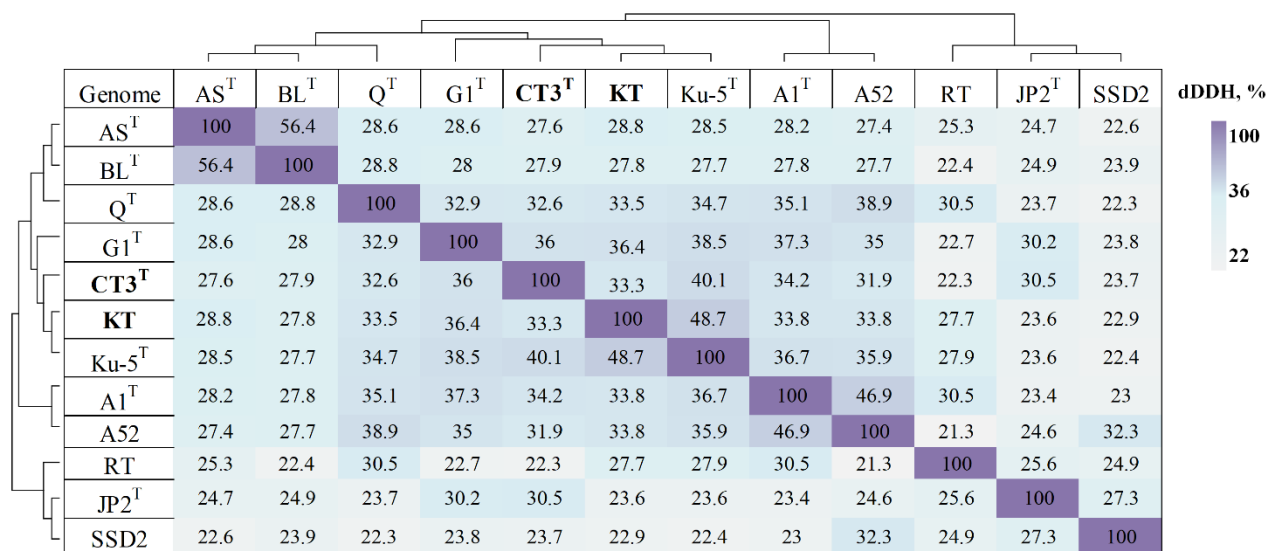
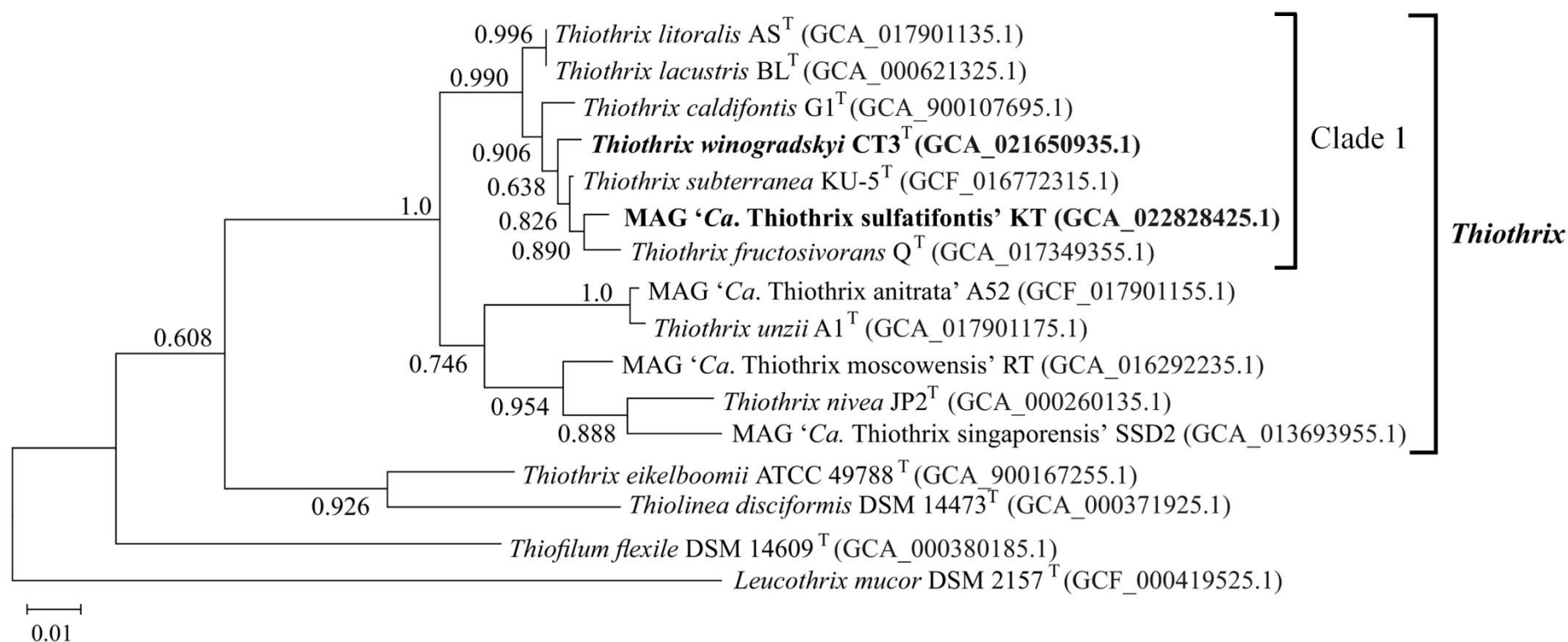




