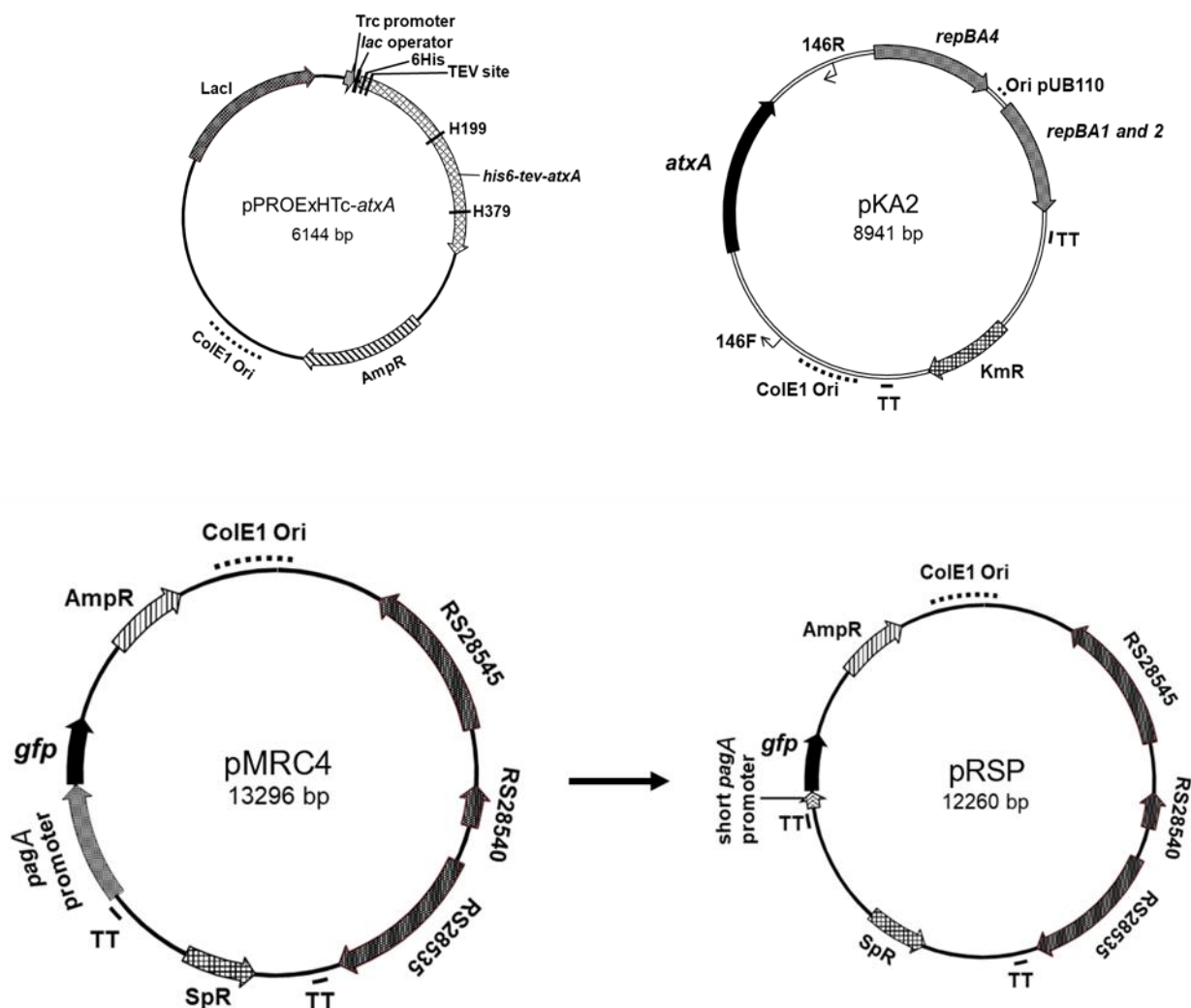
