

## Affymetrix® Transcriptome Analysis Console (TAC) Software

Easy-to-use software for differential expression analysis and visualization

### A NEW analysis solution that transforms data to insight

The Affymetrix GeneChip® platform remains the gold standard for robust comprehensive expression analysis, and for the first time we are providing extensive software tools to take you from microarray data to identifying what is differentially expressed.

Detailed analysis is now at the fingertips of every researcher—regardless of access to bioinformatics resources. The new Affymetrix® Transcriptome Analysis Console (TAC) Software takes the normalized and summarized data from Affymetrix Expression Console™ Software to the next level, providing differential expression analysis and visualization for easy interpretation.

Researchers now have a cost-free solution to quickly analyze their data, enabling discovery and understanding into the biological diversity underpinning their research. These tools were designed with the end user in mind and enable an investigator to analyze and explore data at their own pace. Combined with the comprehensive coverage of Affymetrix' high-density microarray solutions and Expression Console Software, TAC Software provides an easy-to-use, integrated solution to go from raw data to biological results in just a few clicks.

### You decide — gene-level, exon-level, or alternative splicing analysis.

TAC Software supports three types of differential expression analysis for Affymetrix® microarrays, depending upon array type:

#### Gene-level analysis

- 3' IVT arrays, Gene ST arrays, Exon ST arrays, and human transcriptome arrays

#### Exon-level analysis

- Gene ST arrays and Exon ST arrays

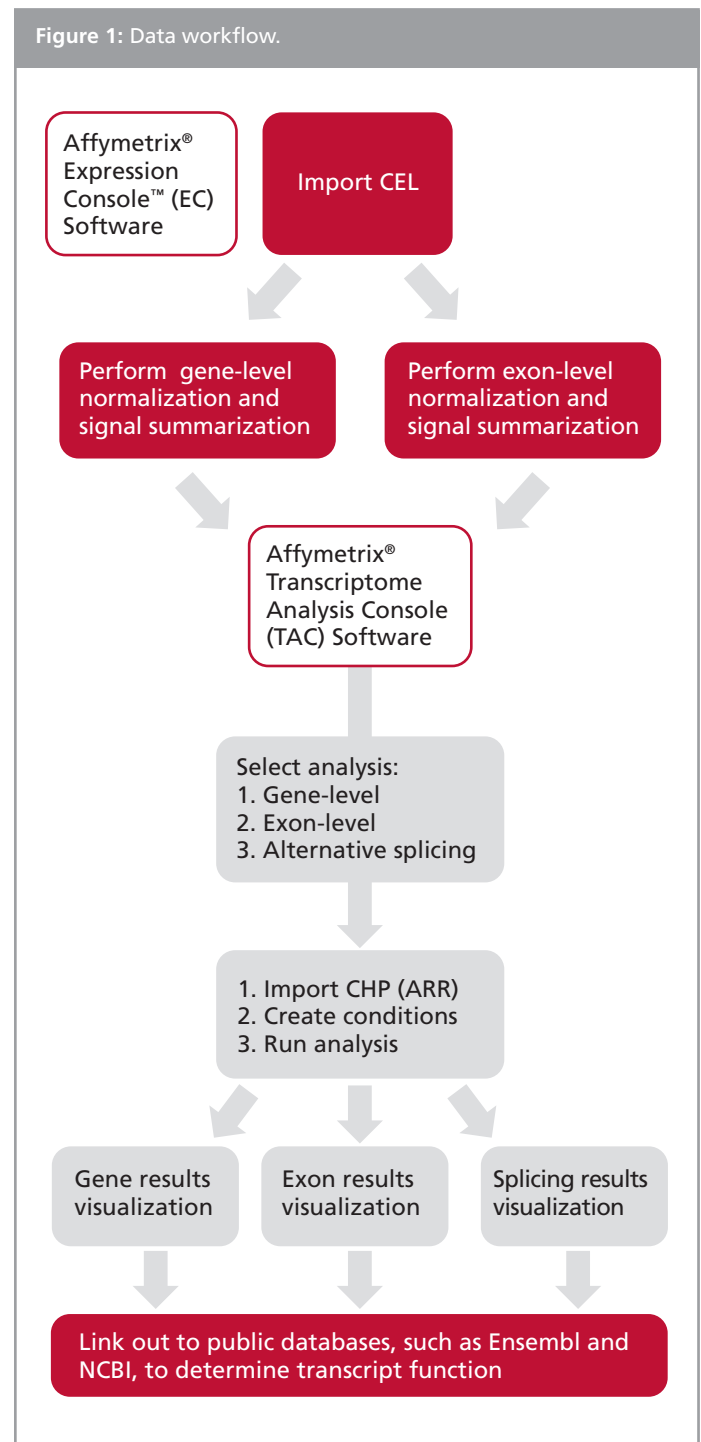
#### Alternative splicing analysis

- Human transcriptome arrays

### Easy-to-use TAC Software provides:

- Sample grouping and cluster visualization
- Statistical tests for differential expression
