

Table S2

Fold change of gene expression of *S. mutans* in dual-species biofilms with *C. albicans* in comparison to gene expression in *S. mutans* biofilm alone at 6 h, 10 h and 24 h of growth.

Name	GeneName	Description	Functional Group	FC 6h	FC 10h	FC 24h
SMU.61	-	putative transcriptional regulator	COM R	1.2	1.6	-4.4
NC_004350	COM S	ComS	COM S	2.9	68.2	6.0
SMU.255	oppA	putative oligopeptide ABC transporter, substrate-binding protein OppA		-1.3	-1.4	3.9
SMU.1997	comX1	putative ComX1, transcriptional regulator of competence-specific genes	MASTER REGULATOR SIGX	2.2	55.8	1.4
SMU.1915	comC	competence stimulating peptide, precursor	BACTERIOCINS AND COMPETENCE REGULATED	1.2	1.8	-2.9
SMU.1916	comD	putative histidine kinase of the competence regulon, ComD		-1.2	3.3	-2.2
SMU.1917	comE	putative response regulator of the competence regulon, ComE; response regulator of sakacin A production		-1.1	3.4	-1.6
SMU.2164	htrA	serine protease HtrA		-1.3	0.3	-2.9
SMU.150	nImA	hypothetical protein	BACTERIOCINS	-1.1	12.1	1.7
SMU.151	nImB	hypothetical protein		-1.1	15.2	1.2
SMU.152	-	hypothetical protein		-1.1	5.4	1.3
SMU.423	-	hypothetical protein		-1.3	14.3	1.3
SMU.299c	-	putative bacteriocin peptide precursor		-1.6	-2.0	-3.0
SMU.925	-	hypothetical protein		-2.4	-1.1	-3.0
SMU.1904c	-	hypothetical protein		-1.1	7.6	1.1
SMU.1905c	-	putative bacteriocin secretion protein		-1.2	8.5	1.7
SMU.1906c	-	hypothetical protein		-2.0	13.3	6.5
SMU.1908c	-	hypothetical protein		-1.2	7.2	1.9
SMU.1909c	-	hypothetical protein		-1.3	5.9	3.6
SMU.1910c	-	hypothetical protein		-1.4	53.0	7.1
SMU.1912c	-	hypothetical protein		-1.2	4.0	1.4
SMU.1913c	-	putative immunity protein, BLpL-like		-1.3	3.0	1.6
SMU.1914c	cipB	hypothetical protein		-2.4	18.0	5.4

SMU.1788c	-	putative bacterocin transport accessory protein, Bta		-2.5	-3.0	-4.8
SMU.1809	scnG	putative bacteriocin operon protein ScnG-like protein		-1.7	-2.8	-7.2
SMU.1810	scnE	putative bacteriocin operon component, ScnE-like protein		-1.5	-2.4	-5.1
SMU.1516	covS/vicK	putative histidine kinase CovS; VicK-like protein	POSSIBLE BACTERIOCINS AND COMPETENCE REGULATORS	1.5	1.2	-3.9
SMU.1517	covR/vicR	putative response regulator CovR; VicR-like protein		1.6	1.1	1.4
SMU.2080	brsR	hypothetical protein		-1.1	-1.1	1.3
SMU.2081	brsM	hypothetical protein		-1.3	-1.2	1.9
SMU.1854	hdrR	hypothetical protein		1.1	1.1	1.7
SMU.1855	hdrM	hypothetical protein		-1.3	-1.2	1.7
SMU.1334	sfp	putative phosphopantetheinyl transferase		1.6	3.7	-1.1
SMU.1335c	-	putative enoyl-(acyl-carrier-protein) reductase	1.7	4.1	-1.5	
SMU.1336	pksD	hypothetical protein	1.6	4.0	-1.1	
SMU.1337c	-	alpha/beta superfamily hydrolase	1.5	4.0	-1.6	
SMU.1338c	-	multidrug ABC transporter permease	1.1	2.0	1.7	
SMU.1339	bacD	putative bacitracin synthetase	2.2	4.3	-1.3	
SMU.1340	bacA2	putative surfactin synthetase	2.6	3.2	1.3	
SMU.1341c	-	putative gramicidin S synthetase	3.4	2.9	-1.1	
SMU.1342	bacA1	putative bacitracin synthetase 1; BacA	3.0	4.0	-1.2	
SMU.1343c	-	putative polyketide synthase	2.3	3.2	1.0	
SMU.1344c	-	putative malonyl-CoA acyl-carrier-protein transacylase	1.3	1.5	1.6	
SMU.1345c	-	putative peptide synthetase MycA	3.1	3.8	-1.2	
SMU.1346	bacT	putative thioesterase BacT	2.2	2.4	1.5	
SMU.1347c	-	permease	1.1	1.7	1.7	
SMU.1348c	-	putative ABC transporter, ATP-binding protein	2.5	4.1	3.3	
SMU.1349	-	hypothetical protein possible transcription regulator of mub gene cluster MubR	1.0	1.0	2.6	
SMU.1361c	-	TetR family transcriptional regulator possible regulator for mub	1.6	1.9	2.2	

