

SUPPLEMENTAL DATA

SUPPLEMENTAL RESULTS AND DISCUSSION

Disruption of a single trans-envelope signaling system during growth in a condition where multiple systems are simultaneously activated—Multiple Sus-like systems involved in host glycan catabolism, including the BT1032-53 system, are simultaneously expressed both *in vitro* during growth on *O*-glycans and *in vivo* in the distal mouse gut (1). The genetic experiments described in the main text demonstrate that the trans-envelope signaling switch encoded within the BT1032-53 PUL is essential for its regulation. We also wished to determine if loss of the positive-acting components of this particular trans-envelope signaling switch (BT1042 and BT1053) influenced other cellular responses to *O*-glycans, such as expression of other PULs. To address this question, we obtained whole genome transcriptional profiles for the $\Delta BT1053$ and $\Omega BT1042$ mutants grown to mid-exponential phase in MM-neutral *O*-glycans and compared them to our previously published GeneChip dataset for wild-type *B. thetaiotaomicron* grown in the same medium (n=2 biological replicates performed/strain). Differences in gene expression were determined by referencing each strain's transcriptional profile to wild-type *B. thetaiotaomicron* grown in MM-glucose and identifying genes with ≥ 5 -fold expression changes. By comparing each of the three MM-neutral *O*-glycan datasets to this common MM-glucose reference, we were able to directly compare all three datasets. A total of 223 genes exhibited ≥ 5 -fold changes in their expression: 195 of these (87.4%) were up-regulated relative to MM-glucose (see Table S5 for a complete list with fold-changes). A Venn diagram comparison of these three strains' responses to neutral *O*-glycans revealed genes present in all 7 sectors (groups) defined in Fig. S4A. However, the largest group of regulated genes (130 up-regulated and 15 down-regulated; 65% of all regulated genes) were contained in Group 5, indicating that their expression changes were similar among all three datasets and therefore not perturbed in either mutant. Notably, this group of shared responses encompasses 8 out of 9 PULs (blue-bracketed genes in Fig. S4B) that were upregulated ≥ 10 -fold during growth in MM-neutral *O*-glycans versus MM-glucose (1), and only excludes the BT1032-53 PUL which belonged to Group 1. Thus, loss of the trans-envelope signaling switch linked to the BT1032-53 locus does not cause noticeable alterations in expression of other PULs. This notion is consistent with the conclusions of our yeast two-hybrid analysis, which suggest that the transcription factors that activate PUL expression function primarily as specific local activators of their adjacent PUL genes.

Two additional groups delineated in Fig. S4A (1 and 3) include particularly interesting sets of genes. Group 1 includes genes that are induced in the wild-type strain, but that lose expression in both the $\Omega BT1042$ and $\Delta BT1053$ mutants. All except three genes in this group belong to the BT1032-53 PUL (blue bracketed genes in the Group 1 section of Fig. S4B), confirming that this system's trans-envelope signaling switch primarily effects the adjacent PUL genes, and suggesting that regulators from the other 8 systems do not compensate for this loss of expression. However, three additional genes encoding proteins of unknown function (BT3221-23) are also in Group 1 and are therefore dependent on the BT1032-53 signaling switch for expression in MM-neutral *O*-glycan medium (red bracketed genes in the Group 1 section of Fig. S4B). Each of these genes encodes a protein with a predicted signal peptide, suggesting that their products are secreted and possibly play a role in assimilating certain *O*-glycan-derived sugars that are specifically imported via the BT1032-53 system. If this were the case, they may be indirectly dependent on ECF- σ^{BT1053} for activation because they would respond to products generated by the ECF- σ^{BT1053} -activated BT1032-53 Sus-like system only when its *O*-glycan substrate(s) was present. Consistent with this notion, BT3221-23 do not exhibit any transcriptional activation during artificial de-repression of ECF- σ^{BT1053} in MM-glucose (Table S4), suggesting that their transcription is not directly dependent on this ECF- σ factor.

Also of interest are 22 of the 24 up-regulated genes belonging to Group 3 (*i.e.*, those up-regulated in response to neutral *O*-glycans but *only* in the $\Delta BT1053$ mutant), which are encompassed within one of *B. thetaiotaomicron*'s eight *CPS* loci, *CPS8* (green bracketed genes in the Group 3 section of Fig. S4B). This

result is notable in light of the results presented in the main text that link four different trans-envelope signaling switches, including the one associated with the *BT1032-50* PUL, with regulation of various *CPS* loci (Fig. 4; note that *CPS8* was induced during de-repression of anti- σ^{BT1052}). In contrast to the anti- σ de-repression experiments described in the main text, which yielded transcriptional responses from ECF- σ -dependent genes in minimal medium lacking complex glycans, specific induction of *CPS8* in the $\Delta BT1053$ mutant reveals that shifting the repertoire of PULs that are simultaneously expressed by the cell can indeed result in alterations in capsule expression. The mechanism through which loss of *BT1053*, but not *BT1042*, uniquely results in increased *CPS8* expression remains unclear. One possibility is that ECF- σ^{BT1053} is essential for priming expression of some genes (*i.e.*, those in the *BT1032-53* PUL), whereas the SusC-like transporter *BT1042* is only essential for subsequent amplification of PUL gene expression upon *O*-glycan recognition. Thus, loss of these two factors could result in slightly different effects on protein expression: *e.g.*, complete lack of *BT1032-53* expression in the $\Delta BT1053$ mutant versus low-level expression that cannot be increased subsequently in response to glycan cues in the $\Omega BT1042$ mutant. Because at least 8 other Sus-like systems are subsequently highly expressed in the same growth condition (MM-neutral *O*-glycans), the resulting differential in *BT1032-53* expression may result in the observed effect on *CPS8*. Future experiments that explore the pathways linking CPS and PUL gene expression will be needed to obtain additional insights into this phenomenon.

SUPPLEMENTAL REFERENCES

1. Martens, E. C., Chiang, H. C., and Gordon, J. I. (2008) *Cell Host & Microbe* **4**(5), 447-457
2. Sonnenburg, E. D., Sonnenburg, J. L., Manchester, J. K., Hansen, E. E., Chiang, H. C., and Gordon, J. I. (2006) *Proc. Natl. Acad. Sci. U.S.A.* **103**(23), 8834-8839
3. D'Elia, J. N., and Salyers, A. A. (1996) *J. Bacteriol.* **178**(24), 7180-7186
4. Xu, J., Bjursell, M. K., Himrod, J., Deng, S., Carmichael, L. K., Chiang, H. C., Hooper, L. V., and Gordon, J. I. (2003) *Science* **299**(5615), 2074-2076
5. Koropatkin, N. M., Martens, E. C., Gordon, J. I., and Smith, T. J. (2008) *Structure* **16**, 1-11
6. Salyers, A.A., Bonheyo, G., and Shoemaker, N.B. (2000) *Methods* **20**, 35-46
7. Sonnenburg, J. L., Xu, J., Leip, D. D., Chen, C. H., Westover, B. P., Weatherford, J., Buhler, J. D., and Gordon, J. I. (2005) *Science* **307**(5717), 1955-1959
8. Bjursell, M. K., Martens, E. C., and Gordon, J. I. (2006) *J. Biol. Chem.* **281**(47), 36269-36279

SUPPLEMENTAL FIGURE LEGENDS

Fig. S1. (A) Housekeeping (σ^{AB}) promoters upstream of ECF- σ genes. Twenty-four out of 26 ECF- σ genes that are coupled to adjacent anti- σ genes are located downstream from putative σ^{AB} promoters. Two others, *BT3993* and *BT2169* appear to be internal genes in operons for which we could not discern potential promoter sequences. The transcription start site for *BT1053* was confirmed using 5'-RACE. Asterisks in *BT1053* mark the two potential initiating bases for this promoter. The nucleotide at which transcription starts is ambiguous because a 3' poly-dC tailing strategy was used during mapping; therefore, we cannot determine if the upstream dC that is marked represents the actual 5' end of the transcript, or the result of enzymatic addition of a dC residue to a transcript end beginning with the marked dA. **(B)** Housekeeping (σ^{AB}) promoters upstream of other classes of PUL regulators. Putative σ^{AB} promoters located upstream of three major classes of inner membrane-spanning transcription factors commonly associated with *B. thetaiotaomicron* PULs: hybrid two-component systems (HTCS); SusR-like regulators; and SARP-family regulators (1-3). A subset of HTCS regulators appears to be subject to auto-regulation in response to glycans such as α -mannan (1). Thus, five representative HTCS regulators were chosen from the 36 present in the *B. thetaiotaomicron* VPI-5482 genome based on the following two

criteria: (i) they are associated with a PUL that was induced in one or more growth conditions; and (ii) they do not exhibit noticeable auto-regulation during PUL induction. The *B. thetaiotaomicron* VPI-5482 genome encodes four SusR-like proteins; one of these (BT3309) is not shown because it is an internal component of an operon. All three SARP-family regulators present in the VPI-5482 strain are presented.

Fig. S2. Signaling domains used in yeast two-hybrid analysis. **(A)** Amino acid sequence alignment of the 5 signal transducing SusC-like transporters analyzed by yeast two-hybrid assay. Major functional domains are color coded as indicated by the legend at the upper right. Sequences highlighted in red ('transducing domain') correspond to the precise peptide segments used for fusions with the GAL4 binding domain. **(B)** Amino acid sequence alignment of the 5 anti- σ factor proteins analyzed in the yeast two-hybrid assay. Major functional domains are color coded as indicated by the legend at the upper right. Sequences highlighted in green ('cytoplasmic domain') and yellow ('periplasmic domain') correspond to the precise peptide sequences fused to the GAL activating domain. Residues highlighted in blue boxes indicate the last residue retained in each anti- σ gene truncation resulting from construction of plasmid insertion mutants. An alignment of the ECF- σ signaling partners is not shown because the entire predicted coding region for each gene was used for our yeast two-hybrid analysis.

Fig. S3. Only BT1042 and not functions encoded by downstream genes are required for trans-envelope signaling. A histogram showing transcriptional activation of three genes (*BT1040*, *BT1043* and *BT1046*) from three different operons in the *BT1032-53* PUL during growth in MM-neutral *O*-glycans. Both wild-type *B. thetaiotaomicron* (yellow bars) and the Ω *BT1043* mutant (orange bars) activate gene expression in response to *O*-glycans, suggesting that the signal transducing SusC-like transporter BT1042 is the only protein encoded by the *BT1042-46* operon that is required for trans-envelope signaling (note that *BT1043* is not expressed in the Ω *BT1043* mutant due to disruption). Data are based on qRT-PCR-based quantification of the expression levels of the three genes indicated. Bars indicate fold-changes in expression during growth in MM-neutral *O*-glycans relative to each strain grown in MM-glucose (n=3 biological replicates per strain in each growth condition; error bars represent one standard deviation).

Fig. S4. Global effects of mutations in the signaling components of a single trans-envelope system. **(A)** Venn diagram showing the distribution of genes with altered expression in response to growth in MM-neutral *O*-glycans for wild-type, Δ *BT1053* and Ω *BT1042* strains (fold-changes for individual genes are summarized by group in Table S5). Note that most genes with altered expression are up regulated and reside in Group 5; these genes are shared among all data sets and indicate that loss of either trans-envelope signaling factor (ECF- σ^{BT1053} or SusC-like transporter BT1042) does not result in global changes in the transcriptional response to neutral *O*-glycans. **(B)** Heatmap illustration of upregulated genes according to the Venn groups illustrated in panel A (gene expression is normalized to the color bars at the bottom of each panel; green represents lower expression and red higher expression). Vertical columns represent the strain and growth conditions listed along the top. Data from duplicate GeneChip experiments are shown for each condition (total of 8 GeneChips from 4 conditions, including the MM-glucose reference). Several gene clusters of interest are labeled along the right of the heatmap (these genes are correspondingly labeled with the same color in Table S5). Labeled genes include: (i) 9 different PULs where the included genes exhibit an average fold-change in response to neutral *O*-glycans that is ≥ 10 -fold [blue brackets and gene labels; (1); note that only expression of the *BT1032-53* PUL (Group 1) is compromised in the Δ *BT1053* and Ω *BT1042* mutants, indicating that loss of this trans-envelope switch only effects its local PUL and not the 8 others]; (ii) a cluster of three genes with no known function (*BT3221-23*; red brackets and gene labels) that also belong to Group 1, indicating that they are induced by neutral *O*-glycans in a Δ *BT1053*/ Ω *BT1042*-dependent manner; and (iii) genes from *CPS8* (green brackets and gene labels), which exhibits increased expression in response to *O*-glycans, but only in the Δ *BT1053* mutant. **(C)** A heatmap similar to the one shown in panel B representing genes with higher expression in MM-glucose relative to MM- neutral *O*-glycans (for a list of these genes, see Table S5).

Fig. S5. Increased capsule thickness in the $\Omega BT3992$ anti- σ mutant. Representative images of India ink-stained *B. thetaiotaomicron* strains: wild-type, $\Omega BT3992$ and $\Omega BT3992/\Delta CPS2$. Bacterial cells appear as a dark shape surrounded by a bright capsular layer, which excludes the dark and particulate India ink. Magnification is 630X; Bar = 2 μm .

Fig. S6. Representative HPAEC-PAD traces. A single HPAEC-PAD trace is shown for each strain and sugar analysis condition presented in Fig. 5C of the main text (note that each experiment was performed in triplicate with similar results): (A) wild-type, neutral monosaccharides; (B) $\Omega BT3992$, neutral monosaccharides; (C) $\Omega BT3992/\Delta CPS2$ neutral monosaccharides; (D) wild-type, acidic monosaccharides; (E) $\Omega BT3992$, acidic monosaccharides; (F) $\Omega BT3992/\Delta CPS2$, acidic monosaccharides. Monosaccharide abbreviations are identical to those used in Fig. 5C of the main text: Fucose, Fuc; N-acetyl-galactosamine, GalNAc; N-acetyl-glucosamine, GlcNAc; galactose, Gal; glucose, Glc; mannose, Man; galacturonic acid, GalA; glucuronic acid, GlcA; and iduronic acid, IdoA (Note the presence of GalNAc and GlcNAc, which are de-acetylated during acid hydrolysis, is inferred from galactosamine and glucosamine standards, respectively). Sugars labeled in red text in panel E correspond to the two unknown sugars that become abundant upon *BT3992* disruption. Note the proximity of ‘unknown 4’ to the peaks corresponding to the acidic monosaccharides GalA and GlcA; this unknown sugar is flanked by these standards, but was clearly distinguishable based on retention time, in each experiment.