**Figure S1.** Bacterial mats of *Thiothrix* in the hydrogen sulfide spring "Sероводородный" in Tatarstan, Russia.



**Figure S2.** dDDH pairwise values for *Thiothrix* genomes. *T. lacustris* BL<sup>T</sup>, (GCF\_000621325.1); *T. litoralis* AS<sup>T</sup> (GCF\_017901135.1); *T. subterranea* Ku-5<sup>T</sup> (GCF\_016772315.1); MAG of *Thiothrix* sp. KT (GCA\_022828425.1); *T. caldifontis* G1<sup>T</sup> (GCF\_900107695.1); *Thiothrix* sp. CT3 (GCA\_021650935.1); *T. fructosivorans* Q<sup>T</sup> (GCA\_017349355.1); *T. unzii* A1<sup>T</sup> (GCA\_017901175.1); MAG of *Thiothrix* sp. A2; MAG of *Thiothrix* sp. A52 (GCF\_017901155.1); ‘*Ca. Thiothrix moscowensis*’ RT (GCA\_016292235.1); *T. nivea* JP2<sup>T</sup> (GCF\_000260135.1); ‘*Ca. Thiothrix singaporensis*’ SSD2 (GCA\_013693955.1).



**Figure S3.** 16S rRNA gene-based maximum-likelihood phylogenetic tree of type strains of *Thiothrix* species. The 16S rRNA gene sequences extracted from genomes (assembly accession numbers are listed after the genome name) were aligned against the SILVA database using SINA v.1.2.11. The alignment had 1535 positions. The best evolutionary model, HKY+G+I (HKY substitution model, estimated proportion of invariable sites, estimated gamma shape parameter), was defined by jModelTest v.2.1.10 with the Bayesian Information Criterion. The maximum likelihood tree was constructed using PhyML v.3.3 with 500 bootstrap replicates; the Log-likelihood of the tree was -5038.18080. The internal branching support levels are specified at the nodes. The genome of *Leucothrix mucor* DSM 2157<sup>T</sup> was used for tree rooting. Scale, 0.01 substitutions per nucleotide position. Note that *Thiothrix eikelboomii* actually should belong to the genus *Thiolinea* but cannot be reclassified because of its absence in two international collections [3].

Table S1. Genes encoding enzymes of metabolic pathways in ‘*Candidatus* Thiothrix sulfatifontis’ KT and *Thiothrix winogradskyi* CT3<sup>T</sup>.

