Table S1. Sequences of oligonucleotide primers used in this study

Primers	Sequences (5′ to 3′)
hfq mutation F	AATGGCTAAGGGGCAATCATTACAAGACCCGTTCTTAAACGCA TTGCGTCG GTGTAGGCTGGAGCTGCTTC
hfq mutation R	GGGGGTCCGGGACACAAAGACTCCCCGTCGTGGAGGAACGGT CACGCTGGTCATATGAATATCCTCCTTA
gcvB mutation F	ATTATAAATTGTCCGTTGAGGAACTGCCAGCAAATACCTATAG TTGCGCCGTGTAGGCTGGAGCTGCTTC
gcvB mutation R	AAGCACCGCAGTTTGCGGTGCTGTAAAAATCAATATGGACAG ACAGGGTACATATGAATATCCTCCTTA
glmZ mutation F	TGAGGTAGAAATTTTCTGCCAGAGTTACCGATATGGCACGTCA TGTGCAGTGTGTAGGCTGGAGCTGCTTC
glmZ mutation R	TGTGTTCACAATCCTATCGCAGATAGCCAGGGCTTATGCTGCT ATAAACCGCATATGAATATCCTCCTTA
micA mutation F	TTTATTTTTGATGCGATGAAACTTTCTCGATCGCCAGACGTCTC AGTATATGTGTAGGCTGGAGCTGCTTC
micA mutation R	AGTGATACGCTTAGCTTCGAAGCCTTTTTACAAAGCAAAAGCT AGCGCCAACATATGAATATCCTCCTTA
omrA mutation F	GTTGCGATTCCGCGGTAGCGGTTTAATGCGGTGCATTGCTACA GTTCAGATGTGTAGGCTGGAGCTGCTTC
omrA mutation R	ACTAACCGGGGTTAGAGAGTTAATTATGATAATTAAACACAAA TTAAGAGCCATATGAATATCCTCCTTA
rprA mutation F	AATGAGATGATTCCTAATGACTCCAAAAACACCTTTTCATACT ATGGTTACGTGTAGGCTGGAGCTGCTTC
rprA mutation R	GTCTGGCAGGCGGCTCTGAATGCCCGGGACGATCGGTTCACCG ATCGTCCTCATATGAATATCCTCCTTA
ryeA mutation F	AGATAATACGTGACGGTAGAACTTTAAGGATCGTGACGTGGCC GGGGAAAGGTGTAGGCTGGAGCTGCTTC
ryeA mutation R	TACCCTCAACGGGCGTGCCGAAAACCTGCAGAGATAGCGGCC ATATGGCATCATATGAATATCCTCCTTA
ryhA mutation F	GACGCCGTTCAACATCACACATTTTAATGAATCTGGTAACATG TGATGAAGGATT GTGTAGGCTGGAGCTGCTTC
ryhA mutation R	AGTTTTACGGCAATGGGTAACAGACGCTGAAAAAAAATGACC CCGACCGAACATATGAATATCCTCCTTA
ryhB mutation F	GGCGTAACACTGCCGCAATAAGGTGAGACAGGCTCACCGCCG CTACCTGAAGTGTAGGCTGGAGCTGCTTC
ryhB mutation R	CTGGAGCTGGGGGCGCTGTTAGCCAGGTTTAAGTGGACTGTAA GGGATAAACATATGAATATCCTCCTTA
spf mutation F	AAGATTGGCCGTATTTTGTGAGCTAAGTTAGATTAAATGTGTC ATTTGCTGGTGTAGGCTGGAGCTGCTTC
spf mutation R	GCCGCACAAGCTTAAAACACGCCAGCGTTTATCAGACAGTGAC TGAGATGACATATGAATATCCTCCTTA
sroB mutation F	TTGATGAATAAATAAGTGGTGAATGATGTCGCTTTAAGCGACA ATCGACACGTGTAGGCTGGAGCTGCTTC
sroB mutation R	GAGGGTAACCTTCCCGGCCTGCTAAGCGGCGGCTAAAAAAAA GGCCAATATCATATGAATATCCTCCTTA

