

Journal: Applied Microbiology and Biotechnology

Supplementary Material

**Growth and gene expression of *Pseudomonas nitroreducens* TX1 on octylphenol
polyethoxylate surfactants**

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16 **Supplemental Table S1** The primers used for the DEGs subjected to qRT-PCR analysis

Gene	Forward primers (5'-3')	Reverse primers (5'-3')	Amplicon length (bp)
<i>aceA</i>	AGTACGATGCGGACTCCTCC	GTTGGTGGTCTTCAGGTGCTTC	107
<i>aceB</i>	GAAAGCCGTGCTGCTCAAG	ACGGAGTCTTCGCAGTCCAT	147
<i>acs2</i>	GAAATCACCTACCGCGAACTG	CGGAATCATCGGCATGTAGAT	111
<i>adh18</i>	AAGGGCTCATCGGTATTCGTT	TCGTTGGAGGGAACATAGAACA	104
<i>adh19</i>	CGGCTTCTTCTACGTCATCGA	CAGTATTCGGCAACCTTTTCG	135
<i>aldh1</i>	GCCTTCGGTGGCTACAAGAAG	GGTTGATGTCGTAGCTCACCAG	106
<i>aldh2</i>	ATCGATCTACACCCGCAACC	CTGCATCGCCTCGAAGTTC	100
<i>c550</i>	GACCTGCGTATGCTCGATCC	ATCTTCGGCATGTACACCGC	101
<i>cheA</i>	ACCTCCAGGAATCGGTGATG	GCCCTGAAGAATCAGCTCGAC	125
<i>fadA1</i>	ATCGTCCTGCTCGACCATG	GCGTTCGACAAAGCTGTACTTG	141
<i>fadB1</i>	TACTTCACCGAGCTCACCACC	CCGACCTTCTTCGTCTGCTG	131
<i>fadB2</i>	TGGTCAACCGTGTGCTGTTT	CCGAACCTTCTCCATGATCTTGTC	100
<i>glcD</i>	CAGATCCGTCCTCGCAGATC	CGACAGTGAGGATGTCCACC	126
<i>glcF</i>	GGAGAACCTGCAGAGCAAGC	CACGCAGCCTTCGAGTATCAG	100
<i>hcp2</i>	AGGTCGAGTACCTGATCATCACC	GATGTTCCAGCCGTACTTGATC	188
<i>mqq2</i>	ACGGCAGTGTTACCGAAACC	GTCCCTGGCTTCTTCGATACC	101
<i>paaJ/fadA2</i>	TCGACAAGATGGAAGAGAAGGTC	CTGCTTCATCACGTTTCAGCAG	113
<i>pqqB</i>	ACTGAGATGGTCCACCAGGAC	ATGGCCGTGATCTGCAGG	149
<i>pqqE</i>	CACCTGCCAGTTCTATGGCTG	CACCACGAAGATCAGTTTGCAC	148
<i>tar</i>	CGTATCGGCGAGATCGACTC	TTCCTGGTTGAGGGTGTGATC	117
<i>16S rRNA</i>	TGGRACCTGAGACACGGYCCA	AARATTCCYYACTGCTGCCT	55

17 The primers for qRT-PCR were designed based on the *Pseudomonas nitroreducens* TX1

18 genome, available under Bioproject PRJNA173805 from the National Center for Biotechnology

19 Information (NCBI)

20

21 **Supplemental Table S2** The differentially expressed genes (DEGs) of *P. nitroreducens* TX1
 22 when grown on MSB/OPEO_n vs. succinate medium

Gene	Product	Log ₂ FC	p. adj	Function group (COGs) ^a
Up-regulated				
<i>orn</i>	Oligoribonuclease (3'-5' exoribonuclease)	3.54	0.028	COG1949A
<i>pflD1</i>	Pyruvate-formate lyase	6.47	0.000	COG1882C
<i>pflD2</i>	Pyruvate-formate lyase	6.47	0.000	COG1882C
<i>pea</i>	Quinohemoprotein amine dehydrogenase	4.45	0.000	COG2010C
<i>actP</i>	Cation/acetate symporter ActP	4.30	0.000	COG4147C
<i>glcE</i>	Glycolate oxidase subunit GlcE	4.24	0.000	COG0277C
<i>cyoB</i>	Heme/copper-type cytochrome/quinol oxidase, subunit 1	4.21	0.000	COG0843C
<i>glcF</i>	Glycolate oxidase iron-sulfur subunit	4.06	0.000	COG0247C
<i>ctaG</i>	Cytochrome c oxidase assembly protein CtaG	4.04	0.000	COG3175C
<i>glcD</i>	Glycolate oxidase subunit GlcD	3.72	0.000	COG0277C
<i>lldP</i>	L-Lactate permease	3.61	0.000	COG1620C
<i>cyoA</i>	Heme/copper-type cytochrome/quinol oxidase, subunit 2	3.60	0.000	COG1622C
<i>aceA</i>	Isocitrate lyase	3.30	0.000	COG2224C
<i>narY</i>	Respiratory nitrate reductase	3.20	0.001	COG1140C
<i>C₅₅₀</i>	Cytochrome C ₅₅₀	3.15	0.001	COG2010C
<i>narJ</i>	Nitrate reductase assembly protein NarJ	3.11	0.001	COG2180C
<i>cyoC</i>	Heme/copper-type cytochrome/quinol oxidase, subunit 3	3.00	0.002	COG1845C
<i>cybB</i>	Cytochrome b561	2.94	0.003	COG3038C
<i>phnB</i>	Zn-dependent glyoxalase, PhnB family	2.85	0.020	COG2764C
<i>narG</i>	Nitrate reductase alpha subunit	2.79	0.004	COG5013C
<i>narI</i>	Nitrate reductase gamma subunit	2.70	0.009	COG2181C
<i>lpdV</i>	Dihydrolipoyl dehydrogenase	2.33	0.023	COG1249C
<i>ydfG</i>	NADP-dependent 3-hydroxy acid dehydrogenase YdfG	2.30	0.026	COG4221C
<i>aceE</i>	Pyruvate dehydrogenase E1 component	2.30	0.027	COG2609C
<i>aceF</i>	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component	2.28	0.029	COG0508C
<i>pqqE</i>	Pyrroloquinoline quinone biosynthesis protein PqqE	4.07	0.000	COG0535D
<i>spoVR</i>	Stage V sporulation protein SpoVR	3.31	0.000	COG2719D
<i>potE</i>	Serine transporter YbeC, amino acid: H ⁺ symporter family	5.76	0.000	COG0531E
<i>potD4</i>	Spermidine/putrescine-binding periplasmic protein	4.30	0.000	COG0687E
<i>dap2</i>	Dipeptidyl aminopeptidase/acylaminoacyl peptidase	3.91	0.000	COG1506E
<i>hisJ4</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	3.79	0.000	COG0834E
<i>ggt</i>	Gamma-glutamyltranspeptidase	3.62	0.000	COG0405E
<i>hisJ5</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	3.39	0.000	COG0834E
<i>eutB</i>	Ethanolamine ammonia-lyase large subunit	3.36	0.000	COG4303E
<i>livK3</i>	ABC-type branched-chain amino acid transport system, periplasmic component	3.26	0.000	COG0683E
<i>livH</i>	Branched-chain amino acid ABC-type transport system, permease component	3.20	0.001	COG0559E