Gene	Predicted function	KT	CT3
		RefSeq (GeneBank) locus_tag	RefSeq (GeneBank) locus_tag
Sulfur metabolism			
<i>sqrA</i>	Sulfide quinone oxidoreductase SqrA (EC 1.8.5.4)	L3K52_05845	L2Y54_RS07100
<i>sqrF</i>	Sulfide quinone oxidoreductase SqrF (EC 1.8.5.4)	L3K52_13295	L2Y54_RS12370 L2Y54_RS12360
<i>fccB</i>	Sulfide dehydrogenase (flavocytochrome c) flavoprotein chain	L3K52_05350 L3K52_18375 L3K52_10900	L2Y54_RS06570 L2Y54_RS06620 L2Y54_RS21270 L2Y54_RS15945
<i>fccA</i>	cytochrome c subunit of flavocytochrome c sulfide dehydrogenase	L3K52_05185	L2Y54_RS06390
<i>soxA</i>	sulfur oxidation c-type cytochrome SoxA (EC 1.8.2.3 )	L3K52_01425	L2Y54_RS05655 L2Y54_RS10175 L2Y54_RS11445
<i>soxZ</i>	thiosulfate oxidation carrier complex protein SoxZ (EC 1.8.2.6 )	L3K52_01420 L3K52_01435	L2Y54_RS05660 L2Y54_RS10180
<i>soxY</i>	thiosulfate oxidation carrier protein SoxY (EC 1.8.2.6 )	L3K52_01415 L3K52_01430	L2Y54_RS05665 L2Y54_RS10185
<i>soxB</i>	thiosulfohydrolase SoxB (EC 3.1.6.20)	L3K52_01470	L2Y54_RS05615
<i>soxX</i>	sulfur oxidation c-type cytochrome SoxX (EC 1.8.2.3 )	L3K52_01410	L2Y54_RS05670 L2Y54_RS10170 L2Y54_RS11440
<i>soeA</i>	sulfite dehydrogenase (quinone) subunit SoeA (EC 1.8.5.6)	L3K52_02785	L2Y54_RS04105
<i>soeB</i>	sulfite dehydrogenase (quinone) subunit SoeB (EC 1.8.5.6)	L3K52_02780	L2Y54_RS04110
<i>soeC</i>	sulfite dehydrogenase (quinone) subunit SoeC (EC 1.8.5.6)	L3K52_02775	L2Y54_RS04115

<i>aprA</i>	adenylylsulfate reductase, subunit A (EC 1.8.4.10)	L3K52_04580	L2Y54_RS05790
<i>aprB</i>	adenylylsulfate reductase, subunit B (EC 1.8.4.10)	L3K52_04575	L2Y54_RS05785
<i>sat</i>	sulfate adenylyltransferase (EC 2.7.7.4)	L3K52_04570	L2Y54_RS05780
<i>dsrA</i>	Dissimilatory sulfite reductase, alpha subunit (EC 1.8.99.5)	L3K52_08855	L2Y54_RS11490
<i>dsrB</i>	Dissimilatory sulfite reductase, beta subunit (EC 1.8.99.5)	L3K52_08860	L2Y54_RS11495
<i>dsrE</i>	tRNA 2-thiouridine synthesizing protein D (EC 2.8.1.-)	L3K52_08865	L2Y54_RS11500
<i>dsrF</i>	tRNA 2-thiouridine synthesizing protein C (EC 2.8.1.-)	L3K52_08870	L2Y54_RS11505
<i>dsrH</i>	tRNA 2-thiouridine synthesizing protein B (EC 2.8.1.-)	L3K52_08875	L2Y54_RS11510
<i>dsrC</i>	tRNA 2-thiouridine synthesizing protein E (EC 2.8.1.-)	L3K52_08835 L3K52_08880	L2Y54_RS11470 L2Y54_RS11515
<i>dsrM</i>	sulfite reduction-associated complex DsrMKJOP protein DsrM	L3K52_08885	L2Y54_RS11520
<i>dsrK</i>	sulfite reduction-associated complex DsrMKJOP protein DsrK	L3K52_08890	L2Y54_RS11525
<i>dsrL</i>	glutamate synthase (NADPH) small chain dsrL/ intracellular sulfur oxidation protein DsrL	L3K52_08895	L2Y54_RS11530
<i>dsrJ</i>	Sulfite reduction-associated complex DsrMKJOP multiheme protein DsrJ	L3K52_08900	L2Y54_RS11535
<i>dsrO</i>	sulfite reduction-associated complex	L3K52_08905	L2Y54_RS11540

