



promoter		motif		Distance to start	e-value
PalpA	GCCGCAAGCT	GCGGGCCGCCGTTTCCCTGATATTTGCA	AGCCCCGAATC	-111bp	9.1e-13
PinR	ACCGCACTGC	GATGGCGCCGGTTTCAGGAGCGACGCT	GACATTCGCG	-175bp	2.8e-8
P88400	TCGGGGCTGG	GCCGGATGCCGTTTCCAACGACGCA	GCGCGGCCCCG	-223bp	8.9e-10
P81655	CTGCCCCCAT	GCCTGCTGACGTTGTCAGCGACATGCC	AGGCAACCAT	-195bp	2.0e-10
P67231	CATGAATCCG	GTCACTCGCGGTTCCCTATTGTTTGCA	GCCTAAAGCA	-59bp	9.8e-9
P58432	CCGCCGAAAT	CCCTGCCGACGTTGTCGGCGACATGCC	CAGGTAGTCC	-190bp	3.4e-10
PtraI	CATGAATGGC	AGGCATGGTGGTTCTCCTGATAGCGAC	ACCACTATGG	-274bp	nan
Pint	ACAGGAATAC	GGGTGAGGCGGCTTCCGGATAGTTGCT	GGGGCTGAGC	-59bp	7.4e-10

Supplementary figure 3. **Common sequence motif in the identified transfer competence promoters of *ICElc*.** Motif identified by MEME [1]. Sequence of P_{traI} added manually to align.

No other similar motif was found on *ICElc*. Distance indicated to the start codon of the downstream gene. Distance to the mapped transcription start site in the P_{inR} -promoter [2]: 152 bp.

- 1) Bailey TL, Boden M, Buske FA, Frith M, Grant CE, Clementi L, et al. MEME SUITE: tools for motif discovery and searching. Nucleic Acids Res. 2009;37(Web Server issue):W202-8. doi: 10.1093/nar/gkp335.
- 2) Minoia M, Gaillard M, Reinhard F, Stojanov M, Sentchilo V, van der Meer JR. Stochasticity and bistability in horizontal transfer control of a genomic island in *Pseudomonas*. Proc Natl Acad Sci U S A. 2008;105(52):20792-7.