SUPPLEMENTARY DOCUMENT TO "THE *FRUB* GENE OF *STREPTOCOCCUS MUTANS* ENCODES AN ENDO-LEVANASE THAT ENHANCES GROWTH ON LEVAN AND INFLUENCES GLOBAL GENE EXPRESSION"

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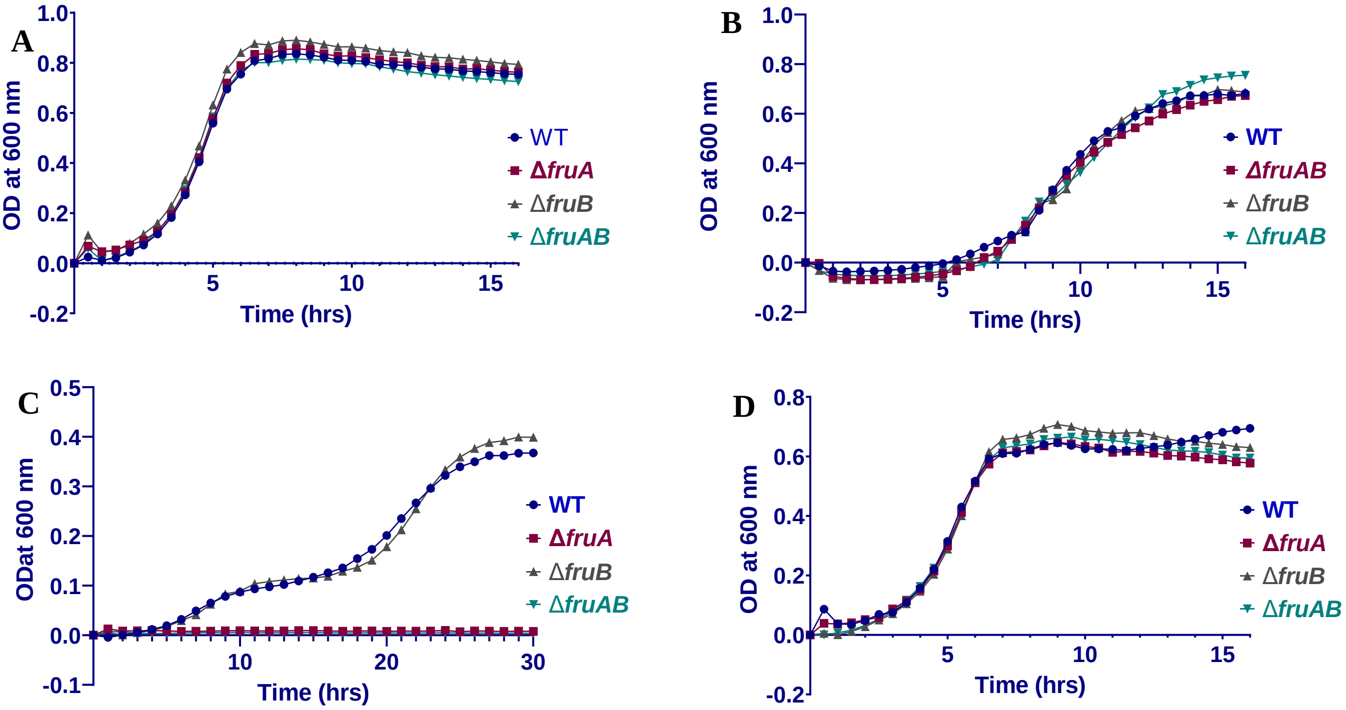
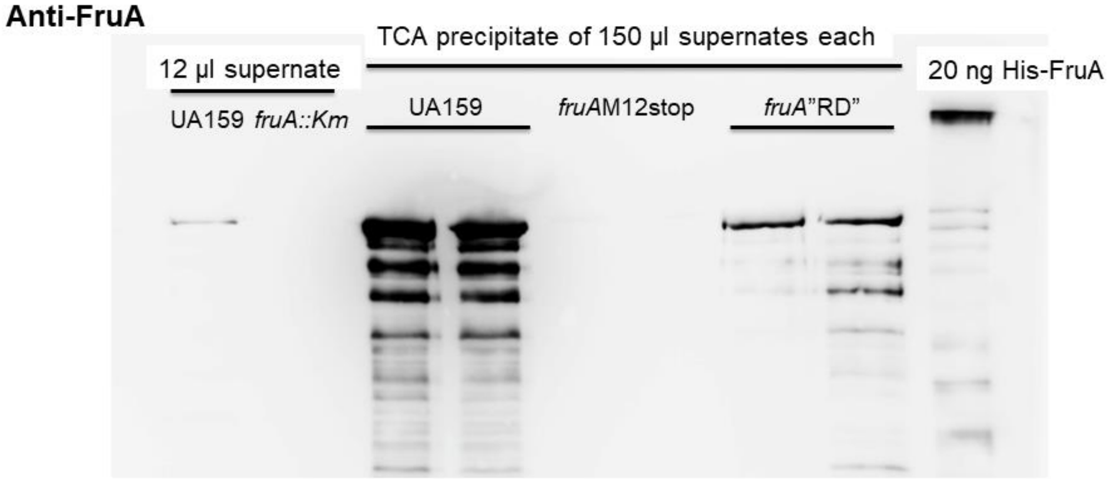


