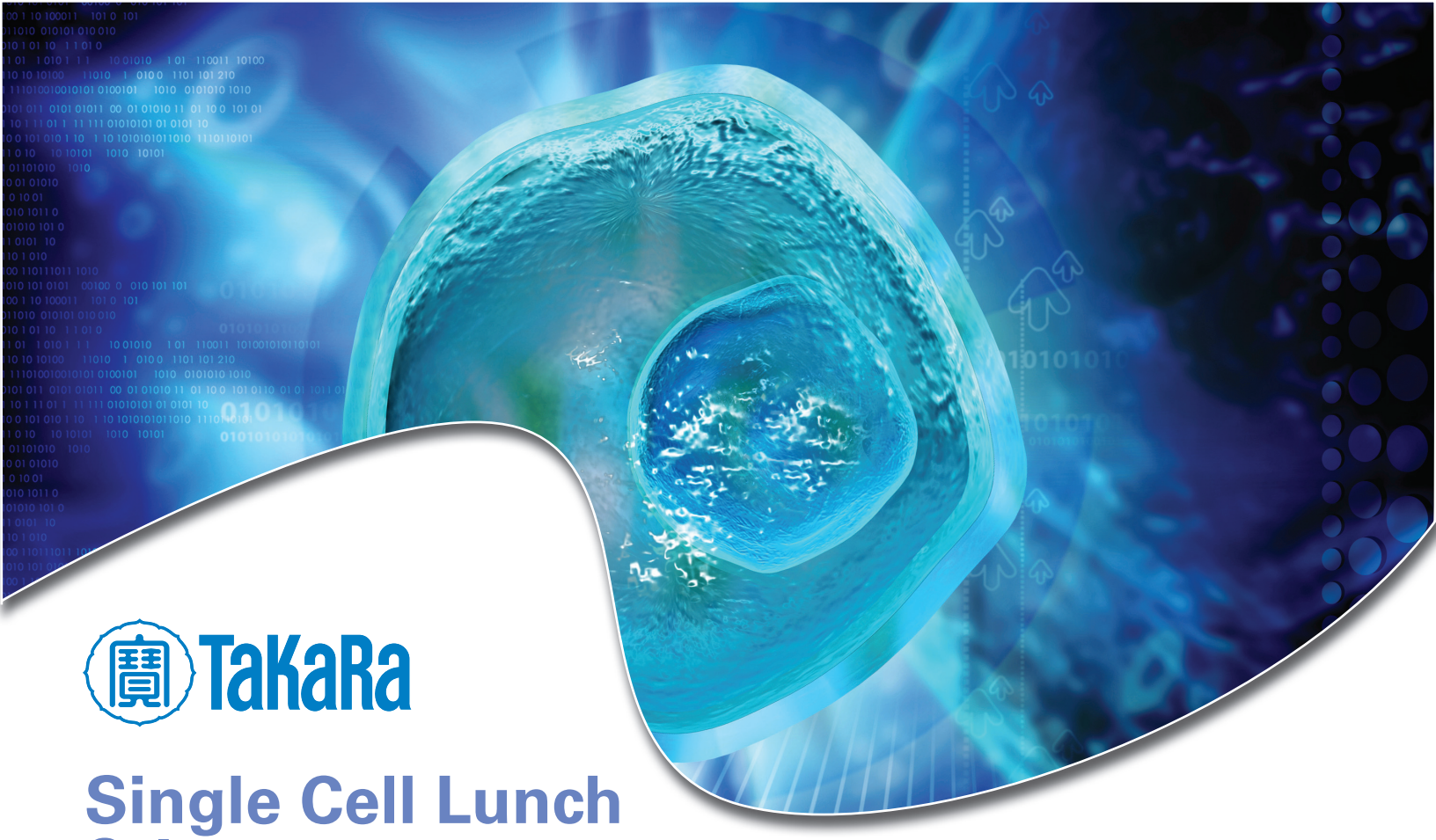

TaKaRa

Single Cell Lunch & 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 to streamline library prep from picograms of FFPE RNA with accuracy powered by UMIs.

Steve Butcher
Senior Territory Manager

Date and time:
December 6, 2022
1:00—2:00 pm CST

Location:
Robert H. Lurie Medical Research Center, Gray Seminar Room, Northwestern University, 303 E. Superior Street, Chicago, IL 60611

Enjoy free
food, drinks, and giveaways!

Register Now!
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