Supplemental Figure Legends

Figure S1. Fold-change responses of *Bt* wild-type and ΔCPS (non-capsulated) strains in response to AP maize and PG potato exposure under the same conditions used in **Fig. 1** of the main text (2 hours after being introduced into glycan-containing medium from mid-exponential growth in MM-glucose). Values represent the mean ± standard deviation of three replicates. *P*-values (*t* test) are shown between the wild-type and ΔCPS strains in each condition.

Figure S2. Histogram plots of fluorescent labeling intensities of cells taken from the various growth conditions shown in **Fig. 2** of the main text. Dashed red lines are used to indicate the threshold used to exclude possible background/non-induced fluorescence levels and correspond to the same threshold shown in the **Fig. 2A** scatter plots. This threshold was set near the high end of the MM-glucose distributions to exclude >97.5% of the cells in the no antibody and glucose conditions.

Figure S3. Representations of the various glycan structures used in this study. Note that for some glycans the structures shown are only representative of some of the possible forms and that other variations are possible, including in the materials used in this study. This is especially true for mucin *O*-linked glycans that may encompass nearly 10^2 different structures, built from the same 5 monosaccharides.

Figure S4. Growth time course experiments in which the concentration of PSM-11 (an earlier version of PSM-12 that lacked mucin *O*-linked glycans) was titrated to determine a level at which glycan concentration was limiting. Although the final mixture used contained mucin *O*-linked glycans the additional glycans added to the 1.1 mg ml^{-1} concentration used were far less than would be needed to increase the total carbohydrate to a level where it is not limiting based on these titration results.

Figure S5. *Bt* PUL expression over time post exposure to PSM-12, second of three replicates.

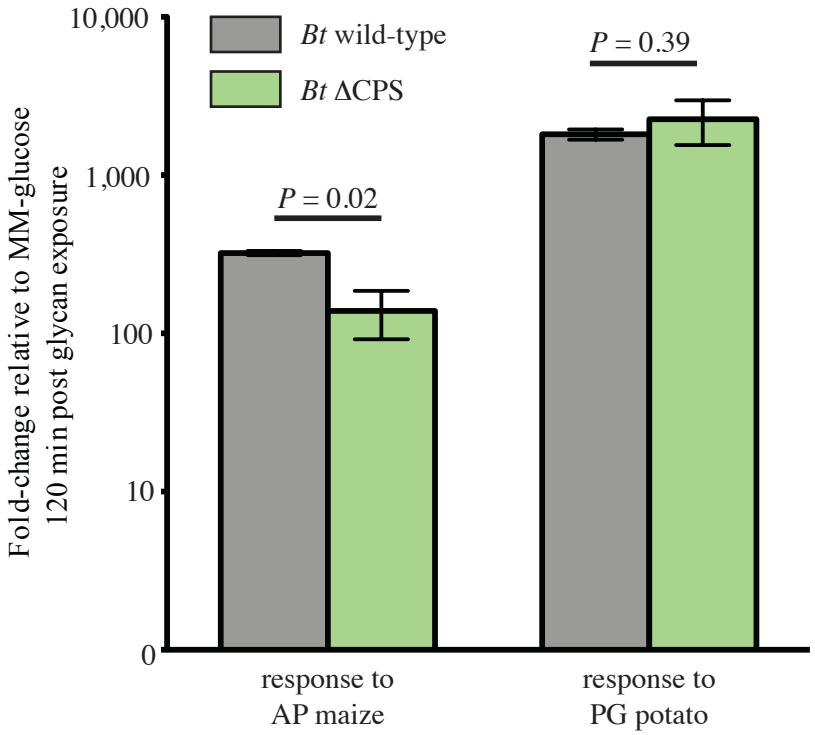
Figure S6. *Bt* PUL expression over time post exposure to PSM-12, third of three replicates.

Figure S7. *Bt* PUL expression over time post exposure to a mixture of PSM-12, and sub-cultured into fresh media at 6 hours post PSM-12, second of three replicates.

