

lncRNA MAGI2-AS3 suppresses castration-resistant prostate cancer proliferation and migration via the miR-106a-5p/RAB31 axis

Nguyen Minh Hoang

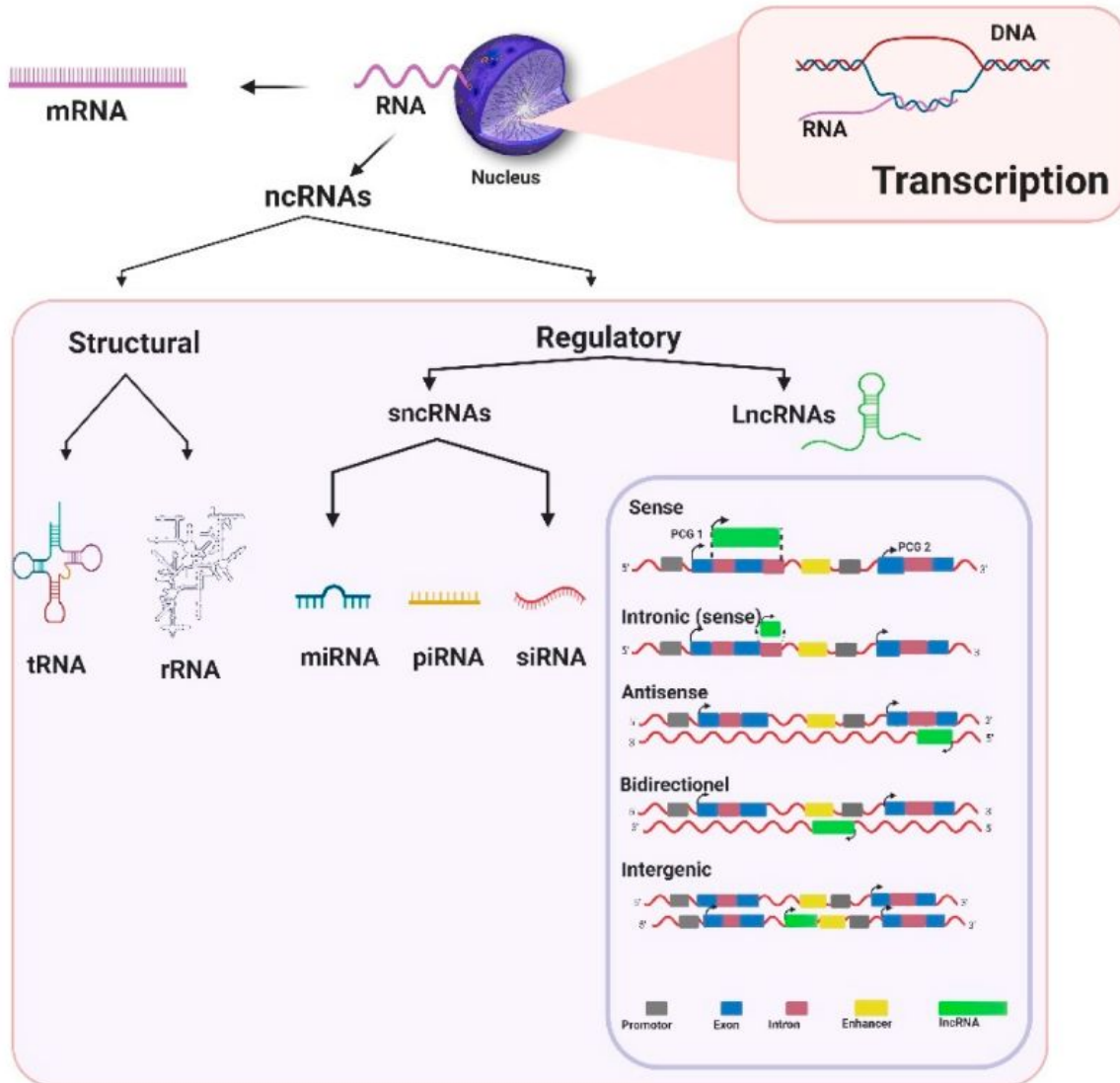
Tran Ba Thien

10/07/2023

Contents

1. What is lncRNA ?
2. Role of lncRNA in human and disease
3. How to detect the expression of lncRNA
4. Example for analysis of lncRNA.

WHAT IS LONG NON-CODING RNAs (lncRNAs)?



lncRNAs are defined as RNAs **longer than 200 nucleotides** that are **not translated** into functional **proteins**.

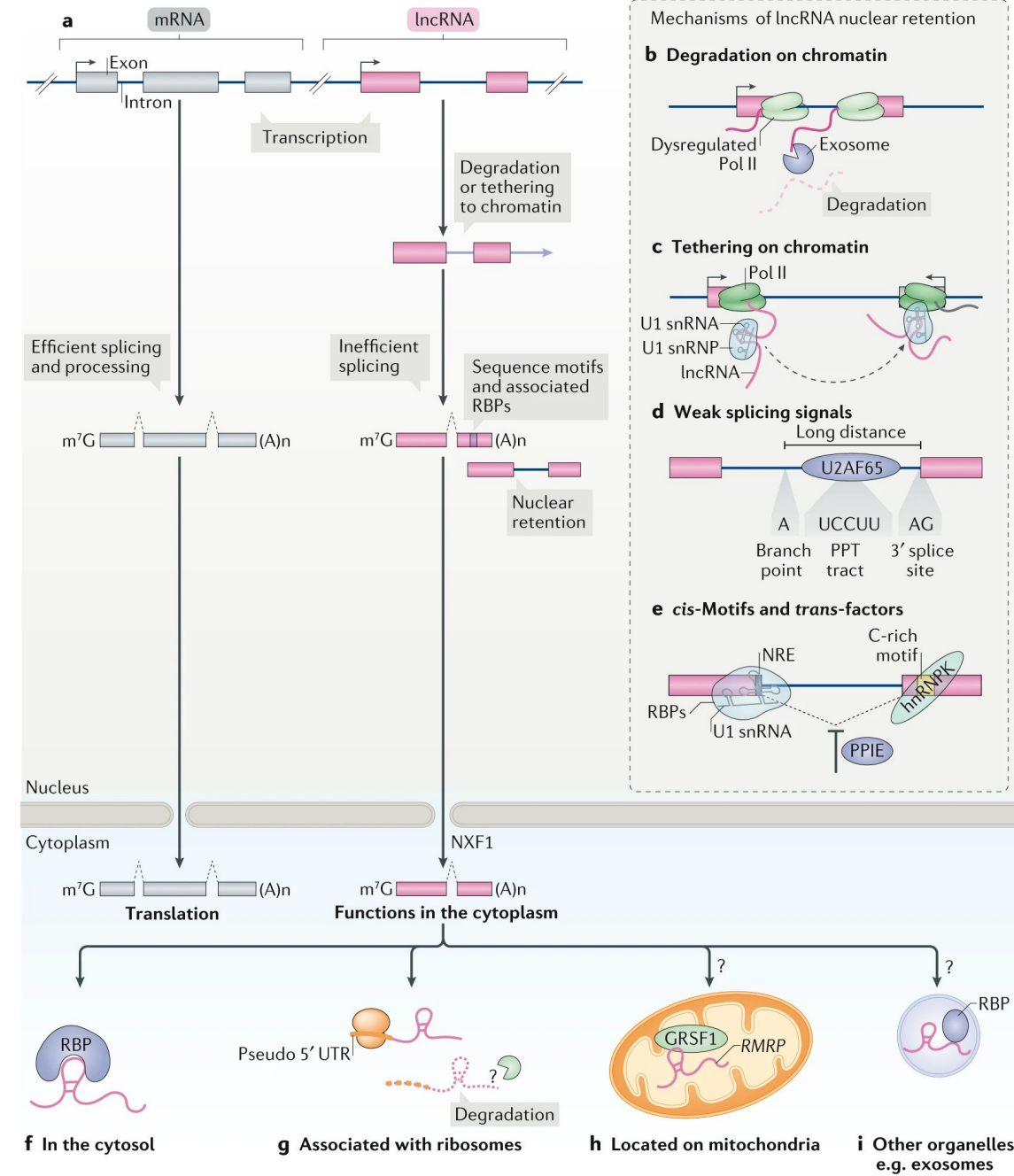
The resulting lncRNAs are often **capped by 7-methyl guanosine (m7G)** at their 5' ends, **polyadenylated** at their 3' ends and **spliced similarly to mRNAs**.

