Table S1 Primers used for construction of deletion mutant phages in this study.

Phage mutant	Primer 1 (5′-3′)	Primer 2 (5′-3′)	Primer 3 (5′-3′)
Δ*modA*	GACTCCCAAGCTTGCGCCTTCTGCTATG	GGATGCATCGGTGCGTGCTTCTATTCGGAAGTAATGATACCAGCTGGAAGTG	ATCTTGCAGATGTTGAACAGT
Δ*srd*	ACGCGTCGACTCATCGTAAATTC	CGTTTAGAGCATACTCAGGCATCTGCCTGAAAAGAGGATATCCGCTAAATTG	ACGCGTCGACATTGAGGTAGTTG
Δ*dda-dda.1*	ACGCGTCGACTTATCGTTTTGTTG	GCGATAGTTTACCGAGACAAAGACGGTGTCACCCGTGGTCGTTATGATGTG	ACGCGTCGACGTAAGATGTGAGAA
Δ*dexA.1-dexA.2*	ACGCGTCGACTTATCGTTTTGTTG	GGAAGCTATTCGTGGAAATAACTAAAGAGGTCAAATTCGTGATTTAGCGAGG	ACGCGTCGACCAATTGCAGGGAAT
Δ*dexA*	ACGCGTCGACTTAGTTTAAGGTA	GGGAAGTGGTGAAAAAGCAGCGGTTGGGTCTTGAAGATGCTCCATCAGAGG	ACGCGTCGACAAATTTGAGGAAG
Δ*motB.2*	TCAACGCCATCTTCCAATCCAT	GACGCTATAACAATACGCCGAGATCTTGGCGGGCATCAAGTAATGTTCCG	GTACCGGAATTCCGATGAATTAGTTTC

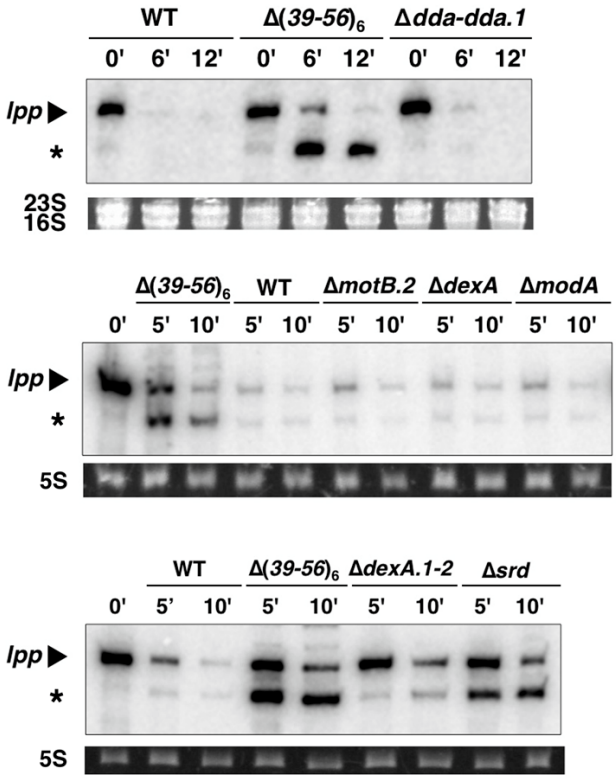

Figure S1 Effect of deleted genes on T4-induced host mRNA degradation. MH1 (wild-type) cells were grown in M9C medium until the OD_{600} reached 0.5 at 37˚, and infected with T4 wild type, Δ(*39-56*)$_6$, Δ*dda-dda.1*, Δ*motB.2*, Δ*dexA*, Δ*modA*, Δ*dexA.1-dexA.2* or Δ*srd* mutant phage. Total RNAs were extracted at the indicated times after infection and then analyzed by northern blotting with a probe for *lpp*. An arrowhead and an asterisk indicate full-length and a decay intermediate of *lpp* mRNA, respectively. Ethidium bromide-stained 5S rRNA or 23S/16S rRNA as a loading control is shown at the bottom of each panel. The Δ*srd* mutant demonstrated that *lpp* mRNA was stabilized and that the decay intermediate was strongly accumulated, as with Δ(*39-56*)$_6$ mutant.

