Table S1. Oligonucleotides used for this study.

Name	Sequence	Use/Products
DegU-Pro-Biotin3	5'-biotin-AAGCCACGCCTCCTTGTAT-3'	EMSA-B0, footprint
DegU-pIS-B1	5'-ATCGGATCCTCATTCGGCTTGCTGGGCA-3'	EMSA-B0, -B1, footprint, U-P2
DegU-Bio-R1	5'-Biotin-AACTGATGGTCGTCGATAAT-3'	EMSA-B1, -B11, B2
DegU-pIS-B2	5'-ATCGGATCCGATTCGAAAATAGGTCTTGG-3'	EMSA-B2
degU-H4	5'-CTATTGTCATCGTTCCTTC-3'	EMSA-H4
degU-mH4	5'-CTATTGTCATAATTCCTTC-3'	EMSA-H4m
degU-Pro-bio4	5'-biotin-TCATTCGGCTTGCTGGGCAT-3'	EMSA-H4, -H4m
ackA-bio	5'-biotin-GAAGACCGGACTTGACGAATT-3'	EMSA-ackA
ackA-down	5'-GATTGACGCTCCTTTATACTC-3'	EMSA-ackA
CtsR-F-bio	5'-biotin-AGGACGCCGCCAAGCAAGCTT-3'	EMSA-PclpC
CtsR-R	5'-GAAATATTATGTCCCACTCA-3'	EMSA-PclpC
Cre-ackA-FB	5'-biotin-TTATTGTAAGCGTTATCAATACGC-3'	EMSA-Fig. S2
Cre-ackA-R	5'-GCGTATTGATAACGCTTACAATAA-3'	EMSA-Fig. S2
Cre-degU-FB	5'-biotin-TTGGAAGGAACGATGACAATAGAT-3'	EMSA-Fig. S2
Cre-degU-R	5'-ATCTATTGTCATCGTTCCTTCCAA-3'	EMSA-Fig. S2
mCre-degU-F	5'-TTGGAAGGAATTATGACAATAGAT-3'	Footprint
mCre-degU-R	5'-ATCTATTGTCATAATTCCTTCCAA-3'	Footprint
degU-H41-bio	5'-biotin-TGCTGGGCATGAAAGAAAGA-3'	EMSA-Fig. S2
degU-H41	5'-TCTTTCTTTCATGCCCAGCA-3'	EMSA-Fig. S2
DegU-pIS-B11	5'-ATCGGATCCGATTTATTGGAAGGAACGATGAC-3'	U-del-11, EMSA-B11
DegU-pIS-B11m	5'-ATCGGATCCGATTTATTGGAAGGAAttATGAC--3'	U-del-11m
DegU-pIS-H3	5'-GATAAGCTTAACTGATGGTCGTCGATAAT-3'	U-del11, -11m
DegU-pIS-H21	5'-GATAAGCTTAATATGCCTTTTGGCTCTA-3'	U-P2
hprK-Sa	5'-ATGGTCGACGTCGTTTTCAGCGGCGATCT-3'	pPhl2-hprK
hprK-E	5'-ATGGAATTCTTCGCACAAAAGACGTAATG-3'	pPhl2-hprK
MecA-F	5'-GTCGGATCCATGGAAATTGAAAGAATTAA-3'	His-MecA
MecA-R	5'-GTCGGATCCTATGATGCAAAGTGTTTTTTTATC-3'	His-MecA

