PNAS

Supporting Information for

Generation of zero-valent sulfur from dissimilatory sulfate reduction in sulfate-reducing microorganisms

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Sulfate reducing bacteria	Abbr.	Collection no.	Origin	Gram-positive/negative	Temp.	Electron donor	Electron acceptor	Medium
Desulfovibrio vulgaris Hildenborough	DvH	DSM 644	Wealden clay	Gram-negative	Mesophilic	DL-Lactate	Sulfate	LS4D
Desulforamulus ruminis DL	DLT	DSM 2154	Rumen of hay-fed sheep	Gram-positive*	Mesophilic	DL-Lactate	Sulfate	LS4D
Desulfomicrobium baculatum X	DMB	DSM 4028	Manganese ore	Gram-negative	Mesophilic	DL-Lactate	Sulfate	LS4D
Pseudodesulfovibrio indicus J2	PDI	DSM 101483	Deep-sea serpentinized peridotite	Gram-negative	Mesophilic	DL-Lactate	Sulfate	LS4D
Thermodesulfatator autotrophicus S606	TDA	DSM 101864	Deep-sea chimney wall	Gram-negative	Thermophilic	Hydrogen	Sulfate	SO4PNsalts
Halodesulfovibrio marinisediminis C/L 2	HDM	DSM 17456	Coastal sediment	Gram-negative	Mesophilic	DL-Lactate	Sulfate	LS4D

Note: * *Desulforamulus ruminis DL* has Gram-positve-type cell wall structure

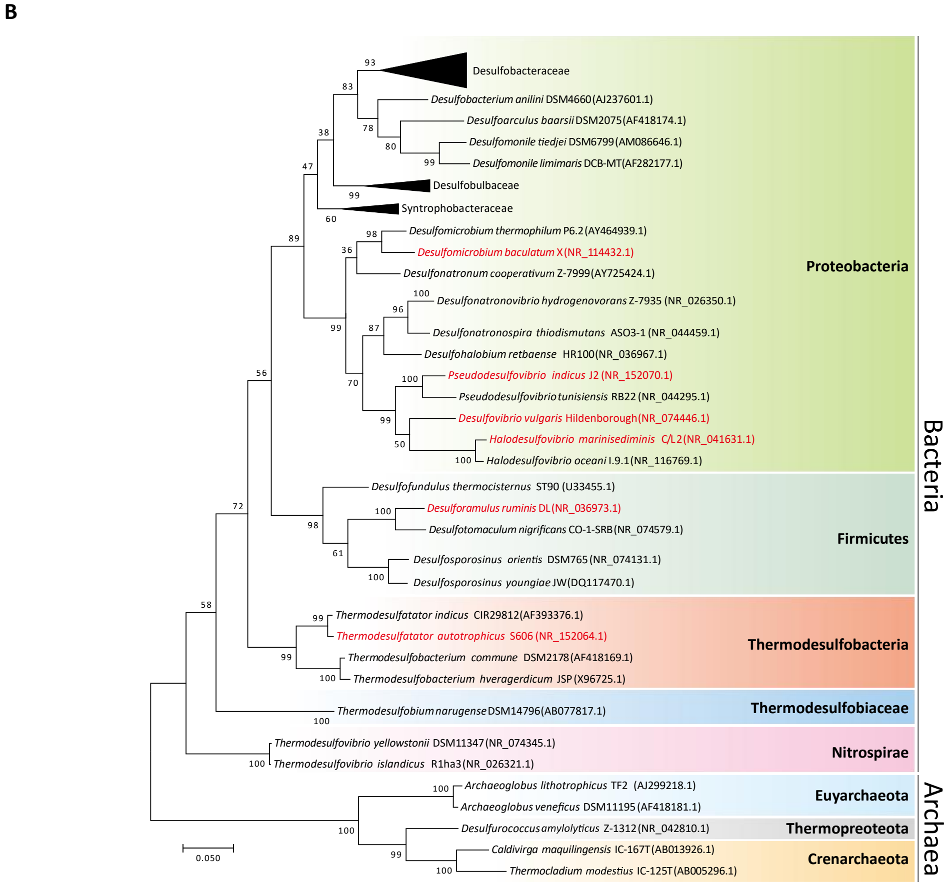

Fig. S1. Phylogenetic and physiological information on the isolated sulfate reducing microorganisms (SRMs) selected in this study. A, Basic phylogenetic and physiological information on the selected SRMs; **B**, Phylogenetic tree based on the full-length 16S rRNA gene sequences of representative SRMs. The SRMs selected in this study are in red font. The sequences were obtained from the NCBI database and the tree was created using MEGA 7 software. The bootstrap values at nodes are based on 1,000 replicates. The scale bar represents a 5 bp substitution per 100 nucleotides.

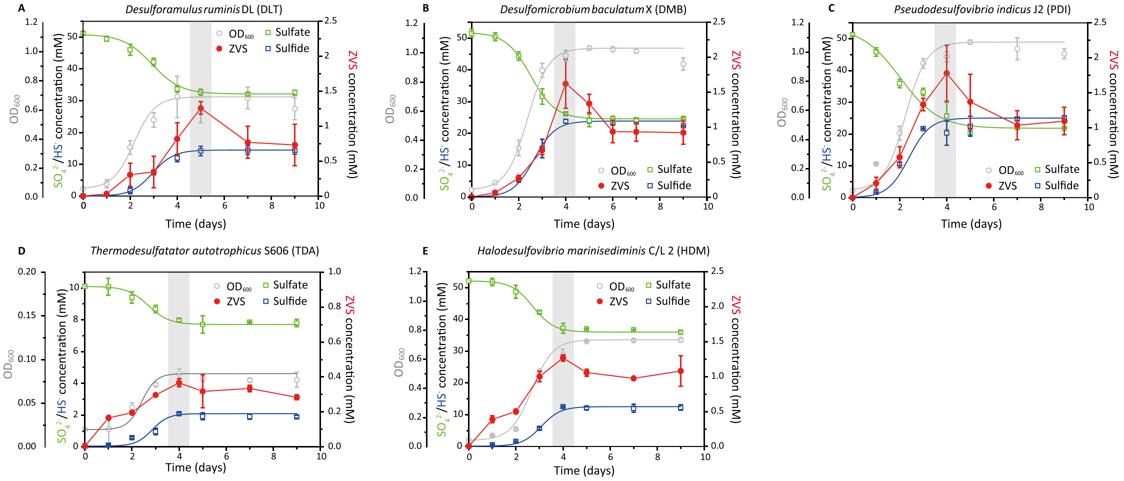

Fig. S2. Dissimilatory sulfate reduction and ZVS generation in five pure cultures of SRMs. **A**, *Desulfotomaculum ruminis* DL (DLT); **B**, *Desulfomicrobium baculatum* X (DMB); **C**, *Pseudodesulfovibrio indicus* J2 (PDI); **D**, *Thermodesulfatator autotrophicus* S606 (TDA); **E**, *Halodesulfovibrio marinisediminis* C/L 2 (HDM). The peak time for accumulation of the highest concentrations of total ZVS (ZVS peak time) in the five SRM cultures were shaded in grey. Error bars represent standard deviations of triplicate cultures.

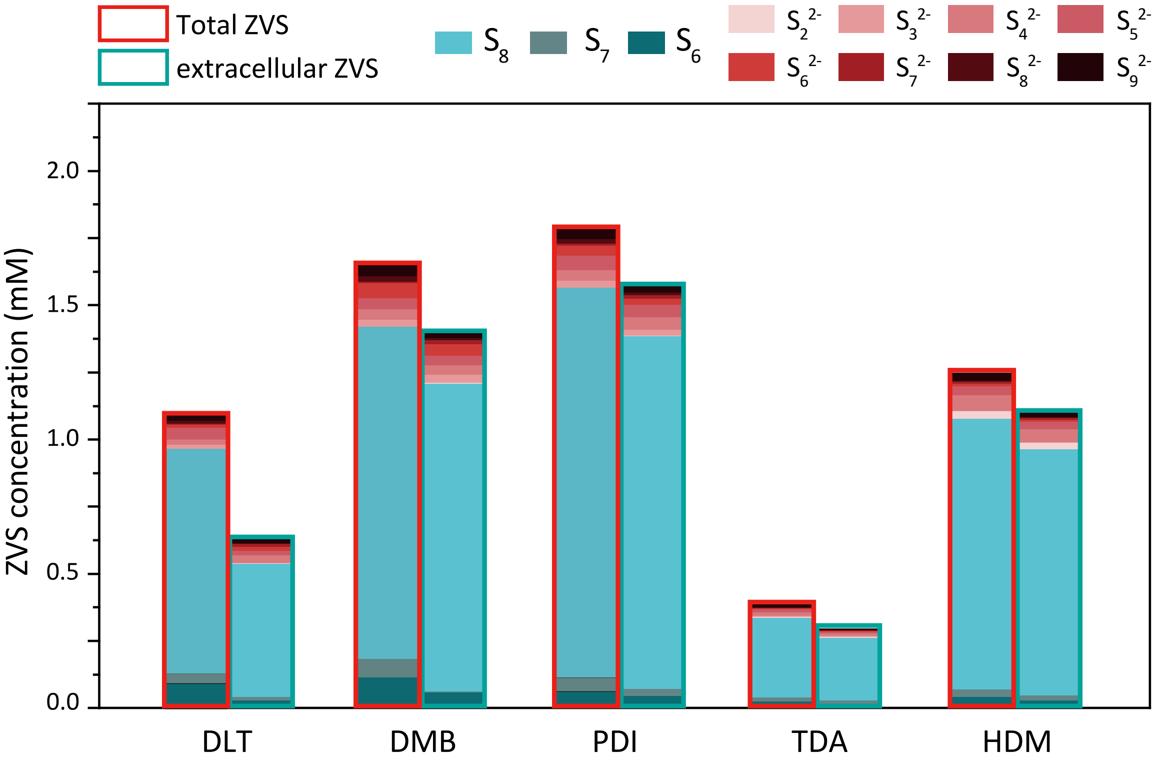

Fig. S3. **The total/extracellular ZVS generation of five SRM pure cultures under their optimum growth conditions.**

