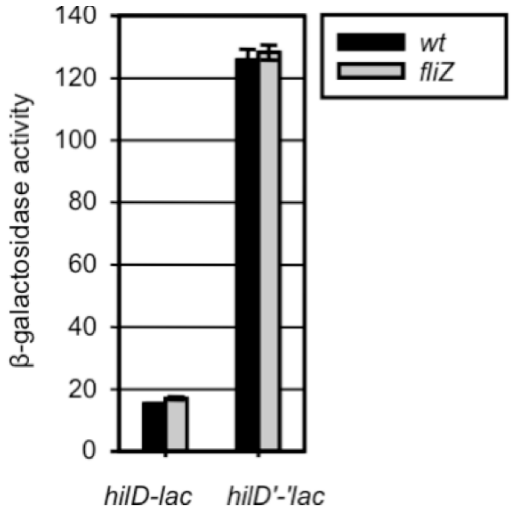

Figure S1 Class I, FliZ has no effect on HilD transcription or translation. For the equivalent of panels A and B (for example in Fig. S2) see FIGURE 3 in our previous publication (Chubiz et al., 2010). The panel above (equivalent to panel C in FIGURE S2) shows the β-galactosidase activity in strains containing a *hilD-lac* transcriptional or a *hilD'-'lac* translational fusion and the indicated mutations after growth under SPI1 inducing conditions. β-galactosidase activity units are defined as (μmol of ONP formed min^{-1}) x 10^3/(OD600 x ml of cell suspension) and are reported as mean ± standard deviation where n=4.

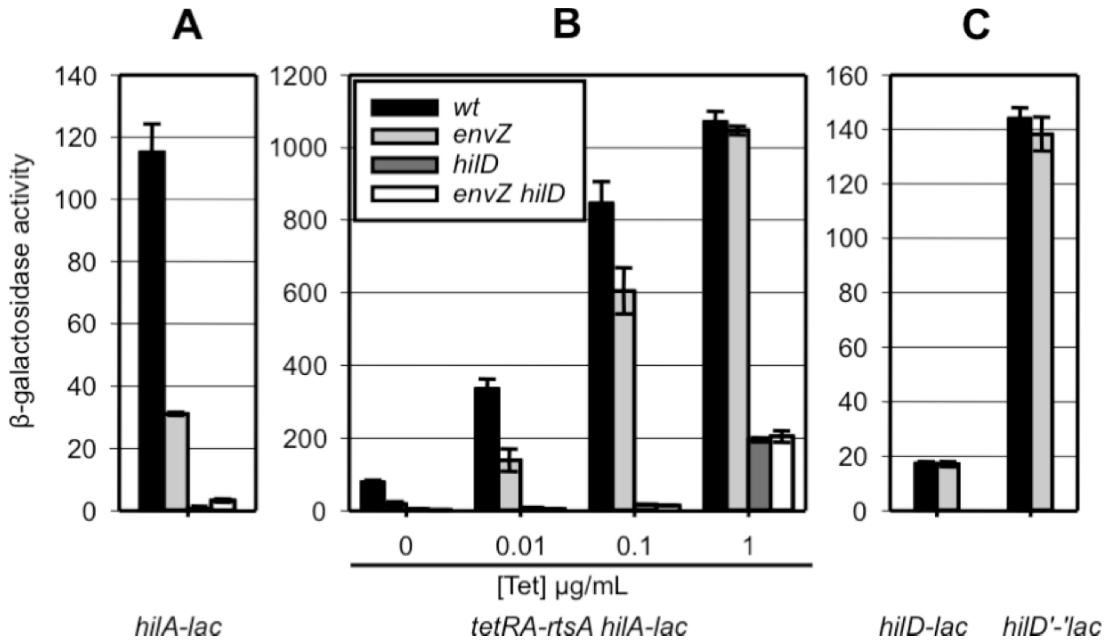

Figure S2 Class I, EnvZ activates *hilA* expression via post-translational control of HilD. (A) β-galactosidase activity in strains containing a *hilA-lac* transcriptional fusion and the indicated mutations after growth under SPI1 inducing conditions. (B) β-galactosidase activity of strains containing a *hilA-lac* transcriptional fusion and indicated mutations with *rtsA* under the control of a tetracycline regulated promoter. Strains were grown under SPI1-inducing conditions with the indicated tetracycline concentrations. (C) β-galactosidase activity in strains containing a *hilD-lac* transcriptional or a *hilD'-'lac* translational fusion and the indicated mutations after growth under SPI1 inducing conditions. β-galactosidase activity units are defined as (µmol of ONP formed min^{-1}) x 10^3/(OD600 x ml of cell suspension) and are reported as mean ± standard deviation where n=4.

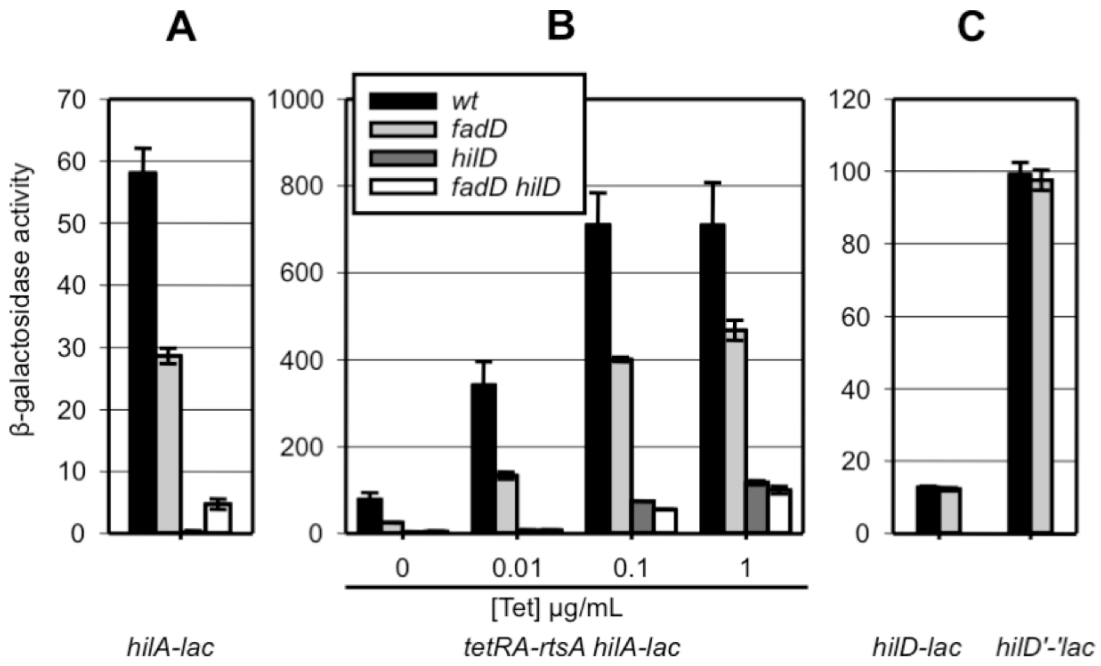

Figure S3 Class I, FadD activates *hilA* expression via the post-translational control of HilD. See FIGURE S2 legend for details.

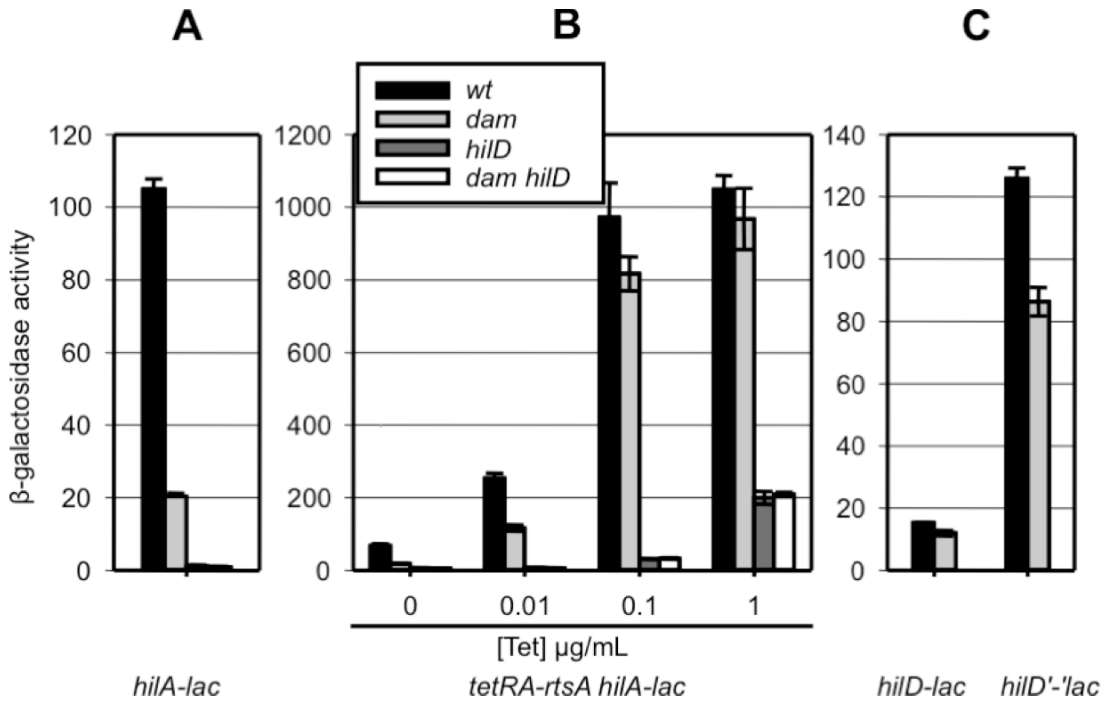

Figure S4 Class II, Dam activates *hilA* expression via the post-transcriptional control of *hilD*. See FIGURE S2 legend for details.

