

Table S5. All annotated genes located on the longest contig containing K23573, the hypothetical protein with the largest difference in relative abundance between the 60 M and deep samples.

Gene	KO	Group	Subgroup1	Subgroup2	Function
c_00000009473_13	K07461	Not Included in Pathway or Brite	Unclassified: genetic information processing	Replication and repair	K07461; putative endonuclease
c_00000009473_14	K13993	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	HSP20; HSP20 family protein
c_00000009473_23	K11927	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	rHE; ATP-dependent RNA helicase RHE [EC:3.6.4.13]
c_00000009473_24	K00254	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	DHODH; pyrD; dihydroorotate dehydrogenase [EC:1.3.5.2]
c_00000009473_37	K00794	Metabolism	Metabolism of cofactors and vitamins	Riboflavin metabolism	riH, RIB4; 6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]
c_00000009473_38	K03564	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers	BCP, PRXQ, DOT5; peroxidoxin Q/BCP [EC:1.11.1.15]
c_00000009473_47	K05307	Metabolism	Metabolism of cofactors and vitamins	Thiamine metabolism	THTPA; thiamine-triphosphatase [EC:3.6.1.28]
c_00000009473_48	K00574	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers	cfa; cyclopropane-fatty-acyl-phospholipid synthase [EC:2.1.1.79]
c_00000009473_59	K01255	Metabolism	Metabolism of other amino acids	Glutathione metabolism	CARP; pepA; leucyl aminopeptidase [EC:3.4.11.1]
c_00000009473_60	K03386	Cellular Processes	Cell growth and death	Apoptosis - fly	PRDX2_4, ahpC; peroxidoxin (alkyl hydroperoxide reductase subunit C) [EC:1.11.1.15]
c_00000009473_63	K01874	Metabolism	Metabolism of other amino acids	Selenocompound metabolism	MARS; metG; methionyl-tRNA synthetase [EC:6.1.1.10]
c_00000009473_63	K01874	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	MARS; metG; methionyl-tRNA synthetase [EC:6.1.1.10]
c_00000009473_64	K03558	Not Included in Pathway or Brite	Poorly characterized	General function prediction only	cvpA; membrane protein required for colicin V production
c_00000009473_65	K03424	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers	tatD; TatD NDNase family protein [EC:3.1.21.-]
c_00000009473_67	K02108	Metabolism	Energy metabolism	Oxidative phosphorylation	ATPF0A; atpB; F-type H ⁺ -transporting ATPase subunit a
c_00000009473_67	K02108	Metabolism	Energy metabolism	Photosynthesis	ATPF0A; atpB; F-type H ⁺ -transporting ATPase subunit a
c_00000009473_68	K02110	Metabolism	Energy metabolism	Oxidative phosphorylation	ATPF0C; atpE; F-type H ⁺ -transporting ATPase subunit c
c_00000009473_68	K02110	Metabolism	Energy metabolism	Photosynthesis	ATPF0C; atpE; F-type H ⁺ -transporting ATPase subunit c
c_00000009473_69	K02109	Metabolism	Energy metabolism	Oxidative phosphorylation	ATPF0B; atpF; F-type H ⁺ -transporting ATPase subunit b
c_00000009473_69	K02109	Metabolism	Energy metabolism	Photosynthesis	ATPF0B; atpF; F-type H ⁺ -transporting ATPase subunit b
c_00000009473_71	K02111	Metabolism	Energy metabolism	Oxidative phosphorylation	ATPF1A; atpA; F-type H ⁺ /Na ⁺ -transporting ATPase subunit alpha [EC:7.1.2.2.2.1]
c_00000009473_71	K02111	Metabolism	Energy metabolism	Photosynthesis	ATPF1A; atpA; F-type H ⁺ /Na ⁺ -transporting ATPase subunit alpha [EC:7.1.2.2.2.1]
c_00000009473_73	K02112	Metabolism	Energy metabolism	Oxidative phosphorylation	ATPF1B; atpD; F-type H ⁺ /Na ⁺ -transporting ATPase subunit beta [EC:7.1.2.2.2.1]
c_00000009473_73	K02112	Metabolism	Energy metabolism	Photosynthesis	ATPF1B; atpD; F-type H ⁺ /Na ⁺ -transporting ATPase subunit beta [EC:7.1.2.2.2.1]
c_00000009473_76	K04566	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	lysK; lysyl-tRNA synthetase, class I [EC:6.1.1.6]
c_00000009473_79	K21929	Genetic Information Processing	Replication and repair	Base excision repair	udg; uracil-DNA glycosylase [EC:3.2.2.27]
c_00000009473_80	K00857	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	tdk, TK; thymidine kinase [EC:2.7.1.21]
c_00000009473_80	K00857	Metabolism	Xenobiotics biodegradation and metabolism	Drug metabolism - other enzymes	tdk, TK; thymidine kinase [EC:2.7.1.21]
