Text S1 Workflow of the mapping and read counting used on Galaxy server

Step 1: FASTQ Groomer

Input FASTQ quality scores type

Sanger & Illumina 1.8+

Use default job resource parameters

Step 2: FASTQ Quality Trimmer

Keep reads with zero length

False

Trim ends

5' and 3'

Window size

5

Step Size

1

Maximum number of bases to exclude from the window during aggregation

0

Aggregate action for window

min score

Trim until aggregate score is

>=

Quality Score

30.0

Step 3: Cutadapt

5' (Front) Adapters

Enter custom 5' adapter sequence

GATCGGAAGAGCACACGTCTGAACTCCAGTCAC

Maximum error rate

0.1

Match times

1

Minimum overlap length

3

Match Read Wildcards

False

Do Not Match Adapter Wildcards

False

Output filtering options

Default (no filtering)

Additional output options

Default

Additional modifications to reads

No Read Modifications

Step 4: FastQC:Read QC

Title for the output file - to remind you what the job was for

FastQC

Step 5: Map with Bowtie for Illumina

Will you select a reference genome from your history or use a built-in index?

Use a built-in index

Select a reference genome

NC_004350.2

Is this library mate-paired?

Single-end

FASTQ file

Output dataset 'output' from step 3

Bowtie settings to use

Full parameter list

Skip the first n reads (-s)

0

Only align the first n reads (-u)

-1

Trim n bases from high-quality (left) end of each read before alignment (-5)

0

Trim n bases from low-quality (right) end of each read before alignment (-3)

0

Maximum number of mismatches permitted in the seed (-n)

2

Maximum permitted total of quality values at mismatched read positions (-e)

70

Seed length (-l)

28

Whether or not to round to the nearest 10 and saturating at 30 (--nomaqround)

Round to nearest 10

Number of mismatches for SOAP-like alignment policy (-v)

-1

Whether or not to try as hard as possible to find valid alignments when they exist (-y)

Do not try hard

Report up to n valid alignments per read (-k)

1

Whether or not to report all valid alignments per read (-a)

Do not report all valid alignments

Suppress all alignments for a read if more than n reportable alignments exist (-m)

-1

Write all reads with a number of valid alignments exceeding the limit set with the -m option to a file (--ma

False

Write all reads that could not be aligned to a file (--un)

False

Whether or not to make Bowtie guarantee that reported singleton alignments are 'best' in terms of stratu

Do not use best

Maximum number of backtracks permitted when aligning a read (--maxbts)

125

Override the offrate of the index to n (-o)

-1

Seed for pseudo-random number generator (--seed)

-1

Suppress the header in the output SAM file

False

Job Resource Parameters

Use default job resource parameters

Step 6: sort

BAM File

Output dataset 'output' from step 5

Sort by

Chromosomal coordinates

Step 7: htseq-count

Aligned SAM/BAM File

Output dataset 'output1' from step 6

GFF File

select at runtime

Mode

Union

Stranded

Reverse

Minimum alignment quality

10

Feature type

gene

ID Attribute

locus_tag

Additional BAM Output

False

Step 8: htseq-count

Aligned SAM/BAM File

Output dataset 'output1' from step 6

GFF File

select at runtime

Mode

Union

Stranded

Yes

Minimum alignment quality

10

Feature type

gene

ID Attribute

locus_tag

Additional BAM Output

False

Table S1 List of genes differentially expressed (fold of change > 1.5) in MMZ1009 when growing in TY supplemented with glucose (Glc), sucrose (Scr) or fructose (Fru).

Gene ID	Log_2 (Scr/Glc)	Log_2 (Fru/Glc)	FDR	Gene description
SMU.29	-1.04	-0.81	6.11E-04	putative SAICAR synthase
SMU.31	-1.00	-0.72	7.76E-04	hypothetical protein
SMU.33	-0.91	-0.82	3.83E-04	hypothetical protein
SMU.36	-0.86	-0.86	4.87E-04	hypothetical protein
SMU.84	0.34	1.31	7.67E-06	putative tRNA pseudouridine synthase A, TruA
SMU.85	0.30	1.26	3.20E-05	putative phosphomethylpyrimidine kinase, ThiD
SMU.86	0.21	1.32	2.70E-04	hypothetical membrane protein
SMU.87	0.26	1.22	5.24E-05	hypothetical protein
SMU.100	0.73	1.88	8.31E-04	PTS system, nigerose-specific enzyme IIB, NigB
SMU.102	0.92	1.73	3.18E-06	PTS system, nigerose-specific enzyme IID, NigD
SMU.104	0.76	1.60	7.26E-06	putative alpha-glucosidase, NigE
SMU.105	0.29	0.89	2.94E-04	transcriptional repressor NigR
SMU.124	0.04	0.82	2.99E-04	putative transcriptional regulator (MarR family)
SMU.125	0.21	1.10	1.48E-05	hypothetical protein
SMU.133c	0.11	0.75	2.11E-04	putative MDR permease
SMU.145	-0.06	0.68	3.01E-04	hypothetical protein
SMU.148	-1.94	-2.60	4.21E-06	putative alcohol-acetaldehyde dehydrogenase, AdhE
SMU.149	-1.17	-1.92	7.92E-04	putative transposase
SMU.179	-1.27	-1.52	1.43E-05	hypothetical protein
SMU.180	-1.62	-1.80	4.36E-07	putative oxidoreductase, IlvC
SMU.237c	0.25	0.91	2.33E-04	putative integral membrane protein
SMU.252	-0.94	-0.61	1.75E-04	hypothetical protein
SMU.260	0.11	0.98	1.89E-04	hypothetical protein
SMU.299c	-0.02	-0.91	2.91E-04	putative bacteriocin peptide precursor
SMU.344	0.11	0.80	1.27E-04	hypothetical protein
SMU.356	-0.34	-0.81	1.58E-04	purine operon repressor