<i>livM</i>	ABC-type branched-chain amino acid transport system, permease component	3.16	0.001	COG4177E
<i>pepD</i>	Dipeptidase	3.12	0.002	COG4690E
<i>hisM2</i>	ABC-type amino acid transport system, permease component	3.11	0.001	COG0765E
<i>eutC</i>	Ethanolamine ammonia-lyase small subunit	3.10	0.001	COG4302E
<i>batB</i>	ABC-type amino acid transport system, permease component	3.02	0.002	COG4597E
<i>hisM1</i>	ABC-type amino acid transport system, permease component	2.98	0.002	COG0765E
<i>potC</i>	ABC-type spermidine/putrescine transport system, permease component II	2.96	0.004	COG1177E
<i>hisJ1</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	2.93	0.003	COG0834E
<i>potD2</i>	Spermidine/putrescine-binding periplasmic protein	2.93	0.002	COG0687E
<i>potA</i>	ABC-type Fe ³⁺ /spermidine/putrescine transport systems, ATPase component	2.89	0.003	COG3842E
<i>livG</i>	ABC-type branched-chain amino acid transport system, ATPase component LivG	2.86	0.004	COG0411E
<i>glnQ1</i>	ABC-type polar amino acid transport system, ATPase component	2.85	0.003	COG1126E
<i>glnQ2</i>	ABC-type polar amino acid transport system, ATPase component	2.81	0.005	COG1126E
<i>hisJ2</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	2.79	0.004	COG0834E
<i>proX</i>	ABC-type proline/glycine betaine transport system, periplasmic component	2.75	0.006	COG2113E
<i>potD3</i>	Spermidine/putrescine-binding periplasmic protein	2.72	0.005	COG0687E
<i>hppD</i>	4-Hydroxyphenylpyruvate dioxygenase and related hemolysins	2.72	0.006	COG3185E
<i>hisM3</i>	ABC-type amino acid transport system, permease component	2.65	0.010	COG0765E
<i>livF</i>	ABC-type branched-chain amino acid transport system, ATPase component LivF	2.55	0.014	COG0410E
<i>dadA2</i>	Glycine/D-amino acid oxidase (deaminating)	2.53	0.012	COG0665E
<i>potB</i>	ABC-type spermidine/putrescine transport system, permease component I	2.50	0.018	COG1176E
<i>soxB</i>	Sarcosine oxidase subunit beta	2.46	0.027	COG0665E
<i>glnA</i>	Glutamine synthetase	2.45	0.015	COG0174E
<i>glyA2</i>	Glycine/serine hydroxymethyltransferase	2.44	0.032	COG0112E
<i>hisJ3</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	2.40	0.029	COG0834E
<i>livK1</i>	ABC-type branched-chain amino acid transport system, periplasmic component	2.34	0.023	COG0683E
<i>hutU</i>	Urocanate hydratase	2.33	0.024	COG2987E
<i>potD1</i>	Spermidine/putrescine-binding periplasmic protein	2.29	0.040	COG0687E
<i>livK2</i>	ABC-type branched-chain amino acid transport system, periplasmic component	2.24	0.035	COG0683E
<i>yobN</i>	Monoamine oxidase	2.22	0.042	COG1231E
<i>dadA1</i>	Glycine/D-amino acid oxidase (deaminating)	2.17	0.043	COG0665E
<i>yiiM</i>	N-Hydroxylaminopurine reductase YiiM, contains MOSC domain	3.03	0.002	COG2258F
<i>codB</i>	Purine-cytosine permease or related protein	2.98	0.003	COG1457F
<i>proP1</i>	MFS family permease, includes anhydromuropeptide permease AmpG	5.84	0.000	COG0477G
<i>adh18</i>	Quinoprotein alcohol dehydrogenase	4.66	0.000	COG4993G
<i>adh19</i>	Quinohemoprotein alcohol dehydrogenase	4.02	0.000	COG4993G
<i>proP2</i>	Proline/betaine transporter	3.25	0.001	COG0477G
<i>yjiC</i>	UDP:flavonoid glycosyltransferase YjiC, YdhE family	2.92	0.002	COG1819G
<i>prpD</i>	2-Methylcitrate dehydratase PrpD	2.84	0.004	COG2079G

<i>rhaT</i>	Permease of the drug/metabolite transporter (DMT) superfamily	2.56	0.012	COG0697G
<i>cite</i>	Citrate lyase beta subunit	2.52	0.019	COG2301G
<i>uhpC</i>	Sugar phosphate permease	2.37	0.019	COG2271G
<i>cyoE1</i>	Protoheme IX farnesyltransferase 1	4.19	0.000	COG0109H
<i>pqqC</i>	Pyrroloquinoline quinone biosynthesis protein C	3.59	0.000	COG5424H
<i>ctaA</i>	Heme A synthase	3.49	0.000	COG1612H
<i>menH1</i>	2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase MenH and related esterases, alpha/beta hydrolase fold	2.62	0.012	COG0596H
<i>menH3</i>	2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase MenH and related esterases, alpha/beta hydrolase fold	2.56	0.013	COG0596H
<i>pncA1</i>	Nicotinamidase-related amidase	2.41	0.022	COG1335H
<i>menH2</i>	2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase MenH and related esterases, alpha/beta hydrolase fold	2.29	0.047	COG0596H
<i>menH4</i>	2-Succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase MenH and related esterases, alpha/beta hydrolase fold	2.29	0.039	COG0596H
<i>est</i>	Esterase	5.26	0.000	COG0657I
<i>aldh4</i>	Aldehyde dehydrogenase	4.78	0.000	COG1012I
<i>aldh2</i>	Aldehyde dehydrogenase	4.70	0.000	COG1012I
<i>aldh3</i>	Acetaldehyde dehydrogenase	4.37	0.000	COG1012I
<i>aldh1</i>	Acetaldehyde dehydrogenase	3.76	0.000	COG1012I
<i>fadB1</i>	3-Hydroxyacyl-CoA dehydrogenase	3.47	0.000	COG1250I
<i>acs1</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	3.34	0.000	COG0365I
<i>caiA5</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	3.10	0.002	COG1960I
<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001	COG0183I
<i>adh1</i>	Alcohol dehydrogenase	3.02	0.002	COG2303I
<i>caiA3</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.96	0.003	COG1960I
<i>fabG</i>	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family	2.84	0.003	COG1028I
<i>caiB</i>	Crotonobetainyl-CoA:carnitine CoA-transferase CaiB and related acyl-CoA transferases	2.81	0.005	COG1804I
<i>caiA4</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.77	0.006	COG1960I
<i>caiA6</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.69	0.005	COG1960I
<i>faa1</i>	Long-chain acyl-CoA synthetase (AMP-forming)	2.63	0.008	COG1022I
<i>acnX1</i>	Mevalonate 5-phosphate dehydratase subunit 1, aconitase superfamily	2.56	0.013	COG1679I
<i>paaJ/fadA2</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	2.53	0.011	COG0183I
<i>scp2</i>	Putative sterol carrier protein, contains SCP2 domain	2.52	0.027	COG3255I
<i>acs2</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	2.41	0.017	COG0365I
<i>menE/fadK</i>	O-Succinylbenzoic acid-CoA ligase MenE or related acyl-CoA synthetase (AMP-forming)	2.38	0.021	COG0318I
<i>fadL</i>	Long-chain fatty acid transport protein	2.30	0.035	COG2067I
<i>erg3</i>	Sterol desaturase/sphingolipid hydroxylase, fatty acid hydroxylase superfamily	2.26	0.030	COG3000I
<i>caiA2</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.19	0.042	COG1960I
<i>caiA1</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.17	0.049	COG1960I
<i>rimI</i>	Ribosomal protein S18 acetylase RimI and related acetyltransferases	2.48	0.019	COG0456J
<i>fusA</i>	Translation elongation factor EF-G, a GTPase	2.47	0.015	COG0480J

