Supplementary information for 1 2 Metagenomic and metatranscriptomic insights into sulfate-reducing bacteria in 3 a revegetated acidic mine wasteland 4 5 Jin-tian Li^{1,2,†}, Pu Jia^{1,†}, Xiao-juan Wang¹, Shu-ning Ou¹, Tao-tao Yang², Shi-wei 6 Feng¹, Jing-li Lu¹, Zhou Fang¹, Jun Liu², Bin Liao², Wen-sheng Shu¹, & Jie-Liang 7 Liang^{1,*} 8 9 ¹Institute of Ecological Science, Guangzhou Key Laboratory of Subtropical 10 Biodiversity and Biomonitoring, Guangdong Provincial Key Laboratory of 11 Biotechnology for Plant Development, School of Life Sciences, South China Normal 12 University, Guangzhou 510631, PR China 13 ²School of Life Sciences, Sun Yat-sen University, Guangzhou 510275, PR China 14 15 16 [†]These authors contributed equally to this work. 17 18 19 *Corresponding author: 20 School of Life Sciences, South China Normal University, Guangzhou 510631, PR 21 China 22 E-mail: Jie-Liang Liang (liangi@m.scnu.edu.cn) 23 Tel.: +86 20 85211850; Fax: +86 20 85211850 24

S1





Supplementary figure 1. Phylogenic analysis of dissimilatory sulfite reductases DsrAB. Concatenated DsrAB protein sequences identified in this study are marked in bold red. Assignment of oxidative/reductive, bacterial/archaeal type DsrAB was according to previous studies^{1, 2}. Bootstrap values were based on 100 replicates, and only bootstrap values higher than 70% are shown with black circles. Tree scale bar = 0.1.



Supplementary figure 2. Phylogenic analysis of the genomes from Acidobacteria 35 phylum. The maximum-likelihood phylogenetic tree was constructed based on a 36 concatenated dataset of 400 universally conserved marker proteins using 37 PhyloPhlAn. Subdivisions are indicated to the right of the tree. The 12 38 metagenome-assembled genomes (MAGs) harboring sequences of dsrAB genes 39 reported in this study are marked in bold red. The 7 MAGs previously reported to 40 have a dissimilatory sulfur metabolism potential are marked in brown. Bootstrap 41 values were based on 100 replicates, and percentages higher than 70% are shown 42 43 with black circles. The MAG (De.bin1) from Deltaproteobacteria was used as an outgroup. Tree scale bar = 1. 44



Supplementary figure 3. Phylogenic analysis of the genomes from *Syntrophobacteraceae* family. The maximum-likelihood phylogenetic tree was constructed using PhyloPhlAn. The *dsrAB*-containing MAG reported in this study (i.e. De.bin4) is marked in bold red. The four reference genomes of the two closest genera to the MAG are marked in brown. The average amino acid identity (AAI) values between the 5 closest genomes are shown in the inset. Bootstrap values were based on 100 replicates, and percentages higher than 70% are shown with black circles. Two genomes (De.bin1 and *Desulfococcus multivorans* DSM 2059) from *Deltaproteobacteria* were used as the outgroup. Tree scale bar = 0.1.

		1	10 20	30	40	50	60	7 <u>0</u>	8 Q
Ac.bin6		MAEVTVES	IAEEMFQYVSEC	AGKKNLKAGD	LTKFAIGKHG	EETCTKDMCK	QAIRQLIDSERCIN	SYLGGSYIQL	PPAPGSEAI
Ac.bin4		MAEVTVES	IAEEMFQYVSEC	AGKKNLKAGD	LTKFAIGKHG	EETCTKDMCK	QAIRQLIDSERCIY	SYL <mark>G</mark> GSYIQL	PPAP <mark>G</mark> SEAI
Ac.bin9		MAEVTVES	IAEEMFQYVSEC	AGKKNLKAGD	LTKFAIGKHG	EETCTKDMCK	QAIRQLIDSERCIY	'SYL <mark>G</mark> GSYIQL	PPAP <mark>G</mark> SEAI
Ac.bin2		MSETAAVPIET	LADEMYQLVAEC	EGKKNLKAGD	LTKAMIAKHG	EAACSKDDCK	KAIRILIDSGRCIY	SYL <mark>G</mark> GSYIQL	PPKE <mark>G</mark> SQQAG
Ac.bin10		MSETAAVPIET	LADEMYQLVAEC	EGKKNLKAGD	LTKAMIAKHG	EAVCSKDDCK	KAIRILIDSGRCIY	SYL <mark>G</mark> GSYIQL	PPKE <mark>G</mark> SQQAG
Ac.bin1		MSETTAVSIET	IAEEMYALVAEC	AGKKNLKPGD	LVKAVIAKHG	EAACSKDDCK	KAIRILIESGRCIY	SYL <mark>G</mark> GSYIQL	PPKE <mark>P</mark> IG
Ac.bin3		MSETTAVSIES	IADEMYALVAEC	AGKKNLKPGD	LIKAVTAKHG	EAACSKDDCK	KAIRILIESGRCIY	SYL <mark>G</mark> GSYIQL	PPKE <mark>P</mark> IG
Ac.bin8		MSETTSVSIET	LAEEMYQLVAEC	EGKKNLKAGD	LIKAMIAKHG	ETACSKEDCK	KAIRILIDSSRCIY	′SYL <mark>G</mark> GSYIQL	PPKQ <mark>G</mark> SQQGA
Ac.bin7		MSDTTAVPVET	LAEEMYQLIAEC	EGKKNLKAGD	LAKAMIAKHG	EAACTKDDCK	KAIRILIDSGRCIY	′SYL <mark>G</mark> GSYIQL	PPKK <mark>G</mark>
Ac.bin11		MSDTTAVPVET	LAEEMYQLIAEC	EGKKNLKAGD	LHKAMIAKHG	EAACTKDDCK	KAIRILIDSGRCIY	'SYL <mark>G</mark> GSYIQL	PPKK <mark>G</mark>
Ac.bin5		MSEATAVPVET	LAEEMYQLVSEC	AGKKNLKAGD	LTKAIIAKHG	EQACGRDECK	KAIRLLIDSGRCIY	′SYL <mark>G</mark> GSYIQL	PPKE <mark>G</mark> SEQAG
GCF_900290245.1		MTETAAVSVET	LAEEMYQLVAEC	AGKKNLKAVD	LTKEMIARHG	DAACGKDDCK	KAIRILIDSGRCIY	'SYL <mark>G</mark> GSYIQL	PSKE <mark>G</mark> TE
GCF_900290345.1		MSEIAVET	LAEEMYQLIAEC	AGKKNLKATD	LTKAMIAKHG	DGACDKDDCK	KAIRVLIDSGRCVY	'SYL <mark>G</mark> GSYIQL	PPKE <mark>G</mark> AAS
GCF_900290315.1		MTITTEA	LADEMYALVSQY	AGKRNLKAGD	LTKEMIARHG	DSACSKDDCK	HAIRTLMDSGRCVY	'SYL <mark>G</mark> GSYIVL	PPKE <mark>G</mark> TLPGA
GCF_900290325.1		MPVTTEA	LADEMYALISQY	AGKRNLKAGD	LTKEMIARHG	EAAT.KDDCK	LAIRALIESGRCVY	'SYL <mark>G</mark> GSYIQL	PPKE <mark>G</mark> AIPG
GCF_900290305.1	M	EVPIATVPIET	LADEMYAMVAEC	AGKRNLKAGD	LTKAMIARHG	EANCGKDECR	QAIRILIDGGRCIY	SYL <mark>G</mark> GSYIQL	PQAEEPQ
GCF_900290255.1		MTDASPLRVEI	VADDMFALVKEC	TGKRKLKAGD	LTKAMIAKHG	EPVCDKETCR	KAIRMLIDSGRCI	TYL <mark>G</mark> GSYIEL	PAPPEDAQQL
De.bin3		MDDAEA	KALIVETLKSKT	N.KSKFYLKD	FYAFLPD	MKKMAVS	KLVNTMVAEGTLEY	WSSGSTTMIG	LKGA <mark>G</mark> KQHATEEGE
De.bin1		MDEAQA	RQHIVDTLKSKT	N.KSKFYLKD	FYAFLPD	MKKMEVG	KLVNKMVAEGTLEY	WSSGSTTMIG	LKGAGKQHATEEGE
De.bin2		MPSE	KEQVLEFLTGKT	G.KSKFYFSD	FCKIFPD	KKQREVK	KILTELVNEGKLEE	WSSGSTTMYG	MIGAGKQKAEEE
De.bin4		MSQEA	KDKIIEWVK.Q	QKKTKHYFND	LCKAVPD	MKMLQAK	KVINELVNEGKLK	WSSGSTTMYM	LPSEGDVEKEEKGMNA
Q46582.1		MEEA	KQKVVDFLNSKS	GSKSKFYFND	FTDLFPD	MKQREVK	KILTALVNDEVLE)	WSSGSTTMYG	LKGAGKQAAAEHED
AAC96109.1	MKIPAQVISIIYE	LERVGLSVEEL	KKAIIEFASN	SKKIRFYFKD	MEKAVQEKI.	. PIAKAREIK	KAASELVNEGILI	FSIGSIIMYG	LKERCASDEPQQ
AAC/8311.1		. MAEEINKEEL	KQKVIEYLQ	. KKPWQVRD	LAKILKVK	KKELD	KIVQELINEGKAA		IPEKLKEMEEKRSGI.
AAB1/215.1	• • • • • • • • • • • • • •	MADYTEED	KUKVLAHVS	· · KKIWKIPE	LAKILKMD	KKVVK	K T VIQ DIL TIN EIG VIAG I	WSS <mark>G</mark> STIYVA	IKEILEELEKKRAEG.
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- 52 Supplementary figure 4. Sequence alignment of DsrD proteins identified in this study with reference sequences. Positions of conserved,
- 53 hydrophobic residues in the DsrD family are marked with asterisks³. Highly conserved residues of the same type are highlighted in red
- 54 background.

