Product Profile

QIAseq Targeted RNA Panels

Digital RNAseq for gene expression analysis

QIAseq Targeted RNA Panels offer:

- Accurate and digital gene expression profiling using molecular barcodes
- Ability to examine hundreds of genes in hundreds of samples
- Disease or pathway-focused genes with 170 panels
- FASTQ to fold change results, using a free online data analysis tool
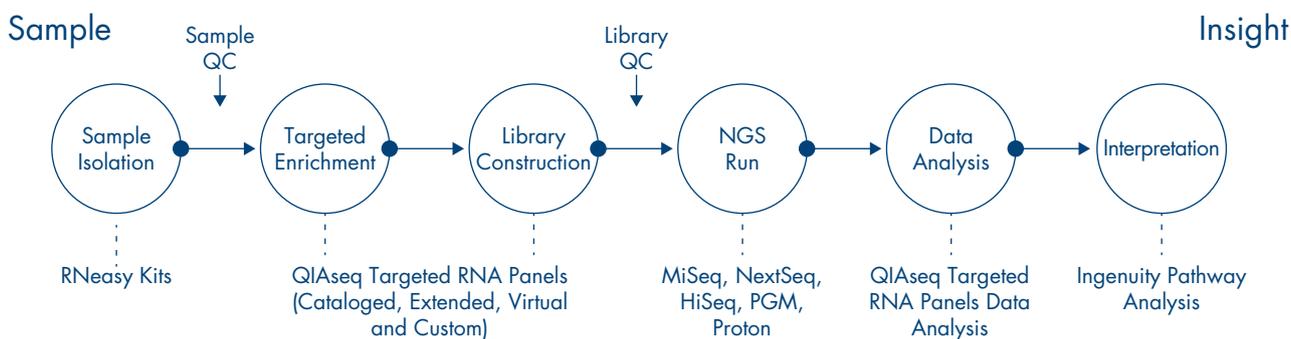
The QIAseq Targeted RNA Panels have been developed as a Sample to Insight® solution for quantitative gene expression profiling using RNAseq. The panels use molecular barcodes and a two-stage PCR-based integrated library preparation to overcome the challenge of PCR duplicates and amplification bias to deliver unbiased, accurate and reproducible gene expression results.