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Gene	-33	-7	start codon	-33/-7 spacing
Consensus:	tttg-----	ta--tttg-----	-----atg	
BT1053:	ttcg-tttctttcattgctttcat-----	tatttttg-ctctgcataaaaaataatgaaga-----	-----atg	19
		**		
BT1617:	cggg-gttcgatacaaaaatttact-----	tatttttg-cagggtttacagcatttacaaaaaaataccacca-----	-----atg	20
BT2562:	tttg-cttttctgcgaaaatatgtg----	ttcttttg-tacgaactaatgaaaatagcctgtaaactcttatgcggtg-----	-----atg	18
BT3010:	tttg-tatcttttaaataatgta-----	tagctttg-ttgtcactaataatttgcacaaat-----	-----atg	19
BT3748:	tata-tttctttgcaatcattaaa-----	gacctttg-gatatacttaactatacgcataagcgccattaatatagatcgaa----	-----atg	19
BT4250:	gttg-cggttaatagttattttctt-----	tatttttg-taacacaattgaaaagag-----	-----atg	19
BT4355:	tctt-tattttattataaaaaagc-----	tataatttg-cagcaaataactatttaataa-----	-----atg	19
BT4402:	tcta-atctttgagaatgtctatttt---	tatacttg-taatcgataataatcttagcggat-----	-----atg	21
BT4636:	tctt-ttattattatttttaataac---	tatctttg-ctttcattgtgtaatgcgacaggcaaatttaagtaataattct-----	-----atg	20
BT0139:	tttg-aaatcattctccggaattgcctt-	tataatttg-catcgtgttcaaaaccgaaaaagatagtatt-----	-----atg	23
BT0188:	tacg-tttgtaacatcataacaa-----	tacctttg-tgccaaaagtaaagaaaat-----	-----atg	18
BT0752:	tttg-agtttctgaattaatcgc-----	tataatttg-cacccgtcccttaaagaaaaagaacga-----	-----atg	18
BT0966:	tgcg-tttttaagcCAAaataattac----	ttcttttg-tcctcactaataaaaaatgaaagtcggacaac-----	-----atg	20
BT1278:	ttcg-tatcttaatttaatttgtt-----	tacatttg-tctttcgatttcaataatctgttaaccg-----	-----atg	19
BT1877:	tatg-ctttaaattcgaataattctc---	taaatttg-tgctattaatctgactggttacattc-----	-----atg	21
BT2198:	tttg-tctttgctgtttcttttgt-----	tacctttg-tgcatctaataatgaggttt-----	-----atg	19
BT2463:	tttg-cgaatcaaataatcatttta-----	tatttttg-tttctcaaaatTTTTaatgaactaaaagaattaaa-----	-----atg	19
BT3037:	ttag-tcgaactcggggaaaagtac----	tatttttg-cagcttcagaatccagataaaga-----	-----atg	20
BT3269:	tttg-taagtcatatctattataacc---	agtttttg-cagtaatttgaagagagctttttattgtttgattaatcttggttgccgt-	atg	21
BT3277:	atag-aacattattatttaatttg-----	tatttttg-gcgcAAAactcccga-----	-----atg	19
BT3517:	tggg-cttttttttgatttattgttt---	tatttttg-tccttgtaaactcataaacttgttatag-----	-----atg	21
BT4643:	aatt-aaaatcagaattgttttct-----	tataatttg-ggaacaatcgtaaaatgatagaagt-----	-----atg	19
BT4705:	ttag-gaaatgctgattttcttatta---	tataatttg-cagtaaaatgaaaactacagaatctcaaaata-----	-----atg	21
BT4722:	cctg-tttctgaccgatggttaaca-----	tacctttg-ttgcaaaattctaagct-----	-----atg	19

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Gene	-33	-7	start codon	-33/-7 spacing
Consensus: tttg-----ta--tttg-----atg				
HTCS regulators:				
BT2391:	ttcg-cctttctgttataatattgat---	tatttttg--	tgacacttaaactaatatgaatatata-----	atg 21
BT2826:	ttta-aatagaatttcctatatatta----	cacctttg--	tacagtattatgtggctattt-----	atg 20
BT3334:	ttcc-cgaaaatcaaataaaaaaaa----	tataattg--	ccattagtaataaccctaaacaaccgaatta-----	gtg 20
BT4137:	tctg-gtaatatTTTTCTCTTAAATGTAG-	tatctttg--	aaaactgaatcttataatctgactata-----	atg 23
BT4663:	catg-gggtatttaaaggaaattac----	tatctttg--	gcgtcattattaatctcgtgaactaata-----	atg 20
SusR-like regulators:				
SusR:	tttc-gTTTTtattactataatcat----	tataattg--	tcacatcttaaaaaagcacctt-----	atg 20
BT3091:	gctg-tcggtttctgaaagacttt-----	tatctttg--	cagatataatacatatggcgct-----	atg 19
BT4069:	tttg-acgaattacccaaagaaaattca-	TTTTTTTg--	caaattgtatataacacattgat-----	atg 23
SARP-family regulators:				
BT1770:	tatg-aatatcatattgTTTTTcg-----	tacttttg--	ccacataggaacagattcaagtagaagtact-----	atg 19
BT2204:	ttag-gcggttatTTTAAATAATCTG--	tataattg--	tgataataaatcgaaagact-----	atg 22
BT3853:	ttgg-tcttagacataagtttct-----	tacttttg--	aacaaggattccggtttt-----	atg 18

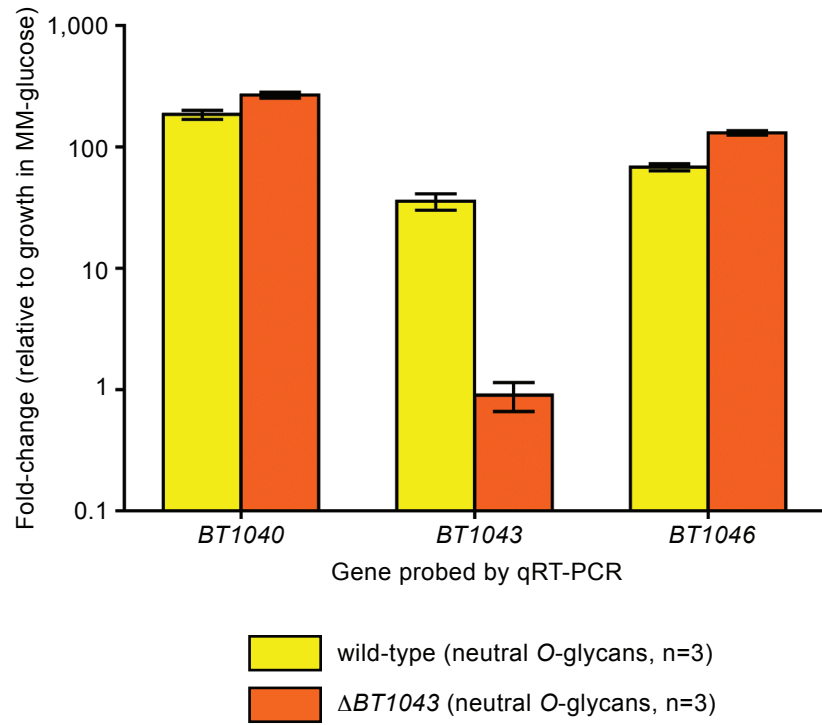
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Accession	Sequence	Position	Color codes
BT1042	MKEI I KHKFPYLL FFLLL FSS FASA	53	
BT1619	MKFKYKLSGI GYPVKI HKFYI LL FALCFYNI A	59	
BT3983	MFNLKFKCMRI NDS CRGSKI FRALLI LMLF ALPAQS	62	
BT4247	MKKNHSYRRRLY KHI ALVLLF YPLS	55	signal peptide
BT4357	MQNNF SI QYLRVV KSFVLT SKKI PRT MRLVI LFL FCFVGLT NATDS	74	
BT1042	MSVVY NTNDVDI NRVI SI KVS KESLT NVMGQLFKGTNI SYSI VDKHI VLST KKEVE QQKK	121	transducing domain
BT1619	FSI AY NQTKLDVK QKVS ANFVREAVS SVLNSVLKGTGFTYRQEGKHI I I I VPAKAEAAP NNTT STQQSI KI RGT	134	
BT3983	YQFFY DDN- LASMRI ES LNVKDVSL KEVLDKALKGNVYKI DDNVVYLSKANASS STKS	131	Ton box
BT4247	YTFYF NAADLEDK QRKDI NCNG- PI DEI LDEVFKDSGI SYI VKNKEVI LNVQKTNTTQQK	122	
BT4357	F SFFYNNAHI NLKRLVI SADRNDI F KVLDEVFKNTNVE YKVI DKKI I LSTELASVEQAH	143	
BT1042	VTDAQGE- PLI GY SI LVKGTA- TGA I TDMDGNFKI QAAKG- DVLEI SYI GYASQSI TLANAQPLKVTMGEDTQT	193	plug domain
BT1619	VTDAQGE- PLI GANVLVDGSK- QATI TDMNGEFS LEVPA N- SKLRVTYI GYVTQEVTVKNKTLFNI QLQEDTQTM	206	
BT3983	VVDANNE- PLI GY SVLE KGTI- NGTI TDFDGNVT LVV TGS NAVLQFS YVGYQTLERAVAGKTAI NI TLKEDAVL	204	TonB β-barrel
BT4247	I I DAVDPSPI I GANI TI KGDKNTGTI SDI DGNFSLSI PDNKTI LVVTYI GYKTREVPVEDLGN I KIVLEGGDHTL	197	
BT4357	VVDAAGE- PVI GASVI EKGS A- NGTI TDMDGNFI LNVGSK EAI LEI SYI GYQGQSLKVTPGKTL SVVLKEDTQSL	216	
BT1042	DEVVV T ALGI KR E QKAL SYN VQVNN DAL T SVK DANFVNS LQGVAGVNI QR- S AS GVGGS TRVT MRGNKSI SG	266	
BT1619	DEVVV I GFGTQK KVNMT GAVAS VNI KESLGRPI TNSV AALQGVVPLKESI- TTGTPGDDMTYNI RGTTSI NG	279	
BT3983	DEVVV T ALGI KR S EKAL SYN VQVNA DAVT TNKDPNFI NSLSGKVAGVNI NA- SS S GVGGS KVV MRGTSI MQ	277	
BT4247	DEVVV V GSGTQK KVSVT GAI TS I KG- ASL KLP S T LNS F AGKLAGVI AKT- NS GEPGS GAE FYI RGI GTF G	268	
BT4357	DEVVV V GFVQVK ANLT GAVSQVKMDV L GSRPVVNAS ALQGAMPGLQI TPNNDAAGPGQSKS FNI RGTTSI NG	291	
BT1042	DNNVL YVVDGVP I GNQADRTGDGTGFSGRSTSGE GI ANF NPDDI ES V SVLT GPSAAALYGASAA NGVI LI NTKKG	341	
BT1619	- GEPLVLVNNVPM D- - - - - I NMI DPQDI ES V SI LKDAASAAI YGARA AFGVI LI TTKQG	332	
BT3983	SSNAL YVVDGVP MYSNAKNVN- GTEFSS- KGNTPEI ADI NPEDI ESMSVLTGAAAAALYGSDAANGAI I I TTKKG	350	
BT4247	RATPLI LLD DVEI SS- - - - - G- D- - - - - LNYVPAENI ESFSI LK DASATAI YGSRGANGVMI VTTKGG	325	
BT4357	GGPLVLI DNVPGD- - - - - I DML NPEDI ES V SVLKDAASAAI YGARA AFGVI LVTTKKA	344	
BT1042	EAGK- MRI DVSS VEFMTPLT MPKFQNRYG- I SGN- - - - - YYSWGDKLENQ- SS YDPKD- FFE LGATFNNSFN	405	
BT1619	KKDMAPRFNYNNNF SFS KASEL PQKASPLE SVLAKEMGWANDTYVDGKNI TQWEGYI RYQANPSNYPN- G- - -	403	
BT3983	KEGR- VNI TVNSNVEFNAPLVMPRFQTRYGTGI GGVKDDNSRSRSGP KLTE ARYFGYNPRDDYFQTGVI GTESVS	424	
BT4247	EYNSKTSI NVTAE NSFNYL DKF PEFVDGAT YMDMYNKAS LARNSSAT PKYS ATDMERTAS G- VNPYLY PDVN- - -	396	
BT4357	KKGDGFHVNYNNNF GFQSSI NRPEQADGLE WMQA YLDGE FNAGKYT QGDI KTWMNYLTERKNPKGK QTTGDGV	419	
BT1042	LSTGNDKNQTYFS I AAVNSDGI VPNNKYHRVNTLRNTAKFLNDKLTLDASASYI REYYNMI SYGTYFNI YVGA	480	
BT1619	YI FDDQGNL FL MR ENDMFADMMDNF GF MQNHSFS VSGS- - - - - QRTSYRLSLGYTGEDGI LVTDKDF DRI NMS	474	
BT3983	FSTGS EKNQTYAS AAVNSKGI VPNNKYDRYFNVRNTT SFLDDKMTLDVNASYI LQKDRNMVNGQTYNNPLVGA	499	
BT4247	- - - WQDVL FKNMS MRQR ANVNI SGGGS KVKYMS LDVSH- - - - - D SGL LNTGKAYS WNNNI NI MNYTFQNNI AYKL	464	
BT4357	YVDPE TGLNYLNEKDL YANML DYGFLQAHHVLSGGT- - - - - DKLAYRLSLGYNS EQGI LI TDKDRYKRLSGSA	490	
BT1042	YL YPRGEDEF EKEKYFERYN- - - SELGYSQQWSP GDFGMDI QNPYWI AYRNI R- - - - - PEVKDRYMLYASLKY	545	
BT1619	FLSVDVKNWLTQLDRIYAN- STQNKVEQGGRNFGVWS AMYLP SYHNI LPYEQDGI EYP AETSATFVRYGEP RV	547	
BT3983	YLFPRGNDWE DI KMYERYD- - - VARKI YTYQWPTGDGNTM QNPYWI YNRNL R- - - - - ENKDRYMLGASLNI	564	
BT4247	TPTTTI LKMNNAQI RQKSPNVSEDLFKQI LTTTPI EFPVTPSPQDGRIMYG- - - - - NNI I S GSTLYTNP YA	532	
BT4357	YI SAEI TSWLTQSVDI RYAQ- S DKNMPVT S DKTGLYDMRLPVVYPE GSLTLP- DGTS LMTNTP SNVLRMATDNN	562	
BT1042	DI TNYLVNAGRVL DNTYTEKE DKRYASTI N- - - TYAS TNGRYTYS NETFRQKYADI MVN- - - FDKQFAEYI HA	613	
BT1619	I KKTNLRTLGRVI I SPLKGLKI TGEYTYNRI TE- - - YNRMVYNYKYI GFNF TGLLNNVENSRYALTQGF TNYNAI	620	
BT3983	QI LDWL NYS GRVRLDNS NNDYTI EKAYASTNTQL- - - TELS DRGLYGI SRSYE KQLYADFLVS- - - VNKT FGEKWSL	634	
BT4247	RMNTS FAETENT LNTVI KI DQDLDFI T KGLKI NAFVNF KTWS SYF DRSI APY YRI KSGSYDETDL ENTEYEL	607	
BT4357	TI RDNARI LSKTVL KPLKGLEVAFEYTFDKTWS- - - NQNVKAS I DYTVELAKI QTATTS S- LETTHQSTDYNAI	634	
BT1042	TI NAG- - - - - TSFE EYDTKG- - - - - RGYGQLLLV PKNFVYSNI DPTQSTASQTGGDSRRRNF AVFSAE L	674	
BT1619	NAFANYDFS I G- KHD I S I MGGYNOEE SHKE S QWS QRTDVLLENLPSL SGTG- TASVTDS FDEYAI RGLFVRVNY	693	
BT3983	QANMGSSFTDMRYDEMAVRGPI ADDS- - - KTFAGEKAGL TNGFYI QNLSTTKSKMQSG- - - WRE QTI YASAEV	704	
BT4247	ELLNS NG- - - SDYI SQS AI GKS SDQT- - - FELQFNLN YARQFGLHNVGAMLLYKQRE YRS DVL PNRNQLS SRLTY	677	
BT4357	NLYANRY S WNDT HNL SLMGGFNQES SDWK KLYT SYSDMI NEKYP SHSTATGENKVI TDDHRVYTVRGA FRYVNY	709	
BT1042	S WNSALYLT LTRGADKPSQLV- - - NSDDPW I FYPVGLSAI VTELLPNNI KEKLEPTL GFLKVRASYTEVG- - - - -	742	
BT1619	TYDGKYMFE ANGRYDGT SRFP- KDSRFGFFPSFS AGWRI SEEA FMKNTK- SFLS- - - - - NLKLRASWGS I GNQI I L	762	
BT3983	FGYSTYLL LTRGNDWP SQLAGRNYSNKSFYPVS VGMSVLSL EMLPKLNKDYLS- - - - - YWKI RGSFASVG- - - - -	770	
BT4247	DYGQRVLYFEFNGYNGT ERLA- KEDRF GFF PAVS LGWVI SNEAFFEP MKNVVDN- - - - - LKIRGSYGLVGSDDL A	746	
BT4357	DYKGYLFE TNGR YDGS SKFP- KKNRFGFFPSVS VGWNI ARENF MKP VAGDWLS- - - - - DLKLRGTWGQI GNQGI D	779	
BT1042	S- - - - - PI PYTGLTPG- - - - - TLT HELEGGTF KPFKYPI S NLK- - - - - AERTRSYEVGLDSKWFNNTI TFGVTY	802	
BT1619	KPDNTPENYPYI PSMSPYLT- - - EWLVDGQKTTLLNAPAMVSSSFS- - - WEKVYTLDFGVDFGF DNRNFNGTFDW	831	
BT3983	T- - - - - AFERYI ANP- - - - - LFAWNTS I GQWSNL TDFPVYDLK- - - - - PERTNSF EVGMNMRFLKN- FELDVTY	828	
BT4247	TAGG- - - - - SYLLYI DKI TNNDLSYLKWT SGNQMDYLQGGPQAMAYY AMSGLGWEVKKLDI GI DFTLFRN- WTTFTDY	818	
BT4357	P- - - - - YKFPVTMSQVEKKDVAWL VNGAKPLT L NAGPLVSDSFT- - - - - WETVETLDFGFDI TALNRLQDGSSTNRI	844	
BT1042	YHSNTYNQLK- - - ATLSG- - - - - NFEYMFVQA GNVQNRGLELSLGFDDKFG- DFNYNTTFTATTNKNKI I QLARD- - -	869	
BT1619	YRRDTKGM LAPGMDLPWVY- - - GATAAKQNAADLKYTGWELELNWRDR I NKDWSYRI GFNL YDSQSEI T KYNNE TN	904	
BT3983	YNAKT MQTFN- - - PELPVG- - - EYARI YI QTGA VRNQGLELALNYNNTWK- DFTWNTGVTYS MNKNKI L TLDN- - -	896	
BT4247	FYDKRYDI F MNRREAWPQSLAYHI AKPWS- - - GKMDNKGEFSI NYANNFSKDL SVLS QANFTY NKNMVYVDEPEY	893	
BT4357	YRRDTKMDLAPGAELPSVV- - - GASAPLQNTADLRTKGWELSLTWRDR I G- AWGYNVGFNL YDSKTVVT KYHNE S K	916	
BT1042	- - - - - VLN PVTNTLI DLDTI QVG- - - - - RFLRLEGGEI G- - - - - TVYANEWLKRDGDNYI DY	916	
BT1619	LLG- - - - - DK IYRKG M KGEI WGYVTD R FYTEDDF NADG- - - - - T LKPGI P I PKGAGKVF PGDVLYKNFD- - - - - TE TI	970	
BT3983	- - - - - AI NPI TREKFSI SSLNMGG- - - - - L GSTRFI LKEGGS MG- - - - - DI YSLMDLKR DANGAVYI	948	
BT4247	P- - - - - TI WKSETGKPY SRI TGYI AEG LFKS QEE I DNS- - - - - PAQNQLGSTPK- V GDI KYRDLNGDG- - - - - I I	951	
BT4357	I I LKS DGTNNYYE GYEI GSI WGYVTDGYT ADDE EDTNT WKLKEGVTV DGVVSPR- PGDI KYQNLRLDDGSSTNRI	990	
BT1042	QPQOALTTETTS P- - - - - YKLGSVNPKWNLGWQHGF SYKGFNLNLF TAR- I GGI AISKTQAMLDRYGVSEASADAR	987	
BT1619	WESGETADNP GQDR- - - - - I GNS TPRFHYGI TAGI SWKGLDLSI FLRG- - - - - VGKRDYWR TQAI AWP- - - - - TGWGS L Y F	1038	
BT3983	DENNSVTE SLEA NNYI KLGSVLPKGNLAWRNNS WKNKI NVAF LVSAR- LGGVVS RTQAVL DNF GVS EASAA R	1022	
BT4247	DSDDQTMISKYGS- - - - - T PRLQYGFGGTVNYK KFDG VFFSGSALRSI MTNGI DPFQEG I AVGNRNVLYK	1017	
BT4357	DTGDGTFDNP GDRK- - - - - I GNNSLRLQYGI NLGVNYKGF DL SVLLQG- - - - - VGKRDVWISDARRWPFNSGQF GSLFK	1060	
BT1042	DAGGVS LG- Y- - - - - FKVDPKTYDDAVSN- - - - - LDAYTY SATNVRLQEARLTYTFPNKWFKGTVNY	1044	
BT1619	ETLNF WPTN- - - - - TNAYPRVYS NDGVTNSYNHWKQSKYL ANAS YLKLQNI TLSYTL PKVWS QRLYFD	1103	
BT3983	DKGYVSVNGN- - - - - DRVNPEGWYSVAVG- - - - - TVPQYI YSATNIRLQEAESI GYTI PRKWL G- NVCD	1082	
BT4247	IADNYWSEEK- - - - - Q- NWDKYPRLGLLATDVAN- TAVNSYVNS RNGS FLRLK NVEVYKI P- - - - -	1073	
BT4357	DQLDYWKPVDSANGDWT AANPNAEYFR I YGQ- GNNSSYNTRAQTKYL MNGS YLRVK NVTL SYNFPKSWLAPI TLT	1134	
BT1042	LSLSVYGTNLWMI YNKAPYDPELTAS TGTG GQGYDYFMLPSQSTYGLSLKFGF	1097	
BT1619	DVKVFFSGE NLTY WDHLPEGLT DMLSK- - - - - GAWEPFMRKFSF GIVTF	1150	
BT3983	I KVS LI GRNLWMI YNKAPDFPE SVAS TDNF YQGI DYFMPSLRNI GRNLSKF	1135	
BT4247	YGRI FVS AANLFT FSPFDLWDELSSWN- - - - - SYPMQKTVNVGI QLQF	1117	
BT4357	SLKAFVSCENLHTFTKL MKGYDPERLS- - - - - WGYPFYRTI SFGNVTL	1178	

