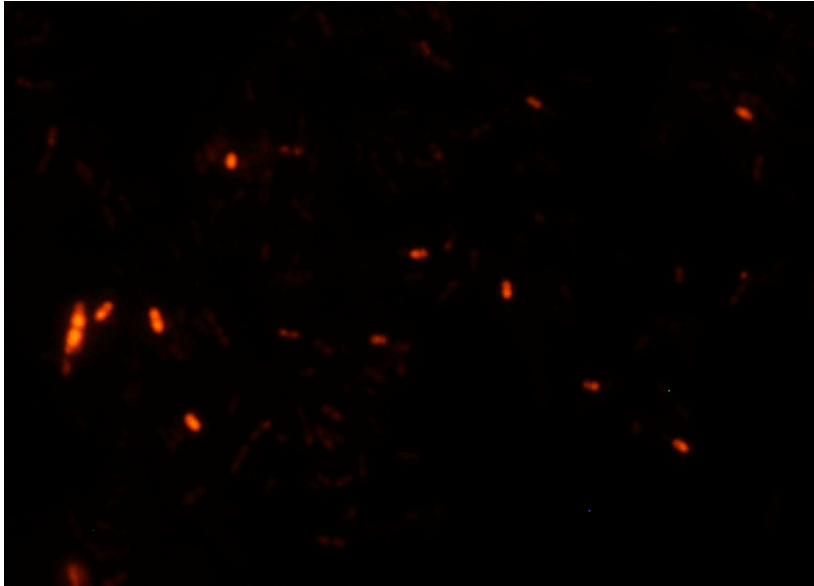
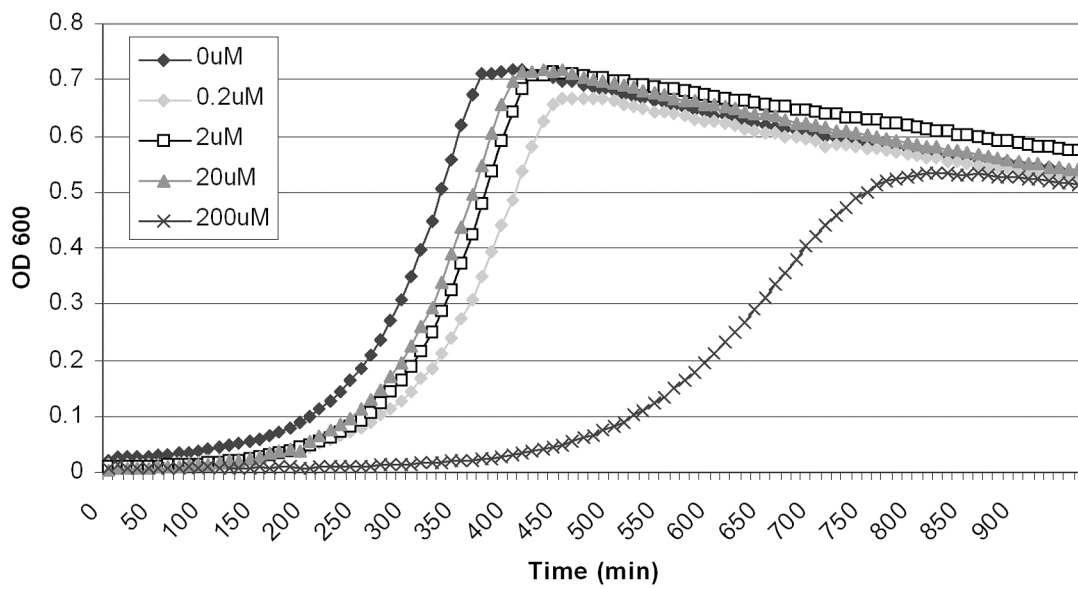


SI Fig. S1

A.



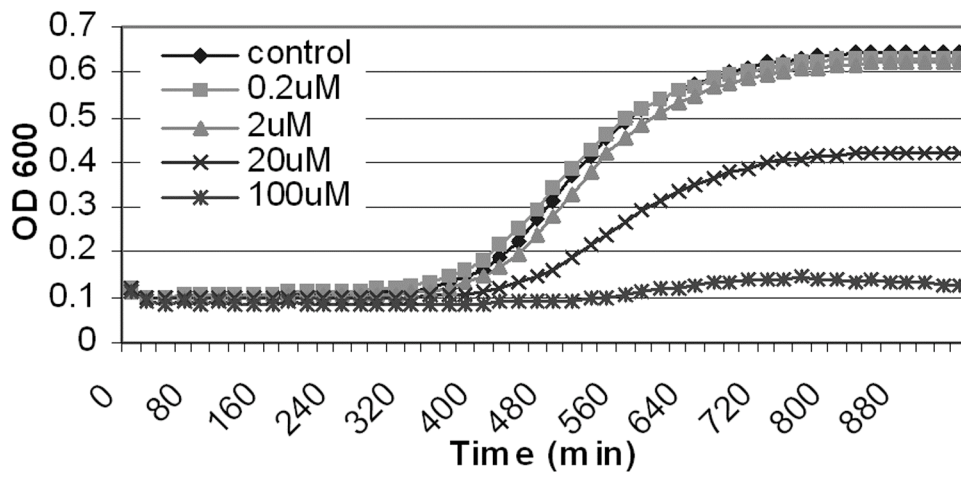
B.