c_00000009473_82	K07043	Not Included in Pathway or Brite	Poorly characterized	Function unknown	K07043; uncharacterized protein
c_00000009473_83	K03657	Genetic Information Processing	Replication and repair	Nucleotide excision repair	uvrD, pcrA; DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.4.12]
c_00000009473_83	K03657	Genetic Information Processing	Replication and repair	Mismatch repair	uvrD, pcrA; DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.4.12]
c_00000009473_89	K05515	Metabolism	Glycan biosynthesis and metabolism	Peptidoglycan biosynthesis	mrda; penicillin-binding protein 2 [EC:3.4.16.4]
c_00000009473_92	K01875	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	SARS; serS; seryl-tRNA synthetase [EC:6.1.1.11]
c_00000009473_93	K03589	Cellular Processes	Cell growth and death	Cell cycle - Caulobacter	ftsQ; cell division protein FtsQ
c_00000009473_95	K09779	Not Included in Pathway or Brite	Poorly characterized	Function unknown	K09779; uncharacterized protein
c_00000009473_97	K01885	Metabolism	Metabolism of cofactors and vitamins	Porphyrin and chlorophyll metabolism	EARS; gtx; glutamyl-tRNA synthetase [EC:6.1.1.17]
c_00000009473_97	K01885	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	EARS; gtx; glutamyl-tRNA synthetase [EC:6.1.1.17]
c_00000009473_106	K01462	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers	PDF; def; peptide deformylase [EC:3.5.1.88]
c_00000009473_107	K00604	Metabolism	Metabolism of cofactors and vitamins	One carbon pool by folate	MTFM; fnt; methionyl-tRNA formyltransferase [EC:2.1.2.9]
c_00000009473_107	K00604	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	MTFM; fnt; methionyl-tRNA formyltransferase [EC:2.1.2.9]
c_00000009473_116	K03328	Not Included in Pathway or Brite	Unclassified: signaling and cellular processes	Transport	TC.PST; polysaccharide transporter, PST family
c_00000009473_117	K02996	Genetic Information Processing	Translation	Ribosome	RP-S9, MRPS9, rpsI; small subunit ribosomal protein S9
c_00000009473_118	K02871	Genetic Information Processing	Translation	Ribosome	RP-L13, MRPL13, rplM; large subunit ribosomal protein L13
c_00000009473_119	K02879	Genetic Information Processing	Translation	Ribosome	RP-L17, MRPL17, rplQ; large subunit ribosomal protein L17
c_00000009473_120	K03040	Genetic Information Processing	Transcription	RNA polymerase	rpoA; DNA-directed RNA polymerase subunit alpha [EC:2.7.7.6]
c_00000009473_121	K02986	Genetic Information Processing	Translation	Ribosome	RP-S4, rpsD; small subunit ribosomal protein S4
c_00000009473_122	K02948	Genetic Information Processing	Translation	Ribosome	RP-S11, MRPS11, rpsK; small subunit ribosomal protein S11
c_00000009473_123	K02952	Genetic Information Processing	Translation	Ribosome	RP-S13, rpsM; small subunit ribosomal protein S13
c_00000009473_125	K01872	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	AARS; alaS; alanyl-tRNA synthetase [EC:6.1.1.7]
c_00000009473_136	K07576	Not Included in Pathway or Brite	Unclassified: genetic information processing	Translation	K07576; metallo-beta-lactamase family protein
c_00000009473_143	K02343	Genetic Information Processing	Replication and repair	DNA replication	dnaX; DNA polymerase III subunit gamma/tau [EC:2.7.7.7]
c_00000009473_143	K02343	Genetic Information Processing	Replication and repair	Mismatch repair	dnaX; DNA polymerase III subunit gamma/tau [EC:2.7.7.7]
c_00000009473_143	K02343	Genetic Information Processing	Replication and repair	Homologous recombination	dnaX; DNA polymerase III subunit gamma/tau [EC:2.7.7.7]
c_00000009473_151	K01883	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	CARS; cysS; cysteinyl-tRNA synthetase [EC:6.1.1.16]
c_00000009473_161	K04043	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	dnaK; HSPA9; molecular chaperone DnaK
c_00000009473_168	K03455	Not Included in Pathway or Brite	Unclassified: signaling and cellular processes	Transport	TC.KEF; monovalent cation:H ⁺ antiporter-2, CPA2 family
c_00000009473_170	K01929	Metabolism	Amino acid metabolism	Lysine biosynthesis	murF; UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase [EC:6.3.2.10]
