

1 **SUPPLEMENTAL MATERIAL**

2 **Histone-like nucleoid-structuring protein (H-NS) paralogue**
3 **StpA activates the type I-E CRISPR-Cas system against**
4 **natural transformation in *Escherichia coli***

5

6 **Running title: StpA regulates the type I-E CRISPR-Cas system**

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1 SUPPLEMENTAL MATERIALS AND METHODS

2

3 1. Construction of *E. coli* mutants

4 *E. coli* mutants were constructed by using the λ -RED recombination system that had
5 been constructed in the temperature sensitive plasmid pKD46 (1). To induce the λ -RED
6 system, arabinose (30 mM) was added to the *E. coli* pKD46 culture at an OD₆₀₀ of 0.2.
7 Chemical competent cells were prepared when the cell culture was grown to an OD₆₀₀
8 of 0.4. The DNA template containing an antibiotic resistant gene (Cm^R or Kan^R) from
9 either pKD3 or pKD4 for double crossover was PCR amplified with a pair of primers
10 (P₀₁-P₀₂ for inactivating *stpA* or P₀₃-P₀₄ for inactivating *hns*) containing short
11 homologous arms. The *stpA* and *hns* null mutants were checked by using colony PCR
12 with primer pairs P₀₅-P₀₆ for Δ *stpA* and P₀₇-P₀₈ for Δ *hns*. The temperature sensitive
13 plasmid pCP20 was transformed into the mutant for eliminating the antibiotic resistance
14 gene in the genome. All primers are shown in Table 2.

15

16 2. Plasmid construction

17 The plasmid pCR1 was constructed by inserting the chemically synthesized DNA
18 fragment (CR1) with four protospacer adjacent motif (PAM)-containing DNA regions,
19 that can be recognized by the CRISPR-Cas system of *E. coli*, into the vector pUC57 at
20 the *Hind* III and *EcoR* I sites. DNA synthesis and cloning were performed by
21 GENEWIZ Biotech Co., LTD. The complete sequence of pCR1 was provided in the
22 section of DNA SEQUENCE INFORMATION at the end of the file.

1 To construct pGLO-P_{cas}-gfp for monitoring transcription of *cas* operon, the promoter of
2 the *cas* operon was fused with the green fluorescence protein (GFP) encoding gene.
3 The fragment of P_{cas} was amplified from *E.coli* genome with primer pairs P₁₁ and P₁₂.
4 The linearized vector, that was obtained by PCR amplification of pGLO with primer
5 pairs P₀₉ and P₁₀, was recombined with the above fragments by using the One Step
6 Cloning Kit (Qingke Biotech Co., LTD).

7 To construct pGLO-P_{rscA}-gfp for checking transcriptional activity of a promoter known
8 to be regulated by H-NS and StpA, the fragment of P_{rscA} was amplified from *E.coli*
9 genome with primer pairs P₁₅ and P₁₆. The linearized vector, that was obtained through
10 PCR amplification of pGLO with primer pairs P₁₃ and P₁₄, was recombined with the
11 above fragments by using the One Step Cloning Kit (Qingke Biotech Co., LTD).

12 The plasmid pGLO-P_{cas}*-gfp carrying mutations in the putative DNA binding site (DBS)
13 for H-NS/StpA was constructed to identify the DBS for H-NS/StpA regulation in P_{cas}.
14 Mutations in DBS was achieved by using site-directed mutagenesis with pGLO-P_{cas}-
15 gfp as the template and the primer pair P₂₅-P₂₆ for amplification.

16 To construct pSUStpA and pSUHNS for ectopic expressing StpA and H-NS on plasmid,
17 DNA fragments containing *stpA* and *hns* together with their original promoters were
18 amplified with primer pairs P₁₇-P₁₈ and P₂₁-P₂₂ from the *E.coli* genome. The linearized
19 vectors, that was obtained by PCR amplification of pSU19 with primer pairs P₁₉-P₂₀
20 and P₂₃-P₂₄, were recombined with the above fragments by using the One Step Cloning
21 Kit (Qingke Biotech Co., LTD).

1 To construct pSU-P_{BAD}-*gfp* which expressed the green fluorescence gene with an
2 arabinose-inducible promoter P_{BAD}, the fragment containing *gfp* together with P_{BAD} was
3 amplified with primer pairs P₃₀-P₃₁ from pGLO-*gfp*. The linearized vector, that was
4 obtained by PCR amplification of pSU19 with primer pairs P₃₂-P₃₃, was recombined
5 with the above fragment by using the One Step Cloning Kit (Qingke Biotech Co., LTD).
6 To construct pSU-P_{BAD}-*stpA* and pSU-P_{BAD}-*hns*, fragments containing *stpA* and *hns*
7 were amplified from *E.coli* genome with primer pairs P₃₆-P₃₇ and P₃₈-P₃₉. The
8 linearized vector, that was obtained by PCR amplification of pSU19 with primer pairs
9 P₃₅-P₃₆, was recombined with the above fragments by using the One Step Cloning Kit
10 (Qingke Biotech Co., LTD).

11

12 **3. Quantification of crRNA with RT-qPCR**

13 Overnight-grown *E. coli* culture (1 ml) was precipitated and the cell pellet was
14 resuspended in 1 ml RNA trizol (TransGen Biotech Co., LTD). The cell resuspension
15 was mixed thoroughly with 0.2 ml chloroform. After incubation at the room
16 temperature for 3 minutes, the mixture was centrifugated at 10, 000 rpm for 15 minutes.
17 The upper layer of the mixture was transferred to the RNA spin column for purifying
18 the total RNA, which was retained in the eluate. Total RNA in the eluate was transferred
19 to a miRNA spin column, in which the resin matrix had high affinity for small RNA
20 (sRNA). The attached sRNA on the resin matrix was washed with ethanol and the
21 washing buffer provided in the EasyPure[®] miRNA Kit (TransGen Biotech Co., LTD).
22 Then, 30 µL RNase-free water was added to the miRNA spin column to dissolve sRNA
23 which was subsequently examined by gel electrophoresis before being stored at -80°C.

1 For quantifying crRNA, the first strand of the corresponding cDNA was obtained with
2 the *TransScript*[®] miRNA First-Strand cDNA Synthesis SuperMix Kit (TransGen
3 Biotech Co., LTD). The reaction system (10 μ l) for reverse transcription was as follows:
4 sRNA (0.2 mg ml⁻¹) 4.5 μ l, *TransScript* miRNA RT Enzyme Mix 0.5 μ l, 2 \times TS miRNA
5 Reaction Mix 5 μ l. The reaction system was left at 37°C for an hour before inactivation
6 of the RT Enzyme Mix at 85°C for 5 seconds. During reverse transcription, the DNA
7 fragment (GATCGCCCTTCTACGTCGTATCGTCATCTGACCGTTATCGCTGCAC
8 GTTTTTTTTTTTTTTTTTTTTT) was simultaneously added to the 3' terminus of the
9 cDNA.

10 To quantify sRNA transcripts, real-time PCR was performed with a pair of primers (P₂₈
11 and P₂₉ for crRNA, P₂₇ and P₂₉ for tRNA) that were complementary to the target cDNA
12 and the added 3' tail respectively, by using the program as follows: 94°C, 30 seconds;
13 94°C, 5 seconds; 57°C, 15 seconds; 72°C, 10 seconds; 72.5°C, 5 seconds for melt curve
14 evaluation; recycle number for 40 times. PCR products were examined by using 2%
15 agar gel electrophoresis.

16

17 **4. Drop-planting**

18 Drop planting was performed according to a documented method (2). The overnight
19 grown culture of *E. coli* carrying pCR1 or pDsRED was serially diluted with LB
20 medium. An aliquot of 10 μ l of the diluted cell suspension was dispensed into LB-agar
21 plate supplemented with 100 μ g ml⁻¹ ampicillin. After drops on the agar dried, the petri
22 plates were inverted and incubated at 30 °C for 24-48 hours.

1

2 **5. Plasmid loss assay in transformants**

3 After natural transformation of *E. coli*, transformant colonies were further grown in LB
4 broth or on LB-agar plates. Cell growth in LB broth was measured in a Spectrumlab
5 S23A Spectrophotometer at 600 nm. To evaluate plasmid loss in transformants, bacteria
6 grown in LB broth were streaked on plates or serial diluted before drop plating (2). To
7 quantify the rate of plasmid loss, numbers of viable counts on LB-agar plates with and
8 without ampicillin ($100 \mu\text{g ml}^{-1}$) were measured by using the track-dilution cfu
9 enumeration technique (3).

10

11 **6. Chemical Transformation**

12 Overnight grown *E.coli* cell culture (1 ml) was inoculated into 50 ml LB medium and
13 incubated at 30°C with shaking to an optical density at 600 nm (OD_{600}) of 0.4. The cell
14 pellet, which had been collected by centrifugation and washed twice with 10 ml 100
15 mM CaCl_2 solution on ice, was resuspended in 500 μl of 100 mM CaCl_2 solution
16 supplemented with 10% (v v^{-1}) glycerol and restored at -80°C. Plasmid pDsRED or
17 pCR1 was added to 50 μl of the competent cell suspension to a final concentration of ~
18 $10 \mu\text{g ml}^{-1}$, which was placed on ice for 30 minutes before a heat shock at 42°C for 90
19 seconds. Then, the cell suspension was placed on ice for ~ 1 minute, followed by the
20 addition of 0.5 mL LB. Transformed cells in LB medium were further incubated at 30°C
21 for 2 hours before being spread on LB-agar plates containing ampicillin at a

1 concentration of 100 $\mu\text{g ml}^{-1}$. The number of transformants on plates were counted and
2 transformation efficiency was calculated as the number of transformants per μg plasmid.

3

4 **7. Protein isolation and purification**

5 *E.coli* BL21 containing pET28a-StpA-His/pET28a-HNS-His was incubated in 50 ml
6 LB medium at 37 °C with shaking. To induce the expression of StpA-His/HNS-His,
7 lactose (0.4%) was added to the cell culture at an OD₆₀₀ of 0.4 and further incubated for
8 6 hours. *E. coli* mutants (ΔstpA , Δhns and $\Delta\text{hns } \Delta\text{stpA}$) and their wildtype parent were
9 grown to the stationary phase in LB broth. Cell pellets were collected by centrifugation
10 and washed with the phosphate-buffered saline (PBS) buffer before being resuspended
11 in 5 mL cold PBS buffer. To obtain total proteins, the cell resuspension was sonicated
12 on ice for 20 min (9 s sonication, 9 s interval) at 33% amplitude. StpA-His/HNS-His
13 was purified from total proteins with Tagged Protein Purification Kit (Soluble Protein)
14 Kit (Beijing ComWin Biotech Co., Ltd).

15

16 **8. Western blot assay**

17 For determination of expression level of StpA/H-NS in cells, total proteins were taken
18 from cultures that had been grown to the stationary phase (10-hour in LB medium and
19 24-hour in M9 medium), and resuspended in the PBS buffer. Samples were subjected
20 to SDS-PAGE (12% polyacrylamide) before being blotted onto a 0.1 μm nitrocellulose
21 transfer membrane (Bio-rad). The chemically synthesized peptide
22 CAAPRAGKKRQPR (Hangzhou HuaAn Biotechnology Co., Ltd.) was used to raise

1 the StpA antibody in rabbits which were reviewed and approved by the Animal
2 Research Committee at Zhejiang University of Technology. The polyclonal StpA
3 antibody was used as the primary antibody. HRP-conjugated Goat anti-Rabbit IgG was
4 used as the secondary antibody at a dilution of 1:2000. The treatment of the membrane
5 was as described in Sambrook and Russell (4).

6

7 **9. Quantification of transcription of *cas* genes with GFP**

8 Cell growth was monitored spectrophotometrically at an optical density of 600 nm
9 (OD_{600}). Intensity of the culture fluorescence, as an indicator of transcription of P_{cas} ,
10 was measured by the SpectraMax Gemini EM microplate reader with excitation and
11 emission wavelengths at 395 and 509 nm respectively. Relative gene expression was
12 calculated through dividing the intensity of the culture fluorescence by OD_{600} .

13

14 **10. Natural transformation of *E. coli hns stpA* carrying pSU- P_{BAD} -*stpA***

15 All experiments were performed at 30 °C. The overnight-grown culture of *E. coli hns*
16 *stpA* mutant carrying pSU- P_{BAD} -*stpA* was added to 50 ml of $1.5 \times$ LB medium with a
17 ratio of 1: 50 ($v v^{-1}$). After 24-hour incubation with shaking at a speed of 180 rpm, 2 ml
18 of the cell culture was added to each glass tube which was supplemented without or
19 with arabinose at concentrations of 0.5, 1 or 2 mM, followed by further incubation with
20 shaking for 1 hour. After centrifugation at room temperature, 90% of the supernatant
21 was discarded and the cell pellet was resuspended in the remaining 10% supernatant
22 before adding the plasmid pCR1 to a final concentration of $40 \mu g ml^{-1}$. The mixture of

1 the cell culture and pCR1 was spread on 5% agar (Bacto Difco)- and ampicillin-
2 containing ($100 \mu\text{g ml}^{-1}$) plates as previously documented (5, 6), without or with
3 arabinose at concentrations of 0.5, 1 or 2 mM. Plates were incubated for two days before
4 counting the number of transformants. Transformation efficiency was calculated as the
5 number of transformants per microgram plasmid DNA.

