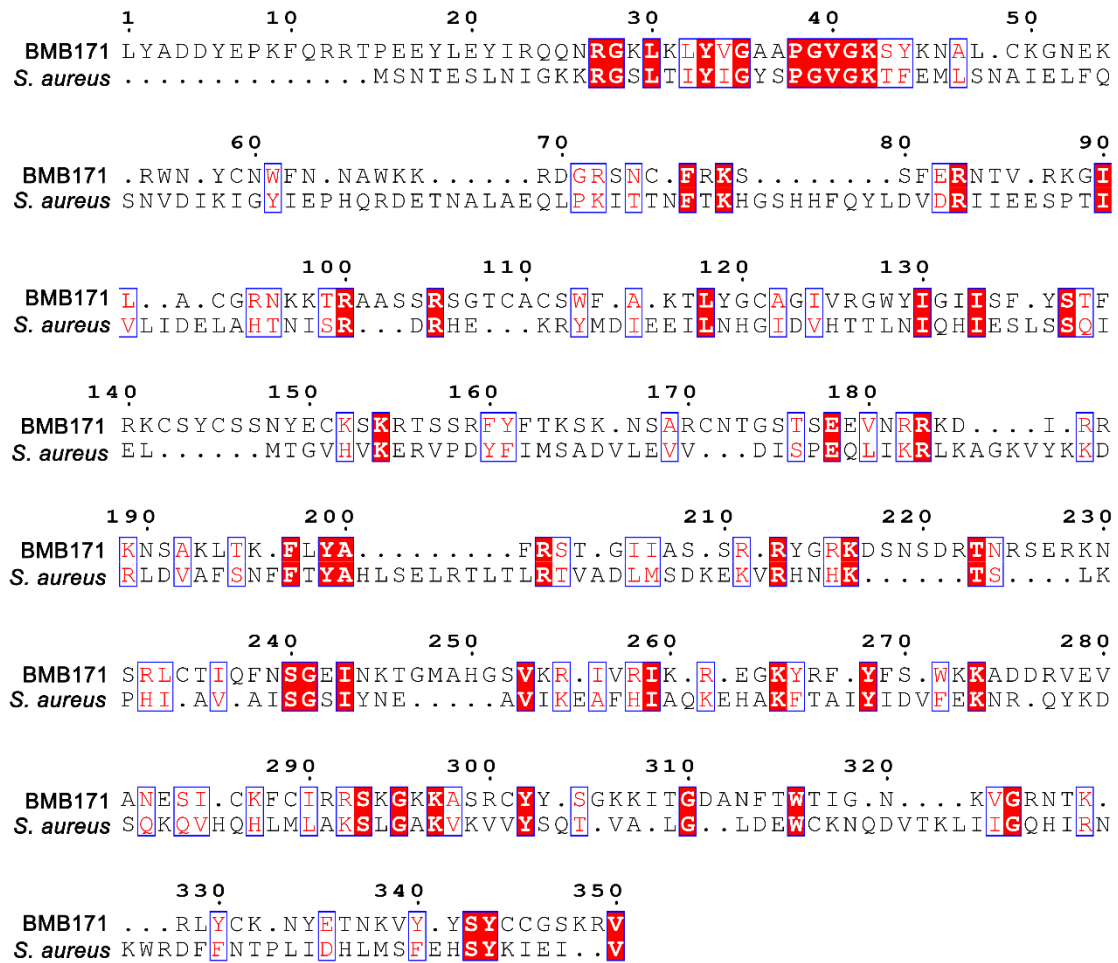
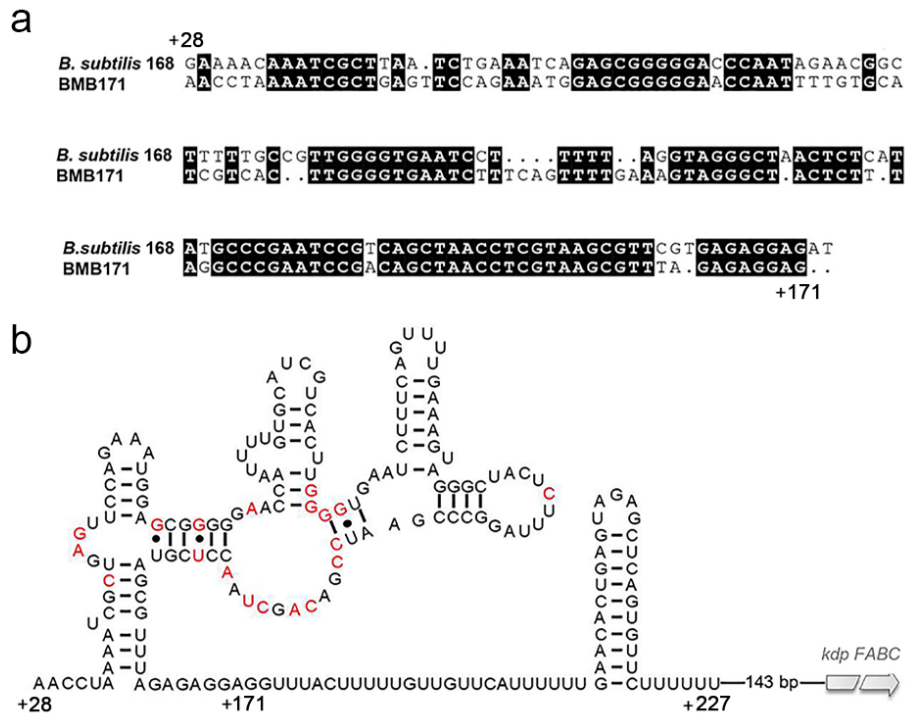


