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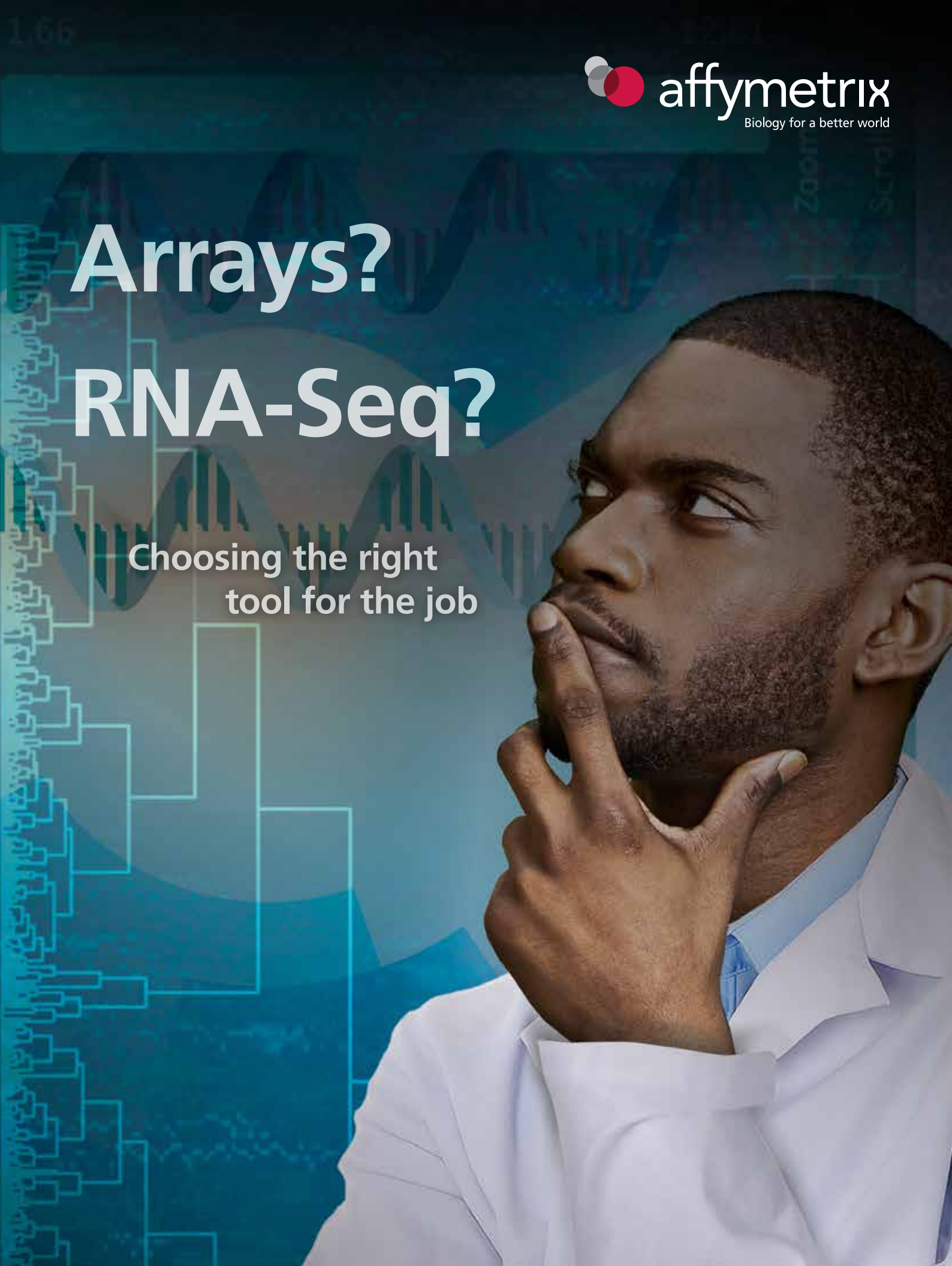
Biology for a better world

Arrays?
RNA-Seq?