SMU.367	-0.03	-0.96	1.20E-04	hypothetical protein
SMU.396	0.75	0.78	6.07E-04	putative glycerol uptake facilitator protein, GlpF
SMU.402	-2.06	-2.89	1.55E-06	pyruvate formate-lyase, Pfl
SMU.493	-0.23	-1.44	1.88E-04	formate acetyltransferase (pyruvate formate-lyase 2)
SMU.495	-0.24	-1.24	2.33E-04	glycerol dehydrogenase, GldA
SMU.498	1.79	-0.35	9.31E-04	putative late competence protein, ComF
SMU.500	-0.62	-1.23	1.13E-06	putative ribosome-associated protein
SMU.510c	0.57	1.30	6.40E-05	hypothetical protein
SMU.542	-0.45	-0.65	3.83E-04	putative glucose kinase, Glk
SMU.564	-0.39	-1.03	4.87E-04	hypothetical protein
SMU.576	-0.85	-0.68	1.78E-04	response regulator LytT
SMU.577	-0.57	-0.55	7.28E-04	histidine kinase LytS
SMU.600c	0.92	1.03	1.12E-04	hypothetical protein
SMU.602	1.14	0.68	1.58E-04	putative sodium-dependent transporter
SMU.609	0.06	1.18	8.68E-05	putative 40K cell wall protein precursor
SMU.610	0.25	0.93	5.13E-04	cell surface antigen, SpaP
SMU.625	2.33	0.95	1.78E-04	putative competence protein, ComEA
SMU.626	2.53	0.46	3.90E-04	putative competence protein, ComEC
SMU.632	0.09	0.96	3.15E-05	MarR-type transcriptional regulator
SMU.633	0.15	1.92	1.27E-07	putative thioesterase
SMU.676	0.33	0.74	3.21E-04	NADP-dependent glyceraldehyde-3-phosphate dehydrogenas
SMU.768c	0.72	-0.03	4.60E-04	hypothetical protein
SMU.848	0.08	0.72	6.62E-05	hypothetical protein
SMU.865	-0.18	-0.76	6.52E-04	30S ribosomal protein S16
SMU.870	1.93	1.89	2.96E-08	transcription regulator for fructose metabolism, FruR
SMU.871	2.02	1.97	6.93E-09	fructose-1-phosphate kinase, FruK
SMU.872	1.90	1.92	5.15E-08	PTS system, fructose-specific enzyme IIABC, FruI
SMU.877	-1.17	-1.64	2.67E-07	alpha-galactosidase, AgaL
SMU.878	-1.22	-1.77	1.37E-06	multiple sugar-binding ABC transporter, MsmE
SMU.879	-1.27	-1.90	3.71E-06	multiple sugar-binding ABC transporter, MsmF

SMU.880	-1.30	-1.84	9.72E-06	multiple sugar-binding ABC transporter, MsmG
SMU.881	-1.29	-1.68	3.11E-07	sucrose phosphorylase, GtfA
SMU.882	-1.15	-1.60	1.43E-05	multiple sugar-binding ABC transporter, MsmK
SMU.883	-1.10	-1.34	6.13E-07	dextran glucosidase, DexB
SMU.886	-0.25	0.78	2.34E-04	galactokinase, GalK
SMU.913	0.97	1.38	3.20E-05	putative NADP-specific glutamate dehydrogenase
SMU.921	0.07	1.05	7.92E-04	Transcriptional regulator MarR-type, RcrR
SMU.922	0.16	0.67	6.23E-04	ABC transporter, RcrP
SMU.923	0.10	0.66	4.33E-04	ABC transporter, RcrQ
SMU.925	-0.07	1.03	5.13E-04	hypothetical protein
SMU.926	-0.06	0.81	1.96E-05	(p)ppGpp synthase, RelP
SMU.927	-0.05	0.78	1.91E-05	response regulator, RelR
SMU.928	-0.06	0.65	5.15E-04	histidine kinase, RelS
SMU.935	0.58	-2.30	6.13E-04	putative amino acid ABC transporter
SMU.940c	-0.55	-3.33	1.65E-08	putative hemolysin III
SMU.941c	-0.45	-3.36	6.91E-08	hypothetical protein
SMU.954	0.14	1.73	2.37E-05	putative pyridoxal kinase
SMU.955	0.34	1.50	7.92E-04	hypothetical membrane protein
SMU.992	-0.18	-0.73	7.36E-04	hypothetical protein
SMU.997	-0.07	1.18	2.26E-04	putative inorganic ion ABC transporter
SMU.998	-0.07	0.95	1.74E-04	putative ABC transporter
SMU.1022	-0.84	-0.37	4.05E-04	hypothetical protein, CitG2
SMU.1023	-0.71	-0.35	2.71E-04	pyruvate carboxylase, PycB
SMU.1048	0.03	0.77	7.19E-04	conserved hypothetical protein
SMU.1077	-1.10	-1.30	8.26E-06	phosphoglucomutase, Pgm
SMU.1078c	0.27	0.84	1.78E-04	multidrug ABC transporter, ATP-binding and permease protein
SMU.1083c	0.21	0.61	6.46E-04	conserved hypothetical protein
SMU.1088	-0.76	-0.56	6.05E-05	putative thiamine biosynthesis lipoprotein, ApbE
SMU.1089	-0.65	-0.23	2.48E-04	conserved hypothetical protein
SMU.1090	-0.76	-0.65	1.43E-04	conserved hypothetical protein

