

AmpliSeq™ for Illumina Transcriptome Human Gene Expression Panel

Targeted panel for simultaneous analysis of the expression levels of > 20,000 human RefSeq genes.

Highlights

- Fast gene expression profiling**
 Prepare libraries in 6 hours with < 1.5 hours hands-on time; results available in < 2 days
- Low-quality, low-quantity sample input**
 Obtain high-quality data even when starting with minimal input from FFPE tissues
- RNA-to-analysis solution**
 Take advantage of a comprehensive workflow that spans library preparation, sequencing, and analysis

Introduction

The AmpliSeq for Illumina Transcriptome Human Gene Expression Panel is a targeted resequencing assay for quantitating gene expression (Table 1). Starting with as little as 1 ng total RNA (10 ng recommended), the AmpliSeq for Illumina Transcriptome Human Gene Expression Panel yields sensitive, accurate results for gene expression studies even from low-quality or limited quantity samples, including formalin-fixed, paraffin-embedded (FFPE) tissues.

The Transcriptome Human Gene Expression Panel is part of a comprehensive workflow that includes AmpliSeq for Illumina PCR-based library preparation, Illumina sequencing by synthesis (SBS) chemistry and next-generation sequencing (NGS) technology, and automated analysis. Taking advantage of this streamlined workflow, researchers can focus their studies on RNA coding regions, decreasing input requirements while obtaining high-sensitivity and accurate results.

Relevant gene coverage

The AmpliSeq for Illumina Transcriptome Human Gene Expression Panel delivers comprehensive coverage of RNA coding sequences. The single-pool, single-tube panel includes > 20,000 amplicons designed against the NCBI37/hg19 reference genome, covering > 95% of RefSeq genes. This ready-to-use panel saves researchers the time and effort of identifying targets, designing amplicons, and optimizing performance.

Table 1: AmpliSeq for Illumina Transcriptome Human Gene Expression Panel at a glance

Parameter	Specification
No. of genes	> 20,000 (> 95% of human RefSeq gene database)
Cumulative target size	2.2 Mb
Variant types	Differential gene expression, gene fusions
Amplicon size	104 bp on average
No. of amplicons	20,802
Input RNA requirement	1-100 ng (10 ng recommended)
No. of pools per panel	1
Supported sample types	FFPE tissue, blood
Percent aligned reads	> 80%
Total assay time ^a	6 hours
Hands-on time	< 1.5 hours
RNA-to-data time	2.5 days

a. Time represents library preparation only and does not include library quantification, normalization, or pooling.

Data on file at Illumina, Inc. 2017

Simple, streamlined workflow

The AmpliSeq for Illumina Transcriptome Human Gene Expression Panel is part of a comprehensive solution that offers streamlined content, easy-to-perform library preparation, push-button sequencing systems, and simplified data analysis.

Library preparation begins with the conversion of total RNA to cDNA, followed by a straightforward, PCR-based protocol that can be completed in as little as 6 hours, with < 1.5 hours hands-on time. Resulting libraries can be normalized, pooled, and then loaded on to a flow cell for sequencing. Prepared libraries are sequenced using proven SBS chemistry on a compatible Illumina sequencing system (Table 2).

Resulting data can be analyzed locally with Local Run Manager or easily streamed into BaseSpace™ bs-name. Local Run Manager and BaseSpace bs-name can access the RNA Amplicon analysis workflow for gene expression profiling.



Learn more about [Illumina sequencing systems](#)



Learn more about [AmpliSeq for Illumina informatics](#)

Table 2: Illumina sequencing systems recommended for use with the AmpliSeq for Illumina Transcriptome Human Gene Expression Panel

Instrument	No. of Samples per Run	Run Time
MiniSeq System (high output)	3	24 hours
MiSeq System (v3 chemistry)	3	32 hours
NextSeq System (mid output)	12	26 hours
NextSeq System (high output)	40	29 hours

Accurate data

The AmpliSeq for Illumina Transcriptome Human Gene Expression Panel enables researchers to analyze differential gene expression across the transcriptome. To demonstrate assay reproducibility, RNA isolated from brain tissue was analyzed in replicate using the Transcriptome panel and the NextSeq™ sys-model System. Results show a high concordance ($R^2 = 0.98$) between the two samples (Figure 1).

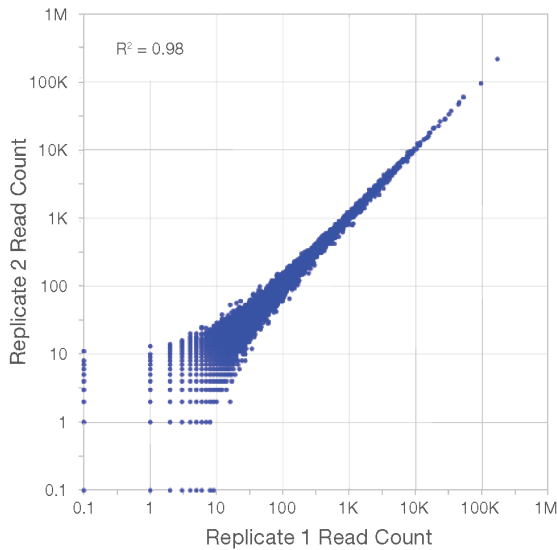


Figure 1: High Concordance Between Replicates—Libraries were prepared using RNA isolated from brain tissue and the AmpliSeq for Illumina Transcriptome Human Gene Expression Panel and sequenced on the NextSeq System. A reproducibility plot shows high correlation between two replicates of the same RNA sample. R^2 is a statistical measurement of data correlation.

Ordering information

Order AmpliSeq for Illumina products online at www.illumina.com

Product	Catalog No.
AmpliSeq for Illumina Transcriptome Human Gene Expression Panel (24 reactions)	20019170
AmpliSeq for Illumina Library PLUS (24 reactions)	20019101
AmpliSeq for Illumina Library PLUS (96 reactions)	20019102
AmpliSeq for Illumina Library PLUS (384 reactions)	20019103
AmpliSeq for Illumina CD Indexes Set A (96 indexes, 96 samples)	20019105
AmpliSeq for Illumina cDNA Synthesis (96 reactions)	20022654
AmpliSeq for Illumina Sample ID Panel	20019162
AmpliSeq for Illumina Direct FFPE DNA	20023378
AmpliSeq for Illumina Library Equalizer	20019171

Learn more

Learn more about the [AmpliSeq for Illumina Transcriptome Human Gene Expression Panel](#)

Learn more about the [AmpliSeq for Illumina targeted sequencing solution](#)