

SI Fig. S1

A.



B.

















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  $\beta$ -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  $\mu$ M sCSP. The OD<sub>600</sub> 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 sCSPunresponsive. Viability staining using propidium iodide indicates less than 10% of the population is dead in the presence of 2  $\mu$ 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  $\mu$ 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  $\mu$ 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 $\mu$ M sCSP

Gene ID	D Putative or assigned function	
Amino acid b	iosynthesis	
SMU.1073	putative formyl-tetrahydrofolate synthetase	-3.3
SMU.1265	putative phosphoribosyl formimino-5-aminoimidazole carboxamide ribonucleotide isomera	-2.0
SMU.1266	putative glutamine amidotransferase HisH	
SMU.1268	putative imidazoleglycerol-phosphate dehydratase	-2.2
SMU. 1269	putative phosphoserine phosphatase	
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 IAB	-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	SMU.954 putative pyridoxal kinase	
Cell envelope	9	
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	
SMU.2081	hypothetical protein	
SMU.539c	signal peptidase type N	
SMU.610	cell surface antigen SpaP	
SMU.627	conserved hypothetical protein	
SMU.63c	conserved hypothetical protein	
SMU.67	putative acyltransferase	4.0
SMU.883	dextran glucosidase DexB	-5.6
Cellular proc	e sse s	
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	
SMU.1346	putative thioesterase BacT	
SMU.150	hypothetical protein	
SMU.1862	hypothetical protein	
SMU. 1897	putative ABC transporter, ATP-binding protein	
SMU.1898	putative ABC transporter, ATP-binding and permease protein	
SMU. 1900	conserved hypothetical protein	
SMU.1905c	putative bacteriocin secretion protein	10.1
SMU.1906c	hypothetical protein	

