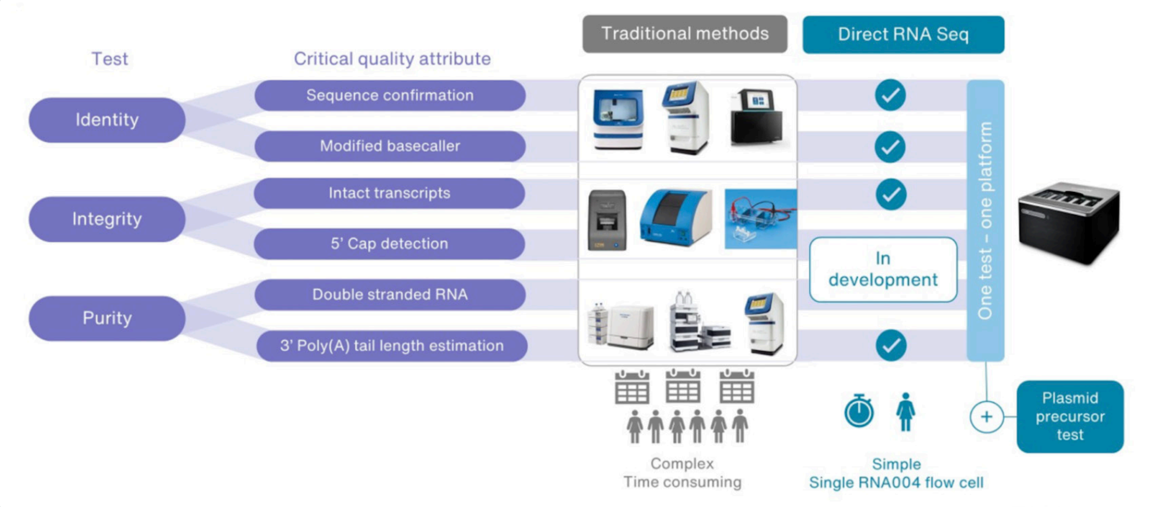
WASATCH.BIOLABS

Streamlining mRNA Quality In A Single Workflow

MRNA VACCINE QC WITH LONG-READ SEQUENCING

From Development to Release: Confidence in Every Molecule

With long reads, single-molecule resolution, and no amplification artifacts, Wasatch BioLabs' Oxford Nanopore mRNA Vaccine QC service delivers a complete and accurate view of vaccine constructs, from early development through lot release and stability studies, all within a single streamlined workflow. As a certified Oxford Nanopore Technologies (ONT) provider, we sequence full-length mRNA molecules directly, preserving critical features such as poly(A) tails, 5′/3′ architecture, and structural heterogeneity to confirm product integrity and support regulatory-ready development.



Sample Requirements

RNA Input Requrement:
300 ng of poly(A)-tailed RNA
or 1 µg of total RNA) in 8 uL

Accepted Sample Types:
100% polyadenalted RNA

Max Number of Transcripts:
Validated up to 16* pooled transcipts

Outputs:

Sequencing & Contamination
% aligned to template, read length distribution, PHRED quality, contamination ID and quantification

Integrity & Accuracy
Intact % and mismatch rates

Relative Quantity:
Observed RNA Abundance

Poly(A) Profiles:
Tail length peaks and degradation signatures

Service Details

Turnaround Times
- 7 business days

Services:

- Standard mRNA QC Report
- Dedicated Project Manager
- Custom Bioinformatic Solutions
- Validation Design
- Lot Release Testing

mRNA Vaccine QC Reporting, Simplified

EXAMPLE REPORT OUTPUTS:

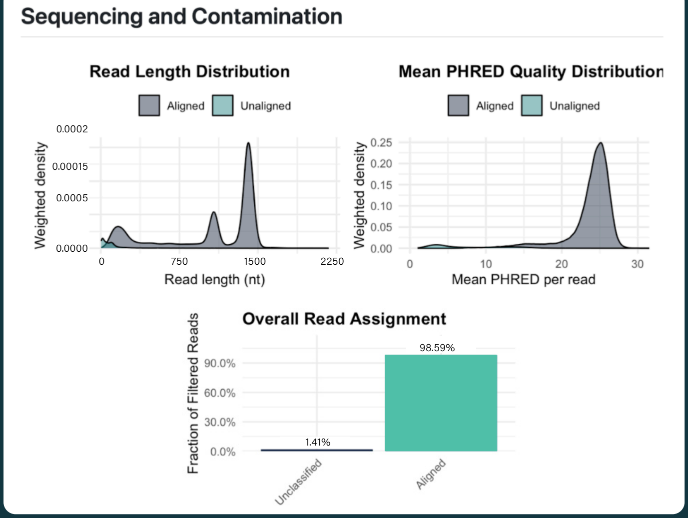


Figure 01: Read length and quality distributions summarize overall sequencing performance, confirming high signal and library integrity. Species-level contamination analysis verifies sample purity and accurate assignment of reads to the expected reference organism.

