

Table S1. General genomic information of strain SS37A-Re^T, *Methylocystis bryophila* DSM21852^T, and *Methylocystis echinoides* LMG27198^T.

Feature	SS37A-Re ^T	<i>M. bryophila</i> DSM21852 ^T	<i>M. echinoides</i> LMG27198 ^T
No. of contigs	7	2	11
No. of plasmids	6	1	N.A.
Total length (bp)	4483149	4715351	5326437
N50	3733946	4540773	4211429
No. of CDS	4276	4330	5174
No. of tRNAs	55	50	54
No. of rRNAs	9	6	8
GC (%)	63.2	63.2	63.9

N.A., not applicable.

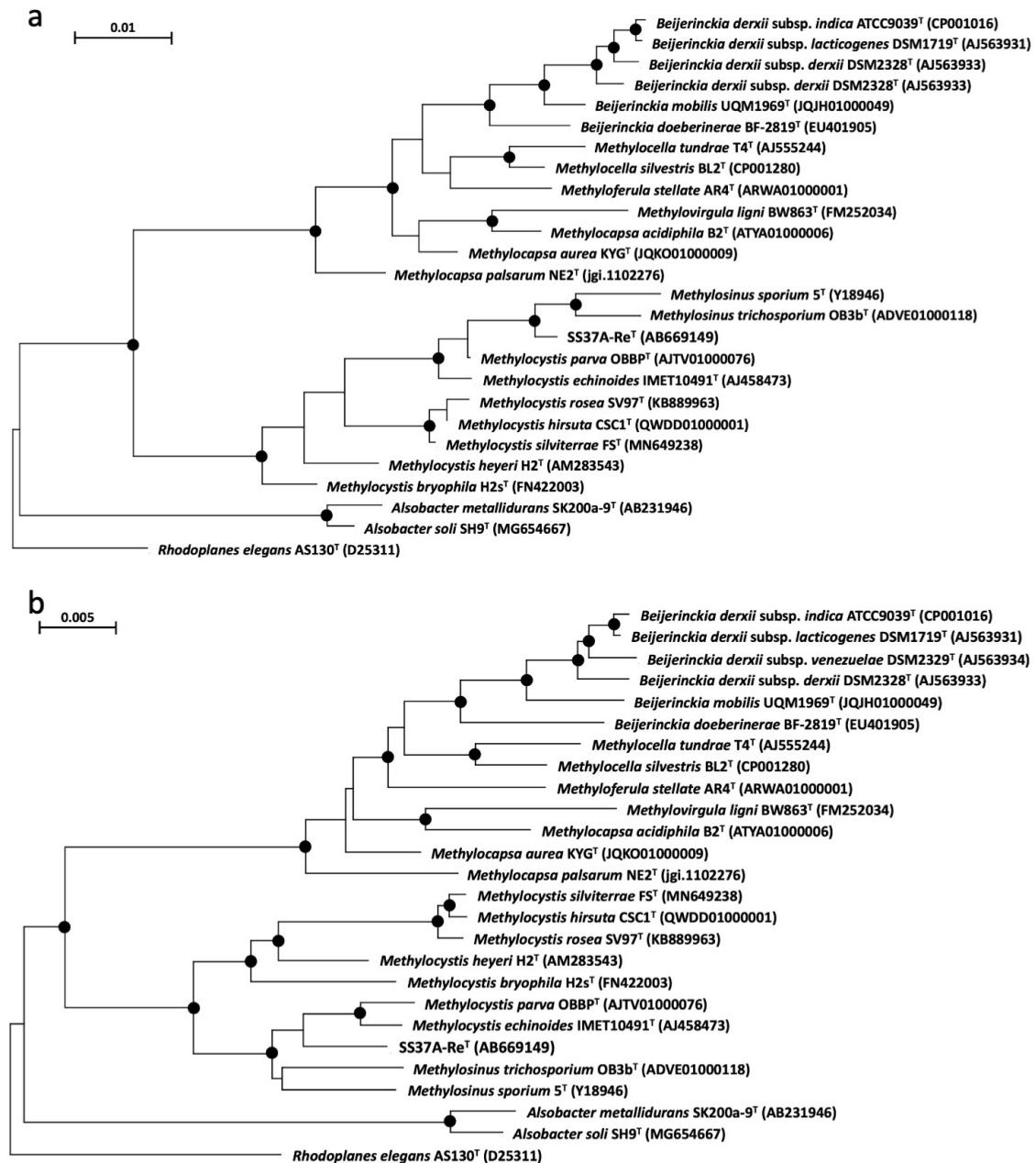


Fig. S1. Phylogenetic trees of 16S rRNA gene sequences showing the relationships between strain SS37A-Re^T and related bacteria by the parsimony (a) and distance (b) methods. Bars represent 0.01 (a) and 0.005 (b) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 data resamplings. The tree was rooted using *Rhodoplanes elegans* AS130^T as the outgroup. GenBank accession numbers are given in parentheses.

