

Table S4. PICRUST analysis of fecal microbiota in WT mice

This table lists genes that are significantly different in abundance based on PICRUST analysis (FDR-corrected $p < 0.05$) in the fecal microbiota of WT mice between at least 2 of the diet groups as determined using a mixed linear model.

Estimate indicates the difference in the least square means of log10 normalized counts of OTUs between:

a) high vs low iron diet (negative = OTU decreased in the high iron diet; positive = OTU increased in the high iron diet),

b) control vs high iron diet (negative = OTU decreased in the control diet; positive = OTU increased in the control diet),

c) control vs low iron diet (negative = OTU decreased in the control diet; positive = OTU increased in control diet).

Comparison	Gene ID	Estimate	FDR p -value	Predicted function
Control vs High Iron Diet	K00002	-1.66	3.7E-03	alcohol dehydrogenase (NADP+) [EC:1.1.1.2]
	K00102	-1.56	2.7E-02	D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]
	K09145	-1.38	1.4E-02	hypothetical protein
	K09144	-1.21	2.8E-02	hypothetical protein
	K05571	-1.21	2.7E-02	multicomponent Na ⁺ :H ⁺ antiporter subunit G
	K05566	-1.21	2.5E-02	multicomponent Na ⁺ :H ⁺ antiporter subunit B
	K04566	-1.17	3.4E-02	lysyl-tRNA synthetase, class I [EC:6.1.1.6]
	K00091	-1.04	5.3E-03	dihydroflavonol-4-reductase [EC:1.1.1.219]
	K06320	-1.02	2.2E-02	spore maturation protein CgeB
	K11104	-0.88	2.0E-02	melibiose permease
	K12700	-0.82	5.0E-03	non-specific ribonucleoside hydrolase [EC:3.2.-.-]
	K05992	-0.63	3.0E-02	None
	K08659	-0.61	6.8E-03	dipeptidase A [EC:3.4.-.-];dipeptidase [EC:3.4.-.-]
	K07741	-0.61	4.5E-02	anti-repressor protein
	K09952	-0.61	4.7E-02	hypothetical protein
	K02076	-0.59	3.5E-02	Fur family transcriptional regulator, zinc uptake regulator
	K01173	-0.59	1.4E-02	endonuclease [EC:3.1.30.-];endonuclease G, mitochondrial
	K04086	-0.58	1.7E-02	ATP-dependent Clp protease ATP-binding subunit ClpL
	K01281	-0.57	2.8E-02	X-Pro dipeptidyl-peptidase [EC:3.4.14.11]
	K13953	-0.56	4.7E-02	alcohol dehydrogenase, propanol-preferring [EC:1.1.1.1]
	K01478	-0.55	4.5E-02	arginine deiminase [EC:3.5.3.6]
	K02246	-0.55	4.4E-02	competence protein ComGD
	K07586	-0.54	5.9E-03	hypothetical protein
	K01575	-0.54	3.8E-02	acetolactate decarboxylase [EC:4.1.1.5]
	K01641	-0.54	1.7E-02	hydroxymethylglutaryl-CoA synthase [EC:2.3.3.10]
	K00054	-0.54	1.7E-02	hydroxymethylglutaryl-CoA reductase [EC:1.1.1.88]
	K00869	-0.54	1.7E-02	mevalonate kinase [EC:2.7.1.36]

K01597	-0.54	1.8E-02	diphosphomevalonate decarboxylase [EC:4.1.1.33]
K00938	-0.54	1.8E-02	phosphomevalonate kinase [EC:2.7.4.2]
K05885	-0.54	1.5E-02	2,5-diketo-D-gluconate reductase [EC:1.1.1.274]
K06198	-0.54	2.0E-02	competence protein CoiA
K01071	-0.53	1.9E-02	oleoyl-[acyl-carrier-protein] hydrolase [EC:3.1.2.14]
K12555	-0.53	2.1E-02	penicillin-binding protein 2A [EC:2.4.1.129 2.3.2.-]
K03476	-0.53	4.5E-02	L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]
K06286	-0.53	4.3E-02	septation ring formation regulator
K02244	-0.53	4.3E-02	competence protein ComGB
K11618	-0.53	2.4E-02	two-component system, NarL family, response regulator LiaR
K00364	-0.53	3.9E-02	GMP reductase [EC:1.7.1.7]
K08987	-0.53	3.5E-02	putative membrane protein
K03095	-0.53	4.3E-02	SprT-like protein
K07177	-0.52	4.1E-02	PDZ domain-containing protein
K03366	-0.51	2.4E-02	(R,R)-butanediol dehydrogenase / diacetyl reductase [EC:1.1.1.4 1.1.1.303]
K09155	-0.51	3.0E-02	hypothetical protein
K07497	-0.50	6.3E-03	putative transposase
K07570	-0.50	2.3E-02	general stress protein 13
K03346	-0.50	3.0E-02	replication initiation and membrane attachment protein
K02086	-0.50	3.0E-02	DNA replication protein
K07668	-0.50	4.1E-02	two-component system, OmpR family, response regulator VicR
K07652	-0.50	4.1E-02	two-component system, OmpR family, sensor histidine kinase VicK [EC:2.7.13.3]
K10108	-0.49	3.4E-02	maltose/maltodextrin transport system substrate-binding protein
K10110	-0.49	3.4E-02	maltose/maltodextrin transport system permease protein
K08728	-0.49	2.7E-02	nucleoside deoxyribosyltransferase [EC:2.4.2.6]
K03709	-0.47	4.0E-02	DtxR family transcriptional regulator, Mn-dependent transcriptional regulator
K00904	-0.47	2.6E-02	deoxyguanosine kinase [EC:2.7.1.113]
K10109	-0.46	4.7E-02	maltose/maltodextrin transport system permease protein
K01621	-0.42	4.7E-02	phosphoketolase [EC:4.1.2.9]
K07023	-0.42	3.5E-02	putative hydrolases of HD superfamily
K00926	-0.41	4.0E-02	carbamate kinase [EC:2.7.2.2]
K03697	-0.39	4.2E-02	ATP-dependent Clp protease ATP-binding subunit ClpE
K09765	-0.38	2.6E-02	hypothetical protein
K02433	-0.16	3.9E-02	aspartyl-tRNA(Asn)/glutamyl-tRNA (Gln) amidotransferase subunit A [EC:6.3.5.6 6.3.5.7]
K03686	-0.13	1.0E-02	molecular chaperone DnaJ
K01534	-0.12	3.3E-03	Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]

K03588	-0.12	1.1E-02	cell division protein FtsW
K08591	-0.12	2.5E-03	glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15]
K04487	-0.11	5.4E-03	cysteine desulfurase [EC:2.8.1.7]
K00948	-0.10	1.1E-02	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
K00942	-0.09	4.8E-02	guanylate kinase [EC:2.7.4.8]
K00789	-0.09	1.7E-03	S-adenosylmethionine synthetase [EC:2.5.1.6]
K10773	-0.09	3.5E-02	endonuclease III [EC:4.2.99.18]
K03545	-0.08	4.6E-03	trigger factor
K02469	-0.08	2.1E-03	DNA gyrase subunit A [EC:5.99.1.3]
K02470	-0.08	1.5E-03	DNA gyrase subunit B [EC:5.99.1.3]
K00762	-0.08	4.4E-02	orotate phosphoribosyltransferase [EC:2.4.2.10]
K00790	-0.07	2.9E-02	UDP-N-acetylglucosamine 1- carboxyvinyltransferase [EC:2.5.1.7]
K01689	-0.06	3.6E-02	enolase [EC:4.2.1.11]
K01874	-0.05	2.4E-02	methionyl-tRNA synthetase [EC:6.1.1.10]
K01887	-0.05	3.3E-02	arginyl-tRNA synthetase [EC:6.1.1.19]
K01265	0.07	9.8E-03	methionyl aminopeptidase [EC:3.4.11.18]
K01448	0.16	7.0E-03	N-acetylmuramoyl-L-alanine amidase [EC:3.5.1.28]
K01935	0.51	3.9E-02	dethiobiotin synthetase [EC:6.3.3.3]
K02011	0.57	3.5E-02	iron(III) transport system permease protein
K06911	0.60	4.5E-02	None
K04773	0.62	4.9E-02	protease IV [EC:3.4.21.-]
K03752	0.64	4.8E-02	molybdopterin-guanine dinucleotide biosynthesis protein A
K02510	0.64	2.2E-02	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [EC:4.1.2.-]
K02619	0.66	1.9E-02	4-amino-4-deoxychorismate lyase [EC:4.1.3.38]
K01744	0.67	2.7E-02	aspartate ammonia-lyase [EC:4.3.1.1]
K02010	0.68	1.1E-02	iron(III) transport system ATP-binding protein [EC:3.6.3.30]
K11203	0.68	1.1E-02	PTS system, fructose-specific IIC-like component
K01805	0.69	2.6E-02	xylose isomerase [EC:5.3.1.5]
K01438	0.70	1.9E-02	acetylornithine deacetylase [EC:3.5.1.16]
K12942	0.71	7.3E-03	aminobenzoyl-glutamate transport protein
K03077	0.71	3.0E-02	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]
K05795	0.71	6.9E-03	tellurium resistance protein TerD
K07085	0.74	4.4E-02	putative transport protein
K03385	0.74	3.6E-02	cytochrome c-552 [EC:1.7.2.2];formate- dependent nitrite reductase, periplasmic
K07217	0.75	4.3E-02	cytochrome c552 subunit [EC:1.7.2.2]
K03694	0.75	3.7E-02	Mn-containing catalase
K03803	0.75	2.2E-02	ATP-dependent Clp protease ATP-binding subunit ClpA
K01993	0.76	3.5E-02	sigma-E factor negative regulatory protein RseC
			HlyD family secretion protein

