IAB
Institute of Applied Biotechnologies

Transcriptomic Services at IAB

RNA sequencing (RNA-Seq) is a powerful and comprehensive method for analyzing the transcriptome of various types of biological samples such as cells, tissues and whole organisms.
Institute of Applied Biotechnologies a.s. (IAB) excels in RNA laboratory sample management, holding unparalleled expertise in RNA isolation, transcriptome library preparation, sample pooling, and data analysis. Our team of dedicated experts guarantees high quality and consistency for every project. Whether you're dealing with high-quality samples or challenging low-quality RNA, IAB's tailored transcriptome sequencing workflows ensure successful finishing and quality results. Trust IAB to transform your RNA samples into meaningful data with precision and reliability.

IAB Transcriptome Workflows

The most common workflows listed below are just a part of services available.

Poly(A) mRNA Selection | **rRNA Depletion** | **Ultra-low Quantity and Quality RNA**

Poly(A) mRNA Selection

Ideal for

High-quality RNA samples

Benefits

Cost-effective, suitable for all organisms with Poly(A) tail on the 3' end of mRNA

Limitations

Does not support non-coding RNA, miRNA, smallRNA, and other untranslated RNAs.

Inapplicable for prokaryotic samples

Sample Requirements

- **RNA Amount:** 10 – 1000 ng
- **Volume:** ≥20 µl
- **RIN Score:** 7 – 10

rRNA Depletion

Ideal for

Lower-quality RNA samples

Benefits

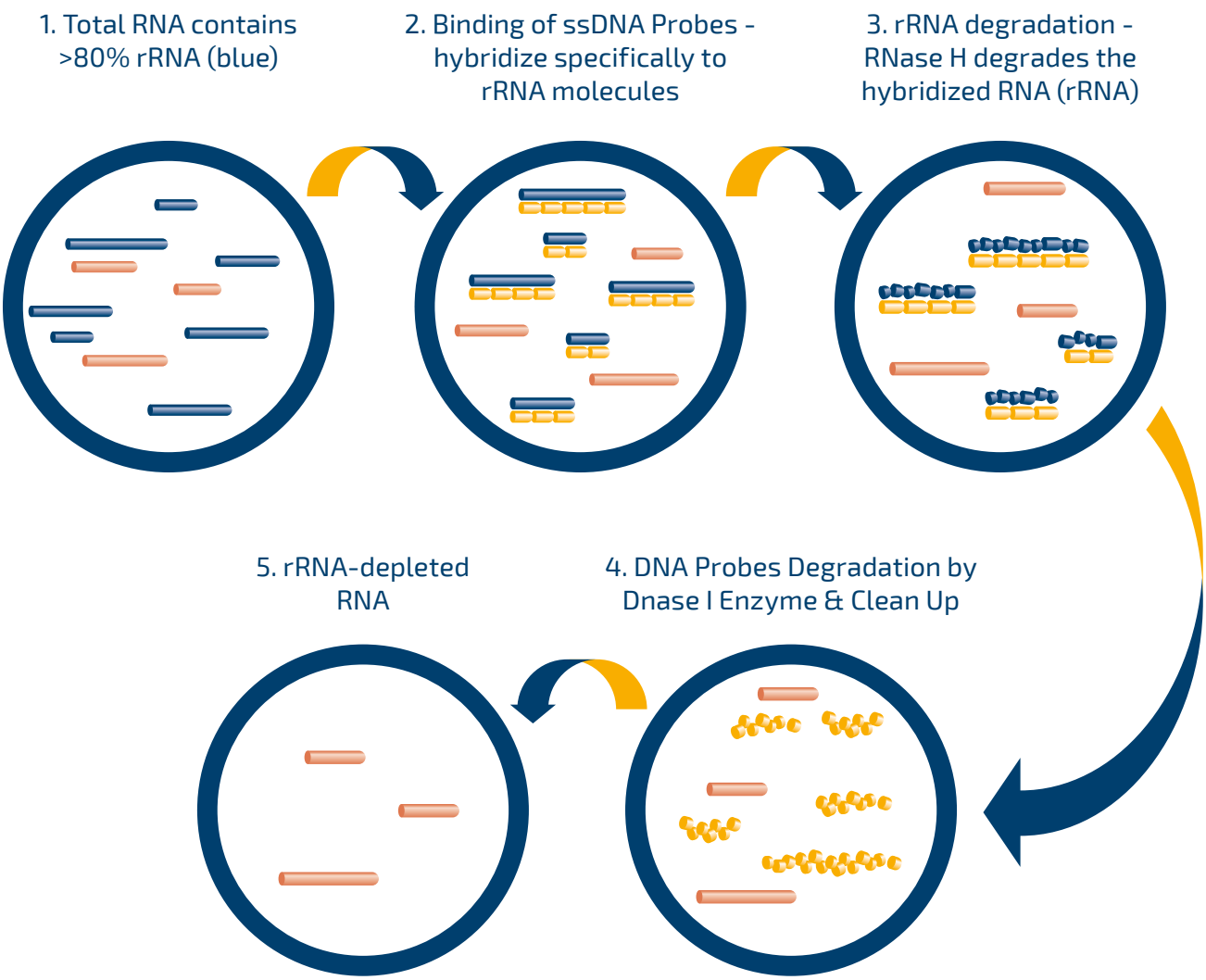
Versatile, species-specific rRNA probes

Limitations

Various rRNA depletion kits; no universal kit for all species of organisms and sample types

Sample Requirements

- **RNA Amount:** >10 – 1000 ng
- **Volume:** ≥20 µl
- **RIN Score:** 2 – 7
- **DV200 (percentage of fragments >200 nucleotides):** >50%



Ultra-low Quantity and Quality RNA

Ideal for

Difficult samples, including FFPE samples

Benefits

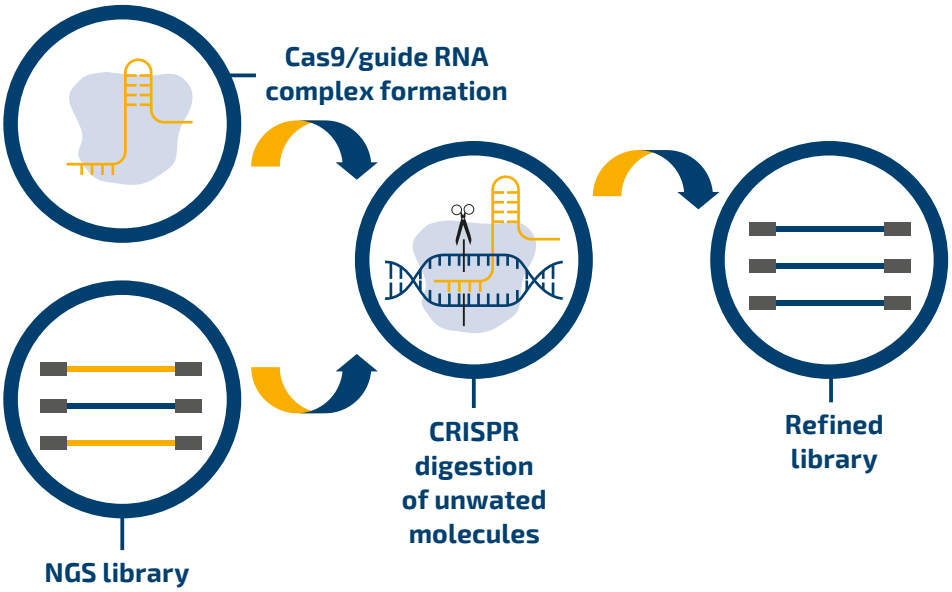
Protocol where rRNA depletion is performed on cDNA (SMARTer) or final libraries (CRISPRclean), enhancing library quality.