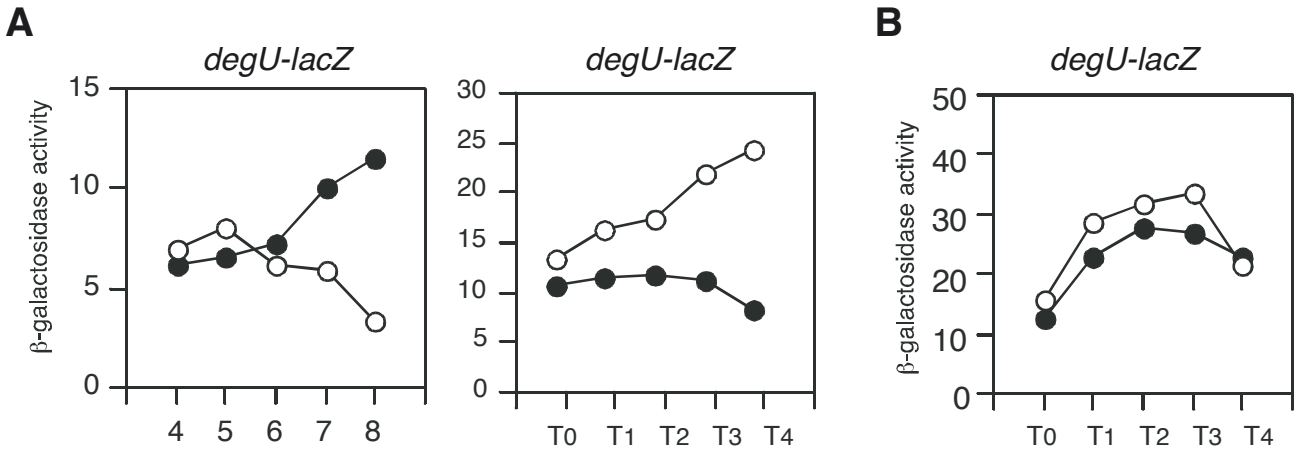


Figure S1. Cells were sampled hourly and β-galactosidase activities are shown in Miller units. (A) Expression of the wild-type *degU-lacZ* fusion. Left, cells were grown in LB medium without (closed symbols) or with (open symbols) 2% glucose. The X-axis represents the growth time after inoculation. Right, cells were grown in glucose-based Modified Competence medium (open symbols, Kunst F, Msadek T, Rapoport G. 1994. p 1-20. *In* Regulation of Bacterial Differentiation. American Society for Microbiology, Washington, DC) or MC medium containing 2% glycerol instead of 2% glucose (closed symbols). (B) Expression of the wild-type *degU-lacZ* fusion in the *ccpA* (Cm^r, closed symbols) and *ccpA clpC* (Cm^rTc^r, open symbols) strains. Cells were grown in sporulation medium. The X-axis represents the growth time in hours relative to the end of vegetative growth (T0). The phenotype of the *clpC* starin was unstable, thus experiments were performed immediately after transformation several times. A typical result is shown.

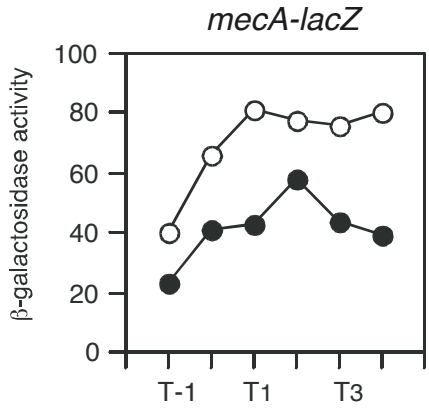
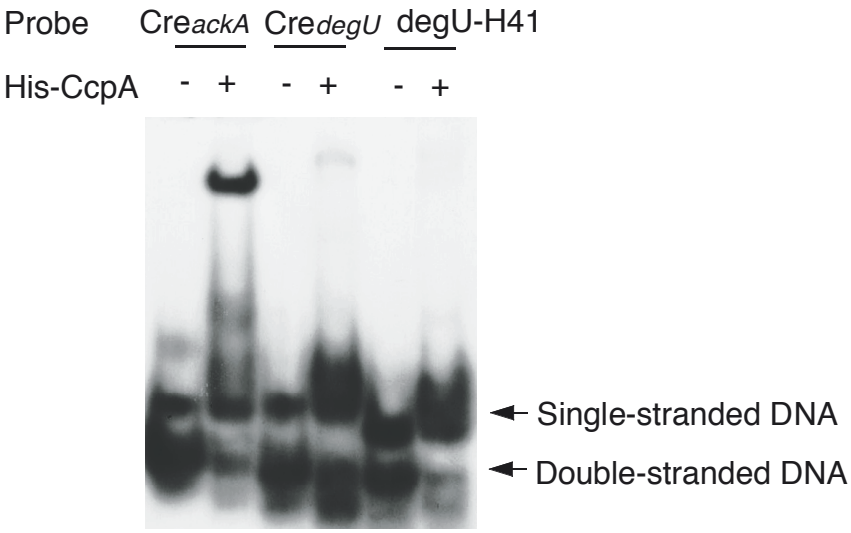


Figure S2. Expression of the *mecA-lacZ* fusion. Cells were grown in sporulation medium without (closed symbols) or with (open symbols) 2% glucose. Cells were sampled hourly and β-galactosidase activities are shown in Miller units. The X-axis represents the growth time in hours relative to the end of vegetative growth (T0). The strain has been constructed in Kong L, Siranosian KJ, Grossman AD, and Dubnau D. 1993. Mol. Microbiol. **9**:365-733.



Cre*ackA* (-68 to -45)	TTATTGTAAGCGTTATCAATACGC
Cre*degU* (-146 to -123)	TTGGAAGGAACGATGACAATAGAT
degU-H41 (-172 to -152)	TGCTGGGCATGAAAGAAAGA

Figure S3. EMSA using His-CcpA. The various probes were prepared by hybridization of the combinations of oligonucleotides indicated in Table S1. The nucleotide sequences of the probes were shown under the panel. The numbers indicate the nucleotide positions relative to the transcription start site. The probes were incubated with His-tagged CcpA (75 nM) as described in Materials and Methods without poly dI-dC. Samples were analyzed in electrophoresis in an 11% non-denaturing polyacrylamide gel.