K00979	0.76	3.1E-02	3-deoxy-manno-octulosonate cytidyltransferase (CMP-KDO synthetase) [EC:2.7.7.38]
K00140	0.77	1.3E-02	malonate-semialdehyde dehydrogenase (acetylating) / methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.18 1.2.1.27];methylmalonate-semialdehyde dehydrogenase [EC:1.2.1.27]
K02014	0.77	1.5E-02	iron complex outermembrane receptor protein
K02428	0.77	2.5E-02	nucleoside-triphosphate pyrophosphatase [EC:3.6.1.19]
K02415	0.78	2.0E-02	flagellar FlhL protein
K01667	0.79	1.4E-02	tryptophanase [EC:4.1.99.1]
K03833	0.79	2.4E-02	selenocysteine-specific elongation factor ATP-dependent Clp protease adaptor protein
K06891	0.80	1.1E-02	ClpS
K06142	0.81	4.8E-02	outer membrane protein
K06167	0.82	2.3E-02	PhnP protein
K06861	0.84	1.8E-02	lipopolysaccharide export system ATP- binding protein [EC:3.6.3.-] anhydro-N-acetylmuramic acid kinase [EC:2.7.1.-];anhydro-N-acetylmuramic acid kinase [EC:2.7.1.170]
K09001	0.84	1.6E-03	tRNA 2-selenouridine synthase [EC:2.9.1.-]
K06917	0.84	1.2E-02	multidrug resistance protein, MATE family
K03327	0.84	3.6E-02	None
K07071	0.85	4.3E-02	uncharacterized protein
K07148	0.87	3.8E-02	PTS system, fructose-specific IIB-like component [EC:2.7.1.69]
K11202	0.88	5.1E-03	cobaltochelataze CobN [EC:6.6.1.2]
K02230	0.88	4.3E-02	
K01205	0.89	3.6E-02	alpha-N-acetylglucosaminidase [EC:3.2.1.50] thiamine-monophosphate kinase [EC:2.7.4.16]
K00946	0.89	2.3E-02	electron transport protein HydN
K05796	0.90	1.5E-02	fumarate hydratase, class I [EC:4.2.1.2]
K01676	0.90	2.8E-02	MFS transporter, PAT family, beta-lactamase induction signal transducer AmpG
K08218	0.91	2.3E-02	pyruvate, water dikinase [EC:2.7.9.2]
K01007	0.91	4.9E-03	outer membrane channel protein TolC
K12340	0.91	2.3E-02	8-amino-7-oxononanoate synthase [EC:2.3.1.47]
K00652	0.91	2.1E-02	FKBP-type peptidyl-prolyl cis-trans isomerase FkIB [EC:5.2.1.8]
K03773	0.92	2.0E-02	lipid A biosynthesis lauroyl acyltransferase [EC:2.3.1.-]
K02517	0.92	1.8E-02	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD [EC:5.2.1.8]
K03775	0.93	1.7E-02	putative lipoprotein
K05807	0.93	1.7E-02	membrane-bound lytic murein transglycosylase D [EC:3.2.1.-]
K08307	0.93	1.7E-02	

			D-alanyl-D-alanine carboxypeptidase / D-alanyl-D-alanine-endopeptidase (penicillin-binding protein 4) [EC:3.4.16.4 3.4.99.-];D-alanyl-D-alanine carboxypeptidase / D-alanyl-D-alanine-endopeptidase (penicillin-binding protein 4) [EC:3.4.16.4 3.4.21.-]
K07259	0.94	1.5E-02	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit C [EC:1.6.5.-]
K00348	0.94	1.7E-02	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit D [EC:1.6.5.-]
K00349	0.94	1.7E-02	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit A [EC:1.6.5.-]
K00346	0.94	1.7E-02	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit B [EC:1.6.5.-]
K00347	0.94	1.7E-02	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit E [EC:1.6.5.-]
K00350	0.94	1.7E-02	Na ⁺ -transporting NADH:ubiquinone oxidoreductase subunit F [EC:1.6.5.-]
K00351	0.94	1.7E-02	glutamate carboxypeptidase [EC:3.4.17.11]
K01295	0.94	3.1E-04	erythronate-4-phosphate dehydrogenase [EC:1.1.1.290]
K03473	0.94	1.7E-02	putative metalloprotease [EC:3.4.24.-]
K07387	0.94	1.6E-02	NADH dehydrogenase I subunit C/D [EC:1.6.5.3];NADH-quinone oxidoreductase subunit C/D [EC:1.6.5.3]
K13378	0.94	1.7E-02	membrane fusion protein
K03585	0.94	1.6E-02	biotin synthesis protein BioC;malonyl-CoA O-methyltransferase [EC:2.1.1.197]
K02169	0.95	1.5E-02	peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]
K03770	0.95	1.7E-02	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]
K00677	0.95	1.8E-02	peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]
K03771	0.95	1.3E-02	bifunctional aspartokinase/homoserine dehydrogenase 1 [EC:2.7.2.4 1.1.1.3];bifunctional aspartokinase / homoserine dehydrogenase 1 [EC:2.7.2.4 1.1.1.3]
K12524	0.96	1.3E-02	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [EC:2.5.1.55]
K01627	0.96	1.3E-02	lipoprotein NlpD
K06194	0.96	1.1E-02	zinc protease [EC:3.4.99.-];zinc protease [EC:3.4.24.-]
K07263	0.96	1.8E-02	glycolate oxidase iron-sulfur subunit
K11473	0.97	4.5E-02	biopolymer transport protein ExbB
K03561	0.97	1.7E-02	lipoyl(octanoyl) transferase [EC:2.3.1.181]
K03801	0.97	1.1E-02	polysaccharide export outer membrane protein
K01991	0.97	1.8E-02	molybdate transport system ATP-binding protein
K05776	0.97	1.1E-02	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.-]
K02535	0.97	1.3E-02	3-deoxy-D-manno-octulosonic-acid transferase [EC:2.-.-.-]
K02527	0.97	1.3E-02	

K07277	0.97	1.3E-02	outer membrane protein
K00912	0.97	1.3E-02	tetraacyldisaccharide 4'-kinase
K00748	0.97	1.3E-02	[EC:2.7.1.130]
			lipid-A-disaccharide synthase [EC:2.4.1.182]
			octaprenyl-diphosphate synthase [EC:2.5.1.-];octaprenyl-diphosphate synthase [EC:2.5.1.90];octaprenyl diphosphate synthase [EC:2.5.1.-]
K02523	0.97	1.3E-02	putative ABC transport system permease protein
K02066	0.97	1.3E-02	putative ABC transport system ATP-binding protein
K02065	0.97	1.3E-02	ribosome-associated heat shock protein
K04762	0.98	1.3E-02	Hsp15
			UDP-2,3-diacylglucosamine hydrolase
K03269	0.98	1.3E-02	[EC:3.6.1.-]
			pyridoxine 5-phosphate synthase
K03474	0.98	1.3E-02	[EC:2.6.99.2]
			NADH dehydrogenase I subunit N
			[EC:1.6.5.3];NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]
K00343	0.98	1.6E-02	NADH-quinone oxidoreductase subunit I
			[EC:1.6.5.3];NADH dehydrogenase I subunit I [EC:1.6.5.3]
K00338	0.98	1.6E-02	NADH-quinone oxidoreductase subunit M
			[EC:1.6.5.3];NADH dehydrogenase I subunit M [EC:1.6.5.3]
K00342	0.98	1.6E-02	NADH-quinone oxidoreductase subunit K
			[EC:1.6.5.3];NADH dehydrogenase I subunit K [EC:1.6.5.3]
K00340	0.98	1.6E-02	NADH dehydrogenase I subunit L
			[EC:1.6.5.3];NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]
K00341	0.98	1.6E-02	NADH dehydrogenase I subunit J
			[EC:1.6.5.3];NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]
K00339	0.98	1.6E-02	NADH-quinone oxidoreductase subunit A
			[EC:1.6.5.3];NADH dehydrogenase I subunit A [EC:1.6.5.3]
K00330	0.98	1.6E-02	NADH dehydrogenase I subunit H
			[EC:1.6.5.3];NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]
K00337	0.98	1.6E-02	NADH dehydrogenase I subunit B
			[EC:1.6.5.3];NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]
K00331	0.98	1.6E-02	chondroitin-sulfate-ABC endolyase/exolyase
K08961	0.99	1.8E-02	[EC:4.2.2.20 4.2.2.21]
			pyruvate dehydrogenase (quinone)
			[EC:1.2.5.1];pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]
K00156	1.00	8.0E-03	hypothetical protein
K09922	1.00	9.0E-03	phosphoribosylglycinamide formyltransferase
			2 [EC:2.1.2.2]
K08289	1.01	8.4E-03	hypothetical protein
K09973	1.01	9.9E-03	