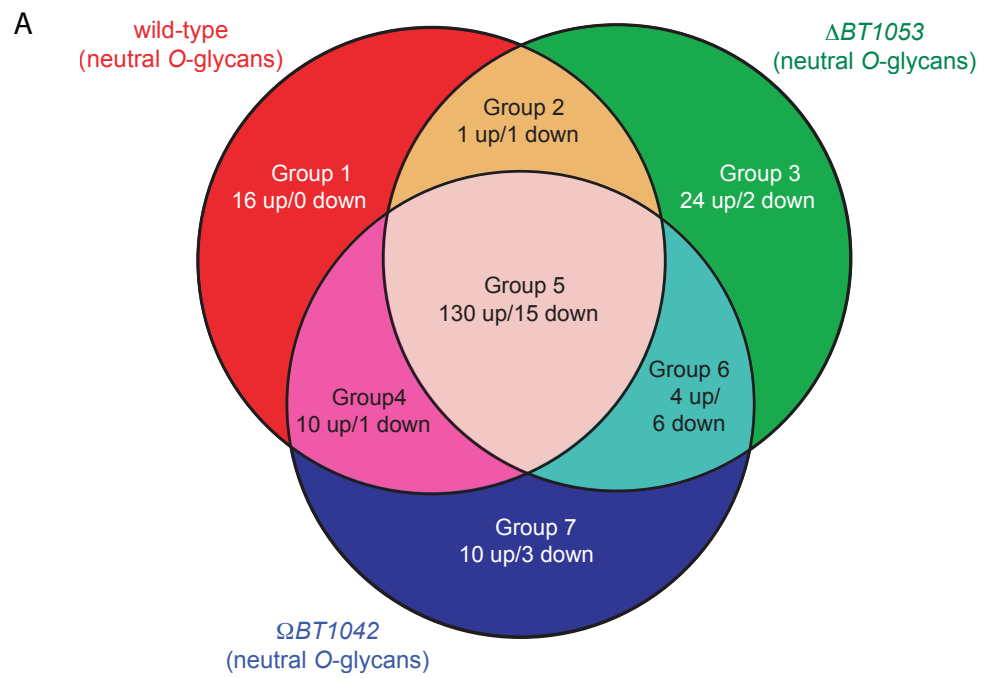
Martens *et al.* Figure S2B

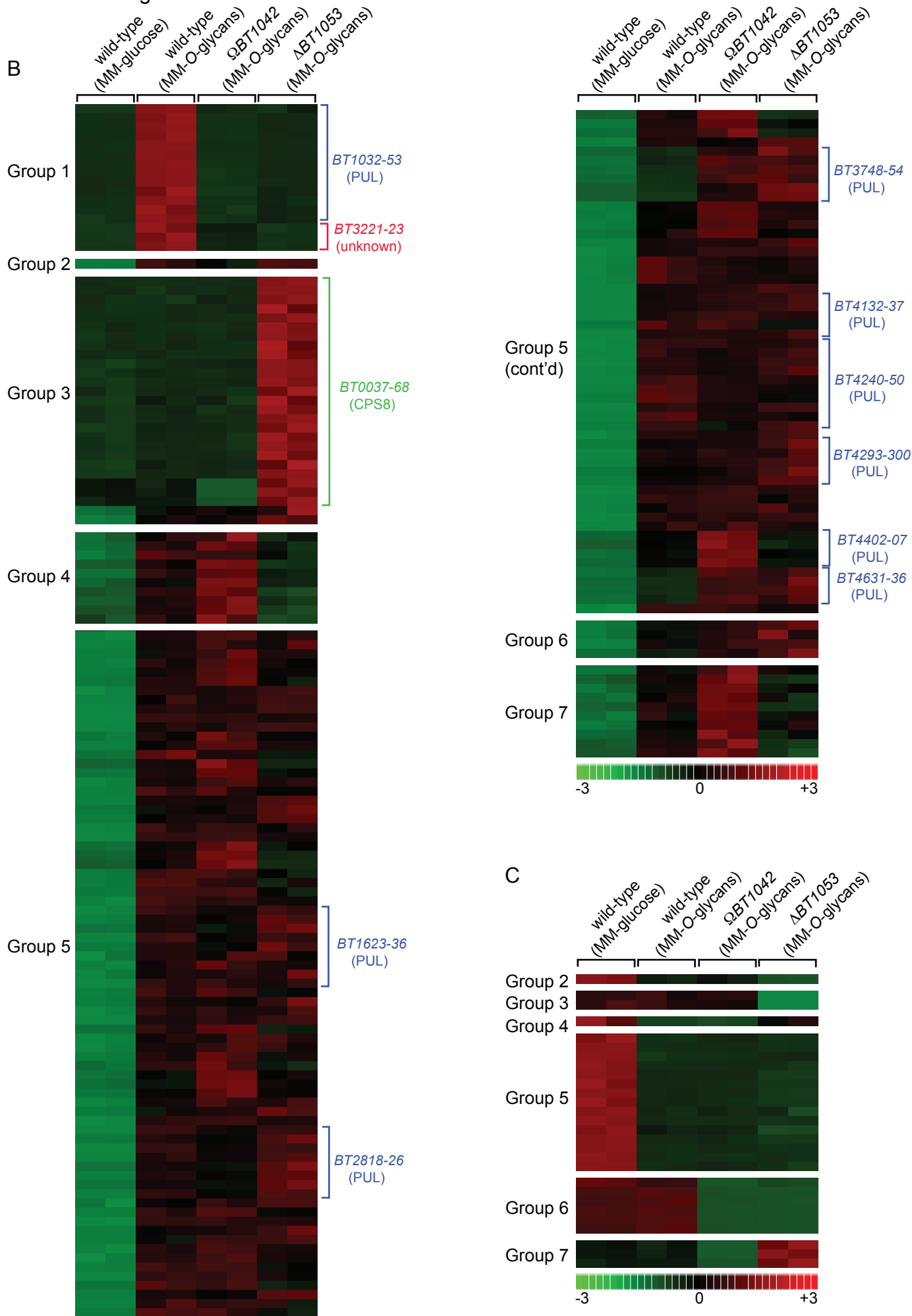
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BT1618	-----MSNAHKIKNF TSDKFSPELKEKLWKWL VDSSEQAKEEALMELWEDQN	49		
BT3992	MKEKKMRNLSEEIINKYLTGQLSEEE LMEVNAWSES DENARQLFRMEEIYHLGK	55	cytoplasmic domain	
BT4248/9	----MDKDTKMSLIGKLAGQLTKK-----Q--RRSYADLESVDRELKIQWNES	43		
BT4356	-MKDLLNNRRIEELLP RYCEGR LSEGERLEVEAWMDESEENKRVATQTFALYLAVD	54	transmembrane	
BT1052	RMVMDAVDTEASLTKFKSLVREKEKAKRRSISVRWGRYASATAAF LAGLVFAG	102		periplasmic domain
BT1618	FKADAGTERS Y--QNFRRKIAPRQRKATARYTLRRW--AQVAVLLIPLLSI VA	99		
BT3992	FDHYADEQRMANAEKRLYKQLS QEKKKKDKVLHMHRW--MRYAAI LAVALLMGGG	108		
BT4248/9	ENKAI DFKIKEQIWEKVKARCVDR-KRNKVLTEL R----WHFAVASLALLLTI GG	93		
BT4356	TVQVMKKVDTEKALLKVKGKMSDREVRRTVWWEWA---QRAAALFIPLLT LFI-	342		
BT1052	GI AWGLLSNKLSDYTVMTT-GGQRAQTVLPDGSKVWLNASTKLIYRNSFWSTDRQ	156		
BT1618	SYLYIQSNEHTELV EYVPRGEQKQITLPGDTTAYLNSGTL LVYPQKFTGDIRS	154		
BT3992	AGYWFYNRPEHQMLVAVAN-EGIVKEVVL PDGTVWLNNAATLKYPREFSEKERN	162		
BT4248/9	FWMNSIRDNI NDEFIKVIA--QQNQMHVLPDSTKVWMESGSSI KYTKAFNKK-RE	145		
BT4356	WQNWKGDTGEVAEMMEVKTSPGMTTSLTLPDGTIAYLNS ESSL SYPSRFNGDFRK	160		
BT1052	IDLSGEAYFEVARDKHAPFIVNT-KHIKTCVLGTFKNVRAREEEDRVVTTLLQGS	210		
BT1618	VYLI GEANFDVKKDKQHPFIVKT-NHLKVKVLGTFKNVHAYAEDEKTTTTLES GS	208		
BT3992	VYLDGEAYFEVTKNRHKPFTVES-DA MRVRVLGTFNFKCDKRCRI AEATLIEGE	216		
BT4248/9	VWLEGNSSF EYVKHEGSFFQVHI-NKAFIEVKGTCFQIKQTN-AEKNEITL FHGK	198		
BT4356	VKLSGEAYFEVAKDPEKKFVLS TTHQSQIEVLGTCFNVEAYEQNTEVITTLIEGK	215		
BT1052	VRMESPRTVNNG-YLLKPGQTLNINTT YQAELEIYAEPTEVLLWNGKLFKQH	264		
BT1618	VVVQKANNE DI--ITLTPNEQL EYDNPSGEFNKKIID A-SVYSGWTRGELNFAAM	260		
BT3992	I EVKGNKDEGQ--IVLAPGQRAELNRNSGR LTVKQVDA-KLDAVWRDNLIPFNKA	268		
BT4248/9	I EFNVESTGK--IIMS PSQV MYNP NNAQTLVE NVMD---I NWKDGRYNFKET	247		
BT4356	VDFMFEKDAVMKHIILS PREKLVYDSETDK VHL YKTS G-KSELAWKDGEVVL DNT	269		
BT1052	SLL EITNIMEKLYDLKFVYDDESLKTERFTGEFSTDNLPDEIL NVLMHTNH-FSY	318		
BT1618	TLSDIFITIERIYDIHI VPPHLATTDVYTIKFKQKAPIKEIMNI VTKTIGNIDY	315		
BT3992	NI FTITKALERFYDVKII LSPDIRSDKTYS GVLKKKSTIESVLKSLQNSIP-IEY	322		
BT4248/9	PLSQLISII NQIYQSNII LEGKFTKQPSFTGSI RYDETLDDVI DKLCFSLN-LTY	301		
BT4356	PLEEALWMLERRY SVK FVIKNEKLKNSSFTGFTTN-QRLEKILEYFKVSSK-IRW	322		
BT1052	KKEGRIRLS-----KK	330		
BT1618	KVEDENI LL IYSPLNKK GGR	335		
BT3992	KIVGNNIFISS---DKK	336		
BT4248/9	KKQNRKIV IYN	312		
BT4356	KHINDDKDGSD---RKKEIEIY	342		

