

Table S1. Identity level of 16S rRNA genes in representatives of the genus *Thiothrix*, %.

	<i>Thiothrix</i> sp. RT	<i>Thiothrix</i> sp.SSD2	<i>T. nivea</i> DSM 5205 ^T	<i>T. unzii</i> A1 ^T	<i>T. lacustris</i> BL ^T	<i>T. caldifontis</i> G1 ^T	<i>T. fructosivorans</i> Q ^T
<i>Thiothrix</i> sp RT	100.0	93.0	97.9	95.9	96.1	96.3	94.9
<i>Thiothrix</i> sp SSD2	94.0	100.0	96.1	94.8	94.6	94.3	93.3
<i>T. nivea</i> DSM 5205 ^T	97.9	96.1	100.0	94.6	95.1	95.1	94.3
<i>T. unzii</i> A1 ^T	95.9	94.8	95.41	100.0	95.4	95.5	95.7
<i>T. lacustris</i> BL ^T	96.1	94.6	94.6	94.8	100.0	98.7	98.6
<i>T. caldifontis</i> G1 ^T	96.3	94.3	95.1	95.5	98.7	100.0	98.9

Table S2. Molecular characteristics of representatives of the genus *Thiothrix*.

Species	<i>T. nivea</i> DSM 5205 ^T	<i>T. lacustris</i> BL ^T	<i>T. caldifontis</i> G1 ^T	<i>Thiothrix</i> sp. RT	<i>Thiothrix</i> sp. SSD2
% Average nucleotide identity (ANI) to:					
<i>T. nivea</i> DSM 5205 ^T	100.0	76.7	75.5	77.5	80.2
<i>T. lacustris</i> BL ^T	76.7	100.0	79.0	76.5	75.9
<i>T. caldifontis</i> G1 ^T	75.5	79.0	100.0	76.7	74.8
<i>Thiothrix</i> sp. RT	77.5	76.5	76.7	100.0	76.7
<i>Thiothrix</i> sp. SSD2	80.2	75.9	74.8	76.7	100.0
% dDDH to:					
<i>T. nivea</i> DSM 5205 ^T	100.0	23.9	23.8	25.6	27.3
<i>T. lacustris</i> BL ^T	23.9	100.0	28.0	24.9	22.4
<i>T. caldifontis</i> G1 ^T	23.8	28.0	100.0	30.2	22.7
<i>Thiothrix</i> sp. RT	25.6	24.9	30.2	100.0	24.9
<i>Thiothrix</i> sp. SSD2	27.3	22.4	22.7	24.9	100.0

Table S3. Genes encoding enzymes of metabolic pathways in *Thiothrix* sp. SSD2 and *Thiothrix* sp. RT.

Gene	Predicted function	<i>Thiothrix</i> sp. RT	<i>Thiothrix</i> sp. SSD2
		RefSeq (GeneBank) ID of gene	RefSeq (GeneBank) ID of gene
Sulfur metabolism			
<i>sqrA</i>	Sulfide quinone oxidoreductase SqrA (EC 1.8.5.4)	fig 6666666.654935.peg.2381	QLQ30307.1
<i>sqrF</i>	Sulfide quinone oxidoreductase SqrF (EC 1.8.5.4)	fig 6666666.654935.peg.1874	QLQ32374.1
<i>fccB</i>	Sulfide dehydrogenase (flavocytochrome c) flavoprotein chain	fig 6666666.654935.peg.278 fig 6666666.654935.peg.268 fig 6666666.654935.peg.1885 fig 6666666.654935.peg.1391	QLQ32594.1
<i>fccA</i>	cytochrome c subunit of flavocytochrome c sulfide dehydrogenase	fig 6666666.654935.peg.269	QLQ32595.1