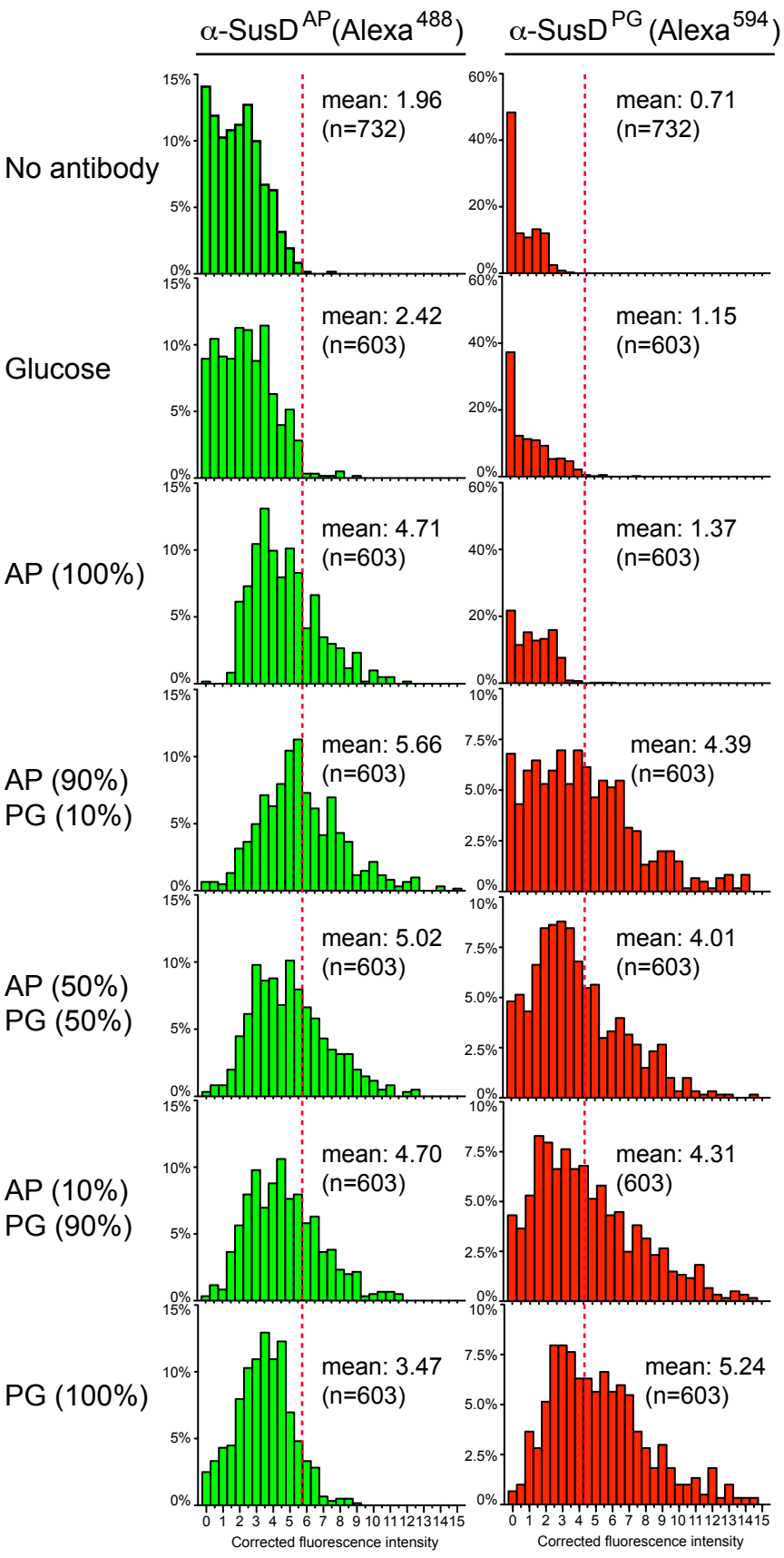
Figure S8. *Bt* PUL expression over time post exposure to PSM-12 and sub-cultured into fresh media at 6 hours post PSM-12, third of three replicates. Note that in this replicate, only the responses of the culture receiving fresh PSM-12 were monitored (dashed lines) and are shown relative to the two time points taken immediately prior to adding new PSM-12 to validate the trends observed in replicates 1 and 2.

Figure S9. Expression of four PULs associated with mucin *O*-linked glycan degradation over the same 12 hr time course depicted in **Fig. 5** of the main text and the time courses in Supplemental Figures S4 and S5.

