

## 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.<sup>1,2</sup>

## 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.<sup>1,2,3</sup> This allows you to determine the length distribution of mRNA molecules as an important determinant for vaccine efficacy.

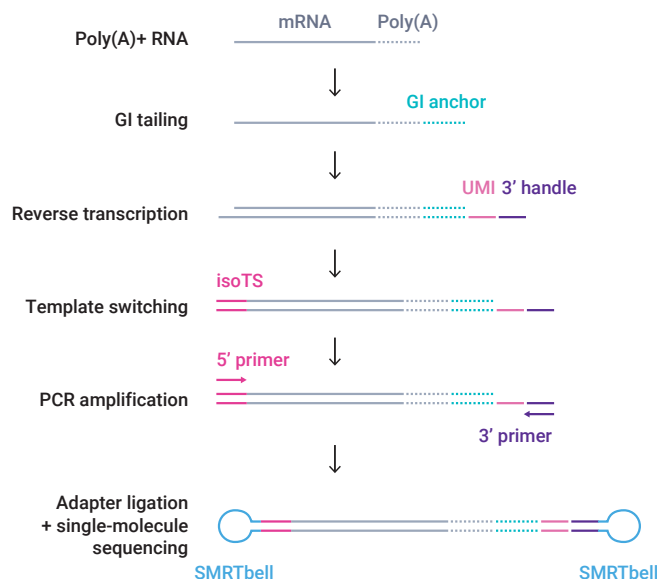


Figure 1: Schematic of Legnini et al's approach to capture full-length mRNA for HiFi long-read sequencing.<sup>1</sup>

### The PacBio® advantage:

- Sequence full-length mRNA molecules at base-level 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.

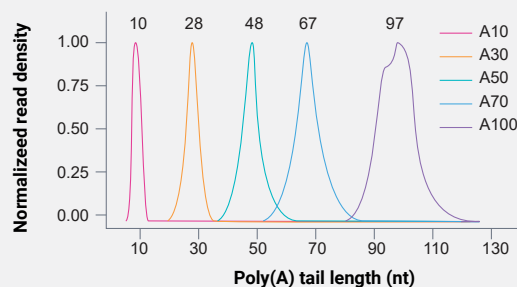


Figure 2: Accurate HiFi sequencing of poly(A) tails of different lengths<sup>2</sup>

### The benefits of HiFi sequencing:



#### Long reads

Up to several kb, capturing full-length mRNA vaccine cDNAs

*Comprehensively characterize full-length vaccine candidates.*



#### Uniform coverage

Accurate coverage in GC-rich and repetitive regions (e.g., homopolymers)

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



#### High accuracy

99.9% accuracy (Q30), ensuring confidence in results

*Have confidence in your results so you can get to answers faster.*



#### Comprehensive data

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](https://pacb.com/biologics-research-and-development)

1. Legnini J, Alles J, Karaikos 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>  
2. Liu Y, Nie H, Liu H, Lu F (2019) **Poly(A) inclusive RNA isoform sequencing (PALISO-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>  
3. 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](https://doi.org/10.1007/978-1-0716-3481-3_13)