SMU.1091	-0.18	-0.83	1.48E-04	possible cell wall protein, WapE
SMU.1095	0.13	0.59	1.20E-04	putative choline ABC transporter
SMU.1096	0.13	0.64	2.55E-04	putative ABC transporter
SMU.1175	1.68	2.35	7.67E-06	putative sodium/amino acid (alanine) symporter
SMU.1243	0.08	0.75	9.62E-04	putative low temperature requirement protein
SMU.1326	0.14	0.58	6.91E-04	putative peptide chain release factor (RF-2)
SMU.1339	0.05	-1.48	5.19E-04	bacitracin synthetase, BacD
SMU.1340	0.06	-1.64	4.13E-04	putative surfactin synthetase, BacA2
SMU.1341c	0.03	-1.49	1.58E-04	putative gramicidin S synthetase
SMU.1342	-0.01	-1.55	2.18E-04	putative bacitracin synthetase 1; BacA1
SMU.1343c	0.04	-1.43	3.97E-05	putative polyketide synthase
SMU.1347c	-0.05	-0.94	8.79E-04	possible permease
SMU.1348c	-0.04	-0.87	2.61E-05	putative ABC transporter
SMU.1365c	-0.04	-0.94	8.48E-04	possible permease
SMU.1366c	0.00	-0.82	2.09E-05	putative ABC transporter
SMU.1389	-0.51	-0.70	6.69E-05	Phosphoenolpyruvate carboxykinase, PckA
SMU.1398	-0.65	-1.13	1.20E-04	transcriptional regulator, IrvR
SMU.1410	-1.53	-2.49	2.11E-04	putative reductase
SMU.1411	-1.55	-2.36	1.84E-05	hypothetical protein
SMU.1419	-0.18	0.64	1.15E-04	putative transcriptional regulator
SMU.1535	-0.97	-1.15	1.91E-06	glycogen phosphorylase, PhsG
SMU.1536	-1.09	-1.45	6.88E-07	bacterial glycogen synthase, GlgA
SMU.1537	-1.20	-1.48	9.79E-06	putative glycogen biosynthesis protein, GlgD
SMU.1538	-1.04	-1.42	3.06E-06	glucose-1-phosphate adenylyltransferase, GlgC
SMU.1539	-0.92	-1.20	1.30E-05	1,4-alpha-glucan branching enzyme, GlgB
SMU.1545c	0.08	0.92	2.00E-05	conserved hypothetical protein
SMU.1550c	0.21	1.01	3.21E-04	hypothetical membrane protein
SMU.1551c	0.22	1.00	5.06E-05	putative ABC transporter
SMU.1552c	0.23	1.10	2.33E-04	hypothetical protein
SMU.1564	-0.80	-1.25	9.72E-06	glycogen phosphorylase, GlgP

SMU.1565	-0.54	-1.26	5.19E-04	putative 4-alpha-glucanotransferase, MalQ
SMU.1568	-0.86	-1.16	2.26E-04	maltose/maltodextrin ABC transporter, MalX
SMU.1569	-0.83	-1.21	3.12E-04	maltose/maltodextrin ABC transporter, MalF
SMU.1570	-0.96	-1.28	1.05E-04	maltose/maltodextrin ABC transporter, MalG
SMU.1571	-0.98	-1.24	3.83E-04	putative ABC transporter, MsmK-like protein
SMU.1591	-0.25	-0.69	2.03E-04	catabolite control protein A, CcpA
SMU.1697c	0.34	0.96	2.33E-04	hypothetical protein
SMU.1699c	0.41	0.87	6.17E-04	hypothetical protein
SMU.1700c	0.99	1.81	9.79E-06	CidB
SMU.1702c	0.03	2.67	6.63E-09	putative phosphatase
SMU.1703c	-0.18	1.49	4.94E-05	hypothetical membrane protein
SMU.1734	-0.16	0.71	3.62E-04	putative acetyl-CoA carboxylase alpha subunit
SMU.1735	-0.11	0.78	1.27E-04	putative acetyl-CoA carboxylase beta subunit
SMU.1737	-0.05	0.66	8.20E-04	putative 3-hydroxymyristoyl-(acyl carrier protein) dehydratase
SMU.1738	-0.09	0.65	1.62E-04	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit
SMU.1739	-0.07	0.76	2.19E-04	putative 3-oxoacyl-(acyl-carrier-protein) synthase
SMU.1740	-0.05	0.80	1.12E-04	putative 3-oxoacyl-acyl-carrier-protein reductase
SMU.1741	-0.09	0.77	6.40E-05	putative malonyl-CoA (acyl-carrier-protein) transacylase
SMU.1742c	0.05	0.62	6.11E-04	putative trans-2-enoyl-ACP reductase
SMU.1758c	0.11	-0.62	5.19E-04	conserved hypothetical protein
SMU.1763c	0.13	-0.67	3.55E-05	CRISPR-associated protein, Cas5
SMU.1828	-0.31	-0.66	3.83E-04	conserved hypothetical protein
SMU.1841	3.38	-0.19	1.02E-09	PTS-system, sucrose-specific enzyme IIABC, ScrA
SMU.1843	0.59	-0.85	3.42E-06	sucrose-6-phosphate hydrolase, ScrB
SMU.1844	0.87	-0.99	9.79E-06	sucrose operon repressor, ScrR
SMU.1853	0.14	0.65	3.83E-04	conserved hypothetical protein
SMU.1927	-0.88	-1.19	1.20E-04	putative ABC transporter
SMU.1928	-0.96	-1.27	1.89E-04	putative ABC transporter, PsaB
SMU.1956c	2.43	2.51	3.21E-06	LevX
SMU.1957	2.42	2.50	1.65E-08	PTS-system, fructose-specific enzyme IID, LevG

SMU.1958c	2.43	2.68	6.91E-08	PTS-system, fructose-specific enzyme IIC, LevF
SMU.1960c	2.24	2.35	6.23E-07	PTS-system, fructose-specific enzyme IIB, LevE
SMU.1961c	2.50	2.47	3.34E-07	PTS-system, fructose-specific enzyme IIA, LevD
SMU.1980c	1.45	0.18	5.81E-04	hypothetical protein
SMU.1981c	1.05	-0.09	2.01E-04	competence protein, ComGF
SMU.1982c	1.23	-0.07	5.34E-04	hypothetical protein
SMU.1983	0.83	-0.20	9.31E-04	competence protein, ComYD
SMU.1985	1.35	0.13	1.89E-04	ABC transporter, ComYB
SMU.1987	1.33	-0.11	2.94E-04	ABC transporter, late competence protein, ComYA
SMU.2027	-0.13	-0.80	7.19E-04	putative transcriptional regulator
SMU.2028	-0.77	-0.83	1.77E-04	beta-D-fructosyltransferase, Ftf
SMU.2042	0.66	0.93	2.29E-04	dextranase precursor, DexA
SMU.2046c	-0.79	-1.03	1.45E-04	Metal-dependent hydrolase
SMU.2047	-0.82	-1.12	9.79E-06	PTS system, maltose-specific IIABC, PtsG
SMU.2127	-1.37	-1.70	4.40E-07	putative succinate semialdehyde dehydrogenase
SMU.2137c	0.00	0.70	4.03E-04	conserved hypothetical protein
SMU.2139c	0.10	0.72	1.85E-04	50S ribosomal protein L9
SMU.2146c	-0.05	-0.70	7.19E-04	hypothetical protein

FDR, false discovery rate; cutoff at 0.001.

