Corrigendum

In vivo cleavage rules and target repertoire of RNase III in *Escherichia coli*

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In the version of this article originally published online, the authors would like to clarify a mistake with one of the figures. In Figure 2A the presented tracks were mistakenly switched, and they did not match the titles of the y-axes. The correct Figure 2A is shown below and has now been corrected online.

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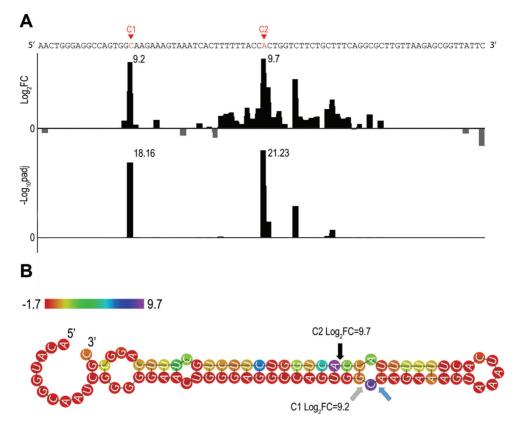


Figure 2. Example of cleavage site detection within *arfA*, a known RNase III target (24). (A). Results of the DESeq2 analysis comparing wt and *rnc-14* read start counts along the *arfA* transcript. Shown are the DESeq2 \log_2 values of the fold change (FC) in read start counts between wt and *rnc-14* (Log₂FC, upper panel) and the DESeq2 adjusted *p* value for multiple hypotheses testing expressed as $-\log_{10}$, (-Log₁₀padj, lower panel). (B) Secondary structure prediction of *arfA* transcript. Arrows designate the cleavage sites detected here and by Garza-Sanchez *et al.* (24): Gray—detected only in our study, blue—detected only by Garza-Sanchez *et al.* (24) and black—detected in both studies. The two cleavage sites detected in our study determine a structural distance of 2 positions, corresponding to dangling ends of 2 n to n both strands. Nucleotide color indicates the \log_2 FC value. Note that C1 and C2 designate the cleavage sites (Panel B) as well as the positions downstream to the cleavage sites (Panel A).