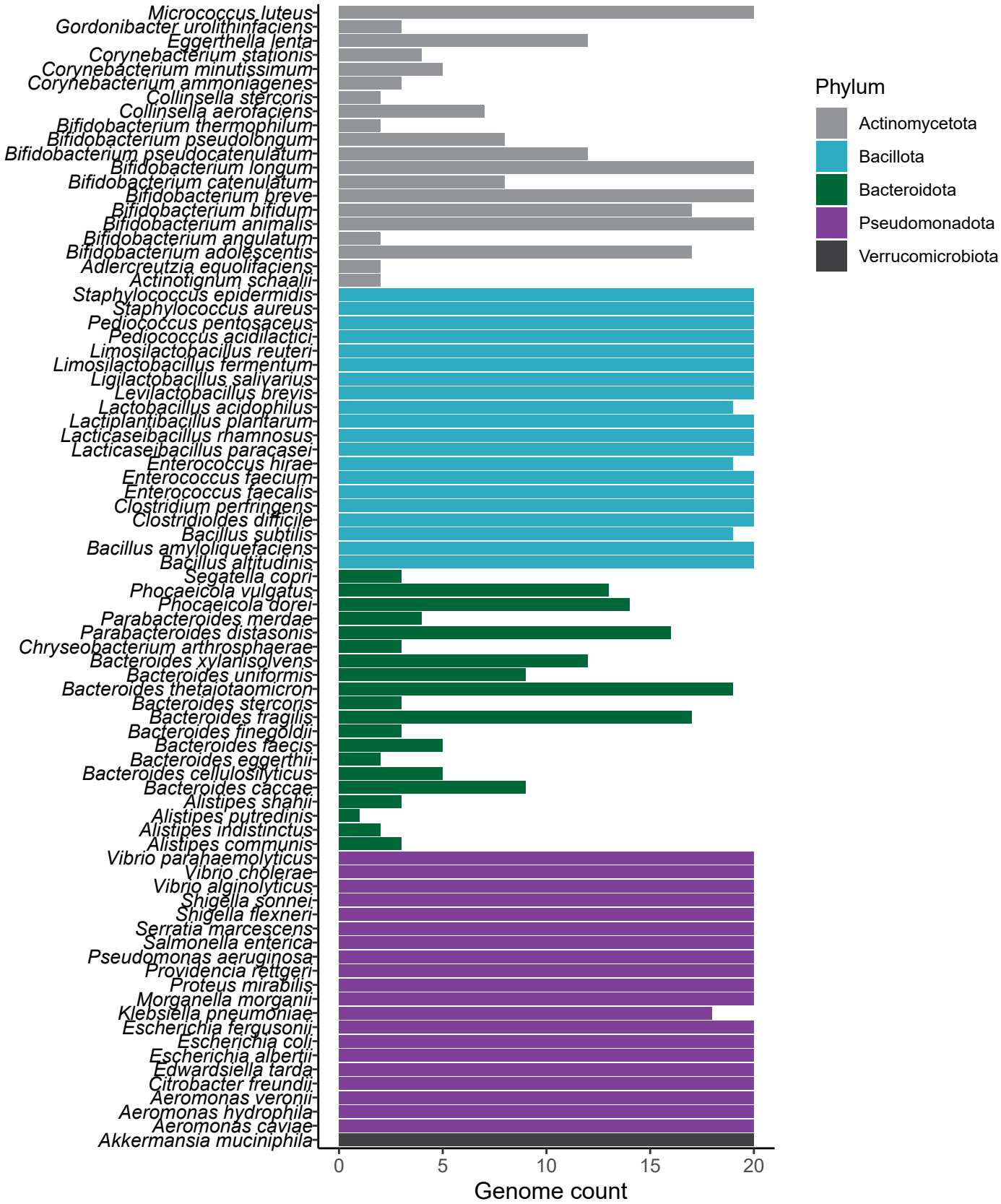
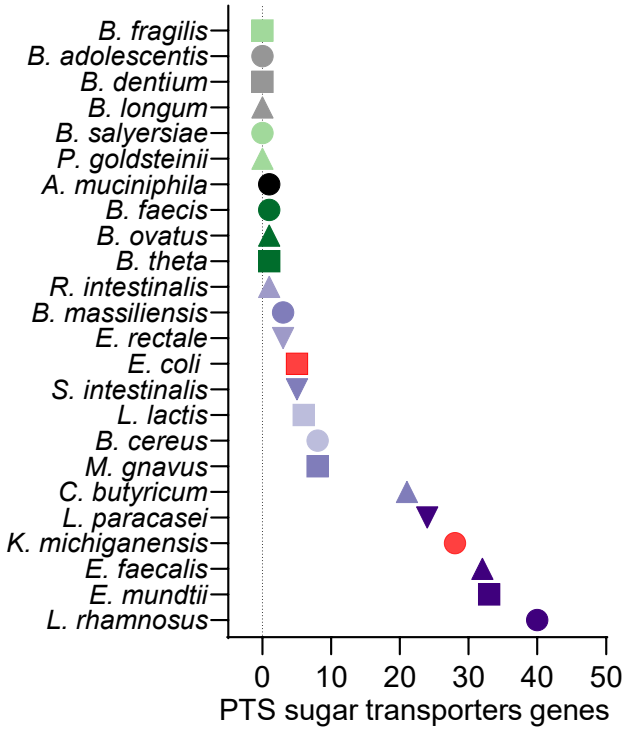
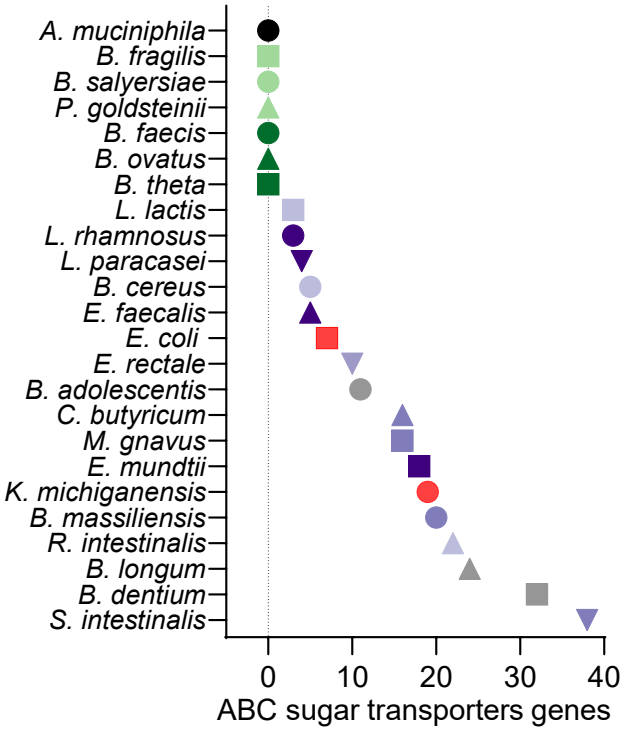
Sugar ABC transporter repertoires predict ecological dynamics in gut microbiome communities

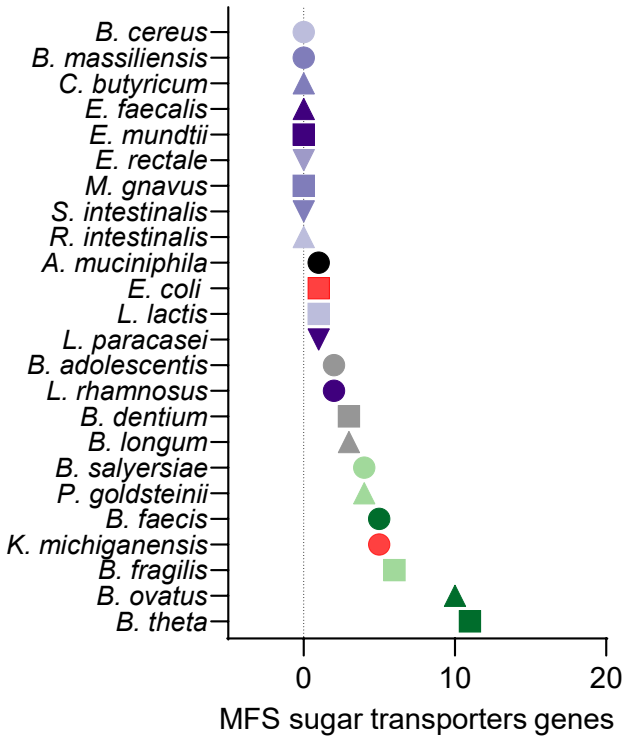
Supplementary Information
Supplementary Figures (1-22)
Supplementary Tables (1- 8)



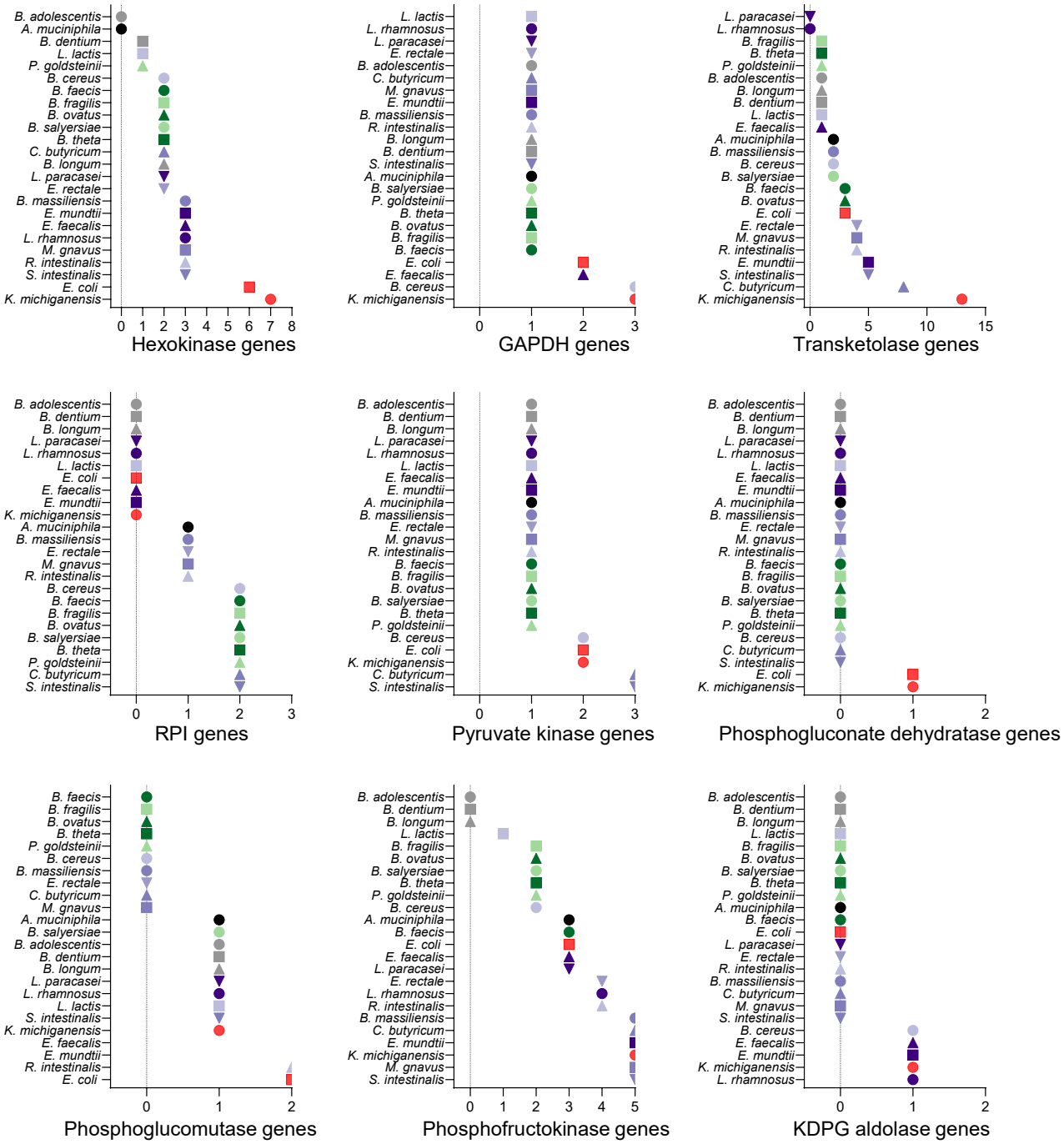
Supplementary Figure. 1. List of genomes used in Fig. 1a. For each phylum (excluding Verrucomicrobiota), 20 species were selected. For species with more than 20 fully sequenced genomes available, a maximum of 20 genomes were randomly chosen. For species with fewer than 20 sequenced genomes available, all available genomes were included.



