APPLICATION NOTE

RNA extraction from mouse tissues using the Omni THQ and 5 mm Omni Tips.

Omni THQ digital tissue homogenizer and 5 mm Omni Tip

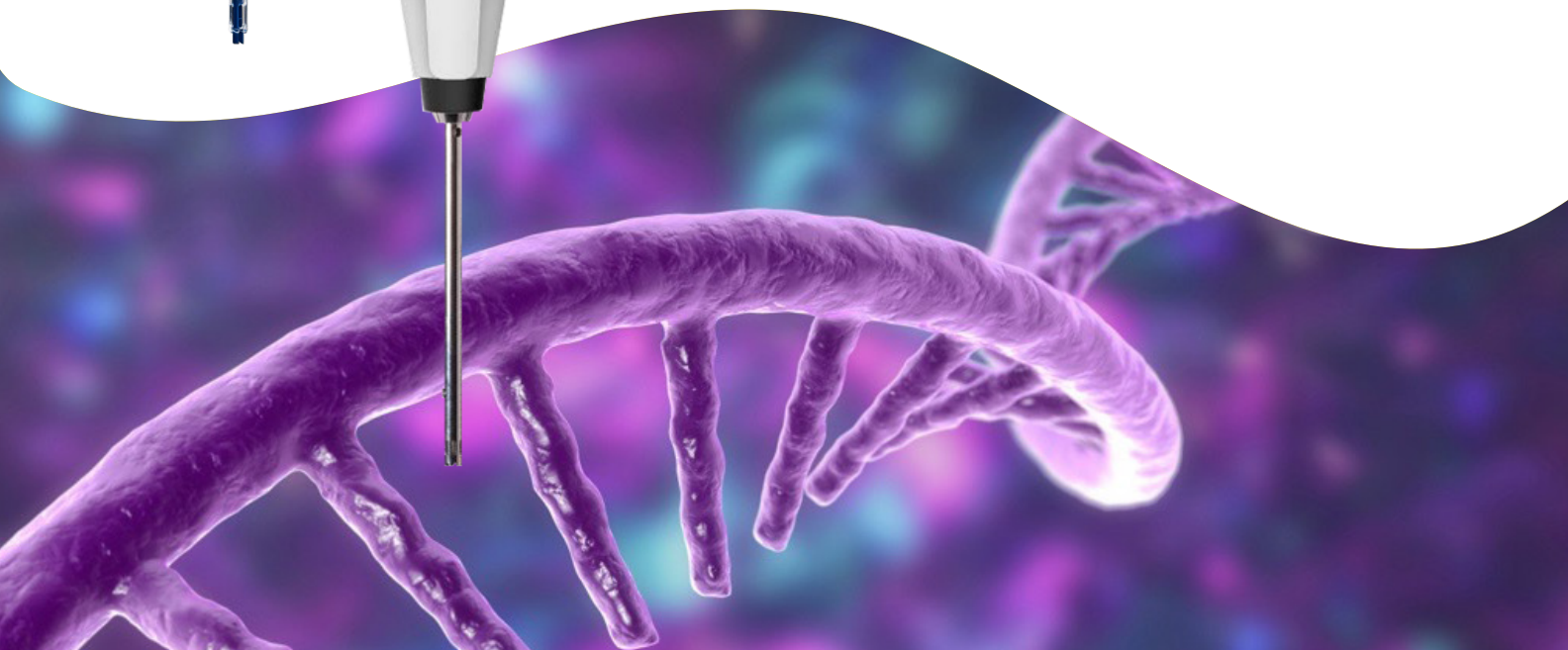
Introduction

High quality RNA extractions are fundamental in modern nucleic acid applications such as qPCR, RNA sequencing, and microarray analysis.[1] Given RNA's inherent instability and susceptibility to degradation by ribonucleases (RNases), minimizing heat exposure and ensuring efficient cellular lysis are critical for reducing excessive shearing and preserving RNA integrity throughout the extraction process.

RNA extractions are also frequently performed in low-throughput laboratory settings, where budget constraints and limited resources create the need for cost effective and accessible solutions. Extensive protocol optimization needed with enzymes and manual homogenization is often impractical in these settings, making simplicity and reliability equally as important as performance.

