

Figure S1. Identification of acetyl-phosphate (AcP) by 2D-TLC. An acid extract of *S. mutans* UA159 was prepared as described in the Methods section. Standard acetyl-[32 P]phosphate was synthesized as following: 4.6 μl of acetic anhydride was slowly added in mixture of 32 % [12 V/] pyridine, 170 mM K $_{2}$ HPO $_{4}$, and 70 μCi [32 P]-orthophosphate, and the mixture was incubated on ice for 2 min. After incubation, 18 μl of 4 M LiOH was added and incubated on ice for 3 min. The synthetic AcP was precipitated by adding 958 μl of ice-cold ethanol. The precipitated AcP was washed twice with 1 ml of ice-cold ethanol by centrifugation and resuspended in 125 μl distilled water. For further purification, 60 μl of ice-cold ethanol was added in the resuspendant, incubated on ice for 15 min, and collected by centrifugation. The purified labeled AcP was dried under vacuum and resuspended in 34 μl of 100 mM Tris-HCl, pH 7.0. The location of AcP was determined by 2D-TLC of either acid extract of *S. mutans* and synthetic acetyl-[32 P]phosphate mixture (A) or only *S. mutans* extract (B). For better detection of the synthetic AcP spot, the labeled acid extract of *S. mutans* UA159 was chromatographed five-fold less (20,000 CPM) than in the Figure 2 and 3. An arrow indicates the location of AcP.

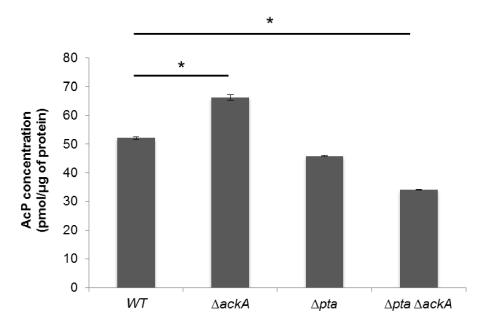


Figure S2. Measurement of intracellular AcP concentration. Exponential cells ($OD_{600} = 0.4$) aerobically grown in 5 ml of FMC supplemented with 25 mM glucose were washed twice with 250 µl of cold buffer A. Cells were resuspended in 250 µl of fresh cold buffer and mechanically disrupted in a Bead Beater-16 cell disrupter (Biospec Products, Inc., Bartlesville, OK) with glass beads (0.1 mm) at 4°C for 30s, twice. After centrifugation at $10,000 \times g$ at 4°C for 5 min, 200 µl of supernatants were mixed with 15 mg of powdered activated charcoal (Sigma) and incubated on ice for 15 min. Aliquots (50 µl) of supernatants were used to determine protein concentration. Charcoal was removed by filtration through 13-mm diameter, 0.22-µm pore size syringe filter (Millipore). For enzymatic conversion of intracellular AcP to ATP, the filtrated extracts of 100 µl were treated with acetate kinase cocktail containing 1 mM MgCl₂, 30 µM ADP, and 4 µg purified *E. coli* acetate kinase (Sigma) per ml and incubated at 30°C for 90 min. Triplicate 50 µl samples of the cell lysate were each mixed with 50 µl of CellTiter-Glo reagent (Promega) in a Costar Cell Culture 96-well flat-bottom plate (Corning, Inc.). The mixtures were incubated at room temperature for 10 min and luminescence was measured using a Synergy™ 2 Multi-Mode Microplate Reader (BioTek® Instruments, Inc., USA). *, differs from the wild-type genetic background at P < 0.01 (Student's t-test).

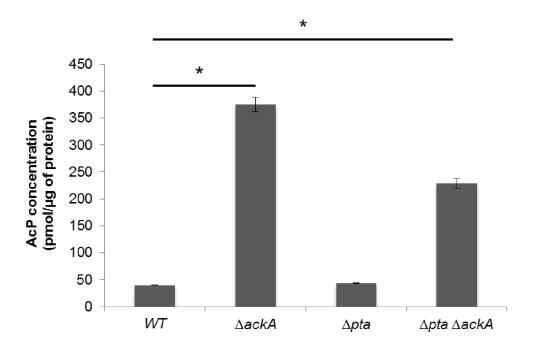


Figure S3. Measurement of intracellular AcP concentration. Experimental procedures were described in the legend of Figure S2. Exponential cells (OD_{600} = 0.4) aerobically grown in 5 ml of FMC supplemented with 25 mM glucose were subjected to 0.003% hydrogen peroxide for 1 hour. *, differs from the wild-type genetic background at P < 0.01 (Student's t-test).

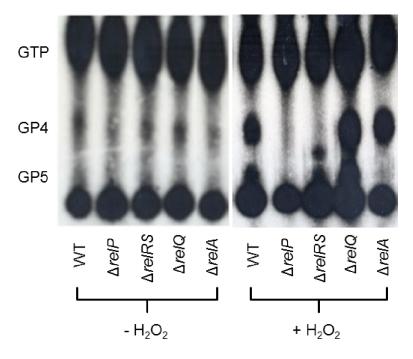


Figure S4. Accumulation of (p)ppGpp in *S. mutans* strains with and without 0.003% hydrogen peroxide. (p)ppGpp accumulation of the wild-type strain was compared with that of the $\Delta relP$, $\Delta relRS$, $\Delta relQ$, and $\Delta relA$ mutants. Exponentially grown cells were labeled with [32 P]-orthophosphate in FMC defined medium and treated with H_2O_2 for 60 min. Nucleotides were extracted by resuspending cells in 10 μl of ice cold 13 M formic acid, followed by three freeze-thaw cycles in a dry ice-ethanol bath. The formic acid extracts were spotted onto PEI-cellulose plates for TLC using 1.5 M KH₂PO₄ buffer.

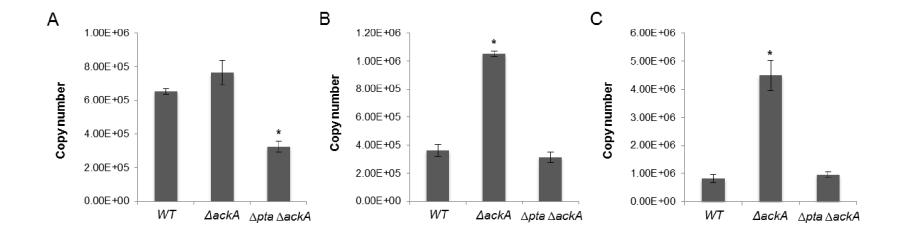


Figure S5. Effects of Pta-Ack pathway in expression of three candidate genes from transcriptome analysis. Cells were grown in triplicate to exponential phase ($OD_{600} = 0.4$) in defined FMC medium at 37°C in a 5% CO_2 aerobic atmosphere. The copy number of the *luxS* (A), *spxA* (B), *wapA* (C) transcripts was determined using Real-time qRT-PCR. qRT-PCR data are reported as the copies of the target RNA derived from 1 μ g of input RNA after normalization to copy number of the 16S rRNA in the same sample. Values shown are the means \pm standard deviations for RNAs from three separate cultures. *, differs from the wild-type genetic background at P < 0.001 (Student's *t*-test).

