

Supplemented figure S1

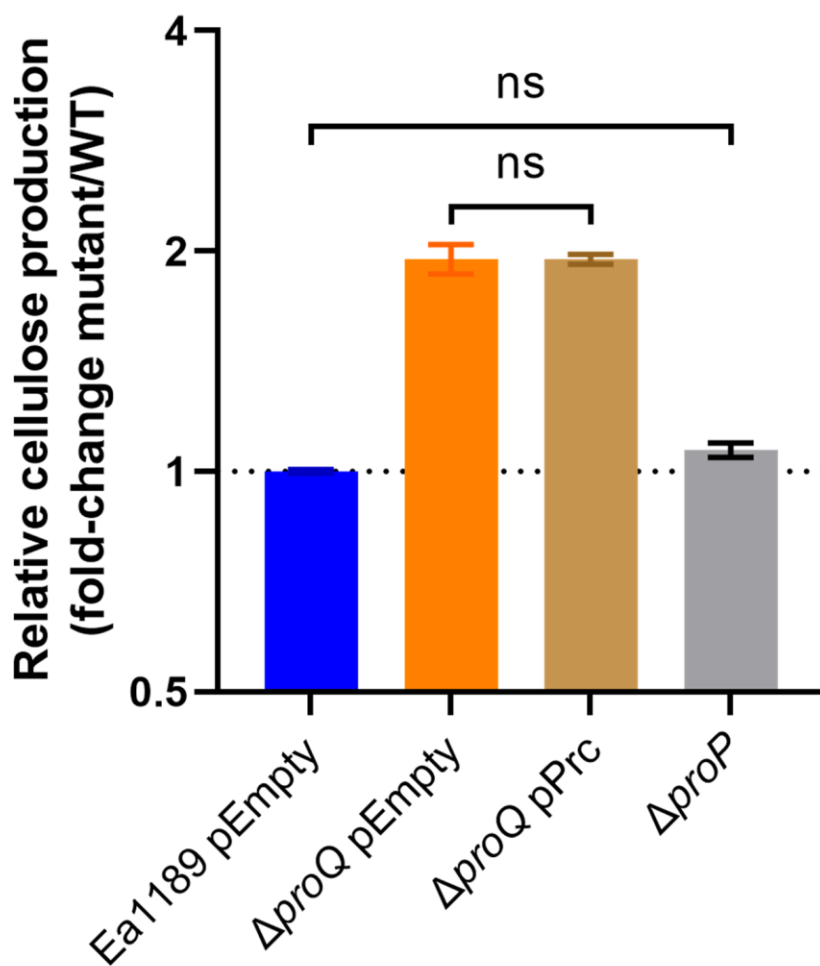


Fig. S1. Prc and ProP are likely not involved in cellulose production in *Erwinia amylovora*. Cellulose production was determined in wild-type Ea1189 harboring the empty vector pBBR1-MCS5, Ea1189ΔproQ harboring pBBR1-MCS5, Ea1189ΔproQ harboring pBBR1-MCS5-prc, and Ea1189ΔproP. Three independent experiments with three replicates were performed. One representative experiment was chosen. Error bars indicate standard errors of the means. ns (not significant), $P > 0.05$ by Student's t-test.