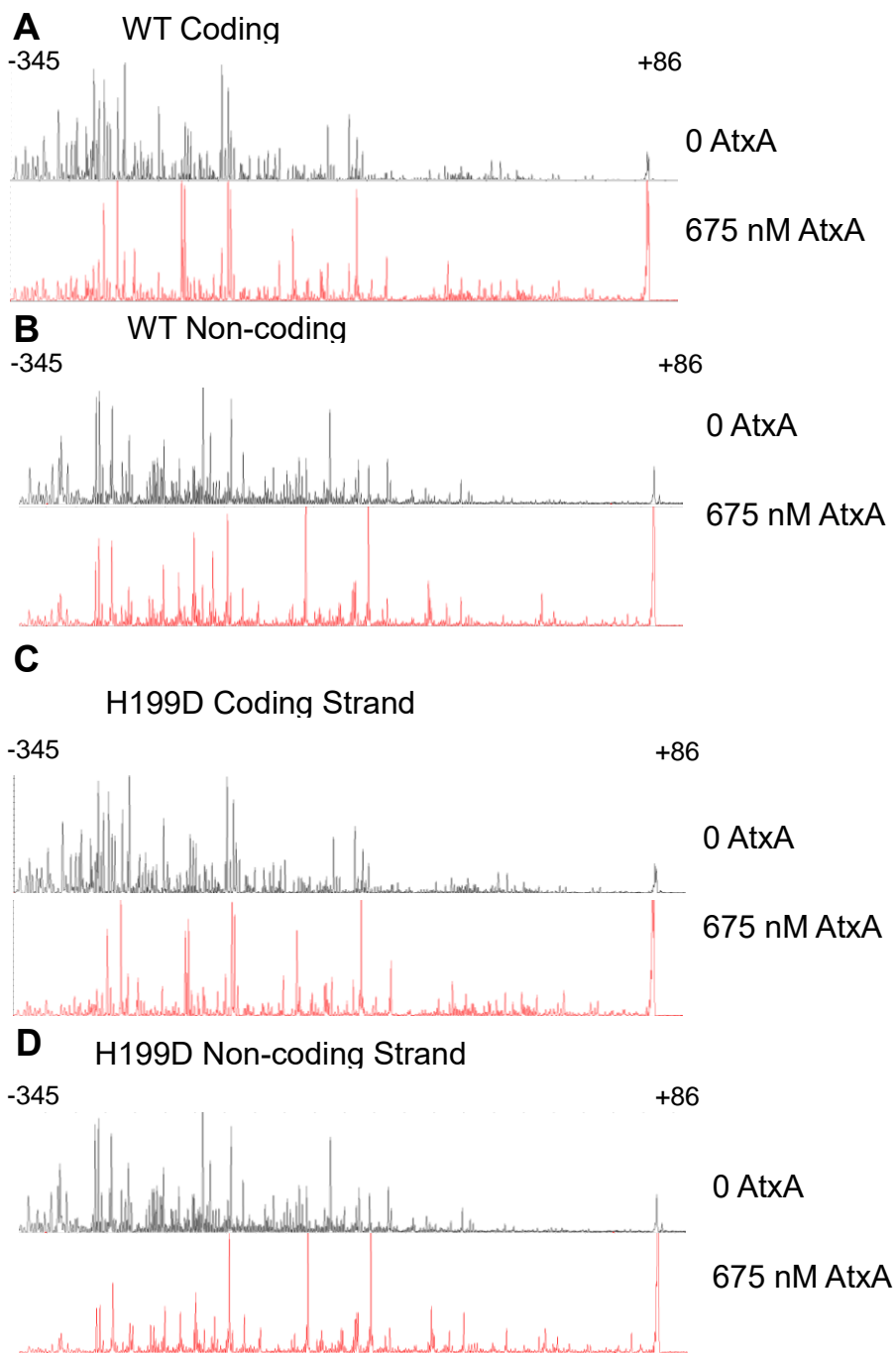