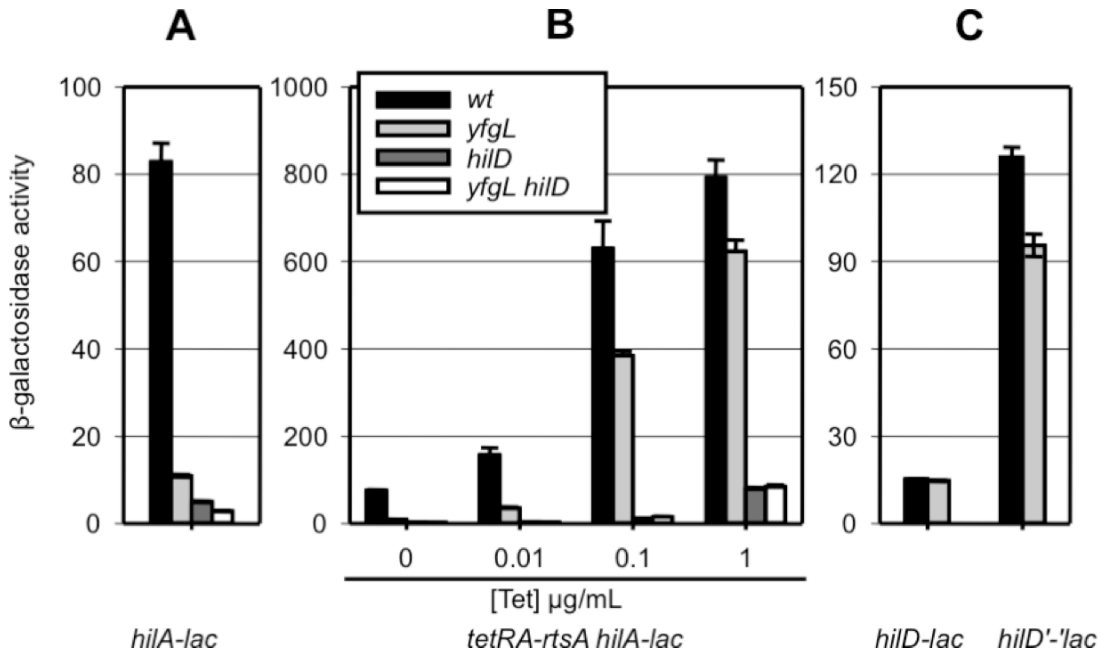

Figure S5 Class II, YfgL activates *hilA* expression via the post-transcriptional control of *hilD*. See FIGURE S2 legend for details.

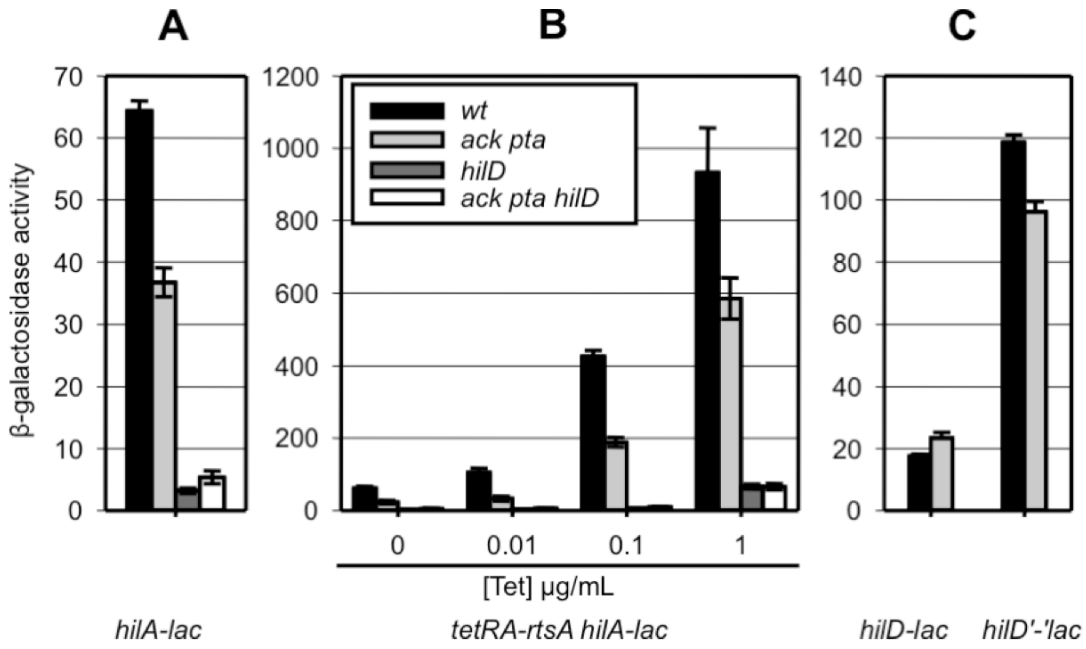

Figure S6 Class II, Ack Pta activates *hilA* expression via the post-transcriptional control of *hilD*. See FIGURE S2 legend for details.

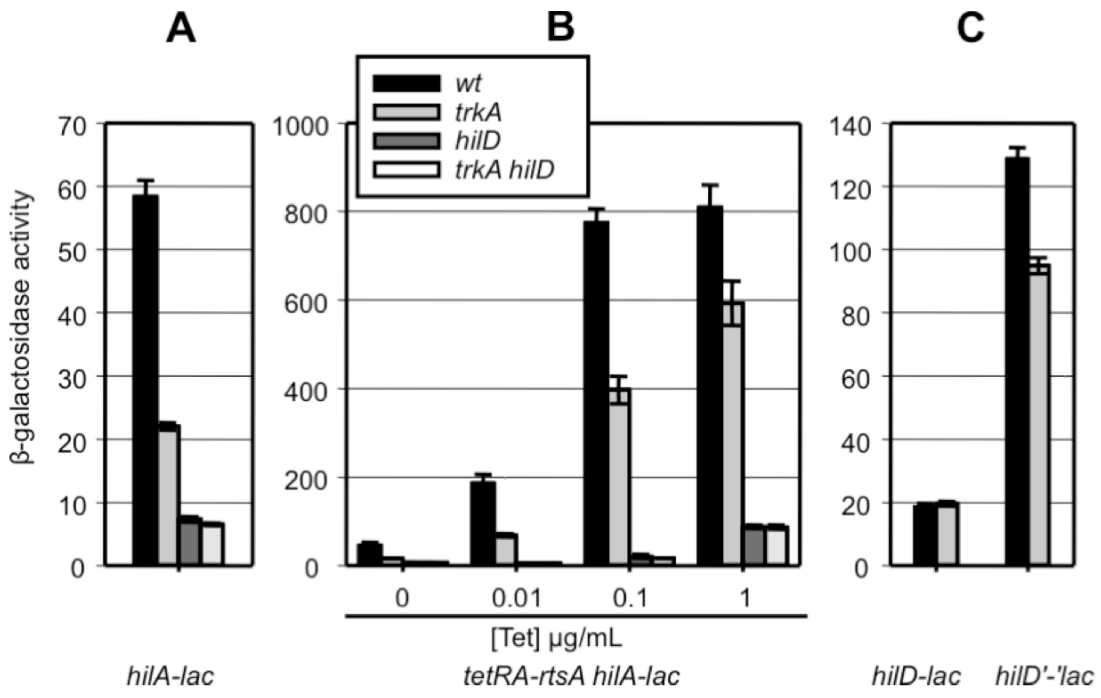

Figure S7 Class II, TrkA activates *hilA* expression via the post-transcriptional control of *hilD*. See FIGURE S2 legend for details.

