfuricurvum</i>	terrestrial oil field, rice mill, coal-tar source, aquifer and hydrothermal vent	<i>S. kujiense</i>	1	1	2	2	-	1	-	1	2	1	1	(Han et al., 2012)	
		<i>S. sp. MLSB</i>	1	1	1	1	-	1	-	1	2	1	1	(Tan and Foght, 2014)	
		<i>S. sp. PC08-66</i>	1	1	-	1	-	1	-	1	1	1	1	(Hamilton et al., 2014)	
<i>Arcobacter</i>	animal and human pathogen, hydrothermal vent, estuarine sediment, marine water, food, sewage and root of the marsh plant	<i>A. butzleri</i> RM4018	-	1	-	1	-	-	-	-	2	1	1	(Miller et al., 2007)	
		<i>A. nitrofigilis</i>	1	1	-	-	-	1	-	1	3	1	1	(Pati et al., 2010)	
<i>Helicobacter</i>	animal and human pathogen	<i>H. pylori</i> 26695	-	-	-	-	-	-	-	-	1	-	-	(Tomb et al., 1997)	
<i>Campylobacter</i>	animal and human pathogen	<i>C. jejuni</i> ATCC700819	-	-	-	-	-	-	-	-	1	-	-	(Parkhill et al., 2000)	
<i>Sulfurospirillum</i>	marine sediments, hydrothermal vent and terrestrial environments	<i>S. barnesii</i>	1	-	-	1	-	-	-	-	1	-	2	(Lucas et al., 2015)	
		<i>S. deleyianum</i>	1	-	-	1	-	-	-	-	1	-	2	(Sikorski et al., 2010a)	
<i>Thiovulum</i>	slough, meromictic lake and marine sediment	<i>T. sp. ES</i>	1	-	-	-	-	1	-	1	-	-	1	(Marshall et al., 2012)	
<i>Wolinella</i>	animal and human	<i>W. succinogenes</i>	1	-	-	1	-	-	-	-	1	-	1	(Baar et al., 2003)	
<i>Sulfurimoans</i>	coastal marine sediment, marine water, hydrothermal vent and terrestrial oil field	<i>S. autotrophica</i>	1	1	1	1	-	1	1	1	1	-	1	(Sikorski et al., 2010b)	
		<i>S. paralvinellae</i>	NR	NR	NR	NR	NR	NR	NR	NR	NR	1	NR	NR	(Takai et al., 2005)
		<i>S. denitrificans</i>	1	1	-	1	1	1	-	-	1	1	1	-	(Sievert et al., 2008)
		<i>S. hongkongensis</i>	1	1	1	2	1	1	-	1	2	1	1	-	(Cai et al., 2014)
		<i>S. gotlandica</i>	1	1	1	2	1	1	-	1	3	1	1	1	(Grote et al., 2012)

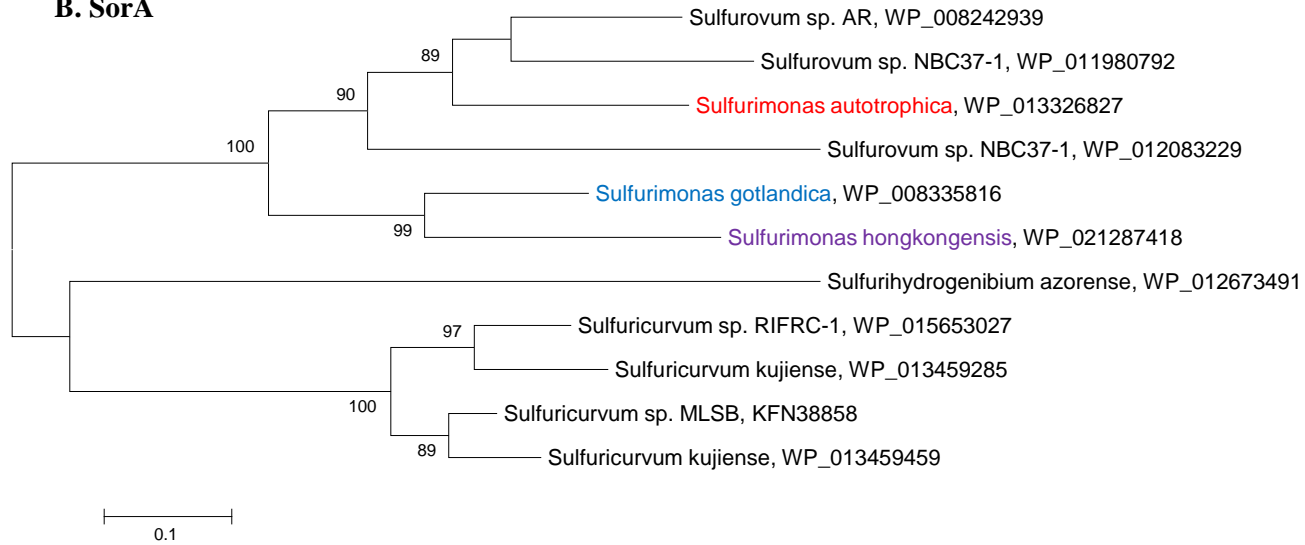
Numbers, the number of enzymes; -, not present; NR, not reported.