	1	10	20	30	40 5	0	60	70	80	90
Ac.bin1		EIAERWLEKTI	ASYPAKVOPE	IAAEODPFRNP	VGNTLRRSLATI	VHESLG		DELIRIRA	VODETPRE	ALRELEHLRSAAA
Ac.bin3		EIAERWLKRTI	ASYPAKVOPE	MAAEPDPFRNP	VGNTLRRSLATI	VRESLG	MDPOALAVAL	DLTRTRA	VODETPRE	ALRELEDIRAAAA
Ac.bin6	MPSED	SIVDAWFLKSI	ETYPPAVRD	LTRTTDOFRNP	LAENLROSLETI	VHOVAD	MNPEAVNKAT	DGIVBLRA	VOECSPSE	AVSFAARLDEVIR
Ac.bin4	MPSFD	SIVDAWFLKSI	EIYPPAVRDI	LIRTTDOFRNP	LAFNLROSLETI	VHOVAD	MNPEAVNKAI	DGIVRLRA	VOECSPSE	AVSFAARLDEVIR
Ac bin9	MPSED	SIVDAWFLKSI	ETYPPAVRD	LIBTTDOFRNP	LAFNLROSLETI	VHOVAD F	MNPEAVNKAT	DGTVRLRA	VOECSPSE	AVSFAARLDEVIR
Ac.bin12		TIAELWMERTI	RSYPVETLSE	LGGEODPFRNP	VGOTLRKSLEVI	AREVIG	MNKDRMMEAT	DALVEMRA	VODESPAC	AVREVETLRAATR
Ac.bin8	MSAEE	TIVELWMERTI	RSYPVETLSE	LGGEODPFRNP	VGÕTLRKSLEVI	AREVIG	MNKDRMMEAT	DALVEMRA	VODESPAC	AVREVETLRAATR
Ac.bin11	MSPAMSTEE	AVVERWVELTI	NSYPAETLSE	LSGEODAFRNP	VGOTLEKSLAAI	AHEVIG	MNKERMLEAT	DALVEMBA	VONESPAC	AVREVEALBAATB
Ac.bin7	MSPVVSPVMSTEE	AVVARWIEOTI	NSYPAETLCE	LSGEODAFRNP	VGOTLRKSLAVI	AHEVLG	MNKORMLEAT	DALVRMRA	VONFTPSE	AVREVEALRAATR
Ac.bin2	MSVEA	VIVERWVDRAI	KSYPSEMHSE	LGGEKDPFRNP	VGNTERENLAAI	VHELLG	MDKEKTAGAT	DGLVRLRA	VONETPGE	ALHEVEDLEPVIG
Ac.bin5	MTGASIGDAVPGTSOIE	AIAERWVSFSN	INSWPGAGRPI	LSTEKDPFRNP	VGSTLRSNLYII	AHEVLG.	MOEAPVAAAI	DAVIHLRA	VODLSPSE	AVREVEDLEVAID
GCF 900290255.1		EILETWIGTL	DSHSOMSASI	LAPKPDPFRNP	VGYAIRTSMGEI	WKOLKGI	MDPOAVDSAI	DVVLRTRA	VODLSVTE	AVGEVVBLBPILBOLS
GCF_900290225.1	MOTGRIAETDWLRLGNAMSSRD	PILEOWIAETI	OSYPASAVPE	LAREDDPFRNP	VGHTLRESLTAI	FDELRG	MEADRIAPAI	DAIIRIRA	VODLTASC	AVGFVFLLKPILREFAP.
GCF ^{-900290345.1}		AILEEWLERTI	ATYPSOTAGE	FRNOKDRFRNP	VGSTLKEGLATI	LDEITG	MDLEKTRPAN	IESLVRM <mark>RA</mark>	VODETAAC	ATSFVFALROILN
GCF_900290325.1		AIAEOWLGRVI	RTYPGÕAAGE	LATEHDAFRNP	IGYTLKRGLAII	LEELLL	MDASRVEAAI	DSIVOIRA	VEDCAPGE	ALEFLFOLKPILS
GCF_900290315.1	MAVÕSKE	GIIEŜWLERVI	RSDPGÖSTAR	LATERDPFRNP	AGSTIROALGII	VDELLL	MDRGRITVAN	IDALMOIRA	VOGLEPGH	ALEFLFÖLKEILR
GCF_900290245.1	MSVSGÃVSE	IVAERWVERTI	AAYPAEILPE	LSGEHDRFRNP	VGOVIOÊSLTTI	ARELLG	MDNRATAPAI	DALVRMRA	VÕDFSPSA	ALRFIFDLRPVIA
De.bin3		AIVORWOHLII	DTYPPETAKI	WKKSSDPYHNP	VGARVRETAEAV	VDYLAAGGDH	AALEPVLDRI	DELVRVRA	VONFAPSC	AAGFLFLLKKVLREGFWO
De.bin1	MNTIEELLAANRK	AIVÕDWYDHII	DTYPAETAKI	WKKGGDPFANP	VAVRSROGAEAV	VSYLIGGEDE	KALAAVLDFI	DEMIRVRA	VONFTPSC	AAGFIFLLKKAMREKLW
De.bin2	MLKLVDYLVLDOO	AVLDAWFDLVI	GTYAESTAVI	WKKRDDPFANP	VRHRFEÄGMRGI	VINLATCGP	APDAATETPLI	DEIVRVRA	VÕDFTPSC	ATSFIFLLKKAIRETLWS
De.bin4		TVITRWFDLVI	ETYVPETAQE	LKKETNRFANP	VGOTTLDGLKDI	TDAFLO	GSSPEDMAKII	DRIIRIRA	IÕEFTPSČ	AVAFVFGLKKIARELLAH
KRT71371.1	MTGAGVGSAOLTGALAARKD	AIVRAWLARTI	ETYPEGTARE	LDKERDPFRNP	VGOGLKEALPAI	FDELLG	AMDPGRLAPLI	DGIVRIRA	VODFSPSC	AVAFVFLLKOVIRHELRH
WP 012611240.1	MTIRDLLAEHKD	AIIHKWIDAMY	GTYPFDTVGE	LRSSRDQFSNP	VGHTTAASAVVI	FDAVAGDH	VDEARLSEAI	EDVIRI <mark>RA</mark>	IONFTPEC	AVGVLFVLKTVLRKMLR/
WP_010938587.1	MTTSTITPELKE	K I S A R W G E F I Y	ATYPFDTTGE	LRSRKNEFSNP	VGHATEKAVTLM	IVAAICGDI	MVDGEVESAI	ADLIRV <mark>RA</mark>	IQQFTPEQ	ATGIIFCVKPILREEILH
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Ac.bin1 Ac.bin3 Ac.bin6	100 SAAVELPA ESGALPT EQQAETLFP	110 DFDARVDEIAI DFTARVDEIAI NLKQHIGQLTE	120 LAFDNYMACH LAFDKFMACH SCALQQYNSCH	130 EQIFNLRTKEL EQIFDLRAREL EEILQIRSRSQ	140 RLRMQSTIMEGI RLRMQSTIMEGI RRLRPLEPWMRQ	QE QE				
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Ac.bin1 Ac.bin3 Ac.bin6 Ac.bin4 Ac.bin9	100 SAAVELPA ESGAALPT EQQAETLFP EQQAETLFP EQQAETLFP	110 DFDARVDEIAI DFTARVDEIAI NLKQHIGQLTE NLKQHIGQLTE NLKQHIGQLTE	120 LAFDNYMACH LAFDKFMACH CALQQYNSCH CALQQYNSCH CALQQYNSCH	130 EQIFNLRTKEL EEQIFDLRAREL EEILQIRSRSQ EEILQIRSRSQ EEILQIRSRSQ	140 RLRMQSTIMEGI RLRMQSTIMEGI RRLRPLEPWMRC RRLRPLEPWMRC RRLRPLEPWMRC	QE QE SL SL SL	· · · · · · · · · · · · · · · · · · ·			
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- 56 Supplementary figure 5. Sequence alignment of DsrT proteins identified in this study with reference sequences. Highly conserved residues of
- 57 the same type are highlighted in red background.