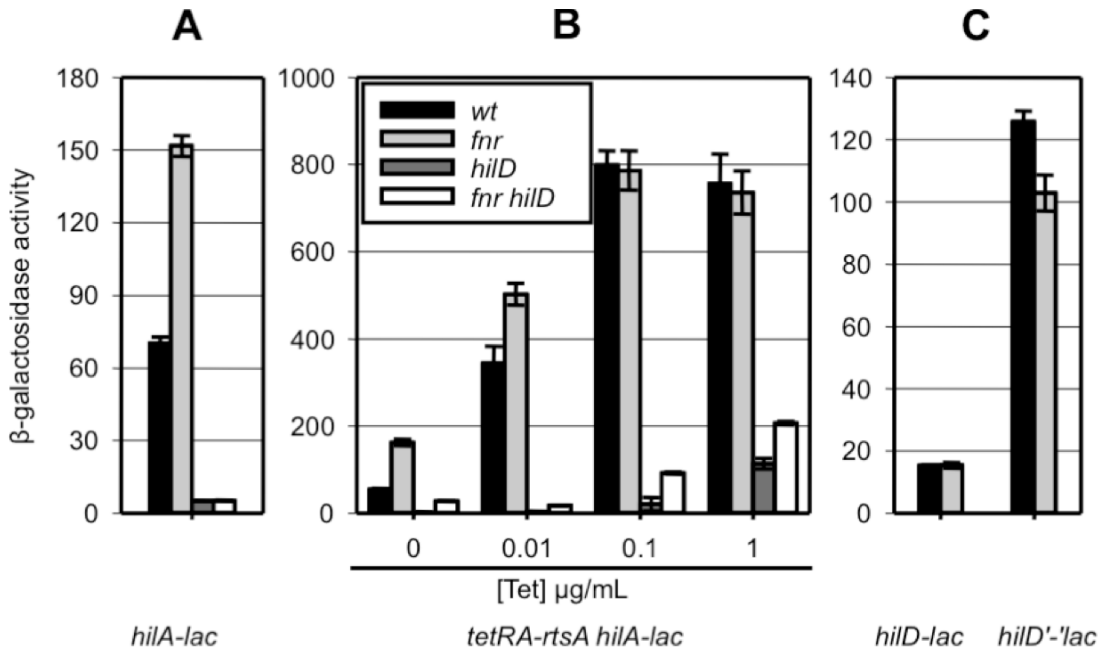

Figure S8 Class III, Fnr represses *hilA* expression independently of HilD. See FIGURE S2 legend for details.

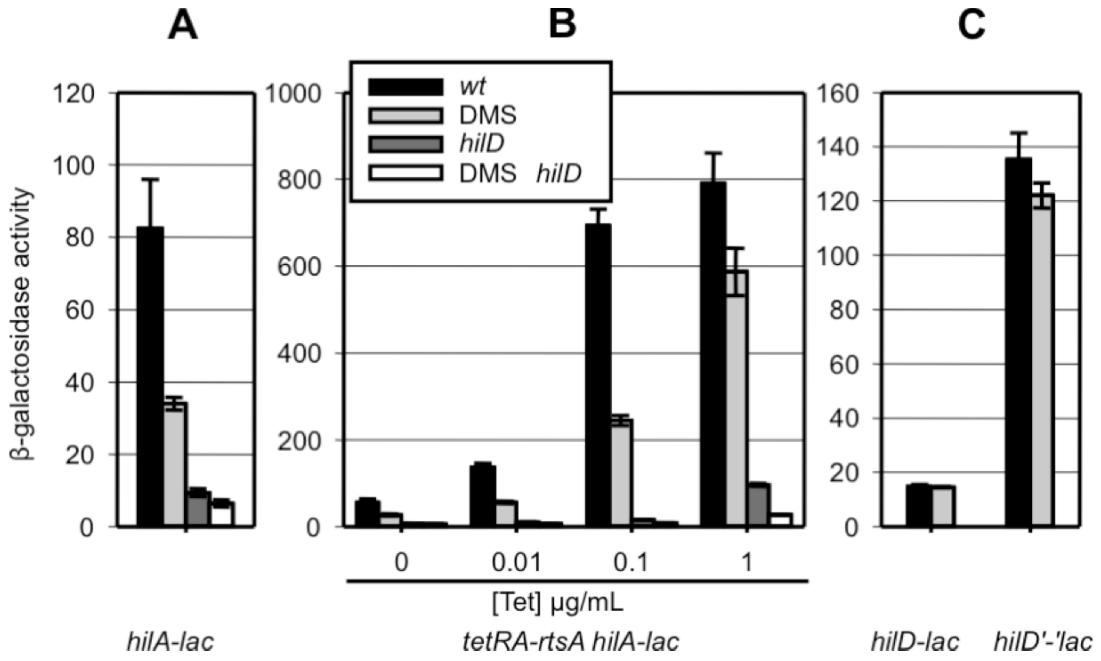

Figure S9 Class III, Dimethyl sulfide (DMS) represses *hilA* expression independently of HilD. See FIGURE S2 legend for details.

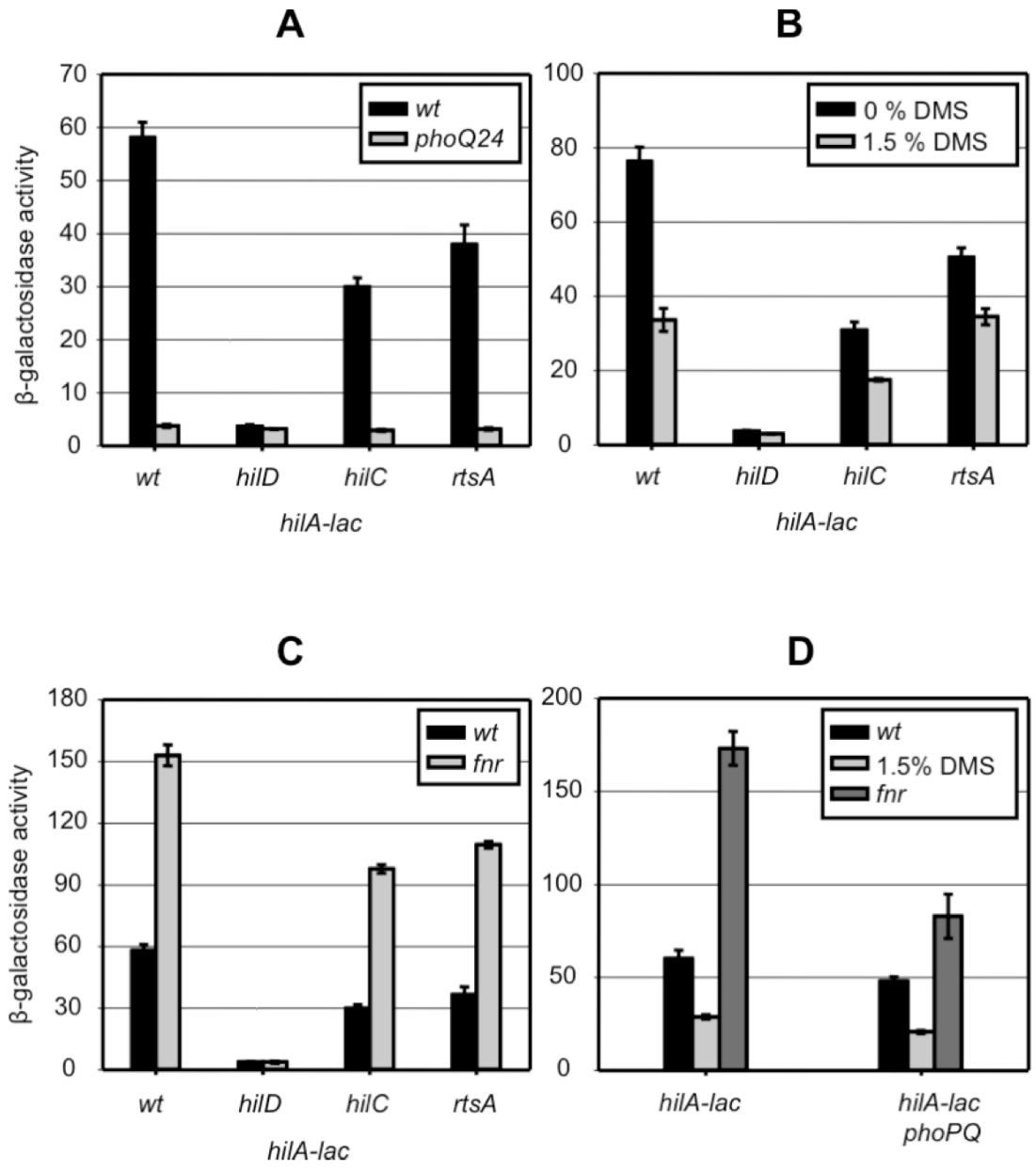

Figure S10 A) PhoPQ , (B) dimethyl sulfide (DMS), and (C) Fnr repress *hilA* expression independently of HilC and RtsA. (D) Dimethyl sulfide (DMS) and Fnr repress *hilA* expression independently of PhoPQ. β-galactosidase activity in strains containing a *hilA-lac* transcriptional fusion and the indicated mutations, or in the presence or absence of the 1.5% dimethyl sulfide, after growth under SPI1 inducing conditions. β-galactosidase activity units are defined as (µmol of ONP formed min^{-1}) x 10^3/(OD600 x ml of cell suspension) and are reported as mean ± standard deviation where n=4.