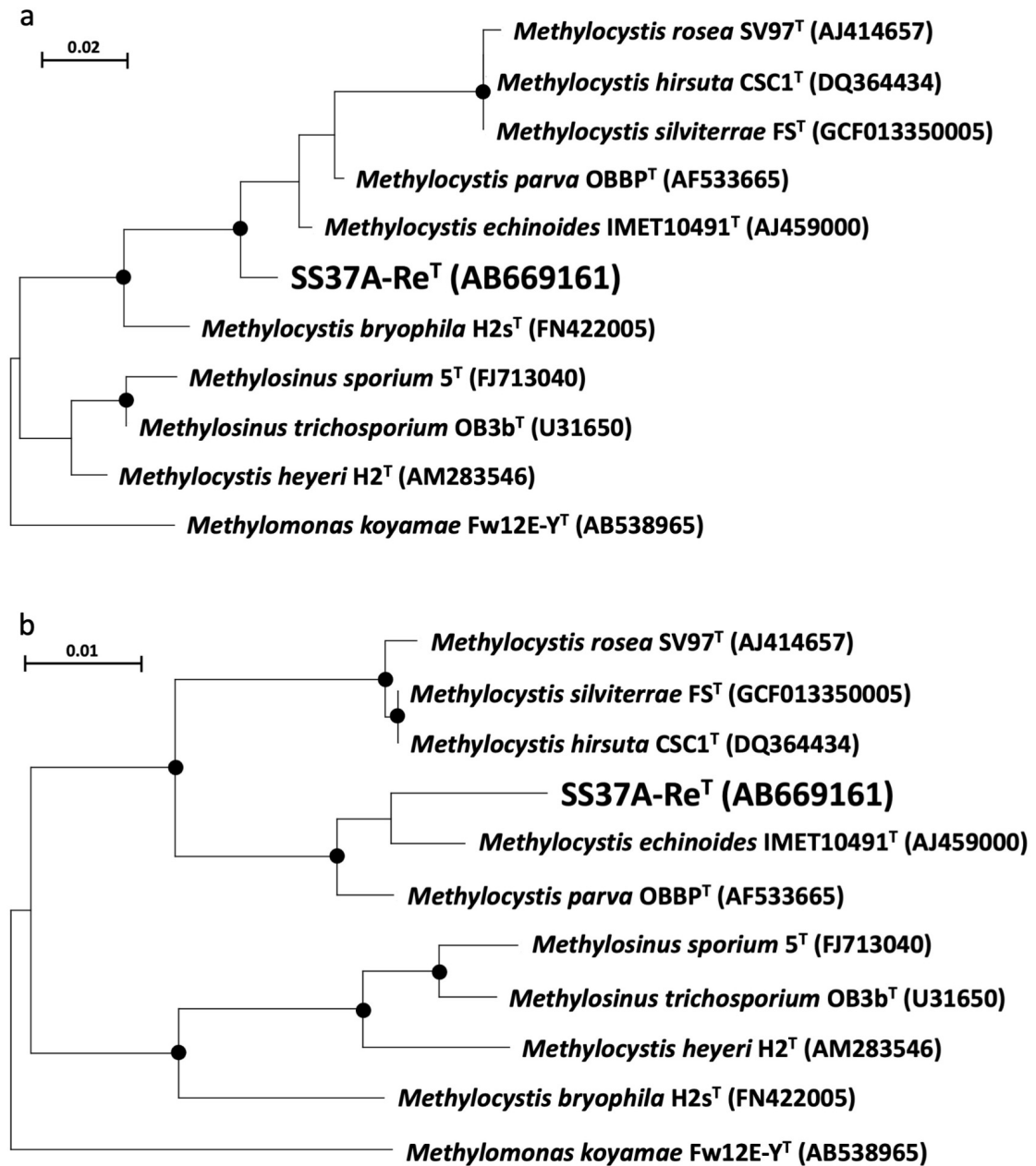


Fig. S2. Phylogenetic trees of *pmoA* gene sequences showing the relationships between strain SS37A-Re^T and related bacteria by the parsimony (a) and distance (b) methods. Bars represent 0.02 (a) and 0.01 (b) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 data resamplings. The tree was rooted using *Methylomonas koyamae* Fw12E-Y^T as the outgroup. GenBank accession numbers are given in parentheses.

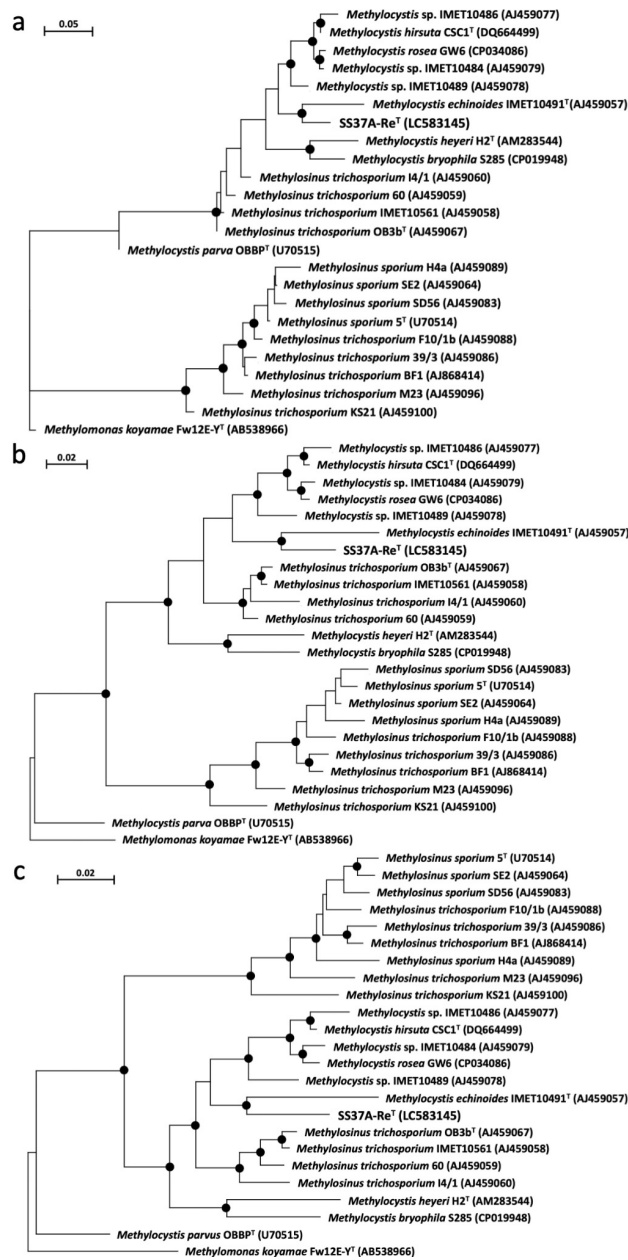


Fig. S3. Phylogenetic trees of *mxoF* gene sequences showing the relationships between strain SS37A-Re^T and related bacteria by the maximum-likelihood (a), parsimony (b), and distance (c) methods. Bars represent 0.05 (a), 0.02 (b) and 0.02 (c) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 data resamplings. The tree was rooted using *Methylomonas koyamae* Fw12E-Y^T as the outgroup. GenBank accession numbers are given in parentheses.