<i>sqrD</i>	Sulfide quinone oxidoreductase SqrD (EC 1.8.5.4)	—	QLQ32934.1
<i>soxA</i>	sulfur oxidation c-type cytochrome SoxA (EC 1.8.2.3)	fig 6666666.654935.peg.3301 fig 6666666.654935.peg.708	QLQ32948.1 QLQ33792.1
<i>soxZ</i>	thiosulfate oxidation carrier complex protein SoxZ (EC 1.8.2.6)	fig 6666666.654935.peg.2874 fig 6666666.654935.peg.709	QLQ33790.1 QLQ33793.1
<i>soxY</i>	thiosulfate oxidation carrier protein SoxY (EC 1.8.2.6)	fig 1947697.4.peg.582 fig 1947697.4.peg.2162	QLQ33791.1 QLQ33794.1
<i>soxB</i>	thiosulfohydrolase SoxB (EC 3.1.6.20)	fig 6666666.654935.peg.2028	QLQ33787.1
<i>soxX</i>	sulfur oxidation c-type cytochrome SoxX (EC 1.8.2.3)	fig 6666666.654935.peg.3302 fig 6666666.654935.peg.572	QLQ32949.1 QLQ33795.1
<i>soeA</i>	sulfite dehydrogenase (quinone) subunit SoeA (EC 1.8.5.6)	fig 6666666.654935.peg.2056	WP_012971673.1 locus_tag="HZT40_19335"
<i>soeB</i>	sulfite dehydrogenase (quinone) subunit SoeB (EC 1.8.5.6)	fig 6666666.654935.peg.2057	QLQ34300.1
<i>soeC</i>	sulfite dehydrogenase (quinone) subunit SoeC (EC 1.8.5.6)	fig 6666666.654935.peg.2058	QLQ33396.1
<i>aprA</i>	adenylylsulfate reductase, subunit A (EC 1.8.4.10)	fig 6666666.654935.peg.3158	QLQ33717.1
<i>aprB</i>	adenylylsulfate reductase, subunit B (EC 1.8.4.10)	fig 6666666.654935.peg.3159	QLQ33716.1
<i>sat</i>	sulfate adenylyltransferase (EC 2.7.7.4)	fig 6666666.654935.peg.3160	QLQ33715.1
<i>dsrA</i>	Dissimilatory sulfite reductase, alpha subunit (EC 1.8.99.5)	fig 6666666.654935.peg.3292	QLQ32927.1
<i>dsrB</i>	Dissimilatory sulfite reductase, beta subunit (EC 1.8.99.5)	fig 6666666.654935.peg.3291	QLQ32926.1
<i>dsrE</i>	tRNA 2-thiouridine synthesizing protein D (EC 2.8.1.-)	fig 6666666.654935.peg.3290	QLQ32925.1
<i>dsrF</i>	tRNA 2-thiouridine synthesizing protein C (EC 2.8.1.-)	fig 6666666.654935.peg.3289	QLQ32924.1
<i>dsrH</i>	tRNA 2-thiouridine synthesizing protein B (EC 2.8.1.-)	fig 6666666.654935.peg.3288	QLQ32923.1
<i>dsrC</i>	tRNA 2-thiouridine synthesizing protein E (EC 2.8.1.-)	fig 6666666.654935.peg.3287 fig 6666666.654935.peg.3296	QLQ32922.1 QLQ30843.1
<i>dsrM</i>	sulfite reduction-associated complex DsrMKJOP protein DsrM	fig 6666666.654935.peg.3286	QLQ34178.1
<i>dsrK</i>	sulfite reduction-associated complex DsrMKJOP protein DsrK	fig 6666666.654935.peg.3285	QLQ32920.1
<i>dsrL</i>	glutamate synthase (NADPH) small chain dsrL/ intracellular sulfur oxidation protein DsrL	fig 6666666.654935.peg.3284	QLQ33191.1