<i>araC2</i>	AraC-type DNA-binding domain and AraC-containing proteins	7.57	0.000	COG2207K
<i>araC1</i>	AraC-type DNA-binding domain and AraC-containing proteins	2.70	0.007	COG2207K
<i>nfxB</i>	HTH-type transcriptional regulator NfxB	2.54	0.012	COG1309K
<i>glxA1</i>	Transcriptional regulator GlxA, contains an amidase domain and an AraC-type DNA-binding HTH domain	2.35	0.022	COG4977K
<i>araC3</i>	AraC-type DNA-binding domain and AraC-containing proteins	2.18	0.044	COG2207K
<i>polC</i>	DNA polymerase III, alpha subunit	2.98	0.004	COG2176L
<i>sphA</i>	Sphingosine uptake channel SphA-related outer membrane channel	6.18	0.000	COG4313M
<i>ompA</i>	Outer membrane protein OmpA and related peptidoglycan-associated (lipo)proteins	2.82	0.003	COG2885M
<i>acrA</i>	Multidrug efflux pump subunit AcrA (membrane-fusion protein)	2.68	0.012	COG0845M
<i>slyB</i>	Outer membrane lipoprotein SlyB	2.47	0.015	COG3133M
<i>mscS</i>	Small-conductance mechanosensitive channel	2.42	0.018	COG0668M
<i>lomR</i>	Opacity protein LomR and related surface antigens	2.38	0.019	COG3637M
<i>tolC</i>	Outer membrane protein TolC	2.25	0.041	COG1538M
<i>pflA1</i>	Pyruvate-formate lyase-activating enzyme	6.38	0.000	COG1180O
<i>pflA2</i>	Pyruvate-formate lyase-activating enzyme	6.38	0.000	COG1180O
<i>aslB</i>	Sulfatase maturation enzyme AslB, radical SAM superfamily	4.76	0.000	COG0641O
<i>shy1</i>	Cytochrome oxidase assembly protein ShyY1	3.40	0.000	COG3346O
<i>ibpA</i>	Small heat shock protein IbpA, HSP20 family	2.57	0.018	COG0071O
<i>surA</i>	Peptidyl-prolyl isomerase, parvulin family	2.25	0.038	COG0760O
<i>czcO1</i>	Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD	4.57	0.000	COG2072P
<i>cirA</i>	Outer membrane receptor protein, Fe transport	4.24	0.000	COG1629P
<i>katG</i>	Catalase-peroxidase	3.12	0.001	COG0376P
<i>pqqB</i>	Coenzyme PQQ synthesis protein B	2.83	0.003	COG1235P
<i>czcO2</i>	Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD	2.78	0.004	COG2072P
<i>afuA</i>	ABC-type Fe ³⁺ transport system, periplasmic component	2.48	0.015	COG1840P
<i>katE</i>	Catalase	2.42	0.017	COG0753P
<i>pksD</i>	Acyl transferase domain in polyketide synthase (PKS) enzymes	2.61	0.009	COG3321Q
<i>paaI</i>	Acyl-CoA thioesterase PaaI, contains HGG motif	2.53	0.023	COG2050Q
<i>yqjQ1</i>	Short-chain dehydrogenase	5.22	0.000	COG0300R
<i>yncE1</i>	DNA-binding beta-propeller fold protein YncE	4.83	0.000	COG3391R
<i>gloB</i>	Glyoxylase or a related metal-dependent hydrolase, beta-lactamase superfamily II	4.10	0.000	COG0491R
<i>yncE2</i>	DNA-binding beta-propeller fold protein YncE	3.96	0.000	COG3391R
<i>yqjQ2</i>	Short-chain dehydrogenase	3.70	0.000	COG0300R
<i>COG4341</i>	Predicted HD phosphohydrolase	3.69	0.000	COG4341R
<i>mmpL</i>	Predicted exporter protein, RND superfamily	3.66	0.000	COG1033R
<i>yeaH</i>	Uncharacterized conserved protein YeaH/YhbH, required for sporulation, DUF444 family	3.21	0.001	COG2718R
<i>dctM</i>	C4-dicarboxylate TRAP transporter large permease protein DctM	2.76	0.004	COG4666R
<i>Imp</i>	TRAP-type uncharacterized transport system, periplasmic component	2.62	0.007	COG2358R
<i>yjgC</i>	Predicted molibdopterin-dependent oxidoreductase YjgC	2.54	0.010	COG3383R

<i>ycf48</i>	Photosystem II assembly lipoprotein Ycf48	2.50	0.012	COG4447R
<i>COG3450</i>	Predicted enzyme of the cupin superfamily	2.41	0.035	COG3450R
<i>SoxYZ</i>	Quinoprotein dehydrogenase-associated SoxYZ-like carrier	4.11	0.000	COG5501S
<i>COG4323</i>	Uncharacterized conserved protein, DUF962 domain	3.23	0.002	COG4323S
<i>yjcH</i>	Inner membrane protein YjcH	3.15	0.001	COG3162S
<i>glcG</i>	Heme-binding protein HbpS, GlcG/HbpS family	4.22	0.002	COG3193T
<i>rscC</i>	Sensor histidine kinase RcsC	3.77	0.000	COG0642T
<i>crp1</i>	cAMP-activated global transcriptional regulator CRP	3.70	0.000	COG2905T
<i>cheY</i>	Chemotaxis protein CheY	3.53	0.001	COG0784T
<i>cheA</i>	Chemotaxis protein histidine kinase CheA	2.92	0.002	COG0643T
<i>prkA</i>	Predicted Ser/Thr protein kinase	2.84	0.003	COG2766T
<i>FIST</i>	FIST domain protein MJ1623, contains FIST_N and FIST_C domains	2.81	0.004	COG3287T
<i>tar/mcpB</i>	Methyl-accepting chemotaxis protein (MCP)	2.72	0.005	COG0840T
<i>rpfG</i>	Response regulator c-di-GMP phosphodiesterase, RpfG family, contains REC and HD-GYP domains	2.71	0.005	COG3437T
<i>COG4191</i>	Signal transduction histidine kinase regulating C4-dicarboxylate transport system	2.70	0.007	COG4191T
<i>COG2206</i>	HD-GYP domain, c-di-GMP phosphodiesterase class II (or its inactivated variant)	2.54	0.013	COG2206T
<i>mcpQ1</i>	Methyl-accepting chemotaxis protein McpQ	2.51	0.012	COG0840T
<i>crp1</i>	cAMP-binding domain of CRP or a regulatory subunit of cAMP-dependent protein kinases	2.47	0.015	COG0664T
<i>cheW</i>	Chemotaxis protein CheW	2.40	0.042	COG0835T
<i>mcpA /tar</i>	Methyl-accepting chemotaxis protein McpA	2.37	0.024	COG0840T
<i>COG2199</i>	GGDEF domain, diguanylate cyclase (c-di-GMP synthetase) or its enzymatically inactive variants	2.32	0.032	COG2199T
<i>fixJ</i>	DNA-binding response regulator, FixJ family, consists of REC and HTH domains	2.25	0.033	COG4566T
<i>tlpQ</i>	Methyl-accepting chemotaxis protein TlpQ	2.22	0.035	COG0840T
<i>mcpQ2</i>	Methyl-accepting chemotaxis protein McpQ	2.13	0.050	COG0840T
<i>hcp1</i>	Type VI protein secretion system component Hcp	3.16	0.004	COG3157U
<i>tssC1</i>	Type VI secretion system sheath protein TssC1	3.12	0.001	COG3517U
<i>tadG</i>	Flp pilus assembly protein TadG, includes N-terminal TadE domain	3.12	0.003	COG4961U
<i>cpaC</i>	Flp pilus assembly protein, secretin CpaC	3.08	0.002	COG4964U
<i>cpaE</i>	Flp pilus assembly ATPase CpaE/TadZ, contains N-terminal REC/TadZ_N domain	2.81	0.005	COG4963U
<i>tssB1</i>	Type VI secretion system sheath protein TssB1	2.77	0.006	COG3516U
<i>cpaB</i>	Flp pilus assembly protein CpaB	2.70	0.007	COG3745U
<i>c39G</i>	Predicted double-glycine leader peptidase, C39-like (CLD) domain	2.50	0.018	COG3271U
<i>fhaB</i>	Large exoprotein involved in heme utilization or adhesion	2.41	0.018	COG3210U
<i>cpaF</i>	Pilus assembly protein, ATPase of CpaF family	2.29	0.048	COG4962U
<i>ccmA</i>	ABC-type multidrug transport system, ATPase component	4.32	0.000	COG1131V
<i>yadH</i>	ABC-type multidrug transport system, permease component	3.81	0.000	COG0842V
<i>acrB</i>	Multidrug efflux pump subunit AcrB	2.36	0.021	COG0841V
<i>emrA</i>	Multidrug resistance efflux pump EmrA	2.25	0.049	COG1566V
<i>tnpA3</i>	Transposase and inactivated derivatives, TnpA family	3.96	0.000	COG4644X