6

7 **11. Quantification of cellular StpA:DNA ratio for transcriptional activation.**

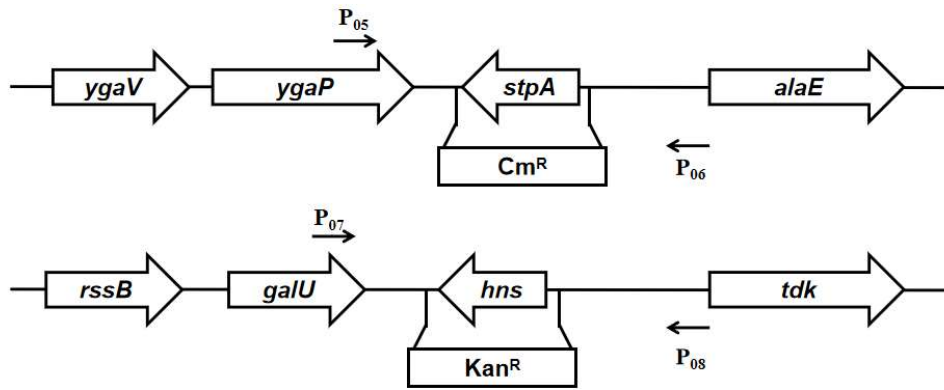
8 The *in vivo* cellular StpA : DNA ratio for activating P_{cas} was estimated from the cell
9 culture grown in M9 medium supplemented with 1 mM arabinose. The concentration
10 of the purified StpA-His was $\sim 0.25 \text{ mg ml}^{-1}$, determined by the BCA protein assay kit
11 (Beijing ComWin Biotech Co., Ltd). According to the Western Blot assay (FIG 5F),
12 the concentration of StpA isolated from the cell culture grown in M9 medium was about
13 10-fold lower than that of the purified StpA-His. Providing that the total protein from
14 50 ml of the cell culture was resuspended in 5 ml of PBS buffer, the amount of StpA in
15 the total protein was estimated to be $0.025 \text{ mg ml}^{-1} \times 5 \text{ ml}$. The viable cell density
16 assayed by plate counting was $\sim 5.4 \times 10^9 \text{ CFU ml}^{-1}$ in M9 medium. Accordingly,
17 cellular concentration of StpA was about $4.6 \times 10^{-16} \text{ g per cell}$. Therefore, each cell
18 contained 1.8×10^4 StpA molecules. Providing the size of the *E. coli* genome is $4.2 \times$
19 10^6 bp , the StpA:DNA ratio was estimated to be $\sim 1: 200$.

20

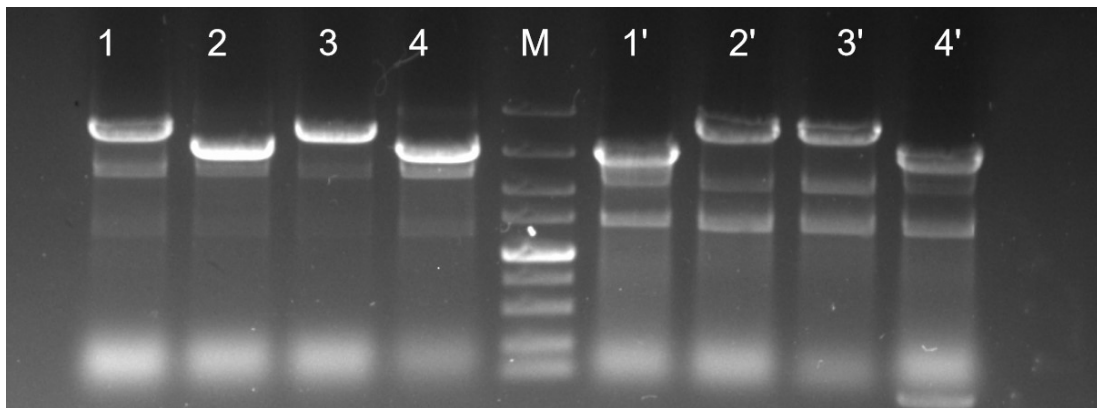
1 **SUPPLEMENTAL RESULTS & DISCUSSION**

2 **1. PCR detection and western blot assay of *E.coli* mutants**

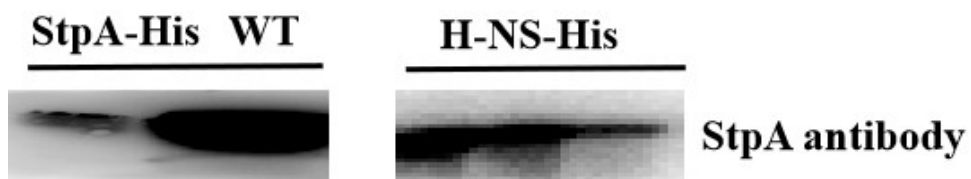
3 **A**



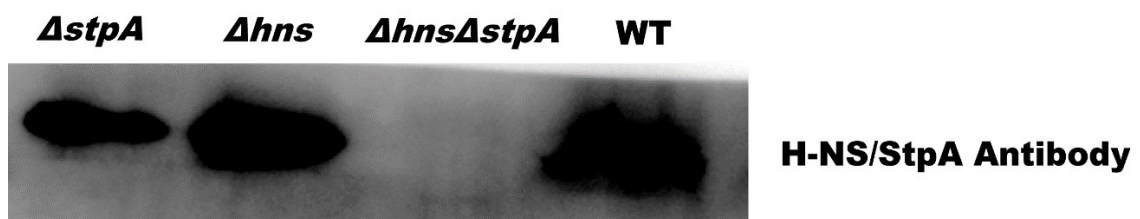
5 **B**



7 **C**



9 **D**



11

1 **FIG S1. Examination of *E. coli* mutants in this work.** (A) Genetic organization of
2 the various chromosomal regions and location of cassette insertion mutants generated
3 in this study (see accompanying TABLE S1). (B) Analysis of PCR fragments for
4 confirmation of the structure of *E. coli* mutant strains. From left to right, each pair of
5 channels compares wild type and mutant strains, as follows. Channel 1/1': $\Delta stpA$ mutant;
6 Channel 2/2': Δhns mutant; Channel 3/3': $\Delta hns \Delta stpA$ mutant; Channel 4/4': wild type;
7 M: 5000 DL marker (from the top down: 5 kb, 3 kb, 2 kb, 1.5 kb, 1 kb, 750 bp, 500 bp,
8 250 bp, 100 bp). (C) Western blot assay was performed to determine interaction
9 between the antibody, raised by a peptide derived from StpA, and purified StpA and H-
10 NS. StpA-His: purified His-tagged StpA protein; H-NS-His: purified His-tagged H-NS
11 protein; WT: Total protein isolated from the wildtype *E. coli* MC4100. (D) Total
12 proteins were isolated from mutants ($\Delta stpA$, Δhns and $\Delta hns \Delta stpA$) and their wildtype
13 parent grown to the stationary phase in LB broth. Western blot assay was performed
14 with the antibody against H-NS or StpA. In *stpA* and *hns* single-deletion mutants, clear
15 bands were detected, showing the presence of H-NS or StpA in these mutants. Whereas,
16 no band was detected in the *hns stpA* null mutant, revealing that neither H-NS nor StpA
17 was present in that mutant.

1 **TABLE S1 Prediction of the structure of *E.coli* mutant strains generated in this**
 2 **work (see accompanying FIG S1C)**

3

Channel ^a	Strain ^b	Primer pair	Size ^c (kb)
1	MC4100 <i>stpA::cat</i>	P ₀₅ +P ₀₆ ^d	3.557
2	MC4100 <i>hns::kan</i>	P ₀₅ +P ₀₆	2.904
3	MC4100 <i>stpA::cat hns::kan</i>	P ₀₅ +P ₀₆	3.557
4	MC4100	P ₀₅ +P ₀₆	2.904
M		DL 5000 marker	
1'	MC4100 <i>stpA::cat</i>	P ₀₇ +P ₀₈ ^e	2.913
2'	MC4100 <i>hns::kan</i>	P ₀₇ +P ₀₈	3.702
3'	MC4100 <i>stpA::cat hns::kan</i>	P ₀₇ +P ₀₈	3.702
4'	MC4100	P ₀₇ +P ₀₈	2.913

4

5 ^a Lane numbers refer to FIG S1.

6 ^b Strains and PCR primers are listed in Table 1 and 2.

7 ^c Sizes predicted on the basis of available DNA sequence information for PCR
 8 fragments generated with primer pairs indicated in the third column.

9 ^d Primer pair for checking *stpA* null mutants.

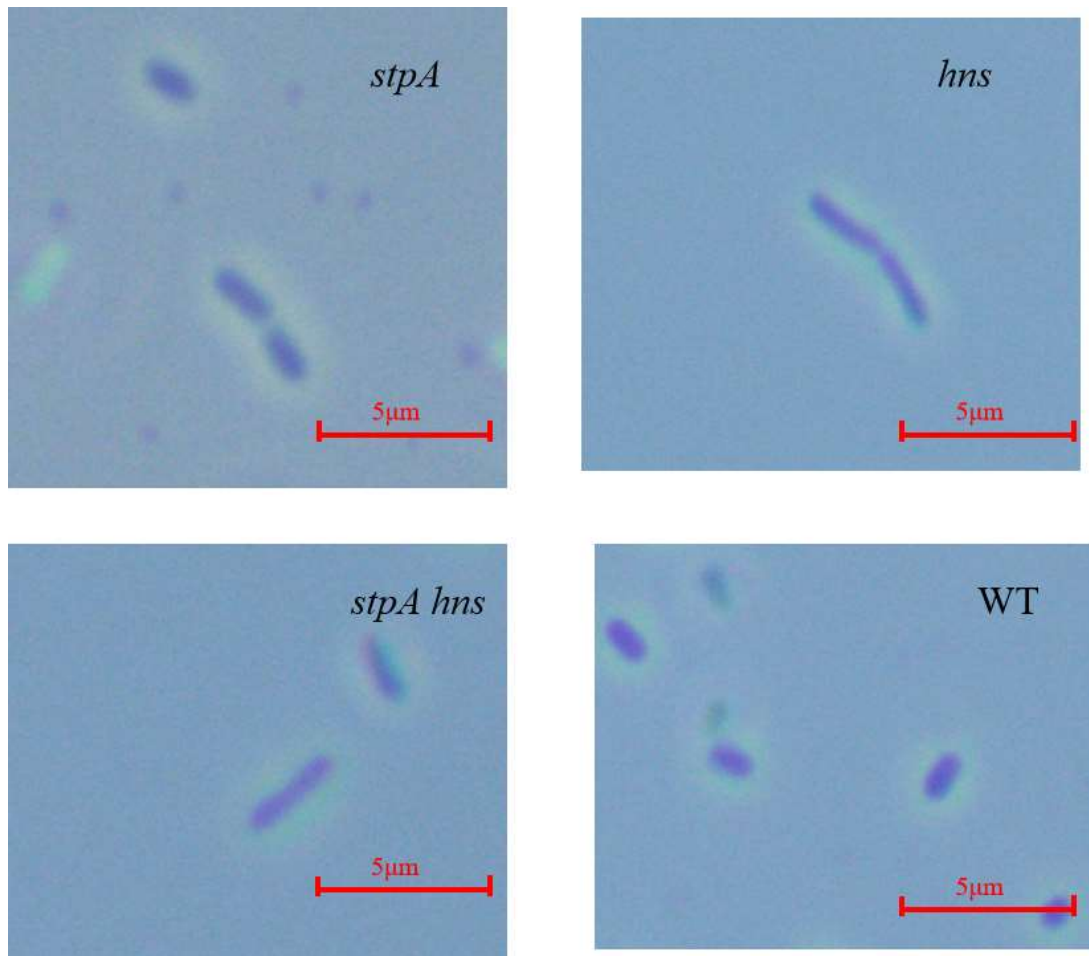
10 ^e Primer pair for checking *hns* null mutants.

11 Sizes of bands detected on the agarose gels shown in FIG S1 are in good agreement
 12 with the prediction.

13

1 **2. Morphology of *E. coli* mutants**

2



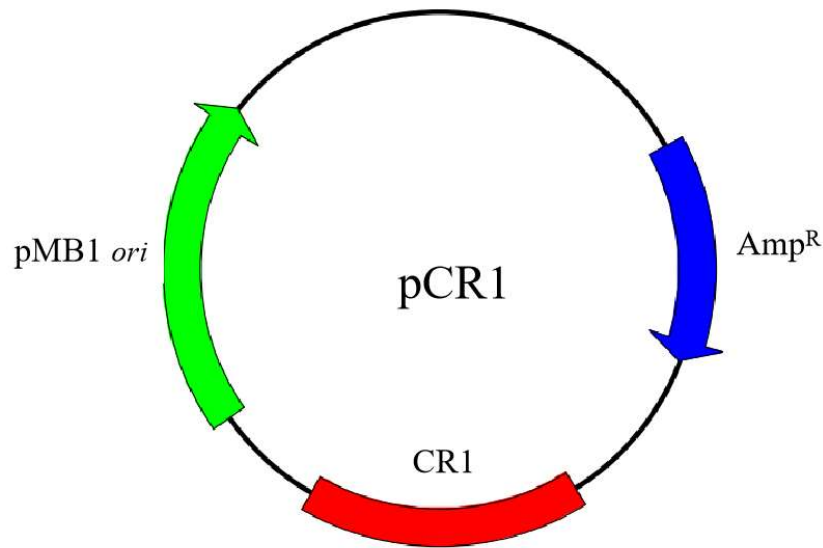
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4

5 **FIG S2 Morphology of constructed *hns* and *stpA* null mutants.** Exponentially
6 growing *E. coli* cells were observed with the phase-contrast microscope (1000 ×). The
7 *hns* null mutant and the *stpA hns* null mutant were obviously longer than the *stpA* null
8 mutant and their WT parent, in line with previous reports (7).

