diagenode
A Hologic Company

D-PLEX SMALL RNA-SEQ LIBRARY PREP KIT

Go deeper with your RNA research & Biomarker discovery

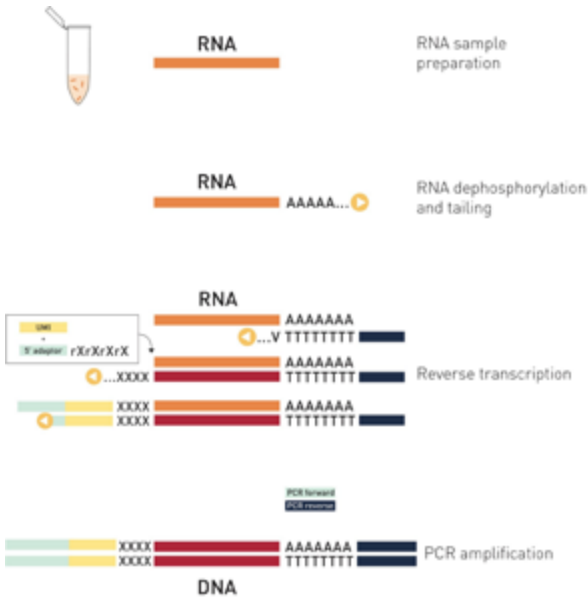
The Diagenode **D-Plex Small RNA-seq Library Prep Kit** is an optimal technology to study the small non-coding RNAs (< 200 nucleotides) that play key roles in the regulation of gene expression at the transcriptional and post-transcriptional levels. This unique ultra-sensitive, ligation-free method uses two innovative mechanisms - **poly(A) tailing** and **template switching** - to generate RNA libraries for next generation sequencing.

ADVANTAGES OF D-PLEX TECHNOLOGY

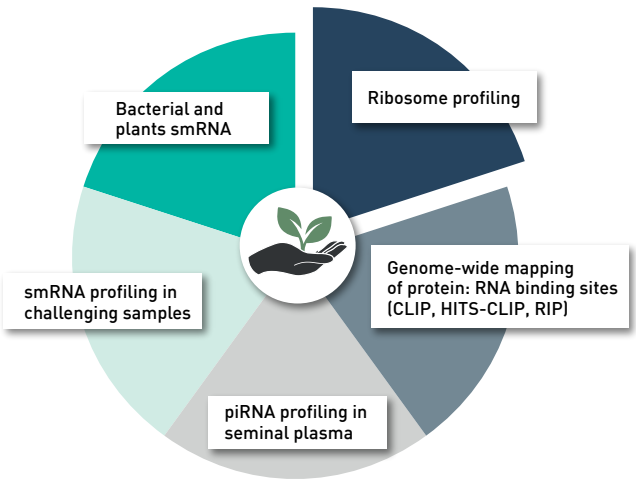
- **Ultra-low input capability: down to 10 pg for small RNA and 100pg for total RNA samples**
- **High library complexity for novel and comprehensive transcript detection**
- **Versatile integration into numerous transcriptomic analysis workflow: ribosome profiling, CLIP-seq, RIP-seq,...**
- **Improved quantification accuracy through the use of unique molecular identifiers (UMIs)**
- **Easy to use with minimal hands-on time: one-day, one-tube protocol**

Maximize information from the regulatory transcriptome using D-Plex small RNA-seq kit for library preparation and MGcount*, quantification software developed at Diagenode, to analyze reads with less multi-alignment and multi-overlaping ambiguity.

WORKFLOW



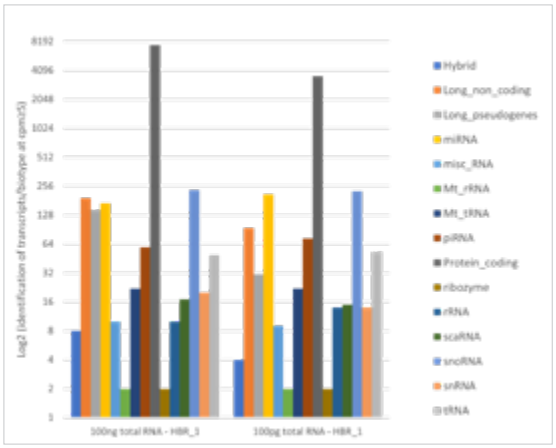
The D-Plex smRNA-seq is a versatile tool for a plethora of transcriptomic analysis