				translation initiation factor 1;translation initiation factor SUI1;translation initiation factor eIF-1
K03113	1.01	8.8E-03		imidazoleglycerol-phosphate dehydratase / histidinol-phosphatase [EC:4.2.1.19
K01089	1.01	8.9E-03		3.1.3.15]
K00281	1.01	8.5E-03		glycine dehydrogenase [EC:1.4.4.2]
K03558	1.02	1.3E-02		membrane protein required for colicin V production
K00029	1.02	1.2E-02		malate dehydrogenase (oxaloacetate-decarboxylating)(NADP+) [EC:1.1.1.40]
K04764	1.02	1.3E-02		integration host factor subunit alpha
K05595	1.02	1.1E-02		multiple antibiotic resistance protein
K06076	1.03	1.2E-02		long-chain fatty acid transport protein
K03832	1.03	8.6E-03		periplasmic protein TonB
K03814	1.04	1.2E-02		monofunctional biosynthetic peptidoglycan transglycosylase [EC:2.4.1.-]
K01241	1.04	1.2E-02		AMP nucleosidase [EC:3.2.2.4]
K13694	1.04	1.2E-02		lipoprotein Spr
K03543	1.04	8.1E-03		multidrug resistance protein A
K02426	1.07	5.5E-03		cysteine desulfuration protein SufE
K03559	1.07	8.1E-03		biopolymer transport protein ExbD
K11537	1.07	7.8E-03		MFS transporter, NHS family, xanthosine permease
K01433	1.07	5.9E-03		formyltetrahydrofolate deformylase [EC:3.5.1.10]
K06177	1.08	5.0E-03		tRNA pseudouridine32 synthase / 23S rRNA pseudouridine746 synthase [EC:5.4.99.28 5.4.99.29];ribosomal large subunit pseudouridine synthase A [EC:5.4.99.12]
K12941	1.08	3.7E-04		aminobenzoyl-glutamate utilization protein B
K01585	1.10	1.6E-03		arginine decarboxylase [EC:4.1.1.19]
K04761	1.10	4.6E-03		LysR family transcriptional regulator, hydrogen peroxide-inducible genes activator
K09181	1.10	4.5E-03		hypothetical protein
K00275	1.10	5.1E-03		pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]
K07735	1.12	4.5E-03		putative transcriptional regulator
K08223	1.13	3.9E-03		MFS transporter, FSR family, fosmidomycin resistance protein
K01932	1.14	1.4E-02		None
K03286	1.19	1.1E-02		OmpA-OmpF porin, OOP family
K05801	1.20	1.2E-02		DnaJ like chaperone protein
K02843	1.20	8.8E-03		heptosyltransferase II [EC:2.4.-.-]
K06894	1.22	1.9E-03		None
K13979	1.22	3.7E-02		uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.-]
K03457	1.22	2.1E-05		nucleobase:cation symporter-1, NCS1 family
K03809	1.31	1.9E-04		Trp repressor binding protein
K05739	1.31	1.3E-03		hypothetical protein
K13821	1.32	9.6E-04		proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]
K07147	1.36	1.8E-02		None

K02439	1.37	7.4E-03	thiosulfate sulfurtransferase [EC:2.8.1.1]
K04771	1.37	1.9E-02	serine protease Do [EC:3.4.21.107]
K02454	1.42	1.4E-02	general secretion pathway protein E
K02456	1.42	1.4E-04	general secretion pathway protein G
K02453	1.43	1.5E-02	general secretion pathway protein D
K06867	1.45	1.1E-03	None
K03673	1.53	3.3E-03	thiol:disulfide interchange protein DsbA
K09798	1.55	1.4E-03	hypothetical protein
K14393	1.56	1.5E-03	cation/acetate symporter
K06204	1.56	3.3E-03	DnaK suppressor protein
K02067	1.56	3.4E-03	putative ABC transport system substrate-binding protein
K04754	1.56	3.3E-03	lipoprotein
K03641	1.56	3.3E-03	TolB protein
K08296	1.57	5.1E-03	phosphohistidine phosphatase [EC:3.1.3.-] geranyltranstransferase [EC:2.5.1.10];farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]
K00795	1.60	2.7E-03	fructose-1,6-bisphosphatase I [EC:3.1.3.11]
K03841	1.61	2.5E-03	lipopolysaccharide export system protein LptA
K09774	1.61	2.5E-03	tRNA 2-thiocytidine biosynthesis protein TtcA
K14058	1.61	2.5E-03	putative toluene tolerance protein
K07323	1.61	2.5E-03	thiol:disulfide interchange protein DsbC [EC:5.3.4.1]
K03981	1.61	2.5E-03	outer membrane lipoprotein carrier protein
K03634	1.61	2.5E-03	lipopolysaccharide export system permease protein
K07091	1.61	2.5E-03	fumarate reductase iron-sulfur protein [EC:1.3.99.1];fumarate reductase iron-sulfur subunit [EC:1.3.99.1]
K00245	1.61	2.5E-03	None
K07000	1.61	2.5E-03	lipopolysaccharide export system permease protein
K11720	1.61	2.4E-03	ADP-L-glycero-D-manno-heptose 6- epimerase [EC:5.1.3.20]
K03274	1.66	2.3E-03	heptosyltransferase I [EC:2.4.-.-]
K02841	1.67	2.1E-03	heptosyltransferase III [EC:2.4.-.-]
K02849	1.67	2.2E-03	MFS transporter, YNFM family, putative membrane transport protein
K08224	1.68	2.3E-03	glutathione S-transferase [EC:2.5.1.18]
K00799	1.76	3.3E-03	protein-L-isoaspartate(D-aspartate) O- methyltransferase [EC:2.1.1.77]
K00573	1.76	1.5E-03	aconitate hydratase 2 [EC:4.2.1.3]
K01682	1.76	1.3E-03	type VI secretion system protein ImpB
K11901	1.76	1.3E-03	type VI secretion system protein ImpC
K11900	1.76	1.3E-03	hypothetical protein
K09794	1.76	1.3E-03	membrane-bound lytic murein transglycosylase C [EC:3.2.1.-]
K08306	1.76	1.3E-03	type VI secretion system protein VasG
K11907	1.76	1.3E-03	putative membrane protein
K08993	1.76	1.3E-03	flagella basal body P-ring formation protein FlgA
K02386	1.76	1.3E-03	spermidine export protein MdtI
K11742	1.76	1.3E-03	

