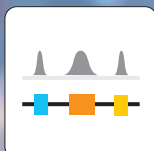


Ovation[®] SoLo[™] RNA-Seq.

PRODUCT SHEET



Whole transcriptome analysis at ultra low input levels

Ovation SoLo RNA-Seq System is a complete end-to-end sample to library preparation solution for stranded, whole transcriptome RNA-Seq analysis of single cells, exosomes, formalin-fixed, paraffin-embedded (FFPE) samples and cell-free RNA. The highly flexible and customizable **AnyDeplete[™]** technology offers depletion of rRNA and other highly abundant, unwanted transcripts. This depletion increases the dynamic range that can be studied, reduces sequencing costs and simplifies data analysis.

Why use the Ovation SoLo RNA-Seq System?

1. Fully integrated workflow for whole transcriptome analysis of as little as 10 pg of precious samples, providing access to complete biological information.
2. Customizable, targeted transcript depletion with AnyDeplete, allowing elimination of unwanted reads after library preparation, even from ultra low inputs.
3. Direct integration with cell lysis protocols, providing an easy-to-use workflow for single cell RNA-Seq.

Benefits

- Whole transcriptome analysis
- 10 pg to 10 ng of isolated RNA or cell lysate from 1-500 cells
- Efficient stranded library preparation without adaptor titration
- Pre-plated adaptors with unique barcodes included for every sample
- Integrated molecular tag for accurate detection of PCR duplicates
- Customizable transcript depletion post-library preparation

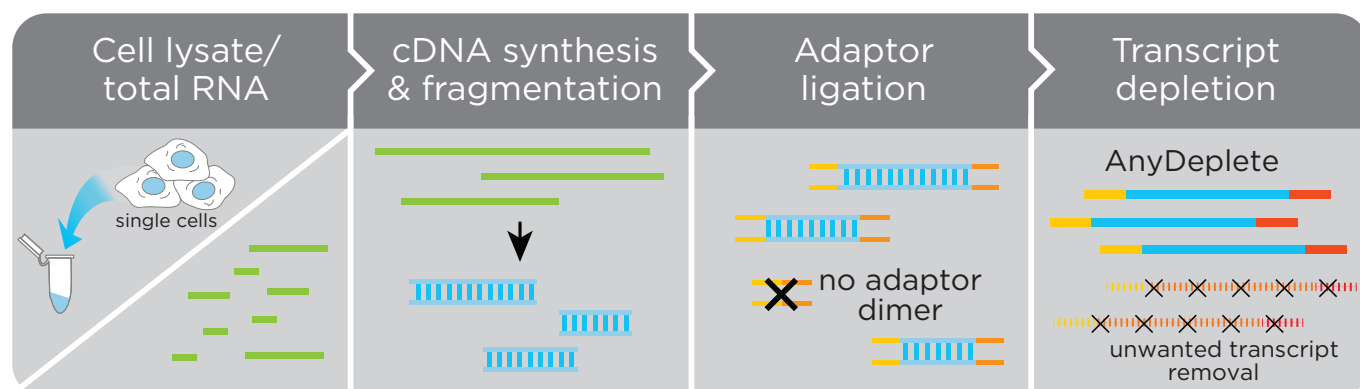


Figure 1: Ovation SoLo RNA-Seq is a complete workflow enabling whole transcriptome analysis from ultra low inputs.



Technical details

- Input range: 10 pg to 10 ng or 1-500 cells
- Excellent correlation down to 10 pg sample input
- Excellent correlation and data from low quality samples

Applications

- Whole transcriptome profiling
- Gene expression
- RNA-Seq from a wide variety of sample sources: liquid biopsy, FFPE samples, exosomes, cell-free RNA, single cells and tissues

Why use AnyDeplete?

- Remove unwanted transcripts after library preparation
- Add new probes to existing probe sets without re-optimization
- Customizable depletion of species- or experiment-specific transcripts

Highly correlated data from 1 ng to 10 pg (single cell input)

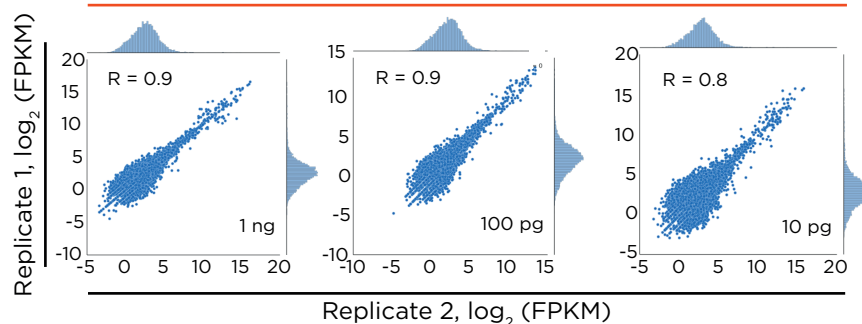


Figure 2: High correlation between technical replicates from inputs as low as 10 pg of total RNA, giving you confidence in your data.

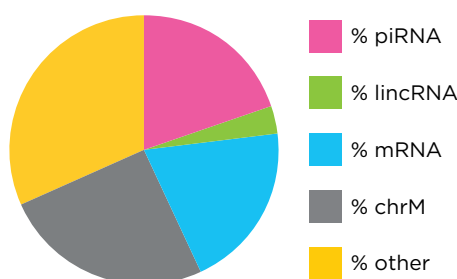


Figure 3: Libraries generated from 5 ng of cell-free plasma RNA with a DV200 score of 10-20 %. Analysis of the whole transcriptome provides complete information from coding, non-coding and regulatory transcripts.

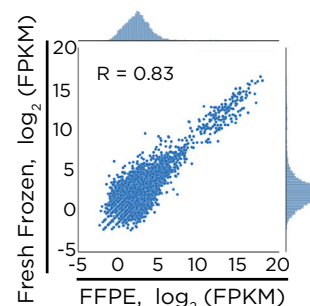


Figure 4: Ovation SoLo RNA Seq provides highly correlated data between fresh frozen and FFPE adenocarcinoma samples.

Référence	Désignation	Conditionnement
TEC0407-32	Ovation SoLo RNA-Seq System Core Kit*	32 rxns
TEC0407-96	Ovation SoLo RNA-Seq System Core Kit*	96 rxns
TEC0500-32	Ovation SoLo RNA-Seq System, Human	32 rxns
TEC0500-96	Ovation SoLo RNA-Seq System, Human	96 rxns
TEC0501-32	Ovation SoLo RNA-Seq System, Mouse	32 rxns
TEC0501-96	Ovation SoLo RNA-Seq System, Mouse	96 rxns
TEC0502-32	Ovation SoLo RNA-Seq System, Drosophila	32 rxns
TEC0502-96	Ovation SoLo RNA-Seq System, Drosophila	96 rxns

* kit sans sondes de déplétion. Les sondes peuvent être commandées à façon pour toutes espèces.

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