Supplementary Material for *Biodegradation*

H_2S biotreatment with Heterotrophic Sulfide-Oxidizing Bacteria

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Contents:

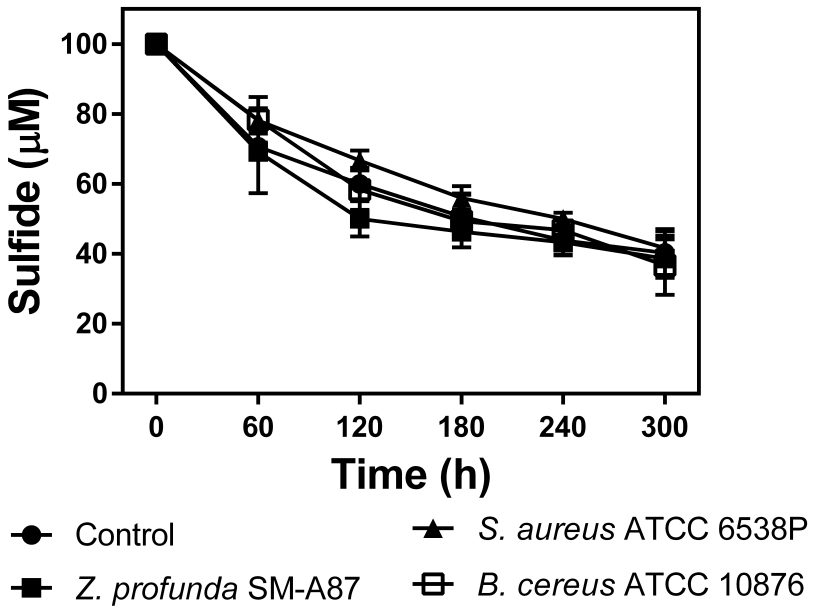

Fig. S1. The heat-inactive cells in FIG 1b did not oxidize sulfide. Cells were cultured, harvested, wash and re-suspended in the same way with FIG. 1. They were then heated in boiling water 30 minutes. NaHS was added to 100 μM to initiate the reaction. Averages ($n \geqslant 3$) with standard deviations (error bar) were shown.

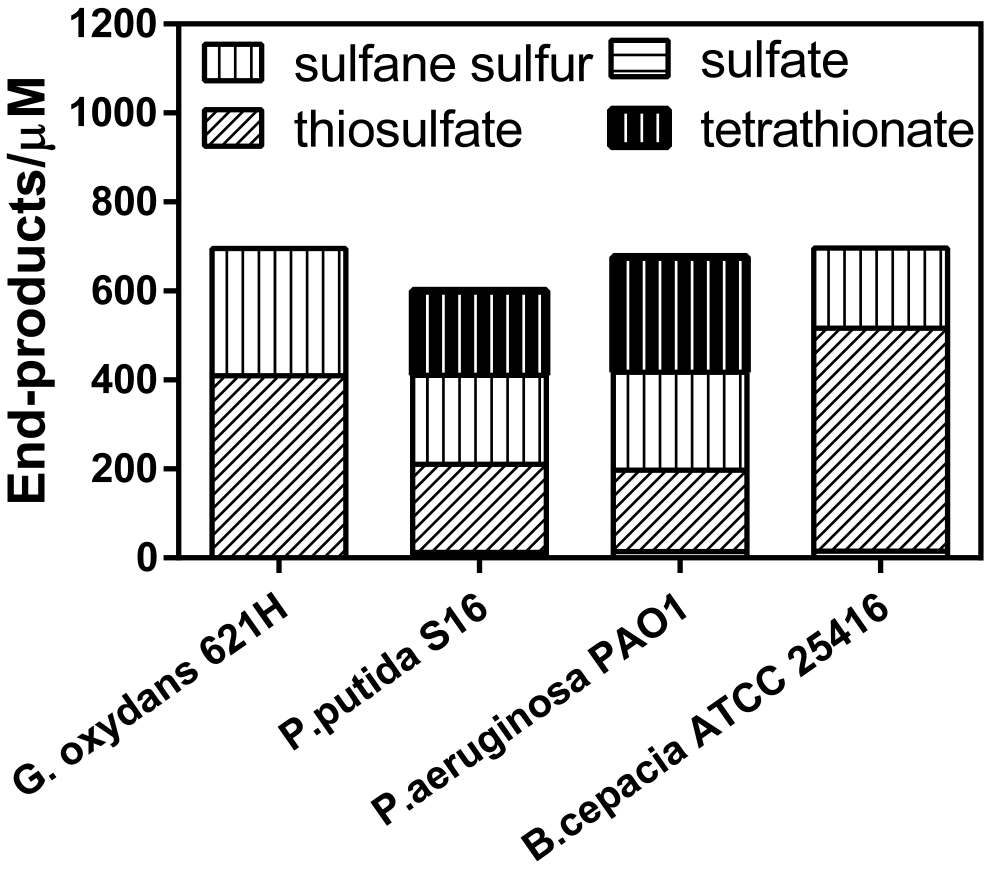

Fig. S2. The end-products of sulfide oxidation by five bacteria after 6-hours reaction. The experiments were done as described in the Figure 1 legend. Thiosulfate contains two sulfur atoms and tetrathionate contains four sulfur atoms, theirs' concentration was adjusted. Sulfane sulfur, zero valence sulfur.

