Supplemental Materials for “Amino Sugars Reshape Interactions between *Streptococcus mutans* and *Streptococcus gordonii*”

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Includes Figures S1 to S8 and Table S1 to S8.

Fig S1. Matrices of correlations across 18 samples from *S. mutans* (A) and *S. gordonii* (B).

Plots show scatter-point ellipses (upper-diagonal) and correlation values (lower-diagonal).

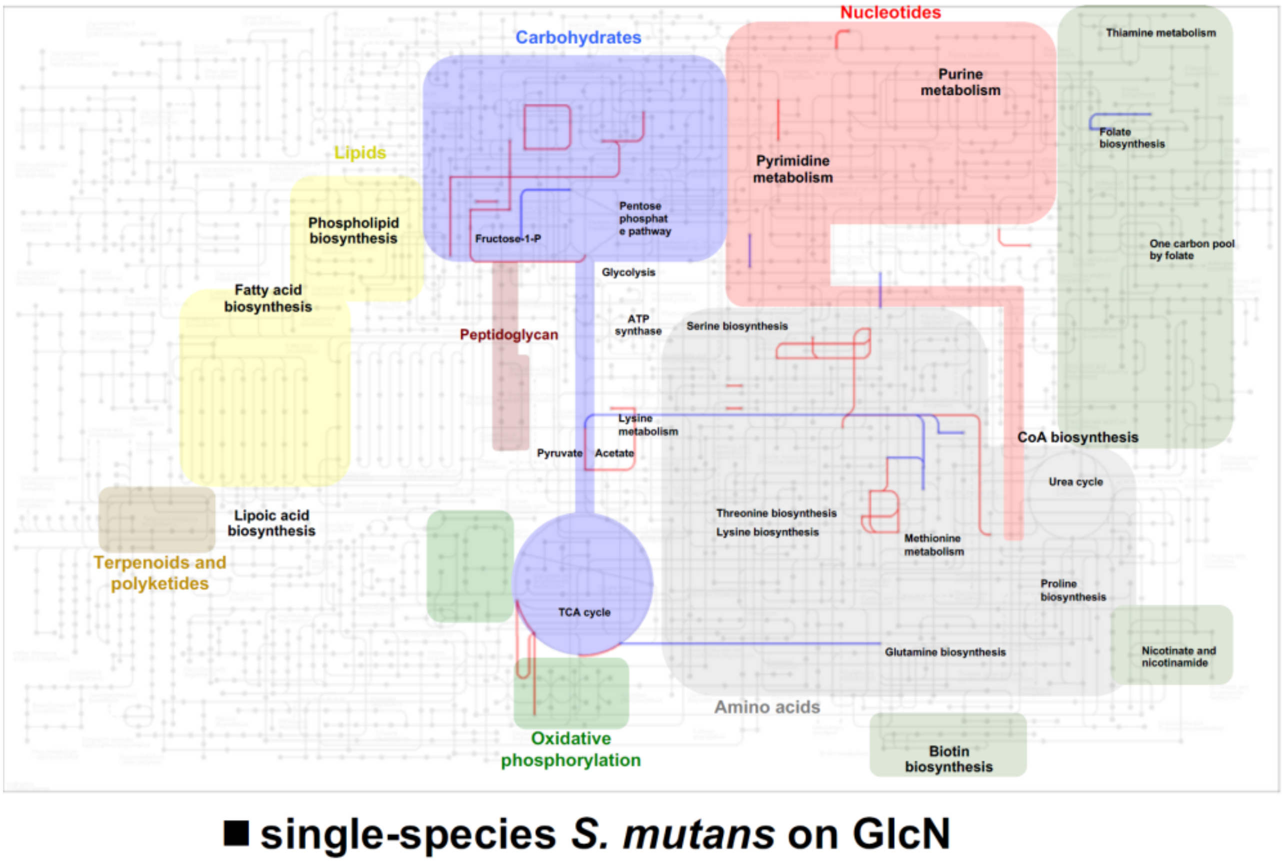


Fig. S2. KEGG visualized map of metabolic pathways showing significant change in gene expression in GlcN-supported, single-species *S. mutans* cultures as compared to glucose-supported cultures. Red lines indicate genes and pathways with increased expression, blue lines denote those with decreased expression.

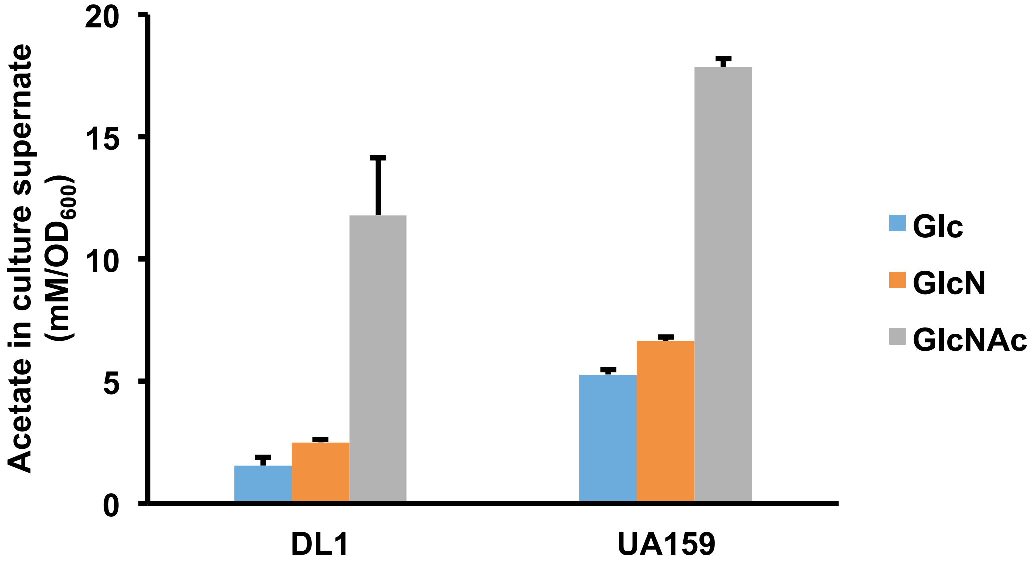
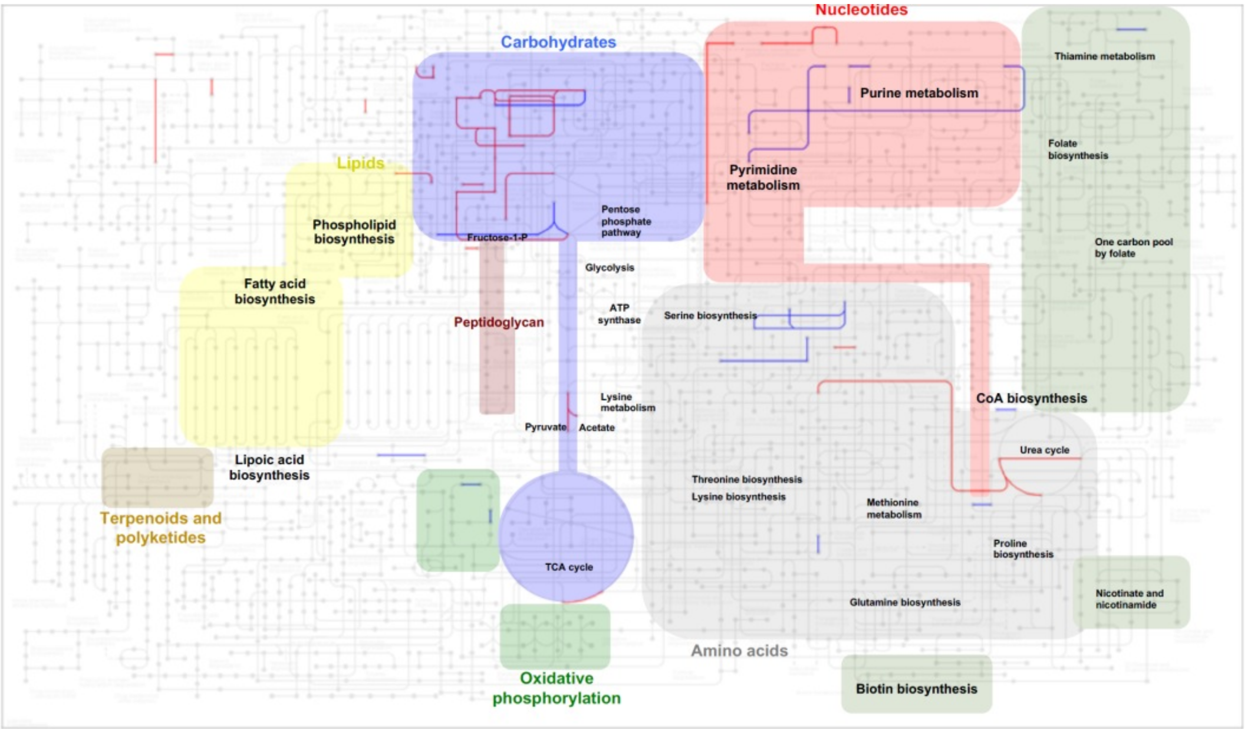


Fig. S3. Measurements of acetate in cultures of UA159 and DL1 on various carbohydrates. Overnight cultures in BHI of each bacterium (n = 3) were diluted 1:20 into TV medium supplemented with 20 mM of Glc, GlcN or GlcNAc and incubated in an aerobic environment maintained with 5% of CO_2. Cultures from the exponential phase were spun down and supernates removed for measurement of acetate, using an acetate colorimetric assay kit (Sigma). Each sample was measured twice, and the TV base medium was used as a blank. The results were normalized against cell density (OD_{600}) at time of harvest.



■ **single-species *S. gordonii* on GlcN**

Fig. S4. KEGG visualized map of metabolic pathways showing significant change in gene expression in GlcN-supported, single-species *S. gordonii* cultures as compared to glucose-supported cultures. Red lines indicate genes and pathways with increased expression, blue lines denote those with decreased expression.

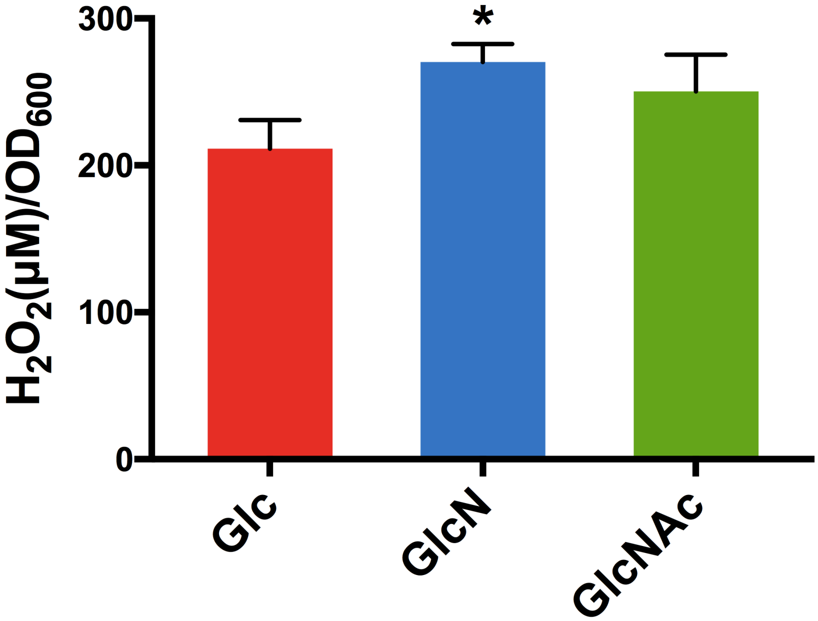


Fig. S5. Measurements of H_2O_2 in liquid cultures of *S. gordonii* DL1 prepared with TV supplemented with 20 mM of specified carbohydrates (1). Each condition was represented by three biological repeats, and each sample measured at least twice. The results were normalized against optical density (OD_{600}) of the culture. The asterisk denotes significant difference relative to the Glc condition according to Students' *t*-test ($p < 0.05$).

