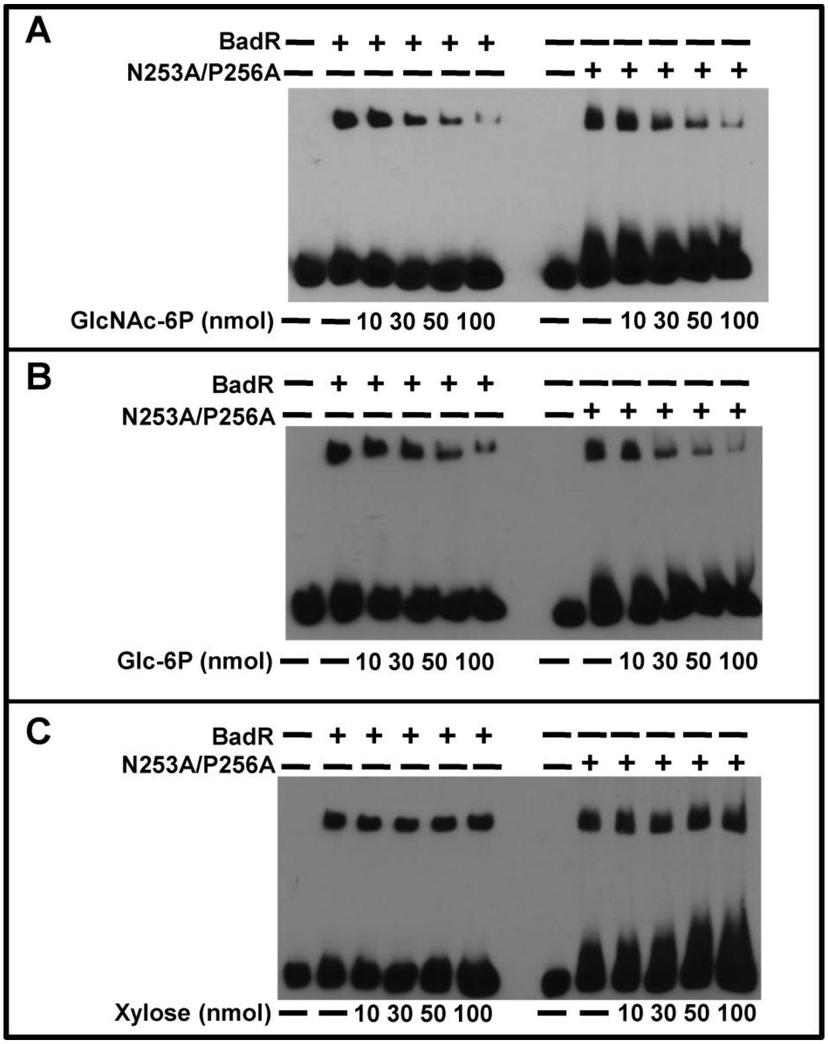

Fig. S1. Effects of site-directed mutations in the BadR putative inducer binding domain on *rpoS* promoter region binding. 5' biotinylated *rpoS* promoter region 1 (20 fmols) was incubated with WT or mutant BadR protein, N253A/P255A (135 pmols), in the absence or presence of various sugars (GlcNAc-6P **(A)**, glucose-6P (Glc-6P) **(B)**, and xylose **(C)**). Binding reactions with various sugar concentrations (10, 30, 50,100mM) determined the influence of each sugar on BadR and N253A/P255A binding to the *rpoS* promoter region.