These mainly include lncRNAs transcribed by **RNA polymerase II (Pol II)**.

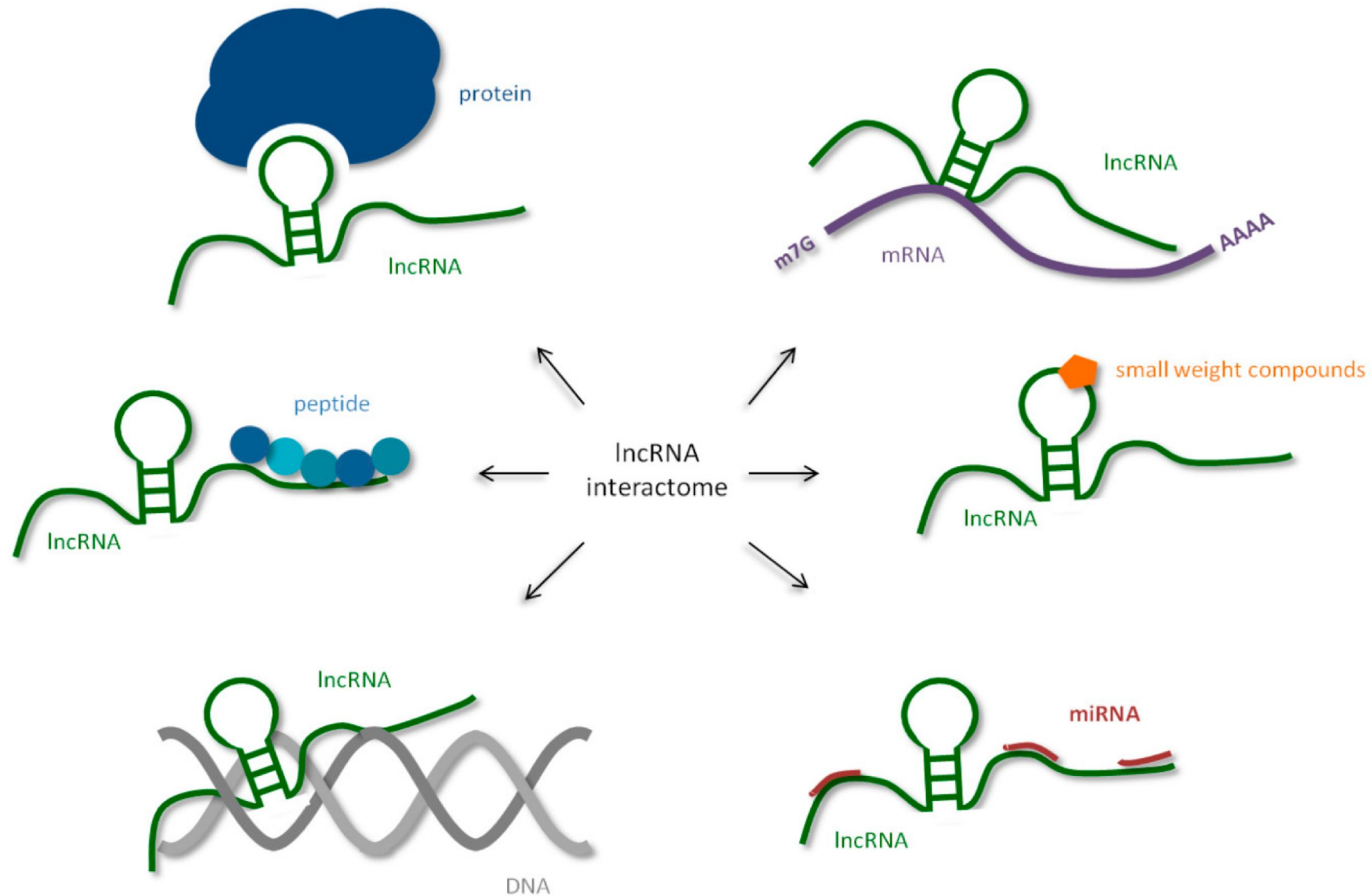
Statistics from **Human GENCODE** suggest that the human genome contains more than **16,000 lncRNA genes**, but other estimates exceed **100,000 human lncRNAs**.

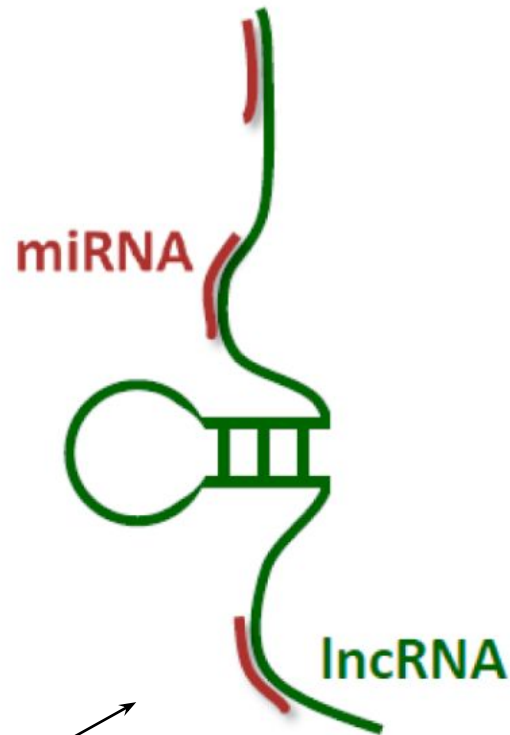
Biogenesis and cellular fates of long non-coding RNAs

- LncRNA is in the nucleus, whereas others are spliced and exported to the cytoplasm. A large fraction of lncRNAs are exported to the cytosol
- lncRNAs are spliced less efficiently than mRNA.



Interaction of human lncRNA with cellular biomolecules.



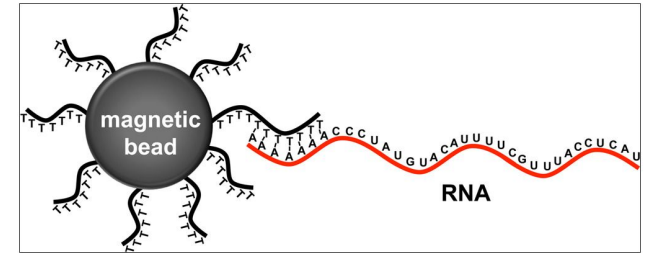


- ncRNAs and miRNAs influence each other -> ceRNA (a competitive, endogenous RNA)
- By sharing identical MREs and competing for common miRNAs, they change miRNA's activity, which results in modified mRNA translation
- lncRNA-associated miRNA have been conducted for many diseases, such as ovarian and prostate cancer, glioblastoma, thyroid carcinoma, as well as breast, lung, kidney and gut cancers