<i>COG3464</i>	Transposase	3.93	0.000	COG3464X
<i>tnpA2</i>	Transposase and inactivated derivatives, TnpA family	2.35	0.021	COG4644X
<i>tnpA1</i>	Transposase	2.27	0.043	COG3464X
<i>porA</i>	Major outer membrane protein	7.69	0.000	NC
<i>rv1313c</i>	Transposase for insertion sequence element IS1557	5.34	0.000	NC
<i>qhnDH</i>	Quinohemoprotein amine dehydrogenase subunit gamma	4.64	0.000	NC
<i>pqqD</i>	pyrroloquinoline quinone biosynthesis protein PqqD	3.95	0.001	NC
<i>MT3584</i>	Putative diacylglycerol O-acyltransferase MT3584	3.80	0.000	NC
<i>nicP</i>	Porin-like protein NicP	3.76	0.000	NC
<i>PA3922</i>	Uncharacterized protein PA3922	3.47	0.000	NC
<i>yip1</i>	Yip1 domain	3.42	0.000	NC
<i>DUF6160</i>	DUF6160 family protein	3.21	0.001	NC
<i>DUF6160</i>	DUF6160 family protein	3.08	0.004	NC
<i>DUF1302</i>	DUF1302 domain-containing protein	3.07	0.002	NC
<i>DUF3015</i>	DUF3015 domain-containing protein	2.96	0.002	NC
<i>Tn3</i>	Tn3 family transposase	2.78	0.004	NC
<i>alkB2</i>	Alkane 1-monooxygenase 2	2.33	0.035	NC
	Hypothetical protein	4.38	0.018	NC
	Hypothetical protein	4.05	0.000	NC
	Hypothetical protein	4.05	0.000	NC
	Hypothetical protein	3.23	0.001	NC
	Hypothetical protein: Type 1 pili tip component	2.63	0.027	NC
	Hypothetical protein	2.52	0.025	NC
	Hypothetical protein	2.48	0.013	NC
	Hypothetical protein	2.46	0.015	NC
	Hypothetical protein	2.46	0.040	NC
	Hypothetical protein	2.43	0.015	NC
	Hypothetical protein	2.32	0.023	NC
Down-regulated				
<i>fpr</i>	Flavodoxin/ferredoxin-NADP reductase	-2.82	0.004	COG1018C
<i>dadA3</i>	D-Amino acid dehydrogenase 2	-2.80	0.007	COG0665E
<i>ansP</i>	L-Asparagine transporter or related permease	-2.84	0.003	COG1113E
<i>aroG1</i>	3-Deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	-3.52	0.000	COG0722E
<i>mgo2</i>	Malate: quinone oxidoreductase 2	-2.63	0.008	COG0579G
<i>gntK</i>	Gluconate kinase	-3.01	0.002	COG3265G
<i>gntT</i>	H ⁺ /gluconate symporter GntT or related permease, GntP/DsdX family	-3.10	0.001	COG2610G
<i>pncA2</i>	Nicotinamidase/pyrazinamidase	-2.78	0.005	COG1335H
<i>desA3</i>	NADPH-dependent stearyl-CoA 9-desaturase	-2.66	0.007	COG3239I
<i>lolD</i>	ABC-type lipoprotein export system, ATPase component	-2.63	0.016	COG1136M
<i>lolE</i>	ABC-type transport system involved in lipoprotein release, permease component LolC	-3.03	0.004	COG4591M
<i>clpA</i>	ATP-dependent Clp protease, ATP-binding subunit ClpA	-2.46	0.015	COG0542O
<i>yfmG</i>	Formylglycine-generating enzyme, required for sulfatase activity, contains SUMF1/FGE domain	-2.46	0.017	COG1262O

<i>pknB</i>	Serine/threonine-protein kinase PknB	-2.69	0.006	COG0515T
<i>prpC</i>	Serine/threonine protein phosphatase PrpC	-3.23	0.007	COG0631T
<i>IcmF</i>	Type VI protein secretion system component VasK	-2.19	0.044	COG3523U
<i>vgrG1a</i>	Type VI secretion system spike protein VgrG1a	-2.21	0.042	COG3501U
<i>hcp2</i>	Type VI protein secretion system component Hcp (secreted cytotoxin)	-2.28	0.047	COG3157U
<i>gpA1</i>	Phage terminase, large subunit GpA	-2.30	0.036	COG5525X
<i>MIMI_R878</i>	Putative KilA-N domain-containing protein R878	-2.77	0.029	NC
	Hypothetical protein	-2.50	0.013	NC
	Hypothetical protein	-2.97	0.014	NC

23 ^aThe proteins were classified into functional categories according to the clusters of orthologous
24 groups (COG). A, RNA processing and modification; C, Energy production and conversion; D,
25 Cell cycle control, cell division, chromosome partitioning; E, Amino acid transport and
26 metabolism; F, Nucleotide transport and metabolism; G, Carbohydrate transport and metabolism;
27 H, Coenzyme transport and metabolism; I, Lipid transport and metabolism; J, Translation,
28 ribosomal structure and biogenesis; K, Transcription; L, Replication, recombination and repair;
29 M, Cell wall/membrane/envelope biogenesis; O, Posttranslational modification, protein turnover,
30 chaperones; P, Inorganic ion transport and metabolism; Q, Secondary metabolites biosynthesis,
31 transport and catabolism; R, General function prediction only; S, Function unknown; T, Signal
32 transduction mechanisms; U, Intracellular trafficking, secretion, and vesicular transport; V,
33 Defense mechanisms; X, Mobilome: prophages, transposons; NC, Proteins not classified into a
34 COG.

35 **Supplemental Table S3** GO enrichment analysis of differentially expressed genes of *P.*
 36 *nitroreducens* TX1 when grown on MSB/OPEO_n vs. succinate medium

Gene	Function	CC membrane	MF cofactor binding	MF FAD binding	MF electron transfer activity	MF heme binding	MF oxidoreductase activity	Log ₂ FC
<i>porA</i>	Major outer membrane protein	1	0	0	0	0	0	7.69
<i>potE</i>	Serine transporter YbeC, amino acid: H ⁺ symporter family	1	0	0	0	0	0	5.76
<i>aldh4</i>	Aldehyde dehydrogenase	0	0	0	0	0	1	4.78
<i>aldh2</i>	Aldehyde dehydrogenase	0	0	0	0	0	1	4.70
<i>qhnDH</i>	Quinohemoprotein amine dehydrogenase subunit gamma	0	0	0	0	0	1	4.64
<i>czcO1</i>	Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD	0	1	1	0	0	1	4.57
<i>peaA</i>	Quinohemoprotein amine dehydrogenase	0	0	0	1	1	0	4.45
<i>aldh3</i>	Acetaldehyde dehydrogenase	0	0	0	0	0	1	4.37
<i>actP</i>	Cation/acetate symporter ActP	1	0	0	0	0	0	4.30
<i>glcE</i>	Glycolate oxidase subunit GlcE	0	1	1	0	0	1	4.24
<i>cyoB</i>	Heme/copper-type cytochrome/quinol oxidase, subunit 1	0	0	0	1	1	1	4.21
<i>adh19</i>	Quinohemoprotein alcohol dehydrogenase	0	0	0	1	1	0	4.02
<i>yadH</i>	ABC-type multidrug transport system, permease component	1	0	0	0	0	0	3.81
<i>aldh1</i>	Acetaldehyde dehydrogenase	0	0	0	0	0	1	3.76
<i>glcD</i>	Glycolate oxidase subunit GlcD	0	1	1	0	0	1	3.72
<i>mmpL</i>	Predicted exporter protein, RND superfamily	1	0	0	0	0	0	3.66
<i>cyoA</i>	Heme/copper-type cytochrome/quinol oxidase, subunit 2	1	0	0	1	1	1	3.60
<i>ctaA</i>	Heme A synthase	0	0	0	0	0	1	3.49
<i>fadB1</i>	3-Hydroxyacyl-CoA dehydrogenase	0	1	0	0	0	1	3.47
<i>yip1</i>	Yip1 domain	1	0	0	0	0	0	3.42
<i>shy1</i>	Cytochrome oxidase assembly protein ShyY1	1	0	0	0	0	0	3.40
<i>c550</i>	Cytochrome c ₅₅₀	0	0	0	1	1	0	3.15
<i>katG</i>	Catalase-peroxidase	0	0	0	0	1	1	3.12
<i>hisM2</i>	ABC-type amino acid transport system, permease component	1	0	0	0	0	0	3.11

