Product Profile

QlAseq[™] UPX 3' Transcriptome Kit

For high-throughput 3' transcriptome NGS from ultralow amounts of RNA

The QIAseq Ultraplex (UPX) 3' Transcriptome Kit enables high-throughput next-generation sequencing (NGS) of polyadenylated RNAs on Illumina® sequencers. The kit is intended for library construction and analysis of single cells, cell pellets and ultralow amounts of purified RNA.

Benefits of QIAseq UPX 3' Transcriptome Kit:

- Start with 1 to 100 cells or 10 pg to 1 ng isolated RNA
- LNA-enhanced chemistry for increased accuracy, specificity and sensitivity
- Integrated unique molecular indexing (UMI) removes amplification bias
- Cell tagging and sample indexing enables simultaneous sequencing of up to 18,432 transcriptomes
- Cloud-based data analysis with the GeneGlobe Data Analysis Center

Innovative, optimized workflow

Purified RNA or single cells are first reverse transcribed and each RNA molecule is given a unique molecular index (UMI) and well-specific IDs are assigned (up to 384 wells; Cell IDs). Following reverse transcription with integrated template switching, all cDNAs are combined, enabling simplified library construction steps to be performed in a single tube (Figures 1 and 2).

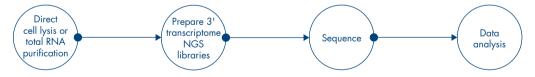


Figure 1. QIAseq UPX 3' Transcriptome workflow.





During subsequent amplification and library construction, up to 48 different library indices (Sample IDs) can be assigned. The combination of Cell IDs and Sample IDs enables up to 18,432 libraries to be sequenced simultaneously.

The QIAseq UPX 3' Transcriptome Kit defines a new generation of high-throughput NGS technologies in QIAGEN's Sample to Insight workflow.

(2 wells shown, up to 96 or 384 wells possible)

RNA AAAA

CDNA Poly-T UMI Cell ID

Pool wells from one plate into one tube

Cell ID

Cell ID

Remaining reactions and library prep from one tube

Perform individual RT reactions in each well

Figure 2. QIAseq UPX 3' Transcriptome Kit handling. Individual reverse transcription reactions are performed for each sample that tag the cDNA with a unique Cell ID and each molecule with a UMI. Following reverse transcription, all wells for a plate, up to 96 or 384 respectively, can be pooled into a single tube. The remaining reactions and library prep associated with that plate are performed in a single tube.

GeneGlobe data analysis

QIAseq UPX cloud-based data analysis is available via the GeneGlobe Data Analysis Center (www.qiagen.com/GeneGlobe) and provides read alignments, UMI and sample de-multiplexing with final single-cell or low-input gene expression analysis.

Ordering Information

Product	Contents	Cat. no.
QIAseq UPX 3' Transcriptome Kit (96)	For 3' transcriptome library prep of 96 cells, cell pellets or ultra-low input RNA samples	333088
QIAseq UPX 3' Transcriptome Kit (96-M)	For 3' transcriptome library prep of 4 \times 96 cells, cell pellets or ultralow input RNA samples	333089
QIAseq UPX 3' Transcriptome Kit (384)	For 3' transcriptome library prep of 384 cells, cell pellets or ultralow input RNA samples	333090

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.

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