Supplemental Table 1: Sequence of the PCR primers used in this study

Gene inactivation of sll0822

sll0822M-FW	GCCTGGGCCAATTGATATCC	
sll0822M-RV	GCTGCCATCCTGTTGCCATT	
sll0822R4	GGGCTTGGTTGCGTT**CCCGGG**AGCCATTCAAGTTTTC	*Sma*I
sll0822A4	AGGTGGGGGCTTGGCT**CCCGGG**AACGTAAGGCTAATT	*Sma*I
KmHinCFW	GGCGCTGAG**GTCGAC**CTCGTGAAGAAG	*Hinc*II
KmHinCRV	ACCTGCAGGGG**GTCGAC**GGAAAGCCAC	*Hinc*II

Cloning of sll0822 coding sequence at NdeI-EcoRI sites of pFC1 for heat inducible overexpression of AbrB2

sll0822FL1:	TCACCGAAAACT**CATATG**GCTAAATCAAACGC
sll0822FL2:	CATTAGTCCCAGC**GAATTC**GCCTTACTCTTCT

Cloning of hox and sll0822 promoter regions in the promoter probe vectors

hox promoter

pSB2A_hox1 Fw	GCGCTGTAAATAAAA**GCCGGC**ATTGATAATTTATTTCTCG	*Nae*I
pSB2A_hox2 Fw	CCCTAGAAATCACTT**GTTAA**CAACACCCAGAACCTAGTAAC	*Hpa*I
pSB2A_hox3 Fw	GGCTAGCAATTGGGGT**CGCGA**CTATTTTC	*Nru*I
pSB2A_hox4 Fw	CACTAAAGGGAAGT**TCGCGA**TATTAATTTAGTTACG	*Nru*I
pSB2A_hox5 Fw	TGATGTAACAAT**GCCGGC**AACCAACTAGAGATTC	*Nae*I
pSB2A_hox7 Rv	CGATCGGTGGCA**GACGTC**ATGGAAAAATCCTCA	*Zra*I

sll0822 promoter

SnaBIFW22	AGCCATCCTT**TACGTA**CAACTATCCCAT	*Sna*BI
SnaBIRV22	CGTTTGATTT**TACGTAT**CAAGTTTTCGG	*Sna*BI

qPCR

HoxE Left	GCCCATCCTAGTGGAGACAA
HoxE Right	GGTAAAAAGTCGCCACTCCA
HoxF Left	TGAAATGACCCCAGAGGAAG
HoxF Right	ATACCTTCGAGGATGCGATG
Hox sll1222 Left	TGCTATGGCTATCCCCTCTG
Hox sll1222 Right	AGCTCCCTTGGTTTTCCATT
HoxU Left	GTTTGTGCATGGTGGAAGTG
HoxU Right	ATTCACAGTTGCCGTTAGCC
HoxY Left	CTCAAGGAATACCCGGACAA
HoxY Right	AGAACCGGATCGCTACCTTT
Hox ssl2420 Left	CCCCAGAGGAGCAAAAGTTA
Hox ssl2420 Right	TCTTGGGTTCTTTCCTCACG
Hox sll1225 Left	TGTCCGACTTCTTGTTGGGTA
Hox sll1225 Right	AGCAATTTGGGCTTGAGTGT
HoxH Left	CTGCGCCGTTTAATGAATTT
HoxH Right	CACTGACCAAGCAGAGTGGA
RnpB Left	GTGAGGACAGTGCCACAGAA
RnpB Right	GGCAGGAAAAAGACCAACCT

Cloning into pET14b for over-expression and purification of 6His-Sll0822 from E.coli

abrB2-NdeI-Fw	GAATTC**CATATG**GCTAAATCAAACGCAACC
abrB2-BamHI-Rv :	CG**GGATCC**TTACTCTTCTTCGTCGTCAGCCC

Promoter fragments for EMSA

***hox* promoter**

Hox_gelshift Fw1	CGATATTAATTTAGTTACGAAATATTAACAAAATCTAGTGC
Hox_gelshift Fw2	ATTAAGTAATCGACATTGAAGAAAGCTAAAGATTT
Hox_gelshift Fw3	CAACCAACTAGAGATTCCATTCGTTATTG
Hox_gelshift Rv4	CCTTCATTGTTACATCAACTTTTAAAAAGTGAG
Hox_gelshift Rv5	CCTTAGTCGGGAAAGAATTTGTGTG
Hox_gelshift Rv6	GTCATGGAAAAATCCTCAAAAAGGAGC