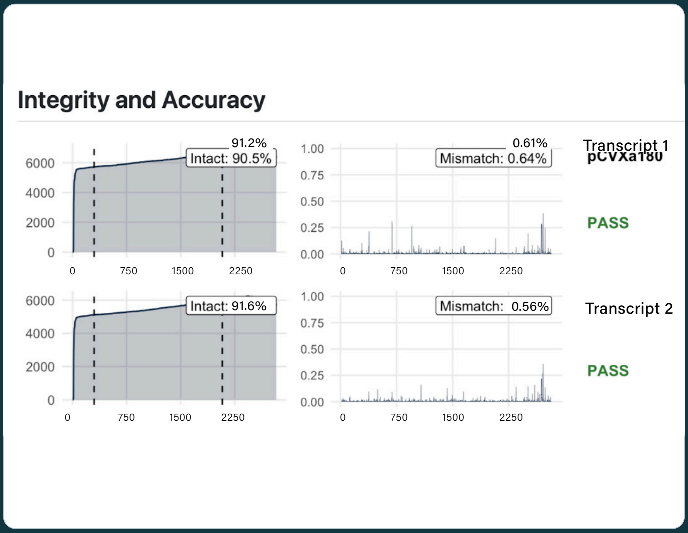


Figure 02: Plots display transcript integrity and base-level mismatch profiles for each transcript, providing an overview of mRNA completeness and sequence accuracy metrics.

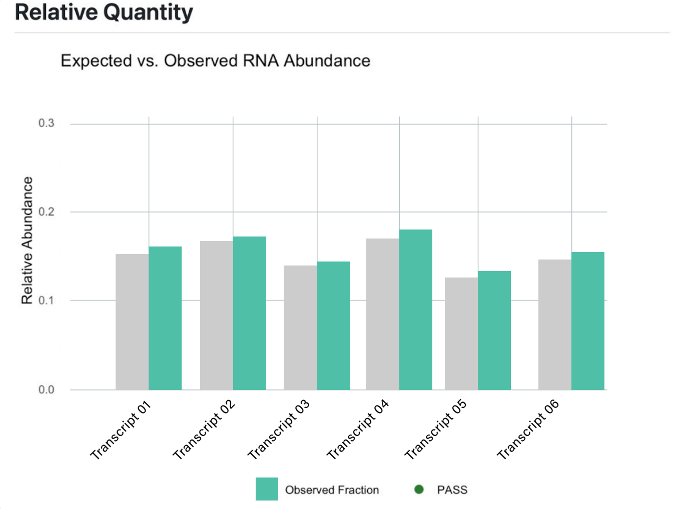


Figure 03: Bar plots compare expected and observed RNA abundance for each transcript, providing an assessment of relative quantity and formulation consistency.

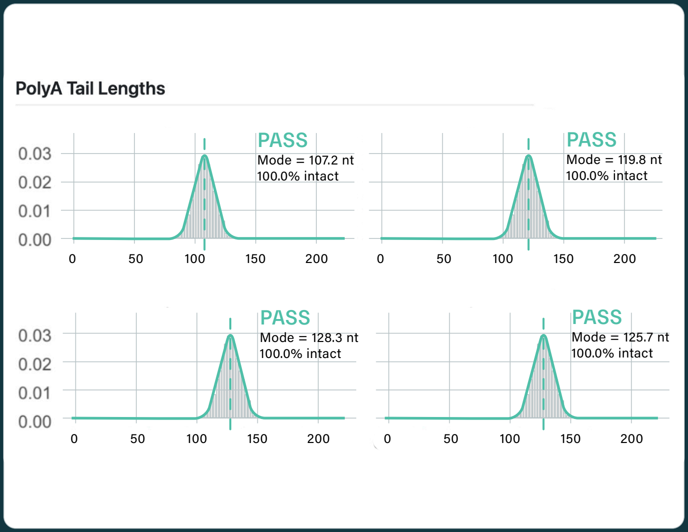


Figure 04: Distributions show measured poly(A) tail lengths for each transcript. A fitted curve represents the expected normal distribution centered on the modal tail length, used to assess tail integrity and uniformity across transcripts.

For more information, visit www.wasatchbiolabs.com
To discuss your project or request a customized quote, contact us at:

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