<i>dsrJ</i>	Sulfite reduction-associated complex DsrMKJOP multiheme protein DsrJ	fig 6666666.654935.peg.3283	QLQ32918.1
<i>dsrO</i>	sulfite reduction-associated complex DsrMKJOP iron-sulfur protein DsrO	fig 6666666.654935.peg.3282	QLQ32917.1
<i>dsrP</i>	sulfite reduction-associated complex DsrMKJOP protein DsrP	fig 6666666.654935.peg.3281	QLQ32917.1
<i>dsrN</i>	Cobyrinic acid A,C-diamide synthase DsrN (EC 6.3.5.11)	fig 6666666.654935.peg.2759	QLQ31889.1
<i>dsrR</i>	protein involved in sulfur oxidation DsrR	fig 6666666.654935.peg.2760	—
<i>dsrS</i>	protein involved in sulfur oxidation DsrS	fig 6666666.654935.peg.40	QLQ31126.1
Nitrogen metabolism			
<i>narG</i>	nitrate reductase alpha subunit (EC 1.7.5.1)	fig 6666666.654935.peg.651	QLQ32018.1
<i>narH</i>	nitrate reductase beta subunit (EC 1.7.5.1)	fig 6666666.654935.peg.652	QLQ32018.1
<i>narI</i>	nitrate reductase gamma subunit (EC 1.7.5.1)	fig 6666666.654935.peg.654	QLQ34178.1
<i>narJ</i>	nitrate reductase delta subunit (EC 1.7.5.1)	fig 6666666.654935.peg.653	WP_020558834.1 locus_tag="HZT40_10965"
<i>nirS</i>	nitrite reductase (NO-forming) (EC 1.7.2.1)	—	QLQ34181.1
<i>cnorB</i>	nitric oxide reductase subunit B (EC 1.7.2.5)	fig 6666666.654935.peg.1942	QLQ32042.1
<i>cnorC</i>	nitric oxide reductase subunit C (EC 1.7.2.5)	fig 6666666.654935.peg.1941	QLQ32043.1
<i>nirB</i>	nitrite reductase (NADH) large subunit (EC 1.7.1.1)	fig 6666666.654935.peg.1096	QLQ33725.1
<i>nirD</i>	nitrite reductase (NADH) small subunit (EC 1.7.1.1)	fig 6666666.654935.peg.1097	WP_002709036.1 locus_tag="HZT40_21300"
<i>nifA</i>	Nif-specific regulatory protein NifA	fig 6666666.654935.peg.634	QLQ31724.1
<i>nifS</i>	cysteine desulfurase NifS (EC 2.8.1.7)	fig 6666666.654935.peg.668	QLQ31672.1
<i>nifU</i>	nitrogen fixation protein NifU and related proteins	fig 6666666.654935.peg.667	QLQ30621.1
<i>nifB</i>	nitrogen fixation protein NifB	fig 6666666.654935.peg.656	QLQ31713.1
<i>nifX</i>	nitrogen fixation protein NifX	fig 6666666.654935.peg.2777	QLQ32343.1
<i>nifX2</i>	nitrogen fixation protein NifX2	fig 6666666.654935.peg.2779	QLQ32343.1
<i>nifB2</i>	nitrogen fixation protein NifB2	—	QLQ31713.1
<i>nifY</i>	nitrogen fixation-related protein, gamma subunit	fig 6666666.654935.peg.3527	—
<i>nifE</i>	nitrogenase molybdenum-cofactor synthesis protein NifE (EC 1.18.6.1)	fig 6666666.654935.peg.2774 fig 6666666.654935.peg.2775	QLQ34086.1
<i>nNifN</i>	nitrogenase molybdenum-iron protein NifN (EC 1.18.6.1.)	fig 6666666.654935.peg.2776	QLQ34087.1
<i>nifQ</i>	nitrogen fixation protein NifQ	fig 6666666.654935.peg.662	QLQ31677.1

