

# ceRNA network analysis & cytoscape



# Important steps

mRNA, miRNA, lncRNA expression data

Hub genes & RNAs selection

Targeting miRNA-genes-lncRNA

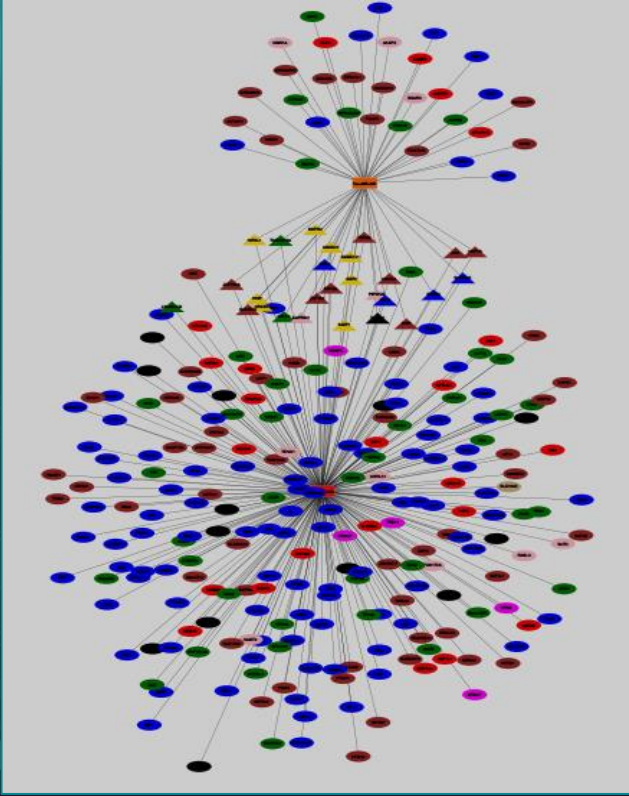
Multimir package of R software

Databases

Cytoscape

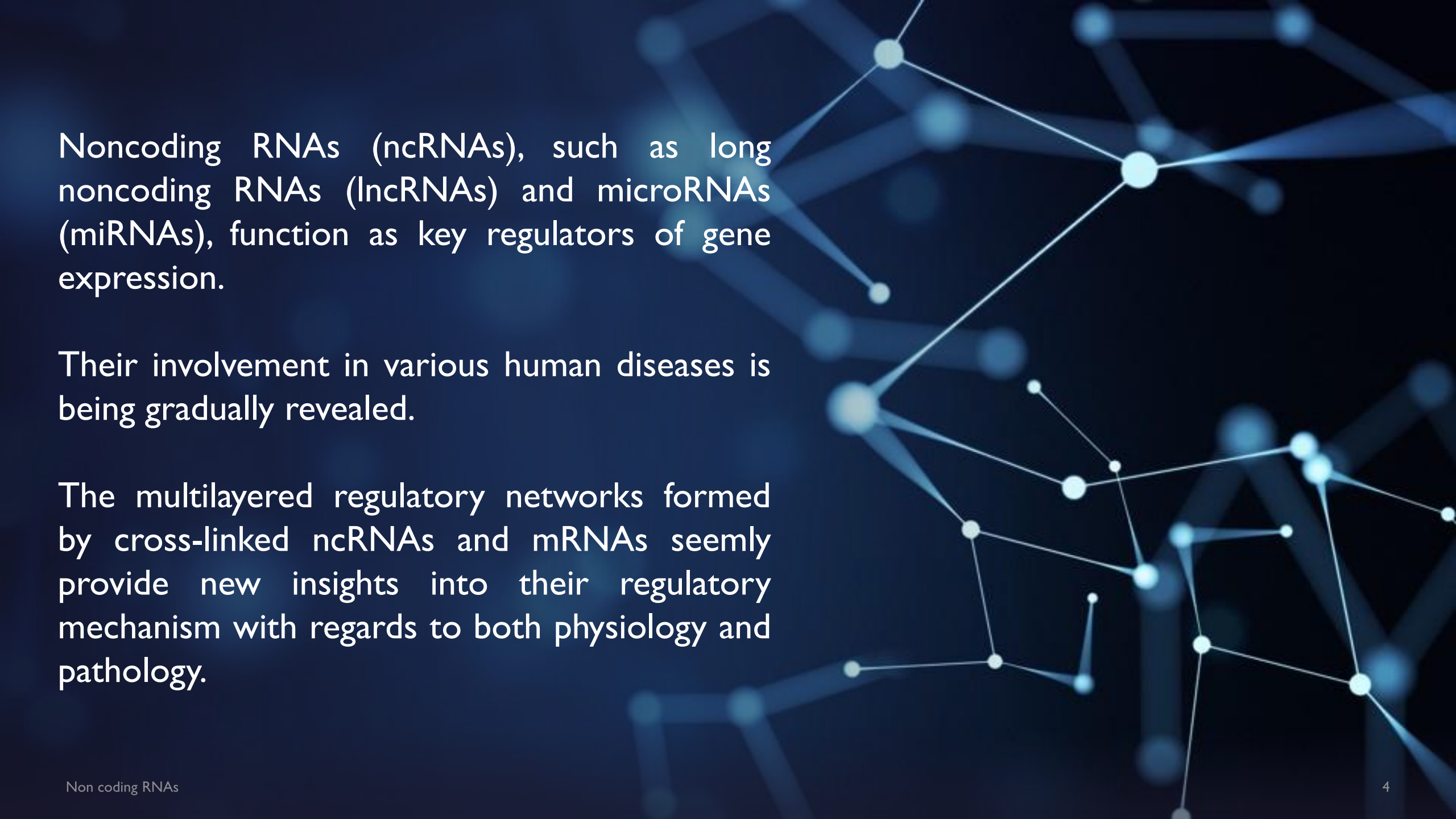






# Introduction

- The competing endogenous RNAs (ceRNAs) have been suggested to be involved in essential biological processes and play crucial roles in the initiation and development of neoplasms, and they potentially serve as diagnostic and prognosis markers or therapeutic targets.



Noncoding RNAs (ncRNAs), such as long noncoding RNAs (lncRNAs) and microRNAs (miRNAs), function as key regulators of gene expression.

Their involvement in various human diseases is being gradually revealed.

The multilayered regulatory networks formed by cross-linked ncRNAs and mRNAs seemly provide new insights into their regulatory mechanism with regards to both physiology and pathology.