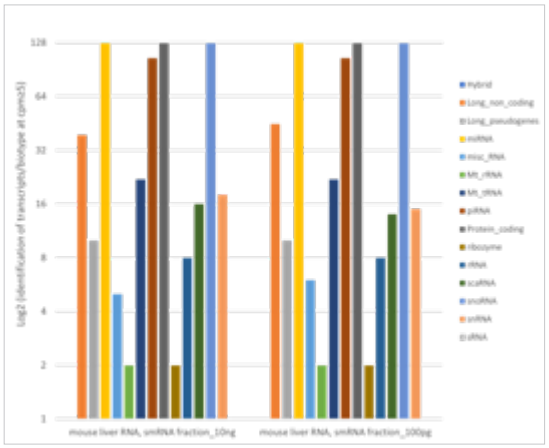
Schematic overview of the D-Plex small RNA-seq Library Prep workflow. RNA molecules are polyadenylated at the 3'-end and primed with a oligo(dT) primer containing part of the ILMN 3'-adapter sequence. The addition of a template-switching oligonucleotide during cDNA synthesis enables to fuse part of the ILMN 5'-adapter sequence during the reverse transcription reaction.

High library diversity for ultra-low inputs

A.



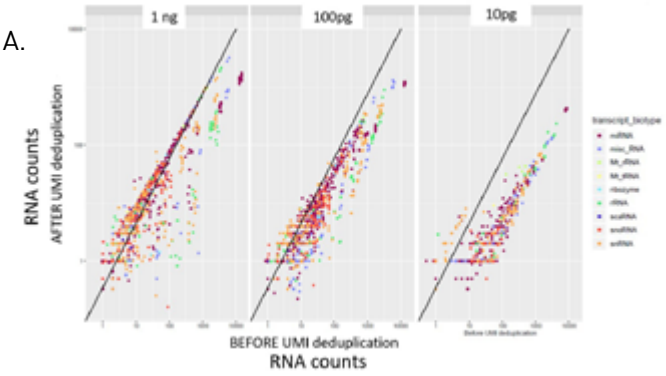
B.



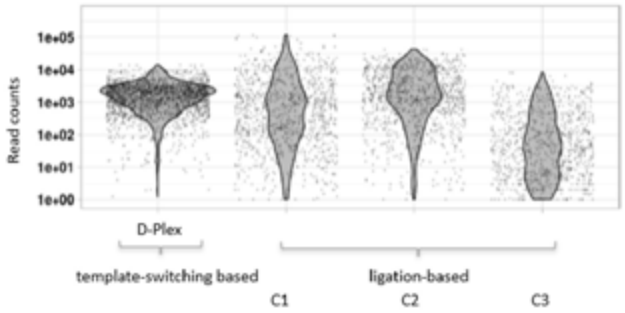
A large number of features detected per biotype at CPM ≥5 in A) human brain RNA and B) mouse liver, using different starting quantities.

Accurate representation of the smRNA content of a sample

A.



B.



A) Accurate identification of PCR duplicates in low-input samples using the unique molecular identifiers (UMIs).
B) D-Plex (template switching) technology enables the recovery of the initial miRNA distribution of the miRXplore Universal Reference (Miltenyi Biotech Inc., Cat. No. 130-093-521). In contrast, ligation-based kits display a strong distortion of the miRNA equimolar distribution initially present in the pool, indicating sample incorporation bias.

ORDERING INFORMATION

ILLUMINA SEQUENCING PLATFORM

Library prep	D-Plex Small RNA-seq Kit	C05030001	24 rxns
Indexes	D-Plex UDI Module - Set A D-Plex UDI Module - Set B D-Plex UDI Module - Set C D-Plex UDI Module - Set D	C05030021 C05030022 C05030023 C05030024	24 UDIs, 24 rxns

MGI SEQUENCING PLATFORM

Library Prep	D-Plex Small RNA DNBSEQ Kit	C05030051	24 rxns
Barcodes	D-Plex DNBSEQ Barcodes Module - Set A D-Plex DNBSEQ Barcodes Module - Set A	C05030060 C05030061	24 barcodes, 24 rxns

*Hita, A., Brocart, G., Fernandez, A. et al. MGcount: a total RNA-seq quantification tool to address multi-mapping and multi-overlapping alignments ambiguity in non-coding transcripts. BMC Bioinformatics 23, 39 (2022). https://doi.org/10.1186/s12859-021-04544-3

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