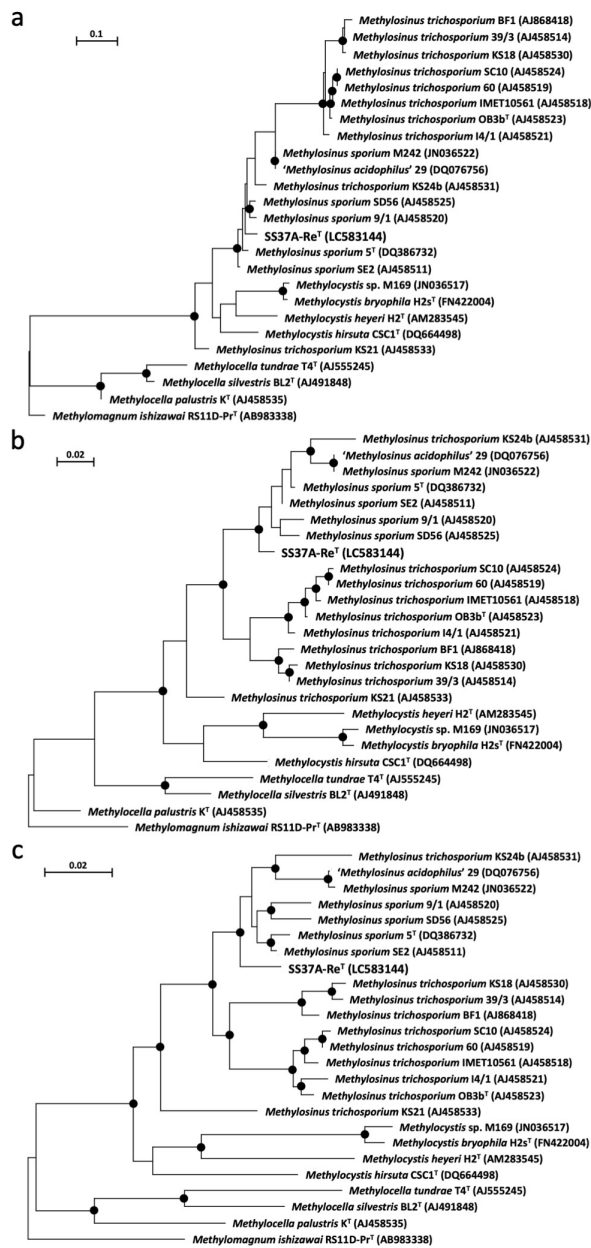
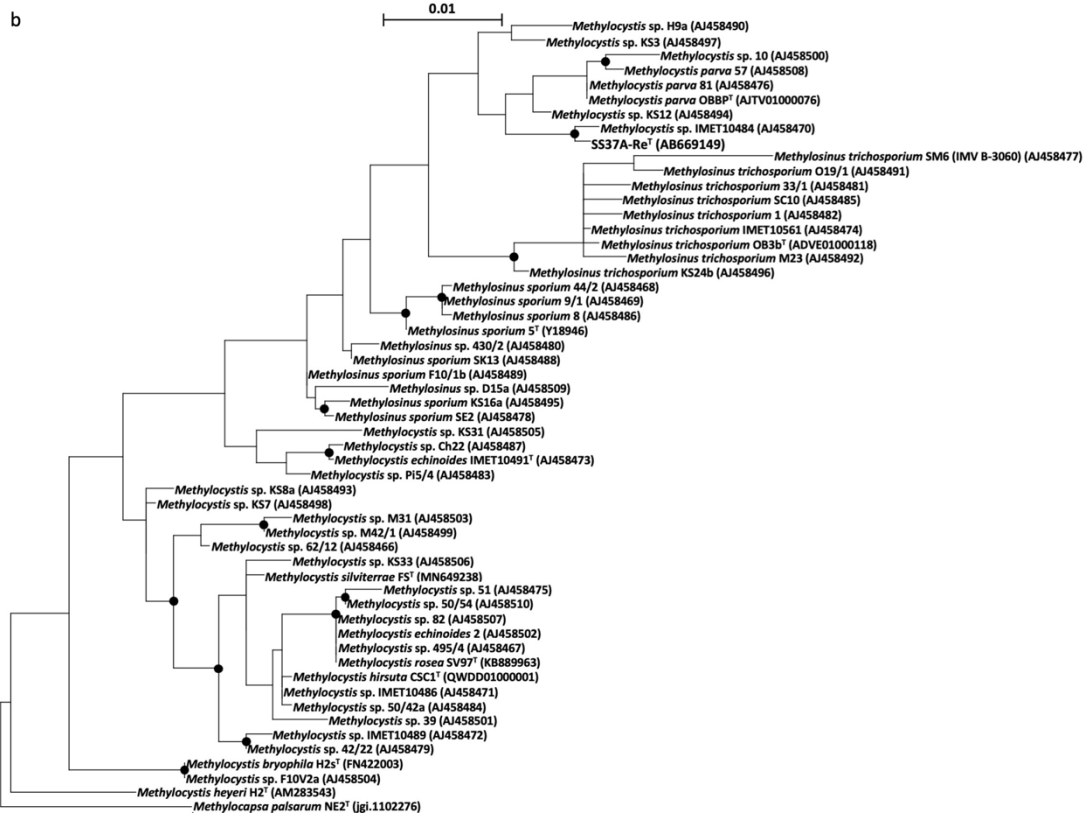
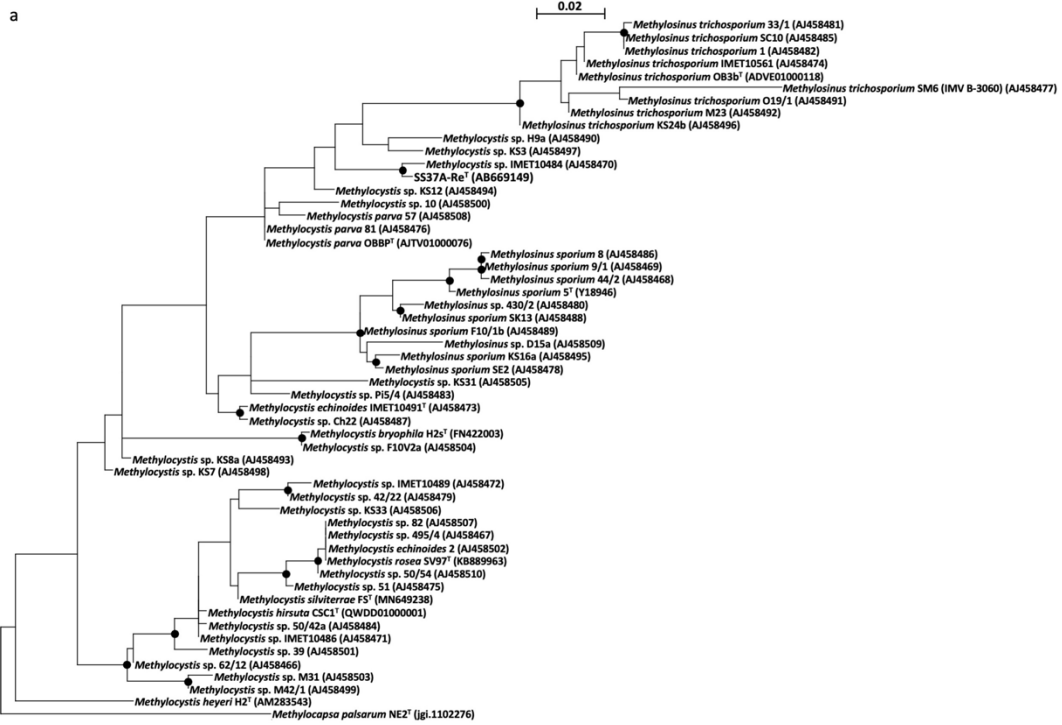


Fig. S4. Phylogenetic trees of *mmoX* gene sequences showing the relationships between strain SS37A-Re^T and related bacteria by the maximum-likelihood (a), parsimony (b), and distance (c) methods. Bars represent 0.1 (a) and 0.02 (b, c) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 data resamplings. The tree was rooted using *Methyloagnum ishizawai* RS11D-Pr^T as the outgroup. GenBank accession numbers are given in parentheses.