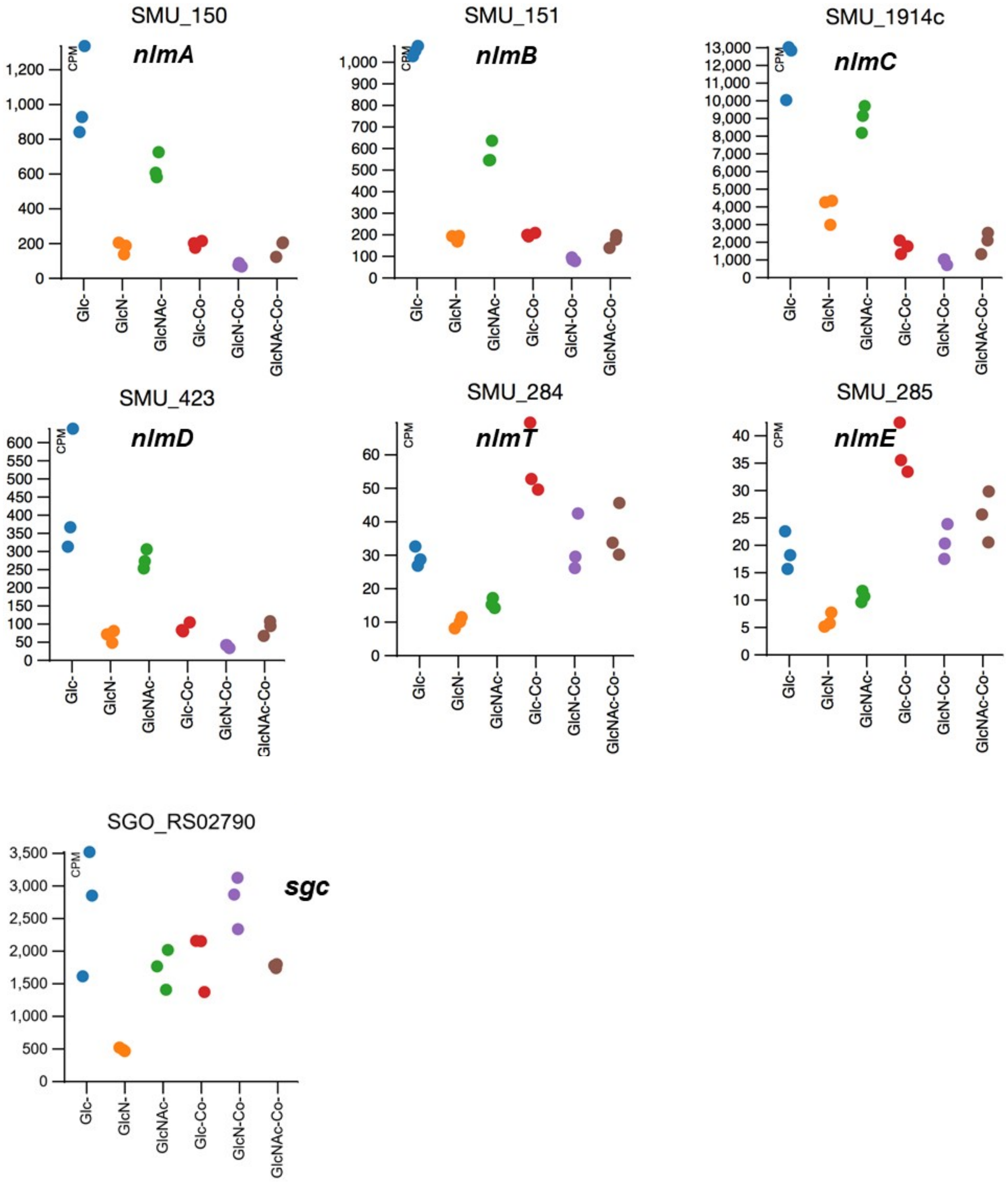


Fig. S6. mRNA levels of genes involved in mutacin production in both bacteria. The results were derived from RNA-Seq analysis using the website http://degust.erc.monash.edu/ and presented in counts per million (CPM). “Co.” denotes mixed-species co-cultures.

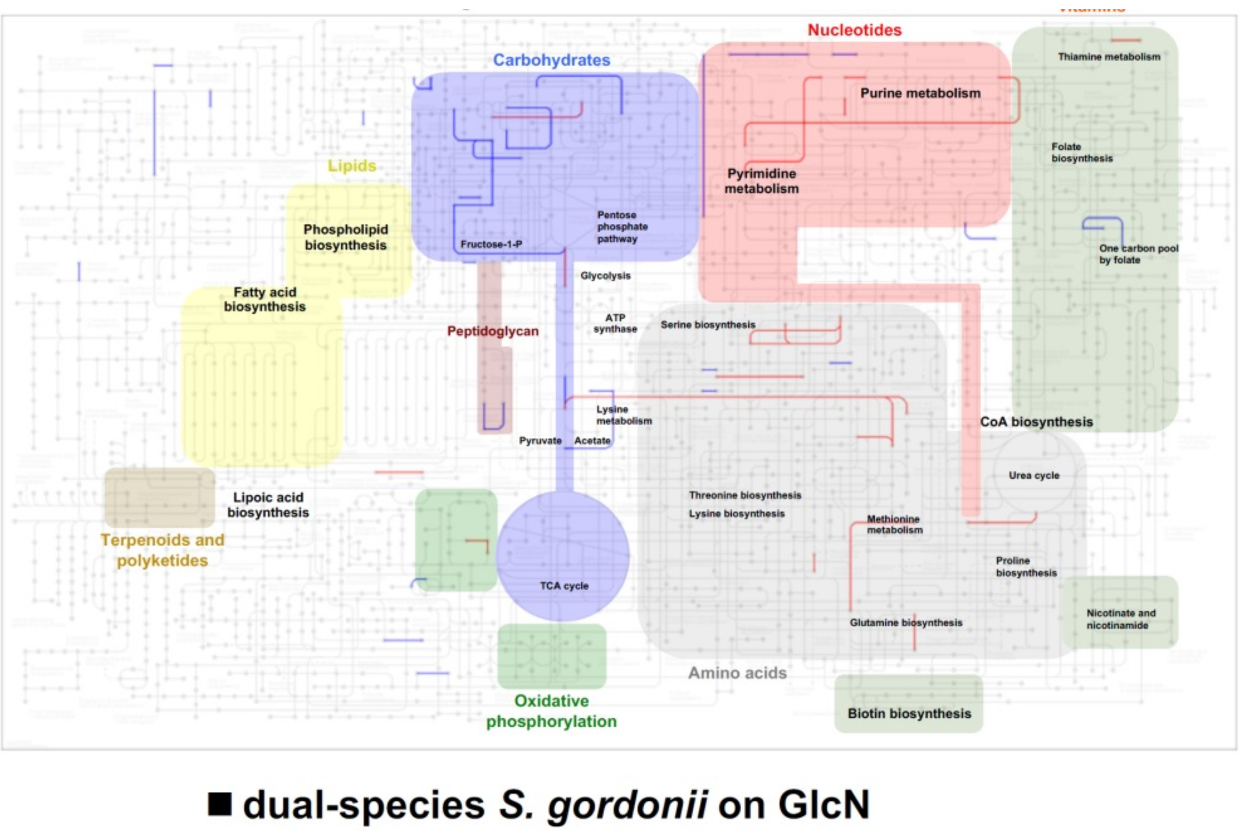


Fig. S7. KEGG visualized map of metabolic pathways showing significant changes in *S. gordonii* gene expression in GlcN-supported, mixed-species cultures together with *S. mutans* as compared to *S. gordonii* grown alone on GlcN. Red lines indicate genes and pathways with increased expression, blue lines denote those with decreased expression.

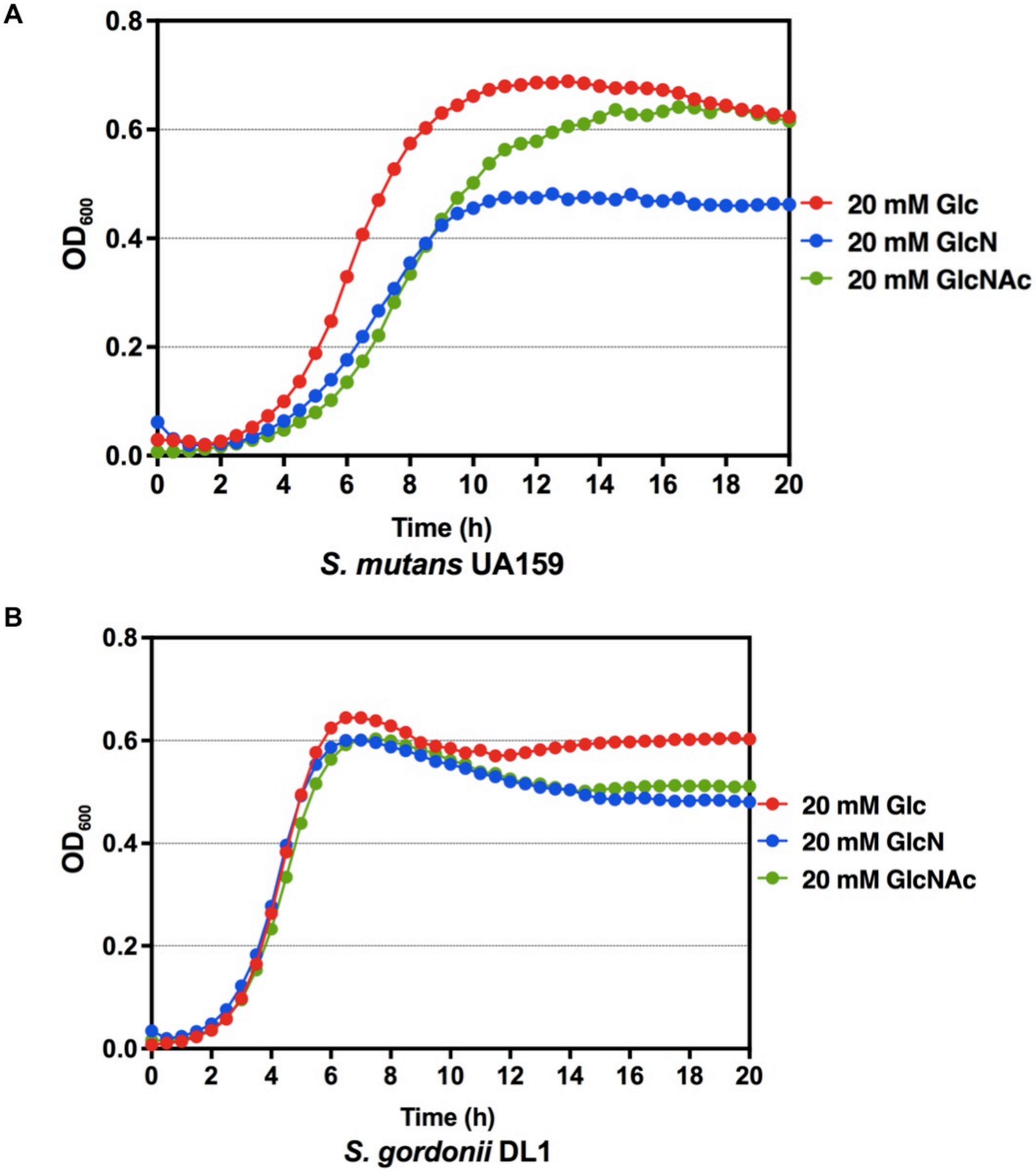


Fig. S8. Growth curves of UA159 (A) and DL1 (B) on TV media supplemented with 20 mM of Glc, GlcN or GlcNAc. The samples were covered with mineral oil and monitored at 37°C using a Bioscreen C system.

Table S1. Differentially expressed genes (DEG) in *S. mutans* grown on GlcN compared to glucose. SMU# in red denotes up-regulation, and SMU# in blue denotes down-regulation.