Choosing the right tool for the job

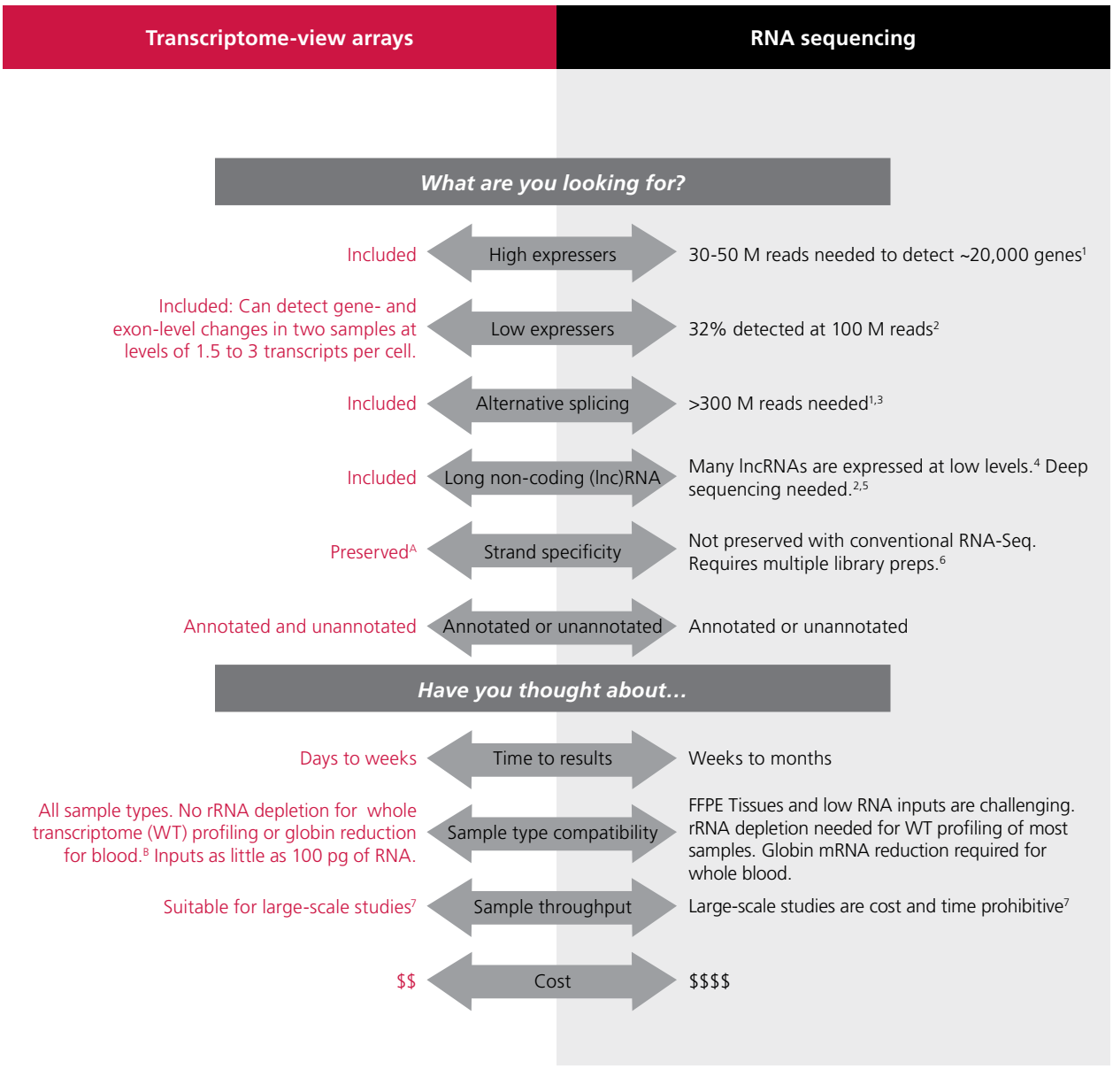


Arrays or sequencing?