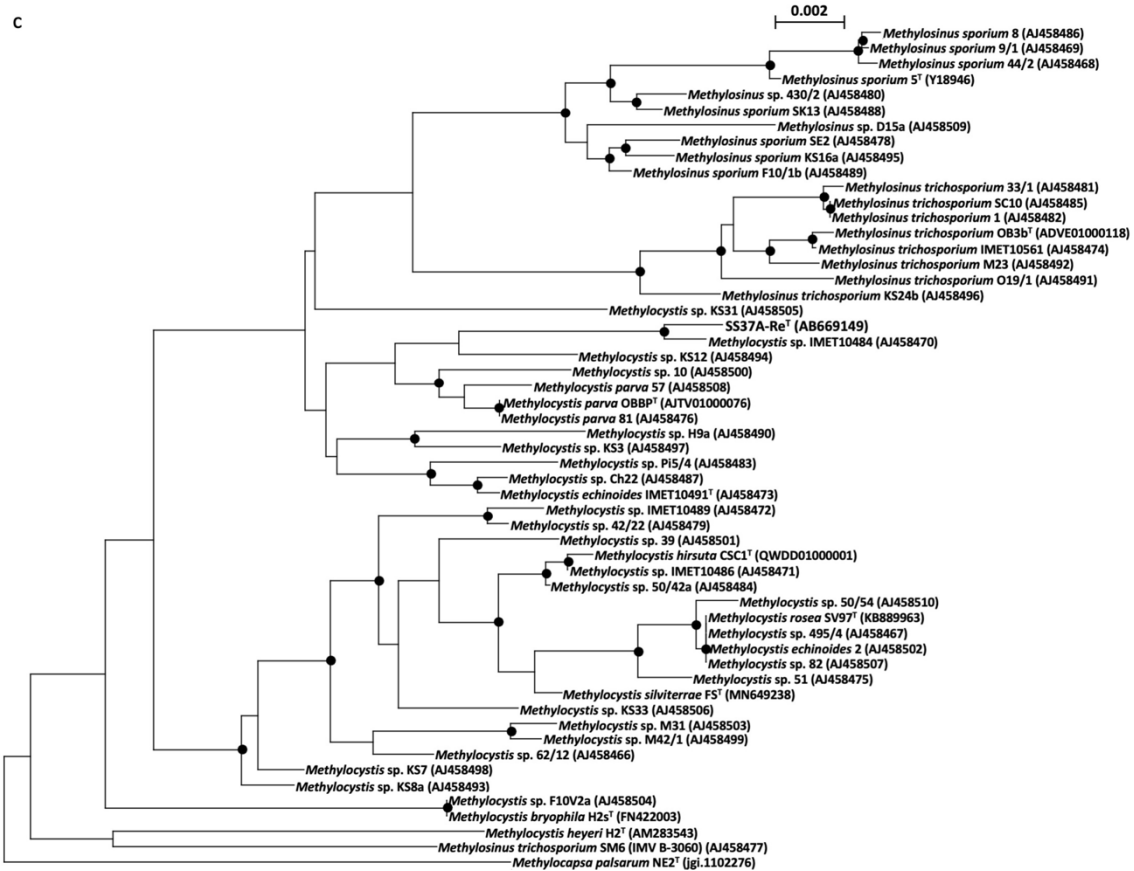
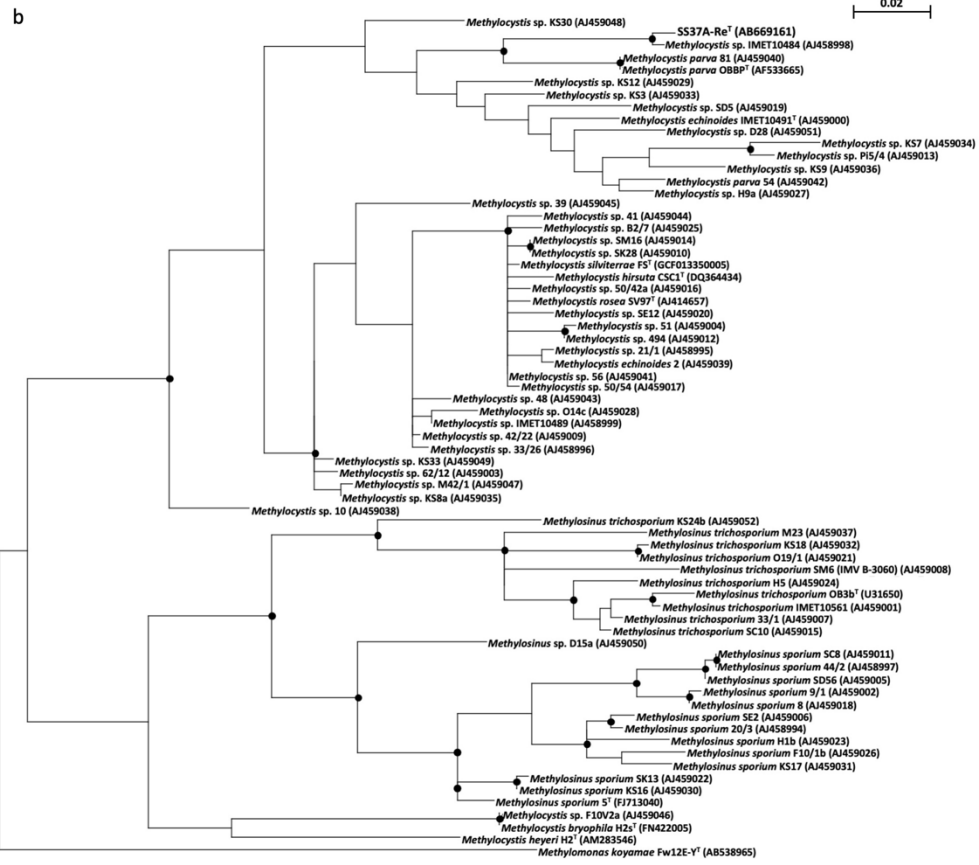
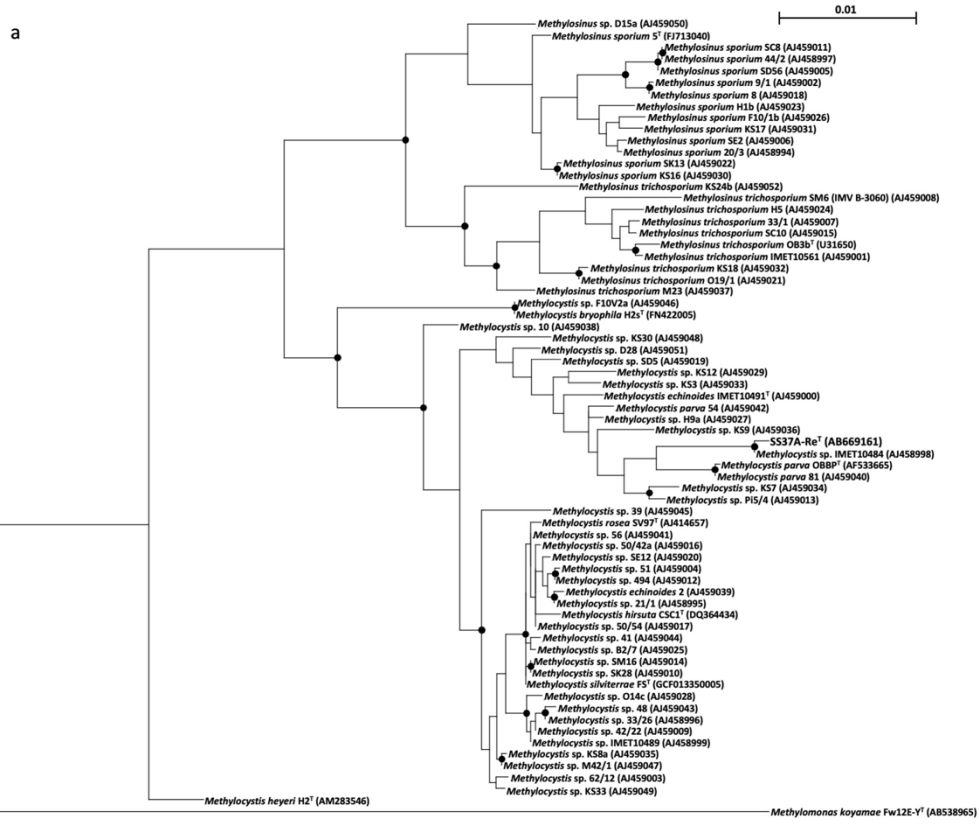