	DsrMKJOP iron-sulfur protein DsrO		
<i>dsrP</i>	sulfite reduction-associated complex DsrMKJOP protein DsrP	L3K52_08910	L2Y54_RS11545
<i>dsrN</i>	Cobyrinic acid A,C-diamide synthase DsrN (EC 6.3.5.11)	L3K52_11740	L2Y54_RS14880
<i>dsrR</i>	protein involved in sulfur oxidation DsrR	L3K52_11745	L2Y54_RS14875
<i>dsrS</i>	protein involved in sulfur oxidation DsrS	L3K52_11645	L2Y54_RS14955
<b>Nitrogen metabolism</b>			
<i>narG</i>	nitrate reductase alpha subunit (EC 1.7.99.4)	-	L2Y54_RS20190
<i>narH</i>	nitrate reductase beta subunit (EC 1.7.5.1)	-	L2Y54_RS20185
<i>narI</i>	nitrate reductase gamma subunit (EC 1.7.5.1)	-	L2Y54_RS20175
<i>narJ</i>	nitrate reductase delta subunit (EC 1.7.5.1)	-	L2Y54_RS20180
<i>nirS</i>	nitrite reductase (NO-forming) (EC 1.7.2.1)	-	L2Y54_RS20045
<i>cnorB</i>	nitric oxide reductase subunit B (EC 1.7.2.5 )	-	L2Y54_RS20040
<i>cnorC</i>	nitric oxide reductase subunit C (EC 1.7.2.5 )	-	L2Y54_RS20035
<i>nirB</i>	nitrite reductase (NADH) large subunit (EC 1.7.1.1)	L3K52_06745	L2Y54_RS07995
<i>nirD</i>	nitrite reductase (NADH) small subunit (EC 1.7.1.1)	L3K52_06750	L2Y54_RS08000
<i>nifA</i>	Nif-specific regulatory protein NifA	L3K52_17530	-
<i>nifS</i>	cysteine desulfurase NifS (EC 2.8.1.7)	L3K52_17560	-
<i>nifU</i>	nitrogen fixation protein NifU and related proteins	L3K52_17565	-
<i>nifB</i>	nitrogen fixation protein NifB	L3K52_17615	-

<i>nifX</i>	nitrogen fixation protein NifX	-	-
<i>nifX2</i>	nitrogen fixation protein NifX2	-	-
<i>nifB2</i>	nitrogen fixation protein NifB2	L3K52_12300	-
<i>nifY</i>	nitrogen fixation-related protein, gamma subunit	-	-
<i>nifE</i>	nitrogenase molybdenum-cofactor synthesis protein NifE (EC 1.18.6.1)	L3K52_08140	-
<i>nifN</i>	nitrogenase molybdenum-iron protein NifN (EC 1.18.6.1.)	L3K52_08145	-
<i>nifQ</i>	nitrogen fixation protein NifQ	L3K52_17585	-
<i>nifV</i>	homocitrate synthase NifV (EC 2.3.3.14)	L3K52_08110	-
<i>nifW</i>	nitrogen fixation protein NifW	L3K52_08070	-
<i>nifM</i>	nitrogen fixation protein NifM	L3K52_08060	-
<i>nifH</i>	nitrogenase iron protein NifH (EC 1.18.6.1)	-	-
<i>nifD</i>	nitrogenase molybdenum-iron protein alpha chain (EC 1.18.6.1)	-	-
<i>nifK</i>	nitrogenase molybdenum-iron protein beta chain (EC 1.18.6.1)	-	-
<i>nifZ</i>	nitrogen fixation protein NifZ	L3K52_08065	-
<i>nifT</i>	nitrogen fixation protein NifT	-	-
<i>nifO</i>	NifO	L3K52_17600	-
<i>nasA</i>	assimilatory nitrate reductase catalytic subunit	L3K52_06755	L2Y54_RS08005
<b>Phosphorus metabolism</b>			
<i>phoU</i>	phosphate transport system protein PhoU	L3K52_14400	L2Y54_RS13770 L2Y54_RS13790

