Erratum

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RNase E-based ribonucleoprotein complexes: mechanical basis of mRNA destabilization mediated by bacterial noncoding RNAs

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In the above-mentioned paper, there were two errors in the reproduction of Figures 1B and 3B, in which the Enolase and RNase E-Flag panels were mistakenly used, respectively. The correct figures appear below, with their legends.

Figure 1. (B) Effect of enolase depletion on the expression of SgrS RNA and *ptsG* mRNA. TM461(Δpgi P_{bla} -*ptsG*) and TM509(Δpgi P_{bla} -*ptsG* P_{BAD} -*eno*) cells were grown in M9 medium containing 0.2% succinate and 0.02% glycerol. At $A_{600} = 0.6$, crude extracts and total RNAs were prepared. The crude extracts corresponding to 0.01 A_{600} unit were subjected to Western blot analysis using anti-enolase antibody. Each RNA sample (15 or 5 μ g) was subjected to Northern blot analysis using *ptsG* or *sgrS* probe, respectively.

Figure 3. (B) Effect of nuclease treatment on the Hfq–RNase E interaction. TM338 (*rne-Flag-cat*) cells were grown in LB medium. At $A_{600} = 0.6$, 1% α MG was added to each culture and incubation was continued for 20 min. (Lanes 4–6) A crude extract was prepared and treated with micrococcal nuclease and subjected to the pull-down assay using anti-Flag agarose. (Lanes 1–3) As a control, the extract without micrococcal nuclease was also subjected to the pull-down assay. The crude extracts, unbound fractions, and bound fractions were analyzed by Western blotting using anti-Flag, anti-enolase, and anti-Hfq antibodies. For analysis of RNAs associated with RNase E analysis, 5 μ L of deproteinized crude extracts, unbound fractions, and bound fractions were subjected to Northern blotting using the *sgrS* probe.

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