

Table S2. Classification of genes identified in LuxS-deficient *S. mutans* biofilms ($P < 0.01$)[@]

Locus	Description and putative functions	Fold Change (lx/wt)*	Parametric P-value	Status in Sztajer's study
Hypothetical proteins:				
SMU.09	conserved hypothetical protein	-2.67	1.55E-05	
SMU.12	conserved hypothetical protein	-2.8	3.85E-05	V
SMU.1284c	conserved hypothetical protein	-1.56	0.004691	
SMU.1402c	conserved hypothetical protein	1.77	0.0014117	
SMU.1403c	conserved hypothetical protein	1.77	0.001963	
SMU.1404c	conserved hypothetical protein	1.77	0.0009305	
SMU.1411	conserved hypothetical protein	1.66	0.001254	
SMU.1574c	conserved hypothetical protein	-1.99	5.19E-05	
SMU.2129c	conserved hypothetical protein	-1.89	0.0002728	
SMU.2147c	conserved hypothetical protein	-1.89	0.0071272	V
SMU.475	conserved hypothetical protein	1.79	7.98E-05	V
SMU.528c	conserved hypothetical protein	-1.51	0.000311	
SMU.600c	conserved hypothetical protein	1.75	9.11E-05	
SMU.63c	conserved hypothetical protein	-1.83	0.0016925	
SMU.66	conserved hypothetical protein	1.63	0.0027803	
SMU.673	conserved hypothetical protein	-1.63	0.0014519	
SMU.730	conserved hypothetical protein	-1.71	0.0008219	V (d)
SMU.86	conserved hypothetical protein	1.93	0.0007914	
SMU.955	conserved hypothetical protein	1.72	0.0055615	
SMU.961	conserved hypothetical protein	-2.46	0.0071689	V
SMU.1249c	hypothetical protein	-1.55	0.0015606	
SMU.1250c	hypothetical protein	-1.66	0.003752	
SMU.1360c	hypothetical protein	-1.53	0.0056236	V
SMU.150	hypothetical protein	4.71	0.0037364	
SMU.151	hypothetical protein	4.07	0.0078298	V
SMU.152	hypothetical protein	4.36	0.0038355	
SMU.1575c	hypothetical protein	-3.46	0.0088639	V
SMU.1576c	hypothetical protein	-3.53	0.0076243	
SMU.1587c	hypothetical protein	1.96	1.90E-05	
SMU.1644c	hypothetical protein	-2.06	0.0026085	
SMU.1882c	hypothetical protein	-1.56	0.0035699	V
SMU.1895c	hypothetical protein	-1.73	0.0002307	V
SMU.1896c	hypothetical protein	-1.91	3.69E-05	V (d)
SMU.1903c	hypothetical protein	3.62	0.0082214	
SMU.1904c	hypothetical protein	3.6	0.0096415	
SMU.1908c	hypothetical protein	3.68	0.0057835	
SMU.1910c	hypothetical protein	4.18	0.0066595	
SMU.1956c	hypothetical protein	4.71	0.0003907	

SMU.503c	hypothetical protein	1.68	0.0003793	
SMU.618	hypothetical protein	1.62	0.0007179	V (d)
SMU.637c	hypothetical protein	-2.21	0.0072757	
SMU.68	hypothetical protein	2.08	0.0009764	V (d)
SMU.735	hypothetical protein	-1.57	0.0005981	
SMU.836	hypothetical protein	2.16	0.0020564	
SMU.925	hypothetical protein	2.35	0.0025068	
SMU.984	hypothetical protein	1.68	0.0004756	V (d)
Stress response				
SMU.1527	FoF1 membrane-bound proton-translocating ATPase, epsilon subunit	1.63	0.0010918	
SMU.1528	FoF1 membrane-bound proton-translocating ATPase, beta subunit	1.59	0.0013416	
SMU.1529	FoF1 membrane-bound proton-translocating ATPase, gamma subunit	1.64	0.0010764	
SMU.1531	FoF1 membrane-bound proton-translocating ATPase, delta subunit	1.74	0.0002825	
SMU.1532	FoF1 membrane-bound proton-translocating ATPase, b subunit	1.68	0.0005269	V (d)
Carbohydrate, energy and central metabolism				
SMU.101	putative sorbose PTS system, IIC component	1.77	0.0001027	V
SMU.102	putative PTS system, IID component	1.83	0.0010273	
SMU.103	putative PTS system, IIA component	1.87	0.0007384	V (d, y)
SMU.104	putative alpha-glucosidase glycosyl hydrolase	1.78	0.0036597	
SMU.1077	putative phosphoglucomutase	1.6	0.0001274	V
SMU.127	putative acetoin dehydrogenase (TPP-dependent), E1 component alpha	-2.24	2.30E-06	
SMU.128	putative acetoin dehydrogenase (TPP-dependent), E1 component beta	-2.79	2.90E-06	
SMU.129	putative dihydrolipoamide acetyltransferase	-2.99	3.80E-06	V
SMU.130	putative dihydrolipoamide dehydrogenase	-2.79	4.60E-06	
SMU.131	putative lipoate-protein ligase	-3.33	3.00E-07	
SMU.132	putative hippurate amidohydrolase	-3.01	2.00E-07	V (d, y)
SMU.1452	alpha-acetolactate synthase	-1.56	0.0003851	V
SMU.148	putative alcohol-acetaldehyde dehydrogenase	2.7	2.00E-07	V
SMU.1568	putative maltose/maltodextrin ABC transporter, sugar-binding protein MalX	1.67	1.61E-05	V
SMU.1569	putative maltose/maltodextrin ABC transporter, permease protein MalF	1.63	7.81E-05	
SMU.1570	putative maltose/maltodextrin ABC transporter, MalG permease	1.66	1.34E-05	
SMU.1598	putative PTS system, cellobiose-specific IIA component	2.82	0.0087769	
SMU.1879	putative PTS system, mannose-specific component IID	2.02	0.0001966	
SMU.1957	putative PTS system, mannose-specific IID component	4.56	0.0002682	
SMU.1958c	putative PTS system, mannose-specific IIC component	4.16	0.0002943	
SMU.1960c	putative PTS system, mannose-specific IIB component	3.27	0.0009091	V
SMU.1961c	putative PTS system, sugar-specific enzyme IIA component	4.23	0.0011744	
SMU.671	citrate synthase	-1.93	0.0020076	
SMU.672	isocitrate dehydrogenase	-2.1	0.0018402	
SMU.878	multiple sugar-binding ABC transporter, sugar-binding protein precursor	1.94	0.0003333	V (d)
SMU.879	multiple sugar-binding ABC transporter, permease protein MsmF	1.7	0.0045663	