RACE RNA linker	GACGAGCACGAGGACACUGACAUGGAGGAGGGAGUAGAAA
ryhA reverse primer for RACE	CAGGGAAATTGGTAACCTGT
rprA reverse primer for RACE	CAGCAATTCTTTAGTTAACTC
arcB qRTPCR F	AAACGGGAATATCTGGATGC
arcB qRTPCR R	CTGGCAATCCCAGTATCCTT
amsG qRTPCR F	GCGACAGGTGGCTAAAGAAT
amsG qRTPCR R	TAAGCCATATCCGTGCCATA
amsK qRTPCR F	TCAACTGAAGACCGCCATT
amsK qRTPCR R	TCTGCTTCATCCAGATAGCG
EAM1647 qRTPCR F	ATTCCTGTCGCTCTTCTGGT
EAM1647 qRTPCR R	CAGTGTAAATCGGGCATTTG
eop1 qRTPCR F	GCCTGTACGAATACGCCAA
eop1 qRTPCR R	GCGGCAATAGCTTTCTATCC
fliC qRTPCR F	CACGTCTGGACGAAATTGAC
fliC qRTPCR R	GTTAGCACCCACCTGGATTT
hrpK qRTPCR F	TCAGATCGTCTCGGGTAAGA
hrpK qRTPCR R	AGCAGCGCATCACTGTAATC
mtgA qRTPCR F	TATCGCAGCAGACGGCTA
mtgA qRTPCR R	CAGACTCTATGCCCAGGGTT
ppsA qRTPCR F	ACGATCCGCTGGAGTTCTAT
ppsA qRTPCR R	AGTCTGACAAGCGCACAATC
recA qRTPCR F	TGTGCTCTCAGCCAGATACC
recA qRTPCR R	GCAACGGAGTCAACAATGAT
hfq-pML123 F	GATGAGCTCCGGCTGGAAAGATGTTCACT
hfq-pML123 R	CGATCTAGAGCCACACTGCGTCAATATCA
rprA-pML123 F	GATGAGCTCCGAAATCATTAGCAAGCAGAA
rprA-pML123 R	CGATCTAGAGTGGTGCAAACCTGGCTTAG
ryhA-pML123 F	GATGAGCTCGGAGAGAAAAAGCGGTTCAA
ryhA-pML123 R	CGATCTAGAGTGGGACAACGTTCAGGAAT

