CeGaT

Research &
Pharma Solutions

Updated Transcriptome Sequencing

New Transcriptome Sequencing Workflow

CeGaT has updated its wet-lab processes for Transcriptome Sequencing by implementing new and innovative library preparation protocols. This update includes efficient ribosomal RNA (rRNA) depletion across a wide range of species, a highly selective mRNA capture, and a precise total RNA determination, establishing a robust foundation for sequencing diverse RNA sample types.

A key technological improvement is the integration of unique molecular identifiers (UMIs) into the transcriptome workflow. The use of UMIs removes PCR duplicates and reduces amplification bias, resulting in greater data accuracy. This enhances the statistical power of downstream analyses, especially when working with low-quality or limited-quantity samples.

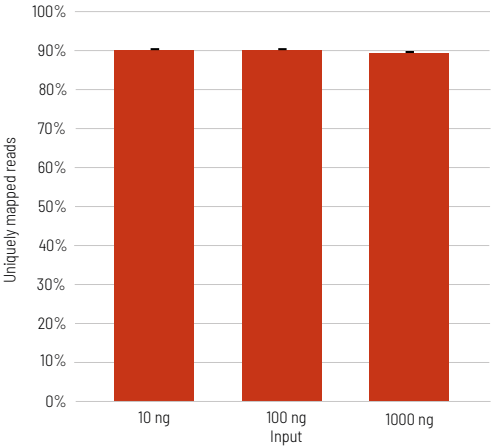

Figure 1 | Percentage of uniquely mapped reads across different input amounts. Independent of the input amount, a high percentage of the sequenced reads are uniquely mapped.

Want to Discover More?

We invite you to take a look at our website.
www.cegat.com/transcriptome-sequencing

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