

SUPPLEMENT 2

List of genes in *E. coli* MG1655 pTrc99A (NOX⁻) whose expression ratio was negatively correlated with NADH/NAD with increasing specific glucose consumption rate. Genes which were determined (by Bioprospector) to contain an ArcA binding site are also indicated (*).

Genes	Functional Category	Gene Product	R
<i>aceK</i> *	Central intermediary metabolism	isocitrate dehydrogenase kinase/phosphatase	-0.93
<i>acnB</i> *	Energy metabolism, carbon	aconitate hydratase B	-0.95
<i>acs</i> *	Fatty acid biosynthesis	acetyl-CoA synthetase	-0.90
<i>add</i> *	Central intermediary metabolism	adenosine deaminase	-0.97
<i>adhP</i> *	Energy metabolism, carbon	alcohol dehydrogenase	-0.97
<i>aldA</i>	Energy metabolism, carbon	aldehyde dehydrogenase, NAD-linked	-0.94
<i>aldB</i>	Degradation of small molecules	aldehyde dehydrogenase B (lactaldehyde dehydrogenase)	-0.99
<i>allP</i> *	Unknown proteins, no known homologs	putative transport protein	-0.95
<i>araG</i> *	Transport/binding proteins	ATP-binding component of high-affinity L-arabinose transport system	-0.92
<i>araF</i> *	Transport/binding proteins	L-arabinose-binding periplasmic protein	-0.94
<i>argT</i> *	Transport/binding proteins	lysine-, arginine-, ornithine-binding periplasmic protein	-0.97
<i>aroM</i> *	Amino acid biosynthesis	protein of <i>aro</i> operon, regulated by <i>aroR</i>	-0.96
b0024*	Unknown proteins, no known homologs	orf, hypothetical protein	-0.99
b1170*	Unknown proteins, no known homologs	putative part of putative ATP-binding component of a transport system	-0.90
b1394	Degradation of small molecules	putative enzyme	-0.91
b1423	Unknown proteins, no known homologs	orf, hypothetical protein	-0.96
b1440	Transport/binding proteins	putative transport protein	-0.90
b1441*	Transport/binding proteins	putative ATP-binding component of a transport system	-0.97
b1443*	Transport/binding proteins	putative transport system permease protein	-0.98
b1444*	Some information, but not classifiable	putative aldehyde dehydrogenase	-0.98
b1486	Transport/binding proteins	putative transport system permease protein	-0.94
b1488*	Unknown proteins, no known homologs	orf, hypothetical protein	-0.93
b1516	Transport/binding proteins	putative LACI-type transcriptional regulator	-0.99
b1775	Some information, but not classifiable	putative transport protein	-0.92
b1972	Unknown proteins, no known homologs	orf, hypothetical protein	-0.94
b2080*	Unknown proteins, no known homologs	orf, hypothetical protein	-1.00
b2228	Unknown proteins, no known homologs	putative membrane protein	-0.90
b2341	Unknown proteins, no known homologs	putative enzyme	-0.92
b2390	Unknown proteins, no known homologs	orf, hypothetical protein	-0.96
b2531	Unknown proteins, no known homologs	orf, hypothetical protein	-0.91
b2659	Unknown proteins, no known homologs	orf, hypothetical protein	-0.99
b2789	Transport/binding proteins	putative transport protein	-0.91
b3001*	Transport/binding proteins	putative reductase	-0.97
b3045*	Laterally acquired elements	IS2 hypothetical protein	-0.91