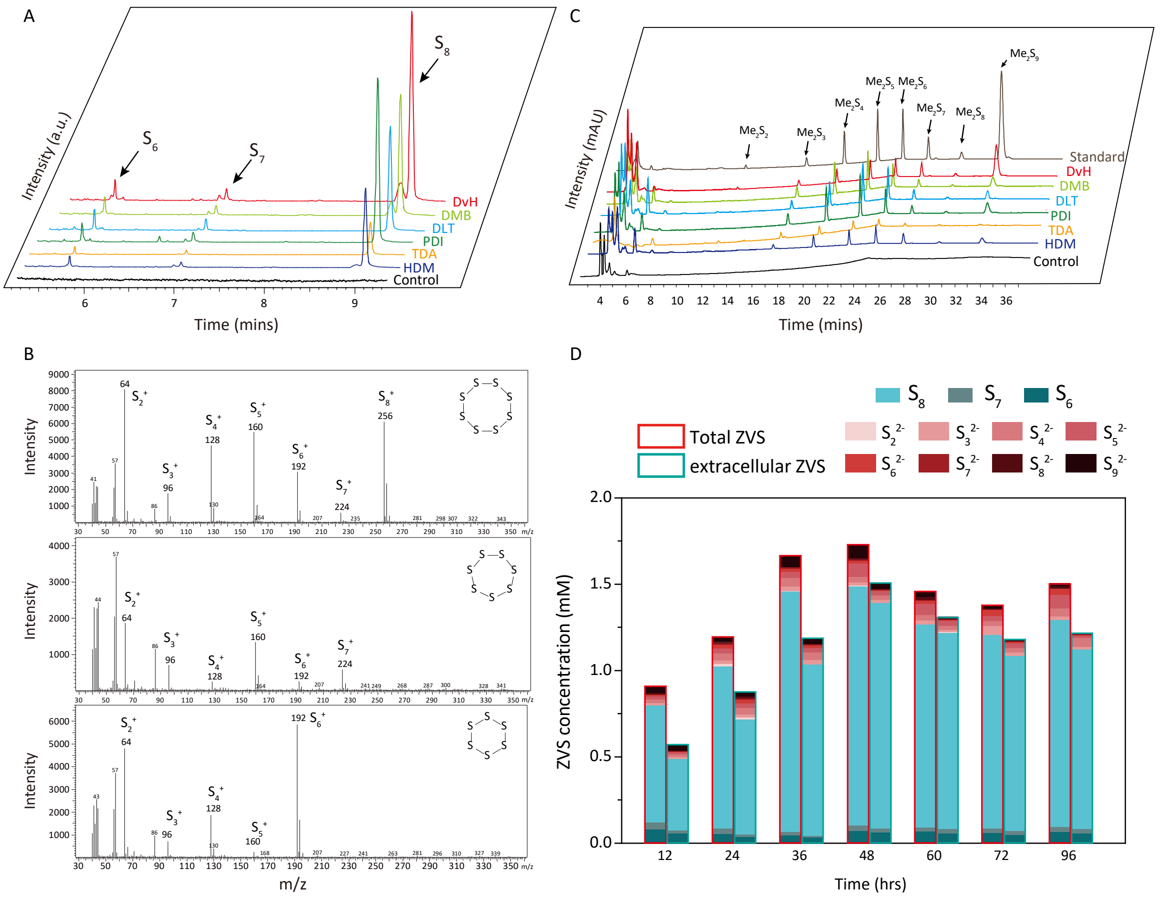

Fig. S4. Identification and characterization of DSR-derived ZVS composition. A, GC-MS chromatogram and **B**, mass spectrum of major elemental sulfur species in the six SRM pure cultures. **C**, HPLC chromatogram of polysulfide species in the six SRM pure cultures. **D**, Temporal change in compositional profiles of total/extracellular ZVS in DvH.

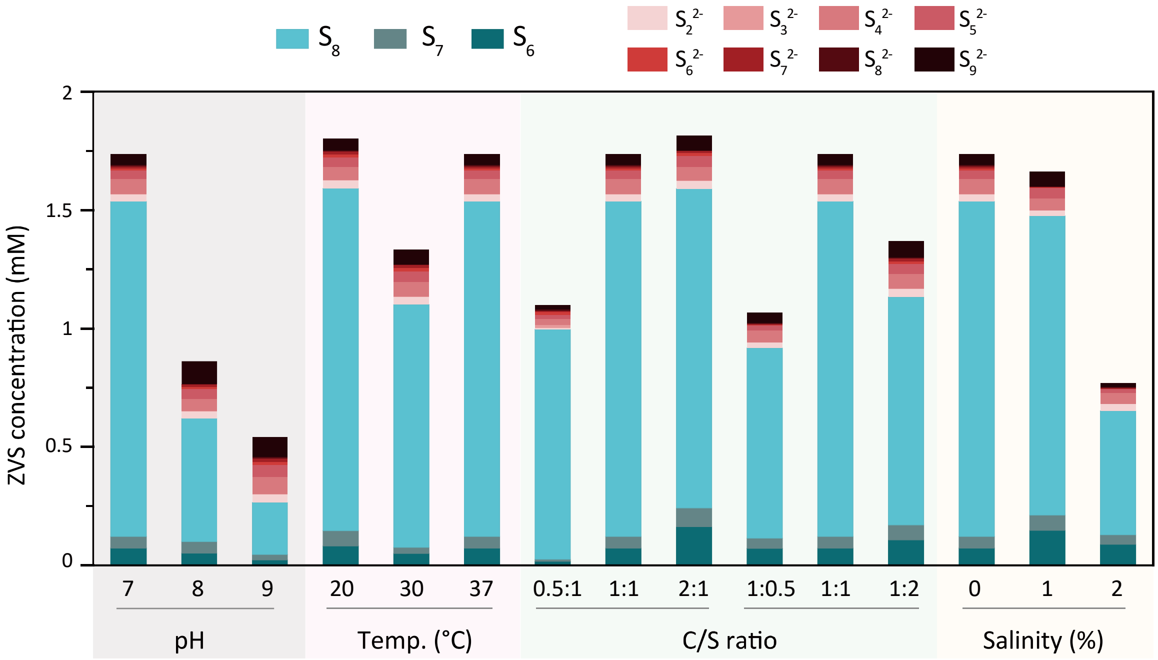

Fig. S5. Compositional profiles of ZVS in DvH cultures under different growth conditions, including different pH (7, 8, and 9), temperature (20, 30, and 37°C), lactate(C) to sulfate(S) ratio (0.5:1, 1:1, 2:1, 1:0.5, 1:1, and 1:2), and Salinity (0, 1, and 2%).