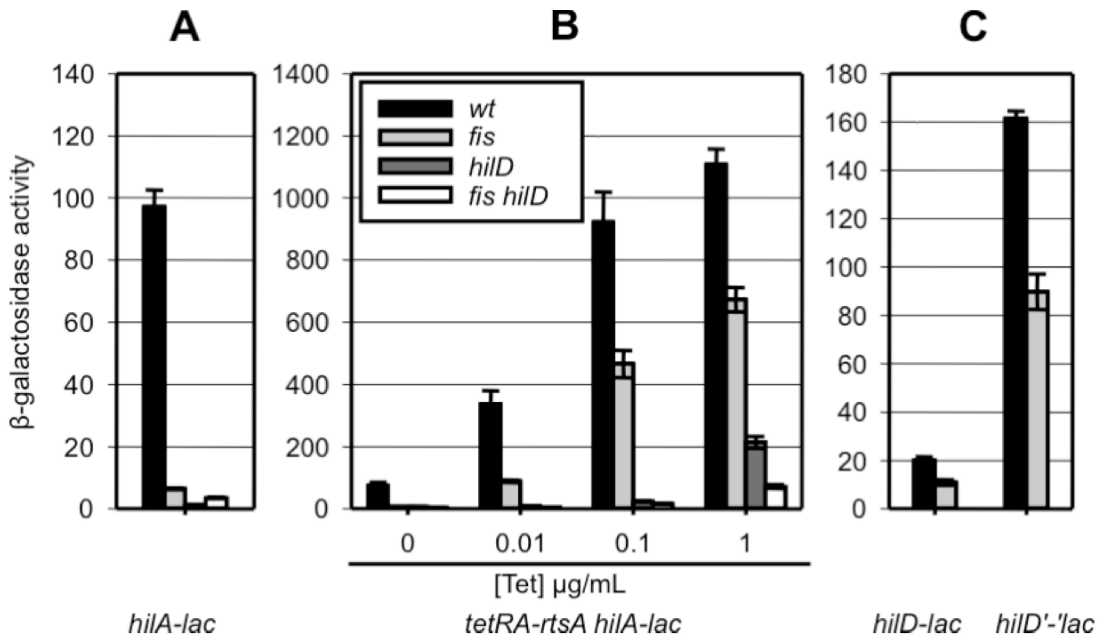

Figure S11 Class IV, Fis activates SPI 1 expression independently of HilD (affect all promoters in the feed-forward loop). See FIGURE S2 legend for details.

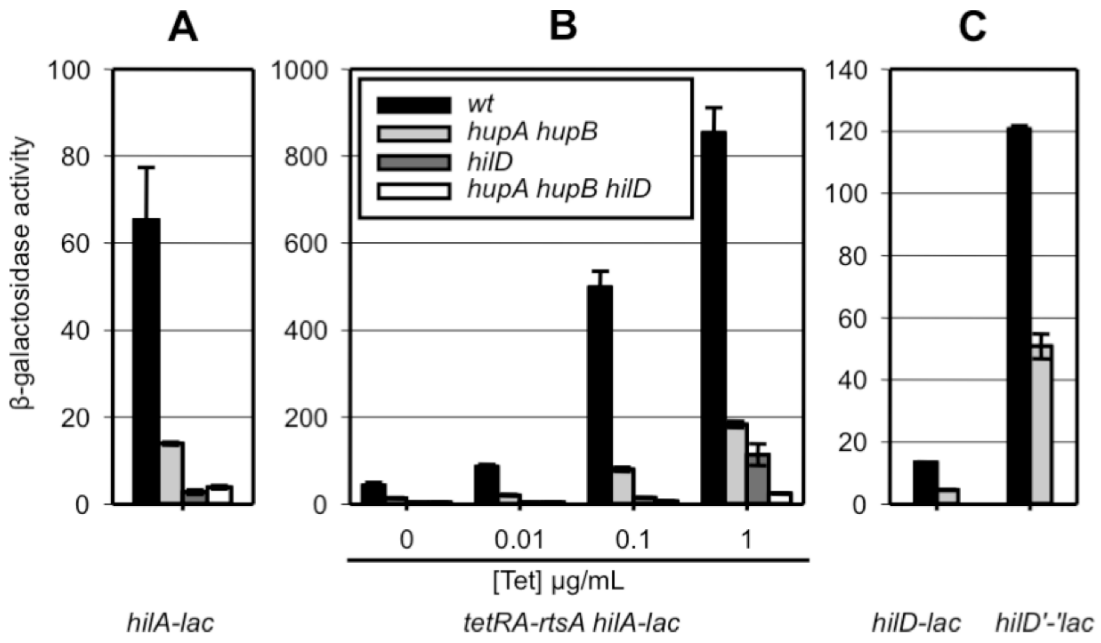

Figure S12 Class IV, HU (encoded by *hupA hupB*) activates SPI 1 expression independently of HilD (affect all promoters in the feed-forward loop). See FIGURE S2 legend for details.

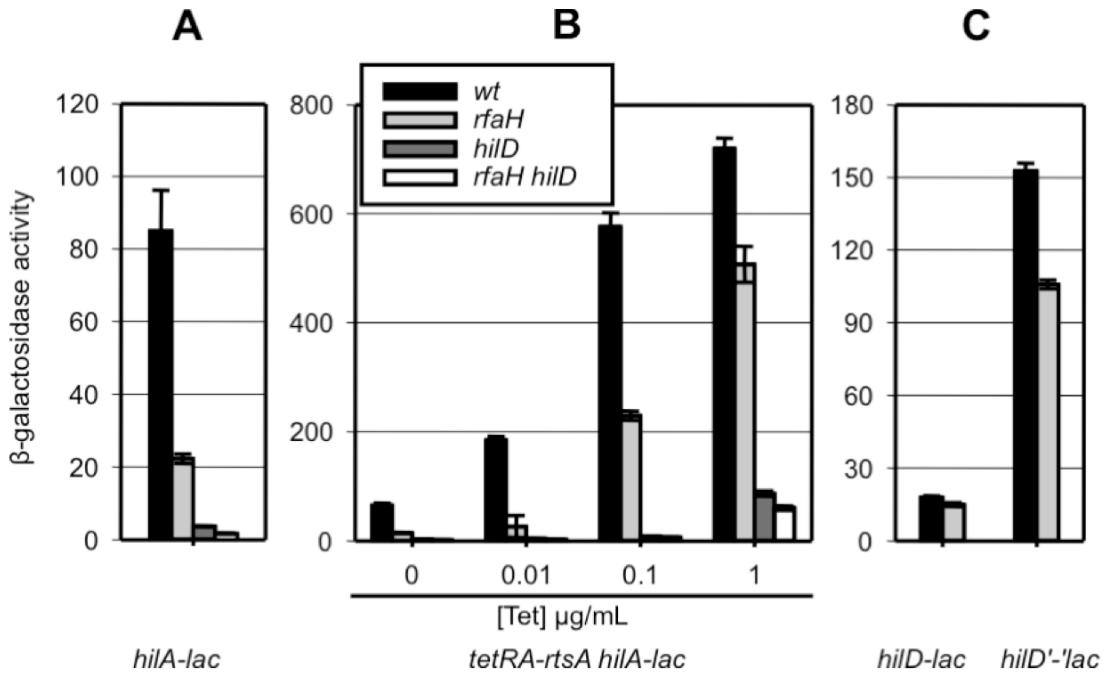

Figure S13 Class IV, RfaH activates SPI 1 expression independently of HilD (affect all promoters in the feed-forward loop). See FIGURE S2 legend for details.

