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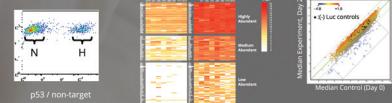
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- Single base-pair resolution
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- High coverage with average $>500x$ and a minimum $100x$

Pyrosequencing Methylation Analysis

- Quantitative, accurate, and cost-effective



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- Represents $\sim 17\%$ of the human genome
- Serves as global methylation markers
- Compatible: MS-HRM, tNGBS, and Pyrosequencing

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- Compatible: MS-HRM, tNGBS, and Pyrosequencing

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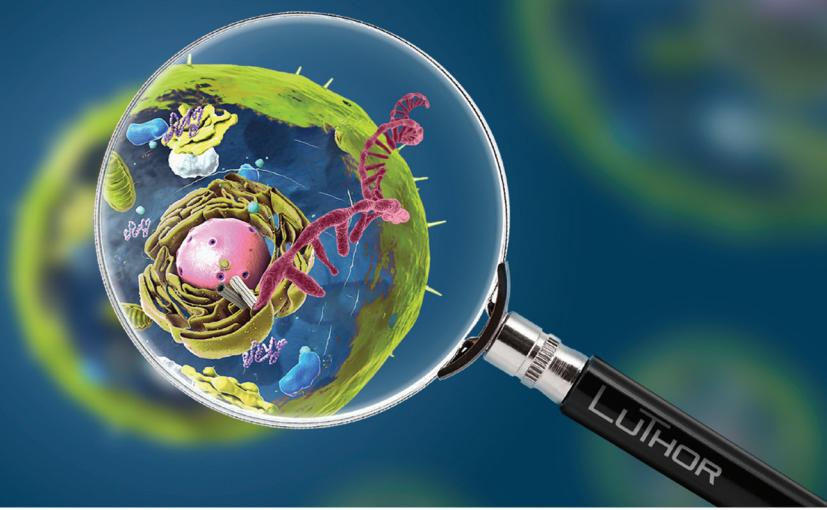
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Take a look at the whole picture

with LUTHOR High-Definition scRNA-Seq kits



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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).

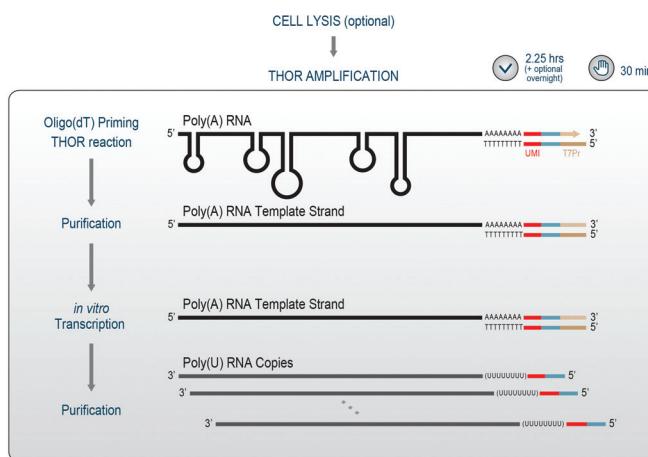


Figure 1 | THOR (T7 High-resolution Original RNA amplification) reaction diagram. Red line: UMI; blue line: Illumina adapter; light brown line: T7 promoter.



Interested to learn more?

Check the *Nature Methods* application note!