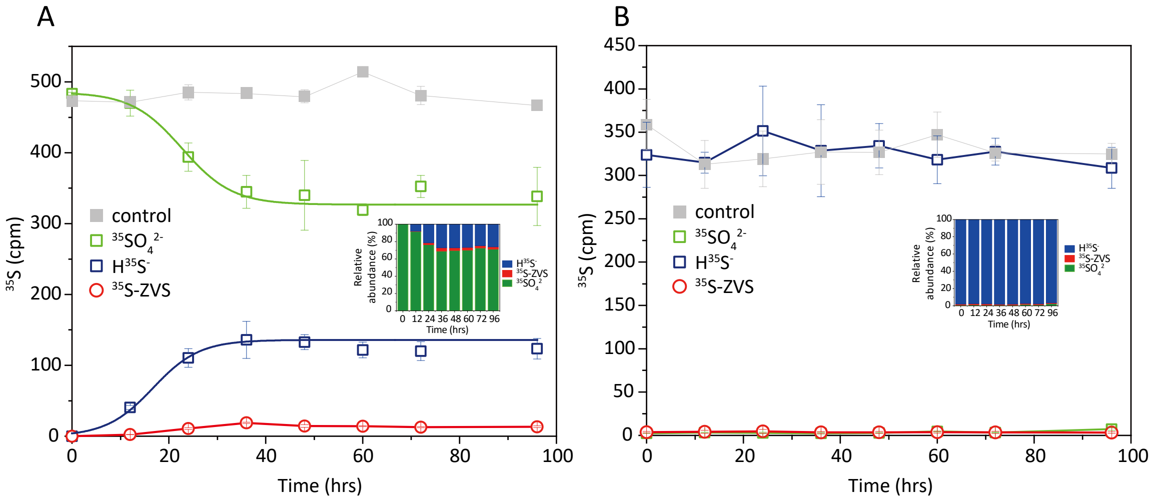

Fig. S6. Temporal changes in ^{35}S-activities of different sulfur species and their relative abundance in DvH cultures fed with ^{35}S-sulfate (A) and ^{35}S-sulfide (B).

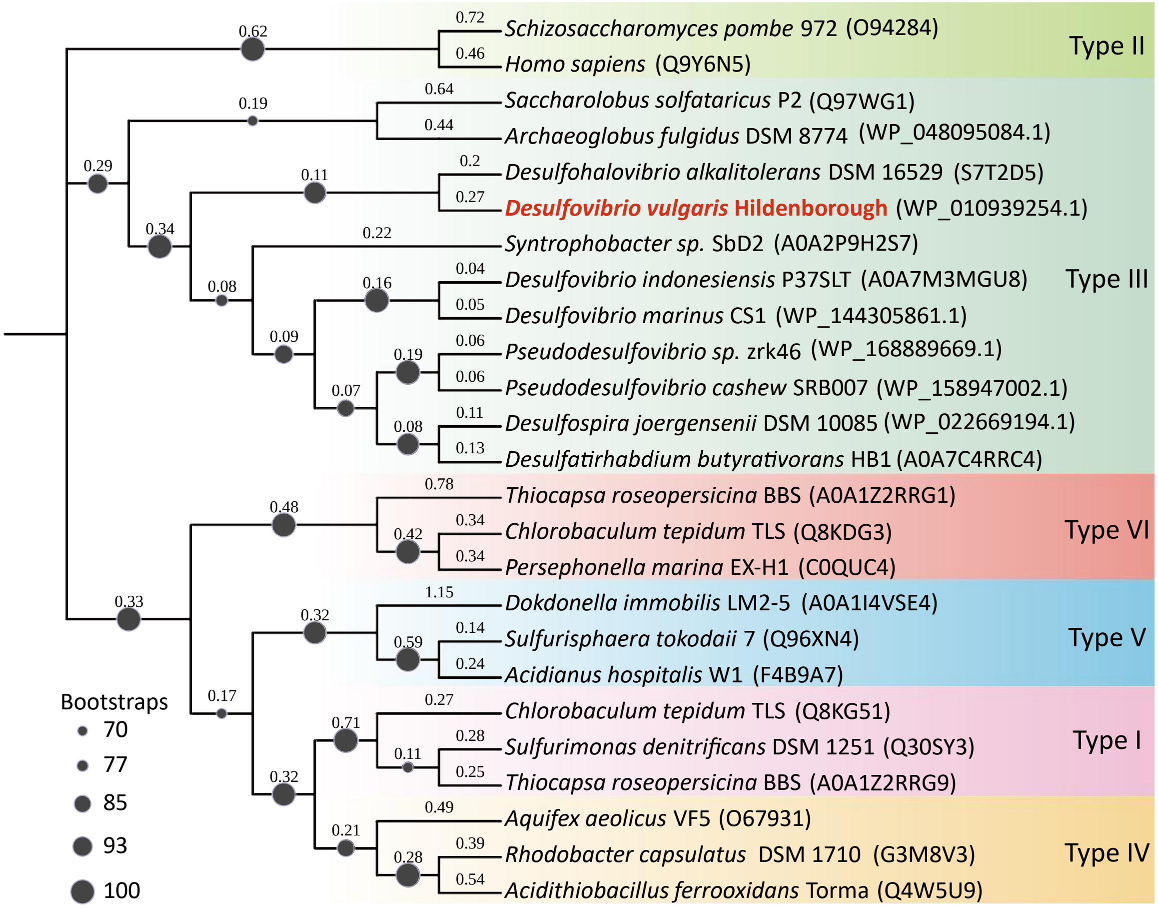

Fig. S7. Phylogeny of *sqr* homologue gene sequences from both SRMs and sulfur-oxidizing bacteria (SOB). Deduced amino acid sequences of the sqr homologue genes are analyzed here, and the phylogenetic tree is inferred and reconstructed under the maximum likelihood criterion using MEGA 7. Bootstrap values (%) >70 are indicated at the base of each node (black nots with different sizes). The numbers along branch represent the tree scale of each branch.

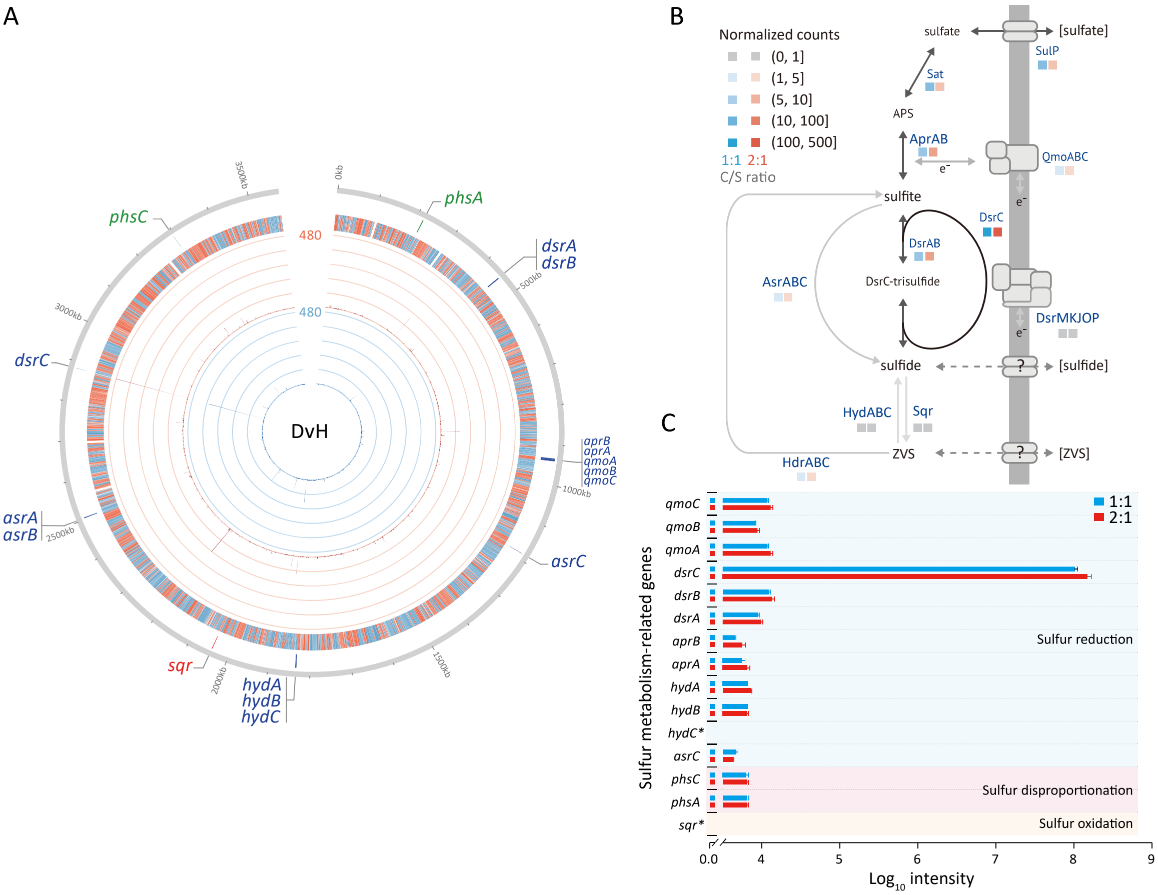

Fig. S8. Transcriptional analyses of DvH under different growth conditions. A, Circos plot showing the transcription levels of all genes for DvH cultures fed with two different molar ratios of lactate to sulfate, i.e., C/S ratios of 1:1 and 2:1. Tracks from inside to outside: track 1 in blue, DvH with the C/S ratio of 1:1; track 2 in red, DvH with the C/S ratio of 2:1; track 3, predicted ORFs in DvH genome (colors: red, forward strand; blue, reverse strand); track 4, predicted sulfur metabolism-related genes (colors: blue, dissimilatory sulfate reduction-related genes; red, sulfur oxidation-related genes; green, sulfur disproportionation-related genes). **B**, Transcription levels of genes encoding the sulfur metabolism-related enzymes in DvH cultures under the two growth conditions. Normalized counts were calculated on the basis of mean change in cycle threshold (ΔCt) compared to the recA. **C**, Translation of key sulfur metabolism-related genes in DvH cultures under the two growth conditions. Protein relative abundances were normalized using RecA as the reference. Enzymes (i.e., Sqr and HydC) with translation levels under the detection limit were marked with asterisks (*). Sat, sulfate adenylyltransferase; Apr, adenosine-5'-phosphosulfate reductase; Dsr, dissimilatory sulfite reductase; DsrMKJOP, transmembrane complex; Asr, anaerobic sulfite reductase; Sqr, sulfide-quinone reductase; Qmo, quinone-interacting membrane bound oxidoreductase; Hdr, heterodisulfide reductase; Hyd, heterotrimeric electron-bifurcating hydrogenase; SulP, Sulfate permease.