## Supplementary Figure 1



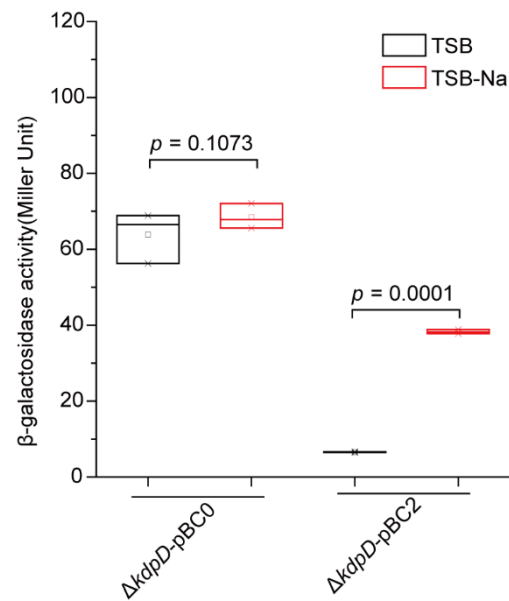
**Supplementary Figure 1. Alignment of KdpD of BMB171 (*Bacillus thuringiensis* BMB171) with N-terminal domain of *S. aureus* (*Staphylococcus aureus* NCTC 8325).** White letters shaded in red denote the conserved nucleotides. The similarity is only 9.1%.

## Supplementary Figure 2



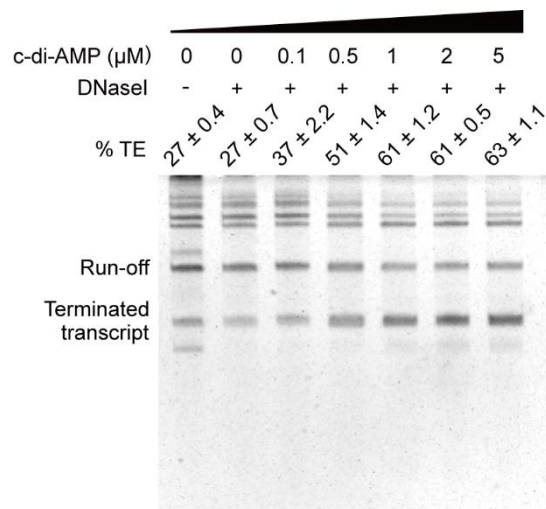
**Supplementary Figure 2. A conserved c-di-AMP riboswitch encoding region within the 5'-UTR encoding region of *kdp* operon. a** Sequence alignment of the aptamer domains in c-di-AMP riboswitch between BMB171 and *B. subtilis* 168, with white letters shaded in black denoting the conserved nucleotides. **b** The predicted secondary structure of c-di-AMP riboswitch. The distance from the 3' terminal of c-di-AMP riboswitch to the first nucleotide of the start codon is 143 bp.