SMU.1978	ackA	putative acetate kinase	LATE COMPETENCE	1.5	8.3	1.2
SMU.1979c	-	hypothetical protein		-1.1	6.1	2.3
SMU.1980c	-	hypothetical protein		1.5	18.7	2.3
SMU.1981c	-	hypothetical protein		3.8	110.1	4.0
SMU.1982c		hypothetical protein		1.9	21.1	2.6
SMU.1983	comYD	putative competence protein ComYD		1.0	9.3	2.9
SMU.1984	comYC	putative competence protein ComYC		11.0	230.8	2.0
SMU.1985	comYB	ABC transporter ComYB		2.4	33.0	8.0
SMU.1987	comYA	putative ABC transporter, ATP-binding protein ComYA; late competence gene		5.7	220.8	165.3
SMU.625	comEA	putative competence protein		3.0	44.8	2.5
SMU.626	-	putative competence protein		1.5	21.3	3.2
SMU.498	comF	putative late competence protein		1.2	8.0	1.6
SMU.499	-	putative late competence protein		-1.2	4.5	1.6
SMU.505	-	putative adenine-specific DNA methylase		1.5	19.1	2.4
SMU.506	-	putative type II restriction endonuclease	1.2	7.1	-1.1	
SMU.1001	smf	putative DNA processing Smf protein	1.3	30.8	1.7	
SMU.1002	topA	DNA topoisomerase I	2.1	11.4	-1.6	
SMU.1003	gid	tRNA (uracil-5-)-methyltransferase Gid	1.4	6.7	1.4	
SMU.1055	radC	DNA repair protein RadC	1.2	9.3	-1.1	
SMU.1967	ssb2	single-stranded DNA-binding protein	1.4	8.0	1.4	
SMU.2085	recA	recombinase A	1.3	6.0	-2.2	
SMU.2086	cinA	competence damage-inducible protein A	1.4	11.9	-1.6	
SMU.1728	greA	transcription elongation factor GreA	2.4	1.7	-3.8	
SMU.1354c	-	putative putative transposase	1.1	1.2	3.3	
SMU.64	ruvB	Holliday junction DNA helicase RuvB	1.3	5.8	1.2	
SMU.1536	glgA	glycogen synthase	-1.7	-1.6	50.3	
SMU.1538	glgC	glucose-1-phosphate adenylyltransferase	-2.2	-2.2	66.0	
SMU.1535	phsG	glycogen phosphorylase	-1.9	-1.7	40.6	
SMU.1537	glgD	putative glycogen biosynthesis protein GlgD	-1.6	-1.7	23.5	
SMU.1539	glgB	glycogen branching enzyme	-1.3	-1.3	23.3	
SMU.82	dnaK	molecular chaperone DnaK	-1.8	-2.0	5.0	
SMU.83	dnaJ	heat shock protein DnaJ (HSP-40)	-1.9	-2.0	3.6	