SI Fig. S2

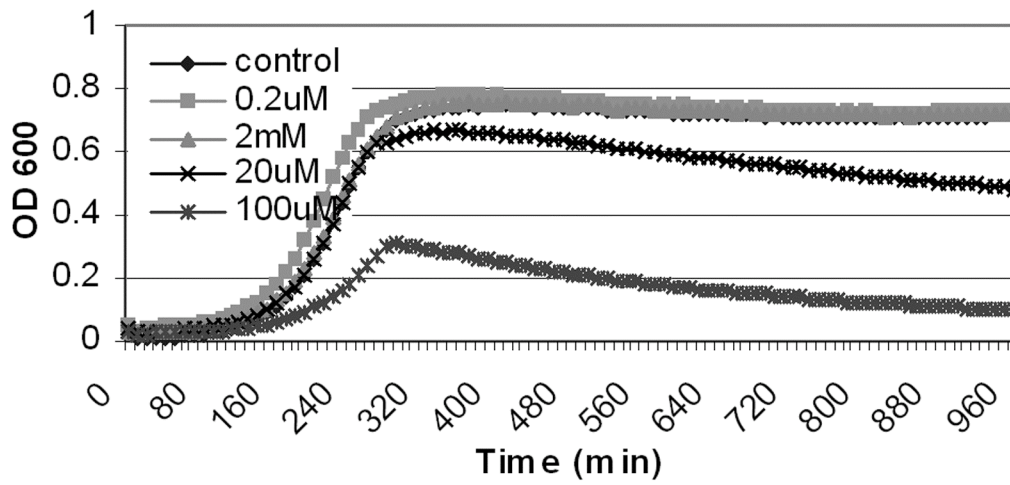
A.

S. thermophilus

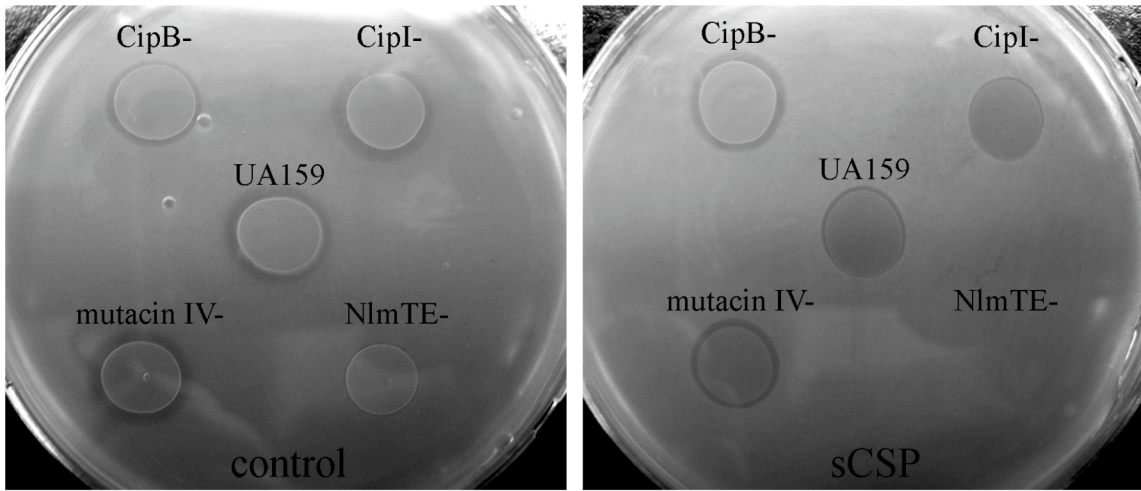


B.