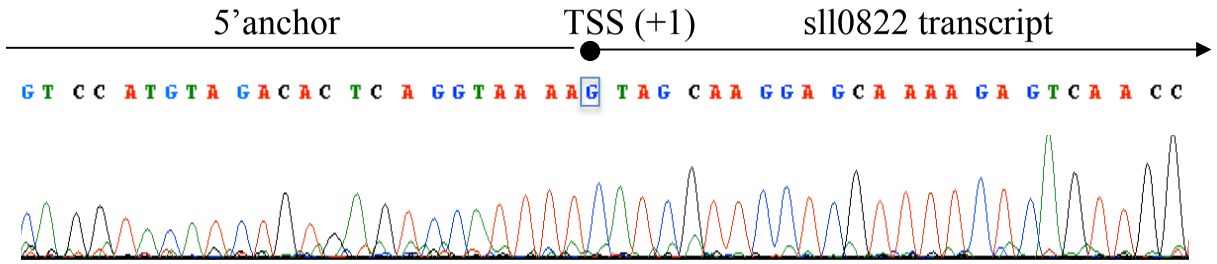
abrB2 promoter:

0822_gelshift Fw	CAACTATCCCATTAAATTAACTATTTATTT
0822_gelshift Rv	TCAAGTTTTCGGTGATTGAG
0822_gelshift mid Fw	AAGCAGGGTAGCAAGGA
0822_gelshift mid Rv	CTACCCTGCTTATATTACACG

Control hoxY protein coding sequence:

hoxY Fw	TTGGTTCTGATCTCAAGGAATACCCG
hoxY Rv	AATACGGTGGGCATCGGG

A



B

-35 like box **-10 box** **TSS**

ACTTCATCCCTTTAGTATAGAAGCCATCCTTGCCCATCAACTATCCCATTAAATTAACTATTTAT**TTGAAC**AAACTAGATAATTATTCCAAGAAACGTG**TAATAT**AAGCAGG**G**TAGCAAGGAGCA

AAAGAGTCAACCATTCCTTCGACTAATCTTCCCTTGCTTACCAATTCTGATCAATCTCAATCACCGAAAACTTGA***ATG***GCTAAATCAAACGCAACCAAGCCCCTAACTGGCGAAGCATTGCTCGA

GAAAGTTAAAGAATTAGGCGATCTGCCCAAAGAAGAGAAAGCTAAAATCTGCGGTTATGTAACTTCCACAAAAAAAGGCCTGCCCCGGGTCAATATGATGAAGTTCTACAACGCC

Fig. S1 Determination of the transcription start site (TSS) of the *abrB2* (sll0822) gene with the 5’RACE technique:
(**A**) Part of the nucleotide sequence of the RT-PCR DNA products amplified with both the 5' anchor and the sll0822 specific reverse primer (sll0822P1; Table S1) whose complementary sequence is written in grey underlined letters in panel B. The first nucleotide immediately downstream the 5' anchor sequence is the sll0822 transcription start site (TSS; the **G** nucleotide noted as +1). (**B**) Nucleotide sequence of the sll0822 promoter region showing the -35-like element (**TTGAAC**), the -10 promoter box (**TATAAT**) and the TSS (**G**) nucleotides in bold cases. The **ATG** start codon and the beginning of the protein coding sequence of sll0822 are written in italics.

