Explore mRNA and miRNA interactions with GeneChip® miRNA 4.0 Array, GeneChip® Human Transcriptome Array 2.0 (HTA 2.0), and Transcriptome Console (TAC) 2.0 Software

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ABSTRACT

The relationship between mRNA and miRNA is extremely complex—one miRNA may target many different genes, and one gene may be targeted by many different miRNA. This many-to-many relationship can be very difficult and time consuming to decipher. To help ease your frustration in analyzing data that includes miRNA and mRNA interactions, Affymetrix is developing Transcriptome Analysis Console (TAC) 2.0 Software, which provides the ability to visualize fold changes of known interactions.

The complete solution. GeneChip® miRNA 4.0 Array and GeneChip® Human Transcriptome Array 2.0 (HTA 2.0), combined with Affymetrix Expression Console™ 1.2.1 Software and Affymetrix® Transcriptome Analysis Console (TAC) 2.0 Software, provide unparalleled resolution in changes in the transcriptome.

GeneChip® miRNA 4.0 Array

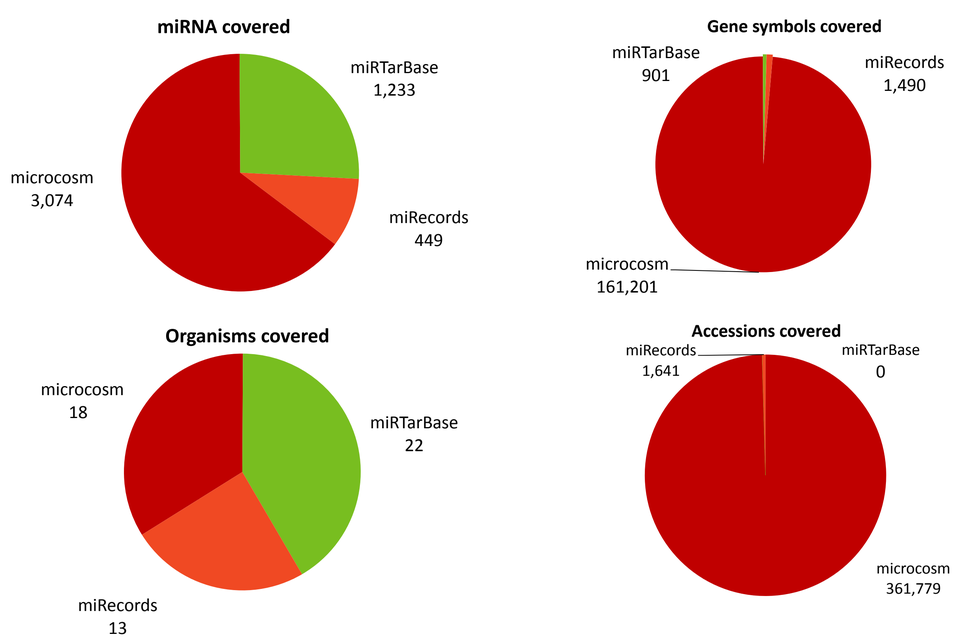
This latest addition to Affymetrix' GeneChip miRNA Array catalog includes design features that make it the most advanced and comprehensive miRNA profiling solution on the market. The array was not only designed using miRBase Release 20, the most current version available, it also includes information that enables the visualization of interactions between mRNA and miRNA.

This information includes:

- Genomic context (the gene where the miRNA comes from)
- Validated miRNA targets (targets validated using a secondary method)
- Predicted miRNA targets (targets predicted by third parties)
- Clustered miRNA (miRNA within 10 kb of one another)

Gene target information on GeneChip® miRNA 4.0 Array

To help advance research and provide investigators with actionable data, GeneChip miRNA 4.0 Array includes target genes from multiple data sources in the annotation file. The charts below summarize the total number of miRNA, organism target genes, and accession numbers covered by each database.



1. microcosm: http://www.ebi.ac.uk/enright- srv/microcosm/htdocs/targets/v5/info.html
   Leverages miRanda for target gene predictions. (Version 5)
2. MTI: http://mirtarbase.mbc.nctu.edu.tw/index.php
   Uses multiple target gene prediction algorithms and only reports a hit when detected by more than one predictor. (Version and download date: Release 4.5 - 11/01/2013)
3. miRecords (validated only): http://mirecords.umn.edu/miRecords/doc.php
   Only the validated targets are reported. (Download date April 27, 2013)

Transcriptome Analysis Console (TAC) 2.0 Software

TAC 2.0 Software, being developed by Affymetrix, delivers more than the identification of differentially expressed genes and exons and the visualization of alternative splicing events. TAC 2.0 Software enables investigators to view the network of interactions between miRNA and the genes they target.