<i>bax</i> *	Some information, but not classifiable	putative ATP-binding protein	-0.94
<i>bcsC</i> *	Macromolecule degradation	putative endoglucanase	-0.93
<i>bfd</i> *	Adaptation	orf, hypothetical protein	-0.93
<i>cdd</i>	Central intermediary metabolism	cytidine/deoxycytidine deaminase	-0.94
<i>cheA</i>	Chemotaxis, motility	sensory transducer kinase between chemosignal receptors and CheB and CheY	-0.95
<i>cirA</i>	Cell envelop	outer membrane receptor for iron-regulated colicin I receptor; porin; requires tonB gene product	-0.93
<i>clpA</i> *	Macromolecule degradation	ATP-binding component of serine protease	-0.97
<i>creD</i>	Global regulatory functions	tolerance to colicin E2	-0.94
<i>cspD</i> *	Some information, but not classifiable	cold shock protein	-0.94
<i>cycA</i>	Transport/binding proteins	transport of D-alanine, D-serine, and glycine	-0.95
<i>dcuC</i> *	Transport/binding proteins	transport of dicarboxylates	-0.93
<i>dgoT</i> *	Transport/binding proteins	D-galactonate transport	-0.95
<i>fadB</i> *	Degradation of small molecules	4-enzyme protein: 3-hydroxyacyl-CoA dehydrogenase; 3-hydroxybutyryl-CoA epimerase; delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase; enoyl-CoA hydratase	-0.99
<i>feaR</i> *	Some information, but not classifiable	regulatory protein for 2-phenylethylamine catabolism	-0.91
<i>fhuA</i>	Cell envelop	outer membrane protein receptor for ferrichrome, colicin M, and phages T1, T5, and phi80	-0.99
<i>fruK</i> *	Energy metabolism, carbon	fructose-1-phosphate kinase	-0.97
<i>fruL</i>	Energy metabolism, carbon	fruR leader peptide	-0.94
<i>fucA</i>	Degradation of small molecules	L-fuculose-1-phosphate aldolase	-0.91
<i>fucO</i> *	Degradation of small molecules	L-1,2-propanediol oxidoreductase	-0.96
<i>fucR</i>	Degradation of small molecules	positive regulator of the <i>fuc</i> operon	-0.92
<i>fumC</i> *	Energy metabolism, carbon	fumarase C= fumarate hydratase Class II; isozyme	-0.92
<i>galS</i> *	Degradation of small molecules	mgl repressor, galactose operon inducer	-0.91
<i>gapC_2</i>	Energy metabolism, carbon	glyceraldehyde-3-phosphate dehydrogenase (second fragment)	-0.94
<i>gatY</i>	Degradation of small molecules	tagatose-bisphosphate aldolase 1	-0.93
<i>glpD</i> *	Energy metabolism, carbon	sn-glycerol-3-phosphate dehydrogenase (aerobic)	-0.90
<i>glpF</i> *	Transport/binding proteins	facilitated diffusion of glycerol	-0.98
<i>glpK</i>	Central intermediary metabolism	glycerol kinase	-0.99
<i>glpQ</i>	Central intermediary metabolism	glycerophosphodiester phosphodiesterase, periplasmic	-0.92
<i>glpT</i>	Transport/binding proteins	sn-glycerol-3-phosphate permease	-0.90

<i>gntP</i>	Transport/binding proteins	gluconate transport system permease 3	-0.94
<i>hcaB*</i>	Degradation of small molecules	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase	-0.97
<i>hcaR</i>	Degradation of small molecules	transcriptional activator of <i>hca</i> cluster	-0.92
<i>hisQ*</i>	Transport/binding proteins	histidine transport system permease protein	-0.90
<i>hyfD</i>	Energy metabolism, carbon	hydrogenase 4 membrane subunit	-0.98
<i>hyfR</i>	Some information, but not classifiable	putative 2-component regulator, interaction with sigma 54	-0.94
<i>idnD</i>	Degradation of small molecules	L-idonate dehydrogenase	-0.90
<i>idnO</i>	Degradation of small molecules	5-keto-D-gluconate 5-reductase	-0.99
<i>kdpD*</i>	Global regulatory functions	sensor for high-affinity potassium transport system	-0.91
<i>lacA</i>	Degradation of small molecules	thiogalactoside acetyltransferase	-0.93
<i>lycV</i>	Laterally acquired elements	bacteriophage lambda lysozyme homolog	-0.90
<i>melB*</i>	Transport/binding proteins	melibiose permease II	-0.91
<i>mhpR</i>	Some information, but not classifiable	transcriptional regulator for mhp operon	-0.95
<i>mopA*</i>	Cell division	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein	-0.91
<i>mtlD</i>	Degradation of small molecules	mannitol-1-phosphate dehydrogenase	-0.95
<i>narK*</i>	Transport/binding proteins	nitrite extrusion protein	-0.93
<i>nrdH</i>	Biosynthesis of cofactors, carriers	glutaredoxin-like protein; hydrogen donor	-0.98
<i>nrdI</i>	Central intermediary metabolism	orf, hypothetical protein	-0.96
<i>paaB*</i>	Degradation of small molecules	orf, hypothetical protein	-0.92
<i>phnF</i>	Some information, but not classifiable	putative transcriptional regulator	-0.99
<i>ppsA</i>	Central intermediary metabolism	phosphoenolpyruvate synthase	-0.91
<i>prpB*</i>	Some information, but not classifiable	putative phosphonmutase 2	-0.91
<i>prpC</i>	Some information, but not classifiable	putative citrate synthase; propionate metabolism?	-0.96
<i>prpD</i>	Degradation of small molecules	orf, hypothetical protein	-0.95
<i>pqqL*</i>	Biosynthesis of cofactors, carriers	putative peptidase	-0.94
<i>rhsD*</i>	Transport/binding proteins	D-ribose high-affinity transport system; membrane-associated protein	-0.95
<i>recN</i>	Macromolecule synthesis, modification	protein used in recombination and DNA repair	-0.95
<i>rhaR*</i>	Degradation of small molecules	positive regulator for <i>rhaRS</i> operon	-0.96
<i>rmf</i>	Ribosome constituents	ribosome modulation factor	-0.90
<i>rpoS*</i>	Global regulatory functions	RNA polymerase, sigma S (sigma38) factor; synthesis of many growth phase related proteins	-0.93
<i>rspA</i>	Global regulatory functions	starvation sensing protein	-0.98