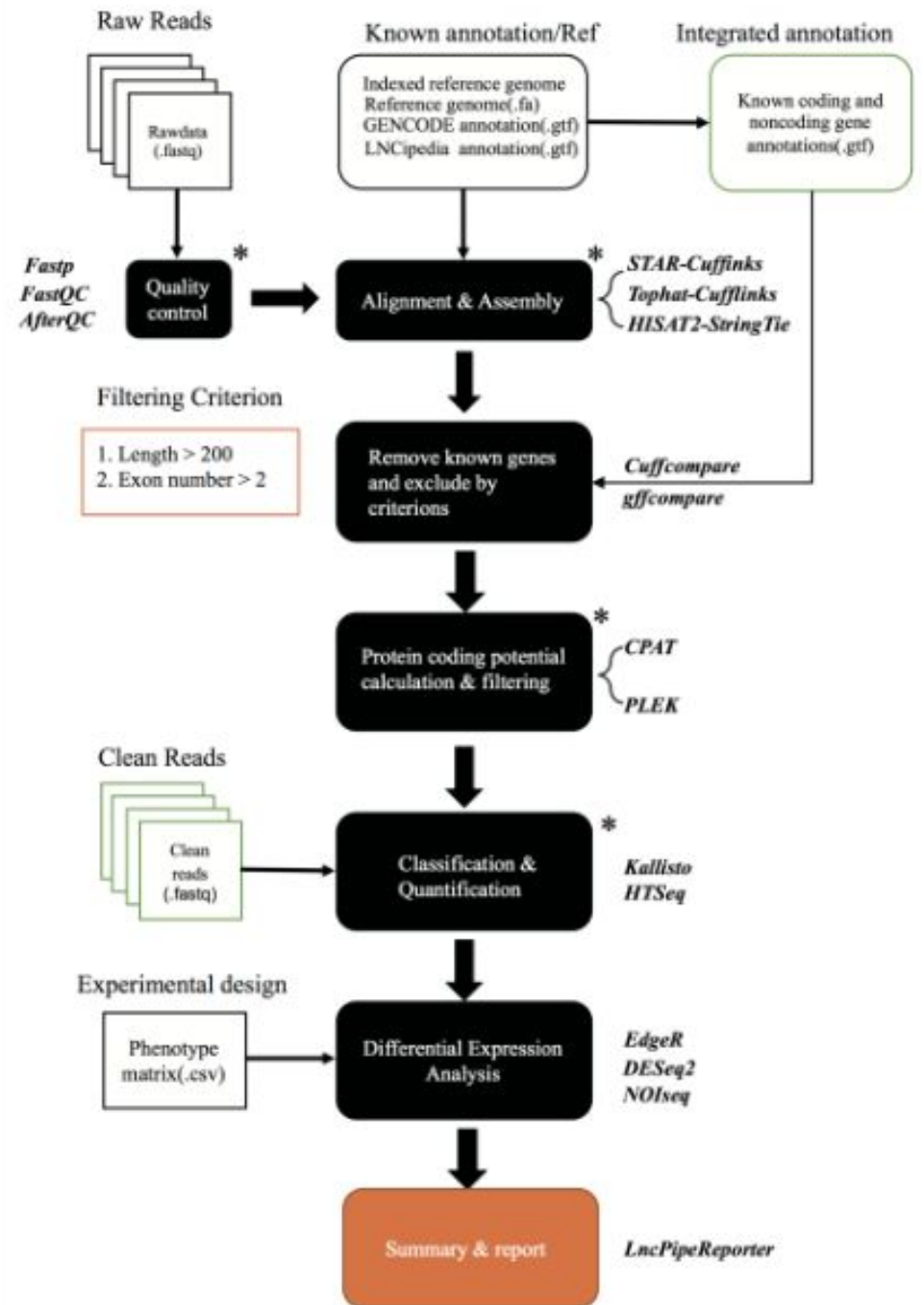
HOW TO DETECT OF LNCRNA

Detecting the expression of long non-coding RNAs (lncRNAs) can be accomplished using various experimental techniques.

- **RNA sequencing (RNA-seq)**
- **Microarray analysis**
- Reverse transcription quantitative polymerase chain reaction (RT-qPCR)
- Northern blotting:
- In situ hybridization (ISH)



PIPELINE FOR ANALYSIS




DATABASES RELATED TO LNCRNAS

TABLE 1. lncRNA databases evaluated

Database	Description	Website	Reference
CHIPBase	Database for decoding the transcriptional regulation of long noncoding RNA and microRNA genes from ChIP-Seq data	deepbase.sysu.edu.cn/chipbase	Yang et al. (2013b)
DIANA-LncBase	Experimentally verified and computationally predicted microRNA targets on long noncoding RNAs	diana.imis.athena-innovation.gr	Paraskevopoulou et al. (2013)
LNCipedia	A database for annotated human lncRNA transcript sequences and structures	www.lncipedia.org	Volders et al. (2013)
lncRNAdb	Database providing comprehensive annotations of eukaryotic long noncoding RNAs	www.lncrnadb.org	Amaral et al. (2011)
lncRNADisease	Experimentally supported lncRNAs-disease associations	cmbi.bjmu.edu.cn/lncrnadisease	Chen et al. (2013)
lncRNome	Comprehensive database of long noncoding RNAs in humans	genome.igib.res.in/lncRNome	Bhartiya et al. (2013)
Noncode v3.0	Integrative annotation of long noncoding RNAs	noncode.org/NONCODERv3	Bu et al. (2012)
The Functional lncRNA Database	Database of lncRNAs manually extracted from the literature along with a parallel database containing all annotated protein-coding human RNAs	www.valadkhanlab.org	Niazi and Valadkhan (2012)

DATABASES RELATED TO LNCRNAS

- ChIPBase



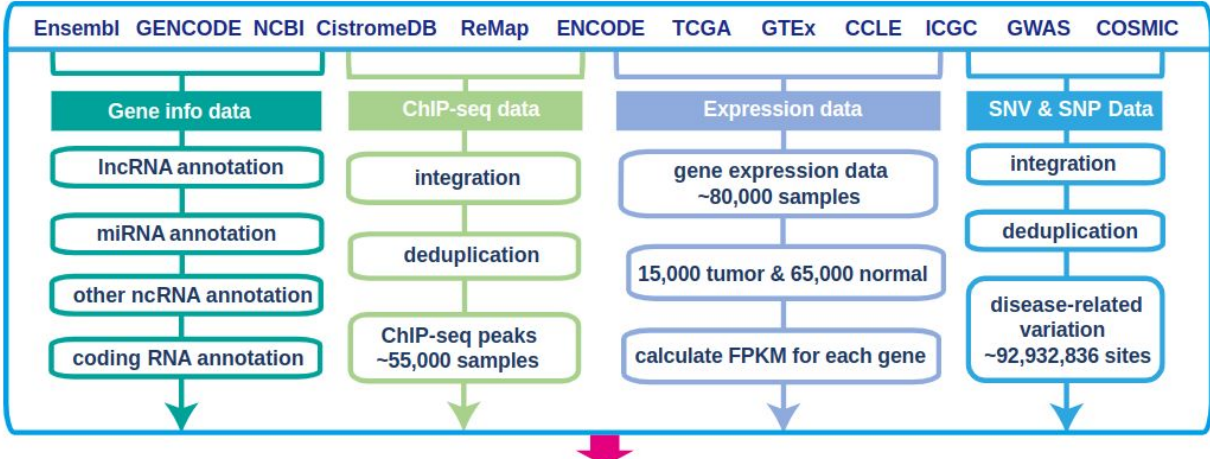

ChIPBase v3.0

The Encyclopedia of Transcriptional Regulation of Non-Coding RNAs

- Home
- lncRNA
- miRNA
- ncRNA
- mRNA
- Enhancer
- Motif
- Function
- Co-Expression
- Disease
- EpiInter
- Network
- Batch-Download
- Contact

Welcome to ChIPBase v3.0 !

ChIPBase v3.0 identified ~151,187,000 regulatory relationships between ~171,600 genes and ~3,000 regulators by analyzing ~55,000 ChIP-seq datasets, which represent a 30-fold expansion. Moreover, we de novo identified ~29,000 motif matrices of transcription factors. In addition, we constructed a novel "Enhancer" module to predict ~1,837,200 regulation regions functioning as poised, active or super enhancers under ~1300 conditions. Importantly, we constructed exhaustive coexpression maps between regulators and their target genes by integrating expression profiles of ~65,000 normal and ~15,000 tumor samples. We built a "Disease" module to obtain an atlas of the disease-associated variations in the regulation regions of genes. We also constructed an "EpiInter" module to explore potential interactions between epitranscriptome and epigenome. Finally, we designed "Network" module to provide extensive and gene-centred regulatory networks.



```
graph TD
    subgraph Inputs
        direction LR
        I1[Ensembl]
        I2[GENCODE]
        I3[NCBI]
        I4[CistromeDB]
        I5[ReMap]
        I6[ENCODE]
        I7[TCGA]
        I8[GTEx]
        I9[CCLL]
        I10[ICGC]
        I11[GWAS]
        I12[COSMIC]
    end

    subgraph Processing
        direction TB
        G1[Gene info data] --> G2[lncRNA annotation] --> G3[miRNA annotation] --> G4[other ncRNA annotation] --> G5[coding RNA annotation]
        G6[ChIP-seq data] --> G7[integration] --> G8[deduplication] --> G9[ChIP-seq peaks ~55,000 samples]
        G10[Expression data] --> G11[gene expression data ~80,000 samples] --> G12[15,000 tumor & 65,000 normal] --> G13[calculate FPKM for each gene]
        G14[SNV & SNP Data] --> G15[integration] --> G16[deduplication] --> G17[disease-related variation ~92,932,836 sites]
    end

    G5 --> Out
    G9 --> Out
    G13 --> Out
    G17 --> Out
```

Release notes

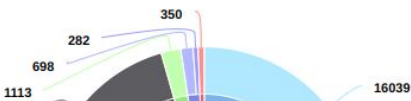
Current version:
Release version 3.0.0 (2022-09-01)
Updated ~55,000 ChIP-seq data from ENCODE, CistromeDB, ReMap.
Updated ~80,000 expression data from ENCODE, TCGA, GTEx, CCLL, ICGC.
Updated genome (human) to GRCh38.
Updated genome (mouse) to GRCh39.
Updated annotation (human) to Release 41.
Updated annotation (mouse) to Release M30.
Constructed novel module "Disease".
Included ~3,993,000 SNP sites from GWAS and COSMIC.
Included ~88,939,000 SNV sites from ICGC and COSMIC.
Constructed novel module "Network".

