HIFI SEQUENCING FOR MRNA VACCINE RESEARCH AND DEVELOPMENT

Comprehensively characterize your mRNA molecules

Following the COVID-19 pandemic, mRNA vaccines have emerged as effective tools against infectious diseases and show potential as cancer treatments. Vital considerations for mRNA-based vaccine stability and efficacy include mRNA sequence integrity and the length of its poly(A) tail.

Characterize your mRNA at full length

PacBio HiFi sequencing allows you to capture the full length of your transcript at single-molecule resolution, giving you comprehensive information at base-level accuracy.^{1,2}

Confidently sequence homopolymers such as poly(A)

In contrast to other methods, HiFi sequencing has the ability to accurately sequence long homopolymers such as full-length poly(A) tails.^{1,2,3} This allows you to determine the length distribution of mRNA molecules as an important determinant for vaccine efficacy.

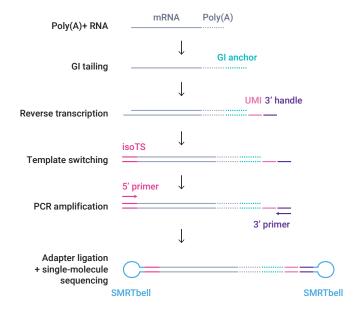


Figure 1: Schematic of Legnini et al's approach to capture full-length mRNA for HiFi long-read sequencing.

The PacBio® advantage:

- · Sequence full-length mRNA molecules at baselevel accuracy to determine size and isoform/ variant distribution to most confidently assess your research products.
- Characterize homopolymers such as poly(A) regions more accurately than with other sequencing methods to optimize your construct and processes.

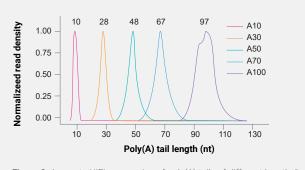


Figure 2: Accurate HiFi sequencing of poly(A) tails of different lengths2

The benefits of HiFi sequencing:



Long reads

Up to several kb, capturing full-

Comprehensively characterize full-

length mRNA vaccine cDNAs

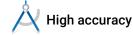
length vaccine candidates.

Uniform coverage

Accurate coverage in GC-rich

Reliable results in challenging regions like poly(A) tails.

and repetitive regions (e.g.,



99.9% accuracy (Q30), ensuring confidence in results

Have confidence in your results so you can get to answers



Increase your productivity compared to other methods

Speed up your process by reducing the need for multiple orthogonal methods



Learn more about HiFi sequencing for Biologics R&D: pacb.com/biologics-research-and-development

homopolymers)

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Legnini I, Alles J, Karaiskos N, et al (2019) FLAM-seq: full-length mRNA sequencing reveals principles of poly(A) tail length control. Nat Methods 16:879-886. https://doi.org/10.1038/s41592-019-0503-y Liu Y, Nie H, Liu H, Lu F (2019) Poly(A) inclusive RNA isoform sequencing (PAlso-seq) reveals wide-spread non-adenosine residues within RNA poly(A) tails. Nat Commun 10:5292. https://doi.org/10.1038/s41467-019-13228-9

Liu, Y., Lu, F. & Wang, J. (2023). Deadenylation, Methods and Protocols. Methods in Molecular Biology, 2723, 215–232. https://doi.org/10.1007/978-1-0716-3481-3_13