Figure S1. Growth curves of *S. mutans* wild type and *ΔfruA*, *ΔfruB* and *ΔfruAB* strains on different carbohydrate sources. (A) Tryptone vitamin (TV) medium supplemented with 10 mM fructose**, (B)** 10 mM glucose, **(C)** 0.2% inulin and 2 mM fructose, and **(D)** BHI medium.



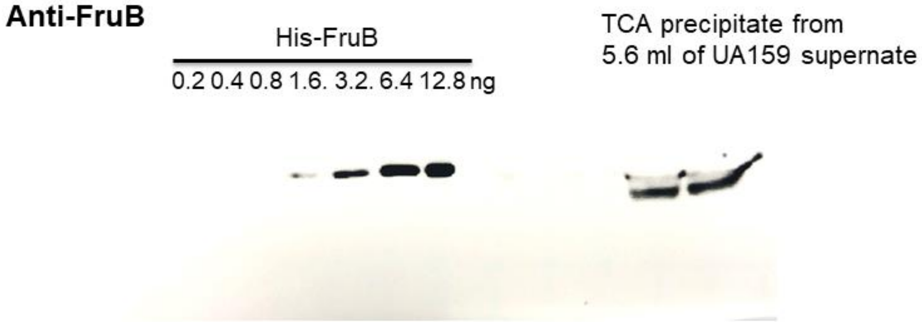


Figure S2. FruA and FruB abundance shown by Western blots. Immunoblotting was carried out using affinity-purified, anti-FruA (top) or anti-FruB (bottom) antiserum against culture supernates of the wild type UA159 and various mutants prepared with TV-inulin. FruA appeared much more abundant than FruB as 12 µl of supernate without TCA treatment (under "Supernate") was sufficient for detection. Estimation based on densitometry of this Western blot put FruA protein copy number at approximately 900/cell, as opposed to 11~26/cell for FruB; a 30~80-fold difference in abundance. *fruA*M12stop is a point mutant of *fruA* that resulted in loss of FruA translation, *fruA*"RD" is a mutant with truncation of the catalytic domain of FruA. Purified recombinant protein His-FruA was loaded as a control and it migrated significantly higher than the wild-type protein in *S. mutans*. The low abundance of the FruA"RD" truncation mutant is caused by insufficient induction of the *fruA* promoter as 0.5% of fructose instead of inulin was used due to loss of growth on inulin, which likely triggered CCR.