Sample Statistics in 5 Species

[View Genome Versions](#)

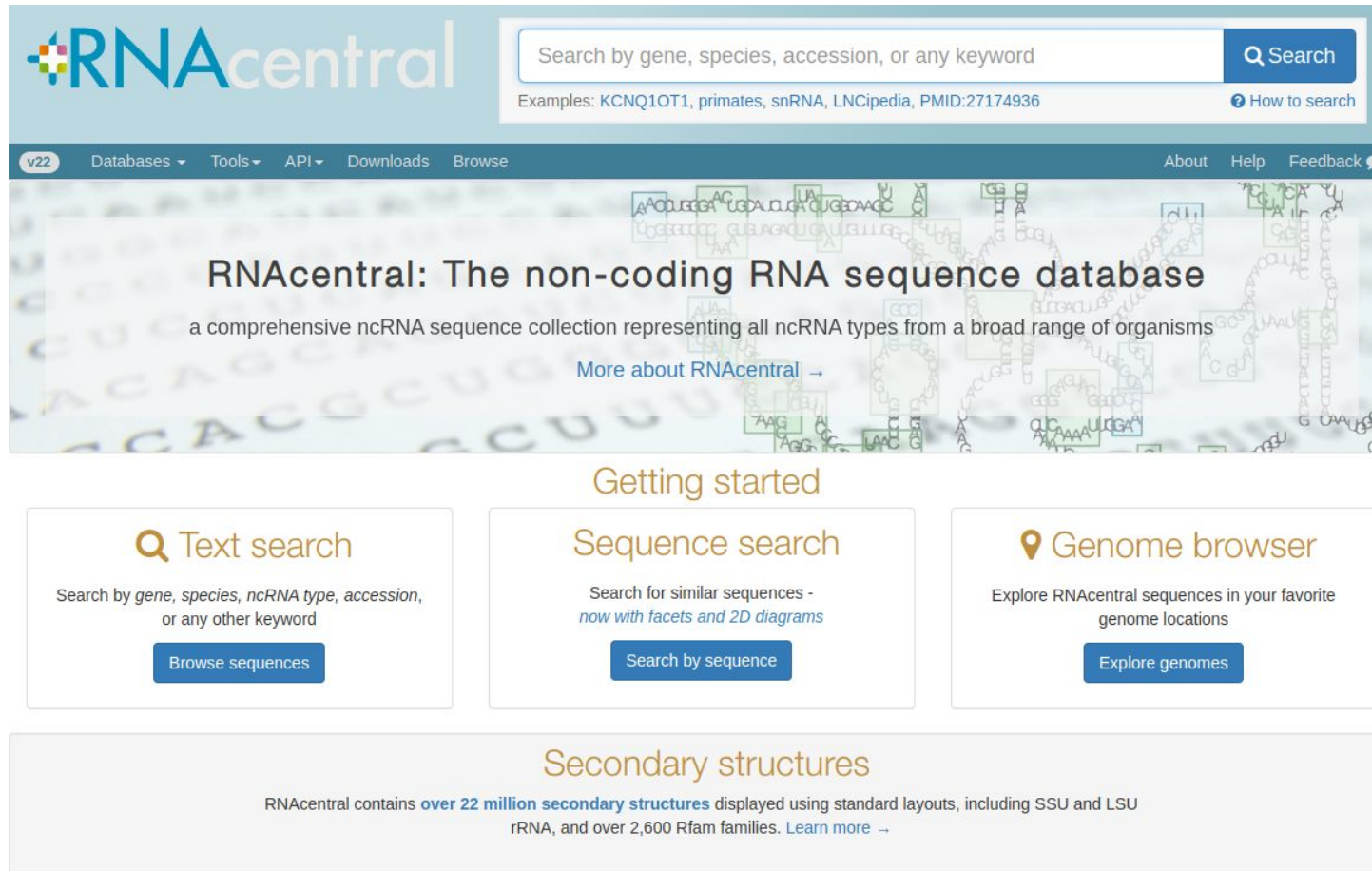
- Human (*Homo sapiens*)
- Mouse (*Mus musculus*)
- Fruitfly (*Drosophila melanogaster*)
- Thale cress (*Arabidopsis thaliana*)
- Worm (*Caenorhabditis elegans*)

Sample Statistics in 5 Species
Total samples: 55,420



DATABASES RELATED TO LNCRNAS

IncRNAdb



The screenshot shows the RNAcentral website homepage. At the top, there is a navigation bar with the RNAcentral logo on the left, a search bar in the center, and links for 'v22', 'Databases', 'Tools', 'API', 'Downloads', 'Browse', 'About', 'Help', and 'Feedback' on the right. The search bar contains the text 'Search by gene, species, accession, or any keyword' and a 'Search' button. Below the search bar, there are examples of search terms: 'KCNQ10T1, primates, snRNA, LNCipedia, PMID:27174936' and a link 'How to search'. The main content area features a large banner with the text 'RNAcentral: The non-coding RNA sequence database' and a subtitle 'a comprehensive ncRNA sequence collection representing all ncRNA types from a broad range of organisms'. Below the banner, there is a link 'More about RNAcentral →'. The 'Getting started' section contains three boxes: 'Text search' (with a magnifying glass icon), 'Sequence search' (with a magnifying glass icon), and 'Genome browser' (with a location pin icon). Each box contains a description of the search type and a 'Browse sequences', 'Search by sequence', or 'Explore genomes' button. The 'Secondary structures' section at the bottom states that RNAcentral contains over 22 million secondary structures and provides a link to learn more.

RNAcentral

Search by gene, species, accession, or any keyword

Search

Examples: KCNQ10T1, primates, snRNA, LNCipedia, PMID:27174936

How to search

v22 Databases Tools API Downloads Browse About Help Feedback

RNAcentral: The non-coding RNA sequence database

a comprehensive ncRNA sequence collection representing all ncRNA types from a broad range of organisms

[More about RNAcentral →](#)

Getting started

Text search

Search by gene, species, ncRNA type, accession, or any other keyword

[Browse sequences](#)

Sequence search

Search for similar sequences - now with facets and 2D diagrams

[Search by sequence](#)

Genome browser

Explore RNAcentral sequences in your favorite genome locations

[Explore genomes](#)

