

# Figure S2

## Full length 302 base pair *cbpA* regulatory DNA

**P6 transcript start**  
ATTTGCAGTGCAACTAATTCCATGTATATTACTACCCATatatagcgtctataaaatttaataataa  
-35 -10 *yccE* start codon

tgacgccctagttaaacttaaagtgcctggttcaactatcaaaaatcgctcacctttttcacctgtt  
-35 -108

**P4 transcript start**  
taaaatagttcagcaaccatcttgatggcgacctctctccgcgatgatttcaataacatattctg  
-10 -94

**P1 & P2 transcript starts**  
tgttggcatatgaaatggaggattaccctacactatagaggttaccttacaggggttccttcaat  
-35 -35 -10 -10

ttgtggtgatttacgcgagataacgctATG  
*cbpA* start codon

## Full length 302 base pair *cbpA* regulatory with -94G and -108C mutations

**P6 transcript start**  
ATTTGCAGTGCAACTAATTCCATGTATATTACTACCCATatatagcgtctataaaatttaataataa  
-35 -10 *yccE* start codon

tgacgccctagttaaacttaaagtgcctggttcaactatcaaaaatcgetcacctttttcacctctt  
-35 -108 \*

\* **P4 transcript start**  
taaaatagttgagcaaccatcttgatggcgacctctctccgcgatgatttcaataacatattctg  
-10 -94

**P1 & P2 transcript starts**  
tgttggcatatgaaatggaggattaccctacactatagaggttaccttacaggggttccttcaat  
-35 -35 -10 -10

ttgtggtgatttacgcgagataacgctATG  
*cbpA* start codon

**Full length 302 base pair *cbpA* regulatory DNA with -217G and -216G mutations**

\*\* P6 transcript start

**ATTTGCAGTGCAACTAATTCCATGGGTATTACTACCCAT**atatagcgtctataaaatttaataataa  
-35 -10 *yccE* start codon

tgacgccctagttaaacttaaagtgcttcaactatcaaaaat**cgctca**ccctttttcacct**gtt**  
-35 -108

P4 transcript start

**taaaat**atggttcagcaacc**c**atcttgatggcgacctcctctccgcgatgatttcaataacatattctg  
-10 -94

P1 & P2 transcript starts

tg**ttggca**at**gaaa**ttttgaggat**taccctacact**a**tagg**agttaccttacaggggttccttcaat  
-35 -35 -10 -10

ttgtggtgatttacgcgagataacgct**ATG**  
*cbpA* start codon

**Full length 302 base pair *cbpA* regulatory DNA with -11G, -7G and -6G mutations**

P6 transcript start

**ATTTGCAGTGCAACTAATTCCATGTATATTACTACCCAT**atatagcgtctataaaatttaataataa  
-35 -10 *yccE* start codon

tgacgccctagttaaacttaaagtgcttcaactatcaaaaat**cgctca**ccctttttcacct**gtt**  
-35 -108

P4 transcript start

**taaaat**atggttcagcaacc**c**atcttgatggcgacctcctctccgcgatgatttcaataacatattctg  
-10 -94

\* \*\* P1 & P2 transcript starts

tg**ttggca**at**gaaa**ttttgaggat**tgccctggact**a**tagg**agttaccttacaggggttccttcaat  
-35 -35 -10 -10

ttgtggtgatttacgcgagataacgct**ATG**  
*cbpA* start codon

**cbpA P4 fragment** (contains a 93 bp deletion between positions -94 and +1)

tcaactatcaaaaat**cgctca**ccctttttcacct**gtt****taaaat**atggttc**atagga**gttaccttacagg  
-35 -108 -10 -94

ggttccttcaatttgtggtgatttacgcgagataacgct**ATG**  
*cbpA* start codon

cbpA P4 -10con fragment

tcaactatcaaaaatcgotca<sup>\*</sup>ccctttttcacctg<sup>\*</sup>ttataat<sup>\*</sup>atggttc<sup>\*</sup>atagga<sup>\*</sup>gttaccttacagg  
-35 -108 -10 -94  
ggttccttcaattt<sup>\*</sup>gtggttgatttacgcgagataacgctATG  
cbpA start codon

cbpA P6 fragment

P6 transcript start  
ATTTGCAGTGCAACTAATTCATGTATATTACTACCCAT<sup>\*</sup>at<sup>\*</sup>atagcgtctataaaat<sup>\*</sup>taataaataa  
-35 -10 yccE start codon  
tgacgccctag<sup>\*</sup>ttaaact<sup>\*</sup>taaagtgcctgg<sup>\*</sup>ttcaactatcaaaaatcg<sup>\*</sup>otcaccctttttcacctg<sup>\*</sup>tt  
-35 -108