Table S1. **Information on genes with a higher transcription level in DvH cultures with the C/S ratio of 2:1 relative to them of DvH cultures with the C/S ratio of 1:1.**

Locus_tag	Start[a]	End	Strand	Length	Annotation	KO assigned	Normalized counts (NC)			P-value
							1:1	2:1	2:1/1:1 ratio	
DVU_RS06585	1466090	1466626	-	537	Bacterioferritin	K03594	4.79	19.43	4.05	0.001
DVU_RS03670	864023	864259	+	237	Hypothetical protein	None	27.94	102.41	3.67	0.006
DVU_RS00100	27468	27635	+	168	Transcriptional regulator	None	9.87	29.60	3.00	0.057
DVU_RS03665	863403	863747	-	345	Hypothetical protein	None	7.89	21.42	2.71	0.026
DVU_RS13930	3071634	3071930	+	297	Hypothetical protein	None	21.76	48.32	2.22	0.011
DVU_RS06695	1495384	1496415	-	1032	OmpA family protein	K03286	8.57	18.80	2.20	0.011
DVU_RS14475	3222373	3222768	+	396	MucR family transcriptional regulator	None	12.68	26.46	2.09	0.000
DVU_RS14535	3236521	3236745	-	225	Rubredoxin	None	8.77	17.90	2.04	0.001
DVU_RS09905	2189295	2189708	-	414	Universal stress protein	None	12.87	24.94	1.94	0.025
DVU_RS06940	1554879	1555124	-	246	Hypothetical protein	None	11.34	21.22	1.87	0.041
DVU_RS01985	455770	456411	+	642	Septal ring lytic transglycosylase RlpA family protein	K03642	11.81	20.48	1.73	0.000
DVU_RS10905	2422628	2422822	+	195	Heavy-metal-associated domain-containing protein	K07213	56.10	96.94	1.73	0.031
DVU_RS14490	3226519	3226902	-	384	MucR family transcriptional regulator	None	17.84	29.33	1.64	0.001
DVU_RS11375	2532470	2532925	-	456	Glycine zipper 2TM domain-containing protein	K06077	22.30	36.03	1.62	0.000
DVU_RS09920	2197893	2198753	-	861	4Fe-4S binding protein	None	109.95	174.79	1.59	0.018
DVU_RS08105	1781209	1781433	-	225	DUF2188 domain-containing protein	None	15.07	22.90	1.52	0.000
DVU_RS04350	1010561	1010887	-	327	ATP synthase F0 subunit C	K02110	20.57	31.18	1.52	0.028
DVU_RS03450	813205	813657	+	453	Hypothetical protein	None	15.56	23.21	1.49	0.016
DVU_RS12420	2765700	2766248	-	549	Hypothetical protein	None	29.77	43.56	1.46	0.002
DVU_RS03785	884382	885779	-	1398	Outer membrane homotrimeric porin	None	16.24	23.31	1.44	0.008
DVU_RS01515	350418	350609	-	192	Ferredoxin	K05337	95.07	136.25	1.43	0.022
DVU_RS14905	3327925	3328311	+	387	Cytochrome c3 family protein	None	34.89	49.94	1.43	0.001
DVU_RS08625	1881750	1882058	-	309	C-type cytochrome	K08738	48.85	64.10	1.31	0.040

Table S1. Information on genes with a higher transcription level in DvH cultures with the C/S ratio of 2:1 relative to them of DvH cultures with the C/S ratio of 1:1. (Continued)

Locus_tag	Start[a]	End	Strand	Length	Annotation	KO assigned	Normalized counts (NC)			P-value
							1:1	2:1	2:1/1:1 ratio	
DVU_RS09040	1980943	1981416	-	474	Purine-binding chemotaxis protein CheW	K03408	18.39	23.82	1.30	0.000
DVU_RS13015	2883462	2883776	+	315	TusE/DsrC/DsvC family sulfur relay protein	K23077	369.83	472.75	1.28	0.058
DVU_RS10470	2314522	2314788	+	267	Hypothetical protein	None	16.39	20.18	1.23	0.068
DVU_RS01970	452427	452660	+	234	Protein DsvD	None	69.03	83.60	1.21	0.037
DVU_RS15420	3452150	3452335	-	186	Ferredoxin family protein	None	270.33	319.14	1.18	0.061
DVU_RS13295	2943651	2944172	+	522	Hypothetical protein	None	17.65	20.30	1.15	0.140
DVU_RS02440	577421	577681	-	261	30S ribosomal protein S15	K02956	21.71	24.70	1.14	0.215
DVU_RS03965	926807	927037	-	231	KH domain-containing protein	K06960	23.36	26.06	1.12	0.020
DVU_RS03950	924560	924904	-	345	50S ribosomal protein L19	K02884	17.99	20.02	1.11	0.196
DVU_RS03970	927124	927360	-	237	30S ribosomal protein S16	K02959	26.86	29.68	1.11	0.060
DVU_RS16690	1016065	1016208	+	144	Hypothetical protein	None	30.09	32.74	1.09	0.094
DVU_RS07410	1650124	1650630	+	507	Ferritin	K02217	21.33	22.48	1.05	0.091
DVU_RS14585	3244295	3244795	+	501	Peptidoglycan-associated lipoprotein Pal	K03640	60.38	61.54	1.02	0.333

Note: a, start and end position of each gene was based on the genome information of *Desulfovibrio vulgaris* Hildenborough (accession: NC_002937.3)

Table S2. Isolated and characterized strains of ZVS-metabolizing microorganisms including ZVS-reducing-microorganisms (S^{0}RMs) and ZVS-disproportionating-microorganisms (S^{0}DMs).

Species of S^{0}RMs	Phylum	Source	Electron donor & Carbon source	References
Desulfuromonas acetoxidans	Proteobacteria	Sea water	Acetate, ethanol, propanol	1
Desulfuromonas acetexigens	Proteobacteria	Freshwater sediment	Acetate	2
Hippea maritima	Proteobacteria	Marine hot vent	Acetate, H_2	3
Geobacter sulfurreducens	Proteobacteria	Freshwater sediment	Acetate	4
Pelobacter carbinolicus	Proteobacteria	Freshwater sediment	Ethanol, H_2	5
Desulfurella acetivorans	Proteobacteria	Hot spring	Acetate	6
Acidianus infernus	Crenarchaeota	Marine hot vent	Glucose, acetate, butyrate, H_2	7
Sulfolobus ambivalens	Crenarchaeota	Solfataric waterhole	CO_2, H_2	8
Pyrodictium occultum	Crenarchaeota	Hot sea floor	CO_2, H_2	9
Pyrobaculum neutrophilum	Crenarchaeota	Hot spring	CO_2, H_2	9
Pyrobaculum maritimus	Crenarchaeota	Hot sea water	CO_2, H_2	9
Stygiolobus azoricus	Crenarchaeota	Solfataric field	CO_2, H_2	10

Species of S^{0}DMs	Phylum	Source	Carbon source	References
Dissulfurimicrobium hydrothermale	Proteobacteria	Hydrothermal pond	Succinate	11
Dissulfurispira thermophila	Nitrospirota	Hot spring	CO_2	12
Dissulfurirhabdus thermomarina	Proteobacteria	Hydrothermal vents	CO_2	13
Dissulfuribacter thermophilus	Proteobacteria	Hydrothermal vents	CO_2	14
Caldimicrobium thiodismutans	Thermodesulfobacteria	Hot spring	CO_2	15
Desulfocapsa sulfoexigens	Proteobacteria	Marine sediment	Acetate	16
Desulfurella amilsii	Proteobacteria	River sediment	Acetate	17
Dethiobacter alkaliphilus	Firmicutes	Soda Lake	Acetate	18
Pantoea agglomerans	Proteobacteria	Marine sediment	Acetate	19
Thermosulfurimonas dismutans	Thermodesulfobacteria	Hydrothermal vents	CO_2	20
Thermosulfuriphilus ammonigenes	Thermodesulfobacteria	Hydrothermal vents	CO_2	21