<i>caiA5</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	0	1	1	0	0	1	3.10
<i>yiiM</i>	<i>N</i> -Hydroxylaminopurine reductase YiiM, contains MOSC domain	0	1	0	0	0	0	3.03
<i>adh1</i>	Alcohol dehydrogenase	0	1	1	0	0	1	3.02
<i>batB</i>	ABC-type amino acid transport system, permease component	1	0	0	0	0	0	3.02
<i>cyoC</i>	Heme/copper-type cytochrome/quinol oxidase, subunit 3	1	0	0	1	0	1	3.00
<i>codB</i>	Purine-cytosine permease or related protein	1	0	0	0	0	0	2.98
<i>hisM1</i>	ABC-type amino acid transport system, permease component	1	0	0	0	0	0	2.98
<i>caiA3</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	0	1	1	0	0	1	2.96
<i>potC</i>	ABC-type spermidine/putrescine transport system, permease component II	1	0	0	0	0	0	2.96
<i>cybB</i>	Cytochrome b561	0	0	0	1	0	0	2.94
<i>narG</i>	Nitrate reductase alpha subunit	0	1	0	0	0	1	2.79
<i>czcO2</i>	Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD	0	1	1	0	0	1	2.78
<i>caiA4</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	0	1	1	0	0	1	2.77
<i>mcpB</i>	Methyl-accepting chemotaxis protein (MCP)	1	0	0	0	0	0	2.72
<i>hisM3</i>	ABC-type amino acid transport system, permease component	1	0	0	0	0	0	2.65
<i>rhaT</i>	Permease of the drug/metabolite transporter (DMT) superfamily	1	0	0	0	0	0	2.56
<i>yjgC</i>	Predicted molibdopterin-dependent oxidoreductase YjgC	0	1	0	0	0	1	2.54
<i>dadA2</i>	Glycine/D-amino acid oxidase (deaminating)	0	0	0	0	0	1	2.53
<i>mcpQ1</i>	Methyl-accepting chemotaxis protein McpQ	1	0	0	0	0	0	2.51
<i>potB</i>	ABC-type spermidine/putrescine transport system, permease component I	1	0	0	0	0	0	2.50
<i>soxB</i>	Sarcosine oxidase subunit beta	0	0	0	0	0	1	2.46

<i>glyA</i>	Glycine/serine hydroxymethyltransferase	0	1	0	0	0	0	2.44
<i>katE</i>	Catalase	0	0	0	0	1	1	2.42
<i>hisJ3</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	1	0	0	0	0	0	2.40
<i>mcpA</i>	Methyl-accepting chemotaxis protein McpA	1	0	0	0	0	0	2.37
<i>acrB</i>	Multidrug efflux pump subunit AcrB	1	0	0	0	0	0	2.36
<i>lpdV</i>	Dihydrolipoyl dehydrogenase	0	0	0	0	0	1	2.33
<i>erg3</i>	Sterol desaturase/sphingolipid hydroxylase, fatty acid hydroxylase superfamily	0	0	0	0	0	1	2.26
<i>tlpQ</i>	Methyl-accepting chemotaxis protein TlpQ	1	0	0	0	0	0	2.22
<i>yobN</i>	Monoamine oxidase	0	0	0	0	0	1	2.22
<i>caiA2</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	0	1	1	0	0	1	2.19
<i>caiA1</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	0	1	1	0	0	1	2.17
<i>dadA1</i>	Glycine/D-amino acid oxidase (deaminating)	0	1	1	0	0	1	2.17
<i>mcpQ2</i>	Methyl-accepting chemotaxis protein McpQ	1	1	1	0	0	1	2.13
<i>mgo2</i>	Malate: quinone oxidoreductase 2	0	0	0	0	0	1	-2.63
<i>dadA3</i>	D-Amino acid dehydrogenase 2	0	0	0	0	0	1	-2.80
<i>fpr</i>	Flavodoxin/ferredoxin-NADP reductase	0	0	0	0	0	1	-2.82
<i>ansP</i>	L-Asparagine transporter or related permease	1	0	0	0	0	0	-2.84
<i>lolE</i>	ABC-type transport system involved in lipoprotein release, permease component LolC	1	0	0	0	0	0	-3.03
<i>gntT</i>	H ⁺ /gluconate symporter GntT or related permease, GntP/DsdX family	1	0	0	0	0	0	-3.10

37 1 means the gene is in GO term, 0 means the gene is not in GO term. CC, cellular component;
38 MF, molecular functions

Supplemental Table S4 KEGG enrichment analysis of differentially expressed genes of *P. nitroreducens* TX1 when grown on MSB/OPEO_n vs. succinate

Pathway	GeneRatio	BgRatio	p-value	p. adj
Pyruvate metabolism	11/112	59/1910	<0.001	0.034
Propanoate metabolism	10/112	58/1910	0.002	0.046
Caprolactam degradation	4/112	10/1910	0.002	0.046
Microbial metabolism in diverse environments	31/112	332/1910	0.003	0.057
Glycolysis / Gluconeogenesis	8/112	45/1910	0.004	0.057
Two-component system	25/112	253/1910	0.004	0.057
Fatty acid degradation	8/112	48/1910	0.006	0.063
Glyoxylate and dicarboxylate metabolism	10/112	72/1910	0.008	0.072
Bacterial secretion system	7/112	41/1910	0.008	0.072
ABC transporters	20/112	199/1910	0.009	0.073

GeneRatio: The number of differential expression genes related to the term/the total number of DEGs

BgRatio: The number of genes related to the term/the total number of genes

44 **Supplemental Table S5** KEGG enrichment analysis of differentially expressed genes of *P.*
 45 *nitroreducens* TX1 when grown on MSB/OPEO_n vs. succinate

KEGG pathway	Gene	Product	Log ₂ FC	p. adj
Pyruvate metabolism	<i>pflD1</i>	Pyruvate-formate lyase	6.47	<0.001
	<i>pflD2</i>	Pyruvate-formate lyase	6.47	<0.001
	<i>aldh2</i>	Aldehyde dehydrogenase	4.70	<0.001
	<i>aldh3</i>	Acetaldehyde dehydrogenase	4.37	<0.001
	<i>aldh1</i>	Acetaldehyde dehydrogenase	3.76	<0.001
	<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001
	<i>acs2</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	2.41	0.017
	<i>lpdV</i>	Dihydrolipoyl dehydrogenase	2.33	0.023
	<i>aceE</i>	Pyruvate dehydrogenase E1 component	2.30	0.027
	<i>aceF</i>	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component	2.28	0.029
	<i>mgo2</i>	Malate: quinone oxidoreductase 2	-2.63	0.008
Caprolactam degradation	<i>est</i>	Esterase	5.26	<0.001
	<i>fadB1</i>	3-Hydroxyacyl-CoA dehydrogenase	3.47	<0.001
	<i>czcO2</i>	Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD	2.78	0.004
	<i>alkB2</i>	Alkane 1-monooxygenase 2	2.33	0.035
Propanoate metabolism	<i>pflD1</i>	Pyruvate-formate lyase	6.47	<0.001
	<i>pflD2</i>	Pyruvate-formate lyase	6.47	<0.001
	<i>fadB1</i>	3-Hydroxyacyl-CoA dehydrogenase	3.47	<0.001
	<i>acs1</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	3.34	<0.001
	<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001
	<i>caiA3</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.96	0.003
	<i>caiA4</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.77	0.006
	<i>acs2</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	2.41	0.017
	<i>lpdV</i>	Dihydrolipoyl dehydrogenase	2.33	0.023
	<i>caiA1</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.17	0.049
Two-component system	<i>rcsC</i>	Sensor histidine kinase RcsC	3.77	<0.001
	<i>nicP</i>	Porin-like protein NicP	3.76	<0.001
	<i>cheY</i>	Chemotaxis protein CheY	3.53	0.001
	<i>ctaA</i>	Heme A synthase	3.49	<0.001
	<i>narY</i>	Respiratory nitrate reductase	3.20	0.001
	<i>hisM2</i>	ABC-type amino acid transport system, permease component	3.11	0.001
	<i>narJ</i>	Nitrate reductase assembly protein NarJ	3.11	0.001
	<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001
	<i>hisM1</i>	ABC-type amino acid transport system, permease component	2.98	0.002
	<i>cheA</i>	Chemotaxis protein histidine kinase CheA	2.92	0.002
	<i>glnQ1</i>	ABC-type polar amino acid transport system, ATPase component	2.85	0.003

