CRP site upstream of *ainS*

VF1038_CATTCTTTACCTTTTTATGTCGCCTTCACAGGCGTCAATTAACTTCTTATTAATCAA
GAGGATGAATAGATAATCCTTCACTCTTAATCACTATCAAATTCTATGAAGCGTGATTATACAA
TATTGTTACTAATAAGCGGTAAGAATTTAATCAAAATTTAATTTTAATTTTTGTCGTAAGACAC
GCAAAGTACTCATAACACCACTACCTATTTTTACTATACTGATTATGCTGAGAAAGTAATTTCC
TCAGCAATTTTAATGACTTATCAATCAATAAGGTAGTAT**TATGA**AAAACT**TCACA**CTTCTTTTA
AATACACTTCCATCTATCTCTCACGAAGAGATAGTCGAAAAAAAACCTGCAATATGAATTTATA
AAAGAGTTG_*ainS*

- Yellow highlight indicates region tested for CRP binding (Figure 5), with key portions of the CRP recognition site in bold
- Green highlight indicates the predicted translational start sites as annotated in Genbank for VF_1038 (on reverse strand at top) and for *ainS* (which appears to lack a typical ATG start)

CRP site upstream in intergenic luxRI region

LuxR_CATTTTTTGTTCACCTAGCTTATTGTTATGTTTTTTGCGTGTTATATAACACCAATTTG
GAGGTTTGGTGATATCGCTTCCAATTAA**TTCGA**TCTGGG**TCACA**TTTATGCATCTTGGTGGAAA
CGTGGTGTTAACATTGCAGCTGTAGGATGGTACAGGTTTCCGTAATGCATCAGTTTGTTATGAT
CATGTAAAATAAGAGAGGTTGCATG_LuxI

- Yellow highlight indicates region tested for CRP binding (Figure 5), with key portions of the CRP recognition site in bold
- Green highlight indicates the predicted translational start sites as annotated in Genbank for LuxR (on reverse strand at top) and *ainS*
- The blue highlighted "A" denotes the transcriptional start site for *luxI* (1)
- Gray shading covers the "*lux* box" target sequence for LuxR
- Underlined bases indicate the predicted -10 promoter element.
- At the site of the pink highlighting, an A is present between the T and G in strain MJ1 (2)

Supplemental Figure S1. Intergenic promoter regions upstream of *ainS* and between *luxR* and *luxI*.

1. **Egland KA, Greenberg EP.** 1999. Quorum sensing in *Vibrio fischeri*: elements of the *luxl* promoter. Mol. Microbiol. **31:**1197-1204.
2. **Bose JL, Wollenberg MS, Colton DM, Mandel MJ, Septer AN, Dunn AK, Stabb EV.** 2011. Contribution of rapid evolution of the *luxR-luxI* intergenic region to the diverse bioluminescence outputs of *Vibrio fischeri* strains isolated from different environments. Appl. Environ. Microbiol. **77:**2445-2457.