The Omni THQ digital tissue homogenizer addresses these challenges with rapid and controlled mechanical disruption of tissue samples. Its digitally controlled speed supports consistent parameters across samples, minimizing variability and reducing the risk of localized heat generation that can accelerate RNase activity and RNA degradation.

The hand-held homogenizer also delivers consistent, high-quality homogenization without requiring complex method development or significant capital investment. This homogenization paired with a commercially available total RNA extraction kit, supports high-purity RNA and high RNA integrity number (RIN) values for reliable downstream analysis.



This technical note evaluates the performance of the Omni THQ equipped with the 5 mm Omni Tip™ for efficient homogenization and cellular lysis in smaller sample sizes and reduced tube formats, expanding accessibility and inclusivity in testing parameters. Our findings determine that this combination achieves complete homogenization without compromising RNA integrity, establishing a reproducible, efficient, and accurate method for high-quality RNA extraction suitable downstream applications.

Methods

Equipment

- Omni THQ digital tissue homogenizer (part number 12-500)
- Soft Tissue Omni Tip Plastic Homogenizing Probes, 5 mm (500/pk) (part number 35550)

Fresh mouse tissues (liver, kidney, and muscle) were excised and sectioned into 10 mg (± 1 mg) samples (n = 4 per tissue type). Each sample was transferred to a 5 mL round bottom tube containing 470 µL of lysis buffer and proteinase K master mix, prepared according to the manufacturer's instructions. Homogenization was performed using the Omni THQ digital tissue homogenizer equipped with 5 mm soft tissue Omni Tip plastic homogenizing probes at 20,000 RPM. Liver and kidney tissues were homogenized for 30 seconds, while muscle tissue was processed for 60 seconds for complete cellular disruption.

All steps of the RNA extraction were carried out on ice following the kit manufacturer's protocol. The extracted RNA was eluted in 100 µL of elution buffer, and RNA concentration was determined using the the Thermo Scientific™ NanoDrop™ 2000 spectrophotometer. RNA integrity was subsequently evaluated using the Agilent 2100 Bioanalyzer® system.

Results

The RNA extraction successfully recovered RNA from fresh homogenized mouse liver, kidney, and muscle tissues. Liver tissue yielded notably higher RNA concentrations compared to kidney and muscle tissues, which is consistent with the high transcriptional activity characteristic of hepatic tissue (Table 1). The corresponding average RNA integrity numbers (RINs) for liver, kidney, and muscle tissues exceeded the benchmark threshold of 7, indicating high RNA quality and integrity across all three tissue types (Figure 1).

The UV absorbance ratios and RIN values were found to be above accepted benchmark values as shown in Figure 1 and 3. No significant shearing or degradation was visible in the electrophoretograms, confirming that the RNA remained intact and was suitable for further downstream analyses (Figure 2).