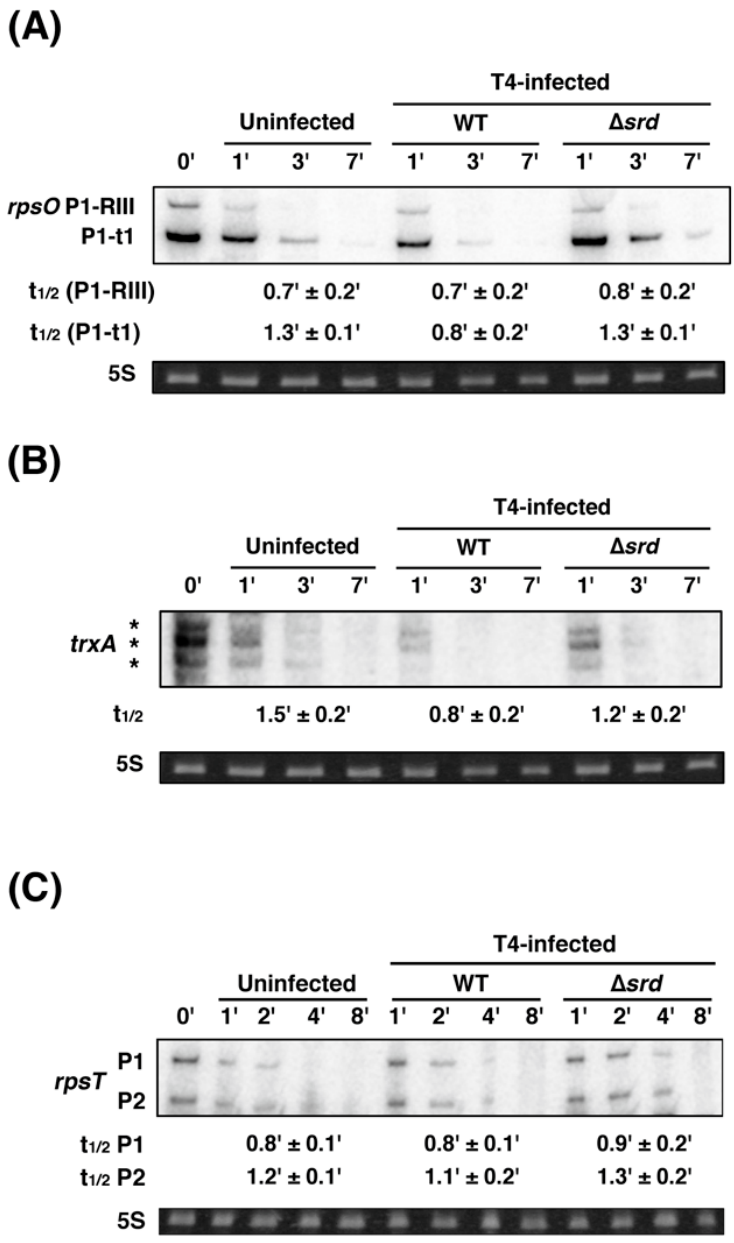

Figure S2 Effect of Srd on stabilities of unstable mRNAs. MH1 (wild-type) cells were grown in M9C medium until the OD_{600} reached 0.5 at 37˚, and infected with wild type T4 or Δ*srd* mutant or treated with rifampicin at a final concentration of 250 μg/ml. Total RNAs were extracted at the indicated times after infection or addition of rifampicin and then analyzed by northern blotting with an oligo-probe for *rpsO* (A, 5′-^{32}P- TTGCTTCAGTACTTAGAGAC), *trxA* (B, 5′-^{32}P-CTGTCGTCAGTCAGGTGAATAATTTTATCGCTC) or *rpsT*(C, 5′-^{32}P-AGAGCGACGGCTTGCGTTGTGCTTACGAGCCTTTTCAGACTGAATGGCGC). The *rpsO*(P1-t1) mRNA corresponds to the monocistronic *rpsO* transcript while the *rpsO*(P1-RIII) mRNA generates from the processing of the *rpsO-pnp* bicistronic transcript by RNase III (Hajnsdorf *et al*. 1994). Asterisks in the figure (B) indicate multiple *trxA* transcripts. Ethidium bromide-stained 5S rRNA as a loading control is shown at the bottom of each panel. Half-lives ($t_{1/2}$) with the mean ± SD of duplicate measurements are shown below the figure. Like *lpp* and *ompA* mRNAs, *trxA* and *rpsO*(P1-t1) mRNAs were destabilized after infection with wild-type T4 and this destabilization was recovered by the deletion of *srd*.