Molecular barcodes: count unique transcripts, not PCR duplicates

PCR duplicates and amplification bias can lead to inaccurate gene expression results using current RNA sequencing approaches. QIAGEN's unique solution to this problem uses molecular barcodes from QIAseq Targeted RNA Panels to tag gene transcripts prior to any amplification steps. By counting these molecular barcodes instead of PCR duplicates, unique gene transcripts can be accurately tallied. The resulting data reflects the original ratios of RNA expression levels (Figure 1).
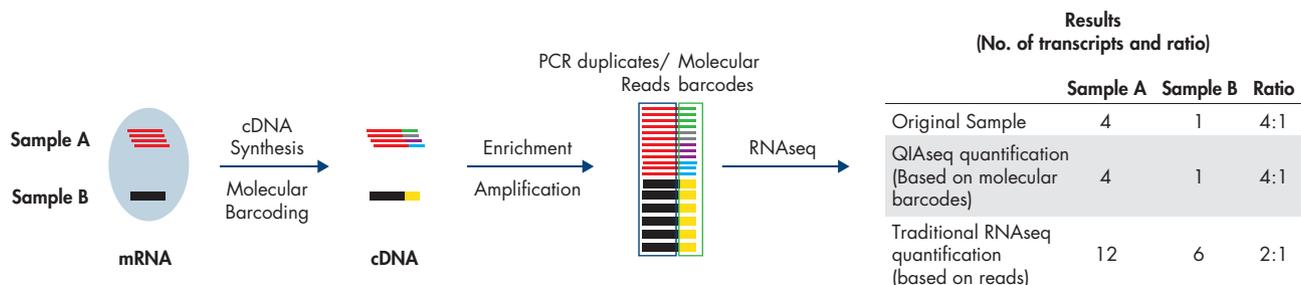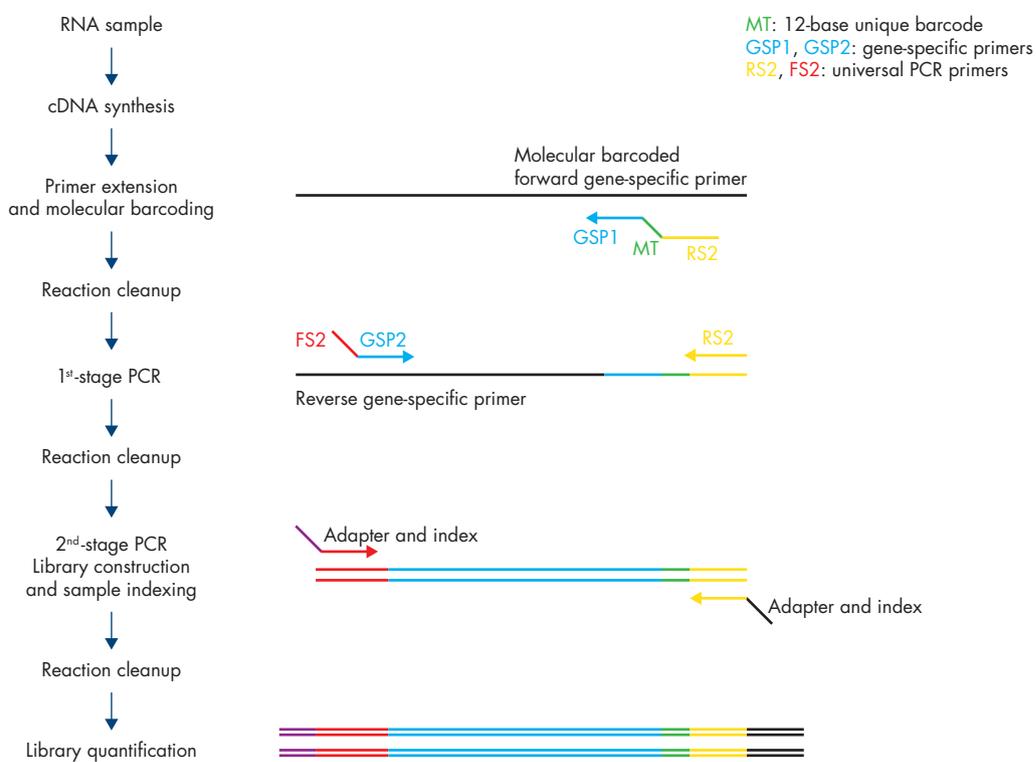
Results (No. of transcripts and ratio)

	Sample A	Sample B	Ratio
Original Sample	4	1	4:1
QIAseq quantification (Based on molecular barcodes)	4	1	4:1
Traditional RNAseq quantification (based on reads)	12	6	2:1

Figure 1. RNA expression levels. QIAseq Targeted RNA Panels use molecular barcodes to preserve the original status of gene levels, thereby reducing PCR amplification bias and duplicates in subsequent steps. The resulting quantification of gene levels is unbiased.

Fast and easy workflow: go from sample to sequencing in one day

Constructing RNA sequencing libraries can be a complicated and lengthy process, ultimately delaying the acquisition of results. QIAseq Targeted RNA Panels combat this issue by offering a fast and easy workflow. Constructing libraries requires only 25 ng of total, unfragmented RNA and six hours of total time (Figure 1). The QIAseq targeted RNA system is an all-in-one solution providing reagents for first strand synthesis, molecular tagging, gene enrichment primer pairs, reaction clean up beads, library preparation adapters and sample indexes (Figure 2).

Figure 2. Simple procedure. Starting with total, unfragmented RNA, cDNA is synthesized. Each cDNA molecule is tagged with a unique molecular barcode immediately after cDNA synthesis and before any amplification occurs. The uniquely tagged cDNA molecules then undergo a two-stage PCR step for enrichment and library construction. The prepared library is then quantified and is ready for sequencing.