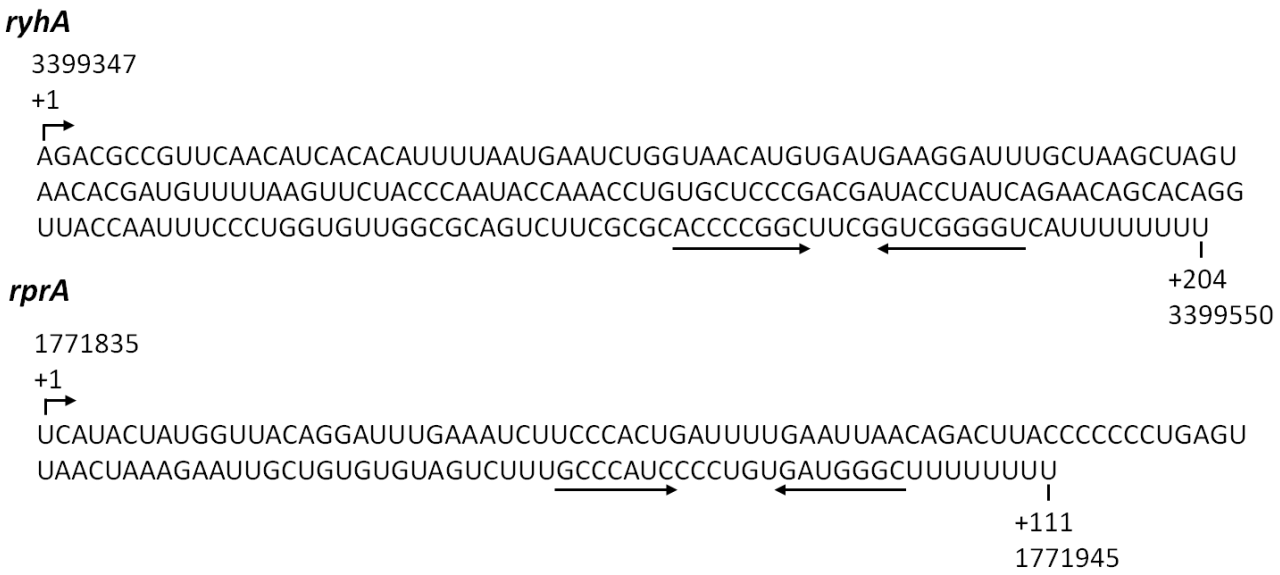

Figure S1. Nucleotide sequences of sRNAs *ryhA* (204 nucleotides) and *rprA* (111 nucleotides) from *E. amylovora* Ea1189. The transcriptional start sites of both *ryhA* and *rprA* were determined using 5' RACE assays and are annotated as +1. Horizontal arrows indicate inverted repeats of the Rho independent terminators.

