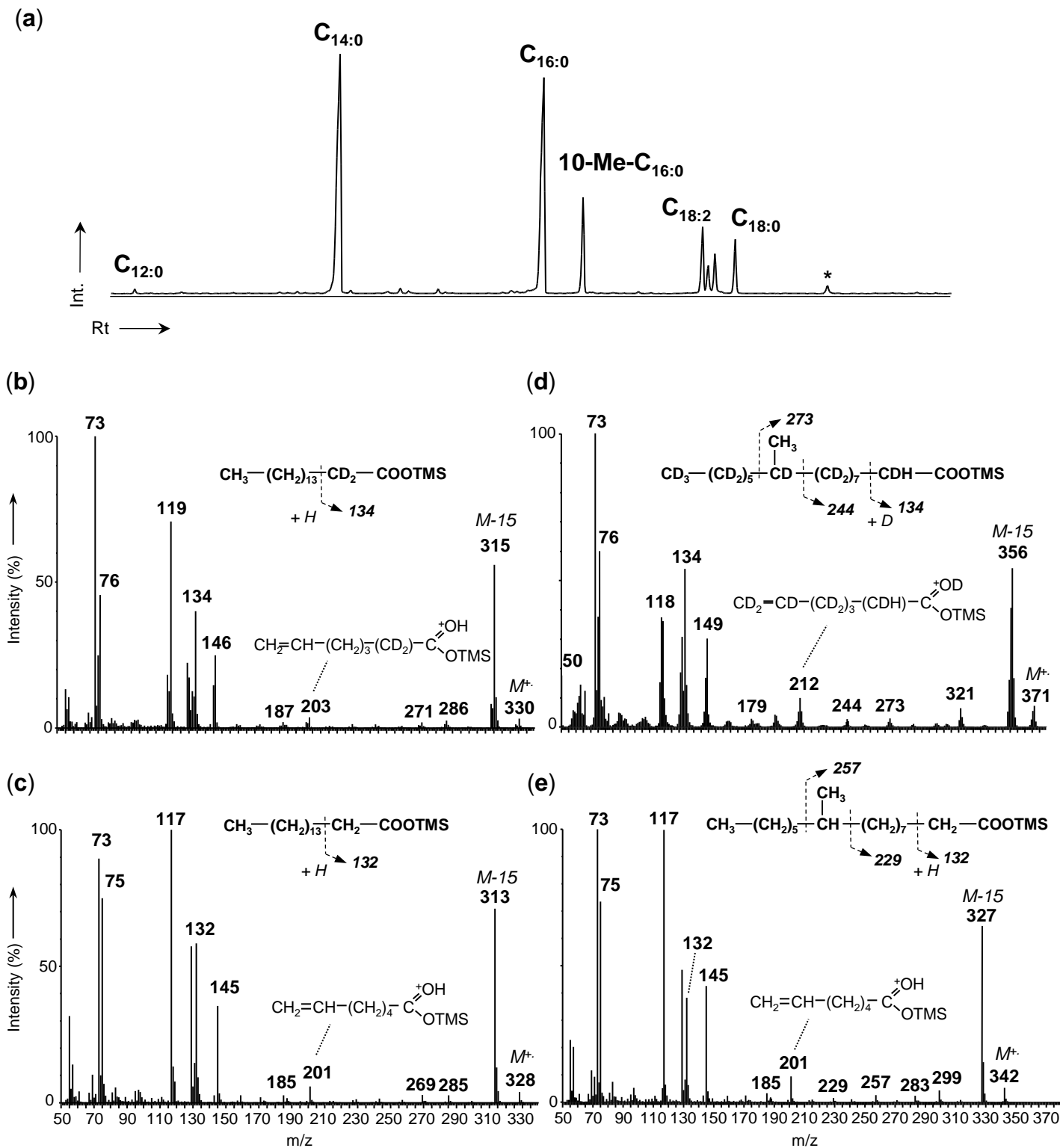




**Figure S1.** Phylogenetic tree based on comparative analyses of 16S rRNA gene sequences (1341 bp) of strain PF2803<sup>T</sup> (in bold) and other sulfate-reducing microorganisms (SRM). Stars indicate hydrocarbon-degrading SRM. Accession numbers are shown in parentheses. The scale bar corresponds to 0.05 substitutions per nucleotide. Percentages of 1000 bootstrap resampling are shown above or near the relevant nodes. Bootstrap values are shown for branches with more than 50% bootstrap support.



**Figure S2.** Total-ion chromatogram of fatty acids (as TMS-derivatives) from saponified cells of *D. alkenivorans* PF2803<sup>T</sup> grown on hexadec-1-ene (a) and mass spectra and structural characteristics of the TMS-derivatives of 2,2-*d*<sub>2</sub>-hexadecanoic acid from a culture grown on 1,1,2,2-*d*<sub>4</sub>-hexadecanol (b), hexadecanoic acid from a culture grown on unlabeled hexadec-1-ene (c), *d*<sub>29</sub>-10-methylhexadecanoic acid from a culture grown on *d*<sub>32</sub>-hexadec-1-ene (d), and 10-methylhexadecanoic acid from a culture grown on unlabeled hexadec-1-ene. \* = contaminants.