SMU#	**Gene name**	**Gene function**
GlcN _Up (114)		
SMU_1088	*apbE*	thiamine biosynthesis lipoprotein
SMU_1089		conserved hypothetical protein
SMU_1090		conserved hypothetical protein
SMU_1116c		hypothetical protein
SMU_1117	*nox*	H_2O-forming NADH oxidase
SMU_113	*pfk*	fructose-1-phosphate kinase
SMU_114	*fruC*	PTS system, fructose-specific IIBC component
SMU_1147c		involved in competence
SMU_115	*fruD*	PTS system, fructose-specific IIA component
SMU_1151c		conserved hypothetical protein
SMU_1152c		conserved hypothetical protein
SMU_1153c		conserved hypothetical protein
SMU_1154c		conserved hypothetical protein
SMU_1156c		hypothetical protein
SMU_1157c		conserved hypothetical protein
SMU_1158c		conserved hypothetical protein
SMU_1159c		hypothetical protein
SMU_116	*lacD1*	tagatose 1,6-aldolase
SMU_1160c		hypothetical protein
SMU_1287	*pmrA tnrA*	transcriptional regulator
SMU_1360c		hypothetical protein
SMU_1361c	*yjjB*	transcriptional regulator
SMU_1421	*acoC yugF*	dihydrolipoamide acetyltransferase (acetoin dehydrogenase E2 component)
SMU_1422	*acoB*	acetoin dehydrogenase E1 component
SMU_1423	*acoA*	acetoin dehydrogenase E1 component
SMU_1424	*acoL adhD*	dihydrolipoamide dehydrogenase
SMU_148	*adhE*	alcohol-acetaldehyde dehydrogenase
SMU_149	*tpn*	transposase fragment (IS605/IS200-like)
SMU_1490	*lacG*	phospho-beta-D-galactosidase
SMU_1491	*lacE*	PTS system, lactose-specific component IIBC
SMU_1493	*lacD*	tagatose-1,6-bisphosphate aldolase
SMU_1535	*glgP*	glycogen phosphorylase
SMU_1536	*glgA*	glycogen synthase
SMU_1537	*glgD*	glycogen biosynthesis protein
SMU_1538	*glgC*	glucose-1-phosphate adenylyltransferase

SMU_1539	*glgB*	1,4-alpha-glucan branching enzyme
SMU_1596	*celD*	PTS system, cellobiose-specific IIC component
SMU_1597c	*celX*	conserved hypothetical protein
SMU_1598	*celC licA*	PTS system IIA component, required for cellobiose uptake and metabolism
SMU_1599	*celR licR*	transcriptional regulator, required for cellobiose uptake and metabolism
SMU_1600	*celB licB*	PTS system IIB component, required for cellobiose uptake and metabolism
SMU_1692	*pflA pflC*	pyruvate-formate lyase activating enzyme
SMU_1770	*syv valS*	valyl-tRNA synthetase
SMU_1772c		hypothetical protein
SMU_179		conserved hypothetical protein (possible oxidoreductase)
SMU_180		oxidoreductase, possible fumarate reductase
SMU_1841	*scrA*	PTS system, sucrose-specific IIABC component
SMU_1843	*scrB*	sucrose-6-phosphate hydrolase
SMU_1844	*scrR*	sucrose operon repressor
SMU_1861c		hypothetical protein
SMU_1956c	*levX*	conserved hypothetical protein
SMU_1957	*levG ptnD*	fructose-specific Enzyme IID component
SMU_1958c	*levF*	fructose-specific Enzyme IIC component
SMU_1960c	*levE*	fructose-specific Enzyme IIB component
SMU_1961c	*levD ptfA*	fructose-specific Enzyme IIA component
SMU_2027		transcriptional regulator/repressor
SMU_2037	*dexS treA*	trehalose-6-phosphate hydrolase
SMU_2038	*pttB treB*	phosphotransferase system, trehalose-specific IIBC component (EIIBC-tre)
SMU_2127	*gabD*	succinic semialdehyde dehydrogenase (NAD-dependent aldehyde dehydrogenase)
SMU_252		hypothetical protein
SMU_270	*rmpC sgaT*	ribulose monophosphate PTS pathway enzyme IIC
SMU_402	*pfl*	pyruvate formate-lyase
SMU_404c		hypothetical protein
SMU_43		conserved hypothetical protein (possible site-specific DNA-methyltransferase/restriction modification enzyme)
SMU_44		conserved hypothetical protein
SMU_45		hypothetical protein
SMU_46		hypothetical protein
SMU_47		hypothetical protein
SMU_51	*purK*	phosphoribosylaminoimidazole carboxylase, ATPase subunit
SMU_574c	*lrgB*	effector of murein hydrolase
SMU_575c	*lrgA*	murein hydrolase regulator
SMU_576	*lytT*	response regulator

SMU_577	*lytS*	sensor histidine kinase
SMU_642		hypothetical protein
SMU_643	*yeeB*	acetyl esterase/ sugar hydrolase
SMU_791c		hypothetical protein
SMU_798c		hypothetical protein
SMU_799c		conserved hypothetical protein
SMU_870	*fruR*	lactose phosphotransferase system repressor/transcriptional repressor of the fructose operon
SMU_871	*fruK*	fructose-1-phosphate kinase
SMU_872	*fruI*	fructose-specific PTS system enzyme IIBC component
SMU_882	*msmK*	multiple sugar-binding transport ATP-binding protein MsmK
SMU_883	*dexB*	glucan 1,6-alpha-glucosidase
SMU_940c	*patB*	hemolysin III-related protein
SMU_941c		conserved hypothetical protein
SMU_956	*clpE clpL*	ATP-dependent Clp protease, ATP-binding subunit
SMU_980	*bglP ptbA*	beta-glucoside-specific EII permease
SMU_981	*bglB*	beta-glucosidase, BglB protein
SMU_982	*bglB*	beta-glucosidase, BglB protein
SMU_1425	*clpB*	ATP-dependent Clp protease, ATP-binding subunit ClpB
SMU_1492	*lacF*	PTS system, lactose-specific IIA component
SMU_1494	*lacC*	tagatose-6-phosphate kinase
SMU_1495	*lacB rpiB*	galactose-6-phosphate isomerase
SMU_1496	*lacA*	galactose-6-phosphate isomerase
SMU_1674	*patB*	aminotransferase class II
SMU_1675	*metB*	cystathionine gamma-synthase
SMU_214c		hypothetical protein
SMU_435	*nagA*	N-acetylglucosamine-6-phosphate deacetylase
SMU_439		transcriptional regulator
SMU_490	*act pflC*	pyruvate formate-lyase activating enzyme
SMU_496	*cysK*	cysteine synthetase A
SMU_636	*nagB*	glucosamine-6-phosphate isomerase
SMU_638	*rsuA*	ribosomal small subunit pseudouridine synthase A
SMU_639	*rimJ*	N-terminal acetyltransferase
SMU_641	*qor*	oxidoreductase
SMU_651c		ABC transporter, periplasmic substrate-binding protein
SMU_652c	*msmK*	ABC transporter, ATP-binding protein (possible nitrate transport system)
SMU_653c	*tauC*	ABC transporter, permease protein (possible taurine transport system permease)
SMU_930c	*cpsY*	transcriptional regulator
SMU_932		conserved hypothetical protein
SMU_933	*atmA*	amino acid ABC transporter, amino acid substrate-binding protein

SMU_934		amino acid ABC transporter, permease protein
SMU_935		amino acid ABC transporter, permease protein
SMU_936		amino acid ABC transporter, ATP-binding protein
GlcN_Down (82)		
SMU_1002	*topA*	DNA topoisomerase I
SMU_1004	*gtfB*	glucosyltransferase-I
SMU_1175	*dagA*	sodium:alanine (or glycine) symporter
SMU_1187	*glmS*	L-glutamine-D-fructose-6-phosphate amidotransferase
SMU_1249c		hypothetical protein
SMU_1250c		hypothetical protein
SMU_1315c		ABC transporter, ATP-binding protein
SMU_1316c		hypothetical protein
SMU_1317c		hypothetical protein
SMU_1342	*mubA bacA*	bacitracin synthetase
SMU_1343c	*mubH pksC*	polyketide synthase
SMU_1344c	*mubG fabD*	malonyl CoA-acyl carrier protein transacylase
SMU_1345c	*mubE ituA*	peptide synthetase similar to mycA
SMU_1346	*mubT bacT*	thioesterase II-like protein
SMU_1390		conserved hypothetical protein
SMU_1396	*gbpC*	glucan-binding protein C
SMU_1419	*acrR2*	Transcriptional regulator
SMU_150	*nlmA*	non-lantibiotic mutacin IV A
SMU_1502c		conserved hypothetical protein
SMU_1505c	*pheT*	conserved hypothetical protein (phenylalanyl-tRNA synthetase fragment)
SMU_151	*nlmB*	non-lantibiotic mutacin IV B
SMU_152		immunity protein for NlmAB
SMU_153		hypothetical protein
SMU_1595	*cah*	carbonic anhydrase (carbonate dehydratase)
SMU_169	*rplM*	50S ribosomal protein L13
SMU_170	*rpsI*	30S ribosomal protein S9
SMU_1884c		conserved hypothetical protein
SMU_1902c	*bsmK*	hypothetical protein
SMU_1903c		hypothetical protein
SMU_1904c		hypothetical protein
SMU_1905c	*bsmL*	hypothetical protein
SMU_1906c	*bsmB*	bacteriocin-related protein
SMU_1908c		hypothetical protein
SMU_1909c		putative mutacin immunity protein
SMU_1910c		hypothetical protein
SMU_1912c		hypothetical protein

SMU_1913c	*blpI*	hypothetical protein; immunity protein, BLpL-like
SMU_1914c	*nlmC cipB*	mutacin V
SMU_1927	*psaA*	PsaA protein/ ABC transporter, ATP-binding protein
SMU_1928	*psaB*	protein secretion ABC transport permease
SMU_1945		conserved hypothetical protein
SMU_1946		conserved hypothetical protein
SMU_1947	*nusG*	transcription antitermination factor
SMU_1966c	*levT rbsB*	ABC transport ribose-binding protein, periplasmic
SMU_1992	*tyrS*	tyrosyl-tRNA synthetase
SMU_1999c	*gshA*	glutamate--cysteine ligase
SMU_2026c	*rps1 rpsJ*	30S ribosomal protein S10 fragment
SMU_2126c		possible phosphorylase
SMU_2129c		conserved hypothetical protein
SMU_2135c	*rpsD rs4*	30S Ribosomal protein S4
SMU_2146c		conserved hypothetical protein
SMU_231	*als ilvB*	acetolactate synthase, large subunit (AHAS)
SMU_232	*ilvH*	acetolactate synthase, small subunit
SMU_233	*ilvC*	ketol-acid reductoisomerase
SMU_277		hypothetical protein
SMU_278		hypothetical protein
SMU_279		hypothetical protein
SMU_281		hypothetical protein
SMU_284	*nlmT*	transport and processing of non-lantibiotic mutacins
SMU_285	*nlmE*	transport and processing of non-lantibiotic mutacins
SMU_365	*gltA gltB*	glutamate synthase, large subunit
SMU_366	*gltD*	glutamate synthase, small subunit
SMU_383c		undetermined reductase or epimerase
SMU_396	*glpF*	glycerol uptake facilitator protein
SMU_42		conserved hypothetical protein
SMU_423	*nlmD*	mutacin VI
SMU_531	*pheA*	chorismate mutase; possible prephenate dehydrogenase
SMU_595	*pyrD*	dihydroorotate dehydrogenase (dihydroorotate oxidase)
SMU_600c		conserved hypothetical protein
SMU_602		sodium-dependent transporter
SMU_63c		conserved hypothetical protein
SMU_711		conserved hypothetical protein
SMU_730		conserved hypothetical protein
SMU_731		ABC transporter, ATP-binding protein
SMU_758c		conserved hypothetical protein
SMU_913	*gdhA*	NADP-specific glutamate dehydrogenase
SMU_914c		conserved hypothetical protein

SMU_915c		conserved hypothetical protein
SMU_916c		conserved hypothetical protein
SMU_917c	*ygcM ykvK*	6-pyruvoyl tetrahydropterin synthase, PTPS
SMU_919c		ATPase, confers aluminum resistance
SMU_1187	*glmS*	L-glutamine-D-fructose-6-phosphate amidotransferase

Table S2. DEG identified in *S. mutans* UA159 grown on GlcNAc compared to glucose.

SMU# in red denotes up-regulation, and SMU# in blue denotes down-regulation.