**Figure S1**

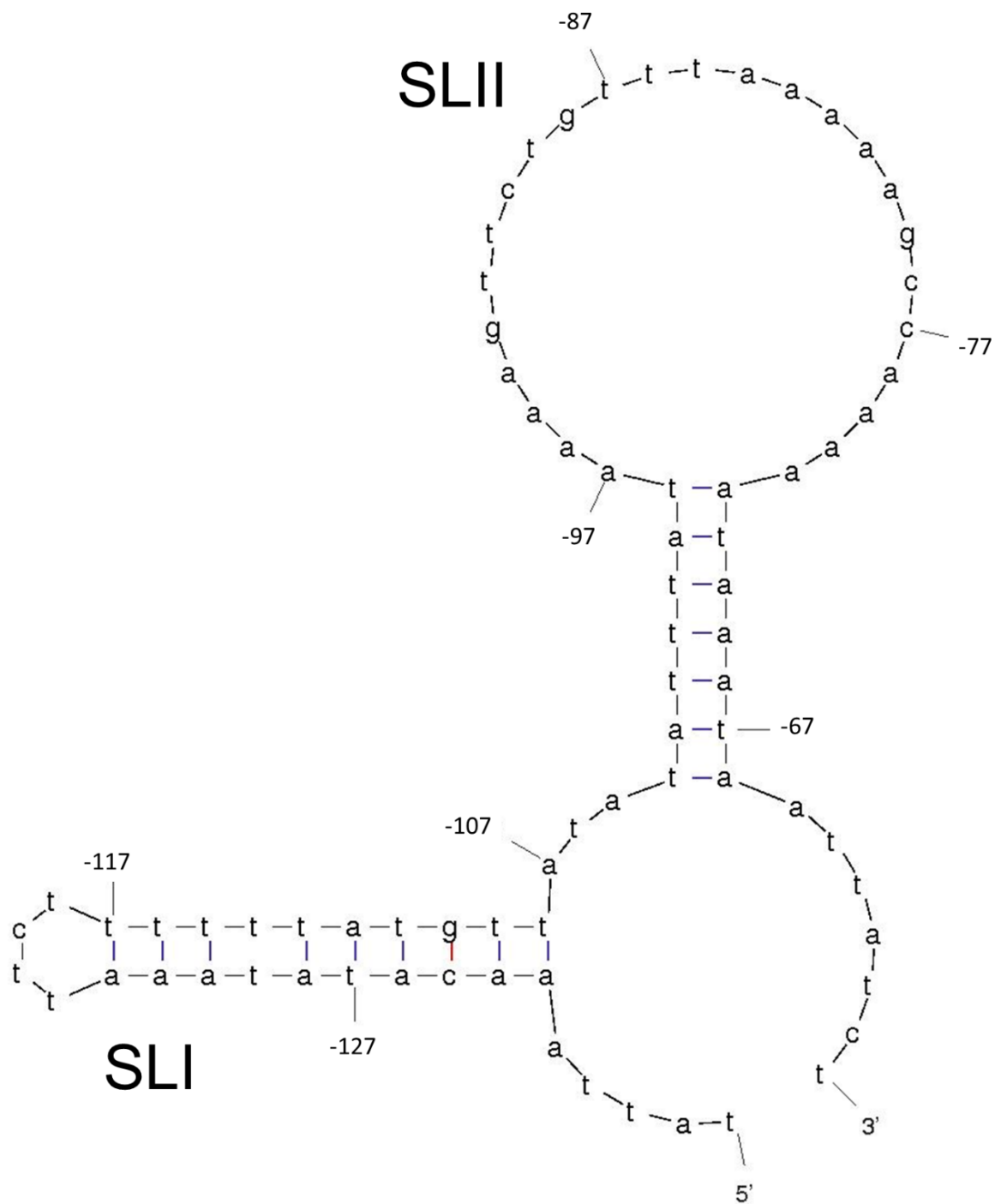


- 1 **Figure S1.** Plasmid pPROExHTc-*atxA*, pKA2, pMRC4 and pRSP maps. Plasmid pPROExHTc-
- 2 *atxA* was used as a source for purification of native AtxA and its H199A, H199D, H379A,
- 3 H379D mutants. Plasmids pKA2 encoding either the native *atxA* gene or its mutant forms
- 4 (H199A, H199D, H379A, H379D) were used for complementation of *atxA* in Ames 35Δ*AtxA*
- 5 strain and for activation of *gfp* expression controlled by full length *pagA* promoter in pMRC4 or
- 6 short *pagA* promoter in pRSP plasmid. TT – transcription terminators, RS28535-28545 represent
- 7 ORFs of pXO1 minireplicon.