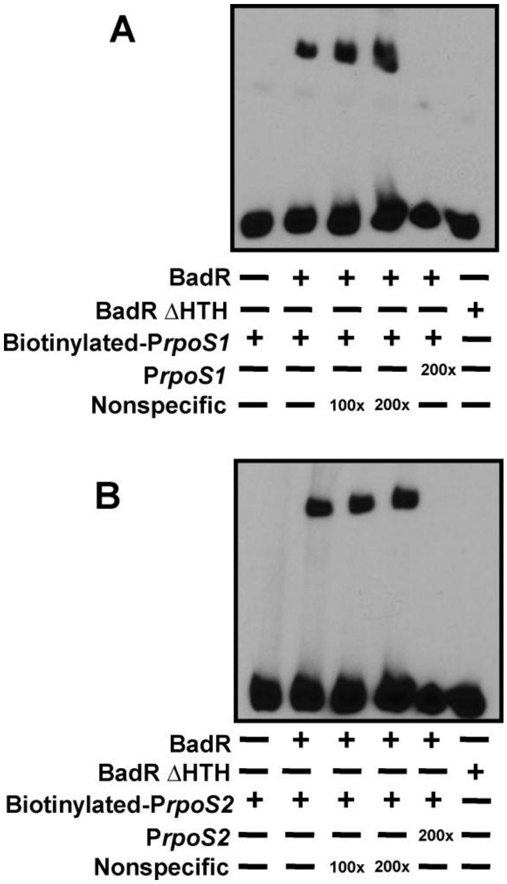

Fig. S2. Non-specific DNA has no effects on the binding of BadR to the *rpoS* promoter regions. 5' biotinylated *rpoS* promoter region 1 or *rpoS* promoter region 2 (20 fmols) and purified WT BadR protein (205 pmols) were incubated in the absence or presence of 100- or 200-fold molar excess of unlabeled nonspecific DNA (corresponding to a DNA region downstream of the *rpoS* gene, coordinates 812305-812517). Additional control reactions were done with specific unlabeled promoter regions (200-fold molar excess) or a N' terminal HTH deficient $\mathrm{BadR}_{(734225\text{-}735289)}$ (BadR Δ HTH).

Supplementary Table 1. Potential of different sugars to inhibit BadR binding to *rpoS* promoter regions.

	% Bound											
	GlcNAc-6P		**Glc-6P**		**Ribose-5P**		**Xylulose5P**		**Xylose**		**Chitobiose**	
Sugar Concentration (nm)	**P*rpoS*1**	**P*rpoS*2**	**P*rpoS*1**	**P*rpoS*2**	**P*rpoS*1**	**P*rpoS*2**	**P*rpoS*1**	**P*rpoS*2**	**P*rpoS*1**	**P*rpoS*2**	**P*rpoS*1**	**P*rpoS*2**
0	100	100	100	100	100	100	100	100	100	100	100	100
10	108	101	128	122	93	93	90	87	90	106	90	108
30	87	75	117	81	52	63	49	50	104	123	115	86
50	56	48	56	72	22	48	41	58	106	112	102	82
100	16	4	30	44	13	18	19	21	102	130	96	99
200	4	1	22	20	0	2	0	0	102	142	100	95

* Densitometry using ImageJ software assessed inhibition of binding by sugars (Schneider, *et al.,* 2012).

† Representative experiment.

‡ The shifted band corresponding to BadR bound to the *rpoS* promoter regions in the absence of sugars was designated as a 100% bound.

Supplementary Table 2. Potential of different sugars to inhibit BadR and BadR mutant (N253A/P255A) binding to *rpoS* promoter region1.

	% Bound					
	GlcNAc-6P		**Glc-6P**		**Xylose**	
Sugar Concentration (nm)	**BadR**	**N253A/P255A**	**BadR**	**N253A/P255A**	**BadR**	**N253A/P255A**
0	100	100	100	100	100	100
10	94	107	85	84	96	98
30	54	73	74	59	87	99
50	35	50	56	31	95	115
100	12	18	27	14	102	116

* Densitometry using ImageJ software assessed inhibition of binding by sugars (Schneider, *et al*., 2012).

† Representative experiment.

‡ The shifted band corresponding to BadR bound to the *rpoS* promoter regions in the absence of sugars was designated as a 100% bound.

Supplementary Table 3. Oligonucleotides used in this study.