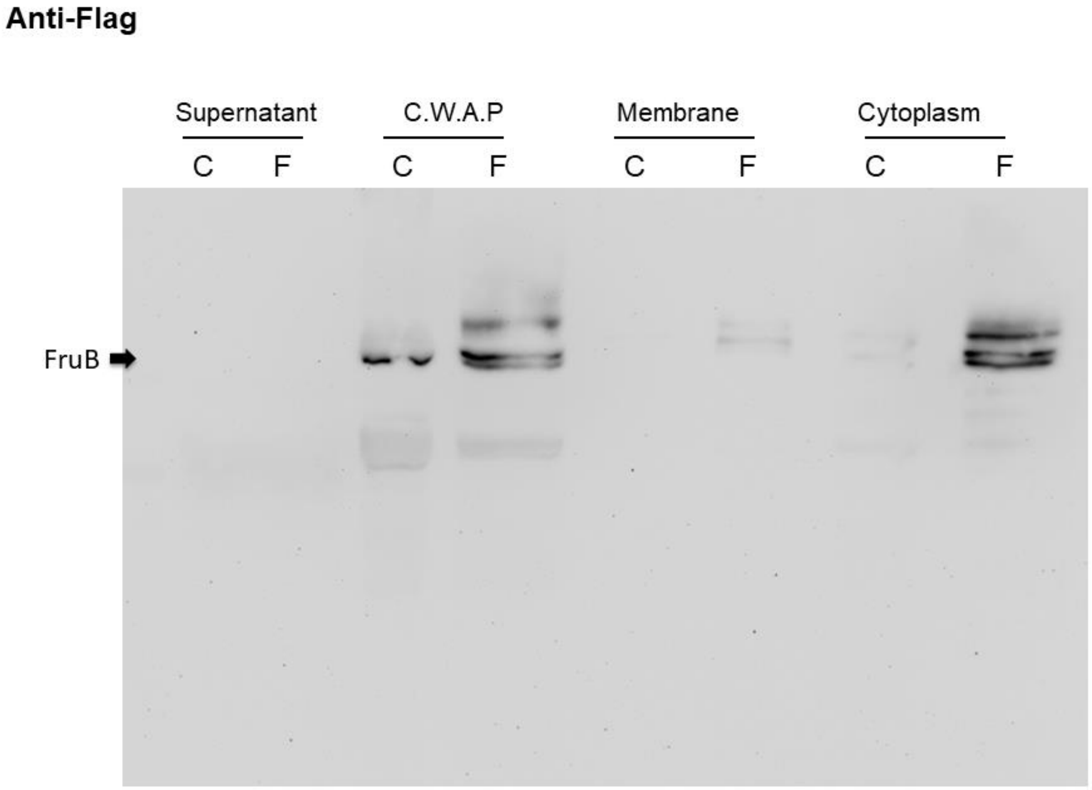


Figure S3. Localization of Flag-tagged recombinant FruB. Western blot with anti-Flag monoclonal antibody (rabbit anti-mouse as secondary). C: UA159; F: FruB-Flag fusion strain; both were cultured in inulin. Signal was detected in cytoplasm and cell wall associated proteins (C.W.A.P).

Table S1. Genes differentially expressed in *fruB* mutant compared to WT UA159

Gene ID	Gene Function	Log2 ∆*fruB*/WT	FDR
SMU_07	peptidyl-tRNA hydrolase	1.92	1.43E-18
SMU_08	transcription-repair coupling factor	1.83	1.19E-15
SMU_09	small RNA binding protein	2.78	1.22E-14
SMU_10	cell-division protein DivIC	2.38	2.38E-07
SMU_11	Streptococcus-specific protein	1.69	0.00016401
SMU_12	conserved hypothetical protein	1.94	8.69E-14
SMU_13	cell-cycle protein, PP-loop superfamily	1.53	1.42E-10
SMU_39	conserved hypothetical protein	-1.07	0.00211954
SMU_43	conserved hypothetical protein (possible site-specific DNA-methyltransferase/restriction modification enzyme)	2.01	7.25E-08
SMU_44	conserved hypothetical protein	2.62	7.23E-13
SMU_45	hypothetical protein	2.39	5.63E-15
SMU_46	hypothetical protein	2.15	0.00011987
SMU_47	hypothetical protein	2.05	9.72E-10
SMU_52	conserved hypothetical protein	1.27	1.20E-07
SMU_53	conserved hypothetical protein	1.15	8.6334E-05
SMU_54	amino acid racemase	1.29	1.1749E-05
SMU_55	hypothetical protein	1.73	1.76E-08
SMU_56	Streptococcus-specific protein	1.95	2.1253E-06
SMU_58	hypothetical protein	1.45	1.44E-08
SMU_63c	conserved hypothetical protein	1.75	1.30E-22
SMU_79	fructan hydrolase; exo-beta-D-fructosidase	-4.84	1.83E-69
SMU_96	DNA-directed RNA polymerase, delta subunit	1.44	4.34E-12
SMU_99	fructose-bisphosphate aldolase	-1.02	0.0012442
SMU_102	PTS system, IID component	1.23	6.1078E-05
SMU_103	PTS system, IIA component	1.61	4.11E-07
SMU_104	glycosyl hydrolase, alpha-glucosidase	1.67	4.33E-11
SMU_120	50S ribosomal protein L28	-1.31	2.04E-09
SMU_125	conserved hypothetical protein	-1.04	0.00015526
SMU_133c	carbohydrate permease; transmembrane efflux protein	-1.12	4.7503E-05
SMU_139	oxalate decarboxylase	-1.01	0.00127343
SMU_140	glutathione reductase	-1.09	0.00040832
SMU_141	conserved hypothetical protein	-1.21	3.01E-05
SMU_152	hypothetical protein	1.59	3.6158E-06
SMU_153	hypothetical protein	2.10	3.57E-09
SMU_162c	conserved hypothetical protein	1.36	2.51E-10
SMU_163c	hypothetical protein	1.37	4.16E-10