59 Supplementary figure 6. Sequence alignment of DcrA proteins identified in this study with reference sequence identified in Desulfovibrio

- 60 *vulgaris* str. Hildenborough. Specific sequences, CHHCH, corresponding to a consensus c-type heme-binding site are marked with asterisks⁴.
- 61 Highly conserved residues of the same type are highlighted in red background.



63 Supplementary figure 7. Operons encoding the *cheA* chemotaxis gene in De.bin1 and *D. vulgaris*⁵. Arrows represented the coding regions. The

64 percentages in grey shadings indicate sequence similarities.



Supplementary figure 8. Virus/host abundance ratio for *Acidobacteria* with a
dissimilatory sulfur metabolism. *Acidobacteria* abundance and the abundance of their
viruses (both calculated as the mean coverage depth from reads mapping, normalized
by the number of reads in each metagenomic dataset) are plotted for each sample.
Pearson correlation analysis was used to correlate the host and viral abundance.



Supplementary figure 9. Correlations between transcript abundance of Ac.bin5 and soil Eh (a) and ferrous iron concentrations (b), and correlations between transcript abundance of *dsrAB* and concentrations of soil total carbon (c), total sulfur (d), sulfate (e) and sulfide (f). Results are based on Pearson correlation analysis.



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Supplementary figure 10. Comparison of Ac.bin5 and De.bin1 on relative expression 78 levels of genes involving in selected metabolic potentials. Relative expression level 79 was calculated based on the reads per kilobase per million mapped reads (RPKM) of a 80 given selected gene normalized by that of the reference gene gyrA. The relative gene 81 expression levels of hydrogenases were selected to indicate the activity of 82 83 fermentation processes occurred in the two SRMs. Values are presented as means \pm SD (n = 3). Kruskal-Wallis rank sum test was performed to determine 84 significant differences in the relative gene expression levels between the two strains. * 85 P < 0.05. The gene abbreviations are in accordance with those in Fig. 2. RC, 86 respiratory complex. The results are based on three soil samples collected from the 87

- unamended layer of the revegetated tailings. Additional details are presented in
- 89 Supplementary Table 2–8 and 13.



Supplementary figure 11. Correlations between transcript abundance of sox*XAYZB*and concentrations of soil total sulfur (a), sulfate (b) and sulfide (c). Results are based
on Pearson correlation analysis.