- Detection of alternative splicing and gene model visualization<sup>1</sup>
- Detailed summary view of comparisons
- Direct links to available public annotations

Figure 1: Data workflow.



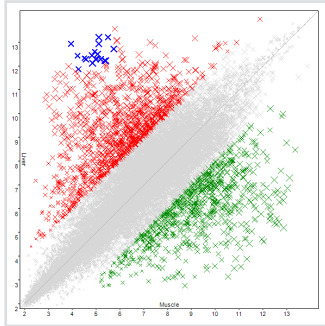
<sup>1</sup> Available for Human Transcriptome Array 2.0

**Powerful visualization tools**

TAC Software provides powerful visualization tools that allow easy interpretation of significant expression changes. Some of the visualization tools in TAC include:

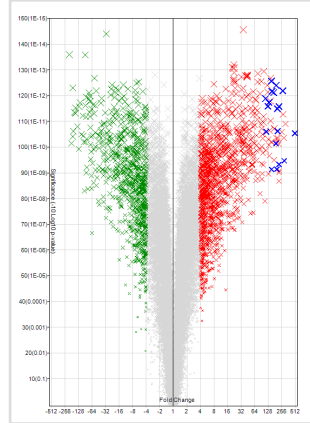
**Scatter plot**

Visualize significant changes in signal between conditions.



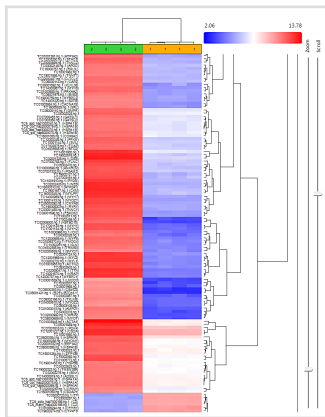
**Volcano plot**

Visualize significant fold-changes between conditions.



**Hierarchical clustering**

Arrange samples and genes into groups based on their expression levels.



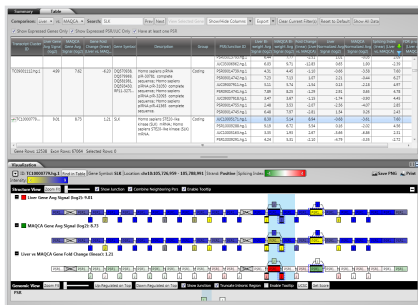
**Chromosome view**

Significant fold-changes visualized along each chromosome (human only).



**Alternative splicing**

Simple visualization of alternatively spliced exons to identify transcript isoforms.



**Export your results and link to external databases**

- Table contents can be exported as tab-delimited text files
- Genes, transcript isoforms, and exons can be linked out to public databases
- Experimental data seamlessly imports into pathway analysis tools

**Download TAC Software today**

To access TAC Software and a complete list of supported arrays, please visit [www.affymetrix.com](http://www.affymetrix.com).

**System requirements**

Microsoft Windows® 7 Professional operating system with Service Pack 1	
Operating system (bits)	64-bit
Processor	8 GHz Intel® Pentium® Quad Core
Memory (RAM)	8 GB (recommended) 16 GB
Web browser	Internet Explorer® 7.0 and above

Microsoft Windows® XP	
Operating system (bits)	64-bit
Processor	4 GHz Intel® Pentium® Quad Core
Memory (RAM)	8 GB (recommended) 16 GB
Web browser	Internet Explorer® 7.0 and above

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