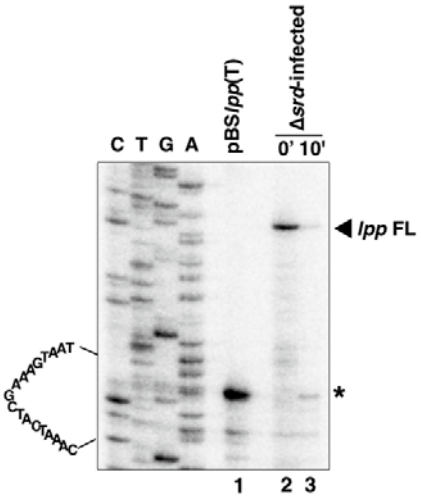

Figure S3 The 5′ end of truncated *lpp* RNA driven from a pBS*lpp*(T) plasmid. Five micrograms of total RNAs extracted from TY1001 (Δ*lpp*::*kan*) cells harboring pBS*lpp*(T) treated with 1 mM IPTG for 10 min (lane 1), from MH1(wild-type) cells at 0 min (lane 2) or at 10 min (lane 3) after infection with Δ*srd* mutant were used for primer extension analysis. FL or an asterisk denotes the full-length *lpp* mRNA or its decay intermediate, respectively. The 5′ end of truncated *lpp* RNA expressed from pBS*lpp*(T) was identical to that of the decay intermediate of *lpp* mRNA accumulated in Δ*srd* mutant-infected cells.