Table S1. Summary of AcP-spot density detected in this study.

Ctualin	AcP-spot density ^a					
Strain	Oxygen (Fig. 2A) ^b	Complementation (Fig. 2B)	H ₂ O ₂ (Fig. 3B)			
WT	86.9 ± 17.9°	52.3 ± 15.5	70.0 ± 11.9			
∆ackA	119.7 ± 9.9, <i>P</i> ≤0.05 ^d	103.2 ± 22.8, <i>P</i> <0.05	148.9 ± 20.7, <i>P</i> <0.05			
Δpta	41.2 ± 11.5, <i>P</i> <0.05	ND^e	74.6 ± 20.5			
Δpta ΔackA	4.6 ± 7.3, <i>P</i> <0.05	ND	91.6 ± 5.8, <i>P</i> <0.05			
<i>∆pta</i> + com	ND	48.8 ± 17.9	ND			
∆ackA + com	ND	43.1 ± 11.2	ND			

^a Sum of pixel in area
^b Parentheses indicate a figure number, from where the spot density has been calculated
^C A numerical value that shows the means ± standard deviations of individual spot density
^d A statistical value, differs from the wild-type genetic background (Student's *t*-test)

^e ND, not determined

Table S2. Genes differentially expressed by loss of ackA gene, compared to the wild-type strain (P < 0.005).

Locus	Description	Gene Symbol	Gene Function	Fold change
SMU.1365c	permease		Transport and binding proteins; ABC Superfamily: membrane spanning permease	2.485
SMU.1941	putative membrane lipoprotein	atmB	Transport and binding proteins; ABC Superfamily: substrate-binding protein	2.141
SMU.506	putative type II restriction endonuclease		DNA metabolism; DNA replication, recombination, and repair	1.916
SMU.987	cell wall-associated protein precursor WapA	wapA	Unassigned	1.914
SMU.549	undecaprenyldiphospho- muramoylpentapeptide beta-N- acetylglucosaminyltransferase	murG	Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan	1.901
SMU.557	putative cell division protein DivIVA	divIVA	Cellular processes; Cell division	1.879
SMU.21	putative cell shape-determining protein MreD	mreD	Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan	1.856
SMU.1089	hypothetical protein		Unknown	1.839
SMU.1206c	hypothetical protein		Unknown	1.815
SMU.454	putative cell division protein	ftsL	Cellular processes; Cell division	1.808
SMU.1050	ribose-phosphate pyrophosphokinase	krpS	Purines, pyrimidines, nucleosides, and nucleotides; Purine ribonucleotide biosynthesis Cellular processes; Chaperones	1.802
SMU.1732c	hypothetical protein		Unknown	1.784
SMU.1091	cell wall protein, WapE	wapE	Hypothetical	1.755
SMU.1923c	transcriptional regulator NrdR	nrdR	Unknown	1.720
SMU.1090	hypothetical protein		Unknown	1.720
SMU.712	phosphoenolpyruvate carboxylase	capP	Central intermediary metabolism; Other metabolism	1.710
SMU.701c	hypothetical protein		Unassigned	1.678
SMU.1706	hypothetical protein		Unknown	1.675
SMU.1366c	putative ABC transporter, ATP-binding protein		Transport and binding proteins; ABC Superfamily: ATP-binding protein	1.661
SMU.2138	replicative DNA helicase	dnaC	DNA metabolism; DNA replication, recombination, and repair	1.659
SMU.716	putative peptidoglycan branched peptide synthesis protein, alanine adding enzyme, beta-lactam resistance factor MurN	murN	Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan Cellular processes; Toxin production and resistance	1.655
SMU.475	hypothetical protein		Unknown	1.638
SMU.2104a	50S ribosomal protein L32	rpmF	Transport and binding proteins; Amino acids, peptides, and amines	1.637
SMU.864	putative ABC transporter, permease		Transport and binding proteins; ABC Superfamily: membrane	1.607

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SMU.1460 putative dTDP-4-keto-L-rhamnose reductase rmlC Cell envelope; Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides 1.350 SMU.418 transcription elongation factor NusA nusA Transcription; Transcription factors 1.344 putative ABC transporter, ATP-binding protein, proline/glycine betaine transport system opuAa protein.	SMU.1083c	hypothetical protein		Unknown	1.388
SMU.418 reductase polysaccharides and lipopolysaccharides polysaccharides and lipopolysaccharides and	SMU.521	hypothetical protein		Unknown	1.359
putative ABC transporter, ATP-binding SMU.1063 protein, proline/glycine betaine transport opuAa system Transport and binding proteins; ABC Superfamily: ATP-binding protein 1.341	SMU.1460	•	rmIC		1.350
SMU.1063 protein, proline/glycine betaine transport opuAa system 1.341	SMU.418		nusA	Transcription; Transcription factors	1.344
,	SMU.1063	protein, proline/glycine betaine transport	opuAa		1.341
	SMU.1122	cytidine deaminase	cdd	Purines, pyrimidines, nucleosides, and nucleotides; Nucleotide	1.320

and nucleoside interconversions

01411400			DATA CLE DATA E C	4.040
SMU.469	Holliday junction-specific endonuclease	recU	DNA metabolism; DNA replication, recombination, and repair	1.316
SMU.331	putative transcriptional regulator		Transcription; Transcription factors	1.314
SMU.1653	putative D-3-phosphoglycerate dehydrogenase	serA	Amino acid biosynthesis; Serine family	1.310
SMU.518	hypothetical protein		Unknown	1.273
SMU.1660c	DNA replication intiation control protein YabA		Unknown	1.269
SMU.1663	thymidylate kinase	tmk	Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine ribonucleotide biosynthesis	1.237
SMU.972	UDP-N-acetylenolpyruvoylglucosamine reductase	murB	Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan	1.230
SMU.1913c	putative immunity protein, BLpL-like		Hypothetical	1.219
SMU.1312	aspartate aminotransferase	aspB	Amino acid biosynthesis; Aspartate family	1.212
SMU.1624	ribosome recycling factor	frr	Protein synthesis; Translation factors	1.187
SMU.1838	preprotein translocase subunit SecA	secA	Protein fate; Protein and peptide secretion and trafficking	1.183
SMU.1054	putative glutamine amidotransferase		Purines, pyrimidines, nucleosides, and nucleotides; Purine ribonucleotide biosynthesis	1.165
SMU.1659c	hypothetical protein		Unknown	1.133
SMU.2165	putative SpoJ		Cellular processes; Cell division	1.126
SMU.86	hypothetical protein		Unknown	0.915
SMU.413	putative ABC transporter, ATP-binding protein		Transport and binding proteins; ABC Superfamily: ATP-binding protein	0.883
SMU.1172c	hypothetical protein		Unknown	0.874
SMU.234	threonine dehydratase	ilvA	Amino acid biosynthesis; Pyruvate family	0.865
SMU.1511c	putative acetyltransferase		Unassigned	0.861
SMU.1429	putative UDP-N-acetylmuramyl tripeptide synthetase MurC	murC2	Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan	0.818
SMU.343	hypothetical protein		Unknown	0.817
SMU.1808c	putative integrase fragment		DNA metabolism; DNA replication, recombination, and repair	0.816
SMU.1592	putative dipeptidase PepQ	pepQ	Protein fate; Degradation of proteins, peptides, and glycopeptides	0.806
SMU.1423	putative pyruvate dehydrogenase, TPP- dependent E1 component alpha-subunit	pdhA	Energy metabolism; Fermentation	0.798
SMU.857	putative uracil permease		Transport and binding proteins; Nucleosides, purines and pyrimidines	0.795
01411.070	putative PTS system, fructose-specific		Transport and binding proteins; Carbohydrates, organic	0.705
SMU.872	enzyme IIABC component		alcohols, and acids Signal transduction; PTS	0.795
SMU.872 SMU.16				0.795