Table S2 List of genes differentially expressed in strain MMZ1196 relative to MMZ1009, when both were cultivated in TY supplemented with glucose.

Gene	$\log_2$ (MMZ1196/MMZ1009)	padj	Description	Abranches study*
SMU.1601	7.91	0.00E+00	*celA*	1
SMU.1596	7.00	0.00E+00	*celD*	1
SMU.1599	6.98	0.00E+00	*celR*	1
SMU.1598	6.96	0.00E+00	*celC*	1
SMU.1600	6.70	1.70E-237	*celB*	1
SMU.1597c	6.62	1.13E-98	*celX*	1
SMU.2127	1.58	3.51E-67	aldehyde dehydrogenase	1
SMU.179	1.51	2.95E-32		1
SMU.1538	1.41	3.18E-43		1
SMU.1539	1.39	1.48E-44	*glgB*	
SMU.252	1.39	4.84E-22	hypothetical	
SMU.1537	1.32	1.28E-36	*glgD*	1
SMU.1536	1.30	1.27E-33	*glgA*	1
SMU.180	1.29	9.31E-45	*ilvC*	1
SMU.1425	1.25	2.72E-22	*clpB*	
SMU.1117	1.24	1.52E-05	*naoX*	
SMU.148	1.19	9.95E-15	*adhE*	1
SMU.402	1.15	8.37E-22	*pfl*	1
SMU.1535	1.03	2.47E-29	*phsG*	1
SMU.980	1.00	2.62E-07	*bglP*	
SMU.1116c	0.93	2.59E-05	hypothetical	
SMU.541	0.92	1.50E-04	hypothetical	
SMU.1411	0.87	8.16E-04	fucose permease	1
SMU.1088	0.86	3.97E-17	*apbE*	
SMU.577	0.84	1.42E-12	*lytS*	
SMU.576	0.83	4.22E-10	*lytT*	
SMU.871	0.81	2.41E-12	*fruK*	1
SMU.1089	0.81	1.97E-12		
SMU.1077	0.77	9.22E-17	*pgm*	1
SMU.1843	0.76	3.28E-10	*scrB*	
SMU.1090	0.75	1.18E-14		
SMU.89c	0.75	3.01E-07	putative nitrite transporter	
SMU.870	0.74	8.49E-10	*fruR*	1
SMU.1410	0.73	1.21E-02	putative reductase	
SMU.542	0.72	1.33E-13	putative glucose kinase	
SMU.872	0.71	4.28E-12	*fruI*	1
SMU.149	0.70	2.81E-02		1

SMU.1841	0.69	1.04E-09	*scrA*	
SMU.543	0.67	5.95E-10	*pspE*	
SMU.1568	0.66	7.97E-07	*malX*	
SMU.1217c	0.65	4.50E-05	ABC transporter	
SMU.545	0.62	3.31E-02	hypothetical	
SMU.1423	0.61	4.17E-02	*pdhA*	
SMU.1978	0.61	3.52E-10	*ackA*	
SMU.1126	0.61	5.39E-02	*coaA*	
SMU.1844	0.59	1.28E-04	*scrR*	
SMU.1569	0.57	2.79E-02	*malF*	
SMU.1125c	0.56	9.80E-05	hypothetical	
SMU.1882c	0.55	1.61E-04		
SMU.1591	0.54	1.74E-08	*ccpA*	
SMU.1692	0.54	1.29E-04	*pflA*	
SMU.2028	0.54	1.69E-07		
SMU.2038	0.52	1.48E-02	*treB*	1
SMU.2037	0.50	1.65E-02	*treA*	
SMU.1590	0.50	3.35E-05	*amyA*	
SMU.1043c	0.49	2.32E-06		
SMU.674	0.49	5.49E-07	*ptsH*	1
SMU.1124	0.49	1.78E-05	*pdp*	
SMU.500	0.48	1.32E-05	ribosome-associated protein	
SMU.88c	0.47	5.71E-03	hypothetical	
SMU.675	0.44	1.28E-04	*EI*	1
SMU.877	0.42	2.04E-03	*agaL*	
SMU.2047	0.40	1.28E-04	*ptsG*	
SMU.1021	0.39	1.05E-02		
SMU.1398	0.37	1.76E-02	*irvR*	
SMU.80	0.36	5.85E-03	*hrcA*	
SMU.879	0.36	2.70E-02	*msmF*	
SMU.1565	0.35	1.64E-02	*malQ*	
SMU.81	0.35	1.50E-02	*grpE*	
SMU.1603	0.34	1.65E-02	*lguL*	1
SMU.1062	0.33	7.78E-03		
SMU.1602	0.33	1.76E-02		1
SMU.1023	0.32	4.43E-02	*pycB*	
SMU.1063	0.32	1.48E-02		
SMU.878	0.32	5.19E-02	*msmE*	
SMU.1564	0.31	3.56E-02	*glgP*	
SMU.1389	0.31	2.65E-02	*pckA*	
SMU.1122	0.30	7.00E-02	*cdd*	
SMU.1121c	0.29	2.51E-02	ABC transporter	
SMU.1954	0.27	1.65E-02	*groEL*	