	K00769	1.76	1.3E-03	xanthine phosphoribosyltransferase [EC:2.4.2.22]
	K02572	1.76	1.3E-03	ferredoxin-type protein NapF
	K03749	1.76	1.3E-03	DedD protein
	K03926	1.77	1.6E-03	periplasmic divalent cation tolerance protein
				molybdopterin biosynthesis protein
	K03831	1.77	1.6E-03	Mog;molybdopterin adenylyltransferase
	K02394	1.77	1.3E-03	flagellar P-ring protein precursor FlgI
	K02393	1.77	1.3E-03	flagellar L-ring protein precursor FlgH
	K01058	1.78	1.2E-03	phospholipase A1 [EC:3.1.1.32]
				type VI secretion system secreted protein
	K11903	1.82	1.0E-03	Hcp
	K03835	1.82	1.0E-03	tryptophan-specific transport protein
Control vs Low Iron Diet	K07495	-2.12	1.0E-03	putative transposase
				arginine-tRNA-protein transferase
	K00685	-2.02	2.7E-04	[EC:2.3.2.8]
				cb-type cytochrome c oxidase subunit I
				[EC:1.9.3.1];cytochrome c oxidase cb-type
	K00404	-2.02	2.8E-04	subunit I [EC:1.9.3.1]
				cb-type cytochrome c oxidase subunit III
				[EC:1.9.3.1];cytochrome c oxidase cb-type
	K00406	-2.02	2.7E-04	subunit III
				cb-type cytochrome c oxidase subunit II
				[EC:1.9.3.1];cytochrome c oxidase cb-type
	K00405	-2.02	2.7E-04	subunit II
	K09792	-2.01	2.8E-04	hypothetical protein
	K02453	-1.86	1.6E-03	general secretion pathway protein D
				uncharacterized zinc-type alcohol
				dehydrogenase-like protein [EC:1.-.-.]
	K13979	-1.82	1.8E-03	general secretion pathway protein E
	K02454	-1.79	2.1E-03	serine protease Do [EC:3.4.21.107]
	K04771	-1.67	4.2E-03	None
	K07147	-1.64	4.7E-03	glycolate oxidase iron-sulfur subunit
	K11473	-1.45	2.4E-03	homoserine O-acetyltransferase
				[EC:2.3.1.31]
	K00641	-1.45	8.1E-03	alkanal monooxygenase (FMN-linked)
				[EC:1.14.14.3]
	K00494	-1.40	2.8E-02	hemoglobin
	K06886	-1.35	2.1E-02	urease subunit beta [EC:3.5.1.5];urease
				beta subunit [EC:3.5.1.5]
	K01429	-1.07	7.7E-03	putative glutathione S-transferase
	K07393	-1.06	1.3E-04	hypothetical protein
	K09967	-1.00	2.1E-02	anthranilate
				synthase/phosphoribosyltransferase
	K13497	-0.99	3.4E-02	[EC:4.1.3.27 2.4.2.18]
	K14623	-0.99	7.1E-03	DNA-damage-inducible protein D
	K11104	-0.89	2.3E-02	melibiose permease
	K07062	-0.89	4.2E-02	None
				guanosine-3',5'-bis(diphosphate) 3'-
	K01139	-0.88	1.7E-02	pyrophosphohydrolase [EC:3.1.7.2]
	K12992	-0.83	2.1E-02	rhamnosyltransferase [EC:2.4.1.-]
	K13954	-0.82	4.5E-02	alcohol dehydrogenase [EC:1.1.1.1]
	K02438	-0.73	2.6E-02	glycogen operon protein GlgX [EC:3.2.1.-]
	K01621	-0.69	1.0E-03	phosphoketolase [EC:4.1.2.9]

K02510	-0.66	2.3E-02	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [EC:4.1.2.-]
K05992	-0.66	2.7E-02	None
K12700	-0.63	3.9E-02	non-specific ribonucleoside hydrolase [EC:3.2.-.-]
K02077	-0.55	3.3E-02	zinc/manganese transport system substrate-binding protein
K05885	-0.54	1.8E-02	2,5-diketo-D-gluconate reductase [EC:1.1.1.274]
K01256	-0.50	3.1E-02	aminopeptidase N [EC:3.4.11.2]
K01589	-0.50	3.7E-02	5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]
K03709	-0.47	4.9E-02	DtxR family transcriptional regulator, Mn-dependent transcriptional regulator
K03549	-0.43	2.8E-02	KUP system potassium uptake protein
K01552	-0.35	3.7E-02	None
K00754	-0.29	4.0E-02	None
K03588	-0.15	1.6E-03	cell division protein FtsW
K03686	-0.13	2.1E-02	molecular chaperone DnaJ
K13292	-0.11	1.4E-02	phosphatidylglycerol:prolipoprotein diacylglycerol transferase [EC:2.-.-.-]
K00003	-0.11	6.0E-03	homoserine dehydrogenase [EC:1.1.1.3]
K00974	-0.11	4.7E-02	tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.25 2.7.7.21 3.1.3.- 3.1.4.-];tRNA nucleotidyltransferase (CCA-adding enzyme) [EC:2.7.7.72 3.1.3.- 3.1.4.-]
K03438	-0.11	1.1E-03	S-adenosyl-methyltransferase [EC:2.1.1.-];16S rRNA (cytosine1402-N4)-methyltransferase [EC:2.1.1.199]
K01534	-0.11	9.9E-03	Cd2+/Zn2+-exporting ATPase [EC:3.6.3.3 3.6.3.5]
K00948	-0.11	9.0E-03	ribose-phosphate pyrophosphokinase [EC:2.7.6.1]
K00925	-0.10	4.0E-02	acetate kinase [EC:2.7.2.1]
K00826	-0.10	5.1E-03	branched-chain amino acid aminotransferase [EC:2.6.1.42]
K08591	-0.09	2.7E-02	glycerol-3-phosphate acyltransferase PlsY [EC:2.3.1.15]
K04487	-0.09	3.0E-02	cysteine desulfurase [EC:2.8.1.7]
K11754	-0.08	6.9E-03	dihydrofolate synthase / folylpolyglutamate synthase [EC:6.3.2.12 6.3.2.17]
K07478	-0.08	4.6E-02	putative ATPase
K01358	-0.08	2.4E-02	ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
K02469	-0.07	1.2E-02	DNA gyrase subunit A [EC:5.99.1.3]
K02470	-0.06	3.0E-02	DNA gyrase subunit B [EC:5.99.1.3]
K07005	0.20	2.0E-02	None
K03522	0.25	5.0E-02	electron transfer flavoprotein alpha subunit
K03521	0.25	4.7E-02	electron transfer flavoprotein beta subunit
K02348	0.43	4.5E-02	ElaA protein
K02768	0.45	4.5E-02	PTS system, fructose-specific IIA component [EC:2.7.1.69]
K03486	0.47	4.1E-02	GntR family transcriptional regulator, trehalose operon transcriptional repressor

K03491	0.48	3.4E-02	lichenan operon transcriptional antiterminator
K01188	0.48	6.5E-03	beta-glucosidase [EC:3.2.1.21]
K01195	0.54	1.7E-02	beta-glucuronidase [EC:3.2.1.31]
K08974	0.54	2.8E-03	putative membrane protein PTS system, fructose-specific IIC-like component
K11203	0.57	4.0E-02	putative RecB family exonuclease
K07464	0.60	2.6E-02	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase [EC:5.3.1.17]
K01815	0.61	5.0E-02	transcriptional activator TenA [EC:3.5.99.2];thiaminase (transcriptional activator TenA) [EC:3.5.99.2]
K03707	0.61	2.2E-02	xanthine dehydrogenase molybdenum-binding subunit [EC:1.17.1.4]
K00087	0.64	3.4E-02	tight adherence protein C
K12511	0.65	4.2E-02	
K09697	0.68	1.0E-02	sodium transport system ATP-binding protein
K09696	0.68	1.0E-02	sodium transport system permease protein
K01048	0.69	2.5E-02	lysophospholipase [EC:3.1.1.5]
K01144	0.70	3.0E-02	exodeoxyribonuclease V [EC:3.1.11.5]
K05919	0.73	3.9E-02	superoxide reductase [EC:1.15.1.2]
K06410	0.74	2.9E-02	dipicolinate synthase subunit A
K01222	0.74	6.0E-04	6-phospho-beta-glucosidase [EC:3.2.1.86]
K10189	0.74	4.9E-02	lactose/L-arabinose transport system permease protein
K00879	0.77	4.9E-02	L-fuculokinase [EC:2.7.1.51]
K13626	0.80	4.9E-02	flagellar assembly factor FliW
K10188	0.80	3.7E-02	lactose/L-arabinose transport system substrate-binding protein
K06215	0.82	1.9E-02	pyridoxine biosynthesis protein [EC:4.-.-.-]
K01492	0.83	3.1E-02	phosphoribosylaminoimidazolecarboxamide formyltransferase [EC:2.1.2.3]
K11689	0.83	3.9E-02	C4-dicarboxylate transporter, DctQ subunit
K06411	0.84	5.3E-03	dipicolinate synthase subunit B
K01212	0.85	2.9E-02	levanase [EC:3.2.1.65]
K00170	0.85	4.8E-02	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]
K02279	0.86	3.4E-03	pilus assembly protein CpaB
K08681	0.88	1.6E-02	glutamine amidotransferase [EC:2.6.-.-]
K01201	0.88	1.9E-02	glucosylceramidase [EC:3.2.1.45]
K01523	0.88	9.8E-03	phosphoribosyl-ATP pyrophosphohydrolase [EC:3.6.1.31]
K12527	0.91	4.1E-03	putative selenate reductase [EC:1.97.1.9]
K00065	0.91	1.8E-02	2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]
K01155	0.93	1.6E-02	type II restriction enzyme [EC:3.1.21.4]
K00619	0.93	2.9E-02	amino-acid N-acetyltransferase [EC:2.3.1.1]
K13479	0.95	4.0E-03	xanthine dehydrogenase FAD-binding subunit [EC:1.17.1.4]
K06408	0.96	8.4E-03	stage V sporulation protein AF
K07181	0.97	1.5E-02	putative signal transduction protein containing EAL and modified HD-GYP domains
K06987	0.98	1.3E-03	None