Limitations

For CRISPR-based rRNA depletion on final libraries, the best results are achieved with libraries with fragment size >450 bp.

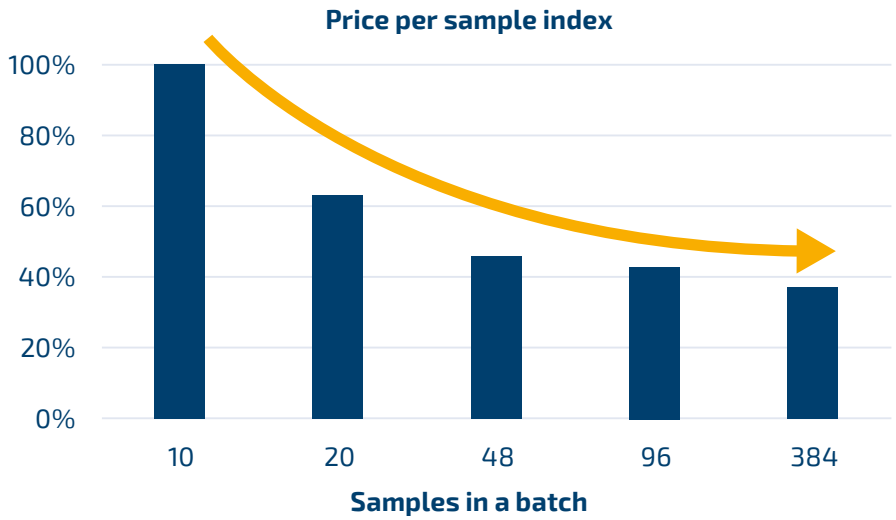
Sample Requirements

- **RNA Amount:** 250 pg – 10 ng
- **Volume:** ≥ 15 ng/µl
- **RIN Score:** 1 – 10 (including FFPE samples)
- **DV200 (percentage of fragments >200 nucleotides):** >50%



Project Cost

Every IAB project is highly customized, so exact pricing varies. However, key factors affecting price per sample include the number of samples processed in a batch.



Reference IAB Projects

Fish tissues

Total RNA was successfully isolated from complicated fish tissues (embryo, liver, brain). 104 RNA-Seq NGS libraries were prepared, although the RNA input of some of the samples was only 1.8–4.9 ng, with the recommended minimum of 10 ng. All NGS data had high quality.

FFPE samples

A problem that users of FFPE tissues face are formalin-induced sequence artifacts. In lower-quality RNA samples, the rRNA is depleted from total RNA isolated by the species-specific rRNA probes. Accurate quantification of nucleic acid enables the selection of sufficient sample amount to be used for library preparation. Three RNA isolates from FFPE samples (human ovaria) of different DV200: 5%, 38% and 58% were used in this study. The libraries were prepared from an input of 10 ng. Although data quality decrease was detected corresponding to the DV200 value, the generated data were all suitable for evaluation.

Ultra-low Quantity and Quality RNA

RNA samples frequently contain up to 90% of ribosomal RNA. Sequencing without removal of these abundant rRNA sequences is inefficient in terms of sequencing capacity and obscures detection of lower expressing, but biologically relevant transcripts. Most depletion methods are performed on samples prior to NGS library preparation. In contrast, cDNA-based and CRISPR-based depletion methods used by IAB are employed on fully prepared NGS libraries. Eight samples of m6A imunoprecipited RNA from rat hipokampus with the lowest inputs of 3.1–3.5 ng were successfully transformed into NGS libraries and treated with Jumpcode CRISPRclean Human Ribosomal RNA Depletion Kit. The required yield of 40 million PE reads/sample was achieved for majority of samples.

IAB - your expert partner providing products, customized solutions, services and advanced bioinformatics for genomic, transcriptomic and proteomic projects
Contact Us Today for more information, details and your custom price quote.

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