<i>phoR</i>	Phosphate regulon sensor protein PhoR (EC 2.7.13.3)	L3K52_14410	L2Y54_RS13780
<i>phoB</i>	Phosphate regulon transcriptional regulatory protein PhoB (EC 2.7.13.3)	L3K52_14170 L3K52_14405	L2Y54_RS12815 L2Y54_RS13775
<i>pstS</i>	phosphate transport system permease protein PstS	L3K52_00885 L3K52_11775 L3K52_14215 L3K52_14360	L2Y54_RS10225 L2Y54_RS13730 L2Y54_RS14835
<i>pstA</i>	phosphate transport system permease protein PstA (EC 7.3.2.1)	L3K52_14390	L2Y54_RS13760
<i>pstC</i>	phosphate transport system permease protein PstC (EC 7.3.2.1)	L3K52_14385	L2Y54_RS13755
<i>pstB</i>	pstA; phosphate transport system permease protein PstB (EC 7.3.2.1)	L3K52_14395	L2Y54_RS13765
<i>ppkI</i>	polyphosphate kinase (EC 2.7.4.1)	L3K52_16915	L2Y54_RS19505
<i>epp</i>	Exopolyphosphatase (EC 3.6.1.11)	L3K52_01755	L2Y54_RS05070
<b>Emden-Meyerhof (EM) pathway and Calvin-Benson-Bassham cycle</b>			
<i>glk</i>	Glucokinase (EC 2.7.1.2)	L3K52_02195	L2Y54_RS04615
<i>pgi</i>	glucose-6-phosphate isomerase (EC 5.3.1.9)	L3K52_02200	L2Y54_RS04610
<i>pfk</i>	6-phosphofructokinase (EC 2.7.1.11)	L3K52_04600	L2Y54_RS05810
<i>fbaA</i>	fructose-bisphosphate aldolase class II (EC 4.1.2.13)	L3K52_04730	L2Y54_RS05940
<i>tpiA</i>	triosephosphate isomerase (EC 5.3.1.1)	L3K52_08945	L2Y54_RS11580
<i>gapA</i>	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	L3K52_04880 L3K52_04715	L2Y54_RS01965 L2Y54_RS10245 L2Y54_RS05925
<i>pgk</i>	Phosphoglycerate kinase (EC 2.7.2.3)	L3K52_04720	L2Y54_RS05930



