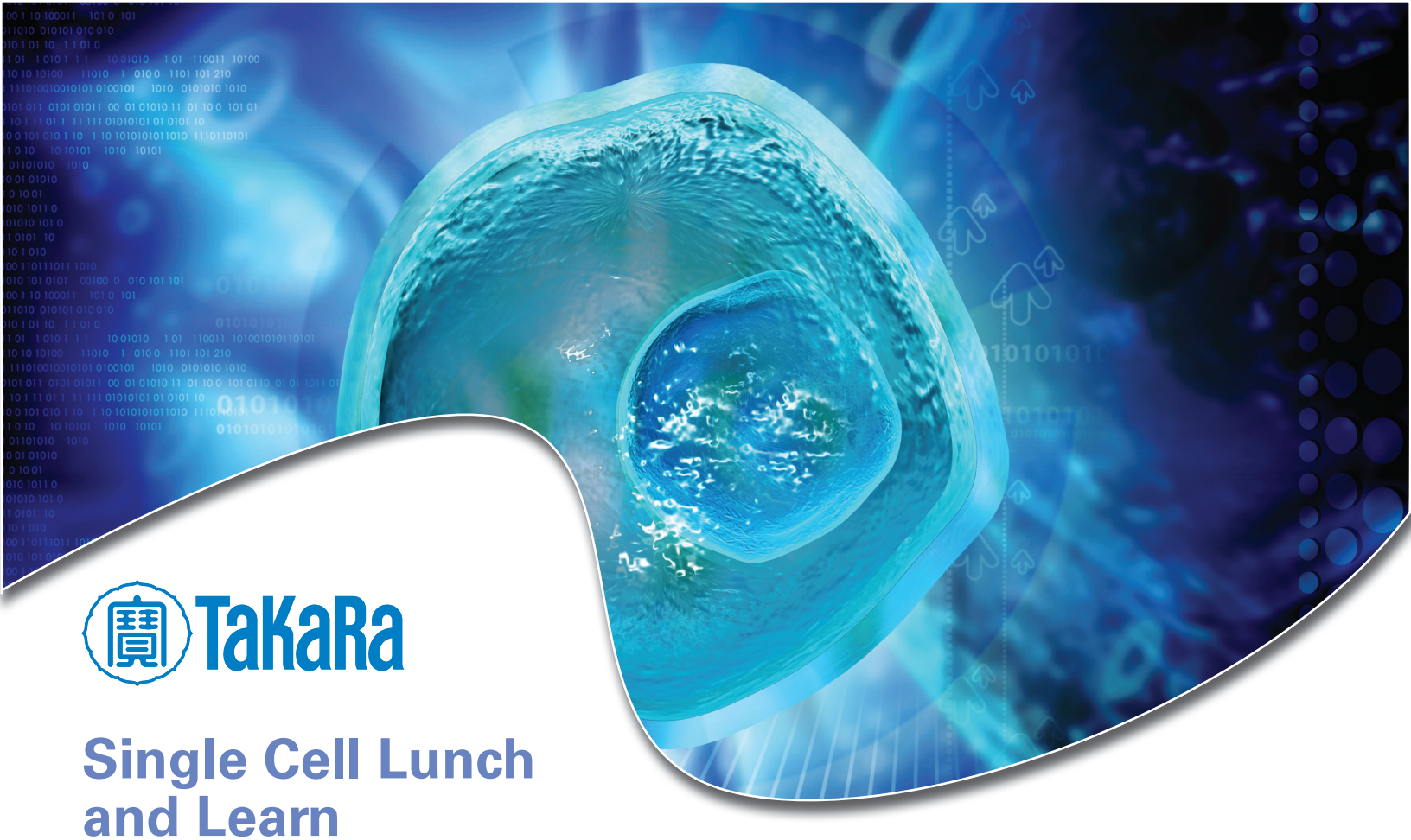

TaKaRa

Single Cell Lunch and Learn

Splice isoforms, gene fusions, and SNPs are not usually at the 5' and 3' ends of your transcript, so you will get incomplete data from your single-cell NGS studies when using a droplet-based approach. See how SMART-Seq® technologies can help you uncover novel biomarkers from the entire full-length transcript.

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:
December 8, 2022
12:00–1:00 pm CST

Location:
Shelby Building, Room 105,
U. of Alabama at Birmingham,
1825 University Blvd,
Birmingham, AL 35233

Enjoy free
food, drinks, and giveaways!

Register Now!
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