An Improved Single-Cell RNA-Sequencing Method

Research Tools

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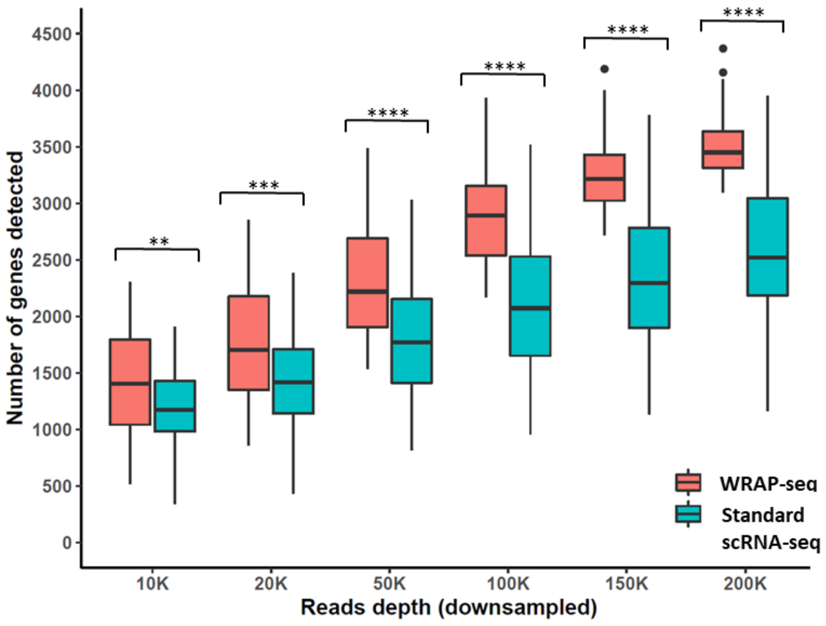
Single-cell RNA sequencing (scRNA-seq) methods enable the detection of only 10%-15% of the cellular transcriptome, rendering low-expressing genes in the dark. WRAP-seq (Well-based RNA Amplification and Pooling) combined with TRAP-seq (Targeted RNA Amplification and Pooling) enable the detection of targeted 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.



WRAP-seq is more sensitive than other scRNA-seq methods

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 'Traps' – panels for targeted genes of interest

DEVELOPMENT STAGE

- WRAP-seq is fully developed
- TRAP-seq POC demonstrated

DIFFERENTIATION

scRNA-seq of targeted genes of interest in parallel to whole transcriptomics analysis

Superior sensitivity compared to commonly used methods

High-throughput and cost-effective