Table S1. *Bacillus subtilis* strains used in this study

Strain	Genotype
B. subtilis	
168	*trpC2*
OC0010	*trpC2 nsrRhis12-tet*
ORB8277	*trpC2 nsrRhis12-tet fur*::*kan*
ORB8278	*trpC2 nsrRhis12-tet resD*::*cat*
ORB8238	*trpC2 resDhis12*
ORB8264	*trpC2 resDhis12 nsrR*::*cat*
ORB8266	*trpC2 resDhis12 fur*::*kan*
ORB8440	*trpC2 furhis12*
ORB8501	*trpC2 furhis12 nsrR*::*cat*
ORB8502	*trpC2 furhis12 resD*::*cat*
ORB8458	*trpC2 ykuN*::pMutin
ORB8461	*trpC2 ykuN*::pMutin *fur*::*kan*
ORB8507	*trpC2 ykuN*::pMutin *resD*::*spc*
ORB8508	*trpC2 ykuN*::pMutin *nsrR*::*cat*
ORB8509	*trpC2 ykuN*::pMutin *fur*::*kan nsrR*::*cat*
ORB8510	*trpC2 ykuN*::pMutin *fur*::*kan resD*::*spc*
ORB8511	*trpC2 ykuN*::pMutin *resD*::*spc nsrR*::*cat*
ORB8512	*trpC2 ykuN*::pMutin *fur*::*kan resD*::*spc nsrR*::*cat*
ORB8620	*trpC2* SPβc2del2::Tn917::pMMN392
ORB8621	*trpC2* SPβc2del2::Tn917::pMMN392 *nsrR*::*cat*
ORB8622	*trpC2* SPβc2del2::Tn917::pMMN392 *resD*::*spc*
ORB8626	*trpC2* SPβc2del2::Tn917::pMMN392 *resD*::*spc nsrR*::*cat*

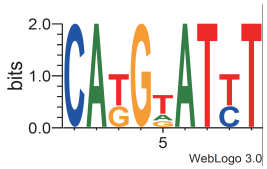
Table S2. Oligonucleotides used in this study

Oligonucleotide	Sequence	Position*	Purpose
oSK203	TAAGTCCAATCCAAATGGTTGAATA	-189	*sdpA* qPCR
oSK204	TTTTGATGTAGATTACCTCCTCTAAGC	-21	*sdpA* qPCR
oSK211	TCAGGAAAATCCATTTTAAAGACAG	-166	*ykuN* qPCR
oSK212	TAGCCATGTTATCACCCCATTAGTT	+7	*ykuN* qPCR
oSK213	GTAAAATGCCCGGTTTTAAGGTATG	-171	*nasD* qPCR
oSK214	GCACAGCAAAAAGGAATATTTAAGA	-40	*nasD* qPCR
oSK223	TCATCTTTGGTAAAATTCATAAAAAGTTC	-154	*ctaB* qPCR
oSK224	AACGTAAACCTCCCTTACAAACCTAAC	-1	*ctaB* qPCR
oSK237	GTATGGTGTCCTATTGACGAAGAAAAAC	-192	*ydhC* qPCR
oSK238	AAAATCATATAACAGATGGTAATGGGAAG	-44	*ydhC* qPCR
oSK240	ATTCGGAGAATGAAGAGAAGATTAAGAAA	-215	*yukE* qPCR
oSK241	AACAGTTTTTCGGCATAGTCAAACAAATA	-76	*yukE* qPCR
oSN86	CATGTTTTTATCACCTAAAAGTTTACCAC	-297	*rpsD* qPCR
oSN87	CGATACACCTTATTGATAAGGAACAAAATG	-112	*rpsD* qPCR
oBH6	CCGTGTTTATCTTCTATCCCTTG	-171	*feuA* qPCR
oBH7	TTCATCTATAGAGCCTCCTGTTCA	+5	*feuA* qPCR
oBH24	TGGTCTCCTCCTTAGTAAACCAT	+21**	*yopS/R* qPCR
oBH25	TGAAATCCATTTGACTATTTTGG	+4**	*yopS/R* qPCR
oBH26	TCCGTTTTTGCTAGGGGATT	-167	*hmp* qPCR
oBH27	TTTCGATTGTTTTGTTATCTAACATTT	+25	*hmp* qPCR
oMMN579	TGACCTCACAGCCACTAATAGT	-70	*ypqP* qPCR
oMMN580	TCCTTTGTTTTGGACGTGGC	+85	*ypqP* qPCR
nsrR-FF	AAAACATGCACCCAGCTGGGTGCATG		*nsrR-his* construct
nsrR-FR	GGTGATGCGATCCTCTCATCTCGAGTTCCTTCATTTTTAAAAGCTTCATG		*nsrR-his* construct
nsrR-BF	CGGAAGGATACTACATCCTGGTAGATTAAGATTCCTTCTTTTTTTATG		*nsrR-his* construct
nsrR-BR	TTCAGTTCCTGCACCGTCATTTTAAACTC		*nsrR-his* construct
12xhis-F	CTCGAGATGAGAGGATCGCATCACCATC		*nsrR-his* construct
rPCR-tetR	CCAGGATGTAGTATCCTTCCGGGGGTTATTGTCTCATGAGCG		*nsrR-his* construct
rPCR-CmF2	GGATAGACTCCACCAGAAGAGCATCATCGGCAATAGTTACCC		*resD-his, fur-his* constuct
rPCR-CmR2	CCAGGATGTAGTATCCTTCCGCGGCGTAGAGGATCTGGAGC		*resD-his, fur-his* constuct
pAPNC-F	CGACAGCGGAATTGACTCAAGC		*resD-his, fur-his* constuct
Cm-R	ATGTACCTGTAAAGATAGCGG		*resD-his, fur-his* constuct
resDCd-1f	ATTGAAGTGTGCCGGCAAATTCGTG		*resD-his* construct
resDCd-1r	GCTCTTCTGGTGGAGTCTATCCTCAAATTTATAACCTACACCCCATAC		*resD-his* construct
resDCd-2f	CGGAAGGATACTACATCCTGGGAGGTCGGCGCTGAATGAAATTTTG		*resD-his* construct
resDCd-2r	GCTTGAGTCAATTCCGCTGTCGGGCAAGCAAAGACTGGGATAAAAAG		*resD-his* construct
resDCH-1r	GTGGTGGTGATGGTGATGGTGGTGCTCAGCACCGACTTCAAATTTATAACCTACACCCCATAC		*resD-his* construct
resDCH-2f	GCACCACCATCACCATCACCACCACCATCATCACCATGAGGTCGGCGCTGAATGAAATTTTG		*resD-his* construct
resD-s3	GAAGCCATTGCCAAAGGGCTTGAAG		*resD-his* construct
resD-s4	ATGTGGTCAGCACAATCGCAATTCC		*resD-his* construct

