Supporting Information

Prioritization of a Plant Polysaccharide over a Mucus Carbohydrate is Enforced by a Bacteroides Hybrid Two-Component System

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Fig. S1. Growth curves of *Bt*, *Bt-ΔBT1754*, and *Bt-ΔBT0366* strains in various carbohydrates.
Bt, *Bt-ΔBT1754*, and *Bt-ΔBT0366* strains were grown in MM supplemented with 0.5% final concentration of the noted carbohydrates. Absorbance measurements were taken at 600nm (OD_{600}). Values shown are mean of triplicates of each condition.

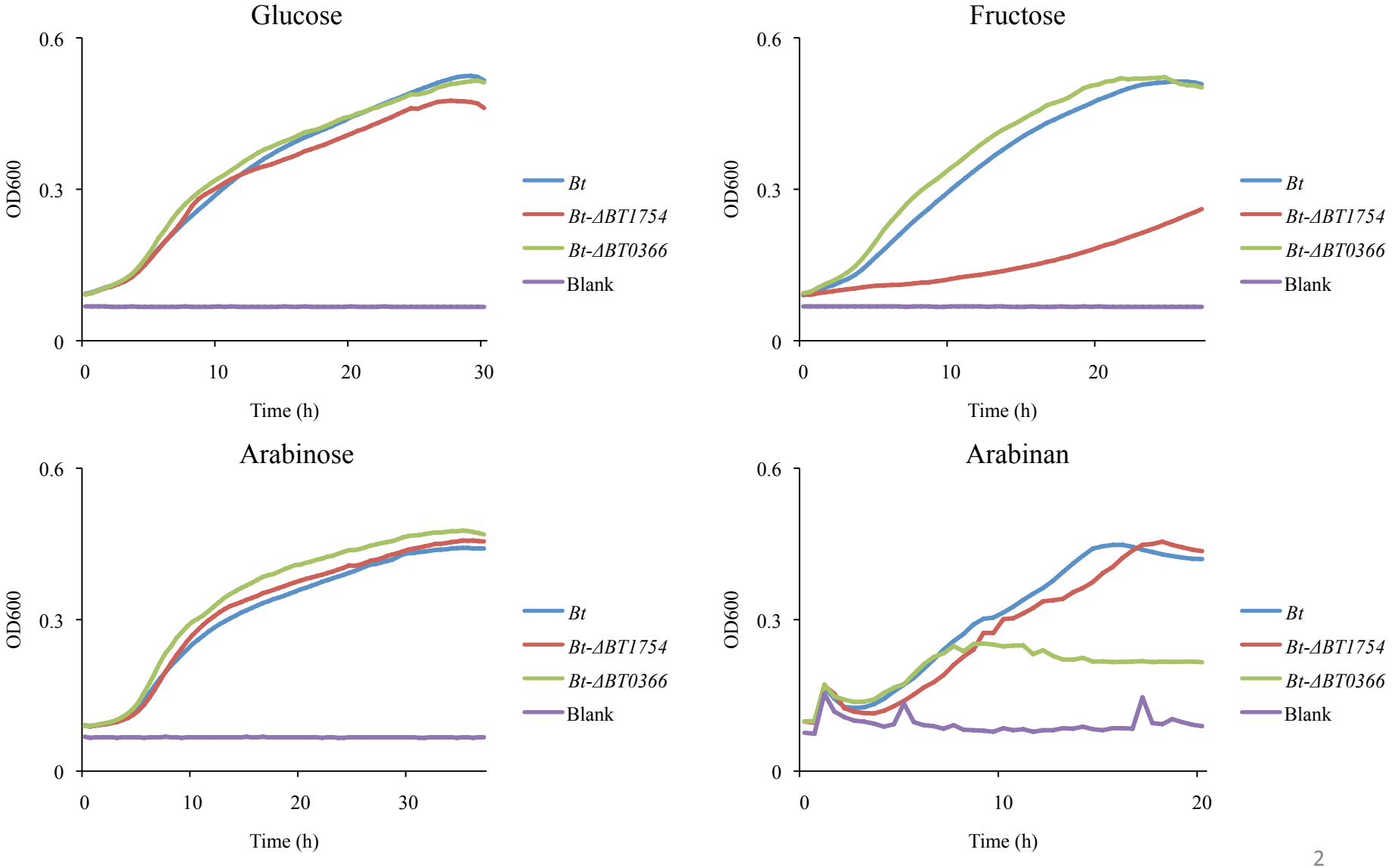

Fig. S2. Deletion of *BT1754* prevents up regulation of the *BT1754*-associated operon during growth in fructose. *Bt* and *Bt-ΔBT1754* were grown in MM supplemented with fructose, arabinan, or both, and expression of the *BT1754*-associated fructokinase *BT1757* was assessed by qRT-PCR. Values shown are mean fold change over *Bt* grown in MM-arabinan. Error bars are +/- SE.