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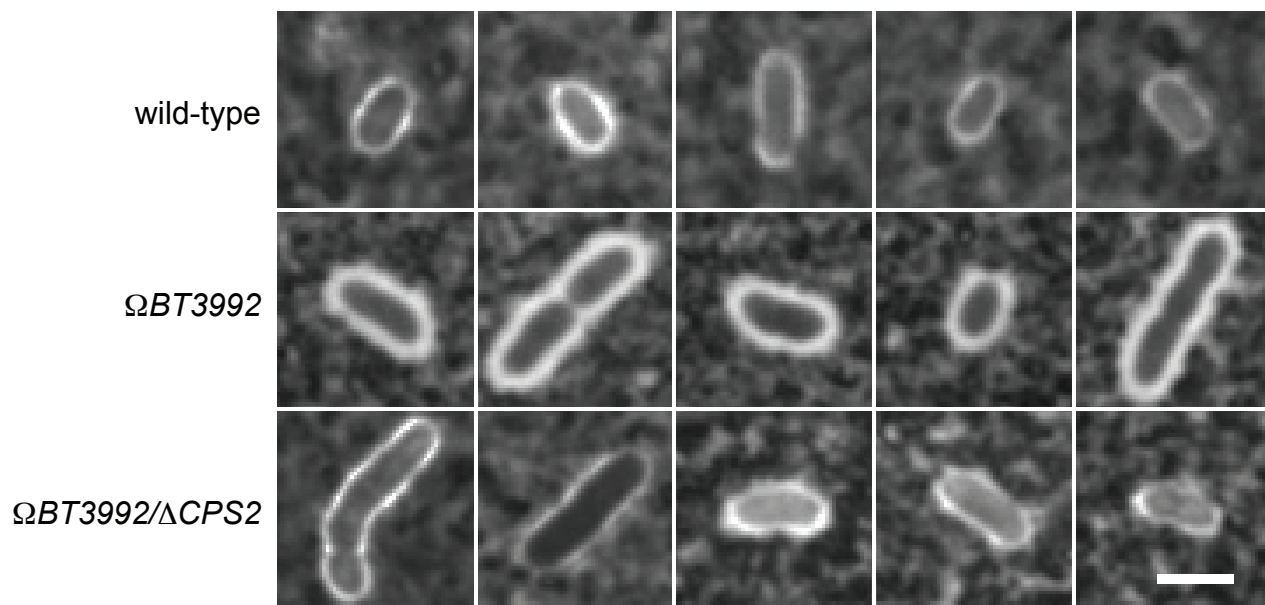


