

# See the invisible with LUTHOR High-Definition scRNA Sequencing



## LUTHOR HD: Introducing High-Definition Single-Cell RNA Sequencing

Classical high-throughput single-cell RNA-Seq (scRNA-Seq) methods rely on sequencing thousands of cells at low read depths. While this approach is sufficient to identify cell types based on the detection of highly expressed signature genes, it gives an incomplete picture of expressed genes, and is insufficient to finely characterize cell subpopulations.

**LUTHOR HD** enables **high-definition scRNA-Seq** with unprecedented sensitivity and resolution. Thanks to the innovative THOR amplification technology, even low-copy genes are captured and sequenced. LUTHOR HD unravels the full, true transcriptome of each cell (typically 95% of expressed genes at 1 M read depth).

LUTHOR HD is a kit for 3' mRNA sequencing, therefore **ideal for gene expression profiling**. Starting material can be single eukaryotic cells, cell biopsies, or purified total RNA down to 1 pg.



### See more genes

The technology behind LUTHOR HD enables exceptional sensitivity and allows access even to lowly expressed transcripts (< 10 copies/cell).



### Ultra-low input, and "less-than-a-cell" input

LUTHOR HD gives the best results with low initial inputs. Standard is 1 to 100 cells or 10 pg to 1 ng of total RNA, down to 0.15 pg is also possible!



### Straightforward and fast

No RNA extraction, mRNA enrichment, or ribosomal RNA depletion. Streamlined workflow takes you from RNA/cell to ready library in only 6 hours.



### Simple data analysis

Thanks to the innovative THOR technology, no more gDNA in your reads. This reduces bias, simplifies the data analysis and saves on read costs.

## Workflow

The LUTHOR HD protocol starts with the “THOR” amplification of the original RNA molecule (Figure 1). aRNA is then reverse transcribed, and the generated cDNA is amplified (not shown), resulting in a library ready to be sequenced with Illumina-compatible chemistries.

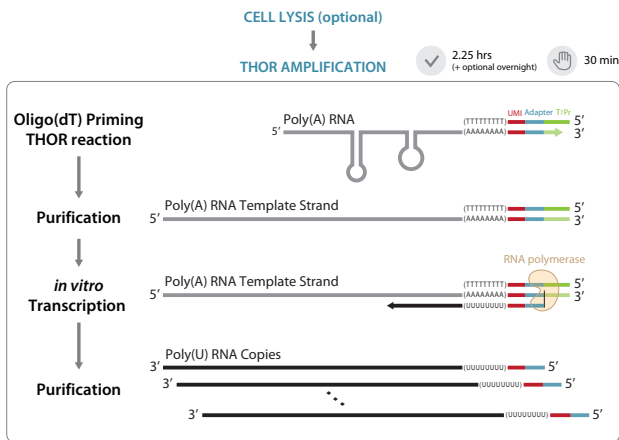


Figure 1 | THOR amplification. Gray: original RNA; black: amplified RNA (aRNA); red: UMI; light blue: P7 Illumina adaptor; light green: T7 promoter.

## See more genes in each cell

One of the challenges of working with very low amounts of RNA is to capture the real transcriptomic diversity. LUTHOR HD provides ultimate performance and enables a more accurate view of gene expression profiles in each individual cell, by allowing more genes to be captured and analyzed (Figure 2).