Table S3. **Gibbs free energy of reactions involving the dissimilatory reduction of sulfate and ZVS.**

Equations	**ΔG°', kJ/mol of**	
	Reaction	**Electron**
$SO_4^{2-} + 2Lactate^- \rightarrow 2Acetate^- + HS^- + 2HCO_3^- + H^+$	-160.67	-20.08
$SO_4^{2-} + 2/3Lactate^- \rightarrow HS^- + 2HCO_3^- + 1/3H^+$	-85.2	-10.65
$SO_4^{2-} + 3/2Lactate^- + 1/2H^+ \rightarrow 3/2Acetate^- + S_0 + 3/2HCO_3^- + H_2O$	-130.725	-21.78
$SO_4^{2-} + 1/2Lactate^- + H^+ \rightarrow S_0 + 3/2HCO_3^- + H_2O$	-74.13	-12.36
$Acetate^- + 4S_0 + 4H_2O \rightarrow 4HS^- + 2HCO_3^- + 5H^+$	-3.29	-6.58
$SO_4^{2-} + 2Lactate^- + 2H^+ \rightarrow 2Acetate^- + H_2S(g) + 2CO_2(g) + 2H_2O$	-175.95	-21.99
$SO_4^{2-} + 2/3Lactate^- + 8/3H^+ \rightarrow H_2S(g) + 2CO_2(g) + 2H_2O$	-100.4	-12.55
$SO_4^{2-} + 3/2Lactate^- + 2H^+ \rightarrow 3/2Acetate^- + S_0 + 2/3CO_2(g) + 5/2H_2O$	-130.93	-21.82
$SO_4^{2-} + 1/2Lactate^- + 5/2H^+ \rightarrow S_0 + 2/3CO_2(g) + 5/2H_2O$	-74.33	-12.39
$Acetate^- + 4S_0 + H^+ + 2H_2O \rightarrow 4H_2S(g) + 2CO_2(g)$	-39.08	-19.54

Table S4. **16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^0MMs (i.e., S^0RMs and S^0DMs) and SRMs.**

No	Type	Location	Coordinates	S^0RB		S^0DB		SRB		Accession	Ref.
				Taxonomy[a]	R.A. (%)[b]	Taxonomy	R.A. (%)	Taxonomy	R.A. (%)		
1	Soil	Antarctica	62.16S, 58.96W	*Geobacter*	6.16E-03	N.A.	N.A.	*Desulforhopalus* *Desulfobacterium* *Desulfobacterium*	5.70E-01	SRR16996395	22
2	Soil	Antarctica	74.76S, 164.01E	*Desulfuromonas*	2.75E-03	N.A.	N.A.	*Desulforhopalus* *Desulfobacterium* *Desulfobulbus*	1.57E+00	SRR16996404	22
3	Soil	Antarctica	62.18S, 58.97W	*Geobacter* *Desulfuromonas*	9.95E-03	N.A.	N.A.	*Desulforhopalus* *Desulfobacterium* *Desulfobacterium*	5.27E-01	SRR16996409	22
4	Soil	Antarctica	72.31S, 170.26E	*Desulfuromonas*	2.33E-02	*Pantoea*	4.89E-03	*Desulforhopalus* *Desulfobacterium* *Desulfobacterium*	8.43E+00	SRR16996416	22
5	Soil	Antarctica	77.21S, 166.44E	*Geobacter* *Desulfuromonas*	7.06E-04	N.A.	N.A.	*Desulforhopalus* *Desulfobacterium* *Desulfobacterium*	2.08E-02	SRR16996428	22
6	Soil	Antarctica	64.89S, 62.87W	*Geobacter*	2.03E-02	N.A.	N.A.	*Desulfosarcina* *Desulfosporosinus*	1.56E-02	SRR17050022	22
7	Soil	Antarctica	68.49S, 78.10E	*Geobacter* *Desulfuromonas*	1.05E-02	N.A.	N.A.	*Desulfosporosinus*	3.28E-02	SRR16979831	22
8	Soil	Petersham, U.S.	42.5 N, 72.19 W	*Geobacter*	2.84E-03	N.A.	N.A.	*Desulfosporosinus*	8.51E-03	c	23
9	Soil	Wheelman, U.S.	39.99N, 105.37 W	*Pelobacter* *Geobacter*	1.13E-02	*Pantoea*	7.99E-02	*Desulfosporosinus*	1.88E-03	c	23
10	Soil	Swaziland	46.63N, 10.37E	*Geobacter*	1.24E-01	N.A.	N.A.	*Desulfosporosinus*	6.10E-03	c	23
11	Soil	Australia	33.47 S, 145.55E	*Geobacter* *Pelobacter*	3.47E-01	N.A.	N.A.	*Desulfobulbus* *Desulfosporosinus*	1.24E-01	c	23
12	Soil	Muztag Ata glacier, China	38.26N, 75.00E	*Geobacter*	4.87E-02	*Pantoea*	1.03E-02	*Desulfosporosinus*	2.80E-02	SRR8156999	24
13	Soil	Barrow Peninsula, US	71.33N, 156.11W	*Geobacter*	8.06E-02	*Desulfocapsa* *Pantoea*	6.69E-02	*Desulfatiglans* *Desulfosporosinus*	5.43E+00	SRR9680643	25
14	Soil	Kirs, Russia	59.23N, 52.23E	*Geobacter* *Desulfuromonas*	1.70E-01	N.A.	N.A.	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	2.56E+00	ERR1779761	26
15	Soil	Al Farafra Desert, Egypt	26.24N, 25.35E	*Geobacter* *Desulfuromonas*	1.00E-01	N.A.	N.A.	*Desulfobulbus* *Desulfuromonas* *Thermodesulfovibrio*	1.59E+00	ERR1779766	26

Table S4. **16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^0MMs (i.e., S^0RMs and S^0DMs) and SRMs. (Continued)**

No	**Type**	**Location**	**Coordinates**	**S^0RB**		**S^0DB**		**SRB**		**Accession**	**Ref.**
				Taxonomy	**R.A. (%)**	**Taxonomy**	**R.A. (%)**	**Taxonomy**	**R.A. (%)**		
16	Soil	Poltava, Ukraine	49.50N, 34.70E	*Geobacter* *Desulfuromonas*	1.44E-01	N.A.	N.A.	*Desulfobulbus* *Thermodesulfovibrio*	3.98E+00	ERR1779774	26
17	Soil	Nalut Province, Libya	30.05N, 10.11E	*Geobacter* *Desulfuromonas*	5.24E-02	N.A.	N.A.	*Desulfobulbus* *Desulfococcus*	2.97E-01	ERR1779777	26
18	Marine sediment	Caspian Sea	39.74 N, 50.48 E	*Geobacter*	8.00E-03	*Desulfocapsa*	6.62E-04	*Desulfobulbus* *Desulfococcus* *Desulfomonile*	6.61E-01	SRR1583209	27
19	Marine sediment	Caspian Sea	39.99 N, 51.50 E	*Geobacter* *Desulfuromonas*	4.37E-02	*Desulfocapsa*	2.95E-04	*Desulfobulbus* *Desulfococcus* *Desulfosarcina* *Desulfomonile*	6.55E-01	SRR1583215	27
20	Marine sediment	Caspian Sea	40.04 N, 51.34 E	*Desulfuromonas*	5.62E-02	*Desulfocapsa*	4.56E-03	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	4.16E-01	SRR1583242	27
21	Marine sediment	Greenland Sea	77.32 N, 15.39 E	*Geobacter* *Desulfuromonas*	3.49E-01	*Desulfosporosinus* *Desulfocapsa*	2.52E-02	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	6.76E+00	SRR7969004	28
22	Marine sediment	French Guiana	5.54 N, 53.17W	*Geobacter* *Desulfuromonas* *Pelobacter*	1.78E+00	*Desulfocapsa*	1.13E-02	*Desulfobulbus* *Desulfobacter* *Desulfococcus*	3.23E+00	SRR027243	29
23	Marine sediment	French Guiana	5.54 N, 52.11W	*Desulfuromonas* *Pelobacter*	1.70E-01	*Desulfocapsa*	1.38E-02	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	3.30E+00	SRR027245	29
24	Marine sediment	Kern River, England	51.87 N, 0.93 E	*Geobacter* *Desulfuromonas* *Pelobacter*	1.06E-01	*Desulfocapsa*	5.62E-02	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	3.21E+00	SRR027362	29
25	Marine sediment	Schimonnik Island, Netherlands	53.49 N, 6.13 E	*Desulfuromonas*	1.01E-01	*Desulfocapsa*	7.17E-02	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	4.11E-01	SRR027371	29
26	Marine sediment	La Parguera Natural Reserve , Puerto Rico	17.87 N, 67.04 W	*Pelobacter*	5.83E-02	*Desulfocapsa*	1.46E-02	*Desulfobulbus* *Desulfococcus*	1.17E-01	SRR027679	29
27	Marine sediment	Peninsula Valdes, Argentina	42.42 S, 64.11 W	*Desulfuromonas* *Pelobacter*	5.75E-02	*Desulfocapsa*	1.44E-02	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	2.97E-01	SRR027686	29