Fig. S5. Phylogenetic trees of 16S rRNA gene sequences showing the relationships between strain SS37A-Re^T and related *Methylocystis* and *Methylosinus* strains isolated from various environments [35] by the maximum-likelihood (a), parsimony (b), and distance (c) methods. Bars represent 0.02 (a), 0.01 (b) and 0.002 (c) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 (a and c) or 100 (b) data resamplings. The tree was rooted using *Methylocapsa palsarum* NE2^T as the outgroup. GenBank accession numbers are given in parentheses.



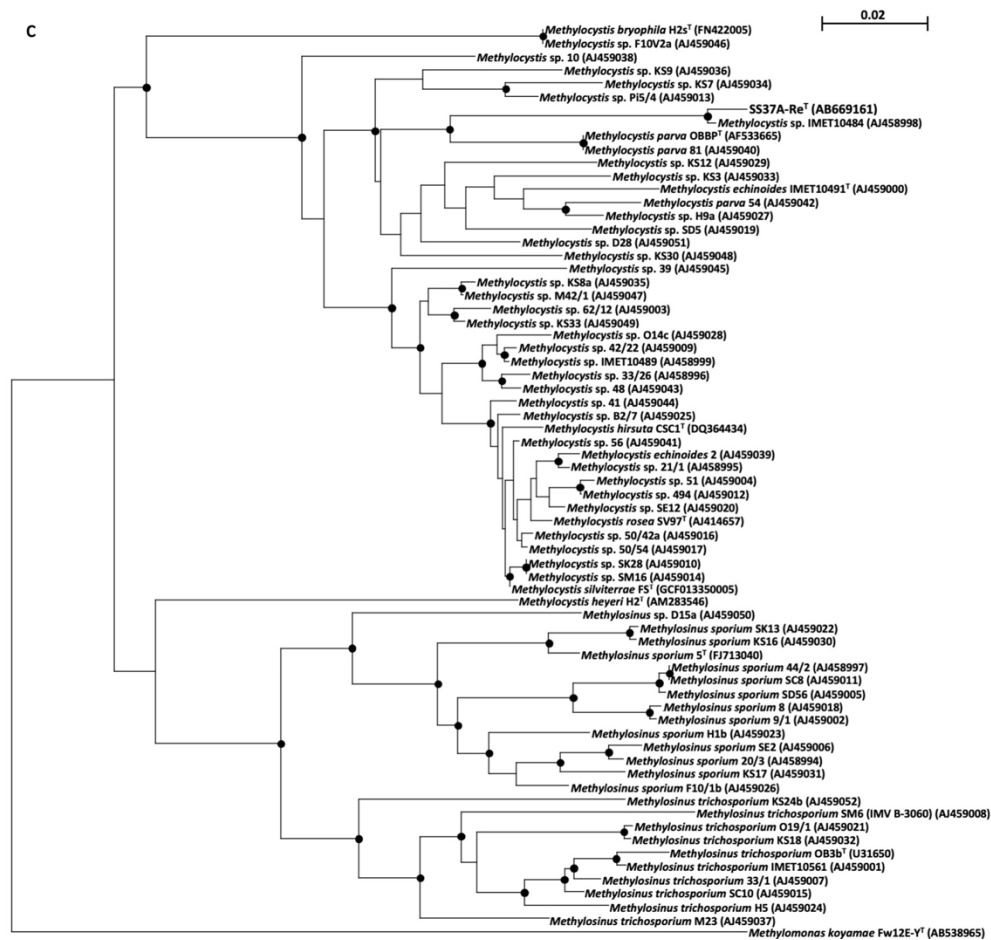
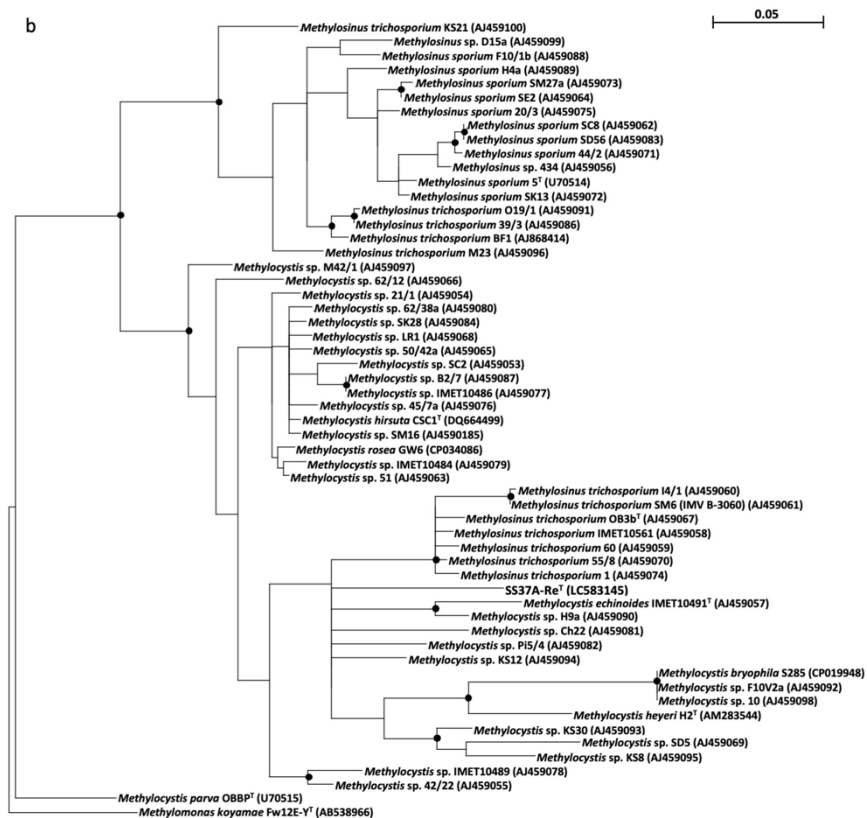