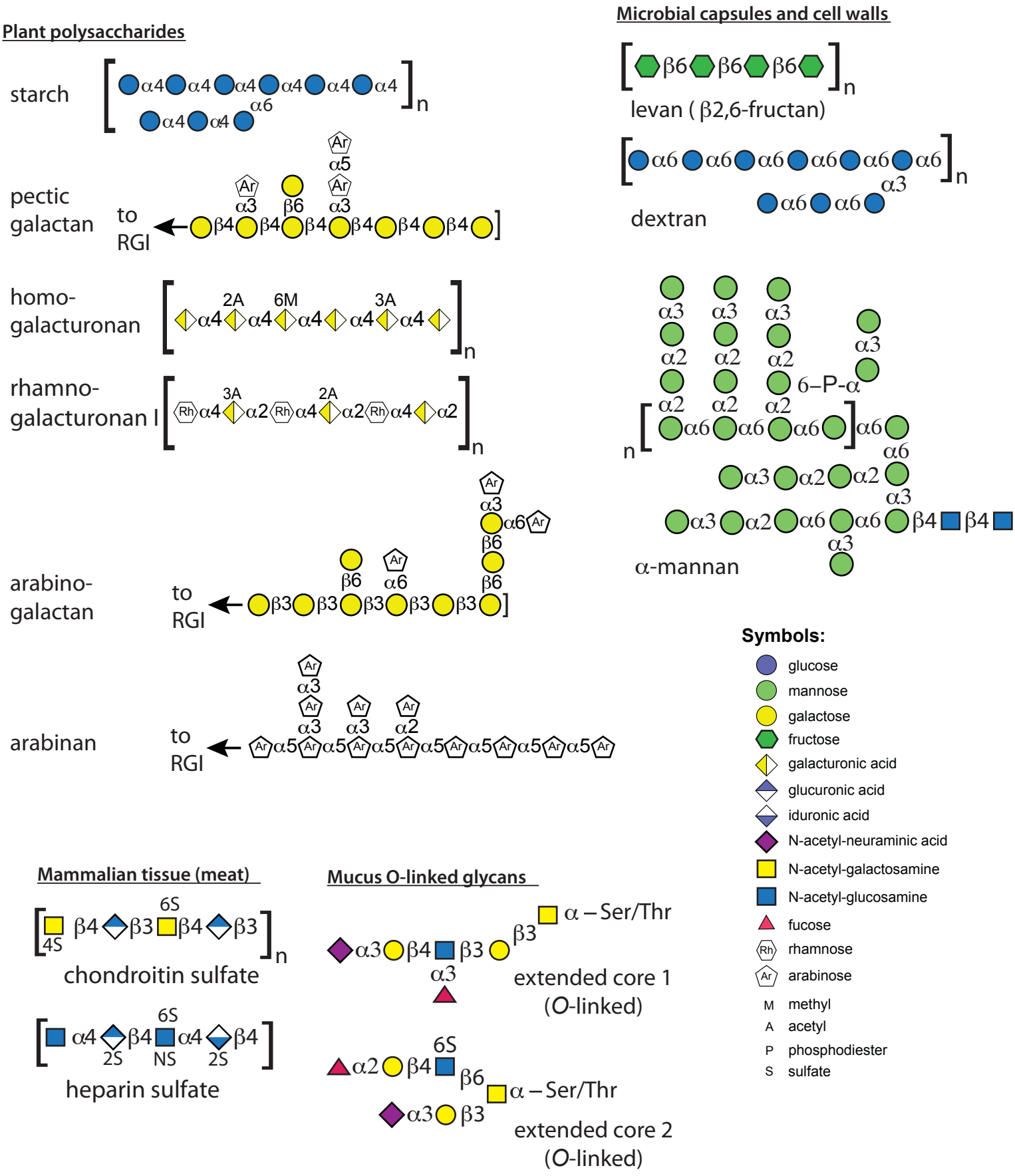
Rogers et al. Figure S1



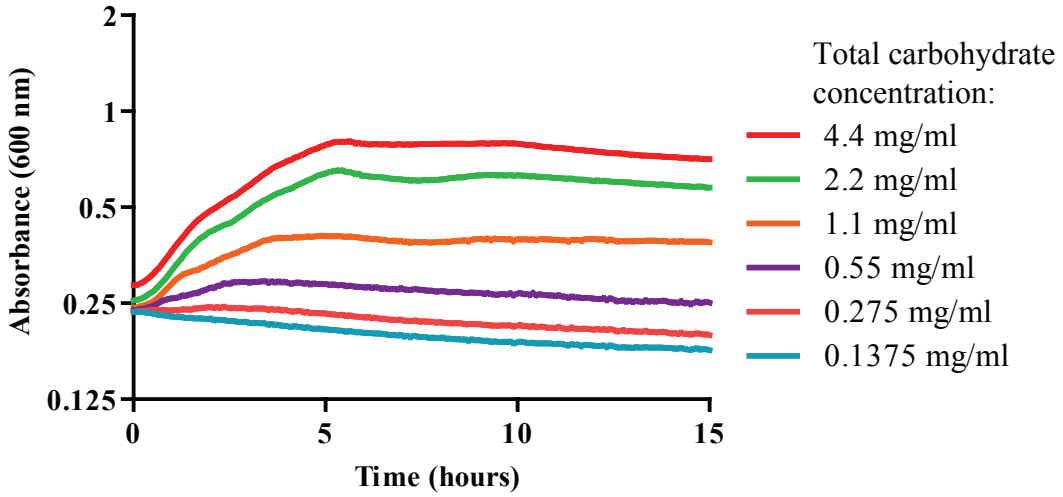
Rogers et al. Figure S2



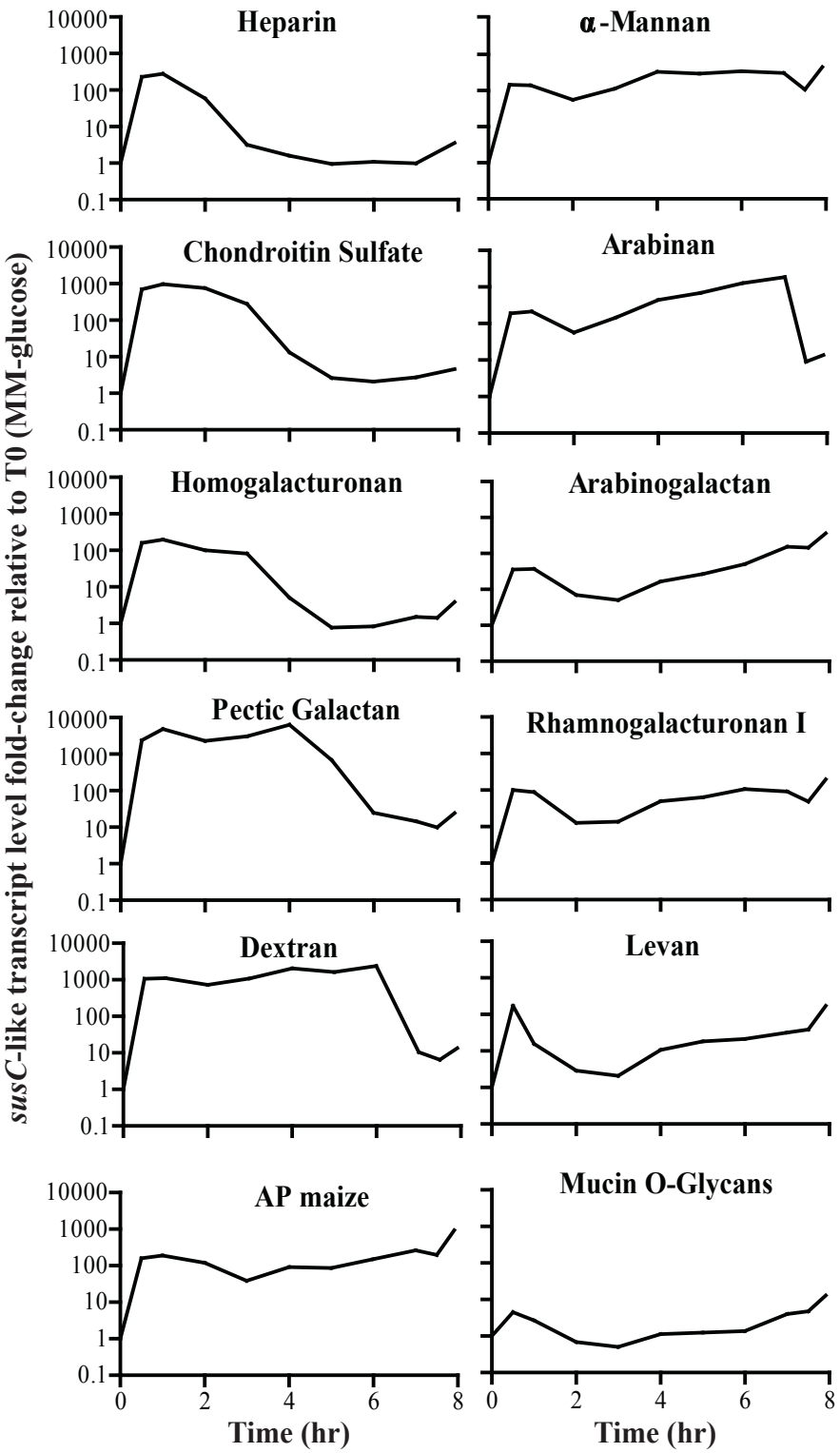
Rogers et al. Figure S3



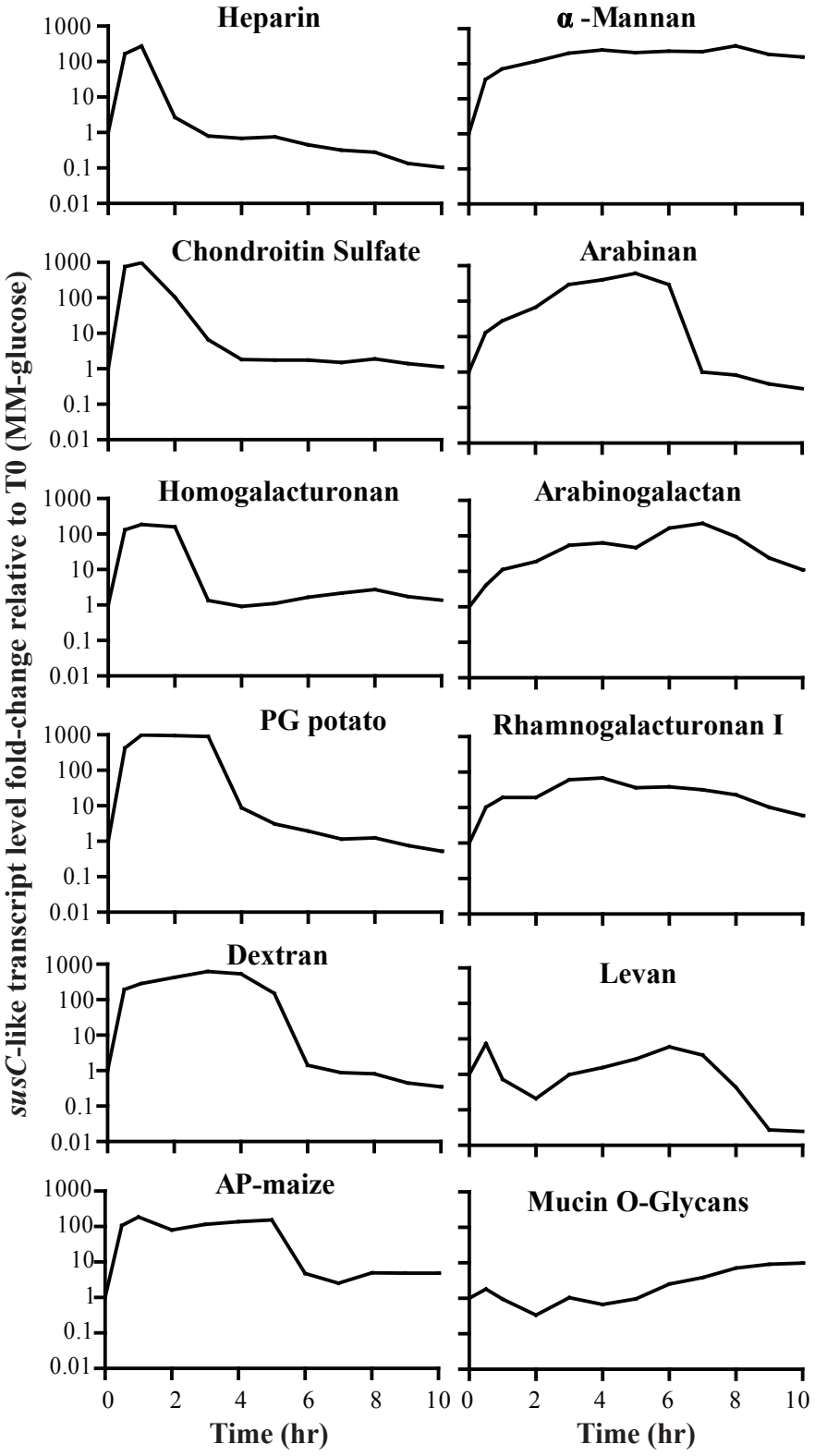
Rogers et al. Figure S4



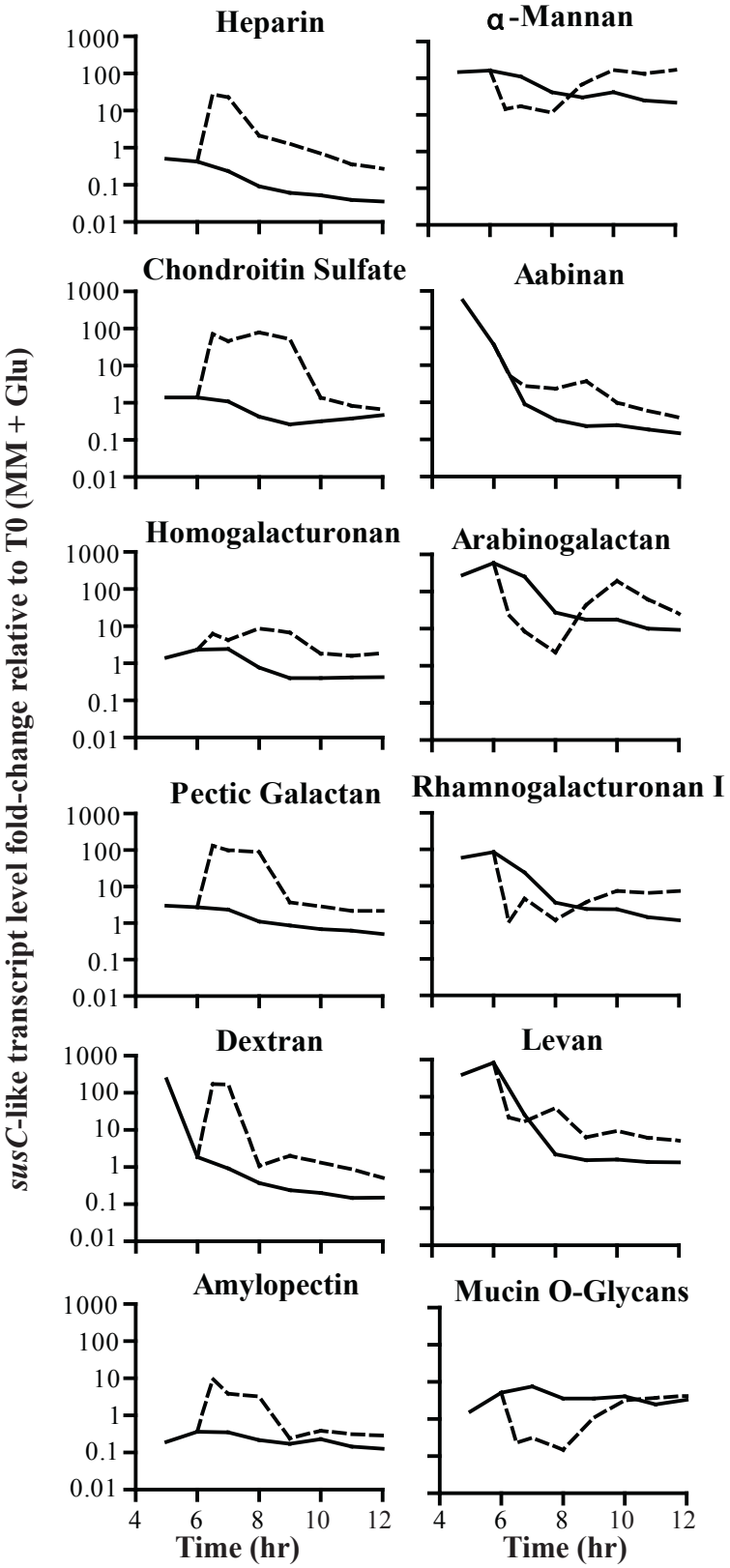
Rogers et al. Figure S5



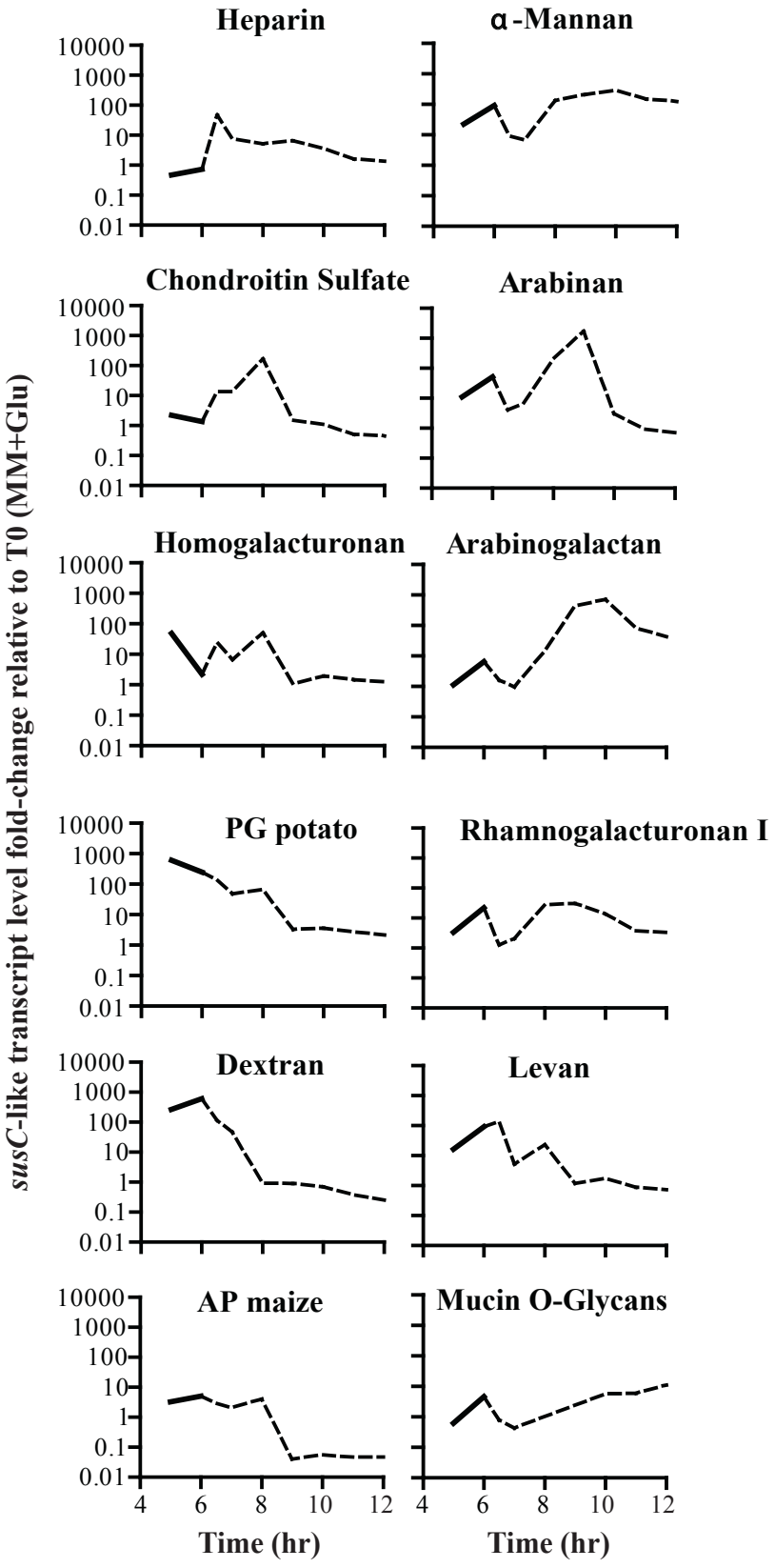
Rogers et al. Figure S6



Rogers et al. Figure S7



Rogers et al. Figure S8



Rogers et al. Figure S9

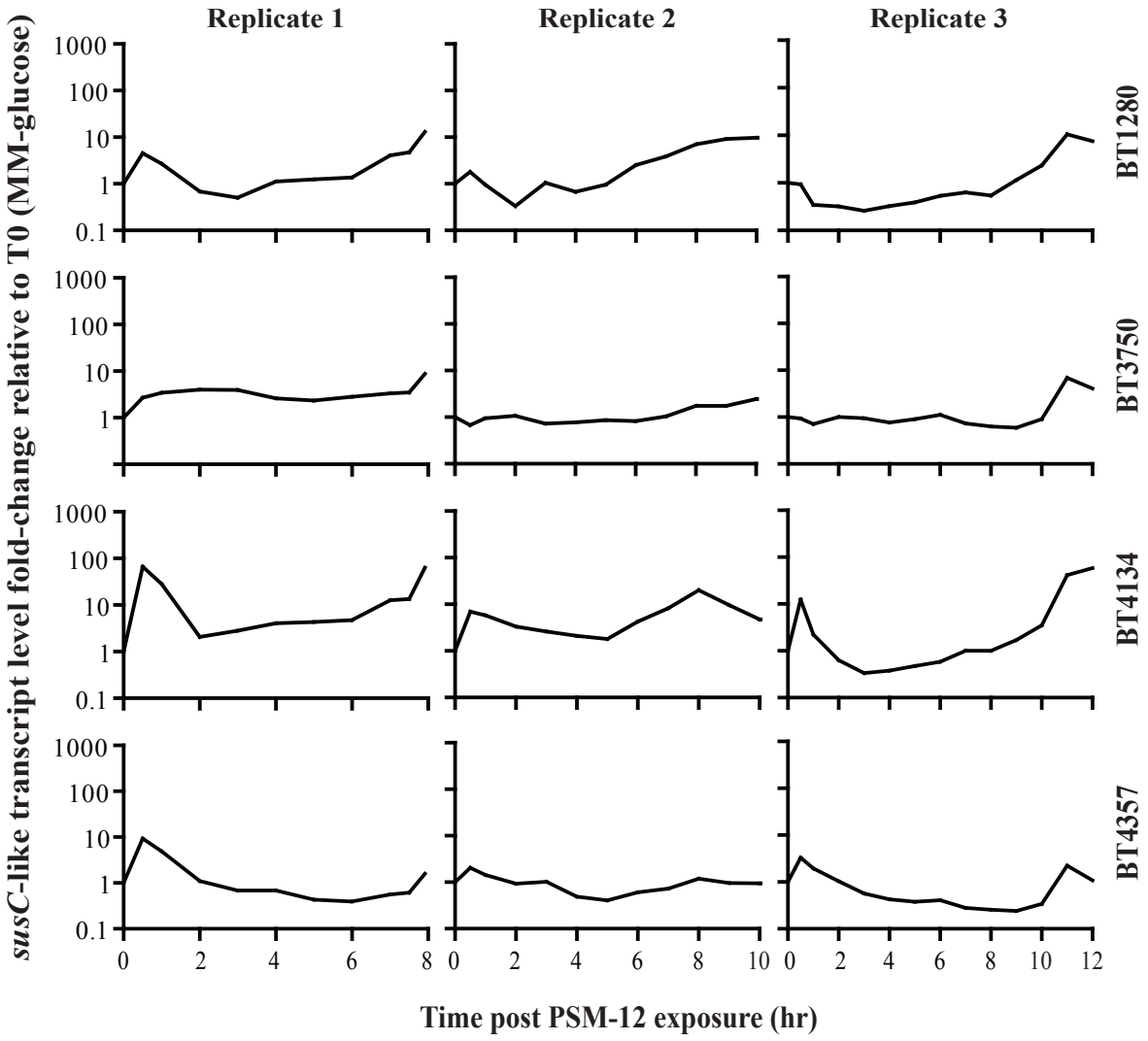


Table S1. Bacterial strains used

Bacterial Strain	**Features**
B. thetaiotaomicron VPI-5482 (ATCC 29148)	Wild-type
B. thetaiotaomicron Δ*tdk*	VPI-5482 with *tdk* deletion (Koropatkin et al., 2008)
B. thetaiotaomicron Δ*BT3701*	*B. thetaiotaomicron* Δ*tdk* with *BT3701* deletion