<i>gpmI</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)	L3K52_04765	L2Y54_RS02070
<i>eno</i>	Enolase (EC 4.2.1.11)	L3K52_10575	L2Y54_RS12835
<i>pyk</i>	Pyruvate kinase (EC 2.7.1.40)	L3K52_14355 L3K52_04725	L2Y54_RS13725 L2Y54_RS05935
<i>porA</i>	pyruvate ferredoxin oxidoreductase alpha subunit [EC:1.2.7.1]	L3K52_02800	L2Y54_RS04055
<i>porB</i>	pyruvate ferredoxin oxidoreductase beta subunit [EC:1.2.7.1]	L3K52_02805	L2Y54_RS04050
<i>porC</i> , <i>porG</i>	pyruvate ferredoxin oxidoreductase gamma subunit [EC:1.2.7.1]	L3K52_02795	L2Y54_RS04060
<i>aceE</i>	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	L3K52_14985	L2Y54_RS17170 L2Y54_RS04245
<i>pdhC</i>	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	L3K52_14980	L2Y54_RS17165 L2Y54_RS04240
<i>pdhD</i>	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)	L3K52_14975	L2Y54_RS17160
		L3K52_10195	L2Y54_RS04235
<i>rpiA</i>	Ribose-5-phosphate isomerase A (EC 5.3.1.6)	L3K52_05760	L2Y54_RS06975
<i>rpe</i>	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	L3K52_15085	L2Y54_RS17270
<i>tktA</i>	Transketolase (EC 2.2.1.1)	L3K52_04710	L2Y54_RS05920
<i>fbp</i>	Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)	L3K52_03050	L2Y54_RS03730

<i>rbcL</i>	Ribulose biphosphate carboxylase large chain (EC 4.1.1.39)	L3K52_12120 L3K52_00755 L3K52_15820	L2Y54_RS00875 L2Y54_RS01010
<i>rbcS</i>	Ribulose biphosphate carboxylase small chain (EC 4.1.1.39)	L3K52_00760 L3K52_15825	L2Y54_RS01015
<i>prkB</i>	Phosphoribulokinase (EC 2.7.1.19)	L3K52_10935 L3K52_04410	L2Y54_RS02325 L2Y54_RS15920
<b>Tricarboxylic acid (TCA) cycle, glyoxylate cycle and a way to anabolism from TCA</b>			
<i>gltA</i>	Citrate synthase (si) (EC 2.3.3.1)	L3K52_10210	L2Y54_RS16985
<i>acnB</i>	Aconitate hydratase 2 (EC 4.2.1.3)	L3K52_10215	L2Y54_RS16980
<i>idh</i>	Isocitrate dehydrogenase (NADP) (EC 1.1.1.42)	L3K52_12060	L2Y54_RS14605 L2Y54_RS18995 L2Y54_RS06290
<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	L3K52_13190 L3K52_11440	L2Y54_RS18995 L2Y54_RS06290
<i>sucB</i>	2-oxoglutarate dehydrogenase E2 complex (EC 2.3.1.61)	L3K52_10190	L2Y54_RS12490
<i>sucD</i>	Succinyl-CoA ligase (ADP-forming) alpha chain (EC 6.2.1.5)	L3K52_10205	L2Y54_RS13255
<i>sucC</i>	Succinyl-CoA ligase (ADP-forming) beta chain (EC 6.2.1.5)	L3K52_10200	L2Y54_RS16995
<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	L3K52_13210	L2Y54_RS12470
<i>sdhB</i>	Succinate dehydrogenase iron- sulfur protein (EC 1.3.99.1)	L3K52_13215	L2Y54_RS12465
<i>sdhC</i>	Succinate dehydrogenase cytochrome b-556 subunit (EC 1.3.99.1)	L3K52_13200	L2Y54_RS12480
<i>sdhD</i>	Succinate dehydrogenase hydrophobic	L3K52_13205	L2Y54_RS10030

