



Unleash the Full Story of Every Cell

- Full-Length
- High-Throughput
- Unmatched Precision

See beyond standard single cell RNA sequencing

- Allele-specific gene expression patterns
- Fusion gene identification
- Mutations/ SNPs detection
- Alternative splicing analysis
- Non-model organisms gene annotation

MobiuSCOPE advantages

- Full length single cell cDNA information with short read sequencing
- Minimal 3' or 5' bias
- More genes detected in each cell with low drop-out rate
- Sensitive detection of splicing junctions
- Easy workflow

Get in touch with us to discuss your project
<https://singleron.bio/consultation/>



Unbiased full-length coverage

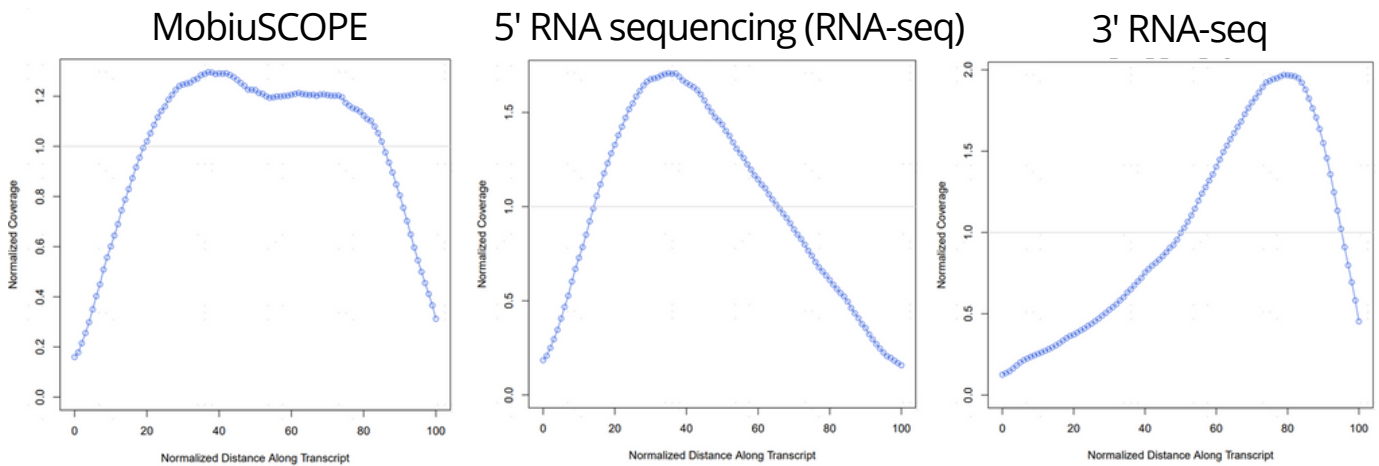


Figure 1. MobiusCOPE showed unbiased full-length coverage across the entire transcript. y-axis: Normalized coverage. x-axis: Normalized distance from the beginning of the transcript on a scale of 1 to 100. 0 represents the 5' end, and 100 represents the 3' end.

Detect gene and splicing junction with higher sensitivity

	MobiusCOPE
Mean splice junctions /cell	71% more than 3' RNA-seq
Average splice junctions /cell	69% more than 3' RNA-seq

Identify fusion genes with higher sensitivity

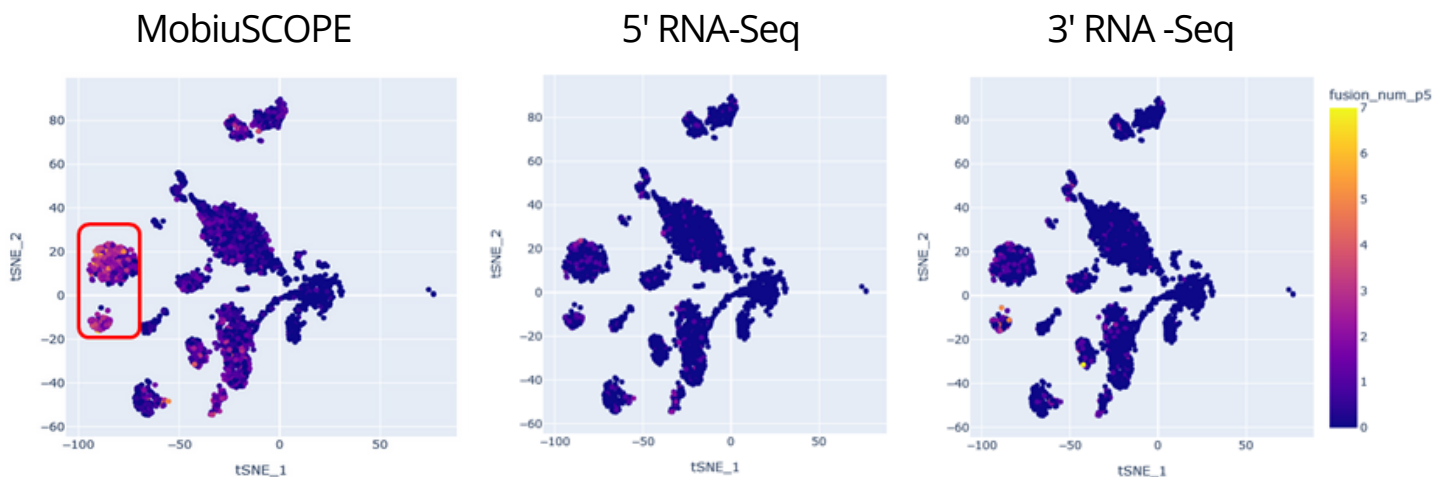


Figure 2. MobiusCOPE detects HLA-C gene fusion effectively in human PBMCs. Scale bar represents the number of fusion events detected per cell.

Unlock full-length insights now!

Europe
 +49 (0) 221 16824777
 Gottfried-Hagen-Strasse 60
 51105 Cologne, Germany
 info@singleron.bio

APAC
 +65 6990 5987
 #02-08, 61 Science Park Rd
 Singapore 117525
 sales.sg@singleron.bio

US
 +1 203-298-0604 (CT) / +1 734-249-0883 (MI)
 1 Bradley Road, Suite 401 Woodbridge, CT 06525
 333 Jackson plaza, Ann Arbor, MI 48103
 info@singleron.bio