			amines	
SMU.441	putative transcriptional regulator		Transcription; Transcription factors	0.780
SMU.764	alkyl hydroperoxide reductase	ahpC	Cellular processes; Detoxification	0.774
SMU.1621c	hypothetical protein		Unknown	0.768
SMU.385	putative glycoprotein endopeptidase		Protein fate; Degradation of proteins, peptides, and glycopeptides	0.767
SMU.595	dihydroorotate dehydrogenase 1A	pyrD	Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine ribonucleotide biosynthesis	0.762
SMU.1611c	putative permease, multi-drug resistance efflux pump		Cellular processes; Detoxification Transport and binding proteins; Other	0.755
SMU.1970c	putative phenylalanyl-tRNA synthetase, beta subunit		Protein synthesis; tRNA aminoacylation	0.752
SMU.1389	hypothetical protein	pckA	Energy metabolism; Glycolysis/gluconeogenesis	0.749
SMU.1789c	hypothetical protein		Unknown	0.748
SMU.181	putative mevalonate kinase		Biosynthesis of cofactors, prosthetic groups, and carriers; Other	0.743
SMU.1267c	hypothetical protein		Hypothetical	0.735
SMU.1578	biotinprotein ligase	birA	Protein fate; Protein modification and repair	0.729
SMU.1548c	putative histidine kinase		Signal transduction; Two-component systems	0.728
SMU.391c	hypothetical protein		Unknown	0.724
SMU.568	putative amino acid ABC transporter, ATP-binding protein		Transport and binding proteins; ABC Superfamily: ATP-binding protein	0.722
SMU.387	putative DNA-binding/iron metalloprotein/AP endonuclease		Protein fate; Degradation of proteins, peptides, and glycopeptides	0.722
SMU.638	putative 16S pseudouridylate synthase		Protein synthesis; tRNA and rRNA base modification	0.719
SMU.2036	putative peptidase	pepO	Protein fate; Degradation of proteins, peptides, and glycopeptides	0.718
SMU.260	hypothetical protein		Unknown	0.714
SMU.634	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	queA	Protein synthesis; tRNA and rRNA base modification	0.700
SMU.952	homocysteine methyltransferase	mmuM	Energy metabolism; Amino acids and amines	0.697
SMU.1073	formatetetrahydrofolate ligase	fthS	Purines, pyrimidines, nucleosides, and nucleotides; Purine ribonucleotide biosynthesis Amino acid biosynthesis; Aspartate family Amino acid biosynthesis; Histidine family	0.692
SMU.435	putative N-acetylglucosamine-6-phosphate deacetylase		Energy metabolism; Other	0.691
SMU.572	putative tetrahydrofolate dehydrogenase/cyclohydrolase	foID	Biosynthesis of cofactors, prosthetic groups, and carriers; Folic acid Amino acid biosynthesis; Aspartate family	0.687
SMU.318	putative hippurate hydrolase		Central intermediary metabolism; Other metabolism Protein synthesis; Degradation of proteins, peptides, and	0.685

			glycopeptides	
SMU.1646c	hemolysis inducing protein		Unknown	0.683
SMU.2127	putative succinate semialdehyde dehydrogenase		Central intermediary metabolism; Other metabolism	0.675
SMU.1931	16S rRNA methyltransferase GidB	gidB	Cellular processes; Cell division	0.668
SMU.151	hypothetical protein		Unassigned	0.657
SMU.1109c	putative integral membrane protein, permease		Unknown	0.650
SMU.349	dimethyladenosine transferase	ksgA	Cellular processes; Toxin production and resistance	0.642
SMU.1573	S-adenosylmethionine synthetase	metK	Central intermediary metabolism; Other metabolism	0.641
SMU.913	glutamate dehydrogenase		Amino acid biosynthesis; Glutamate family	0.638
SMU.1869	putative thioredoxin	trxA	Energy metabolism; Electron transport	0.626
SMU.18	hypothetical protein		Hypothetical	0.625
SMU.390	hypothetical protein		Hypothetical	0.618
SMU.1867c	putative alcohol dehydrogenase		Energy metabolism; Fermentation	0.603
SMU.951	putative amino acid permease		Transport and binding proteins; Amino acids, peptides, and amines	0.590
SMU.493	formate acetyltransferase (pyruvate formate-lyase 2)	pfl2	Energy metabolism; Fermentation	0.589
SMU.530c	hypothetical protein		Unknown	0.580
SMU.125	hypothetical protein		Unknown	0.567
SMU.1399	hypothetical protein		Hypothetical	0.560
SMU.925	hypothetical protein		Hypothetical	0.557
SMU.1298	50S ribosomal protein L31 type B	rpmE2	Protein synthesis; Ribosomal proteins: synthesis and modification	0.553
SMU.1203	branched-chain amino acid aminotransferase	ilvE	Amino acid biosynthesis; Pyruvate family	0.541
SMU.564	hypothetical protein		Unknown	0.529
SMU.1702c	putative phosphatase		Unassigned	0.505
SMU.924	thiol peroxidase	tpx	Cellular processes; Adaptations to atypical conditions	0.442
SMU.929c	hypothetical protein		Unknown	0.430
SMU.1978	putative acetate kinase	ackA	Energy metabolism; Anaerobic	0.036

Table S3. Genes differentially expressed by loss of both pta and ackA genes, compared to the wild-type strain (P < 0.005).