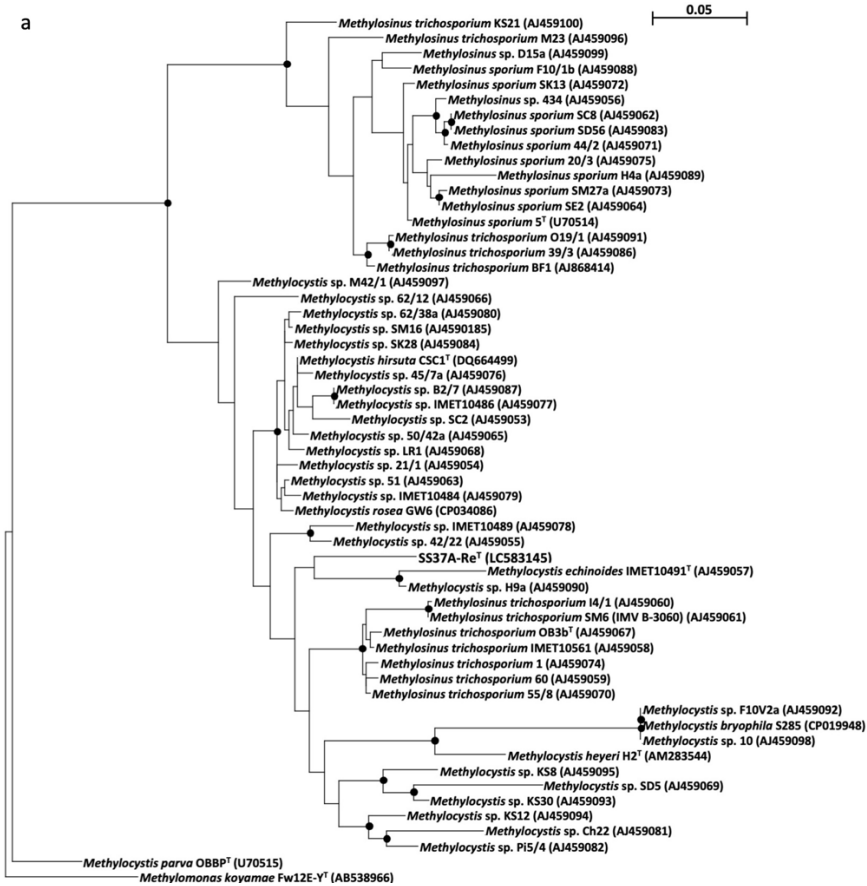


Fig. S6. Phylogenetic trees of *pmoA* gene sequences showing the relationships between strain SS37A-Re^T and related *Methylocystis* and *Methylosinus* strains isolated from various environments [35] by the maximum-likelihood (a), parsimony (b), and distance (c) methods. Bars represent 0.01 (a), 0.02 (b) and 0.02 (c) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 (a and c) or 100 (b) data resamplings. The tree was rooted using *Methylomonas koyamae* Fw12E-Y^T as the outgroup. GenBank accession numbers are given in parentheses.