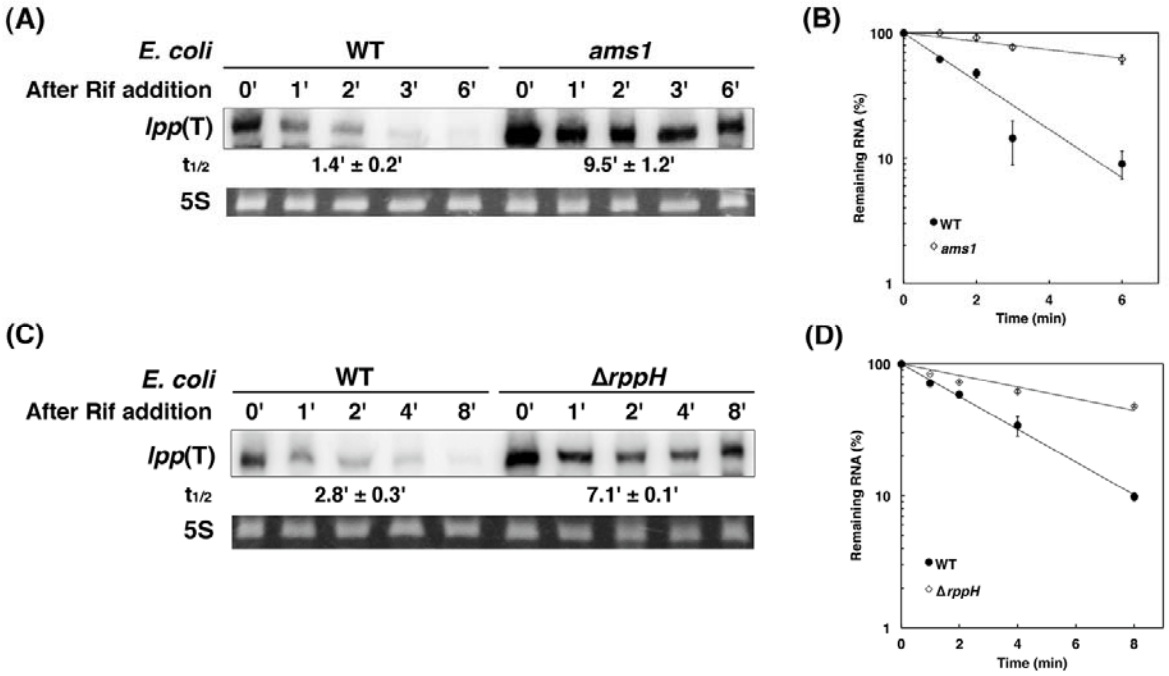

Figure S4 Degradation of *lpp*(T) RNA under normal growth condition. (A) TY1001 (Δ*lpp*::*kan*) or TY1002 (Δ*lpp*::*kan ams1*) cells harboring pBS*lpp*(T) were grown in LB medium until the OD_{600} reached 0.3 at 30˚ and shifted to 44˚ for another 30 min. After cells were treated with 1 mM IPTG for 10 min to induce expression of *lpp*(T) RNA, total RNAs extracted at the indicated times after addition of rifampicin were subjected to northern blotting with a probe for *lpp*. The RNA with a sequence identical to the truncated intermediate of *lpp* mRNA is labeled as *lpp*(T)(upper panel). (B) Quantification analysis of *lpp*(T) RNA in the figure (A) was performed. Data points represent the mean ± SD of triplicate measurements. A half-life ($t_{1/2}$) of each mRNA is shown below the figure (A). (C) TY1001 or TY1006 (Δ*lpp*::*kan* Δ*rppH*) harboring pBS*lpp*(T) were treated with 1 mM IPTG for 10 min when the OD_{600} reached 0.5 at 30˚. Total RNAs extracted at the indicated times after addition of rifampicin were subjected to northern blotting with a probe for *lpp*. (D) Quantification analysis of *lpp*(T) RNA in the figure (C) was performed. Data points represent the mean ± SD of triplicate measurements. *lpp*(T) RNA was degraded by RNase E in RppH-dependent manner under normal growth condition.

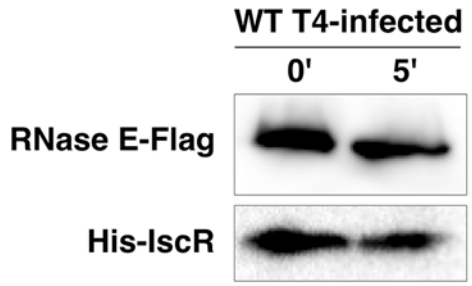

Figure S5 Amount of RNase E before and after T4 infection. TY1007 (*rne-FLAG-cat*) cells harboring pQ-orf2-95 were grown in LB medium until the OD_{600} reached 0.3 and treated with 0.02 mM IPTG for 30 min to induce expression of IscR. Cells were harvested immediately before (0 min) or 5 min after T4 infection. Equal amount of cell extracts were electrophoresed through a 10% polyacrylamide gel containing SDS, followed by western blotting with antibodies against FLAG-tag and His-tag. The amount of RNase E did not change after T4 infection.

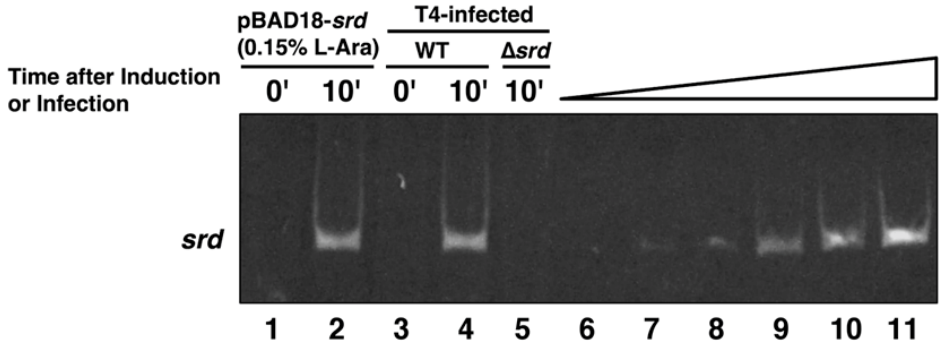

Figure S6 Semi-quantitative RT-PCR analysis to detect *srd* mRNA from T4 genome. Total RNAs from TY0807 cells harboring pBAD18-*srd* at 0 or 10 min after induction of 0.15% arabinose (lanes 1 and 2), or from MH1 cells after infection with wild-type phage (lanes 3 and 4) or Δ*srd* mutant (lane 5) were used for RT-PCR. RT-PCR analyses for *srd* mRNA were performed by incubation at 42° for 50 min with 2 μg of total RNA, 80 units of ReverTra Ace reverse transcriptase (TOYOBO), 1 mM of dNTPs, and 2.5 pmol of *srd*-RT primer (5′-ACGCGTCGACTTATCCTCGGATAAG) in 10 μl of reverse transcription buffer. PCR amplification was performed with 0.2 mM dNTPs, 1 μl of reverse transcription mixture, 10 pmol of sense primer (5′-CGCATAGCAGAAGGCGCTGAAG) and antisense primer (5′-GCGGATATCCTCTTTTCAGTTT), and 1 unit of KOD Dash (TOYOBO) in 25 μl of PCR Buffer. A thermal cycle of 94° for 30 s, 54° for 15 s, and 72° for 20 s was repeated 15 times. The products were separated through a 5% polyacrylamide gel. Various amounts of pBAD18-*srd* were used as a template to demonstrate a semi-quantitative profile of PCR conditions; lane 6: 0.1 ng; lane 7: 0.5 ng; lane 8: 1 ng; lane 9: 2.5 ng; lane 10: 5 ng; lane 11: 10 ng. The level of *srd* mRNA during T4 infection was almost same as that derived from the plasmid.