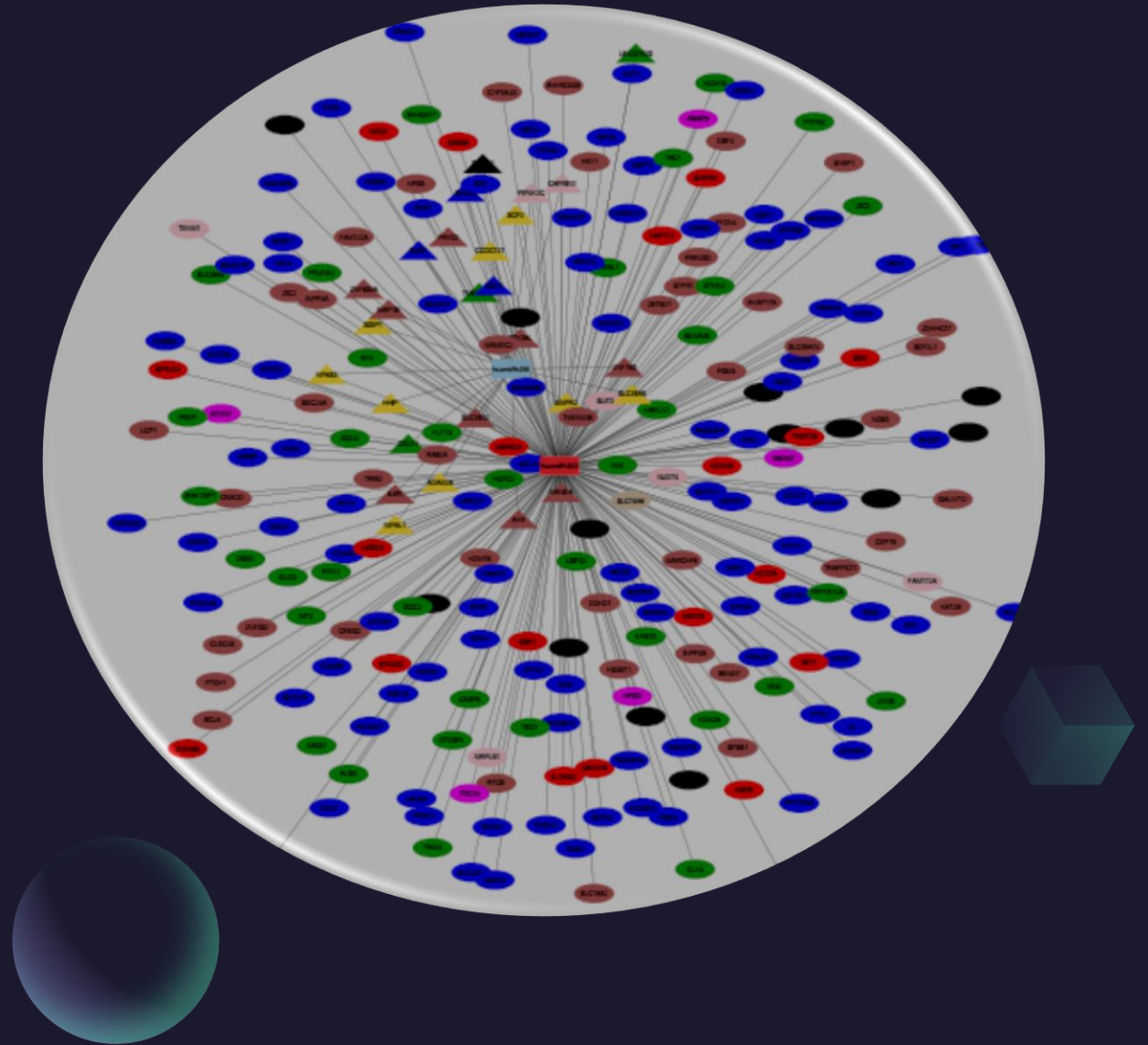


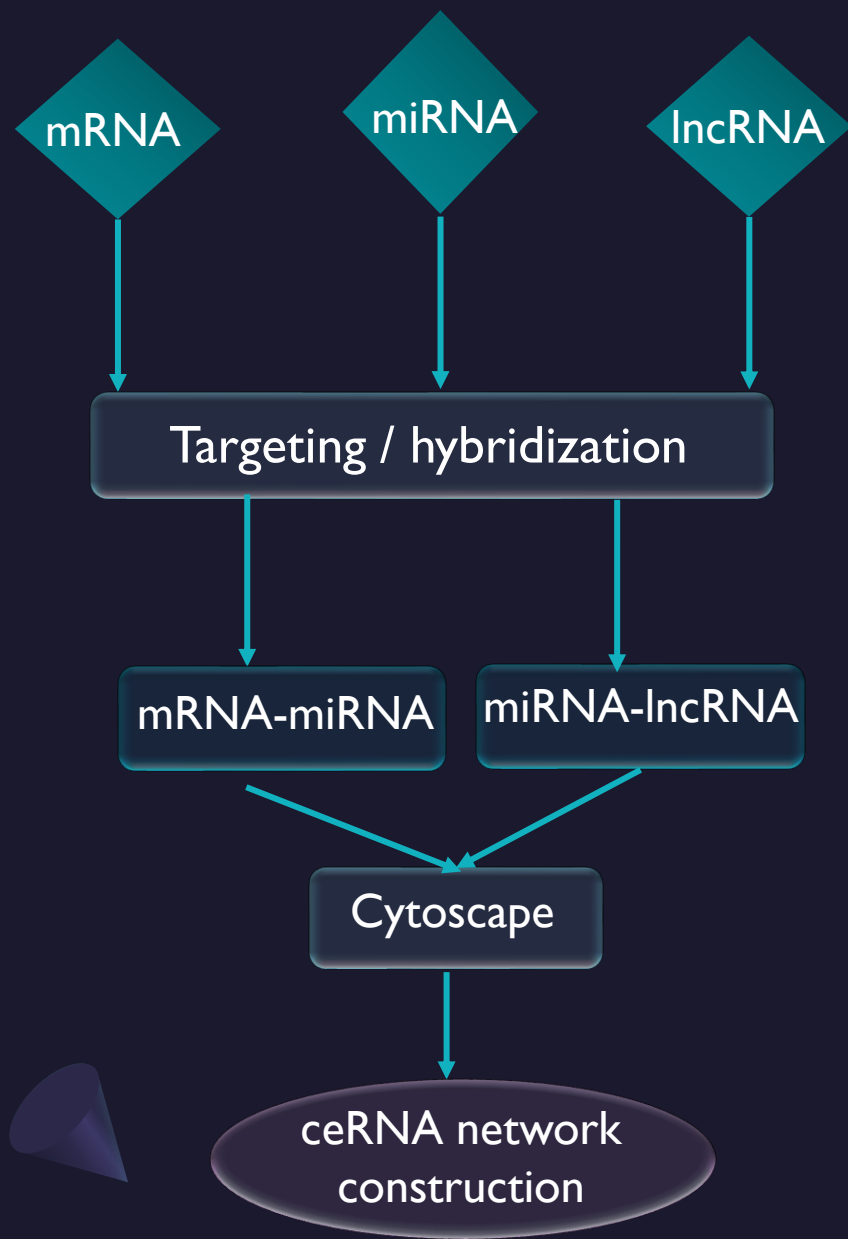
The complexity of the human genome has been revealed by advanced RNA sequencing analysis.