MT: 12-base unique barcode
GSP1, GSP2: gene-specific primers
RS2, FS2: universal PCR primers

NGS power: economical gene expression profiling from many samples

Gene expression methods such as qPCR and digital qPCR are either rigid in gene multiplexing or expensive if hundreds of samples are to be profiled. QIAseq Targeted RNA Panels bypass the rigidity and economic burden of these approaches by enabling the simultaneous profiling of thousands of genes in hundreds of samples. For instance, the expression levels of 500 genes can be profiled in 25 samples on the MiSeq® and 400 samples on the NextSeq platforms.

qPCR accuracy: digital quantification

Current targeted RNA sequencing methods for gene expression profiling are challenging due to the introduction of PCR duplicates during amplification steps. PCR duplicates can result in inaccurate and biased gene expression quantification. The QIAseq Targeted RNA Panel tags each cDNA molecule with a unique molecular barcode prior to amplification, thereby generating quantification results that are as accurate as traditional qPCR methods (HBRR and UHRR are reference RNA samples) (Figure 3).
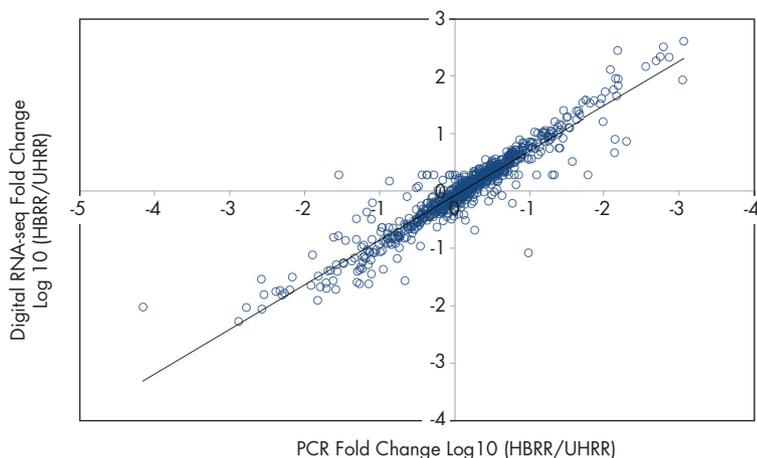

Figure 3. Concordance with qPCR. Expression levels for 384 genes were determined using both QIAseq Targeted RNA Panels and qPCR for Human Brain Reference RNA (HBRR) and Universal Human Reference RNA (UHRR) samples. The expression levels were normalized, fold change between the samples was calculated (HBRR/UHRR) for each gene and compared.

Valuable insight: easy-to-use data analysis

Analysis of RNAseq data can be overwhelming. QIAseq Targeted RNA Panels simplify data analysis by providing automated, free-of-charge online solutions. Just upload your FASTQ or BAM files to the online portal and it will perform base calling, QC scores, read mapping and alignment, molecular barcode counting and conversion into fold changes – all automatically. As outputs, you will get digital gene counts and fold changes. These analyses can then be fed into Ingenuity® Pathway Analysis (IPA) (sold separately) to gain valuable biological insight.