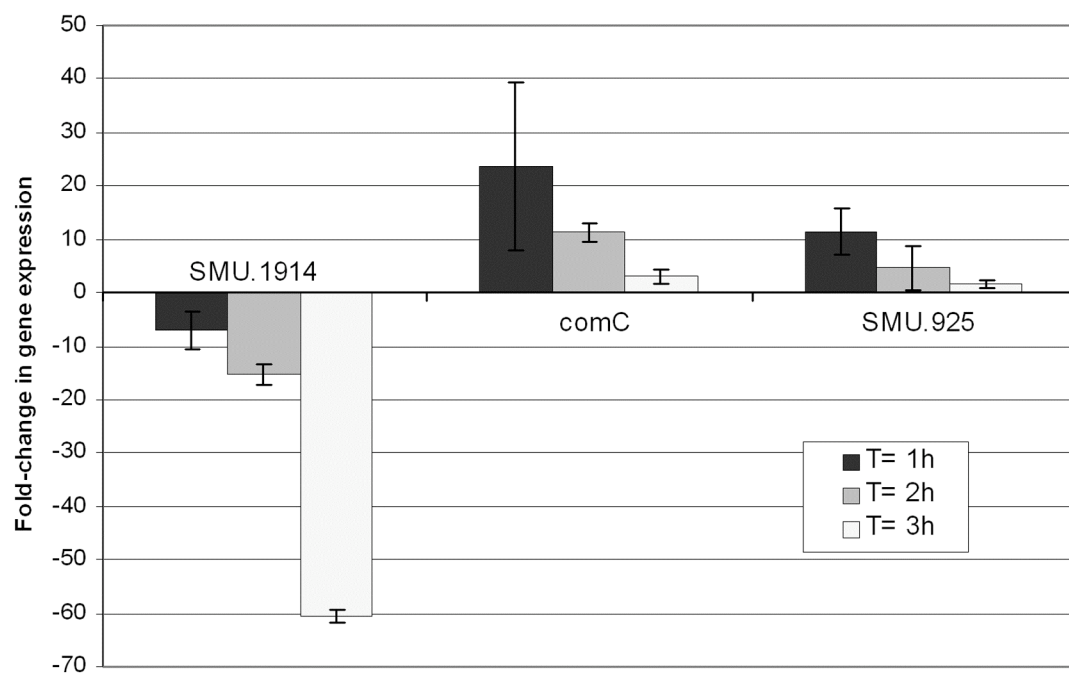
S. salivarius



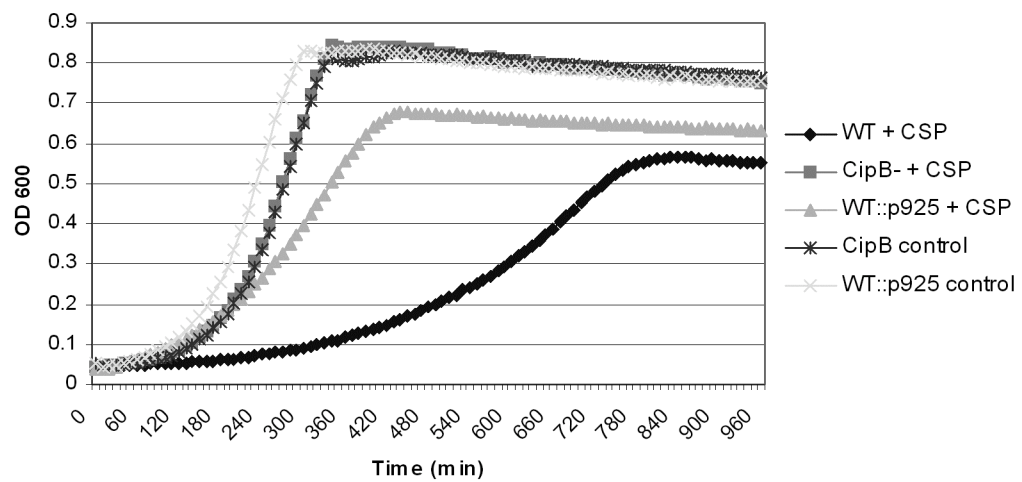
SI Fig. S3



SI Fig. S4



SI Fig. S5



SI Fig. S6

Supporting Information: Figure Legends

SI Fig. S1. Effect of sCSP on culture density and cell lysis. The culture-wide graded response to increasing concentrations of sCSP could be due to an identical bacteriostatic response in the whole population, or to an ‘all-or-none’ induction of cell lysis in a fraction of the population. To distinguish between the two, the release of the cytoplasmic enzyme β -glucuronidase (GUS) into the supernatant of growing cultures was quantified as a measure of cell lysis. The observed increase in GUS activity in presence of sCSP favors the induction of lysis in a fraction of the population. ‘Control’ cultures were grown in THYE without sCSP, while ‘+ sCSP’ cultures were supplemented with 2 μ M sCSP. The OD₆₀₀ of the culture is plotted at time points corresponding to times at which GUS activity in the supernatant was assayed. GUS activity is normalized to the optical density of the culture at each time point, and is expressed in Miller units (MU).

SI Fig. S2. A sub-set of the population undergoes cells lysis, while the majority remains sCSP-unresponsive. Viability staining using propidium iodide indicates less than 10% of the population is dead in the presence of 2 μ M sCSP (A). Growth of cells when re-suspended in fresh THYE after overnight exposure to sCSP at the concentrations indicated. Growth resumes after sCSP exposure even at 200 μ M, suggesting that a sub-population of cells is always resistant to sCSP-mediated cell lysis (B).

SI Fig. S3. Growth of *Streptococcus thermophilus* (A) and *Streptococcus salivarius* (B) in increasing concentrations of their species-specific signaling peptides. In these two non-competence species of streptococci, the peptide signaling system is composed of CSP-ComDE

paralogues BIP (bacteriocin-inducing peptide) and BlpRH, known to induce expression of bacteriocins. The similarity between these BIP-induced growth curves and the CSP-induced growth curves in *S. mutans* strongly suggests the involvement of a bacteriocin in the *S. mutans* cell death cascade.