B. thetaiotaomicron Δ*BT4670*	*B. thetaiotaomicron* Δ*tdk* with *BT4670* deletion
B. thetaiotaomicron Δ*BT3701*, Δ*BT4670*	*B. thetaiotaomicron* Δ*tdk* with *BT3701* and *BT4670* deletions
B. thetaiotaomicron ΔCPS	*B. thetaiotaomicron* Δ*tdk* with deletions in all eight capsule synthesis loci
B. thetaiotaomicron ΔCPS, Δ*BT3701* (*susD*)	*B. thetaiotaomicron* ΔCPS all with *BT3701* deletion
B. thetaiotaomicron ΔCPS, Δ*BT4670*	*B. thetaiotaomicron* ΔCPS all with *BT4670* deletion
E. coli S17-1 λ *pir*	Donor for conjugation of suicide plasmids into *B. thetaiotaomicron*

Table S2. Oligonucleotides used in this study

Primers	Sequence (written 5' to 3')	Source/Use
***Bt* gene deletions**	(Restriction sites are indicated as underlined text)	
cps1 left 750 SalI	gcggtcgacggttcaataatcgtctgaagaga	cps1 deletion using pExchange-*tdk*
cps1 left internal	ggatttcttgctggacaggaac	cps1 deletion using pExchange-*tdk*
cps1 right 750 XbaI	gcgtctagacatgtgcgtggatttaacaggc	cps1 deletion using pExchange-*tdk*
cps1 right internal	gttcctgtccagcaagaaatccgtcattaacggcgtagacctg	cps1 deletion using pExchange-*tdk*
cps2 left 750 SalI	gcggtcgacagctgaaaaagaactccatacag	cps2 deletion using pExchange-*tdk*
cps2 left internal	cattatcacccattacccctttg	cps2 deletion using pExchange-*tdk*
cps2 right 750 XbaI	gcgtctagacttgcgttttaccgctcatcc	cps2 deletion using pExchange-*tdk*
cps2 right internal	caaggggtaatgggtgataatgctaaatcgtaatccggttctaag	cps2 deletion using pExchange-*tdk*
cps3 left 750 SalI	gcggtcgacgaatatcagtctgcacttcgc	cps3 deletion using pExchange-*tdk*
cps3 left internal	attctcaatccccaccttgttc	cps3 deletion using pExchange-*tdk*