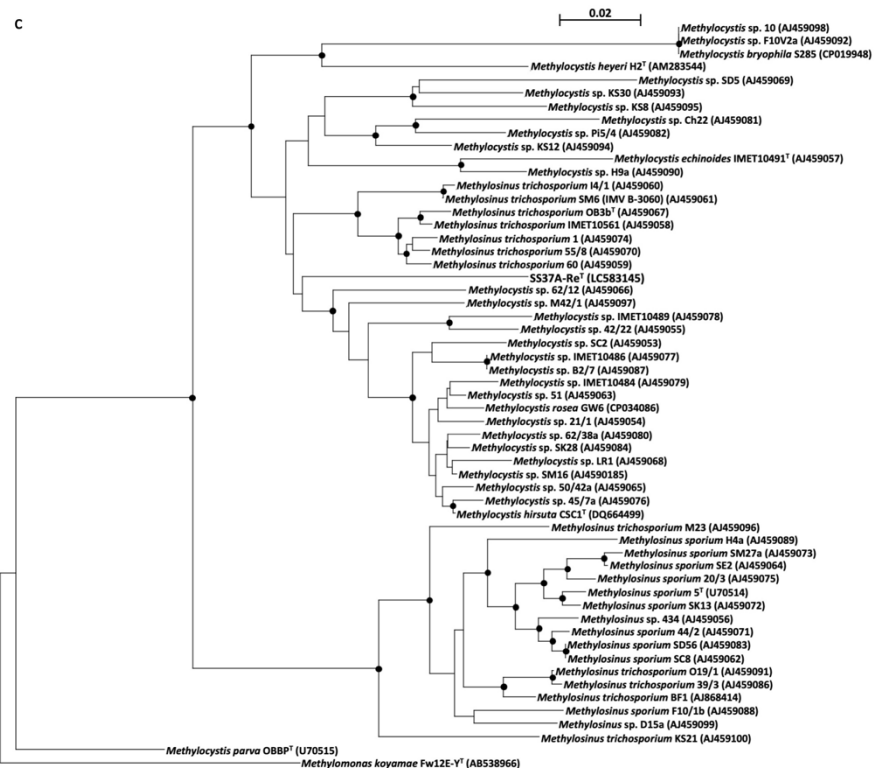
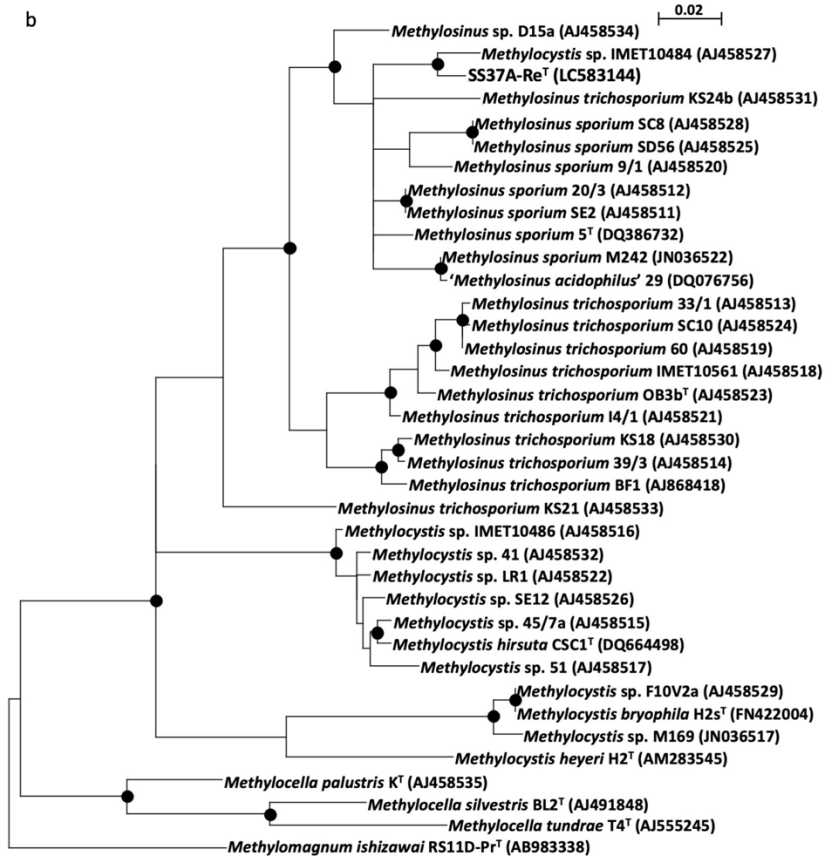
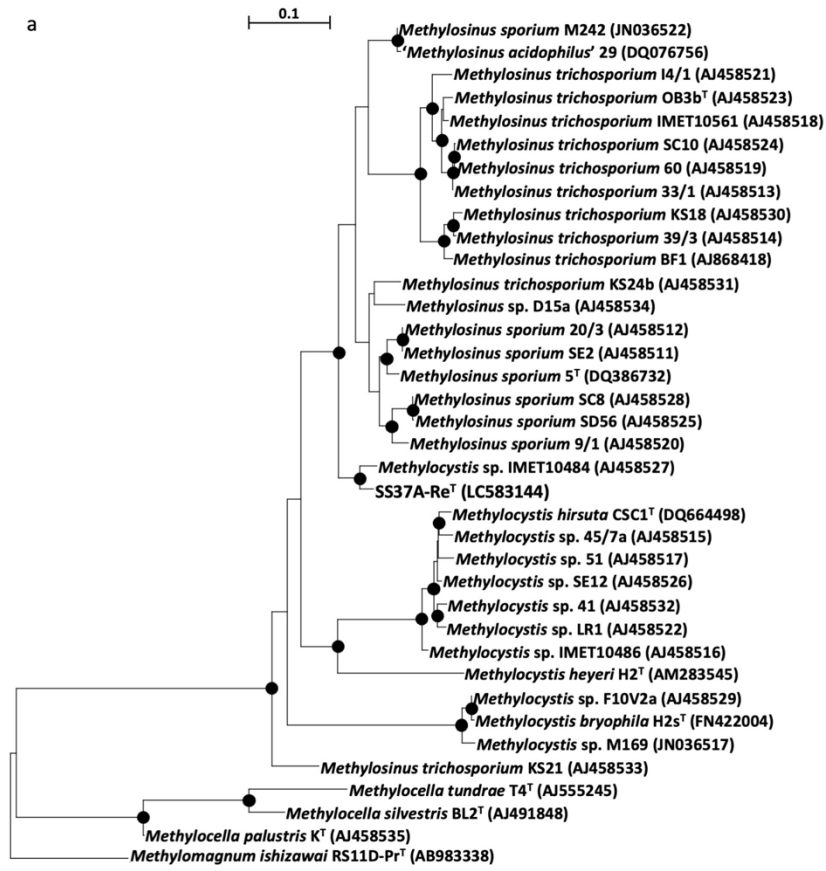


Fig. S7. Phylogenetic trees of *mxoF* gene sequences showing the relationships between strain SS37A-Re^T and related *Methylocystis* and *Methylosinus* strains isolated from various environments [35] by the maximum-likelihood (a), parsimony (b), and distance (c) methods. Bars represent 0.05 (a), 0.05 (b) and 0.02 (c) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 (a and c) or 100 (b) data resamplings. The tree was rooted using *Methylomonas koyamae* Fw12E-Y^T as the outgroup. GenBank accession numbers are given in parentheses.