	K00171	0.99	3.5E-02	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
	K00603	0.99	2.4E-02	glutamate formiminotransferase [EC:2.1.2.5]
	K00172	1.00	1.4E-02	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]
	K00169	1.00	1.4E-02	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]
	K03338	1.01	4.2E-02	5-dehydro-2-deoxygluconokinase [EC:2.7.1.92]
	K09749	1.02	5.9E-03	hypothetical protein
	K00050	1.05	3.4E-02	hydroxypyruvate reductase [EC:1.1.1.81]
	K04061	1.06	4.5E-03	flagellar biosynthesis protein
	K00358	1.06	1.0E-03	None
				2-C-methyl-D-erythritol 4-phosphate cytidyltransferase / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:2.7.7.60]
	K12506	1.07	6.0E-03	4.6.1.12]
				ferredoxin hydrogenase large subunit [EC:1.12.7.2]
	K00533	1.07	4.0E-02	LuxR family transcriptional regulator, maltose regulon positive regulatory protein
	K03556	1.09	1.3E-02	galactoside O-acetyltransferase [EC:2.3.1.18]
	K00633	1.10	3.5E-04	multicomponent Na ⁺ :H ⁺ antiporter subunit C
	K05567	1.14	3.0E-02	two-component system, chemotaxis family, response regulator CheV
	K03415	1.14	3.1E-03	spore germination protein KA
	K06295	1.14	2.6E-03	multicomponent Na ⁺ :H ⁺ antiporter subunit E
	K05569	1.15	3.2E-02	multicomponent Na ⁺ :H ⁺ antiporter subunit D
	K05568	1.15	3.8E-03	hypothetical protein
	K09988	1.15	6.3E-03	streptomycin 3"-adenylyltransferase [EC:2.7.7.47]
	K00984	1.15	7.8E-03	N-acylneuraminate cytidyltransferase [EC:2.7.7.43]
	K00983	1.16	2.1E-02	restriction system protein
	K07448	1.18	3.7E-03	transcriptional pleiotropic regulator of transition state genes
	K06284	1.20	4.6E-04	nondiscriminating aspartyl-tRNA synthetase [EC:6.1.1.23]
	K09759	1.34	1.9E-03	C4-dicarboxylate-binding protein DctP
	K11688	1.35	3.3E-02	hypothetical protein
	K09116	1.56	2.0E-02	
	K12452	1.73	1.1E-03	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase
High vs Low Iron Diet	K02453	-3.29	2.0E-07	general secretion pathway protein D
	K02454	-3.21	2.5E-07	general secretion pathway protein E
	K09792	-3.07	1.6E-07	hypothetical protein
				arginine-tRNA-protein transferase [EC:2.3.2.8]
	K00685	-3.07	1.6E-07	cb-type cytochrome c oxidase subunit I [EC:1.9.3.1];cytochrome c oxidase cb-type subunit I [EC:1.9.3.1]
	K00404	-3.07	1.6E-07	

K00406	-3.07	1.6E-07	cb-type cytochrome c oxidase subunit III [EC:1.9.3.1];cytochrome c oxidase cb-type subunit III
K00405	-3.07	1.6E-07	cb-type cytochrome c oxidase subunit II [EC:1.9.3.1];cytochrome c oxidase cb-type subunit II
K07495	-3.07	3.9E-06	putative transposase
K04771	-3.04	8.2E-07	serine protease Do [EC:3.4.21.107]
K13979	-3.04	6.9E-07	uncharacterized zinc-type alcohol dehydrogenase-like protein [EC:1.-.-.]
K07147	-3.00	8.8E-07	None
K03831	-2.70	4.0E-06	molybdopterin biosynthesis protein Mog;molybdopterin adenyllyltransferase
K03926	-2.70	4.1E-06	periplasmic divalent cation tolerance protein
K00573	-2.69	3.8E-06	protein-L-isoaspartate(D-aspartate) O-methyltransferase [EC:2.1.1.77]
K02849	-2.58	5.9E-06	heptosyltransferase III [EC:2.4.-.]
K02841	-2.58	5.7E-06	heptosyltransferase I [EC:2.4.-.]
K03274	-2.57	5.9E-06	ADP-L-glycero-D-manno-heptose 6-epimerase [EC:5.1.3.20]
K08296	-2.49	1.7E-05	phosphohistidine phosphatase [EC:3.1.3.-]
K14393	-2.46	2.1E-06	cation/acetate symporter
K11473	-2.42	1.2E-06	glycolate oxidase iron-sulfur subunit
K06867	-2.28	1.3E-06	None
K03835	-2.18	1.1E-04	tryptophan-specific transport protein
K11903	-2.18	1.1E-04	type VI secretion system secreted protein Hcp
K01058	-2.14	1.3E-04	phospholipase A1 [EC:3.1.1.32]
K02394	-2.12	1.4E-04	flagellar P-ring protein precursor FlgI
K02393	-2.12	1.4E-04	flagellar L-ring protein precursor FlgH
K11742	-2.11	1.4E-04	spermidine export protein MdtI
K00769	-2.11	1.4E-04	xanthine phosphoribosyltransferase [EC:2.4.2.22]
K08306	-2.11	1.4E-04	membrane-bound lytic murein transglycosylase C [EC:3.2.1.-]
K08993	-2.11	1.4E-04	putative membrane protein
K02572	-2.11	1.5E-04	ferredoxin-type protein NapF
K02386	-2.11	1.4E-04	flagella basal body P-ring formation protein FlgA
K03749	-2.11	1.4E-04	DedD protein
K11907	-2.11	1.4E-04	type VI secretion system protein VasG
K00799	-2.11	4.6E-04	glutathione S-transferase [EC:2.5.1.18]
K11901	-2.11	1.4E-04	type VI secretion system protein ImpB
K11900	-2.11	1.4E-04	type VI secretion system protein ImpC
K01682	-2.11	1.4E-04	aconitate hydratase 2 [EC:4.2.1.3]
K09794	-2.11	1.4E-04	hypothetical protein
K08224	-2.02	2.8E-04	MFS transporter, YNFM family, putative
K03642	-1.95	2.5E-03	membrane transport protein
K00245	-1.93	3.2E-04	rare lipoprotein A
K07091	-1.93	3.2E-04	fumarate reductase iron-sulfur protein [EC:1.3.99.1];fumarate reductase iron-sulfur subunit [EC:1.3.99.1]
K03634	-1.93	3.2E-04	lipopolysaccharide export system permease protein
			outer membrane lipoprotein carrier protein

K03981	-1.93	3.2E-04	thiol:disulfide interchange protein DsbC [EC:5.3.4.1]
K07323	-1.93	3.2E-04	putative toluene tolerance protein
K14058	-1.93	3.2E-04	tRNA 2-thiocytidine biosynthesis protein TtcA
K09774	-1.93	3.2E-04	lipopolysaccharide export system protein LptA
K07000	-1.93	3.2E-04	None
K11720	-1.93	3.2E-04	lipopolysaccharide export system permease protein
K03841	-1.93	3.2E-04	fructose-1,6-bisphosphatase I [EC:3.1.3.11]
K00795	-1.92	3.6E-04	geranyltranstransferase [EC:2.5.1.10];farnesyl diphosphate synthase [EC:2.5.1.1 2.5.1.10]
K03641	-1.89	4.3E-04	TolB protein
K04754	-1.89	4.3E-04	lipoprotein
K06204	-1.88	4.3E-04	DnaK suppressor protein
K02067	-1.88	4.6E-04	putative ABC transport system substrate-binding protein
K09798	-1.86	1.5E-04	hypothetical protein
K03673	-1.83	4.9E-04	thiol:disulfide interchange protein DsbA
K00494	-1.81	3.4E-03	alkanal monooxygenase (FMN-linked) [EC:1.14.14.3]
K13821	-1.81	1.3E-05	proline dehydrogenase / delta 1-pyrroline-5-carboxylate dehydrogenase [EC:1.5.99.8 1.5.1.12]
K02017	-1.76	2.8E-03	molybdate transport system ATP-binding protein [EC:3.6.3.29]
K03635	-1.75	1.2E-03	molybdenum cofactor biosynthesis protein E;molybdopterin synthase catalytic subunit [EC:2.-.-.-]
K03636	-1.75	1.2E-03	molybdopterin synthase sulfur carrier subunit;molybdenum cofactor biosynthesis protein D
K02456	-1.68	1.1E-05	general secretion pathway protein G
K00116	-1.66	6.2E-03	malate dehydrogenase (quinone) [EC:1.1.5.4]
K06886	-1.64	4.0E-03	hemoglobin
K03820	-1.63	1.7E-03	apolipoprotein N-acyltransferase [EC:2.3.1.-]
K03559	-1.63	8.0E-05	biopolymer transport protein ExbD
K06894	-1.62	5.6E-05	None
K07062	-1.57	1.8E-04	None
K03457	-1.52	4.3E-07	nucleobase:cation symporter-1, NCS1 family
K02439	-1.51	2.9E-03	thiosulfate sulfurtransferase [EC:2.8.1.1]
K00641	-1.47	6.0E-03	homoserine O-acetyltransferase [EC:2.3.1.31]
K03179	-1.44	1.9E-03	4-hydroxybenzoate octaprenyltransferase [EC:2.5.1.-]
K14623	-1.38	1.4E-04	DNA-damage-inducible protein D
K03809	-1.37	9.9E-05	Trp repressor binding protein
K03561	-1.36	7.6E-04	biopolymer transport protein ExbB
K03640	-1.33	4.4E-02	peptidoglycan-associated lipoprotein
K07735	-1.33	8.2E-04	putative transcriptional regulator

