Product Comparison Report

RNase R (Cat. E049)

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MM02060001-202606

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Introduction

RNase R is a highly processive 3'→5' exoribonuclease that selectively degrades linear RNA while largely preserving circular RNA species. This selective activity makes RNase R an essential tool for researchers aiming to remove unwanted linear transcripts and enrich circular RNAs for downstream analyses such as qPCR or RNA-seq.

In this study, we evaluated the performance of **abm** RNase R in comparison to a commercially available RNase R from Competitor N. Total human RNA was treated with each enzyme, and the resulting samples were analyzed using qPCR with primers targeting both linear RNA and circular RNA targets. This dual assessment allows simultaneous evaluation of linear RNA digestion efficiency and circular RNA preservation, highlighting **abm** RNase R's utility in studies of RNA biology.

Method

1. RNA Extraction and Quality Assessment

Total RNA was extracted from HEK293 cells using standard protocols. The integrity and purity of the RNA were carefully evaluated through agarose gel electrophoresis and NanoDrop spectrophotometry to ensure that only high-quality RNA was used for downstream applications.

2. RNase R Treatment

Aliquots of 10 µg total RNA were treated with **abm** RNase R or Competitor N RNase R following the respective manufacturer's recommended conditions. Untreated RNA samples were maintained as controls to provide baseline measurements for comparison.

3. RNA Purification

Following digestion, RNA samples were purified via ethanol precipitation to remove enzymes and reaction components. This step ensured that the RNA was clean and ready for reliable reverse transcription.

4. Reverse Transcription

Purified RNA was reverse-transcribed into cDNA using **abm All-in-One 5X RT MasterMix (Cat. G592)**. This approach generated high-quality cDNA suitable for subsequent qPCR analysis of both linear and circular RNA targets.

5. qPCR Analysis

The resulting cDNA samples were amplified by qPCR using primers targeting human GAPDH to assess linear RNA degradation, as well as three circRNA-specific primer sets to evaluate circular RNA enrichment using **BlasTaq 2X qPCR Mastermix (Cat. G891)**. Amplification curves were recorded with **abm** RNase R shown in orange, Competitor N RNase R in red, and untreated control in green, providing a clear visual representation of RNA digestion efficiency and circRNA preservation.

This product is for research use only and is not intended for therapeutic or diagnostic applications. Please contact a technical service representative for more information.

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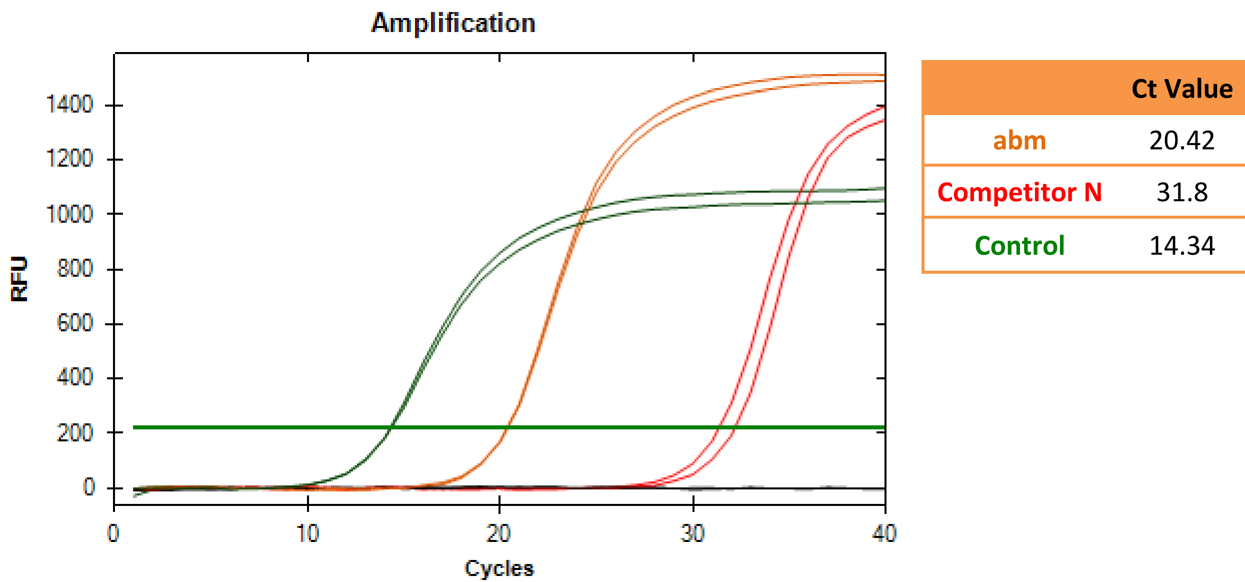
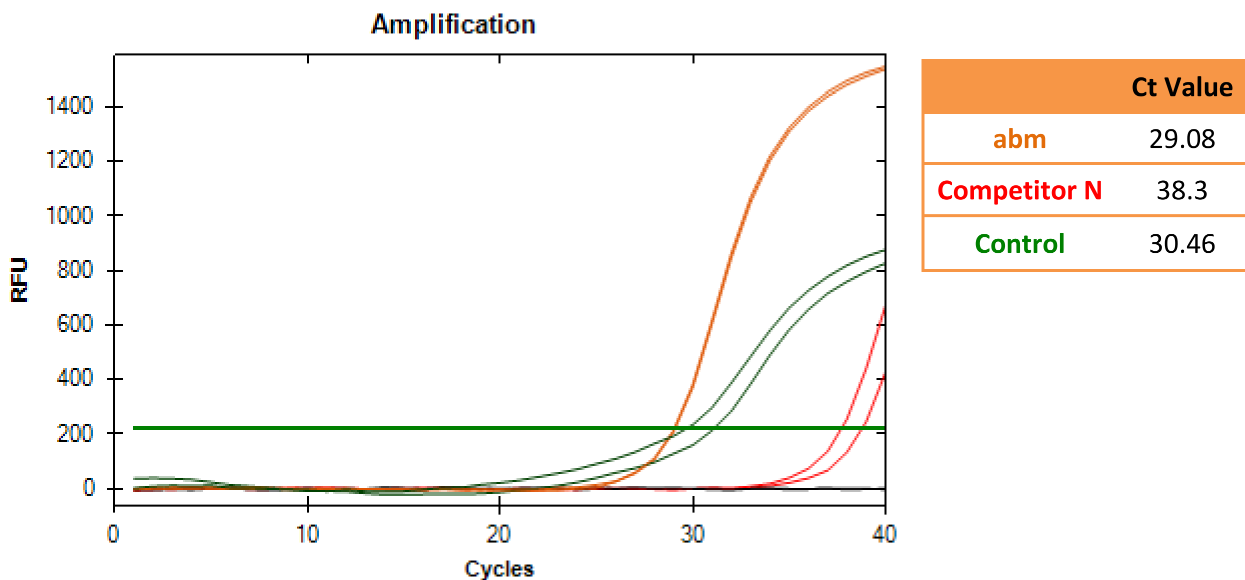
Results