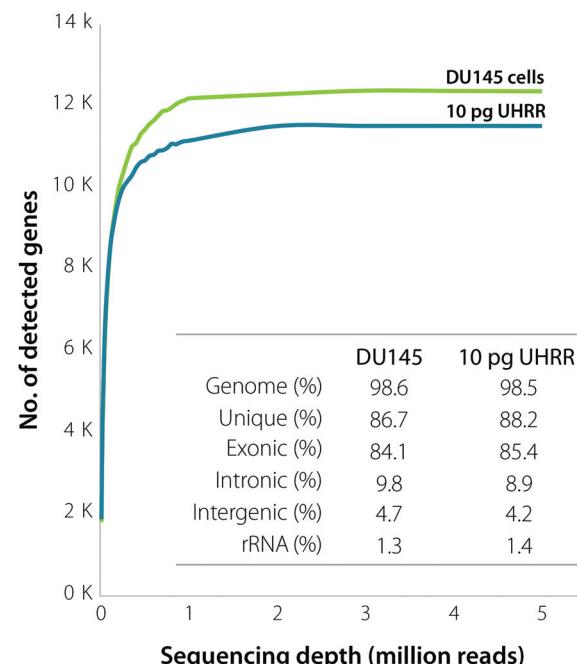
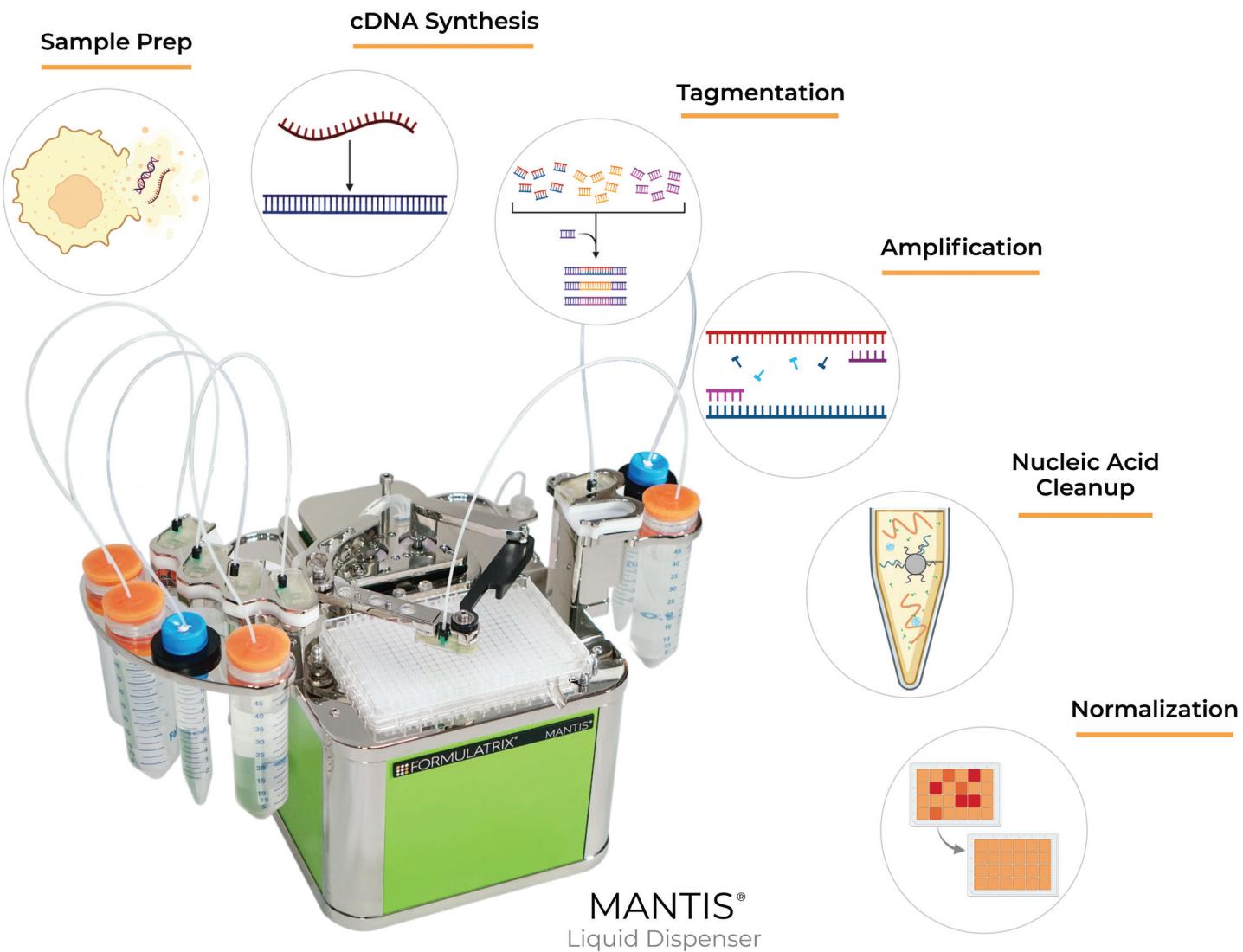


Figure 2 | Sensitivity of LUTHOR. Scatter plots of the average number of genes detected per DU145 human cell (contains 18.3 ± 1.5 pg of total RNA) and 10 pg Universal Human Reference RNA (UHRR) inferred across four replicates at stepwise-reduced read fractions (CPM > 1). Table shows sequencing alignment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

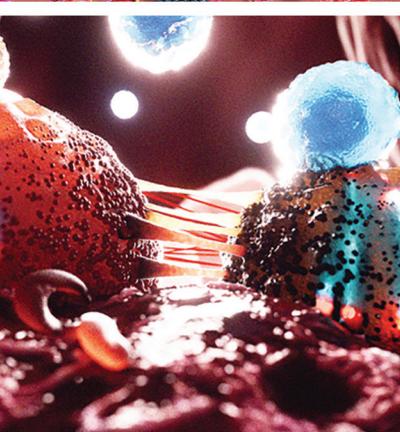
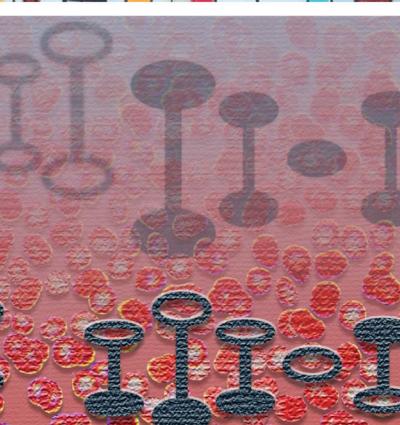
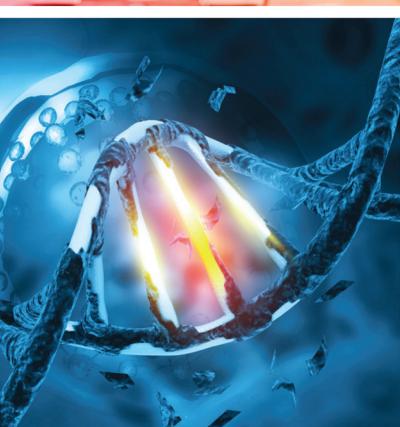
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