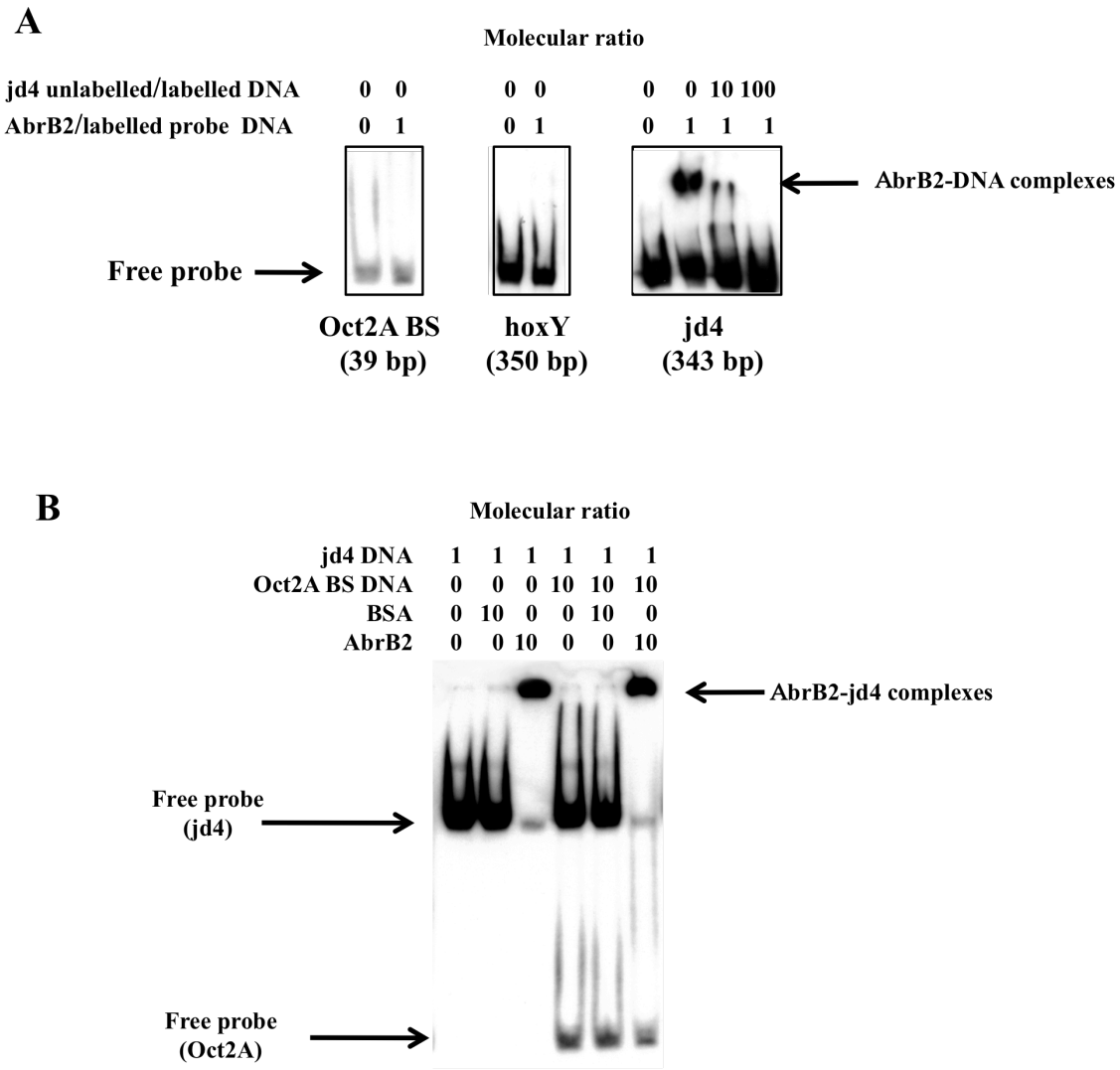


Fig. S2. Electrophoretic migration-shift assay showing that AbrB2 binds specifically onto the *hox*-promoter DNA.

(A) Analysis of the electrophoretic mobility of various DIG-labelled DNA fragments following incubation with or without the 6xHis-tagged AbrB2 regulator or the BSA control protein. The tested DNA probes are namely: Oct2A DNA binding sequence (control DNA provided by Roche), segment of hoxY protein coding sequence (prepared with the PCR primers presented in Table S1) and the jd4 segment of the *hox*-operon promoter, which was also used as an un-labelled specific DNA competitor. The size of the three DNA fragments used as probes of AbrB2 binding are indicated underneath. Arrows indicate the positions of free DNA probes and the jd4-AbrB2 retarded complexes.

(B) Analysis of the electrophoretic mobility of the DIG-labelled jd4 promoter region in presence (competition) or absence of Oct2A DNA binding sequence, following incubation with or without the 6xHis-tagged AbrB2 regulator or the BSA control protein. Arrows indicate the positions of free DNA probes and the jd4-AbrB2 retarded complexes.