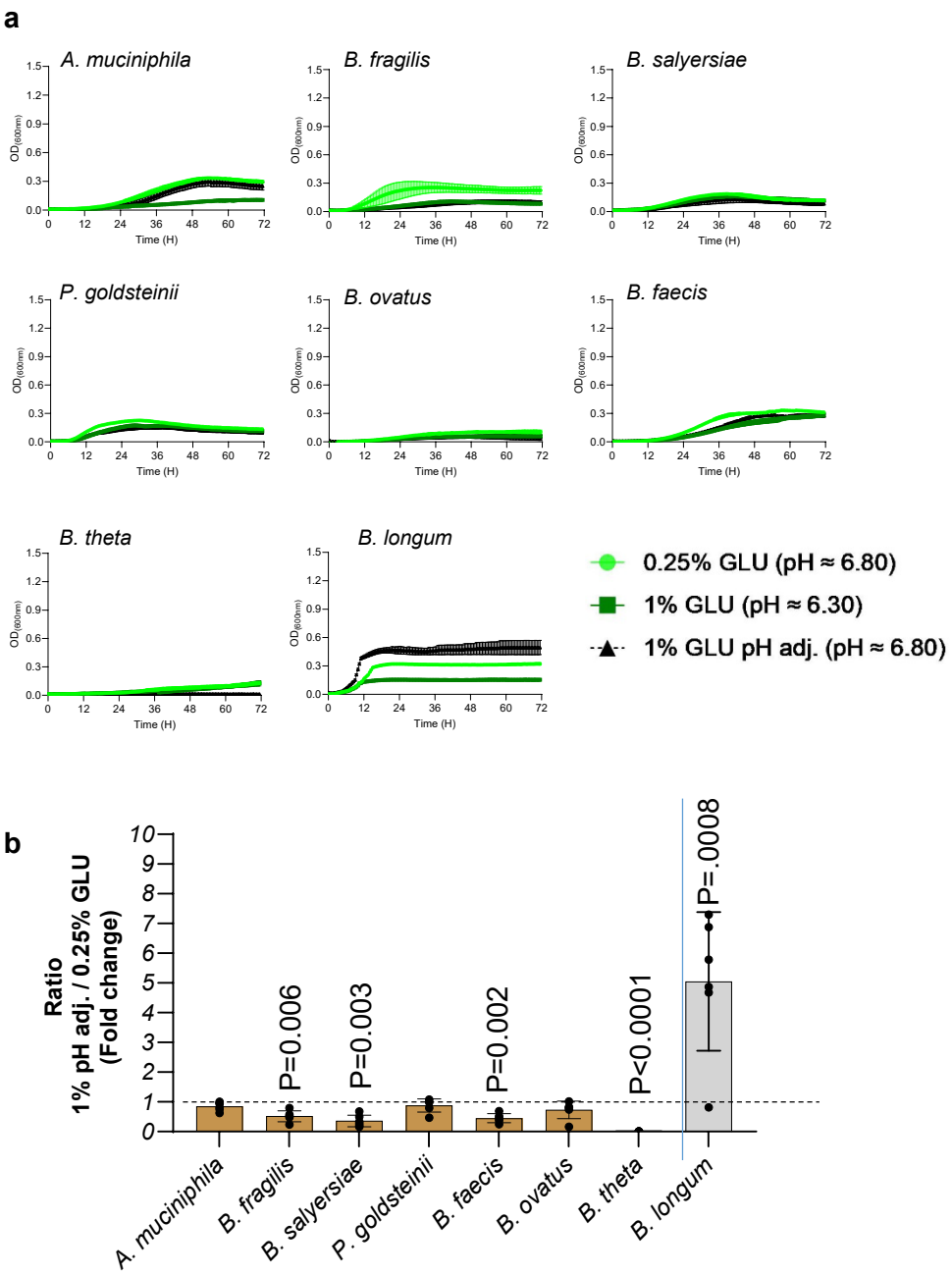




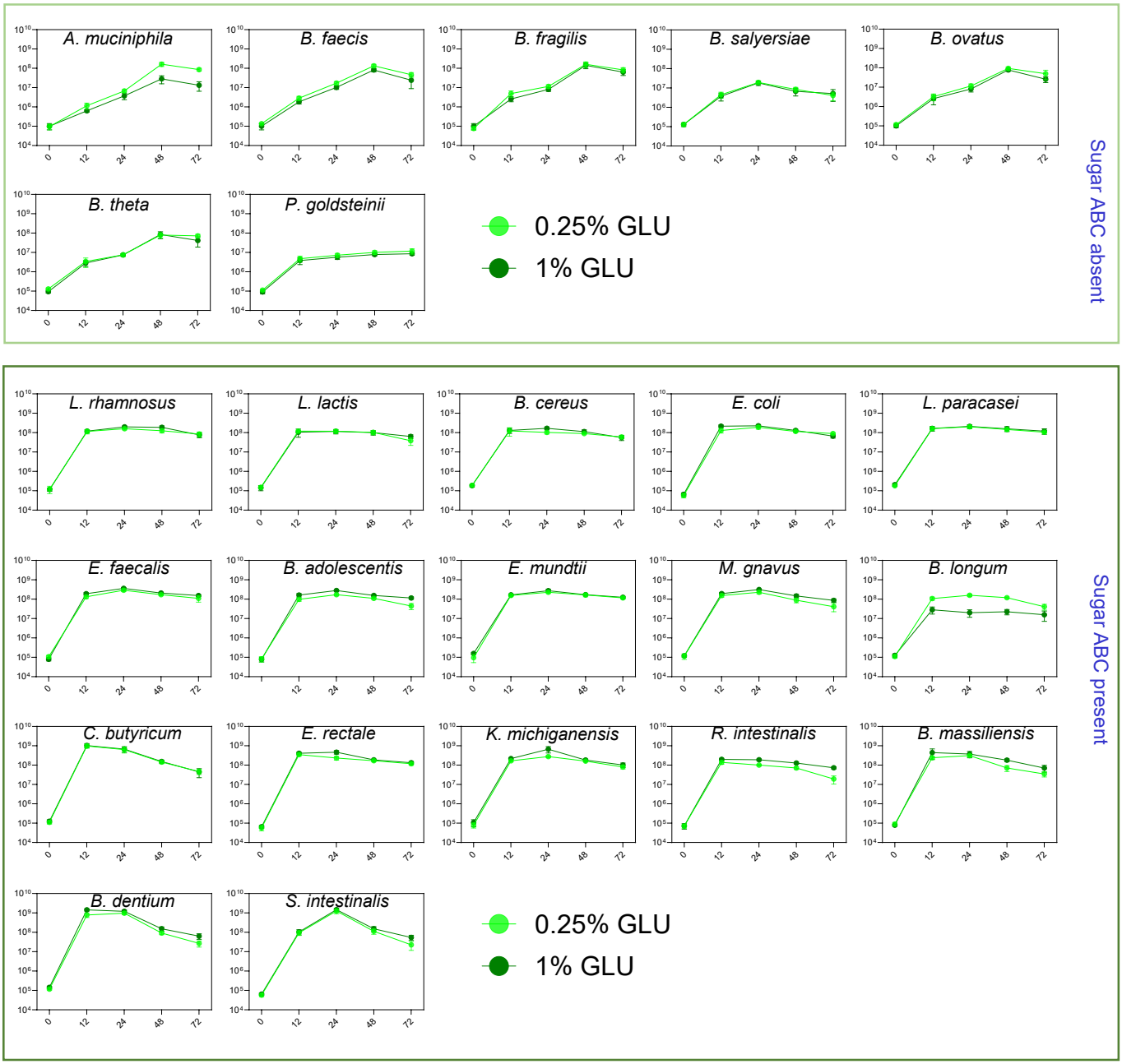
Supplementary Figure 2. Enumeration of genes involved in ABC, PTS and MFS sugar transporters of the indicated bacteria.



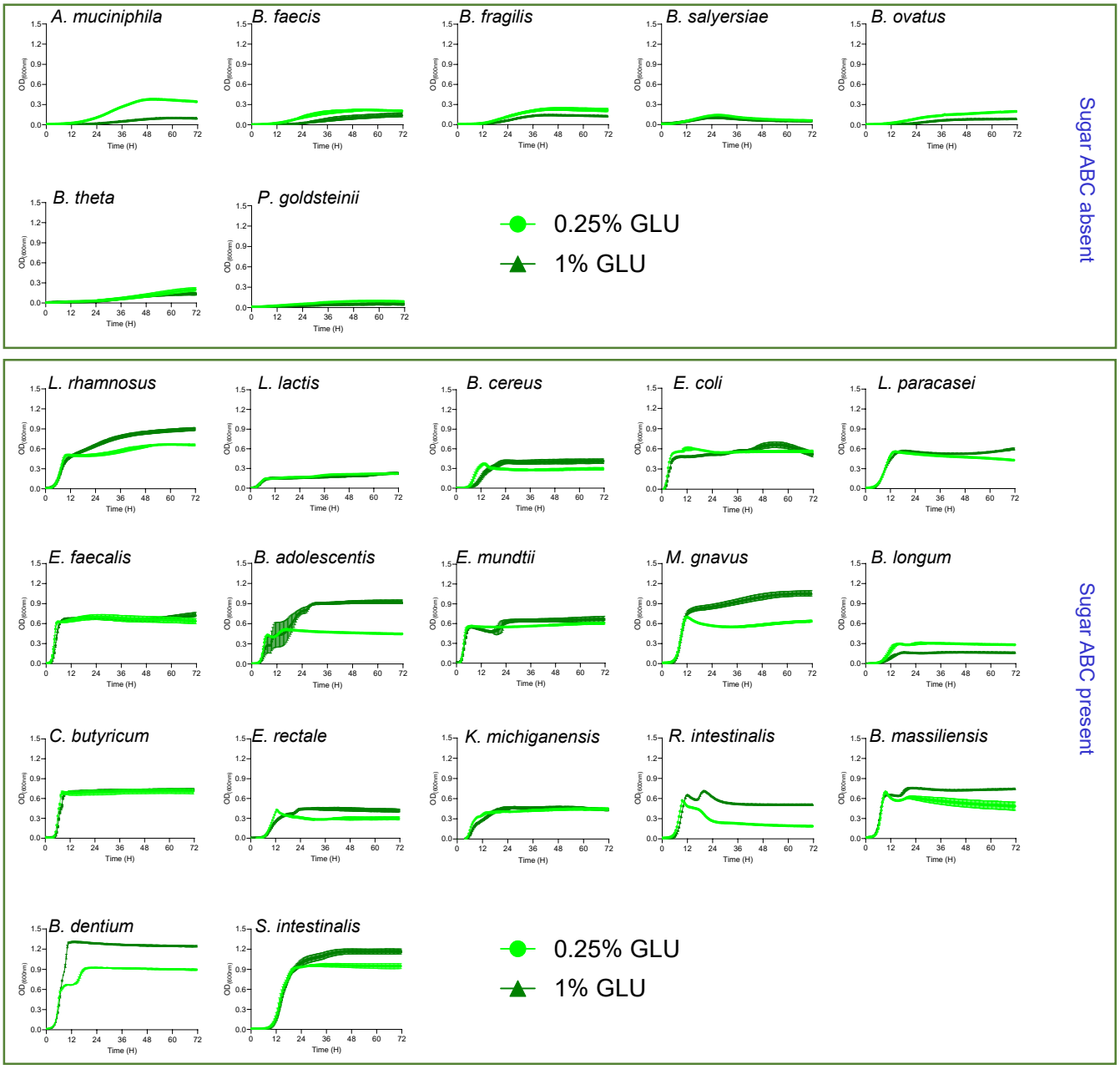
Supplementary Figure 3. Enumeration of genes involved in the glycolytic pathways of the indicated bacteria.