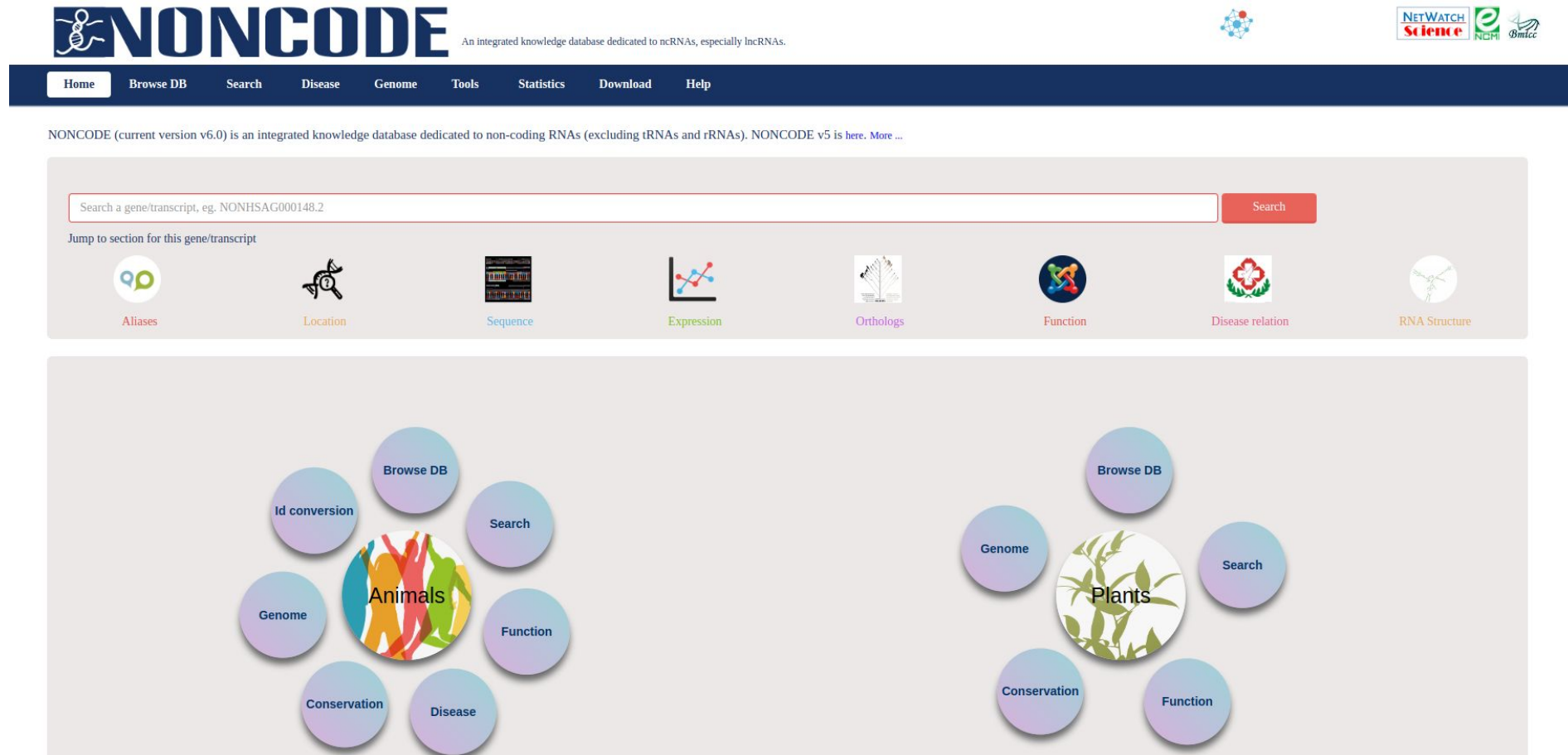
Secondary structures

RNAcentral contains over 22 million secondary structures displayed using standard layouts, including SSU and LSU rRNA, and over 2,600 Rfam families. [Learn more →](#)

<https://rnacentral.org/>

DATABASES RELATED TO LNCRNAS

NONCODE



The screenshot displays the NONCODE database homepage. At the top, the NONCODE logo is accompanied by the tagline "An integrated knowledge database dedicated to ncRNAs, especially lncRNAs." and logos for partner institutions: NETWATCH Science, NCI, and Bmcc. A dark blue navigation bar contains links to Home, Browse DB, Search, Disease, Genome, Tools, Statistics, Download, and Help. Below this, a text line states: "NONCODE (current version v6.0) is an integrated knowledge database dedicated to non-coding RNAs (excluding tRNAs and rRNAs). NONCODE v5 is [here](#). [More ...](#)".

The main content area features a search bar with the placeholder text "Search a gene/transcript, eg. NONHSAG000148.2" and a red "Search" button. Below the search bar, a prompt "Jump to section for this gene/transcript" is followed by eight icons representing different data categories: Aliases, Location, Sequence, Expression, Orthologs, Function, Disease relation, and RNA Structure.

At the bottom, two circular navigation diagrams are shown. The "Animals" diagram has a central circle with silhouettes of people and is surrounded by seven nodes: Browse DB, Search, Function, Disease, Conservation, Genome, and Id conversion. The "Plants" diagram has a central circle with a leaf pattern and is surrounded by four nodes: Browse DB, Search, Function, and Conservation.

<http://www.noncode.org/>

DATABASES RELATED TO LNCRNAS

LncRNADisease

LncRNADisease v2.0

The LncRNA and Disease Database (version 2.0)

[HOME](#)[SEARCH](#)[BROWSE](#)[STATISTICS](#)[DOWNLOAD](#)[SUBMIT](#)[HELP](#)

About LncRNADisease v2.0

The LncRNADisease v2.0 now hosts disease associated **LncRNAs** and **CircRNAs**.

Statistics

- LncRNAs: **19,166**
- CircRNAs: **823**
- Disease: **529**
- LncRNA-disease Associations: **205,959**
- CircRNA-disease Associations: **1,004**
- LncRNA Causative Associations: **2,297**
- CircRNA Causative Associations: **198**
- Literature: **3,878**

News

- Causality information was attached ...

Welcome to LncRNADisease v2.0

Posted by [PKU](#) & [ECNU](#) on May 10, 2018 •



Long non-coding RNAs (lncRNAs) are an important category of non-coding RNAs (ncRNAs) which range from 200 nucleotides to multiple kilobases in length, with little or no protein-coding capacity. Circular RNAs (circRNAs) are widely expressed in diverse eukaryotic species and are characterized by covalently closed RNA loops through backsplicing events. Increasing evidence has highlighted the critical roles of lncRNAs and circRNAs in plenty of diseases development and progression. Here, we have updated the LncRNADisease database to version 2.0 by integrating comprehensive experimentally supported and predicted ncRNA-disease associations curated from manual literatures and other resources. The new developments in LncRNADisease v2.0 include (I) over 40-fold ncRNA-disease associations enhancement compare to the previous version; (II) integrating experimentally supported circRNA-disease associations; (III) providing regulatory relationship among ncRNA, mRNA and miRNA; (IV) mapping disease name to the Disease Ontology and Medical Subject Headings (MeSH); (V) providing a confidence score for each ncRNA-disease association.

Database Summary

Experimental lncRNA-disease associations



Species	Associations
Homo sapiens	~10000
Mus musculus	~500
Rattus norvegicus	~100
Gallus gallus	~10

Experimental circRNA-disease associations



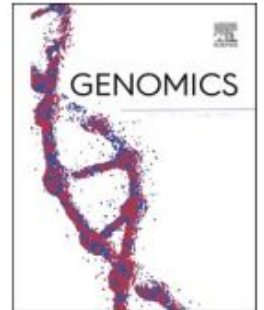
Species	Associations
Homo sapiens	~900
Mus musculus	~100
Rattus norvegicus	~20
Gallus gallus	~10



Contents lists available at [ScienceDirect](https://www.sciencedirect.com)

Genomics

journal homepage: www.elsevier.com/locate/ygeno



lncRNA MAGI2-AS3 suppresses castration-resistant prostate cancer proliferation and migration via the miR-106a-5p/RAB31 axis

Guo Yang^a, Ting Li^b, Jiayu Liu^a, Zhen Quan^a, Miao Liu^c, Yuan Guo^a, Yingying Wu^b, Liping Ou^b, Xiaohou Wu^{a,*}, Yongbo Zheng^{a,*}

^a Department of Urology, The First Affiliated Hospital of Chongqing Medical University, 400042 Chongqing, China

^b Key Laboratory of Laboratory Medical Diagnostics, Ministry of Education, Chongqing Medical University, 400016 Chongqing, China

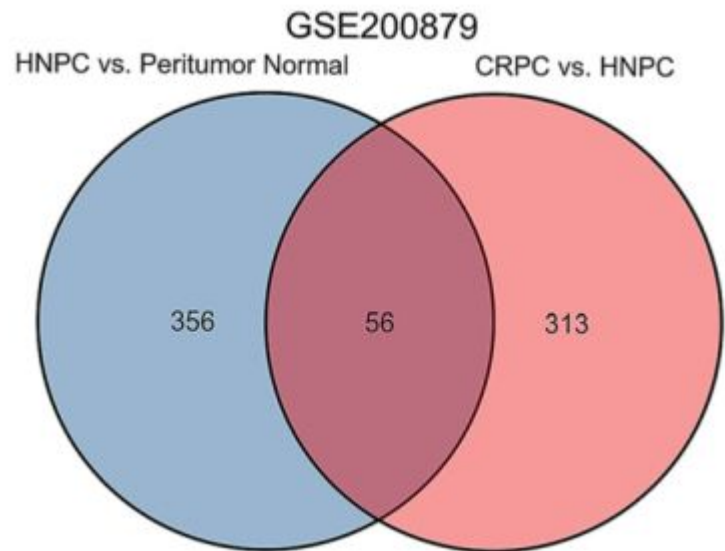
^c Gastrointestinal Cancer Center, Chongqing University Cancer Hospital, 400030 Chongqing, China