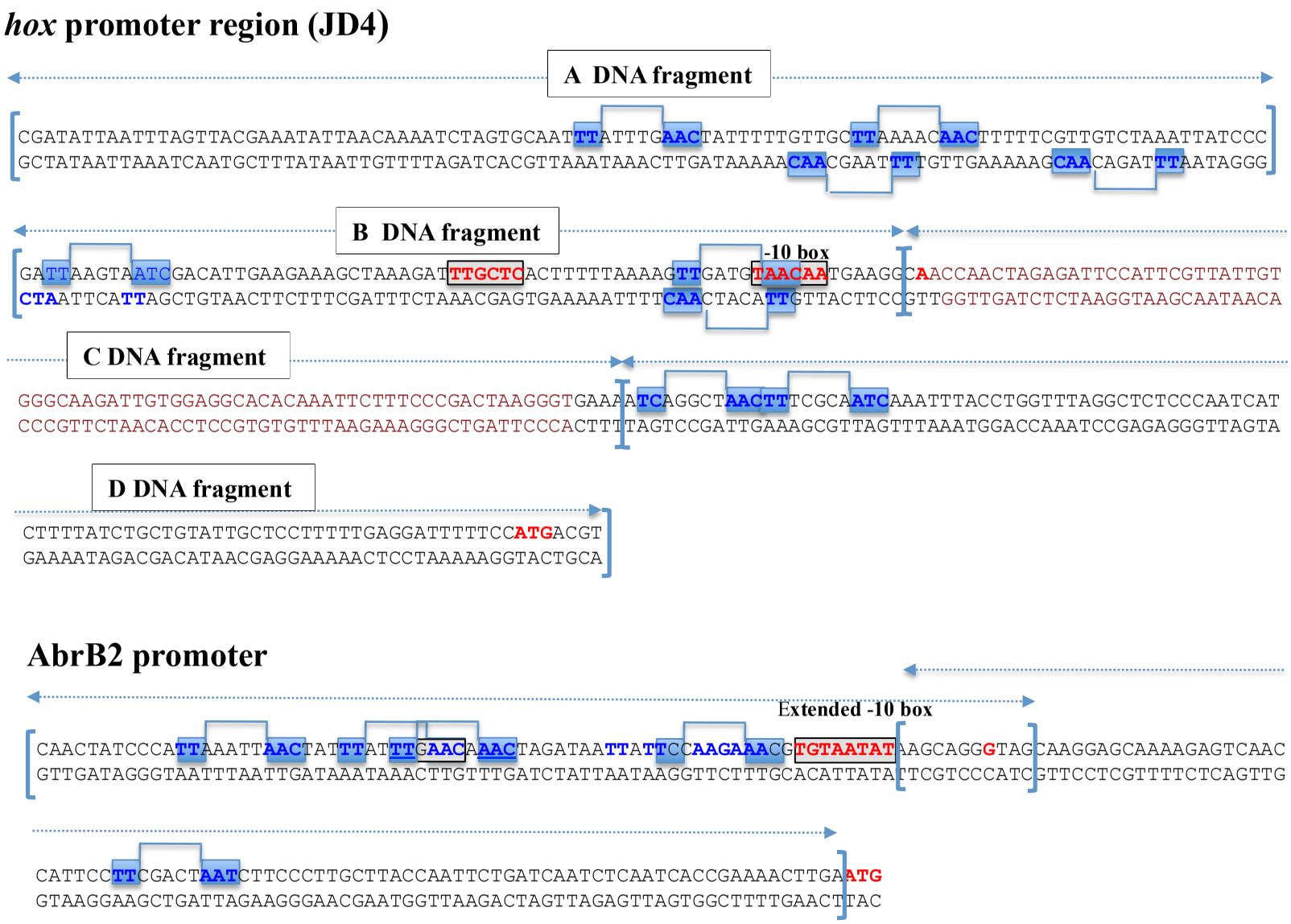


Fig.S3. Nucleotide sequence of the promoters of the *abrB2* gene and the *hoxEFUYH* operon (jd4 DNA segment) showing in red cases, the promoter boxes (enlighted in grey), the transcription start sites and the ATG start codon of the *abrB2* and *HoxE* genes, and in blue the TTn5AAC repeated. Note that this motif is absent from the sequence (written in purple) of C subfragment of the
jd4 hox-operon promoter which does not bind AbrB2. Furthermore, our assumption that the consensus TTn5AAC motif is negatively acting on promoter activity in binding the AbrB2 repressor is supported by our finding that the TT to GG transversion mutagenesis of the TTn5AAC motif (***TT****GAAC*A**AAC**) overlapping the *TTGAAC* motif resembling a -35 promoter box led to an increase (not decrease) in the abrB2 promoter activity.