CANOPY BIOSCIENCES

NanoString nCounter vs RNA Seq in Gene Expression Studies: How Do You Choose?

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SELECTING THE RIGHT ASSAY

In the last 15 years, we have witnessed remarkable technological advances in the field of gene expression profiling. These innovations have allowed researchers to obtain gene expression information from virtually any sample type, even down to the single cell level. At Canopy Biosciences, we recognize that every experimental question is unique and there is no one-size-fits-all approach when it comes to measuring transcript expression. As a result, we offer both NanoString nCounter technology and RNA-Seq which gives us access to the full breadth of speed, sensitivity, and transcriptome coverage that may be needed for specific customer requirements.

A common misconception is that NanoString and RNA-Seq are competitive technologies. We view them as truly unique offerings that can complement one another to provide researchers with an assay from discovery through diagnostic, prognostic, or predictive endpoints. In this article we will help determine which of these experimental approaches may be best suited to address your specific experimental needs.

1. Do you need coverage of the full transcriptome or do your hypotheses involve specific pathways or genes?

If your work is hypothesis-driven and you know which genes or signaling pathways are of interest to your project, then NanoString nCounter is a great choice. NanoString nCounter gene expression assays offer an extensive list of gene panels which cover many disease areas including oncology, neuroscience, and immunology. NanoString nCounter technology can accurately quantify up to 800 targets per run, and all panels reserve space for a minimum of 20-30 additional targets. If you have a panel in mind that is lacking a couple of your favorite genes, let us know and we can easily customize the panel for you!

If you are in the discovery phase of your project, we have got you covered! With our comprehensive RNA sequencing offerings, you can quantify virtually any type of transcript from a wide range of sample types.

2. How quickly do you need results?

Fast turnaround times are one of the NanoString nCounter's greatest advantages. Due to a low-complexity wet-lab workflow and fast data acquisition, we can deliver full data analysis for projects <24 samples in two weeks or less. Standard turnaround times for RNA-Seq experiments start at 4-6 weeks.

3. Do you have bioinformatics support?

If performing your own analysis is important, NanoString offers free access to software programs (e.g. nSolver and Advanced Analysis) that make data normalization and downstream result visualization very straightforward. RNA sequencing data analysis is complex and requires an understanding of programming languages.

Alternatively, we offer interactive data analysis using ROSALIND powered by OnRamp for both NanoString and RNA-Seq. Leave the heavy lifting to us and we will provide you with an intuitive data analysis visualization space that you can share with your colleagues.

4. Are you interested in gene fusions or transcript isoforms?

Accurate fusion gene detection is essential for diagnostic and research purposes. Due to detection constraints, many platforms have low throughput when quantifying these rearrangements. RNA-Seq can overcome these limitations by providing genome-wide detection as well as discovery of novel fusion genes. The NanoString nCounter platform can also be used to sensitively detect known fusion transcripts, but is limited to the specific fusion partners included in the panel design.

Both platforms are capable of quantifying expression of gene isoforms, but RNA-Seq has the added advantage of being able to analyze at a genome-wide scale.

5. Are you working with FFPE-derived RNA or other sample types with degraded RNA?

Working with degraded RNA presents challenges for all technologies, particularly when the RNA also contains base modifications that result from fixation (e.g. FFPE samples). At Canopy, we have optimized FFPE extraction procedures to yield RNA that is acceptable for use in RNA-Seq or NanoString experiments, including core needle biopsies. If a target approach is desired, NanoString's enzyme-free workflow provides a great way to capture a diverse set of transcripts. If a whole transcriptome approach is needed, we have a number of FFPE-specific RNA-Seq workflows to suit your needs. Both platforms are capable of quantifying expression of gene isoforms, but RNA-Seq has the added advantage of being able to analyze at a genome-wide scale.

6. Are you interested in developing RNA-based classifiers of patient populations for future use as an LTD or CDx?

We are uniquely positioned to help with these experiments. Our RNA-Seq services can provide a global snapshot of transcriptional changes which can then lead to the selection of a reduced set of genes that are necessary to stratify patient populations. Once completed, NanoString nCounter experiments can be expediently run in our CLIA-certified lab to provide real time data during ongoing clinical trials.

References:

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Heyer, EE et. al. Nat Commun 10, 1388 (2019).

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