Virtual panels: content for any application

Research Area	Apoptosis Research	Biomarker Research	Cancer Research	Cell Cycle Research
The QIAseq Targeted RNA Virtual Panels, each containing 84 genes and 5 housekeeping genes, build on QIAGEN's know-how to deliver more than 170 panels with biologically- and disease-relevant gene content. The content of the panels has been curated over several years by mining the literature and accessing the proprietary QIAGEN Knowledge database.	Apoptosis	Alzheimer's Disease	Angiogenesis	Apoptosis
	Autophagy	Angiogenesis	Apoptosis	Autophagy
	Cancer PathwayFinder	Breast Cancer and Estrogen Receptor Signaling	Breast Cancer and Estrogen Receptor Signaling	Cancer PathwayFinder
	Cell Cycle	Cancer PathwayFinder	Cancer Drug Resistance and Metabolism	Cell Cycle
	DNA Damage Signaling Pathway	Cell Surface Markers	Cancer PathwayFinder	DNA Damage Signaling Pathway
	DNA Repair	Dendritic and Antigen Presenting Cell	Cell Cycle	DNA Repair
	Endothelial Cell Biology	Epigenetic Chromatin Modification Enzymes	DNA Damage Signaling Pathway	Epithelial to Mesenchymal Transition (EMT)
	Heat Shock Proteins	Epigenetic Chromatin Remodeling Factors	EGF/PDGF Signaling Pathway	MAP Kinase Signaling Pathway
	NFκB Signaling Pathway	Epithelial to Mesenchymal Transition (EMT)	Epithelial to Mesenchymal Transition (EMT)	mTOR Signaling
	Oxidative Stress and Antioxidant Defense	Extracellular Matrix and Adhesion Molecules	MAP Kinase Signaling Pathway	Neurogenesis and Neural Stem Cell
	p53 Signaling Pathway	Glucose Metabolism	p53 Signaling Pathway	NFκB Signaling Pathway
	PI3K-AKT Signaling Pathway	Hematopoietic Stem Cells and Hematopoiesis	PI3K-AKT Signaling Pathway	p53 Signaling Pathway
	Stress and Toxicity PathwayFinder	Homeobox (HOX) Genes	Protein Phosphatases	PI3K-AKT Signaling Pathway
	TNF Ligand and Receptor	Mesenchymal Stem Cell	TGFβ BMP Signaling Pathway	Protein Phosphatases
	Tumor Suppressor Genes	Stem Cell	Tumor Metastasis	Signal Transduction PathwayFinder
	Ubiquitination Pathway	T-cell and B-cell Activation	Tumor Suppression Genes	Transcription Factors
	Unfolded Protein Response	Th1-Th2-Th3	WNT Signaling Pathway	Ubiquitination Pathway

Inflammation Research	ECM/Adhesion Research	Neuroscience Research	Signal Transduction Research	Stem Cell Research	Toxicology/Drug ADME Research
Chemokines & Receptors	Angiogenic Growth Factors & Angiogenesis Inhibitors	Alzheimer's Disease	cAMP/Ca2+ Signaling PathwayFinder	Adipogenesis	Cancer Drug Resistance and Metabolism
Common Cytokine	Atherosclerosis	Apoptosis	EGF/PDGF Signaling Pathway	Dendritic and Antigen Presenting Cell	Cancer PathwayFinder
Inflammasomes	Chemokines and Receptors	Autophagy	G Protein Coupled Receptors	Embryonic Stem Cells	Cardiotoxicity
Inflammatory Cytokines and Receptors	Common Cytokine	Drug Transporters	GPCR Signaling PathwayFinder	Hedgehog Signaling Pathway	Cell Cycle
Inflammatory Response and Autoimmunity	Embryonic Stem Cells	Embryonic Stem Cells	Heat Shock Proteins	Hematopoietic Stem Cells and Hematopoiesis	DNA Damage Signaling Pathway
Interferon α, β Response	Endothelial Cell Biology	GPCR Signaling PathwayFinder	Hedgehog Signaling Pathway	Homeobox (HOX) Genes	Drug Metabolism
Interferon and Receptor	Extracellular Matrix and Adhesion Molecules	Heat Shock Proteins	Insulin Signaling Pathway	Lipoprotein Signaling and Cholesterol Metabolism	Drug Metabolism: Phase I Enzymes
JAK/STAT Signaling Pathway	Glycosylation	Hedgehog Signaling Pathway	JAK/STAT Signaling Pathway	Mesenchymal Stem Cell	Drug Metabolism: Phase II Enzymes
NFκB Signaling Pathway	MAP Kinase Signaling Pathway	Huntington's Disease	MAP Kinase Signaling Pathway	Neurogenesis and Neural Stem Cell	Drug Transporters
T Cell Anergy & Immune Tolerance	Mesenchymal Stem Cell	Hypoxia Signaling Pathway	mTOR Signaling	Neurotrophin and Receptors	GPCR Signaling PathwayFinder
T-cell and B-cell Activation	NFκB Signaling Pathway	Mesenchymal Stem Cell	NFκB Signaling Pathway	Notch Signaling Pathway	Hepatoxicology
TGFβ BMP Signaling Pathway	Osteogenesis	Neurogenesis and Neural Stem Cell	Nuclear Receptors and Coregulators	Osteogenesis	Lipoprotein Signaling and Cholesterol Metabolism
Th17 for Autoimmunity and Inflammation	TGFβ BMP Signaling Pathway	Neuroscience Ion Channels and Transporters	PI3K-AKT Signaling Pathway	Stem Cell Signaling	Mitochondria
Th1-Th2-Th3	TNF Ligand and Receptor	Neurotransmitters Receptors and Regulators	Signal Transduction PathwayFinder	T-cell and B-cell Activation	Molecular Toxicology 384HT
TNF Ligand and Receptor	Tumor Metastasis	Neurotrophin and Receptors	TGFβ BMP Signaling Pathway	Terminal Differentiation Marker	Nephrotoxicity
Toll-Like Receptor Signaling Pathway	VEGF Signaling	Nitric Oxide Signaling Pathway	Transcription Factors	TGFβ BMP Signaling Pathway	Oxidative Stress and Antioxidant Defense
Tumor Necrosis Factor (TNF) Ligand and Receptor	Wound Healing	Notch Signaling Pathway	Wnt Signaling Pathway	Wnt Signaling Pathway	Stress and Toxicity PathwayFinder