	membrane anchor protein (EC 1.3.5.1)		
<i>fumA</i>	Fumarate hydratase class I, aerobic (EC 4.2.1.2)	L3K52_13100	L2Y54_RS12610
<i>mgo</i>	Malate:quinone oxidoreductase (EC 1.1.5.4)	L3K52_16865	L2Y54_RS19455
<i>pckA</i>	Phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49)	L3K52_10325	L2Y54_RS16795
<i>aspB</i>	Aspartate aminotransferase (EC 2.6.1.1)	L3K52_11185 L3K52_15490 L3K52_15450	L2Y54_RS15595 L2Y54_RS17995
<i>gltB</i>	Glutamate synthase (NADPH) large chain (EC 1.4.1.13)	L3K52_15405	L2Y54_RS17900
<i>gltD</i>	Glutamate synthase (NADPH) small chain (EC 1.4.1.13)	L3K52_15410	L2Y54_RS17905
<i>aceA</i>	Isocitrate lyase (EC 4.1.3.1)	L3K52_16860	L2Y54_RS19450
<i>aceB</i>	Malate synthase G (EC 2.3.3.9)	L3K52_01335	L2Y54_RS06200
<i>maeB</i>	NADP-dependent malic enzyme (EC 1.1.1.40)	L3K52_01365	L2Y54_RS06165
<i>ppc</i>	phosphoenolpyruvate carboxylase (EC 4.1.1.31)	L3K52_06505	L2Y54_RS07775
<i>pyc</i>	Pyruvate carboxylase (EC 6.4.1.1)	L3K52_11710	L2Y54_RS14905
<b>Antioxidant protection</b>			
<i>SOD2</i>	Superoxide dismutase [Fe] (EC 1.15.1.1)	L3K52_00175	L2Y54_RS00165
<i>CAT2</i>	catalase/oxidase HPI (EC 1.11.1.21)	L3K52_09360	L2Y54_RS11910
<i>CAT</i>	Catalase (EC 1.11.1.6)	L3K52_07200	-
<i>ccp</i>	Cytochrome c551 peroxidase (EC 1.11.1.5)	L3K52_05920 L3K52_09275	L2Y54_RS07160 L2Y54_RS11850 L2Y54_RS11925
<b>Respiratory Electron Transfer Chain</b>			
<b>Complex 1 NADH-dehydrogenase</b>			
<i>nuoA</i>	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)	L3K52_08960	L2Y54_RS11595

<i>nuoB</i>	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)	L3K52_08965	L2Y54_RS11600
<i>nuoC</i>	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)	L3K52_08970	L2Y54_RS11605
<i>nuoD</i>	NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)	L3K52_08975	L2Y54_RS11610
<i>nuoE</i>	NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)	L3K52_08980	L2Y54_RS11615
<i>nuoF</i>	NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)	L3K52_08985	L2Y54_RS11620
<i>nuoG</i>	NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3)	L3K52_08990	L2Y54_RS11625
<i>nuoH</i>	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)	L3K52_08995	L2Y54_RS11630
<i>nuoI</i>	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)	L3K52_09000	L2Y54_RS11635
<i>nuoJ</i>	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)	L3K52_09005	L2Y54_RS11640
<i>nuoK</i>	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)	L3K52_09010	L2Y54_RS11645
<i>nuoL</i>	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)	L3K52_09015 L3K52_01510	L2Y54_RS11650
<i>nuoM</i>	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)	L3K52_09020 L3K52_01500 L3K52_01515 L3K52_01520	L2Y54_RS11655 L2Y54_RS00890 L2Y54_RS00915 L2Y54_RS00920
<i>nuoN</i>	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)	L3K52_09025	L2Y54_RS11660
<b>Complex II (succinate dehydrogenase)</b>			
<i>sdhC</i>	Succinate dehydrogenase, cytochrome b556 subunit (EC 1.3.99.1)	L3K52_13210	L2Y54_RS12470
<i>sdhD</i>	Succinate dehydrogenase, hydrophobic	L3K52_13215	L2Y54_RS12465