SMU. 1916      putative response regulator of the competence regulon, ComE      11.3        SMU. 1937      putative competence protein ComYC      26.6        SMU. 1984      putative competence protein ComYC      26.8        SMU. 1987      putative competence protein ComYC      26.9        SMU. 1987      putative ABC transporter ComYE; probably part of the DNA transport machinery      23.9        SMU. 1987      putative ABC transporter ComYE; probably part of the DNA transport machinery      23.8        SMU.2084      conserved hypothetical protein      5.6        SMU.400      putative scoreted esterase      2.8        SMU.423      hypothetical protein      18.0        SMU.632      putative competence protein      18.0        SMU.6425      putative competence protein      14.1        SMU.626      putative transcriptional regulator      2.4        SMU.632      putative transcriptional regulator      2.4        SMU.632      putative transcriptional regulator      2.4        SMU.632      putative MutE      3.9        SMU.633      putative Nacetylgucosamine-6-phosphate isomerase      3.1        SMU.636      putative MutE      3.2	SMU.1914c	hypothetical protein		
SMU.1917      putative response regulator of the competence protein ComYD      28.6        SMU.1983      putative competence protein ComYC      26.2        SMU.1984      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.402      optative Safe Camsporter as e      2.8        SMU.423      hypothetical protein      14.6        SMU.424      potative scienced esterase      2.8        SMU.425      putative amino acid recemase      3.5        SMU.541      putative competence protein      14.1        SMU.625      putative manganese-type superoxide dismutase, Fe/Mn-SOD      2.2        SMU.632      putative transcriptional regulator      2.4        SMU.635      putative manganese-type superoxide dismutase, Fe/Mn-SOD      2.7        SMU.636      putative competence protein      4.0        Central interme diary metabolism      3.9        SMU.703      conserved hypothetical protein      4.0        Central interme diary metabolism      3.9        <	SMU. 1916	putative histidine kinase of the competence regulon, ComD	10.5	
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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    stative N-acetylglucosamine-6-phosphate isomerase    3.1      DNA metabolism    stative N-acetylglucosamine-6-phosphate isomerase    3.1      DNA metabolism    stative N-acetylglucosamine-6-phosphate isomerase    3.1      SMU.1002    putative Integrase/recombinase; XerC-like    2.2      SMU.1035    putative integrase/recombinase; XerC-like    14.1      SMU.2085    putative onpetence and damage inducible protein    16.4      SMU.2085    recombination protein RecA    6.7      SMU.2086    putative onpetence and damage inducible protein CinA    10.2      SMU.2085    putative integrase/recombinates RuvB    9.0      SMU.505    putative type II restriction endonuclease    9.0      SMU.64    Holliday junction DNA helicase RuvB    8.0      Energy metabolism    stative acetoin dehydrogenase (TPP-dependent), E1 component alpha subunit    -2.2      SMU.122    putative dihydrolipoamide acetyltransferase    -2.6      SMU.123    putative dihydrolipoamide	SMU.632	putative transcriptional regulator	2.4	
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SMU.753    conserved hypothetical protein    4.0      Central intermediary metabolism    SMU.636    putative N-acety/glucosamine-6-phosphate isomerase    3.1      DNA metabolism    SMU.1032    putative DNA topoisomerase I    8.2      SMU.1034c    putative integrase/recombinase; XerC-like    2.2      SMU.1055    putative integrase/recombinase; XerC-like    2.2      SMU.1056    putative integrase/recombinase; XerC-like    6.7      SMU.2086    putative competence and damage inducible protein CinA    10.2      SMU.505    putative adenine-specific DNA methylase    11.8      SMU.505    putative type Il restriction endonuclease    9.0      SMU.64    Holliday junction DNA helicase Ru/B    8.0      SMU.104    glucosyltransferase-I    6.0      SMU.127    putative acetoin dehydrogenase (TPP-dependent), E1 component alpha subunit    -2.2      SMU.128    putative dihydrolipoamide acetyltransferase    -2.6      SMU.129    putative dihydrolipoamide dehydrogenase    -2.7      SMU.129    putative dihydrolipoamide dehydrogenase    -2.7      SMU.129    putative dihydrolipoamide dehydrogenase    2.9      SMU.130    putative dihydroli	SMU 655	putative MutF	3.9	
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DNA metabolismImage: Construction of the second	SMU.636	putative N-acetylolucosamine-6-phosphate isomerase	3.1	
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Energy metabolismComposition between the second and the	SMU 64	Holliday junction DNA helicase RuvB	8.0	
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SMU.79 fructan hydrolase; exo-beta-D-fructosidase; FruB -4.5	SMU.772	alucan-binding protein D with lipase activity: BalB-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 a	nd phospholipid metabolism	
SMU. 1344c	putative malonyl-CoA acyl-carrier-protein transacylase	-2.9
SMU. 1345c	putative peptide synthetase similar to MycA	-2.7
Hypothetica	I 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 e	xtrachromosomal 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 lipoate-protein ligase	-2.4
SMU.645	putative oligopeptidase	10.4
Protein synth	esis	
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, pvrir	nidines, nucleosides, and nucleotides	
SMU.30	putative phosphoribosylformylglycinamidine 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		
SMU.51	putative phosphoribosylaminoimidazole carboxylase, ATPase subunit		
SMU.668c	ribonucleotide reductase, large subunit		
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		
SMU. 1409c	putative transcriptional regulator		
SMU. 1509	9 putative transcriptional regulator		
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 trans	sduction		
SMU. 1957	putative PTS system, mannose-specific IID component	-5.1	
SMU 1958c	nutative 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	
Transcriptio	n	0.0	
SMU.2001	DNA-directed RNA polymerase, alpha subunit	-2.2	
Transport a	nd hinding proteins		
SMU. 1006	putative ABC transporter. ATP-binding protein	2.9	
SMU 1067c	nutative ABC transporter, permease protein	27	
SMU 1068c	putative ABC transporter, ATP-binding protein	3.0	
SMU 1148	nutative transporter ATP-binding protein: bacteriocin immunity protein	24	
SMU 1185	PTS system, mannitol-specific enzyme IIBC component	2.4	
SMU 1194	nutative ABC transporter ATP-binding protein	22	
SMU 1195	conserved hypothetical protein: possible permease	2.0	
SMU 1848	hypothetical protein	2.0	
SMU 1878	nutative PTS system mannose-specific component IIC	-3.0	
SMU 1879	nutative PTS system, mannose-specific component IID	-3.0	
SMU 1899	putative ABC transporter ATP-binding and permease protein (fragment)	5.2	
SMU 1963c	nutative sugar-binding periplasmic protein	4.0	
SMU 1966c	nutative periolasmic sugar-binding protein	7.0	
SMLL 2038	nutative PTS system trehalose-specific IIABC component	5.2	
SMU 242c	nutative amino acid ABC transporter permease protein diutamine transport system	_2 0	
SMU 427	putative comper chaperone	-2.0	
SMU 862	conserved hypothetical protein: putative permease	0.0	
SMI1 962	nutative ARC transporter. ATD binding protoin	2.1	
SIVIU.003	pulative ABC transporter permease component	1.9	
CMI 1 070	putative ABO transporter, permease component	2.0	
SIVIU.0/2	putative FTS system, illuctose-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 fu	nction	
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