Choose the right tool for the job

Are you leveraging the appropriate technology for your research? The scientific community is now widely acknowledging that there are specific applications best served by arrays and others by RNA sequencing (RNA-Seq). Additionally, many see opportunities to harness the power of both technologies for expression studies.

What specifics have you considered when choosing the best technology for your study?



Look beyond the gene

Expand your biomarker discovery universe

Due to the complexity of the transcriptome, scientists are now aware of the importance of expanding their scope beyond the gene level. Gaining attention as critical regulators of coding RNA and alternative splicing, lncRNA have been implicated in a wide range of diseases, opening up the possibility of their use as biomarkers and therapeutic targets.[8] In addition, because an estimated **95%** of human genes undergo alternative splicing,[9,10] and the disruption of such events is known to be highly associated with many diseases,[9] alternatively spliced variants are also promising candidates for biomarkers.[11]

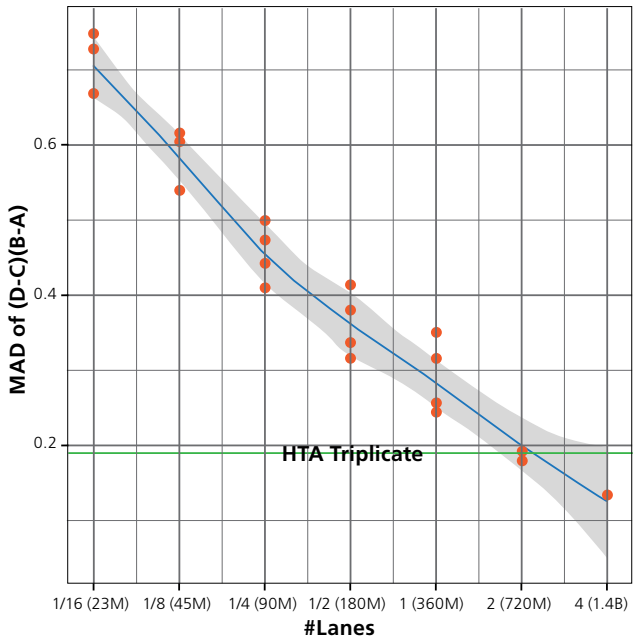
A growing body of evidence has shown that identifying lncRNA and alternative splicing events can be very challenging with RNA-Seq.

- To reveal low-abundance transcripts and splice junctions, very deep sequencing is required— which is not cost effective.[12]
- Detection of alternative splicing events with RNA-Seq is challenging due to sampling noise, requiring >300 million reads providing only 80% confidence.[1,3]
- Due to significant biases introduced in library preparation, interpreting exon-level RNA-Seq results—especially when looking for alternative splicing events—should be done with caution.[13]

Go beyond gene-level with transcriptome-view solutions

Precise results

Accuracy for RNA-Seq is read-depth dependent. GeneChip® transcriptome-view solutions deliver accurate results equivalent to **two full lanes of RNA-Seq.**

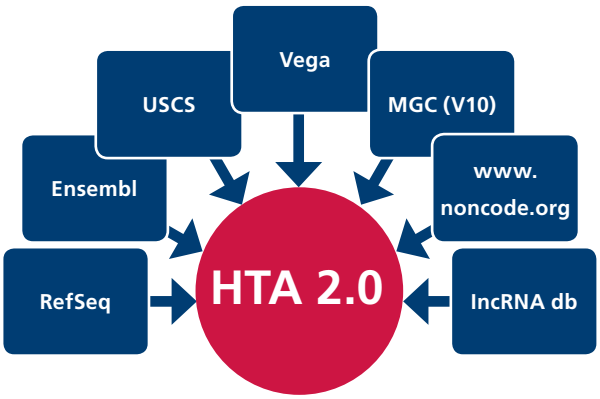


By evaluating a linear tissue mixture model in which RNA from two samples are mixed in known proportions, the accuracy of expression was evaluated across all measured exons.