1 **3. Plasmids constructed in this study**

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3

4

5 **Sequences of the CR1 fragment:**

6 5'-GAATTCGAGTTCCCCGCGCCAGCGGGGATAAA **AAG**CTTTCGCAGACGCG
7 **CGGCGATACGCTCACGCA**GAGTTCCCCGCGCCAGCGGGGATAAA **AAGCAG**
8 **CCGAAGCCAAAGGTGATGCCGAACACGCT**GAGTTCCCCGCGCCAGCGGGG
9 ATAAA **AAG**GGCTCCCTGTCGGTTGTAATTGATAATGTTGA GAGTTCCCCGC
10 GCCAGCGGGGATAAAA **AAG**TTTGATCGGGTCTGGAATTTCTGAGCGGTTCGC
11 GAGTTCCCCGCGCCAGCGGGGATAAAA **AAG**AAGCTT-3'

12

13 **FIG S3 Schematic map and sequence of the CRISPR-Cas-targeted plasmid pCR1.**

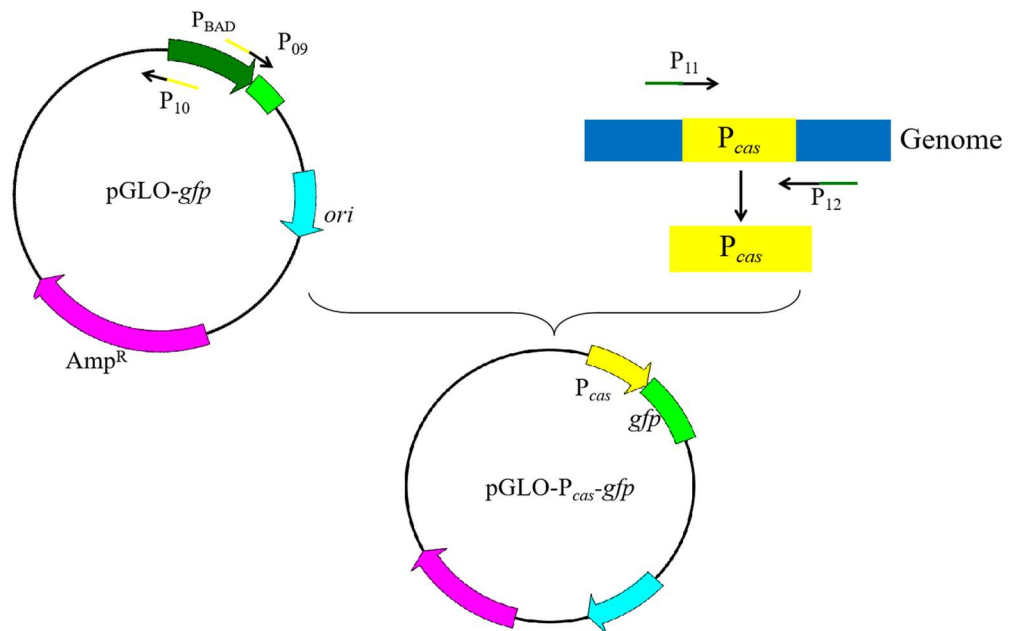
14 PAM sequences are indicated with black letters on green background. Sequences of

15 protospacers are indicated with black letters on red background. The complete sequence

16 of pCR1 is available at the end of the file.

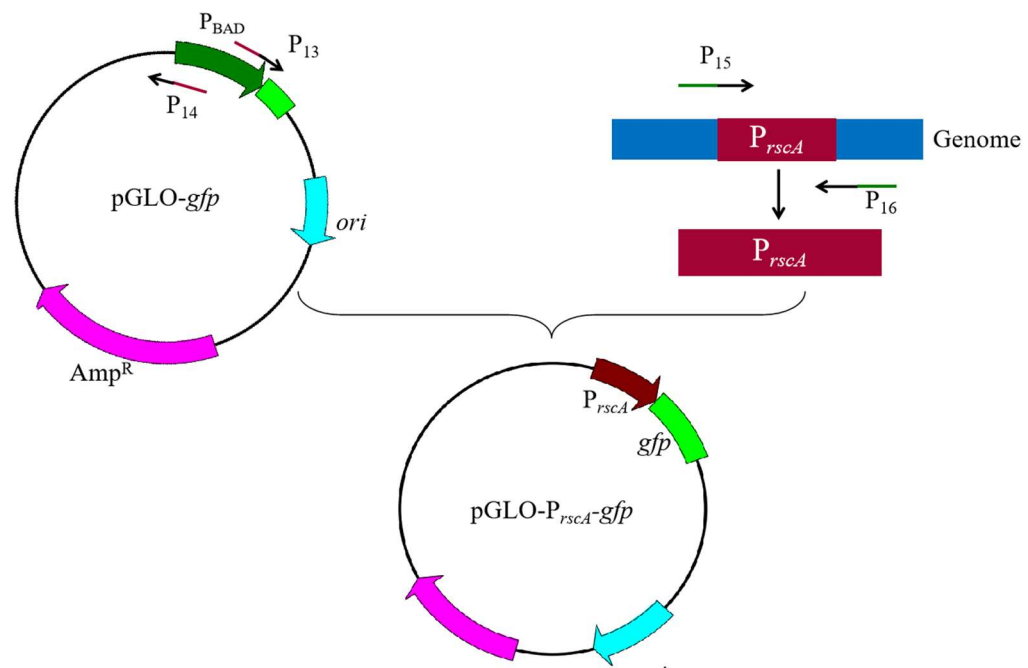
17

1 **A**



2

3 **B**

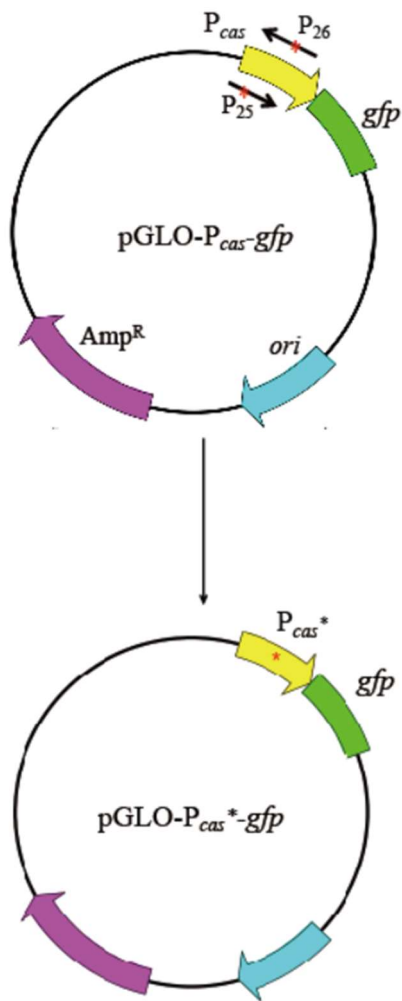


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5

6 **FIG S4 Construction of reporter plasmids pGLO-P_{cas}-gfp and pGLO-P_{rscA}-gfp.**

7



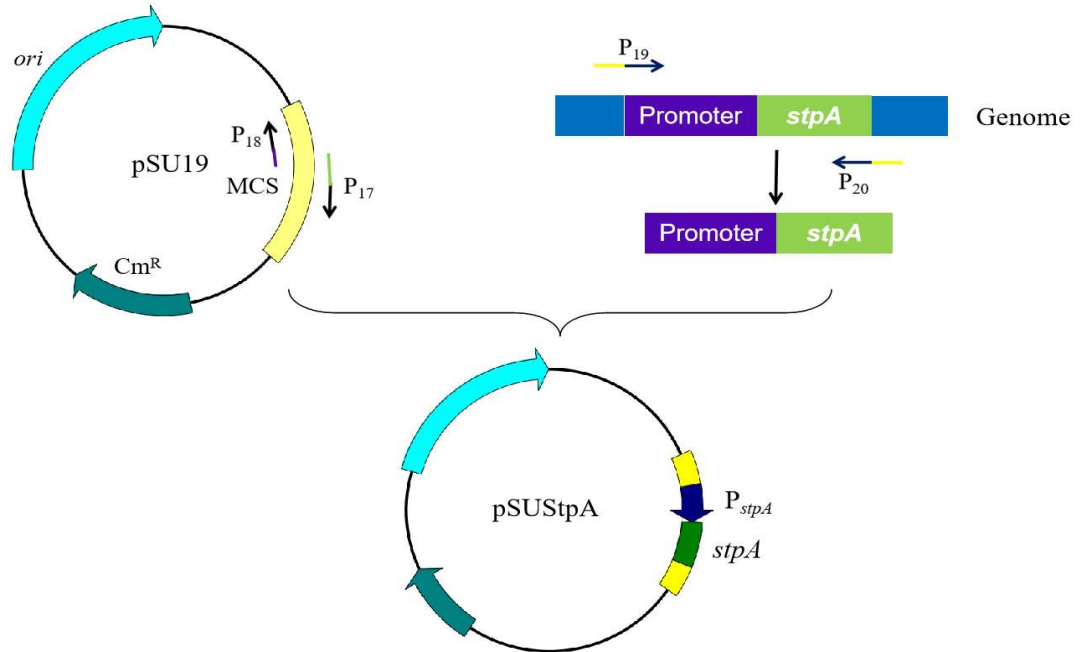
1

2

3 **FIG S5 Construction of pGLO- P_{cas}^* -gfp for identifying DBS for H-NS/StpAin P_{cas} .**

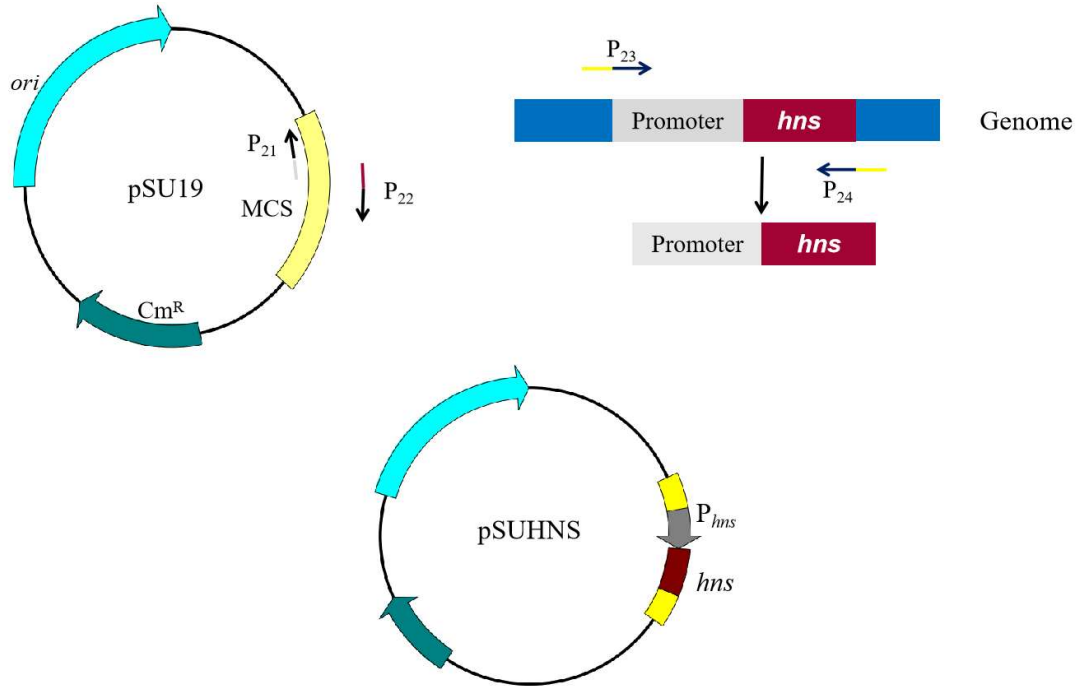
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1 **A**