	Ct Value
abm	20.42
Competitor N	31.8
Control	14.34

Figure 1. Linear RNA degradation by **abm** RNase R. Total RNA was treated with **abm** RNase R (orange) or Competitor N RNase R (red), then reverse-transcribed and analyzed by qPCR using human GAPDH primers. Untreated RNA (green) serves as control. Amplification curves show Ct values of 14.34 (control), 20.42 (**abm**), and 31.8 (Competitor N), illustrating efficient linear RNA digestion



	Ct Value
abm	29.08
Competitor N	38.3
Control	30.46

Figure 2. Circular RNA preservation by **abm** RNase R. Total RNA was treated with **abm** RNase R (orange) or Competitor N RNase R (red), then reverse-transcribed and analyzed by qPCR using circRNA primer 1 (Cssp1). Untreated RNA (green) serves as control. Amplification curves show Ct values of 30.46 (control), 29.08 (**abm**), and 38.3 (Competitor N), with **abm** RNase R producing a stronger and earlier amplification signal, highlighting its superior ability to preserve circular RNA while removing linear transcripts.

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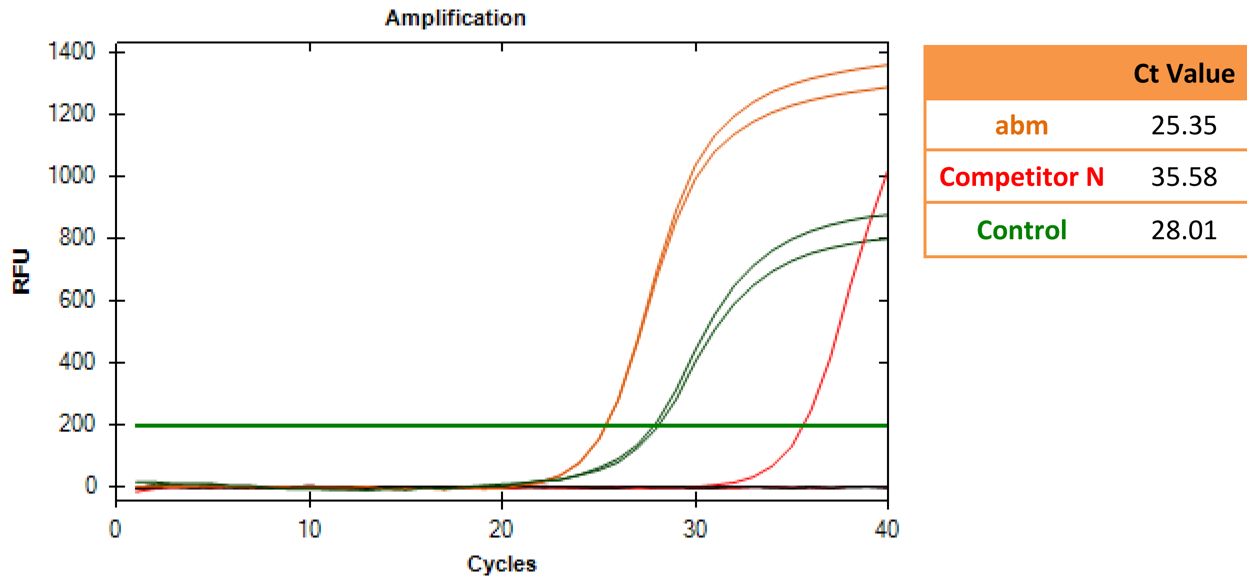
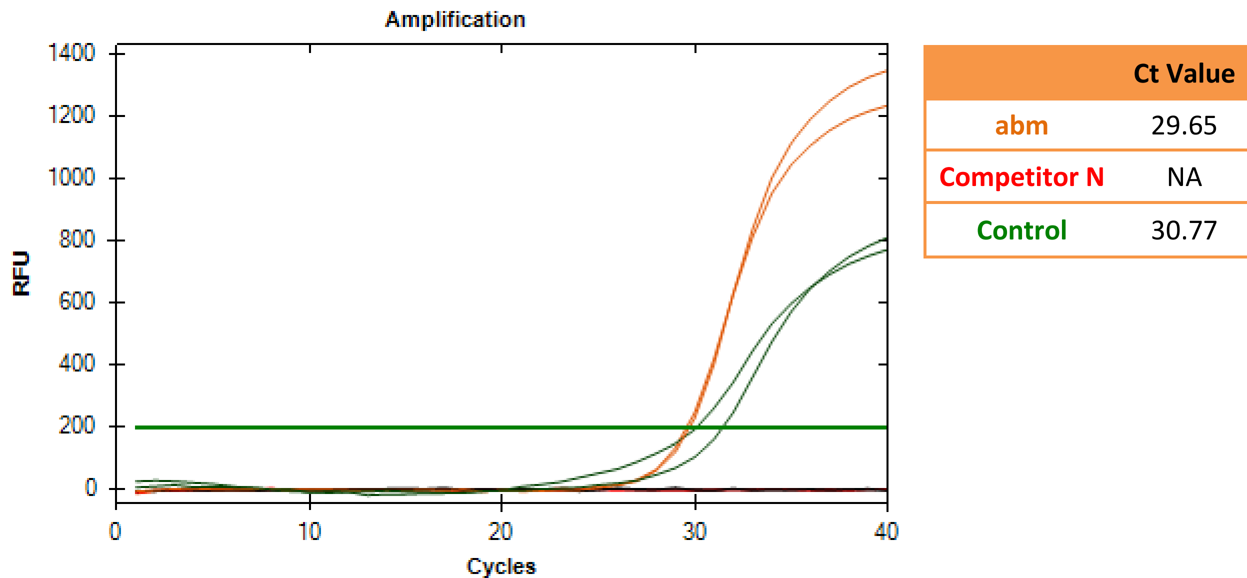


	Ct Value
abm	25.35
Competitor N	35.58
Control	28.01

Figure 3. Circular RNA preservation by **abm** RNase R. Total RNA was treated with **abm** RNase R (orange) or Competitor N RNase R (red), then reverse-transcribed and analyzed by qPCR using circRNA primer 2 (HIPK3). Untreated RNA (green) serves as control. Amplification curves show Ct values of 28.01 (control), 25.35 (**abm**), and 35.58 (Competitor N, only 1 of 2 replicates amplified).