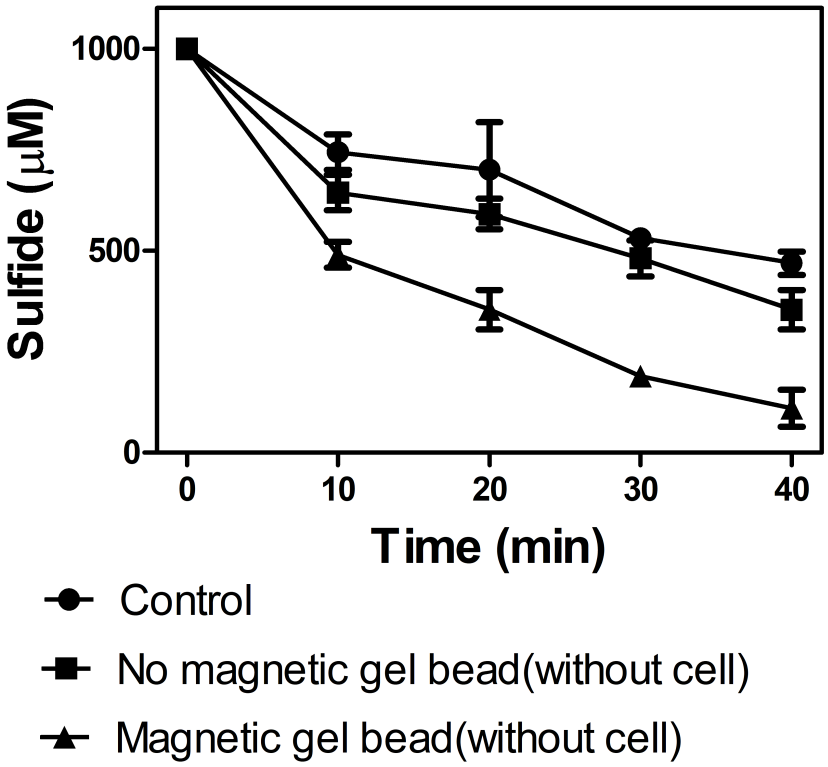

Fig. S3. Gel beads coated Fe_3O_4 nanoparticles without cells oxidize sulfide. The experiments were carried out in 50-ml centrifuge tube containing 10 ml of HEPES buffer (pH=7.4) at 30°C on a reciprocal shaker at 180 r.p.m.. Averages ($n \geq 3$) with standard deviations (error bar) were shown.

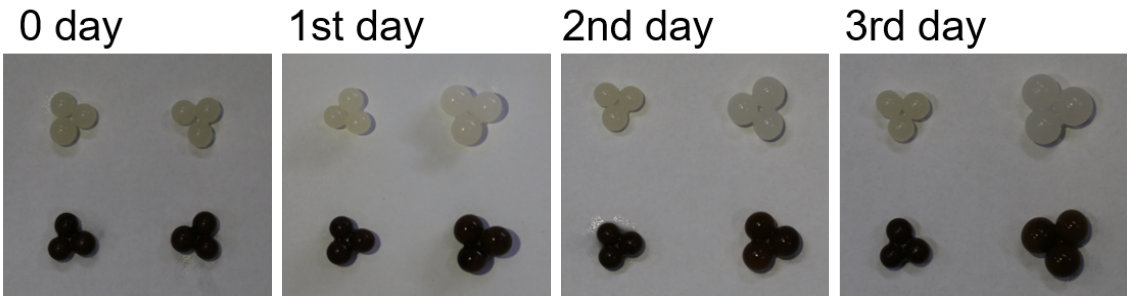

Fig. S4. The change of diameters of beads with immobilized *G. oxydans* 621H cells during culturing in water or MM. The cells were immobilized in alginate gel beads with (black) or without (white) Fe_3O_4 nanoparticles. The experiments were carried out in 50-ml centrifuge tube containing 10 ml of distilled water or MM at 30°C on a reciprocal shaker at 180 r.p.m. On the left is the immobilized-cell beads incubated in distilled water; on the right is the immobilized-cell beads incubated in MM with glucose.

Table S1. Tested heterotrophic bacteria and SQR and PDO accession numbers

Strains	SQR accession No.	PDO accession No.
G. oxydans 621H	WP_011252149.1 WP_011252513.1	WP_011252150.1
P. putida S16	WP_013970253.1	WP_013970252.1
P. aeruginosa PAO1	NP_251256.1 NP_251035.1	NP_251605.1
B. cepacia ATCC 25416	WP_027787303.1	WP_027790374.1 WP_027787304.1
B. cereus ATCC10876	WP_000857315.1	WP_000925319.1
Z. profunda SM-A87	WP_009779527.1	WP_009779529.1
S. aureus ATCC 6538P	WP_001033018.1	WP_000465474.1
S. marcescens ATCC13880	WP_033641274.1 WP_033640364.1	WP_033640361.1
E. coli BL21	None	None

Table S2. Distribution of TsdA in different bacterial phyla.

	TsdA couts
Betaproteobacteria	553
Gammaproteobacteria	294
Alphaproteobacteria	115
Epsilonproteobacteria	91
Bacilli	11
Synechococcales	9
Flavobacteriia	8
Sphingobacteriia	7
Deltaproteobacteria	6
Nitrospirales	4
Acidobacteriales	3
Parachlamydiales	2
Aquificales	2
Chitinophagia	2
Deinococci	2
Gemmatimonadales	2
Cytophagia	1