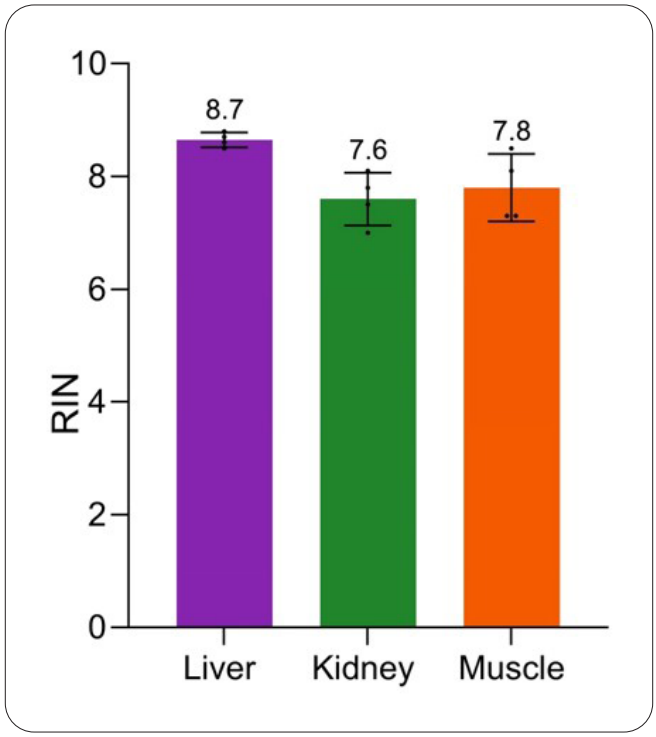
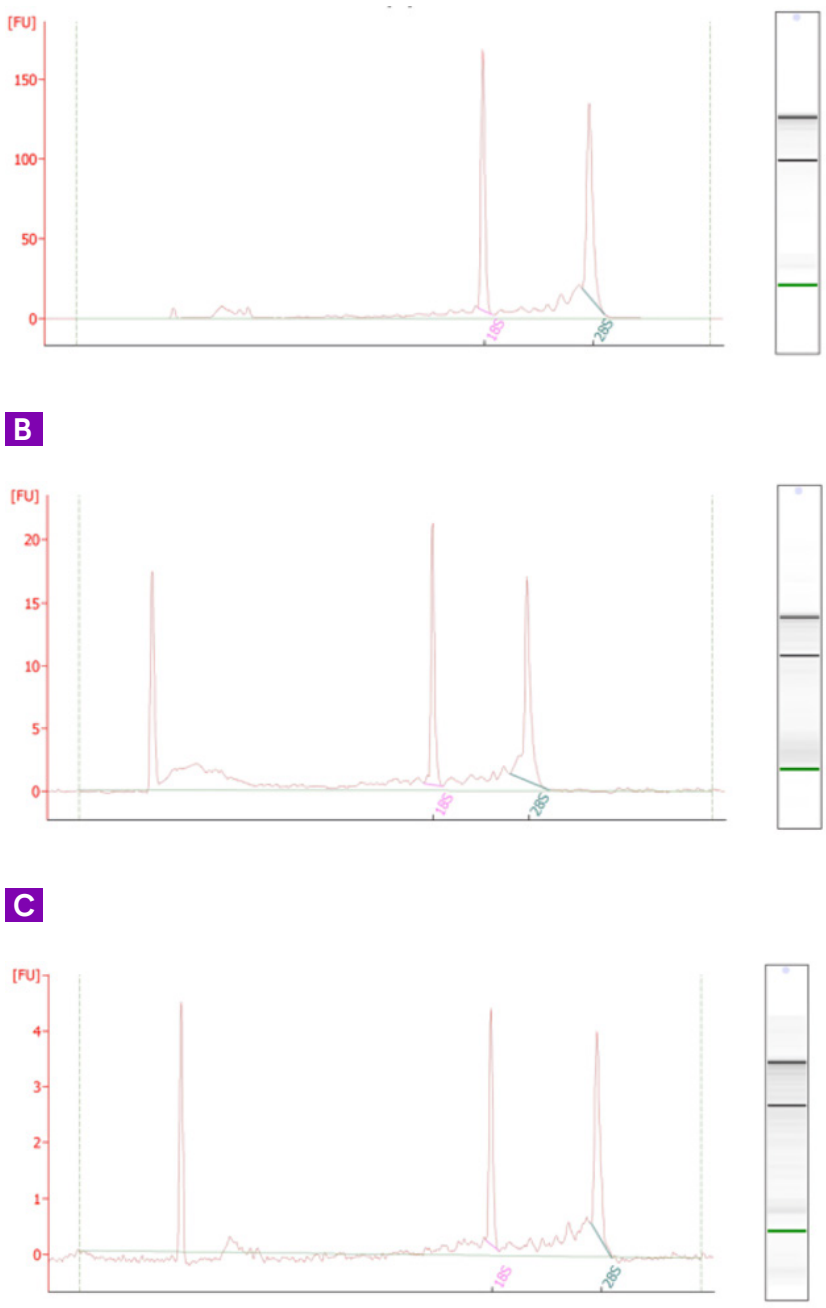


Figure 1: RNA integrity numbers (RIN) obtained from fresh mouse liver, kidney, and muscle tissues following homogenization with the Omni THQ digital tissue homogenizer paired with 5 mm Omni Tips and RNA extraction according to the kit manufacturer's protocol. The error bars represent the spread of RIN values across the samples, with the average RIN value indicated at the top of each error bar.