	<i>hisJ2</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	2.79	0.004
	<i>narG</i>	Nitrate reductase alpha subunit	2.79	0.004
	<i>mcpB</i>	Methyl-accepting chemotaxis protein (MCP)	2.72	0.005
	<i>narI</i>	Nitrate reductase gamma subunit	2.70	0.009
	<i>hisM3</i>	ABC-type amino acid transport system, permease component	2.65	0.010
	<i>citE</i>	Citrate lyase beta subunit	2.52	0.019
	<i>mcpQ1</i>	Methyl-accepting chemotaxis protein McpQ	2.51	0.012
	<i>glnA</i>	Glutamine synthetase	2.45	0.015
	<i>cheW</i>	Chemotaxis protein CheW	2.40	0.042
	<i>mcpA</i>	Methyl-accepting chemotaxis protein McpA	2.37	0.024
	<i>tolC</i>	Outer membrane protein TolC	2.25	0.041
	<i>fixJ</i>	DNA-binding response regulator, FixJ family, consists of REC and HTH domains	2.25	0.033
	<i>tlpQ</i>	Methyl-accepting chemotaxis protein TlpQ	2.22	0.035
	<i>mcpQ2</i>	Methyl-accepting chemotaxis protein McpQ	2.13	0.050
Glycolysis / Gluconeogenesis	<i>adh18</i>	Quinoprotein alcohol dehydrogenase	4.66	<0.001
	<i>aldh3</i>	Acetaldehyde dehydrogenase	4.37	<0.001
	<i>adh19</i>	Quinohemoprotein alcohol dehydrogenase	4.02	<0.001
	<i>aldh1</i>	Acetaldehyde dehydrogenase	3.76	<0.001
	<i>acs2</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	2.41	0.017
	<i>lpdV</i>	Dihydrolipoyl dehydrogenase	2.33	0.023
	<i>aceE</i>	Pyruvate dehydrogenase E1 component	2.30	0.027
	<i>aceF</i>	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component	2.28	0.029
Microbial metabolism in diverse environments	<i>pflD1</i>	Pyruvate-formate lyase	6.47	<0.001
	<i>pflD2</i>	Pyruvate-formate lyase	6.47	<0.001
	<i>aldh4</i>	Aldehyde dehydrogenase	4.78	<0.001
	<i>aldh2</i>	Aldehyde dehydrogenase	4.70	<0.001
	<i>adh18</i>	Quinoprotein alcohol dehydrogenase	4.66	<0.001
	<i>peaA</i>	Quinohemoprotein amine dehydrogenase	4.45	<0.001
	<i>aldh3</i>	Acetaldehyde dehydrogenase	4.37	<0.001
	<i>glcE</i>	Glycolate oxidase subunit GlcE	4.24	<0.001
	<i>SoxYZ</i>	Quinoprotein dehydrogenase-associated SoxYZ-like carrier	4.11	<0.001
	<i>glcF</i>	Glycolate oxidase iron-sulfur subunit	4.06	<0.001
	<i>adh19</i>	Quinohemoprotein alcohol dehydrogenase	4.02	<0.001
	<i>aldh1</i>	Acetaldehyde dehydrogenase	3.76	<0.001
	<i>glcD</i>	Glycolate oxidase subunit GlcD	3.72	<0.001
	<i>yqjQ2</i>	Short-chain dehydrogenase	3.70	<0.001
	<i>fadB1</i>	3-Hydroxyacyl-CoA dehydrogenase	3.47	<0.001
	<i>aceA</i>	Isocitrate lyase	3.30	<0.001
	<i>narY</i>	Respiratory nitrate reductase	3.20	0.001
	<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001
	<i>narG</i>	Nitrate reductase alpha subunit	2.79	0.004
	<i>czcO2</i>	Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD	2.78	0.004

	<i>narI</i>	Nitrate reductase gamma subunit	2.70	0.009
	<i>yjgC</i>	Predicted molibdopterin-dependent oxidoreductase YjgC	2.54	0.010
	<i>fadA2</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	2.53	0.011
	<i>glnA</i>	Glutamine synthetase	2.45	0.015
	<i>glyA</i>	Glycine/serine hydroxymethyltransferase	2.44	0.032
	<i>acs2</i>	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	2.41	0.017
	<i>lpdV</i>	Dihydrolipoyl dehydrogenase	2.33	0.023
	<i>aceE</i>	Pyruvate dehydrogenase E1 component	2.30	0.027
	<i>aceF</i>	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component	2.28	0.029
	<i>mqa2</i>	Malate: quinone oxidoreductase 2	-2.63	0.008
	<i>gntK</i>	Gluconate kinase	-3.01	0.002
Fatty acid degradation	<i>yqjQ2</i>	Short-chain dehydrogenase	3.70	<0.001
	<i>fadB1</i>	3-Hydroxyacyl-CoA dehydrogenase	3.47	<0.001
	<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001
	<i>caiA3</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.96	0.003
	<i>caiA4</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.77	0.006
	<i>fadA2</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	2.53	0.011
	<i>alkB2</i>	Alkane 1-monooxygenase 2	2.33	0.035
	<i>caiA1</i>	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	2.17	0.049
Bacterial secretion system	<i>hcp1</i>	Type VI protein secretion system component Hcp	3.16	0.004
	<i>IcmF</i>	Type VI protein secretion system component VasK	-2.19	0.044
	<i>vgrG1a</i>	Type VI secretion system spike protein VgrG1a	-2.21	0.042
	<i>hcp2</i>	Type VI protein secretion system component Hcp (secreted cytotoxin)	-2.28	0.047
	<i>clpA</i>	ATP-dependent Clp protease, ATP-binding subunit ClpA	-2.46	0.015
	<i>pknB</i>	Serine/threonine-protein kinase PknB	-2.69	0.006
	<i>prpC</i>	Serine/threonine protein phosphatase PrpC	-3.23	0.007
Glyoxylate and dicarboxylate metabolism	<i>aldh2</i>	Aldehyde dehydrogenase	4.70	<0.001
	<i>glcE</i>	Glycolate oxidase subunit GlcE	4.24	<0.001
	<i>glcF</i>	Glycolate oxidase iron-sulfur subunit	4.06	<0.001
	<i>glcD</i>	Glycolate oxidase subunit GlcD	3.72	<0.001
	<i>aceA</i>	Isocitrate lyase	3.30	<0.001
	<i>fadA1</i>	Acetyl-CoA acetyltransferase/3-ketoacyl-CoA thiolase	3.06	0.001
	<i>glnA</i>	Glutamine synthetase	2.45	0.015
	<i>glyA</i>	Glycine/serine hydroxymethyltransferase	2.44	0.032
	<i>katE</i>	Catalase	2.42	0.017
	<i>lpdV</i>	Dihydrolipoyl dehydrogenase	2.33	0.023
ABC transporters	<i>potD4</i>	Spermidine/putrescine-binding periplasmic protein	4.30	<0.001
	<i>hisJ5</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	3.39	<0.001
	<i>livK3</i>	ABC-type branched-chain amino acid transport system, periplasmic component	3.26	<0.001
	<i>livH</i>	Branched-chain amino acid ABC-type transport system, permease component	3.20	0.001

<i>livM</i>	ABC-type branched-chain amino acid transport system, permease component	3.16	0.001
<i>hisM2</i>	ABC-type amino acid transport system, permease component	3.11	0.001
<i>batB</i>	ABC-type amino acid transport system, permease component	3.02	0.002
<i>hisM1</i>	ABC-type amino acid transport system, permease component	2.98	0.002
<i>potC</i>	ABC-type spermidine/putrescine transport system, permease component II	2.96	0.004
<i>potA</i>	ABC-type Fe ³⁺ /spermidine/putrescine transport systems, ATPase component	2.89	0.003
<i>livG</i>	ABC-type branched-chain amino acid transport system, ATPase component LivG	2.86	0.004
<i>glnQ1</i>	ABC-type polar amino acid transport system, ATPase component	2.85	0.003
<i>glnQ2</i>	ABC-type polar amino acid transport system, ATPase component	2.81	0.005
<i>hisJ2</i>	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	2.79	0.004
<i>proX</i>	ABC-type proline/glycine betaine transport system, periplasmic component	2.75	0.006
<i>potD3</i>	Spermidine/putrescine-binding periplasmic protein	2.72	0.005
<i>hisM3</i>	ABC-type amino acid transport system, permease component	2.65	0.010
<i>livF</i>	ABC-type branched-chain amino acid transport system, ATPase component LivF	2.55	0.014
<i>potB</i>	ABC-type spermidine/putrescine transport system, permease component I	2.50	0.018
<i>potD1</i>	Spermidine/putrescine-binding periplasmic protein	2.29	0.040