Martens *et al.* Figure S4A

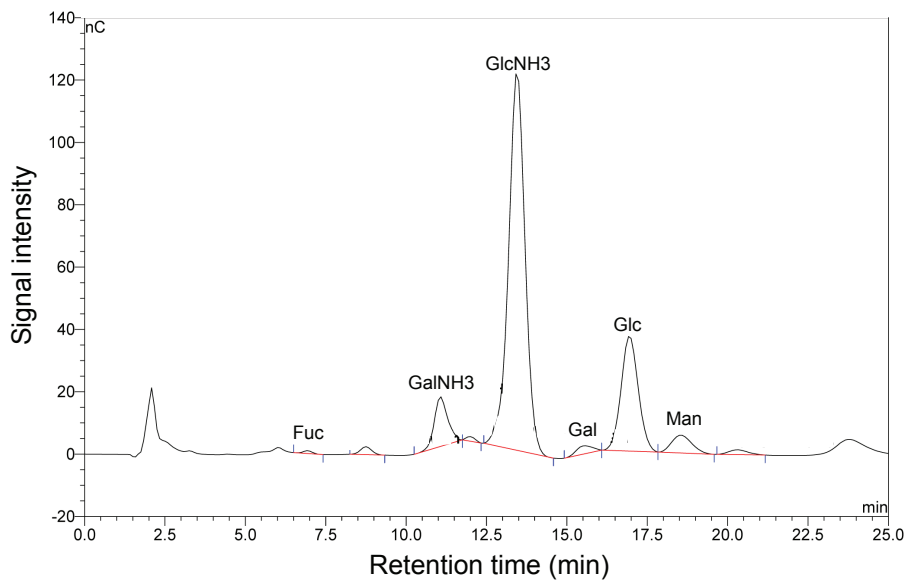




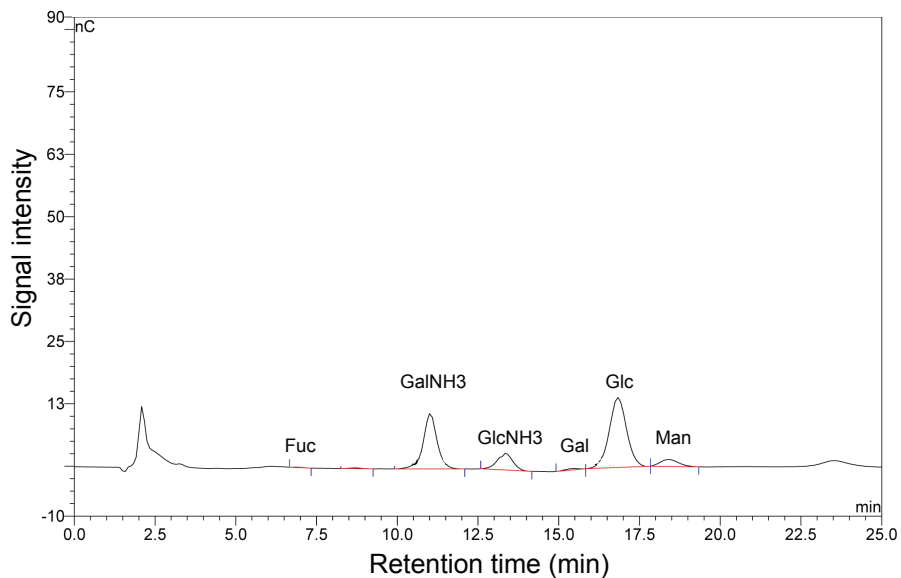
Martens *et al.* Figure S5



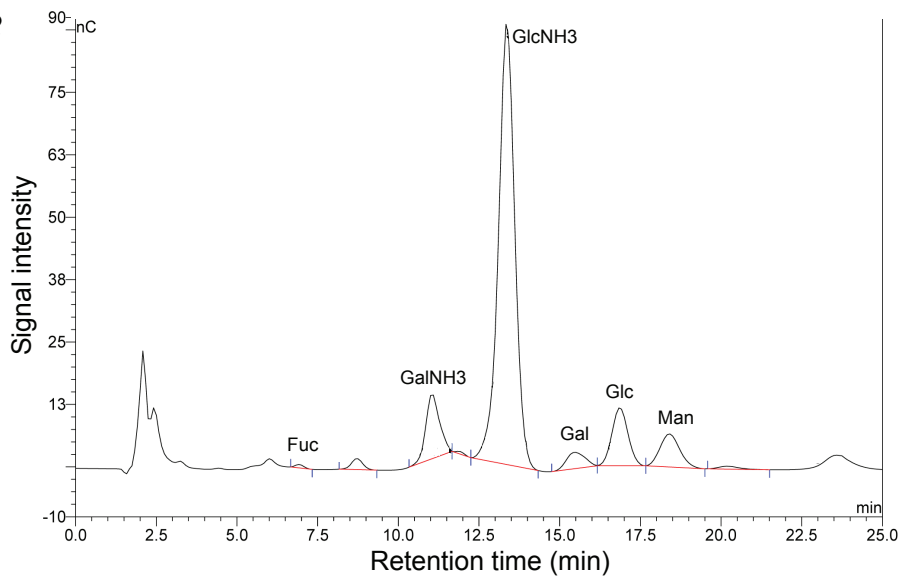
A wild-type



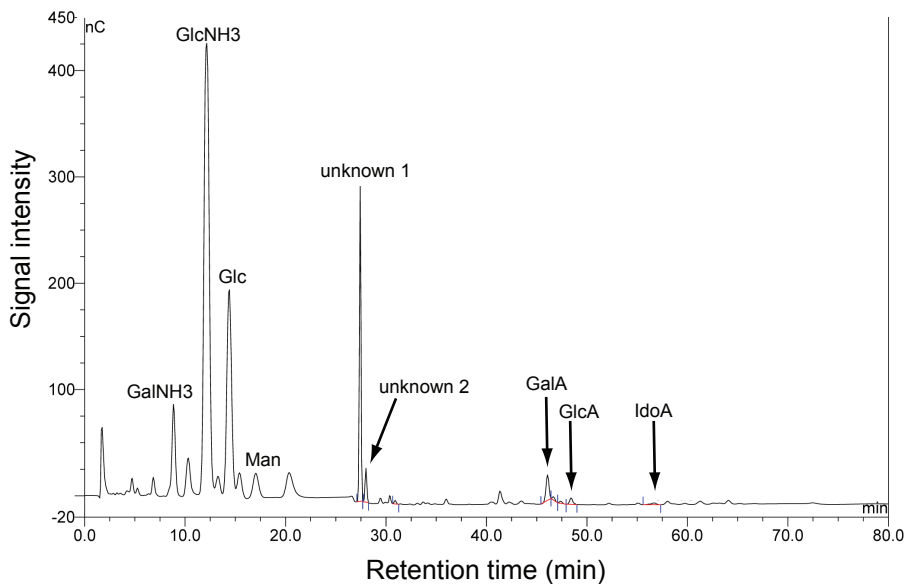
B $\Omega BT3992$



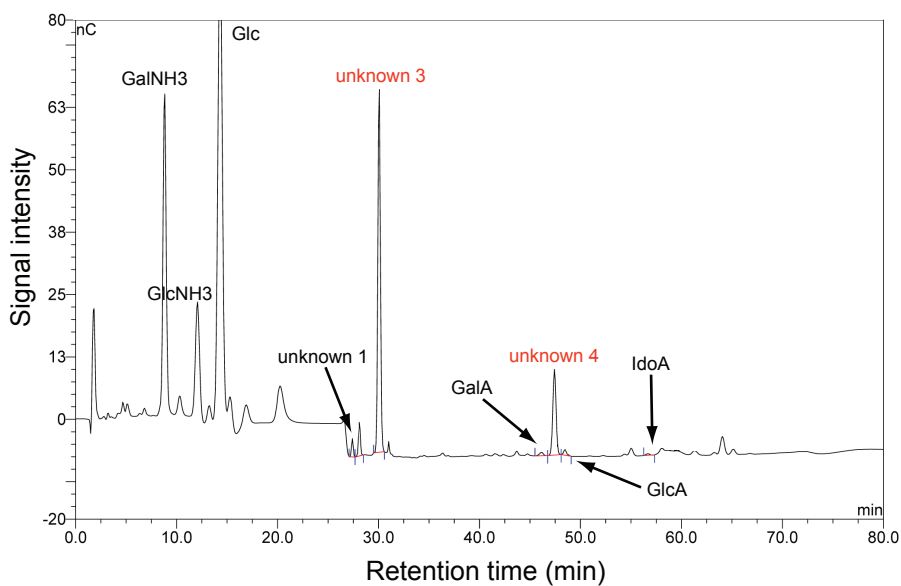
C $\Omega BT3992/\Delta CPS2$



D wild-type



E $\Omega BT3992$



F $\Omega BT3992/\Delta CPS2$

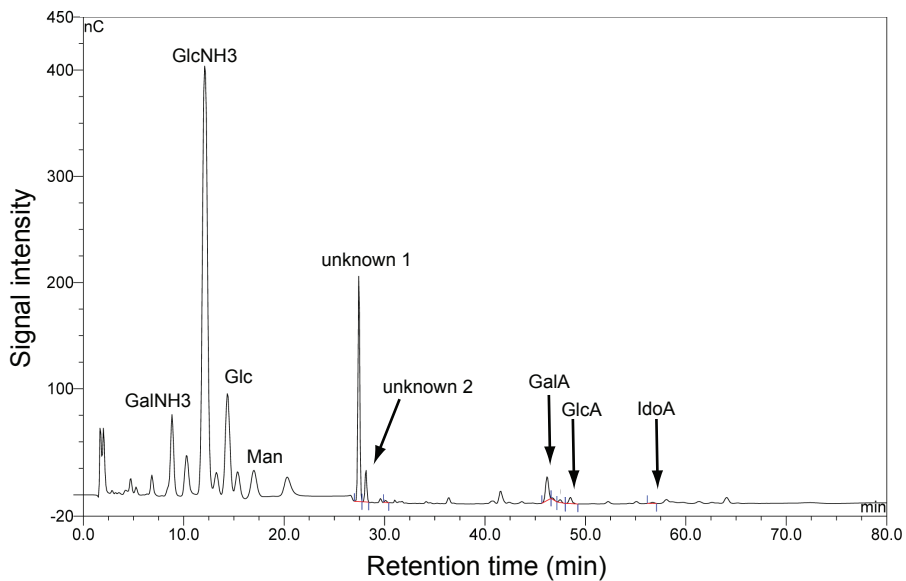


Table S1. Strains and plasmids used in this study

Strain or plasmid	Relevant feature(s)	Use	Source or reference
<i>B. thetaiotaomicron</i> strains:			
ATCC 29148	wild-type strain; VPI-5482	wild-type strain	(4)
ATCC 29148 <i>tdk</i>	Tdk ^R , FUdR ^R	"wild-type" strain for gene deletion by allelic exchange	(5)
Ω BT1052	Erm ^R , lacks anti- σ BT1052	ATCC 29148 with pGERM insertion in <i>BT1052</i>	This study
Ω BT1052:: <i>NBU2-BT1052</i>	Erm ^R , Tet ^R	Ω BT1052 with complementing copy of <i>BT1052</i> inserted into <i>att NBU2</i> site 1 via p <i>NBU2-bla-tetQb</i>	This study
Ω BT1618	Erm ^R , lacks anti- σ BT1618	ATCC 29148 with pGERM insertion in <i>BT1618</i>	This study
Ω BT3992	Erm ^R , lacks anti- σ BT3992	ATCC 29148 with pGERM insertion in <i>BT3992</i>	This study
Ω BT4249	Erm ^R , lacks anti- σ BT4249	ATCC 29148 with pGERM insertion in <i>BT4249</i>	This study
Ω BT4356	Erm ^R , lacks anti- σ BT4356	ATCC 29148 with pGERM insertion in <i>BT4356</i>	This study
Ω BT1042	Erm ^R , lacks SusC-like protein BT1042	ATCC 29148 with pGERM insertion in <i>BT1042</i>	This study
Ω BT1043	Erm ^R , lacks SusD-like protein BT1043	ATCC 29148 with pGERM insertion in <i>BT1043</i>	This study
Δ BT1053	Tdk ^R , FUdR ^R , lacks ECF- σ BT1053	ATCC 29148 <i>tdk</i> with deletion of <i>BT1053</i>	This study
Ω BT3992/ Δ BT3993	Tdk ^R , FUdR ^R , Erm ^R , lacks ECF- σ BT3993 and anti- σ BT3992	ATCC 29148 <i>tdk</i> with deletion of <i>BT3993</i> and pGERM insertion in <i>BT3992</i>	This study
Ω BT3992/ Δ BT3983-88	Tdk ^R , FUdR ^R , Erm ^R , lacks Sus-like system encoded by <i>BT3983-88</i> and anti- σ BT3992	ATCC 29148 <i>tdk</i> with deletion of <i>BT3983-88</i> and pGERM insertion in <i>BT3992</i>	This study
Ω BT3992/ Δ CPS2	Tdk ^R , FUdR ^R , Erm ^R lacks CPS2 genes and anti- σ BT3992	ATCC 29148 <i>tdk</i> with deletion of CPS2 (<i>BT0462-82</i>) and pGERM insertion in <i>BT3992</i>	This study
Plasmids:			
pGERM	<i>Bacteroides</i> spp. suicide vector	construction of insertion-duplication mutants	(6)
pExchange- <i>tdk</i>	Derivative of pKNOCK- <i>bla-ermGb</i> carrying cloned <i>tdk</i> for counter-selection	construction of gene deletions	(5)
p <i>NBU2-bla-tetQb</i>	Targets cloned fragments to <i>NBU2 att1</i> and/or <i>att2</i> sites, Tet ^R , Amp ^R	<i>NBU2</i> -based complementation and tagging vector	(1)

Table S2. GeneChip experiments used in this study

GEO series	GEO number	GEO platform	Strain genotype (all ATCC 29148)	Experiment description	Culture type/volume	Growth phase/OD600	Reference
New microarrays:							
GSE14592	GSM364877	GPL1821	$\Omega BT1052$	anti- σ <i>BT1052</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.62	This work
GSE14592	GSM364878	GPL1821	$\Omega BT1052$	anti- σ <i>BT1052</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.59	This work
GSE14592	GSM364879	GPL1821	$\Omega BT1052$	anti- σ <i>BT1052</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.64	This work
GSE14592	GSM364880	GPL1821	$\Omega BT1052::NBU2-BT1052$ (complemented)	complemented anti- σ <i>BT1052</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.65	This work
GSE14592	GSM364881	GPL1821	$\Omega BT1052::NBU2-BT1052$ (complemented)	complemented anti- σ <i>BT1052</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.60	This work
GSE14592	GSM364882	GPL1821	$\Omega BT1052::NBU2-BT1052$ (complemented)	complemented anti- σ <i>BT1052</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.62	This work
GSE14592	GSM364883	GPL1821	$\Omega BT1618$	anti- σ <i>BT1618</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.66	This work
GSE14592	GSM364884	GPL1821	$\Omega BT1618$	anti- σ <i>BT1618</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.62	This work
GSE14592	GSM364885	GPL1821	$\Omega BT1618$	anti- σ <i>BT1618</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.60	This work
GSE14592	GSM364886	GPL1821	$\Omega BT4249$	anti- σ <i>BT4247</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.66	This work
GSE14592	GSM364887	GPL1821	$\Omega BT4249$	anti- σ <i>BT4247</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.70	This work
GSE14592	GSM364888	GPL1821	$\Omega BT4249$	anti- σ <i>BT4247</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.67	This work
GSE14592	GSM364889	GPL1821	$\Omega BT4356$	anti- σ <i>BT4356</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.64	This work
GSE14592	GSM364890	GPL1821	$\Omega BT4356$	anti- σ <i>BT4356</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.60	This work
GSE14592	GSM364891	GPL1821	$\Omega BT4356$	anti- σ <i>BT4356</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.61	This work
GSE14592	GSM364892	GPL1821	$\Omega BT3992$	anti- σ <i>BT3992</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.63	This work
GSE14592	GSM364893	GPL1821	$\Omega BT3992$	anti- σ <i>BT3992</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.63	This work
GSE14592	GSM364896	GPL1821	$\Omega BT3992$	anti- σ <i>BT3992</i> mutant grown in MM-glucose	Chemostat/800ml	mid-log/0.59	This work
GSE14592	GSM364897	GPL1821	$\Omega BT1042$	SusC-like transporter <i>BT1042</i> mutant grown in MM-neutral O-	Tube/5ml	mid-log/0.64	This work

GSE14592	GSM364898	GPL1821	<i>ΩBT1042</i>	SusC-like transporter <i>BT1042</i> mutant grown in MM-neutral O-	Tube/5ml	mid-log/0.62	This work
GSE14592	GSM364899	GPL1821	<i>ΔBT1053</i>	ECF-σ <i>BT1053</i> mutant grown in MM-neutral O- glycans	Tube/5ml	mid-log/0.6	This work
GSE14592	GSM364900	GPL1821	<i>ΔBT1053</i>	ECF-σ <i>BT1053</i> mutant grown in MM-neutral O- glycans	Tube/5ml	mid-log/0.63	This work
Published microarrays:							
GSE11980	GSM40886	GPL1821	wild-type	Cecal bacterial population from adult NMRI inbred mouse fed simple sugar diet; replicate 1/3	N/A	N/A	(7)
GSE11980	GSM40887	GPL1821	wild-type	Cecal bacterial population from adult NMRI inbred mouse fed simple sugar diet; replicate 2/3	N/A	N/A	(7)
GSE11980	GSM40888	GPL1821	wild-type	Cecal bacterial population from adult NMRI inbred mouse fed simple sugar diet; replicate 3/3	N/A	N/A	(7)
GSE11980	GSM119522	GPL1821	wild-type	Pooled cecal bacterial populations from 17 day- old NMRI inbred mice suckling on mother's milk; replicate 1/6	N/A	N/A	(8)
GSE11980	GSM119523	GPL1821	wild-type	Pooled cecal bacterial populations from 17 day- old NMRI inbred mice suckling on mother's milk; replicate 2/6	N/A	N/A	(8)

GSE11980	GSM119524	GPL1821	wild-type	Pooled cecal bacterial populations from 17 day-old NMRI inbred mice suckling on mother's milk; replicate 3/6	N/A	N/A	(8)
GSE11980	GSM119525	GPL1821	wild-type	Pooled cecal bacterial populations from 17 day-old NMRI inbred mice suckling on mother's milk; replicate 4/6	N/A	N/A	(8)
GSE11980	GSM119526	GPL1821	wild-type	Pooled cecal bacterial populations from 17 day-old NMRI inbred mice suckling on mother's milk; replicate 5/6	N/A	N/A	(8)
GSE11980	GSM119527	GPL1821	wild-type	Pooled cecal bacterial populations from 17 day-old NMRI inbred mice suckling on mother's milk; replicate 6/6	N/A	N/A	(8)
GSE11980	GSM301635	GPL1821	wild-type	Minimal medium plus glucose 0.5% (w/v); replicate 1/3; reference for anti- σ mutant	Chemostat/ 800ml	middle logarithmic growth phase/ 0.645	(1)
GSE11980	GSM301637	GPL1821	wild-type	Minimal medium plus glucose 0.5% (w/v); replicate 2/3; reference for anti- σ mutant	Chemostat/ 800ml	middle logarithmic growth phase/ 0.62	(1)
GSE11980	GSM301639	GPL1821	wild-type	Minimal medium plus glucose 0.5% (w/v); replicate 3/3; reference for anti- σ mutant	Chemostat/ 800ml	middle logarithmic growth phase/ 0.635	(1)
GSE11980	GSM301720	GPL1821	wild-type	Minimal medium plus glucose 0.5% (w/v); replicate 1/2, reference for <i>BT1042</i> and <i>BT1053</i> mutant profiles	Tube/5ml	middle logarithmic growth phase/0.62	(1)
GSE11980	GSM301721	GPL1821	wild-type	Minimal medium plus glucose 0.5% (w/v); replicate 2/2, reference for <i>BT1042</i> and <i>BT1053</i> mutant profiles	Tube/5ml	middle logarithmic growth phase/0.64	(1)

GSE11980	GSM301722	GPL1821	wild-type	Minimal medium plus 0.5% (w/v) neutral PMG glycans; replicate 1/2	Tube/5ml	middle logarithmic growth phase/0.59	(1)
GSE11980	GSM301731	GPL1821	wild-type	Minimal medium plus 0.5% (w/v) neutral PMG glycans; replicate 2/2	Tube/5ml	middle logarithmic growth phase/0.63	(1)
GSE11980	GSM302149	GPL1821	wild-type	Minimal medium plus 0.5% (w/v) 100mM fraction PMG glycans; earlt phase, replicate	Tube/5ml	mid 1st log phase/0.3	(1)
GSE11980	GSM302150	GPL1821	wild-type	Minimal medium plus 0.5% (w/v) 100mM fraction PMG glycans; early phase, replicate	Tube/5ml	mid 1st log phase/0.3	(1)

Table S3. Oligonucleotides used in this study

Primer name	Sequence (5'-3')	Use
IDM mutants:		
<i>BT1052</i> IDM fwd (<i>Sall</i>)	gcggtcgcgaggggaggatgcaatgacg	<i>BT1052</i> ::pGERM
<i>BT1052</i> IDM rev (<i>KpnI</i>)	gcgggtaccgcaatccccacgcaattccg	<i>BT1052</i> ::pGERM
<i>BT1042</i> IDM fwd (<i>Sall</i>)	gcggtcgcactgtcagtagtatacaacacaaatg	<i>BT1042</i> ::pGERM
<i>BT1042</i> IDM rev (<i>KpnI</i>)	gcgggtaccctgcttatcgactattgaataactg	<i>BT1042</i> ::pGERM
<i>BT1043</i> IDM fwd (<i>Sall</i>)	gcggtcgcaccctagttgacaactggacctg	<i>BT1043</i> ::pGERM
<i>BT1043</i> IDM rev (<i>KpnI</i>)	gcgggtaccttctgatatgcataattcattctac	<i>BT1043</i> ::pGERM
<i>BT1618</i> IDM fwd (<i>SmaI</i>)	gcgccccgggcccgcataagtttcagtcctgaac	<i>BT1618</i> ::pGERM
<i>BT1618</i> IDM rev (<i>EcoRI</i>)	gcggaattccactatagagagtaggggaatc	<i>BT1618</i> ::pGERM
<i>BT3992</i> IDM fwd (<i>Sall</i>)	gcggtcgcacgcatggaagaaattatcatctgg	<i>BT3992</i> ::pGERM
<i>BT3992</i> IDM rev (<i>KpnI</i>)	gcgggtaccgatacacattacgttcttttcgg	<i>BT3992</i> ::pGERM
<i>BT4248</i> IDM fwd (<i>Sall</i>)	gcggtcgcaccgaattataaaggatagtagcac	<i>BT4248</i> ::pGERM
<i>BT4248</i> IDM rev (<i>KpnI</i>)	gcgggtaccctcaaaaaatgagttgccttc	<i>BT4248</i> ::pGERM
<i>BT4356</i> IDM fwd (<i>Sall</i>)	gcggtcgcgcttctcctgattgtgaggg	<i>BT4356</i> ::pGERM
<i>BT4356</i> IDM rev (<i>KpnI</i>)	gcgggtaccgggataaacagaattgcagc	<i>BT4356</i> ::pGERM
Yeast two-hybrid domains:		
<i>BT1619</i> YTH fwd (<i>NdeI</i>)	gcgcatatgtatgggcaaaatcagccaataac	<i>BT1619</i> N-terminal domain
<i>BT1619</i> YTH rev (<i>SmaI</i>)	gcgccccgggatcttctgtagctgtatgtga	<i>BT1619</i> N-terminal domain
<i>BT4357</i> YTH fwd (<i>NdeI</i>)	gcgcatatgtatgcccaatctgcaaaggtt	<i>BT4357</i> N-terminal domain
<i>BT4357</i> YTH rev (<i>SmaI</i>)	gcgccccgggtcctctttcagcactaccga	<i>BT4357</i> N-terminal domain
<i>BT4247</i> YTH fwd (<i>NdeI</i>)	gcgcatatggctcttgagctcaaggacac	<i>BT4247</i> N-terminal domain
<i>BT4247</i> YTH rev (<i>SmaI</i>)	gcgccccgggtctcctccagtacaattttgat	<i>BT4247</i> N-terminal domain
<i>BT1042</i> YTH fwd (<i>NdeI</i>)	gcgcatatgtatggcaggaacgaatgattac	<i>BT1042</i> N-terminal domain
<i>BT1042</i> YTH rev (<i>SmaI</i>)	gcgccccgggtcttaccattgtgacttttag	<i>BT1042</i> N-terminal domain
<i>BT3983</i> YTH fwd (<i>NdeI</i>)	gcgcatatggcaatagcacagtaacaattag	<i>BT3983</i> N-terminal domain
<i>BT3983</i> YTH rev (<i>SmaI</i>)	gcgccccgggagcatcttctttaaagtgatattaat	<i>BT3983</i> N-terminal domain
<i>BT1617</i> YTH fwd (<i>NdeI</i>)	gcgcatatggaaacctttgacgaaaacaac	<i>BT1617</i> entireORF
<i>BT1617</i> YTH rev (<i>SmaI</i>)	gcgccccgggttagaaaaatagaataaaggttatgaat	<i>BT1617</i> entireORF
<i>BT4355</i> YTH fwd (<i>NdeI</i>)	gcgcatatggaagaactacgcataaagag	<i>BT4355</i> entire ORF