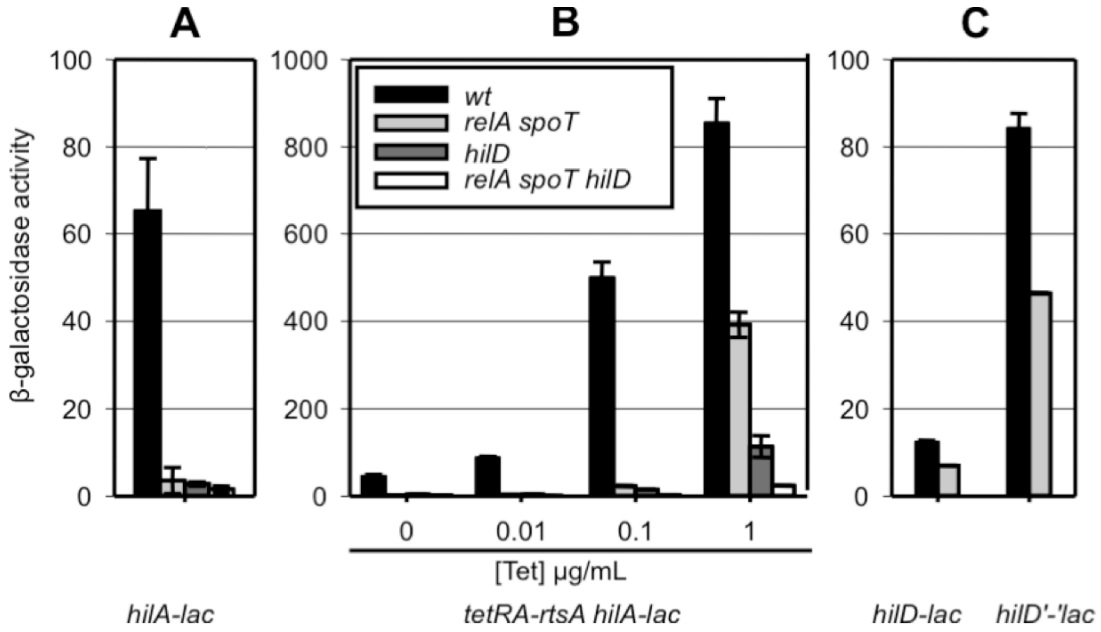

Figure S14 Class IV, ppGpp (produced by RelA and SpoT) activates SPI 1 expression independently of HilD (affect all promoters in the feed-forward loop). See FIGURE S2 legend for details.

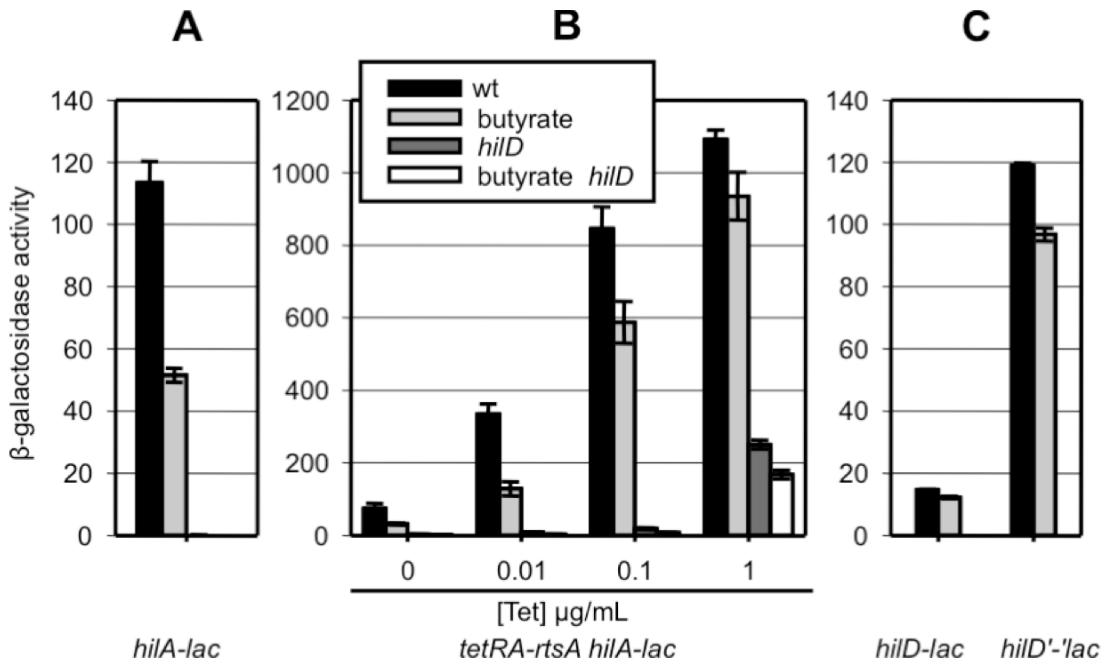

Figure S15 Class IV, Butyrate represses SPI1 expression independently of HilD (affect all promoters in the feed-forward loop). See FIGURE S2 legend for details.

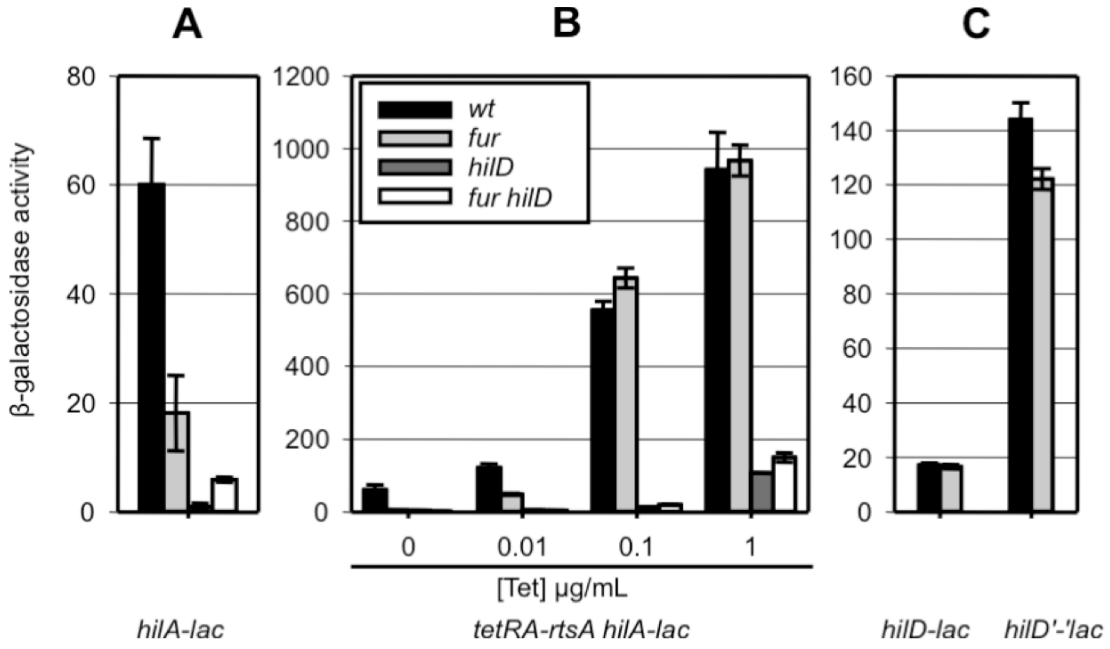

Figure S16 Class V, Fur activates *hilA* expression via HilD. See FIGURE S2 legend for details.