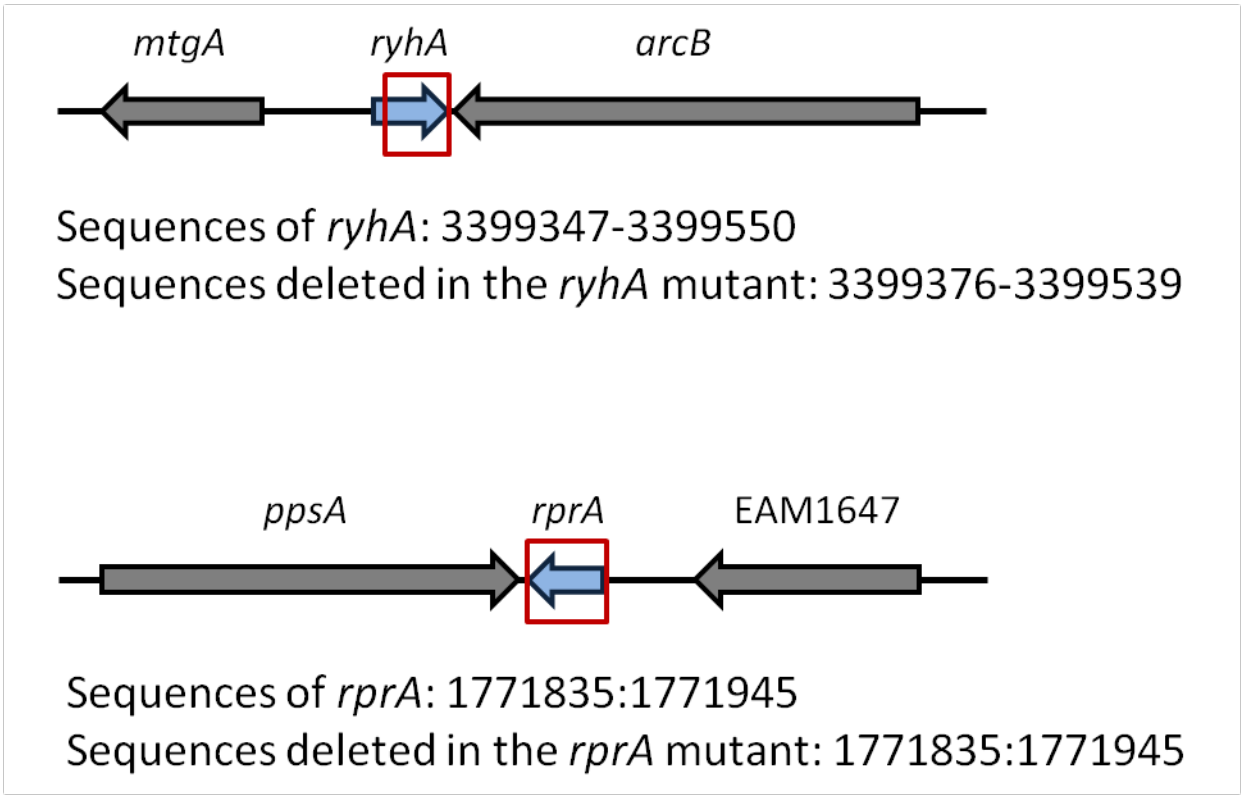

Figure S2. Illustration of the sequences deleted in Ea1189Δ*ryhA* and Ea1189Δ*rprA* and the genomic context of these sRNAs. The 5' end and 3' end of the *ryhA* and *rprA* genes were determined using a 5' RACE assay and the location of the Rho-independent terminator sequences, and annotated on the genome of *E. amylovora.* Red boxes indicate sequences deleted in the Δ*ryhA* and Δ*rprA* mutants. Specific sequences deleted in Δ*ryhA* and Δ*rprA* as well as the genome location of *ryhA* and *rprA* are also indicated.

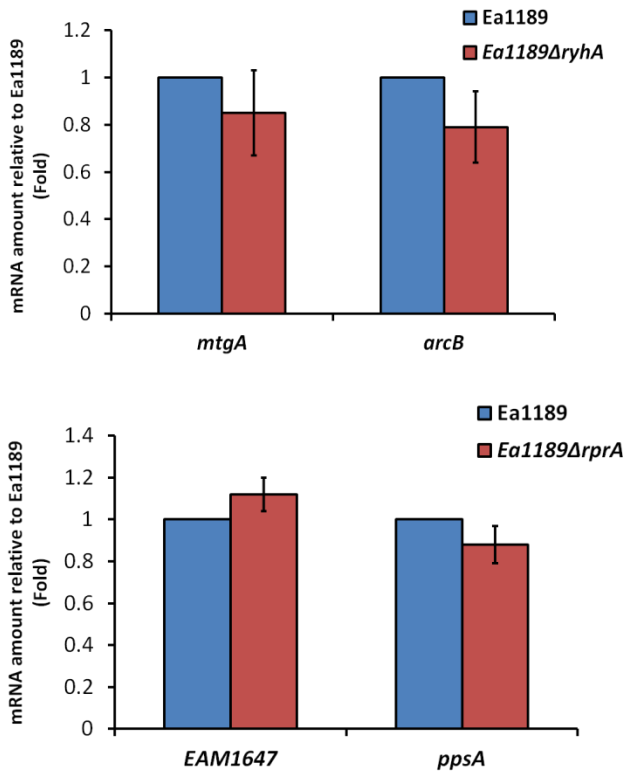

Figure S3. (A) Relative mRNA amount of *mtgA* and *arcB* in Ea1189 and Ea1189Δ*ryhA*. (B) Relative mRNA amount of EAM1647 and *ppsA* in Ea1189 and Ea1189Δ*rprA*. mRNA amount was quantified by qRT-PCR. Experiments contained three replicates and were conducted twice. Data from one representative experiment are shown. No significant differences were observed between wild type and the sRNA mutants ($P > 0.05$).

Figure S4. Virulence of *E. amylovora* Ea1189, Ea1189Δ*hfq*, Ea1189Δ*rprA*, Ea1189Δ*ryhA*, Ea1189Δ*hfq*(pMLhfq), Ea1189Δ*rprA* (pMLrprA), and Ea1189Δ*ryhA*(pMLryhA) in immature pears, at 5 days post inoculation (DPI).