c_00000009473_170	K01929	Metabolism	Glycan biosynthesis and metabolism	Peptidoglycan biosynthesis	murF; UDP-N-acetylmuramoyl-tripeptide-D-alanyl-D-alanine ligase [EC:6.3.2.10]
c_00000009473_171	K03587	Metabolism	Glycan biosynthesis and metabolism	Peptidoglycan biosynthesis	ftsI; cell division protein FtsI (penicillin-binding protein 3) [EC:3.4.16.4]
c_00000009473_175	K19221	Metabolism	Metabolism of cofactors and vitamins	Porphyrin and chlorophyll metabolism	cobA, btuR; cob(I)alamin adenosyltransferase [EC:2.5.1.17]
c_00000009473_178	K00525	Metabolism	Nucleotide metabolism	Purine metabolism	E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
c_00000009473_178	K00525	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	E1.17.4.1A, nrdA, nrdE; ribonucleoside-diphosphate reductase alpha chain [EC:1.17.4.1]
c_00000009473_183	K00382	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle)	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Carbohydrate metabolism	Pyruvate metabolism	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Carbohydrate metabolism	Glyoxylate and dicarboxylate metabolism	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Carbohydrate metabolism	Propanoate metabolism	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Amino acid metabolism	Glycine, serine and threonine metabolism	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Amino acid metabolism	Valine, leucine and isoleucine degradation	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Amino acid metabolism	Lysine degradation	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_183	K00382	Metabolism	Amino acid metabolism	Tryptophan metabolism	DLD, lpd, pdhD; dihydroloamide dehydrogenase [EC:1.8.1.4]
c_00000009473_194	K23170	Metabolism	Metabolism of other amino acids	D-Glutamine and D-glutamate metabolism	murL; UDP-N-acetyl-alpha-D-muramoyl-L-alanyl-L-glutamate epimerase [EC:5.1.1.23]
c_00000009473_205	K05770	Environmental Information Processing	Signaling molecules and interaction	Neuroactive ligand-receptor interaction	TSP0, BZRP; translocator protein
c_00000009473_205	K05770	Cellular Processes	Cell growth and death	Apoptosis - fly	TSP0, BZRP; translocator protein
c_00000009473_213	K00134	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
c_00000009473_213	K00134	Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
c_00000009473_213	K00134	Environmental Information Processing	Signal transduction	HIF-1 signaling pathway	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
c_00000009473_214	K03455	Not Included in Pathway or Brite	Unclassified: signaling and cellular processes	Transport	TC.KEF; monovalent cation:H ⁺ antiporter-2, CPA2 family
c_00000009473_230	K00793	Metabolism	Metabolism of cofactors and vitamins	Riboflavin metabolism	ribE, RIB5; riboflavin synthase [EC:2.5.1.9]
c_00000009473_237	K01921	Metabolism	Metabolism of other amino acids	D-Alanine metabolism	ddi; D-alanine-D-alanine ligase [EC:3.6.2.4]
c_00000009473_237	K01921	Metabolism	Glycan biosynthesis and metabolism	Peptidoglycan biosynthesis	ddi; D-alanine-D-alanine ligase [EC:3.6.2.4]
c_00000009473_238	K17686	Environmental Information Processing	Signal transduction	MAPK signaling pathway - plant	copA, ctpA, ATP7; P-type Cu ⁺ transporter [EC:7.2.2.8]
c_00000009473_238	K01533	Not Included in Pathway or Brite	Unclassified: metabolism	Enzymes with EC numbers	copB; P-type Cu ²⁺ transporter [EC:7.2.2.9]
c_00000009473_239	K09792	Not Included in Pathway or Brite	Poorly characterized	Function unknown	K09792; uncharacterized protein
c_00000009473_243	K01803	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
c_00000009473_243	K01803	Metabolism	Carbohydrate metabolism	Fructose and mannose metabolism	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
c_00000009473_243	K01803	Metabolism	Carbohydrate metabolism	Inositol phosphate metabolism	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
c_00000009473_243	K01803	Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms	TPI, tpiA; triosephosphate isomerase (TIM) [EC:5.3.1.1]