furCd-1f	GCTTACATCTAGACTTTTTTAAAATCAT	*fur-his* construct
furCd-1r	GCTCTTCTGGTGGAGTCTATCCTTCAGTTTCTTTTCCGTTACAGC	*fur-his* construct
furCd-2f	CGGAAGGATACTACATCCTGGTAGACGGTGCCGAGCGCGAACCTT	*fur-his* construct
furCd-2r	GCTTGAGTCAATTCCGCTGTCGGGATAATATGTATGCGGGTAAC	*fur-his* construct
furCH-1r	GATGATGGTGGTGGTGATGGTGATGGTGGTGTTCAGTTTCTTTTCCGTTACAGC	*fur-his* construct
furCH-2f	CATCACCATCACCACCACCATCATCACCATTAGACGGTGCCGAGCGCGAACCTT	*fur-his* construct
fur-s3	GGTCATTCTGTTTTTAGCGCTGATTT	*fur-his* construct
fur-s4	ATGCCAAATGCCGCGCCGATGTCTT	*fur-his* construct

Underlines indicate his-coding regions.
*Listed is the position of 5'-end nucleotide relative to the translation start site.
**As for oBH24 and oBH25, the position of 5'-end nucleotide is shown relative to the last nucleotide of the stop codon of conversely transcribed *yopS* and *yopR*, respectively.

A



Consensus I CATR**TA**TYTT*AAAT**A**TATV

Consensus II CAKGDATYT

B

hmp	CATG**TA**TTTTAAAG**A**TATA
nasD	CATG**TA**TCTTAAAT**A**TTCC
ydhC	**CA**G**G**G**AT**C**T**GACAAGGCAG
yopS-yopR	**CA**T**G**T**AT**T**T**AAAGTGATTA
feuA	**CA**G**GAATT**TGTCCATGGTG
ykuN	**CA**G**GAA**AA**T**CCATTTTAAA

Fig. S1. Motifs found in promoter regions targeted by NsrR. A. The consensus sequence for NsrR-binding was previously proposed by base substitution analysis of the *nasD* promoter (15). The asterisk shows the center of the dyad symmetry and the nucleotides in bold play critical roles in repressor activity. The half site of the previously proposed consensus sequence for NsrR is found from the sequence logo (http://meme.nbcr.net) of high- and middle-level NsrR-binding sites identified by ChAP-chip experiment in this study. B. Nucleotides marked in blue correspond to conserved residues in the NsrR-binding sequence and those marked in red correspond to conserved residues in the half site. Highly conserved nucleotides are shown in bold.