2. Supplementary Figure S1

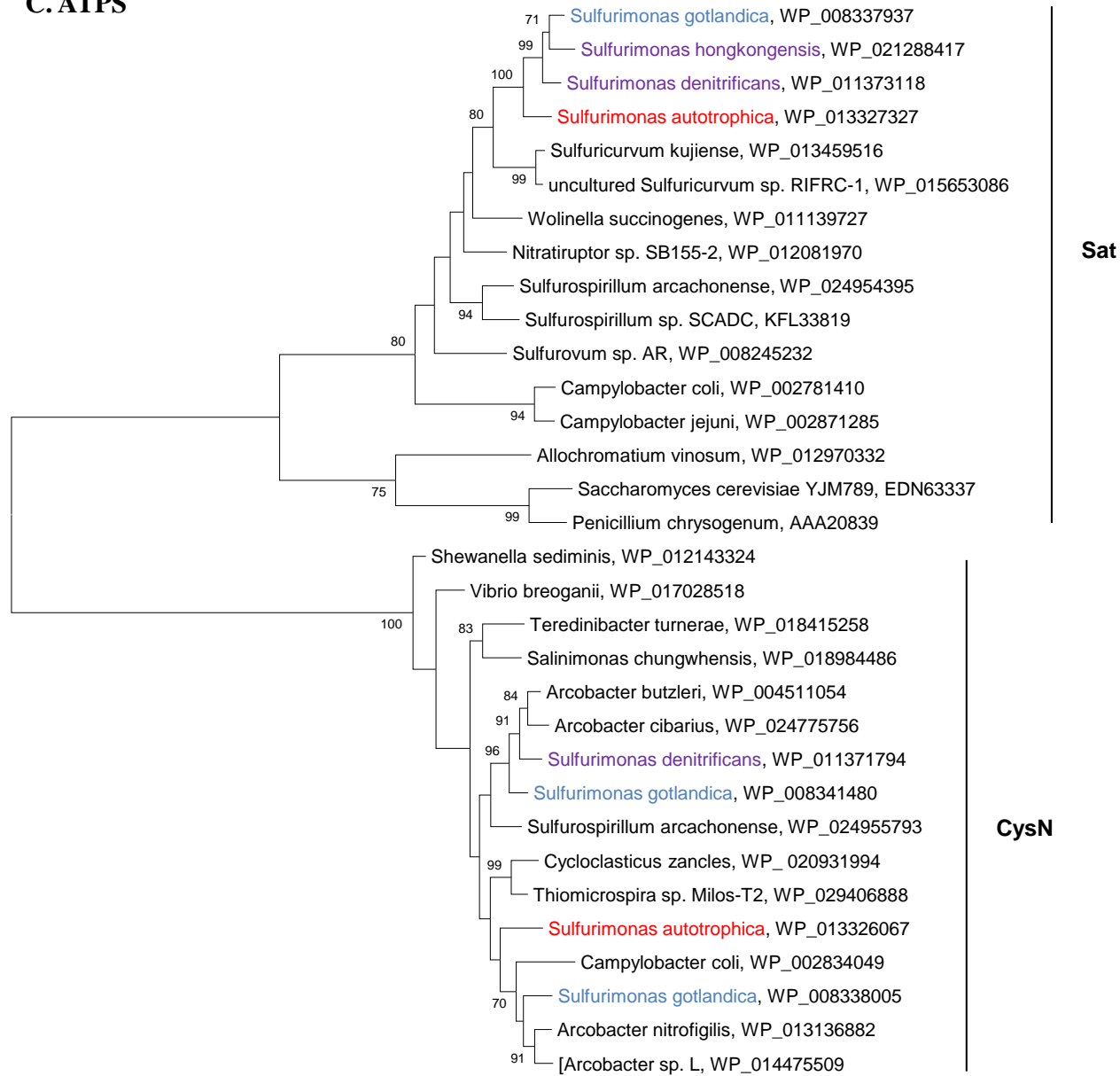
A. SoxB



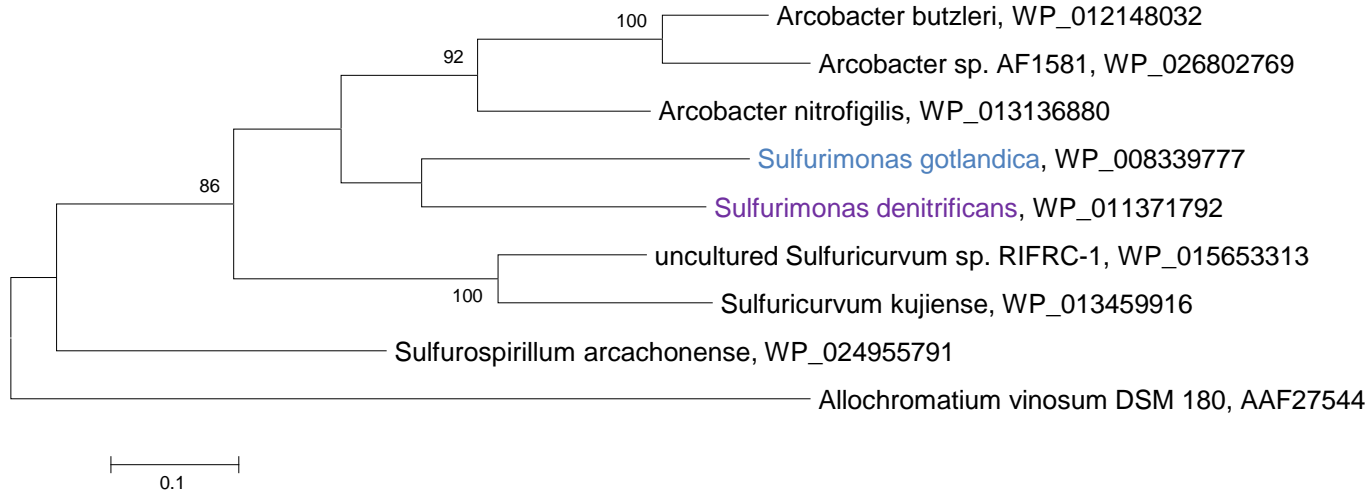
B. SorA



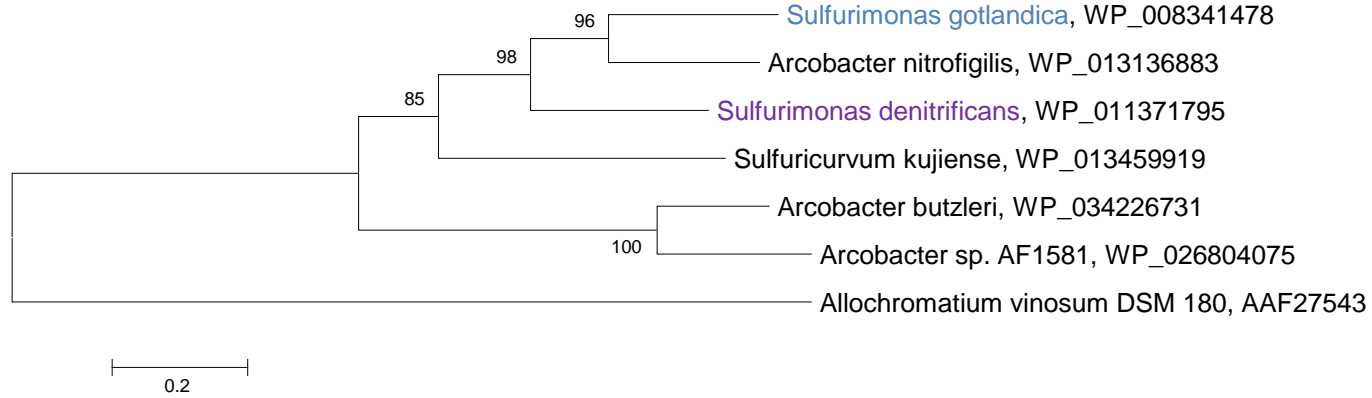
C. ATPS



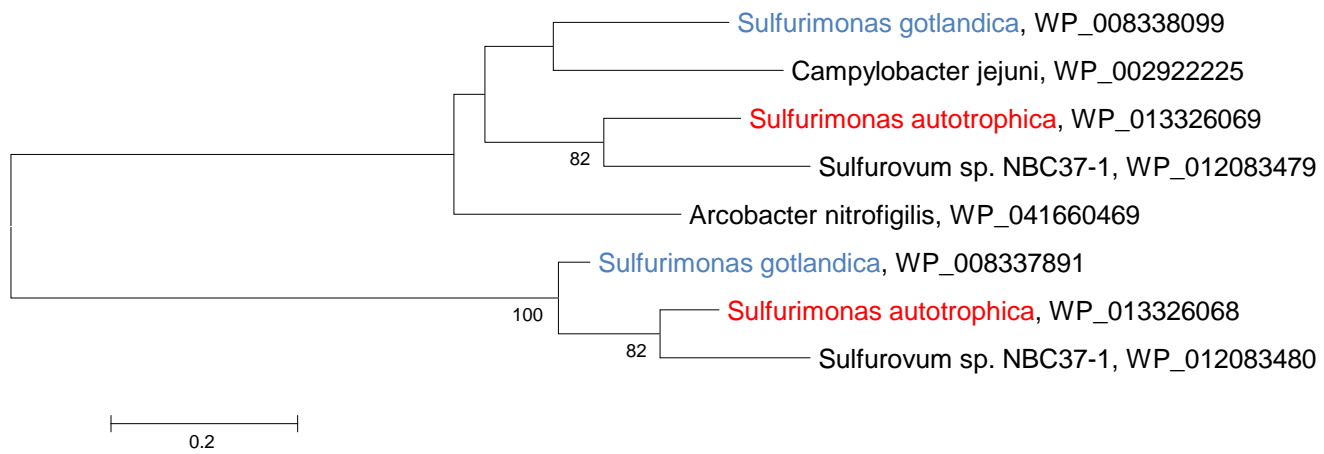
D. CysH



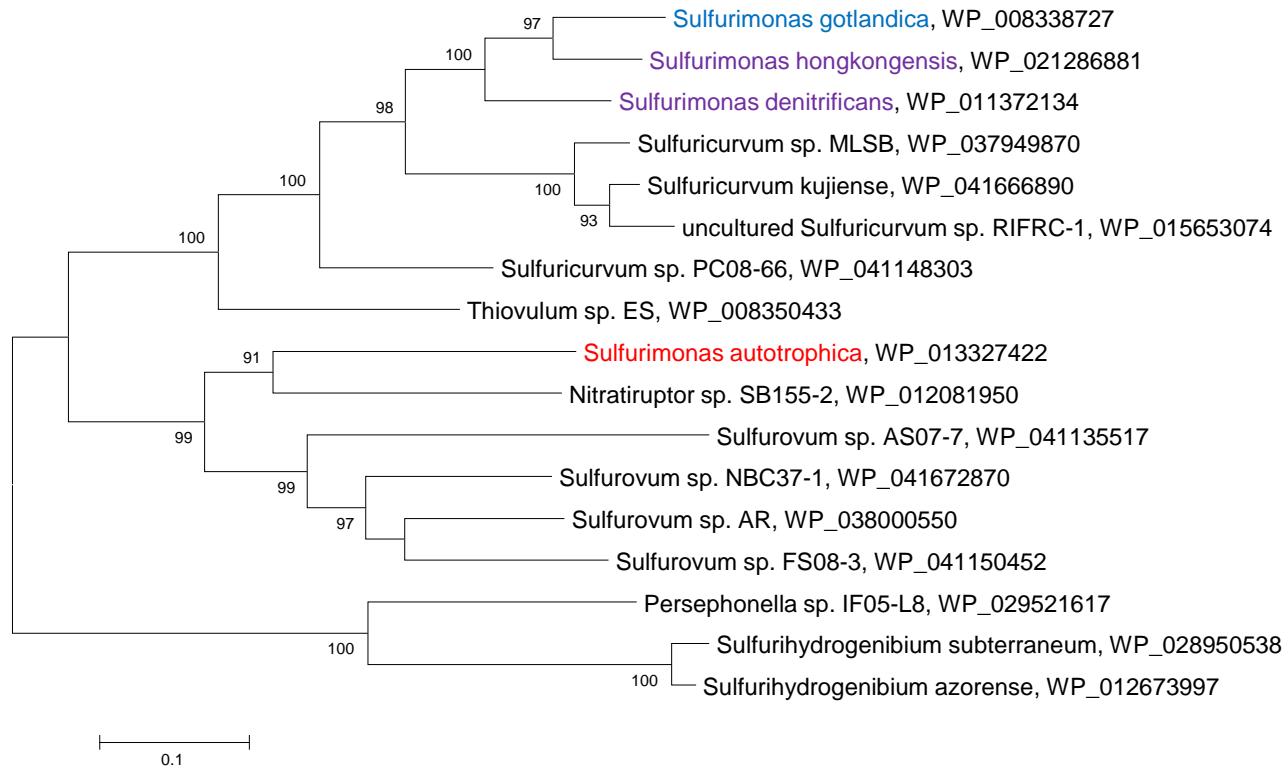