Supplemented figure S2

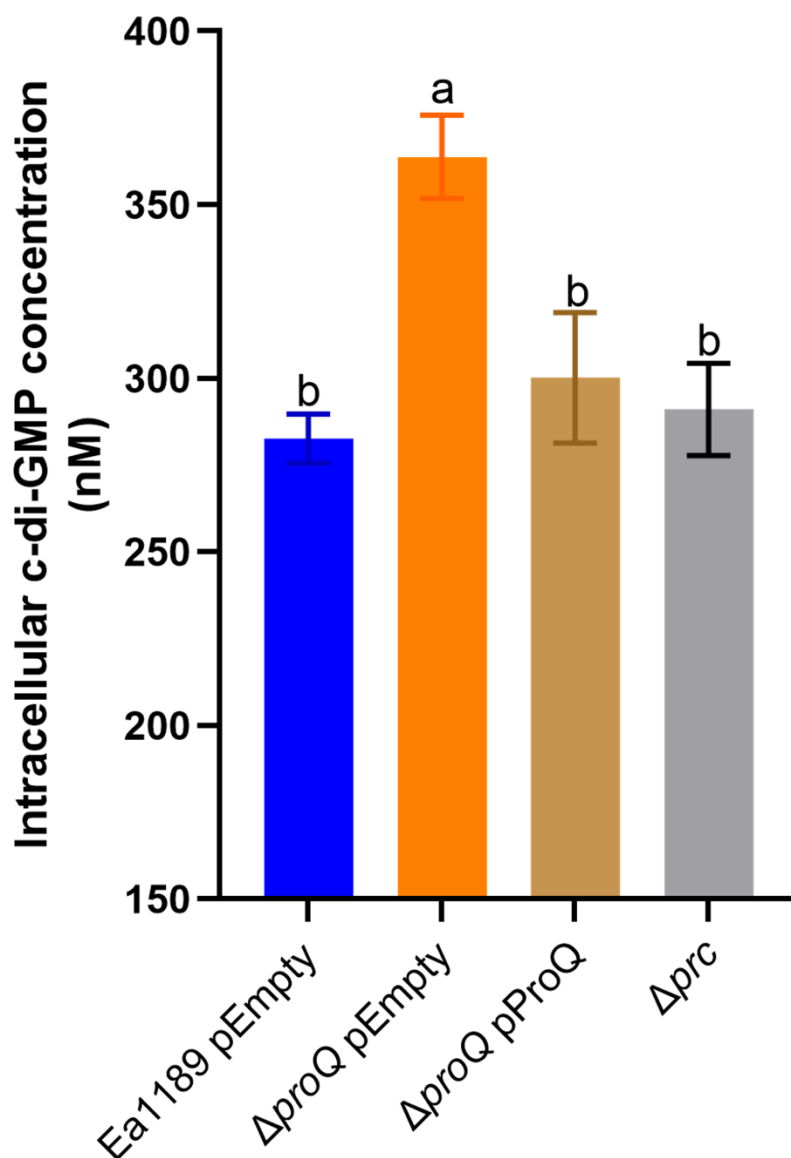


Fig. S2. ProQ represses intracellular c-di-GMP levels in *Erwinia amylovora*. Intracellular levels of c-di-GMP were measured in wild-type Ea1189 harboring the empty vector pCL1920, Ea1189Δ*proQ* harboring pCL1920, Ea1189Δ*proQ* harboring pCL1920-*proQ*, and Ea1189Δ*prc*. One representative experiment was chosen, and two independent experiments with three replicates were performed. Error bars indicate standard errors of the means. Different lowercase letters above the bars indicate statistically significant differences between treatments (Fisher's least significant difference, $P < 0.05$).

Supplemented Table S1

Table S1. Detailed information for transposon mutants.