SI Fig. S4. Agar overlay assays showing bacteriocin production in the UA159 wild-type and mutants defective in the CipB bacteriocin, the CipI immunity protein, the bacteriocin mutacin IV and the bacteriocin transporter NImTE. Bacteriocin expression is measured against the indicator strain *Lactococcus lactis* I6 by cells grown in the absence (control) and presence of sCSP.

SI Fig. S5. Quantitative real-time RT-PCR gene expression profiles of SMU.1914 (encoding CipB), *comC* (encoding CSP) and SMU.925 (encoding CipI) at 1-h, 2-h, and 3-h intervals following 1:100 dilution from an overnight culture. Gene expression was normalized to the expression of the constitutively expressed 16S rRNA gene.

SI Fig S6. Growth of the wild-type and a wild-type strain over-expressing SMU.925 from a multi-copy plasmid in the absence and presence of 2 μ M sCSP. The sCSP-resistant CipB mutant was used as a control.

SI Table S1. Genes showing a minimum \pm 2-fold difference in expression when *S. mutans* UA159 cells were exposed to 2 μ M sCSP

Gene ID	Putative or assigned function	Fold
Amino acid biosynthesis		
SMU.1073	putative formyl-tetrahydrofolate synthetase	-3.3
SMU.1265	putative phosphoribosyl formimino-5-aminoimidazole carboxamide ribonucleotide isomerase	-2.0
SMU.1266	putative glutamine amidotransferase HisH	-2.1
SMU.1268	putative imidazoleglycerol-phosphate dehydratase	-2.2
SMU.1269	putative phosphoserine phosphatase	-1.9
SMU.1270	putative histidinol dehydrogenase	-2.3
SMU.1271	putative ATP phosphoribosyltransferase	-2.1
SMU.1273	putative histidinol-phosphate aminotransferase	-2.4
SMU.1877	putative PTS system, mannose-specific component IIB	-2.9
SMU.531	putative chorismate mutase	4.3
SMU.532	putative anthranilate synthase, alpha subunit	3.4
SMU.534	putative phosphoribosyl anthranilate transferase	3.4
SMU.535	putative indoleglycerol phosphate synthase	3.7
SMU.536	putative phosphoribosyl anthranilate isomerase	2.5
SMU.537	putative tryptophan synthase, beta subunit	2.5
SMU.538	putative tryptophan synthase, alpha subunit	2.8
Biosynthesis of cofactors, prosthetic groups, and carriers		
SMU.1996	putative isopentenyl monophosphate kinase	3.3
SMU.353	conserved hypothetical protein	5.3
SMU.838	glutathione reductase	6.5
SMU.954	putative pyridoxal kinase	2.3
Cell envelope		
SMU.109	conserved hypothetical protein; possible permease (efflux protein)	5.7
SMU.1196c	conserved hypothetical protein	2.3
SMU.1677	putative UDP-N-acetylmuramoylananine-D-glutamate-2,6- diaminopimelate ligase; UDP-I	2.4
SMU.196c	putative transfer protein	3.0
SMU.2075c	conserved hypothetical protein	2.9
SMU.2081	hypothetical protein	7.5
SMU.539c	signal peptidase type IV	22.4
SMU.610	cell surface antigen SpaP	-2.5
SMU.627	conserved hypothetical protein	4.5
SMU.63c	conserved hypothetical protein	5.3
SMU.67	putative acyltransferase	4.0
SMU.883	dextran glucosidase DexB	-5.6
Cellular processes		
SMU.1001	putative DNA processing Smf protein	19.0
SMU.1279c	putative cell division protein (cell shape determining protein)	2.0
SMU.1343c	putative polyketide synthase	-3.4
SMU.1346	putative thioesterase BacT	-2.5
SMU.150	hypothetical protein	11.2
SMU.1862	hypothetical protein	2.4
SMU.1897	putative ABC transporter, ATP-binding protein	9.2
SMU.1898	putative ABC transporter, ATP-binding and permease protein	4.2
SMU.1900	conserved hypothetical protein	5.9
SMU.1905c	putative bacteriocin secretion protein	10.1
SMU.1906c	hypothetical protein	11.4

