Transcriptomics: Open Access
ISSN: 2329-8936
OPEN ACCESS Freely available online
Commentary

RNA Sequencing-Based Transcriptomics in Precision Medicine Applications

Sofia Martinez*

Department of Genomic Medicine, National Autonomous University, Mexico, Mexico

DESCRIPTION

Ribonucleic acid (RNA) sequencing-based transcriptomics has become one of the most transformative technologies in modern biomedical science, reshaping how diseases are understood, diagnosed, and treated. By capturing the complete set of RNA transcripts expressed within a cell, tissue, or organism, RNA sequencing provides a dynamic view of gene activity that reflects both genetic background and environmental influences. At its core, RNA sequencing enables high-throughput quantification of gene expression across thousands of genes simultaneously. Unlike earlier microarray-based methods, RNA sequencing does not rely on predefined probes, allowing for unbiased detection of known and novel transcripts. This includes messenger RNAs, long non-coding RNAs, microRNAs, and alternatively spliced isoforms. The ability to capture this broad spectrum of RNA species makes RNA sequencing particularly valuable for understanding the complexity of human diseases, many of which are driven by subtle but coordinated changes in gene expression rather than single genetic mutations. In precision medicine, the integration of RNA sequencing data with clinical information has enabled the identification of molecular disease subtypes that are not distinguishable using traditional diagnostic approaches. In oncology, tumors that appear similar under a microscope may exhibit distinct transcriptomic profiles that influence their aggressiveness, metastatic potential, and response to therapy. By analyzing gene expression signatures, clinicians can classify cancers into molecular subtypes, allowing for more accurate prognosis and personalized treatment selection. This approach has been particularly successful in breast cancer, lung cancer, and hematological malignancies.

One of the most important applications of RNA sequencing in precision medicine is biomarker discovery. Transcriptomic biomarkers are genes or gene expression patterns that correlate with disease states or therapeutic responses. By comparing RNA expression profiles between healthy and diseased individuals, researchers can identify differentially expressed genes that serve as diagnostic or prognostic markers. These biomarkers can be used to detect diseases at early stages, monitor disease progression, or predict patient response to specific treatments. Another critical application is in the field of pharmacogenomics, where RNA sequencing helps understand how genetic and transcriptional variation influences drug response. Patients often respond differently to the same medication due to differences in gene expression levels affecting drug metabolism, transport, and target interaction. RNA sequencing allows researchers to identify these variations and predict which patients are more likely to benefit from a particular drug or experience adverse effects. RNA sequencing also plays a major role in immunotherapy, particularly in cancer treatment. Single-cell RNA sequencing has further expanded the role of transcriptomics in precision medicine by enabling gene expression profiling at the level of individual cells. This has revealed that many diseases are extreme cellular heterogeneity, where different cell populations within the same tissue behave differently. In cancer, rare drug-resistant cell populations can be identified using single-cell transcriptomics, allowing for more therapeutic interventions. In autoimmune diseases, single-cell analysis helps identify specific immune cell subsets responsible for pathological inflammation. Spatial transcriptomics, when combined with RNA sequencing, provides additional context by preserving the spatial organization of gene expression within tissues. RNA sequencing-based transcriptomics generates large and complex datasets that require advanced bioinformatics tools for analysis. The process involves quality control, alignment of sequencing reads to reference genomes, quantification of gene expression, and statistical analysis to identify differentially expressed genes. Machine learning techniques are increasingly being used to analyze these datasets, enabling pattern recognition, patient stratification, and outcome prediction. These computational approaches are essential for translating raw sequencing data into clinically actionable insights. One major issue is data variability, which can arise from differences in sample collection, sequencing platforms, and experimental protocols. Batch effects and technical noise can obscure true biological signals, making standardization and normalization critical steps in data analysis. The interpretation of transcriptomic data requires careful consideration, as changes in gene expression do not always directly translate into functional biological effects.

Correspondence to: Sofia Martinez, Department of Genomic Medicine, National Autonomous University, Mexico, Mexico, E-mail: sofia.martinez@unam.mx

Received: 01-Sep-2025, Manuscript No. TOA-25-41964; **Editor assigned:** 03-Sep-2025, PreQC No. TOA-25- 41964 (PQ); **Reviewed:** 16-Sep-2025, QC No. TOA-25-41964; **Revised:** 23-Sep-2025, Manuscript No. TOA-25- 41964 (R); **Published:** 30-Sep-2025, DOI: 10.35248/2329-8936.25.11.222.

Citation: Martinez S (2025). RNA Sequencing-Based Transcriptomics in Precision Medicine Applications. Transcriptomics. 11:222.

Copyright: © 2025 Martinez S. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.