

## May 11, 2011 – LC Sciences Launches V17 MicroRNA Microarrays

Houston, TX - Taking advantage of its flexible  $\mu$ Paraflo<sup>®</sup> Chip Technology, Houston based LC Sciences today announced immediate availability of probe content from miRBase 17 for their microRNA (miRNA) microarray customers. This announcement comes just a few days after the announcement of the update to version 17 at miRBase.org (<u>http://www.mirbase.org/blog/2011/04/mirbase-17-released/</u>).

The public miRBase sequence database serves as the primary probe content for many commercially available miRNA profiling microarrays. However, the continued updating of the database can be problematic for researchers using pre-made microarrays as the probe content of the arrays immediately goes out of date whenever a new miRBase version is released. Especially, in a rapidly evolving field as miRNA research it is important to scientists to have the most complete picture of miRNAs expressed in their experimental samples.

This miRBase release marks yet another significant update with the addition of close to 2400 experimentally verified novel mature miRNA sequences as well as large additions of deep sequencing data revealing a wealth of information about individual miRNA sequence isoforms. These numbers represent an increase in the number of unique Human miRNA sequences of 43%.

LC Sciences miRNA microarrays make use of a microfluidics on-chip synthesis platform, termed  $\mu$ ParaFlo<sup>®</sup>, *versus* a traditional spotted array based on pre-synthesized oligonucleotides. This on-chip synthesis platform solves the issue of out of date microarrays because made-to-order microarrays can be produced on demand, delivering the most up-to-date research tools to researchers.



Chris Hebel, Vice President of Business Development at LC Sciences says, "We're excited to be able to offer our customers the most up-to-date and complete coverage of known miRNAs. Many other providers claim complete coverage of miRNA sequences, but the fact is that some have only

recently been able to update their arrays to version 16 and others, only to version 15. This is due to the inflexibility of their microarray platforms. Compared with probe content based on miRBase versions as recent as 15, our arrays cover 59% more Human, 57% more Mouse, and 76% more Rat sequences. These are big numbers and they represent information that I don't think researchers would want to miss."

**About microRNA (miRNA)** – miRNAs are small non-protein-coding RNA molecules that function as negative regulators of gene expression by base pairing with specific mRNAs. This either inhibits translation or promotes mRNA degradation.

**About miRBase -** The miRBase sequence database is a comprehensive database of miRNA sequence data, annotation, and predicted gene targets and is the primary public repository for these data. Release 17 of the database contains 16,772 entries representing hairpin precursor miRNAs, expressing 19,724 mature miRNA products, in primates, rodents, birds, fish, worms, flies, plants and viruses (<u>miRBase release summary</u>). The miRBase Registry also provides a gene-naming service for assigning official miRNA names to novel miRNAs before they are published. It is freely available to all at <u>http://www.mirbase.org/registry.shtml.</u>

**About LC Sciences** - LC Sciences offers discovery, profiling and validation services for microRNA and other small RNAs. Services include deep sequencing for discovery applications, microarrays for differential expression profiling and validation/confirmation of newly discovered microRNAs, and qRT-PCR for quantitation of microRNA expression levels. These comprehensive services are designed to be one-stop and produce the results needed to quickly advance your biological and biomedical research. Combining the latest deep sequencing technology with our µParaflo® on chip synthesis technology offers unprecedented flexibility and customization capability.

1. Griffiths-Jones S, Grocock R, van Dongen S, Bateman A, Enright A. miRBase: microRNA sequences, targets and gene nomenclature. *Nucleic Acids Res* 34(Database issue), D140–D144.

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