Supplementary Table 1. Overview of the reductive dsrAB -containing MAGs recovered from the mine wasteland.

MAG IDs	Genome bins#	Completeness (%)	Contamination (%)	Genome size (Mb)	Gene no.	Taxonomy (based on GTDB-Tk annotation)	16S rRNA sequence predicted	Relative abundance (%)
Ac.bin1	ULRT4_3.bins.75	98.06	0.86	4.75	3947	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	Yes	0.055
Ac.bin2	ULRT4_1.bins.77	95.53	1.72	5.11	4196	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	Yes	0.054
Ac.bin3	ULRT3_2.bins.110	95.47	7.76	6.53	5817	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	Yes	0.030
De.bin1	ULRT4_3.bins.101	94.64	0.79	3.68	3325	$Desulfobacterota_A; Desulfovibrionia; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio_N;$	No	0.051
Ac.bin4	UT3_2.bins.71	94.02	0	4.23	3399	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Granulicella_A;	No	0.031
Ac.bin5	ULRT4_2.bins.48	92.67	0	5.82	5139	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Palsa-343;	Yes	0.036
Ac.bin6	UT4_3.bins.137	92.65	0.43	3.73	3093	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Granulicella_A;	No	0.031
Ac.bin7	ULRT3_3.bins.30	89.78	0.43	4.28	3682	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	Yes	0.028
Ac.bin8	ULRT3_2.bins.77	88.69	7.76	4.51	4019	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	No	0.046
Ac.bin9	UT3_3.bins.87	78.4	0	3.15	2801	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Granulicella_A;	No	0.031
De.bin2	ULRT4_3.bins.66	75.17	0.86	3.02	2975	Desulfobacterota_A;Desulfovibrionia;Desulfovibrionales;Desulfovibrionaceae;Desulfovibrio_F;	Yes	0.024
Ac.bin10	ULRT3_2.bins.124	66.11	0	3.61	3559	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	Yes	0.020
De.bin3	ULRT4_2.bins.47	65.41	0	2.45	2585	$Desulfobacterota_A; Desulfovibrionia; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio_N;$	No	0.036
De.bin4	ULRT4_2.bins.61	63.39	0.81	2.50	2589	Desulfobacterota;Syntrophobacteria;Syntrophobacterales;Syntrophobacteraceae;;	No	0.018
Ac.bin11	ULRT3_2.bins.142	59.77	0	3.15	2649	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	Yes	0.039
Ac.bin12	ULRT4_2.bins.123	53.76	0	2.58	2618	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;	No	0.046

[#]The bins were named after the sample from which they were assembled and binned. For example, the name 'ULRT4_3.bins.75' meant that this bin was generated from the metagenomic dataset of the sample ULRT4_3 (representing the third replicate sample collected from the unamended layer of the reclaimed tailings at four years after ecological restoration initiation), as the 75th bin of the genome bins recovered from the mine wasteland.

Putative functions	Genes	MAG No.	MAGs
Sulfate reduction (to sulfide)	aprBA, sat are present, DsrAB cluster with reductive DsrAB, dsrD gene is present, and dsrEFH are absent	11	Ac.bin1, Ac.bin2, Ac.bin3, Ac.bin4, Ac.bin5, Ac.bin6, Ac.bin7, Ac.bin11, De.bin1, De.bin2, De.bin3
Sulfite reduction (to sulfide)	DsrAB cluster with reductive DsrAB, <i>dsrD</i> gene is present, and <i>dsrEFH</i> are absent	2	Ac.bin9, Ac.bin10
Sulfite reduction (to sulfide) incomplete	DsrAB cluster with reductive DsrAB, <i>dsrD</i> or <i>aprAB</i> , <i>sat</i> genes are not entirely present, and <i>dsrEFH</i> are absent	3	Ac.bin8, Ac.bin12, De.bin4

Supplementary Table 2. Directions of dissimilatory sulfur metabolism for the MAGs recovered in this study.

Supplementary	v Tahle 3	Genes encoding	alveoside	hydrolace	s for the sulfate	-reducing	hacteria an	d reference s	necies consider	ed in this study
Supprementar	y rable 5	. Genes encoung	z grycosiuc	inyui olases	s for the suitate	-reducing	Datter la al	iu reference s	pecies consider	cu m uns study.

Glyappiementary Table 3. Gene	A a hin1	A a bin?	A a hin?	A a bind	A a bin5	A a bind	Tarracidinkilus adhretonsis \$55	Do hir 1	Dogulfonibrio nulgaria Hildonboronab	Desulfaceagus multivergns DSM 2050
GH3	AC.DIII1	AC.01112	AC.01115	AC.01114	AC.DIII3	AC.DIIIO	10	1	1	1
CH13	9 11	12	12	10	15	7 5	10	1	1	1
CH13	11	0	12	0	2	2	7	4	2	5
GH25 GH2	4	2	5	2	3	2	5	0	8	4
CH21	4	5	4	5	6	0	3	0	0	0
CH20	5	5	5	3	0	2	3	0	0	0
CH29	0	0	2	4	7	5	3	0	0	0
CH28	4	0	3	0	2	5	5	0	0	0
GH2/	3	1	2	1	3	0	4	0	0	0
CH92	2	0	2	3	4	3	5	0	0	0
GH35	5	4	5	3	2	3	3	0	0	0
GH/8	2	6	2	5	2	5	0	0	0	0
GH39	3	0	4	3	3	3	5	0	0	0
GH51	4	2	3	2	0	2	2	0	0	0
GH20	3	4	3	3	3	3	3	0	0	0
GH38	1	5	2	3	2	4	2	0	0	0
GHI05	2	5	1	2	5	2	2	0	0	0
GH18	3	2	3	2	3	3	4	0	0	0
GH42	3	3	3	3	1	2	1	0	0	0
GH5	I	3	3	2	3	I	3	0	0	0
GH36	2	2	2	1	5	1	4	0	0	0
GH15	2	2	2	2	2	2	2	0	0	0
GH144	2	2	3	2	1	2	1	0	0	0
GH106	0	3	0	4	2	3	1	0	0	0
GH79	1	4	1	2	2	2	1	0	0	0
GH57	1	1	1	2	1	2	1	2	1	0
GH146	1	3	1	2	2	1	1	0	0	0
GH54	1	2	1	2	1	2	2	0	0	0
GH8	2	0	2	1	1	1	2	1	0	0
GH33	0	3	0	2	2	1	0	0	0	0
GH1	1	1	2	1	1	1	1	0	0	0
GH125	1	1	1	1	2	1	1	0	0	0
GH9	3	0	2	0	2	0	1	0	0	0
GH77	1	1	1	1	1	0	1	0	1	0
GH43	1	3	1	0	0	1	5	0	0	0
GH116	0	2	0	3	0	1	3	0	0	0
GH130	1	1	1	1	1	0	1	0	0	0
GH95	1	2	0	1	0	1	2	0	0	0
GH32	1	0	1	1	1	1	2	0	0	0
GH74	2	0	2	0	1	0	0	0	0	0
GH55	1	1	1	0	1	0	2	0	0	0
GH37	1	1	1	0	1	0	0	0	0	0
GH24	0	1	0	1	0	1	1	0	0	1
GH76	0	2	0	1	0	1	2	0	0	0
GH16	0	0	1	2	1	0	0	0	0	0
GH103	0	0	0	0	0	0	0	2	1	1
GH59	0	1	0	1	1	1	0	0	0	0
GH97	1	1	1	0	0	0	1	0	0	0
GH115	0	1	1	0	1	0	1	0	0	0
GH67	1	0	1	0	1	0	0	0	0	0