SMU#	**Gene name**	**Gene function**
GlcNAc_Up (43)		
SMU_132	*hipO*	amino acid amidohydrolase (hippurate amidohydrolase)
SMU_201c		conserved hypothetical protein
SMU_209c		hypothetical protein
SMU_210c		hypothetical protein
SMU_211c		hypothetical protein
SMU_2133c		conserved hypothetical protein (possible transmembrane protein)
SMU_213c		hypothetical protein
SMU_29	*purC*	phosphoribosylaminoimidazole-succinocarboxamide synthase
SMU_30	*purL*	phosphoribosylformylglycinamidine synthase
SMU_31		conserved hypothetical protein
SMU_32	*purB purF*	amidophosphoribosyltransferase
SMU_33		hypothetical protein
SMU_34	*purM*	phosphoribosylformylglycinamide cyclo-ligase (AIRS)
SMU_35	*purN*	phosphoribosylglycinamide formyltransferase
SMU_36		conserved hypothetical protein (eukaryotic-like)
SMU_37	*purH*	phosphoribosylaminoimidazolecarboxamide formyltransferase / IMP cyclohydrolase
SMU_961		macrophage infectivity potentiator-related protein
SMU_962	*mmgC*	acyl-CoA dehydrogenase
SMU_1425	*clpB*	ATP-dependent Clp protease, ATP-binding subunit ClpB
SMU_1492	*lacF*	PTS system, lactose-specific IIA component
SMU_1494	*lacC*	tagatose-6-phosphate kinase
SMU_1495	*lacB rpiB*	galactose-6-phosphate isomerase
SMU_1496	*lacA*	galactose-6-phosphate isomerase
SMU_1674	*patB*	aminotransferase class II
SMU_1675	*metB*	cystathionine gamma-synthase
SMU_214c		hypothetical protein
SMU_435	*nagA*	N-acetylglucosamine-6-phosphate deacetylase
SMU_439		transcriptional regulator
SMU_490	*act pflC*	pyruvate formate-lyase activating enzyme
SMU_496	*cysK*	cysteine synthetase A
SMU_636	*nagB*	glucosamine-6-phosphate isomerase
SMU_638	*rsuA*	ribosomal small subunit pseudouridine synthase A
SMU_639	*rimJ*	N-terminal acetyltransferase
SMU_641	*qor*	oxidoreductase
SMU_651c		ABC transporter, periplasmic substrate-binding protein

SMU_652c	*msmK*	ABC transporter, ATP-binding protein (possible nitrate transport system)
SMU_653c	*tauC*	ABC transporter, permease protein (possible taurine transport system permease)
SMU_930c	*cpsY*	transcriptional regulator
SMU_932		conserved hypothetical protein
SMU_933	*atmA*	amino acid ABC transporter, amino acid substrate-binding protein
SMU_934		amino acid ABC transporter, permease protein
SMU_935		amino acid ABC transporter, permease protein
SMU_936		amino acid ABC transporter, ATP-binding protein
GlcNAc_Down (2)		
SMU_637c		hypothetical protein
SMU_1187	*glmS*	L-glutamine-D-fructose-6-phosphate amidotransferase

Table S3. DEG identified in *S. mutans* UA159 common to both GlcN and GlcNAc cultures.

SMU# in red denotes up-regulation, and SMU# in blue denotes down-regulation.

SMU#	**Gene name**	**Gene function**
Up (25)		
SMU_1425	*clpB*	ATP-dependent Clp protease, ATP-binding subunit ClpB
SMU_1492	*lacF*	PTS system, lactose-specific IIA component
SMU_1494	*lacC*	tagatose-6-phosphate kinase
SMU_1495	*lacB rpiB*	galactose-6-phosphate isomerase
SMU_1496	*lacA*	galactose-6-phosphate isomerase
SMU_1674	*patB*	aminotransferase class II
SMU_1675	*metB*	cystathionine gamma-synthase
SMU_214c		hypothetical protein
SMU_435	*nagA*	N-acetylglucosamine-6-phosphate deacetylase
SMU_439		transcriptional regulator
SMU_490	*act pflC*	pyruvate formate-lyase activating enzyme
SMU_496	*cysK*	cysteine synthetase A
SMU_636	*nagB*	glucosamine-6-phosphate isomerase
SMU_638	*rsuA*	ribosomal small subunit pseudouridine synthase A
SMU_639	*rimJ*	N-terminal acetyltransferase
SMU_641	*qor*	oxidoreductase
SMU_651c		ABC transporter, periplasmic substrate-binding protein
SMU_652c	*msmK*	ABC transporter, ATP-binding protein (possible nitrate transport system)
SMU_653c	*tauC*	ABC transporter, permease protein (possible taurine transport system permease)
SMU_930c	*cpsY*	transcriptional regulator
SMU_932		conserved hypothetical protein
SMU_933	*atmA*	amino acid ABC transporter, amino acid substrate-binding protein
SMU_934		amino acid ABC transporter, permease protein
SMU_935		amino acid ABC transporter, permease protein
SMU_936		amino acid ABC transporter, ATP-binding protein
Down (1)		
SMU_1187	*glmS*	L-glutamine-D-fructose-6-phosphate amidotransferase

Table S4. DEG identified in *S. gordonii* DL1 grown on GlcN compared to glucose. SGO# in red denotes up-regulation, and SGO# in blue denotes down-regulation. Also indicated are the 30 upregulated DEG shared by GlcN and GlcNAc.

SGO_R#	SGO#	Gene name	Function
GlcN (129)			
SGO_RS00105	SGO_0021		conserved domain protein
SGO_RS00170	SGO_0035		phosphoribosylformylglycinamidine synthase
SGO_RS00175	SGO_0036	*purF*	amidophosphoribosyltransferase
SGO_RS00180	SGO_0037	*purM*	phosphoribosylformylglycinamidine cyclo-ligase
SGO_RS00215	SGO_0045		PTS system, IIC component
SGO_RS00220	SGO_0046		PTS system, IID component
SGO_RS00225	SGO_0047		PTS system, IIA component
SGO_RS00230	SGO_0048		tagatose-6-phosphate ketose/aldose isomerase
SGO_RS00235	SGO_0049	*galM*	aldose 1-epimerase
SGO_RS00495	SGO_0099	*pulA-2*	pullulanase, type I
SGO_RS00500	SGO_0100		maltose operon transcription repressor
SGO_RS00505	SGO_0101	*malA*	Maltodextrose utilization protein malA
SGO_RS00510	SGO_0102		Maltodextrin transport system permease protein malD
SGO_RS00515	SGO_0103		Maltodextrin transport system permease protein malC
SGO_RS00520	SGO_0104		Maltose/maltodextrin-binding protein precursor
SGO_RS00585	SGO_0118		N-acetylmannosamine-6-phosphate epimerase, putative
SGO_RS00590	SGO_0119		conserved hypothetical protein subfamily
SGO_RS00595	SGO_0120		Bacterial extracellular solute-binding protein domain protein
SGO_RS00600	SGO_0121		ABC transporter, permease protein SP1689
SGO_RS00605	SGO_0122		ABC transporter, permease protein SP1688
SGO_RS00610	SGO_0123		oxidoreductase, Gfo/Idh/MocA family SP1325
SGO_RS00615	SGO_0124		N-acetylneuraminate lyase
SGO_RS00620	SGO_0125	*xylR*	glucokinase
SGO_RS00625	SGO_0126		BlpT protein, fusion
SGO_RS00630	SGO_0127		phosphosugar-binding transcriptional regulator, RpiR family
SGO_RS00800	SGO_0162	*abpB*	amylase-binding protein B
SGO_RS00960	SGO_0196		protease, putative
SGO_RS01230	SGO_0249		hypothetical protein
SGO_RS01240	SGO_0251		CAAX amino terminal protease family
SGO_RS01315	SGO_0267		amino acid permease family protein
SGO_RS01385	SGO_0281		PTS system, beta-glucoside-specific IIABC component
SGO_RS01425	SGO_0289		CopAB ATPases metal-fist type repressor
SGO_RS01430	SGO_0290		copper -translocating P-type ATPase
SGO_RS01435	SGO_0291		copper-translocating P-type ATPase

SGO_RS01440	SGO_0292	*spxB*	pyruvate oxidase
SGO_RS01445	SGO_0293		glyoxalase family protein superfamily
SGO_RS01480	SGO_0300		membrane protein, putative
SGO_RS01485	SGO_0301		ABC transporter ATP-binding protein-like protein
SGO_RS01490	SGO_0302		membrane protein, putative
SGO_RS01495	SGO_0303		ABC transporter ATP-binding protein-like protein
SGO_RS01500	SGO_0304		membrane protein, putative
SGO_RS01515	SGO_0307	*pabB*	chorismate binding enzyme
SGO_RS01540	SGO_0313		HAD superfamily hydrolase
SGO_RS01545	SGO_0314		phosphoglycerate mutase family protein
SGO_RS01550	SGO_0315		phosphoglycerate mutase family protein
SGO_RS01555	SGO_0316		LPXTG cell wall surface protein, serine protease, subtilase family
SGO_RS01560	SGO_0317		LPXTG cell wall surface protein, serine protease, subtilase family
SGO_RS01685	SGO_0341		lipoprotein, putative
SGO_RS01740	SGO_0352		ABC transporter, ATP-binding protein SP1580
SGO_RS01750	SGO_0354		membrane spanning protein
SGO_RS01920	SGO_0385		exo-beta-D-fructosidase
SGO_RS01930	SGO_0387		conserved hypothetical protein
SGO_RS01935	SGO_0388		LPXTG cell wall surface protein, zinc carboxypeptidase family
SGO_RS02020	SGO_0405		Beta-N-acetylhexosaminidase precursor
SGO_RS02045	SGO_0410		integral membrane protein
SGO_RS02050	SGO_0411		conserved hypothetical protein TIGR01440
SGO_RS02180	SGO_0440		L-iditol 2-dehydrogenase BH3949
SGO_RS02360	SGO_0477		cell wall binding protein
SGO_RS02365	SGO_0478		cell wall binding protein
SGO_RS02465	SGO_0498	*dsg*	putative permease
SGO_RS03100	SGO_0630		Glycerol uptake facilitator protein
SGO_RS03105	SGO_0631		alpha-glycerophosphate oxidase
SGO_RS03110	SGO_0632	*glpK*	glycerol kinase
SGO_RS03115	SGO_0633		conserved hypothetical protein
SGO_RS03380	SGO_0686		Transcriptional regulator, DeoR family
SGO_RS03390	SGO_0688		ATP dependent Clp protease, ATP-binding subunit, ClpE
SGO_RS03550	SGO_0721		abpB-like dipeptidase lipoprotein
SGO_RS03560	SGO_0724		dipeptidase
SGO_RS03565	SGO_0725		conserved hypothetical protein
SGO_RS04560	SGO_0932	*galK*	Galactokinase
SGO_RS04565	SGO_0933	*galT*	galactose-1-phosphate uridylyltransferase
SGO_RS04725	SGO_0965		integral membrane protein
SGO_RS05455	SGO_1111	*fruR*	phosphotransferase system repressor
SGO_RS05535	SGO_1126		Tyrosine recombinase xerC

SGO_RS05555	SGO_1130		dihydrolipoamide dehydrogenase
SGO_RS05560	SGO_1131	*sucB*	dihydrolipoamide S-acetyltransferase
SGO_RS05565	SGO_1132		acetoin dehydrogenase
SGO_RS05570	SGO_1133	*acoA*	acetoin dehydrogenase
SGO_RS05615	SGO_1142		hypothetical protein
SGO_RS05745	SGO_1167	*nox*	NADH oxidase
SGO_RS05815	SGO_1182		LPXTG cell wall surface protein
SGO_RS06270	SGO_1277		conserved hypothetical protein
SGO_RS06305	SGO_1285		ABC transporter, ATP-binding protein SP1282
SGO_RS06460	SGO_1317		hypothetical protein
SGO_RS06940	SGO_1415		LPXTG cell wall surface protein, X-prolyl dipeptidylaminopeptidase, putative
SGO_RS07290	SGO_1486		beta-galactosidase
SGO_RS07300	SGO_1488		putative methyltransferase
SGO_RS07345	SGO_1497		ABC-type transporter, ATPase component
SGO_RS07590	SGO_1549		PAP2 family protein
SGO_RS07595	SGO_1550	*glgP-1*	glycogen phosphorylase
SGO_RS07600	SGO_1551	*glgA*	Glycogen synthase
SGO_RS07605	SGO_1552	*glgD*	glucose-1-phosphate adenylyltransferase, GlgD subunit
SGO_RS07610	SGO_1553	*glgC*	glucose-1-phosphate adenylyltransferase
SGO_RS07615	SGO_1554	*glgB*	1,4-alpha-glucan branching enzyme
SGO_RS07755	SGO_1583		hypothetical protein
SGO_RS07785	SGO_1589	*arcT*	putative transaminase/peptidase
SGO_RS07790	SGO_1590	*arcD*	arginine-ornithine antiporter
SGO_RS07795	SGO_1591	*arcC*	carbamate kinase
SGO_RS07800	SGO_1592	*arcB*	ornithine carbamoyltransferase
SGO_RS07805	SGO_1593	*arcA*	arginine deiminase
SGO_RS08080	SGO_1649	*act*	pyruvate formate-lyase-activating enzyme
SGO_RS08520	SGO_1738		conserved hypothetical protein
SGO_RS08525	SGO_1739		LytTr DNA-binding domain family
SGO_RS08660	SGO_1766		Glycosyl hydrolase family 20, catalytic domain family
SGO_RS08665	SGO_1767		ROK family protein
SGO_RS08670	SGO_1768		glycosyl hydrolase, family 38
SGO_RS08675	SGO_1769		Protein of unknown function (DUF1237) superfamily
SGO_RS08855	SGO_1805	*hutU*	urocanate hydratase
SGO_RS09090	SGO_1856		ATP-dependent proteinase ATP-binding chain
SGO_RS09250	SGO_1889		conserved hypothetical protein
SGO_RS09255	SGO_1890		PTS system, fructose(mannose)-specific IID
SGO_RS09260	SGO_1891		PTS system, IIC component
SGO_RS09270	SGO_1893		PTS system, fructose(mannose)-specific IIA component
SGO_RS09460	SGO_1932		conserved hypothetical protein