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_184	ABC transporter element, iron predicted binding protein	2.11	0.00313516
SMU_185	hypothetical protein	2.12	0.00295715
SMU_191c	phage-related integrase	1.11	0.00115441
SMU_198c	conjugative transposon protein	1.14	6.3065E-05
SMU_199c	hypothetical protein	2.01	2.51E-10
SMU_200c	hypothetical protein	1.41	0.00041505
SMU_201c	conserved hypothetical protein	1.26	5.5067E-05
SMU_202c	conserved hypothetical protein/Streptococcus-specific protein	1.39	4.4461E-05
SMU_204c	hypothetical protein	1.78	2.90E-07
SMU_205c	conserved hypothetical protein	1.13	0.00036885
SMU_206c	hypothetical protein	1.37	0.00013065
SMU_207c	transcriptional regulator	1.21	9.0092E-06
SMU_209c	hypothetical protein	1.31	0.00073285
SMU_210c	hypothetical protein	1.12	0.00133386
SMU_219	hypothetical protein	1.38	2.80E-08
SMU_220c	hypothetical protein	1.26	1.8535E-06
SMU_221c	phage-related integrase, truncated	1.84	2.44E-16
SMU_223c	hypothetical protein	1.08	0.00021367
SMU_236c	transcriptional regulator	-1.31	6.53E-07
SMU_237c	ABC transporter multidrug permease protein	-1.88	1.99E-07
SMU_238c	ABC transporter, ATP-binding protein	-1.91	4.67E-07
SMU_287	ABC transport protein ComB, accessory factor for ComA	1.44	1.37E-14
SMU_299c	bacteriocin peptide precursor	-1.81	2.88E-09
SMU_338	conserved hypothetical protein, Jag protein	1.04	5.2064E-05
SMU_353	thiamine pyrophosphokinase	1.01	0.0001306
SMU_360	glyceraldehyde-3-phosphate dehydrogenase; plasmin receptor	-1.08	0.00138028
SMU_372	hypothetical protein	1.54	4.75E-08
SMU_373	hypothetical protein	1.27	1.161E-06
SMU_374	oxidoreductase/ dehydrogenase	1.41	4.10E-09
SMU_375	hypothetical protein	1.28	1.1396E-05
SMU_376	aminotransferase	1.56	6.46E-13
SMU_378	hypothetical protein	1.60	7.47E-08
SMU_379	hypothetical protein	1.16	4.9022E-06
SMU_390	hypothetical protein	-1.06	0.00499521
SMU_391c	conserved hypothetical protein	-1.15	3.432E-05
SMU_396	glycerol uptake facilitator protein	-1.08	3.0428E-05
SMU_419	conserved hypothetical protein	1.40	2.45E-07
SMU_420	ribosomal protein L7A family	1.55	1.072E-05

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_421	translation initiation factor IF-2	1.17	6.53E-10
SMU_422	ribosome binding factor A	1.64	1.91E-13
SMU_442	conserved hypothetical protein	-1.08	0.0002314
SMU_447	conserved hypothetical protein	1.78	4.13E-14
SMU_473	conserved hypothetical protein	1.31	1.32E-12
SMU_474	S-ribosylhomocysteine lyase (S-ribosylhomocysteinase)	-1.01	0.000163
SMU_496	cysteine synthetase A	-1.21	0.00024987
SMU_502	conserved hypothetical protein	1.30	1.19E-09
SMU_504	site-specific DNA-adenine methyltransferase	2.13	1.02E-21
SMU_505	adenine-specific DNA methylase (DpnIIB)	2.57	8.08E-27
SMU_506	type II restriction endonuclease	2.17	2.40E-20
SMU_526c	transcriptional regulator	1.01	4.9721E-06
SMU_532	anthranilate synthase, component I	1.34	5.65E-07
SMU_540	peroxide resistance protein / iron binding protein	-1.08	8.3407E-05
SMU_549	undecaprenyl-PP-MurNAc-pentapeptide-UDPGlcNAc GlcNAc transferase	1.18	3.46E-10
SMU_550	cell division protein	1.53	1.22E-14
SMU_554	conserved hypothetical protein	1.13	7.11E-11
SMU_555	conserved hypothetical protein	1.31	3.16E-10
SMU_556	conserved hypothetical protein	1.82	3.36E-21
SMU_557	cell division initiation protein	1.45	2.95E-17
SMU_564	conserved hypothetical protein	-1.15	3.3906E-06
SMU_574c	effector of murein hydrolase	-1.10	0.00654374
SMU_583	probable hemolysin A	1.31	1.06E-07
SMU_584	arginine repressor	1.48	1.13E-08
SMU_587	lipase/acylhydrolase with GDSL-like domain	1.25	1.55E-07
SMU_588	conserved hypothetical protein	1.32	3.21E-09
SMU_589	histone-like DNA-binding protein	-1.18	8.131E-05
SMU_595	dihydroorotate dehydrogenase (dihydroorotate oxidase)	-1.16	0.00017926
SMU_600c	conserved hypothetical protein	-1.73	1.009E-05
SMU_602	sodium-dependent transporter	-2.20	4.11E-07
SMU_604	conserved hypothetical protein	1.20	0.0019887
SMU_605	hypothetical protein	2.84	6.06E-19
SMU_606	hypothetical protein	2.32	6.76E-21
SMU_616	hypothetical protein	-1.41	7E-05
SMU_618	hypothetical protein	-1.45	1.3896E-05
SMU_629	superoxide dismutase	-1.41	1.1813E-06
SMU_633	thioesterase	-1.05	3.9336E-06
SMU_642	hypothetical protein	1.37	0.00017309
SMU_643	acetyl esterase/ sugar hydrolase	1.18	2.3089E-06