Table S4. **16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^{0}MMs (i.e., S^{0}RMs and S^{0}DMs) and SRMs. (Continued)**

No	Type	Location	Coordinates	S^{0}RB		S^{0}DB		SRB		Accession	Ref.
				Taxonomy	R.A. (%)	Taxonomy	R.A. (%)	Taxonomy	R.A. (%)		
28	Marine sediment	Talcahuano, Chile	36.69 S, 73.07 W	*Desulfuromonas*	1.27E-02	*Desulfocapsa*	4.13E-02	*Desulfobulbus* *Desulfobacter* *Desulfococcus*	2.38E+00	SRR027975	29
29	Marine sediment	Talcahuano, Chile	36.64 S, 73.04 W	*Geobacter*	2.51E-02	*Desulfocapsa*	2.19E-02	*Desulfobulbus* *Desulfococcus* *Desulfobacterium*	1.42E+00	SRR027976	29
30	Marine sediment	Arabian sea	10.10 N, 59.29 E	*Geobacter*	4.76E-02	*Desulfocapsa*	4.04E-03	*Desulfobulbus* *Desulfococcus*	1.62E-01	ERR1779755	26
31	Marine sediment	Arabian sea	10.43 N, 57.46 E	*Geobacter* *Desulfuromonas*	8.36E-02	*Desulfocapsa*	4.19E-03	*Desulfobulbus* *Desulfococcus*	2.93E-01	ERR1779758	26
32	Marine sediment	Gulf of Aden	15.51 N, 44.97 E	*Geobacter* *Desulfuromonas*	6.25E-02	*Desulfocapsa*	4.39E-02	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	1.80E+00	ERR1779761	26
33	Marine sediment	Atlantic Ocean	52.16 S, 14.17 E	*Geobacter* *Desulfuromonas*	3.21E-02	*Desulfocapsa*	3.94E-02	*Desulfatiglans* *Desulforhopalus* *Desulfobulbus*	3.06E-01	S_PRJEB23821	30
34	Marine sediment	Bering Sea	55.64 N, 179.46 E	*Pelobacter*	3.30E-01	*Pantoea*	4.77E-02	*Desulfatiglans* *Desulfobulbus* *Desulfococcus*	3.88E+00	SRR1631774	31
35	Marine sediment	Pacific Ocean	4.88 N, 141.75 W	*Geobacter*	6.91E-03	N.A.	N.A.	*Desulfofrigus*	4.87E-03	SRR12576035	32
36	Marine sediment	Pacific Ocean	13.76 N, 116.45 W	*Geobacter*	8.38E-03	N.A.	N.A.	*Desulfofrigus*	8.38E-03	SRR1257636	32
37	Marine sediment	Forlandsundet	78.59 N, 11.39 E	*Desulfuromonas*	1.23E-01	*Desulfocapsa*	4.28E-01	*Desulforhopalus* *Desulfobulbus* *Desulfococcus*	9.15E+00	SRR4237752	33
38	Marine sediment	Atlantic Ocean	33.48 N, 54.16 W	*Desulfuromonas*	7.13E-03	*Desulfocapsa*	6.19E-02	*Desulfatiglans* *Desulfobulbus*	1.56E+00	SRR6396235	34
39	Marine sediment	Okinawa Trough	30.53 N, 128.00 E	*Geobacter* *Desulfuromonas*	7.25E-02	*Desulfocapsa*	4.86E-03	*Desulfatiglans* *Desulfobulbus* *Thermodesulfovibrio*	3.61E+00	SRR3416391	35
40	Marine sediment	Okinawa Trough	29.84 N, 127.63 E	*Geobacter* *Desulfuromonas*	2.23E-02	*Desulfocapsa*	2.52E-03	*Desulfatiglans* *Desulfobulbus*	3.08E+00	SRR3416505	35

Table S4. 16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^{0}MMs (i.e., S^{0}RMs and S^{0}DMs) and SRMs. (Continued)

No	**Type**	**Location**	**Coordinates**	**S^{0}RB**		**S^{0}DB**		**SRB**		**Accession**	**Ref.**
				Taxonomy	**R.A. (%)**	**Taxonomy**	**R.A. (%)**	**Taxonomy**	**R.A. (%)**		
41	Marine sediment	Indian Ocean	26.94 S, 67.32 E	*Geobacter*	2.19E-03	*Pantoea*	1.83E-03	*Desulfovibrio* *Desulfobulbus*	2.16E+00	SRR5007323	36
42	Marine sediment	Indian Ocean	26.76 S, 67.71 E	*Geobacter*	1.10E-03	*Pantoea*	7.34E-04	*Desulfovibrio*	3.13E-01	SRR5007326	36
43	Marine sediment	South China Sea	16.89 N,112.35 E	*Geobacter*	3.50E-02	*Desulfocapsa*	4.07E-03	*Desulfovibrio* *Desulfococcus* *Desulfatiglans*	6.02E-01	SRR101434571	37
44	Marine sediment	South China Sea	16.97 N, 112.19 E	*Geobacter*	2.46E-02	*Pantoea*	2.00E-03	*Desulfovibrio* *Desulfococcus* *Desulfatiglans*	5.79E-01	SRR101434831	37
45	Marine sediment	North Pacific	47.45 N, 127.76 W	*Desulfuromonas*	5.30E-03	*Pantoea*	2.01E-03	*Desulfatiglans* *Desulfobulbus*	1.03E+00	DRR179137	38
46	Marine sediment	Gulf of Mexico	28.09 N, 89.02 W	*Desulfuromonas*	7.83E-03	*Pantoea*	7.57E-03	*Desulfatiglans*	1.43E+00	DRR179159	38
47	Marine sediment	North Pacific	33.22 N, 136.72 E	*Desulfuromonas*	5.14E-03	*Pantoea*	8.53E-03	*Desulfatiglans* *Desulfosporosinus*	5.09E-01	DRR179195	38
48	Marine sediment	Baltic Sea	58.62 N, 18.25 E	*Desulfuromonas*	1.61E-02	*Pantoea*	1.20E-02	*Desulfatiglans* *Desulfococcus*	5.48E-01	DRR179296	38
49	Marine sediment	Baltic Sea	55.46 N, 15.47 E	*Desulfuromonas*	3.44E-03	*Pantoea*	9.06E-02	*Desulfatiglans*	4.78E-01	DRR179305	38
50	Marine sediment	Bay of Bengal	14.00 N, 84.82 E	*Desulfuromonas*	5.26E-03	*Pantoea*	5.26E-03	*Desulfatiglans* *Desulfobulbus* *Desulfomonile*	1.09E+00	DRR179324	38
51	Marine sediment	North Atlantic ocean	33.48 N, 54.16 W	*Desulfuromonas*	3.07E-03	N.A.	N.A.	*Desulfatiglans* *Desulfobulbus*	1.90E-01	DRR179368	38
52	Marine sediment	Pacific Ocean	9.11 S, 80.58 W	*Desulfuromonas*	6.72E-03	*Desulfocapsa*	2.94E-03	*Desulfatiglans* *Desulfobulbus*	3.77E+00	DRR181262	38
53	Hot spring sediment	Tibet, China	28.52 N, 91.88 E	*Geobacter* *Sulfolobus*	3.06E-02	*Caldimicrobium* *Desulfurella*	2.79E-02	*Thermodesulfovibrio* *Desulfosporosinus*	1.19E+00	SRR5313425	39
54	Hot spring sediment	Tibet, China	29.62 N, 85.74 E	*Geobacter* *Sulfolobus*	2.92E-02	*Caldimicrobium* *Desulfurella*	1.48E-02	*Thermodesulfovibrio* *Desulfovibrio* *Desulfosporosinus*	3.82E-01	SRR5313441	39

Table S4. 16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^0MMs (i.e., S^0RMs and S^0DMs) and SRMs. (Continued)