<i>BT4355</i> YTH rev (<i>Sma</i> I)	<u>gcgccccgggtaaggaaacagtaaaggaagcag</u>	<i>BT4355</i> entire ORF
<i>BT4250</i> YTH fwd (<i>Nde</i> I)	<u>gcgcatatggaggagacaataattctgga</u>	<i>BT4250</i> entire ORF
<i>BT4250</i> YTH rev (<i>Sma</i> I)	<u>gcgccccgggtatcccataaatacgcacaaataaag</u>	<i>BT4250</i> entire ORF
<i>BT1053</i> YTH fwd (<i>Nde</i> I)	<u>gcgcatatgcaacaacctctatatacct</u>	<i>BT1053</i> entire ORF
<i>BT1053</i> YTH rev (<i>Sma</i> I)	<u>gcgccccgggtcatgattgtttgaatatgtcaagc</u>	<i>BT1053</i> entire ORF
<i>BT3993</i> YTH fwd (<i>Nde</i> I)	<u>gcgcatatgatgaatgaaaacttcgacttaacc</u>	<i>BT3993</i> entire ORF
<i>BT3993</i> YTH rev (<i>Sma</i> I)	<u>gcgccccgggccccaaaaacacttatctttaatc</u>	<i>BT3993</i> entire ORF
<i>BT1618c</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggataacaatcgaa</u> tgaagagcataca	<i>BT1618</i> C-terminal domain
<i>BT1618c</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcatcggcctccttcttatttagg</u>	<i>BT1618</i> C-terminal domain
<i>BT1052c</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggctttccaataaa</u> ctttctgattata	<i>BT1052</i> C-terminal domain
<i>BT1052c</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcatttttagacaatcgaataatccg</u>	<i>BT1052</i> C-terminal domain
<i>BT4356c</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggaaaggggata</u> cgggagaggtta	<i>BT4356</i> C-terminal domain
<i>BT4356c</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcaataaatctctattatctcttttttc</u>	<i>BT4356</i> C-terminal domain
<i>BT4248c</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggatgaattcaatc</u> agagataatattaac	<i>BT4248</i> C-terminal domain
<i>BT4248c</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcaattatataattactattttctattctg</u>	<i>BT4248</i> C-terminal domain
<i>BT3992c</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcatcatttctatctgaagagataaag</u> at	<i>BT3992</i> C-terminal domain
<i>BT3992c</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggaaccggccgg</u> aacatcagatg	<i>BT3992</i> C-terminal domain
<i>BT1618n</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggatgtcgaacgc</u> tcataaaataattaaa	<i>BT1618</i> N-terminal domain
<i>BT1618n</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcatctgcgtaaggtataaccttgcg</u>	<i>BT1618</i> N-terminal domain
<i>BT1052n</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggatggatgaatct</u> atcttgatgaac	<i>BT1052</i> N-terminal domain
<i>BT1052n</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcaacgtccccatcgaaccgatat</u>	<i>BT1052</i> N-terminal domain
<i>BT4356n</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggatgaaagattta</u> aataataatagaatag	<i>BT4356</i> N-terminal domain
<i>BT4356n</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcaacgtgtgcccactcccaccaca</u>	<i>BT4356</i> N-terminal domain
<i>BT4249n</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccggggatggataaaga</u> tacaagatgagtttg	<i>BT4248</i> N-terminal domain
<i>BT4249n</i> YTH rev CDSIII	<u>tctagaggccgaggcgccgacatgtcatcaactaagtctcttagaacttg</u>	<i>BT4248</i> N-terminal domain

<i>BT3992n</i> YTH rev CDSIII	<u>tctagaggccgaggcggccgacatgtcatctcatccagcgatgcatatgc</u>	<i>BT3992</i> N-terminal domain
<i>BT3992n</i> YTH fwd SM3	<u>aagcagtggatcaacgcagagtggccattatggccgggatggaggtaaa</u>	<i>BT3992</i> N-terminal domain
	tgcttgatca	

Gene deletions:

<i>BT3983-88</i> upstream (<i>Sall</i>)	<u>gcggtcgacggaagatgaactgaatacggg</u>	<i>BT3983-88</i> deletion, upstream flank
<i>BT3983-88</i> 5' out	cattagttttatataaatattagaatcg	<i>BT3983-88</i> deletion, upstream flank
<i>BT3983-88</i> 3' out	<u>cgattctaataattatataaaaactaatgaattctaaataaatcaagataggtat</u>	<i>BT3983-88</i> deletion, downstream flank
<i>BT3983-88</i> downstream (<i>SmaI</i>)	<u>gcgcccgggtattcactacttttgccggac</u>	<i>BT3983-88</i> deletion, downstream flank
CPS2 upstream (<i>Sall</i>)	<u>gcggtcgacagctgaaaaagaactccatacag</u>	CPS2 deletion, upstream flank
CPS2 5' out	cattatcaccattacccttg	CPS2 deletion, upstream flank
CPS2 3' out	<u>caaggggtaatgggtgataatgctaaatcgtaatccggttctaag</u>	CPS2 deletion, downstream flank
CPS2 downstream (<i>XbaI</i>)	<u>gcgctagacttgctttaccgctcatcc</u>	CPS2 deletion, downstream flank

Complementation alleles:

<i>BT1052</i> comp fwd (<i>XbaI</i>)	<u>gcgctagatgtaatatctaggtatataggag</u>	<i>BT1052</i> complementation
<i>BT1052</i> comp rev (<i>Sall</i>)	<u>gcggtcgacacataccttttttaacattctc</u>	<i>BT1052</i> complementation

qRT-PCR primers:

<i>BT1040</i> fwd	tcagcgtttgcgtcagtctcctaa
<i>BT1040</i> rev	attccatccctccaagcaacactac
<i>BT1043</i> fwd	gtaaaccaaccggactcactg
<i>BT1043</i> rev	ttttgcgtaataattttctgtaactg
<i>BT1046</i> fwd	ctaccggacggatacgatgacga
<i>BT1046</i> rev	cagtacagccgataagccgacaga
<i>BT3983</i> fwd	gaaatggctgtacgcgacctat
<i>BT3983</i> rev	ttacggcctgccaactgtgaag
<i>BT3984</i> fwd	ggggtgcagacgggtgga
<i>BT3984</i> rev	cgataatgcttcttctctctct
<i>BT0463</i> fwd	ctatttcggtattgatgttgctggta
<i>BT0463</i> rev	tctccgataataaatgcttgggcta
<i>BT0482</i> fwd	attaaccgacgagaagaacgaaaaaga
<i>BT0482</i> rev	tgatggctaaattggcggagataa

BT0206 fwd
BT0206 rev
BT4404 fwd
BT4404 rev
BT3992 fwd
BT3992 rev

gctgaaagtgggcacgaatacaat
acataaagcgtgaaccggaaatagg
ggtcgctggcaagaggctaca
accgggagttccagtcattacga
gcggtcgacgcatggaagaaattatcatctgg
gcgggtaccgatacacattacgttcttttcgg

Table S4. Genes with increased (+) or decreased (-) expression in anti- σ mutants

Up-regulated genes:

Gene	Description	Ω BT1052 folds (P-value)	Ω BT1052 complement folds (P-value)	Ω BT1618 folds (P-value)	Ω BT3992 folds (P- value)	Ω BT4249 folds (P-value)	Ω BT4356 folds (P-value)
BT0037	putative transcriptional regulatory protein (CPS8)	+16.0 (9.4E-06)					
BT0038	hypothetical protein (CPS8)	+20.5 (1.5E-03)					
BT0039	hypothetical protein (CPS8)	+8.5 (1.8E-04)					
BT0041	F420H2:quinone oxidoreductase (CPS8)	+15.1 (4.1E-04)					
BT0042	hypothetical protein (CPS8)	+8.3 (1.5E-03)					
BT0044	putative glycosyltransferase (CPS8)	+8.5 (8.6E-04)					
BT0046	putative glycosyltransferase (CPS8)	+8.9 (4.8E-03)					
BT0047	putative glycosyltransferase (CPS8)	+12.9 (5.0E-05)					
BT0048	hypothetical protein (CPS8)	+21.1 (3.4E-05)		+3.2 (2.0E-03)	+3.2 (1.6E-03)	+2.6 (7.6E-03)	+2.5 (3.8E-03)
BT0049	putative glycosyltransferase (CPS8)	+15.7 (4.4E-05)					
BT0050	putative glycosyltransferase (CPS8)	+15.1 (2.5E-05)					
BT0051	putative glycosyltransferase (CPS8)	+10.4 (4.8E-03)					
BT0053	glycosyltransferase (CPS8)	+11.2 (1.4E-04)					
BT0054	putative glycosyltransferase (CPS8)	+6.0 (9.8E-05)					
BT0055	putative glycosyltransferase (CPS8)	+8.7 (2.9E-03)					
BT0056	putative glycosyltransferase (CPS8)	+14.1 (1.6E-04)					
BT0057	hypothetical protein (CPS8)	+12.6 (1.1E-04)					
BT0058	hypothetical protein (CPS8)	+12.1 (7.3E-04)					
BT0059	hypothetical protein (CPS8)	+19.1 (2.0E-03)					
BT0060	putative polysaccharide export protein (CPS8)	+21.9 (1.7E-03)					
BT0061		+11.8 (4.2E-04)					
	putative tyrosine-protein kinase ptk (CPS8)						
BT0062	hypothetical protein (CPS8)	+13.8 (1.7E-05)					
BT0063	hypothetical protein (CPS8)	+12.4 (3.5E-05)					
BT0064	hypothetical protein (CPS8)	+15.3 (5.4E-04)					
BT0065	Glycoside Hydrolase Family 27 (CPS8)	+10.9 (1.3E-04)					
BT0066	major outer membrane protein OmpA (CPS8)	+13.7 (4.9E-04)					
BT0067	hypothetical protein (CPS8)	+6.7 (2.1E-03)					
BT0068	hypothetical protein (CPS8)	+17.6 (1.2E-04)					
BT0106	hypothetical protein	+2.9 (1.4E-03)			+3.3 (1.3E-03)		+2.5 (3.4E-03)
BT0134	hypothetical protein		+2.8 (2.2E-03)				
BT0206	susC-like				+6.9 (8.2E-03)		

BT0207	susD-like			+7.1 (7.0E-03)		
BT0208	hypothetical protein			+5.4 (8.2E-03)		
BT0209	hypothetical protein			+6.5 (1.1E-03)		
BT0212	protease			+4.4 (3.6E-03)		
BT0213	hypothetical protein			+4.7 (2.9E-03)		
BT0377	hypothetical protein (CPS1)	+3.9 (3.1E-05)		+3.1 (2.7E-04)		+3.9 (2.0E-04)
BT0378	capsular polysaccharide biosynthesis protein capD (CPS1)	+3.8 (4.6E-05)		+4.2 (4.2E-05)		
BT0380	nucleotide sugar epimerase (CPS1)	+3.6 (6.4E-03)				
BT0381	capsular polysaccharide biosynthesis protein capD (CPS1)	+4.0 (2.2E-03)		+3.3 (7.0E-04)		
BT0383	putative UDP-N-acetylglucosamine 2-epimerase (CPS1)	+3.1 (5.7E-04)				
BT0384	hypothetical protein (CPS1)	+4.5 (3.8E-03)		+4.0 (4.0E-03)		
BT0385	hypothetical protein (CPS1)	+5.2 (9.3E-03)		+5.9 (8.1E-03)		
BT0386	putative F420H2-dehydrogenase (CPS1)	+7.0 (1.5E-04)		+6.6 (6.6E-05)	+2.8 (5.4E-04)	+2.6 (2.2E-03)
BT0388	galactoside O-acetyltransferase (CPS1)	+4.8 (1.1E-04)		+2.8 (2.1E-03)		
BT0389	putative galactoside acetyltransferase (CPS1)	+4.6 (5.6E-03)		+4.1 (6.7E-03)		
BT0390	putative O-antigen export protein (CPS1)	+4.1 (3.7E-04)				
BT0391	putative protein involved in capsular polysaccharide biosynthesis (CPS1)	+5.8 (2.0E-03)		+5.7 (2.2E-03)		
BT0392	lipopolysaccharide biosynthesis RfbU-related protein (CPS1)	+3.8 (9.4E-04)		+3.3 (1.0E-04)		
BT0393	serine acetyltransferase (CPS1)	+4.3 (7.0E-03)				
BT0394	capsular polysaccharide biosynthesis glycosyltransferase (CPS1)	+3.6 (5.6E-03)		+3.7 (5.1E-03)		
BT0396	putative UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase (CPS1)	+3.8 (1.5E-03)		+3.6 (1.1E-04)		
BT0397	hypothetical protein (CPS1)	+5.6 (1.3E-03)		+4.5 (4.5E-03)		
BT0398	polysaccharide export outer membrane protein (CPS1)	+3.3 (6.5E-06)		+3.4 (4.2E-05)		
BT0399	tyrosine-protein kinase ptk involved in exopolysaccharide biosynthesis (CPS1)			+3.0 (5.7E-03)		
BT0400	putative tyrosine-protein kinase in capsular polysaccharide biosynthesis region (CPS1)	+3.0 (5.9E-03)		+4.2 (2.2E-03)		
BT0456	Glycoside Hydrolase Family 20			+2.9 (2.4E-03)		
BT0459	Glycoside Hydrolase Family 20	+3.9 (2.1E-05)		+6.4 (1.3E-04)		
BT0460	Glycoside Hydrolase Family 20	+3.5 (1.4E-03)		+4.6 (5.9E-05)		
BT0461	Glycoside Hydrolase Family 2	+5.4 (4.4E-03)		+8.0 (3.5E-04)		