CHAPERONES

SMU.1954	groEL	chaperonin GroEL	CHAPERONES	-2.7	-5.4	-1.8
SMU.1955	groES	co-chaperonin GroES		-2.6	-4.2	-2.6
SMU.881	gtfA	sucrose phosphorylase, GtfA	SUGAR METABOLISM; EPS	-1.8	1.0	9.2
SMU.882	mSmK	multiple sugar-binding ABC transporter, ATP-binding protein, MsmK		-1.5	1.0	6.3
SMU.1004	gtfB	glucosyltransferase-I		-1.1	-5.6	-9.7
SMU.1005	gtfC	glucosyltransferase-Si		-1.3	-4.0	-3.2
SMU.1840	scrK	putative fructokinase		-1.2	-1.9	2.3
SMU.1841	scrA	putative PTS system, sucrose-specific IIABC component		1.2	-1.1	1.6
SMU.1843	scrB	sucrose-6-phosphate hydrolase		1.1	-1.1	2.4
SMU.1844	scrR	sucrose operon repressor		1.2	1.0	2.7
SMU.1396	gbpC	glucan-binding protein C, GbpC		GLUCAN BINDING PROTEINS	-3.2	-8.1
SMU.772	gbpD	putative glucan-binding protein D; BglB-like protein	1.1		3.5	-1.1
SMU.1869	trxA	putative thioredoxin	OXIDATIVE STRESS	-1.6	-2.1	-17.5
SMU.924	tpx	thiol peroxidase		-2.5	-4.2	-13.3
SMU.838	gshR	glutathione reductase		-2.2	1.2	-12.5
SMU.629	sod	putative manganese-type superoxide dismutase, Fe/Mn-SOD		-3.5	-7.1	-6.0
SMU.463	trxB	putative thioredoxin reductase (NADPH)		-1.5	-1.8	-3.6
SMU.764	ahpC	alkyl hydroperoxide reductase		-2.4	-4.8	-2.3
SMU.765	ahpF	oxidase/alkyl hydroperoxidase reductase peroxide-		-2.6	-6.1	-2.8
SMU.540	dpr	peroxide resistance protein Dpr		-1	-2.3	2.1
SMU.1117	naoX	NADH oxidase (H2O-forming)		-1.4	-2.7	-2.5
SMU.645	pepB	putative oligopeptidase		1.1	7.7	-2.0
SMU.644	-	putative competence protein/transcription factor		1.0	7.4	1.7
SMU.1337c	-	alpha/beta superfamily hydrolase		1.5	4.0	-1.6
SMU.104	-	putative alpha-glucosidase; glycosyl hydrolase		1.6	2.8	8.5
SMU.456	mraY	phospho-N-acetylmuramoyl-pentapeptide-transferase		3.0	1.8	-1.9

SMU.1425	clpB	putative Clp proteinase, ATP-binding subunit ClpB	CELL WALL RELATED	-1.2	-1.1	3.2
SMU.548	murD	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase		1.6	-1.1	-4.8
SMU.956	clp	putative Clp-like ATP-dependent protease, ATP-binding subunit		-1.9	-1.7	7.2
SMU.1784c	-	membrane-associated Zn-dependent protease		1.2	-1.6	-4.3
SMU.2164	htrA	serine protease HtrA		-1.3	-3.0	-2.9
SMU.610	spaP	cell surface antigen SpaP		-1.8	-3.2	-2.2
SMU.836	-	hypothetical protein CbpD gene		1.2	12.2	1.9
SMU.837	CUST_2274_PI415924990			1.2	13.9	1.1
SMU.716	murN	putative peptidoglycan branched peptide synthesis protein; alanine adding enzyme; beta-lactam resistance factor MurN		1.3	1.2	1.0
SMU.717	murM	putative peptidoglycan branched peptide synthesis protein MurM		1.0	1.0	2.0
SMU.689	-	hypothetical protein		1.1	-1.2	-2.0
SMU.562	clpE	ATP-dependent protease ClpE		-1.3	-1.8	-1.7
SMU.1425	clpB	putative Clp proteinase, ATP-binding subunit ClpB		Protease	-1.2	-1.1
SMU.1672	clpP	ATP-dependent Clp protease proteolytic subunit	-1.3		-1.5	-2.4
SMU.2029	clpC	class III stress response-related ATP-dependent Clp protease, ATP-binding subunit	1.1		-1.5	2.5
SMU.949	clpX	ATP-dependent protease ATP-binding subunit ClpX	1.9		-1.2	-2.8
SMU.956	clp	putative Clp-like ATP-dependent protease, ATP-binding subunit	-1.9		-1.7	7.2
SMU.1591	ccpA	catabolite control protein A, CcpA	1.8		1.6	4.2