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_682	hypothetical protein	2.52	9.63E-26
SMU_683	conserved hypothetical protein	2.07	2.42E-26
SMU_684	hypothetical protein	2.62	1.73E-30
SMU_685	hypothetical protein	2.83	4.56E-26
SMU_688	conserved hypothetical protein	1.82	9.47E-14
SMU_694c	ferredoxin	-1.50	1.0202E-05
SMU_706c	conserved hypothetical protein	-1.13	1.4053E-05
SMU_727	mercury resistance operon negative regulator	1.03	3.1457E-05
SMU_730	conserved hypothetical protein	1.80	4.0405E-05
SMU_731	ABC transporter, ATP-binding protein	1.72	7.37E-13
SMU_742	conserved hypothetical protein, Cof family	1.10	0.00030165
SMU_743	hydrolase, haloacid dehalogenase-like family	1.07	0.00031278
SMU_758c	conserved hypothetical protein	-1.22	9.46E-09
SMU_766	transposase	2.09	0.00210798
SMU_767	transposase	1.39	0.00059646
SMU_768c	conserved hypothetical protein	1.01	0.00383396
SMU_790	conserved hypothetical protein	1.91	0.00011667
SMU_804	hypothetical protein	1.72	5.80E-12
SMU_812	hypothetical protein	1.00	0.00261132
SMU_813	hypothetical protein (possible transcriptional regulator)	1.52	4.79E-12
SMU_815	amino acid ABC transporter, periplasmic amino acid-binding protein	1.04	5.1004E-05
SMU_817	amino acid ABC transporter, substrate-binding protein	1.06	2.2076E-05
SMU_838	glutathione reductase	-1.11	1.5968E-05
SMU_856	bifunctional protein: pyrimidine operon regulatory protein and uracil phosphoribosyltransferase	-1.01	0.00014361
SMU_865	30S ribosomal protein S16	-1.23	1.6522E-05
SMU_866	conserved hypothetical protein	-1.26	1.1472E-06
SMU_891	type I restriction-modification system DNA methylase	1.20	5.91E-07
SMU_892	type I restriction-modification system specificity determinant	2.26	3.08E-21
SMU_893	anticodon nuclease	2.39	3.62E-23
SMU_895	conserved hypothetical protein	1.69	2.2471E-05
SMU_896	conserved hypothetical protein	1.83	2.54E-08
SMU_897	type I restriction-modification system,helicase subunits	2.50	1.51E-30
SMU_911c	hypothetical protein	-1.23	4.5245E-05
SMU_913	NADP-specific glutamate dehydrogenase	-1.10	2.2076E-05
SMU_924	thiol peroxidase	-1.71	1.44E-08
SMU_929c	conserved hypothetical protein	-1.54	2.18E-09
SMU_954	pyridoxal kinase	-1.17	4.8042E-06