SMU.2005	-0.27	5.35E-02	*adK*	
SMU.2074	-0.34	2.40E-03	*nrdD*	
SMU.363	-0.34	2.20E-02		
SMU.365	-0.37	7.85E-04		
SMU.393	-0.39	8.42E-03		
SMU.1502c	-0.39	1.23E-02	hypothetical	
SMU.299c	-0.39	5.39E-02	bacteriocin	
SMU.233	-0.41	4.06E-04	*ilvC*	
SMU.232	-0.41	1.08E-03	*ilvH*	
SMU.231	-0.42	9.98E-05	*ilvB*	
SMU.2042	-0.44	2.36E-04	*dexA*	1
SMU.2072c	-0.47	7.18E-02	hypothetical	
SMU.633	-0.47	2.06E-04	thioesterase	
SMU.1073	-0.53	2.29E-02	*fthS*	
SMU.1700c	-0.54	5.58E-02	*cidB*	
SMU.1961c	-0.57	1.05E-02	*levD*	
SMU.1960c	-0.62	1.85E-04	*levE*	
SMU.1956c	-0.68	1.73E-03	*levX*	
SMU.1957	-0.69	7.39E-10	*levG*	
SMU.49	-0.71	1.25E-07		
SMU.600c	-0.72	4.89E-03	hypothetical	
SMU.1958c	-0.73	1.36E-10	*levF*	
SMU.52	-0.74	1.55E-08		
SMU.50	-0.80	1.16E-02		
SMU.55	-0.81	4.78E-09		
SMU.396	-0.81	5.28E-11	*glpF*	
SMU.58	-0.82	1.70E-03		
SMU.53	-0.83	1.73E-03		
SMU.54	-0.87	3.78E-04		
SMU.31	-0.90	1.96E-05		
SMU.29	-0.91	9.40E-06		
SMU.36	-0.91	2.40E-07		
SMU.59	-0.92	4.82E-03		
SMU.56	-0.92	9.65E-05		
SMU.30	-1.01	1.31E-03		
SMU.33	-1.03	4.59E-05		
SMU.35	-1.03	4.41E-03		
SMU.37	-1.04	1.18E-04		
SMU.34	-1.04	9.39E-03		
SMU.1881c	-1.45	8.39E-25	*sunT*	
SMU.1175	-1.66	7.22E-09	alanine symporter	
SMU.602	-2.13	9.67E-19	Na$^+$-dependent transporter	1
SMU.1877	-2.51	1.15E-123	*manL*	

SMU.1878	-9.21	6.20E-277	*manM*
SMU.1879	-9.68	0.00E+00	*manN*

- * Presence of a number 1 indicates that this ORF was previously identified as being regulated by glucose-PTS in a similar study (*J Bacteriol* 188: 3748-3756).

Table S3 List of genes differentially expressed in strain MMZ1196 growing in TY-sucrose (Scr), in comparison to TY-glucose (Glc).

Gene	Log_2(Scr/Glc)	padj	1009GlcvScr*
SMU.1175	3.45	5.05E-49	1
SMU.602	3.36	1.08E-188	1
SMU.1958c	3.10	5.59E-49	1
SMU.1957	3.07	1.85E-61	1
SMU.1956c	3.01	1.88E-65	1
SMU.1961c	2.94	2.18E-20	1
SMU.1960c	2.88	2.57E-27	1
SMU.1841	2.77	0.00E+00	1
SMU.499	2.67	9.19E-10	1
SMU.626	2.60	9.80E-09	1
SMU.625	2.37	1.42E-08	1
SMU.498	2.04	1.45E-10	1
SMU.1980c	1.84	1.54E-10	1
SMU.600c	1.69	5.17E-20	1
SMU.396	1.68	2.18E-144	1
SMU.1700c	1.60	1.17E-21	1
SMU.1981c	1.55	3.74E-05	1
SMU.1987	1.44	5.13E-11	1
SMU.1982c	1.38	1.91E-03	1
SMU.1985	1.36	5.52E-06	1
SMU.913	1.34	1.55E-82	1
SMU.1701c	1.32	2.46E-07	1
SMU.871	1.20	2.02E-59	1
SMU.872	1.19	1.61E-80	1
SMU.870	1.18	1.92E-51	1
SMU.1983	1.15	1.59E-04	1
SMU.2042	1.10	2.13E-63	1
SMU.1984	1.09	1.50E-03	1
SMU.768c	1.01	1.10E-06	1
SMU.233	0.97	2.36E-57	1
SMU.231	0.96	1.57E-54	1
SMU.232	0.93	2.01E-38	1
SMU.836	0.90	3.38E-05	1
SMU.365	0.90	1.46E-46	1
SMU.438c	0.86	1.81E-09	
SMU.1967	0.85	1.65E-04	1
SMU.644	0.84	1.39E-02	

SMU.366	0.81	4.76E-29	1
SMU.05	0.75	1.15E-02	1
SMU.1699c	0.74	9.63E-19	1
SMU.633	0.72	1.70E-17	
SMU.84	0.71	1.33E-04	
SMU.46	0.71	4.61E-03	1
SMU.1862	0.71	7.82E-02	
SMU.363	0.69	8.96E-20	1
SMU.47	0.68	3.28E-03	1
SMU.364	0.67	2.45E-20	1
SMU.09	0.67	2.27E-03	
SMU.85	0.62	3.49E-04	
SMU.916c	0.61	5.66E-05	
SMU.1520	0.60	2.38E-04	1
SMU.1109c	0.57	1.17E-13	
SMU.1521	0.57	8.36E-05	1
SMU.510c	0.57	5.24E-02	1
SMU.954	0.56	5.76E-02	
SMU.393	0.56	4.15E-10	
SMU.1595	0.56	1.61E-12	
SMU.87	0.56	4.60E-04	
SMU.873	0.55	8.52E-02	
SMU.10	0.54	1.39E-03	
SMU.1502c	0.54	1.81E-07	
SMU.914c	0.54	2.99E-02	
SMU.1519	0.54	5.44E-04	
SMU.632	0.53	1.40E-05	
SMU.915c	0.52	2.65E-02	
SMU.394c	0.51	2.32E-02	
SMU.102	0.51	8.09E-02	1
SMU.1375c	0.51	5.24E-02	
SMU.1317c	0.51	7.64E-02	
SMU.917c	0.50	5.93E-02	
SMU.1078c	0.50	7.25E-11	
SMU.941c	-0.50	6.19E-09	1
SMU.1869	-0.50	9.29E-04	1
SMU.1954	-0.51	3.69E-11	1
SMU.1746c	-0.51	5.85E-14	1
SMU.1602	-0.52	2.06E-08	
SMU.1017	-0.52	4.36E-03	
SMU.2119	-0.52	4.67E-06	
SMU.618	-0.52	7.01E-05	1
SMU.803c	-0.53	1.60E-02	