### Supplementary Figure 3



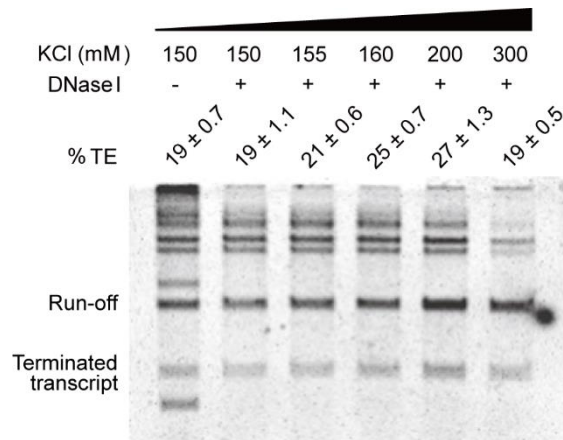
**Supplementary Figure 3** The  $\beta$ -galactosidase activities for  $\Delta kdpD$  carrying plasmids with (pBC2) and without the c-di-AMP riboswitch encoding region (pBC0) at different  $K^+$  concentrations. Data are expressed as box-and-whisker plots, where the central lines denote medians, edges represent upper and lower quartiles and whiskers show minimum and maximum values. Data were subjected to one-way analysis of variance (ANOVA) using the Bonferroni test,  $n = 3$ ,  $p$ -values are shown above each panel.

## Supplementary Figure 4



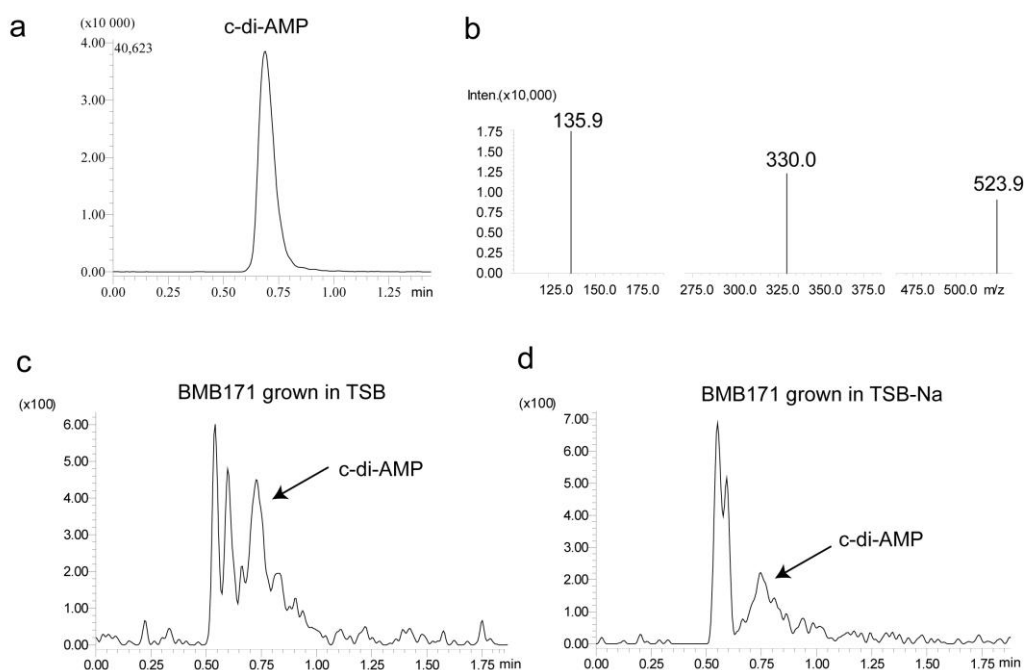
Supplementary Figure 4. *In vitro* transcription assay conducted in the presence of various c-di-AMP concentrations ranging from 0 to 5  $\mu\text{M}$ .