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_955	conserved hypothetical protein	-1.17	3.06E-07
SMU_986c	conserved hypothetical protein	1.01	0.00442369
SMU_991	conserved hypothetical protein (similar to ribonucleotide reductase alpha subunit)	-1.12	3.368E-05
SMU_1011	citG protein	1.17	8.212E-06
SMU_1012c	transcriptional regulator	1.08	0.00010368
SMU_1013c	Mg2+/citrate complex transporter	1.12	1.5512E-05
SMU_1016	biotin carboxyl carrier protein	1.07	3.368E-05
SMU_1025	transcriptional regulator	1.03	0.00441991
SMU_1026	conserved hypothetical protein	1.32	0.00040701
SMU_1027	transcriptional regulator (TetR/AcrR family)	2.02	4.86E-10
SMU_1028	hydrolase or acyltransferase	1.68	1.33E-10
SMU_1037c	histidine kinase	1.14	2.27E-07
SMU_1038c	response regulator	1.17	1.26E-07
SMU_1045c	NAD(+) kinase (ATP-NAD kinase)	1.27	1.93E-08
SMU_1046c	GTP pyrophosphokinase	1.79	3.33E-12
SMU_1063	amino acid ABC transporter, ATP-binding protein	1.04	6.9147E-06
SMU_1069c	hypothetical protein	1.19	4.576E-05
SMU_1070c	conserved hypothetical protein	1.08	0.0012031
SMU_1080c	conserved hypothetical protein	1.38	2.85E-09
SMU_1081c	conserved hypothetical protein	1.15	3.7164E-06
SMU_1107c	conserved hypothetical protein	1.27	2.67E-09
SMU_1116c	hypothetical protein	1.60	2.16E-11
SMU_1117	H2O-forming NADH Oxidase	1.09	1.0648E-05
SMU_1125c	conserved hypothetical protein	1.04	0.00142196
SMU_1126	pantothenate kinase	1.15	5.8729E-05
SMU_1127	30S ribosomal protein S20	-1.07	8.5666E-06
SMU_1129	two-component response regulator	1.11	2.5958E-05
SMU_112c	transcriptional regulator, RpiR family	1.09	1.3456E-05
SMU_1133	phosphate uptake regulatory protein	1.66	2.16E-15
SMU_1134c	phosphate ABC transporter, ATP-binding protein	1.36	4.33E-11
SMU_1154c	conserved hypothetical protein	1.35	3.42E-11
SMU_1156c	hypothetical protein	1.70	9.64E-13
SMU_1157c	conserved hypothetical protein	2.13	1.57E-19
SMU_1158c	conserved hypothetical protein	1.86	5.25E-20
SMU_1159c	hypothetical protein	2.03	9.49E-12
SMU_1160c	hypothetical protein	2.30	1.41E-25
SMU_1161c	conserved hypothetical protein	1.83	3.10E-15
SMU_1175	sodium:alanine (or glycine) symporter	-1.95	4.18E-07
SMU_1193	transcriptional regulator, GntR family	1.44	5.56E-08

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_1194	ABC transporter, ATP-binding protein	1.23	3.64E-09
SMU_1205c	hypothetical protein	1.49	4.92E-11
SMU_1206c	conserved hypothetical protein	1.62	2.51E-11
SMU_1207	cell filamentation / mobilization protein	1.25	5.00E-10
SMU_1208c	hypothetical protein	1.48	2.95E-13
SMU_1209c	hypothetical protein	1.48	6.23E-12
SMU_1211	conserved hypothetical protein	-1.06	0.00025629
SMU_1249c	hypothetical protein	1.48	4.33E-11
SMU_1250c	hypothetical protein	2.00	1.15E-11
SMU_1254	phosphatase	-1.08	8.6312E-05
SMU_1296	glutathione S-transferase	-1.33	1.761E-06
SMU_1298	50S ribosomal protein L31	-1.41	4.8042E-06
SMU_1322	acetoin reductase	-1.06	1.5699E-05
SMU_1323	conserved hypothetical protein (possible hydrolase)	-1.08	0.00032294
SMU_1330c	transposase, IS1167, fragment	-1.03	0.0046045
SMU_1334	phosphopantetheinyl transferase	1.33	3.5267E-05
SMU_1335c	enoyl-acyl carrier protein(ACP) reductase; dioxygenase related to 2-nitropropane dioxygenase	1.77	1.95E-12
SMU_1337c	alpha/beta superfamily hydrolases	1.32	0.00041505
SMU_1339	bacitracin synthetase; surfactin synthetase	3.20	3.87E-46
SMU_1340	bacitracin synthetase 1/ tyrocidin synthetase III	3.71	1.51E-52
SMU_1341c	gramicidin S synthase/mycosubtilin synthetase chain mycB	3.50	1.05E-45
SMU_1342	bacitracin synthetase	3.48	1.89E-47
SMU_1343c	polyketide synthase	3.53	1.83E-69
SMU_1344c	malonyl CoA-acyl carrier protein transacylase	2.93	2.81E-43
SMU_1345c	peptide synthetase similar to mycA	3.42	4.19E-62
SMU_1346	thioesterase II-like protein	2.75	4.69E-36
SMU_1347c	Permease-ABC-type antimicrobial peptide transport system, Permease component	2.38	2.90E-30
SMU_1348c	ABC transporter ATP-binding Protein	2.02	1.69E-13
SMU_1351	transposase fragment	1.59	2.87E-11
SMU_1354c	transposase	1.19	7.9709E-05
SMU_1355c	transposase	1.19	0.00122165
SMU_1356c	transposase	1.55	1.6997E-06
SMU_1360c	hypothetical protein	1.97	1.01E-12
SMU_1361c	transcriptional regulator	2.19	2.87E-19
SMU_1363c	transposase fragment (IS605/IS200-like)	1.23	5.12E-07
SMU_1365c	Permease-FtsX-like permease	2.34	4.27E-28
SMU_1366c	ABC transporter ATP-binding Protein	1.94	1.14E-13