SMU.1914c	hypothetical protein	20.4
SMU.1916	putative histidine kinase of the competence regulon, ComD	10.5
SMU.1917	putative response regulator of the competence regulon, ComE	11.3
SMU.1983	putative competence protein ComYD	26.6
SMU.1984	putative competence protein ComYC	26.2
SMU.1985	putative ABC transporter ComYB; probably part of the DNA transport machinery	23.9
SMU.1987	putative ABC transporter, ATP-binding protein ComYA; late competence gene	17.5
SMU.1997	16S ribosomal RNA	14.3
SMU.2084c	conserved hypothetical protein	5.6
SMU.400	putative secreted esterase	2.8
SMU.423	hypothetical protein	14.6
SMU.426	copper-transporting ATPase; P-type ATPase	7.3
SMU.499	putative late competence protein	18.0
SMU.54	putative amino acid recemase	-3.5
SMU.625	putative competence protein	14.1
SMU.626	putative competence protein	25.6
SMU.629	putative manganese-type superoxide dismutase, Fe/Mn-SOD	-2.2
SMU.632	putative transcriptional regulator	2.4
SMU.644	putative competence protein/transcription factor	27.2
SMU.655	putative MutE	3.9
SMU.753	conserved hypothetical protein	4.0
Central intermediary metabolism		
SMU.636	putative N-acetylglucosamine-6-phosphate isomerase	3.1
DNA metabolism		
SMU.1002	putative DNA topoisomerase I	8.2
SMU.1034c	putative integrase/recombinase; XerC-like	2.2
SMU.1055	putative DNA repair protein RadC	14.1
SMU.1967	putative single-stranded DNA-binding protein	16.4
SMU.2085	recombination protein RecA	6.7
SMU.2086	putative competence and damage inducible protein CinA	10.2
SMU.327	putative DNA repair protein	3.2
SMU.505	putative adenine-specific DNA methylase	11.8
SMU.506	putative type II restriction endonuclease	9.0
SMU.64	Holliday junction DNA helicase RuvB	8.0
Energy metabolism		
SMU.1004	glucosyltransferase-I	6.0
SMU.127	putative acetoin dehydrogenase (TPP-dependent), E1 component alpha subunit	-2.2
SMU.128	putative acetoin dehydrogenase (TPP-dependent), E1 component beta subunit	-2.5
SMU.129	putative dihydrolipoamide acetyltransferase	-2.6
SMU.130	putative dihydrolipoamide dehydrogenase	-2.7
SMU.1327c	conserved hypothetical protein; possible 4Fe-4S ferredoxin	3.0
SMU.1424	putative dihydrolipoamide dehydrogenase	2.9
SMU.148	putative alcohol-acetaldehyde dehydrogenase	3.4
SMU.1978	putative acetate kinase	9.0
SMU.2037	putative trehalose-6-phosphate hydrolase TreA	6.7
SMU.352	putative ribulose-phosphate-3-epimerase	6.0
SMU.402	pyruvate formate-lyase	-2.2
SMU.772	glucan-binding protein D with lipase activity; BglB-like protein	10.0
SMU.79	fructan hydrolase; exo-beta-D-fructosidase; FruB	-4.5

SMU.877	alpha-galactosidase	-3.3
SMU.881	sucrose phosphorylase, GtfA	-5.8
SMU.886	galactokinase, GalK	-2.6
SMU.887	galactose-1-P-uridyl transferase, GalT	-2.6
SMU.888	UDP-galactose 4-epimerase, GalE	-2.7
Fatty acid and phospholipid metabolism		
SMU.1344c	putative malonyl-CoA acyl-carrier-protein transacylase	-2.9
SMU.1345c	putative peptide synthetase similar to MycA	-2.7
Hypothetical proteins		
SMU.108	hypothetical protein	4.9
SMU.1197	tRNA-Arg	2.6
SMU.1267c	hypothetical protein	-2.1
SMU.1438c	putative Zn-dependent protease	2.1
SMU.151	hypothetical protein	12.4
SMU.1651	putative arsenate reductase	2.4
SMU.167	hypothetical protein	10.0
SMU.1904c	hypothetical protein	12.2
SMU.1915	competence stimulating peptide, precursor	3.8
SMU.1956c	hypothetical protein	-5.0
SMU.1979c	conserved hypothetical protein	22.0
SMU.1980c	conserved hypothetical protein	24.6
SMU.1982c	conserved hypothetical protein	22.3
SMU.199c	hypothetical protein	2.8
SMU.202c	hypothetical protein	2.8
SMU.205c	hypothetical protein	3.5
SMU.2076c	hypothetical protein	10.1
SMU.2077c	conserved hypothetical protein	2.7
SMU.2078c	conserved hypothetical protein	2.4
SMU.2079c	conserved hypothetical protein	2.8
SMU.2080	conserved hypothetical protein	3.3
SMU.209c	hypothetical protein	3.8
SMU.212c	hypothetical protein	3.8
SMU.217c	hypothetical protein	2.5
SMU.326	conserved hypothetical protein	3.3
SMU.470	conserved hypothetical protein	2.4
SMU.503c	hypothetical protein	-2.2
SMU.53	conserved hypothetical protein	-3.5
SMU.56	conserved hypothetical protein	-3.1
SMU.649	conserved hypothetical protein	-2.0
SMU.840c	hypothetical protein	2.1
SMU.959c	hypothetical protein	-2.2
SMU.1047c	hypothetical protein	6.2
SMU.1056	hypothetical protein	5.7
SMU.1069c	hypothetical protein	3.7
SMU.1147c	hypothetical protein	5.0
SMU.1250c	hypothetical protein	1.9
SMU.152	hypothetical protein	16.1
SMU.153	hypothetical protein	12.2
SMU.166	hypothetical protein	9.1
SMU.1902c	hypothetical protein	9.8