E. CysI



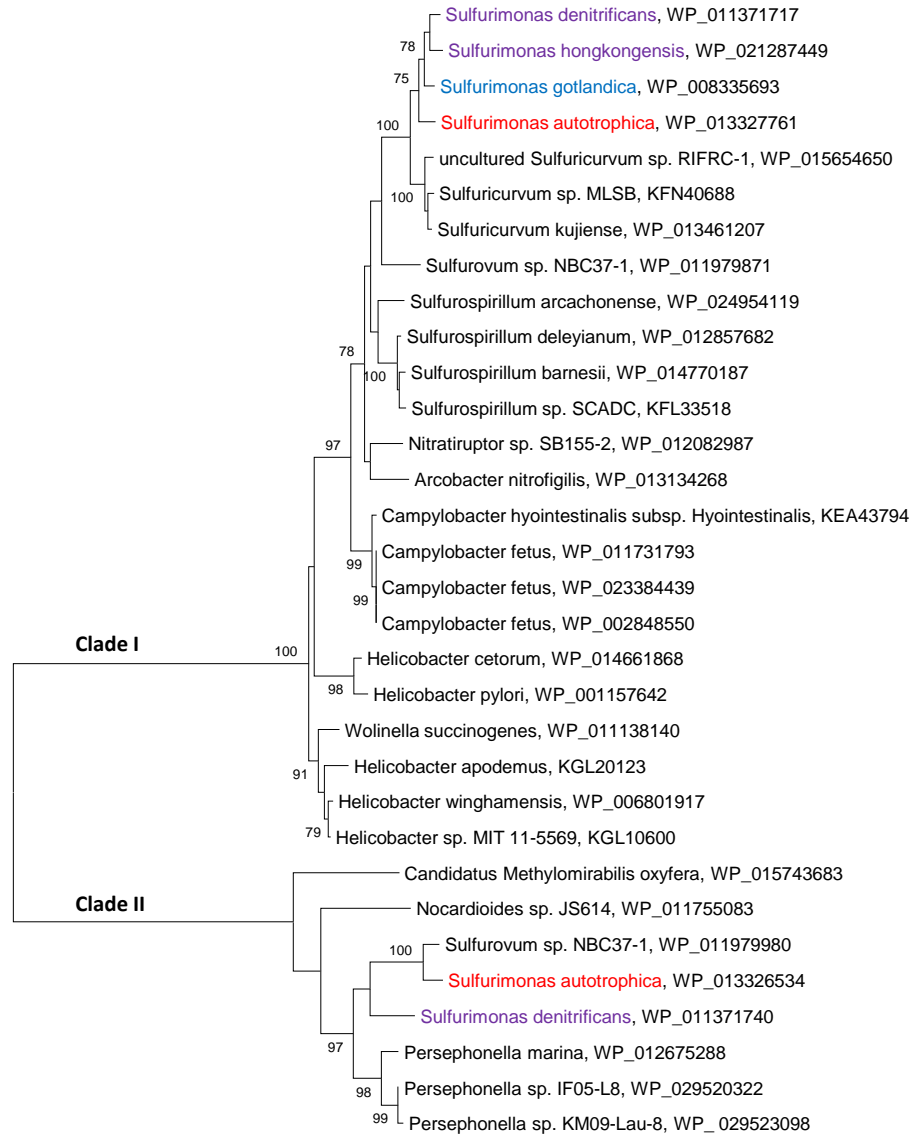
F. CysC



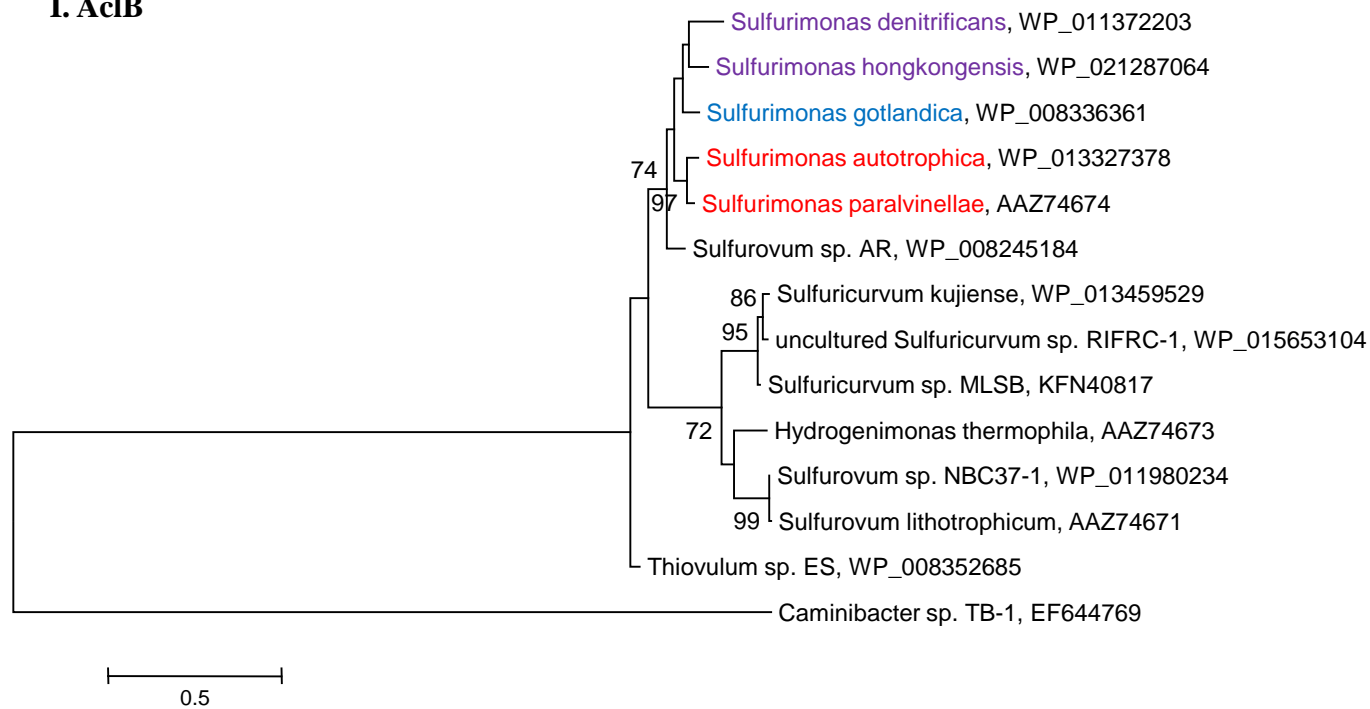
G. PsrA



H. CcoN



I. AclB



Supplementary Figure S1. Phylogenetic relationships of SoxB (A), SorA (B), ATPS (C), CysH (D), CysI (E), CysC (F), PsrA (G), CcoN (H) and AclB (I) protein sequences from *Sulfurimonas* species.

The SoxB, SorA, ATPS (CysN and Sat-type), CysH, CysI, CysC, PsrA, CcoN and AclB amino acid sequences were compared with the non-redundant protein database of NCBI by using BLASTP. The phylogenetic tree was constructed with MEGA6 (Tamura et al., 2013) based on the Maximum-likelihood method with 1000 bootstrap replications after multiple alignments with ClustalW (Larkin et al., 2007). The percentage of bootstrap resamplings ≥ 70 is indicated on the branches. The scale bar represents the expected number of changes per amino acids position. Isolation sources of *Sulfurimonas* species are indicated in different colors: blue, marine non-vent water system; purple, marine sediments; red, hydrothermal environments.

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