An Improved Single-Cell RNA-Sequencing Method

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Overview

Single-cell RNA sequencing (scRNA-seq) methods enable the detection of only 10%-15% of the cellular transcriptome, rendering low-expressing genes in the dark. WRAP-seq (Well-based RNA Amplification and Pooling) combined with TRAP-seq (Targeted RNA Amplification and Pooling) enable the detection of targeted sets of low-expressing genes of interest on top of the whole transcriptome. These gene sets can be tailored to provide in-depth analysis of specific biological pathways.

Applications and Differentiation

Applications

- Dissecting cell subpopulations
- Deciphering cell state within the tumor microenvironment
- TCR/BCR analysis linked with the whole transcriptome
- Identifying specific isoforms
- Tailored applications supported by â€˜Trapsâ€™ â€“ panels for targeted genes of interest

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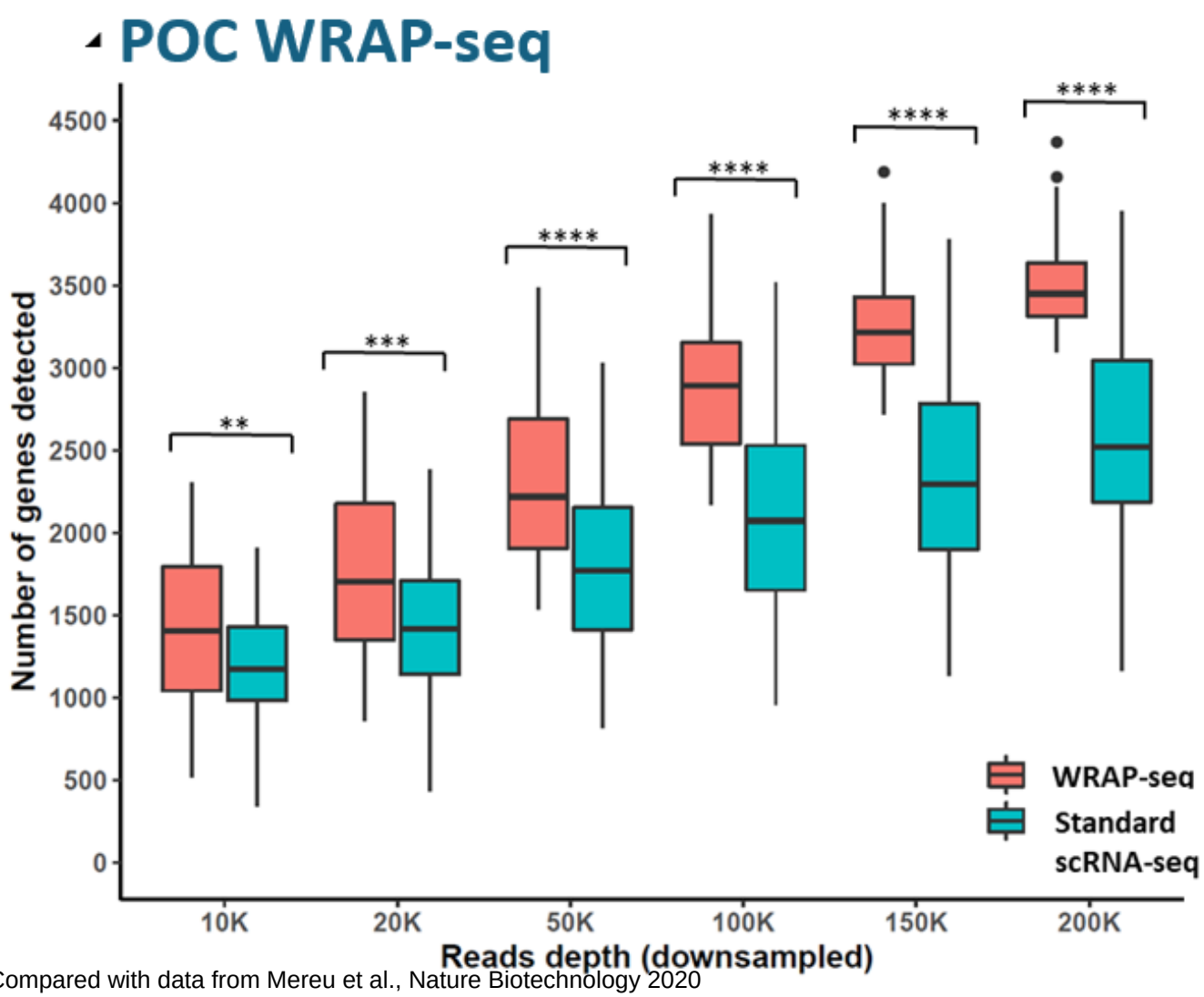
Differentiation

- Single-cell sequencing of targeted genes of interest in parallel to whole transcriptomics analysis
- Superior sensitivity compared to commonly used methods
- High-throughput and cost-effective

Development Stage

- WRAP-seq is fully developed
- TRAP-seq has a POC of several target genes, and is in validation stages for additional targets
- A proof-of-concept study demonstrated superior sensitivity compared to a standard scRNA-seq method.



Compared with data from Mereu et al., Nature Biotechnology 2020

Patent Status

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