	Ct Value
abm	29.65
Competitor N	NA
Control	30.77

Figure 4. Circular RNA preservation by **abm** RNase R. Total RNA was treated with **abm** RNase R (orange) or Competitor N RNase R (red), then reverse-transcribed and analyzed by qPCR using circRNA primer 3 (MLLT3). Untreated RNA (green) serves as control. Amplification curves show Ct values of 30.77 (control), 29.65 (**abm**), and No detectable amplification form Competitor N.

Conclusion

abm RNase R efficiently degrades linear RNA while selectively preserving circular RNA, enabling reliable circRNA enrichment for downstream analyses. In linear RNA qPCR assays (human GAPDH), **abm**-treated samples showed clear digestion of linear transcripts, with amplification curves reflecting robust RNA removal. For circular RNA targets (Cssp1, HIPK3, and MLLT3), **abm**-treated RNA consistently produced stronger and earlier amplification curves compared to both untreated controls and Competitor N-treated samples, highlighting superior circRNA preservation. Competitor N-treated RNA, in contrast, showed delayed or inconsistent amplification, and in some cases failed to produce detectable signals, indicating reduced circular RNA retention. Overall, **abm** RNase R delivers reliable linear RNA digestion while maintaining and enriching circular RNA, offering a powerful tool for circRNA-focused studies.