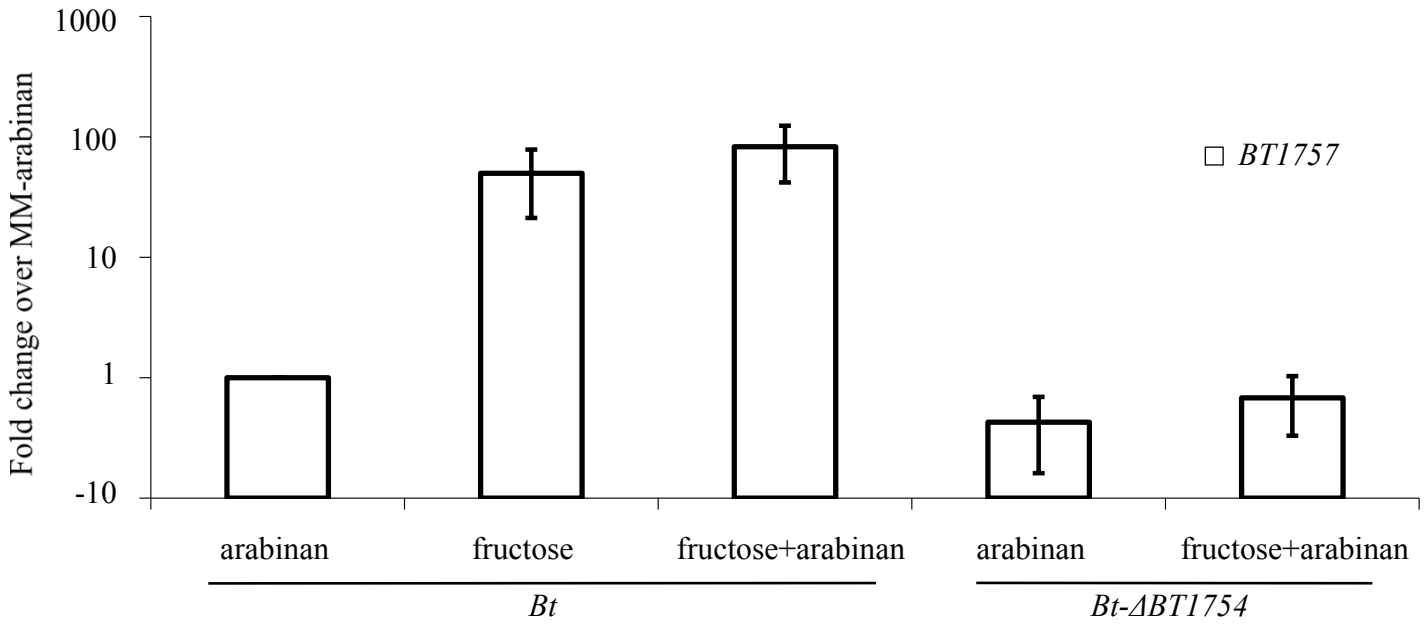

Fig. S3. The *BT1754/BT0366* chimera does not affect *BT1754*-associated genes.
Relative expression of the *BT1754*-associated PUL gene, *BT1757*, in *Bt*, *Bt-ΔBT1754*, and *Bt-ΔBT1754-BT1754/BT0366* grown in MM supplemented with fructose, arabinose, or both; assessed by qRT-PCR. Values represent mean fold change in expression over *Bt* grown in MM-arabinose. Error bars are +/- SE.