## Supplementary Figure 5



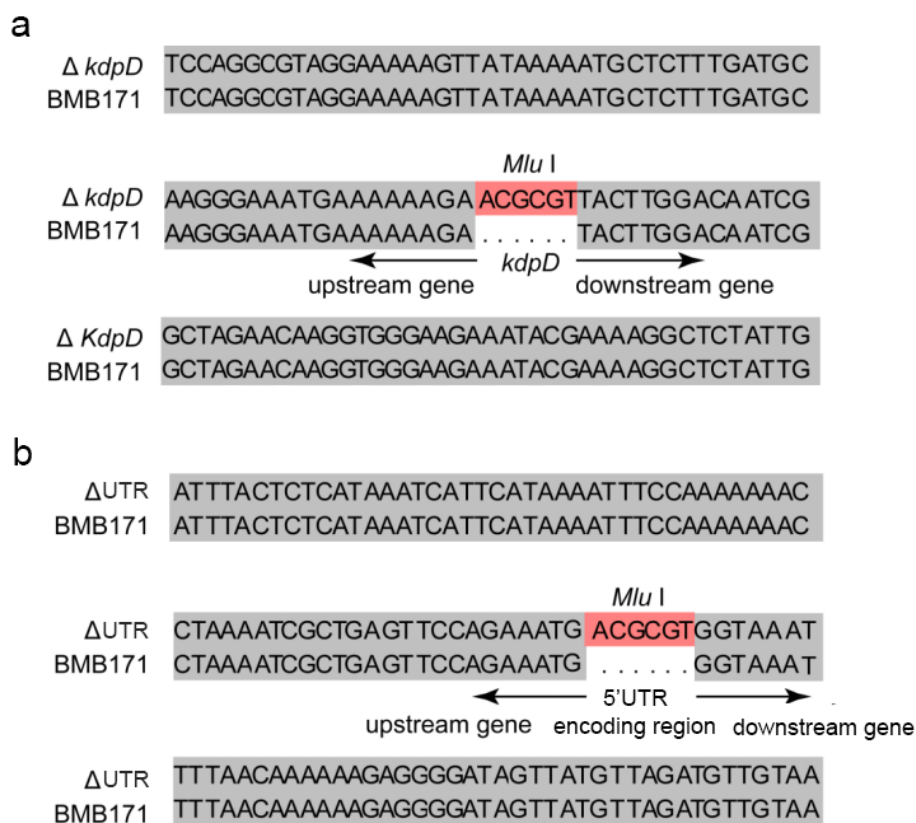
Supplementary Figure 5. *In vitro* transcription assay conducted in the presence of various  $K^+$  concentrations ranging from 150 to 300 mM.

## Supplementary Figure 6



**Supplementary Figure 6. Quantification of intracellular c-di-AMP concentration by LC-MS/MS.** **a** LC-MS/MS chromatogram of the c-di-AMP standard detected using the  $m/z$  fragments at 135.9, 330.0 and 523.9. **b** Mass spectrum of daughter ions  $m/z$  135.9, 330.0 and 523.9 from parent ions  $m/z$  659.0 and 660.0. **c** and **d** Determination of c-di-AMP extracted from BMB171 strain grown in TSB and TSB-Na, respectively.

## Supplementary Figure 7



**Supplementary Figure 7.** Verification of  $\Delta kdpD$  and  $\Delta UTR$  by sequencing. **a** Sequence alignment of PCR products amplified from the  $\Delta kdpD$  genomic DNA and the BMB171 genomic DNA using primer pair *kdpC-F/ kdpD-DR* (*Bam*H I). The PCR products (about upstream 100 bp and downstream 100 bp sequences of *kdpD*) were shown. **b** Sequence alignment of PCR products amplified from the  $\Delta UTR$  genomic DNA and the BMB171 genomic DNA using primer pair UTR-UUF/UTR-DR (*Bam*H I). The PCR products (about upstream 100 bp and downstream 100 bp sequences of c-di-AMP riboswitch) were shown.