GH141	1	0	0	1	0	1	0	0	0	0
GH154	0	2	0	0	1	0	0	0	0	0
GH137	0	1	0	1	0	1	0	0	0	0
GH138	0	1	0	1	0	1	0	0	0	0
GH10	0	1	0	0	1	0	1	0	0	0
GH89	0	0	0	1	0	1	1	0	0	0
GH102	0	0	0	0	0	0	0	0	1	1
GH63	1	0	0	0	1	0	0	0	0	0
GH44	1	0	1	0	0	0	1	0	0	0
GH85	0	0	0	1	0	1	0	0	0	0
GH94	0	0	0	0	1	0	1	0	0	0
GH140	0	0	0	0	1	0	0	0	0	0
GH26	1	0	0	0	0	0	0	0	0	0
GH136	0	1	0	0	0	0	0	0	0	0
GH120	0	1	0	0	0	0	0	0	0	0
GH127	0	0	0	0	1	0	0	0	0	0
GH93	0	1	0	0	0	0	0	0	0	0
GH142	0	1	0	0	0	0	1	0	0	0
GH139	0	0	0	0	1	0	0	0	0	0
GH4	0	0	0	0	1	0	0	0	0	0
GH50	0	0	0	0	0	0	0	1	0	0
GH11	1	0	0	0	0	0	0	0	0	0

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Supplementary Table 4. Genes encoding hydrogenases for the sulfate-reducing bacteria and reference species considered in this study.

Hydrogenases	Ac.bin1	Ac.bin2	Ac.bin3	Ac.bin4	Ac.bin5	Ac.bin6	Terracidiphilus gabretensis S55	De.bin1	Desulfovibrio vulgaris Hildenborough	Desulfococcus multivorans DSM 2059
FeFe Group A1	0	0	0	0	0	0	0	0	1	0
FeFe Group A2	0	0	0	0	0	0	0	0	1	0
NiFe Group 1a	0	0	0	0	0	0	0	0	2	0
NiFe Group 1b	0	0	0	0	0	0	0	1	1	0
NiFe Group 1d	1	0	1	0	1	0	0	0	0	0
NiFe Group 3d	1	1	1	0	1	0	0	0	0	1
NiFe Group 4c	0	0	0	0	0	0	0	1	1	0
NiFe Group 4e	0	0	0	0	0	0	0	1	1	0

Supplementary Table 5. Genes encoding respiratory complexs for the sulfate-reducing bacteria and reference species considered in this study.

COG	Gene	Function	Ac.bin1	Ac.bin2	Ac.bin3	Ac.bin4	Ac.bin5	Ac.bin6	Terracidiphilus gabretensis S55	De.bin1	Desulfovibrio vulgaris Hildenboroug	h Desulfococcus multivorans DSM 2059
COG0838	nuoA	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	2	2	2	2	0	1
COG0852	nuoC	respiratory complex I (NADH dehydrogenase 1)	2	2	2	2	2	2	2	3	2	1
COG0649	nuoD	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	2	2	2	2	0	0
COG1005	nuoH	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	2	2	2	2	0	1
COG0839	nuoJ	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	2	2	2	2	0	1
COG0713	nuoK	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	2	2	2	2	0	1
COG1009	nuoL	respiratory complex I (NADH dehydrogenase 1)	2	2	4	3	2	3	2	2	1	2
COG1008	nuoM	respiratory complex I (NADH dehydrogenase 1)	3	3	4	3	3	3	3	3	0	1
COG1007	nuoN	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	2	2	2	2	0	1
COG1905	nuoE	respiratory complex I (NADH dehydrogenase 1)	2	3	3	1	2	1	1	1	0	4
COG1894	nuoF	respiratory complex I (NADH dehydrogenase 1)	2	3	3	1	3	1	1	1	0	4
COG3383	nuoG	respiratory complex I (NADH dehydrogenase 1)	4	4	6	5	5	5	1	3	0	7
COG0377	nuoB	respiratory complex I (NADH dehydrogenase 1)	2	2	3	2	1	2	2	1	0	0
COG1143	nuoI	respiratory complex I (NADH dehydrogenase 1)	3	4	4	3	4	3	2	5	6	1
COG1034	nuoG_a	respiratory complex I (NADH dehydrogenase 1)	0	0	1	0	0	0	0	1	0	1
COG1252	ndh	respiratory complex I (NADH dehydrogenase 2)	1	1	1	0	1	0	1	1	2	1
COG0029	sdhA/frdA	respiratory complex II (succinate dehydrogenase)	1	1	1	1	1	1	1	1	1	1
COG0479	sdhB/frdB	respiratory complex II (succinate dehydrogenase)	1	1	3	1	1	1	1	2	2	1
COG2009	sdhC	respiratory complex II (succinate dehydrogenase)	1	1	1	0	0	0	1	0	0	0
COG1053	sdhA	respiratory complex II (succinate dehydrogenase)	2	3	2	1	2	1	1	3	4	2
COG0723	petC	respiratory complex III (quinol-cytochrome-c reductase)	6	5	7	2	5	2	1	0	0	1
COG1290	petB/petD	respiratory complex III (quinol-cytochrome-c reductase)	5	4	6	2	6	2	1	0	0	0
COG0243	actB1	respiratory complex III (quinol-cytochrome-c reductase)	2	2	3	2	3	2	1	6	9	5
COG0437	actB	respiratory complex III (quinol-cytochrome-c reductase)	4	3	12	3	4	4	0	3	10	7
COG5557	actC	respiratory complex III (quinol-cytochrome-c reductase)	2	2	2	2	2	2	1	2	3	5
COG1622	coxM	respiratory complex IV (low-affinity terminal oxidase)	0	0	0	0	2	0	1	1	0	0
COG0843	coxN	respiratory complex IV (low-affinity terminal oxidase)	3	2	4	2	3	1	2	1	1	0
COG1845	coxO	respiratory complex IV (low-affinity terminal oxidase)	4	3	4	3	3	3	3	1	1	0
COG3125	ctaF	respiratory complex IV (low-affinity terminal oxidase)	0	0	0	0	0	0	0	1	0	0
COG1271	cydA	respiratory complex IV (bd-type high-affinity terminal oxidase)	2	2	3	2	3	2	0	2	3	4
COG1294	cydB	respiratory complex IV (bd-type high-affinity terminal oxidase)	1	1	2	1	2	1	0	1	1	2
COG3278	ccoN	respiratory complex IV (cbb3-type high-affinity terminal oxidase)	0	1	1	1	0	1	0	0	0	1
COG2993	ccoO	respiratory complex IV (cbb3-type high-affinity terminal oxidase	0	0	1	0	0	0	0	0	0	0
COG0056	atpA	respiratory complex V (F-type ATP synthase)	1	2	1	1	1	1	1	1	1	2
COG0055	atpD	respiratory complex V (F-type ATP synthase)	1	2	1	1	1	1	1	1	1	2
COG0712	atpH	respiratory complex V (F-type ATP synthase)	1	2	1	1	1	1	1	1	1	1
COG0355	atpC	respiratory complex V (F-type ATP synthase)	1	2	1	1	1	1	1	1	1	2
COG0224	atpG	respiratory complex V (F-type ATP synthase)	1	2	1	1	1	1	1	1	2	2
COG0356	atpB	respiratory complex V (F-type ATP synthase)	1	2	1	1	1	1	1	1	1	3
COG0711	atpF	respiratory complex V (F-type ATP synthase)	1	2	1	2	2	2	2	2	2	5