Biology-driven content

The contents of several panels have been curated by scientists from many resources such as external databases, scientific publications and QIAGEN's proprietary Knowledgebase, all expertly reviewed (Figure 4). Panel content is relevant to many biological applications: cancer, molecular toxicology, immuno-oncology, signal transduction, apoptosis, inflammation and stem cells. By concentrating on a set of biologically-relevant, research-focused targets, you can achieve a higher level of sample multiplexing, with actionable insights as compared to whole transcriptome sequencing (WTS).

Define your own content, build your unique panel

Building a panel specific to your requirements has never been easier. Through the easy-to-use QIAseq Targeted RNA custom builder accessible at **www.qiagen.com/MyRNAPanel**, you can create your own panel. The only piece of information you need to provide is the list of genes to be quantified. Using the builder, you can also extend the contents of an existing panel by adding up to 25 additional genes.
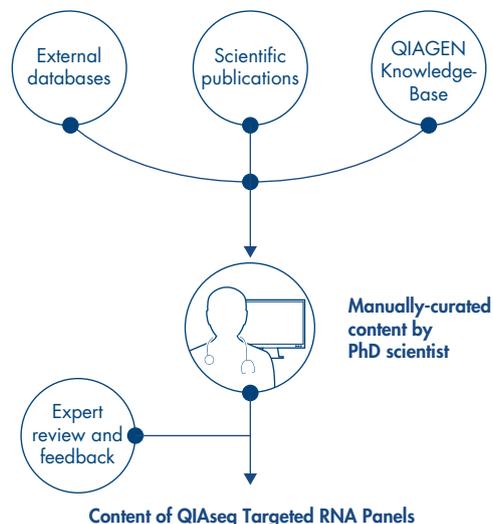

Content of QIAseq Targeted RNA Panels

Figure 4. Panel content is biology-driven. The contents of several panels have been curated by scientists from many resources such as external databases, scientific publications and QIAGEN's proprietary Knowledgebase.