**Supplementary Table 1. Primers used in this study**

Primers	Consequence	Purposes	Origins
<i>kdpA</i> -F	CGTTAGATGGGGCGGTTACA		This work
<i>kdpA</i> -R	GTGACACGAAAAGGATGCGG		This work
<i>kdpB</i> -F	GGCGGTGATTTTGTTCGGT	RT-qPCR	This work
<i>kdpB</i> -R	AAATCGGCAACGTCACAACG		This work
<i>kdpC</i> -F	AATCGGGCAAACTTCACGG		This work
<i>kdpC</i> -R	ATATGCGATCCACCTGCACA		This work
<i>gapdh</i> -F	TTTTGCTAGCGCTTTCGCAG		This work
<i>gapdh</i> -R	TAGCGCCTGTTGTGAAGGTG	RT-qPCR, internal control	This work
16S-F	CCGCCCTTTAGTGCTGAAG		This work
16S-R	CTTGTGCGGGCCCCCGTCAATTC		This work
Primer-8	TTTTTTTTTTTTTTTT	5'-RACE	
UTR-R(5'-RACE)	AACTGAAAGATTACCCCAAGTGACGA		This work
<i>Pkdp</i> -F ( <i>Nco</i> I)	CATGCCATGGAATAACAGTAATAATCTTCA ATGTA	Plasmids pBC0 and pBC2 construction	This work
<i>Pkdp</i> -R1 ( <i>Bam</i> H I)	CGGGATCCGAGAGTAAATATACTCCTCTAT AT	Plasmid pBC0 construction	This work
0647-R ( <i>Bam</i> HI)	CGGGATCCTTTTTGTAAAAATTACCATT AAATATTAATA	Plasmid pBC2 construction	This work
UTR-UF( <i>Hind</i> III)	CCCAAGCTT GAGGATGAGGTACATGGAECTA		This work
UTR-UR ( <i>Mlu</i> I)	CGACGCGT CATTCTGGAACCTCAGCGATTTTAG	Plasmid pRP1028-UTR-UD construction	This work
UTR-DF ( <i>Mlu</i> I)	CGACGCGTGGTAAATTTAACAAAAAGAG GGGA		This work
UTR-DR( <i>Bam</i> H I)	CG GGATCC ATCCACCGCGTTATTTCCAAG		This work
UTR-UUF	CTTCGTAAGCGTCTTGAGAGAGGAC	For c-di-AMP riboswitch encoding region deleted candidate screening	This work
pRP1028-R	GTGCGAATAAGGGACAGTGAAGAAGG		This work
<i>kdpD</i> -UF ( <i>Sma</i> I)	TCCCCGGG AATTAACATCACCCTGTCAGCG		This work
<i>kdpD</i> -UR ( <i>Mlu</i> I)	CG ACGCGT TCTTTTTTCATTTCCCTTGCATC	Plasmid pRP1028- <i>kdpD</i> -UD construction	This work
<i>kdpD</i> -DF ( <i>Mlu</i> I)	CGACGCGT TACTTGGACAATCGGCTAGAACA		This work
<i>kdpD</i> -DR( <i>Bam</i> H I)	CG GGATCC ATTATGCAGCTCGTATATGGACC		This work
<i>kdpC</i> -F	AATCGGGCAAACTTCACGG	For chromosomal <i>kdpD</i> gene deleted candidate screening	
pRP1028-R	GTGCGAATAAGGGACAGTGAAGAAGG		This work
Eco-P	CAATGTAAGCGTTTAAATGAATG	<i>In vitro</i> transcription	This work
ZL-2R	TCCTTCTTTCACAACCTTATCTGACCAACT		This work



**Supplementary Table 2. Strains used in this study**

<b>Strains</b>	<b>Relevant characteristics</b>	<b>Origins</b>
<i>E. coli</i> DH5 $\alpha$	F- $\Phi$ 80 <i>lacZ</i> $\Delta$ M15 $\Delta$ ( <i>lacZYA-argF</i> ) U169 <i>recA1 endA1 hsdR17</i> (rk <sup>-</sup> , mk <sup>+</sup> ) <i>phoA supE44 thi-1 gyrA96 relA1</i> $\lambda$ -	Beijing TransGen Biotech Co., Ltd
BMB171	<i>B. thuringiensis</i> strain BMB171; an acrySTALLIFEROUS mutant strain; high transformation frequency	3, 4
$\Delta$ <i>cdaA</i>	In frame deletion of <i>cdaA</i> in BMB171	5
$\Delta$ <i>disA</i>	In frame deletion of <i>disA</i> in BMB171	5
$\Delta$ UTR	In frame deletion of c-di-AMP riboswitch in BMB171	This work
$\Delta$ <i>kdpD</i>	In frame deletion of <i>kdpD</i> in BMB171	This work
BMB171-pBC0	Derivate strain of BMB171 carrying the pBC0 plasmid	This work
BMB171-pBC2	Derivate strain of BMB171 carrying the pBC2 plasmid	This work
$\Delta$ <i>cdaA</i> -pBC0	Derivate strain of $\Delta$ <i>cdaA</i> carrying the pBC0 plasmid	This work
$\Delta$ <i>cdaA</i> -pBC2	Derivate strain of $\Delta$ <i>cdaA</i> carrying the pBC2 plasmid	This work
$\Delta$ <i>disA</i> -pBC0	Derivate strain of $\Delta$ <i>disA</i> carrying the pBC0 plasmid	This work
$\Delta$ <i>disA</i> -pBC2	Derivate strain of $\Delta$ <i>disA</i> carrying the pBC2 plasmid	This work

