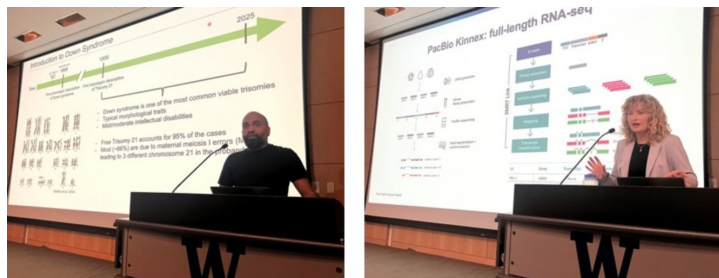


## LONG READ SEQUENCING

# Long-Read Symposium: Two Presenters Share Their Research and Impressions

Sophie Kogut, a graduate student in the Blanco-Melo lab at the Fred Hutchinson Cancer Center, and F. Kumara Mastrorosa, Ph.D., a Post-doctoral Scholar, in the Eichler Lab at the UW, offer insights

By: BBI Communications on September 24, 2025



**F. Kumara Mastrorosa, Ph.D. (left) and Sophie Kogut: 'Long-read sequencing is changing the field of genomics and the symposium was a great occasion to share my work and discuss future applications and limitations with other experts.'**

*EDITOR'S NOTE: The third annual long read symposium on September 16th, hosted by BBI's Danny Miller, M.D., Ph.D., included presentations by Sophie Kogut, a graduate student in the Blanco-Melo lab at the Fred Hutchinson Cancer Center, and F. Kumara Mastrorosa, Ph.D., a Post-doctoral Scholar, in the Eichler Lab at the UW. Here is a Q&A exploring their research and impressions of the event.*

*Why did you choose to participate in the long read symposium?*

**KOGUT:** I am new to the long-read field and also the only person in my lab working with long-read data, so I thought it would be a good opportunity to learn from experts in the field and catch up on the latest tools and methods.

**MASTROROSA:** Long-read sequencing is changing the field of genomics and the symposium was a great occasion to share my work and discuss future applications and limitations with other experts working in the field. It's also a good occasion to receive feedback on my own work and how to structure the next steps.

*What did you want the audience to come away with from your presentation?*

KOGUT: The main takeaway from my presentation is that Human Endogenous Retroviruses (HERVs) are tricky to study, but long-read is opening up new ways to explore their transcriptional dynamics and coding potential. Each type of RNAseq I talked about adds something unique to our understanding of HERV biology, and I wanted to convince people that this is an area worth studying.

MASTROROSA: I wanted to provide a real-case application of long-read sequencing and how this technology is helping answer biological questions related to human health and evolution that remained unsolved for many years. Trisomy 21 is one of those human conditions for which we still do not know the genetic factors that predispose to it and long-read sequencing is revealing more and more biological information on structures of the genome, such as the centromeres, that might play a crucial role in its aetiology.

*What changes would you like to see in next year's symposium?*

KOGUT: I thought the symposium was well organized and appropriately paced. I learned so much!

MASTROROSA: It would be great to have even more students presenting their work, maybe with a larger poster session and an interactive session with the speakers.

*Symposium Chair Dr. Danny Miller stated: "The momentum for wider use of long-read sequencing and collaboration among researchers and clinicians is growing in the Puget Sound." Do you agree or disagree? Why?*

KOGUT: I strongly agree! As long-read technologies gain popularity and become more affordable, more local clinicians and researchers will use them. That's why it's important to establish networks through events like this, so we can share our experience and expertise with others in Seattle.

MASTROROSA: I agree. The decreasing cost of long-read sequencing and more standardized workflows are helping make this technology and its application more widely accessible and applicable to an increasing number of scenarios. Also, symposia and similar events encourage connections and make collaborations easier to establish.

*What is one thing you learned, or one talk that you found especially exciting, at the symposium?*

KOGUT: As someone on the research side, it was really cool to learn about the clinical applications of long-read sequencing directly from physicians. I also thought it was very interesting to hear about what the Miller lab is doing, applying these technologies to resolve unresolved rare disease cases.

MASTROROSA: It is always interesting to participate in this type of event because you can appreciate real-case applications showing that the technology and its applications are always evolving and improving. It was very interesting to see novel applications of long-read sequencing that were not used just a few years ago and how many improvements there have been in the quality of data.

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## Long-Read Symposium Set for September 16; Registration Closes September 5

August 27, 2025 | By BBI Communications

'The momentum for wider use of long-read sequencing and collaboration among researchers and clinicians is growing in the Puget Sound.' Danny Miller, M.D., Ph.D.

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