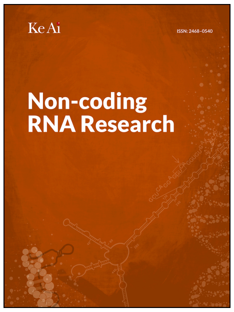

# Unraveling long non-coding RNAs through analysis of high-throughput RNA-sequencing data

Rashmi Tripathi, Pavan Chakraborty, Pritish Kumar Varadwaj

PII: S2468-0540(17)30020-3
DOI: 10.1016/j.ncrna.2017.06.003
Reference: NCRNA 23

To appear in: *Non-Coding RNA Research*

Received Date: 1 June 2017
Revised Date: 19 June 2017
Accepted Date: 21 June 2017

Please cite this article as: R. Tripathi, P. Chakraborty, P.K. Varadwaj, Unraveling long non-coding RNAs through analysis of high-throughput RNA-sequencing data, *Non-Coding RNA Research* (2017), doi: 10.1016/j.ncrna.2017.06.003.

# Unraveling long non-coding RNAs through analysis of high-throughput RNA-sequencing data

## Abstract

Extensive genome-wide transcriptome study mediated by high throughput sequencing technique has revolutionized the study of genetics and epigenetic at unprecedented resolution. The research has revealed that besides protein-coding RNAs, large proportions of mammalian transcriptome includes a heap of regulatory non protein-coding RNAs, the number encoded within human genome is enigmatic. Many taboos developed in the past categorized these non-coding RNAs as ‘‘dark matter” and “junks”. Breaking the myth, *RNA-seq*-- a recently developed experimental technique is widely being used for studying non-coding RNAs which has acquired the limelight due to their physiological and pathological significance. The longest member of the ncRNA family-- *long non-coding RNAs*, acts as stable and functional part of a genome, guiding towards the important clues about the varied biological events like cellular-, structural- processes governing the complexity of an organism. Here, we review the most recent and influential computational approach developed to identify and quantify the long non-coding RNAs serving as an assistant for the users to choose appropriate tools for their specific research.

**Keywords**: transcriptome; high throughput sequencing; genetic and epigenetic; long non-coding RNA; RNA-sequencing; RNA-seq