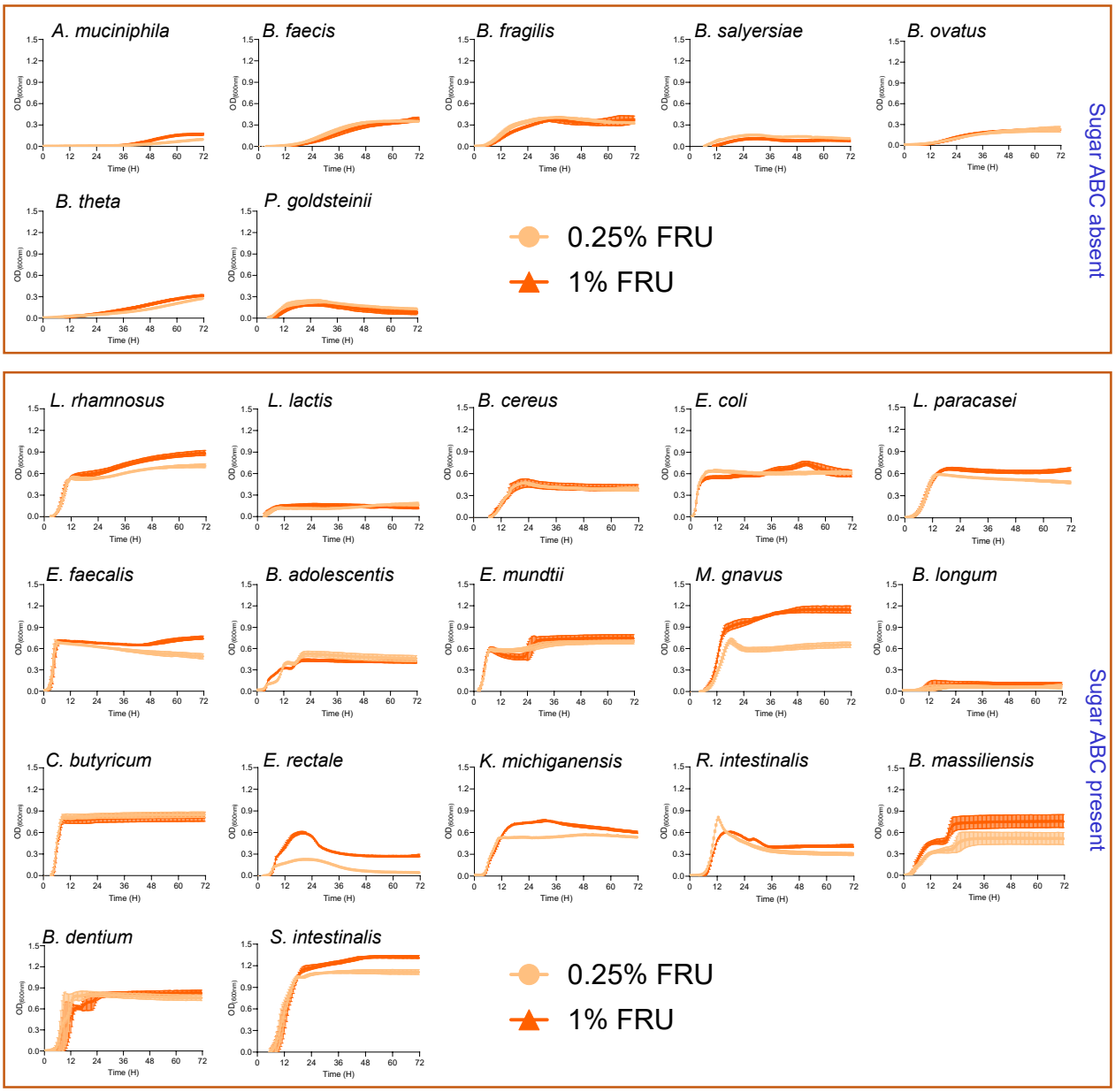
Supplementary Figure 4. a) Analysis of the growth (OD_{600}) of the indicated strains. Growth was monitored in BHI-NG medium supplemented with 0.25% , 1% and 1% (pH adjusted to 0.25% medium) glucose. Graphs represent mean ± SD from two independent experiments (n = 6). **b)** The fold change between the CFUs obtained at 1% pH adjusted and 0.25% glucose at 48 hours for each indicated species, derived from two independent experiments ($n = 6$). Bacteria were cultured in BHI medium supplemented with 0.25% or 1% pH adjusted glucose and harvested at 24 hours post inoculation. Data are presented as mean ± SD (with individual data points). Statistical analysis was performed using a two-tailed one-sample ratio t-test against a fold change of 1. $P < 0.05$ was considered statistically significant. The dashed line represents a fold change of 1, indicating no difference in growth between the two glucose concentrations.



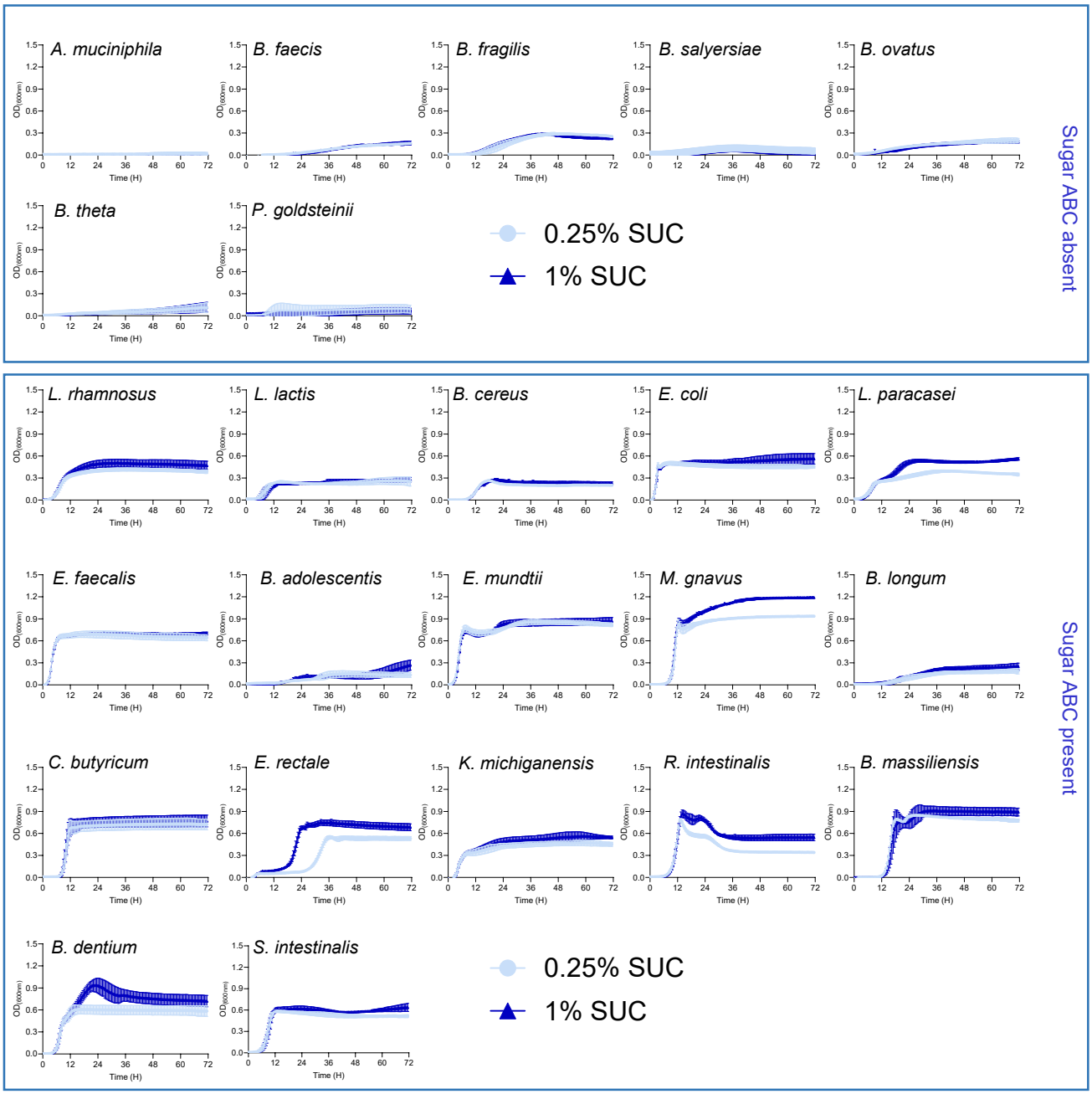
Supplementary Figure 5. Growth analysis of the indicated bacteria. Bacteria were cultured in BHI-NG medium supplemented with 0.25% or 1% glucose (GLU) and harvested at 12, 24, 48 and 72 hours post inoculation and colony-forming units (CFU) were counted. Initial inoculum at 0 hour was 10^5 CFU/mL ± 0.3 Graphs represent mean ± SD from two independent experiments (n = 6).



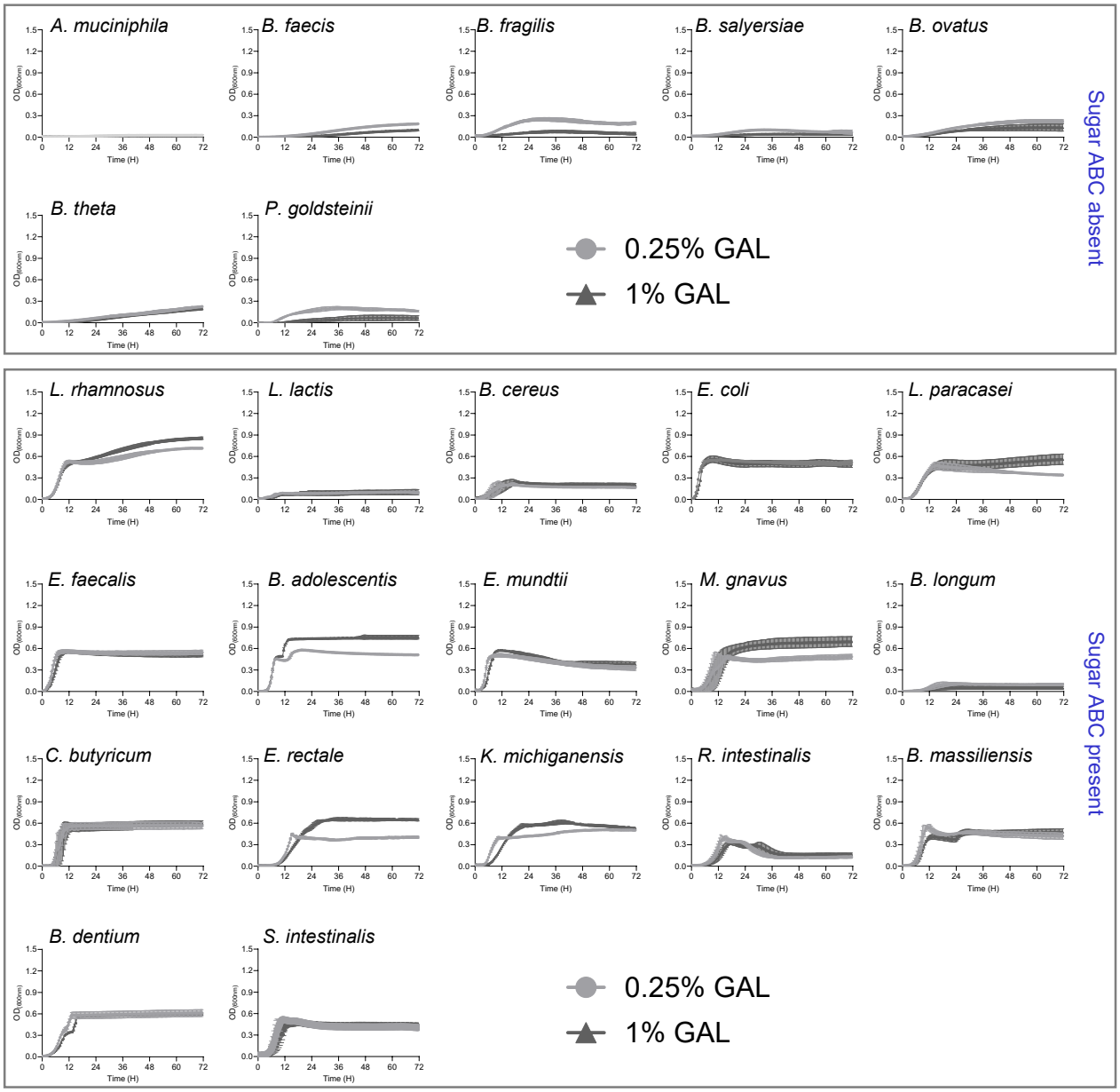
Supplementary Figure 6. Analysis of the growth (OD_{600}) of the indicated strains. Bacteria were cultured in BHI medium-NG supplemented with 0.25% and 1% glucose (GLU). Graphs represent mean ± SD from two independent experiments (n = 6).



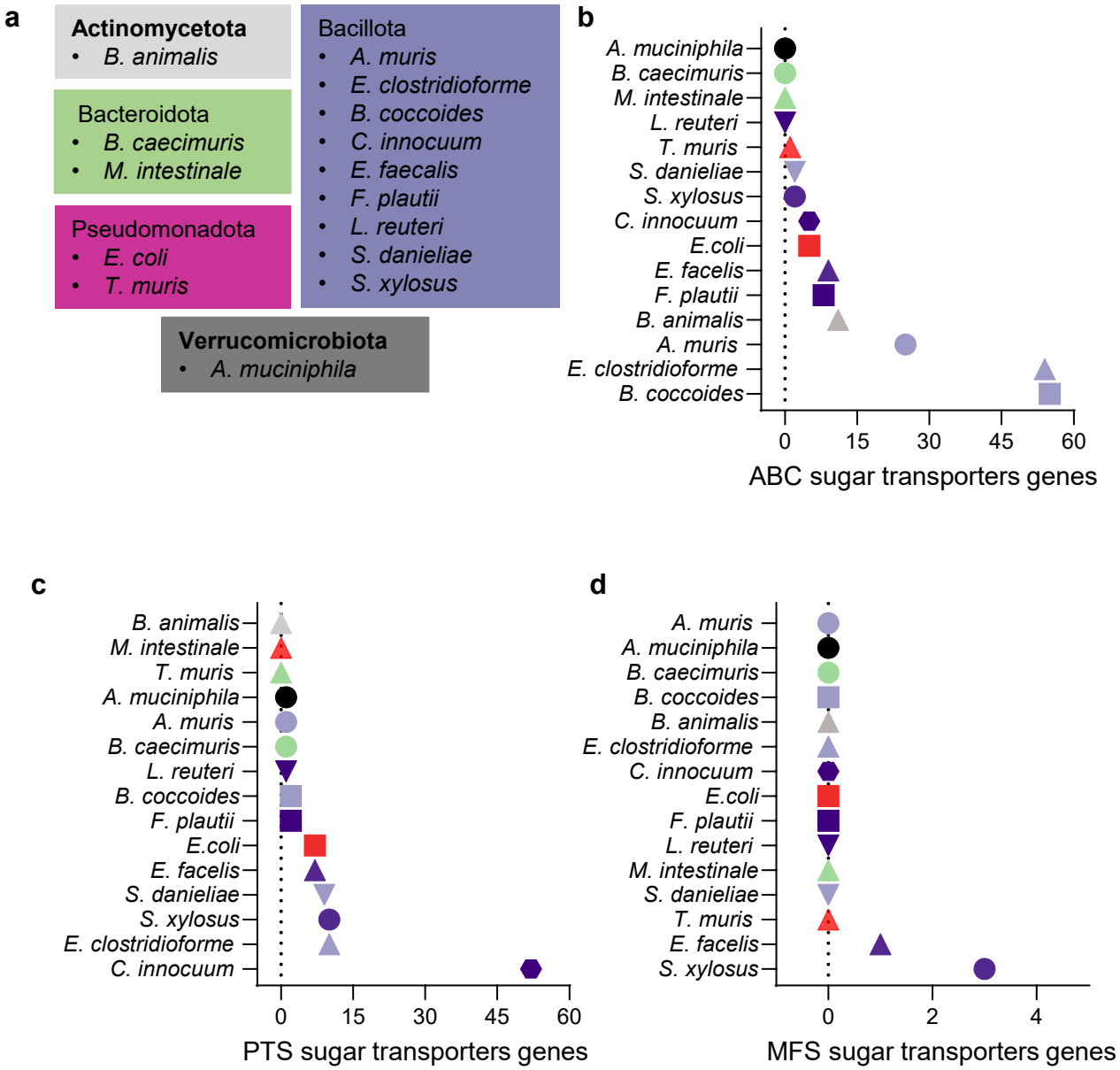
Supplementary Figure 7. Analysis of the growth (OD_{600}) of the indicated strains. Bacteria were cultured in in BHI-NG medium supplemented with 0.25% and 1% fructose (FRU). Graphs represent mean ± SD from two independent experiments (n = 6)