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_1379	hypothetical protein-HTH XRE domain	3.79	0.00021888
SMU_1392c	conserved hypothetical protein; possible acetyltransferase	1.12	1.3006E-05
SMU_1397c	possible transcriptional repressor	-1.35	4.1095E-06
SMU_1399	hypothetical protein	-2.14	0.00910997
SMU_1402c	conserved hypothetical protein	1.04	9.4741E-06
SMU_1403c	conserved hypothetical protein	1.05	1.5631E-06
SMU_1404c	conserved hypothetical protein	1.20	2.10E-07
SMU_1405c	conserved hypothetical protein	2.06	7.70E-23
SMU_1442c	conserved hypothetical protein	1.43	1.19E-10
SMU_1443c	tributyrin esterase	1.03	9.51E-08
SMU_1479	conserved hypothetical protein	-1.24	2.8019E-06
SMU_1485c	conserved hypothetical protein (possible endonuclease)	1.07	4.46E-07
SMU_1502c	conserved hypothetical protein	-1.31	1.21E-07
SMU_1508c	coenzyme PQQ synthesis protein /possible oxidoreductase	1.04	3.8839E-06
SMU_1509	transcriptional regulator	1.26	9.11E-08
SMU_1513	chromosome segregation SMC protein	1.51	6.75E-17
SMU_1560	conserved hypothetical protein	-1.09	0.00010095
SMU_1574c	conserved hypothetical protein	1.82	3.67E-11
SMU_1575c	hypothetical protein	1.62	0.00035979
SMU_1576c	hypothetical protein	1.92	1.1813E-06
SMU_1577c	conserved hypothetical protein	1.51	6.84E-09
SMU_1602	NAD(P)H-flavin oxidoreductase	-1.33	1.1491E-05
SMU_1603	lactoylglutathione lyase	-1.51	9.42E-07
SMU_1604c	conserved hypothetical protein	1.14	0.00049711
SMU_1609c	preprotein translocase, SecG subunit	-1.01	3.6357E-06
SMU_1628	conserved hypothetical protein	-1.32	1.3456E-05
SMU_1642c	conserved hypothetical protein	1.15	2.97E-07
SMU_1643c	conserved hypothetical protein	1.17	0.00096135
SMU_1644c	conserved hypothetical protein	1.12	0.00330123
SMU_1648c	hypothetical protein	-1.12	1.8675E-05
SMU_1649	exodeoxyribonuclease III/ Smx nuclease	-1.11	0.00037979
SMU_1650	endonuclease III (DNA repair)	-1.16	0.0001169
SMU_1657c	nitrogen regulatory protein PII	-1.54	3.0894E-06
SMU_1700c	LrgB-like protein; possible murein hydrolase regulator	-1.68	4.38E-07
SMU_1701c	conserved hypothetical protein	-1.76	1.66E-07
SMU_1711	ribosomal large subunit pseudouridine synthase B	1.13	2.0246E-06
SMU_1712c	segregation and condensation protein B	1.20	2.7075E-05
SMU_1713c	segregation and condensation protein A	1.05	0.00013065

