Isolation | Expression Analysis | Localization | Functional Analysis

miRCURY LNA™ microRNA Array Analysis Software

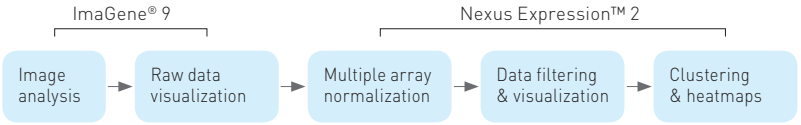
At a glance

- Fast and accurate analysis of miRCURY LNA™ microRNA Array data
- ImaGene® 9 and Nexus Expression™ 2 in a package specifically adapted to Exiqon's microarrays
- Easy workflow – no bioinformatics skills required
- Best-in-class grid placement, automatic analysis and quality check of all spots
- Quick and easy identification of differentially expressed microRNAs
- Direct links to microRNAs in miRBase and TargetScan

Leading-edge microarray analysis software

This comprehensive microarray data analysis package is ideal for use with the miRCURY LNA™ microRNA Arrays. It consists of the well-known ImaGene® 9 and Nexus Expression™ 2 from BioDiscovery, as well as settings files for rapid and easy analysis of Exiqon microarrays. Go from raw data to publication-ready results in an easy, step-by-step process without the need for advanced bioinformatics skills.

Overview of ImaGene® 9 and Nexus Expression™ 2.



ImaGene® 9

ImaGene® is a very powerful tool for microarray image analysis. Through an intuitive interface, it lets the user extract signal intensities from the scanned array and flag (poor) spots either automatically or manually (Figure 1). In addition, ImaGene® can be used for easy visualization of microarray data in scatter or M-A plots (Figure 2).

Highlights include:

- Advanced spot finding and grid placement
- Automatic analysis and quality check of all spots
- Interactive spot checking
- Intuitive interface and navigation
- Scanner, array and system independent
- Integrated settings file for convenient analysis of Exiqon's miRCURY LNA™ microRNA Arrays
- A quality control template specifically designed for Exiqon's microarrays

Figure 1

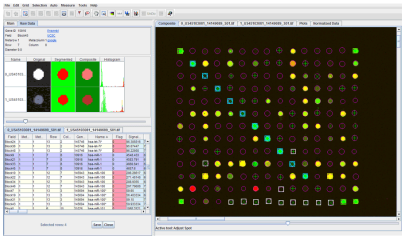


Figure 1. Fast and accurate spot identification. Squares indicate the different spots available on miRCURY LNA™ microRNA Arrays: Landing lights (green), Spike-ins (blue), Spike-ins v.2 (yellow) and empty spots (grey).

Figure 2

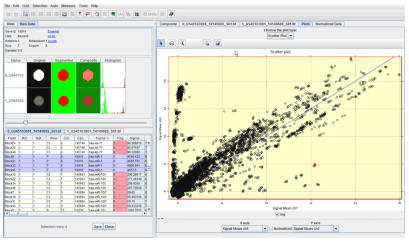


Figure 2. Excellent data visualization. This scatter plot clearly shows that most of the spots occur in groups of four (the four replicates printed on the slides), illustrating the good uniform hybridization of the arrays. The lasso tool can be used to select groups of spots, which are then highlighted in the list to the left.

LNA™

EXIQON
Seek Find Verify

Nexus Expression™ 2

Nexus Expression™ is a very feature-packed but easy-to-use program for the analysis of microarray experiments. Using a simple workflow, raw data from ImaGene® is background-subtracted and normalized, after which the data can be visualized in heat maps and differentially expressed microRNAs identified (Figures 3 & 4).

Highlights include:

- Simple but powerful workflow – No bioinformatics/programming skills required
- One click workflow, with direct links to microRNAs in miRBase and TargetScan
- Combines replicate measurements
- Identifies differentially expressed microRNAs
- Cluster analysis: clusters sample groups or microRNAs

System requirements

ImaGene® 9

- Platforms Supported: Windows 9x/Nt4/Win2k/WinXP, Linux, OS X
- Minimum: 700 MHz Pentium or G4, 256 MB RAM
- Recommended: 2.0 GHz or faster Intel® Core™ 2 Duo processor, 1024 or more MB RAM

Nexus Expression™ 2

- Platforms Supported: Windows Win2k/WinXP, OS X
- Minimum: 1.0 GHz Pentium or G4, 512 MB RAM
- Recommended: 2.0 GHz or faster Intel® Core™ 2 Duo processor, 1024 or more MB RAM

Ordering information

Product number	Product name	Product description
208221	ImaGene®/Nexus™ - 30 day license/24 slides	Microarray Analysis Software
208220	ImaGene®/Nexus™ - Perpetual license	Microarray Analysis Software

Figure 3

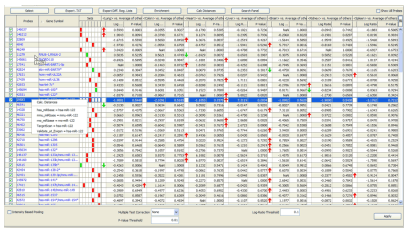


Figure 3. Up or down regulated microRNAs are easily identified. Probes are listed with both p-values and log values. Direct links to miRBase, TargetScan and relevant Exiqon products are available by clicking on the probe ID.

Figure 4

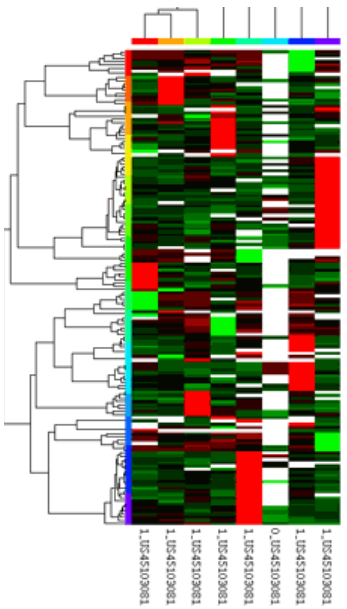


Figure 4. Flexible clustering of data. Heat maps are easily generated using different clustering algorithms.

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