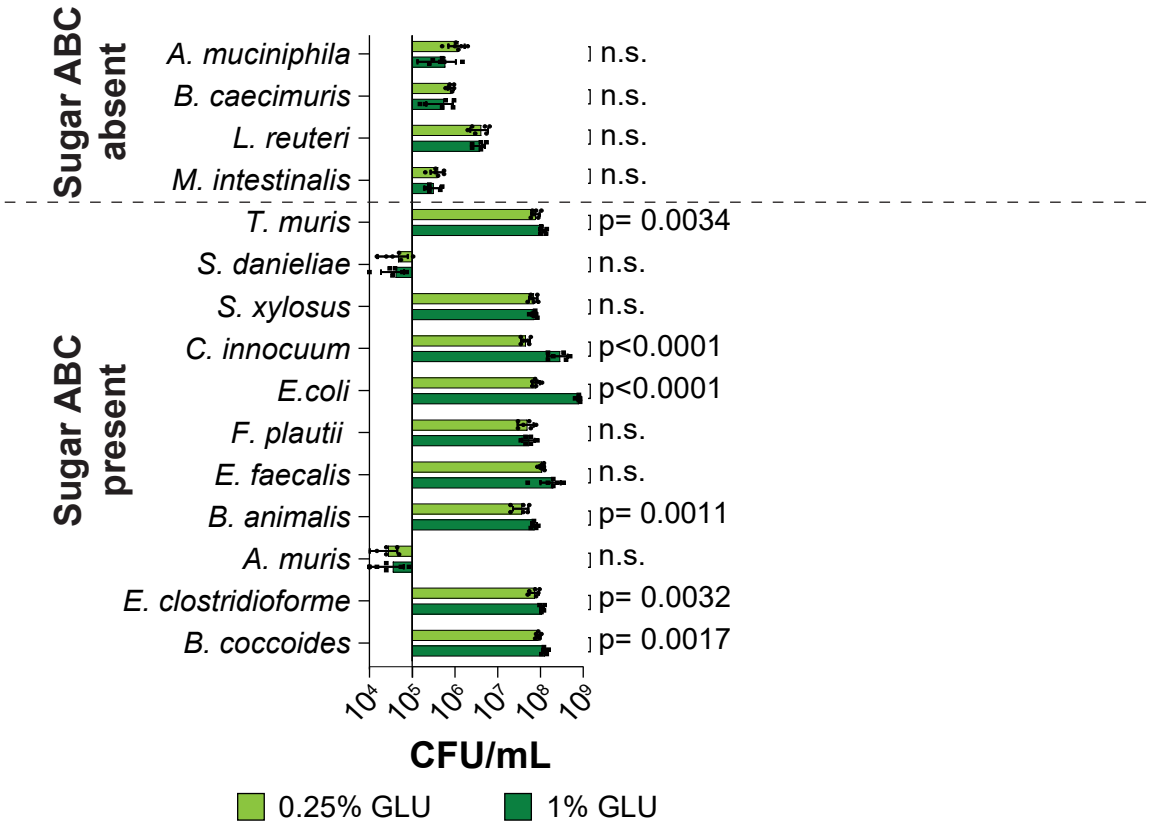
Supplementary Figure 8. Analysis of the growth (OD_{600}) of the indicated strains. Bacteria were cultured in BHI-NG medium supplemented with 0.25% and 1% fructose (SUC). Graphs represent mean ± SD from two independent experiments (n = 6)



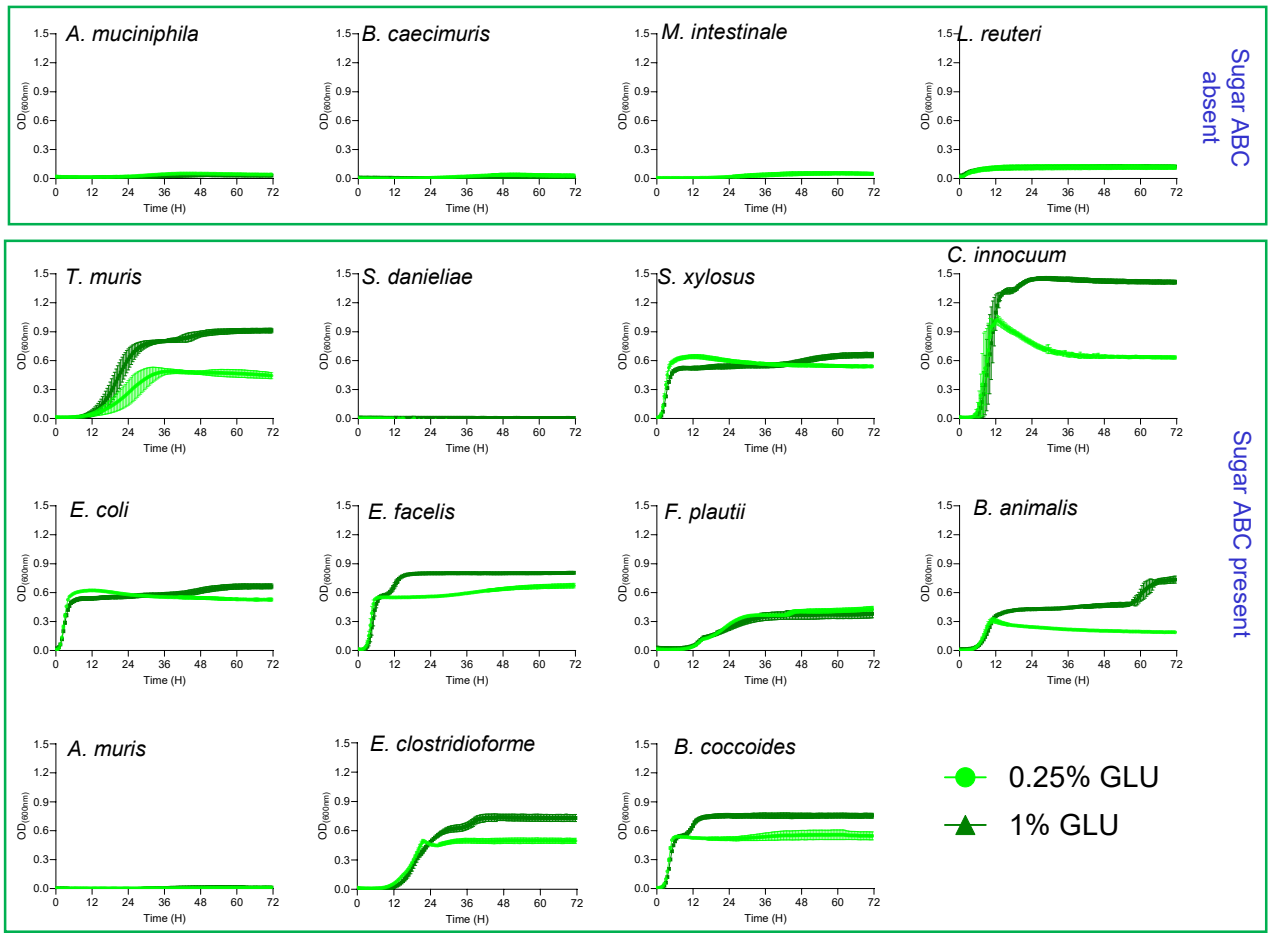
Supplementary Figure 9. Analysis of the growth (OD_{600}) of the indicated strains. Bacteria were cultured in BHI-NG medium supplemented with 0.25% and 1% galactose (GAL). Graphs represent mean ± SD from two independent experiments (n = 6)



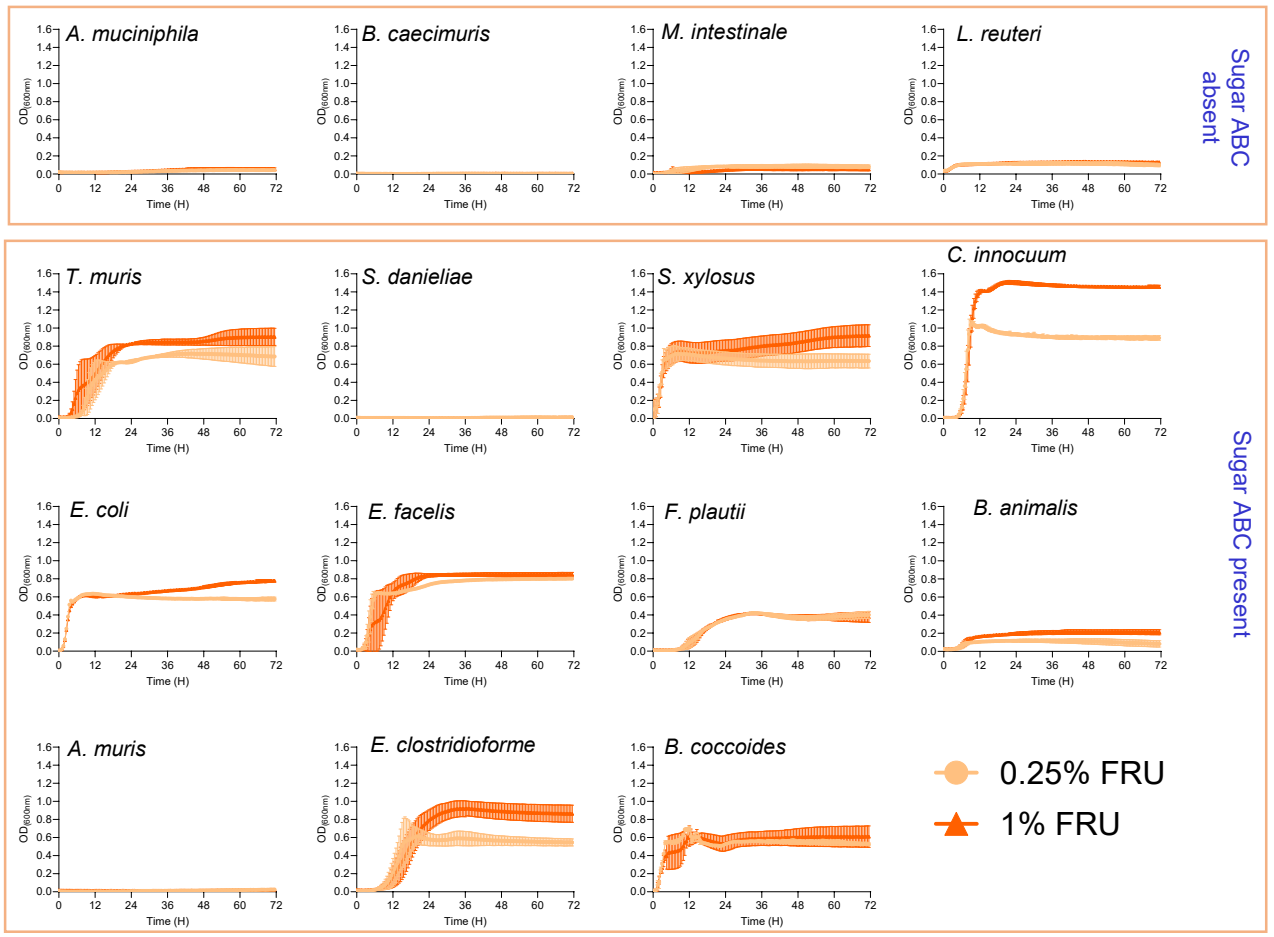
Supplementary Figure 10. a) Table showing the OMM[15] strains categorized based on their phylum. **b), c), d)** Enumeration of genes involved in sugar ABC, PTS and MFS transporters of the indicated bacteria.