K08223	-1.33	7.5E-04	MFS transporter, FSR family, fosmidomycin resistance protein
K00275	-1.31	9.1E-04	pyridoxamine 5'-phosphate oxidase [EC:1.4.3.5]
K09181	-1.30	8.1E-04	hypothetical protein
K02510	-1.30	7.3E-06	2,4-dihydroxyhept-2-ene-1,7-dioic acid aldolase [EC:4.1.2.-]
K01971	-1.30	3.3E-03	DNA ligase (ATP) [EC:6.5.1.1]
K04761	-1.30	8.9E-04	LysR family transcriptional regulator, hydrogen peroxide-inducible genes activator
K01433	-1.28	1.1E-03	formyltetrahydrofolate deformylase [EC:3.5.1.10]
K08311	-1.25	1.0E-02	putative (di)nucleoside polyphosphate hydrolase [EC:3.6.1.-]
K02426	-1.25	1.3E-03	cysteine desulfuration protein SufE
K07071	-1.24	2.5E-03	None
K03585	-1.23	1.6E-03	membrane fusion protein
K09973	-1.21	1.8E-03	hypothetical protein
K00281	-1.19	1.9E-03	glycine dehydrogenase [EC:1.4.4.2]
K03113	-1.19	1.9E-03	translation initiation factor 1;translation initiation factor SUI1;translation initiation factor eIF-1
K08289	-1.19	1.8E-03	phosphoribosylglycinamide formyltransferase 2 [EC:2.1.2.2]
K05801	-1.19	1.3E-02	DnaJ like chaperone protein
K09922	-1.19	2.0E-03	hypothetical protein
K07263	-1.18	3.4E-03	zinc protease [EC:3.4.99.-];zinc protease [EC:3.4.24.-]
K03286	-1.16	1.3E-02	OmpA-OmpF porin, OOP family
K04762	-1.16	3.0E-03	ribosome-associated heat shock protein Hsp15
K03269	-1.16	3.0E-03	UDP-2,3-diacylglycerol glucosamine hydrolase [EC:3.6.1.-]
K03474	-1.16	3.0E-03	pyridoxine 5-phosphate synthase [EC:2.6.99.2]
K00331	-1.16	3.9E-03	NADH dehydrogenase I subunit B [EC:1.6.5.3];NADH-quinone oxidoreductase subunit B [EC:1.6.5.3]
K00330	-1.16	3.9E-03	NADH-quinone oxidoreductase subunit A [EC:1.6.5.3];NADH dehydrogenase I subunit A [EC:1.6.5.3]
K00337	-1.16	3.9E-03	NADH dehydrogenase I subunit H [EC:1.6.5.3];NADH-quinone oxidoreductase subunit H [EC:1.6.5.3]
K00341	-1.16	3.9E-03	NADH dehydrogenase I subunit L [EC:1.6.5.3];NADH-quinone oxidoreductase subunit L [EC:1.6.5.3]
K00339	-1.16	3.9E-03	NADH dehydrogenase I subunit J [EC:1.6.5.3];NADH-quinone oxidoreductase subunit J [EC:1.6.5.3]
K00342	-1.16	3.9E-03	NADH-quinone oxidoreductase subunit M [EC:1.6.5.3];NADH dehydrogenase I subunit M [EC:1.6.5.3]

K00340	-1.16	3.9E-03	NADH-quinone oxidoreductase subunit K [EC:1.6.5.3];NADH dehydrogenase I subunit K [EC:1.6.5.3]
K00338	-1.16	3.9E-03	NADH-quinone oxidoreductase subunit I [EC:1.6.5.3];NADH dehydrogenase I subunit I [EC:1.6.5.3]
K00343	-1.16	3.9E-03	NADH dehydrogenase I subunit N [EC:1.6.5.3];NADH-quinone oxidoreductase subunit N [EC:1.6.5.3]
K02523	-1.16	2.9E-03	octaprenyl-diphosphate synthase [EC:2.5.1.-];octaprenyl-diphosphate synthase [EC:2.5.1.90];octaprenyl diphosphate synthase [EC:2.5.1.-]
K02066	-1.16	2.9E-03	putative ABC transport system permease protein
K02065	-1.16	2.9E-03	putative ABC transport system ATP-binding protein
K02535	-1.16	2.9E-03	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase [EC:3.5.1.-] 3-deoxy-D-manno-octulosonic-acid
K02527	-1.16	2.9E-03	transferase [EC:2.-.-.-]
K07277	-1.16	2.9E-03	outer membrane protein
K00912	-1.16	2.9E-03	tetraacyldisaccharide 4'-kinase [EC:2.7.1.130]
K00748	-1.16	3.0E-03	lipid-A-disaccharide synthase [EC:2.4.1.182]
K00677	-1.15	4.0E-03	UDP-N-acetylglucosamine acyltransferase [EC:2.3.1.129]
K02230	-1.15	7.0E-03	cobaltochelatase CobN [EC:6.6.1.2]
K09979	-1.15	2.9E-02	hypothetical protein
K00895	-1.14	9.9E-03	pyrophosphate--fructose-6-phosphate 1-phosphotransferase [EC:2.7.1.90]
K01627	-1.14	3.0E-03	2-dehydro-3-deoxyphosphooctonate aldolase (KDO 8-P synthase) [EC:2.5.1.55]
K03771	-1.13	3.1E-03	peptidyl-prolyl cis-trans isomerase SurA [EC:5.2.1.8]
K00123	-1.13	4.3E-03	formate dehydrogenase, alpha subunit [EC:1.2.1.2]
K03770	-1.13	4.2E-03	peptidyl-prolyl cis-trans isomerase D [EC:5.2.1.8]
K02843	-1.13	1.4E-02	heptosyltransferase II [EC:2.4.-.-]
K01295	-1.12	2.4E-05	glutamate carboxypeptidase [EC:3.4.17.11]
K00428	-1.10	9.0E-03	cytochrome c peroxidase [EC:1.11.1.5]
K03453	-1.10	7.3E-04	bile acid:Na ⁺ symporter, BASS family
K13895	-1.09	1.7E-02	microcin C transport system permease protein
K13894	-1.09	1.7E-02	microcin C transport system permease protein
K05835	-1.09	1.8E-02	threonine efflux protein
K14261	-1.09	1.8E-02	alanine-synthesizing transaminase [EC:2.6.1.-]
K13893	-1.08	1.9E-02	microcin C transport system substrate-binding protein
K13954	-1.08	5.8E-03	alcohol dehydrogenase [EC:1.1.1.1]
K01585	-1.08	2.0E-03	arginine decarboxylase [EC:4.1.1.19]