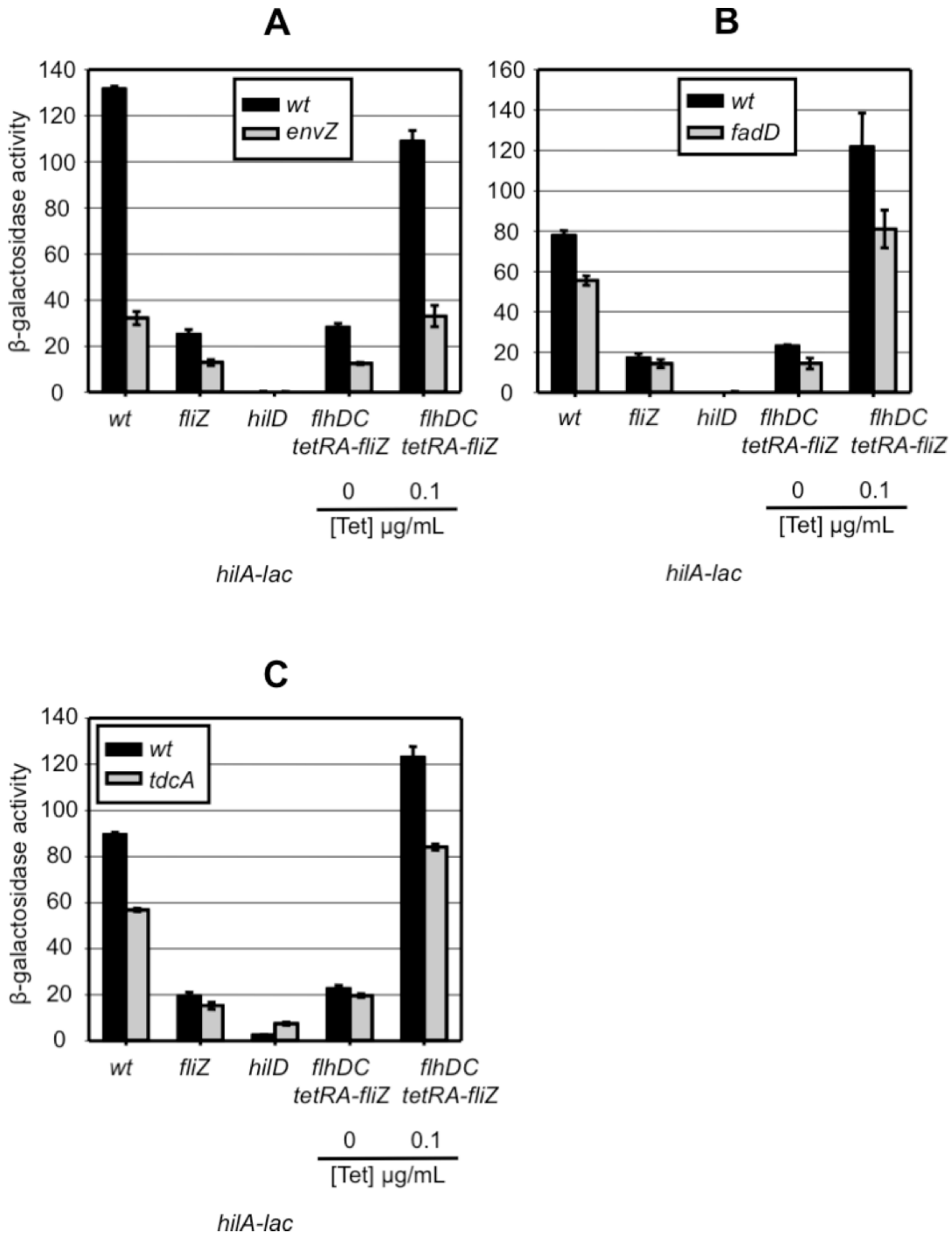

Figure S17 A) EnvZ, (B) FadD, and (C) TdcA affect *hilA* expression independently of FliZ. β-galactosidase activity in strains containing a *hilA-lac* transcriptional fusion and the indicated mutations after growth under SPI1 inducing conditions. β-galactosidase activity units are defined as (µmol of ONP formed min^{-1}) x 10^3/(OD600 x ml of cell suspension) and are reported as mean ± standard deviation where n=4.

TABLE S1 Regulatory factors/conditions affecting expression of SPI1

Regulator	Description	Mechanism of action/comments	References
HilA	Transcriptional activator, OmpR/ToxR family	Direct activation of *prg/org* and *inv/spa* operons	(8; 23; 27; 56; 57)
HilD	AraC-like transcriptional activator	Direct activation of *hilA*, *hilD*, *hilC*, and *rtsA*	(29; 88)
HilC	AraC-like transcriptional activator	Direct activation of *hilA*, *hilD*, *hilC*, and *rtsA*	(28; 29; 46; 88)
RtsA	AraC-like transcriptional activator	Direct activation of *hilA*, *hilD*, *hilC*, and *rtsA*	(29; 30)
HilE		Repression of *hilA* by binding to and preventing HilD function	(11); Chubiz JE (unpublished)
FliZ	Enhancer of class II flagellar genes expression	Activation of *hilA* via post-translational regulation of HilD	(20; 45; 54; 59; 85; 102)
EnvZ/OmpR	Two-component regulatory system; regulation of outer membrane porin genes, and virulence	Activation of *hilA* via HilD	(29; 58)
FadD	Acyl-CoA synthetase; degradation of long-chain fatty acids	Activation of *hilA* via an unknown mechanism	(59);Ellermeier JR (unpublished)
SirA	Transcriptional regulator; two-component regulatory system BarA/SirA; regulation of carbohydrate metabolism, motility, biofilm formation, and invasion	Activation of *hilA* via activation of *csrB/csrC* to block CsrA repression of *hilD*	(1; 29; 46; 52; 62; 99; 102);Ellermeier JR (unpublished)
Dam	DNA methylase	Activation of *hilA* via post-transcriptional regulation of *hilD*	(55)
Ack Pta	acetate kinase and phosphotransacetylase	Activation of *hilA* and *hilD* by formate via an unknown mechanism	(43)

TABLE S1 Regulatory factors/conditions affecting expression of SPI1

Regulator	Description	Mechanism of action/comments	References
YfgL	Outer membrane lipoprotein; assembly of the outer membrane β-barrel proteins in complex with YaeT, YfiO, and NlpB	Activation of SPI1genes via an unknown mechanism	(2; 37)
Trk (potassium)	Potassium transporter	Activation of SPI1 genes via an unknown mechanism	(94)
Fnr	Transcriptional regulator; cytoplasmic oxygen sensor	Repression of *hilA* via an unknown mechanism	(102);Ellermeier JR (unpublished)
PhoPQ (PhoQ24)	Two-component regulatory system; response to divalent cation limitation, pH and antimicrobial peptides	Repression of *hilA*, most likely direct	(9; 10; 14; 78; 111);Ellermeier JR (unpublished)
H-NS	Nucleoid protein	Direct repression of *hilA*, *hilC*, *hilD* and *rtsA*	(73; 74; 89)
Hha	Nucleoid protein	Direct repression of *hilA*, *hilC*, *hilD* and *rtsA*	(36; 73; 74; 102)
Fis	Nucleoid protein	Activation of SPI1 genes	(22; 48; 89; 110)}
HU	Nucleoid protein	Activation of SPI1 genes	(60; 89)
RfaH	Transcriptional anti-terminator; long operons for LPS core and O-antigen biosynthesis	Activation of SPI1genes via an unknown mechanism	(60; 67)
Fur	Transcriptional regulator; response to iron	Activation of *hilA* via an unknown regulation of HilD; repression of H-NS; direct binding of Fur to *hilD* promoter	(32; 98; 101)
TdcA	Transcriptional regulator of *tdc* operon; transport and metabolism of L-	Activation of *fliZ* and SPI1 genes expression	(50)

TABLE S1 Regulatory factors/conditions affecting expression of SPI1

Regulator	Description	Mechanism of action/comments	References
	threonine and L-serine		
FlhDC	Transcriptional regulator; activation of class II flagellar genes	Activation of *hilA* via activation of *fliZ*	(20; 54)
DsbA	Periplasmic disulfide bond oxidase	Activation of *hilA* via activation of FliZ, including repression of RcsCDB	(31; 54)
RcsCDB	phosphorelay system: sensor RcsC, response regulator RcsB, and phosphotransfer protein RcsD; regulation of capsule synthesis and biofilm formation	Repression of *hilA* via repression of FliZ and an independent unknown regulation of HilD	(54)
Lon	ATP-dependent protease	Repression of *hilA* via degradation of HilD, HilC, and FliZ	(16; 20; 95; 97)
ClpXP	ATP-dependent protease	Repression of SPI1 genes via FliZ	(47)
Formate	Short chain fatty acid	Activation of *hilA* and *hilD* (see Ack Pta)	(43)
Dimethyl sulfide/ DMSO		Repression of SPI1 genes via an unknown mechanism	(4)
Temperature		Activation of SPI1 genes when shifted from 25^{o} to 37^{o}C in H-NS-dependent manner	(75)
Butyrate	Short chain fatty acid	Repression of SPI1 genes via an unknown mechanism	(41)
ppGpp	Small signaling molecule; stringent response during starvation	Activation of *hilA* via an unknown mechanism	(79; 92; 93; 100);Ellermeier JR (unpublished)

TABLE S1 Regulatory factors/conditions affecting expression of SPI1

Regulator	Description	Mechanism of action/comments	References
FimZY	Transcriptional regulators; control of type 1 fimbriae gene expression	Repression of *hilA* via activation of *hilE*	(12; 87)
FimW	negative regulator of type 1 fimbriae	Activation of SPI1 genes via an unknown mechanism	(38)
Mlc	Transcriptional regulator; regulation of sugar uptake and metabolism	Repression of *hilA* via activation of *hilE*	(53)
CRP	cAMP-receptor protein	Activation of invasion via an unknown mechanism	(17)
CpxA	Sensor kinase, two-component regulatory system CpxRA; periplasmic stress responce	Activation of *hilA* via an unknown mechanism, apparently independent of CpxR	(68)
Lrp	Transcriptional regulator	Overproduction of Lrp represses SPI1 genes via an unknown mechanism	(6)
PmrM	Part of the *pmrHFIJKLM* operon	Activation of *hilA* via an unknown mechanism	(61; 65; 102)
ApaH/YgdP	Dinucleoside polyphosphate hydrolases	Activation of invasion via an unknown mechanism	(44)
PreAB (QseBC)	Two-component regulatory system; regulation of motility and virulence in response to quorum-sensing and hormonal signals	Activation of SPI1 genes via an unknown mechanism	(64; 66)
LuxS	Autoinducer 2 synthase	Activation of *invF*	(19)
PhoBR	Two-component regulatory system; phosphate limitation	Repression of *hilA* via PhoBR	(59)