SGO_RS09465	SGO_1933		copper transport protein CopZ-related protein
SGO_RS09470	SGO_1934		copper-translocating P-type ATPase
SGO_RS09475	SGO_1935		negative transcriptional regulator, CopY
SGO_RS09785			hypothetical protein
SGO_RS10100	SGO_2067		conserved membrane protein, putative multidrug efflux associated
SGO_RS10105	SGO_2068		Protein of unknown function (DUF990) superfamily
SGO_RS10110	SGO_2069		ATP-binding protein of ABC transporter
SGO_RS10230	SGO_2089	*purK*	phosphoribosylaminoimidazole carboxylase, ATPase subunit
SGO_RS10235	SGO_2090	*purE*	phosphoribosylaminoimidazole carboxylase, catalytic subunit
SGO_RS10240	SGO_2091		conserved hypothetical protein
SGO_RS10245	SGO_2092	*purD*	phosphoribosylamine--glycine ligase
SGO_RS10275	SGO_2100		ABC transporter substrate-binding protein
SGO_RS10280	SGO_2101		ABC transporter, permease protein SP2198
SGO_RS10285	SGO_2102		conserved hypothetical protein
SGO_RS10720			hypothetical protein
GlcN_GlcNAc (30)			
SGO_RS00205	SGO_0043		beta-galactosidase
SGO_RS00210	SGO_0044		PTS system, IIB component
SGO_RS01020	SGO_0208	*endoD*	LPXTG cell wall surface protein, glycosyl hydrolase family
SGO_RS01220	SGO_0247	*pfl*	formate acetyltransferase
SGO_RS02715	SGO_0549	*nagA*	N-acetylglucosamine-6-phosphate deacetylase
SGO_RS02720	SGO_0551		hypothetical protein
SGO_RS02725	SGO_0552		oxidoreductase, aldo/keto reductase family
SGO_RS02730	SGO_0553		acetyltransferase
SGO_RS07410	SGO_1512	*lacG*	6-phospho-beta-galactosidase
SGO_RS07415	SGO_1513	*lacE*	PTS system, lactose-specific IIBC component
SGO_RS07420	SGO_1514	*lacF*	PTS system, lactose-specific IIa component
SGO_RS07425	SGO_1515		antiterminator protein
SGO_RS07430	SGO_1516	*lacD-2*	tagatose 1,6-diphosphate aldolase
SGO_RS07435	SGO_1517	*lacC*	tagatose-6-phosphate kinase
SGO_RS07440	SGO_1518	*lacB-2*	galactose-6-phosphate isomerase, LacB subunit
SGO_RS07445	SGO_1519	*lacA-1*	galactose-6-phosphate isomerase, LacA subunit
SGO_RS07450	SGO_1520		PTS system, IIC component
SGO_RS07455	SGO_1521		PTS system IIB component (galactitol/fructose specific)
SGO_RS07460	SGO_1522		PTS system enzyme IIBC component (galactitol/fructose specific)
SGO_RS07465	SGO_1523	*lacD-1*	tagatose 1,6-diphosphate aldolase
SGO_RS07470	SGO_1524	*lacC-2*	tagatose-6-phosphate kinase
SGO_RS07475	SGO_1525	*lacB-1*	galactose-6-phosphate isomerase, LacB subunit
SGO_RS07480	SGO_1526	*lacA-2*	galactose-6-phosphate isomerase, LacA subunit

SGO_RS07770	SGO_1586	*nagB*	glucosamine-6-phosphate isomerase
SGO_RS08095	SGO_1652	*treA*	intracellular glycosyl hydrolase
SGO_RS08100	SGO_1653	*treB*	trehalose PTS enzyme II
SGO_RS08645	SGO_1763		ABC transporter, substrate-binding protein SP0092
SGO_RS08650	SGO_1764		ABC transporter, permease protein SP0091
SGO_RS08655	SGO_1765		ABC transporter sugar binding protein
SGO_RS10270	SGO_2099		ABC transporter ATP-binding protein
GlcN (144)			
SGO_RS00045	SGO_0009	*recF*	DNA replication and repair protein RecF
SGO_RS00050	SGO_0010		conserved hypothetical protein
SGO_RS00315	SGO_0065		hypothetical protein
SGO_RS00365	SGO_0075		hypothetical protein
SGO_RS00435	SGO_0087		transporter, major facilitator family
SGO_RS00440	SGO_0088		transcription regulator, AcrR family
SGO_RS00450	SGO_0090		transcriptional regulator, TetR family
SGO_RS01115	SGO_0226		methyltransferase
SGO_RS01160	SGO_0235		glycerol uptake facilitator protein-like protein
SGO_RS01410	SGO_0286		DNA mismatch repair protein MutS, putative
SGO_RS01415	SGO_0287		haloacid dehalogenase-like hydrolase, putative
SGO_RS01420	SGO_0288		GDSL-like lipase/acylhydrolase
SGO_RS01745	SGO_0353		transport protein
SGO_RS01755	SGO_0355		RNA methyltransferase, TrmH family, group 3
SGO_RS01760	SGO_0356		hypothetical protein
SGO_RS01765	SGO_0357	*degV*	DegV family fatty acid binding protein
SGO_RS01770	SGO_0358	*rplM*	ribosomal protein L13
SGO_RS01775	SGO_0359	*rpsI*	ribosomal protein S9
SGO_RS01860			hypothetical protein
SGO_RS01865	SGO_0374		response regulator of the LytR/AlgR family
SGO_RS01870			hypothetical protein
SGO_RS02290	SGO_0463	*cydD*	putative ABC transporter (ATP-binding protein)
SGO_RS02295	SGO_0464	*cydC*	putative ABC transporter (ATP-binding protein)
SGO_RS02300	SGO_0465		conserved hypothetical protein
SGO_RS02305	SGO_0466		membrane protein, putative
SGO_RS02310	SGO_0467		ATP binding protein of ABC transporter
SGO_RS02330	SGO_0471		DNA-binding protein
SGO_RS02335	SGO_0472		hypothetical protein
SGO_RS02340	SGO_0473		hypothetical protein
SGO_RS02345	SGO_0474		abortive infection protein
SGO_RS02350	SGO_0475		conserved hypothetical protein
SGO_RS02790	SGO_0566	*sgc*	serine protease challisin
SGO_RS02795	SGO_0568	*glyQ*	glycyl-tRNA synthetase, alpha subunit

SGO_RS02800	SGO_0569	*glyS*	glycyl-tRNA synthetase, beta subunit
SGO_RS02805	SGO_0570		conserved hypothetical protein
SGO_RS02985	SGO_0606	*cysK*	cysteine synthase A
SGO_RS03070	SGO_0623		tRNA-Pro
SGO_RS03135	SGO_0637		acetyltransferase, GNAT family
SGO_RS03140	SGO_0638		membrane protein, putative
SGO_RS03145	SGO_0639	*valS*	valyl-tRNA synthetase
SGO_RS03355	SGO_0681	*ileS*	isoleucyl-tRNA synthetase
SGO_RS03495	SGO_0710		tRNA-Thr
SGO_RS03655	SGO_0744		conserved hypothetical protein
SGO_RS03770	SGO_0766		esterase of alpha/beta hydrolase superfamily, putative
SGO_RS03775	SGO_0767		transport protein
SGO_RS03780	SGO_0769		iron compound ABC transporter, ATP-binding protein
SGO_RS03785	SGO_0770		FecCD transport family
SGO_RS04495	SGO_0917		membrane protein, putative
SGO_RS04500	SGO_0918		Cobalt transport protein superfamily
SGO_RS04505	SGO_0919		abc transporter, ATP-binding protein
SGO_RS04510	SGO_0920		cobalt ABC transporter, ATP-binding protein
SGO_RS04535			hypothetical protein
SGO_RS05135	SGO_1046		conserved hypothetical protein
SGO_RS05285	SGO_1076	*rpsT*	ribosomal protein S20
SGO_RS05290	SGO_1077	*coaA*	pantothenate kinase
SGO_RS05715	SGO_1161	*tatA*	twin-arginine translocation protein, Tat A/E family
SGO_RS05720	SGO_1162	*tatC*	Sec-independent protein translocase TatC
SGO_RS05725	SGO_1163		Iron permease FTR1 family
SGO_RS05730	SGO_1164		tat translocated dye-type peroxidase family
SGO_RS05735	SGO_1165		lipoprotein, putative
SGO_RS05945	SGO_1211		hypothetical protein
SGO_RS06005	SGO_1223		Adenylate cyclase
SGO_RS06065	SGO_1235		tRNA-Gln
SGO_RS06075	SGO_1237		conserved hypothetical protein
SGO_RS06085	SGO_1239	*parC*	DNA topoisomerase IV, A subunit
SGO_RS06090	SGO_1240		CAAX amino terminal protease family
SGO_RS06095	SGO_1241		aminoglycoside adenylyltransferase
SGO_RS06100	SGO_1242		lipoprotein, putative
SGO_RS06110	SGO_1244		conserved hypothetical protein
SGO_RS06230	SGO_1268		murein hydrolase export regulator
SGO_RS06235	SGO_1269		murein hydrolase exporter
SGO_RS06440	SGO_1313		pneumococcal histidine triad A protein
SGO_RS06445	SGO_1314		metal binding lipoprotein
SGO_RS06585	SGO_1342		ABC transporter, ATP-binding protein SP1715

SGO_RS06590	SGO_1343		ABC transporter, ATP-binding protein SP1715
SGO_RS06735	SGO_1374	*aroE*	shikimate 5-dehydrogenase
SGO_RS06740	SGO_1375	*aroD*	3-dehydroquinate dehydratase, type I
SGO_RS06775	SGO_1382		tRNA-Arg
SGO_RS06820	SGO_1391		conserved hypothetical protein
SGO_RS07170	SGO_1461		putative stress-responsive transcriptional regulator PspC
SGO_RS07310	SGO_1490		NrdI protein, putative
SGO_RS07385	SGO_1506		membrane protein, putative
SGO_RS07670	SGO_1566	*argD*	acetylornithine aminotransferase (ACOAT)
SGO_RS07890	SGO_1610		hypothetical protein
SGO_RS07910	SGO_1614		magnesium and cobalt transporter CorA family
SGO_RS07915	SGO_1615		CAAX amino terminal protease family
SGO_RS07920	SGO_1616		methyltransferase
SGO_RS07925	SGO_1617	*prfC*	peptide chain release factor 3
SGO_RS07965	SGO_1626		branched-chain amino acid ABC transporter, ATP-binding protein
SGO_RS08235	SGO_1679		phosphotransferase system enzyme II
SGO_RS08240	SGO_1680		phosphotransferase system enzyme II
SGO_RS08255	SGO_1683	*serS*	seryl-tRNA synthetase
SGO_RS08345	SGO_1702		tRNA-Asn
SGO_RS08555	SGO_1745	*fba*	fructose-1,6-bisphosphate aldolase, class II
SGO_RS08755	SGO_1785		nickel-cobalt-cadmium resistance protein; NccN
SGO_RS08840	SGO_1802		metal ABC transporter substrate-binding lipoprotein precursor
SGO_RS08975	SGO_1829		tRNA-Lys
SGO_RS08980	SGO_1830	*Mga*	Mga-like regulatory protein
SGO_RS09015	SGO_1838		ABC transporter domain protein
SGO_RS09345	SGO_1909		membrane protein, putative
SGO_RS09505	SGO_1941		tRNA-Leu
SGO_RS09515	SGO_1943		tRNA-His
SGO_RS09525	SGO_1945		tRNA-Tyr
SGO_RS09585	SGO_1957		conserved hypothetical protein
SGO_RS09590	SGO_1958	*rplQ*	ribosomal protein L17
SGO_RS09595	SGO_1959	*rpoA*	DNA-directed RNA polymerase, alpha subunit
SGO_RS09600	SGO_1960	*rpsK*	ribosomal protein S11
SGO_RS09605	SGO_1961	*rpsM*	ribosomal protein S13p/S18e
SGO_RS09610			hypothetical protein
SGO_RS09615	SGO_1964	*adk*	adenylate kinase (ATP-AMP transphosphorylase)
SGO_RS09620	SGO_1965		preprotein translocase secY subunit
SGO_RS09625	SGO_1966	*rplO*	ribosomal protein L15
SGO_RS09630	SGO_1967		50S ribosomal protein L30 -related protein
SGO_RS09635	SGO_1968	*rpsE*	ribosomal protein S5

