Selected Publications:

Arraystar LncRNA microarray & service

Fibrogenic Activity of MECP2 is Regulated by Phosphorylation in Hepatic Stellate Cells. Moran-Salvador E, et al. Gastroenterology, 2019

Loss of RNA-binding protein GRSF1 activates mTOR to elicit a proinflammatory transcription-al program. Noh J H, et al. Nucleic Acids Research, 2019

NKILA lncRNA promotes tumor immune evasion by sensitizing T cells to activation-induced cell death. Huang D, et al. Nature immunology, 2018

GUARDIN is a p53-responsive long non-coding RNA that is essential for genomic stability. Hu W L, et al. Nature Cell Biology, 2018

Long Non-coding RNA GMAN, Upregulated in Gastric Cancer Tissues, is Associated with Metastasis in Patients and Promotes Translation of Ephrin A1 by Competitively Binding GMAN-AS. Zhuo W, et al. Gastroenterology, 2018

Long noncoding RNA lnc-TSI inhibits renal fibrogenesis by negatively regulating the TGF-β/S-mad3 pathway. Wang P, et al. Science translational medicine, 2018

Arraystar circRNA microarray & service

A Noncoding Regulatory RNAs Network Driven by Circ-CDYL Acts Specifically in the Early Stages Hepatocellular Carcinoma. Wei Y, et al. Hepatology,2019

Circular RNA CircFndc3b modulates cardiac repair after myocardial infarction via FUS/VEGF-A axis. Garikipati V., et al. Nature Communications, 2019

FOXP1 circular RNA sustains mesenchymal stem cell identity via microRNA inhibition. Cherubini A, et al. Nucleic acids research, 2019

A Circular RNA Protects Dormant Hematopoietic Stem Cells from DNA Sensor cGAS-Mediat-ed Exhaustion. Xia P, et al. Immunity, 2018

PRMT5 circular RNA promotes metastasis of urothelial carcinoma of the bladder through sponging miR-30c to induce epithelial-mesenchymal transition. Chen X, et al. Clinical Cancer Research, 2018

circEPSTI1 as a prognostic marker and mediator of triple-negative breast cancer progression. Chen B, et al. Theranostics, 2018

Arraystar Epitranscriptomic microarray & service

Transient Focal Ischemia Significantly Alters the m6A Epitranscriptomic Tagging of RNAs in the Brain. Chokkalla A K, et al. Stroke, 2019

nrStar™ ncRNA PCR Arrays

tRNA-based prognostic score in predicting survival outcomes of lung adenocarcinomas. Kuang M, et al. International journal of cancer, 2019

DNA damage-induced cell death relies on SLFN11-dependent cleavage of distinct type II tRNAs. Li M, et al. Nature Structural & Molecular Biology, 2018

Saturated fatty acid alters embryonic cortical neurogenesis through modulation of gene expression in neural stem cells. Ardah M T, et al. The Journal of Nutritional Biochemistry, 2018

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Go Beyond RNA

With the discovery of non-coding RNA (ncRNA) regulatory activities beyond protein coding transcripts, a pursuit to uncover the pivotal roles of novel ncRNAs has attracted intense scientific interest with alluring opportunities of finding new disease regulators, biomarkers, and therapeutic targets. Arraystar Inc. is dedicated to empower the understanding of ncRNAs, including lncRNAs, circular RNAs, microRNAs, tRNAs, tRFs, tiRNAs, snoRNAs and more. Our innovative products, strong experimental knowledge, and bioinformatics expertise in the field of ncRNAs has supported more than one thousand high impact publications since our 2009 inception. While the industry of RNA analysis is still predominantly covering only mRNAs, our customers are taking new paths advancing science with us.