SMU.1903c	hypothetical protein	16.0
SMU.1907	hypothetical protein	8.9
SMU.1908c	hypothetical protein	18.3
SMU.1909c	hypothetical protein	19.6
SMU.1910c	hypothetical protein	18.3
SMU.1912c	hypothetical protein	22.2
SMU.1913c	putative immunity protein, BLpL-like	15.2
SMU.1976c	hypothetical protein	3.6
SMU.200c	hypothetical protein	2.8
SMU.204c	hypothetical protein	3.0
SMU.2083c	hypothetical protein	4.0
SMU.210c	hypothetical protein	3.2
SMU.215c	hypothetical protein	3.2
SMU.216c	hypothetical protein	2.5
SMU.378	hypothetical protein	2.5
SMU.41	hypothetical protein	2.7
SMU.49	hypothetical protein	-2.9
SMU.55	hypothetical protein	-3.6
SMU.58	hypothetical protein	-3.1
SMU.637c	hypothetical protein	2.9
SMU.68	hypothetical protein	2.9
SMU.735	hypothetical protein	2.1
SMU.771c	hypothetical protein	8.0
SMU.925	hypothetical protein	18.2
Mobile and extrachromosomal element functions		
SMU.149	putative transposase	4.1
SMU.195c	hypothetical protein; similar to ORF 5 of bacteriophage SPP1	3.3
SMU.198c	putative conjugative transposon protein	2.6
SMU.2027	putative transcriptional regulator	4.7
Protein fate		
SMU.131	putative lipocate-protein ligase	-2.4
SMU.645	putative oligopeptidase	10.4
Protein synthesis		
SMU.1044c	putative pseudouridylate synthase	2.5
SMU.1512	putative phenylalanyl-tRNA synthetase (alpha subunit)	-2.3
SMU.154	30S ribosomal protein S15	2.2
SMU.1886	putative seryl-tRNA synthetase	-2.1
SMU.2000	50S ribosomal protein L17	-2.3
SMU.2002	30S ribosomal protein S11	-2.1
SMU.2012	30S ribosomal protein S8	-2.1
SMU.2014	30S ribosomal protein S14	-2.0
SMU.2015	50S ribosomal protein L5	-2.5
SMU.2016	50S ribosomal protein L24	-2.1
SMU.2017	50S ribosomal protein L14	-2.1
SMU.2022	50S ribosomal protein L22	-2.3
SMU.500	putative ribosome-associated protein	2.7
SMU.558	isoleucine-tRNA synthetase	-2.1
Purines, pyrimidines, nucleosides, and nucleotides		
SMU.30	putative phosphoribosylformylglycinamide synthase, (FGAM synthase)	-2.6
SMU.325	putative dUTPase	4.1
SMU.356	purine operon repressor	3.8

SMU.48	putative phosphoribosylamine-glycine ligase; phosphoribosyl glycinamide synthetase (G/	-2.4
SMU.50	putative phosphoribosylaminoimidazole carboxylase, catalytic subunit	-2.6
SMU.51	putative phosphoribosylaminoimidazole carboxylase, ATPase subunit	-3.4
SMU.668c	ribonucleotide reductase, large subunit	-2.0
Regulatory functions		
SMU.1048	conserved hypothetical protein	2.4
SMU.1145c	putative histidine kinase; homolog of RumK and ScnK (HK3)	2.4
SMU.1193	putative transcriptional regulator	2.5
SMU.1409c	putative transcriptional regulator	2.4
SMU.1509	putative transcriptional regulator	2.2
SMU.168	putative transcriptional regulator	8.7
SMU.1964c	putative response regulator (RR9)	4.8
SMU.1977c	putative transcriptional regulator	3.8
SMU.207c	putative transposon protein	4.4
SMU.424	negative transcriptional regulator, CopY	8.4
SMU.507	putative transcriptional regulator (DeoR family)	6.0
SMU.61	putative transcriptional regulator	3.1
SMU.65	putative protein tyrosine-phosphatase	6.6
SMU.80	transcriptional regulator; repressor (HrcA) of class I heat shock genes	3.0
SMU.927	putative response regulator (RR4)	4.8
SMU.928	putative histidine kinase (HK4)	5.3
Signal transduction		
SMU.1957	putative PTS system, mannose-specific IID component	-5.1
SMU.1958c	putative PTS system, mannose-specific IIC component	-4.4
SMU.1960c	putative PTS system, mannose-specific IIB component	-3.4
SMU.1961c	putative PTS system, sugar-specific enzyme IIA component	-3.2
SMU.1965c	putative histidine kinase (HK9)	5.5
Transcription		
SMU.2001	DNA-directed RNA polymerase, alpha subunit	-2.2
Transport and binding proteins		
SMU.1006	putative ABC transporter, ATP-binding protein	2.9
SMU.1067c	putative ABC transporter, permease protein	2.7
SMU.1068c	putative ABC transporter, ATP-binding protein	3.0
SMU.1148	putative transporter, ATP-binding protein; bacteriocin immunity protein	2.4
SMU.1185	PTS system, mannitol-specific enzyme IIBC component	2.4
SMU.1194	putative ABC transporter, ATP-binding protein	2.2
SMU.1195	conserved hypothetical protein; possible permease	2.0
SMU.1848	hypothetical protein	2.1
SMU.1878	putative PTS system, mannose-specific component IIC	-3.0
SMU.1879	putative PTS system, mannose-specific component IID	-3.9
SMU.1899	putative ABC transporter, ATP-binding and permease protein (fragment)	5.2
SMU.1963c	putative sugar-binding periplasmic protein	4.0
SMU.1966c	putative periplasmic sugar-binding protein	7.1
SMU.2038	putative PTS system, trehalose-specific IABC component	5.3
SMU.242c	putative amino acid ABC transporter, permease protein, glutamine transport system	-2.0
SMU.427	putative copper chaperone	6.5
SMU.862	conserved hypothetical protein; putative permease	2.1
SMU.863	putative ABC transporter, ATP-binding protein	1.9
SMU.864	putative ABC transporter, permease component	2.0
SMU.872	putative PTS system, fructose-specific enzyme IABC component	-2.1