Supplemental Table S6 DEGs of genes in the DNA region containing NAD(P)-independent ADH cluster of *P. nitroreducens* TX1 when grown on MSB/OPEO_n vs. succinate

Gene	Product	log ₂ FC	p. adj
<i>c550</i>	Cytochrome c ₅₅₀	3.15	0.001
<i>ABC</i>	Amino acid ABC transporter substrate-binding protein	3.79	<0.001
<i>SoxYZ</i>	Quinoprotein dehydrogenase-associated SoxYZ-like carrier	4.11	<0.001
<i>?</i>	MBL fold metallo-hydrolase	4.10	<0.001
<i>adh18</i>	Quinoprotein alcohol dehydrogenase	4.66	<0.001
<i>aldh1</i>	Aldehyde dehydrogenase	3.76	<0.001
<i>adh19</i>	Quinohemoprotein alcohol dehydrogenase	4.02	<0.001
<i>aldh2</i>	Aldehyde dehydrogenase	4.70	<0.001
<i>R</i>	Sigma 54 specific transcriptional regulator	1.42	0.373
<i>pqqA</i>	Pyrroloquinoline quinone precursor peptide PqqA	2.65	<0.001
<i>pqqB</i>	Pyrroloquinoline quinone biosynthesis protein PqqB	2.83	0.003
<i>pqqC</i>	Pyrroloquinoline-quinone synthase PqqC	3.59	<0.001
<i>pqqD</i>	Pyrroloquinoline quinone biosynthesis peptide chaperone PqqD	3.95	0.001
<i>pqqE</i>	Pyrroloquinoline quinone biosynthesis protein PqqE	4.07	<0.001
<i>pqqF</i>	Pyrroloquinoline quinone biosynthesis protein PqqF	3.91	<0.001
<i>adh17</i>	Alcohol dehydrogenase	0.83	0.930

51 **Supplemental Table S7** The expression of PQQ-ADH genes is increased when *P. nitroreducens*

52 TX1 is exposed to OPEO_n compared to succinate

Gene	Counts per million mapped reads (CPM)									
	OPEO _n				Succinate				OPEO _n /Succinate	
	(1)	(2)	(3)	Average	(1)	(2)	(3)	Average	Log ₂ FC	padj
<i>adh18</i>	735.61	2053.19	2388.49	1725.76 ± 873.73	84.22	141.50	43.85	89.86 ± 49.07	4.7	4.1E-07
<i>adh19</i>	6.40	96.19	46.44	49.67 ± 44.98	4.64	1.88	4.57	3.70 ± 1.58	4.0	4.0E-05

(1), (2), (3) correspond to experimental repetitions.

53

Supplemental Table S8 Amino acid sequence similarity among the ADHs from *P. nitroreducens* TX1, the PQQ-ADHs from *P. aeruginosa* PAO1, and the PQQ-ADHs from *P. putida* KT2440.

Protein	Homology (%)				
	<i>P. nitroreducens</i> TX1		<i>P. aeruginosa</i> PAO1	<i>P. putida</i> KT2440	
	adh18	adh19	exaA	peaE	peaH
adh18	-	36.3	54.0	52.8	81.6
adh19		-	37.2	36.1	37.5
exaA			-	83.7	53.0
peaE				-	51.9
peaH					-

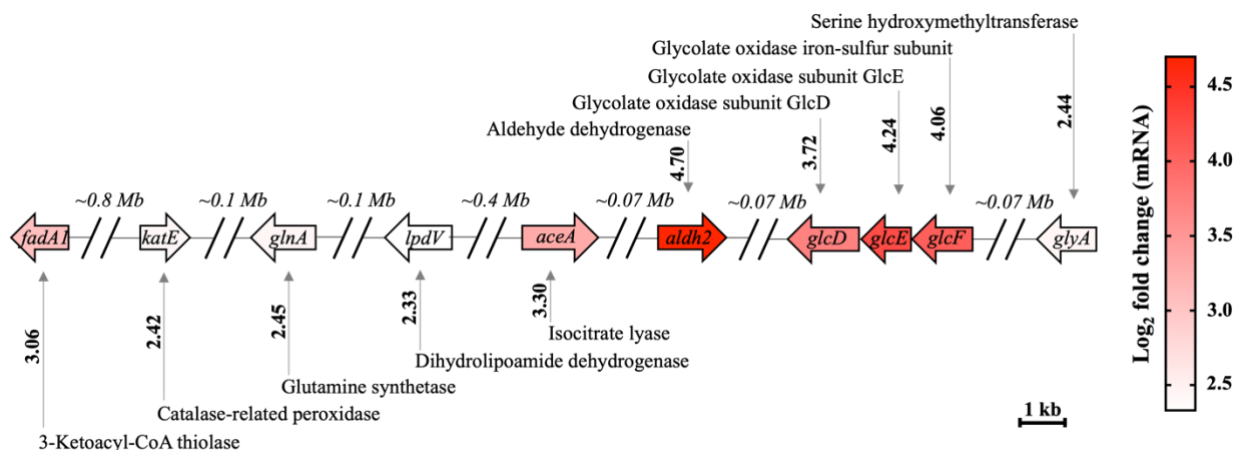


Fig. S1 Upregulation of genes related to the glyoxylate and dicarboxylate metabolism in *P.*

nitroreducens TX1 when grown on OPEO_n vs. succinate. Arrows indicate gene position and

orientation of transcription of the gene. The mRNA expression level is presented in log₂ fold

change, and the bold number indicates the up-regulated mRNA. Color intensity indicates the

expression level of the corresponding genes

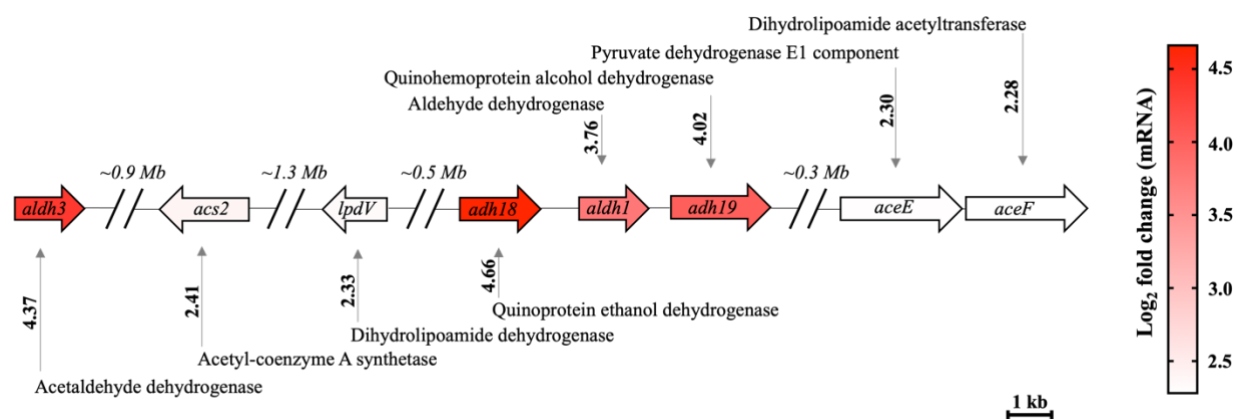


Fig. S2 Upregulation of genes related to glycolysis/gluconeogenesis in *P. nitroreducens* TX1

when grown on OPEO_n vs. succinate. Arrows indicate gene position and orientation of

transcription of the gene. The mRNA expression level is presented in log₂ fold change, and the

bold number indicates the up-regulated mRNA. Color intensity indicates the expression level of