c_00000009473_245	K01880	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	GARS; glyS1; glycyl-tRNA synthetase [EC:6.1.1.14]
c_00000009473_267	K02864	Genetic Information Processing	Translation	Ribosome	RP-L10, MRPL10, rplJ; large subunit ribosomal protein L10
c_00000009473_268	K02935	Genetic Information Processing	Translation	Ribosome	RP-L7, MRPL7, rplL; large subunit ribosomal protein L7/L12
c_00000009473_271	K09903	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	pyrH; uridylyl kinase [EC:2.7.4.22]
c_00000009473_272	K08972	Not Included in Pathway or Brite	Poorly characterized	General function prediction only	K08972; putative membrane protein
c_00000009473_273	K03602	Genetic Information Processing	Replication and repair	Mismatch repair	xseB; exodeoxyribonuclease VII small subunit [EC:3.1.11.6]
c_00000009473_274	K03601	Genetic Information Processing	Replication and repair	Mismatch repair	xseA; exodeoxyribonuclease VII large subunit [EC:3.1.11.6]
c_00000009473_287	K00116	Metabolism	Carbohydrate metabolism	Citrate cycle (TCA cycle)	mqo; malate dehydrogenase (quinone) [EC:1.1.5.4]
c_00000009473_287	K00116	Metabolism	Carbohydrate metabolism	Pyruvate metabolism	mqo; malate dehydrogenase (quinone) [EC:1.1.5.4]
c_00000009473_291	K00789	Metabolism	Amino acid metabolism	Cysteine and methionine metabolism	metK; S-adenosylmethionine synthetase [EC:2.5.1.6]

c_00000009473_299	K03657	Genetic Information Processing	Replication and repair	Nucleotide excision repair	uvrD, pcrA; DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.4.12]
c_00000009473_299	K03657	Genetic Information Processing	Replication and repair	Mismatch repair	uvrD, pcrA; DNA helicase II / ATP-dependent DNA helicase PcrA [EC:3.6.4.12]
c_00000009473_301	K07082	Not Included in Pathway or Brite	Poorly characterized	General function prediction only	K07082; UPF0755 protein
c_00000009473_302	K00971	Metabolism	Carbohydrate metabolism	Fructose and mannose metabolism	manC, cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
c_00000009473_302	K00971	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	manC, cpsB; mannose-1-phosphate guanylyltransferase [EC:2.7.7.13]
c_00000009473_304	K15633	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	gpmI; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]
c_00000009473_304	K15633	Metabolism	Energy metabolism	Methane metabolism	gpmI; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]
c_00000009473_304	K15633	Metabolism	Amino acid metabolism	Glycine, serine and threonine metabolism	gpmI; 2,3-bisphosphoglycerate-independent phosphoglycerate mutase [EC:5.4.2.12]
c_00000009473_305	K01689	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	ENO, eno; enolase [EC:4.2.1.11]
c_00000009473_305	K01689	Metabolism	Energy metabolism	Methane metabolism	ENO, eno; enolase [EC:4.2.1.11]
c_00000009473_305	K01689	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	ENO, eno; enolase [EC:4.2.1.11]
c_00000009473_305	K01689	Environmental Information Processing	Signal transduction	HIF-1 signaling pathway	ENO, eno; enolase [EC:4.2.1.11]
c_00000009473_306	K00927	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
c_00000009473_306	K00927	Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms	PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
c_00000009473_306	K00927	Environmental Information Processing	Signal transduction	HIF-1 signaling pathway	PGK, pgk; phosphoglycerate kinase [EC:2.7.2.3]
c_00000009473_307	K07098	Not Included in Pathway or Brite	Poorly characterized	Function unknown	K07098; uncharacterized protein
c_00000009473_308	K00134	Metabolism	Carbohydrate metabolism	Glycolysis / Gluconeogenesis	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
c_00000009473_308	K00134	Metabolism	Energy metabolism	Carbon fixation in photosynthetic organisms	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
c_00000009473_308	K00134	Environmental Information Processing	Signal transduction	HIF-1 signaling pathway	GAPDH, gapA; glyceraldehyde 3-phosphate dehydrogenase [EC:1.2.1.12]