SMU.878	multiple sugar-binding ABC transporter, sugar-binding protein precursor MsmE	-4.4
SMU.879	multiple sugar-binding ABC transporter, permease protein MsmF	-5.4
SMU.880	multiple sugar-binding ABC transporter, permease protein MsmG	-5.6
SMU.882	multiple sugar-binding ABC transporter, ATP-binding protein, MsmK	-5.9
Unclassified		
SMU.1111c	conserved hypothetical protein	2.0
SMU.1342	putative bacitracin synthetase 1; BacA	-2.9
SMU.1372c	hypothetical protein	2.2
SMU.193c	conserved hypothetical protein	2.9
SMU.1981c	conserved hypothetical protein	25.9
SMU.1988c	putative DNA binding protein	2.0
SMU.2057c	putative cadmium-transporting ATPase; P-type ATPase	4.0
SMU.214c	hypothetical protein	2.2
SMU.219	hypothetical protein	2.0
SMU.52	conserved hypothetical protein	-3.6
SMU.73	conserved hypothetical protein	-2.7
SMU.758c	conserved hypothetical protein	3.3
SMU.769	conserved hypothetical protein	9.5
SMU.78	fructan hydrolase; exo-beta-D-fructosidase; fructanase, FruA	-5.5
SMU.836	hypothetical protein	18.3
Unknown function		
SMU.1003	putative glucose-inhibited division protein	7.1
SMU.1046c	putative GTP pyrophosphokinase	2.4
SMU.1053	conserved hypothetical protein	6.4
SMU.1054	putative glutamine amidotransferase	6.0
SMU.1070c	conserved hypothetical protein	3.4
SMU.1322	putative acetoin dehydrogenase	2.0
SMU.1323	conserved hypothetical protein; possible hydrolase	2.0
SMU.1340	putative surfactin synthetase	-2.0
SMU.1341c	putative gramicidin S synthetase	-2.4
SMU.1400c	conserved hypothetical protein	4.7
SMU.1975c	conserved hypothetical protein; possible membrane protein	2.5
SMU.208c	putative transposon protein; possible DNA segregation ATPase	3.3
SMU.328	putative carbonic anhydrase	2.2
SMU.354	conserved hypothetical protein	6.2
SMU.355	putative CMP-binding factor	6.8
SMU.399	conserved hypothetical protein	2.5
SMU.401c	conserved hypothetical protein	2.5
SMU.498	putative late competence protein	22.4
SMU.508	conserved hypothetical protein	7.2
SMU.641	putative oxidoreductase	2.1
SMU.646	putative phosphatase	9.5
SMU.647	putative methyltransferase	2.7
SMU.66	conserved hypothetical protein	5.0
SMU.72	conserved hypothetical protein	-2.4
SMU.807	putative membrane protein	2.1
SMU.837	putative reductase	14.1
SMU.890	conserved hypothetical protein	2.0
SMU.926	conserved hypothetical protein; possible GTP-pyrophosphokinase	5.4

SI Table S2. *S. mutans* genes showing a minimum \pm 2-fold difference in expression when *S. mutans* $\Delta comX$ cells were exposed to 2 μ M sCSP