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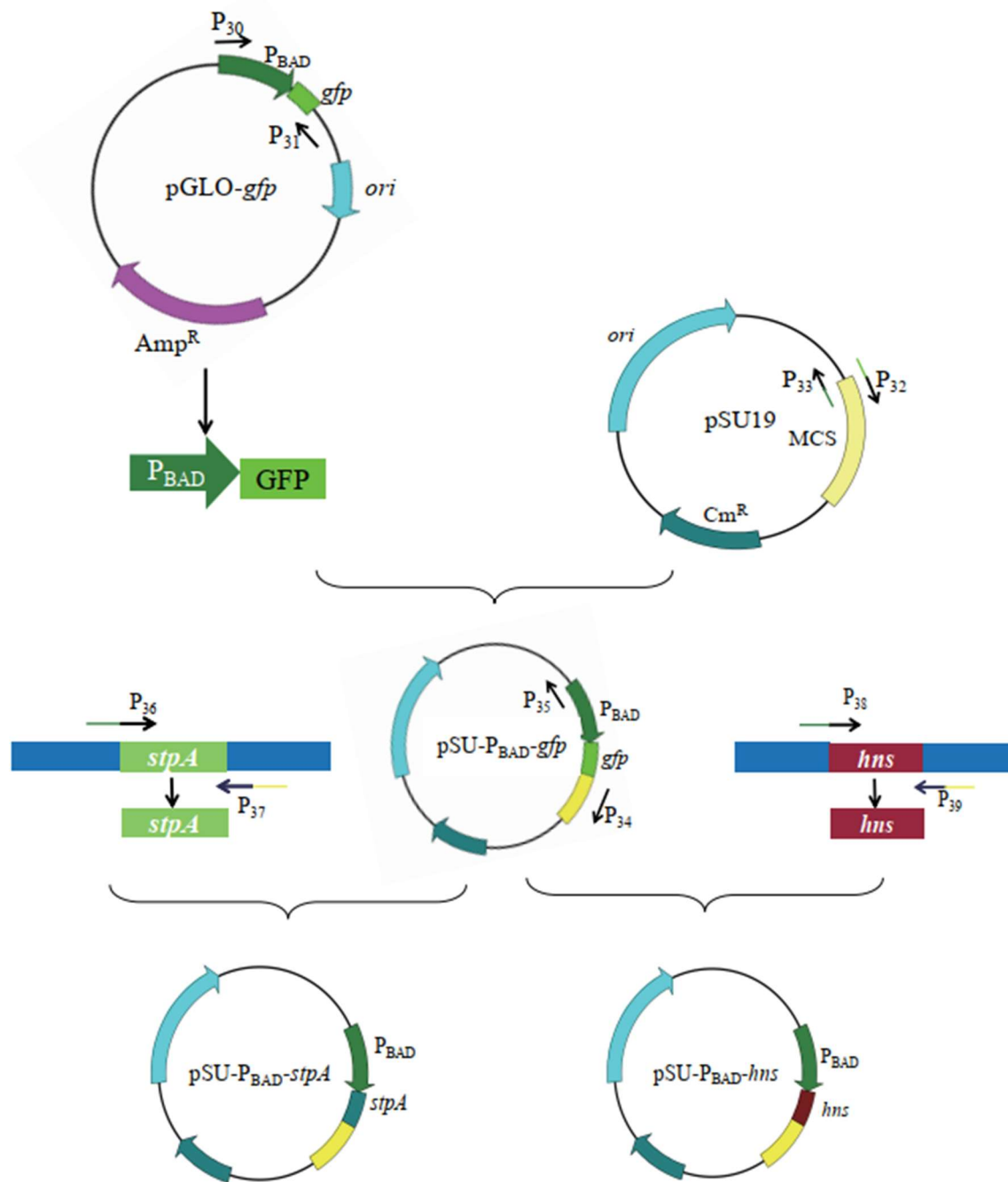
3 **B**



4

5

6 **FIG S6 Construction of pSUStpA and pSUHNS.**



1

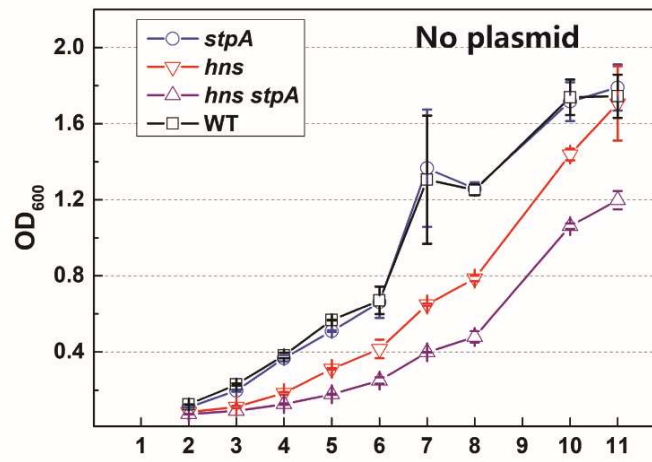
2

3 **FIG S7 Construction of pSU- P_{BAD} -*stpA* and pSU- P_{BAD} -*hns*.**

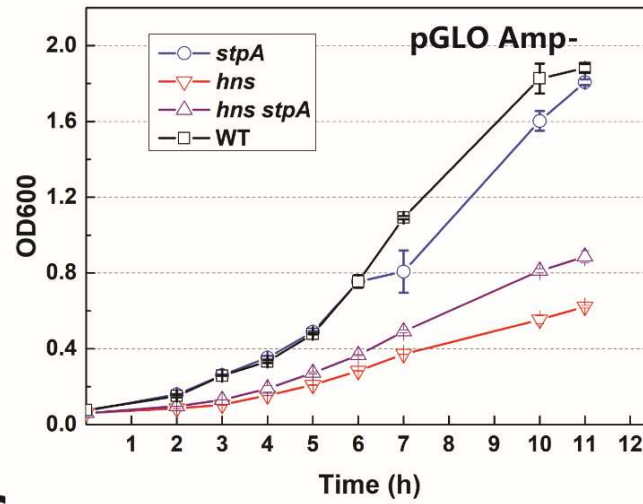
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1 4. Growth of *E. coli* strains in the absence or presence of plasmid.

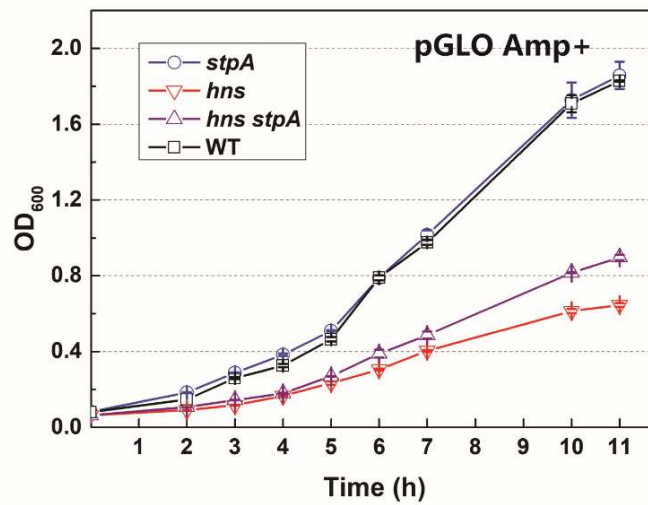
A



B



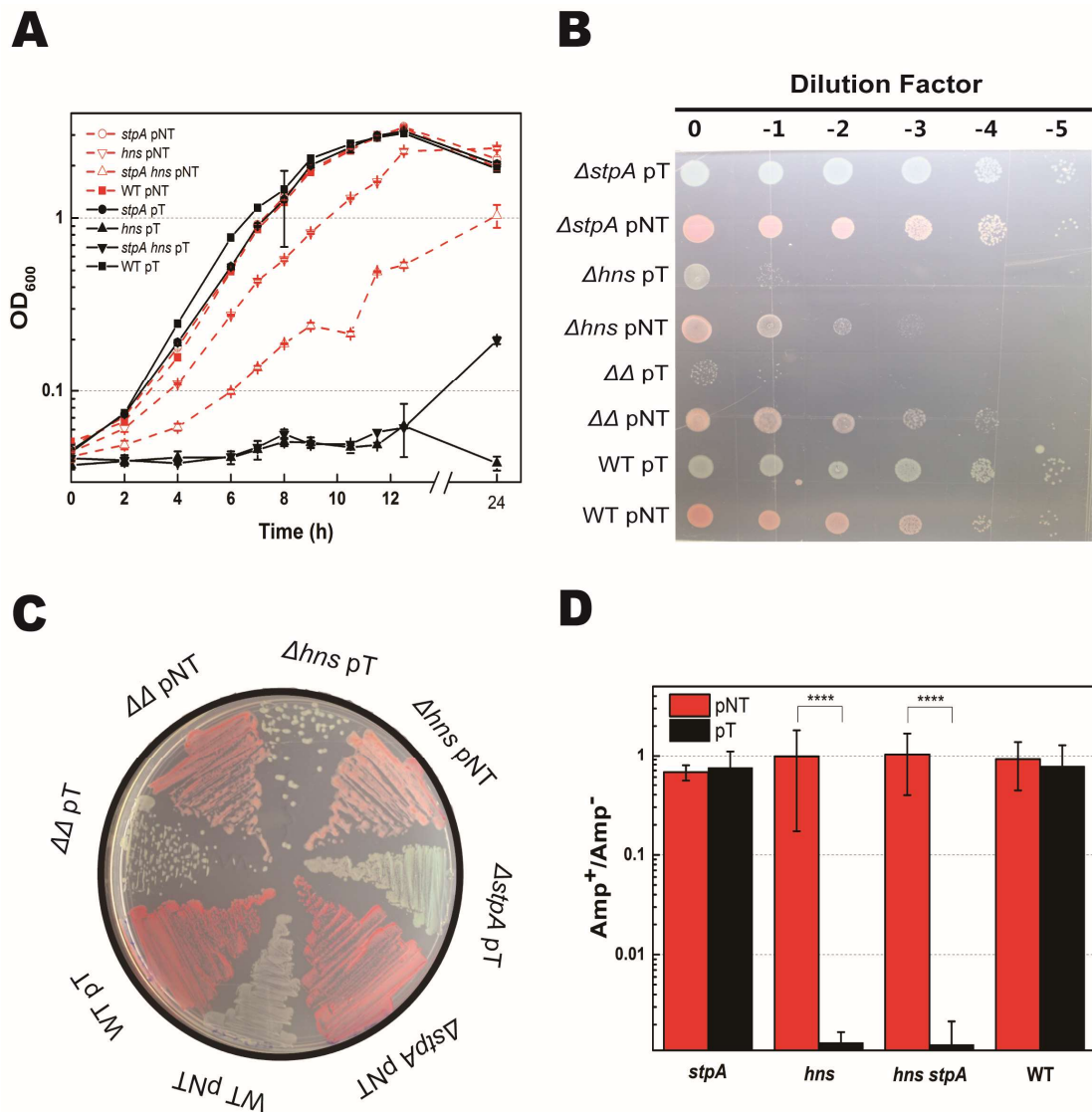
C



1 **FIG S8 Plasmid affects the growth of the *hns* null mutant.** In agreement with
2 previous reports (8, 9), the *hns stpA* null mutant (purple line) grew obviously slower
3 than the *hns* null mutant (red line) in LB broth (A). When a multi-copy-plasmid (pGLO-
4 P_{cas}) was transferred into these strains, growths of the *stpA* mutant, the *stpA hns* null
5 mutant and their parent were not obviously affected in LB supplemented without (B)
6 or with (C) ampicillin (100 µg ml⁻¹). However, the growth of the *hns* null mutant
7 carrying pGLO-P_{cas} was remarkably reduced in LB broth supplemented with or without
8 ampicillin (B, C).

1 **5. CRISPR-Cas-mediated DNA interference after natural transformation**

2



3

4 **FIG S9 Plasmid loss assay in transformants.** (A) Cell growths of transformants

5 carrying the CRISPR-Cas-targeted (pT, black solid lines) and non-targeted (pNT, red

6 dash lines) in LB broth supplemented with ampicillin (100 $\mu\text{g ml}^{-1}$).

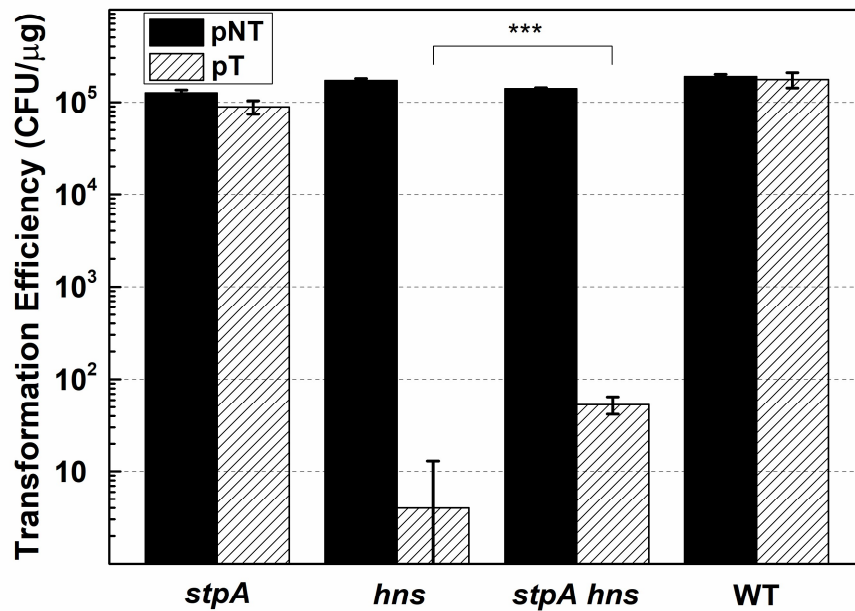
7 (B) Overnight-grown cell cultures with no antibiotic added were serially diluted followed by drop-

8 plating. (C) Overnight-grown cell cultures with no antibiotic added were streaked on

9 LB-agar plates. (D) The ratio of the number of ampicillin resistant colonies to

- 1 ampicillin sensitive colonies in the overnight-grown cell culture (no antibiotic added)
- 2 was calculated. pT: pCR1; pNT: pDsRED. **** $P < 0.001$.
- 3

1 **6. CRISPR-Cas-mediated DNA interference during chemical transformation**



2

3 **FIG S10 Effect of *stpA* inactivation on chemical transformation with CRISPR-**

4 **Cas-targeted plasmid.** Chemically competent cells were prepared by washing

5 exponentially growing cells (OD₆₀₀ 0.4 ~ 0.5) twice with the CaCl₂ solution (100 mM).