Locus	Description	Gene Symbol	Gene Function	Fold-change
SMU.1013c	putative Mg2+/citrate transporter	_	Transport and binding proteins; Carbohydrates, organic alcohols, and acids	5.127
SMU.1023	oxaloacetate decarboxylase	русВ	Amino acid biosynthesis; Pyruvate family	4.962
SMU.1016	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	bcc	Fatty acid and phospholipid metabolism; Other	4.896
SMU.1022	2'-(5"-triphosphoribosyl)-3'-dephospho- CoA:apo- citrate lyase	citX	Unknown	4.723
SMU.1018	hypothetical protein		Hypothetical	4.561
SMU.1365c	permease		Transport and binding proteins; ABC Superfamily: membrane spanning permease	3.989
SMU.1366c	putative ABC transporter, ATP- binding protein		Transport and binding proteins; ABC Superfamily: ATP-binding protein	3.522
SMU.1020	putative citrate lyase CilB, citryl-CoA lyase, beta subunit	cilB	Energy metabolism; Fermentation Energy metabolism; TCA cycle	3.504
SMU.1360c	hypothetical protein		Hypothetical	3.302
SMU.1012c	putative transcriptional regulator		Transcription; Transcription factors	2.686
SMU.1342	putative bacitracin synthetase 1, BacA	bacA1	Cellular processes; Toxin production and resistance	2.349
SMU.53	hypothetical protein		Unknown	2.009
SMU.671	citrate synthase	citZ	Energy metabolism; TCA cycle	1.895
SMU.58	hypothetical protein		Hypothetical	1.863
SMU.2005	adenylate kinase	adk	Purines, pyrimidines, nucleosides, and nucleotides; Nucleotide and nucleoside interconversions	1.687
SMU.131	putative lipoate-protein ligase	IpIA	Protein fate; Protein modification and repair	1.656
SMU.129	branched-chain alpha-keto acid dehydrogenase subunit E2	adhC	Energy metabolism; Glycolysis/gluconeogenesis	1.631
SMU.52	hypothetical protein		Unknown	1.604
SMU.287	putative ComB, accessory factor for ComA		Transport and binding proteins; ABC Superfamily: substrate-binding protein Cellular processes; Competence	1.505
SMU.1081c	hypothetical protein		Unknown	1.436
SMU.1910c	hypothetical protein		Hypothetical	1.426
SMU.521	hypothetical protein		Unknown	1.391
SMU.2033c	hypothetical protein		Unknown	1.362
SMU.419	hypothetical protein		Unknown	1.353
SMU.1392c	putative acetyltransferase		Unknown	1.328

