



RNA-Seq
misses

HTA
Delivers!

Volume 2

RNA-Seq misses what

HTA

Delivers!

RNA-Seq promises a great deal, but bottlenecks in informatics and data analysis continue to delay your discovery, your answers, and your publications.

Accelerate publishing your discovery with a solution that distills the vast amounts of genetic data generated by GeneChip® Human Transcriptome Array (HTA) into relevant, useful information in minutes. Affymetrix® Transcriptome Analysis Console (TAC) Software provides intuitive interactive visualization tools that easily and rapidly show you what has changed in the expression profile—at the gene and exon level—as well as allowing you to drill down into alternatively spliced exons.

RNA-Seq means big costs, not big results.

As reported by Sboner, *et al.*¹, the real cost of sequencing is higher than you think. Investigators using RNA-Seq are allocating larger proportions of funding to informatics rather than to biology and medicine. Despite the recent decrease in cost of generating sequence data, overhead costs for NGS continue to increase². With limited budgets, paying for infrastructure or cloud computing and storage means you have to compromise on your science.

Spend your funding on what really matters – your scientific discoveries!

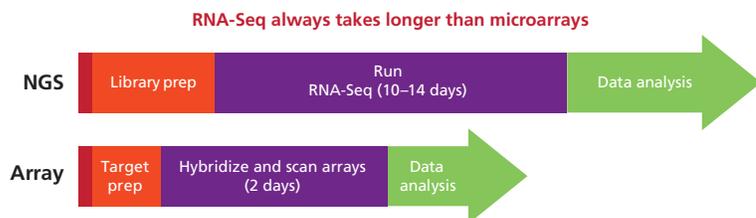
Spend your grant money on science, not overhead! TAC Software, provided at no charge, requires no cloud storage or computing and no need to build infrastructure or hire special bioinformatics staff.

Waiting for answers?

Investigators using RNA-Seq are losing efficiency from lengthy study cycles. RNA-Seq experiments take many weeks to complete. RNA-Seq investigators are left waiting for bioinformatics resources to begin analyzing their sequencing data. Circumvent the handling and analysis bottlenecks of NGS applications, and stop being confused about the RNA-Seq analysis pipeline choices.

Discover more, faster.

By using TAC Software, you can quickly start finding your answers. Impact your research, discover more, and publish faster. Analyze your data in minutes, easily interpret your results, and get answers FASTER.

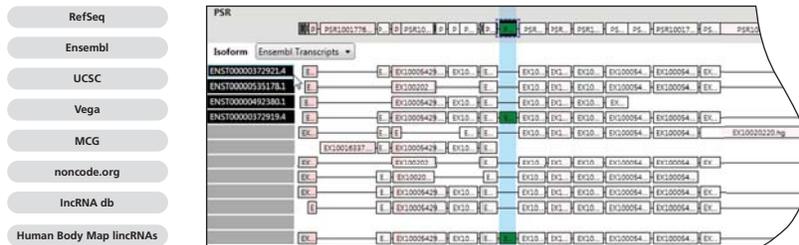


RNA-Seq misses what

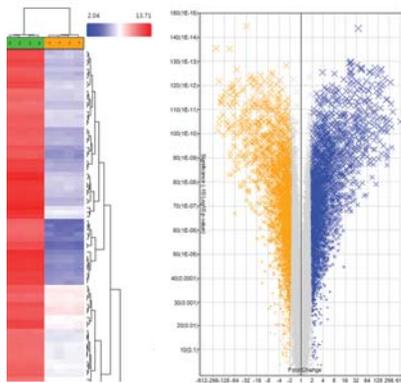
HTA

Delivers!

A complete solution for your gene expression profiling: GeneChip® Human Transcriptome Array (HTA) and Affymetrix® Transcriptome Analysis Console (TAC) Software

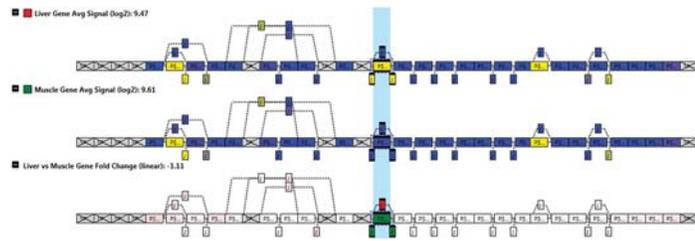


The most comprehensive gene models available, at your fingertips. The HTA design is based on a thorough model of the entire human transcriptome including all known coding and non-coding transcripts. The array contains all known exons and splice junctions and 40,000 non-coding RNAs. TAC Software provides you with a complete view of the transcriptome and allows quick further analysis of transcripts of interest by providing integrated links to public databases and annotation sources.



Your data, your analysis, your view.

Whether you prefer hierarchical clustering, volcano plots, or scatter plots, TAC Software provides interactive visualization tools for fast and easy data interpretation on your laptop or desktop computer.



Alternative splicing is critical to understanding disease mechanisms.

In the human transcriptome, almost 95% of multi-exon genes are known to be alternatively spliced³. A large proportion of genetic diseases can be attributed to aberrant splicing events⁴. TAC Software allows you to quickly and comprehensively analyze all transcript isoforms, assuring you don't miss important regulatory events. Please visit us at www.affymetrix.com/hta to view video tutorials and learn how easy it is to perform gene-level and alternative splicing analysis using TAC Software.

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Delivers!

See how HTA can deliver for you!

Contact your local Affymetrix Account Manager or sales@affymetrix.com for more information.

Ordering information

Part number	Description
902309	Kit, GeneChip® Human Transcriptome Array 2.0 and GeneChip® WT PLUS Reagent Kit, 10 samples
902310	Kit, GeneChip® Human Transcriptome Array 2.0 and GeneChip® WT PLUS Reagent Kit, 30 samples
902311	Kit, GeneChip® Human Transcriptome Array 2.0 and SensationPlus™ FFPE Amplification and WT Labeling Kit, 12 samples
902312	Kit, GeneChip® Human Transcriptome Array 2.0 and SensationPlus™ FFPE Amplification and WT Labeling Kit, 24 samples

References

1. Sboner A., *et al.* The real cost of sequencing: higher than you think! *Genome Biology* **12**:125 (2011).
2. Khemani A., Jaju G. Contracting sequencing costs could mean ballooning informatics prices. *Genetic Engineering & Biotechnology News* (blog post, May 9, 2012). <http://www.genengnews.com/gen-articles/contracting-sequencing-costs-could-mean-ballooning-informatics/4388/>
3. Pan Q., *et al.* Deep surveying of alternative splicing complexity in the human transcriptome by high-throughput sequencing. *Nature Genetics* **40**(12):1413–1415 (2008). doi:10.1038/ng.259. PMID 18978789.
4. Matlin A. J., Clark F., Smith C. W. Understanding alternative splicing: towards a cellular code. *Nature Reviews Molecular Cell Biology* **6**(5):386–398 (2005). doi:10.1038/nrm1645. PMID 15956978.

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