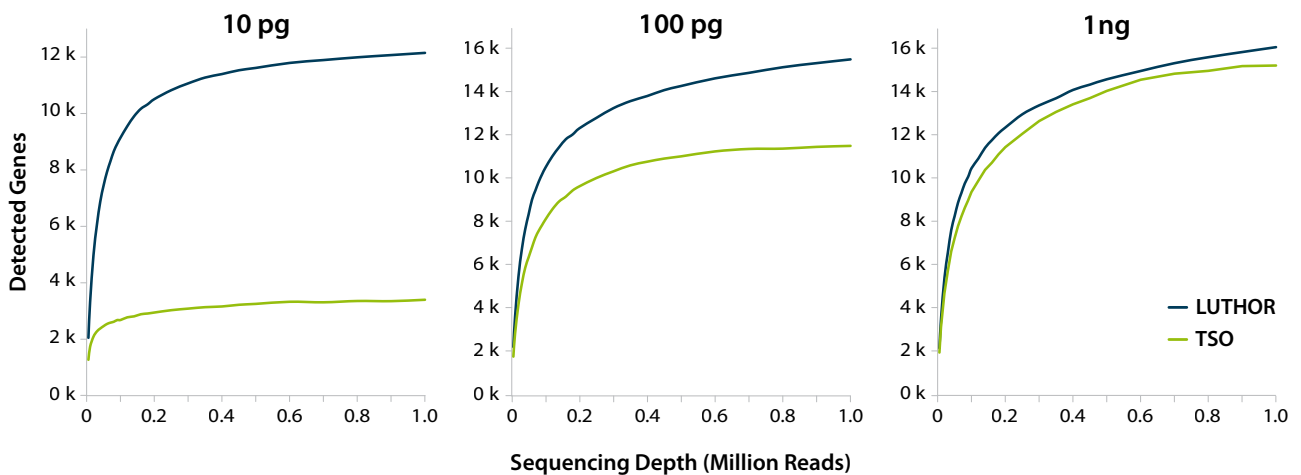


Figure 2 | Average number of genes detected for 10 pg, 100 pg and 1 ng of UHRR, inferred at stepwise-reduced fractions (CPM > 1). Data is based on duplicates (LUTHOR HD) and triplicates (TSO). UHRR: Universal Human Reference Control. TSO is a 3' mRNA-Seq method based on template-switching during initial reverse transcription.



Is LUTHOR HD the right solution for your RNA research? Let's find out!

[www.lexogen.com/luthor-configurator](http://www.lexogen.com/luthor-configurator)

For more information and additional resources, please visit our [website](http://www.lexogen.com).

## Ordering Information

Cat. №	Product Name
221.24	LUTHOR High-Definition Single-Cell 3' mRNA-Seq Library Prep Kit with UDI 12 nt Set B1, (UDI12B_0001-0024), 24 preps
221.96	LUTHOR High-Definition Single-Cell 3' mRNA-Seq Library Prep Kit with UDI 12 nt Set B1, (UDI12B_0001-0096), 96 preps



## Dive into high-definition RNA-Seq

Classical scRNA-Seq approaches targeting thousands of cells at once provide scientists with an overview of cell populations, yet they are far from revealing the full picture of each cell's transcriptomic profile. With LUTHOR HD, you will uncover the “unseen”, deep-dive into each cell's full transcriptome, and gain an exquisite understanding of each cell's unique diversity.

## Explore new frontiers

LUTHOR's exceptional sensitivity enables working with even less than a cell, thereby opening the door to cutting-edge approaches (e.g., cytoplasmic extraction of RNA from live cells). Even 1/100th of a cell-equivalent still consistently leads to detection of thousands of genes (Figure 3).

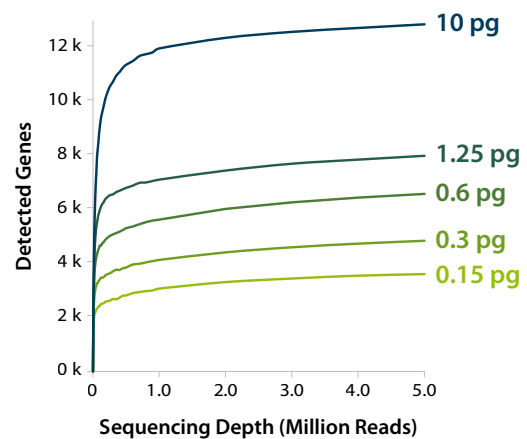


Figure 3 | Average number of genes detected for 10 pg, 1.25 pg, 0.6 pg, 0.3 pg, and 0.15 pg of RNA dilutions (purified RNA from human Panc-1 cells). LUTHOR HD libraries, CPM > 1.