SMU.1714c	-0.54	7.61E-09	
SMU.1895c	-0.55	4.37E-02	
SMU.1422	-0.57	6.38E-02	
SMU.1349	-0.58	5.65E-04	
SMU.1603	-0.58	2.07E-09	
SMU.401c	-0.58	9.25E-02	
SMU.1402c	-0.61	8.17E-03	
SMU.1019	-0.62	5.32E-02	
SMU.1071c	-0.63	1.40E-05	1
SMU.1590	-0.67	2.25E-14	
SMU.804	-0.67	4.32E-09	
SMU.1421	-0.71	4.97E-03	
SMU.1293c	-0.72	5.06E-24	1
SMU.1124	-0.74	5.17E-22	
SMU.88c	-0.78	9.17E-09	
SMU.21	-0.78	6.90E-02	
SMU.1591	-0.79	7.17E-36	
SMU.798c	-0.80	7.29E-02	
SMU.1125c	-0.82	6.69E-14	
SMU.1389	-0.83	1.19E-30	1
SMU.1020	-0.87	1.42E-06	1
SMU.674	-0.93	7.18E-48	1
SMU.132	-0.93	6.83E-05	
SMU.799c	-0.95	3.10E-03	
SMU.1043c	-0.96	4.42E-44	1
SMU.1398	-0.97	5.16E-23	1
SMU.2046c	-0.99	4.07E-20	1
SMU.675	-1.00	6.40E-62	1
SMU.1023	-1.01	4.71E-26	1
SMU.1022	-1.02	1.12E-05	1
SMU.1021	-1.04	1.11E-28	
SMU.1565	-1.08	5.57E-39	1
SMU.1978	-1.09	2.54E-66	1
SMU.1425	-1.10	1.39E-03	
SMU.114	-1.11	5.24E-03	
SMU.1564	-1.11	2.80E-53	1
SMU.130	-1.11	2.16E-05	
SMU.131	-1.12	1.87E-05	
SMU.1217c	-1.12	9.76E-13	
SMU.1126	-1.13	5.10E-06	
SMU.1571	-1.14	8.33E-09	1
SMU.2047	-1.15	2.97E-76	1
SMU.1692	-1.15	7.74E-11	1

SMU.500	-1.15	1.05E-59	1
SMU.116	-1.17	1.77E-03	
SMU.129	-1.23	1.39E-03	
SMU.89c	-1.24	1.83E-19	1
SMU.542	-1.26	7.13E-78	1
SMU.543	-1.27	1.24E-61	1
SMU.981	-1.28	3.67E-03	
SMU.2028	-1.34	1.89E-78	1
SMU.128	-1.35	5.54E-04	
SMU.883	-1.35	4.36E-59	1
SMU.882	-1.35	1.08E-37	1
SMU.1927	-1.35	2.06E-09	1
SMU.545	-1.36	2.89E-08	
SMU.1089	-1.36	2.80E-60	1
SMU.1570	-1.37	2.51E-07	1
SMU.1568	-1.38	2.67E-27	1
SMU.127	-1.38	1.18E-03	
SMU.982	-1.39	1.16E-02	
SMU.1928	-1.43	1.63E-63	1
SMU.1569	-1.46	2.76E-11	1
SMU.1090	-1.46	5.62E-102	1
SMU.881	-1.47	1.88E-75	1
SMU.878	-1.52	5.04E-67	1
SMU.1088	-1.54	6.80E-100	1
SMU.877	-1.56	1.11E-75	1
SMU.577	-1.58	6.11E-71	1
SMU.879	-1.61	2.92E-64	1
SMU.880	-1.61	9.19E-63	1
SMU.1116c	-1.72	2.91E-16	
SMU.541	-1.73	1.68E-12	
SMU.576	-1.75	3.00E-38	1
SMU.980	-1.79	5.18E-18	1
SMU.1077	-1.81	4.44E-198	1
SMU.1535	-1.93	6.25E-203	1
SMU.1410	-2.10	2.47E-15	1
SMU.149	-2.12	1.63E-14	1
SMU.1539	-2.20	2.17E-198	1
SMU.1411	-2.28	1.37E-18	1
SMU.252	-2.31	2.20E-45	1
SMU.1117	-2.38	9.11E-14	
SMU.1536	-2.39	1.91E-79	1
SMU.1538	-2.49	1.09E-222	1
SMU.1537	-2.49	3.15E-213	1

SMU.179	-2.80	4.94E-90	1
SMU.180	-2.87	0.00E+00	1
SMU.2127	-2.98	0.00E+00	1
SMU.148	-3.09	1.42E-136	1
SMU.402	-3.44	0.00E+00	1
SMU.1597c	-6.50	1.20E-93	
SMU.1600	-6.77	1.61E-245	
SMU.1599	-6.88	0.00E+00	
SMU.1598	-6.94	0.00E+00	
SMU.1596	-6.97	0.00E+00	
SMU.1601	-8.11	0.00E+00	

* Presence of a number 1 indicates that this ORF has been identified as differentially expressed in strain MMZ1009, when growing similarly under glucose and sucrose conditions (Table 2). Note: the fold-of-change cutoff here is smaller, therefore more ORFs are retained, than that in Table 2.