<i>nifV</i>	homocitrate synthase NifV (EC 2.3.3.14)	fig 6666666.654935.peg.675	QLQ30738.1
<i>nifW</i>	nitrogen fixation protein NifW	fig 6666666.654935.peg.614	QLQ30752.1
<i>nifM</i>	nitrogen fixation protein NifM	fig 6666666.654935.peg.616	QLQ30754.1
<i>nifH</i>	nitrogenase iron protein NifH (EC 1.18.6.1)	fig 6666666.654935.peg.3522	QLQ32348.1
<i>nifD</i>	nitrogenase molybdenum- iron protein alpha chain (EC 1.18.6.1)	fig 6666666.654935.peg.3523	QLQ32347.1
<i>nifK</i>	nitrogenase molybdenum- iron protein beta chain (EC 1.18.6.1)	fig 6666666.654935.peg.3524	QLQ32346.1
<i>nifZ</i>	nitrogen fixation protein NifZ	fig 6666666.654935.peg.615	QLQ30753.1
<i>nifT</i>	nitrogen fixation protein NifT	fig 6666666.654935.peg.3525	QLQ32345.1
<i>nifO</i>	NifO	—	QLQ31710.1
Phosphorus metabolism			
<i>phoU</i>	phosphate transport system protein PhoU	fig 6666666.654935.peg.2604	QLQ33978.1
<i>phoR</i>	Phosphate regulon sensor protein PhoR (EC 2.7.13.3)	fig 6666666.654935.peg.2602	QLQ32508.1
<i>phoB</i>	Phosphate regulon transcriptional regulatory protein PhoB (EC 2.7.13.3)	fig 6666666.654935.peg.1341 fig 6666666.654935.peg.2603	QLQ32507.1
<i>pstS</i>	phosphate transport system permease protein PstS	fig 6666666.654935.peg.1741 fig 6666666.654935.peg.260	QLQ31375.1
<i>pstA</i>	phosphate transport system permease protein PstA (EC 7.3.2.1)	fig 6666666.654935.peg.2606	QLQ31376.1 QLQ32506.1
<i>pstC</i>	phosphate transport system permease protein PstC (EC 7.3.2.1)	fig 6666666.654935.peg.2607	QLQ32505.1
<i>pstB</i>	pstA; phosphate transport system permease protein PstB (EC 7.3.2.1)	fig 6666666.654935.peg.2605	QLQ31377.1
<i>ppk1</i>	polyphosphate kinase (EC 2.7.4.1)	fig 6666666.654935.peg.1345	QLQ34227.1
<i>epp</i>	Exopolyphosphatase (EC 3.6.1.11)	fig 6666666.654935.peg.540	QLQ33092.1
Embden-Meyerhof (EM) pathway and Calvin-Benson-Bassham cycle			
<i>glk</i>	Glucokinase (EC 2.7.1.2)	fig 6666666.654935.peg.695 fig 6666666.654935.peg.2090	QLQ32326.1
<i>pgi</i>	glucose-6-phosphate isomerase (EC 5.3.1.9)	fig 6666666.654935.peg.2089	QLQ33478.1
<i>pfk</i>	6-phosphofructokinase (EC 2.7.1.11)	fig 6666666.654935.peg.3154	QLQ33720.1
<i>fbaA</i>	fructose-bisphosphate aldolase class II (EC 4.1.2.13)	fig 6666666.654935.peg.2989	QLQ33878.1
<i>tpiA</i>	triosephosphate isomerase (EC 5.3.1.1)	fig 6666666.654935.peg.1194	QLQ32910.1
<i>gapA</i>	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	fig 6666666.654935.peg.1302 fig 6666666.654935.peg.2986	QLQ33881.1
<i>pgk</i>	Phosphoglycerate kinase (EC 2.7.2.3)	fig 6666666.654935.peg.2987	QLQ33880.1