One solution to overcome the challenges of gene expression profiling

	Disadvantages	QIAseq Targeted RNA Panels
Whole transcriptome sequencing (WTS)	• Expensive • Complex data analysis	• Cost-effective • Simplified data analysis • Compatible with FFPE samples
Microarrays	• High background noise • Low dynamic range • High RNA requirement	• High specificity • High dynamic range • Low RNA requirement
qPCR and ddPCR	• Limited sample and assay throughput • Requires lots of RNA	• High sample and assay throughput • Requires as little as 25 ng RNA
Traditional targeted RNAseq	• Inaccurate gene expression profiling due to PCR duplicates and amplification bias	• Digital quantification enabled by molecular barcodes for precise gene expression profiling

Ordering Information

Product	Contents	Cat. no.
QIAseq Targeted RNA Panel (12)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment and library amplification) to enrich predefined genes and construct libraries from up to 12 samples to be sequenced on either Illumina or Ion Torrent™ platforms	333002
QIAseq Targeted RNA Panel (96)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment and library amplification) to enrich predefined genes and construct libraries from up to 96 samples to be sequenced on either Illumina or Ion Torrent platforms	333005
QIAseq Targeted RNA Extended Panel (12)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment, and library amplification) to enrich predefined and extended genes and construct libraries from up to 12 samples to be sequenced on either Illumina or Ion Torrent platforms	333012
QIAseq Targeted RNA Extended Panel (96)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment, and library amplification) to enrich predefined and extended genes and construct libraries from up to 96 samples to be sequenced on either Illumina or Ion Torrent platforms	333015
QIAseq Targeted Virtual Panels	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment and library amplification) to enrich 84 predefined, biologically-relevant, genes and construct libraries to be sequenced on either Illumina or Ion Torrent platforms	Varies
QIAseq Targeted Custom Panel (12)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment, and library amplification) to enrich user-defined genes and construct libraries from up to 12 samples to be sequenced on either Illumina or Ion Torrent platforms	333022
QIAseq Targeted Custom Panel (96)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment, and library amplification) to enrich user-defined genes and construct libraries from up to 96 samples to be sequenced on either Illumina or Ion Torrent platforms	333025
QIAseq Targeted Custom Panel (384)	Complete set of reagents (cDNA synthesis, molecular tags, gene-specific enrichment, and library amplification) to enrich user-defined genes and construct libraries from up to 384 samples to be sequenced on either Illumina or Ion Torrent platforms	333027

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Ordering Information

Product	Contents	Cat. no.
QIAseq Targeted RNA 12-Index I (48)	Sample indexes in tube format to support indexing of up to 12 samples for Illumina platforms; enough for processing 48 samples	333114
QIAseq Targeted RNA 96-Index I (384)	Sample indexes in tube format to support indexing of up to 96 samples for Illumina platforms; enough for processing 384 samples	333117
QIAseq Targeted RNA 96-Index HT I (384)	Sample indexes in plate format to support indexing of up to 96 samples for Illumina platforms; enough for processing 384 samples	333127
QIAseq Targeted RNA 12-Index L (48)	Sample indexes in tube format to support indexing of up to 12 samples for Ion Torrent platforms; enough for processing 48 samples	333214
QIAseq Targeted RNA 96-Index HT L (384)	Sample indexes in plate format to support indexing of up to 96 samples for Ion Torrent platforms; enough for processing 384 samples	333217

QIAseq Targeted RNA Panels, QIAseq Targeted RNA Extended Panels, QIAseq Targeted Custom Panels and QIAseq Targeted RNA Indexes are intended for molecular biology use only. These products are not intended for the diagnosis, prevention or treatment of a disease.

For up-to-date licensing information and product-specific disclaimers, see the respective QIAGEN kit handbook or user manual. QIAGEN kit handbooks and user manuals are available at **www.qiagen.com** or can be requested from QIAGEN Technical Services or your local distributor.

For personal consultation, please contact **DigitalRNAseq@qiagen.com**.

Ordering **www.qiagen.com/contact** | Technical Support **support.qiagen.com** | Website **www.qiagen.com**