<i>sodA</i>	Protection responses	superoxide dismutase, manganese	-0.90
<i>spr</i> *	Some information, but not classifiable	putative lipoprotein	-0.93
<i>thiD</i> *	Biosynthesis of cofactors, carriers	phosphomethylpyrimidine kinase	-0.92
<i>thrS</i>	Macromolecule synthesis, modification	threonine tRNA synthetase	-0.91
<i>tra5_2</i>	Some information, but not classifiable	IS3 putative transposase	-0.97
<i>tra5_3</i>	Some information, but not classifiable	IS3 putative transposase	-0.91
<i>trkH</i> *	Transport/binding proteins	potassium uptake, requires TrkE	-0.91
<i>ttdA</i> *	Energy metabolism, carbon	L-tartrate dehydratase, subunit A	-0.90
<i>ugpE</i>	Transport/binding proteins	sn-glycerol 3-phosphate transport system, integral membrane protein	-0.96
<i>ugpQ</i>	Central intermediary metabolism	glycerophosphodiester phosphodiesterase, cytosolic	-0.98
<i>wzxC</i> *	Transport/binding proteins	probable export protein	-0.94
<i>xylF</i>	Transport/binding proteins	xylose binding protein transport system	-0.91
<i>xylG</i>	Transport/binding proteins	putative ATP-binding protein of xylose transport system	-0.98
<i>xylH</i> *	Transport/binding proteins	putative xylose transport, membrane component	-0.95
<i>xylR</i> *	Some information, but not classifiable	putative regulator of <i>xyl</i> operon	-0.90
<i>yafH</i>	Some information, but not classifiable	putative acyl-CoA dehydrogenase (EC 1.3.99.-)	-0.93
<i>yafL</i>	Unknown proteins, no known homologs	putative lipoprotein	-0.98
<i>yaiC</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.93
<i>yajO</i> *	Unknown proteins, no known homologs	putative NAD(P)H-dependent xylose reductase	-0.98
<i>ybeR</i> *	Unknown proteins, no known homologs	orf, hypothetical protein	-0.92
<i>ybgG</i>	Some information, but not classifiable	putative sugar hydrolase	-0.91
<i>ybhI</i>	Transport/binding proteins	putative membrane pump protein	-0.90
<i>ybiX</i> *	Some information, but not classifiable	putative enzyme	-0.92
<i>yehA</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.92
<i>ycjC</i> *	Unknown proteins, no known homologs	orf, hypothetical protein	-0.90
<i>ycjT</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.97
<i>ydbC</i> *	Unknown proteins, no known homologs	putative dehydrogenase	-0.94
<i>ydbD</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.93
<i>ydcA</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.92
<i>ydcF</i> *	Unknown proteins, no known homologs	orf, hypothetical protein	-0.92
<i>yddA</i>	Transport/binding proteins	putative ATP-binding component of a transport system	-0.91
<i>yeaL</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.95
<i>yeaW</i>	Some information, but not classifiable	orf, hypothetical protein	-0.94
<i>yebG</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.95
<i>yeeE</i> *	Some information, but not classifiable	putative transport system permease protein	-0.94
<i>yehZ</i>	Some information, but not classifiable	putative transport system permease protein	-0.94
<i>yeiC</i> *	Some information, but not classifiable	putative kinase	-0.96

<i>yfeH</i>	Some information, but not classifiable	putative cytochrome oxidase	-0.97
<i>yfhH*</i>	Transport/binding proteins	orf, hypothetical protein	-0.95
<i>ygbF</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.94
<i>ygcE</i>	Some information, but not classifiable	putative kinase	-0.93
<i>ygfR*</i>	Unknown proteins, no known homologs	putative oxidoreductase	-0.92
<i>ygfT*</i>	Some information, but not classifiable	putative oxidoreductase, Fe-S subunit	-0.90
<i>yhfO*</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.90
<i>yidK*</i>	Some information, but not classifiable	putative cotransporter	-0.93
<i>yeC*</i>	Transport/binding proteins	putative receptor protein	-0.94
<i>yigF*</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.98
<i>yigN*</i>	Some information, but not classifiable	putative alpha helix chain	-0.94
<i>yihU*</i>	Some information, but not classifiable	putative dehydrogenase	-0.92
<i>yihV*</i>	Some information, but not classifiable	putative kinase	-0.91
<i>yjcG</i>	Transport/binding proteins	putative transport protein	-0.93
<i>yjcH*</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.96
<i>yjhI</i>	Some information, but not classifiable	putative regulator	-0.93
<i>yjiI</i>	Central intermediary metabolism	orf, hypothetical protein	-0.94
<i>ylaC*</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.91
<i>ymfN</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.92
<i>yncB</i>	Some information, but not classifiable	putative oxidoreductase	-0.96
<i>ynjA</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.91
<i>ytfJ*</i>	Unknown proteins, no known homologs	orf, hypothetical protein	-0.94
<i>ytfQ</i>	Transport/binding proteins	putative LACI-type transcriptional regulator	-0.99