Supplementary Table 6. Core genes responsible for chemotavis and moti-	ty for the sultate-reducing bacteria and reference si	necies considered in this study
Supprementary rable 6. Core genes responsible for enemotiaxis and moti	ty for the sunate-reducing bacteria and reference sp	sectes considered in this study.

KO	Gene	Function	Ac.bin1	Ac.bin2	Ac.bin3	Ac.bin4	Ac.bin5	Ac.bin6	Terracidiphilus gabretensis S55	De.bin1	Desulfovibrio vulgaris Hildenborough	Desulfococcus multivorans DSM 2059
PF00015	MCP	methyl-accepting chemotaxis protein	2	1	0	1	6	1	1	34	28	0
K03412	cheB	protein-glutamate methylesterase/glutaminase	2	1	1	1	5	1	1	5	2	0
K00575	cheR	chemotaxis protein methyltransferase CheR	1	1	0	1	5	1	1	4	2	0
K13924	cheBR	vo-component system, chemotaxis family, CheB/CheR fusion protei	1	0	2	0	2	0	0	2	1	1
K03407	cheA	two-component system, chemotaxis family, sensor kinase CheA	2	1	0	1	4	1	1	4	3	0
K03408	cheW	purine-binding chemotaxis protein CheW	1	1	0	1	4	1	1	4	4	0
K03413	cheY	wo-component system, chemotaxis family, chemotaxis protein Che?	2	1	1	3	6	3	2	9	5	0
K02387	flgB	flagellar basal-body rod protein FlgB	1	1	1	0	2	1	1	1	1	0
K02388	flgC	flagellar basal-body rod protein FlgC	1	1	1	0	2	0	1	1	2	0
K02389	flgD	flagellar basal-body rod modification protein FlgD	1	1	1	0	1	0	1	2	1	0
K02390	flgE	flagellar hook protein FlgE	1	1	1	0	2	1	1	2	2	0
K02391	flgF	flagellar basal-body rod protein FlgF	0	0	0	0	1	0	0	0	0	0
K02392	flgG	flagellar basal-body rod protein FlgG	1	1	1	0	2	0	1	2	2	0
K02396	flgK	flagellar hook-associated protein 1 FlgK	1	1	1	0	2	0	1	2	1	0
K02397	flgL	flagellar hook-associated protein 3 FlgL	1	1	1	0	2	0	1	2	1	0
K02400	flhA	flagellar biosynthesis protein FlhA	1	1	1	0	3	0	1	1	1	0
K02401	flhB	flagellar biosynthetic protein FlhB	1	1	1	0	2	0	1	1	1	0
K02406	fliC	flagellin	2	1	2	0	2	0	1	3	4	0
K02407	fliD	flagellar hook-associated protein 2	1	1	1	0	2	0	1	2	1	0
K02408	fliE	flagellar hook-basal body complex protein FliE	1	1	1	0	2	0	1	1	1	0
K02409	fliF	flagellar M-ring protein FliF	1	1	1	0	2	0	1	1	1	0
K02410	fliG	flagellar motor switch protein FliG	1	1	1	0	2	0	1	1	1	0
K02411	fliH	flagellar assembly protein FliH	1	2	1	0	2	0	1	1	1	0
K02412	fliI	flagellum-specific ATP synthase	1	1	1	0	2	0	1	1	1	0
K02416	fliM	flagellar motor switch protein FliM	1	1	1	0	2	0	1	1	1	0
K02417	fliN	flagellar motor switch protein FliN	2	1	1	0	3	0	1	1	1	0
K02419	fliP	flagellar biosynthetic protein FliP	1	1	1	0	2	0	1	1	1	0
K02420	fliQ	flagellar biosynthetic protein FliQ	1	1	1	0	2	0	1	1	1	0
K02421	fliR	flagellar biosynthetic protein FliR	1	1	1	0	2	0	1	1	1	0
K02556	motA	chemotaxis protein MotA	2	2	2	2	4	1	2	5	4	0
K02557	motB	chemotaxis protein MotB	2	2	2	1	3	0	2	5	5	0
K02650	pilA	type IV pilus assembly protein PilA	0	0	0	1	0	1	0	0	0	1
K02652	pilB	type IV pilus assembly protein PilB	1	1	1	1	1	1	1	1	1	0
K02653	pilC	type IV pilus assembly protein PilC	1	1	1	1	1	1	1	1	1	1
K02654	oilD, ppp.	A leader peptidase (prepilin peptidase) / N-methyltransferase	1	1	1	2	1	2	1	1	2	1
K02662	pilM	type IV pilus assembly protein PilM	1	1	1	1	1	1	1	0	0	1
K02663	pilN	type IV pilus assembly protein PilN	1	1	1	1	0	1	1	0	0	0
K02651	flp, pilA	pilus assembly protein Flp/PilA	1	1	1	0	5	0	0	0	2	1
K02669	pilT	twitching motility protein PiIT	0	0	0	1	1	1	0	3	1	2
K02664	pilO	type IV pilus assembly protein PilO	0	0	0	0	0	0	0	0	0	1
K02665	pilP	type IV pilus assembly protein PilP	0	0	0	0	0	0	0	0	0	1
K02666	pilO	type IV pilus assembly protein PilO	0	0	0	0	0	0	0	1	1	1

]	la	Ib	П	IIIm	IIIc	IVa	IVb
	Cluster I	Cluster II	10	11	mm	me	Iva	100
Ac.bin1	0	0	0	0	0	0	1	1
Ac.bin2	1	0	0	0	0	0	0	0
Ac.bin3	0	0	0	0	0	0	0	0
Ac.bin4	0	0	0	0	0	0	1	0
Ac.bin5	2	0	0	0	0	0	1	3
Ac.bin6	0	0	0	0	0	0	1	0
Terracidiphilus gabretensis S55	1	0	0	0	0	0	0	0
De.bin1	18	9	0	0	2	2	0	3
Desulfovibrio vulgaris Hildenborough	17	10	0	0	1	0	0	0
Desulfococcus multivorans DSM 2059	0	0	0	0	0	0	0	0

Supplementary Table 7. Classification* of methyl-accepting chemotaxis proteins (MCP) for the sulfate-reducing bacteria and reference species considered in this study.