No	Type	Location	Coordinates	S^0RB		S^0DB		SRB		Accession	Ref.
				Taxonomy	R.A. (%)	Taxonomy	R.A. (%)	Taxonomy	R.A. (%)		
55	Hot spring sediment	Tibet, China	31.61 N, 91.83 E	*Geobacter* *Sulfolobus*	3.15E-02	*Caldimicrobium* *Dethiobacter*	8.27E-02	*Thermodesulfovibrio* *Desulfomicrobium* *Desulfovibrio*	1.62E-01	SRR5313461	39
56	Hot spring sediment	Tibet, China	28.25 N, 91.81 E	*Geobacter* *Sulfolobus*	1.93E-01	*Caldimicrobium* *Dethiobacter*	3.63E-02	*Desulfotomaculum* *Thermodesulfovibrio* *Desulfomicrobium*	1.01E+00	SRR5313524	39
57	Hot spring sediment	Yunnan, China	24.95 N, 98.44 E	*Geobacter* *Sulfolobus*	7.76E-01	*Caldimicrobium* *Desulfurella*	5.65E-01	*Thermodesulfovibrio* *Thermodesulfobacterium* *Desulfomicrobium*	6.18E-01	CRR144043	40
58	Hot spring sediment	Iceland	64.68N, 21.40W	*Geobacter*	5.52E-03	*Caldimicrobium* *Dethiobacter*	2.79E-03	*Desulfobulbus* *Desulfovibrio* *Thermodesulfovibrio*	1.58E-03	SRR11066918	41
59	Hot spring sediment	Iceland	64.13N, 20.30 W	*Geobacter*	1.59E-03	*Caldimicrobium* *Dethiobacter*	1.05E-02	*Desulfobulbus* *Desulfovibrio* *Thermodesulfovibrio*	8.73E-03	SRR11066925	41
60	Hot spring sediment	New Zealand	38.05 S, 176.36 E	*Geobacter*	3.36E-01	*Desulfurella*	1.35E-02	*Thermodesulfovibrio* *Thermodesulfobium*	1.62E-01	SRR129639161	42
61	AMD[d] sediment	Shaoguan, China	25.04 N, 113.66 E	*Geobacter* *Desulfuromonas*	9.31E-03	*Dethiobacter*	3.52E-02	*Desulfomonile* *Desulfosporosinus* *Desulfotomaculum*	3.57E-01	SRR8455939	43
62	AMD sediment	Guizhou, China	25.80N, 107.61E	*Geobacter* *Desulfuromonas*	2.85E+00	*Desulfocapsa* *Dethiobacter*	1.28E-01	*Desulfomonile* *Thermodesulfobium* *Desulfovibrio* *Desulfobulbus*	3.92E+00	SRR12726967	44
63	AMD sediment	Shaoguan, China	24.55 N, 113.74 E	*Geobacter*	2.82E-03	*Desulfocapsa*	2.04E-03	*Desulfovibrio* *Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	5.18E-01	SRR12737887	44

Table S4. 16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^{0}MMs (i.e., S^{0}RMs and S^{0}DMs) and SRMs. (Continued)

No	Type	Location	Coordinates	S^{0}RB		S^{0}DB		SRB		Accession	Ref.
				Taxonomy	R.A. (%)	Taxonomy	R.A. (%)	Taxonomy	R.A. (%)		
64	AMD sediment	Guangxi, China	25.14N, 107.50E	*Geobacter*	4.60E-02	*Dethiobacter* *Pantoea*	1.07E-02	*Desulfovibrio* *Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	9.42E-02	SRR12744846	44
65	AMD sediment	Shangrao, Jiangxi, China	29.00 N, 117.72 E	*Geobacter*	3.86E-03	*Dethiobacter*	1.94E-03	*Desulfosporosinus* *Desulfotomaculum*	1.23E-02	SRR12745062	44
66	AMD sediment	Fankou, Guangdong, China	25.04 N, 113.66 E	*Geobacter*	1.42E-03	N.A.	N.A.	*Desulfovibrio* *Desulfomonile*	5.68E-02	SRR12768936	44
67	AMD sediment	Huangshaping, Hunan, China	25.67N, 112.70E	*Geobacter*	4.71E-03	*Dethiobacter* *Pantoea*	4.68E-03	*Desulfotomaculum* *Desulfosporosinus*	1.15E-02	SRR12769161	44
68	AMD sediment	Jiuan, Guizhou, China	26.52 N, 106.57 E	*Geobacter* *Desulfuromonas*	3.87E-03	*Dethiobacter* *Pantoea*	3.97E-03	*Desulfotomaculum* *Desulfosporosinus*	8.43E-03	SRR12769163	44
69	AMD sediment	Longli, Guizhou, China	26.38 N, 106.97 E	*Geobacter*	2.00E-01	*Desulfocapsa* *Pantoea*	5.67E-03	*Desulfovibrio* *Desulfobulbus*	8.92E-02	SRR12769170	44
70	AMD sediment	Longshenao, Guangxi, China	24.83 N, 107.56 E	*Geobacter*	3.23E-02	*Desulfocapsa*	8.32E-04	*Desulfovibrio* *Desulfobulbus*	3.90E-02	SRR12769176	44
71	AMD sediment	Manshan, Anhui, China	31.67 N, 118.62 E	*Geobacter*	1.56E-02	*Desulfocapsa*	9.94E-04	*Desulfovibrio* *Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	2.62E-02	SRR12808556	44
72	AMD sediment	Shuikoushan, Hunan, China	26.53 N, 112.60 E	*Geobacter* *Desulfuromonas*	7.31E-01	*Desulfocapsa* *Desulfurella* *Dethiobacter* *Pantoea*	5.08E-02	*Desulfotomaculum* *Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	7.48E-01	SRR12808561	44
73	AMD sediment	Tongling, Anhui, China	30.94 N, 117.98 E	*Geobacter*	1.28E-02	*Desulfocapsa*	4.66E-03	*Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	2.23E-02	SRR12808565	44
74	AMD sediment	Wuhu, Anhui, China	31.08 N, 118.25 E	*Geobacter*	3.33E-03	*Desulfocapsa*	1.12E-03	*Desulfovibrio* *Desulfobulbus*	4.13E-02	SRR12816447	44
75	AMD sediment	Wuyi, Guangxi, China	25.14 N, 107.50 E	*Geobacter*	6.32E-01	*Desulfocapsa* *Dethiobacter* *Pantoea*	4.01E-02	*Desulfovibrio* *Desulfobulbus* *Desulfomonile*	9.75E-01	SRR12816452	44

Table S4. **16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^0MMs (i.e., S^0RMs and S^0DMs) and SRMs. (Continued)**

No	Type	Location	Coordinates	S^0RB		S^0DB		SRB		Accession	Ref.
				Taxonomy	R.A. (%)	Taxonomy	R.A. (%)	Taxonomy	R.A. (%)		
76	AMD sediment	Yunfu, Guangdong, China	22.96 N, 112.01E	*Geobacter*	4.77E-03	*Dethiobacter*	3.39E-03	*Desulfotomaculum* *Desulfomonile* *Desulfosporosinus*	1.24E-02	SRR12816507	44
77	AMD sediment	Yongping, Jiangxi, China	28.19 N, 117.76 E	*Geobacter*	4.43E-03	*Dethiobacter* *Pantoea*	4.40E-03	*Desulfotomaculum* *Desulfosporosinus*	9.87E-03	SRR12816510	44
78	AMD sediment	Zhijin, Guizhou, China	26.60 N, 105.72 E	*Geobacter*	1.35E-02	*Pantoea* *Desulfurella*	4.94E-03	*Desulfotomaculum* *Desulfosporosinus*	2.81E-02	SRR12834021	44
79	AMD sediment	YInshan, Jiangxi, China	28.97N, 117.60 E	*Geobacter*	6.21E-03	*Dethiobacter* *Pantoea*	6.31E-03	*Desulfotomaculum* *Desulfosporosinus*	1.83E-02	SRR12834185	44
80	AMD sediment	Rio Tinto, Spain	37.59N, 6.55W	*Geobacter*	1.87E-02	N.A.	N.A.	*Desulfobulbus* *Desulfosporosinus*	1.11E-02	QFIRB012AB	45
81	AMD sediment	Rio Tinto, Spain	37.31N, 6.82W	*Geobacter* *Desulfuromonas*	3.51E+00	N.A.	N.A.	*Desulfotomaculum* *Desulfobulbus* *Desulfosporosinus*	1.29E+01	QFIRB010AC	45
82	Freshwater sediment	Enshi, Hubei, China	31.04 N, 110.4 E	*Geobacter* *Desulfuromonas*	1.18E-01	*Desulfocapsa*	1.06E-03	*Desulfobacterium* *Desulfosporosinus* *Desulfovibrio*	1.78E-01	SRR3944723	46
83	Freshwater sediment	Changshou, Jiangsu, China	31.77 N, 120.96 E	*Geobacter* *Desulfuromonas*	1.05E-01	*Desulfocapsa*	1.12E-03	*Desulfobulbus* *Desulfomonile*	1.09E-01	SRR3944727	46
84	Freshwater sediment	Yibing, Sichuan, China	28.8 N, 104.42 E	*Geobacter* *Desulfuromonas*	2.38E-01	*Desulfocapsa*	1.27E-03	*Desulfobulbus* *Desulfobacter* *Desulfomonile* *Desulfosporosinus*	2.45E-01	SRR3944737	46
85	Freshwater sediment	Guangan, Sichuan	30.35 N, 106.28 E	*Geobacter* *Desulfuromonas*	3.97E-01	*Desulfocapsa*	1.48E-03	*Desulfovibrio* *Desulfobulbus* *Desulfobacterium*	4.69E-01	SRR3944744	46
86	Freshwater sediment	Beipei, Chongqing	29.81 N, 106.46 E	*Geobacter* *Desulfuromonas*	3.51E-01	*Desulfocapsa*	1.06E-03	*Desulfobulbus* *Desulfomonile*	2.70E-01	SRR3944753	46
87	Freshwater sediment	Panzihua, Sichuan	26.57 N, 101.7 E	*Geobacter* *Desulfuromonas*	7.55E-01	*Desulfocapsa*	2.75E-03	*Desulfobulbus* *Desulfovibrio*	2.91E-01	SRR3944771	46
88	Freshwater sediment	Wushen, Chongqing	29.33 N, 107.76 E	*Geobacter* *Desulfuromonas*	4.05E-01	*Desulfocapsa*	3.35E-03	*Desulfobulbus* *Desulfovibrio*	1.02E-01	SRR3944777	46