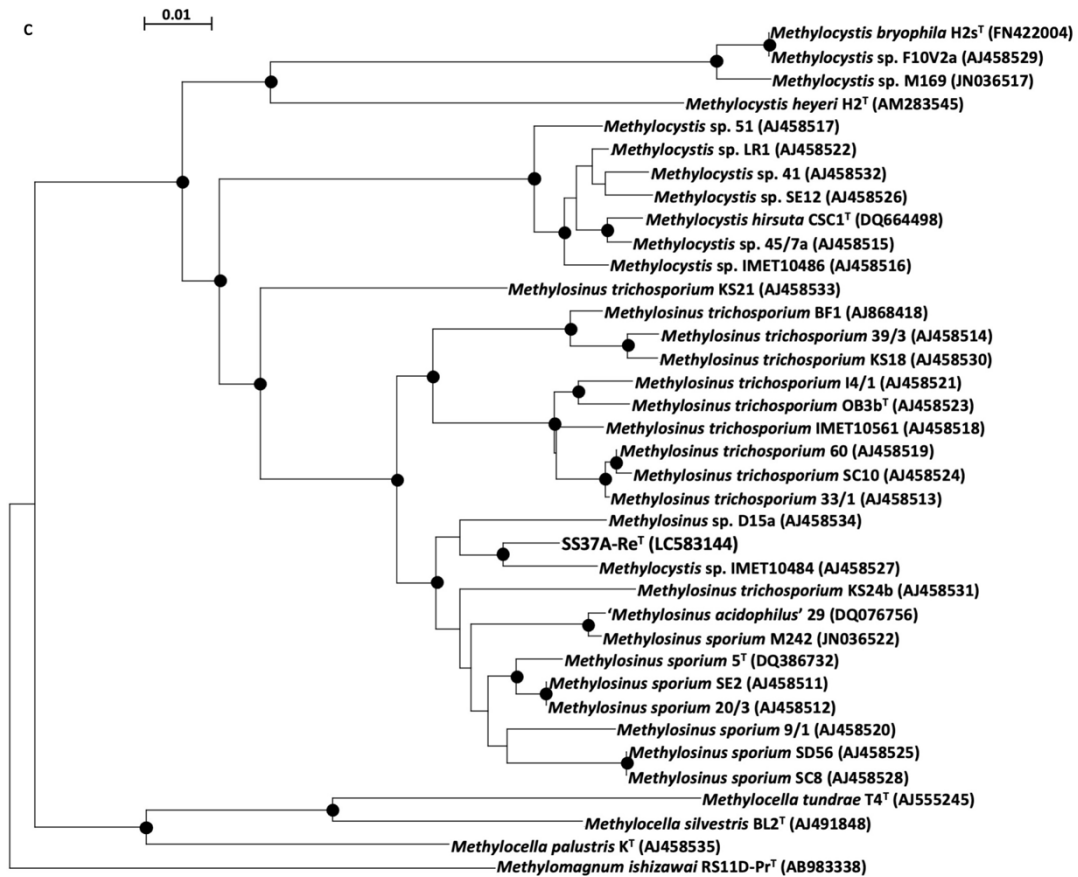


Fig. S8. Phylogenetic trees of *mmoX* gene sequences showing the relationships between strain SS37A-Re^T and related *Methylocystis* and *Methylosinus* strains isolated from various environments [35] by the maximum-likelihood (a), parsimony (b), and distance (c) methods. Bars represent 0.1 (a), 0.02 (b) and 0.01 (c) substitutions per nucleotide sequence position. Closed circles indicate internal nodes with at least 50% bootstrap support from 1000 (a and c) or 100 (b) data resamplings. The tree was rooted using *Methylomagnium ishizawai* RS11D-Pr^T as the outgroup. GenBank accession numbers are given in parentheses.

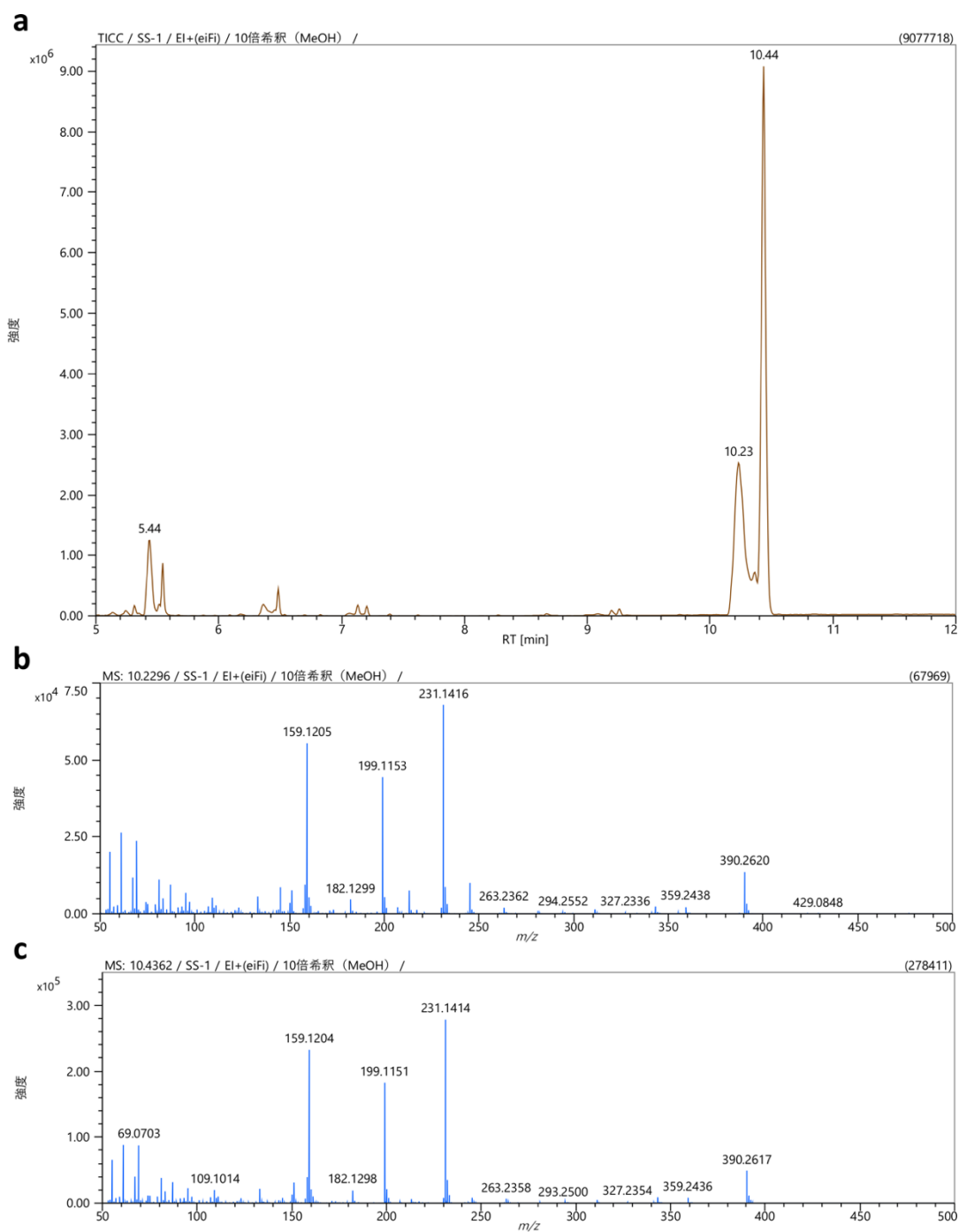


Fig. S9. (a) Total ion current chromatogram of dimethyl disulphide adducts from strain SS37A-Re^T monounsaturated fatty acids. Mass spectra of dimethyl disulphide adducts of C_{18:1} fatty acids eluted at the retention times 10.23 min (b) and 10.44 min (c), respectively, on the chromatogram (a). Ions at m/z 159, 231, and 390 correspond to ω -fragment, Δ -fragment, and M⁺ of the dimethyl disulphide adduct of C_{18:1} ω 8 [49].