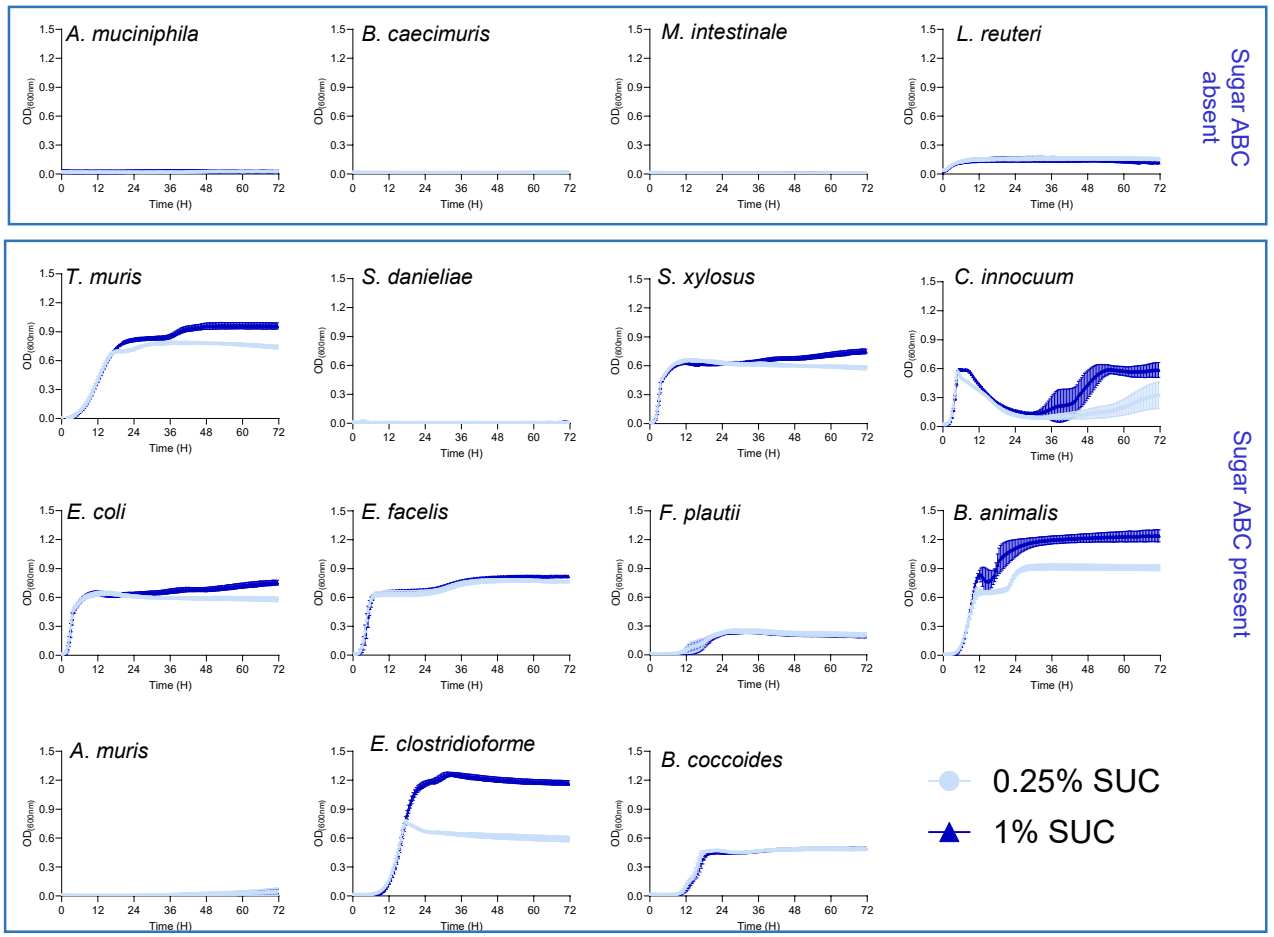
Supplementary Figure 11. Mean ± SD CFUs of the indicated species after 48 h. Statistical comparison was performed between 0.25% and 1% GLU for each species using an unpaired t-test with Welch's correction. Bacteria were cultured in BHI-NG medium supplemented with 0.25% and 1% glucose. Graphs represent mean ± SD from two independent experiments (n = 6).



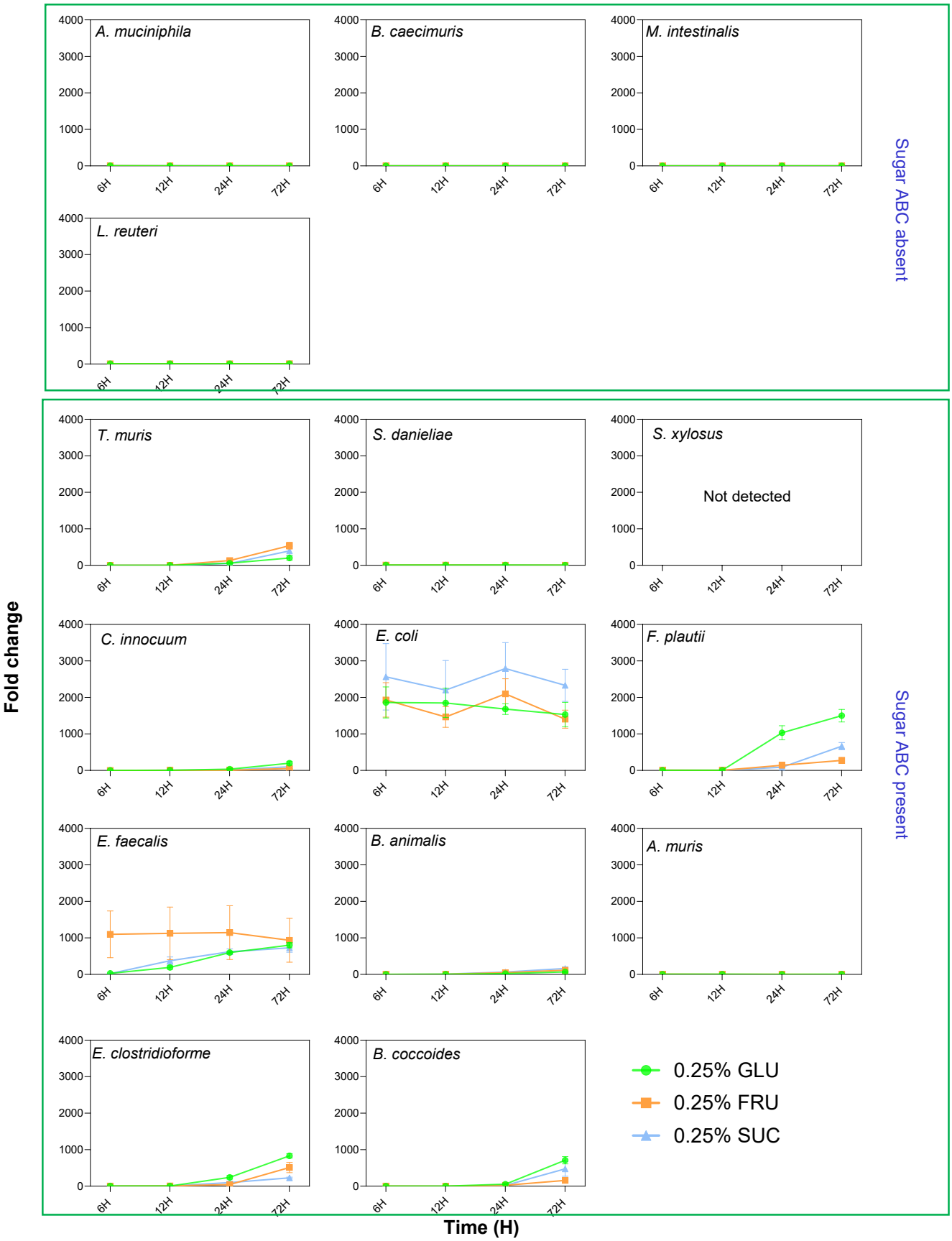
Supplementary Figure 12. Analysis of the growth (OD_{600}) of the indicated OMM^{15} strains. Bacteria were cultured in BHI-NG medium supplemented with 0.25% and 1% glucose. Graphs represent mean ± SD from two independent experiments (n = 6).



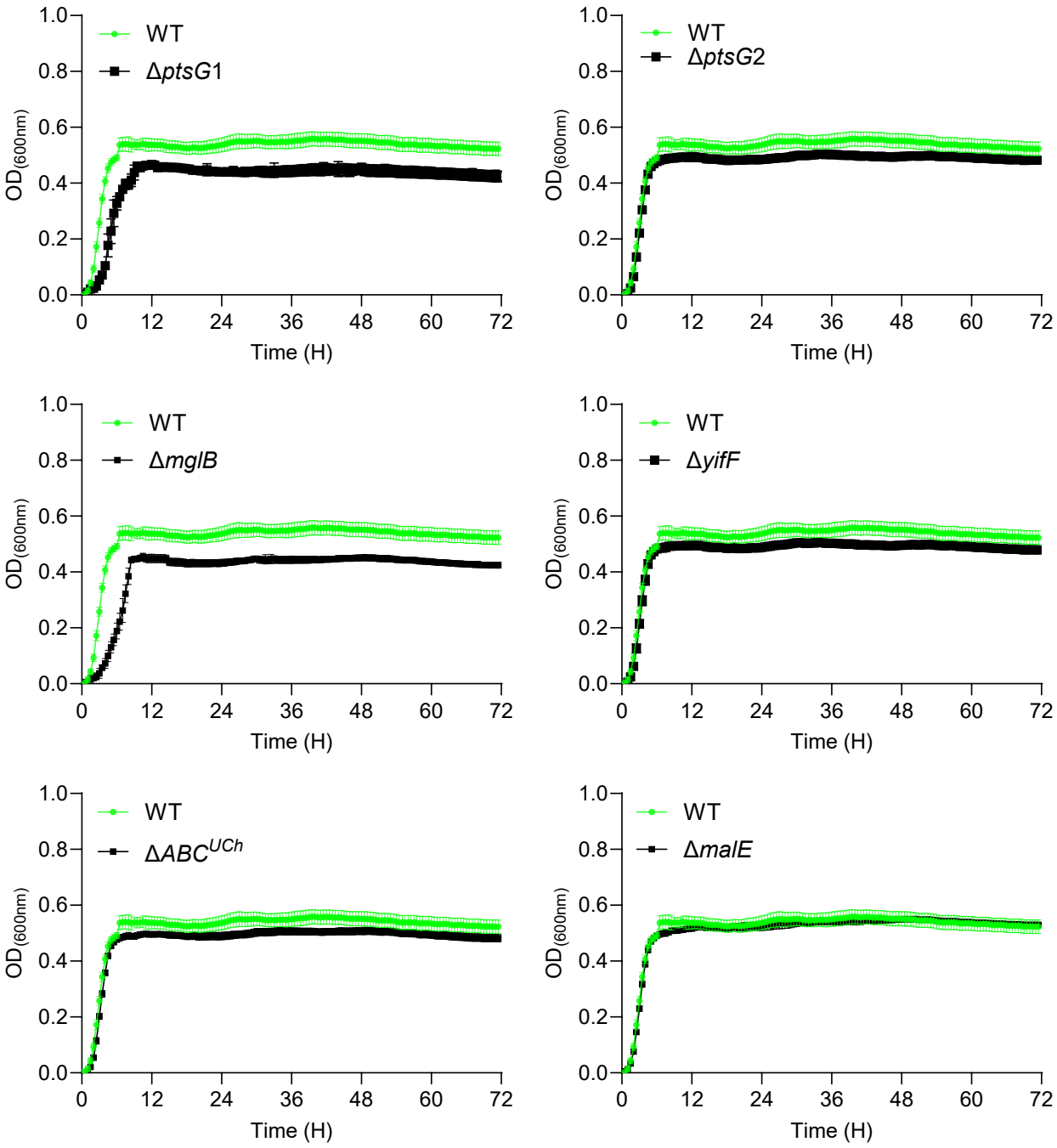
Supplementary Figure 13. Analysis of the growth (OD_{600}) of the indicated OMM^{15} strains. Bacteria were cultured in BHI-NG medium supplemented with 0.25% and 1% fructose. Graphs represent mean ± SD from two independent experiments (n = 6)