the corresponding genes

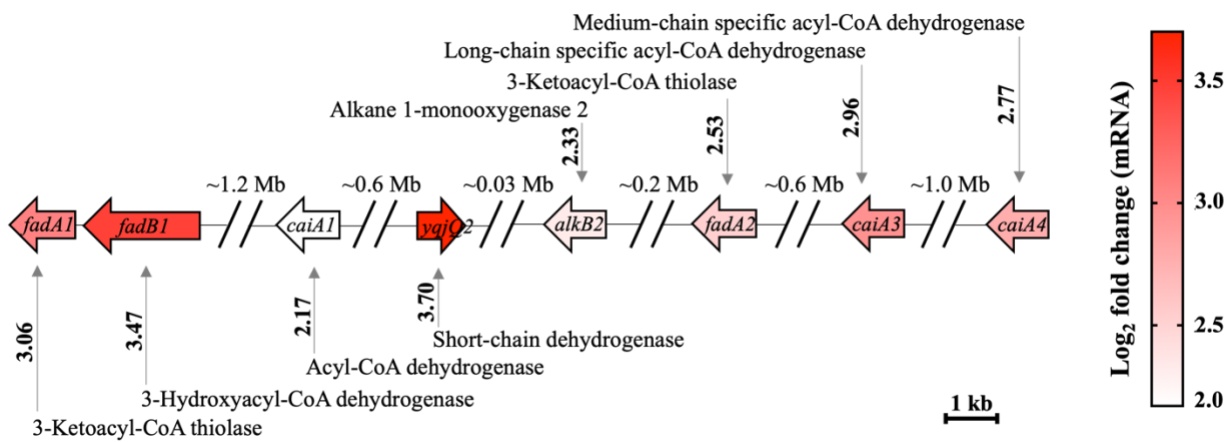


Fig. S3 Upregulation of genes related to fatty acid degradation in *P. nitroreducens* TX1 when grown on OPEO_n vs. succinate. Arrows indicate gene position and orientation of transcription of the gene. The mRNA expression level is presented in log₂ fold change, and the bold number indicates the up-regulated mRNAs. Color intensity indicates the expression level of the corresponding genes

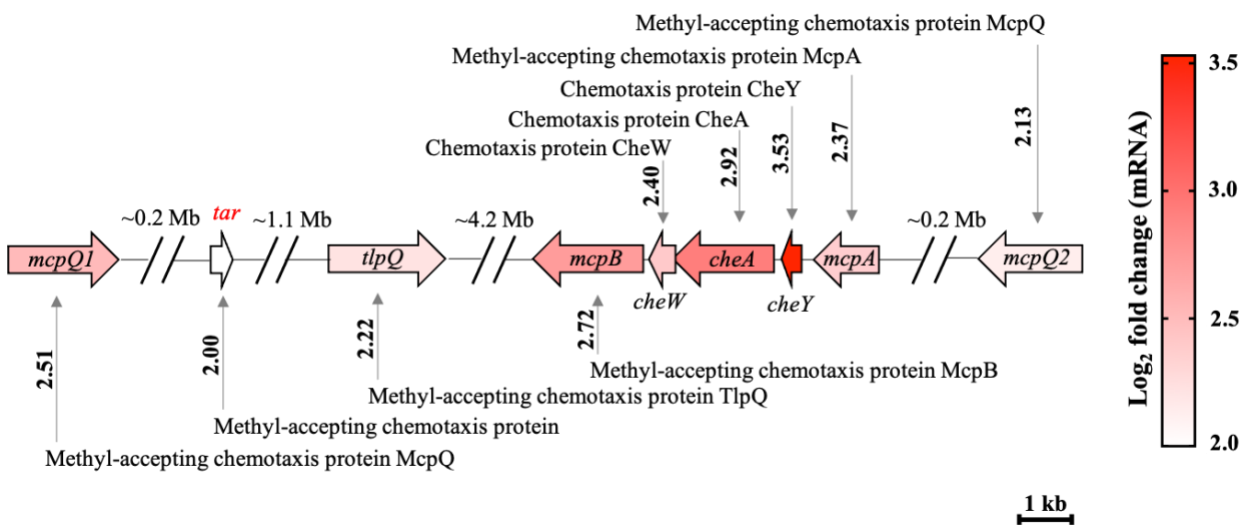
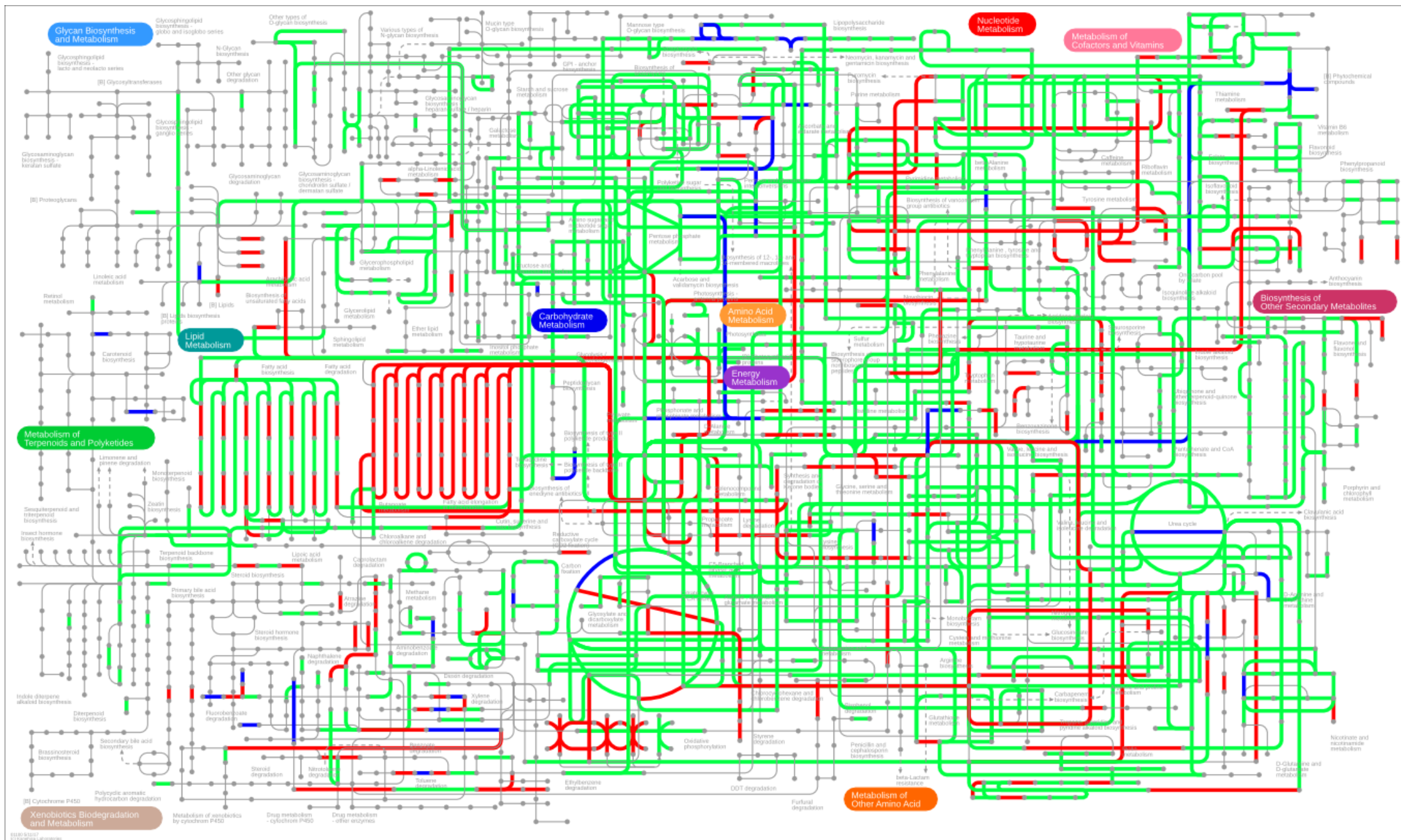


Fig. S4 Upregulation of genes related to chemotaxis pathway in *P. nitroreducens* TX1 when grown on OPEO_n vs. succinate. Arrows indicate gene position and orientation of transcription of the gene. The mRNA expression level is presented in log₂ fold change, and the bold number indicates the up-regulated mRNAs. Color intensity indicates the expression level of the corresponding genes



114 **Fig. S5** Pathway map of the complete metabolism in biological systems as determined using
115 Interactive Pathways Explorer (iPath) v3 (<https://pathways.embl.de/>) when TX1 strain grown on
116 OEPO_n vs. succinate. A gray node symbolizes a compound; the gray line represents a metabolic
117 pathway; the red line indicates upregulation; the blue line shows downregulation; the green line
118 designates no significant difference in expression genes on OPEO_n vs. succinate