Arraystar LncRNA Microarrays

2019 New Releases: Human V5.0, Mouse V4.0, Rat V3.0

Highlights

- Most sensitive and best technology for lncRNA profiling, superior to RNA-seq
- Comprehensive and robust full-length lncRNA* collection curated from all major latest databases and landmark publications
- Systematic and specialized lncRNA annotation, including genomic context, epigenomic context*, completeness*, subcellular localization**, miRNA recognition site...
- Unambiguous, reliable and accurate detection and quantification of lncRNA transcript isoforms otherwise difficult by RNA-seq
- Simultaneous lncRNA and mRNA profiling on the same array for co-expressional and correlational expression and regulation

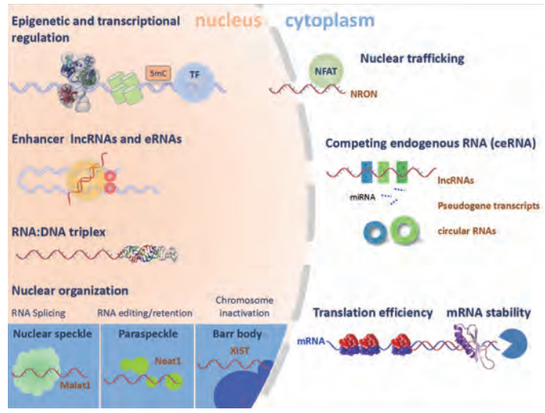

Fig 2. LncRNAs may regulate gene expression by various mechanisms, such as recruiting chromatin modifiers/remodelers to epigenetically regulate gene expression; by enhancer RNAs; by nuclear substructures; by nuclear-cytoplasmic transport; by competing endogenous RNAs via miRNAs; or by mRNA stability and translation; in cis or in trans, at transcription or post-transcriptional levels.

Introduction

LncRNAs are a major RNA class in the transcriptome [1]. These noncoding RNAs are transcribed from genomic sites either in association with a protein coding gene nearby or in the intergenic regions as lincRNAs (Fig. 1), with functions in gene expression regulation by multiple mechanisms, either in cis or in trans, at transcriptional or post-transcriptional levels (Fig. 2). LncRNAs are a key player in a wide range of biological systems and diseases. Cutting edge lncRNA science has resolved many long standing mysteries in, for example, chromosomal inactivation, developmental and differentiation programming, and diseases of unknown etiology. In general, lncRNAs exhibit more restricted cell type-specific expression compared to mRNAs, making lncRNAs a class of higher specificity biomarker. With the broadened horizon and modern paradigm of studying gene regulation, the science of gene expression profiling has now gone beyond past mRNA-only to encompass both classes of the coding and non-coding RNAs.

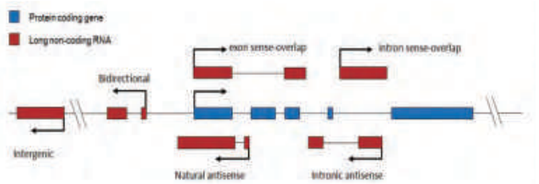

Fig1. LncRNA classification based on genomic contexts with the closest protein coding gene.

* Applicable to Human V5.0 ** Applicable to Human V5.0 and Mouse V4.0

Arraystar is the leader in lncRNA expression profiling technologies, using LncRNA Microarrays as the best performing platform to systematically profile lncRNAs together with mRNAs. To date, these microarrays have been an empowering tool and invaluable resource in lncRNA research touting many high impact publications. To incorporate rapid scientific advances and new data, Arraystar has now released new Human V5.0 and Mouse V4.0, and Rat V3.0 LncRNA Expression Microarrays.

Consolidated, comprehensive, robust, most up-to-date full-length lncRNA contents*

Unlike well-established protein coding genes, publically available lncRNAs are often sparsely annotated, partial in scope and scattered in collection. Large proportions of reported "lncRNAs" tend to be incomplete at 5′ or 3′ ends. Also, RNA-seq reads are not uniform in covering the 5′ and 3′ ends. These inaccurate and truncated lncRNA annotations can have a profound impact on downstream uses of the data, such as misinterpreting mRNA fragments as lncRNAs, unreliable transcript abundance estimate by FPKM, and misidentification of lncRNA promoter sites [1,2]