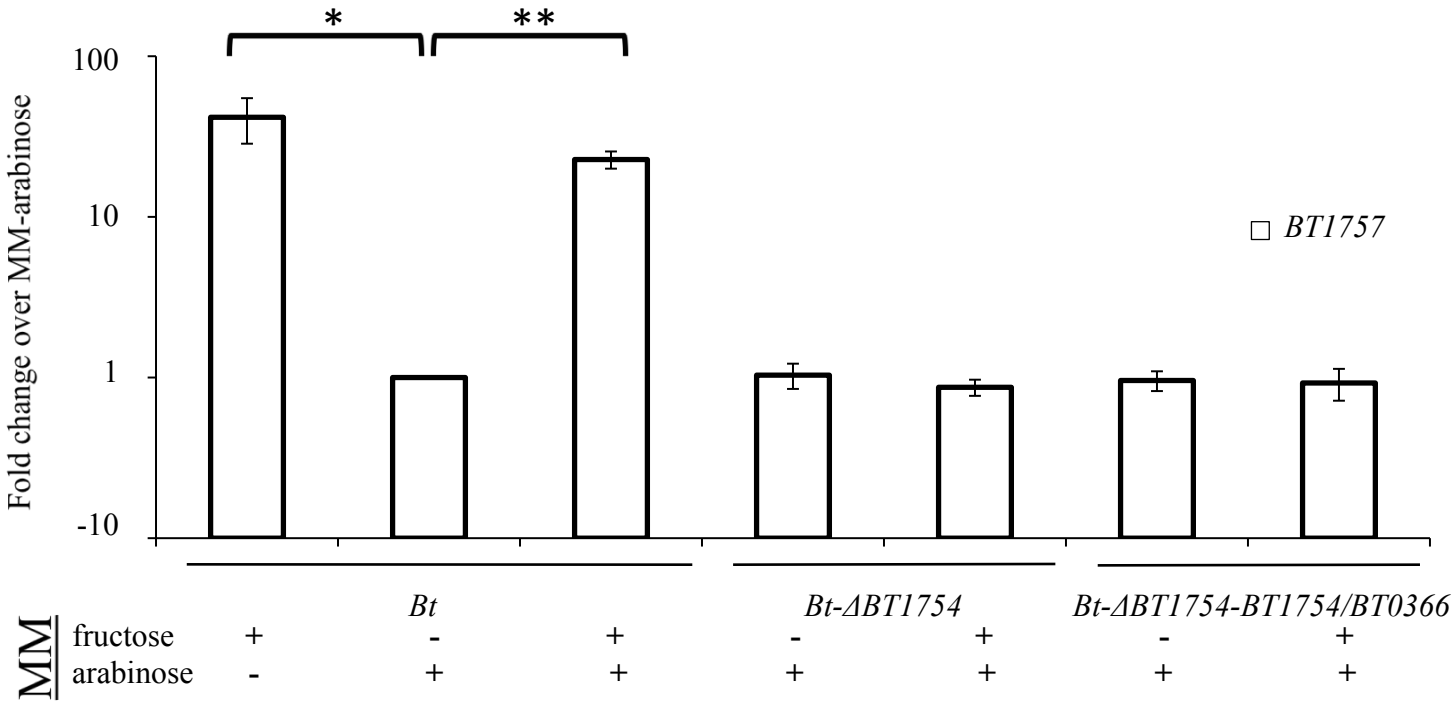

Table S1. List of BT0366 binding loci. Chromatin Immunoprecipitation followed by high throughput sequencing (ChIP-seq) was used to enrich for BT0366 binding loci using an antibody against the periplasmic domain of BT1754 in the *Bt-ΔBT1754-BT1754/BT0366* strain. Enrichment was determined via comparison with sequences derived from the same immunoprecipitation performed in the *Bt* strain. Datasets were analyzed with CLC Genomics Workbench using the ChIP-seq toolkit.

Genomic coordinates	False discovery %	Gene name
431842-431855	1.7e-3	BT0359-BT0360 intergenic region
1973275-1973282	1.35e-13	BT1602-BT1603 intergenic region
2336929-2336949	1.58e-4	BT1862-5S intergenic region
2345070-2345092	4.71e-18	BT1866-BT1867 intergenic region
2993445-2993459	0.03	BT2397-BT2398 intergenic region
3190619-3190676	1.6e-15	BT2557-BT2558 intergenic region
3192445-3192449	2.56e-9	BT2558-BT2559 intergenic region
4399596-4399610	6.37e-4	BT3415
4484457-4484472	1.6e-10	BT3478-BT3479 intergenic region
4709598-4709605	4.01e-10	BT3633-BT3634 intergenic region
4816848-4816869	6.86e-6	SusR-BT3706 intergenic region
4930604-4930612	8.06e-13	BT3794-BT3795 intergenic region
4976427-4976442	3.77e-21	BT3824-BT3825 intergenic region
5439702-5439710	1.89e-8	BT4143-BT4144 intergenic region
5650981-5650988	2.43e-5	BT4289-BT4290 intergenic region
5784589-5784597	4.89e-10	BT4391-BT4392 intergenic region
5999278-5999322	5.73e-6	BT4579-BT4580 intergenic region
6220119-6220127	4.82e-14	BT4740-BT4741 intergenic region