SGO_RS09640	SGO_1969	*rplR*	ribosomal protein L18
SGO_RS09645	SGO_1970	*BL10*	50S ribosomal protein L6
SGO_RS09650	SGO_1971	*rpsH*	ribosomal protein S8
SGO_RS09655	SGO_1972	*rpsN*	ribosomal protein S14p/S29e
SGO_RS09660	SGO_1973	*BL6*	50S ribosomal protein L5
SGO_RS09855	SGO_2015		possible polysaccharide transport protein
SGO_RS09860	SGO_2016		nucleotide sugar dehydratase, putative
SGO_RS09865	SGO_2017		nucleotidyl transferase, putative
SGO_RS09870	SGO_2018		extrracellular polysaccharide polymerase putative
SGO_RS09875	SGO_2019	*licD*	licD3 protein
SGO_RS09880	SGO_2020		glycosyltransferase
SGO_RS09885	SGO_2021		extracellular polysaccharide glycosyltransferase
SGO_RS09890	SGO_2022		UDP-glucose 4-epimerase BH3715
SGO_RS09895	SGO_2023		galactosyltransferase
SGO_RS09900	SGO_2024		extracellular polysaccharide biosynthesis
SGO_RS09905	SGO_2025	*wze*	putative autophosphorylating protein tyrosine kinase
SGO_RS10090	SGO_2065	*rpmF*	ribosomal protein L32
SGO_RS10095	SGO_2066	*rpmG*	ribosomal protein L33
SGO_RS10120			hypothetical protein
SGO_RS10125	SGO_2070		conserved hypothetical protein
SGO_RS10130	SGO_2071		hypothetical protein
SGO_RS10145	SGO_2073		FtsK/SpoIIIE family subfamily, putative
SGO_RS10350	SGO_2114		tRNA-Ser
SGO_RS10355	SGO_2115		tRNA-Met
SGO_RS10360	SGO_2116		tRNA-Met
SGO_RS10500	SGO_2145	*comE*	competence response regulator ComE
SGO_RS10510	SGO_2147	*comC*	competence factor-related protein ComC
SGO_RS10515	SGO_2148		tRNA-Arg
SGO_RS10600			hypothetical protein
SGO_RS10795	SGO_1962	*rpmJ*	ribosomal protein L36

Table S5. DEG identified in *S. mutans* UA159 and *S. gordonii* DL1 when co-cultured on glucose, in comparison to UA159 and DL1, respectively, growing alone on glucose. Gene# in red indicates up-regulation, and Gene# in blue indicates down-regulation.

Gene#	**Gene name**	**Function**
UA159		
Glc_GlcN_ GlcNAc (5)		
SMU_182	*sloA*	ABC transporter, ATP-binding protein, iron and/or manganese
SMU_183	*sloB*	manganese ABC transporter permease element
SMU_184	*fimA lraI*	ABC transporter element, iron predicted binding protein
SMU_185		hypothetical protein
SMU_186	*sloR*	metalloregulatory protein
Glc_GlcNAc (1)		
SMU_770c	*mntH hitA*	manganese transporter
Glc (1)		
SMU_768c		hypothetical protein
Glc_GlcN_ GlcNAc (8)		
SMU_1906c	*bsmB*	bacteriocin-related protein
SMU_1914c	*nlmC cipB*	mutacin V
SMU_196c		immunogenic secreted protein (transfer protein)
SMU_200c		hypothetical protein
SMU_201c		conserved hypothetical protein
SMU_202c		conserved hypothetical protein/Streptococcus-specific protein
SMU_205c		conserved hypothetical protein
SMU_206c		hypothetical protein
Glc_GlcNAc (13)		
SMU_150	*nlmA*	non-lantibiotic mutacin IV A
SMU_151	*nlmB*	non-lantibiotic mutacin IV B
SMU_153		hypothetical protein
SMU_1902c	*bsmK*	hypothetical protein
SMU_1903c		hypothetical protein
SMU_1904c		hypothetical protein
SMU_1905c	*bsmL*	hypothetical protein
SMU_1908c		hypothetical protein
SMU_1909c		putative mutacin immunity protein
SMU_1910c		hypothetical protein
SMU_1912c		hypothetical protein
SMU_1913c	*blpI*	hypothetical protein; immunity protein, BLpL-like

SMU_423	*nlmD*	mutacin VI
Glc (1)		
SMU_152		immunity protein for NlmAB
Glc_GlcN (1)		
SMU_575c	*lrgA*	murein hydrolase regulator
DL1		
Glc_GlcN (2)		
SGO_RS03070		tRNA-Pro
SGO_RS09530		tRNA-Phe
Glc_GlcN_GlcNAc (2)		
SGO_RS09525		tRNA-Tyr
SGO_RS10225		hypothetical protein
Glc_GlcN (2)		
SGO_RS00565	*acdH*	alcohol-acetaldehyde dehydrogenase
SGO_RS03180		conserved hypothetical protein

Table S6. DEG identified in *S. mutans* UA159 and *S. gordonii* DL1 when co-cultured on GlcN, in comparison to UA159 and DL1, respectively, growing alone on GlcN. Gene# in red indicates up-regulation, and Gene# in blue indicates down-regulation.

Gene#	***Gene* name**	**Function**
UA159		
Glc_GlcN_GlcNAc (5)		
SMU_182	*sloA*	ABC transporter, ATP-binding protein, iron and/or manganese
SMU_183	*sloB*	manganese ABC transporter permease element
SMU_184	*fimA lraI*	ABC transporter element, iron predicted binding protein
SMU_185		hypothetical protein
SMU_186	*sloR*	metalloregulatory protein
GlcN (29)		
SMU_1315c		ABC transporter, ATP-binding protein
SMU_1316c		hypothetical protein
SMU_1317c		hypothetical protein
SMU_1341c	*mubB grs mycB*	gramicidin S synthase/mycosubtilin synthetase chain mycB
SMU_1342	*mubA bacA*	bacitracin synthetase
SMU_1343c	*mubH pksC*	polyketide synthase
SMU_1344c	*mubG fabD*	malonyl CoA-acyl carrier protein transacylase
SMU_1345c	*mubE ituA*	peptide synthetase similar to mycA
SMU_1346	*mubT bacT*	thioesterase II-like protein
SMU_1390		conserved hypothetical protein
SMU_1884c		conserved hypothetical protein
SMU_1947	*nusG*	transcription antitermination factor
SMU_1992	*tyrS*	tyrosyl-tRNA synthetase
SMU_2026c	*rps1NA rpsJ*	30S ribosomal protein S10 fragment
SMU_2146c		conserved hypothetical protein
SMU_277		hypothetical protein
SMU_278		hypothetical protein
SMU_279		hypothetical protein
SMU_281		hypothetical protein
SMU_284	*nlmT*	transport and processing of non-lantibiotic mutacins
SMU_285	*nlmE*	transport and processing of non-lantibiotic mutacins
SMU_396	*glpF*	glycerol uptake facilitator protein
SMU_531	*pheA*	chorismate mutase; possible prephenate dehydrogenase
SMU_595	*pyrD*	dihydroorotate dehydrogenase (dihydroorotate oxidase)
SMU_709		conserved hypothetical protein
SMU_730		conserved hypothetical protein

SMU_732		conserved hypothetical protein
SMU_734		conserved hypothetical protein (probable membrane protein)
SMU_758c		conserved hypothetical protein
Glc_GlcN_GlcNAc (8)		
SMU_1906c	*bsmB*	bacteriocin-related protein
SMU_1914c	*nlmC cipB*	mutacin V
SMU_196c		immunogenic secreted protein (transfer protein)
SMU_200c		hypothetical protein
SMU_201c		conserved hypothetical protein
SMU_202c		conserved hypothetical protein/Streptococcus-specific protein
SMU_205c		conserved hypothetical protein
SMU_206c		hypothetical protein
GlcN (43)		
SMU_113	*pfk*	fructose-1-phosphate kinase
SMU_114	*fruC*	PTS system, fructose-specific IIBC component
SMU_1147c		involved in competence
SMU_115	*fruD*	PTS system, fructose-specific IIA component
SMU_1152c		conserved hypothetical protein
SMU_1153c		conserved hypothetical protein
SMU_1154c		conserved hypothetical protein
SMU_1156c		hypothetical protein
SMU_1157c		conserved hypothetical protein
SMU_1158c		conserved hypothetical protein
SMU_1159c		hypothetical protein
SMU_116	*lacD1*	tagatose 1,6-aldolase
SMU_1287	*pmrA tnrA*	transcriptional regulator
SMU_1360c		hypothetical protein
SMU_1421	*acoC yugF*	dihydrolipoamide acetyltransferase (acetoin dehydrogenase E2 component)
SMU_1422	*acoB*	acetoin dehydrogenase E1 component
SMU_1423	*acoA*	acetoin dehydrogenase E1 component
SMU_1424	*acoL adhD*	dihydrolipoamide dehydrogenase
SMU_1494	*lacC*	tagatose-6-phosphate kinase
SMU_1495	*lacB rpiB*	galactose-6-phosphate isomerase
SMU_1561	*trkB*	potassium uptake protein B
SMU_1562	*trkA*	potassium uptake protein A
SMU_1563	*pacL*	cation-transporting P-ATPase
SMU_1889c		hypothetical protein (possible relation to bacteriocin BlpU)
SMU_194c		conserved hypothetical protein, phage-related
SMU_1956c	*levX*	conserved hypothetical protein
SMU_1957	*levG ptnD*	fructose-specific Enzyme IID component

SMU_1958c	*levF*	fructose-specific Enzyme IIC component
SMU_1960c	*levE*	fructose-specific Enzyme IIB component
SMU_1961c	*levD ptfA*	fructose-specific Enzyme IIA component
SMU_2027		transcriptional regulator/repressor
SMU_212c		hypothetical protein
SMU_490	*act pflC*	pyruvate formate-lyase activating enzyme
SMU_651c		ABC transporter, periplasmic substrate-binding protein
SMU_652c	*msmK*	ABC transporter, ATP-binding protein (possible nitrate transport system)
SMU_653c	*tauC*	ABC transporter, permease protein (possible taurine transport system permease)
SMU_930c	*cpsY*	transcriptional regulator
SMU_932		conserved hypothetical protein
SMU_933	*atmA*	amino acid ABC transporter, amino acid substrate-binding protein
SMU_934		amino acid ABC transporter, permease protein
SMU_935		amino acid ABC transporter, permease protein
SMU_936		amino acid ABC transporter, ATP-binding protein
SMU_956	*clpE clpL*	ATP-dependent Clp protease, ATP-binding subunit
GlcN_GlcNAc (18)		
SMU_1674	*patB*	aminotransferase class II
SMU_1675	*metB*	cystathionine gamma-synthase
SMU_191c		phage-related integrase
SMU_193c		conserved hypothetical protein
SMU_195c		hypothetical protein
SMU_197c		hypothetical protein
SMU_198c	*tpn*	conjugative transposon protein
SMU_199c		hypothetical protein
SMU_204c		hypothetical protein
SMU_207c		transcriptional regulator
SMU_208c		conserved hypothetical protein, FtsK/SpoIIIE family
SMU_209c		hypothetical protein
SMU_210c		hypothetical protein
SMU_211c		hypothetical protein
SMU_214c		hypothetical protein
SMU_216c		hypothetical protein
SMU_496	*cysK*	cysteine synthetase A
SMU_574c	*lrgB*	effector of murein hydrolase
Glc_GlcN (1)		
SMU_575c	*lrgA*	murein hydrolase regulator
DL1		
GlcN (162)		

SGO_RS00045	*recF*	DNA replication and repair protein RecF
SGO_RS00050		conserved hypothetical protein
SGO_RS00315		hypothetical protein
SGO_RS00585		N-acetylmannosamine-6-phosphate epimerase, putative
SGO_RS00590		conserved hypothetical protein subfamily
SGO_RS00750	*tgt*	queuine tRNA-ribosyltransferase
SGO_RS01000	*rpsL*	ribosomal protein S12
SGO_RS01005	*rpsG*	ribosomal protein S7
SGO_RS01015	*gap*	glyceraldehyde-3-phosphate dehydrogenase, type I
SGO_RS01160		glycerol uptake facilitator protein-like protein
SGO_RS01165		membrane protein, putative
SGO_RS01535	*xfp*	D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase
SGO_RS01735		leucine-rich protein
SGO_RS01745		transport protein
SGO_RS01755		RNA methyltransferase, TrmH family, group 3
SGO_RS01760		hypothetical protein
SGO_RS01765	*degV*	DegV family fatty acid binding protein
SGO_RS01770	*rplM*	ribosomal protein L13
SGO_RS01775	*rpsI*	ribosomal protein S9
SGO_RS02035	*zmpB*	zinc metalloproteinase B
SGO_RS02140		GTP-sensing transcriptional pleiotropic repressor codY
SGO_RS02165	*gatB*	glutamyl-tRNA(Gln) amidotransferase, B subunit
SGO_RS02330		DNA-binding protein
SGO_RS02335		hypothetical protein
SGO_RS02340		hypothetical protein
SGO_RS02345		abortive infection protein
SGO_RS02350		conserved hypothetical protein
SGO_RS02460	*gtfG*	glucosyltransferase G
SGO_RS02600	*ilvB*	acetolactate synthase, large subunit, biosynthetic type
SGO_RS02605	*ilvN*	acetolactate synthase, small subunit
SGO_RS02790	*sgc*	serine protease challisin
SGO_RS02795	*glyQ*	glycyl-tRNA synthetase, alpha subunit
SGO_RS02800	*glyS*	glycyl-tRNA synthetase, beta subunit
SGO_RS02805		conserved hypothetical protein
SGO_RS02985	*cysK*	cysteine synthase A
SGO_RS03355	*ileS*	isoleucyl-tRNA synthetase
SGO_RS03740	*tuf*	translation elongation factor Tu
SGO_RS03815		hypothetical protein
SGO_RS03820	*thrS*	threonyl-tRNA synthetase
SGO_RS04190	*cshA*	surface-associated protein CshA
SGO_RS04200		ABC transporter, substrate binding protein