● = individual RNA-Seq experiment
— = RNA-Seq, best fit
— = GeneChip® Human Transcriptome Array (HTA) 2.0, triplicate data

One experiment; multiple layers of biology

GeneChip® Human Transcriptome Array (HTA) 2.0 content* is derived from **eight databases,** greatly exceeding the number used in most RNA-Seq analysis pipelines. This allows exploration of all known coding and non-coding genes, exons, and isoforms.



*The same design approach is taken for rat and mouse transcriptome-view arrays.

Choose GeneChip® transcriptome-view solutions

Simple workflow. Fast analysis. Cost effective.

Human, mouse, and rat transcriptome arrays from Affymetrix allow researchers to

- Generate comprehensive datasets quickly across known pathways and genes, allowing time-consuming RNA-Seq experiments to be focused on discovery of unknown transcripts
- Perform global gene expression profiling with as little as 100 pg of RNA or 500 pg of degraded formalin-fixed, paraffin-embedded (FFPE) RNA— sample inputs which are not easily amenable to RNA-Seq
- Better quantify low-abundance transcripts[7]
- Validate complex RNA-Seq data quickly and easily
- Quickly and cost-effectively complete high-volume studies[7]
- Analyze data in minutes with free Transcriptome Analysis Console (TAC) software

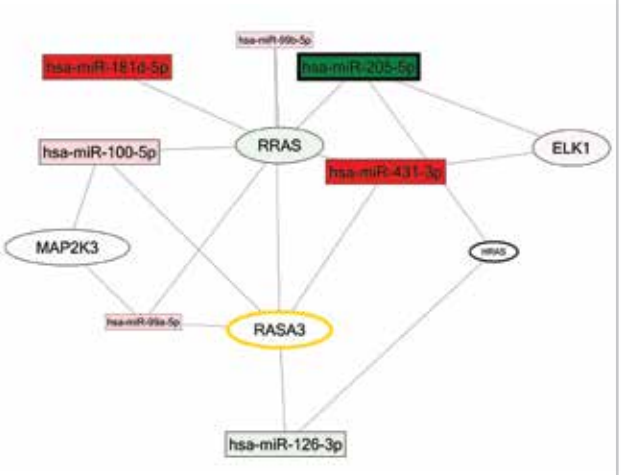
> "We have done comparisons between the data quality using microarrays and RNA-Seq. For our purposes, we have found the results to be more or less comparable. But when you consider the time and cost savings, microarrays come out ahead."
>
> **Dr. Jay Tiesman**
> The Procter & Gamble Company

Improve turnaround time. Data to insight in minutes.

