

**Table S1. Classification of genes identified in LuxS-deficient *S. mutans* planktonic cultures ( $P < 0.01$ )<sup>@</sup>**

Locus	Description and putative function	Fold-difference*	Parametric <i>P</i> value	Status in Sztajer's study
Hypothetic proteins				
SMU.1141c	conserved hypothetical protein	1.64	6.60E-03	
SMU.1151c	conserved hypothetical protein	1.72	4.70E-03	
SMU.1347c	conserved hypothetical protein, possible permease	-3.4	1.40E-05	
SMU.1716c	conserved hypothetical protein	1.79	1.50E-03	
SMU.1780	conserved hypothetical protein	-1.57	5.60E-03	
SMU.1972c	conserved hypothetical protein	1.75	1.60E-03	
SMU.2155	conserved hypothetical protein	-1.8	6.10E-03	
SMU.613	hypothetical protein	-1.68	6.90E-03	v
Chaperone				
SMU.188c	33 kD chaperonin (heat shock protein)	1.72	2.80E-03	
Carbohydrate, energy and central intermediate metabolism				
SMU.1420	putative oxidoreductase, NADPH-quinone reductase	1.56	7.30E-03	
SMU.1664c	putative acetoin utilization protein, acetoin dehydrogenase	-1.51	5.50E-03	
SMU.1687	putative manganese-dependent inorganic pyrophosphatase	1.72	2.40E-03	
SMU.1877	PTS system, mannose-specific component IIB	-3.63	2.00E-07	v
SMU.1878	PTS system, mannose-specific component IIC	-3.1	3.90E-05	v
SMU.1879	PTS system, mannose-specific component IID	-4.77	1.00E-07	
SMU.1960c	PTS system, fructose-specific IIB component, LevE	-1.57	3.80E-03	v
SMU.78	fructan hydrolase exo-beta-D-fructosidase; fructanase, FruA	2.7	4.80E-03	
SMU.870	transcriptional regulator of sugar metabolism, FruR	-3.39	3.90E-03	
SMU.871	fructose-1-phosphate kinase	-4.02	6.10E-03	
SMU.872	fructose-specific enzyme IABC component	-7.67	2.70E-06	v
SMU.985	beta-glucosidase BglA	1.79	7.70E-03	
Nucleic acid metabolism				
SMU.322c	glucose-1-phosphate uridylyltransferase	1.64	9.10E-03	
SMU.1054	putative glutamine amidotransferase	2.05	4.10E-04	v
Amino acid and protein synthesis				
SMU.1950	putative pseudouridylate synthase	1.58	4.70E-03	
SMU.2007	50S ribosomal protein L15	-1.87	3.40E-03	v
SMU.2008	50S ribosomal protein L30	-1.64	5.20E-03	v
SMU.2011	50S ribosomal protein L6 (BL10)	-1.6	2.50E-03	v
SMU.364	glutamine synthetase type 1 glutamate—ammonia ligase	-1.62	1.80E-03	v
Fatty acid and phospholipid metabolism				
SMU.1734c	acetyl-CoA carboxylase alpha subunit	-1.48	4.60E-03	
SMU.1735c	acetyl-CoA carboxylase beta subunit	-1.67	6.00E-04	
SMU.1739c	3-oxoacyl-(acyl-carrier-protein) synthase	-2.03	7.90E-05	

SMU.1740c	3-oxoacyl-acyl-carrier-protein reductase / 3-ketoacyl-acyl carrier protein	-2	2.00E-04	v
SMU.1741c	malonyl-CoA (acyl-carrier-protein) transacylase	-1.94	6.60E-05	v
SMU.1744c	3-oxoacyl-[acyl-carrier-protein] synthase III	-1.88	1.40E-03	
SMU.1745c	putative transcriptional regulator	-1.79	1.10E-03	v
Transcription regulator				
SMU.1361c	putative transcriptional regulator (TetR family)	-3.94	3.10E-03	
Cell envelop related				
SMU.1340	putative surfactin synthetase	-2.05	3.50E-03	v
SMU.610	cell surface antigen SpaP	1.61	4.50E-03	v
SMU.987	cell wall-associated protein precursor WapA	2.04	5.00E-03	v
Cellular process				
SMU.1050	phosphoribosylpyrophosphate synthetase, PRPP synthetase	1.92	8.10E-03	
SMU.1342	putative bacitracin synthetase 1 BacA	-1.62	6.30E-03	
Other				
SMU.1363c	putative transposase	-7.15	7.30E-05	

@, Genes identified in the LuxS-deficient mutant at the level of  $P < 0.01$  are grouped based upon the description and putative functions of the *S. mutans* genome database. \* Defined as levels of expression in the LuxS-deficient mutant relative to those of the wild-type, with “-“ representing down-regulation. \*\*, Genes that were also identified in the LuxS-deficient mutants by the Sztajer group were marked with “v”, with a “d” and a “y” in parentheses representing those that were density-dependent and those that were reverted to the wild-type level with inclusion of synthetic AI-2, respectively.