K00946	-1.06	5.9E-03	thiamine-monophosphate kinase [EC:2.7.4.16]
K03304	-1.06	2.0E-02	tellurite resistance/dicarboxylate transporter, TDT family
K01130	-1.06	8.4E-03	arylsulfatase [EC:3.1.6.1]
K03272	-1.06	7.8E-03	D-beta-D-heptose 7-phosphate kinase / D- beta-D-heptose 1-phosphate
K03833	-1.03	2.9E-03	adenosyltransferase [EC:2.7.1.- 2.7.7.-]
K03543	-1.03	8.6E-03	selenocysteine-specific elongation factor
K00658	-1.03	1.3E-02	multidrug resistance protein A
K01902	-1.02	1.3E-02	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
K01903	-1.02	1.3E-02	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
K01991	-1.02	1.3E-02	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
K03832	-1.02	9.6E-03	polysaccharide export outer membrane protein
K06861	-1.01	4.1E-03	periplasmic protein TonB
K06891	-1.01	1.3E-03	lipopolysaccharide export system ATP- binding protein [EC:3.6.3.-]
K03149	-0.95	1.3E-03	ATP-dependent Clp protease adaptor protein ClpS
K00652	-0.95	1.6E-02	thiamine biosynthesis ThiG
K02428	-0.94	5.8E-03	8-amino-7-oxononanoate synthase [EC:2.3.1.47]
K01007	-0.94	3.6E-03	nucleoside-triphosphate pyrophosphatase [EC:3.6.1.19]
K04773	-0.91	3.0E-03	pyruvate, water dikinase [EC:2.7.9.2]
K11996	-0.91	3.8E-02	protease IV [EC:3.4.21.-]
K00979	-0.90	1.0E-02	adenylyltransferase and sulfurtransferase;adenylyltransferase and sulfurtransferase MOCS3/UBA4 [EC:2.7.7.- 2.8.1.-]
K03327	-0.89	2.7E-02	3-deoxy-manno-octulosonate cytidyltransferase (CMP-KDO synthetase) [EC:2.7.7.38]
K00241	-0.89	3.0E-02	multidrug resistance protein, MATE family
K09808	-0.88	4.1E-02	succinate dehydrogenase cytochrome b556 subunit;succinate dehydrogenase cytochrome b-556 subunit [EC:1.3.99.1];succinate dehydrogenase cytochrome b-556 subunit
K06177	-0.88	2.3E-02	lipoprotein-releasing system permease protein
K00390	-0.88	1.7E-03	tRNA pseudouridine32 synthase / 23S rRNA pseudouridine746 synthase [EC:5.4.99.28 5.4.99.29];ribosomal large subunit
K03593	-0.87	2.6E-02	pseudouridine synthase A [EC:5.4.99.12]
K06911	-0.86	3.1E-03	phosphoadenosine phosphosulfate reductase [EC:1.8.4.8]
			ATP-binding protein involved in chromosome partitioning
			None

K02014	-0.86	6.3E-03	iron complex outermembrane receptor protein
K02481	-0.85	4.1E-02	two-component system, NtrC family, response regulator
K01805	-0.84	5.7E-03	xylose isomerase [EC:5.3.1.5]
K00860	-0.82	2.5E-02	adenylylsulfate kinase [EC:2.7.1.25]
K11527	-0.82	3.8E-02	two-component system, unclassified family, sensor histidine kinase and response regulator [EC:2.7.13.3]
K01993	-0.82	2.1E-02	HlyD family secretion protein
K01847	-0.82	5.0E-02	methylmalonyl-CoA mutase [EC:5.4.99.2]
K01596	-0.81	6.7E-03	phosphoenolpyruvate carboxykinase (GTP) [EC:4.1.1.32]
K03273	-0.81	2.7E-02	D-glycero-D-manno-heptose 1,7-bisphosphate phosphatase [EC:3.1.3.-]
K00156	-0.81	3.6E-02	pyruvate dehydrogenase (quinone) [EC:1.2.5.1];pyruvate dehydrogenase (cytochrome) [EC:1.2.2.2]
K02536	-0.81	1.5E-02	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase [EC:2.3.1.-]
K01579	-0.80	1.0E-02	aspartate 1-decarboxylase [EC:4.1.1.11]
K02048	-0.80	4.9E-02	sulfate transport system substrate-binding protein
K03297	-0.80	3.3E-02	small multidrug resistance protein, SMR family
K02379	-0.80	3.8E-02	FdhD protein
K01918	-0.80	1.0E-02	pantoate--beta-alanine ligase [EC:6.3.2.1]
K06167	-0.77	3.3E-02	PhnP protein
K01911	-0.76	2.8E-02	O-succinylbenzoic acid--CoA ligase [EC:6.2.1.26]
K07214	-0.75	2.9E-02	enterochelin esterase and related enzymes
K06402	-0.75	1.6E-02	stage IV sporulation protein FB [EC:3.4.24.-]
K12992	-0.70	5.0E-02	rhamnosyltransferase [EC:2.4.1.-]
K01438	-0.70	2.0E-02	acetylornithine deacetylase [EC:3.5.1.16]
K01661	-0.69	4.4E-02	naphthoate synthase [EC:4.1.3.36]
K02053	-0.69	4.5E-02	putative spermidine/putrescine transport system permease protein
K03077	-0.68	4.0E-02	L-ribulose-5-phosphate 4-epimerase [EC:5.1.3.4]
K00956	-0.68	4.7E-02	sulfate adenylyltransferase subunit 1 [EC:2.7.7.4]
K06920	-0.67	3.3E-02	queuosine biosynthesis protein QueC
K03752	-0.66	3.9E-02	molybdopterin-guanine dinucleotide biosynthesis protein A
K09001	-0.66	1.3E-02	anhydro-N-acetylmuramic acid kinase [EC:2.7.1.-];anhydro-N-acetylmuramic acid kinase [EC:2.7.1.170]
K03446	-0.66	2.9E-02	MFS transporter, DHA2 family, multidrug resistance protein B
K01744	-0.65	3.2E-02	aspartate ammonia-lyase [EC:4.3.1.1]
K00833	-0.64	2.7E-02	adenosylmethionine-8-amino-7-oxononanoate aminotransferase [EC:2.6.1.62]
K05795	-0.64	1.6E-02	tellurium resistance protein TerD

K01912	-0.63	2.4E-02	phenylacetate-CoA ligase [EC:6.2.1.30]
K01487	-0.61	4.8E-02	guanine deaminase [EC:3.5.4.3]
K02058	-0.60	4.6E-02	simple sugar transport system substrate-binding protein
K03154	-0.58	4.5E-02	sulfur carrier protein;thiamine biosynthesis ThiS
K07393	-0.57	3.5E-02	putative glutathione S-transferase
K00998	-0.54	3.6E-02	phosphatidylserine synthase [EC:2.7.8.8]
K00789	0.08	5.1E-03	S-adenosylmethionine synthetase [EC:2.5.1.6]
K07238	0.14	4.8E-02	zinc transporter, ZIP family
K07005	0.29	7.1E-04	None
K07727	0.31	2.5E-03	putative transcriptional regulator
K01188	0.39	2.2E-02	beta-glucosidase [EC:3.2.1.21]
K05993	0.43	4.8E-02	isochorismatase [EC:3.3.2.1]
K01812	0.45	3.1E-02	glucuronate isomerase [EC:5.3.1.12]
K01222	0.46	3.0E-02	6-phospho-beta-glucosidase [EC:3.2.1.86]
K07497	0.47	1.1E-02	putative transposase
K03758	0.48	4.3E-02	arginine:ornithine antiporter
K02819	0.49	2.3E-02	PTS system, trehalose-specific IIC component
K01531	0.53	3.7E-02	Mg2+-importing ATPase [EC:3.6.3.2]
K00756	0.55	1.8E-02	pyrimidine-nucleoside phosphorylase [EC:2.4.2.2]
K01226	0.55	1.2E-02	trehalose-6-phosphate hydrolase [EC:3.2.1.93]
K04518	0.56	3.8E-02	prephenate dehydratase [EC:4.2.1.51]
K03930	0.57	9.6E-03	putative tributyrin esterase [EC:3.1.1.-]
K09696	0.58	2.6E-02	sodium transport system permease protein
K09697	0.58	2.5E-02	sodium transport system ATP-binding protein
K08986	0.59	2.8E-02	putative membrane protein
K02348	0.62	2.6E-03	ElaA protein
K07464	0.63	1.6E-02	putative RecB family exonuclease
K01819	0.64	1.5E-02	galactose-6-phosphate isomerase [EC:5.3.1.26]
K03486	0.66	2.9E-03	GntR family transcriptional regulator, trehalose operon transcriptional repressor
K09134	0.66	2.0E-03	hypothetical protein
K07443	0.67	2.2E-02	methylated-DNA-protein-cysteine methyltransferase related protein
K09167	0.68	1.2E-02	hypothetical protein
K01686	0.69	4.3E-03	mannonate dehydratase [EC:4.2.1.8]
K03322	0.70	3.9E-03	manganese transport protein
K11618	0.70	2.5E-03	two-component system, NarL family, response regulator LiaR
K01815	0.71	1.8E-02	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase [EC:5.3.1.17]
K10109	0.74	1.1E-03	maltose/maltodextrin transport system permease protein
K01478	0.75	5.3E-03	arginine deiminase [EC:3.5.3.6]
K10110	0.77	7.7E-04	maltose/maltodextrin transport system permease protein
K01422	0.77	1.3E-03	None
K08352	0.78	3.7E-02	thiosulfate reductase [EC:1.-.-.-]

