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Ion AmpliSeq RNA Custom Panels

Targeted quantitative gene expression analysis

Ion AmpliSeq™ Designer is a free online tool that allows researchers to create and order Ion AmpliSeq™ RNA Custom Panels (ampliseq.com) designed to gene expression targets. Leveraging more than a decade of expertise powering the Applied Biosystems™ Custom TaqMan® Assay design pipeline, Ion AmpliSeq Designer produces optimized primer designs. You now have full flexibility to analyze hundreds of genes of your choice, such as those implicated in particular disease states or representing specific biochemical pathways.

Ion AmpliSeq RNA Custom Panels	
Targets	Choose from over 20,000 quantitative gene expression assays and over 1,000 well-annotated fusion genes
Amplicon length	150 bp amplicons per single pool, 12 to 1,200 primer pairs
Input RNA required	500 pg of unfixed RNA or 1 ng of formalin-fixed, paraffin-embedded (FFPE) RNA
Performance	
Target design rate	Amplicons designed to over 20,000 genes with thorough coverage of the coding genome, plus over 1,000 assays targeting the junctions of well-annotated gene fusion events
Coverage uniformity	Amplicons designed for maximal transcript detection
On-target bases*	>90%

* On-target bases = bases that mapped to target regions, out of total mapped bases per run

- As little as 500 pg of unfixed RNA or 1 ng of FFPE RNA required
- High correlation with Applied Biosystems™ TaqMan® Assay results
- Thorough coverage of the human coding genome
- Specific amplicon design for optimal inclusion of target gene transcripts

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Confirm expression using TaqMan Assays

RNA isolated from FFPE lung tumor and normal adjacent lung tissue from the same sample source was used to generate libraries using the Ion AmpliSeq™ RNA Apoptosis Panel for differential expression research. For comparison, a subset of the 267 genes of the Ion AmpliSeq™ RNA Apoptosis Panel was also assayed using the corresponding Applied Biosystems™ TaqMan® Gene Expression Assays. The high correlation value of 0.949, as shown in Figure 1, highlights the accuracy of the gene expression data obtained with the Ion AmpliSeq™ RNA workflow. Find TaqMan Assays corresponding to the same gene regions interrogated by Ion AmpliSeq™ RNA amplicons at **thermofisher.com/confirmrna**

Simple workflow

The 1.5-day workflow from RNA to annotated genes produces targeted libraries in 5.5 hours, after which the template is prepared using the Ion OneTouch™ 2 or Ion Chef™ System and then sequenced using the Ion S5™ or Ion PGM™ Sequencer. Automated analysis is then performed using Torrent Suite™ Software with the Ion AmpliSeq RNA plug-in (Figure 2). Gene expression data can be easily exported in a simple CSV format for further analysis in third-party software such as Excel™, Bioconductor, or Partek™ Flow™ software.

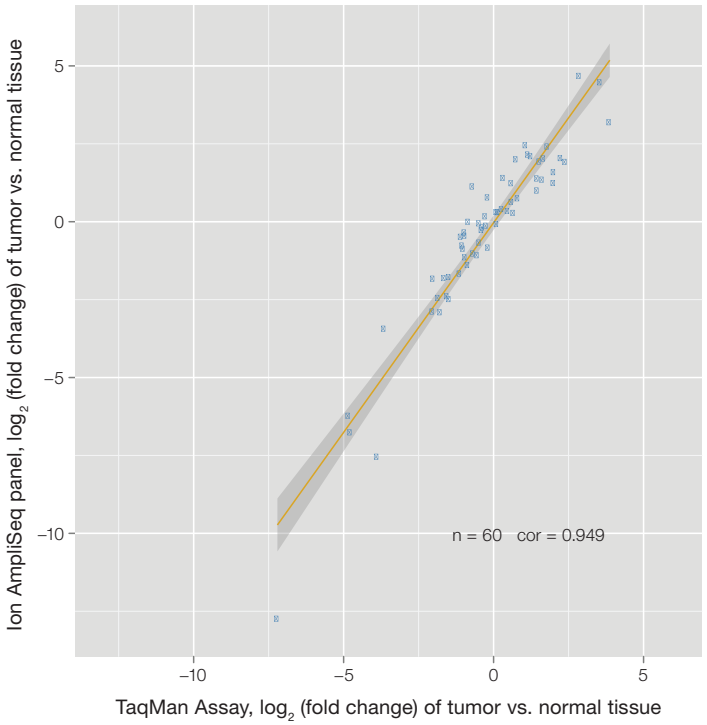

Figure 1. Correlation of Ion AmpliSeq RNA Apoptosis Panel with TaqMan Assays. Fold change between FFPE lung tumor and normal tissue was determined for 60 target genes, by the two methods of targeted gene expression analysis.

Figure 2. Ion AmpliSeq RNA Custom Panel workflow using an Ion 318™ Chip and 4.5-hour, 1 x 200-base sequencing run.

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Ideal for FFPE sequencing—requires only 1 ng of RNA

Ion AmpliSeq™ technology is designed to use as little as 1 ng of FFPE RNA input per primer pool to accommodate the sample quality variability and low sample amounts that are typical of FFPE tissues. All Ion AmpliSeq RNA Custom Panels are compatible with FFPE samples. Targeted selection is completed using standard PCR equipment.

Expanded offering of Ion AmpliSeq panels for your targeted DNA and RNA sequencing

Ion AmpliSeq technology enables simple and fast library construction for affordable targeted sequencing of specific human genes, and human and mouse genomic regions.

	Human DNA	Human RNA	Nonhuman DNA*
Custom panels	√	√	√
Ready-to-use panels	√	√	
Community panels	√	√	

* See **ampliseq.com** for full listing of supported species

Learn more about Ion AmpliSeq RNA panels at **thermofisher.com/ampliseq**

For Ion AmpliSeq Custom Panels, go to **ampliseq.com**

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