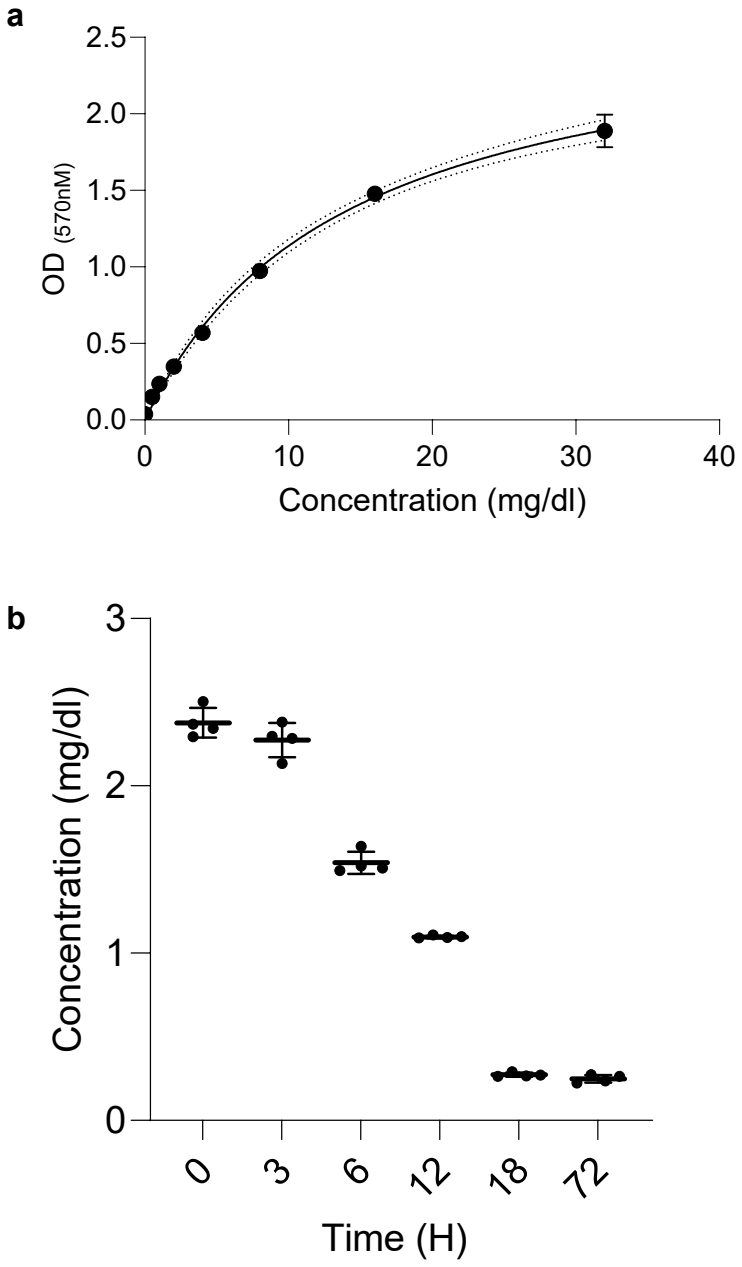
Supplementary Figure 14. Analysis of the growth (OD_{600}) of the indicated OMM^{15} strains. Bacteria were cultured in BHI-NG medium supplemented with 0.25% and 1% fructose. Graphs represent mean ± SD from two independent experiments (n = 6)



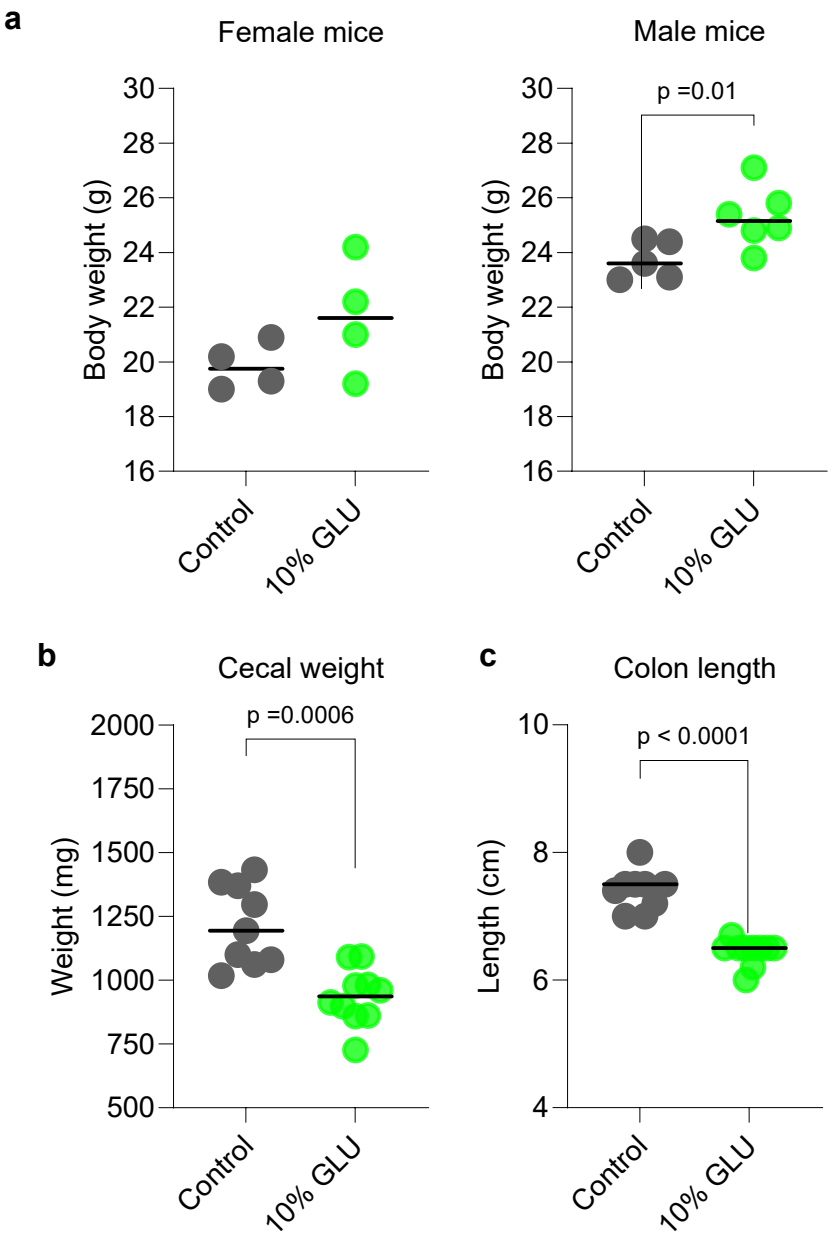
Supplementary Figure 15. Comparing the fold change in growth for each OMM[15] species when grown together as an *in vitro* community over a 72-hour period, as determined by quantitative PCR (qPCR). The 0-hour time point (inoculation) was selected as the baseline, and fold change was calculated based on comparisons between 0 to 6, 0 to 12, 0 to 24, and 0 to 72 hours. Bacteria were grown in BHI-NG medium supplemented with 0.25% glucose (GLU), fructose (FRU), or sucrose (SCU). Graphs represent mean ± SD from two independent experiments (n = 6). Data are combined from two independent biological experiments and qPCR was performed in technical duplicate for each species (n = 4).



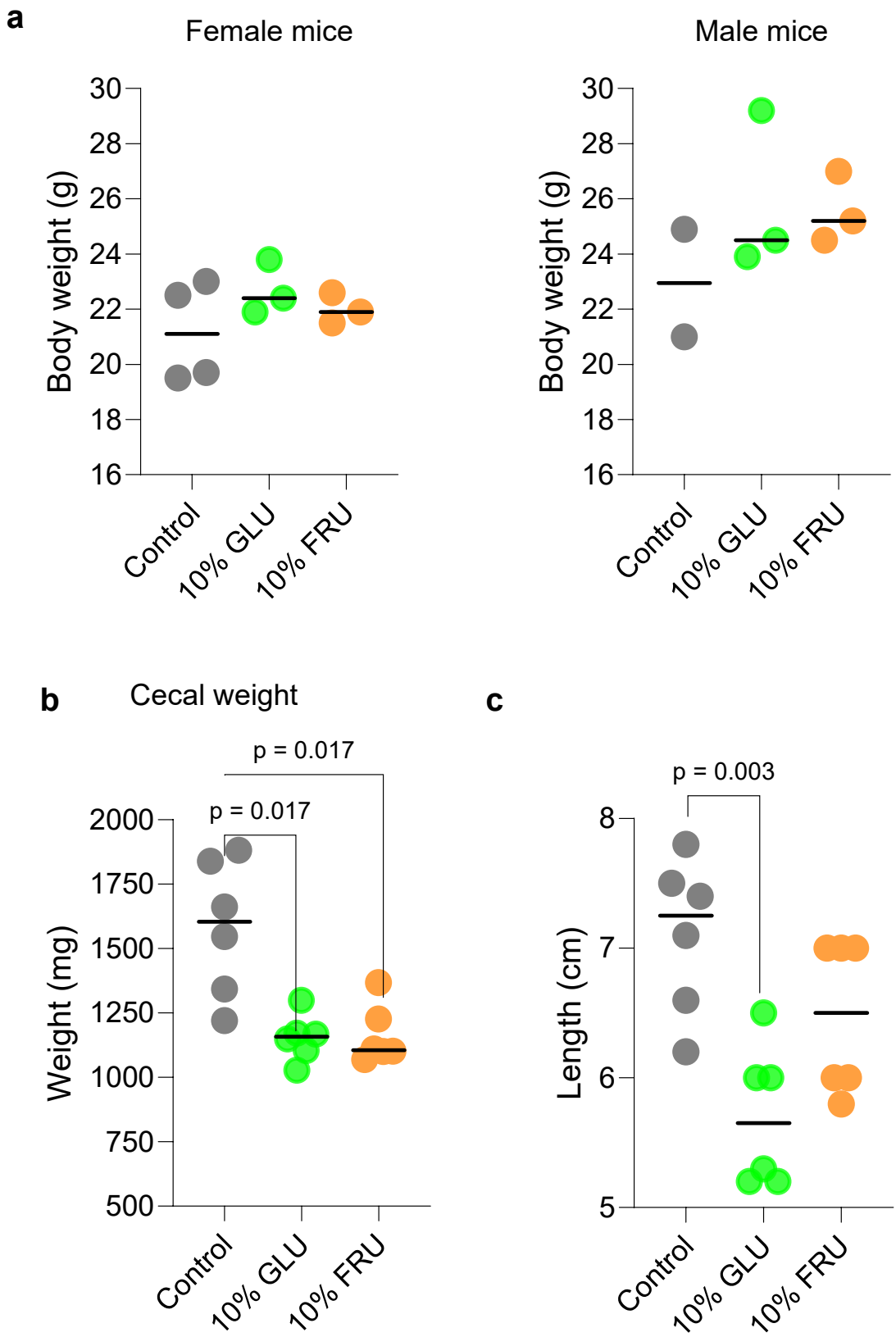
Supplementary Figure 16. Analysis of the growth (OD_{600}) of WT *E. coli* MT1B1 and its indicated sugar ABC and PTS transporters permease mutants. Bacteria were cultured in BHI-NG medium supplemented with 0.25% glucose. Graphs represent mean ± SD from two independent experiments (n = 6).



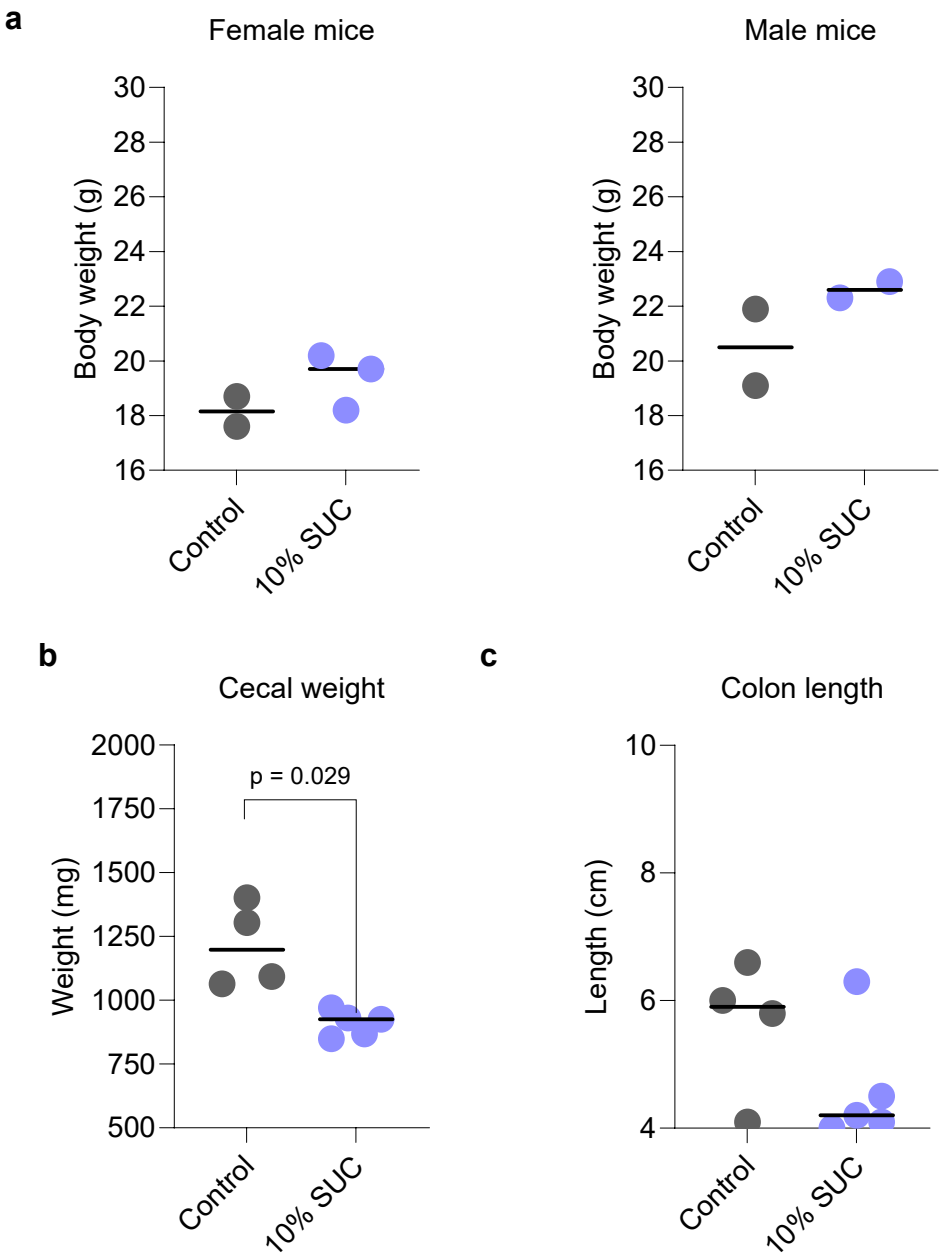
Supplementary Figure 17. a) Standard curve generated using the Invitrogen glucose colorimetric detection kit. Standards were used in in duplicates (n=2). **b)** Graph showing glucose concentrations over a period of 72-hour in an OMM[15] community cultured in 0.25%glucose (GLU). Samples were diluted 100 folds. Graphs represent mean ± SD from two independent experiments (n = 6)