BT0462	putative transcriptional regulator (CPS2)			+27.2 (1.8E-03)	
BT0463	glucose-1-phosphate thymidyltransferase (CPS2)			+37.3 (2.0E-06)	
BT0464	dTDP-4-dehydrorhamnose 3,5-epimerase (CPS2)			+99.9 (2.3E-03)	
BT0465	dTDP-4-dehydrorhamnose reductase (CPS2)			+80.2 (2.4E-04)	
BT0466	dTDP-glucose 4,6-dehydratase (CPS2)			+92.2 (1.6E-03)	
BT0467	hypothetical protein (CPS2)			+60.0 (4.6E-07)	
BT0468	putative F420H2-dehydrogenase 40 kDa subunit (CPS2)			+110.1 (2.8E-03)	
BT0470	hypothetical protein (CPS2)			+99.7 (1.8E-03)	
BT0472	putative acyltransferase in colanic acid biosynthesis (CPS2)			+85.9 (6.1E-04)	
BT0473	putative glycosyltransferase (CPS2)			+69.5 (2.7E-03)	
BT0474	D-glycero-D-manno-heptose 1-phosphate kinase (CPS2)			+56.2 (3.6E-04)	
BT0475				+130.5 (4.3E-04)	
BT0476	putative phosphoheptose isomerase (CPS2)				
BT0476	D-mannose-1-phosphate guanylyltransferase (CPS2)			+98.2 (8.2E-04)	
BT0477	putative phosphatase (CPS2)			+111.6 (1.4E-03)	
BT0478	hypothetical protein (CPS2)			+101.9 (2.4E-03)	
BT0479	putative glycosyltransferase (CPS2)			+100.3 (3.6E-06)	
BT0480	glycosyltransferase (CPS2)			+51.3 (9.1E-04)	
BT0481	polysaccharide export outer membrane protein (CPS2)			+102.4 (6.0E-03)	
BT0506	Glycoside Hydrolase Family 20	+37.5 (2.1E-05)		+18.4 (1.7E-05)	
BT0567	putative protein involved in barrier function of the cell envelope		+2.6 (4.6E-04)		
BT0597	hypothetical protein (CPS3)			+3.6 (3.8E-04)	+4.4 (3.8E-04)
BT0599	UDP-glucose 6-dehydrogenase (CPS3)	+2.9 (3.9E-03)		+4.6 (4.1E-03)	+7.2 (2.8E-03)
BT0600	nucleotide sugar epimerase (CPS3)	+2.9 (1.6E-03)	+2.6 (4.5E-03)	+3.0 (1.8E-03)	+7.7 (1.7E-03)
BT0601	UDP-N-acetylglucosamine 2-epimerase (CPS3)			+3.1 (1.2E-03)	+5.0 (1.7E-03)
BT0603	hypothetical protein (CPS3)			+3.2 (2.4E-03)	+5.8 (1.0E-03)
BT0604	putative coenzyme F420-reducing hydrogenase (CPS3)			+3.0 (5.6E-03)	+7.0 (3.0E-03)
BT0607	serine O-acetyltransferase (CPS3)			+3.1 (2.4E-04)	+5.9 (2.4E-04)
BT0608	glycosyltransferase (CPS3)				+9.1 (7.3E-04)
BT0609	glycosyltransferase (CPS3)			+4.9 (4.8E-07)	+7.6 (4.8E-04)

BT0610	lipopolysaccharide biosynthesis protein, putative glycosyltransferase (CPS3)			+2.7 (1.7E-03)	+5.5 (1.6E-03)
BT0683	Glycoside Hydrolase Family 97	+30.2 (7.4E-05)		+161.9 (5.6E-07)	
BT0840	hypothetical protein			+2.5 (4.3E-03)	
BT0842	hypothetical protein			+3.1 (8.7E-04)	+2.9 (9.1E-04)
BT0890	hypothetical protein		+2.6 (4.7E-03)		+2.8 (4.3E-03)
BT0931	hypothetical protein		+2.6 (8.2E-03)	+2.5 (7.9E-03)	()
BT0942	putative dinitrogenase reductase activating glycohydrolase		+3.3 (3.7E-04)		+2.7 (6.2E-04) +3.3 (3.7E-04)
BT0943	penicillin-binding protein 2B (PBP-2B)		+3.5 (3.5E-05)		+3.3 (6.0E-05) +3.5 (4.1E-05)
BT1032	Glycoside Hydrolase Family 92	+11.3 (1.2E-06)		+24.3 (1.3E-05)	
BT1033	hypothetical protein	+14.2 (1.2E-04)		+16.6 (6.1E-04)	
BT1034		+202.7 (2.3E-04)		+358.1 (6.7E-06)	
	putative signal transducer				
BT1035	hypothetical protein	+40.8 (1.6E-03)		+11.6 (5.2E-03)	
BT1036	hypothetical protein	+14.4 (1.2E-03)			
BT1037	hypothetical protein	+11.5 (7.2E-03)			
BT1038	hypothetical protein	+18.5 (1.2E-03)			
BT1039	susD-like	+15.8 (1.2E-03)			
BT1040	susC-like	+12.3 (2.9E-03)			
BT1042		+120.0 (1.4E-03)			
	susC-like				
BT1043		+123.2 (6.8E-07)			
	susD-like				
BT1044		+187.5 (9.2E-04)			
	Glycoside Hydrolase Family 18				
BT1045	hypothetical protein	+97.6 (7.5E-04)			
BT1486	hypothetical protein		+11.7 (1.1E-04)		
BT1487	hypothetical protein		+14.4 (4.7E-04)		
BT1488	hypothetical protein		+21.8 (9.2E-05)		
BT1489	vitamin B12 receptor, outer membrane		+11.9 (2.0E-04)		
BT1490	conserved hypothetical protein, putative surface protein		+10.6 (3.8E-04)		
BT1491	hypothetical protein		+16.1 (5.0E-04)		
BT1624	putative secreted sulfatase	+7.2 (6.4E-06)			
BT1625	Glycoside Hydrolase Family 29	+7.4 (8.4E-05)			
BT1951	Fe ³⁺ ABC transporter, permease protein		+3.7 (1.8E-03)		
BT1952	Fe ³⁺ ABC transporter, periplasmic iron-binding protein		+7.8 (2.3E-04)		
BT1953	putative TonB-linked outer membrane receptor		+5.2 (5.7E-04)		
BT1954	putative surface layer protein		+4.7 (1.7E-04)		
BT1955	putative cell wall biogenesis protein		+7.2 (2.0E-04)		

BT1956	putative cell surface protein		+9.4 (1.5E-04)			
BT1957	hypothetical protein		+7.2 (7.2E-04)			
BT1995	hypothetical protein			+2.8 (1.3E-03)	+3.0 (1.1E-04)	+2.7 (8.8E-06)
BT1997	hypothetical protein	+5.4 (9.0E-04)			+29.2 (1.3E-05)	
BT2094	TonB-dependent receptor		+8.2 (6.6E-03)			
BT2095	putative surface layer protein		+5.0 (1.7E-03)			
BT2561	putative anti-sigma factor	+5.3 (9.2E-04)			+3.3 (1.1E-03)	
BT2569	RNA polymerase ECF-type sigma factor		+2.6 (8.0E-03)			
BT2656	hypothetical protein		+4.1 (1.2E-03)		+5.7 (3.3E-04)	
BT2657	hypothetical protein	+3.2 (5.7E-03)	+6.3 (1.5E-03)		+8.4 (5.1E-03)	
BT3011	putative anti-sigma factor	+2.8 (1.2E-03)				
BT3149	hypothetical protein			+2.5 (5.7E-03)		
BT3169	Glycoside Hydrolase Family 31	+2.9 (4.7E-04)			+3.7 (1.1E-03)	
BT3344	hypothetical protein		+29.3 (5.6E-05)			
BT3345	susD-like		+16.1 (2.9E-03)			
BT3346	susC-like		+16.3 (1.4E-03)			
BT3347	hypothetical protein		+49.7 (4.5E-04)			
BT3574	hypothetical protein				+3.1 (3.0E-03)	
BT3743	hypothetical protein				+2.8 (5.6E-05)	
BT3868	Glycoside Hydrolase Family 20				+2.6 (1.5E-04)	
BT3983	susC-like				+366.0 (4.0E-03)	
BT3984	susD-like				+188.1 (1.4E-06)	
BT3985	hypothetical protein				+353.6 (7.9E-03)	
BT3986	putative patatin-like protein				+575.0 (4.7E-03)	
BT3987	Glycoside Hydrolase Family 18				+282.8 (7.5E-04)	
BT3988	putative peptidoglycan bound protein				+249.7 (9.6E-07)	
BT3990	Glycoside Hydrolase Family 92	+4.8 (4.6E-03)				
BT3991	Glycoside Hydrolase Family 92	+3.7 (1.1E-04)				
BT3992	putative anti-sigma factor	+3.9 (2.9E-04)				
BT3993	RNA polymerase ECF-type sigma factor				+5.6 (1.6E-03)	
BT3994	Glycoside Hydrolase Family 92				+4.8 (2.3E-04)	
BT4240					+2.8 (3.4E-05)	
	conserved hypothetical protein, with a phosphotransferase enzyme family domain					
BT4241	Glycoside Hydrolase Family 2				+3.1 (3.3E-03)	
BT4245	hypothetical protein			+4.2 (2.9E-03)		
BT4246	susD-like			+3.3 (3.9E-03)		
BT4247	susC-like			+3.0 (1.8E-04)		
BT4248	putative anti-sigma factor			+3.6 (2.9E-03)		
BT4393	hypothetical protein	+3.4			+3.8 (8.0E-03)	
BT4395	Glycoside Hydrolase Family 84				+2.9 (5.5E-04)	
BT4403	putative anti-sigma factor				+11.9 (2.1E-04)	
BT4404	susC-like				+5.7 (7.2E-03)	

BT4405	susD-like				+14.5 (3.3E-03)		
BT4406	hypothetical protein				+10.5 (5.7E-04)		
BT4407	hypothetical protein		+3.9 (8.2E-03)		+36.7 (8.5E-04)	+2.5 (9.7E-03)	
BT4515	hypothetical protein			+2.6 (4.5E-03)			
BT4523	Type I restriction enzyme EcoR124II specificity protein	+6.3 (1.3E-03)					
BT4638	hypothetical protein		+3.1 (3.6E-03)	+3.5 (3.4E-03)	+3.1 (1.8E-03)	+3.2 (1.2E-03)	+3.5 (4.5E-03)
BT4690	Glycoside Hydrolase Family 13		+2.6 (4.2E-03)				+2.7 (5.3E-03)
p5482_27	VPI-5482 plasmid ORF_27	+8.3 (2.5E-05)	+16.9 (6.4E-05)	+15.3 (8.4E-06)	+11.8 (1.5E-05)		
p5482_28	VPI-5482 plasmid ORF_28	+7.7 (2.2E-03)	+14.5 (2.5E-03)	+16.1 (7.1E-04)	+16.3 (2.8E-03)		
p5482_29	VPI-5482 plasmid ORF_29	+7.2 (1.8E-04)	+8.8 (1.8E-04)	+8.8 (2.1E-04)	+14.4 (3.8E-07)		

Down-regulated genes:

Gene	Description	Ω BT1052 folds (P-value)	Ω BT1052 complement folds (P-value)	Ω BT1618 folds (P-value)	Ω BT3992 folds (P-value)	Ω BT4249 folds (P-value)	Ω BT4356 folds (P-value)
BT0174	hypothetical protein			-2.5 (1.60E-04)			
BT1338	dTDP-4-dehydrorhamnose 3,5-epimerase (CPS4)				-7.6 (4.80E-05)		-2.9 (5.60E-04)
BT1339	undecaprenyl-phosphatealpha-N-acetylglucosaminyl transferase (CPS4)				-6.3 (6.90E-04)		-2.6 (2.50E-04)
BT1340	putative lipopolysaccharide biosynthesis glycosyltransferase (CPS4)				-5.1 (4.70E-04)		
BT1341	UDP-glucose 6-dehydrogenase (CPS4)				-5.4 (1.90E-05)		
BT1342	putative UDP-glucuronic acid epimerase (CPS4)				-11.9 (9.90E-05)		-3 (1.50E-04)
BT1343	putative capsule biosynthesis protein (CPS4)				-6.8 (2.00E-03)		
BT1344	putative glycosyltransferase (CPS4)				-5.8 (1.60E-04)		
BT1345	glycosyltransferase (CPS4)				-6.6 (1.30E-03)		
BT1346	capsule biosynthesis protein capA (CPS4)				-7.6 (8.90E-05)		
BT1347	hypothetical protein (CPS4)				-6.2 (2.40E-05)		-2.6 (5.50E-04)
BT1348	CDP-abequose synthase (CPS4)				-6.7 (1.40E-04)		
BT1349	hypothetical protein (CPS4)				-7.5 (2.60E-03)		
BT1350	CDP-glucose 4,6-dehydratase (CPS4)				-7.3 (1.00E-05)		-3.1 (4.60E-04)
BT1351	glucose-1-phosphate cytidyltransferase (CPS4)				-7.6 (6.00E-04)		-3.3 (3.60E-03)
BT1352	putative glycosyltransferase HI1698 (CPS4)				-6.3 (2.80E-05)		
BT1353	glycosyltransferase (CPS4)				-3.8 (5.90E-04)		
BT1354	putative flippase (CPS4)				-9.3 (3.00E-04)		-3.1 (3.50E-03)

BT1355	hypothetical protein (CPS4)				-11.9 (7.10E-04)		-2.9 (2.80E-03)
BT1356	putative capsule polysaccharide export protein (CPS4)				-12.7 (1.40E-05)		-3.2 (2.10E-03)
BT1357	hypothetical protein (CPS4)				-18.1 (6.40E-03)		
BT1358	putative transcriptional regulator (CPS4)				-9.5 (3.20E-03)		
BT1871	Glycoside Hydrolase Family 97				-78.1 (1.50E-06)		
BT1872	Glycoside Hydrolase Family 3				-133.3 (5.50E-05)	-2.9 (7.60E-06)	
BT1970	glutamate dehydrogenase					-190.8 (2.90E-06)	-2.7 (1.00E-05)
BT2032	susC-like					-2.5 (4.70E-03)	-2.7 (3.80E-06)
BT2033	susD-like					-2.9 (8.70E-03)	
BT2163	30S ribosomal protein S6					-2.8 (3.30E-04)	
BT2259	hypothetical protein						-3 (9.00E-03)
BT2268	susC-like					-4.7 (3.10E-03)	
BT2269	susD-like					-3.2 (5.50E-03)	
BT2675	hypothetical protein					-4.9 (7.80E-03)	
BT2676	hypothetical protein					-3.2 (5.50E-03)	
BT2737	50S ribosomal protein L1					-4.1 (1.20E-04)	
BT2740	elongation factor Tu						-2.5 (1.20E-03)
BT2790							-2.6 (2.60E-05)
	phosphoenolpyruvate carboxykinase [ATP]						-2.7 (6.80E-06)
BT2989	hypothetical protein	-3.8 (1.80E-03)	-3.3 (4.60E-03)				
BT3240	susC-like					-3 (3.70E-03)	
BT3243	hypothetical protein					-8.3 (6.00E-03)	
BT3244	hypothetical protein					-13.9 (8.90E-03)	
BT3603	susD-like					-8.6 (4.00E-03)	
BT3875	50S ribosomal protein L13						
BT3991	Glycoside Hydrolase Family 92					-2.5 (4.80E-03)	
BT4037	hypothetical protein					-2.5 (2.50E-04)	
BT4058	NADH dehydrogenase I, chain N					-5.8 (3.90E-03)	
BT4059	NADH dehydrogenase I, chain M					-6.5 (2.40E-03)	
BT4060	NADH dehydrogenase I, chain L						-2.6 (3.80E-05)
BT4062	NADH dehydrogenase I, chain J						-3.5 (1.40E-05)
BT4063	NADH dehydrogenase I, chain I					-2.8 (6.40E-03)	
BT4065	NADH dehydrogenase I, chain D					-2.6 (5.30E-03)	
BT4066	NADH dehydrogenase I, chain B					-2.8 (8.60E-03)	
p5482_21	VPI-5482 plasmid ORF_21					-2.6 (4.40E-04)	-2.7 (4.40E-05)
							-2.7 (5.70E-03)
						-2.9 (6.00E-03)	
						-3.1 (3.60E-03)	
						-4.8 (7.00E-04)	-2.8 (9.00E-04)

Table S5. Neutral O-glycan-responsive genes in wild-type, $\Delta BT1053$ and $\Omega BT1042$ mutants

Up-regulated genes:

Gene	Description	wild-type fold-change	$\Delta BT1053$ fold-change	$\Omega BT1042$ fold-change
Group 1				
BT1035	hypothetical protein	+8.9		
BT1036	hypothetical protein	+37.7		
BT1037	hypothetical protein	+54.4		
BT1038	hypothetical protein	+62.0		
BT1039	susD-like	+37.2		
BT1040	susC-like	+48.0		
BT1042	susC-like	+20.4		
BT1043	susD-like	+17.8		
BT1044	Glycoside Hydrolase Family 18	+20.7		
BT1045	hypothetical protein	+13.1		
BT1046	susC-like	+78.3		
BT1048	Glycoside Hydrolase Family 18	+11.5		
BT1049	putative patatin-like protein	+20.5		
BT3221	hypothetical protein	+27.0		+5.1
BT3222	hypothetical protein	+15.9		
BT3223	hypothetical protein	+10.4		
Group2				
p5482_18	VPI-5482 plasmid ORF_18		+5.0	
Group 3				
BT0037	putative transcriptional regulatory protein (CPS8)		+8.3	
BT0038	hypothetical protein (CPS8)		+7.1	
BT0040	hypothetical protein (CPS8)		+5.8	
BT0041	F420H2:quinone oxidoreductase (CPS8)		+6.3	
BT0044	putative glycosyltransferase (CPS8)		+6.3	
BT0048	hypothetical protein (CPS8)		+6.1	

BT0049	putative glycosyltransferase (CPS8)		+5.4	
BT0050	putative glycosyltransferase (CPS8)		+6.7	
BT0052	hypothetical protein (CPS8)		+5.3	
BT0054	putative glycosyltransferase (CPS8)		+6.4	
BT0056	putative glycosyltransferase (CPS8)		+5.1	
BT0057	hypothetical protein (CPS8)		+5.8	
BT0059	hypothetical protein (CPS8)		+5.7	
BT0060	putative polysaccharide export protein (CPS8)		+5.3	
BT0061	putative tyrosine-protein kinase ptk (CPS8)		+6.4	
BT0062	hypothetical protein (CPS8)		+8.1	
BT0063	hypothetical protein (CPS8)		+7.6	
BT0064	hypothetical protein (CPS8)		+5.7	
BT0065	Glycoside Hydrolase Family 27 (CPS8)		+6.3	
BT0066	major outer membrane protein OmpA (CPS8)		+7.0	
BT0067	hypothetical protein (CPS8)		+5.4	
BT0068	hypothetical protein (CPS8)		+9.6	
BT3171	sialic acid-specific 9-O-acetylerase		+5.0	
BT4357	susC-like	+36.4	+58.7	+38.0
Group 4				
BT1209	cytochrome D ubiquinol oxidase subunit II			+5.1
BT1285	Glycoside Hydrolase Family 18	+8.2		+11.4
BT1532	ABC transporter permease	+14.2	+6.9	+12.8
BT2131	hypothetical protein			+7.2
BT2451	putative pyrogenic exotoxin B	+12.2	+7.0	+15.8
BT3059	hypothetical protein			+5.4
BT3958	susC-like	+11.6		+16.4
BT3960	hypothetical protein			+5.6
BT3961	hypothetical protein	+5.3		+8.7
BT4690	Glycoside Hydrolase Family 13			+5.1
Group 5				
BT0124	NADH:ubiquinone oxidoreductase subunit			+5.7
BT0125	NADH:ubiquinone oxidoreductase subunit	+5.6	+6.6	+6.8
BT0284	putative peptidoglycan binding protein (LPXTG motif)	+5.2	+5.9	+7.5
BT0317	susC-like	+5.1		+6.7

BT0318	susD-like	+5.7	+5.4	+8.0
BT0319	hypothetical protein	+7.5	+5.2	+9.9
BT0455	Glycoside Hydrolase Family 33		+5.3	
BT0456	Glycoside Hydrolase Family 20		+5.5	
BT0459	Glycoside Hydrolase Family 20	+11.2	+13.0	+10.6
BT0460	Glycoside Hydrolase Family 20	+8.7	+7.3	+8.2
BT0461	Glycoside Hydrolase Family 2	+9.8	+11.8	+10.2
BT0483	susC-like			+5.4
BT0484	susD-like	+5.2	+5.4	+7.3
BT0506	Glycoside Hydrolase Family 20	+11.2	+5.4	+7.8
BT0787	succinyl-CoA synthetase alpha chain	+5.3		+8.7
BT0788	succinyl-CoA synthetase beta chain	+5.4		+7.7
BT0902	hypothetical protein			+5.4
BT1272	FucR	+8.4	+6.0	+8.1
BT1273	L-fucose isomerase	+21.6	+30.3	+21.3
BT1274	L-fuculose-1-phosphate aldolase	+15.6	+28.0	+18.0
BT1275	L-fuculose kinase	+20.3	+31.6	+22.2
BT1276	hypothetical protein	+25.4	+21.7	+26.5
BT1277	L-fucose permease	+33.2	+27.4	+35.2
BT1448	biotin carboxyl carrier protein	+6.0	+5.1	+10.0
BT1449	biotin carboxylase	+7.7		+13.1
BT1450	propionyl-CoA carboxylase beta chain	+8.4		+15.7
BT1533	hypothetical protein	+7.5		+7.6
BT1534	hypothetical protein	+22.6	+13.1	+18.7
BT1535	ABC transporter ATP-binding protein	+9.4	+5.5	+9.6
BT1536	ABC transporter permease	+9.7	+7.4	+8.8
BT1624	putative secreted sulfatase	+6.9	+6.9	+5.5
BT1625	Glycoside Hydrolase Family 29	+8.2	+10.9	+7.3
BT1626	Glycoside Hydrolase Family 2	+12.1	+18.0	+8.7
BT1627	Glycoside Hydrolase Family 20	+20.0	+18.6	+14.0
BT1628	putative sulfatase yidJ	+17.2	+22.3	+12.9
BT1630	susD-like	+6.6	+6.7	+6.8
BT1631	susC-like			+5.1
BT1632	Glycoside Hydrolase Family 18	+5.5	+6.7	+5.8
BT1636	arylsulfatase precursor	+5.6	+5.4	+5.7
BT1918	choline-sulfatase	+5.1		+5.6

BT2038	cation efflux system protein	+5.2	+6.8	
BT2039	cation efflux system protein, AcrB/AcrD/AcrF family protein	+9.4	+9.8	+9.2
BT2040	hypothetical protein		+5.6	+5.0
BT2167	elongation factor G	+31.6	+17.8	+42.4
BT2450	hypothetical protein	+5.9	+6.7	+6.6
BT2452	hypothetical protein	+10.0	+10.8	+12.8
BT2559	susD-like	+6.8	+5.9	+9.1
BT2560	susC-like	+5.6		+6.6
BT2624	hypothetical protein			+7.2
BT2625	susD-like		+5.1	+8.7
BT2627	putative cell surface protein, have conserved domain	+5.3	+5.3	+8.6
BT2690	histidine ammonia-lyase		+5.5	+5.7
BT2692	imidazolonepropionase	+5.6	+9.6	+7.1
BT2810	hypothetical protein	+5.2		+5.6
BT2818	susC-like	+368.2	+355.0	+281.7
BT2819	susD-like	+416.8	+584.4	+321.0
BT2820	susC-like	+4216.0	+4319.0	+3163.0
BT2821	susD-like	+433.0	+536.3	+363.0
BT2822	hypothetical protein	+139.5	+224.2	+105.6
BT2823	hypothetical protein	+3671.0	+5053.0	+2919.0
BT2824	Glycoside Hydrolase Family 16	+1264.0	+2106.0	+993.3
BT2825	Glycoside Hydrolase Family 18	+77.7	+89.2	+54.8
BT3015	hypothetical protein		+5.5	
BT3057	N-acetylgalactosamine-6-sulfatase precursor	+6.9	+5.4	+8.3
BT3169	Glycoside Hydrolase Family 31	+5.4		+5.3
BT3173	Glycoside Hydrolase Family 95	+6.7	+10.0	+7.7
BT3322	putative thioredoxin family protein		+6.8	+6.5
BT3411	pyrophosphate-energized vacuolar membrane proton pump			+5.3
BT3418	putative thiol:disulfide interchange protein			+5.3
BT3571	hypothetical protein	+203.9	+130.0	+212.0
BT3572	hypothetical protein	+182.1	+145.3	+186.0
BT3573	hypothetical protein	+297.4	+139.9	+281.5
BT3574	hypothetical protein	+75.6	+106.3	+65.2
BT3575	hypothetical protein	+54.7	+40.0	+52.4
BT3619	hypothetical protein	+6.8		+6.3
BT3735	hypothetical protein	+5.4		+8.5

BT3736	hypothetical protein	+5.0		+6.7
BT3737	hypothetical protein	+5.4		+7.1
BT3739	Na ⁺ /dicarboxylate or sulfate symporter		+6.0	
BT3749	putative anti-sigma factor		+8.6	+6.2
BT3750	susC-like	+132.0	+302.5	+331.2
BT3751	outer membrane protein	+15.8	+44.6	+41.3
BT3752	susD-like	+19.1	+60.1	+59.1
BT3753	endo-beta-N-acetylglucosaminidase F2 precursor (mannosyl-glyco	+12.7	+60.8	+35.5
BT3754	hypothetical protein	+13.1	+68.6	+44.0
BT3787	hypothetical protein	+5.5	+6.3	+8.6
BT3789	susD-like		+5.4	+7.1
BT3791	hypothetical protein			+5.3
BT3792	Glycoside Hydrolase Family 76			+6.1
BT3868	Glycoside Hydrolase Family 20	+7.1	+9.4	+7.6
BT3990	Glycoside Hydrolase Family 92		+5.7	+5.7
BT4038	susD-like	+8.4	+6.5	+6.5
BT4039	susC-like	+9.3	+7.2	+7.6
BT4040	putative galactose oxidase precursor	+8.7	+6.6	+7.0
BT4050	Glycoside Hydrolase Family 2	+9.2	+11.9	+10.4
BT4132	putative chitinase	+100.7	+129.5	+121.5
BT4133	hypothetical protein	+395.8	+518.5	+448.8
BT4134	susD-like	+303.6	+309.3	+364.5
BT4135	susC-like	+723.8	+415.0	+723.4
BT4136	Glycoside Hydrolase Family 29	+1136.0	+1275.0	+1127.0
BT4240	conserved hypothetical protein, with a phosphotransferase enzyme	+8.5	+7.8	+8.1
BT4241	Glycoside Hydrolase Family 2	+7.7	+8.2	+6.7
BT4242	putative transporter	+7.3	+7.9	+6.5
BT4243	putative oxidoreductase (putative secreted protein)	+7.8	+9.2	+7.0
BT4244	hypothetical protein	+49.3	+40.3	+39.2
BT4245	hypothetical protein	+36.0	+24.6	+27.6
BT4246	susD-like	+38.9	+23.0	+29.1
BT4247	susC-like	+36.7	+40.4	+30.5
BT4248	putative anti-sigma factor	+34.6	+24.6	+25.4
BT4249	hypothetical protein	+12.9	+14.3	+8.7
BT4251	hypothetical protein	+6.2	+7.2	+5.8
BT4294	hypothetical protein	+24.3	+37.3	+26.7

BT4295	putative chitinase	+30.8	+37.1	+34.3
BT4296	hypothetical protein	+32.8	+46.4	+38.3
BT4297	susD-like	+37.3	+65.4	+43.5
BT4298	susC-like	+33.5	+51.9	+37.6
BT4299	hypothetical protein	+38.0	+39.3	+43.5
BT4311	glucose/galactose transporter	+6.1	+5.2	+6.4
BT4393	hypothetical protein	+14.9	+18.1	+18.3
BT4394	Glycoside Hydrolase Family 20	+10.7	+11.9	+11.0
BT4395	Glycoside Hydrolase Family 84	+6.7	+6.4	+7.4
BT4404	susC-like	+5.1		+10.1
BT4405	susD-like	+9.3	+6.6	+21.6
BT4406	hypothetical protein	+7.6	+7.5	+14.9
BT4407	hypothetical protein	+12.6	+10.5	+25.3
BT4631	putative arylsulfatase precursor	+12.4	+26.5	+29.2
BT4632	putative galactose oxidase precursor	+13.9	+43.0	+38.7
BT4633	susD-like	+12.4	+36.7	+32.3
BT4634	susC-like	+17.1	+39.9	+43.5
BT4681	Glycoside Hydrolase Family 20	+5.5		+5.4
Group 6				
BT3013	susD-like		+6.9	+5.5
BT3983	susC-like		+5.0	
BT4408	hypothetical protein		+5.6	+5.1
BT4683	arylsulfatase		+6.1	
Group 7				
BT2453	hypothetical protein		+5.0	+7.4
BT2500	hypothetical protein			+5.2
BT2623	Glycoside Hydrolase Family 76	+6.9	+6.2	+12.5
BT2626	susC-like	+5.1		+7.8
BT3784	Glycoside Hydrolase Family 92			+6.2
BT3788	susC-like			+5.4
BT3790	hypothetical protein	+5.9	+6.7	+10.2
BT3793	hypothetical protein	+7.3	+5.6	+13.3
BT3959	susD-like			+6.3
BT4689	Glycoside Hydrolase Family 13			+6.0

Down-regulated genes:

Gene	Description	wild-type fold-change	$\Delta BT1053$ fold-change	$\Omega BT1042$ fold-change
Group 1				
Group 2				
BT1915	pyruvate carboxylase subunit A		-5.1	
Group 3				
BT1053	RNA polymerase ECF-type sigma factor		-21.2	
BT2275	thymidine kinase		-134.2	
Group 4				
BT1886	hypothetical protein	-5.9		-7
Group 5				
BT0490	hypothetical protein	-9.4	-9.7	-6.5
BT0970	haloacid dehalogenase-like hydrolase	-6.6	-7.5	-6.1
BT1419	hypothetical protein	-73.5	-11	-17.3
BT1420	hypothetical protein	-12.5	-20.7	-11.6
BT1563	hypothetical protein	-6.7	-20	-7.3
BT1564	hypothetical protein	-6.6	-12.3	-7.4
BT1566	putative aluminum resistance protein	-5.1	-9.1	-5.6
BT1567	hypothetical protein	-5.6	-11	-6.9
BT1999	anaerobic ribonucleoside-triphosphate reductase activating protein		-5.5	
BT2156	putative sugar phosphate isomerase/epimerase	-5.4	-6.8	-6
BT2158	putative dehydrogenases and related proteins		-5.4	
BT2159	putative oxidoreductase	-5.1	-7.6	-5.2
BT2178	hypothetical protein	-9.7	-11.8	-7.9
BT3113	putative transmembrane efflux protein	-11.9	-14	-14.7
BT4499	conserved hypothetical protein, putative membrane protein	-10.6	-28.7	-7.5

Group 6

BT2675	hypothetical protein	-5.4	-7.5
BT3240	susC-like	-11.2	-10.1
BT3241	susD-like	-12.7	-9.9
BT3242	hypothetical protein	-13.6	-12.6
BT3243	hypothetical protein	-13.1	-11.4
BT3244	hypothetical protein	-10.2	-9.4

Group 7

BT2987	hypothetical protein		-8.8
BT2988	hypothetical protein		-8.5
BT2989	hypothetical protein		-9.6