6 Washed cells were then resuspended in the CaCl₂ solution. The competent cell

7 suspension was mixed with plasmid on ice before a heat shock at 42 °C for 90 seconds.

8 Transformed cells were recovered in LB medium and spread onto selective LB-agar

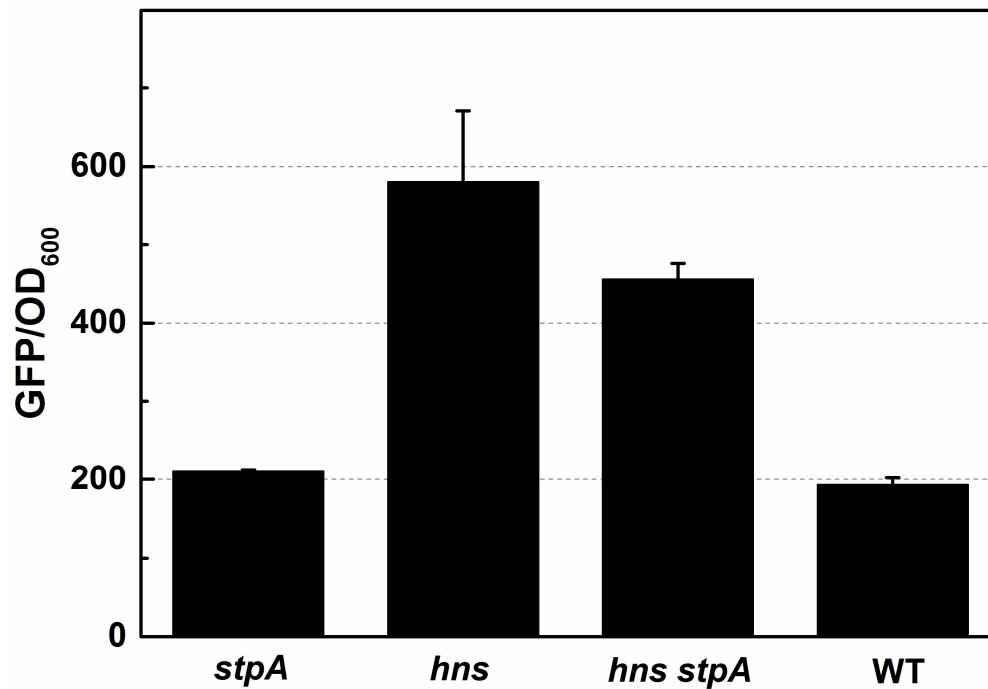
9 plates. Levels of chemical transformation with the CRISPR-Cas-targeted plasmid pCR1

10 (pT) or non-targeted plasmid pDsRED (pNT) was measured in Δhns , $\Delta stpA$, $\Delta hns \Delta stpA$

11 and WT. pT: pCR1; pNT: pDsRED. *** $P < 0.005$.

1 **7. Evaluation of *E. coli* mutants and the reporter system**

2



3

4

5 **FIG S11 Quantification of transcription of *rscA* with the reporter plasmid pGLO-**

6 **P_{rscA} -*gfp*.** By fusing the promoter P_{rscA} with *gfp*, the reporter plasmid pGLO- P_{rscA} -*gfp*

7 was constructed (FIG S4B). We transformed pGLO- P_{rscA} -*gfp* into the *stpA*, *hns*, *hns*

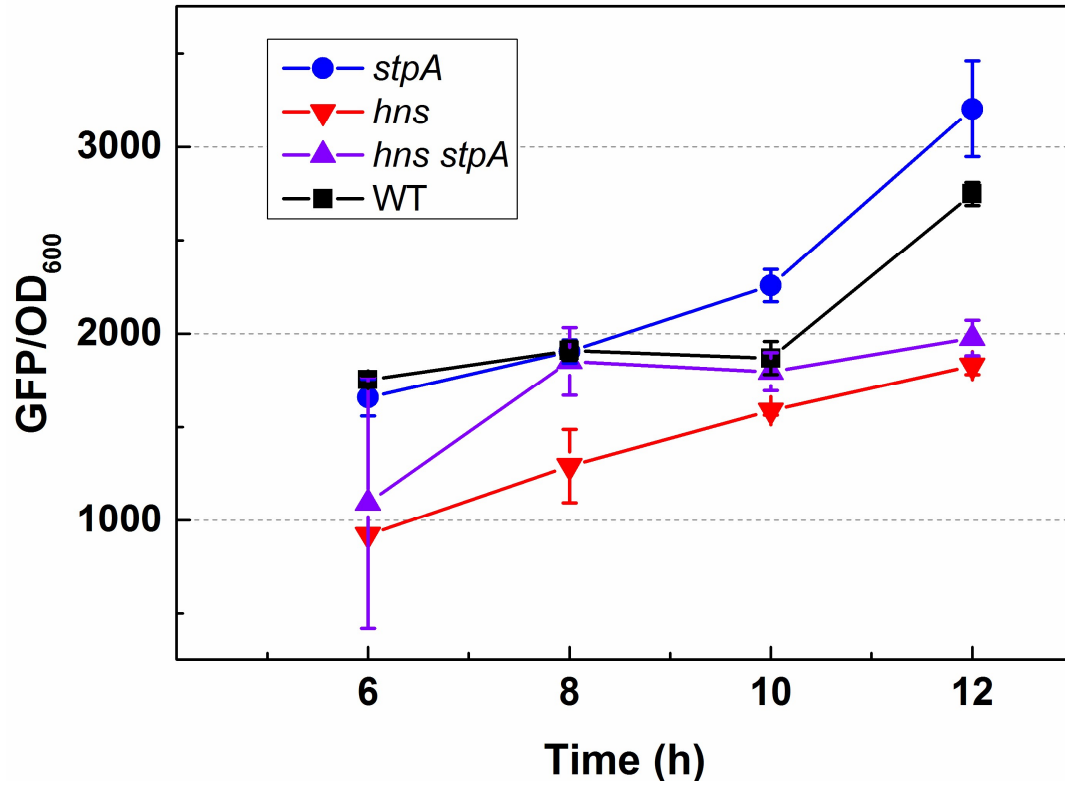
8 *stpA* null mutants and their wildtype parent. Green fluorescence was measured in the

9 cell culture incubated in LB for 24 hours. Data are shown as mean ± SD (n = 3).

10

1 **8. Expression of GFP with a constitutive promoter in *E. coli* strains**

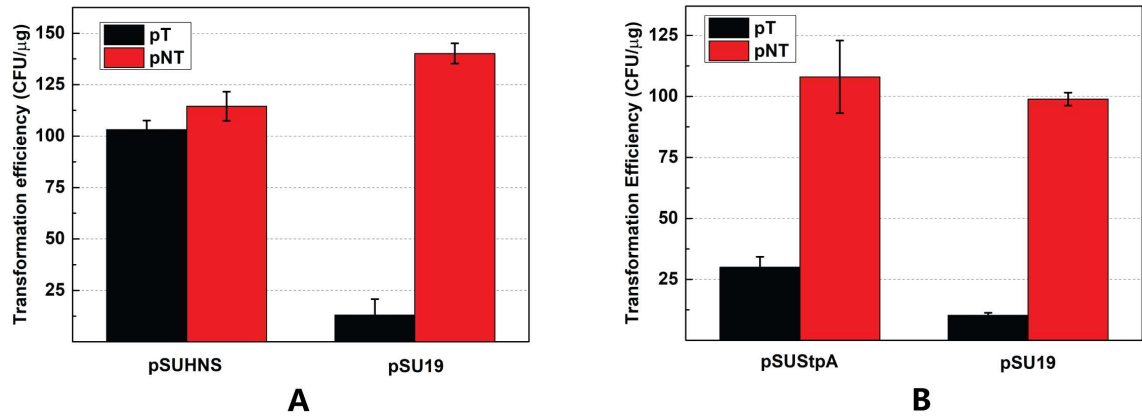
2
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4



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6

7 **FIG S12 Expression of GFP by using P_{J23119} in the *hns* and *stpA* null mutants and**
8 **their wild type parent.** Expression of GFP with the constitutive promoter P_{J23119} were
9 monitored in the *hns*, *stpA* and *hns stpA* null mutants, as well as their wildtype parent
10 (WT). Obviously, intensities of green fluorescence in the *hns* and *hns stpA* null mutants
11 were not higher than that in the *stpA* null mutant and WT.

1 **9. Impact of ectopic expression of H-NS and StpA on CRISPR-Cas-mediated**
2 **immunity against natural transformation during natural transformation**



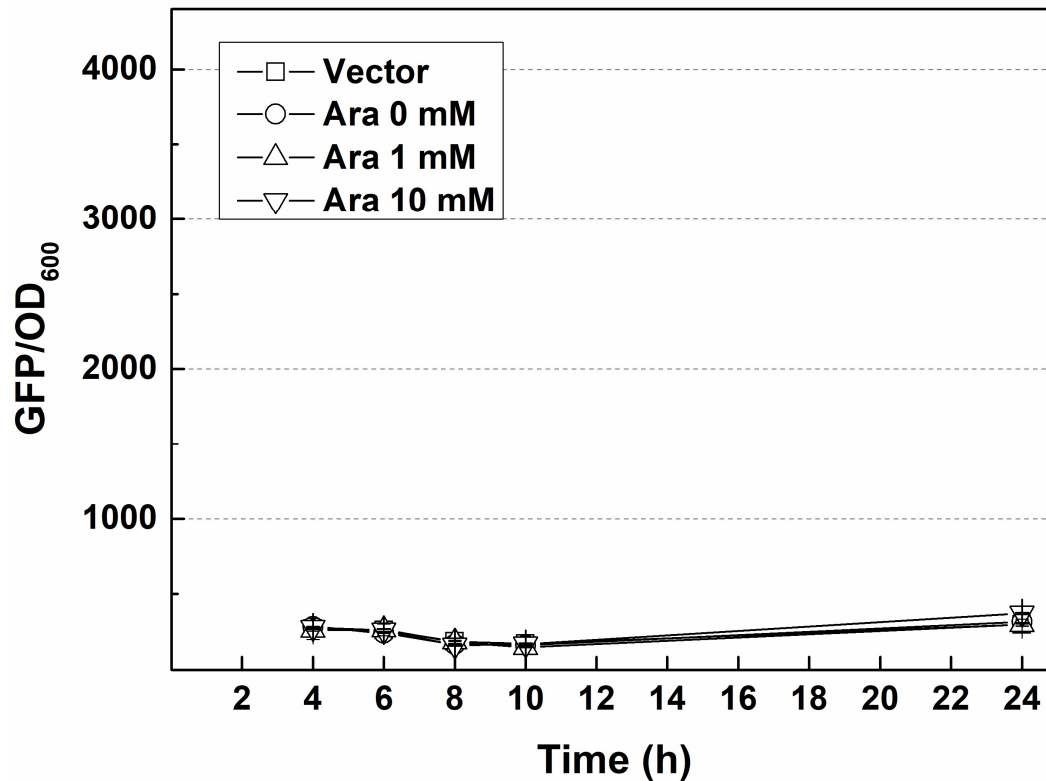
3 **A**

4 **FIG S13 Effect of complementing H-NS and StpA on CRISPR-Cas-mediated DNA**
5 **interference during natural transformation of the *hns stpA* mutant.** Natural
6 transformation was performed by spreading the mixture of the 24-hour incubated of *E.*
7 *coli* culture and plasmid onto LB plates containing 5% (w v⁻¹) agar supplemented with
8 ampicillin (100 μg ml⁻¹). Levels of natural transformation with the CRISPR-Cas-
9 targeted plasmid pCR1 (pT) or non-targeted plasmid pDsRED (pNT) were measured in
10 $\Delta hns \Delta stpA$ carrying either pSUHNS (A) or pSUStpA (B), with the empty vector as the
11 control.

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1 **10. Effect of H-NS expression on the activity of P_{cas} in the *hns stpA* null mutant.**

2



3

4 **FIG S14 Expressing H-NS failed to induce transcription of the *cas* operon.** StpA

5 was found to promote the activity of P_{cas} when it was expressed at a low level in the

6 *hns stpA* null mutant (FIG 5). To evaluate potential effect of H-NS on the activity of

7 P_{cas} in the *hns stpA* null mutant, pSU-P_{BAD}-HNS was constructed to control the

8 expression of H-NS with arabinose (FIG S6) with the empty vector as the control.