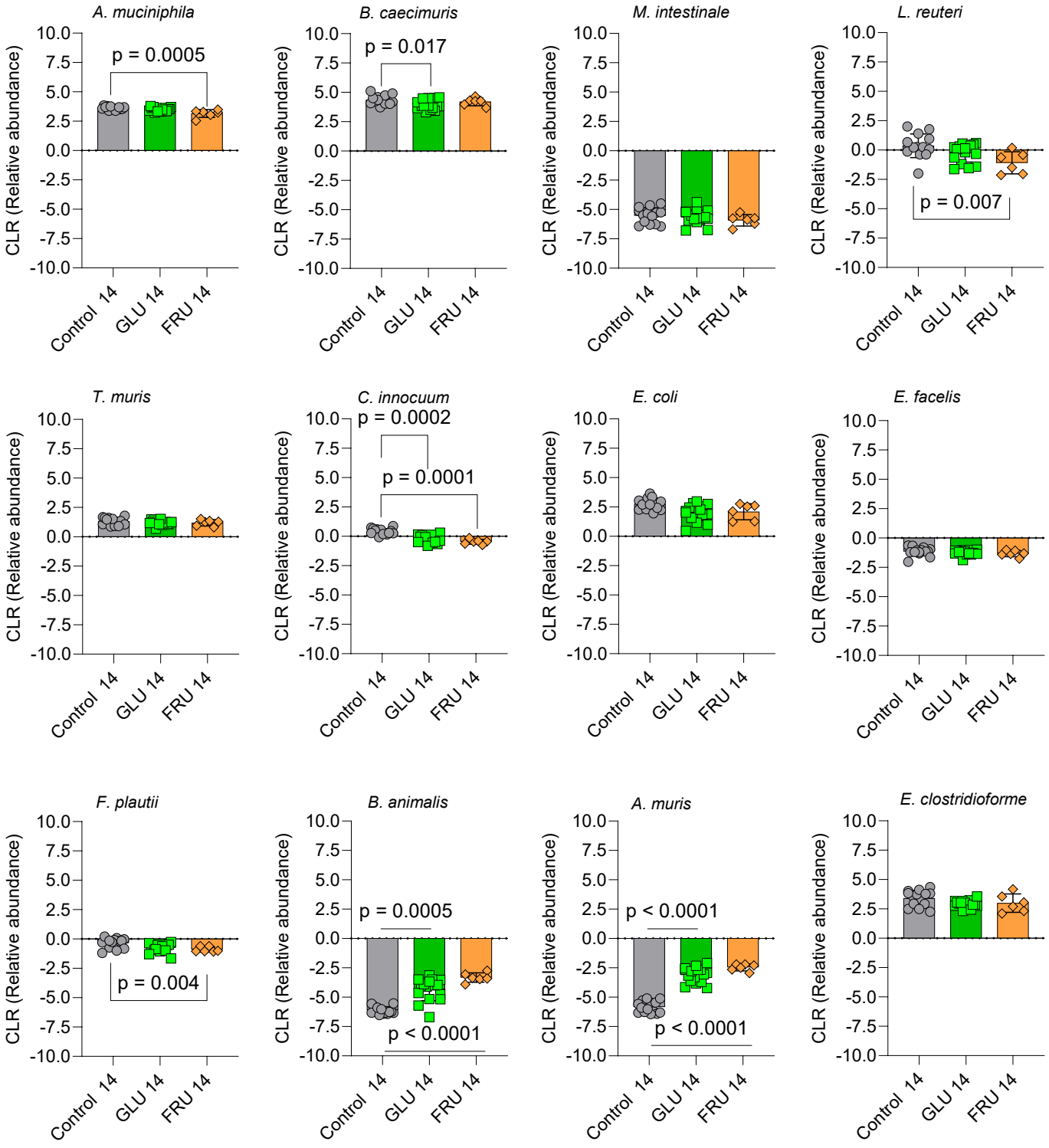
Supplementary Figure 18. Comparison of **a)** body weight, **b)** cecal weight, and **c)** colon length at day 14 between control mice and mice provided with 10% glucose (GLU) supplemented water. Graphs depict the mean and individual data points for each mouse from one experiment (n = 4 control female mice, n = 4 10% GLU female mice, n = 5 control male mice, and n = 6 10% GLU male mice). Statistical analysis was performed using an unpaired *t*-test with Welch's correction. $p < 0.05$ was considered statistically significant.



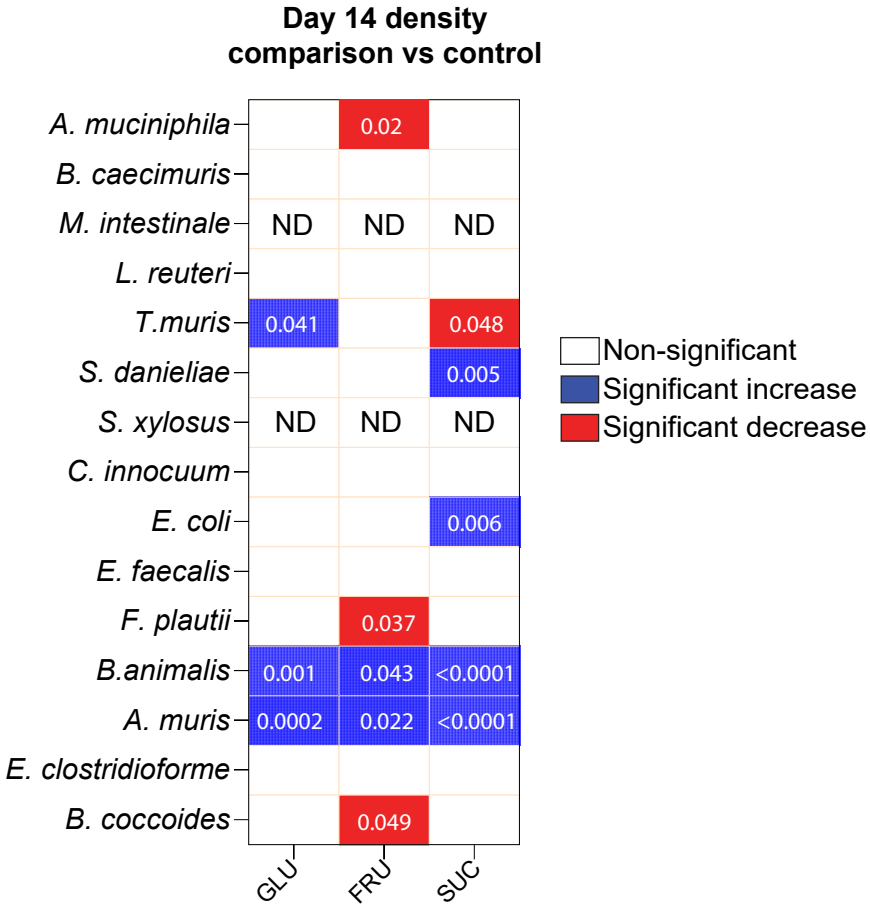
Supplementary Figure 19. Comparison of **a)** body weight, **b)** cecal weight, and **c)** colon length at day 14 between control mice and mice provided with 10% glucose (GLU) and 10% fructose (FRU) supplemented water. Graphs depict the mean and individual data points for each mouse from one experiment (n = 4 control female mice, n = 3 10% FRU female mice, n = 3 10% GLU female mice n = 2 control male mice, n = 3 10% FRU male mice and n = 3 10% GLU male mice). Statistical analysis was performed using an unpaired *t*-test with Welch's correction. $p < 0.05$ was considered statistically significant.



Supplementary Figure 20. Comparison of **a)** body weight, **b)** cecal weight, and **c)** colon length at day 14 between control mice and mice provided 10% sucrose (SUC) supplemented water. Graphs depict the mean and individual data points for each mouse from one experiment (n = 2 control female mice, n= 3 10% SUC female mice, n = 2 control male mice, n = 2 10% SUC male mice). Statistical analysis was performed using unpaired *t*-test with Welch's correction. $p < 0.05$ was considered statistically significant.



Supplementary Figure 21. Comparison of the CLR-transformed relative abundance of OMM[15] community members on day 14 between control mice and those provided with 10% GLU or FRU supplemented water. Data are combined from two independent experiments (n = 8 control female mice, n = 7 control male mice, n = 7 GLU female mice, n = 9 GLU male mice, n = 3 FRU female mice, n = 3 FRU male mice). Statistical analysis was performed using the Kruskal–Wallis test with Dunn's multiple comparisons, with adjusted p values reported. *S. danieliae* and *S. xylosus* were undetectable by 16S rRNA sequencing. $P < 0.05$ was considered statistically significant.



Supplementary Figure 22. Differences in density of OMM[15] species using normalized cT values (cT / fecal weight) from qPCR data of OMM[15] community members on day 14 between control mice and those provided with 10% glucose (GLU), fructose (FRU), or sucrose (SUC) supplemented water. Data were combined from three independent experiments (control: n = 10 females, n = 9 males; GLU: n = 7 females, n = 9 males; FRU: n = 3 females, n = 3 males; SUC: n = 3 females, n = 2 males). ND, not detected, *M. intestinale* and *S. xylosus* were below the qPCR detection limit. Statistical analysis was performed using the Kruskal–Wallis test with Dunn's multiple comparisons. Directionality of differences with adjusted p-values < 0.05 is indicated by color.

Supplementary table 1: List of bacterial species

Strain	Strain ID	Description/Source
Bifidobacterium adolescentis	ao_0067_0069_a1	BIO-ML
Bifidobacterium dentium	cx_0004_0053_g2	BIO-ML
Bifidobacterium longum	af_0058_0067_a1	BIO-ML
Bacteroides faecis	aa_0143_0089_f9	BIO-ML
Bacteroides fragilis	bf_0095_0017_a11	BIO-ML
Bacteroides salyersiae	bk_0021_0020_d1	BIO-ML
Bacteroides ovatus	af_0058_0006_c3	BIO-ML
Bacteroides thetaiotaomicron	af_0058_0071_a4	BIO-ML
Parabacteroides goldsteinii	aa_0143_0055_a8	BIO-ML
Bacillus cereus	af_0058_0034_c11.1	BIO-ML
Blautia massiliensis	af_0058_0067_h4.1	BIO-ML
Clostridium butyricum	bj_0095_0031_f8.1	BIO-ML
Enterococcus faecalis	av_0103_0014_c3	BIO-ML
Eubacterium rectale	aa_0143_098_a3	BIO-ML
Enterococcus mundtii	am_0171_0068_d4	BIO-ML
Leuconostoc lactis	aa_0143_0055_c12	BIO-ML
Lactobacillus paracasei	av_0103_0073_c8	BIO-ML
Lactobacillus rhamnosus	aa_0143_0087_g1	BIO-ML

Strain	Strain ID	Description/Source
Mediterraneibacter gnavus (Ruminococcus gnavus)	ATCC 29149	
Roseburia intestinalis	aa_0143_098_d11	BIO-ML
Sellimonas intestinalis	am_0224_0084_c8.2	BIO-ML
Klebsiella michiganensis	AD 9	The TaxUMAP atlas
Escherichia coli	AD 24	The TaxUMAP atlas
Akkermansia muciniphila	ATCC BAA-835	
Gordonibacter pamelaeae	aa_0143_0087_b9	BIO-ML
Bittarella massiliensis	am_0224_0084_d8.2	BIO-ML
Finegoldia sp.	am_0052_0084_f1.1	BIO-ML
Veillonella dispar	bj_0095_0068_g5	BIO-ML

BIO-ML
Broad Institute-OpenBiome Microbiome Library

Poyet, M. *et al.* A library of human gut bacterial isolates paired with longitudinal multiomics data enables mechanistic microbiome research. *Nat Med* **25**, 1442–1452 (2019).

The TaxUMAP atlas
Schluter, J. *et al.* The TaxUMAP atlas: Efficient display of large clinical microbiome data reveals ecological competition in protection against bacteremia. *Cell Host & Microbe* **31**, 1126-1139.e6 (2023).

