

Table S1. General features and genomic comparison between *A. ferrooxidans* YQ-N3 and the other published genomes *A. ferrooxidans*.

Strain	Geographic origin	GenBank accession no	Genome size (Mb)	GC%	CDS	Plasmids	Scaffolds
<i>A. ferrooxidans</i> YQ-N3	Shanxi, China	GCA_020221655.1	3.21772	58.7316%	3132	5	6
<i>A. ferrooxidans</i> YNTRS-40	-	GCA_013462805.1	3.25704	58.4696%	3168	1	2
<i>A. ferrooxidans</i> ATCC23270	Bituminous coal mine effluent	GCA_000021485.1	2.9824	58.8%	2927	-	1
<i>A. ferrooxidans</i> BYM	Baiyin, China	GCA_019856615.1	3.2555	58.4696%	3134	1	2
<i>A. ferrooxidans</i> NFP31	Volcanic ash deposits on Miyakejima, Japan	GCA_020887015.1	3.24985	58.4724%	3193	1	2
<i>A. ferrooxidans</i> ATCC53993	-	GCA_000020825.1	2.88504	58.9%	2811	-	1
<i>A. ferrooxidans</i> CCM4253	Mine waters, Czech Republic	GCA_003233765.1	3.19656	58.6%	3073	-	15
<i>A. ferrooxidans</i> DSM16786	Wudalianchi Heilongjiang, China	GCA_018853455.1	3.67579	58.4%	3636	-	49
<i>A. ferrooxidans</i> YQH-1	Wudalianchi volcano water, China	GCA_001418795.1	3.11122	58.60%	3012	-	96
<i>A. ferrooxidans</i> Hel18	Flue dust	GCA_001559335.1	3.10916	58.6%	3065	-	123
<i>A. ferrooxidans</i> PQ506	Santiago, Chile	GCA_018854475.1	3.37146	58.3%	3342	-	277
<i>A. ferrooxidans</i> PQ505	Santiago, Chile	GCA_018854395.1	3.51657	58.4%	3534	-	305
<i>A. ferrooxidans</i> CF3	Santiago, Chile	GCA_018854495.1	3.01139	58.7%	3057	-	310
<i>A. ferrooxidans</i> F221	-	GCA_018854265.1	3.00995	58.7%	3006	-	360
<i>A. ferrooxidans</i> BY0502	-	GCA_001652185.1	2.97667	56.8%	3026	-	295
<i>A. ferrooxidans</i> BY-3	Gansu, China	GCA_010577825.1	3.83234	57.8%	3777	-	194
<i>A. ferrooxidans</i> RVS1	Andacollo gold mining area, Argentina	GCA_003931975.1	2.82631	58.8%	2705	-	49
<i>A. ferrooxidans</i> DLC-5	-	GCA_000732185.1	4.18422	57.6%	-	-	2090
<i>A. ferrooxidans</i> COP1	-	GCA_018854355.1	3.008	58.8%	3855	-	1561
<i>A. ferrooxidans</i> S10	Santiago, Chile	GCA_018854365.1	2.953	58.8%	3998	-	1827
<i>A. ferrooxidans</i> TFBk		GCA_024626545.1	3.62032	57.9%	3640	-	159
<i>A. ferrooxidans</i> GD-A		GCA_024606825.1	2.7863	58.9%	2776		135
<i>A. ferrooxidans</i> GD-B		GCA_024606715.1	2.79519	58.9%	2806		155
<i>A. ferrooxidans</i> GD-0		GCA_024592575.1	2.77163	58.9%	2765		139
<i>A. ferrooxidans</i> BN		GCA_024606725.1	3.41125	58.5%	3489		171
<i>A. ferrooxidans</i> ZBY		GCA_024606765.1	3.40092	58.5%	3476		159
<i>A. ferrooxidans</i> DX		GCA_024606705.1	3.15885	58.5%	3216		201

Note: “-” indicates no data.

Table S2. List of selected genes identified in strain YQ-N3 strain via KEGG annotation, including genes for iron and sulfur metabolism.

Gene name	Gene length	KEGG gene ID	KEGG orthology description
fdxA	327bp	afr: AFE_0014	ferredoxin
feoA	288bp	afr:AFE_2523	ferrous iron transport protein A
feoB	2349bp	afr:AFE_2524	ferrous iron transport protein B
hemH	1014bp	afr:AFE_0179	protoporphyrin/coproporphyrin ferrochelatase
cyc2	1458bp	afr:AFE_3153	iron: rusticyanin reductase
resB	1845bp	afr:AFE_3112	cytochrome c biogenesis protein
hyaC	756bp	afr:AFE_2429	Ni/Fe-hydrogenase 1 B-type cytochrome subunit
coxA	1884bp	afe:Lferr_2747	cytochrome c oxidase subunit I
coxB	765bp	afe:Lferr_2748	cytochrome c oxidase subunit II
coxC	555bp	afr:AFE_3148	cytochrome c oxidase subunit III
porA	984bp	tth:THITH_06955	pyruvate ferredoxin oxidoreductase alpha subunit
porB	1164bp	tig:THII_3692	pyruvate ferredoxin oxidoreductase beta subunit
porC	603bp	tth:THITH_06960	pyruvate ferredoxin oxidoreductase gamma subunit
-	2340bp	afe:Lferr_1935	iron complex outer membrane receptor protein
fdxA	621bp	afr:AFE_1844	ferredoxin
fdx	306bp	afr:AFE_1541	ferredoxin, 2Fe-2S
rus	564bp	afr:AFE_3146	rusticyanin
-	1035bp	afe:Lferr_1212	iron complex transport system substrate-binding protein
petA	621bp	afe:Lferr_2707	ubiquinol-cytochrome c reductase iron-sulfur subunit
petB	1209bp	afe:Lferr_2708	ubiquinol-cytochrome c reductase cytochrome b subunit
petC	729bp	afr:AFE_3111	ubiquinol-cytochrome c reductase cytochrome c1 subunit
erpA	372bp	afj:AFERRID_10140	iron-sulfur cluster insertion protein
moaD	243bp	afr:AFE_0975	sulfur-carrier protein
iscA	324bp	afr:AFE_0675	iron-sulfur cluster assembly protein
doxDA	1083bp	afe:Lferr_0045	thiosulfate dehydrogenase (quinone)
doxA	1083bp	afj:AFERRID_13680	thiosulfate dehydrogenase (quinone) small subunit
cysN	1353bp	afr:AFE_3125	sulfate adenylyltransferase subunit 1
cysD	939bp	afe:Lferr_2723	sulfate adenylyltransferase subunit 2
cysJ	1767bp	afr:AFE_3121	sulfite reductase (NADPH) flavoprotein alpha-component
cysI	1692bp	afr:AFE_3122	sulfite reductase (NADPH) hemoprotein beta-component
cysH	738bp	afr:AFE_3123	phosphoadenosine phosphosulfate reductase
sqr	1140bp	afr:AFE_2601	sulfide:quinone oxidoreductase
hdrA2	1056bp	afr:AFE_2553	heterodisulfide reductase subunit A2
hdrB2	912bp	afr:AFE_2550	heterodisulfide reductase subunit B2
hdrC2	720bp	afr:AFE_2551	heterodisulfide reductase subunit C2
tusA	231 bp	[EC:2.8.1.-]	sulfurtransferase TusA family protein
dsrE	342bp	afr:AFE_2556	tRNA 2-thiouridine synthesizing protein D
thiS	201bp	afr:AFE_0642	sulfur carrier protein