INTRODUCTION

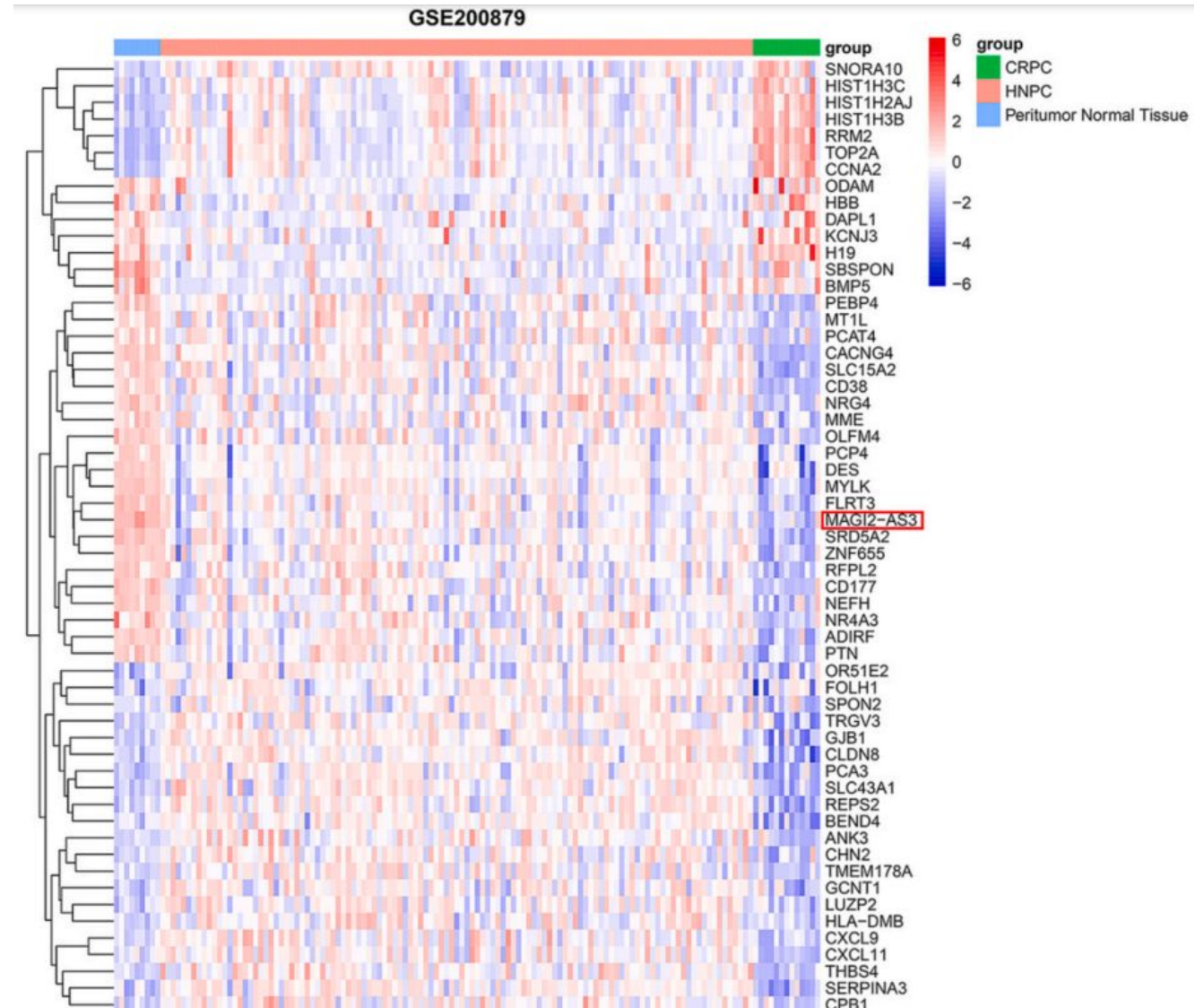
- **Prostate cancer (PCa)** is a **common malignant cancer** in elderly males in **Western countries**
- Despite remarkable progress in **early diagnosis and prevention**, **most cases of PCa** are diagnosed in the *advanced stages of metastasis and castration-resistant prostate cancer (CRPC) develops*, ultimately accounting for the second leading cause of **cancer-related death among men**.
- Several molecular mechanisms related to **castration resistance** have been identified. These mechanisms are mainly involved in **androgen receptor (AR) signal** transduction, including AR amplification, mutation, activation, co-regulation, selective clipping, and aberrant post-translational modifications.
- Some **aberrantly expressed lncRNAs** have been identified in **PCa** clinical samples and cell lines, which may be ubiquitously involved in **multiple biological processes**, such as infarction, autophagy, apoptosis, cell senescence, resistance to chemotherapy, and cancer cell metastasis.

STEP 1: To screen for **abnormally expressed lncRNAs**, They selected **two GEO datasets** to identify the lncRNAs involved in **CRPC development**

Benign prostate hyperplasia (BPH) and adjacent normal tissues -> hormone-naïve PCa (HNPc) -> CRPC and metastatic PCa tissues