	membrane anchor protein (EC 1.3.5.1)		
<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	L3K52_13200	L2Y54_RS12480
<i>sdhB</i>	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	L3K52_13205	L2Y54_RS10030
<b>Complex III</b>			
<i>cytB</i>	ubiquinol-cytochrome c reductase cytochrome b subunit (EC 7.1.1.8)	L3K52_16505	L2Y54_RS19170
<i>cyc1</i>	ubiquinol-cytochrome c reductase cytochrome c1 subunit (EC 7.1.1.8)	L3K52_16500	L2Y54_RS19165
<i>rip1</i> ( <i>ISP</i> )	ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 7.1.1.8)	L3K52_16510 L3K52_10880	L2Y54_RS15965 L2Y54_RS19175
<b>Complex IV (terminal oxydases)</b>			
<i>cyoE</i>	Heme A synthase, cytochrome oxidase biogenesis protein Cox15-CtaA (EC 2.5.1.141)	L3K52_00155	L2Y54_RS00145
<i>cox11</i>	cytochrome c oxidase assembly protein subunit 11 (EC 7.1.1.9)	L3K52_00125	L2Y54_RS00115
<i>cox15</i>	cytochrome c oxidase assembly protein subunit 15 (EC 7.1.1.9)	L3K52_00100 L3K52_00155	L2Y54_RS00085
<i>coxB</i>	cytochrome c oxidase subunit II (EC 7.1.1.9)	L3K52_00115	L2Y54_RS00100
<i>coxA</i>	cytochrome c oxidase subunit I (EC 7.1.1.9)	L3K52_00120	L2Y54_RS00105
<i>coxC</i>	cytochrome c oxidase subunit III (EC 7.1.1.9)	L3K52_00130	L2Y54_RS00120

<i>coxD</i>	cytochrome c oxidase subunit IV (EC 7.1.1.9)	-	L2Y54_RS20060
<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit I (EC 7.1.1.7)	L3K52_15575	-
<i>cydB</i>	Cytochrome d ubiquinol oxidase subunit II (EC 7.1.1.7)	L3K52_15570	-
<i>cydC</i>	Transport ATP-binding protein CydC	L3K52_15555	-
<i>cydD</i>	Transport ATP-binding protein CydD	L3K52_15560	-
<i>ccoN</i>	cytochrome c oxidase cbb3-type subunit I (EC 1.9.3.1)	L3K52_14130	L2Y54_RS16310 L2Y54_RS19630
<i>ccoO</i>	cytochrome c oxidase cbb3-type subunit II (EC 7.1.1.9)	L3K52_14125	L2Y54_RS16305 L2Y54_RS19625
<i>ccoP</i>	cytochrome c oxidase cbb3-type subunit III (EC 7.1.1.9)	L3K52_14115	L2Y54_RS16295 L2Y54_RS19615
<i>ccoG</i> ( <i>FixG</i> )	Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation	L3K52_14635	L2Y54_RS19610 L2Y54_RS17630
<i>ccoQ</i>	CcoQ/FixQ family Cbb3-type cytochrome c oxidase assembly chaperone (EC 1.9.3.1)	-	L2Y54_RS19620
<i>ccoS</i>	cbb3-type cytochrome oxidase assembly protein CcoS	L3K52_14620	L2Y54_RS17615
<b>ATPase</b>			
<i>atpA</i>	F-type H <sup>+</sup> -transporting ATPase subunit alpha (EC 7.1.2.2)	L3K52_00430	L2Y54_RS00385 L2Y54_RS09295
<i>atpD</i>	F-type H <sup>+</sup> -transporting ATPase subunit beta (EC 7.1.2.2)	L3K52_00420	L2Y54_RS00375
<i>atpH</i>	F-type H <sup>+</sup> -transporting ATPase	L3K52_00435	L2Y54_RS00390

	subunit delta (EC 7.1.2.2)		
<i>atpC</i>	F-type H <sup>+</sup> -transporting ATPase subunit epsilon (EC 7.1.2.2)	L3K52_00415	L2Y54_RS00370
<i>atpG</i>	F-type H <sup>+</sup> -transporting ATPase subunit gamma (EC 7.1.2.2)	L3K52_00425	L2Y54_RS00380
<i>atpB</i>	F-type H <sup>+</sup> -transporting ATPase subunit a (EC 7.1.2.2)	L3K52_00450	L2Y54_RS00405
<i>atpF</i>	F-type H <sup>+</sup> -transporting ATPase subunit b (EC 7.1.2.2)	L3K52_00440	L2Y54_RS00395
<i>atpE</i>	ATP synthase F <sub>0</sub> sector subunit c (EC 7.1.2.2)	L3K52_00445	L2Y54_RS00400