TABLE S1 Regulatory factors/conditions affecting expression of SPI1

Regulator	Description	Mechanism of action/comments	References
SprB	Transcriptional regulator	Repression of *hilA* via repression of *hilD* transcription	(86)
RamA	AraC/XylS family transcriptional activator; regulation of multidrug resistance	Repression of SPI1 genes via an unknown mechanism	(7)
PPK	Polyphosphate kinase	Activation of invasion via an unknown mechanism	(49)
PNPase	Polynucleotide phosphorylase	Repression of SPI1 genes via an unknown mechanism	(21)
Hfq	RNA shaperone	Activation of SPI1 genes	(3; 90; 91)
SmpB	RNA-binding protein	Activation of SPI1 genes	(3)
IHF	Nucleoid protein	Activation of *hilA*; counteraction of H-NS mediated silencing	(35; 83)
RNAseE	5 -end-dependent endoribonuclease; part of degradosome complex	Repression of SPI1genes; exact mechanism unclear	(35)
Pag		Repression of SPI1 genes via an unknown mechanism	(35)
SirB		Activation of *hilA*; exact mechanism unclear	(84)
Sig32	Sigma factor; heat shock responce	Repression of *hilA* via degradation of HilD by Lon protease	(63)
TolC/AcrAB	Multidrug efflux pump	Activation of SPI1 genes via an unknown mechanism	(15; 103; 107)
AsmA	Outer membrane protein	Required for invasion; unknown mechanism	(80)
CorA	Mg^{2+} channel	Activation of SPI1 genes via an unknown mechanism	(76; 77)

TABLE S1 Regulatory factors/conditions affecting expression of SPI1

Regulator	Description	Mechanism of action/comments	References
PoxA	paralog of lysyl tRNA-synthetase	Repression of SPI1 genes via an unknown mechanism	(70)
YjeK	putative 2,3-β-lysine aminomutase	Repression of SPI1 genes via an unknown mechanism	(70)
Antimicrobial peptides		Repression of SPI1 genes via PhoPQ	(5)
Macrophages		Repression of SPI1 genes	(33; 96)
Epithelial cells		Activation of SPI1 genes	(42)
Bile	Role in lipid digestion	Repression of *hilA* via SirA	(81; 82)
Propanediol	Product of decomposition of rhamnose and fucose	Repression of *hilA* via an unknown mechanism	(69)
Microgravity	low-shear modeled microgravity	Repression of SPI1 genes	(109)
Lactobacillus supernatant; probiotics		Repression of SPI1 genes via an unknown mechanism	(25); (13)
Tetracycline		Activation of SPI1 genes	(108)
Nalidixic acid		Repression of SPI1 genes	(26)
Salicylidene acylhydrasides		Repression of SPI1 genes	(71)
Fluoroquinolone resistance		Repression of SPI1 genes	(34)

TABLE S2 Strains and plasmids

Name	Genotype [a]	Deletion endpoints [b]	Source or reference [c]
14028	Wild type		ATCC [d]
JS564	Δ*hilD138*::Kn		(32)
JS253	Δ*hilD114*::Cm		(30)
JS749	*attλ*::pDX1::*hilA'-lacZ*		(54)
JS951	Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		(20)
JS576	Δ*hilD114*::Cm *attλ*::pDX1::*hilA'-lacZ*		(32)
JS953	*tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		(20)
JS955	Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		(20)
JS488	Φ(*hilD'*-lac$^+$)*114*		
JS892	Φ(*hilD'-'lacZ*)*hyb139*		(20)
JS996	Δ*hilE115*::Cm	4763527-4764108	
JS997	Δ*hilE115*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS998	Δ*hilE115*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS999	Δ*hilE115*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1000	Δ*hilE115*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1001	Φ(*hilD'*-lac$^+$)*114* Δ*hilE115*::Cm		
JS1002	Φ(*hilD'-'lacZ*)*hyb139* Δ*hilE115*::Cm		
JS950	Δ*fliZ8042*::Cm *attλ*::pDX1::*hilA'-lacZ*		(20)
JS1003	Φ(*hilD'*-lac$^+$)*114* Δ*fliZ8042*::Cm		
JS1004	Φ(*hilD'-'lacZ*)*hyb139* Δ*fliZ8042*::Cm		
JS1006	Δ*envZ182*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1007	Δ*envZ182*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1008	Δ*envZ182*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1009	Δ*envZ182*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1010	Φ(*hilD'*-lac$^+$)*114*Δ*envZ182*::Cm		
JS1011	Φ(*hilD'-'lacZ*)*hyb139* Δ*envZ182*::Cm		
JS1012	Δ*fadD21*::Kn	1915235-1916908	
JS1013	Δ*fadD21*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1014	Δ*fadD21*::Kn Δ*hilD114*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1015	Δ*fadD21*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1016	Δ*fadD21*::Kn Δ*hilD114*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1017	Φ(*hilD'*-lac$^+$)*114* Δ*fadD21*		
JS1018	Φ(*hilD'-'lacZ*)*hyb139* Δ*fadD21*		
JS1019	*sirA3*::Cm *attλ*::pDX1::*hilA'-lacZ*		

Name	Genotype [a]	Deletion endpoints [b]	Source or reference [c]
JS1020	*sirA3*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1021	*sirA3*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1022	*sirA3*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1023	Φ(*hilD'*-lac$^+$)*114 sirA3*::Cm		
JS1024	Φ(*hilD'-'lacZ*)*hybb139 sirA3*::Cm		
JS1025	Δ*dam241*::Cm	3638689-3639527	
JS1026	Δ*dam241*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1027	Δ*dam241*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1028	Δ*dam241*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1029	Δ*dam241*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1030	Φ(*hilD'*-lac$^+$)*114* Δ*dam241*::Cm		
JS1031	Φ(*hilD'-'lacZ*)*hyb139* Δ*dam241*::Cm		
JS1032	Δ(*ack-pta)4202*::Cm	2447938-2451363	
JS1033	Δ(*ack-pta)4202*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1034	Δ(*ack-pta)4202*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1035	Δ(*ack-pta)4202*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1036	Δ(*ack-pta)4202*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1037	Φ(*hilD'*-lac$^+$)*114* Δ(*ack-pta)4202*::Cm		
JS1038	Φ(*hilD'-'lacZ*)*hyb139* Δ(*ack-pta)4202*::Cm		
JS1180	Δ*trkA*::Cm	3579771-3581196	
JS1181	Δ *trkA*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1182	Δ *trkA*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1183	Δ *trkA*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1184	Δ *trkA*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1185	Φ(*hilD'*-lac$^+$)*114* Δ*trkA*::Cm		
JS1186	Φ(*hilD'-'lacZ*)*hyb139* Δ*trkA*::Cm		
JS1039	Δ*yfgL611*::Cm	2653048-2654226	
JS1040	Δ*yfgL611*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1041	Δ*yfgL611*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1042	Δ*yfgL611*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1043	Δ*yfgL611*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1044	Φ(*hilD'*-lac$^+$)*114* Δ*yfgL611*::Cm		
JS1045	Φ(*hilD'-'lacZ*)*hyb139* Δ*yfgL611*::Cm		

Name	Genotype [a]	Deletion endpoints [b]	Source or reference [c]
JS1046	Δ*fnr1*::Cm	1754380-1755116	
JS1047	Δ*fnr1*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1048	Δ*fnr1*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1049	Δ*fnr1*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1050	Δ*fnr1*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1051	Φ(*hilD'*-lac^{+})*114* Δ*fnr1*::Cm		
JS1052	Φ(*hilD'-'lacZ*)*hyb139* Δ*fnr1*::Cm		
JS1053	Δ*ycfD612*::Kn	1316880	
JS1054	*phoQ24 ΔycfD612*::Kn		
JS1055	*phoQ24 ΔycfD612*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1056	*phoQ24 ΔycfD612*::Kn Δ*hilD114*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1057	*phoQ24 ΔycfD612*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1058	*phoQ24 ΔycfD612*::Kn Δ*hilD114*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1059	Φ(*hilD'*-lac^{+})*114 phoQ24 ΔycfD612*		
JS1060	Φ(*hilD'-'lacZ*)*hyb139 phoQ24 ΔycfD612*		
JS577	Δ*hilC113*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS579	Δ*rtsA5 attλ*::pDX1::*hilA'-lacZ*		
JS1061	*phoQ24 ΔycfD612*::Kn Δ*hilC113*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1062	*phoQ24 ΔycfD612*::Kn Δ*rtsA5 attλ*::pDX1::*hilA'-lacZ*		
JS1063	Δ*fnr2*::Tet	1754321-1755129	
JS1064	Δ*fnr2*::Tet *attλ*::pDX1::*hilA'-lacZ*		
JS1065	Δ*fnr2*::Tet Δ*hilD114*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1066	Δ*fnr2*::Tet Δ*hilC113*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1067	Δ*fnr2*::Tet Δ*rtsA5 attλ*::pDX1::*hilA'-lacZ*		
JS1068	Δ*phoPQ*::Cm	1317242-1319310	
JS1069	Δ*phoPQ*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1070	Δ*fnr2*::Tet Δ*phoPQ*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1071	Δ*hha1*::Cm	528131-528349	
JS1072	Δ*hha1*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1073	Δ*hha1*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1074	Δ*hha1*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1075	Δ*hha1*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1076	Φ(*hilD'*-lac^{+})*114* Δ*hha1*::Cm		
JS1077	Φ(*hilD'-'lacZ*)*hyb139* Δ*hha1*::Cm		