c_00000009473_310	K02967	Genetic Information Processing	Translation	Ribosome	RP-S2, MRPS2, rpsB; small subunit ribosomal protein S2
c_00000009473_314	K02909	Genetic Information Processing	Translation	Ribosome	RP-L31, rpmE; large subunit ribosomal protein L31
c_00000009473_318	K02897	Genetic Information Processing	Translation	Ribosome	RP-L25, rplY; large subunit ribosomal protein L25
c_00000009473_326	K03073	Genetic Information Processing	Folding, sorting and degradation	Protein export	secE; preprotein translocase subunit SecE
c_00000009473_326	K03073	Environmental Information Processing	Membrane transport	Bacterial secretion system	secE; preprotein translocase subunit SecE
c_00000009473_326	K03073	Cellular Processes	Cellular community - prokaryotes	Quorum sensing	secE; preprotein translocase subunit SecE
c_00000009473_328	K02867	Genetic Information Processing	Translation	Ribosome	RP-L11, MRPL11, rplK; large subunit ribosomal protein L11
c_00000009473_329	K02863	Genetic Information Processing	Translation	Ribosome	RP-L1, MRPL1, rplA; large subunit ribosomal protein L1
c_00000009473_331	K01494	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	dcd, dCTP deaminase [EC:3.5.4.13]
c_00000009473_332	K01493	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	comEB, dCMP deaminase [EC:3.5.4.12]
c_00000009473_333	K00943	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	tmk, dTYMK, dTMP kinase [EC:2.7.4.9]
c_00000009473_336	K02434	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	gatB, PET112; aspartyl-tRNA(Asn)/glutamy-tRNA(Gln) amidotransferase subunit B [EC:6.3.5.6 6.3.5.7]
c_00000009473_337	K00791	Metabolism	Metabolism of terpenoids and polyketides	Zeatin biosynthesis	miaA, TRIT1; tRNA dimethylallyltransferase [EC:2.5.1.75]
c_00000009473_339	K01868	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	TARS, thrS; threonyl-tRNA synthetase [EC:6.1.1.3]
c_00000009473_343	K02337	Genetic Information Processing	Replication and repair	DNA replication	dnaE; DNA polymerase III subunit alpha [EC:2.7.7.7]
c_00000009473_343	K02337	Genetic Information Processing	Replication and repair	Mismatch repair	dnaE; DNA polymerase III subunit alpha [EC:2.7.7.7]
c_00000009473_343	K02337	Genetic Information Processing	Replication and repair	Homologous recombination	dnaE; DNA polymerase III subunit alpha [EC:2.7.7.7]
c_00000009473_356	K01890	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	FARSB, pheT; phenylalanyl-tRNA synthetase beta chain [EC:6.1.1.20]
c_00000009473_357	K01889	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	FARSA, pheS; phenylalanyl-tRNA synthetase alpha chain [EC:6.1.1.20]
c_00000009473_358	K11749	Cellular Processes	Cell growth and death	Cell cycle - Caulobacter	rseP; regulator of sigma E protease [EC:3.4.24.-]
c_00000009473_361	K03744	Not Included in Pathway or Brite	Poorly characterized	General function prediction only	lemA; LemA protein
c_00000009473_370	K00560	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	thyA, TYMS; thymidylate synthase [EC:2.1.1.45]
c_00000009473_370	K00560	Metabolism	Metabolism of cofactors and vitamins	One carbon pool by folate	thyA, TYMS; thymidylate synthase [EC:2.1.1.45]
c_00000009473_371	K03655	Genetic Information Processing	Replication and repair	Homologous recombination	recG; ATP-dependent DNA helicase RecG [EC:3.6.4.12]
c_00000009473_389	K01784	Metabolism	Carbohydrate metabolism	Galactose metabolism	galE, GALE; UDP-glucose 4-epimerase [EC:5.1.3.2]
c_00000009473_389	K01784	Metabolism	Carbohydrate metabolism	Amino sugar and nucleotide sugar metabolism	galE, GALE; UDP-glucose 4-epimerase [EC:5.1.3.2]
c_00000009473_392	K04077	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	groEL, HSPD1; chaperonin GroEL
c_00000009473_396	K03217	Genetic Information Processing	Folding, sorting and degradation	Protein export	yidC, spoIIJ, OXA1, ccfA; YidC/Oxa1 family membrane protein insertase
c_00000009473_396	K03217	Environmental Information Processing	Membrane transport	Bacterial secretion system	yidC, spoIIJ, OXA1, ccfA; YidC/Oxa1 family membrane protein insertase