*Results are based on membrane topology and ligand-binding domain.

G I 4 TILOG P		
Supplementary Table 8. Genes encodin	I oxidative stress for the sulfate-reducin	g bacteria and reference species considered in this study
Supprementary ruble of Genes encount	, oundative bureas for the sumate reducing	g bucteria and reference species considered in this stady

КО	Key proteins	Function	Ac.bin1	Ac.bin2	Ac.bin3	Ac.bin4	Ac.bin5	Ac.bin6	Terracidiphilus gabretensis S55	De.bin1	Desulfovibrio vulgaris Hildenborough	Desulfococcus multivorans DSM 2059
K03781	catalase (EC 1.11.1.6)	hydrogen peroxide:hydrogen peroxide oxidoreductase	0	0	0	0	2	0	0	1	1	1
K00425	ente desente del conserve en de store (FC 7.1.1.7)	Cytochrome bd oxygen reductase (cydA)	1	1	2	1	3	1	0	1	1	2
K00426	cytochrome bd oxygen reductase (EC 7.1.1.7)	Cytochrome bd oxygen reductase (cydB)	1	1	2	1	2	1	0	1	1	2
K02274		coxA, ctaD; cytochrome c oxidase subunit I	2	2	3	2	3	1	2	0	1	0
K02275	cytochrome c oxidase (ferrocytochrome c:oxygen oxidoreductase. EC 7.1.1.9)	coxB, ctaC; cytochrome c oxidase subunit II	3	2	3	2	6	1	3	0	1	0
K02276	,	coxC, ctaE; cytochrome c oxidase subunit III	3	2	3	2	3	2	3	0	1	0
K01738	cysteine synthase (CysK; EC 2.5.1.47)	cysK; cysteine synthase	2	1	2	2	3	1	1	1	1	1
K00533	E 11 1 (EC 1 12 7 A)	ferredoxin hydrogenase large subunit	0	0	0	0	0	0	0	0	2	0
K00534	[Fe] hydrogenase (EC 1.12.7.2)	ferredoxin hydrogenase small subunit	0	0	0	0	0	0	0	0	1	0
K00428	cytochrome c peroxidase (Ccp; EC 1.11.1.5)	cytochrome c peroxidase	0	1	0	0	1	0	0	0	0	0
COG1592;PF02915		Rubrerythrin1;Nigerythrin	3	1	3	0	2	0	1	5	5	7
COG0491;PF00753	NADH peroxidases (EC 1.11.1.1)	Rubrerythrin2	2	2	2	2	5	2	5	2	2	3
K00432	glutathione peroxidase (EC 1.11.1.9)	gpx, btuE, bsaA; glutathione peroxidase	2	1	2	1	0	1	4	0	0	0
K11065	thioredoxin peroxidase (Tpx; EC 1.11.1.15)	tpx; thioredoxin-dependent peroxiredoxin	0	0	0	0	0	0	0	1	1	1
K03564	thioredoxin-dependent peroxiredoxin (EC 1.11.1.24)	BCP	1	2	2	2	2	2	2	1	1	1
PF00753;PF00258;COG0426	rubredoxin-oxygen oxireductase	rubredoxin-oxygen oxireductase (ROO)	1	0	0	0	0	0	0	2	1	4
K05919	superoxide reductase (EC 1.15.1.2)	dfx; superoxide reductase	0	0	0	0	0	0	0	1	1	1
K16627		Copper/zinc superoxide dismutase	0	0	0	0	0	0	0	0	0	0
K04565	superovide disputtors (EC 1.15.1.1)	Copper/zinc superoxide dismutase	0	0	0	1	0	1	1	0	0	0
K04564	superoxide distilutase (EC 1.15.1.1)	Iron/manganese superoxide dismutase	1	1	1	1	1	1	1	1	1	2
K00518		Nickel-containing superoxide dismutase	0	0	0	0	0	0	0	0	0	1

Supplementary Table 9. Virus-host linkages information for the sulfate-reducing bacteria and reference species considered in this study.

Supplementary Table	9. Virus-nost mikaş	ges information for	r the suitate-reduc	ing bacteria and reference s	species considered in this study.				
Viral sequence ID#	VirSorter_category	vContact2_cluster	No. of sequences in the cluster	Taxonomy	Virion-associated gene (i.e., capsid, terminase or portal) detected in viral sequences	Phage transposase & integrase detected in viral sequences	Phage tail component in viral sequences	Host genome bin	Host taxonomy (based on GTDB-Tk annotation)
Ac bin1.1	Category_5	VC_335_0	5	unassigned	+	-	-	Ac hin1	A cidobacteriota: A cidobacteriae: A cidobacteriales: A cidobacteriaceae: Terracidinbilus:
AC.0111.1	Category_5	singleton	-	unassigned	+	+	-	Acourt	Actionateriola, Actionateriae, Actionateriaes, Actionateriaes, Terractalphilus,
Ac.bin2.1	Category_5	VC_335_0	5	unassigned	+	-	-	Ac.bin2	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;
Ac.bin3.1	Category_5	VC_335_0	5	unassigned	+		-	Ac.bin3	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;
Ac.bin5.1	Category_5	VC_335_0	5	unassigned	+	-	-	Ac.bin5	Acidobacteriota;Acidobacteriae;Acidobacteriales;Acidobacteriaceae;;
Ac.bin11.1	Category_5	singleton	-	unassigned	+	+	-	Ac.bin11	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;
T. gabretensis.1	Category_5	VC_335_0	5	unassigned	+		-	Terracidiphilus gabretensis S55	Acidobacteriota; Acidobacteriae; Acidobacteriales; Acidobacteriaceae; Terracidiphilus;
D. vulgaris.1	Category_4	singleton	-	Caudovirales	+	+	+		
D. vulgaris.2	Category_4	singleton	-	Caudovirales	+	+	+		
D. vulgaris.3	Category_5	VC_61_0	9	Caudovirales; Myoviridae	+		+		
D. vulgaris.4	Category_5	VC_336_0	3	Caudovirales	+	+	+	Desulfovibrio vulgaris Hildenborough	Desunobacterola; Desunovibrionia; Desunovibrionales; Desunovibrionaceae; Nitratidesunovibrio; Nitratidesunovibrio
D. vulgaris.5	Category_5	singleton	-	Caudovirales	-	+	+		virgans
D. vulgaris.6	Category_5	VC_336_0	3	Caudovirales	-	+	+		
D. vulgaris.7	Category_5	VC_336_0	3	Caudovirales	+	+	+		
D. multivorans.1	Category_5	singleton	-	unassigned	-	+	-		
D. multivorans.2	Category_5	singleton	-	Caudovirales	-		+	Desulfococcus multivorans DSM 2059	Desulfobacterota; Desulfobacteria; Desulfobacterales; Desulfococcaceae; Desulfococcus; Desulfococcus multivorans
D. multivorans.3	Category_5	singleton	-	unassigned	-	+	-		