SMU.880	multiple sugar-binding ABC transporter, permease protein MsmG	1.87	0.0010886	
SMU.881	sucrose phosphorylase, GtfA	2.07	0.0006337	
SMU.882	multiple sugar-binding ABC transporter, ATP-binding protein, MsmK	2.05	0.0005783	
SMU.883	dextran glucosidase DexB	2.06	0.0001632	
SMU.985	putative beta-glucosidase	1.73	0.0006083	
Nucleic acid metabolism and DNA repair				
SMU.08	putative transcription-repair coupling factor	-1.78	0.0037726	V
SMU.356	purine operon repressor	-2.18	0.0006405	V
SMU.44	conserved hypothetical protein, (possible DNA mismatch repair)	-6.67	1.87E-05	V (d, y)
SMU.43	putative site-specific DNA-methyltransferase restriction-modification protein	-4.62	1.94E-05	V
SMU.47	hypothetical protein, (putative HNH-type endonuclease)	-4.41	0.0015788	V
SMU.504	putative site-specific DNA-methyltransferase	-1.7	0.0079468	
SMU.64	Holliday junction DNA helicase RuvB	1.67	0.0068071	
Protein synthesis				
SMU.07	putative peptidyl-tRNA hydrolase	-1.63	0.0092027	
SMU.1510	putative phenylalanyl-tRNA synthetase (beta subunit)	1.84	0.0005145	
SMU.1586	putative threonyl-tRNA synthetase	2.09	0.0003764	V
SMU.1821c	putative glutamyl-tRNA (Gln) amidotransferase subunit C	1.71	0.0013321	
SMU.558	isoleucine-tRNA synthetase	2.11	8.91E-05	V
SMU.84	putative tRNA pseudouridine synthase A	1.68	0.0001738	
Transporters				
SMU.1063	putative ABC transporter, ATP-binding protein, proline/glycine betaine	-1.67	0.00198	
SMU.1119c	putative sugar ABC transporter, permease protein	1.88	0.0030978	
SMU.1121c	putative ABC transporter	1.68	0.0052076	
SMU.1788c	putative bacterocin transport accessory protein, Bta	-1.57	0.0014281	
SMU.602	putative sodium-dependent transporter	1.52	0.0024142	
Transcriptional regulators				
SMU.1027	putative transcription regulator	-2.05	0.0003367	
SMU.105	putative transcriptional regulator repressor of sugar transport	1.66	0.0047994	
SMU.1282	putative transcriptional regulator	-1.96	0.0069287	V
SMU.144c	putative transcriptional regulator	-1.51	0.0002565	
SMU.46	hypothetical protein, (putative LuxR-type of regulator)	-6.57	0.0004281	V
SMU.930c	putative transcriptional regulator	-2.59	0.0003519	
SMU.953c	putative transcriptional regulator/aminotransferase	-1.55	0.0002725	V
Cell envelop related				
SMU.609	putative 40K cell wall protein precursor	1.6	0.0072096	
SMU.1437	putative UDP-N-acetylglucosamine 2-epimerase	-1.56	0.0012153	
SMU.574c	putative membrane protein	4.47	0.0052827	
SMU.732	conserved hypothetical protein possible inner membrane protein	-1.58	0.0005442	

Cellular process				
SMU.13	putative cell-cycle protein	-1.77	0.0022179	V
SMU.65	putative protein tyrosine-phosphatase	1.93	0.0025818	
SMU.299c	putative bacteriocin peptide precursor	-1.62	0.0009831	
SMU.926	conserved hypothetical protein possible GTP-pyrophosphokinase, RelP	1.6	0.0015504	
SMU.423	hypothetical protein, mutacin-like protein	5.23	0.002112	
Unknown and unsigned				
SMU.1337c	putative alpha/beta superfamily hydrolase	2.08	0.0036599	V
SMU.1511c	putative acetyltransferase	1.72	0.0005328	V (d, y)
SMU.2154c	putative peptidase	-1.71	0.0022015	V
SMU.67	putative acyltransferase	1.79	0.0002638	
Fatty acids				
SMU.1336	conserved hypothetical protein PksD, involved in polyketide	-2.69	0.0097701	V
Other				
SMU.149	putative transposase	1.93	0.0048977	V
Signal transduction				
SMU.928	putative histidine kinase, RelS	1.56	0.0051509	

[@], 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. See Table S1 for more information.