**Supplementary Table 3. Plasmids used in this study**

Plasmids	Relevant characteristics	Purposes	Origins
pHT1K- <i>lacZ</i>	<i>B. thuringiensis-E. coli</i> shuttle plasmid; Amp <sup>R</sup> Erm <sup>R</sup> , pHT1K plasmid harboring the promoter-less <i>lacZ</i> gene, for $\beta$ -galactosidase activity assay	$\beta$ -Galactosidase assays	1
pBC0	<i>Kdp</i> promoter cloned between <i>Nco</i> I and <i>Bam</i> H I sites of pHT1K- <i>lacZ</i> , for $\beta$ -galactosidase activity assay	$\beta$ -Galactosidase assays	This work
pBC2	<i>Kdp</i> promoter and c-di-AMP riboswitch coding region cloned between <i>Nco</i> I and <i>Bam</i> H I sites of pHT1K- <i>lacZ</i> , for $\beta$ -galactosidase activity assay	$\beta$ -Galactosidase assays	This work
pRP1028	<i>B. thuringiensis-E. coli</i> shuttle plasmid; Amp <sup>R</sup> Erm <sup>R</sup> ; containing <i>turbo-rfp</i> gene and an I- <i>Sce</i> I recognition site	Gene deletion	2
pSS4332	<i>B. thuringiensis-E. coli</i> shuttle plasmid; Km <sup>R</sup> ; containing <i>gfp</i> and I- <i>Sce</i> I restriction enzyme encoding gene	Gene deletion	2
pSS1827	The helper plasmid for conjugative transfer; Amp <sup>R</sup>	Gene deletion	2
pRP1028-UTR-UD	pRP1028 with the upstream and downstream regions of c-di-AMP riboswitch, an intermediate plasmid in gene deletion experiments	c-di-AMP riboswitch encoding region deletion	This work
pRP1028- <i>kdpD</i> -UD	pRP1028 with the upstream and downstream regions of <i>kdpD</i> gene, an intermediate plasmid in gene deletion experiments	<i>kdpD</i> deletion	This work

### Supplementary References

1. Wang, J. P., Ai, X. L., Mei, H., Fu, Y., Chen, B., Yu, Z.N. & He, J. High-throughput identification of promoters and screening of highly active promoter-5' UTR DNA region with different characteristics from *Bacillus thuringiensis*. *PLoS ONE*, **8**, e62960 (2013).
2. Janes, B. K. & Stibitz, S. Routine markerless gene replacement in *Bacillus anthracis*. *Infect Immun*, **74**, 1949-1953 (2006).
3. Li, L., Shao, Z., & Yu, Z. Transformation of *Bacillus thuringiensis* recipient BMB171 by electroporation. *Wei Sheng Wu Xue Tong Bao*, **27**, 331-334 (2000).
4. Li, L., Yang, C., Liu, Z., Li, F., & Yu, Z. Screening of acrySTALLIFEROUS mutants from *Bacillus thuringiensis* and their transformation properties. *Wei Sheng Wu Xue Bao*, **40**, 85-90 (2000).
5. Zheng, C., Ma, Y., Wang, X., Xie, Y., Ali, M. K., & He, J. Functional analysis of the sporulation-specific diadenylate cyclase CdaS in *Bacillus thuringiensis*. *Front Microbiol*, **6**, 908 (2015).