SGO_RS04205		ABC transporter, permease protein
SGO_RS04210		ABC transporter, ATP-binding protein
SGO_RS04495		membrane protein, putative
SGO_RS04500		Cobalt transport protein superfamily
SGO_RS04505		abc transporter, ATP-binding protein
SGO_RS04510		cobalt ABC transporter, ATP-binding protein
SGO_RS04535		hypothetical protein
SGO_RS04785		conserved hypothetical protein
SGO_RS04815		amino acid ABC transporter, amino acid-binding protein
SGO_RS04820		amino acid ABC transporter, ATP-binding protein SP0709
SGO_RS04825		amino acid ABC transporter, permease protein SP0710
SGO_RS04830		amino acid ABC transporter, permease protein SP0711
SGO_RS05065	*infC*	translation initiation factor IF-3
SGO_RS05135		conserved hypothetical protein
SGO_RS05285	*rpsT*	ribosomal protein S20
SGO_RS05835		ABC transporter, permease/ATP-binding protein
SGO_RS05850	*rplL*	ribosomal protein L7/L12
SGO_RS05855	*BL5*	50S ribosomal protein L10
SGO_RS06060	*rpsA*	30S ribosomal protein S1
SGO_RS06065		tRNA-Gln
SGO_RS06075		conserved hypothetical protein
SGO_RS06085	*parC*	DNA topoisomerase IV, A subunit
SGO_RS06090		CAAX amino terminal protease family
SGO_RS06095		aminoglycoside adenylyltransferase
SGO_RS06100		lipoprotein, putative
SGO_RS06110		conserved hypothetical protein
SGO_RS06230		murein hydrolase export regulator
SGO_RS06235		murein hydrolase exporter
SGO_RS06440		pneumococcal histidine triad A protein
SGO_RS06445		metal binding lipoprotein
SGO_RS06485		KH domain protein
SGO_RS06490	*rpsP*	ribosomal protein S16
SGO_RS06585		ABC transporter, ATP-binding protein SP1715
SGO_RS06590		ABC transporter, ATP-binding protein SP1715
SGO_RS06740	*aroD*	3-dehydroquinate dehydratase, type I
SGO_RS06820		conserved hypothetical protein
SGO_RS07145	*rplK*	ribosomal protein L11
SGO_RS07295		LPXTG cell wall surface protein, Cna protein B-type domain
SGO_RS07310		NrdI protein, putative
SGO_RS07315		hypothetical protein
SGO_RS07385		membrane protein, putative

SGO_RS07670	*argD*	acetylornithine aminotransferase (ACOAT)
SGO_RS07675	*argB*	acetylglutamate kinase
SGO_RS07680	*argJ*	arginine biosynthesis bifunctional protein ArgJ
SGO_RS07965		branched-chain amino acid ABC transporter, ATP-binding protein
SGO_RS07970		branched-chain amino acid ABC transporter, ATP-binding protein
SGO_RS07975	*braE*	branched-chain amino acid ABC transporter, permease protein
SGO_RS07980	*livH*	branched-chain amino acid ABC transporter, permease protein
SGO_RS07985		branched-chain amino acid ABC transporter, amino acid-binding protein
SGO_RS08235		phosphotransferase system enzyme II
SGO_RS08240		phosphotransferase system enzyme II
SGO_RS08245		PTS system, mannose/fructose/sorbose family, IID component
SGO_RS08255	*serS*	seryl-tRNA synthetase
SGO_RS08260		acyl-CoA dehydrogenase family
SGO_RS08265		putative peroxidase / antioxidase
SGO_RS08345		tRNA-Asn
SGO_RS08375	*amiF*	oligopeptide transport ATP-binding protein amiF
SGO_RS08380	*amiE*	oligopeptide transport ATP-binding protein
SGO_RS08385	*amiD*	oligopeptide transport system permease protein
SGO_RS08390	*hppB*	oligopeptide transport system permease
SGO_RS08755		nickel-cobalt-cadmium resistance protein; NccN
SGO_RS08975		tRNA-Lys
SGO_RS09200	*rpsR*	ribosomal protein S18
SGO_RS09210	*rpsF*	ribosomal protein S6
SGO_RS09345		membrane protein, putative
SGO_RS09505		tRNA-Leu
SGO_RS09510		tRNA-Gln
SGO_RS09515		tRNA-His
SGO_RS09520		tRNA-Trp
SGO_RS09540		tRNA-Ser
SGO_RS09590	*rplQ*	ribosomal protein L17
SGO_RS09595	*rpoA*	DNA-directed RNA polymerase, alpha subunit
SGO_RS09600	*rpsK*	ribosomal protein S11
SGO_RS09605	*rpsM*	ribosomal protein S13p/S18e
SGO_RS09610		hypothetical protein
SGO_RS09615	*adk*	adenylate kinase (ATP-AMP transphosphorylase)
SGO_RS09620		preprotein translocase secY subunit
SGO_RS09625	*rplO*	ribosomal protein L15
SGO_RS09630		50S ribosomal protein L30 -related protein
SGO_RS09635	*rpsE*	ribosomal protein S5
SGO_RS09645	*BL10*	50S ribosomal protein L6

SGO_RS09650	*rpsH*	ribosomal protein S8
SGO_RS09655	*rpsN*	ribosomal protein S14p/S29e
SGO_RS09660	*BL6*	50S ribosomal protein L5
SGO_RS09665	*rplX*	ribosomal protein L24
SGO_RS09670	*rplN*	ribosomal protein L14
SGO_RS09675	*BS16*	30S ribosomal protein
SGO_RS09680	*rpmC*	ribosomal protein L29
SGO_RS09685	*rplP*	ribosomal protein L16
SGO_RS09690	*rpsC*	ribosomal protein S3
SGO_RS09695	*rplV*	ribosomal protein L22
SGO_RS09855		possible polysaccharide transport protein
SGO_RS09860		nucleotide sugar dehydratase, putative
SGO_RS09865		nucleotidyl transferase, putative
SGO_RS09870		extrracellular polysaccharide polymerase putative
SGO_RS09875	*licD*	licD3 protein
SGO_RS09880		glycosyltransferase
SGO_RS09885		extracellular polysaccharide glycosyltransferase
SGO_RS09890		UDP-glucose 4-epimerase BH3715
SGO_RS09895		galactosyltransferase
SGO_RS09900		extracellular polysaccharide biosynthesis
SGO_RS09905	*wze*	putative autophosphorylating protein tyrosine kinase
SGO_RS09910	*wzd*	polysaccharide export protein, MPA1 family
SGO_RS09915	*wzh*	wzh/Putative phosphotyrosine-protein phosphatase
SGO_RS09920	*wzg*	transcriptional regulator
SGO_RS10090	*rpmF*	ribosomal protein L32
SGO_RS10095	*rpmG*	ribosomal protein L33
SGO_RS10265	*rpsD*	ribosomal protein S4
SGO_RS10300	*abpA*	amylase-binding protein AbpA
SGO_RS10315		hypothetical protein
SGO_RS10320	*mreC*	cell shape-determining protein MreC
SGO_RS10325		tRNA-Ser
SGO_RS10350		tRNA-Ser
SGO_RS10355		tRNA-Met
SGO_RS10360		tRNA-Met
SGO_RS10435		tRNA-Asn
SGO_RS10500	*comE*	competence response regulator ComE
SGO_RS10510	*comC*	competence factor-related protein ComC
SGO_RS10610		hypothetical protein
SGO_RS10700		hypothetical protein
SGO_RS10795	*rpmJ*	ribosomal protein L36
Glc_GlcN (2)		

SGO_RS03070		tRNA-Pro
SGO_RS09530		tRNA-Phe
Glc_GlcN_GlcNAc (2)		
SGO_RS09525		tRNA-Tyr
SGO_RS10225		conserved hypothetical protein
GlcN_GlcNAc (4)		
SGO_RS08830	*troB*	manganese ABC transporter, ATP-binding protein SP1648
SGO_RS08835	*scaA*	ABC transporter, manganese transport
SGO_RS08840		metal ABC transporter substrate-binding lipoprotein precursor
SGO_RS09640	*rplR*	ribosomal protein L18
GlcN (101)		
SGO_RS00105		conserved domain protein
SGO_RS00165	*purC*	phosphoribosylaminoimidazole-succinocarboxamide synthase
SGO_RS00170		phosphoribosylformylglycinamidine synthase
SGO_RS00175	*purF*	amidophosphoribosyltransferase
SGO_RS00180	*purM*	phosphoribosylformylglycinamidine cyclo-ligase
SGO_RS00185	*purN*	phosphoribosylglycinamide formyltransferase
SGO_RS00205		beta-galactosidase
SGO_RS00210		PTS system, IIB component
SGO_RS00215		PTS system, IIC component
SGO_RS00220		PTS system, IID component
SGO_RS00225		PTS system, IIA component
SGO_RS00230		tagatose-6-phosphate ketose/aldose isomerase
SGO_RS00490		ribonucleotide reductase-like protein
SGO_RS00525	*malQ*	4-alpha-glucanotransferase
SGO_RS00530	*glgP-2*	maltodextrin phosphorylase
SGO_RS00800	*abpB*	amylase-binding protein B
SGO_RS01240		CAAX amino terminal protease family
SGO_RS01315		amino acid permease family protein
SGO_RS01370	*msrA*	peptide methionine sulfoxide reductase msrA/msrB
SGO_RS01425		COPAB ATPases metal-fist type repressor
SGO_RS01430		copper -translocating P-type ATPase
SGO_RS01435		copper-translocating P-type ATPase
SGO_RS01480		membrane protein, putative
SGO_RS01485		ABC transporter ATP-binding protein-like protein
SGO_RS01490		membrane protein, putative
SGO_RS01495		ABC transporter ATP-binding protein-like protein
SGO_RS01570		conserved hypothetical protein
SGO_RS01740		ABC transporter, ATP-binding protein SP1580
SGO_RS01750		membrane spanning protein

SGO_RS01920		exo-beta-D-fructosidase
SGO_RS01925		multidrug-efflux transporter 2 regulator
SGO_RS01930		conserved hypothetical protein
SGO_RS01935		LPXTG cell wall surface protein, zinc carboxypeptidase family
SGO_RS02000	*grpE*	co-chaperone GrpE
SGO_RS02005	*dnaK*	DnaK chaperone protein
SGO_RS02020		beta-N-acetylhexosaminidase precursor
SGO_RS02045		integral membrane protein
SGO_RS02050		conserved hypothetical protein TIGR01440
SGO_RS02360		cell wall binding protein
SGO_RS02365		cell wall binding protein
SGO_RS02395		sensor histidine kinase
SGO_RS02455	*rgg*	transcriptional regulator Rgg
SGO_RS02465	*dsg*	putative permease
SGO_RS02785	*adhA*	alcohol dehydrogenase
SGO_RS03115		conserved hypothetical protein
SGO_RS03175		conserved hypothetical protein
SGO_RS03185		ImpB/MucB/SamB family protein
SGO_RS03190		putative transcriptional repressor
SGO_RS03360		transcription regulator
SGO_RS03380		Transcriptional regulator, DeoR family
SGO_RS03975	*ppdK*	pyruvate, phosphate dikinase
SGO_RS04075	*uvrC*	excinuclease ABC, C subunit
SGO_RS04135		carboxypeptidase
SGO_RS04725		integral membrane protein
SGO_RS05455	*fruR*	phosphotransferase system repressor
SGO_RS05535		Tyrosine recombinase xerC
SGO_RS05615		hypothetical protein
SGO_RS05690		4-oxalocrotonate tautomerase -related protein
SGO_RS05815		LPXTG cell wall surface protein
SGO_RS06175		probable transcriptional regulator (LysR family)
SGO_RS06460		hypothetical protein
SGO_RS06800	*sufB-2*	FeS assembly protein SufB
SGO_RS07075		Ser/Thr protein phosphatase family
SGO_RS07290		beta-galactosidase
SGO_RS07300		putative methyltransferase
SGO_RS07400		LacX protein, aldolase 1 epimerase
SGO_RS07410	*lacG*	6-phospho-beta-galactosidase
SGO_RS07415	*lacE*	PTS system, lactose-specific IIBC component
SGO_RS07420	*lacF*	PTS system, lactose-specific IIa component
SGO_RS07425		antiterminator protein

