



Supplementary information S1 (figure) | **Comparison of the genome of *Desulfovibrio vulgaris* Hildenborough with those of other sulphate-reducing microorganisms (SRMs).** Only gene categories related to stress responses are shown, including those encoding enzymes involved in hydrogen cycling, hydrogenases, cytochromes, and transmembrane complexes. The heat map indicates the percent identity of *D. vulgaris* Hildenborough orthologues in sequenced SRM genomes as indicated by BlastP comparison (red, 80-100%; yellow, 60-80%; white, 40-60%; blue, <40%). Heat maps were generated in R v 2.11.0. Species abbreviations are as follows: Afu, *Archaeoglobus fulgidus*; Apr, *Archaeoglobus profundus*; Dco, *Desulfococcus oleovorans*; Dba, *Desulfobacterium autotrophicum*; Daa, *Desulfatibacillum alkenivorans*; Dtp, *Desulfotalea psychrophila*; Sfu, *Syntrophobacter fumaroxidans*; Dsa, *Desulfovibrio salexigens*; Dae, *Desulfovibrio aespoensis*; Dma, *Desulfovibrio magneticus*; DFW, *Desulfovibrio* sp. FW1012B; Dhr, *Desulfohalobium retbaense*; Dmb, *Desulfomicrobium baculatum*; Dnt, *Desulfonatronospira thiodismutans*; Dpi, *Desulfovibrio piger*; Dde, *Desulfovibrio desulfuricans* subsp. *desulfificans* str. ATCC 27,774; Ddg, *Desulfovibrio desulfuricans* subsp. *desulfuricans* str. G20; Dvm, *Desulfovibrio vulgaris* str. Miyazaki F; Dvp, *Desulfovibrio vulgaris* str. DP4; Dvr, *Desulfovibrio vulgaris* str. RCH1; Dra, '*Candidatus Desulforudis audaxviator*'; Doa, *Desulfotomaculum acetoxidans*; Dor, *Desulfotomaculum reducens*; Tye, *Thermodesulfovibrio yellowstoneii*.