<i>gpmI</i>	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1)	fig 6666666.654935.peg.974	QLQ34313.1
<i>gpmB</i>	alpha-ribazole-5'-phosphate phosphatase (EC 3.1.3.73)	fig 6666666.654935.peg.1632	—
<i>eno</i>	Enolase (EC 4.2.1.11)	fig 6666666.654935.peg.2493	QLQ31148.1
<i>pyk</i>	Pyruvate kinase (EC 2.7.1.40)	fig 6666666.654935.peg.2988	QLQ33879.1 QLQ31383.1
<i>aceE</i>	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)	fig 6666666.654935.peg.745 fig 6666666.654935.peg.2843	QLQ33197.1 QLQ31452.1
<i>pdhC</i>	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)	fig 6666666.654935.peg.746 fig 6666666.654935.peg.2844	QLQ33196.1
<i>pdhD</i>	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4)	fig 6666666.654935.peg.747 fig 6666666.654935.peg.1364 fig 6666666.654935.peg.2845	QLQ33195.1 QLQ31603.1 WP_019023766.1 locus_tag="HZT40_07365"
<i>rpiA</i>	Ribose 5-phosphate isomerase A (EC 5.3.1.6)	fig 6666666.654935.peg.1410	QLQ30286.1
<i>rpe</i>	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)	—	QLQ31009.1
<i>tktA</i>	Transketolase (EC 2.2.1.1)	fig 6666666.654935.peg.2985	QLQ33882.1
<i>fbp</i>	Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)	fig 6666666.654935.peg.1039	present, but not annotated
<i>rbcL</i>	Ribulose bisphosphate carboxylase large chain (EC 4.1.1.39)	fig 6666666.654935.peg.1163 fig 6666666.654935.peg.900	QLQ31332.1
<i>rbcS</i>	Ribulose bisphosphate carboxylase small chain (EC 4.1.1.39)	fig 6666666.654935.peg.901 fig 6666666.654935.peg.1164	QLQ31406.1
<i>prkB</i>	Phosphoribulokinase (EC 2.7.1.19)	fig 6666666.654935.peg.948	QLQ33508.1
Tricarboxylic acid (TCA) cycle, glyoxylate cycle and a way to anabolism from TCA			
<i>gltA</i>	Citrate synthase (si) (EC 2.3.3.1)	fig 6666666.654935.peg.1367	QLQ31602.1
<i>acnB</i>	Aconitate hydratase 2 (EC 4.2.1.3)	fig 6666666.654935.peg.1368	QLQ31601.1
<i>idh</i>	Isocitrate dehydrogenase (NADP) (EC 1.1.1.42)	fig 6666666.654935.peg.2560 fig 6666666.654935.peg.1253	QLQ31348.1 QLQ31637.1
<i>sucA</i>	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)	fig 6666666.654935.peg.1361 fig 6666666.654935.peg.2190	QLQ31177.1 QLQ31079.1
<i>sucB</i>	2-oxoglutarate dehydrogenase E2 complex (EC 2.3.1.61)	fig 6666666.654935.peg.1363	QLQ31604.1
<i>sucD</i>	Succinyl-CoA ligase (ADP-forming) alpha chain (EC 6.2.1.5)	fig 6666666.654935.peg.1366	WP_002706977.1 locus_tag="HZT40_08370"
<i>sucC</i>	Succinyl-CoA ligase (ADP-forming) beta chain (EC 6.2.1.5)	fig 6666666.654935.peg.1365	WP_002706976.1 locus_tag="HZT40_08375"
<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	fig 6666666.654935.peg.1357	QLQ31174.1

<i>sdhB</i>	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	fig 6666666.654935.peg.1356	QLQ31173.1
<i>sdhC</i>	Succinate dehydrogenase cytochrome b-556 subunit (EC 1.3.99.1)	fig 6666666.654935.peg.1359	QLQ31175.1
<i>sdhD</i>	Succinate dehydrogenase hydrophobic membrane anchor protein (EC 1.3.5.1)	fig 6666666.654935.peg.1358	WP_002706930.1 locus_tag="HZT40_05675"
<i>fumA</i>	Fumarate hydratase class I, aerobic (EC 4.2.1.2)	fig 6666666.654935.peg.2555	QLQ31155.1
<i>fumC</i>	Fumarate hydratase class I, aerobic (EC 4.2.1.2)	—	QLQ31685.1
<i>mgo</i>	Malate:quinone oxidoreductase (EC 1.1.5.4)	fig 6666666.654935.peg.2675	QLQ32494.1
<i>pckA</i>	Phosphoenolpyruvate carboxykinase (ATP) (EC 4.1.1.49)	fig 6666666.654935.peg.3025	QLQ31415.1
<i>aspB</i>	Aspartate aminotransferase (EC 2.6.1.1)	fig 6666666.654935.peg.2488	QLQ34144.1
<i>gltB</i>	Glutamate synthase (NADPH) large chain (EC 1.4.1.13)	—	QLQ32096.1
<i>gltD</i>	Glutamate synthase (NADPH) small chain (EC 1.4.1.13)	fig 6666666.654935.peg.751	QLQ32571.1 WP_010871407.1 locus_tag="HZT40_11410"
<i>aceA</i>	Isocitrate lyase (EC 4.1.3.1)	fig 6666666.654935.peg.2674	WP_002554010.1 locus_tag="HZT40_13880"
<i>aceB</i>	Malate synthase G (EC 2.3.3.9)	fig 6666666.654935.peg.2950	QLQ33085.1
<i>maeB</i>	NADP-dependent malic enzyme (EC 1.1.1.40)	fig 6666666.654935.peg.1819 fig 6666666.654935.peg.2001	QLQ33532.1 QLQ33315.1
<i>ppc</i>	phosphoenolpyruvate carboxylase (EC 4.1.1.31)	—	QLQ32413.1
<i>pyc</i>	Pyruvate carboxylase (EC 6.4.1.1)	fig 6666666.654935.peg.1183	QLQ31324.1
Antioxidant protection			
<i>SOD2</i>	Superoxide dismutase [Fe] (EC 1.15.1.1)	fig 6666666.654935.peg.134	QLQ30489.1
<i>CAT2</i>	catalase/peroxidase HPI (EC 1.11.1.21)	—	QLQ32619.1
Respiratory Electron Transfer Chain			
Complex 1 NADH-dehydrogenase			
<i>nuoA</i>	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)	fig 6666666.654935.peg.1196	WP_012982121.1 locus_tag="HZT40_16395"
<i>nuoB</i>	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)	fig 6666666.654935.peg.1197	QLQ32569.1 WP_004630808.1 locus_tag="HZT40_16390"
<i>nuoC</i>	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3)	fig 6666666.654935.peg.1198	QLQ32570.1 QLQ32909.1
<i>nuoD</i>	NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)	fig 6666666.654935.peg.1199	QLQ32908.1 WP_002707159.1 locus_tag="HZT40_14375"
<i>nuoE</i>	NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)	fig 6666666.654935.peg.1200	QLQ34262.1

