Revealing insights of noncoding RNA in gene expression regulation

Back in 2003, when the first draft of the human genome had been sequenced, many in the scientific community envisioned a quick and easy path to a complete understanding of human biology. After some analysis, the community came to realize that we have only ~20,000 coding genes representing ~4% of the genome. The initial assumption was that coding elements of DNA were the most important part of the genome, and we erroneously concluded that genes that are transcribed into RNA but not translated to protein (noncoding RNA [ncRNA]) were "junk".

Turning junk into treasure

It is now well established that ncRNA actually plays a critical role in regulating the expression of coding RNA. There are two main subtypes of ncRNA based on size. Small ncRNA, defined as <200 nucleotides, has diverse functions in cellular processes and includes miRNA, snoRNA, siRNA, exRNA, piRNA, and gRNA. Probably the most widely studied types of small ncRNA are miRNAs, which downregulate expression by either blocking translation or causing degradation of mRNA. Studies indicate that miRNAs play an important role in complex diseases such as cancer.

The second and most recently discovered class of ncRNA is long noncoding RNA (lncRNA), which is defined as >200 nucleotides and is now recognized as the largest group of transcripts overall. The function of lncRNA is steadily being uncovered, with fewer than 200 characterized so far but tens of thousands already identified. For this reason, lncRNA is an active area for basic research, fueling more than 1,600 publications in 2016. lncRNAs have also been identified as valuable sources of diagnostic biomarkers (such as PCA3 for potential diagnosis of prostate cancer) and potential targets in drug discovery programs.

Simplifying the study of coding and ncRNA interactions

Recognizing the importance of ncRNA in gene expression regulation, we incorporated ncRNA as well as coding RNA content onto the classic 3´ IVT arrays more than a decade ago. This has allowed researchers to better understand the interactions between coding and ncRNA and gain new perspectives into biology while discovering novel associations. However, the relationships between coding and ncRNA are extremely complex and have been challenging to understand and visualize. To address these challenges, we now provide complete solutions, including data analysis tools, to help understand the complexity and interplay of coding and ncRNA.

The next generation of transcriptome profiling solutions, Applied Biosystems™ Clariom™ D assays, allow researchers to identify global gene- and exon-level coding and lncRNA expression patterns, which can be combined with genome-wide small ncRNA analysis assays to accurately measure the expression of pre- and mature miRNA, as well as sno- and scaRNA. To simplify the analysis of gene expression and its regulation, we also provide intuitive, free analysis software to rapidly combine mRNA and ncRNA data and visualize complex interaction networks.

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Find important relationships between coding and ncRNA quickly and easily

Profile transcriptome-wide coding and lncRNA in a single assay:

- **Applied Biosystems™ Clariom™ D assays, human**
- **Applied Biosystems™ Clariom™ D assays, mouse**
- **Applied Biosystems™ Clariom™ D assays, rat**

Measure genome-wide expression of small ncRNA:

- **Applied Biosystems™ GeneChip™ miRNA 4.0 Assay**

Analyze, explore, and visualize regulatory networks with free analysis software:

- **Applied Biosystems™ Transcriptome Analysis Console (TAC) Software**

Find out more at **thermofisher.com/microarrays**

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