c_00000009473_396	K03217	Cellular Processes	Cellular community - prokaryotes	Quorum sensing	yidC, spoIIJ, OXA1, ccfA; YidC/Oxa1 family membrane protein insertase
c_00000009473_399	K07460	Not Included in Pathway or Brite	Unclassified: genetic information processing	Replication and repair	yraN; putative endonuclease
c_00000009473_405	K01887	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	RARS, argS; arginyl-tRNA synthetase [EC:6.1.1.19]
c_00000009473_406	K01866	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	YARS, tyrS; tyrosyl-tRNA synthetase [EC:6.1.1.1]
c_00000009473_407	K01873	Genetic Information Processing	Translation	Aminoacyl-tRNA biosynthesis	VARS, valS; valyl-tRNA synthetase [EC:6.1.1.9]
c_00000009473_414	K00945	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	cnk; CMP/dCMP kinase [EC:2.7.4.25]
c_00000009473_415	K02884	Genetic Information Processing	Translation	Ribosome	RP-L19, MRPL19, rplS; large subunit ribosomal protein L19
c_00000009473_417	K03701	Genetic Information Processing	Replication and repair	Nucleotide excision repair	uvrA; excinuclease ABC subunit A
c_00000009473_420	K03075	Genetic Information Processing	Folding, sorting and degradation	Protein export	secG; preprotein translocase subunit SecG
c_00000009473_420	K03075	Environmental Information Processing	Membrane transport	Bacterial secretion system	secG; preprotein translocase subunit SecG
c_00000009473_420	K03075	Cellular Processes	Cellular community - prokaryotes	Quorum sensing	secG; preprotein translocase subunit SecG
c_00000009473_421	K02035	Cellular Processes	Cellular community - prokaryotes	Quorum sensing	ABC.P.E.S. peptide/nickel transport system substrate-binding protein
c_00000009473_422	K12574	Genetic Information Processing	Folding, sorting and degradation	RNA degradation	rj; ribonuclease J [EC:3.1.-.-]
c_00000009473_423	K09815	Environmental Information Processing	Membrane transport	ABC transporters	znuA; zinc transport system substrate-binding protein
c_00000009473_424	K09817	Environmental Information Processing	Membrane transport	ABC transporters	znuC; zinc transport system ATP-binding protein [EC:7.2.2.-]
c_00000009473_425	K09816	Environmental Information Processing	Membrane transport	ABC transporters	znuB; zinc transport system permease protein
c_00000009473_427	K04564	Environmental Information Processing	Signal transduction	MAPK signaling pathway - fly	SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
c_00000009473_427	K04564	Environmental Information Processing	Signal transduction	FoxO signaling pathway	SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
c_00000009473_427	K04564	Cellular Processes	Transport and catabolism	Peroxisome	SOD2; superoxide dismutase, Fe-Mn family [EC:1.15.1.1]
c_00000009473_430	K01937	Metabolism	Nucleotide metabolism	Pyrimidine metabolism	pyrG, CTPS; CTP synthase [EC:6.3.4.2]
c_00000009473_431	K23573	Environmental Information Processing	Signaling molecules and interaction	ECM-receptor interaction	DSPP; dentin sialophosphoprotein
c_00000009473_433	K03685	Genetic Information Processing	Translation	Ribosome biogenesis in eukaryotes	rnc, DROSHA, RNT1; ribonuclease III [EC:3.1.26.3]
c_00000009473_445	K02945	Genetic Information Processing	Translation	Ribosome	RP-S1, rpsA; small subunit ribosomal protein S1
c_00000009473_464	K13993	Genetic Information Processing	Folding, sorting and degradation	Protein processing in endoplasmic reticulum	HSP20; HSP20 family protein
c_00000009473_466	K18346	Environmental Information Processing	Signal transduction	Two-component system	vanW; vancomycin resistance protein VanW
c_00000009473_469	K01358	Cellular Processes	Cell growth and death	Cell cycle - Caulobacter	clpP, CLPP; ATP-dependent Clp protease, protease subunit [EC:3.4.21.92]
c_00000009473_470	K06881	Metabolism	Energy metabolism	Sulfur metabolism	nnaA; bifunctional oligoribonuclease and PAP phosphatase NnaA [EC:3.1.3.7 3.1.13.3]
c_00000009473_474	K02959	Genetic Information Processing	Translation	Ribosome	RP-S16, MRPS16, rpsP; small subunit ribosomal protein S16
c_00000009473_477	K06960	Not Included in Pathway or Brite	Poorly characterized	Function unknown	K06960; uncharacterized protein