SGO_RS07430	*lacD-2*	tagatose 1,6-diphosphate aldolase
SGO_RS07435	*lacC*	tagatose-6-phosphate kinase
SGO_RS07445	*lacA-1*	galactose-6-phosphate isomerase, LacA subunit
SGO_RS07465	*lacD-1*	tagatose 1,6-diphosphate aldolase
SGO_RS07475	*lacB-1*	galactose-6-phosphate isomerase, LacB subunit
SGO_RS07480	*lacA-2*	galactose-6-phosphate isomerase, LacA subunit
SGO_RS07600	*glgA*	glycogen synthase
SGO_RS07605	*glgD*	glucose-1-phosphate adenylyltransferase, GlgD subunit
SGO_RS07610	*glgC*	glucose-1-phosphate adenylyltransferase
SGO_RS07755		hypothetical protein
SGO_RS08520		conserved hypothetical protein
SGO_RS08525		LytTr DNA-binding domain family
SGO_RS08645		ABC transporter, substrate-binding protein SP0092
SGO_RS08855	*hutU*	urocanate hydratase
SGO_RS08865		serine cycle enzyme, putative
SGO_RS08925		CAAX amino terminal protease family
SGO_RS08930		conserved hypothetical protein
SGO_RS09090		ATP-dependent proteinase ATP-binding chain
SGO_RS09230	*groL*	60 kDa chaperonin/groEL protein
SGO_RS09235	*groES*	chaperonin, 10 kDa
SGO_RS09250		conserved hypothetical protein
SGO_RS09255		PTS system, fructose(mannose)-specific IID
SGO_RS09260		PTS system, IIC component
SGO_RS09265		PTS system, fructose(mannose)-specific IIB
SGO_RS09270		PTS system, fructose(mannose)-specific IIA component
SGO_RS09460		conserved hypothetical protein
SGO_RS09465		copper transport protein CopZ-related protein
SGO_RS09470		copper-translocating P-type ATPase
SGO_RS09475		negative transcriptional regulator, CopY
SGO_RS09785		hypothetical protein
SGO_RS10100		putative multidrug efflux associated
Glc_GlcN (2)		
SGO_RS00565	*acdH*	alcohol-acetaldehyde dehydrogenase
SGO_RS03180		conserved hypothetical protein
GlcN_GlcNAc (4)		
SGO_RS07440	*lacB-2*	galactose-6-phosphate isomerase, LacB subunit
SGO_RS07470	*lacC-2*	tagatose-6-phosphate kinase
SGO_RS08095		intracellular glycosyl hydrolase
SGO_RS08100		trehalose PTS enzyme II

Table S7. DEG identified in *S. mutans* UA159 and *S. gordonii* DL1 when co-cultured on GlcNAc, in comparison to UA159 and DL1, respectively, growing alone on GlcNAc. Gene# in red indicates up-regulation, and Gene# in blue indicates down-regulation.

Gene#	Gene name	Function
UA159		
Glc_GlcN_ GlcNAc (5)		
SMU_182	*sloA*	ABC transporter, ATP-binding protein, iron and/or manganese
SMU_183	*sloB*	manganese ABC transporter permease element
SMU_184	*fimA lraI*	ABC transporter element, iron predicted binding protein
SMU_185		hypothetical protein
SMU_186	*sloR*	metalloregulatory protein (27, 28)
Glc_GlcNAc (1)		
SMU_770c	*mntH hitA*	putative manganese transporter
Glc_GlcN_ GlcNAc (8)		
SMU_1906c	*bsmB*	bacteriocin-related protein
SMU_1914c	*nlmC cipB*	mutacin V
SMU_196c		immunogenic secreted protein (transfer protein)
SMU_200c		hypothetical protein
SMU_201c		conserved hypothetical protein
SMU_202c		conserved hypothetical protein/Streptococcus-specific protein
SMU_205c		conserved hypothetical protein
SMU_206c		hypothetical protein
GlcNAc (5)		
SMU_1927	*psaA*	PsaA protein/ ABC transporter, ATP-binding protein
SMU_1928	*psaB*	protein secretion ABC transport permease
SMU_2133c		conserved hypothetical protein (possible transmembrane protein)
SMU_213c		hypothetical protein
SMU_215c		hypothetical protein
Glc_GlcNAc (13)		
SMU_150	*nlmA*	non-lantibiotic mutacin IV A
SMU_151	*nlmB*	non-lantibiotic mutacin IV B
SMU_153		hypothetical protein
SMU_1902c	*bsmK*	hypothetical protein
SMU_1903c		hypothetical protein
SMU_1904c		hypothetical protein

SMU_1905c	*bsmL*	hypothetical protein
SMU_1908c		hypothetical protein
SMU_1909c		putative mutacin immunity protein
SMU_1910c		hypothetical protein
SMU_1912c		hypothetical protein
SMU_1913c	*blpI*	hypothetical protein; immunity protein, BLpL-like
SMU_423	*nlmD*	mutacin VI
GlcN_GlcNAc (18)		
SMU_1674	*patB*	aminotransferase class II
SMU_1675	*metB*	cystathionine gamma-synthase
SMU_191c		phage-related integrase
SMU_193c		conserved hypothetical protein
SMU_195c		hypothetical protein
SMU_197c		hypothetical protein
SMU_198c	*tpn*	conjugative transposon protein
SMU_199c		hypothetical protein
SMU_204c		hypothetical protein
SMU_207c		transcriptional regulator
SMU_208c		conserved hypothetical protein, FtsK/SpoIIIE family
SMU_209c		hypothetical protein
SMU_210c		hypothetical protein
SMU_211c		hypothetical protein
SMU_214c		hypothetical protein
SMU_216c		hypothetical protein
SMU_496	*cysK*	cysteine synthetase A
SMU_574c	*lrgB*	effector of murein hydrolase
DL1		
Glc_GlcN_GlcNAc (2)		
SGO_RS09525		tRNA-Tyr
SGO_RS10225		conserved hypothetical protein
GlcN_GlcNAc (4)		
SGO_RS08830	*troB*	manganese ABC transporter, ATP-binding protein SP1648
SGO_RS08835	*scaA*	ABC transporter, manganese transport
SGO_RS08840		metal ABC transporter substrate-binding lipoprotein precursor
SGO_RS09640	*rplR*	ribosomal protein L18
GlcNAc (1)		
SGO_RS01860		hypothetical protein
GlcN_GlcNAc (4)		

SGO_RS07440	*lacB-2*	galactose-6-phosphate isomerase, LacB subunit
SGO_RS07470	*lacC-2*	tagatose-6-phosphate kinase
SGO_RS08095		intracellular glycosyl hydrolase
SGO_RS08100		trehalose PTS enzyme II

Table S8. Primers used in this study for RT-qPCR.

Primers	Sequence
SMU.641-AS	TTG ACT GTC TTT CGG TGC TG
SMU.641-S	ATC CTG ATG GTT TCG ACC AC
SMU.638-AS	TCA GCT GCT TAC CTG ACA CG
SMU.638-S	AAA GTT CAT TCG CAG CCA AC
SMU.770c-AS	TCC CGG ATC CAT ATA ACC AA
SMU.770c-S	CAA TCA CTC AGC GAG GTC AA
SMU.127-AS	GCA TAG AAC CAC CAC GAC CT
SMU.127-S	TTT TCA AAT CAC CGT GGA CA
SMU.930c-AS	CAT CAT CTG TTA GGC GAG CA
SMU.930c-S	CAC ACA GCC CAA TCT TTC CT
SMU.932-AS	ACC TGA GCC GGA TAA TCC TT
SMU.932-S	AGC TCA GCA AGC TCA AGG TC
SMU.936-AS	CGC GTC CTG TCT TCT TTA GG
SMU.936-S	AGA TGT GGC CAA TCA TGT CA
SMU.1346-AS	TCT GGG AAT ATC CCA CCT TG
SMU.1346-S	CCA GGT ATC CCT CCC AAT TT
SMU.1424-AS	GCC AAC AAT AAC AGC CCC TA
SMU.1424-S	CAT CAA CAG AGA CGC AAG GA
Sm_lrgA-AS	TGC CTG ATG GGA CAA ACA TA
Sm_lrgA-S	TGT CCT TTT GTG CAG CCA TA
Sm_sloA-AS	ACG AGC CAA GAG CAT ACG TT
Sm_sloA-S	TGG CAA TGT GTT CAA GAA GC
Sm_lacA-S	TAT GAC ACG CGG CCA TAA TA
Sm_lacA-AS	CGC CGT CAT ATT TAG CCT CTA
Sm_gyrA-S	CCA AGA ATC TGC TGT CCG
Sm_gyrA-AS	TTG CGA CTA TCT GCT ATG TG

Sm_lytS-S	AGC TGC GCT TTC CTG ATA AA
Sm_lytS-AS	ATG ACG CAC TGC ATT TTC AA
Sm_nlmA-S	AAT GGA CAG CCA AAC ACT TTC
Sm_nlmA-AS	TAA CAA GAG TCG CAC CTG CC
Sm_nlmB-S	TGT CAG AAG TTT TTG GTG G
Sm_nlmB-AS	ACT CCA GCA CAT CCA GCA AG
Sm_nlmD-S	CAA CTG TTG AGG GTG GTG GTA TG
Sm_nlmD-AS	AAG CCG CTC CAG ATA CTG TAC C
Sm_glgD-S	GCT ATC GGA TTC CCA GAA ATG G
Sm_glgD-AS	CAC GAC CGC TTC TGA TAT GAT C
Sm_pfl-S	AAG GAA CTG ACT GGA AAG AC
Sm_pfl-AS	CGT GTT TCT TCG TAA TGC G
Sm_cipB-S	TTG TGC AGC AGG TAT TGC TC
Sm_cipB-AS	AAA GGC ACC AGT GCC AAT AG
Sgo_lpdA-AS	TGC GTC TGA AGC AAT AGC AC
Sgo_lpdA-S	GCA GCA GTT GGT TTG ACA GA
Sg_endoD-AS	CGG GTT TGG TGA TAG CTG TT
Sg_endoD-S	TTC TGG ACA GGT TTC CAA GG
Sg_troB-AS	CAA TCA AGA CCC GTT GGA AT
Sg_troB-S	ACT GGG ACA AGG TCA ACC AG
Sg_lrgA-AS	CTG CAC GGT ATA GGC AAT GA
Sg_lrgA-S	CCG GCA GCA GTT GGT ATT AT
SGO_1133-AS	CAC CGA GGT TAC CAG CAT CT
SGO_1133-S	TCA ATG GAA TGA TGG CTG AA
SGO_gyrA-S	GTT GGT GCA GGT GTT GTG TC
SGO_gyrA-AS	GGC CTT TTG TCG GAT ATT CA
SGO_lacA1-S	GGT CAG GAT TTT GTT GAT GTG ACC C
SGO_lacA1-AS	GGA CCA GCC CCA TAA GCA TCG AT
SGO_lacA2-S	GGT GCA GAT GCT GCT GGA AAT

SGO_lacA2-AS	CAC CTC AGC TGC AAC TGC CAA T
SGO_bgaA-S	CGT CGT CTC AAG CAA ATG AA
SGO_bgaA-AS	TCC TAA CTC TGC CGC AAT CT
SGO_bgaC-S	GGC AGA GCC TGT TCA AAG TC
SGO_bgaC-AS	ATC TGC ATC CCA GTC AGC TT
SGO_arcA-S	CGC TCC AGG TGT TGT TGT TGT G
SGO_arcA-AS	GAC CGC GAA CCA ATT CAC TTC C
SGO_NAgA-S	AGC GCA AAA TCC TTC CTA CA
SGO_NAgA-AS	ATT CAG CAA GCC ATT TGA GG
SGO_spxB-S	AAT CCT TGG TGA TGC AGG TC
SGO_spxB-AS	CGC CAG TTT TGG TTG TTC TT

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