Table S2. List of BT1754 binding loci. Chromatin Immunoprecipitation followed by high throughput sequencing (ChIP-seq) was used to enrich for BT1754 binding loci using an antibody against the periplasmic domain of BT1754 in the *Bt* strain. Enrichment was determined via comparison with sequences derived from the same immunoprecipitation performed in the *Bt-ΔBT1754-BT1754/BT0366* strain. Datasets were analyzed with CLC Genomics Workbench using the ChIP-seq toolkit.

Genomic coordinates	False discovery %	Gene name
2165495-2165595	0.00	BT1754
4399582-4399606	2.68e-24	BT3415
5439720-5439726	4.3e-8	BT4143-BT4144 intergenic region

Table S3. Strains referenced in this paper

Name	Description	Reference
Bt	Parent *Bt* strain VPI-5482 Δ*tdk*	(Koropatkin *et al.*, 2008)
Bt-ΔBT0366	Parent w/ in frame deletion of HTCS *BT0366*	This paper
Bt-ΔBT1754	Parent w/ in-frame deletion of HTCS *BT1754*	(Sonnenburg *et al.*, 2010)
Bt-BT1754/BT0366	Parent containing *BT1754/BT0366* chimera integrated next to genomic Ser-tRNA$_{UGA}$ site	This paper
Bt-ΔBT1754-BT1754/BT0366	*Bt-ΔBT1754* strain with *BT1754/BT0366* chimera integrated at genomic Ser-tRNA$_{UGA}$ site	This paper

Table S4. Cloning primers used in this paper

Primer name	Sequence
BT1754 forward primary	GGAAACGCTACACTATTGATGGTAAA
BT1754/BT0366 sewing reverse	TTCTAACAGATGCTTTTGCTGTTCAAGCTCTTTATTCAAGCGATTCTTAG
BT0366 reverse primary	CCCAATCCTGACAAGAACTCAT
BT1754/BT0366 sewing forward	CTAAGAATCGCTTGAATAAAGAGCTTGAACAGCAAAAGCATCTGTTAGAA
BT1754 forward secondary	GAAAAGGAATGGGATCCAAACTAA
BT0366 reverse secondary	GCTGAGAACGTCTAGAATTGCCAT
0366FragAfwrd	CTGTTTGATCTGTTCCGGAGAC
0366sewR	GCCCTTATTAATACGTACATATATATGTAACTGATATAAGGGTTGCTATTATGAAAC
0366sewF	GTTTCATAATAGCAACCCTTATATCAGTTACATATATGCACGTATTAATAAGGGGC
0366FragBrev	TTATTTGATTCTTTTTCCCCAGAC
0366F. secondary	CCCGGATCGGGATCCCCCCAGTCG
0366R.secondary	GTTTCCTTCACCGTCTAGAAAAGACGGC

Table S5. qRT-PCR primers used in this paper

BT16S-F4	GTGTAGCGGTGAAATGCTTAGATATC
BT16S-R4	CAGTGTCAGTTGCAGTCCAGTGA
BT1757-1F	ATGGGATAACATTCCTTTCACG
BT1757-1R	AGACTCGCGCAATACTTCTTTC
BT1763-1F	AGTAGGCAAACATCGTGGAGAT
BT1763-1R	GAGCGAGTGAATACCCCTCAC
BT0360.1F	GTCAAACGGGGATTCTGCTA
BT0360.1R	GTTGGCAAGGTTCCAGTCAT
BT0365.1F	CCGCACAAAATGAGAAAGGT
BT0365.1R	GCCGATACTGTCCATGAGT
BT4294aF	TAGACTCCACCCGAAAATGC
BT4294aR	TGCATATCTTTGGCAGCTTG
BT4299aF	GGCAAAGCAGGAAGTGACTC
BT4299aR	AGCCCTTCCCGTTCATAACT
BT4404aF	CTATTCTGAGCGGACCTTCG
BT4404aR	AGTTGGTTCCGGTGTTGAAG
BT4406aF	GCGGTAAGATCACGGTTTGT
BT4406aR	CTGCGATATGGTCTTCAGCA