cps3 right 750 XbaI	gcgtctagacaatcagaagtacaaaaggaattatg	cps3 deletion using pExchange-*tdk*
cps3 right internal	gaacaaggtggggattgagaatgtgcagatgaaaaactggatttga	cps3 deletion using pExchange-*tdk*
cps4 left 750 SalI	gcggtcgacgaaaccagctagctttttgtagc	cps4 deletion using pExchange-*tdk*
cps4 left internal	taggatattactccaattacctgc	cps4 deletion using pExchange-*tdk*
cps4 right 750 XbaI	gcgtctagagtgtaggacgttacgaagaatcc	cps4 deletion using pExchange-*tdk*
cps4 right internal	gcaggtaattggagtaatatcctaactaaaaatcatctatttaccccac	cps4 deletion using pExchange-*tdk*
cps5 left 750 SalI	gcggtcgacggagacgaagaggcacc	cps5 deletion using pExchange-*tdk*
cps5 left internal	gaattatcccgaacgttttgctc	cps5 deletion using pExchange-*tdk*
cps5 right 750 XbaI	gcgtctagagaccagctccggaaccgac	cps5 deletion using pExchange-*tdk*
cps5 right internal	gagcaaaacgttcgggataattcgccttcccctgtcccattaat	cps5 deletion using pExchange-*tdk*
cps6 left 750 SalI	gcggtcgacggctgaaacgactggtaaaac	cps6 deletion using pExchange-*tdk*
cps6 left internal	gcaagtttggcaaggtcg	cps6 deletion using pExchange-*tdk*
cps6 right 750 XbaI	gcgtctagactgcgctacaatcgtgtc	cps6 deletion using pExchange-*tdk*
cps6 right internal	cgaccttgccaaacttgcgcaacataccagcgttttgag	cps6 deletion using pExchange-*tdk*
cps7 left 750 SalI	gcggtcgacccagattcaagtcgaacgc	cps7 deletion using pExchange-*tdk*
cps7 left internal	cacaaactcactaatatggcgg	cps7 deletion using pExchange-*tdk*
cps7 right 750 XbaI	gcgtctagactttggagagggcaacag	cps7 deletion using pExchange-*tdk*
cps7 right internal	ccgccatattagtgagtttgtgcgacgtgtttcttcctgtaac	cps7 deletion using pExchange-*tdk*
cps8 left 750 SalI	gcggtcgaccctgacccattacgtgg	cps8 deletion using pExchange-*tdk*