<i>nuoF</i>	NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)	fig 6666666.654935.peg.1201	QLQ32907.1 QLQ32567.1
<i>nuoG</i>	NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3)	fig 6666666.654935.peg.1202	QLQ32906.1
<i>nuoH</i>	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)	fig 6666666.654935.peg.1203	QLQ32905.1 QLQ32568.1
<i>nuoI</i>	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)	fig 6666666.654935.peg.1204	QLQ32904.1
<i>nuoJ</i>	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)	fig 6666666.654935.peg.1205	QLQ32903.1
<i>nuoK</i>	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)	fig 6666666.654935.peg.1206	QLQ32902.1 QLQ32566.1
<i>nuoL</i>	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)	fig 6666666.654935.peg.1207	QLQ32901.1 QLQ33633.1
<i>nuoM</i>	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)	fig 6666666.654935.peg.1208	QLQ33636.1 QLQ33632.1 WP_008291478.1 locus_tag="HZT40_16335"
<i>nuoN</i>	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)	fig 6666666.654935.peg.1209	QLQ32900.1
Complex II (succinate dehydrogenase)			
<i>sdhC</i>	Succinate dehydrogenase, cytochrome b556 subunit (EC 1.3.99.1)	fig 6666666.654935.peg.1359	QLQ31175.1
<i>sdhD</i>	Succinate dehydrogenase, hydrophobic membrane anchor protein (EC 1.3.5.1)	fig 6666666.654935.peg.1358	WP_002706930.1 locus_tag="HZT40_05675"
<i>sdhA</i>	Succinate dehydrogenase flavoprotein subunit (EC 1.3.99.1)	fig 6666666.654935.peg.1357	QLQ31174.1
<i>sdhB</i>	Succinate dehydrogenase iron-sulfur protein (EC 1.3.99.1)	fig 6666666.654935.peg.1356	QLQ31173.1
Complex III			
<i>cytB</i>	ubiquinol-cytochrome c reductase cytochrome b subunit (EC 7.1.1.8)	fig 6666666.654935.peg.1086 fig 6666666.654935.peg.277	QLQ31660.1
<i>cyc1</i>	ubiquinol-cytochrome c reductase cytochrome c1 subunit (EC 7.1.1.8)	fig 6666666.654935.peg.1085	QLQ31659.1
<i>rip1</i> (ISP)	ubiquinol-cytochrome c reductase iron-sulfur subunit (EC 7.1.1.8)	fig 6666666.654935.peg.1087	QLQ31661.1 QLQ31570.1
Complex IV (terminal oxydases)			
<i>cyoE</i>	Heme A synthase, cytochrome oxidase biogenesis protein Cox15- CtaA (EC 2.5.1.141)	fig 6666666.654935.peg.115	QLQ31913.1
<i>cox11</i>	cytochrome c oxidase assembly protein subunit 11 (EC 7.1.1.9)	fig 6666666.654935.peg.109	QLQ31908.1 QLQ31900.1