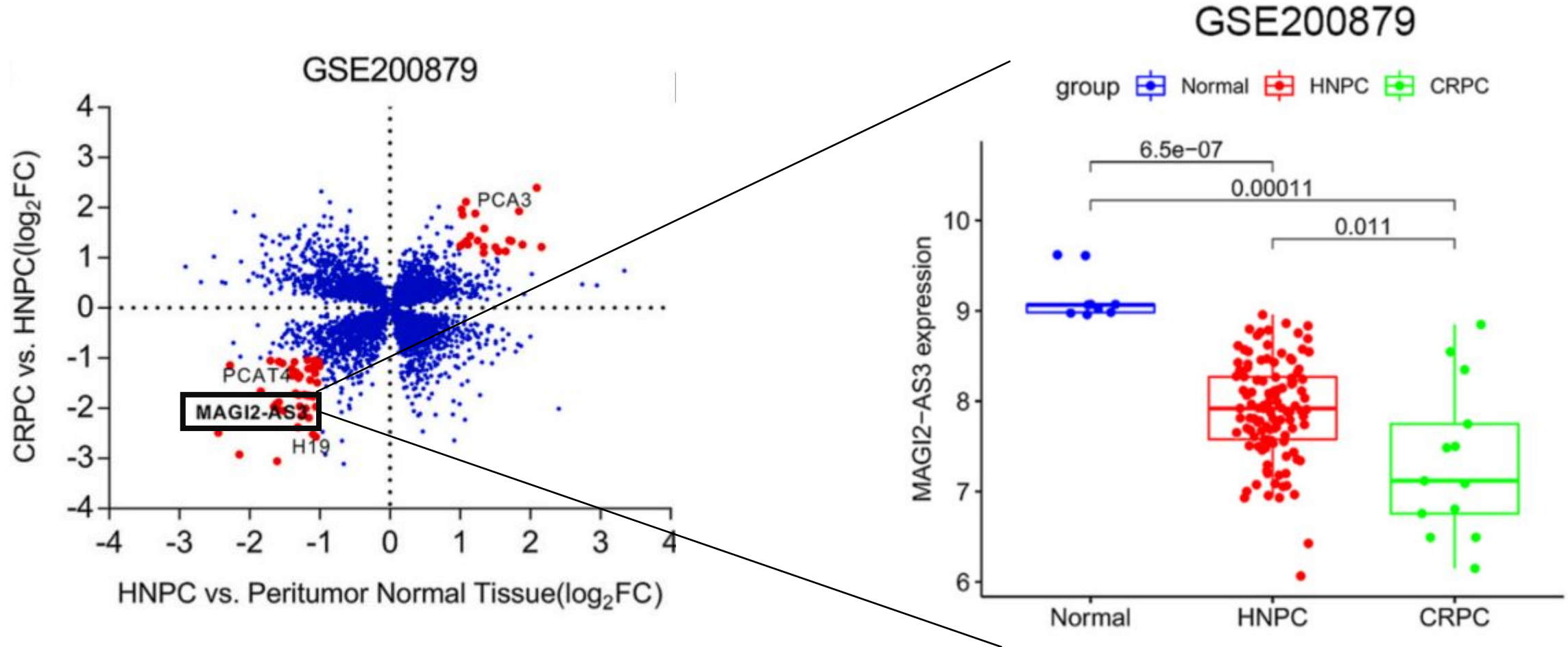
Venn Diagram depicting the common DEGs



Heatmap of all DEGs analyzed with GSE200879

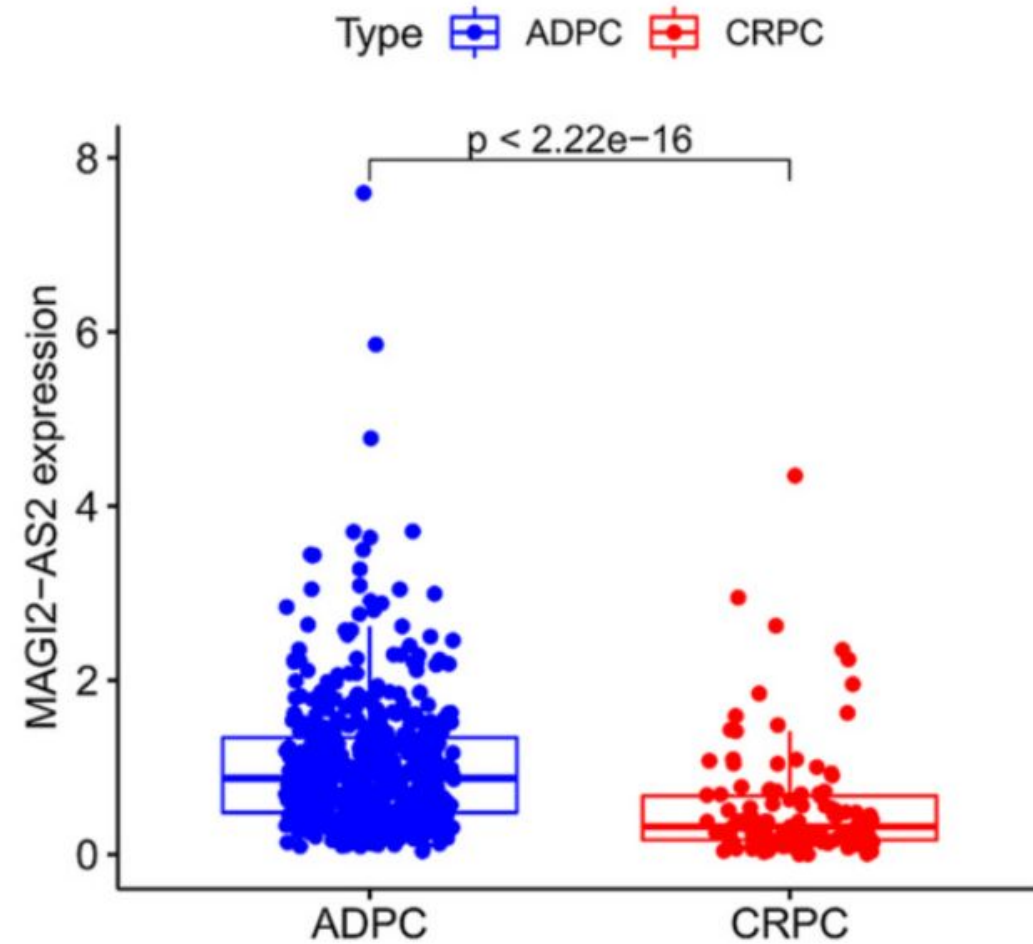
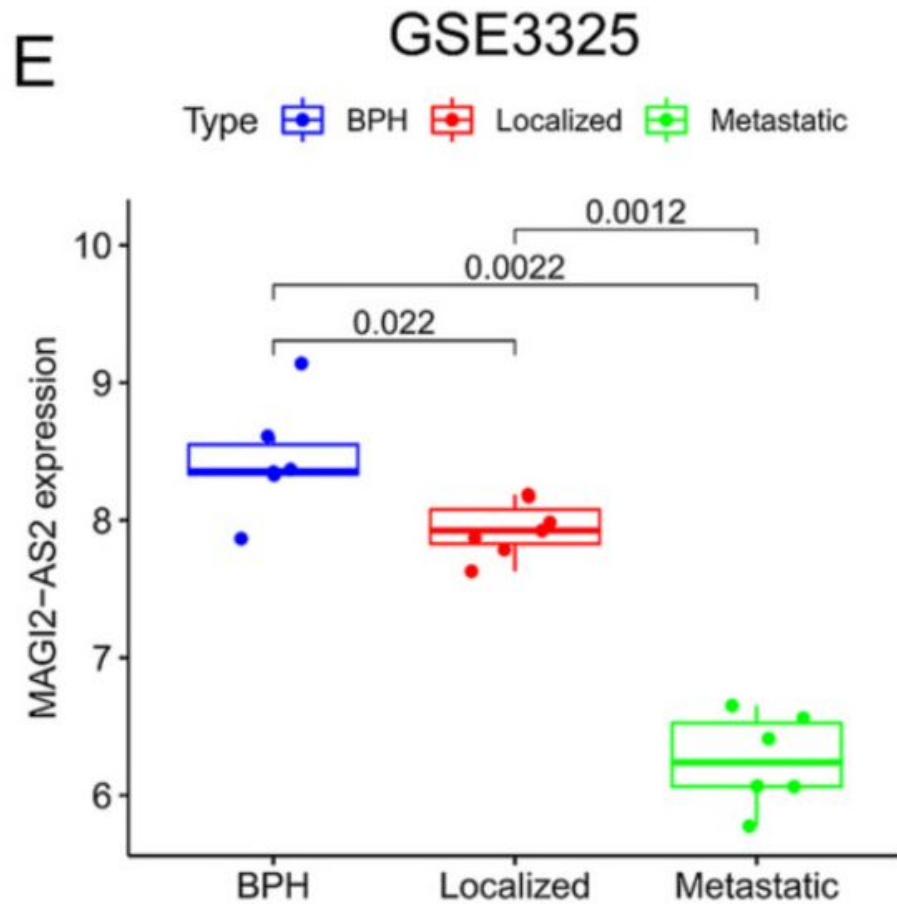
STEP 1: To screen for **abnormally expressed lncRNAs**, They selected **two GEO datasets** to identify the lncRNAs involved in **CRPC development**

Benign prostate hyperplasia (BPH) and adjacent normal tissues -> hormone-naïve PCa (HNPC) -> CRPC and metastatic PCa tissues



STEP 1: To screen for **abnormally expressed lncRNAs**, They selected **two GEO datasets** to identify the lncRNAs involved in **CRPC development**

Benign prostate hyperplasia (BPH) and adjacent normal tissues -> hormone-naïve PCa (HNPC) -> CRPC and metastatic PCa tissues



STEP 1: To screen for **abnormally expressed lncRNAs**, They selected **two GEO datasets** to identify the lncRNAs involved in **CRPC development**