Detailed analysis is now available for every researcher, regardless of their access to bioinformatics resources, with Expression Console Software and TAC 2.0 Software. With these easy-to-use yet powerful analysis tools, investigators will be able to:

- Visualize relationships between miRNA and the genes they target
- Perform statistical tests for differential expression
- Identify differentially expressed genes, exons, and alternative splicing events
- Visualize gene models with exon and junction signal
- Link directly to available public annotations

Visualize miRNA and target RNA fold change

Visualize a single miRNA and its target genes: The oval at the center of Figure 1 is the miRBase accession number for a human miRNA. The rectangles connected to each miRNA are the predicted and validated targets of the miRNA. The fold change is depicted using color-coding for each oval and rectangle (red: up regulated; green: down regulated).

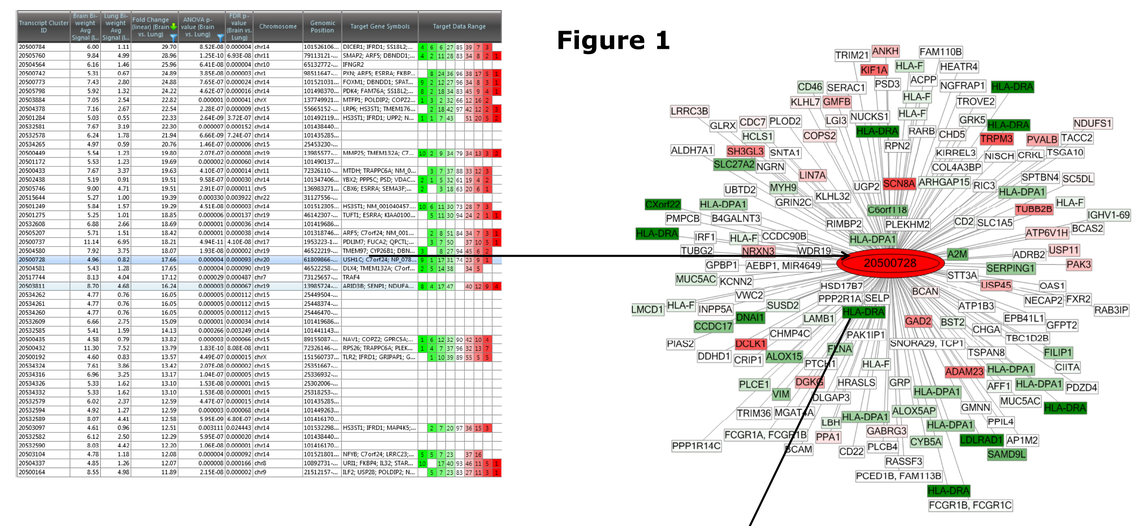


Figure 1

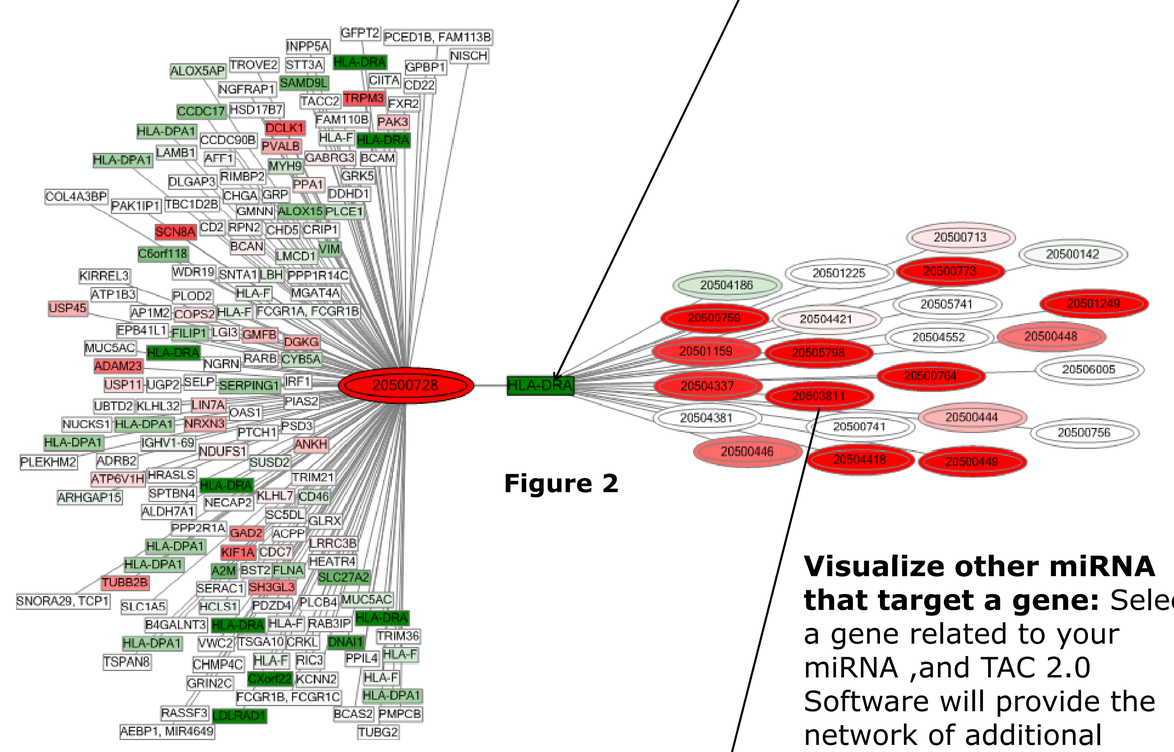


Figure 2

Visualize other miRNA that target a gene: Select a gene related to your miRNA ,and TAC 2.0 Software will provide the network of additional miRNA that interact with that gene, as shown in Figure 2.

Visualize the network of relationships between miRNA and genes: Select another miRNA that interacts with your gene to expand the network of interactions to include common genes as wells as the genes unique to the miRNA.

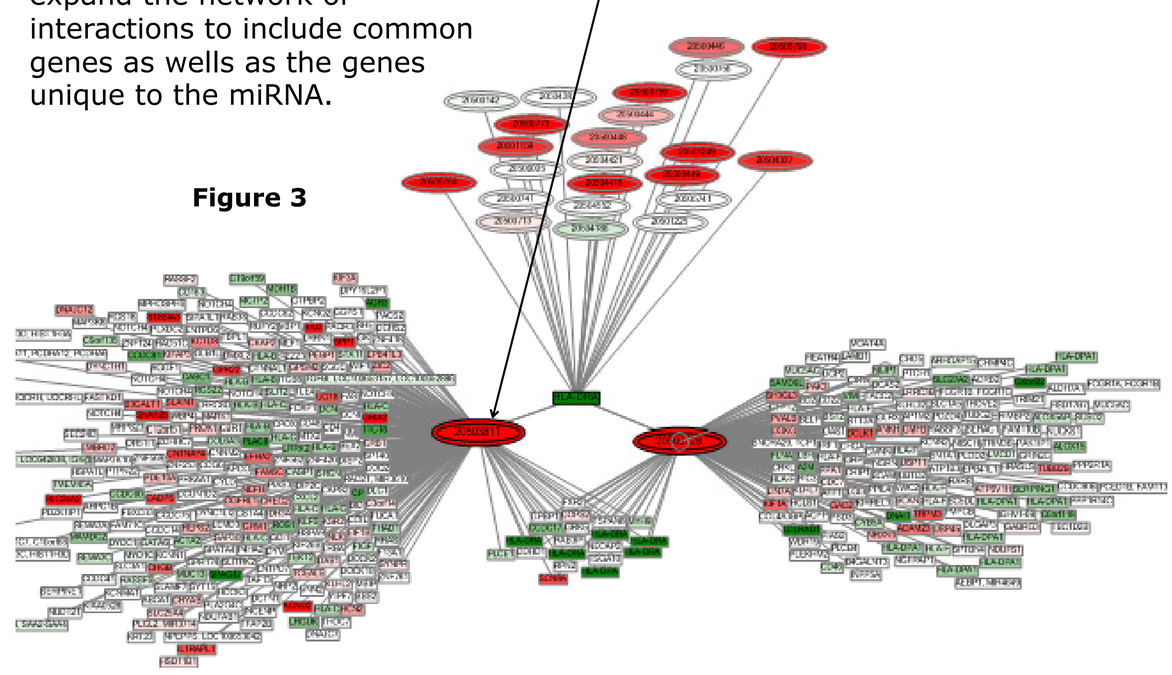


Figure 3

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