

# Ion AmpliSeq Transcriptome Human Gene Expression Kit



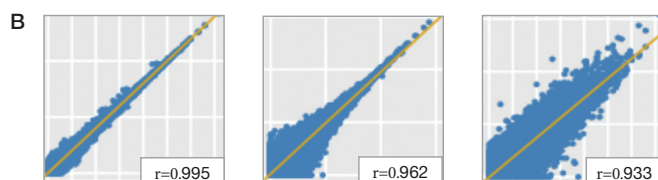
## Easy gene-level transcriptome sequencing

The Ion AmpliSeq™ Transcriptome Human Gene Expression Kit with the Ion S5™ System enables fast and affordable gene expression analysis from limited or degraded samples, such as formalin-fixed paraffin-embedded (FFPE) tissues (Figure 1). With simultaneous amplification of more than 20,000 RefSeq genes in a single tube starting from as little as 100 pg of high-quality RNA or 10 ng of FFPE RNA, the Ion AmpliSeq Transcriptome Human Gene Expression Kit transforms cancer and translational research in tumor profiling and biomarker discovery.

Leveraging the speed and simplicity of Ion AmpliSeq™ technology, this ultrahigh-multiplex PCR enrichment approach enables rapid gene expression profiling with minimal hands-on time, allowing you to go from RNA to quantitated gene expression in less than 2 days. This research method provides a wider quantitative dynamic range and improved transcript detection compared to conventional microarray analysis. The Ion AmpliSeq Transcriptome Human Gene Expression Kit completes the continuum of Ion Torrent™ RNA sequencing solutions, from targeted RNA research panels to global unbiased whole-transcriptome profiling.

**A**

| Sample name     | Mapped reads | Valid reads | Targets detected |
|-----------------|--------------|-------------|------------------|
| Fresh frozen #1 | 11.6 M       | 88.0%       | 73.9%            |
| Fresh frozen #2 | 11.6 M       | 88.0%       | 73.9%            |
| FFPE #1         | 9.2 M        | 77.8%       | 67.3%            |
| FFPE #2         | 9.8 M        | 77.7%       | 67.9%            |



**Figure 1. 10 ng of total RNA was used in sample preparation and 8 resulting libraries were barcoded and run on a single chip.** Shown are **(A)** sequencing results for fresh frozen and FFPE tissue samples and **(B)** correlations between fresh frozen replicates, FFPE replicates, and fresh frozen tissue vs. FFPE samples.

## Survey precious FFPE samples

Start with as little as 10 ng input RNA from FFPE tissue.

## Fast and affordable gene expression profiling in under 2 days

Minimize the cost and complexity of gene expression analysis with about 1 hour of hands-on time for library preparation. Maximize sample processing without waiting to batch samples.

## Better research performance

Detect more genes, at lower expression levels, than can be detected with microarrays.

## Leverage existing microarray or other next-generation sequencing analysis pipelines

Utilize straightforward analysis tools to obtain unambiguous gene expression data compatible with current downstream analysis packages.

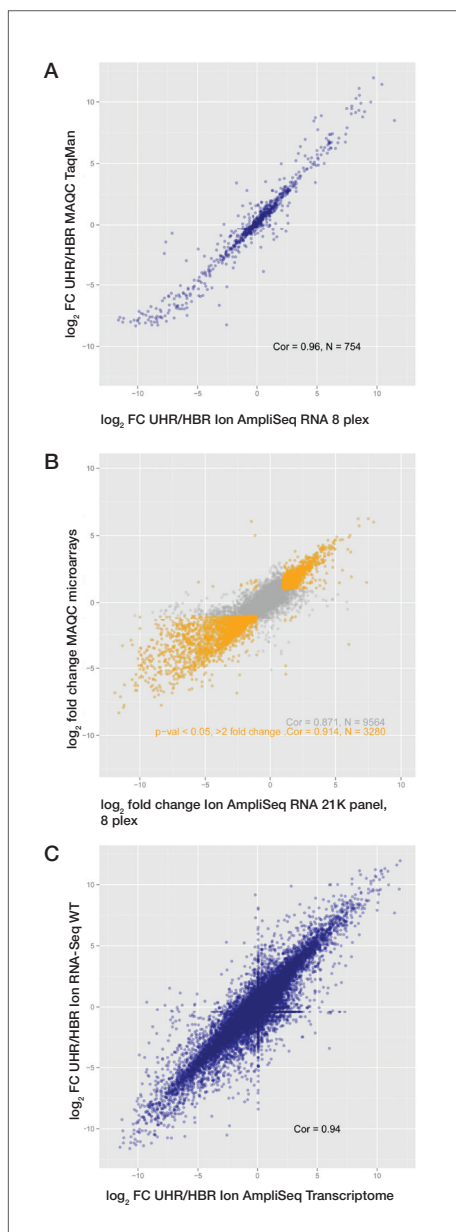
"The Ion AmpliSeq transcriptome technology is a very useful tool for any group analyzing low-input or FFPE samples using RNA-Seq. Our highly degraded, low-yield, or microdissected samples that could not be successfully processed in the past now have a dependable and efficient conduit for library preparation."