Table S4 Primers used in this study.

Name	Sequence	Purpose
fruB-5’	5’- GGG TAA ACG AAT CAA TGA TGA TCA AT -3’	*fruB*M1stop
fruBM1stop-3’	5’- CAA ACT AAT TTT TTC TTT AGC TAA AGA CAC CTC TAT CTA TTG -3’	*fruB*M1stop
fruBM1stop-5’	5’- CAA TAG ATA GAG GTG TCT TTA GCT AAA GAA AAA ATT AGT TTG -3’	*fruB*M1stop
fruBdelta113-3’	5’- GGT AGG TAA ATC TTT GAA AAA TTG ATT-3’	*fruB*M1stop
gyrA-S	5’- CCA AGA ATC TGC TGT CCG -3’	*gyrA*
gyrA-AS	5’- TTG CGA CTA TCT GCT ATG TG -3’	*gyrA*
SMU.180-S	5'- TTT TAG ATG CTC CGG GTG TC -3'	SMU.180
SMU.180-AS	5'- GAC TTG AGG TTG CCT GCT TC -3'	SMU.180
SMU.1927-S	5'- CGA GGT CCG TGC CAA TAA TA -3'	SMU.1927
SMU.1927-AS	5'- TTG AGC AGG GTT GAT TTT CC -3'	SMU.1927
comEA-S	5'- CGG TGA GAA GAA AGC TCA GG -3'	*comEA*
comEA-AS	5'- TTT ATC GCC AAT CCC TGA AA -3'	*comEA*
SMU.1175-S	5'- TCA TGG CTG CAG CTT ACA TC -3'	SMU.1175
SMU.1175-AS	5'- TTG TTC AAT GGC AGG AAT GA -3'	SMU.1175
dacA-S	5'- GTC CCC ATG GAT GCT AGA GA -3'	*dacA*
dacA-AS	5'- CCA ACT TTT TCA GCC AAA GC -3'	*dacA*
purC-S	5'- TGG TTC CAT CAA ATC GGA CT -3'	*purC*
purC-AS	5'- GCA TCC CAA AGA CGA CAG TT -3'	*purC*
SMU.101-S	5'- TTA GGT GTT GCT GGG CTA GG -3'	SMU.101
SMU.101-AS	5'- CAA ACC CGA TCC TGT CCT AA -3'	SMU.101
rcrR-S	5'-TGT TTT AAC GCC ATT AGG TCA GG -3'	*rcrR*
rcrR-AS	5'- TCC GAG CAA CTG ATA AGT CTT CC -3'	*rcrR*
ptsG-S	5’- CGG ATT CAG TTG AAA GAG CCA AG -3’	*ptsG*
ptsG-AS	5’- GAC GAT AAT ACC GCC GAA CAC C -3’	*ptsG*
levD-S	5’- GCC CTT TGA CAA CAG CTT GC -3’	*levD*
levD-AS	5’- CTG CCA TTG GTA AGT TCA TCC C -3’	*levD*
glgD-S	5’- GCT ATC GGA TTC CCA GAA ATG G -3’	*glgD*
glgD-AS	5’- CAC GAC CGC TTC TGA TAT GAT C -3’	*glgD*
ftf-S	5’- AAA TAT GAA GGC GGC TAC AAC G -3’	*ftf*
ftf-AS	5’- CTT CAC CAG TCT TAG CAT CCT GAA -3’	*ftf*
pfl-S	5’- AAG GAA CTG ACT GGA AAG AC -3’	*pfl*
pfl-AS	5’- CGT GTT TCT TCG TAA TGC G -3’	*pfl*
scrA-S	5’- TGC AGC AAA TAA GGC ACA AG -3’	*scrA*
scrA-AS	5’- ATC CCC TTA CCC ATT GCT TC -3’	*scrA*
scrB-S	5’- TGA TGC ATC GGA AAT TCA AA -3’	*scrB*
scrB-AS	5’- ATA AAC ACG GCC ATC AGG AG -3’	*scrB*
scrK-S	5’- AGC GGG TCC TAG CTT AGA GG -3’	*scrK*

scrK-AS	5’- GGA CAG TCG CTT GAA TAG CC -3’	*scrK*
fruR-S	5’- GCT GGG ACA ACA ACT GCT CTT C -3’	*fruR*
fruR-AS	5’- GCC AAC TGA CCT ATG CTC GC -3’	*fruR*
pgm-S	5’- ATT GGC GCT GGA ACT AAT CG -3’	*pgm*
pgm-AS	5’- TTG AGA GAA ATG ACG GGA ATC G-3’	*pgm*
bacD-S	5’- TTC TGA AAT GCC GTT GAT GA -3’	*bacD*
bacD-AS	5’- CGC CGA TAA TTC TTC GAC AT -3’	*bacD*
lytS-S	5’- AGC TGC GCT TTC CTG ATA AA -3’	*lytS*
lytS-AS	5’- ATG ACG CAC TGC ATT TTC AA -3’	*lytS*
comYA-S	5’- GGC ATC GTC CGG ATA TTT TA -3’	*comYA*
comYA-AS	5’- TTG CCC CTG TAA GAC TTG CT -3’	*comYA*
cidB-S	5’- GTT TTG GGG CCA ACT CTT TT -3’	*cidB*
cidB-AS	5’- AGC CGT TCC AGT ACC AAC AG -3’	*cidB*
gtfD-S	5’- CAC AGG CAA AAG CTG AAT TAA C -3’	*gtfD*
gtfD-AS	5’- GAA TGG CCG CTA AGT CAA CA -3’	*gtfD*
ptsH-S	5’- CAT GCA CGC CCA GCT ACT TTG -3’	*ptsH*
ptsH-AS	5’- CAT CAG CAC CTT GAC CAA CAC C -3’	*ptsH*
ptsI-S	5’- GCA GTA GAT ACC CTT GGT GAA G -3’	*ptsI*
ptsI-AS	5’- TCT GTC ACT TCT TTG AGA GCA C -3’	*ptsI*
SMU.1349-S	5’- TGA CTA AGG GAA CAA GGG AAA A -3’	SMU.1349
SMU.1349-AS	5’- AGG CTT CCT CAG CAA TTT CA -3’	SMU.1349

FIG S1 Sucrose pulsing leads to release of fructose by *S. mutans.* Strains MMZ952 (*gtfABCD/ftf/fruA*, dark) and MMZ993 (*gtfABCD/ftf/fruA/scrA*, light) were cultivated in TV medium supplemented with 0.5% of galactose into exponential phase, followed by pulsing for 30 min with sucrose at final concentrations ranging from 0 to 10 mM. Supernates of the bacterial cultures were collected and free fructose was measured. Results are the averages of three independent cultures, with error bars representing the standard deviations.