Gene ID	Putative or assigned function	Fold
SMU.925	hypothetical protein	2.7
SMU.150	hypothetical protein	5.3
SMU.151	hypothetical protein	4.9
SMU.152	hypothetical protein	5.4
SMU.153	hypothetical protein	5.2
SMU.1902c	hypothetical protein	2.5
SMU.1903c	hypothetical protein	5.0
SMU.1904c	hypothetical protein	5.1
SMU.1905c	putative bacteriocin secretion protein	5.1
SMU.1906c	hypothetical protein	4.8
SMU.1908c	hypothetical protein	4.9
SMU.1909c	hypothetical protein	5.7
SMU.1910c	hypothetical protein	5.6
SMU.1912c	hypothetical protein	4.9
SMU.1913c	putative immunity protein, BLpL-like	5.2
SMU.1914c	hypothetical protein	4.5
SMU.2037	putative trehalose-6-phosphate hydrolase TreA	2.1
SMU.2038	putative PTS system, trehalose-specific IIABC component	2.3
SMU.41	hypothetical protein	-3.3
SMU.423	hypothetical protein	5.8
SMU.424	negative transcriptional regulator, CopY	2.0
SMU.426	copper-transporting ATPase; P-type ATPase	2.5
SMU.427	putative copper chaperone	2.1
SMU.63c	conserved hypothetical protein	2.7
SMU.64	Holliday junction DNA helicase RuvB	2.7
SMU.65	putative protein tyrosine-phosphatase	2.8
SMU.66	conserved hypothetical protein	2.1
SMU.78	fructan hydrolase; exo-beta-D-fructosidase; fructanase, FruA	-2.0
SMU.799c	conserved hypothetical protein	2.6
SMU.877	alpha-galactosidase	-2.2
SMU.878	multiple sugar-binding ABC transporter, sugar-binding protein precursor MsmE	-2.7
SMU.879	multiple sugar-binding ABC transporter, permease protein MsmF	-2.6
SMU.880	multiple sugar-binding ABC transporter, permease protein MsmG	-2.5
SMU.881	sucrose phosphorylase, GtfA	-2.8
SMU.882	multiple sugar-binding ABC transporter, ATP-binding protein, MsmK	-2.4
SMU.883	dextran glucosidase DexB	-2.8
SMU.887	galactose-1-P-uridyl transferase, GalT	-2.2

SI Table S3. Bacterial strains used in this study

Strain	Description*	Reference
<i>S. mutans</i>		
UA159	Wild-type	ATCC
$\Delta comC$	$\Delta smu.1915$; Em ^r	This work
$\Delta comC$ complemented	$\Delta smu.1915(pcomC)$; Em ^r , Spc ^r	This work
$\Delta comE$	$\Delta smu.1917$; Em ^r	This work
$\Delta comDE$	$\Delta smu.1916-smu.1917$; Em ^r	This work
$\Delta comX$	$\Delta smu.1997$; Em ^r	This work
Δ mutacin IV	$\Delta smu.150-smu.151$; Em ^r	This work
$\Delta cipB$	$\Delta smu.1914$; Em ^r	This work
$\Delta cipI$	$\Delta smu.925$; Em ^r	This work
$\Delta 1913$	$\Delta smu.1913$; Em ^r	This work
$\Delta 423$	$\Delta smu.423$; Em ^r	This work
$\Delta 1906$	$\Delta smu.1906$; Em ^r	This work
$\Delta nlmTE$	$\Delta smu.286-smu.287$; Em ^r	Hale <i>et al.</i> , 2005
$\Delta luxS$	$\Delta smu.474$; Em ^r	Sztajer <i>et al.</i> , 2008
UA159(pIB187)	Theta-replicating plasmid with the <i>gusA</i> reporter gene under the control of the <i>P23</i> constitutive promoter	Biswas <i>et al.</i> , 2008
UA159(<i>PcomX-gfp</i>)	<i>PcomX-gfp</i> fusion into pDL277; Spc ^r	Aspiras <i>et al.</i> , 2004
UA159(pDL277)	pDL277; Spc ^r	This work
UA159(<i>Pmsm-1914</i>)	<i>Pmsm-1914</i> into pDL277; Spc ^r	This work
$\Delta cipI(Pmsm-1914)$	<i>Pmsm-1914</i> into pDL277; Em ^r , Spc ^r	This work
UA159(p925)	<i>Smu.925</i> into pDL277; Spc ^r	This work
<i>E. coli</i>		
BL21(pET28a(+))	T7 expression vector, non-expression host; Kan ^r	Novagen
BL213DE3 (pET28a(+))	T7 expression vector, expression host; Kan ^r	Novagen
BL21(His ₆ -fullCipB)	CipB precursor cloned into pET28a(+), non-expression host; Kan ^r	This work
BL21(His ₆ -GGCipB)	Mature form of CipB cloned into pET28a(+), non-expression host; Kan ^r	This work
BL21DE3(His ₆ -fullCipB)	CipB precursor cloned into pET28a(+), expression host; Kan ^r	This work
BL21DE3(His ₆ -GGCipB)	Mature form of CipB cloned into pET28a(+), expression host; Kan ^r	This work
<i>L. lactis</i> I6	Indicator strain, susceptible to CipB	Hale <i>et al.</i> , 2005
<i>S. salivarius</i> 25975	Wild-type	M. Frenette, U. Laval
<i>S. thermophilus</i> LMG18311	Wild-type	S. Moineau, U. Laval

*Em^r, erythromycin resistance; Spc^r, spectinomycin resistance; Kan^r, kanamycin resistance