SMU.1096 putative ABC transporter, ATP-binding protein, choline transporter putative ABC transporter, ATP-binding protein, choline transporter putative ABC transporter, ATP-binding protein, choline transporter putative ABC transporter, ATP-binding protein, choline transport putative ABC transporter, ATP-binding protein, proline/glycine betaine transport system protein protein, proline/glycine betaine transport system protein p	SMU.915c	7-cyano-7-deazaguanine reductase		Unknown	1.319
SMU.1085 protein, choline transporter opublish protein system opublish putative ABC transporter, ATP-binding protein system opublished by the system of the system opublished by the system opublished by the system of the system opublished by the system of the system opublished by the system of the system of the system opublished by the system of the system of the system opublished by the system	SMU.782	hypothetical protein		Unknown	1.309
SMU.1063 protein, proline/glycine betaine transport system SMU.691 peptidase T pepT Protein fate; Degradation of proteins, peptides, and glycopeptides groups, and binding proteins; ABC Superfamily: ATP-binding protein system SMU.2142 hypothetical protein permease (efflux protein) putative aminopeptidase P pepP Protein fate; Degradation of proteins, peptides, and glycopeptides groups, and binding proteins; Other 1.186 SMU.892 putative BglB fragment bglB2 Energy metabolism; Pentose phosphate pathway 1.218 SMU.1850 putative aminopeptidase P pepP Protein fate; Degradation of proteins, peptides, and glycopeptides (Protein Glycopeptides) (Protein G	SMU.1096		ориВа		1.307
SMU.1063 protein, proline/glycine betaine transport system SMU.691 peptidase T pepT SMU.2142 hypothetical protein SMU.109 permease (efflux protein) SMU.820 putative BglB fragment bglB2 Energy metabolism; Pentose phosphate pathway SMU.1850 putative aminopeptidase P pepP SMU.1850 hypothetical protein SMU.613 hypothetical protein SMU.613 hypothetical protein SMU.614 hypothetical protein SMU.615 hypothetical protein SMU.841 putative aminotransferase SMU.841 putative aminotransferase SMU.841 putative aminotransferase SMU.841 putative aminotransferase SMU.843 hypothetical protein SMU.840 hypothetical protein SMU.841 putative aminotransferase SMU.843 hypothetical protein SMU.841 putative aminotransferase SMU.842 hypothetical protein SMU.843 hypothetical protein SMU.844 putative aminotransferase SMU.845 hypothetical protein SMU.846 hypothetical protein SMU.850 hypothetical protein SMU.867 hypothetical protein SMU.868 hypothetical protein SMU.870 hypothetical protein SMU.880 hypothetical protein SMU.881 putative protein SMU.882 hypothetical protein SMU.883 hypothetical protein SMU.884 hypothetical protein SMU.885 hypothetical protein SMU.886 hypothetical protein	SMU.365	glutamate synthase (large subunit)	gltA	Amino acid biosynthesis; Glutamate family	1.297
SMU.2142 hypothetical protein pitality protein	SMU.1063	protein, proline/glycine betaine transport	opuAa		1.249
SMU.109 permease (efflux protein) SMU.982 putative BglB fragment SMU.1850 putative aminopeptidase P SMU.1936c hypothetical protein SMU.1936c hypothetical protein SMU.613 hypothetical protein SMU.1851 hypothetical protein SMU.841 putative aminotransferase SMU.841 putative aminotransferase SMU.842 hypothetical protein SMU.843 putative ABC transporter, ATP-binding protein SMU.1957 hypothetical protein SMU.1957 hypothetical protein SMU.1958 hypothetical protein SMU.1959 ferrichrome ABC transporter permease protein SMU.996 ferrichrome ABC transporter permease SMU.781 hypothetical protein SMU.782 hypothetical protein SMU.996 ferrichrome ABC transporter permease protein SMU.783 hypothetical protein SMU.996 ferrichrome ABC transporter permease SMU.1821 hypothetical protein SMU.996 ferrichrome ABC transporter permease SMU.1821 hypothetical protein SMU.781 putative protease SMU.782 hypothetical protein SMU.996 ferrichrome ABC transporter permease protein SMU.783 putative protease SMU.784 putative protease SMU.785 hypothetical protein SMU.996 ferrichrome ABC transporter permease SMU.786 putative protease SMU.781 putative protease SMU.782 dijustrogratate debuttrogenese 4B putative SMU.783 dijustrogratate debuttrogenese 4B putative SMU.784 putative protease SMU.784 putative protease SMU.785 putative protease SMU.786 hypothetical protein SMU.7879 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine	SMU.691	peptidase T	pepT		1.226
SMU.982 putative BglB fragment bglB2 Energy metabolism; Sugars 1.097 SMU.1850 putative aminopeptidase P pepP Protein fate; Degradation of proteins, peptides, and glycopeptides SMU.1936c hypothetical protein Unknown 0.868 SMU.613 hypothetical protein Unknown 0.857 SMU.1612c hypothetical protein Unknown 0.857 SMU.1612c hypothetical protein Unknown 0.855 SMU.841 putative aminotransferase Biosynthesis of cofactors, prosthetic groups, and carriers; O.844 SMU.1802c hypothetical protein Unknown 0.831 SMU.413 putative ABC transporter, ATP-binding protein putative PTS system, mannose-specific IID component Unknown 1.0820 SMU.1957 lypothetical protein Unknown 1.0820 SMU.1992c hypothetical protein Unknown 1.0820 SMU.1993 transporter, ATP-binding protein Unknown 1.0830 SMU.1655c hypothetical protein Unknown 1.0830 SMU.996 ferrichrome ABC transporter permease protein 1.0904 SMU.761 putative protease 1.0904 SMU.7621 hypothetical protein Unknown 1.0799 SMU.1621c hypothetical protein Unknown 1.0779 SMU.1621c hypothetical grotein Unknown 1.0779 SMU.1621c hypothetical protein Unknown 1.0779 SMU.1621c hypothetical grotein Unknown 1.0779	SMU.2142	hypothetical protein	rpiB	Energy metabolism; Pentose phosphate pathway	1.218
SMU.1850 putative aminopeptidase P pepP Protein fate; Degradation of proteins, peptides, and glycopeptides MU.1936c hypothetical protein Unknown 0.868 MU.613 hypothetical protein Hypothetical O.868 MU.73 hypothetical protein Unknown 0.857 MU.1612c hypothetical protein Unknown 0.852 MU.841 putative aminotransferase Biosynthesis of cofactors, prosthetic groups, and carriers; O.844 MU.1802c hypothetical protein Unknown 0.831 MU.413 putative ABC transporter, ATP-binding protein Unknown 0.828 MU.1957 putative PTS system, mannose-specific IID component Unknown 0.820 MU.1958 hypothetical protein Unknown 0.820 MU.1990 hypothetical protein Unknown 0.820 MU.996 ferrichrome ABC transporter permease protein Putative protease Unassigned Unknown 0.779 MU.1621c hypothetical protein Unknown 0.800 MU.1621c hypothetical protein Unknown 0.779 MU.1623 dibustroportate debustrogenase 18 purpB Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.772	SMU.109	permease (efflux protein)		Transport and binding proteins; Other	1.186
SMU.1936c hypothetical protein Unknown 0.868 SMU.613 hypothetical protein Hypothetical Description Unknown 0.868 SMU.73 hypothetical protein Unknown 0.857 SMU.1612c hypothetical protein Unknown 0.852 SMU.841 putative aminotransferase Biosynthesis of cofactors, prosthetic groups, and carriers; Other Unknown 0.831 SMU.413 putative ABC transporter, ATP-binding protein Unknown 0.831 SMU.413 putative PTS system, mannose-specific IID component SMU.1957 putative PTS system, mannose-specific IID component Unknown 0.820 SMU.1957 bypothetical protein Unknown 0.810 SMU.973 putative Spermidine/putrescine ABC transporter, ATP-binding protein Unknown 0.810 SMU.965c hypothetical protein Hypothetical Forcein Hypothetical Protein Unknown 0.800 SMU.966 protein Unknown 0.800 SMU.761 putative protease Unassigned 0.799 SMU.1621c hypothetical protein Unknown 0.779 SMU.1233 dibydrocratate debydrocenase 4B purples	SMU.982	putative BglB fragment	bglB2	Energy metabolism; Sugars	1.097
SMU.613 hypothetical protein Hypothetical SMU.73 hypothetical protein Unknown 0.857 SMU.1612c hypothetical protein Unknown 0.852 SMU.841 putative aminotransferase Biosynthesis of cofactors, prosthetic groups, and carriers; Other Unknown 0.831 SMU.1802c hypothetical protein Unknown 0.831 SMU.413 putative ABC transporter, ATP-binding protein Putative PTS system, mannose-specific IID component SMU.1957 Unknown 0.820 SMU.1957 putative PTS system, mannose-specific IID component Unknown 0.810 SMU.973 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1655c hypothetical protein Unknown 0.800 SMU.1655c hypothetical protein Hypothetical protein Unknown 0.800 SMU.996 ferrichrome ABC transporter permease protein Unknown 0.799 SMU.761 putative protease Unassigned 0.799 SMU.1621c hypothetical protein Unknown 0.779 SMU.1323 dibydrocostate debydrocepase 1B purQB Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.773	SMU.1850	putative aminopeptidase P	pepP	·	1.077
SMU.73 hypothetical protein SMU.1612c hypothetical protein SMU.841 putative aminotransferase SMU.842 hypothetical protein SMU.843 putative ABC transporter, ATP-binding protein SMU.1957 putative PTS system, mannose-specific IID component SMU.1957 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1958 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1958 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1959 putative spermidine/putrescine ABC transporter permease protein SMU.1950 hypothetical protein SMU.1951 putative spermidine/putrescine ABC transporter permease protein SMU.1950 hypothetical protein SMU.1951 putative protease SMU.1952 hypothetical protein SMU.1953 putative protease SMU.1954 putative protease Unknown Transport and binding proteins; ABC Superfamily: ATP-binding protein Hypothetical Transport and binding proteins; ABC Superfamily: ATP-binding protein Unknown Transport and binding proteins; ABC Superfamily: ATP-binding protein Unknown Unk	SMU.1936c	hypothetical protein		Unknown	0.868
SMU.1612c hypothetical protein Unknown 0.852 SMU.841 putative aminotransferase Dissynthesis of cofactors, prosthetic groups, and carriers; Other 0.844 SMU.1802c hypothetical protein Unknown 0.831 SMU.413 putative ABC transporter, ATP-binding protein putative PTS system, mannose-specific IID component SMU.1957 putative spermidine/putrescine ABC transporter, ATP-binding protein putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.973 putative spermidine/putrescine ABC transporter ATP-binding protein PotA SMU.996 ferrichrome ABC transporter permease protein SMU.761 putative protease Unassigned 0.799 SMU.1621c hypothetical protein Unknown 0.772 SMU.1233 dibydrocrotate debydrogenase 18 purps	SMU.613	hypothetical protein		Hypothetical	0.868
SMU.841 putative aminotransferase Biosynthesis of cofactors, prosthetic groups, and carriers; Other Other 0.844 SMU.1802c hypothetical protein Unknown 0.831 SMU.413 putative ABC transporter, ATP-binding protein putative PTS system, mannose-specific IID component SMU.1957 putative spermidine/putrescine ABC transporter, ATP-binding protein Putative spermidine/putrescine ABC transporter, ATP-binding protein Putative spermidine/putrescine ABC transporter, ATP-binding protein PotA SMU.996 ferrichrome ABC transporter permease protein Putative protease Unassigned 0.799 SMU.761 putative protease Unassigned 0.779 SMU.1233 dibydrocrotate debydrogenase 1B put DB Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.773	SMU.73	hypothetical protein		Unknown	0.857
SMU.1802c hypothetical protein putative ABC transporter, ATP-binding protein putative PTS system, mannose-specific IID component hypothetical protein putative spermidine/putrescine ABC transporter, ATP-binding protein putative spermidine/putrescine ABC transporter, ATP-binding protein PMU.1655c hypothetical protein SMU.996 ferrichrome ABC transporter permease protein putative protease SMU.621c hypothetical protein SMU.621c hypothetical protein putative protease SMU.623 dibydrogreptate debydrogenase 18 putative all minutatisterase Other Unknown Transport and binding proteins; ABC Superfamily: ATP-binding protein 0.800 Transport and binding proteins; ABC Superfamily: ATP-binding protein 0.800 Transport and binding proteins; ABC Superfamily: membrane spanning permease Unassigned 0.799 SMU.621c hypothetical protein Unknown 0.779 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.773	SMU.1612c	hypothetical protein		Unknown	0.852
SMU.413 putative ABC transporter, ATP-binding protein SMU.1957 putative PTS system, mannose-specific IID component SMU.1957 putative PTS system, mannose-specific IID component SMU.1920 hypothetical protein SMU.973 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1655c hypothetical protein SMU.1655c hypothetical protein SMU.996 ferrichrome ABC transporter permease protein SMU.761 putative protease SMU.762 hypothetical protein SMU.763 putative ABC transporter permease protein SMU.764 hypothetical protein SMU.765 hypothetical protein SMU.765 hypothetical protein SMU.766 hypothetical protein SMU.767 putative protease SMU.768 hypothetical protein SMU.769 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine	SMU.841	putative aminotransferase			0.844
SMU.1957 protein putative PTS system, mannose-specific IID component Signal transduction; PTS 0.820 SMU.1292c hypothetical protein putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1655c hypothetical protein Hypothetical protein Hypothetical protein SMU.996 ferrichrome ABC transporter permease protein SMU.761 putative protease SMU.1621c hypothetical protein Unknown 0.800 SMU.1233 dibydrogrotate debydrogenase 18 purps SMU.1623 dibydrogrotate debydrogenase 18 protein Protein Unknown 0.773	SMU.1802c	71			0.831
SMU.1292c hypothetical protein SMU.973 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.996 ferrichrome ABC transporter permease protein SMU.761 putative protease SMU.1621c hypothetical protein SMU.1233 dibydrocretate debydrogenase 1B Signal transduction, PTS Unknown Transport and binding proteins; ABC Superfamily: ATP-binding protein Hypothetical Transport and binding proteins; ABC Superfamily: membrane spanning permease Unassigned Unknown 0.800 Transport and binding proteins; ABC Superfamily: membrane spanning permease Unassigned Unknown 0.779 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine	SMU.413	protein			0.828
SMU.973 putative spermidine/putrescine ABC transporter, ATP-binding protein SMU.1655c hypothetical protein SMU.996 ferrichrome ABC transporter permease protein SMU.761 putative protease SMU.1621c hypothetical protein SMU.1223 dibydrogrotate debydrogenase 18 putative proteins; ABC Superfamily: ATP-binding proteins; ABC Superfamily: Membrane spanning permease Unassigned Unknown Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine	SMU.1957			Signal transduction; PTS	0.820
transporter, ATP-binding protein protein protein protein protein Hypothetical protein Hypothetical protein protein Hypothetical protein SMU.996 ferrichrome ABC transporter permease protein spanning permease SMU.761 putative protease Unassigned Unassigned 0.796 Unknown 0.779 SMU.1223 dibydrogrotate debydrogenase 18 pyrD8 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.772	SMU.1292c	**			0.810
SMU.996 ferrichrome ABC transporter permease protein SMU.761 putative protease SMU.1621c hypothetical protein SMU.1323 dibydrogrotate debydrogenase 1B DyrDB Transport and binding proteins; ABC Superfamily: membrane spanning permease Unassigned Unknown O.799 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine	SMU.973		potA		0.800
SMU.761 putative protease Unassigned 0.796 SMU.1621c hypothetical protein Unknown 0.779 SMU.1323 dibydrogrotate debydrogenase 18 pyrD8 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.773	SMU.1655c	hypothetical protein		Hypothetical	0.800
SMU.1621c hypothetical protein Unknown 0.779 SMU.1223 dibydrogrotate debydrogenase 18 pyrD8 Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine 0.772	SMU.996	• •		· · · · · · · · · · · · · · · · · · ·	0.799
SMIL 1223 dibydrogrotate debydrogenase 1B pyrDR Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine	SMU.761	putative protease		Unassigned	0.796
	SMU.1621c	hypothetical protein			0.779
	SMU.1223	dihydroorotate dehydrogenase 1B	pyrDB	Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine ribonucleotide biosynthesis	
SMU.67 putative acyltransferase Unassigned 0.765	SMU.67	putative acyltransferase		Unassigned	0.765