Name	**Sequence 5'→ 3'**
BadRExpF_NheI	ACGCGCTAGCATGCAGGGTGAAAATATGG
BadRExpR_XhoI	ACGCCTCGAGATCAATATCTCCTCCTGTCAAAT
BadRExpF_BamHI	ACGCGGATCCATGCAGGGTGAAAATATGG
BadRExpR_SalI	ACGCGTCGACATTATCAATATCTCCTCCTGTCAAAT
BadRExpFNoHTH_BamHI	ACGCGGATCCATGATAAAAGAAAATCTTTTGATTG
BadRExpRNoHTH_SalI	ACGCGTCGACTTAATCAATATCTCCTCCAGTCAAATA
BadRExpFNoIBD_BamHI	ACGCGGATCCATGCAGGGTGAAAATATGG
BadRExpFNoIBD_SalI	ACGCGTCGACTTAACTTTCAAGATTACTGTTAGTG
BadRSDMF_H243A	TAAATCAGGTATGGTTAGTGCCATGATAATTGATTATGA
BadRSDMR_H243A	TCATAATCAATTATCATGGCACTAACCATACCTGATTTA
BadRSDMF_C254A/C257A	TATGAGGGAGAAAAAAATGCTCCAACTGCTGGTAATAAGGGTTGTGTC
BadRSDMR_C254A/C257A	GACACAACCCTTATTACCAGCAGTTGGAGCATTTTTTTCTCCCTCATA
BadRSDMF_N253A/P255A	GATTATGAGGGAGAAAAAGCTTGTGCAACTTGTGGTAATAAGG
BadRSDMR_N253A/P255A	CCTTATTACCACAAGTTGCACAAGCTTTTTCTCCCTCATAATC
BadRDel1F	CCGGTTGTTTTAATGTCTGTTGAG
BadRDel2R_Sal	CAAATAAAATGTCGACTTTTCACCCTGCATAATACACCTC
BadRDel3F_Sal	AGGGTGAAAAGTCGACATTTTATTTGACTGGAGGAGATATTG
BadRDel4R	CTACAAGACTAACAACATCCCCC
BadRInternalF	TCTTTTGATTGAAGTTGGCTCTAGG
BadRInternalR	GAAGCGGGCCCTACAACAGAAAC
NagAExpF_NheI	ACGCGCTAGCATGCCAAATTTTTGCTTATTTAAC
NagAExpF_XhoI	ACGCCTCGAGGAGATTGTTAAAATTTATTTTAGATTC
NagBExpF_NdeI	ACGCCATATGAGATTAATAATCAGACCCACATAC
NagBExpR_XhoI	ACGCCTCGAGTTTTAAGTCATTATTAAAGTTTTTTC
XylR2ExpF_NdeI	ACG CCA TAT GTT GAG GAT AAA TAT GAA AA
XylR2ExpR_XhoI	ACG CCT CGA GAA ATG AGG TAT TAT TTT G
PtsGExpF_NdeI	ACGCCATATGATAAATAAGTTTGATTTTAAAACTCCG
PtsGExpR_XhoI	ACGCCTCGAGAGCCTCTAGCAATTCTCCTATTTCATTC
ChbAExpF_NdeI	ACGCCATATGAATAAAAAAATATATAGCATAG
ChbAExpF_XhoI	ACGCCTCGAGTTTTTTTATTTCTTTTATTATTTTG
XylulokinaseExpF_NdeI	ACGCCATATGAATGCTCTTAGTATTGATATTG
XylulokinaseExpR_XhoI	ACGCCTCGAGCCCGTTAACAAATAGACTATAAT3'
BBI41ExpF_NdeI	ACGCCATATGAATGCTAATAAAGCTTATAAGTGCAG
BBI41ExpR_XhoI	ACGCCTCGAGTTGAATTAAGTTGGAGAATTTTTC
RpoS1F_813088	CGCAAGTTTGCATTTATCATCTTG
RpoS1R_813282	ACTTAATCACAATATTCAAGAAAGGGG
RpoS2F_813258	CCTTTCTTGAATATTGTGATTAAG
RpoS2R_813471	GCGAACAAAGAGCAAAACAAATG
NonspecificF_812305	AAATACAAACATTCATGACCACTGAC
NonspecificR_812517	AGAACTTGGAATATCTATCAGAAACTG
RpoSLFq_813419	AAATACTCCCCCTAAACTCAAAA
RpoSLqR_813290	TTCCATGCAAAAACTGTGC
RpoSqF	AGATATGCGGGTAAAGGGTTAAAA
RpoSqR	CAGCAGCTCTTATTAATCCCAAGTT
BBB05qF	AAGGCCCATGAAGCACACA
BBB05qR	GCGTTTTGACAGAGTTTGGATTAG
BB0240qF	AGAAATGGATCCTGGCTTAGAAAA
BBB0240qR	TCCAGGAACAGCAGGGAAAG
BBI42qF	TTATGCGTATAGTTCGTTGGCTGTA
BBI42qR	CTCCCCTCTTCGCCAGAATACT
BBA07qF	GCAATCCCGACAAGTTTAATCAA
BBA07qR	GCAATCCCGACAAGTTTAATCAA
BBP27qF	CGGCCAAATTAGCAGCGTTA
BBP27qR	TTGAAATATCCTGATCCTTGTCAGTAA
BBP28qF	CAGACCAACAAAAAACCACTTTCA
BBP28qR	AATCCATCTATCCCCCCACTAAG
BBB29qF	GGGAACATTGGAAATAAATAACGAA
BBB29qR	GGGATCTGCAAGTTGTTTGAAAA
BBI16qF	ATGTAAAAAGTATGGAAAAAGAACCTGAAG
BBI16qR	CCCCCAATTCAATCCCCTAA
BB0019qF	GAATAAGGCTTTGAATCTTGAGAATGA
BB0019qR	GATCCAATACTAATAGCTGAAAACCTAAAA
BB0198qF	TGTTTACACCCCAGAAGGAGAAG
BB0198qR	GCATAAAGAGCTTGATCTCCAATATCT

[a]. Restriction sites are underlined.

q. Quantitative RT-PCR primers.