Name	Genotype [a]	Deletion endpoints [b]	Source or reference [c]
JS1078	*fis-3*::Cm		(72), listed as JG1160)
JS1079	*fis-3*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1080	*fis-3*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1081	*fis-3*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1082	*fis-3*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1083	Φ(*hilD'*-lac$^+$)*114 fis-3*::Cm		
JS1084	Φ(*hilD'-'lacZ*)*hyb139 fis-3*::Cm		
JS1085	Δ*hupA121*::Cm	4386709-4386981	
JS1086	Δ*hupB122*::Cm	508105-508378	
JS1087	Δ*hupA121*:: Δ*hupB122*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1088	Δ*hupA121*:: Δ*hupB122*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1089	Δ*hupA121*:: Δ*hupB122*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1090	Δ*hupA121*:: Δ*hupB122*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1091	Φ(*hilD'*-lac$^+$)*114* Δ*hupA121*:: Δ*hupB122*::Cm		
JS1092	Φ(*hilD'-'lacZ*)*hyb139* Δ*hupA121*:: Δ*hupB122*::Cm		
JS1093	Δ*rfaH4531*::Cm	4182923-4183411	
JS1094	Δ*rfaH4531*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1095	Δ*rfaH4531*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1096	Δ*rfaH4531*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1097	Δ*rfaH4531*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1098	Φ(*hilD'*-lac$^+$)*114* Δ*rfaH4531*::Cm		
JS1099	Φ(*hilD'-'lacZ*)*hyb139* Δ*rfaH4531*::Cm		
JS1100	Δ*relA81*::Kn	3102853-3105080	
JS1101	Δ*relA81* Δ*spoT292*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1102	Δ*relA81* Δ*spoT292*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1103	Δ*relA81* Δ*spoT292*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1104	Δ*relA81* Δ*spoT292*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1105	Φ(*hilD'*-lac$^+$)*114* Δ*relA81* Δ*spoT292*::Cm		
JS1106	Φ(*hilD'-'lacZ*)*hyb139* Δ*relA81* Δ*spoT292*::Cm		
JS1107	Δ*fur41*::Cm *attλ*::pDX1::*hilA'-lacZ*		
JS1108	Δ*fur41*::Cm Δ*hilD138*::Kn *attλ*::pDX1::*hilA'-lacZ*		
JS1109	Δ*fur41*::Cm *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		

Name	Genotype [a]	Deletion endpoints [b]	Source or reference [c]
JS1110	Δ*fur41*::Cm Δ*hilD138*::Kn *tetRA-rtsA attλ*::pDX1::*hilA'-lacZ*		
JS1111	Φ(*hilD'*-lac^{+})*114* Δ*fur41*::Cm		
JS1112	Φ(*hilD'-'lacZ*)*hyb139* Δ*fur41*::Cm		
JS1113	*attλ*::pDX1::*hilA'-lacZ hilD138*		
JS1114	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042*		
JS1115	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ*		
JS1116	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*hilE115*::Cm		
JS1117	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*hilE115*::Cm		
JS1118	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*hilE115* ::Cm		
JS1119	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*envZ182*::Cm		
JS1120	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*envZ182*::Cm		
JS1121	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*envZ182*::Cm		
JS1122	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*fadD21*::Kn		
JS1123	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*fadD21*::Kn		
JS1124	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*fadD21*::Kn		
JS1125	*attλ*::pDX1::*hilA'-lacZ hilD138 sirA3*::Cm		
JS1126	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042 sirA3*::Cm		
JS1127	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ sirA3*::Cm		
JS1128	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*dam241*::Cm		
JS1129	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*dam241*::Cm		
JS1130	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*dam241*::Cm		
JS1131	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ(*ack-pta)4202*::Cm		
JS1132	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ(*ack-pta)4202*::Cm		
JS1133	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ(*ack-pta)4202*::Cm		
JS1134	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*yfgL611*::Cm		
JS1135	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*yfgL611*::Cm		
JS1136	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*yfgL611*::Cm		
JS1137	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*hha1*::Cm		
JS1138	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*hha1*::Cm		
JS1139	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*hha1*::Cm		
JS1140	*attλ*::pDX1::*hilA'-lacZ hilD138* fis-3::Cm		
JS1141	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*fis*::Cm:		
JS1142	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ fis-3*::Cm		
JS1143	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*hupA121* Δ*hupB122*::Cm		
JS1144	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*hupA121* Δ*hupB122*::Cm		
JS1145	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*hupA121* Δ*hupB122*::Cm		
JS1146	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*rfaH4531*::Cm		

Name	Genotype [a]	Deletion endpoints [b]	Source or reference [c]
JS1147	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*rfaH4531*::Cm		
JS1148	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*rfaH4531*::Cm		
JS1149	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*relA81*::Kn Δ*spoT292*::Cm		
JS1150	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*relA81*::Kn Δ*spoT292*::Cm		
JS1151	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*relA81*::Kn Δ*spoT292*::Cm		
JS1152	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*fur41*::Cm		
JS1153	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*fur41*::Cm		
JS1154	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*fur41*::Cm		
JS1155	Δ*flhDC8045*::Cm	2022064-2021175	
JS1156	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045*::Cm		
JS1157	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*flhDC8045*::Cm		
JS1158	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*flhDC8045*::Cm		
JS1159	Δ*tdcA51*::Cm	3412473-3413411	
JS1160	*attλ*::pDX1::*hilA'-lacZ* Δ*tdcA51*::Cm		
JS1161	*attλ*::pDX1::*hilA'-lacZ hilD138* Δ*tdcA51*::Cm		
JS1162	*attλ*::pDX1::*hilA'-lacZ* Δ*fliZ8042* Δ*tdcA51*::Cm		
JS1163	*attλ*::pDX1::*hilA'-lacZ* Δ*flhDC8045 tetRA-fliZ* Δ*tdcA51*::Cm		

Plasmids	Relevant Characteristics	Cloned End Points	
pKD46	*bla* P_{BAD} *gam bet exo* pSC101 oriTS		(24)
pCP20	*bla cat cI*857 λP_R *flp* pSC101 oriTS		(18)
pKD3	*bla* FRT *cat* FRT PS1 PS2 oriR6K		(24)
pKD4	*bla* FRT *aph* FRT PS1 PS2 oriR6K		(24)
pWKS30	pSC101 ori, Ap^r		(106)
pRfaH (pKG115)	pWKS30::*rfaH*$^+$	4182924-4183440	

[a] All strains are isogenic derivatives of ATCC 14028.
[b] The numbers indicate the base pairs that are deleted (strains) or cloned (plasmids) (inclusive) as defined in the *S. enterica* serovar Typhimurium LT2 genome sequence in the National Center for Biotechnology Information database.
[c] This study unless specified otherwise.
[d] ATCC, American Type Culture Collection.

TABLE S3 Transcriptomic datasets that reveal co-regulation of SPI 1 and flagellar genes in *Salmonella* Typhimurium

Global response to a regulatory system or specific environmental stimuli	Reference	Regulates *hilA* through FliZ?[a]	Class of SPI1 regulator
Macrophage	(33)	ND	
CsrA [b]	(51)	no	II
Antimicrobial peptides	(5)	ND	
Bile	(81)	no	
Swarming	(104; 105)	ND	
Fis	(48)	no	IV
RfaH	(67)	no	IV
YfgL	(37)	no	II
Fnr	(39)	no	III
Hydrogen peroxide	(40)	ND	

[a] No indicates that the factor regulates *hilA* in a *fliZ* null background and when FliZ is ectopically expressed. ND - Not Determined

[b] Effect of the loss of SirA was tested

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