9 Transcription of the *cas* operon in the *hns stpA* null mutant harboring pSU-P_{BAD}-HNS

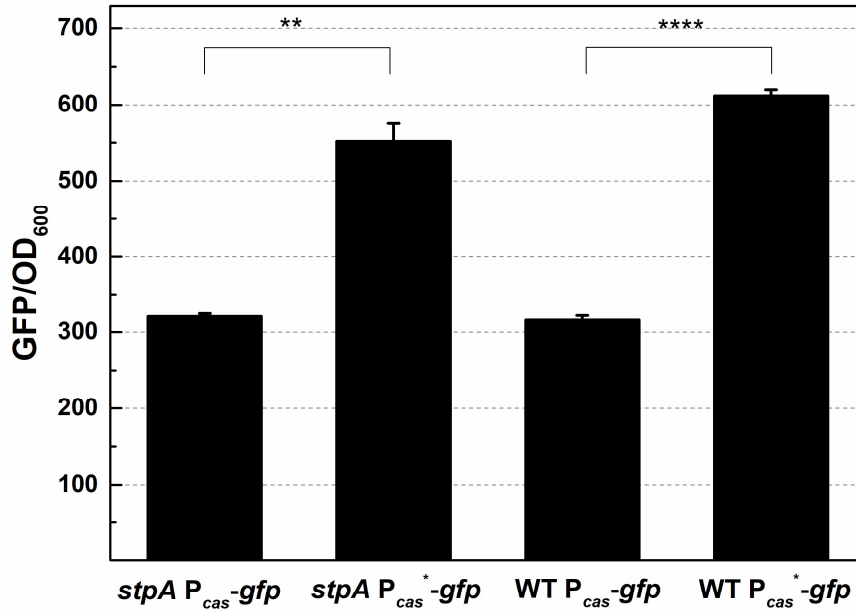
10 was low in M9 medium supplemented with arabinose at any tested concentrations (0

11 mM, 1 mM or 10 mM). Therefore, unlike StpA, expressing H-NS at low or high level

12 failed to promote the activity of P_{cas} in the *hns stpA* null mutant.

13

1 **11. Examination of the DNA binding site of H-NS in the *stpA* null mutant and its**
2 **wildtype parent.**



3

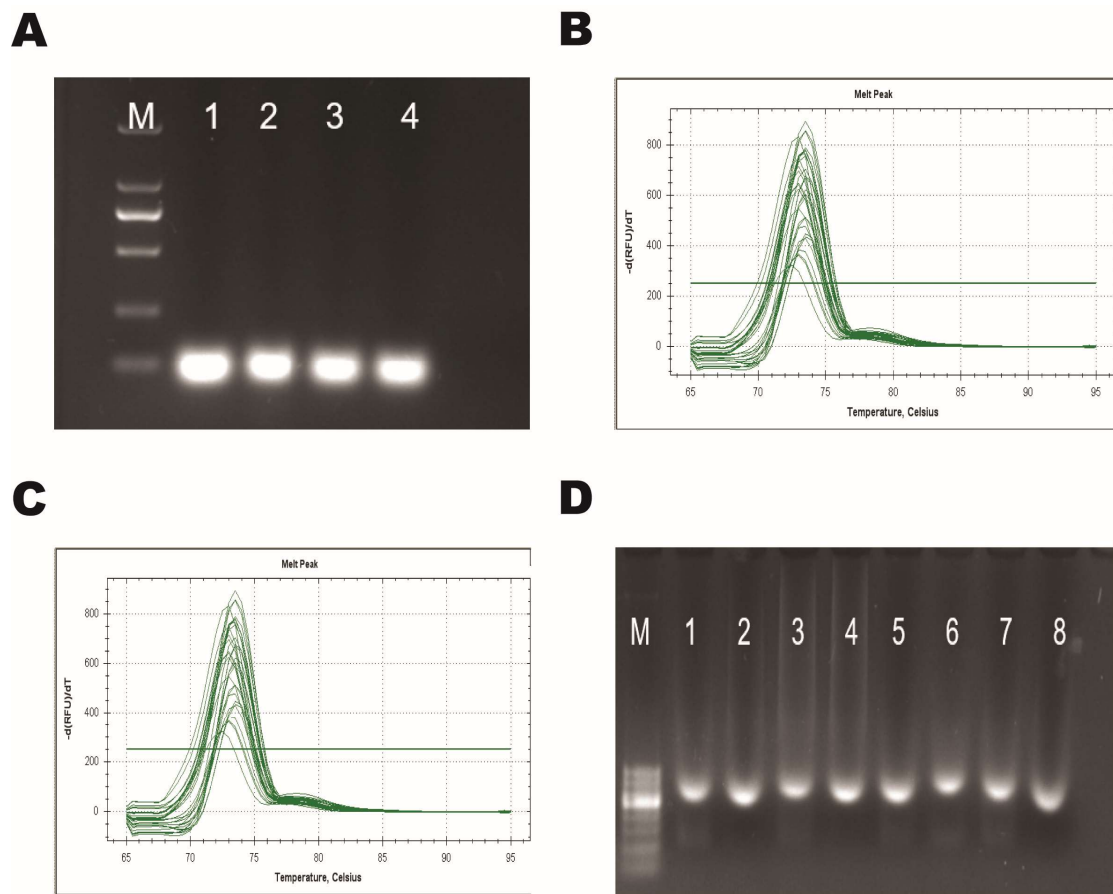
4 **FIG S15 DNA binding site for transcriptional regulation by H-NS.** Activities of
5 *P_{cas}-gfp* and *P_{cas}*-gfp* were compared in the *stpA* null mutant and its wildtype parent
6 that were grown at 30 °C for 24-hour in M9 minimal medium supplemented with 0.32%
7 (w v⁻¹) fructose. Statistical significance was determined using a two tailed Student's
8 test. ** $P \leq 0.01$, **** $P \leq 0.001$.

9

10

1 **12. Evaluation of qPCR-based assays for crRNA quantification**

2



3

4

5 **FIG S16 Examination of purified sRNA and PCR products of transcripts of**

6 **crRNA and tRNA by real-time PCR.** (A) Gel electrophoresis of total RNA. M: 50 bp

7 marker; Lane 1: total sRNA from *ΔstpA*; Lane 2: total sRNA isolated from *Δhns*; Lane

8 3: total sRNA from *ΔstpA Δhns*; Lane 4: total sRNA from WT. (B) Melt curve of reverse

9 transcripts of crRNA. (C) Melt curve of reverse transcripts of tRNA. (D) Gel

10 electrophoresis of RT-PCR products. Lane 1: tRNA of *ΔstpA*; Lane 2: tRNA of *Δhns*;

11 Lane 3: tRNA of *ΔstpA Δhns*; Lane 4: tRNA of WT; Lane 5: crRNA of *ΔstpA*; Lane 6:

12 crRNA of *Δhns*; Lane 7: crRNA of *ΔstpA Δhns*; Lane 8: crRNA of WT; M: 50 bp marker.

13

14

1 **TABLE S2 Natural transformation of *hns stpA* pSU-P_{BAD}-*stpA* with CRISPR-**
 2 **targeted plasmid**
 3

Arabinose (mM)	0	0.5	1	2
TE ^{&} (CFU μg^{-1})	35.5 \pm 7.0	5 \pm 4	N. D.*	N. D.

4

5 [&] TE, Transformation Efficiency.

6 * N. D., Not Detected, < 1 CFU μg^{-1}

7

1 **TABLE S3 Calculation of the cellular concentration of StpA**

Item	Method/Reference	Result
Concentration of StpA-His	Protein assay kit	0.25 mg ml ⁻¹
Concentration of StpA for WB	FIG 5F in the main text	~ 0.025 mg ml ⁻¹
Amount of StpA in 1 ml culture	Proteins from 50 ml culture resuspended in 5 ml PBS	~ 0.0025 mg ml ⁻¹
Viable cell density	Plate counting	~ 5.4 × 10 ⁹ CFU ml ⁻¹
Amount of StpA in each cell	Calculation: 0.0025 mg ml ⁻¹ ÷ 5.4 × 10 ⁹ CFU ml ⁻¹	4.6 × 10 ⁻¹⁶ g
Number of StpA in each cell	Calculation: (4.6 × 10 ⁻¹⁶ g) ÷ (15.3 × 10 ³ Da) × (6.022 × 10 ²³ molecules/mol)	1.8 × 10 ⁴ molecules
StpA : DNA	Calculation: 1.81 × 10 ⁴ molecules : 4.2 × 10 ⁶ bp	~ 1 : 200

2

3

1 SUPPLEMENTAL REFERENCES

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25

26

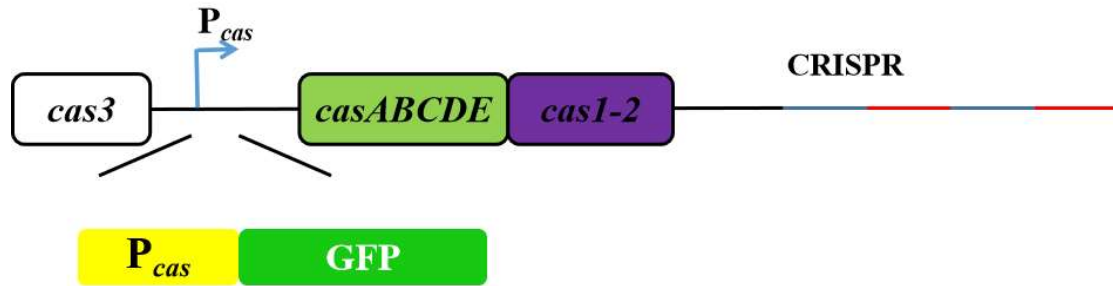
1 **DNA SEQUENCE INFORMATION**

2 **1. Sequence of the type I-E CRISPR-Cas system** (GenBank accession number:

3 NC_000913)

4

5 **From 5' to 3':**



6

7 **FIG S17 Sketch map of type I-E CRISPR-Cas system**

8

9 **The Gene encoding the nuclease**

10 ***cas3* (*ygcB*)**

11 ATGGAACCTTTTAAATATATATGCCATTACTGGGGAAAATCCTCAAAAAGCT
12 TGACGAAAGGAAATGATATTCATCTGTTAATTTATCATTGCCTTGATGTTGCT
13 GCTGTTGCAGATTGCTGGTGGGATCAATCAGTCGTACTGCAAAATACTTTTT
14 GCCGAAATGAAATGCTATCAAACAGAGGGTGAAGGCCTGGCTGTTATTTT
15 TCATTGCTCTTCATGATATTGGAAAGTTTGATATACGATTCCAATATAAATCA
16 GCAGAAAGTTGGCTGAAATTAATCCTGCAACGCCATCACTTAATGGTCCA
17 TCAACACAAATGTGCCGTAATTTAATCATGGTGCAGCCGGTCTGTATTGGT
18 TTAACCAGGATTCACTTTCAGAGCAATCTCTCGGGGATTTTTTCAGTTTTTT
19 TGATGCCGCTCCTCATCCTTATGAGTCCTGGTTTCCATGGGTAGAGGCCGTT
20 ACAGGACATCATGGTTTTATATTACATCCCAGGATCAAGATAAGTCGCGTT
21 GGGAAATGCCAGCTTCTCTGGCATCTTATGCTGCGCAAGATAAACAGGCTC
22 GTGAGGAGTGGATATCTGTAAGCATTATTTTTAACGCCAGCGGGGT
23 TATCTATAAACGATATAACCCTGATTGTTTCATCACTGTTAGCAGGTTTTTGC
24 TCGCTTGCTGACTGGTTAGGCTCCTGGACTACAACGAATACCTTTCTGTTA
25 ATGAGGATGCGCCTTCCGACATAAATGCTCTGAGAACGTATTTCCAGGACC
26 GACAGCAGGATGCGAGCCGGGTATTGGAGTTGAGTGGACTTGTATCAAATA
27 AGCGATGTTATGAAGGTGTTTCATGCACTACTGGACAATGGCTATCAACCCA
28 GACAATTACAGGTGTTAGTTGATGCTCTTCCAGTAGCTCCCGGGCTGACGG
29 TAATAGAGGCACCTACAGGCTCCGGTAAAACGGAAACAGCGCTGGCCTATG
30 CTTGGAAACTTATTGATCAACAAATTGCGGATAGTGTTATTTTTGCCCTCCC
31 AACACAAGCTACCGCGAATGCTATGCTTACGAGAATGGAAGCGAGCGCGA
32 GCCACTATTTTTCATCCCCAAATCTTATTCTTGCTCATGGCAATTCACGGTTT
33 AACCACCTCTTTCAATCAATAAAATCACGCGCGATTACTGAACAGGGGCAA
34 GAAGAAGCGTGGGTTTCAGTGTTGTCAGTGGTTGTCACAAAGCAATAAGAA