SMU.1467	adenine phosphoribosyltransferase	apt	Purines, pyrimidines, nucleosides, and nucleotides; Salvage of nucleosides and nucleotides	0.762
SMU.1676c	hypothetical protein		Transport and binding proteins; Carbohydrates, organic alcohols, and acids	0.757
SMU.942	putative hydroxymethylglutaryl-CoA reductase	mvaA	Energy metabolism; Other	0.745
SMU.2126c	putative purine-nucleoside phosphorylase		Purines, pyrimidines, nucleosides, and nucleotides; Salvage of nucleosides and nucleotides	0.738
SMU.1288	50S ribosomal protein L19	rpIS	Protein synthesis; Ribosomal proteins: synthesis and modification	0.736
SMU.1446c	putative ABC transporter, permease protein		Transport and binding proteins; ABC Superfamily: membrane spanning permease Transport and binding proteins; Carbohydrates, organic	0.734
SMU.880	multiple sugar-binding ABC transporter, permease protein MsmG	msmG	alcohols, and acids Energy metabolism; Sugars Transport and binding proteins; ABC Superfamily: membrane spanning permease	0.715
SMU.725c	hypothetical protein		Unknown	0.713
SMU.929c	hypothetical protein		Unknown	0.711
SMU.857	putative uracil permease		Transport and binding proteins; Nucleosides, purines and pyrimidines	0.705
SMU.1119c	putative sugar ABC transporter, permease protein		Transport and binding proteins; ABC Superfamily: membrane spanning permease	0.704
SMU.133c	putative MDR permease, transmembrane efflux protein		Transport and binding proteins; Carbohydrates, organic alcohols, and acids	0.701
SMU.1593c	putative CDP-diglyceride synthetase		Unknown	0.696
SMU.838	glutathione reductase	gshR	Biosynthesis of cofactors, prosthetic groups, and carriers; Glutathione and analogs Cellular processes; Detoxification	0.686
SMU.1324	putative cell-division protein FtsX	ftsX	Cellular processes; Cell division Transport and binding proteins; ABC Superfamily: membrane spanning permease	0.681
SMU.1389	hypothetical protein	pckA	Energy metabolism; Glycolysis/gluconeogenesis	0.678
SMU.1950	putative pseudouridylate synthase		Protein synthesis; tRNA and rRNA base modification	0.673
SMU.1587c	hypothetical protein		Hypothetical	0.668
SMU.387	putative DNA-binding/iron metalloprotein/AP endonuclease		Protein fate; Degradation of proteins, peptides, and glycopeptides	0.664
SMU.1203	branched-chain amino acid aminotransferase	ilvE	Amino acid biosynthesis; Pyruvate family	0.660
SMU.2146c	hypothetical protein		Unknown	0.657
SMU.1570	putative maltose/maltodextrin ABC transporter, MalG permease	malG	Transport and binding proteins; ABC Superfamily: membrane spanning permease	0.657
SMU.1958c	putative PTS system, mannose-		Signal transduction; PTS	0.656

