

A Comparative Analysis of RNA-Seq and NanoString Technologies in Deciphering Viral Infection Response in Upper Airway Lung Organoids

Background

Respiratory viruses induce complex immune responses in the human airways, making it critical to have robust models and reliable profiling tools to study infection dynamics. This study uses a 3D airway organoid (OTE) model maintained at an air-liquid interface to study infections by influenza A virus (IAV), human metapneumovirus (MPV), or parainfluenza virus (PIV3). Researchers compared both RNA-Seq and the nCounter® platform to capture immune-related genes during active versus control infections. The aim was to evaluate method agreement while identifying key antiviral responses.

Research Questions

- Do RNA-seq and the nCounter platform provide concordant gene expression results when studying viral infections in 3D lung organoids?
- Which immune signatures, particularly those related to interferon pathways, are most predictive of an effective antiviral response?

Results & Conclusions

- Strong data agreement:** RNA-seq and the nCounter platform demonstrated high congruence (Spearman correlations >0.86) across multiple infection conditions.
- Highly reliable:** Both platforms resulted in >96% of data points within acceptable limits across all conditions (Bland-Altman).
- Key antiviral genes identified:** Both RNA-seq and nCounter detected similar interferon-stimulated genes (IFIT, ISG15, MX1, OAS family) highlighting an active immune response to viral infections.
- Biologically relevant nCounter content:** Gene ontology analysis linked immune signatures to viral defense pathways to confirm biological relevance.
- nCounter excelled at early MPV infection:** Direct detection enabled subtle, early MPV infection changes missed by RNA-seq.

Experimental Setup

Sample Type	3D airway organoid cultures
Tissue Type	Human bronchial epithelial cells in a hydrogel-based model that recapitulates the upper airway
Assay	nCounter® probe set targeting 773 genes related to immune and antiviral responses
Analyte	RNA
Instrument	nCounter® Analysis System, Illumina NovaSeq® 6000

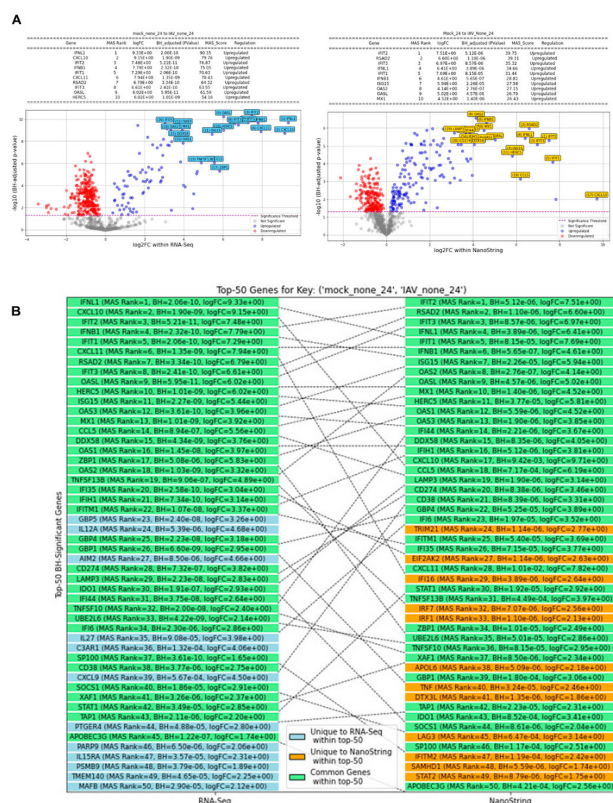


Figure 5: Technology congruence.

Volcano plots and top differentially expressed genes demonstrating concordance in the findings identified by each technology.

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