Table 1: Average RNA yield and standard deviation between the four replicates for each tissue processed on the Omni THQ digital tissue homogenizer using the 5 mm Omni Tips.

Organ	Average RNA concentration (ng/µL)	Standard deviation
Liver	493.25	123.04
Kidney	27.25	8.02
Muscle	32.00	10.98



Liver	
RNA concentration	619 ng/µl
RIN	8.70

Kidney	
RNA concentration	96 ng/µl
RIN	8.10

Muscle	
RNA concentration	17 ng/µl
RIN	8.10

Figure 2: RNA extracted by homogenizing liver, kidney, and muscle tissue samples on the Omni THQ and analyzed using the Agilent Bioanalyzer® 2100 system. Electropherograms showing the lower marker, 18S and 28S peaks for one replicate of (a) liver, (b) kidney, and (c) muscle tissue, respectively (n = 4). Each electropherogram is labeled with its corresponding tissue type, along with overall results including RNA concentration and RIN.

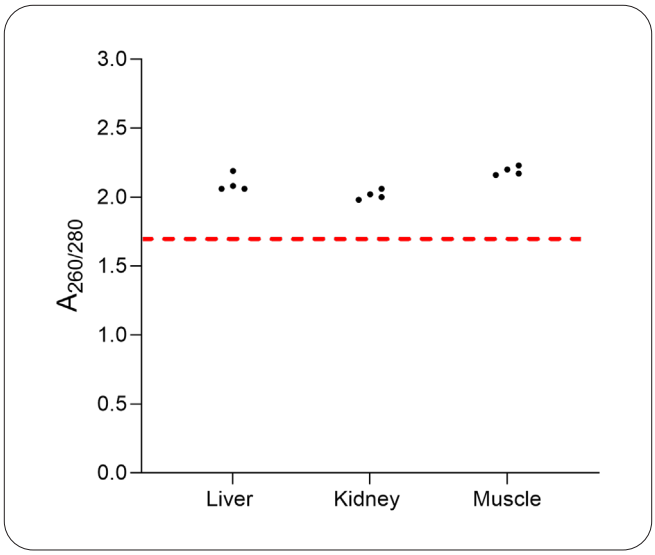


Figure 3: Absorbance ratio ($A_{260}/_{280}$) of RNA extracted from liver, kidney, and muscle tissues. Each dot represents an individual replicate. The red dashed line indicates the minimum accepted QC threshold ($A_{260}/_{280}$ = 1.7). All replicates met or exceeded the QC threshold, indicating acceptable RNA purity.

Conclusions

The Omni THQ equipped with the 5 mm Omni Tip, achieved consistent and reproducible homogenization of liver, kidney, and muscle tissues. RNA extracted from all tissue types met established quality thresholds for concentration, $A_{260}/_{280}$ ratio, and RIN value, confirming compatibility with downstream applications including gene expression profiling and RNA sequencing[2].

The 5 mm Omni Tip adds on to the existing 7 mm and 12 mm Omni Tip portfolio, expanding the range of processable sample types and compatible buffer volumes. This broader selection allows researchers to better match homogenization needs. The disposable tip design drastically reduces cross-sample contamination, a critical advantage when working with limited or irreplaceable material. Rapid processing further reduces the risk of heat-induced RNA degradation, and minimal protocol optimization was required to achieve high-quality yields.

Collectively, these findings support the Omni THQ as an efficient and accessible homogenization platform suitable for low-throughput laboratory settings. Furthermore, its compatibility with the Omni LH96 automated homogenizer workstation provides a scalable pathway for high-throughput applications, positioning the Omni THQ and the 5 mm Omni Tips as a versatile solution across a broad spectrum of research and analytical workflows.

References

1. Opitz L et al., Impact of RNA degradation on gene expression profiling. *BMC Med Genomics*. 2010 Aug 9;3:36. doi: 10.1186/1755-8794-3-36. PMID: 20696062.
2. Texas A&M University. (2025). TxGen sample requirements. Texas A&M University. https://www.txgen.tamu.edu/wp-content/uploads/txgen/TxGen_Sample_Requirements.pdf