Supplementary table 2: Glycolytic genes and their function

Gene	Pathway	Function	Reference
Glyceraldehyde 3-phosphate dehydrogenase **GAPDH**	EMP	Conversion of glyceraldehyde-3-phosphate to 1,3-bisphosphoglycerate	1,2
Hexokinase (ROK protein family) **HK**	EMP, PPP, ED	catalyzes the phosphorylation of glucose by ATP to glucose-6-phosphate	1,2
Pyruvate kinase **PK**	EMP	conversion of phosphoenolpyruvate to pyruvate	1,2
Phosphoglucomutase **PGM**	EMP, PPP, ED	PGM converts Glucose-1-Phosphate released from glycogen into Glucose-6-Phopsphate, which can then be used in the glycolytic pathways	1,2,3,4
Phosphofructokinase **PFK**	EMP	conversion of fructose-6-phosphate to fructose-1,6-diphosphate	1,2
Ribose-5-phosphate isomerase **RPI**	PPP	conversion of ribose-5-phosphate to ribulose-5-phosphate	1,4
Transketolase **TK**	EMP, PPP	Linking EMP to PPP pathway	1,4
Phosphogluconate dehydratase **6PGDH**	ED	6-phosphogluconate (6-PG) is dehydrated to 2-keto-3-deoxy-6-phosphogluconate	1,3
2-dehydro-3-deoxy-phosphogluconate aldolase **KDPG**	ED	Conversion of 2-Keto-3-deoxy-6-phosphogluconate (KDPG) to pyruvate and D-glyceraldehyde-3-phosphate	1,3

1.Wolfe, A. J. Glycolysis for the Microbiome Generation. *Microbiol Spectr* **3**, 10.1128/microbiolspec.MBP-0014–2014 (2015).

2.Sánchez-Pascuala, A., de Lorenzo, V. & Nikel, P. I. Refactoring the Embden–Meyerhof–Parnas Pathway as a Whole of Portable GlucoBricks for Implantation of Glycolytic Modules in Gram-Negative Bacteria. *ACS Synth. Biol.* **6**, 793–805 (2017).

3.Peekhaus, N. & Conway, T. What's for Dinner?: Entner-Doudoroff Metabolism in Escherichia coli. *Journal of Bacteriology* **180**, 3495 (1998).

4.Rashida, Z. & Laxman, S. The pentose phosphate pathway and organization of metabolic networks enabling growth programs. *Current Opinion in Systems Biology* **28**, 100390 (2021).

Supplementary table 3: MM[15] strains used in the study

Strain	Strain ID
Acutalibacter muris	MM12 KB18 (DSM 26090)
Akkermansia muciniphila	MM12 YL44 (DSM 26127)
Bacteroides caecimuris	MM12 I48 (DSM 26085)
Bifidobacterium animalis subsp. animalis	MM12 YL2 (DSM 26074)
Blautia coccoides	MM12 YL58 (DSM 26115)
Clostridium innocuum	MM12 I46 (DSM 26113)
Enterocloster clostridioforme	MM12 YL32 (DSM 26114)
Enterococcus faecalis	MM12 KB1 (DSM 32036)
Escherichia coli	Mt1B1 (DSM 28618)
Flavonifractor plautii	MM12 YL31 (DSM 26117)
Limosilactobacillus reuteri	MM12 I49 (DSM 32035)
Muribaculum intestinale	MM12 YL27 (DSM 28989)
Staphyloccocus xylosus	33-ERD13C (DSM 28566)
Streptococcus danieliae	ERD01G (DSM 22233)
Turicimonas muris	MM12 YL45 (DSM 26109)

Supplementary table 4: List of *Escherichia coli* MT1B1 mutants

Mutant	Description	Reference
ΔptsG1 (EIIC1)	Permease of first PTS transporter responsible for the transport of sugar molecules. Cm^r	1
ΔptsG2 (EIIC2)	Permease of second PTS transporter responsible for the transport of sugar molecules. Cm^r	1
ΔmglB	*mglB* is a high affinity uptake system of the MglBAC ABC transporter system, which is responsible for the uptake of D-galactose, glucose and methyl-D-galactoside. Cm^r	2
ΔABC^{Uch}	Unknown sugar ABC permease. Cm^r	This study
ΔyjfF	*yjfF* is a permease of YtfQRT-YjfF ABC transporter system which is responsible for the uptake of Galactofuranose. Cm^r	3
ΔmalE	*malE* is a high affinity uptake system of the MalEFGK ABC transporter system which is responsible for the uptake of maltose and maltodextrin. Cm^r	3

This strain possesses six putative genes encoding components of active sugar transporters, including two PTS permeases (EIIC1 and EIIC2), both annotated as *ptsG* in our screen but referred to here as *ptsG1* and *ptsG2* for clarity. Additionally, it contains four sugar ABC transporter components: two high affinity transport systems *mglB* and *malE*; *yjfF,* an inner membrane sugar ABC protein; and one uncharacterized gene functionally assigned as a sugar ABC permease (*ABC^{UCh}*).

1.McCoy, J. G., Levin, E. J. & Zhou, M. Structural insight into the PTS sugar transporter EIIC. *Biochimica et biophysica acta* **1850**, 577 (2014).

2.Ferenci, T. Adaptation to life at micromolar nutrient levels: the regulation of Escherichia coli glucose transport by endoinduction and cAMP. *FEMS Microbiology Reviews* **18**, 301–317 (1996).

3.Blattner, F. R. *et al.* The complete genome sequence of Escherichia coli K-12. *Science* **277**, 1453–1462 (1997).

Supplementary table 5: Sugar - sweetened beverages consumed by HCT patients

FNDDS Food Code	Description	Prevalence in 1009 samples	Sugars per g (g)
92410610	Soft drink, ginger ale	206	1.01
95320200	Sports drink (Gatorade G)	142	0.79
92410310	Soft drink, cola	93	0.93
92309000	Tea, iced, bottled, black	88	0.86
95103000	Nutritional drink or shake, ready−to−drink (Ensure)	83	0.38
92410510	Soft drink, fruit flavored, caffeine free	50	0.88
92513000	Fruit flavored smoothie drink, frozen, no dairy	46	0.86
95103010	Nutritional drink or shake, ready−to−drink (Ensure Plus)	35	0.18
95104000	Nutritional drink or shake, ready−to−drink, sugar free (Glucerna)	8	0.13
95101010	Nutritional drink or shake, ready−to−drink (Boost Plus)	6	0.23
95322200	Sports drink, low calorie (Gatorade G2)	5	0.63
95220000	Nutritional powder mix, NFS	5	0.24
92510610	Fruit juice drink	3	1.00
92530610	Fruit juice drink, with high vitamin C	3	0.90
92101900	Coffee, Latte	3	0.45
92510955	Lemonade, fruit juice drink	2	0.96
92306800	Tea, hot, chai, with milk	1	0.74
95330100	Fluid replacement, electrolyte solution	1	0.69
95106000	Nutritional drink or shake, ready−to−drink (Muscle Milk)	1	0.07
95202000	Nutritional powder mix (Muscle Milk)	1	0.07

Sugar-sweetened beverages were defined as beverages with added sugar, not including enteral formulae. Sugars per gram of food are reported, as they appear in the FNDDS database.

Supplementary table 6: List of plasmids used to generate *Escherichia coli* MT1B1 mutants

Plasmid	Resistance	Reference
pkd46	Amp^r	1
pkd3	Amp^r, Cm^r	1

Amp^r– tetracycline resistance, Cm^r – chloramphenicol resistance

1.One-step inactivation of chromosomal genes in Escherichia coli K-12 using PCR products | PNAS.

Supplementary table 7: List of primers used to generate *Escherichia coli* MT1B1 mutants

Mutant	Primers
Δ*ptsG*1 (*EIIC*1)	Forward 5' GTTCTATCGTCTACGGCGCACCGCGTAATTTCAGCATTACCGGCACGTATCAGTTCTGAAT AACACCTGTAAAAAAGGCAGCCATCTGGCTGCCTTAGTCTCCCCAACGTCTTACGGAGCCA TGGTCCATATGAATATCCTCCTTAG - '3 Reverse 3' - CGGCACTGAATTATTTTACTCTGTGTAATAAATAAAGGGCGCTTAGATGCCCTGTACACGG CGAGGCACTCCCCCCTTGCCACGCGTGAGAACGTAAAAAAAGCACCCATACTCAGGAGCA CTCTCAATTGTGTAGGCTGGAGCTGCTTC- '5
Δ*ptsG*2 (*EIIC*2)	Forward 5' GAATCTAATATTATTAAACTATTACCTGAACTAACTTTTCACACATCATAAAATGGATATGGC ATACATGCTTTATTGGGATGTATAAATATCCAGGACAACAGGGCCATGGTCCATATGAATAT CCTCCTTAG - '3 Reverse 3' - GCCCGGCACAACGTATGGCTTCCATCGCATCAGAACGAGCCTGTCCCGCGTTGATCAGTA ACTCCATAACAAGTTCTTCATCTGCAAACATCACAATCTCCTTCCTGGGTAAATGGTGTAGG CTGGAGCTGCTTC- '5
Δ*mglB*	Forward 5' GTGAGCTTCGGCGTTCAGTAACACTTCATTAACTCTACTGCCCCGCCGAGCATTTATCTCA AGCACTACCCTGCATAAGAAAAACCGGAGATACGCCATGGTCCATATGAATATCCTCCTTA G - '3 Reverse 3' - CCGCTCATTTCCAACAAGTATTCCCCGGAAGACGGAGTCGTTGAGCTGACCATATAATTTT ACCTTGTTGGTCATACAATAAGGGCGCAGTAAACGACTGCGCCCAATCAGTCGTGTAGGC TGGAGCTGCTTC- '5
Δ*ABC*^{UK}	Forward 5' CCACGGATGAAACCACCGACACCACCATGCTGTTACGGAAGTAGTCGACAAACGGGAAAA TCACCGGATTAAAAATGTCGACGTAATGCTCCAGCGTGCCATGGTCCATATGAATATCCTC CTTAG - '3 Reverse 3' - GCCGAATCAGCTAATCAGCGAACTGCCAAATATTCAGGTCTTTGGCGCAGTAGGGGATAAA AACTTTACCCGCATGGGCGATGTCACGGGGTCTGGTGTGGTGAGTTCAATGGGTGTAGGC TGGAGCTGCTTC- '5
Δ*yjfF*	Forward 5' GAGTGCAACCCGATGGCATTCCTGGCGGAACAAGCGGGCGGTAAAGCGAGCGATGGCAA AGAGCGTATTCTGGATATTATCCCGGAAACCCTGCACCAGCGCCGCCATGGTCCATATGA ATATCCTCCTTAG - '3 Reverse 3' - GCTTTCTGGCTTTCCGCCGGAGATGAACCAGGTGGTGAAAGCGGTGGTGGTGCTTTGCGT GCTGATTGTCCAGTCGCAACGCTTTATCAGTCTGATTAAAGGGGTACGTAACCGTGTAGGC TGGAGCTGCTTC- '5
Δ*malE*	Forward 5' CACACAAAGCAACGATGGGGCGTAGGGGCAAGGAGGATGGAAAGAGGTTGCCGTATAAA GAAACTAGAGTCCGTTTAGGTGTTTTCACGAGCACTTCACCAACAAGGACCATAGATTGCC ATGGTCCATATGAATATCCTCCTTAG - '3 Reverse 3' - GGCTTTCATACCTTATCCGACAACAACTGCCTGATGCGACGCTGACGCGTCTTATCAGGCC TACATACGTTTCAATTTCGTAGGCCGGATAAGGCGTTCACGCCGCATCCGGCATTTCACAG CAGTGTAGGCTGGAGCTGCTTC- '5

Supplementary table 8: List of MM[15] qPCR primers used in this study

Strain	Primers
Acutalibacter muris	FW - TGGCAAGTCAGTAGTGAAATCCA RV - TCACTCAAGCTCGACAGTTTCAA
Akkermansia muciniphila	FW - CGGGATAGCCCTGGGAAA RV - GCGCATTGCTGCTTTAATCTTT
Bacteroides caecimuris	FW - GGCAGCATGGGAGTTTGCT RV - TTATCGGCAGGTTGGATACGT
Bifidobacterium animalis subsp. animalis	FW - GGGTGAGTAATGCGTGACCAA RV - CGGAGCATCCGGTATTACCA
Blautia coccoides	FW - GAAGAGCAAGTCTGATGTGAAAGG RV - CGGCACTCTAGAAAAACAGTTTCC
Clostridium innocuum	FW - CGGATCGTAAAGCTCTGTTGTAAG RV - GCTACCGTCACTCCCATAGCA
Enterocloster clostridioforme	FW - AATACCGCATAAGCGCACAGT RV - CCATCTCACACCACCAAAGTTTT
Enterococcus faecalis	FW - CTTCTTTCCTCCCGAGTGCTT RV - CCCCTCTGATGGGTAGGTTACC
Escherichia coli	FW - GGACCTTCGGGCCTCTTG RV -CCTTTACCCCACCTACTAGCTAATCC
Flavonifractor plautii	FW - AGGCGGGATTGCAAGTCA RV - CCAGCACTCAAGAACTACAGTTTCA
Limosilactobacillus reuteri	FW - GCACTGGCTCAACTGATTGATG RV - CCGCCACTCACTGGTGATC
Muribaculum intestinale	FW - TCAAGTCAGCGGTAAAAATTCG RV - CCCACTCAAGAACATCAGTTTCAA
Staphyloccocus xylosus	FW - GGAGCTAATACCGGATAACATTTAGAA RV - CCATCTATAAGTGATAGCAAAACCATCT
Streptococcus danieliae	FW - CAACTGCATCACTACCAGATGGA RV - CGCCTAGGTGAGCCTTTACCT
Turicimonas muris	FW - AGACGGCCTTCGGGTTGTA RV - CGTCATCGTCTATCGGTATTATCAA

Reference

Brugiroux, S. *et al.* Genome-guided design of a defined mouse microbiota that confers colonization resistance against Salmonella enterica serovar Typhimurium. *Nat Microbiol* **2**, 1–12 (2016).