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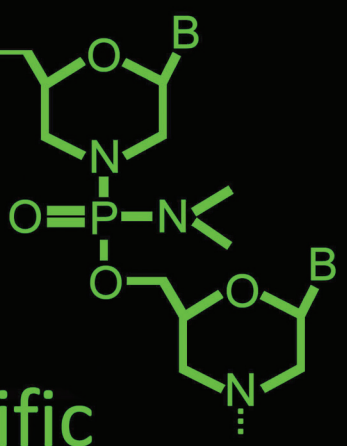

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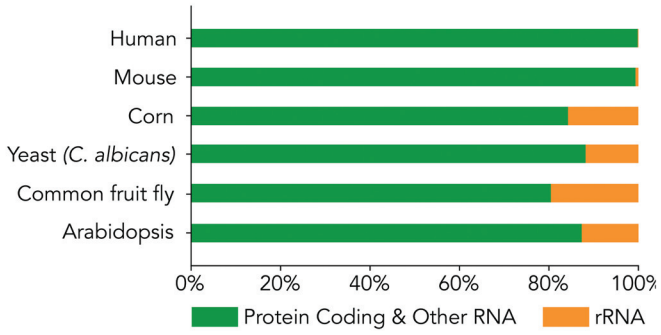

The Zymo-Seq RiboFree Kit Produces Dense Coverage of Protein Coding and Other Transcripts. Classification of the STAR-aligned reads was based on Ensembl annotations and RepeatMasker rRNA tracks from UCSC genome browser when applicable.

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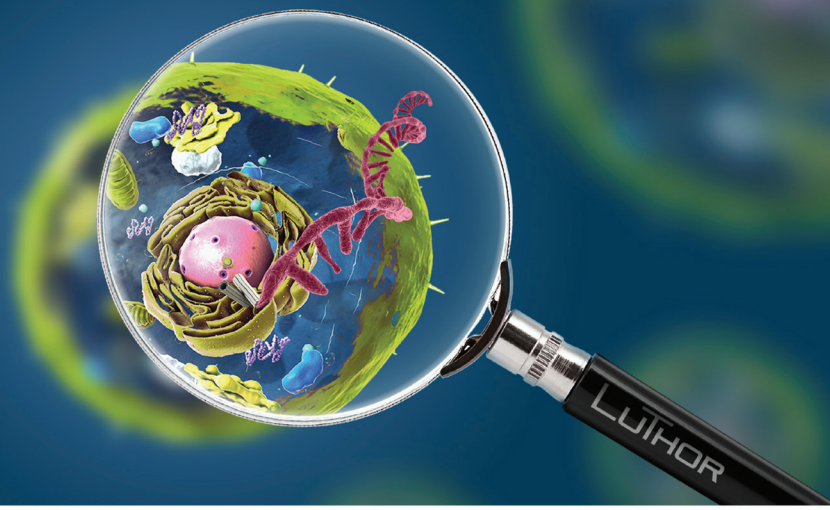
Take a look at the whole picture

with LUTHOR High-Definition scRNA-Seq kits



LUTHOR: your gateway to High-Definition Single-Cell RNA sequencing

When you need to handle subnanogram RNA amounts, you can count on LUTHOR to help! Ideally designed for samples ranging from 100 cells down to a single cell, from 1 ng down to 10 pg total RNA - and even lower - the THOR in vitro transcription step will open up new possibilities and allow you to see many more genes and to determine their expression levels. LUTHOR HD focuses on 3' ends of each gene, hence simplifying the data analysis to the sequences that matter for gene identification and gene count.

Library preparation starts with generation of a double-stranded template for T7-promoted *in vitro* transcription, at the gene 3' end (Fig. 1). Amplified RNA is then prepared by random-primed reverse transcription and subsequent library amplification (not shown).

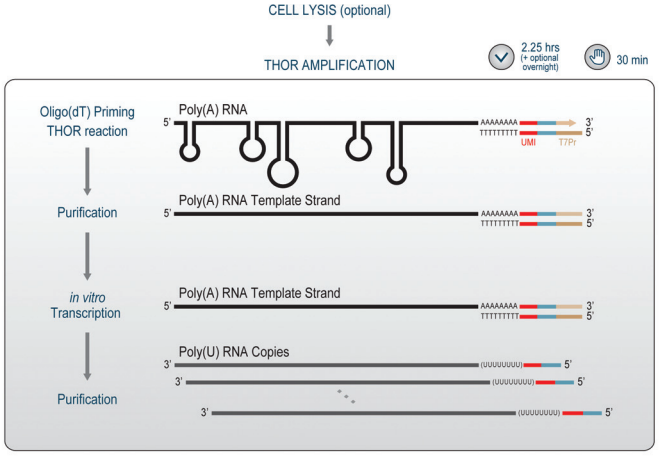
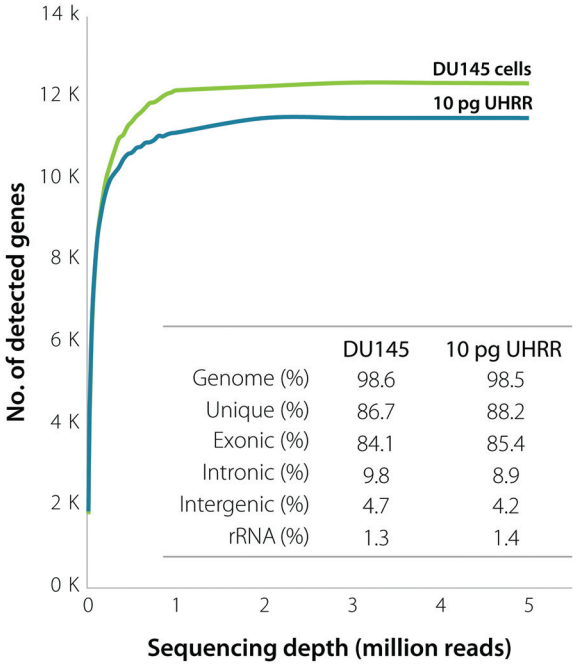


*Figure 1 | THOR (**T**7 **H**igh-resolution **O**riginal **R**NA amplification) reaction diagram. Red line: UMI; blue line: Illumina adapter; light brown line: T7 promoter.*



	DU145	10 pg UHRR
Genome (%)	98.6	98.5
Unique (%)	86.7	88.2
Exonic (%)	84.1	85.4
Intronic (%)	9.8	8.9
Intergenic (%)	4.7	4.2
rRNA (%)	1.3	1.4

Figure 2 | Sensitivity of LUTHOR. Scatter plots of the average number of genes detected per DU145 human cell (contains 18.3 ± 1.5 pg of total RNA) and 10 pg Universal Human Reference RNA (UHRR) inferred across four replicates at stepwise-reduced read fractions (CPM > 1). Table shows sequencing alignment metrics across four DU145 cells and 10 pg UHRR replicates at 1 million read depth.

Interested to learn more?

Check the *Nature Methods* application note!