8 **Figure S2**

9 Figure S2. DNase I Footprinting analysis of the entire PAG4 fragment. Footprinting was done  
10 with FAM/VIC end-labeled fragments generated using labeled primers in PCR amplification.  
11 Mixtures of protein and DNA were incubated with 0.07 U of DNase I for 10 min at room  
12 temperature. Reactions were heat inactivated, purified, and sent to OSU-PMGF for analysis on  
13 the 3730 DNA Analyzer. Figure shows resulting peaks generated by incubation of the PAG4  
14 fragment both with and without protein. (A) Coding strand of PAG4 incubated with AtxA WT.  
15 (B) Non-coding strand of PAG4 incubated with AtxA WT. (C) Coding strand of PAG4  
16 incubated with AtxA H199D. (D) Non-coding strand of PAG4 incubated with AtxA H199D.

Figure S3



17 Figure S3. Predicted secondary structure of part of *pagA* promoter containing stem loops. Figure  
18 displays basepairs -137 to -59 from transcriptional start site and each of the hypothesized stem  
19 loops are labeled. This structure contains the lowest Gibbs Free Energy of all possible structures  
20 for this region and was created using the mfold web server  
21 (<http://unafold.rna.albany.edu/?q=mfold/DNA-Folding-Form>).

## Figure S4

Bacillus anthracis str. 'Ames Ancestor' plasmid pXO1, complete sequence

Sequence ID: [AE017336.2](#)

Range 1: 143622 to 143662 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
76.8 bits(41)	4e-14	41/41(100%)	0/41(0%)	Plus/Plus

```

Query 1      AACATATAAATTCTTTTTTATGTTATATATTTATAAAAGTT 41
             |||
Sbjct 143622 AACATATAAATTCTTTTTTATGTTATATATTTATAAAAGTT 143662

```

Bacillus anthracis str. Sterne plasmid pXO1, complete sequence

Sequence ID: [CP009540.1](#) Length: 181624 Number of Matches: 1

Range 1: 31793 to 31833 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
75.2 bits(82)	4e-11	41/41(100%)	0/41(0%)	Plus/Minus

```

Query 1      AACATATAAATTCTTTTTTATGTTATATATTTATAAAAGTT 41
             |||
Sbjct 31833  AACATATAAATTCTTTTTTATGTTATATATTTATAAAAGTT 31793

```

Bacillus cereus G9241 plasmid pBCX01, complete sequence

Sequence ID: [CP009592.1](#) Length: 190860 Number of Matches: 1

Range 1: 83110 to 83151 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
68.9 bits(75)	6e-09	41/42(98%)	1/42(2%)	Plus/Plus

```

Query 1      AACATATAAATTCTTTT-TTATGTTATATATTTATAAAAGTT 41
             |||
Sbjct 83110  AACATATAAATTCTTTTTTATGTTATATATTTATAAAAGTT 83151

```

Bacillus cereus biovar anthracis str. CI plasmid pCI-XO1, complete sequence

Sequence ID: [CP001747.1](#) Length: 181907 Number of Matches: 1

Range 1: 143876 to 143917 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
68.9 bits(75)	6e-09	41/42(98%)	1/42(2%)	Plus/Plus

```

Query 1      AACATATAAATTCTTTT-TTATGTTATATATTTATAAAAGTT 41
             |||
Sbjct 143876 AACATATAAATTCTTTTTTATGTTATATATTTATAAAAGTT 143917

```

22

23 Figure S4. BLAST analysis of DNA region responsible for *pagA* promoter activation.

24