Table S4. **16S rRNA gene amplicon sequencing-based metadata of global marine/terrestrial sites with presence of S^0MMs (i.e., S^0RMs and S^0DMs) and SRMs. (Continued)**

No	Type	Location	Coordinates	S^0RB		S^0RB		SRB		Accession	Ref.
				Taxonomy	R.A. (%)	Taxonomy	R.A. (%)	Taxonomy	R.A. (%)		
89	Freshwater sediment	Zhengjiang, Jiangsu	32.18 N, 119.66 E	*Geobacter* *Desulfuromonas*	1.37E-01	*Desulfocapsa* *Pantoea*	4.13E-01	*Desulfobulbus* *Desulfomonile*	1.13E-01	SRR3944998	46
90	Freshwater sediment	Yichang, Hubei	30.77 N, 111.31 E	*Geobacter* *Desulfuromonas*	9.66E-02	*Desulfocapsa*	4.90E-03	*Desulfobacterium* *Desulfomonile* *Desulfobacterium*	3.00E-01	SRR3944785	46
91	Freshwater sediment	Dongtinghu, Hunan,	29.42 N, 113.13 E	*Geobacter* *Desulfuromonas*	2.72E-01	*Pantoea*	7.06E-03	*Desulfobulbus* *Desulfomonile* *Desulfobacterium*	1.46E-01	SRR3944798	46
92	Freshwater sediment	Yiyang, Hunan	29.07 N, 112.29 E	*Geobacter* *Desulfuromonas*	1.33E-01	*Desulfocapsa*	8.85E-03	*Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	3.40E-01	SRR3944806	46
93	Freshwater sediment	Changde, Hunan	28.91 N, 112.06 E	*Geobacter* *Desulfuromonas*	1.71E-01	*Desulfocapsa*	1.11E-02	*Desulfobulbus* *Desulfomonile* *Desulfosporosinus*	2.10E-01	SRR3944815	46
94	Hydrothermal vent sediment	Atlantic Ocean	37.84 N, 31.51 W	*Hippea* *Desulfuromonas*	7.81E-02	*Desulfocapsa*	2.50E-02	*Desulfovibrio* *Desulfobulbus*	7.43E-02	ERR10783031	47
95	Hydrothermal vent sediment	Atlantic Ocean	37.81 N, 31.58 W	*Geobacter*	1.75E-02	*Dissulfuribacter*	8.62E-02	*Desulfobulbus*	1.75E-02	ERR9954321	47
96	Hydrothermal vent sediment	Pacific Ocean, Dorado Outcrop	9.08 N, 87.10 W	*Geobacter* *Desulfuromonas* *Pelobacter*	8.47E-02	*Dethiobacter*	4.69E-05	*Desulfovibrio* *Desulfobulbus* *Desulfobacter* *Thermodesulfovibrio*	8.65E-02	SRR6715662	48
97	Hydrothermal vent sediment	Guaymas Basin, Mexico	27.26 N, 111.50 W	*Geobacter* *Desulfuromonas*	1.32E-01	*Desulfocapsa*	5.34E-03	*Desulfobulbus* *Desulfobacterium*	1.15E+00	SRR11568399	49
98	Hydrothermal vent sediment	Guaymas Basin, Mexico	27.35 N, 111.28 W	*Geobacter* *Desulfuromonas*	7.40E-02	*Desulfocapsa*	5.23E-01	*Desulfobulbus* *Desulfococcus* *Desulfosarcina*	3.20E+00	SRR19201761	50
99	Hydrothermal vent sediment	Pacific Ocean	20.05 S, 176.13 W	*Hippea*	1.35E-01	*Desulfocapsa*	4.58E-02	*Desulfobulbus* *Thermodesulfatator*	1.26E+01	SRR027260	51
100	Hydrothermal vent sediment	Atlantic Ocean	38.23 N, 26.63 W	*Desulfuromonas*	2.93E-02	*Desulfocapsa* *Dissulfuribacter*	1.04E-01	*Desulfobacter*	1.17E02	SRR027592	51

Note: a, major genera of S^0RMs, S^0DMs, and SRMs were provided based on the taxonomy information of each sample. The following SRMs were included to calculate the relative abundance of SRMs: *Desulfotomaculum, Desulfovibrio, Desulfobulbus, Desulfobacter, Desulfobacterium, Desulfococcus, Desulfosarcina, Thermodesulfovibrio, Thermodesulfobacterium, Archaeoglobus, Thermodesulfatator, Desulfosporomusa, Desulfohalobium, Desulfocaldus, Desulfomicrobium, Desulfonatronovibrio, Desulfonatronum, Desulfomonile, Desulfarculus, Desulfosporosinus, Thermodesulfobium, Thermocladium*. See Table S2 for the list of S^0RMs and S^0DMs.

b, relative abundance (R.A.) of S^0RMs, S^0DMs, and SRMs were calculated by using following equation: Relative abundance (%)=$I_{si}/\Sigma N_{si} \times 100$, where Isi was the total sequencing reads of S^0RMs, S^0DMs, and SRMs, and ΣN_{si} was the total sequencing reads of the sample.

c, sequencing data for sample 8-11 were provided on the following website: https://figshare.com/s/82a2d3f5d38ace925492

d, Acid mine drainage

Table S5. Metagenome sequencing-based metadata of global marine/terrestrial sites with the presence of both S^0RMs and SRMs.

No	Type	Location	Coordinates	*psrA/dsrC*[a]	Accession	Reference
1	Marine sediment	Atlantic Ocean	30.34S, 7.81W	1.63E-03	ERR3363723	52
2	Marine sediment	Atlantic Ocean	34.79S, 18.96W	1.17E-02	ERR3363725	52
3	Marine sediment	Atlantic Ocean	32.53S, 13.55W	1.81E-03	ERR3363726	52
4	Marine sediment	Pacific Ocean	39.8S, 139.8W	3.94E-03	SRR2605792	53
5	Marine sediment	Pacific Ocean	39.8S, 139.8W	4.14E-03	SRR2605793	53
6	Marine sediment	Pacific Ocean	66.4S, 140.5W	1.59E-03	SRR5486138	54
7	Marine sediment	Pacific Ocean	66.4S, 140.5W	1.70E-03	SRR5486139	54
8	Marine sediment	Ross Sea	75.20 S, 176.59 W	1.71E-03	SRR10156264	55
9	Marine sediment	Ross Sea	72.46 S, 104.36 W	3.41E-03	SRR10156265	55
10	Marine sediment	Pacific Ocean	71.45 S, 102.16 W	2.07E-03	SRR10156269	55
11	Marine sediment	Pacific Ocean	70.48 S, 95.20 W	2.84E-03	SRR10156270	55
12	Marine sediment	Ross Sea	75.50 S, 166.30 W	3.13E-03	SRR10156272	55
13	Marine sediment	Philippine Sea	9.86 N, 138.66 E	1.50E-03	SRR7467837	56
14	Marine sediment	Philippine Sea	9.65 N, 138.82 E	1.69E-03	SRR7467840	56

a, the ratio of *prsA*/*dsrC* represent the ratio between S^0RMs and SRMs, where the reads of *psrA* and *dsrC* was employed to represent abundance of S^0RMs and SRMs, respectively. *psrA*: polysulfide reductase subunit A; *dsrC*: dissimilatory sulfite reductase subunit C.

Table S6. Primers for qPCR amplification of target genes.

Target gene or primer name	Forward primer	Reverse primer	Length	Reference
recA	GCCCTGTTCGACATCCTCTA	GGAGTCATGCCAAGGTGTTC	222	57
dsrC	GCTGAAGTCACTTACAAGGGC	CCGGTGTTCTTCGAGAGGAT	218	58
Geo196F/535R	GAATATGCTCCTGATTC	TAAATCCGAACAACGCTT	340	59
DSV691F/826R	CCGTAGATATCTGGAGGAACATCAG	ACATCTAGCATCCATCGTTTACAGC	136	60
sqr	ACGACTACGACTGGCTTGTG	GCAGCATCTTCTTGCGAAGG	141	This study

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