cps8 left internal	ggcgttaggttgagtttctg	cps8 deletion using pExchange-*tdk*
cps8 right 750 XbaI	gcgtctagacctaaagaagatcgggagcac	cps8 deletion using pExchange-*tdk*
cps8 right internal	cagaaactcaacctaacgcccttacatcaacgaggcgaaag	cps8 deletion using pExchange-*tdk*
Δ*BT4670* fwd NotI	ATGCGTCGCGGCCGCGACAGACTGGCAACATGCAGTGC	*BT4670* deletion
Δ*BT4670* 5' out	CTAACAATAATC GTATGGTGCATGTAAAAAGATACGATATGAAAG	*BT4670* deletion
Δ*BT4670* 3' out	CATGCACCATACGATTATTGTTAG	*BT4670* deletion
Δ*BT4670* rev SpeI	CCGACACTAGTTCTGTTACCGGACACATCATC	*BT4670* deletion
Δ*susD* fwd SalI	gcggtcgacgtcatcatacacaaacttcaagtc	*susD* deletion
Δ*susD* upstream rev	catgataaattgatttaatgaatgttag	*susD* deletion
Δ*susD* downstream fwd	ctaacattcattaaatcaatttatcatgtaaccaagagttc atccttatataaaag	*susD* deletion
Δ*susD* rev XbaI	gcgtctagatccgcatcctccagtatctgc	*susD* deletion
BT4670 expression in *E. coli*		
BT4670 NheI fwd	CCGACTGCTAGCACAGATGTTCTTGATCAAATGCCG	BT4670 expression
BT4670 XhoI rev	CCGCTCGAGTTAATAGAGTGGATTATGTAGATTAG	BT4670 expression
qPCR Primers		
16S F (Bt/Bo)	GGTAGTCCACACAGTAAACGATGAA	16S rDNA normalization
16S R (Bt/Bo)	CCCGTCAATTCCTTTGAGTTTC	16S rDNA normalization
BT4671F	ATGGTTTCATCGCCCGAAGAG	PG PUL expression
BT4671R	GCGTATGGTTGAGACAGATGTAGG	PG PUL expression
BT4114F	cgcaacggaagcactaacagg	homogalacturonan PUL expression
BT4114R	gggaagccgtctacaataaataaa	homogalacturonan PUL expression
BT1763F	tgccgcatccgcttctatct	levan PUL expression
BT1763R	cgtccgtattgctcagtgttcagt	levan PUL expression
BT3332F	tgttcccggagccagtgttc	chondroitin sulfate PUL expression
BT3332R	ttcgtccagcgttttagtatcttcttt	chondroitin sulfate PUL expression
BT4660F	agcccgacaaatacttccaacct	heparin PUL expression
BT4660R	tgtgcggcaaagtgtatcctaaag	heparin PUL expression
BT4671F	cagcgtggattggaatgtaagatgggtaa	pectic galactan PUL expression
BT4671R	gtaattcttttgcgggccgtatgtgtagtc	pectic galactan PUL expression
BT3090F	atgctgaatgccgcccaata	dextran PUL expression
BT3090R	cgagaaaaccgccggatacata	dextran PUL expression

BT3702F	gctattggcggggcattgg	starch PUL expression
BT3702R	cagcggattttggggagagttcg	starch PUL expression
BT3788F	aagcgtggggaaaaaggtaagg	α-mannan PUL expression
BT3788R	gctaaacgcgcccaatcataac	α-mannan PUL expression
BT4164F	gaaatgtaatgaatgatgcaaaaggtaga	rhamnogalacturonan I PUL expression
BT4164R	cgaaacgtccgtggaagaaagta	rhamnogalacturonan I PUL expression
BT3680F	cgggaaattaaatatactgctacgaaact	arabinogalactan PUL expression
BT3680R	ctgccgggtctacattggtga	arabinogalactan PUL expression
BT0364F	tgaatggcggtaaggtaaaagaaca	arabinan
BT0364R	cgggccggaagcgagtag	arabinan
BT4134F	accgggacccagtggacgatgta	Mucin O-glycan PUL expression
BT4134R	ccgcttttgctattggttgggtgat	Mucin O-glycan PUL expression
BT3750F	cgatgccggtgccagttatattcttcag	Mucin O-glycan PUL expression
BT3750R	aggccagtattgctccatcaggtccat	Mucin O-glycan PUL expression
BT1280F	tgcgcggtacaaaatccatc	Mucin O-glycan PUL expression
BT1280R	ggcggctgcggctgctc	Mucin O-glycan PUL expression
BT4357F	ttggcgtacagaagaaagcgaacct	Mucin O-glycan PUL expression
BT4357R	cggaccggcagcatcattattag	Mucin O-glycan PUL expression