transposon mutant names	insertion sites relative to gene 5' to 3'	gene name (ID)	gene encoding protein function
pQ2-4	1285 bp	<i>bcsA</i> (EAM_3387)	cellulose synthase catalytic subunit [UDP-forming]
pQ17-2	171 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ20-2	1850 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ32-1	1254 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ64-2	119 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ66-2	2100 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ69-2	1771 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ71-2	797 bp	<i>bcsA</i>	cellulose synthase catalytic subunit [UDP-forming]
pQ6-3	1016 bp	<i>bcsB</i> (EAM_3386)	putative cellulose synthase protein
pQ11-2	808 bp	<i>bcsB</i>	putative cellulose synthase protein
pQ12-2	495 bp	<i>bcsB</i>	putative cellulose synthase protein
pQ15-2	1047 bp	<i>bcsB</i>	putative cellulose synthase protein
pQ18-1	2019 bp	<i>bcsB</i>	putative cellulose synthase protein
pQ29-2	1858 bp	<i>bcsB</i>	putative cellulose synthase protein
pQ30-1	1978 bp	<i>bcsB</i>	putative cellulose synthase protein
pQ13-1	2589 bp	<i>bcsC</i> (EAM_3385)	putative cellulose synthase protein
pQ21-1	2004 bp	<i>bcsC</i>	putative cellulose synthase protein
pQ24-1	3569 bp	<i>bcsC</i>	putative cellulose synthase protein
pQ26-1	3992 bp	<i>bcsC</i>	putative cellulose synthase protein
pQ54-1	40 bp	<i>bcsE</i> (EAM_3382)	conserved hypothetical protein
pQ48-2	333 bp	<i>bcsQ</i> (EAM_3388)	putative cellulose biosynthesis protein
pQ49-2	400 bp	<i>bcsQ</i>	putative cellulose biosynthesis protein
pQ47-2	103 bp	<i>clpX1</i> (EAM_0991)	ATP-dependent Clp protease ATP-binding subunit
pQ55-2	108 bp	<i>clpX1</i>	ATP-dependent Clp protease ATP-binding subunit
pQ7-2	153 bp	<i>csrA</i> (EAM_2637)	carbon storage regulator
pq14-2	573 bp	<i>edcB</i> (EAM_0564)	putative signal transduction protein
pQ19-1	52 bp	<i>edcB</i>	putative signal transduction protein
pQ22-1	374 bp	<i>edcB</i>	putative signal transduction protein
pQ43-1	439 bp	<i>edcB</i>	putative signal transduction protein

pQ53-1	1097 bp	<i>fliC</i> (EAM_2562)	flagellin
pQ65-2	255 bp	<i>gmhA</i> (EAM_0891)	phosphoheptose isomerase (D-sedoheptulose 7-phosphate isomerase)
pQ39-2	1178 bp	<i>hldE</i> (EAM_2994)	bifunctional protein [includes: D-beta-D-heptose 7-phosphate kinase; D-beta-D-heptose 1-phosphate adenosyltransferase]
pQ40-1	272 bp	<i>hldE</i>	bifunctional protein [includes: D-beta-D-heptose 7-phosphate kinase; D-beta-D-heptose 1-phosphate adenosyltransferase]
pQ58-2	502 bp	<i>ispZ</i> (EAM_1886)	putative intracellular septation protein
pQ4-2	1592 bp	<i>lon</i> (EAM_0994)	ATP-dependent protease La
pQ5-1	230 bp	<i>lon</i>	ATP-dependent protease La
pQ8-2	2324 bp	<i>lon</i>	ATP-dependent protease La
pQ9-2	1192 bp	<i>lon</i>	ATP-dependent protease La
pQ45-1	1 bp	<i>lrhA</i> (EAM_2993)	NADH dehydrogenase operon transcriptional regulator (LysR-family transcriptional regulator)
pQ51-1	2508 bp	<i>mdoH</i> (EAM_1418)	glucans biosynthesis glucosyl transferase H
pQ70-2	1 bp	<i>mdtA</i> (EAM_2183)	multidrug resistance protein
pQ68-2	169 bp	<i>murQ</i> (EAM_2506)	putative phosphosugar-binding protein
pQ27-1	224 bp	<i>nth</i> (EAM_1688)	endonuclease III
pQ42-2	42 bp	<i>rfaC</i> (EAM_0088)	lipopolysaccharide heptosyltransferase-1
pQ62-2	487 bp	<i>rfaC</i>	lipopolysaccharide heptosyltransferase-1
pQ1	141 bp	<i>waaE</i> (EAM_0077)	lipopolysaccharide core biosynthesis glycosyl transferase
pQ36-1	300 bp	<i>waaE</i>	lipopolysaccharide core biosynthesis glycosyl transferase
pQ57-2	536 bp	<i>walW</i> (EAM_0080)	glycosyl transferase
pQ63-2	923 bp	<i>wbnF</i> (EAM_1916)	putative uridine diphosphate galacturonate 4-epimerase (nucleotide sugar epimerase)
pQ50-2	496 bp	<i>wzyE</i> (EAM_0174)	putative ECA polymerase