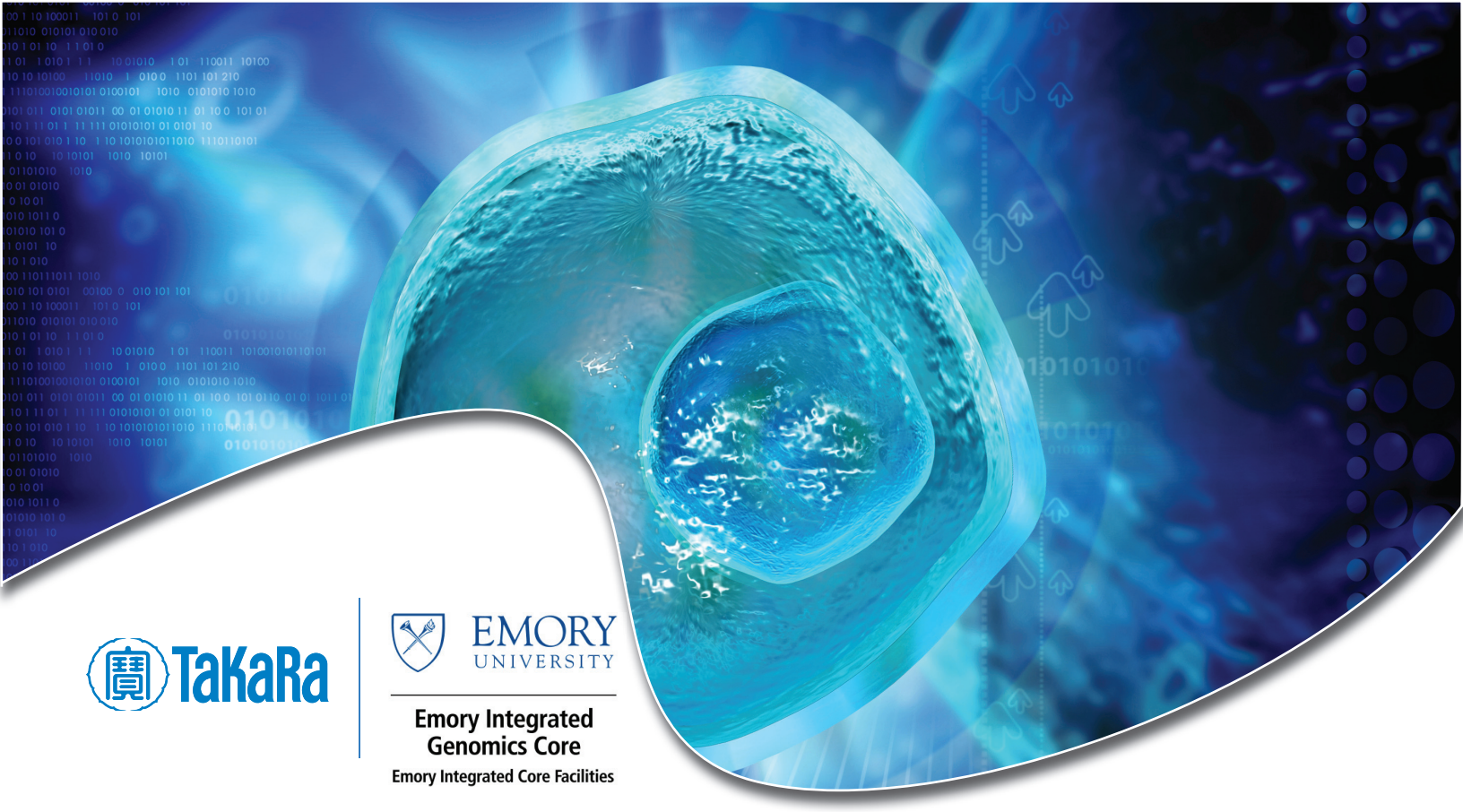

TaKaRa

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Single Cell Seminar

Splice isoforms, gene fusions, and SNVs are not usually found at the 5' or 3' ends of transcripts and can be missed if you use a droplet-based approach for your single-cell NGS studies. See how SMART-Seq® technologies can help you uncover novel biomarkers from entire, full-length transcripts.

A complete, end-to-end automation solution with superior sensitivity to detect critical biomarkers such as splice variants, gene fusions, and SNVs.

Bill Warble
Senior Business Development Manager, Automation

An easy, plate-based solution for full-length single-cell sequencing that minimizes sample loss and handling errors.

Kunj Pathak, PhD
Territory Manager II

Date and time:
April 20, 2023
11:00 am—12:00 pm EST

Location:
Emory University, HSRB Auditorium, 1760 Haygood Dr. NE, Atlanta, GA 30322

Sponsored by:
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Unable to make it in person?
Join us on Zoom: https://zoom.us/j/294261547

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