1 AGTGTTCCTTGGGCAAATCGGCGTTTGCACGATTGATCAGGTGTTGATATCG
2 GTATTGCCAGTTAAACACCGCTTTATCCGTGGTTTGGGAATTGGTCGAAGTG
3 TTTAATTGTTGATGAAGTTCATGCTTACGACACCTATATGAACGGCTTGCT
4 GGAGGCAGTGCTCAAGGCTCAGGCTGATGTGGGAGGGAGTGTTATTCTTCT
5 TTCCGCAACCCTACCAATGAAACAAAAACAGAACTTCTGGATACTTATGG
6 TCTGCATACAGATCCAGTGGAAAATAACTCCGCATATCCACTCATTAACTGG
7 CGAGGTGTGAATGGTGCGCAACGTTTTGATCTGCTAGCTCATCCAGAACAA
8 CTCCCGCCCCGCTTTTCGATTCAGCCAGAACCTATTTGTTAGCTGACATGT
9 TACCTGACCTTACGATGTTAGAGCGAATGATCGCAGCGGCAAACGCGGGTG
10 CACAGGTCTGTCTTATTTGCAATTTGGTTGACGTTGCACAAGTATGCTACCA
11 ACGGCTAAAGGAGCTAAATAACACGCAAGTAGATATAGATTTGTTTCATGC
12 GCGCTTTACGCTGAACGATCGTCGTGAAAAAGAGAATCGAGTTATTAGCAA
13 TTTCGGCAAAAATGGGAAGCGAAATGTTGGACGGATACTTGTCGCAACCC
14 AGGTCGTGGAACAATCACTCGACGTTGATTTTGATTGGTTAATTACTCAGCA
15 TTGTCCTGCAGATTTGCTTTTCCAACGATTGGGCCGTTTACATCGCCATCAT
16 CGCAAATATCGTCCCCTGGTTTTGAGATTCCCTGTTGCCACCATTTTGCTGC
17 CTGATGGCGAGGGTTACGGACGACATGAGCATATTTATAGCAACGTTAGAG
18 TCATGTGGCGGACGCAGCAACATATTGAGGAGCTTAATGGAGCATCCTTATT
19 TTTCCCTGATGCTTACCGGCAATGGCTGGATAGCATTACGATGATGCGGAA
20 ATGGATGAGCCAGAATGGGTCGGCAATGGCATGGATAAATTTGAAAGCGCC
21 GAGTGTGAAAAAAGGTTCAAGGCTCGCAAGGTCCTGCAGTGGGCTGAAG
22 AATATAGCTTGCAGGATAACGATGAAACCATTCTTGCGGTAACGAGGGATG
23 GGGAAATGAGCCTGCCATTATTGCCCTTATGTACAAACGTCTTCAGGTAAAC
24 AACTGCTCGATGGCCAGGTCTACGAGGACCTAAGTCATGAACAGCAGTATG
25 AGGCGCTTGC ACTTAATCGCGTCAATGTACCCTTCACCTGGAAACGTAGTT
26 TTTCTGAAGTAGTAGATGAAGATGGGTTACTTTGGCTGGAAGGGAAACAGA
27 ATCTGGATGGATGGGTCTGGCAGGGTAACAGTATTGTTATTACCTATACAGG
28 GGATGAAGGGATGACCAGAGTCATCCCTGCAAATCCCAAATAA

29

30 **Genes encoding components of Cascade**

31 *casA (ygcL)*

32 ATGAATTTGCTTATTGATAACTGGATCCCTGTACGCCCGCGAAACGGGGGG
33 AAAGTCCAAATCATAAATCTGCAATCGCTATACTGCAGTAGAGATCAGTGG
34 CGATTAAGTTTGCCCCGTGACGATATGGAACCTGGCCGCTTTAGCACTGCTG
35 GTTTGCATTGGGCAAATTATCGCCCCGGCAAAGATGACGTTGAATTTCGA
36 CATCGCATAATGAATCCGCTCACTGAAGATGAGTTTCAACAACTCATCGCG
37 CCGTGGATAGATATGTTCTACCTTAATCACGCAGAACATCCCTTTATGCAGA
38 CCAAAGGTGTCAAAGCAAATGATGTGACTCCAATGGAAAACTGTTGGCT
39 GGGGTAAGCGGCGCGACGAATTGTGCATTTGTCAATCAACCGGGGCAGGG
40 TGAAGCATTATGTGGTGGATGCACTGCGATTGCGTTATTCAACCAGGCGAAT
41 CAGGCACCAGGTTTTGGTGGTGGTTTTAAAGCGGTTTACGTGGAGGAAC
42 ACCTGTAACAACGTTTCGTACGTGGGATCGATCTTCGTTCAACGGTGTTACTC

1 AATGTCCTCACATTACCTCGTCTTCAAAAACAATTTCTAATGAATCACATA
2 CGGAAAACCAACCTACCTGGATTAAACCTATCAAGTCCAATGAGTCTATAC
3 CTGCTTCGTCAATTGGGTTTGTCCGTGGTCTATTCTGGCAACCAGCGCATAT
4 TGAATTATGCGATCCATTGGGATTGGTAAATGTTCTTGCTGTGGACAGGAA
5 AGCAATTTGCGTTATACCGGTTTTCTTAAGGAAAAATTTACCTTTACAGTTA
6 ATGGGCTATGGCCCCATCCGCATTCCCCTTGTCTGGTAACAGTCAAGAAAG
7 GGGAGGTTGAGGAAAAATTTCTTGCTTTCACCACCTCCGCACCATCATGGA
8 CACAAATCAGCCGAGTTGTGGTAGATAAGATTATTCAAATGAAAATGGAA
9 ATCGCGTGGCGGCGGTTGTGAATCAATTCAGAAATATTGCGCCGCAAAGTC
10 CTCTTGAATTGATTATGGGGGGATATCGTAATAATCAAGCATCTATTCTTGAA
11 CGGCGTCATGATGTGTTGATGTTTAATCAGGGGTGGCAACAATACGGCAAT
12 GTGATAAACGAAATAGTGACTGTTGGTTTGGGATATAAACAGCCTTACGC
13 AAGGCGTTATATACCTTTGCAGAAGGGTTTAAAAATAAAGACTTCAAAGGG
14 GCCGGAGTCTCTGTTTCATGAGACTGCAGAAAGGCATTTCTATCGACAGAGT
15 GAATTATTAATTCCCGATGTAAGTGGCGAATGTTAATTTTTCCAGGCTGATGA
16 GGTAATAGCTGATTTACGAGACAACTTCATCAATTGTGTGAAATGCTATTT
17 AATCAATCTGTAGCTCCCTATGCACATCATCCTAAATTAATAAGCACATTAGC
18 GCTTGCCCGCGCCACGCTATACAAACATTTACGGGAGTTAAAACCGCAAGG
19 AGGGCCATCAAATGGCTGA

20

21 *casB (ygcK)*

22 ATGGCTGATGAAATTGATGCAATGGCTTTATATCGAGCCTGGCAACAACCTGG
23 ATAATGGATCATGTGCGCAAATTAGACGTGTTTCAGAACCTGATGAATTACG
24 CGATATCCCTGCGTTTTATAGGCTGGTGCAACCTTTTGGTTGGGAAAACCCA
25 CGTACCAGCAGGCTCTTTTGCGCATGGTGTGTTTGCCTGAGCGCAGGAAAG
26 AATGTCATCCGACATCAGGACAAAAAATCGGAGCAAACAACAGGTATCTC
27 GTTGGGAAGAGCTTTAGCCAATAGTGGAAGAATTAACGAGCGCCGTATCTT
28 TCAATTAATTCGGGCTGACAGAACAGCCGATATGGTCCAGTTACGTCGATTA
29 CTTACTCACGCCGAACCCGTACTTGACTGGCCATTAATGGCCAGGATGTTG
30 ACCTGGTGGGGAAAGCGCGAACGCCAGCAACTTCTGGAAGATTTGTATT
31 GACCACAAACAAAAATGCGTAA

32

33 *casC (ygcJ)*

34 ATGTCTAACTTTATCAATATTCATGTTCTGATCTCTCACAGCCCTTCATGTCT
35 GAACCGCGACGATATGAACATGCAGAAAGACGCTATTTTCGGCGGCAAAA
36 GACGAGTAAGAATTTCAAGTCAAAGCCTTAAACGTGCGATGCGTAAAAGT
37 GGTTATTACGCACAAAATATTGGTGAATCCAGTCTCAGAACCATTTCATCTTG
38 CACAATTACGTGATGTTCTTCGGCAAAAACCTTGGTGAACGTTTTGACCAAA
39 AAATCATCGATAAGACATTAGCGCTGCTCTCCGGTAAATCAGTTGATGAAGC
40 CGAAAAGATTTCTGCCGATGCGGTTACTCCCTGGGTTGTGGGAGAAATAGC
41 CTGGTTCTGTGAGCAGGTTGCAAAAGCAGAGGCTGATAATCTGGATGATAA
42 AAAGCTGCTCAAAGTTCTTAAGGAAGATATTGCCGCCATACGTGTGAATTT
43 ACAGCAGGGTGTGATATTGCGCTTAGTGGAAGAATGGCAACCAGCGGCAT
44 GATGACTGAGTTGGGAAAAGTTGATGGTGAATGTCCATTGCGCATGCGAT

1 CACTACTCATCAGGTTGATTCTGATATTGACTGGTTCACCGCTGTAGATGAT
2 TTACAGGAACAAGGTTCTGCACATCTGGGAACTCAGGAATTTTCATCGGGT
3 GTTTTTTATCGTTATGCCAACATTAACCTCGCTCAACTTCAGGAAAATTTAG
4 GTGGTGCCTCCAGGGAGCAGGCTCTGGAAATTGCAACCCATGTTGTTTATA
5 TGCTGGCAACAGAGGTCCCTGGAGCAAAACAGCGTACTTATGCCGCTTTTA
6 ACCCTGCGGATATGGTAATGGTTAATTTCTCCGATATGCCACTTTCTATGGCA
7 AATGCTTTTGAAAAAGCGGTTAAAGCGAAAGATGGCTTTTTTGCAACCGTCT
8 ATACAGGCGTTAATCAATATTGGGATCGCGTTGCCAATGGATATGGTCTGA
9 ACGGAGCTGCTGCGCAATTCAGCTTATCTGATGTAGACCCAATTACTGCTCA
10 AGTTAAACAAATGCCTACTTTAGAACAGTTAAAATCCTGGGTTTCGTAATAAT
11 GGCGAGGCGTGA

12

13 *casD (ygcI)*

14 GTGAACATGAGATCTTATTTGATCTTGCGGCTTGCTGGGCCAATGCAAGCCT
15 GGGGGCAGCCGACCTTTGAAGGAACGCGACCTACCGGAAGATTTCCGACC
16 CGAAGCGGGTTATTAGGGCTACTCGGGGCTTGTCTTGGGATCCAACGTGAT
17 GATACTTCTTCATTACAGGCGTTATCAGAGAGTGTGCAATTTGCAGTGCCT
18 GCGATGAACTCATTCTTGACGATCGTCGTGTGTCTGTAACGGGGTTGCGTG
19 ATTACCATACAGTCCTTGGAGCGCGAGAAGATTACCGTGGTTTGAAAAGTC
20 ATGAAACGATTCAAACATGGCGCGAATATTTATGTGATGCCTCCTTTACCGT
21 CGCTCTCTGGTTAACACCCCATGCAACGATGGTTATCTCAGAACTTGAAAA
22 AGCAGTATTAAGCCTCGGTATACACCTTACCTGGGGCGGAGAAGTTGCCC
23 ACTAACACACCCGCTTTTTTTGGGGACATGTCAGGCATCGGATCCTCAGAA
24 GGCGCTATTAATTATGAGCCCGTTGGCGGCGATATATATAGTGAGGAATCA
25 GTTACAGGGCATCATTTAAAATTTACGGCGCGCGACGAACCGATGATCACC
26 TTGCCTCGACAATTTGCTTCCCGAGAATGGTATGTGATTAAGGAGGTATGG
27 ATGTATCTCAGTAA

28

29 *casE (ygcH)*

30 ATGTATCTCAGTAAAGTCATCATTGCCAGGGCCTGGAGCAGGGATCTTTACC
31 AACTTCACCAGGGATTATGGCATTATTTCCAAACAGACCGGATGCTGCTCG
32 TGATTTTCTTTTTTCATGTTGAGAAGCGAAACACACCAGAAGGCTGTCATGT
33 TTTATTGCAGTCAGCGCAAATGCCTGTTTCAACTGCCGTTGCGACAGTCATT
34 AAAACTAAACAGGTTGAATTTCAACTTCAGGTTGGTGTTCCTACTTATTTTC
35 GGCTTCGGGCAAATCCGATCAAACTATTCTCGACAATCAAAGCGCCTGG
36 ACAGTAAAGGGAATATTAACGCTGTCGGGTTCCGTTAATAAAAAGAAGCAG
37 AACAAATCGCGTGGTTGCAACGTAAATTGGGCAATGCGGCGCGCGTTGAA
38 GATGTGCATCCCATATCGGAACGGCCACAGTATTTTTCTGGTGATGGTAAAA
39 GTGGAAAGATCCAAACGGTTTGCTTTGAAGGTGTGCTCACCATCAACGAC
40 GCGCCAGCGTTAATAGATCTTGTACAGCAAGGTATTGGGCCAGCTAAATCG
41 ATGGGATGTGGCTTGCTATCTTTGGCTCCACTGTGA

42

43 **Genes encoding Cas1 and Cas2 which are involved in adaption**

1 *cas1 (ygbT)*
2 ATGACCTGGCTTCCCCTTAATCCCATTCCACTCAAAGATCGCGTCTCCATGA
3 TCTTTCTGCAATATGGGCAGATCGATGTAATAGATGGCGCGTTTGTACTTATC
4 GACAAGACAGGGATCCGCACTCATATTCCTGTTGGCTCGGTTGCCTGCATC
5 ATGCTGGAACCTGGTACACGGGTTTCGCATGCAGCTGTACGCCTGGCTGCG
6 CAAGTTGGAACATTGTTGGTATGGGTGGGGGAAGCGGGCGTTCGTGTTTAT
7 GCTTCTGGTCAGCCTGGAGGTGCGCGTTCAGATAAGCTGCTCTATCAGGCA
8 AAAGTTGCTCTGGATGAAGATTTGCGTCTGAAGGTCGTACGTAAAATGTTT
9 GAACTTCGGTTTGGAGAACCTGCGCCTGCCCGGCGCTCCGTAGAGCAACT
10 CAGAGGTATAGAAGGCAGTCGCGTGCGGGCAACCTACGCACTTCTGGCGA
11 AGCAATACGGCGTGACATGGAATGGACGTCGCTACGATCCGAAAGACTGG
12 GAAAAGGGCGATACGATCAACCAATGCATTAGCGCTGCAACTTCTGTTTA
13 TACGGCGTAACTGAAGCGGGGATACTTGCAGCTGGTTATGCACCAGCTATT
14 GGGTTTGTGCATACAGGAAAGCCTCTTTCCTTTGTTTACGATATTGCAGACA
15 TCATTAATTTGACACTGTTGTACCGAAAGCTTTTGAGATAGCGCGTCGTAA
16 CCCTGGTGAGCCGGACCGGGAAGTCCGTTTGGCGTGCAGGGATATTTTTCG
17 CAGTAGTAAAACATTAGCCAAATTGATTCCGCTTATAGAGGACGTGCTTGCC
18 GCTGGAGAAATACAACCGCCGGCCCCACCTGAAGATGCACAGCCTGTTGC
19 CATTCCGCTTCTGTTTCACTGGGAGATGCAGGCCATCGGAGTAGCTGA

20
21 *cas2 (ygbF)*
22 ATGAGTATGTTGGTCGTGGTCACTGAAAATGTACCTCCGCGCTTACGAGGC
23 AGATTAGCCATCTGGTTGTTGGAGGTACGTGCAGGGGTATATGTAGGTGATG
24 TATCCGCAAAAATTCGTGAAATGATCTGGGAACAAATAGCTGGACTGGCGG
25 AAGAAGGCAATGTAGTGATGGCATGGGCAACGAATACGGAAACGGGATTT
26 GAGTTCCAGACATTTGGGTTAAACAGGCGTACCCCGGTAGATTTGGATGGT
27 TTAAGGTTGGTGTCTTTTTTACCTGTTTGA

28
29 **CRISPR array I** (Repeats are indicated with black letters on yellow background.

