

SUPPLEMENTAL SECTION

Table S1. Single copy genes used to evaluate the completeness of the *Thiobacillus* sp. RG5 draft genome.

Description	COG	Count
Arginyl-tRNA synthetase	COG0018	1
DNA-directed RNA polymerase subunit alpha	COG0202	1
DNA-directed RNA polymerase subunit beta	COG0085	2
GTP-binding protein YchF	COG0012	1
Histidyl-tRNA synthetase	COG0124	1
Isoleucyl-tRNA synthetase	COG0060	1
Leucyl-tRNA synthetase	COG0495	1
Methionyl-tRNA synthetase	COG0143	2
O-sialoglycoprotein endopeptidase	COG0533	0
Phenylalanyl-tRNA synthetase, alpha subunit	COG0016	1
Protein translocase subunit secY alpha	COG0201	1
Ribosomal protein L1P	COG0081	1
Ribosomal protein L22	COG0091	1
Ribosomal protein L2P	COG0090	1
Ribosomal protein L3P	COG0087	1
Ribosomal protein L4P	COG0088	1
Ribosomal protein L5P	COG0094	1
Ribosomal protein L6P	COG0097	1
Ribosomal protein L11P	COG0080	1
Ribosomal protein L13P	COG0102	1
Ribosomal protein L14P	COG0093	1
Ribosomal protein L15P	COG0200	1
Ribosomal protein L16P	COG0197	1
Ribosomal protein L18	COG0256	1
Ribosomal protein S2P	COG0052	1
Ribosomal protein S3P	COG0092	1
Ribosomal protein S4P	COG0522	1

Description	COG	Count
Ribosomal protein S5P	COG0098	1
Ribosomal protein S7P	COG0049	1
Ribosomal protein S8P	COG0096	1
Ribosomal protein S9P	COG0103	1
Ribosomal protein S11P	COG0100	1
Ribosomal protein S12P	COG0048	1
Ribosomal protein S13P	COG0099	1
Ribosomal protein S15P/S13E	COG0184	1
Ribosomal protein S17P	COG0186	1
Ribosomal protein S19P	COG0185	1
Ribosomal protein alanyl-tRNA synthetase	COG0525	0
Seryl-tRNA synthetase	COG0172	1
Signal recognition particle subunit FFH	COG0541	1

Table S2. Model parameters describing logistic SO_4^{2-} production in cultures of *Thiobacillus* sp. RG4 incubated at 5 or 15 °C. Values represent the average of triplicate biotic assays. Errors are 2σ .

	Oxidant	$t_{\text{half}}^{\text{a}}$ (h)	$C_{\text{max}}^{\text{b}}$ (mM)	α^{c} (mM h⁻¹)	R²
5 °C	O ₂	223 ± 4	11.3 ± 0.2	1.7 x 10 ⁻² ± 0.1 x 10 ⁻²	0.99
	NO ₃ ⁻	630 ± 22	7.9 ± 0.4	7.6 x 10 ⁻³ ± 0.9 x 10 ⁻³	0.99
	NO ₂ ⁻	1508 ± 44	4.6 ± 0.4	5.1 x 10 ⁻³ ± 0.8 x 10 ⁻³	0.98
15 °C	O ₂	243 ± 18	12.5 ± 0.8	1.3 x 10 ⁻² ± 0.3 x 10 ⁻²	0.98
	NO ₃ ⁻	826 ± 18	7.5 ± 0.4	8.8 x 10 ⁻³ ± 1.1 x 10 ⁻³	0.99
	NO ₂ ⁻	--	--	--	--

^a Time (t) at which half the total SO_4^{2-} is produced. ^b Maximum SO_4^{2-} concentration predicted to accumulate. ^c Maximum rate of sulfate production observed.

Table S3. Parameters describing cell production via $S_2O_3^{2-}$ oxidation coupled to O_2 and NO_3^- reduction in cultures of *Thiobacillus* sp. RG5 incubated at 5 or 15 °C. Values represent the average of triplicate biotic assays and errors are 2σ unless otherwise noted.

<i>Oxidant</i>	°C	$t_{half}^{a,d}$ (h)	$C_{max}^{b,d}$ (cells ml ⁻¹)	$\alpha^{c,d}$ (cells h ⁻¹)	R^2	t_D (h)	E_c^e (μJ cell ⁻¹)	p (E _c)
O ₂	5	247 ± 46	5.6 x 10 ⁸ ± 1.2 x 10 ⁸	1.5 x 10 ⁻² ± 0.8 x 10 ⁻²	0.95	140	3.2 ± 0.6	< 0.01
	15	176 ± 55	2.3 x 10 ⁸ ± 0.4 x 10 ⁸	1.2 x 10 ⁻² ± 0.8 x 10 ⁻²	0.89	294	7.7 ± 2.4	
NO ₃ ⁻	5	<i>n.a.</i>	<i>n.a.</i>	<i>n.a.</i>	<i>n.a.</i>	154	2.3 ± 1.7	0.07
	15	<i>n.a.</i>	<i>n.a.</i>	<i>n.a.</i>	<i>n.a.</i>	197	7.6 ± 3.4	

^a Time (t) at which half the total cells are produced. ^b Maximum predicted cell density.

^c Maximum rate of cell production. ^d Values derived from logistic model. ^e Errors are 1σ .