	specific IIC component			
SMU.621c	hypothetical protein		Unknown	0.653
SMU.119	putative alcohol dehydrogenase class III	adh	Energy metabolism; Fermentation	0.653
SMU.1109c	putative integral membrane protein, permease		Unknown	0.651
SMU.2056	recombination factor protein RarA		Cellular processes; Cell division	0.647
SMU.1323	hydrolase		Unknown	0.645
SMU.523	hypothetical protein		Unknown	0.644
SMU.1722c	putative integral membrane protein		Unknown	0.644
SMU.1266	imidazole glycerol phosphate synthase subunit HisH	hisH	Amino acid biosynthesis; Histidine family	0.639
SMU.636	putative N-acetylglucosamine- 6-phosphate isomerase		Central intermediary metabolism; Amino sugars	0.632
SMU.570	putative ferrous ion transport protein B	feoB	Transport and binding proteins; Cations and iron carrying compounds	0.631
SMU.856	bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	pyrR	Regulatory functions; DNA interactions Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine ribonucleotide biosynthesis	0.623
SMU.2055	putative acetyltransferase		Unassigned	0.622
SMU.1828	hypothetical protein		Unknown	0.617
SMU.2075c	hypothetical protein		Unknown	0.606
SMU.771c	hypothetical protein		Hypothetical	0.604
SMU.1902c	hypothetical protein		Hypothetical	0.603
SMU.474	S-ribosylhomocysteinase	luxS	Cellular processes; Other	0.601
SMU.321	hypothetical protein		Unknown	0.600
SMU.495	glycerol dehydrogenase	gldA	Energy metabolism; Sugars	0.599
SMU.1807c	putative integral membrane protein, permease		Unassigned	0.592
SMU.388	putative integral membrane protein, branched-chain amino acid permease		Transport and binding proteins; Amino acids, peptides, and amines	0.592
SMU.291	transketolase	tkt	Energy metabolism; Pentose phosphate pathway	0.587
SMU.1399	hypothetical protein		Hypothetical	0.582
SMU.911c	hypothetical protein		Hypothetical	0.582
SMU.1115	L-lactate dehydrogenase	ldh	Energy metabolism; Glycolysis/gluconeogenesis	0.580

SMU.1649	putative exodeoxyribonuclease III	exoA	DNA metabolism; DNA replication, recombination, and repair	0.572
SMU.303	hypothetical protein		Unknown	0.561
SMU.564	hypothetical protein		Unknown	0.544
SMU.1450	putative amino acid permease		Unassigned	0.491
SMU.1545c	hypothetical protein		Unknown	0.474
SMU.493	formate acetyltransferase (pyruvate formate-lyase 2)	pfl2	Energy metabolism; Fermentation	0.454
SMU.1043c	phosphotransacetylase	pta	Energy metabolism; Fermentation	0.243
SMU.1978	putative acetate kinase	ackA	Energy metabolism; Anaerobic	0.040

Table S4. Genes differentially expressed by loss of ackA versus both pta and ackA genes (P < 0.005).

Locus	Description	Gene symbol	Gene Function	Fold-change
SMU.1043c	phosphotransacetylase	pta	Energy metabolism; Fermentation	4.88
SMU.1419	putative transcriptional regulator		Transcription; Transcription factors	2.23
SMU.935	putative amino acid ABC transporter, permease protein		Transport and binding proteins; ABC Superfamily: membrane spanning permease	2.21
SMU.81	heat shock protein GrpE (HSP-70 cofactor)	grpE	Protein fate; Protein folding and stabilization	2.18
SMU.80	heat-inducible transcription repressor	hrcA	Regulatory functions; DNA interactions	2.15
SMU.1941	putative membrane lipoprotein	atmB	Transport and binding proteins; ABC Superfamily: substrate-binding protein	1.99
SMU.932	hypothetical protein		Unknown	1.94
SMU.496	putative cysteine synthetase A, O- acetylserine lyase	cysK	Amino acid biosynthesis; Serine family	1.91
SMU.880	multiple sugar-binding ABC transporter, permease protein MsmG	msmG	Transport and binding proteins; Carbohydrates, organic alcohols, and acids Energy metabolism; Sugars Transport and binding proteins; ABC Superfamily: membrane spanning permease	1.9
SMU.01	chromosomal replication initiation protein	dnaA	DNA metabolism; DNA replication, recombination, and repair	1.89
SMU.987	cell wall-associated protein precursor WapA	wapA	Unassigned	1.85
SMU.1412c	putative ABC transporter, membrane protein subunit and ATP-binding protein		Transport and binding proteins; ABC Superfamily: membrane spanning permease Transport and binding proteins; ABC Superfamily: ATP-binding protein	1.77
SMU.459	putative ABC transporter, amino acid binding protein		Transport and binding proteins; ABC Superfamily: substrate-binding protein	1.76
SMU.1206c	hypothetical protein		Unknown	1.67
SMU.2084c	transcriptional regulator Spx	spxA	Unknown	1.62
SMU.1050	ribose-phosphate pyrophosphokinase	krpS	Purines, pyrimidines, nucleosides, and nucleotides; Purine ribonucleotide biosynthesis Cellular processes; Chaperones	1.6
SMU.864	putative ABC transporter, permease component		Transport and binding proteins; ABC Superfamily: membrane spanning permease	1.6
SMU.1938c	putative ABC transporter, permease protein		Transport and binding proteins; ABC Superfamily: membrane spanning permease	1.6
SMU.1659c	hypothetical protein		Unknown	1.59