Gene ID	Putative or assigned function	Fold
SMU.925	hypothetical protein	2.7
SMU.150	hypothetical protein	
SMU.151	hypothetical protein	
SMU.152	hypothetical protein	
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	
SMU.2037	putative trehalose-6-phosphate hydrolase TreA	
SMU.2038	putative PTS system, trehalose-specific IIABC component	
SMU.41	hypothetical protein	-3.3
SMU.423	hypothetical protein	
SMU.424	negative transcriptional regulator, CopY	
SMU.426	copper-transporting ATPase; P-type ATPase	
SMU.427	putative copper chaperone	
SMU.63c	conserved hypothetical protein	2.7
SMU.64	Holliday junction DNA helicase RuvB	2.7
SMU.65	putative protein tyrosine-phosphatase	
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	
SMU.878	multiple sugar-binding ABC transporter, sugar-binding protein precursor MsmE	
SMU.879	multiple sugar-binding ABC transporter, permease protein MsmF	-2.6
SMU.880	multiple sugar-binding ABC transporter, permease protein MsmG	
SMU.881	sucrose phosphorylase, GtfA	
SMU.882	multiple sugar-binding ABC transporter, ATP-binding protein, MsmK	-2.4
SMU.883	dextran glucosidase DexB	
SMU.887	galactose-1-P-uridyl transferase, GalT	-2.2

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

Strain	Description*	Reference
S. mutans		
UA159	Wild-type	ATCC
$\Delta comC$	$\Delta$ smu.1915; Em <sup>r</sup>	This work
$\Delta comC$ complemented	$\Delta$ smu.1915(pcomC); Em <sup>r</sup> , Spc <sup>r</sup>	This work
$\Delta comE$	$\Delta$ smu.1917; Em <sup>r</sup>	This work
$\Delta comDE$	Δsmu.1916-smu.1917; Em <sup>r</sup>	This work
$\Delta com X$	$\Delta$ smu.1997; Em <sup>r</sup>	This work
∆mutacin IV	$\Delta$ smu.150-smu.151; Em <sup>r</sup>	This work
$\Delta cipB$	$\Delta$ smu.1914; Em <sup>r</sup>	This work
$\Delta cipI$	$\Delta$ smu.925; Em <sup>r</sup>	This work
Δ1913	$\Delta$ smu.1913; Em <sup>r</sup>	This work
Δ423	$\Delta$ smu.423; Em <sup>r</sup>	This work
Δ1906	$\Delta$ smu.1906; Em <sup>r</sup>	This work
$\Delta nlmTE$	$\Delta$ smu.286-smu.287; Em <sup>r</sup>	Hale et al., 2005
$\Delta luxS$	$\Delta$ smu.474; Em <sup>r</sup>	Sztajer et al., 2008
UA159(pIB187)	Theta-replicating plasmid with the	Biswas et al., 2008
	gusA reporter gene under the control	,
	of the <i>P23</i> constitutive promoter	
UA159(PcomX–gfp)	<i>PcomX–gfp</i> fusion into pDL277; Spc <sup>r</sup>	Aspiras et al., 2004
UA159(pDL277)	pDL277; Spc <sup>r</sup>	This work
UA159( <i>Pmsm</i> -1914)	<i>Pmsm</i> -1914 into pDL277; Spc <sup>r</sup>	This work
$\Delta cipI(Pmsm-1914)$	<i>Pmsm</i> -1914 into pDL277; Em <sup>r</sup> , Spc <sup>r</sup>	This work
UA159(p925)	Smu.925 into pDL277; Spc <sup>r</sup>	This work
E. coli		
BL21(pET28a(+))	T7 expression vector, non-expression	Novagen
(}())	host: Kan <sup>r</sup>	
BL213DE3 (pET28a(+))	T7 expression vector expression host	Novagen
	Kan <sup>r</sup>	1.00,000
BL21(Hise-fullCipB)	CipB precursor cloned into	This work
	pET28a(+) non-expression host: Kan <sup>r</sup>	
BL21(Hise-ccCipB)	Mature form of CipB cloned into	This work
	pET28a(+) non-expression host: Kan <sup>r</sup>	
BL21DE3(Hise-fullCinB)	CipB precursor cloped into	This work
	pET28a(+) expression host: Kan <sup>r</sup>	
BL21DE3(Hise-ccCipB)	Mature form of CipB cloned into	This work
	pET28a(+) expression host: Kan <sup>r</sup>	
L. lactis 16	Indicator strain susceptible to CinB	Hale <i>et al</i> 2005
S. salivarius 25975	Wild-type	M Frenette U Laval
S. thermophilus LMG18311	Wild-type	S. Moineau, U. Laval

SI Table S3. Bacterial strains used in this study

\*Em<sup>r</sup>, erythromycin resistance; Spc<sup>r</sup>, spectinomycin resistance; Kan<sup>r</sup>, kanamycin resistance