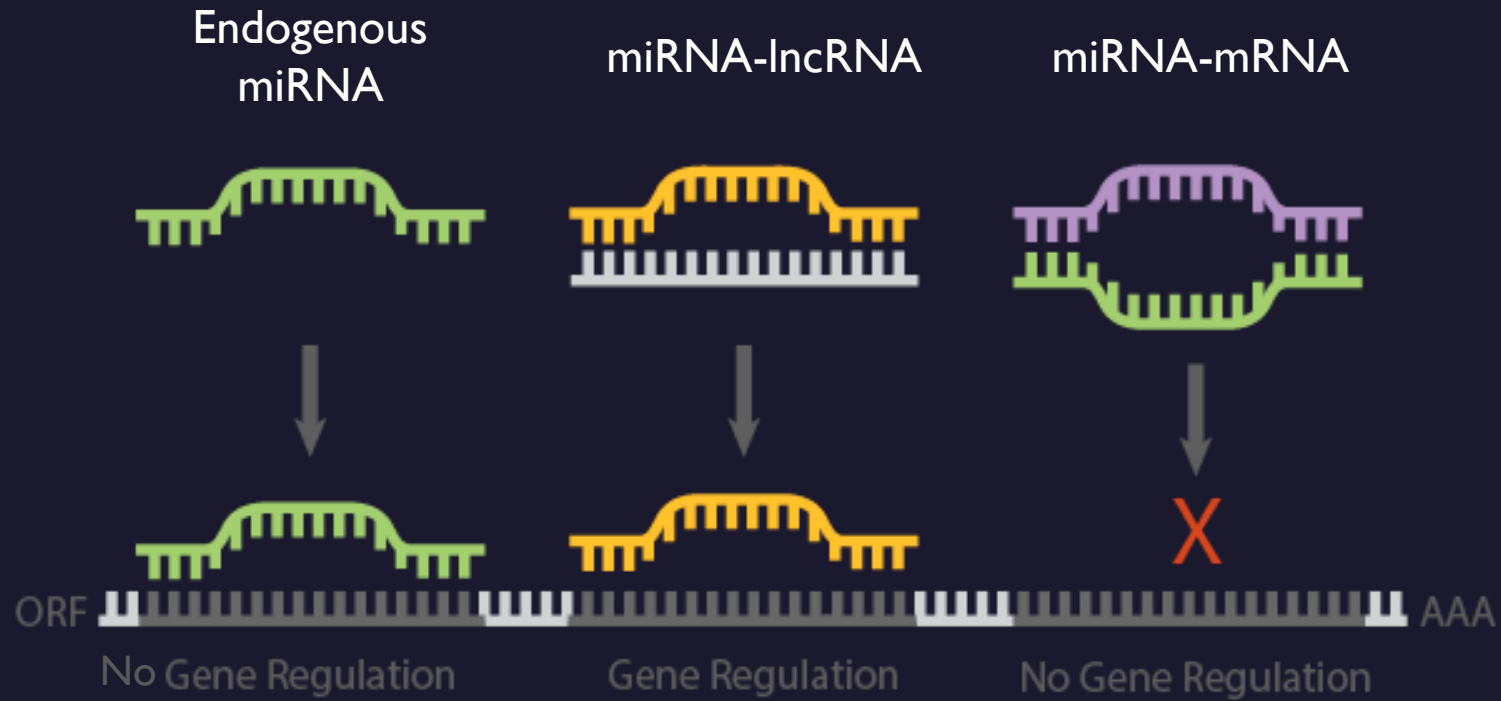
Competing endogenous RNA (ceRNA) analyses have demonstrated that lncRNAs can communicate with common miRNA response elements.

miRNAs to construct an intricate interconnected network and ultimately crosstalk with mRNA.

The involvement of the ceRNA regulatory network in tumour initiation and progression has been validated in previous studies







Endogenous miRNA interact with its target ( based on complementary sequence) and causes gene silence. No gene regulation.

Interaction of lncRNA and miRNA can cause the main gene regulation.

Interaction of mRNA (protein coding RNA) and miRNA can inhibit gene regulation. No protein coding.