BioSkryb GENOMICS

Investigate Cancer Heterogeneity and Evolution with Single-Cell Multiomics Using ResolveDNA® and ResolveOME™

Wednesday, 31st January, 9:00 AM - 1:00 PM GMT

Queen Mary University of London
Ground Floor Lobby, John Vane Science Centre

Your contact:
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As the local BioSkryb account manager supporting QMUL, James helps researchers to apply ResolveDNA and ResolveOME technologies in their translational research and to plan experiments with maximum information from precious patient samples.

While single-cell transcriptomics has flourished with a vast amount of data available in cancer research, single-cell genomics has struggled with some challenges.

BioSkryb's primary template-directed amplification (PTA) overcomes many of the challenges associated with single-cell whole genome amplification (scWGA), drastically improving genome coverage and accuracy of copy number variation and single nucleotide variant calling. With our technology, you can profile the whole genome of individual cells, or the whole genome and full-length transcriptome of the same cell. We will be in the foyer to discuss your research to see where single-cell genomics and multiomics can help you discover more.

What could your lab do with the power to fully analyze the complete genome and transcriptome from individual single cells?

- Advantages of PTA in genome coverage and uniformity
- Cellular heterogeneity and the value of profiling individual cells
- How complete genome and transcriptome profiling from individual single-cells can enhance your research aims