



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 μ g 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 μ l of reverse transcription buffer. PCR amplification was performed with 0.2 mM dNTPs, 1 μ l 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 μ l 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.