With simple and free TAC software you can

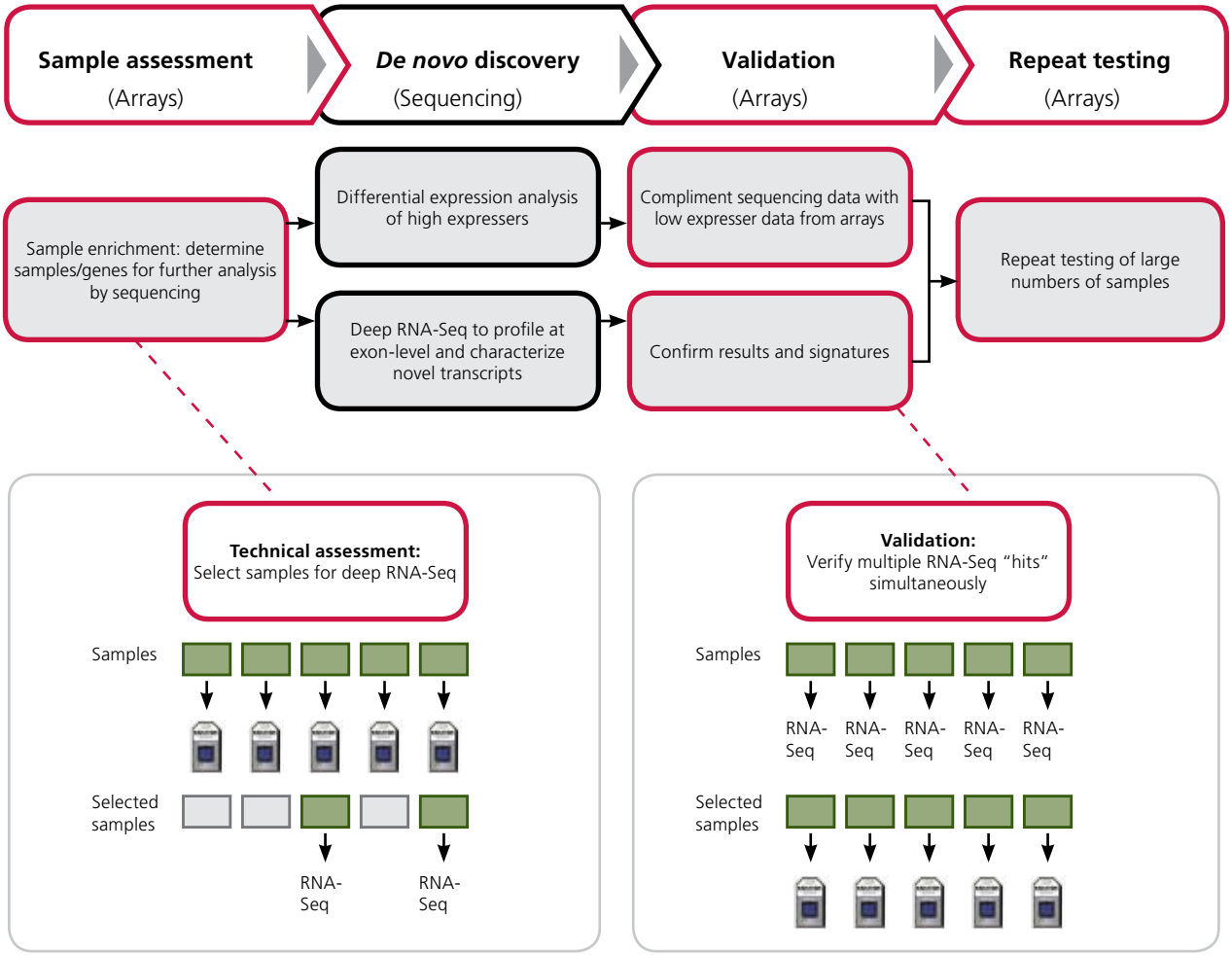
- Identify genes, exons, and alternative splicing events
- Explore expression changes across networks of miRNA and target genes
- Visualize gene models with exon and junction signals
- Filter on genes and pathways of interest
- Link directly to multiple public databases
- View data in multiple formats—volcano and scatter plots; mRNA-miRNA interaction networks; chromosome summaries; hierarchical clustering and transcript isoform views; WikiPathways integration

miRNA regulation of the MAPK pathway



Take gene expression studies further, faster

Combine sequencing with arrays



"As for the future, I really see RNA-Seq and microarrays as complementing each other. There's an extra bit of confidence I get from using both technologies."

Dr. Jeremy Murray
John Innes Centre

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A. Strandedness is preserved in the following sample preparation kits: GeneChip® WT Pico Kit; GeneChip® WT PLUS Reagent Kit; GeneChip® 3′ IVT PLUS Reagent Kit; SensationPlus™ FFPE Amplification and 3′ IVT Labeling Kit.

B. No rRNA or globin mRNA reduction required for the following sample preparation kits: GeneChip® WT Pico Kit; GeneChip® WT PLUS Reagent Kit; GeneChip® IVT Pico Kit; SensationPlus™ FFPE Amplification and WT Labeling Kit; SensationPlus™ FFPE Amplification and 3′ IVT Labeling Kit. GeneChip® 3′ IVT PLUS Reagent Kit requires globin mRNA reduction.

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