### Brad Hancock

Laboratory of Milan Radovich, PhD  
Department of Surgery, Indiana University School of Medicine, USA

See the data comparing FFPE and fresh-frozen samples (under Datasets tab) at [thermofisher.com/ioncommunity](http://thermofisher.com/ioncommunity)

**ThermoFisher**  
SCIENTIFIC

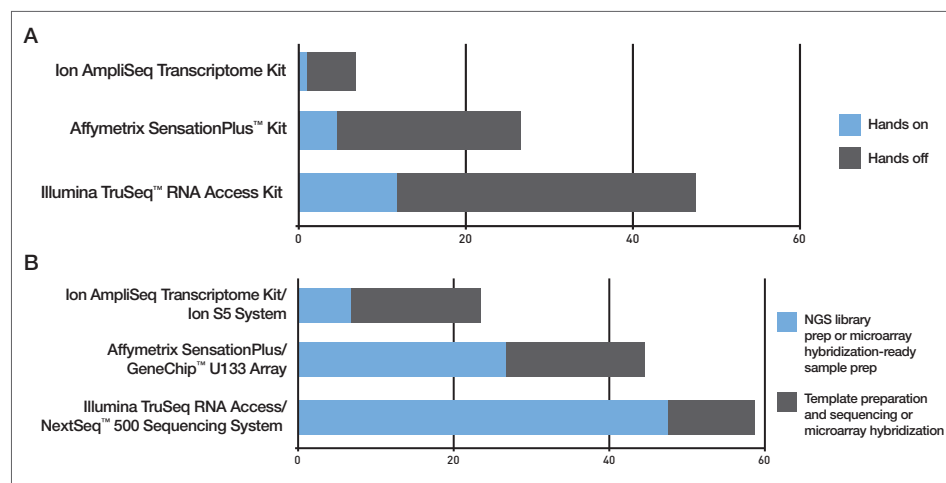


**Figure 2. Correlation of DEGs between Ion AmpliSeq Transcriptome Human Gene Expression Kit data and (A) qPCR, (B) MAQC array, and (C) whole-transcriptome data.**

## Automated data analysis

Point-and-click data analysis with Torrent Suite™ Software provides run metrics on technical reproducibility, read alignment, and detection of on-target transcripts automatically. A list of differentially expressed genes (DEGs) is then easily generated using the Ion Torrent™ ampliSeqRNA plugin and is highly correlated with MAQC array, qPCR, and whole-transcriptome data (Figure 2). The resulting data files are compatible with existing offline analysis tools.

The simplicity and speed of PCR-based library preparation enable a rapid method for gene expression profiling with a less than 2-day workflow from sample to analysis (Figure 3).



**Figure 3: Comparison of hands-on and total turnaround time (in hours). (A) NGS library prep or microarray hybridization-ready sample step only. (B) Entire workflow, from sample to data files.**

## Ion AmpliSeq Transcriptome Human Gene Expression Panel

|                                     |                                                 |
|-------------------------------------|-------------------------------------------------|
| Targets                             | >95% representation of human RefSeq genes       |
| No. of genes designed               | 20,802                                          |
| Input total RNA required per sample | 100 pg of high-quality RNA or 10 ng of FFPE RNA |
| Recommended sample multiplexing     | 8 samples per Ion 540™ Chip                     |

## Ordering information

| Product                                               | Quantity | Cat. No. |
|-------------------------------------------------------|----------|----------|
| Ion AmpliSeq Transcriptome Human Gene Expression Kit* | 24 rxns  | A26325   |
| Ion AmpliSeq Transcriptome Human Gene Expression Kit* | 96 rxns  | A26326   |
| Ion AmpliSeq Transcriptome Human Gene Expression Kit* | 384 rxns | A26327   |
| Ion Xpress Barcode Adapters 1-16 Kit                  | 1 kit    | 4471250  |

Get fast and affordable gene expression analysis from your most precious samples at [thermofisher.com/ampliseqtranscriptome](https://thermofisher.com/ampliseqtranscriptome)

**ThermoFisher**  
SCIENTIFIC

\*Includes Ion AmpliSeq™ Transcriptome Human Gene Expression Core Panel, Ion AmpliSeq™ Library Plus Kit, and Invitrogen™ SuperScript™ VILO™ cDNA Synthesis Kit.

**For Research Use Only. Not for use in diagnostic procedures.** © 2015 Thermo Fisher Scientific Inc. All rights reserved. All trademarks are the property of Thermo Fisher Scientific and its subsidiaries unless otherwise specified. GeneChip and SensationPlus are trademarks of Affymetrix, Inc. NextSeq and TruSeq are trademarks of Illumina, Inc. TaqMan is a trademark of Roche Molecular Systems, Inc., used under permission and license. **CO018753 0915**