*Viral sequences were named according to their host. For example, Ac.bin1.1 represents the first viral sequence of Ac.bin1.

Supplementary Table 10. Glycoside hydrolases (GHs) encoded by viruese infecting the sulfate-reducing bacteria and reference speci	cies considered in this study.
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Viral sequence ID	Gene	Host	CAZy family	Signalp	Phyre2 Annotation	Protein Data Bank Best Hit ID	Model Confidence %	Sequence % Identity	Query Coverage (% of protein aligned)	Protein Phyre ID	Protein Model Organism
Ac.bin3.1	NODE_263_length_121426_cov_5.268051_26	Ac.bin3	GH105	Ν	D-4,5-unsaturated β-glucuronyl hydrolase (EC: 3.2.1.172)	4CE7	100	42	72	6219b7372294dff3	Nonlabens ulvanivorans
D. vulgaris.2	NZ_CABHLV010000001.1_980	Desulfovibrio vulgaris Hildenborough	GH23	Y (1-32)	chitinase (EC 3.2.1.14)	3W6D	100	18	78	cab4a76fdc34f6f0	Ralstonia sp. A-471
D. vulgaris.5	NZ_CABHLV010000001.1_1306	Desulfovibrio vulgaris Hildenborough	GH23	Y (1-31)	chitinase (EC 3.2.1.14)	3W6D	100	16	79	99acf6a7696aa132	Ralstonia sp. A-471

Supplementary Table 11. Viral methyl-accepting chemotaxis proteins (MCPs) and superoxide dismutase (SOD) encoded by viruese infecting the sulfate-reducing bacteria and reference species considered in this study.

Virus	Gene	Host	size (aa)	MCP_Category	Interpro Annotation	Function	start_aa	end_aa	Phyre2 Annotation	Protein Data Bank Best Hit ID	Model Confidence %	Sequence % Identity	Query Coverage (% of protein aligned)	Protein Phyre ID	Protein Model Organism
					PF17201	Cache 3/Cache 2 fusion domain	34	318							
D vulgaris 1	NZ CARHI V01000001 1, 2202		813	Ia (Cluster II)	PF00672	HAMP domain	341	390	Cache domain of methyl-	3080	99.7	17	34	97c8efb277d8aa81	Vibrio cholerae
D. Migarbit	N2_CABIL V01000001.1_2702		015	in (cluster ii)	PF08448	PAS fold	405	513	accepting chemotaxis protein	3686	//	.,	54	7765615277401401	nono choicrae
					PF00015	Methyl-accepting chemotaxis protein (MCP) signalling domain	590	773							
					PF08269	Cache domain 2	54	227	Cache-like sensor domain						
D. vulgaris.1	NZ_CABHLV010000001.1_2799 Desulfe	fovibrio vulgaris Hildenborough	626	Ia (Cluster I)	PF00672	HAMP domain	251	301	acetate) and C3 (propionate and pyruvate) carboxylates	5G4Y	99.5	43	23	74ba713b5a5e3de9	Pseudomonas syringae
					PF00015	Methyl-accepting chemotaxis protein (MCP) signalling domain	409	591	sensing						
					PF02743	Double Cache domain 1	49	284							
D vulgarie 2	NZ CARUI V01000001 1 943		804	In (Chustar II)	PF00672	HAMP domain	338	384	Double CACHE (dCACHE)	SWPE	99.9	24		6cm65165d56m22c	Helicobaster pylori 26605
D. 10. 00.2	http://www.interforces.com/		004	in (cluster ii)	PF13426	PAS domain	405	507	domain mediating lactate sensing	51151	5 39.9	34	11	000000000000000000000000000000000000000	neucobacter pytori 20095
					PF00015	Methyl-accepting chemotaxis protein (MCP) signalling domain	587	768							
D. multivorans.2	CP015381.1_2500 Desulfe	fococcus multivorans DSM 2059	157	/	PF09055	Nickel-containing superoxide dismutase	27	150	Nickel-containing superoxide dismutase, NiSOD	1T6U	100	16	75	ee61aa0bf878be49	Streptomyces coelicolor

	ULRT1	ULRT2	ULRT3
рН	7.65	7.80	7.75
Eh (mV)	190	191	194
Total C (mg g ⁻¹)	5.18	1.90	2.71
Total S (mg g ⁻¹)	144	120	138
$SO_4^{2-} (mg g^{-1})$	14.8	12.9	11.1
$S^{2-}(\mu g g^{-1})$	1.83	18.7	7.60
Fe^{2+} (µg g ⁻¹)	10.6	9.19	5.22

Supplementary Table 12. Selected physico-chemical properties of soil samples used for metatranscriptomic analysis of this study.

KO	Function	Ac.bin5	De.bin1
K00370	nitrate reductase 1	0	0
K00371	nitrate reductase 1	0	0
K00374	nitrate reductase 1	0	0
K02567	nitrate reductase (cytochrome)	0	0
K02568	nitrate reductase (cytochrome)	0	0
K00368	nitrate reductase (NO-forming)	0	0
K15864	nitrate reductase (NO-forming)	0	0
K04561	nitric oxide reductase	2	1
K02305	nitric oxide reductase	0	0
K00376	nitrous-oxide reductase	0	0

Supplementary Table 13. Genes responsible for denitrification and fermentation illustraed in Supplementary Figure 10 in this study.

Supplementary Table 14. The mormation of metal ansemptonic datasets used in this study.							
ULRT1	ULRT2	ULRT3					
42179613	89679037	47502326					
40357389	86004585	43953294					
32042524	48888842	34021435					
66601	136109	214175					
	ULRT1 42179613 40357389 32042524 66601	ULRT1 ULRT2 42179613 89679037 40357389 86004585 32042524 48888842 66601 136109					

Supplementary Table 14. The information of metatranscriptomic datasets used in this study.

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