Supplemental material

Table S1 RNA-Seq data showing the downregulation of the A1S_2091- A1S_2088 operon when bacterial cells were cultured in SB at 24°C in the presence of light

Gene Identifier[a]	Fold Change	*P* value	Predicted function
A1S_2088	-2.75	0.0008	Hypothetical
A1S_2089	-4.41	0.0001	Fimbrial usher protein
A1S_2090	-3.08	0.0014	P pilus assembly protein
A1S_2091	-5.67	0.0001	Hypothetical

[a]The A1S_2091-A1S_2088 operon is described as the *prpABCD* operon in this report.

Table S2 Primers used in this study

Primer number	Nucleotide Sequence[a]
4100	5'-GCAAACTTAAGAGTGTGTTG-3'
4101	5'-CCTTTAGTAACGTGTAACTTTC-3'
4151	5'-CGAAGCATTGTCTTTAGACC-3'
4152	5'-GGCTACTAAATCCTCAGAAGG-3'
4153	5'-ATTGGAGTTGCAACAACTGC-3'
4154	5'-CCACCAATCATACGACGTTG-3'
4413	5'-ATGGTAGGATCCGTATGATGCCAAAAATAGAG-3'
4419	5'-GTCCACCATCAAATGACAAAGTCC-3'
4420	5'-CTGTGTCCTGAATACCTCAGC-3'
4465	5'-TGATGTGGATCCTTAATAAGTTACTGTGACTGTCAC-3'
4470	5'-CACATTCGTATTGTCCTGTAACTG-3'
4471	5'- ACTTGTAGTCGATCTTCTTGATC-3'
4488	5'-GCCCAGAAACTACCACTGG-3'
4489	5'-GCTTCTTTAAACGGAGGAGCC-3'
4615	5'-GGTAATGTCCAGACAGTTAACG-3'
4618	5'-TGCATCACTATTAATATTTGCTGC-3'

[a]Underlined nucleotides identify *Bam*HI restriction sites.

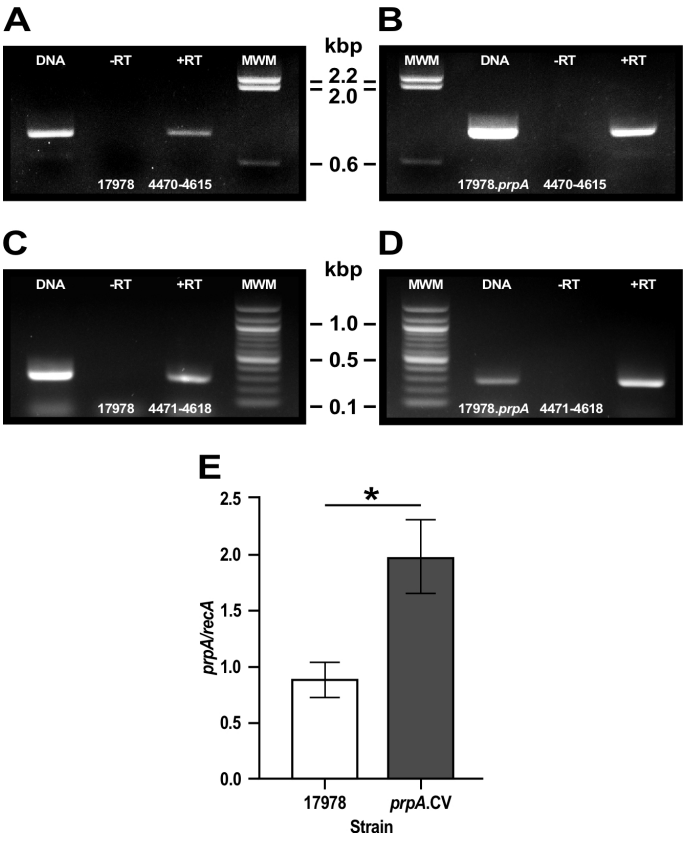

Figure S1. Transcriptional analyses of the *prpABCD* operon. RT-PCR with the intergenic primer pairs shown in Fig. 1A using as templates DNA, RNA and cDNA samples obtained from cells of the 17978 parental strain (A and C) or the 17978.*prpA* mutant (B and D) cultured in SB at 24°C in darkness. Numbers in the panels represent primer pairs used to amplify the sequences located between coding regions as displayed in Fig. 1A. λ *Hin*dIII-digested DNA and a 100-bp ladder were used as molecular weight markers in panels A/B and C/D, respectively. (E) qRT-PCR analysis of RNA isolated from 17978 and 17978.*prpA*.CV (*prpA*.CV) cells cultured in SB at 24°C in darkness until they reached on OD_{600} of 0.8. *recA* was used as a constitutively expressed control gene. Horizontal bars identify statistically different values ($P \leq 0.05$, ∗) and error bars represent the standard error of each data set.

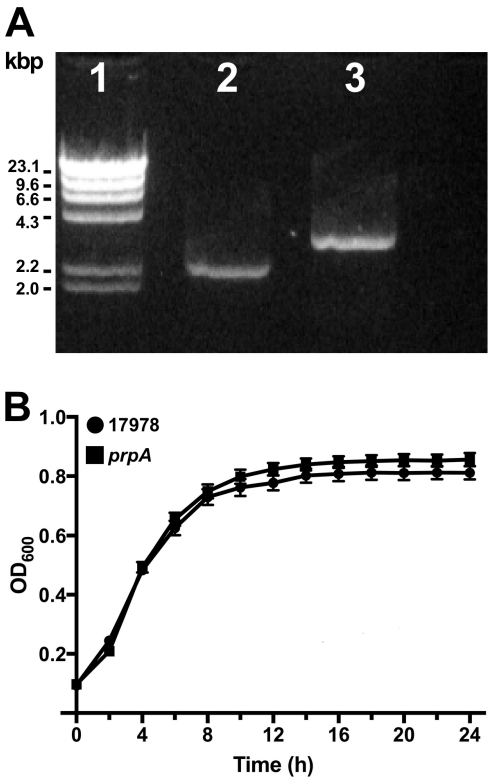

Figure S2. Analysis of the 17978.*prpA* insertion derivative. (A) Agarose gel electrophoresis of the amplicons generated using primers 4151 and 4152 (Fig. 1A and Table S1) and total DNA isolated from 17978 (lane 2) or 17978.*prpA* cells (lane 3). Lane 1, λ *Hin*dIII-digested DNA. (B) Growth curves of 17978 and 17978.*prpA* cells cultured in LB broth at 37°C in a shaking plate reader set at 200 rpm. Error bars represent the standard error of each data set.