SMU.1727	OxaA-like protein precursor		Cell envelope; Other	1.57
SMU.353	hypothetical protein		Biosynthesis of cofactors, prosthetic groups, and carriers; Thiamine	1.51
SMU.712	phosphoenolpyruvate carboxylase	capP	Central intermediary metabolism; Other metabolism	1.5
SMU.1958c	putative PTS system, mannose-specific IIC component		Signal transduction; PTS	1.47
SMU.244	undecaprenyl pyrophosphate phosphatase	иррР	Cellular processes; Detoxification Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan	1.44
SMU.2086	competence damage-inducible protein A	cinA	Cellular processes; DNA transformation DNA metabolism; DNA replication, recombination, and repair	1.42
SMU.551	cell division protein FtsA	ftsA	Cellular processes; Cell division	1.42
SMU.1457	putative dTDP-glucose-4,6-dehydratase	rmIB	Cell envelope; Surface polysaccharides, lipopolysaccharides and antigens	1.41
SMU.1570	putative maltose/maltodextrin ABC transporter, MalG permease	malG	Transport and binding proteins; ABC Superfamily: membrane spanning permease	1.4
SMU.586	hypothetical protein		Unknown	1.39
SMU.1324	putative cell-division protein FtsX	ftsX	Cellular processes; Cell division Transport and binding proteins; ABC Superfamily: membrane spanning permease	1.39
SMU.1204	DNA topoisomerase IV subunit A	parC	DNA metabolism; DNA replication, recombination, and repair	1.39
SMU.1195	permease		Transport and binding proteins; ABC Superfamily: membrane spanning permease	1.35
SMU.1957	putative PTS system, mannose-specific IID component		Signal transduction; PTS	1.33
SMU.1663	thymidylate kinase	tmk	Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine ribonucleotide biosynthesis	1.32
SMU.1936c	hypothetical protein		Unknown	1.31
SMU.1935c	hypothetical protein		Unknown	1.31
SMU.469	Holliday junction-specific endonuclease	recU	DNA metabolism; DNA replication, recombination, and repair	1.29
SMU.1460	putative dTDP-4-keto-L-rhamnose reductase	rmIC	Cell envelope; Biosynthesis and degradation of surface polysaccharides and lipopolysaccharides	1.26
SMU.1653	putative D-3-phosphoglycerate dehydrogenase	serA	Amino acid biosynthesis; Serine family	1.26
SMU.1655c	hypothetical protein		Hypothetical	1.25
SMU.858	aspartate carbamoyltransferase catalytic subunit	pyrB	Purines, pyrimidines, nucleosides, and nucleotides; Pyrimidine ribonucleotide biosynthesis	1.25
SMU.1054	putative glutamine amidotransferase		Purines, pyrimidines, nucleosides, and nucleotides; Purine	1.25

ribonucleotide biosynthesis

			riboriucieotide biosyritriesis	
SMU.2074	anaerobic ribonucleoside triphosphate reductase	nrdD	Purines, pyrimidines, nucleosides, and nucleotides; 2'- Deoyribonucleotide metabolism	1.25
SMU.1801c	GTP-binding protein YqeH	yqeH	Unknown	1.21
SMU.841	putative aminotransferase		Biosynthesis of cofactors, prosthetic groups, and carriers; Other	1.19
SMU.972	UDP-N-acetylenolpyruvoylglucosamine reductase	murB	Cell envelope; Biosynthesis and degradation of murein sacculus and peptidoglycan	1.16
SMU.328	putative carbonic anhydrase		Unknown	0.87
SMU.1573	S-adenosylmethionine synthetase	metK	Central intermediary metabolism; Other metabolism	0.75
SMU.53	hypothetical protein		Unknown	0.73
SMU.59	adenylosuccinate lyase	purB	Purines, pyrimidines, nucleosides, and nucleotides; Purine ribonucleotide biosynthesis	0.73
SMU.764	alkyl hydroperoxide reductase	ahpC	Cellular processes; Detoxification	0.72
SMU.952	homocysteine methyltransferase	mmuM	Energy metabolism; Amino acids and amines	0.72
SMU.349	dimethyladenosine transferase	ksgA	Cellular processes; Toxin production and resistance	0.71
SMU.1808c	putative integrase fragment		DNA metabolism; DNA replication, recombination, and repair	0.7
SMU.530c	hypothetical protein		Unknown	0.67
SMU.1702c	putative phosphatase		Unassigned	0.65
SMU.125	hypothetical protein		Unknown	0.64
SMU.365	glutamate synthase (large subunit)	gltA	Amino acid biosynthesis; Glutamate family	0.64
SMU.367	hypothetical protein		Unassigned	0.64
SMU.1073	formatetetrahydrofolate ligase	fthS	Purines, pyrimidines, nucleosides, and nucleotides; Purine ribonucleotide biosynthesis Amino acid biosynthesis; Aspartate family Amino acid biosynthesis; Histidine family	0.63
SMU.925	hypothetical protein		Hypothetical	0.61
SMU.36	hypothetical protein		Unknown	0.61
SMU.128	putative acetoin dehydrogenase (TPP-dependent), E1 component beta subunit	adhB	Energy metabolism; Fermentation	0.57
SMU.924	thiol peroxidase	tpx	Cellular processes; Adaptations to atypical conditions	0.52
SMU.671	citrate synthase	citZ	Energy metabolism; TCA cycle	0.47
SMU.1366c	putative ABC transporter, ATP-binding protein		Transport and binding proteins; ABC Superfamily: ATP-binding protein	0.47

SMU.129	branched-chain alpha-keto acid dehydrogenase subunit E2	adhC	Energy metabolism; Glycolysis/gluconeogenesis	0.46
SMU.1012c	putative transcriptional regulator		Transcription; Transcription factors	0.42
SMU.1017	putative oxaloacetate decarboxylase, sodium ion pump subunit	oadB	Amino acid biosynthesis; Pyruvate family	0.37
SMU.1360c	hypothetical protein		Hypothetical	0.35
SMU.1020	putative citrate lyase CilB, citryl-CoA lyase, beta subunit	cilB	Energy metabolism; Fermentation Energy metabolism; TCA cycle	0.29
SMU.1018	hypothetical protein		Hypothetical	0.24
SMU.1023	oxaloacetate decarboxylase	русВ	Amino acid biosynthesis; Pyruvate family	0.23
SMU.1022	2'-(5"-triphosphoribosyl)-3'-dephospho- CoA:apo- citrate lyase	citX	Unknown	0.21
SMU.1013c	putative Mg2+/citrate transporter		Transport and binding proteins; Carbohydrates, organic alcohols, and acids	0.21
SMU.1016	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	bcc	Fatty acid and phospholipid metabolism; Other	0.15