t<sup>\*</sup>aaaat<sup>\*</sup>atg<sup>\*</sup>ttc<sup>\*</sup>atag<sup>\*</sup>gattac<sup>\*</sup>cttacagg<sup>\*</sup>ggttc<sup>\*</sup>ccttca<sup>\*</sup>attt<sup>\*</sup>gtg<sup>\*</sup>ttgatt<sup>\*</sup>acgcgagataacg  
-10 -94  
ctATG  
cbpA start codon

cbpA P6 Δ10

P6 transcript start  
ATTTGCAGTGCAACTAATTCATGTATATTACTACCCAT<sup>\*</sup>ata<sup>\*</sup>aaat<sup>\*</sup>taataa<sup>\*</sup>aatgacgccctag  
-35 -10 yccE start codon  
ttaaact<sup>\*</sup>taaagtgcctgg<sup>\*</sup>ttcaactatcaaaaatcg<sup>\*</sup>otcaccctttttcacctg<sup>\*</sup>tt<sup>\*</sup>aaaat<sup>\*</sup>atg<sup>\*</sup>tt  
-35 -108 -10

catag<sup>\*</sup>gattac<sup>\*</sup>cttacagg<sup>\*</sup>ggttc<sup>\*</sup>ccttca<sup>\*</sup>attt<sup>\*</sup>gtg<sup>\*</sup>ttgatt<sup>\*</sup>acgcgagataacgctATG  
-94 cbpA start codon

cbpA P6 Δ20

P6 transcript start  
ATTTGCAGTGCAACTAATTCATGTATATTACTACCCAT<sup>\*</sup>ata<sup>\*</sup>aaat<sup>\*</sup>aatgacgccctag<sup>\*</sup>ttaaact<sup>\*</sup>taa  
-35 -10 yccE start codon  
agtgcctgg<sup>\*</sup>ttcaactatcaaaaatcg<sup>\*</sup>otcaccctttttcacctg<sup>\*</sup>tt<sup>\*</sup>aaaat<sup>\*</sup>atg<sup>\*</sup>ttc<sup>\*</sup>atag<sup>\*</sup>gatt  
-35 -108 -10 -94

accttacagg<sup>\*</sup>ggttc<sup>\*</sup>ccttca<sup>\*</sup>attt<sup>\*</sup>gtg<sup>\*</sup>ttgatt<sup>\*</sup>acgcgagataacgctATG  
cbpA start codon

cbpA P6 Δ30

P6 transcript start  
ATTTGCAGTGCAACTAATTCATGTATATTACTACCCAT<sup>\*</sup>acg<sup>\*</sup>ccctag<sup>\*</sup>ttaaact<sup>\*</sup>taaagtgcctgg<sup>\*</sup>t  
-35 -10 yccE start codon  
tcaactatcaaaaatcg<sup>\*</sup>otcaccctttttcacctg<sup>\*</sup>tt<sup>\*</sup>aaaat<sup>\*</sup>atg<sup>\*</sup>ttc<sup>\*</sup>atag<sup>\*</sup>gattac<sup>\*</sup>cttacagg  
-35 -108 -10 -94

ggttccttca<sup>\*</sup>attt<sup>\*</sup>gtg<sup>\*</sup>ttgatt<sup>\*</sup>acgcgagataacgctATG  
cbpA start codon

**cbpA P6 Δ60**

P6 transcript start  
ATTTCAGTGCAACTAATTCCATGTATATTACTACCCATcaactatcaaaaatcggtcacccctttt  
-35 -10 yccE start codon -35

cacctggtttaaaatgatgttcataggagttaccttacaggggttccttcaatttggttgatttacg  
-108 -10 -94

cgagataacgctATG  
cbpA start codon

**cbpA P6 Δ80**

P6 transcript start  
ATTTCAGTGCAACTAATTCCATGTATATTACTACCCATccctttttcacctggtttaaaatgatgttc  
-35 -10 yccE start codon -108 -10 -94

taggagttaccttacaggggttccttcaatttggttgatttacgagataacgctATG  
cbpA start codon

**cbpA P6 Δ100**

P6 transcript start  
ATTTCAGTGCAACTAATTCCATGTATATTACTACCCATataggttcataggagttaccttacagggg  
-35 -10 yccE start codon -94

ttccttcaatttggttgatttacgagataacgctATG  
cbpA start codon

**Figure S2: *cbpA* regulatory region DNA fragments.** The figure shows DNA sequences for *cbpA* regulatory region DNA fragments. The P6, P4, P1 and P2 promoters and transcription start sites are highlighted in purple, orange, red and blue respectively. Coding DNA sequences for the *yccE* and *cbpA* genes are shown in upper case. The Fis binding element between position -108 and -94 with respect to the P1 promoter is underlined. Note that the -10 hexamers for the P1 and P2 promoters overlap by 1 bp. Mutations in different promoter elements are highlighted by a star.