30 Spacers are indicated with black letters on green background)

31
32 **From 5' to 3':**

33 TGGGAACAAATAGCTGGACTGGCAGGAAAGAAGGCAATGTAGTGATGGCATG
34 GGCAACGAATACGGAAACGGGATTTGAGTTCCAGACATTTGGGTTAAACA
35 GCGTACCCCGGTAGATTTGGATGGTTTAAAGGTTGGTGTCTTTTTTACCTGT
36 TTGAAAACAAAGAATTAGCTGATCTTTAATAATAAGGAAATGTTACATTAAG
37 GTTGGTGGGTTGTTTTTATGGGAAAAAATGCTTTAAGAACAAATGTATACTT
38 TTAGA**GAGTTCCCCGCGCCAGCGGGGATAAACCGCTTTCGCAGACGCGCG**
39 **GCGATACGCTCACGCA**GAGTTCCCCGCGCCAGCGGGGATAAACCG**CAGCC**
40 **GAAGCCAAAGGTGATGCCGAACACGCT**GAGTTCCCCGCGCCAGCGGGGAT
41 **AAACCGGGCTCCCTGTCGGTTGTAATTGATAATGTTGAGAGTTCCCCGCGC**
42 **CAGCGGGGATAAACCGTTTGGATCGGGTCTGGAATTTCTGAGCGGTCGCGA**
43 **GTTCCCCGCGCCAGCGGGGATAAACCGCGAATCGCGCATAACCTGCGCGTC**

1 GCCGCCTGC GAGTTC CCGCGCCAGCGGGGATAAACCG TCAGCTTTATAAA
2 TCCGGAGATACGGAAACTAGAGTTC CCGCGCCAGCGGGGATAAACCGGA
3 CTCACCCCGAAAGAGATTGCCAGCCAGCTT GAGTTC CCGCGCCAGCGGG
4 GATAAACCG CTGCTGGAGCTGGCTGCAAGGCAAGCCGCCA GAGTTC CCG
5 GCGCCAGCGGGGATAAACCG GGGGGCGCATGACCGTAAACATTATCCCCCG
6 GGAGTTC CCGCGCCAGCGGGGATAAACCG GGAGTTCAGACATAGGTGGA
7 ATGATGGACTACGAGTTC CCGCGT TAGCGGGGATAAACCGCCCGGTAGCC
8 AGGTTTGCAACGCCTGAACCGAGAGTTC CCGCGCCAGCAGGGATAAACCC
9 GGCAACGACGGTGAGATTTACGCCTGACGCTGGTGTTCCCGCATCAGC
10 GGGGATAAACCGGGCGCACTGGATGCGATGATGGATATCACTTGGAGTTCC
11 CCCGCCTCTGCGGTAGAACTCCCAGCTCCCATTTTCAAACCCATCAAGACG
12 CCTTCGCCAACTCCTTCACCAGAGGTAGCATTATCCGCATA
13

1 **3. Sequence of the promoter of the *cas* operon** (GenBank accession number:
2 NC_000913; TSS: Transcription Start Site)

3
4 **From 5' to 3':**

5 TTAT CAATG ACGAT AATAA GACCA ATAAC GGTTT ATCCC TACTT AAGTA

6 ⁻³⁵⁰
GGGAA GGTGC ACAAT GTACA TCTTC TTTA ATTTC CCGGT ATGAG

7 ⁻³⁰⁰
ATTTT ATATT CACAG TATGA ATATTT TATGTA ATAAA ATTCAT GGTA

8 ⁻²⁵⁰ **H-NS Binding Site**
TTATT ATAAC TAAAA GTTTC TTTAA TAATA AAACG AATAA CTTGC

9 ⁻²⁰⁰ **TSS**
AGATT TGAAA TGCAT GCATT ATTGT CTTTA ACAA TTCAA CACAT

10 ⁻¹⁵⁰
CTTAA TATAT GTATA GGTTA ATTGT ATTAA ACCAA TGAAT ATATT TTTGC

11 ⁻¹⁰⁰
AGTGA ATGTG ATTAT TGAAT TAATT ACGCC GTATT TTTTC TTTGT TTTA

12 ⁻⁵⁰
CCGAT AACGG AAGTG TGCCG ACGTA TAGAA ATGCA GGAGA AATGT

13 ⁻¹
CGGAG CATAT GAAGG AGAACAA

14

15

16

1 **4. Complete Sequence of pCR1** (AddGene accession number: 154270; repeats
2 and PAMs are on red and green backgrounds respectively)

3

4 **From 5' to 3':**

5 TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGG
6 AGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGT
7 CAGGGCGCGTCAGCGGGTGTGGCGGGTGTTCGGGGCTGGCTTAACTATGC
8 GGCATCAGAGCAGATTGTAAGTGCACCATATGCGGTGTGAAATACC
9 GCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAG
10 GCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACG
11 CCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGC
12 CAGGGTTTTCCAGTCACGACGTTGTAACGACGGCCAGTGGAATTCGA
13 GTTCCCCGCGCCAGCGGGGATAAAAGCTTTCGCAGACGCGCGGGCGATAC
14 GCTCACGCAAGTTCCCCGCGCCAGCGGGGATAAAAGCAGCCGAAGCCA
15 AAGGTGATGCCGAACACGCTGAGTTCCCCGCGCCAGCGGGGATAAAAGG
16 GCTCCCTGTCGGTTGTAATTGATAATGTTGAGAGTTCCCCGCGCCAGCGGG
17 GATAAAAGTTTGGATCGGGTCTGGAATTTCTGAGCGGTCGCAGTTCCCC
18 CGCCAGCGGGGATAAAAGAAAGCTTAGCTTGGCGTAATCATGGTCATAGC
19 TGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCACACAACATACGAGC
20 CGGAAGCATAAAGTGTAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA
21 CATTAAATTGCGTTGCGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCGT
22 GCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTTCGT
23 ATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTT
24 GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA
25 CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA
26 AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGC
27 TCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGG
28 CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCC
29 CTCGTGCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCT
30 TTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCT
31 CAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC
32 CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAC
33 CCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT
34 AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC
35 TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA
36 GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA

1 CCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA
2 GAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG
3 CTCAGTGGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGAGATTATCAA
4 AAAGGATCTTCACCTAGATCCTTTTAAATTA AAAATGAAGTTTTAAATCAAT
5 CTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGT
6 GAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTCCATAGTTGCCTGAC
7 TCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCA
8 GTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAG
9 CAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACT
10 TTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTA
11 GTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGT
12 GGTGTCACGCTCGTCGTTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACG
13 ATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTC
14 CTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACT
15 CATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGAT
16 GCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTAT
17 GCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCC
18 ACATAGCAGA ACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCG
19 AAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCAC
20 TCGTGCACCCA ACTGATCTTCAGCATCTTTTACTTTACCAGCGTTTCTGGG
21 TGAGCAAAAACAGGAAGGCAAAAATGCCGCAAAAAGGGAATAAGGGCGA
22 CACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATT
23 TATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAA
24 TAAACAAATAGGGGTTCGCGCACATTTCCCCGAAAAGTGCCACCTGACGT
25 CTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACG
26 AGGCCCTTTCGTC

27

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1 **5. Complete Sequence of pDsRed** (sequence of *rfp* marked on red background)

2 Available in the website: <http://www.biofeng.com/zaiti/dachang/pDsRed-Express2.html>

3

4 **From 5' to 3':**

5 AGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAAT
6 GCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCAA
7 CGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTT
8 ATGCTTCCGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACA
9 CAGGAAACAGCTATGACCATGATTACGCCAAGCTTGCATGCCTGCAGGTCG
10 ACTCTAGAGGATCCCCGGGTACCGGTCGCCACC **ATGGATAGCACTGAGAAC**
11 **GTCATCAAGCCCTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAAC**
12 **GGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCAAGCCCTACGAGG**
13 **GCACCCAGACCGCCAAGCTGCAGGTGACCAAGGGCGGCCCCCTGCCCTTC**
14 **GCCTGGGACATCCTGTCCCCCAGTTCCAGTACGGCTCCAAGGTGTACGTG**
15 **AAGCACCCCGCCGACATCCCCGACTACAAGAAGCTGTCTTCCCCGAGGG**
16 **CTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGTTGACCG**
17 **TGACCCAGGACTCCTCCCTGCAGGACGGCACCTTCATCTACCACGTGAAGT**
18 **TCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACTC**
19 **TGGGCTGGGAGCCCTCCACCGAGCGCTGTACCCCCGCGACGGCGTGCTG**
20 **AAGGGCGAGATCCACAAGGCGCTGAAGCTGAAGGGCGGCGGCCACTACCT**
21 **GGTGGAGTTCAAGTCAATCTACATGGCCAAGAAGCCCGTGAAGCTGCCCG**
22 **GCTACTACTACGTGGACTCCAAGCTGGACATCACCTCCACAACGAGGACT**
23 **ACACCGTGGTGGAGCAGTACGAGCGCGCCGAGGCCCGCCACCACCTGTTT**
24 **CAGTAG**CGGCCGCGACTCTAGAATTCCAAGTGAAGCGCCGGTTCGCTACCATT
25 ACCAACTTGTCTGGTGTCAAAAATAATAGGCCTACTAGTCGGCCGTACGGG
26 CCCTTTCGTCTCGCGCGTTCGGTGTGACGGTGAAAACCTCTGACACATG
27 CAGCTCCCGGAGACGGTACAGCTTGTCTGTAAGCGGATGCCGGGAGCAG
28 ACAAGCCCGTCAGGGCGCGTACGCGGGTGTGGCGGGTGTCCGGGGCTGGC
29 TTAATATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT
30 GTGAAATACCGCACAGATGCGTAAGGAGAAAATAACCGCATCAGGCGGCCTT
31 AAGGGCCTCGTGATACGCCTATTTTTATAGGTTAATGTCATGATAATAATGGT
32 TTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTAT
33 TTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAAC
34 CCTGATAAATGCTTCAATAATATTGAAAAGGAAGAGTATGAGTATTCAACA
35 TTTCCGTGTCGCCCTTATCCCTTTTTTGCGGCATTTCCTTCCCTGTTTTTG
36 CTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGGT
37 GCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAG
38 AGTTTTCGCCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTG
39 CTATGTGGCGCGGTATTATCCCGTATTGACGCCGGGCAAGAGCAACTCGGT
40 CGCCGCATACACTATTCTCAGAATGACTTGGTTGAGTACTACCAGTCACA
41 GAAAAGCATCTTACGGATGGCATGACAGTAAGAGAATTATGCAGTGCTGCC
42 ATAACCATGAGTGATAACACTGCGGCCAACTTACTTCTGACAACGATCGGA
43 GGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAAC

1 CGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGA
2 GCGTGACACCACGATGCCTGTAGCAATGGCAACAACGTTGCGCAAACCTATT
3 AACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGAT
4 GGAGGCGGATAAAGTTGCAGGACCCTTCTGCGCTCGGCCCTTCCGGCTG
5 GCTGGTTTATTGCTGATAAATCTGGAGCCGGTGAGCGTGGGTCTCGCGGTAT
6 CATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTAC
7 ACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGA
8 GATAGGTGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTC
9 ATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAAGGATCTAGGT
10 GAAGATCCTTTTTGATAATCTCATGACCAAATCCCTAACGTGAGTTTTTCG
11 TTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGAT
12 CCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTA
13 CCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAG
14 GTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTTCTTCTAGTGTAG
15 CCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTC
16 GCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGT
17 CTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCG
18 GGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTA
19 CACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCC
20 CGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACA
21 GGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAG
22 TCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCG
23 TCAGGGGGGCGGAGCCTATGGAAAACGCCAGCAACGCGGCCTTTTTACG
24 GTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCC
25 CTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCTGATACCGCTCG
26 CCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAA
27 G
28
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