K10108	0.78	6.5E-04	maltose/maltodextrin transport system substrate-binding protein
K05845	0.79	1.6E-03	osmoprotectant transport system substrate-binding protein
K04516	0.79	1.1E-03	chorismate mutase [EC:5.4.99.5]
K09155	0.80	5.0E-04	hypothetical protein
K00041	0.80	8.8E-03	tagaturonate reductase [EC:1.1.1.58]
K00633	0.81	7.0E-03	galactoside O-acetyltransferase [EC:2.3.1.18]
K01195	0.82	2.4E-04	beta-glucuronidase [EC:3.2.1.31]
K02279	0.82	4.1E-03	pilus assembly protein CpaB
K01201	0.83	2.4E-02	glucosylceramidase [EC:3.2.1.45]
K00358	0.85	7.2E-03	None
K00283	0.85	2.4E-02	glycine dehydrogenase subunit 2 [EC:1.4.4.2]
K00282	0.85	2.4E-02	glycine dehydrogenase subunit 1 [EC:1.4.4.2]
K04029	0.85	1.0E-02	ethanolamine utilization protein EutP
K10188	0.86	2.2E-02	lactose/L-arabinose transport system substrate-binding protein
K06410	0.86	8.5E-03	dipicolinate synthase subunit A
K07498	0.87	3.1E-03	putative transposase
K00968	0.87	1.9E-02	choline-phosphate cytidyltransferase [EC:2.7.7.15]
K06987	0.88	3.0E-03	None
K08974	0.89	1.9E-06	putative membrane protein
K01218	0.90	2.6E-02	mannan endo-1,4-beta-mannosidase [EC:3.2.1.78]
K01144	0.91	3.4E-03	exodeoxyribonuclease V [EC:3.1.11.5]
K06411	0.93	1.7E-03	dipicolinate synthase subunit B
K03476	0.93	3.3E-04	L-ascorbate 6-phosphate lactonase [EC:3.1.1.-]
K07741	0.93	1.7E-03	anti-repressor protein
K00224	0.95	1.3E-02	None
K07216	0.96	3.7E-02	hemerythrin
K03707	0.98	1.9E-04	transcriptional activator TenA [EC:3.5.99.2];thiaminase (transcriptional activator TenA) [EC:3.5.99.2]
K00065	0.98	9.0E-03	2-deoxy-D-gluconate 3-dehydrogenase [EC:1.1.1.125]
K00603	0.99	2.2E-02	glutamate formiminotransferase [EC:2.1.2.5]
K09163	0.99	1.6E-03	hypothetical protein
K06882	1.00	7.4E-03	None
K11689	1.02	8.3E-03	C4-dicarboxylate transporter, DctQ subunit
K01666	1.02	1.7E-02	4-hydroxy 2-oxovalerate aldolase [EC:4.1.3.39]
K12527	1.03	8.3E-04	putative selenate reductase [EC:1.97.1.9]
K12506	1.03	6.4E-03	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase / 2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase [EC:2.7.7.60 4.6.1.12]
K13479	1.06	1.1E-03	xanthine dehydrogenase FAD-binding subunit [EC:1.17.1.4]

K03415	1.10	3.6E-03	two-component system, chemotaxis family, response regulator CheV
K00662	1.10	3.4E-02	aminoglycoside N3'-acetyltransferase [EC:2.3.1.81]
K00170	1.11	7.3E-03	pyruvate ferredoxin oxidoreductase, beta subunit [EC:1.2.7.1]
K01523	1.12	9.0E-04	phosphoribosyl-ATP pyrophosphohydrolase [EC:3.6.1.31]
K03079	1.13	4.0E-03	L-ribulose-5-phosphate 3-epimerase [EC:5.1.3.22]
K07448	1.14	4.6E-03	restriction system protein
K06295	1.15	1.9E-03	spore germination protein KA
K06215	1.17	7.1E-04	pyridoxine biosynthesis protein [EC:4.-.-.]
K00171	1.17	9.7E-03	pyruvate ferredoxin oxidoreductase, delta subunit [EC:1.2.7.1]
K13640	1.18	7.4E-03	MerR family transcriptional regulator, heat shock protein HspR
K09988	1.18	4.3E-03	hypothetical protein
K08681	1.19	8.6E-04	glutamine amidotransferase [EC:2.6.-.-]
K06284	1.22	3.0E-04	transcriptional pleiotropic regulator of transition state genes
K04061	1.23	9.0E-04	flagellar biosynthesis protein
K09749	1.23	7.8E-04	hypothetical protein
K08077	1.25	2.3E-03	UDP-sugar diphosphatase [EC:3.6.1.45]
K07181	1.25	1.4E-03	putative signal transduction protein containing EAL and modified HD-GYP domains
K01654	1.27	3.6E-03	N-acetylneuraminate synthase [EC:2.5.1.56]
K06331	1.28	1.7E-03	spore coat protein I
K03336	1.30	9.6E-03	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase [EC:3.7.1.-]
K11688	1.31	3.8E-02	C4-dicarboxylate-binding protein DctP
K00172	1.32	9.3E-04	pyruvate ferredoxin oxidoreductase, gamma subunit [EC:1.2.7.1]
K00984	1.33	1.9E-03	streptomycin 3"-adenylyltransferase [EC:2.7.7.47]
K00169	1.33	9.3E-04	pyruvate ferredoxin oxidoreductase, alpha subunit [EC:1.2.7.1]
K06408	1.35	1.8E-04	stage V sporulation protein AF
K13922	1.37	3.6E-03	propionaldehyde dehydrogenase
K07814	1.37	3.5E-03	putative two-component system response regulator
K03338	1.40	3.3E-03	5-dehydro-2-deoxygluconokinase [EC:2.7.1.92]
K03337	1.40	4.4E-03	5-deoxy-glucuronate isomerase [EC:5.3.1.-]
K09759	1.42	9.0E-04	nondiscriminating aspartyl-tRNA synthetase [EC:6.1.1.23]
K01608	1.42	1.7E-03	tartronate-semialdehyde synthase [EC:4.1.1.47]
K03556	1.43	9.9E-04	LuxR family transcriptional regulator, maltose regulon positive regulatory protein
K02590	1.47	5.5E-03	nitrogen regulatory protein PII 2
K02589	1.47	5.5E-03	nitrogen regulatory protein PII 1
K10709	1.48	1.7E-03	protein FrlC

K00983	1.53	1.7E-03	N-acylneuraminate cytidyltransferase [EC:2.7.7.43]
K06320	1.57	3.8E-04	spore maturation protein CgeB
K05568	1.62	5.4E-05	multicomponent Na ⁺ :H ⁺ antiporter subunit D
K00002	1.63	4.3E-03	alcohol dehydrogenase (NADP ⁺) [EC:1.1.1.2]
K01134	1.65	1.8E-03	arylsulfatase A [EC:3.1.6.8]
K00096	1.67	2.6E-03	glycerol-1-phosphate dehydrogenase [NAD(P)] [EC:1.1.1.261]
K00958	1.69	9.0E-03	sulfate adenylyltransferase [EC:2.7.7.4]
K00533	1.70	7.6E-04	ferredoxin hydrogenase large subunit [EC:1.12.7.2]
K00091	1.73	9.5E-06	dihydroflavonol-4-reductase [EC:1.1.1.219]
K06306	1.74	3.8E-03	spore germination protein
K04566	1.76	1.1E-03	lysyl-tRNA synthetase, class I [EC:6.1.1.6]
K00050	1.86	1.3E-04	hydroxypyruvate reductase [EC:1.1.1.81]
K12452	1.87	3.8E-04	CDP-6-deoxy-D-xylo-4-hexulose-3-dehydrase
K09981	1.93	1.5E-02	hypothetical protein
K07084	1.94	1.4E-04	None
K05566	2.09	1.1E-04	multicomponent Na ⁺ :H ⁺ antiporter subunit B
K05571	2.11	1.2E-04	multicomponent Na ⁺ :H ⁺ antiporter subunit G
K05567	2.12	4.8E-05	multicomponent Na ⁺ :H ⁺ antiporter subunit C
K05569	2.13	5.9E-05	multicomponent Na ⁺ :H ⁺ antiporter subunit E
K09144	2.22	6.2E-05	hypothetical protein
K09116	2.31	4.9E-04	hypothetical protein
K09145	2.40	3.0E-05	hypothetical protein
K00102	2.62	2.1E-04	D-lactate dehydrogenase (cytochrome) [EC:1.1.2.4]