<i>cox15</i>	cytochrome c oxidase assembly protein subunit 15 (EC 7.1.1.9)	fig 6666666.654935.peg.1879	QLQ31913.1
<i>coxB</i>	cytochrome c oxidase subunit II (EC 7.1.1.9)	fig 6666666.654935.peg.106	QLQ31902.1 QLQ31910.1
<i>coxA</i>	cytochrome c oxidase subunit I (EC 7.1.1.9)	fig 6666666.654935.peg.107	QLQ31901.1 QLQ31909.1
<i>coxC</i>	cytochrome c oxidase subunit III (EC 7.1.1.9)	fig 6666666.654935.peg.110	QLQ31907.1 QLQ31899.1 QLQ34175.1
<i>coxD</i>	cytochrome c oxidase subunit IV (EC 7.1.1.9)		QLQ32013.1
<i>cydA</i>	Cytochrome d ubiquinol oxidase subunit I (EC 7.1.1.7)	fig 6666666.654935.peg.2173	QLQ31581.1
<i>cydB</i>	Cytochrome d ubiquinol oxidase subunit II (EC 7.1.1.7)	fig 6666666.654935.peg.2172	QLQ31580.1
<i>cydC</i>	Transport ATP-binding protein CydC	fig 6666666.659398.peg.1687 fig 6666666.659398.peg.1690	WP_002706844.1 locus_tag="HZT40_08230"
<i>cydD</i>	Transport ATP-binding protein CydD	fig 6666666.654935.peg.2171	QLQ31578.1
<i>cydX</i>	cytochrome bd-I ubiquinol oxidase subunit X (EC 7.1.1.7)		QLQ31579.1
<i>ccoN</i>	cytochrome c oxidase cbb3-type subunit I (EC 1.9.3.1)	fig 6666666.654935.peg.811 fig 6666666.654935.peg.1292	QLQ32538.1 QLQ30879.1 QLQ32042.1 locus_tag="HZT40_10230"
<i>ccoO</i>	cytochrome c oxidase cbb3-type subunit II (EC 7.1.1.9)	fig 6666666.654935.peg.810 fig 6666666.654935.peg.1293	QLQ30880.1 QLQ32537.1
<i>ccoP</i>	cytochrome c oxidase cbb3-type subunit III (EC 7.1.1.9)	fig 6666666.654935.peg.808 fig 6666666.654935.peg.1295	QLQ30881.1 QLQ34081.1 QLQ32536.1
<i>ccoG</i> (<i>FixG</i>)	Type cbb3 cytochrome oxidase biogenesis protein CcoG, involved in Cu oxidation	fig 6666666.659398.peg.1742 fig 6666666.659398.peg.2266 fig 6666666.659398.peg.805	QLQ30882.1 QLQ31613.1
<i>ccoQ</i>	CcoQ/FixQ family Cbb3-type cytochrome c oxidase assembly chaperone (EC 1.9.3.1)	fig 6666666.659398.peg.803	QLQ34234.1
<i>ccoS</i>	cbb3-type cytochrome oxidase assembly protein CcoS	fig 6666666.659398.peg.1739	WP_020559959.1 locus_tag="HZT40_08450"
ATPase			
<i>atpA</i>	F-type H ⁺ -transporting ATPase subunit alpha (EC 7.1.2.2)	fig 6666666.654935.peg.180	QLQ32745.1
<i>atpD</i>	F-type H ⁺ -transporting ATPase subunit beta (EC 7.1.2.2)	fig 6666666.654935.peg.178	QLQ32743.1
<i>atpH</i>	F-type H ⁺ -transporting ATPase subunit delta (EC 7.1.2.2)	fig 6666666.654935.peg.181	QLQ32746.1
<i>atpC</i>	F-type H ⁺ -transporting ATPase subunit epsilon (EC 7.1.2.2)	fig 6666666.654935.peg.177	QLQ32742.1
<i>atpG</i>	F-type H ⁺ -transporting ATPase subunit gamma (EC 7.1.2.2)	fig 6666666.654935.peg.179	QLQ32744.1

<i>atpB</i>	F-type H ⁺ -transporting ATPase subunit a (EC 7.1.2.2)	fig 6666666.654935.peg.184	QLQ32712.1 QLQ32748.1
<i>atpF</i>	F-type H ⁺ -transporting ATPase subunit b (EC 7.1.2.2)	fig 6666666.654935.peg.182	QLQ32747.1
<i>atpE</i>	ATP synthase F0 sector subunit c (EC 7.1.2.2)	fig 6666666.654935.peg.183	QLQ34252.1