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_1728	transcription elongation factor GreA	1.89	1.56E-17
SMU_1729c	aminodeoxychorismate lyase-like protein (fragment)	1.85	7.70E-23
SMU_1730c	arylalkylamine n-acetyltransferase	1.36	4.66E-11
SMU_1752c	hypothetical protein	-1.13	1.7884E-05
SMU_1758c	conserved hypothetical protein	1.13	1.43E-07
SMU_1760c	conserved hypothetical protein	1.89	1.30E-16
SMU_1761c	conserved hypothetical protein	2.35	7.78E-22
SMU_1762c	conserved hypothetical protein	2.32	3.78E-20
SMU_1763c	conserved hypothetical protein	1.88	4.89E-14
SMU_1764c	conserved hypothetical protein	1.81	2.75E-14
SMU_1771c	hypothetical protein	1.15	0.0026122
SMU_1772c	hypothetical protein	2.05	1.68E-11
SMU_1773c	conserved hypothetical protein	1.54	4.10E-09
SMU_1775c	hypothetical protein	1.66	1.50E-08
SMU_1780	RecA regulator RecX	1.67	1.10E-11
SMU_1827	biotin biosynthesis protein	-1.22	0.00555715
SMU_1828	universal stress protein family	-1.07	1.2645E-05
SMU_1869	thioredoxin	-1.06	4.01E-08
SMU_1889c	hypothetical protein (possible relation to bacteriocin BlpU)	-1.26	0.00011409
SMU_1897	ABC transporter, ATP-binding protein; similar to BlpA	-1.01	0.00035319
SMU_1900	ABC transporter	1.16	0.00694273
SMU_1903c	hypothetical protein	2.70	8.78E-19
SMU_1904c	hypothetical protein	2.77	1.00E-29
SMU_1905c	hypothetical protein	2.78	4.15E-28
SMU_1906c	bacteriocin-related protein	2.01	7.75E-20
SMU_1908c	hypothetical protein	2.23	6.06E-19
SMU_1909c	hypothetical protein	2.73	6.89E-28
SMU_1910c	hypothetical protein	3.19	1.33E-45
SMU_1912c	hypothetical protein	3.07	1.83E-50
SMU_1913c	hypothetical protein; immunity protein, BLpL-like	2.55	1.31E-24
SMU_1922	chromosome replication initiation and membrane attachment protein	1.44	2.80E-08
SMU_1923c	conserved hypothetical protein	1.07	1.4324E-05
SMU_1927	PsaA protein/ ABC transporter, ATP-binding protein	1.74	5.66E-13
SMU_1928	protein secretion ABC transport permease	1.79	1.00E-15
SMU_1941	ABC transporter solute-binding protein	1.26	3.46E-09
SMU_1969c	probable transcriptional regulator	1.29	1.42E-07
SMU_2002	30S ribosomal protein S11	1.08	4.8663E-05
SMU_2003	30S ribosomal protein S13, N-terminal fragment	1.06	0.00019621

Gene ID	Gene Function	Log2 △*fruB*/WT	FDR
SMU_2059c	conserved hypothetical protein; possible membrane protein	-1.38	0.00010017
SMU_2061	hypothetical protein	1.21	6.18E-07
SMU_2085	recombinase A	1.26	2.09E-13
SMU_2086	competence damage-inducible protein A	1.44	1.55E-15
SMU_2087	3-methyladenine DNA glycosylase I	1.34	4.87E-08
SMU_2088	Holliday junction DNA helicase	1.18	3.65E-07
SMU_2096c	conserved hypothetical protein	1.21	0.00124779
SMU_2113c	conserved hypothetical protein	1.62	6.27E-11
SMU_2114c	probable transcriptional regulator, MerR family	1.08	0.00017515
SMU_2135c	30S Ribosomal protein S4	-1.09	0.00070484
SMU_2137c	conserved hypothetical protein	1.42	8.89E-08
SMU_2138	replicative DNA helicase	1.16	2.86E-09
SMU_2139c	50S ribosomal protein L9	2.10	2.40E-20
SMU_2147c	conserved hypothetical protein	1.39	4.98E-13
SMU_2150c	ABC transporter, ATP-binding protein	1.09	6.4044E-06
SMU_2152c	conserved hypothetical protein	1.33	2.87E-11
SMU_2153c	peptidase, M16 family	1.91	6.02E-18
SMU_2154c	peptidase, M16 family	1.03	3.3352E-06
SMU_2155	conserved hypothetical protein	1.02	3.0316E-06
SMU_2156	recombination protein F (DNA replication and repair ATPase)	1.16	6.31E-08
SMU_2164	serine protease	1.62	9.64E-15
SMU_2165	chromosome segregation protein, ParB-like nuclease domain	1.74	4.13E-14