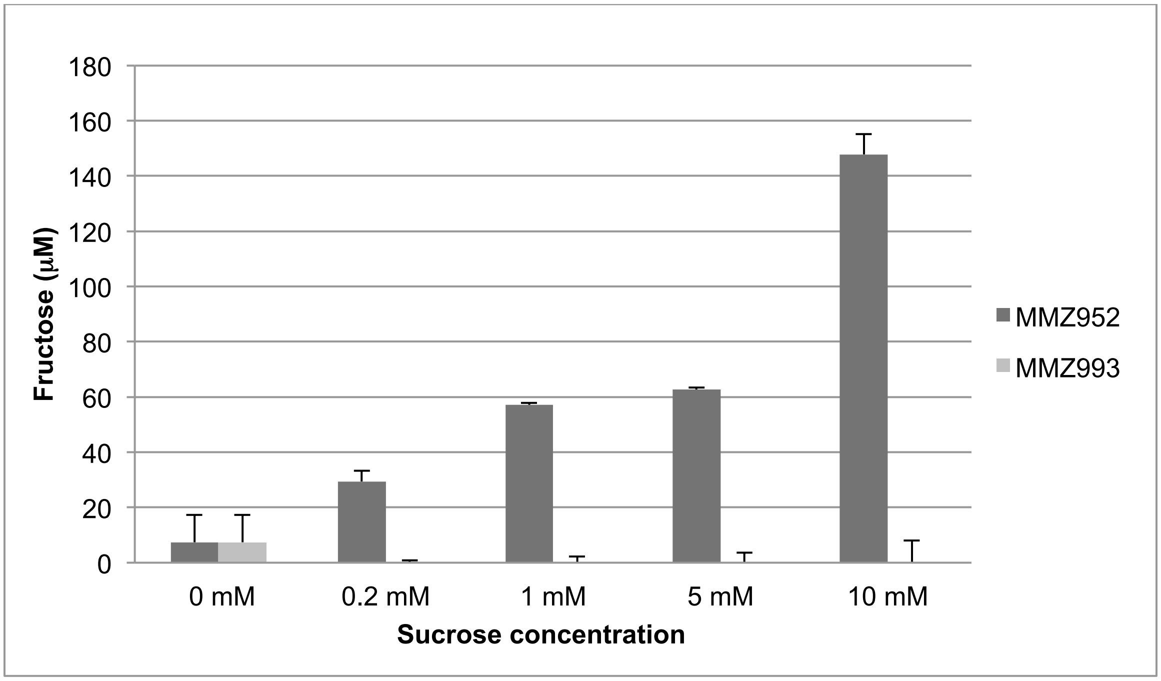
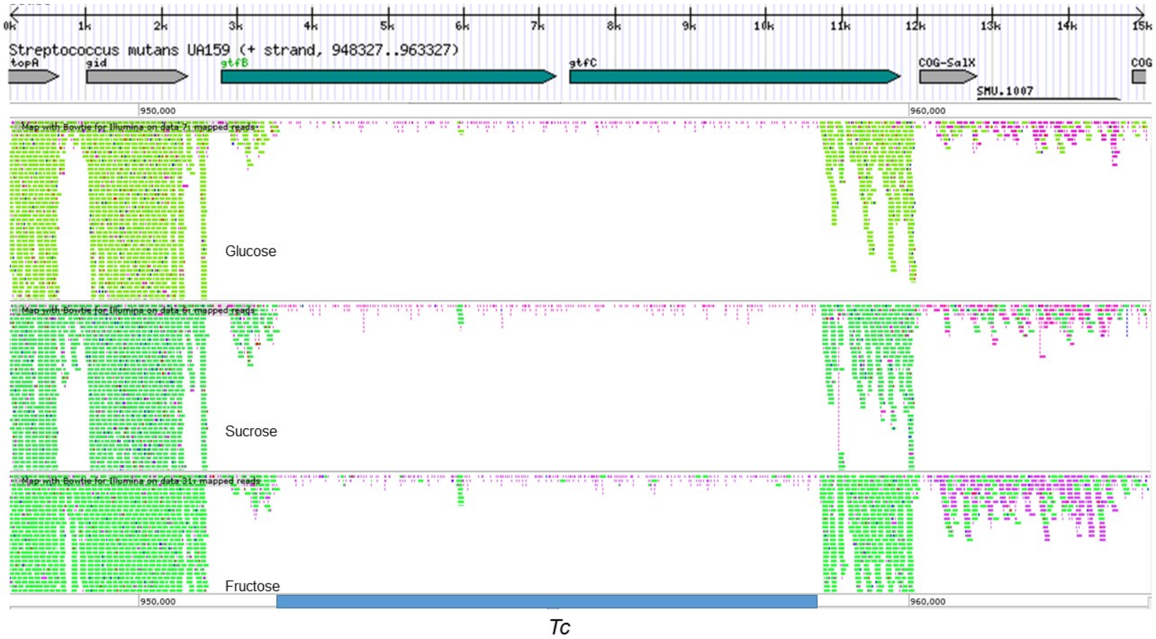


FIG S2 Comparison of the cDNA levels in the region of *gtfBC:Tc* (A) and *gtfD* (B) in strain MMZ1009 growing in TY media supported solely by glucose, sucrose or fructose.

A



B