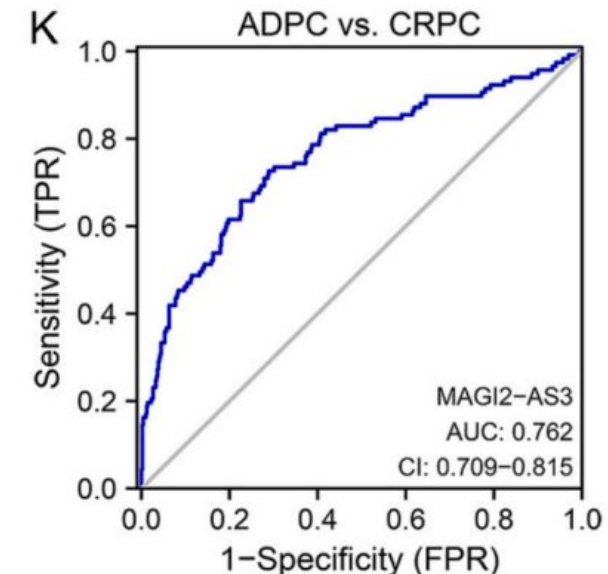
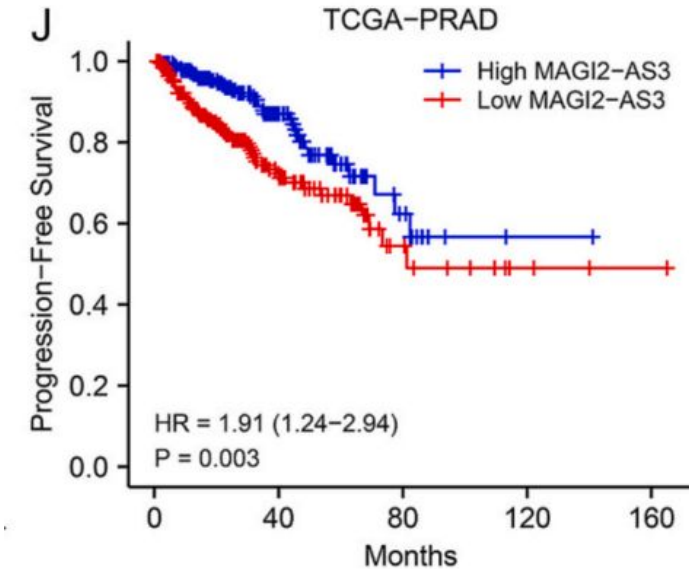
Benign prostate hyperplasia (BPH) and adjacent normal tissues -> hormone-naïve PCa (HNPC) -> CRPC and metastatic PCa tissues

Table 1

Association between MAGI2-AS3 and the clinicopathological features of prostate cancer patients in TCGA.

Variables	Cases	MAGI2-AS3 expression		P-value
		Low (n = 177)	High (n = 177)	
Age (year)				
<60	136	74(41.8%)	62(35.0%)	0.190
≥60	218	103(58.2%)	115(65.0%)	
Postoperative PSA (ng/mL)				
<10	341	170(96.0%)	171(96.6%)	0.777
≥10	13	7(4.0%)	6(3.4%)	
TNM stage				
I/II	123	54(30.5%)	69(39.0%)	0.094
III/IV	231	123(69.5%)	108(61.0%)	
Gleason score				
≤7 (3 + 4)	124	46 (26.0%)	78(44.1%)	<0.001*
≥7 (4 + 3)	230	131 (74.0%)	99 (55.9%)	
Lymph-node Metastases				
Negative	288	136 (76.8%)	152 (85.9%)	0.029*
Positive	66	41 (23.4%)	25 (14.1%)	

* Statistically significant ($P < 0.05$).



RESULT STEP 1:

MAGI2-AS3 was abundant in benign prostate hyperplasia (BPH) and adjacent normal tissues, downregulated in localized or hormone-naïve PCa (HNPC), and more significantly downregulated in CRPC and metastatic PCa tissues

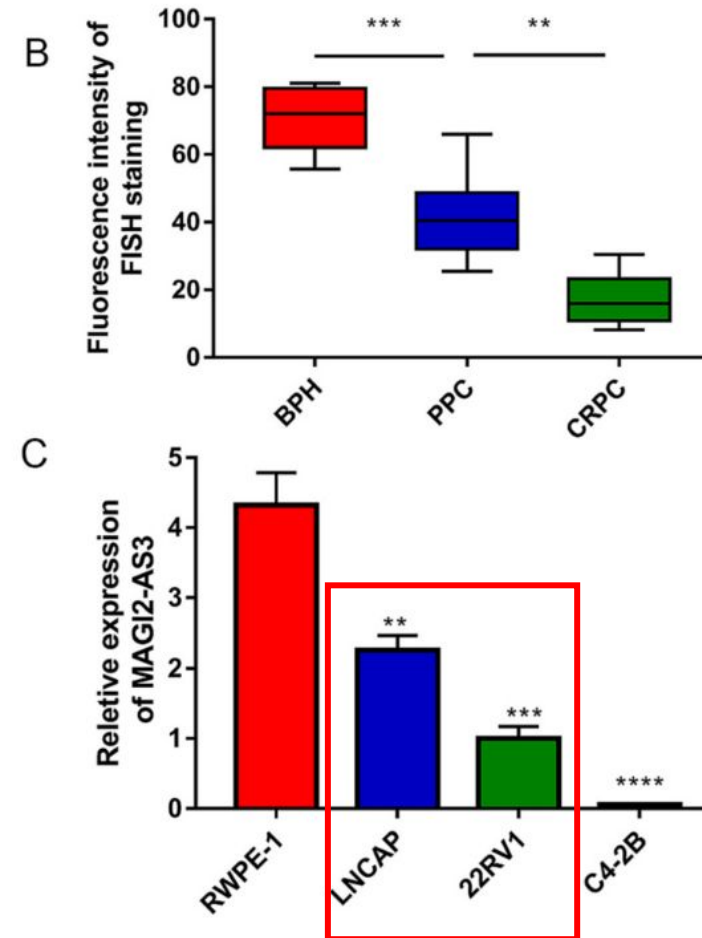
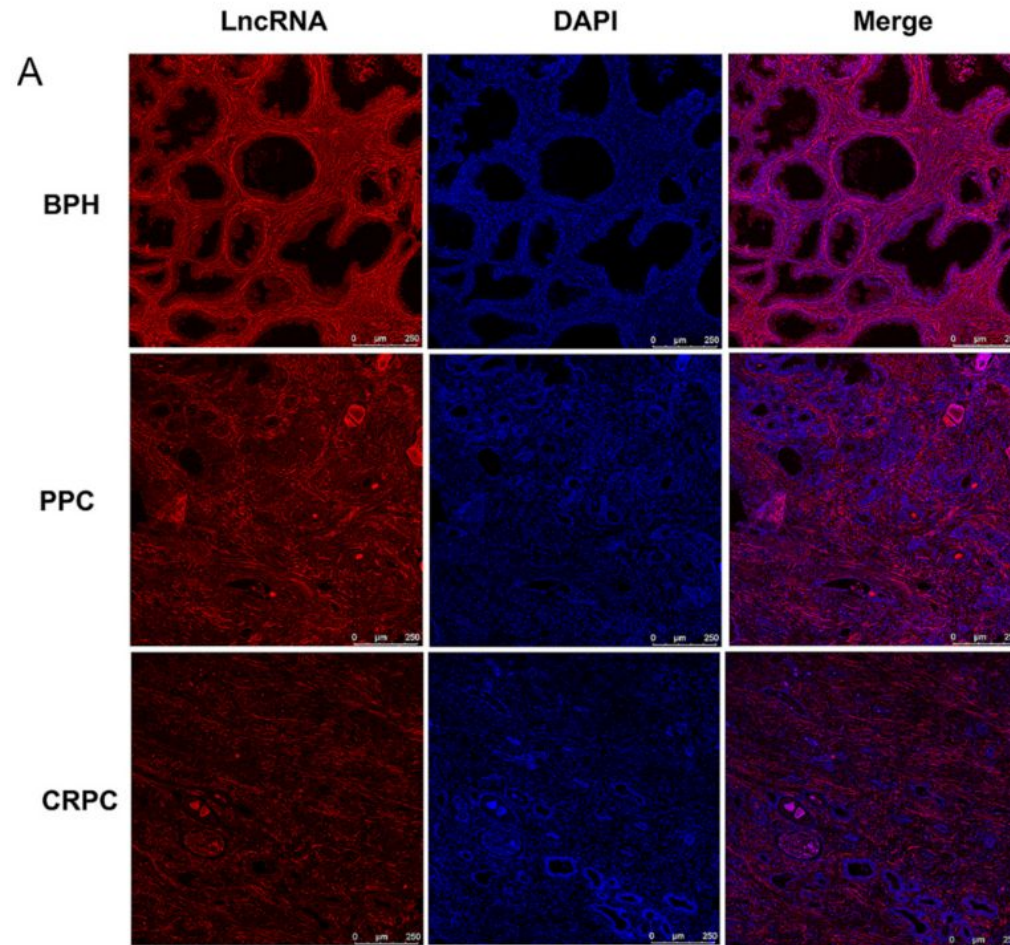
MAGI2-AS3 is **downregulated in CRPC** and can be a **prognostic biomarker** based on **RNA-sequencing analysis**

STEP 2: To determine the expression levels of MAGI2-AS3

Tissue specimens: 7 BPH, 35 PPC, and 6 CRPC

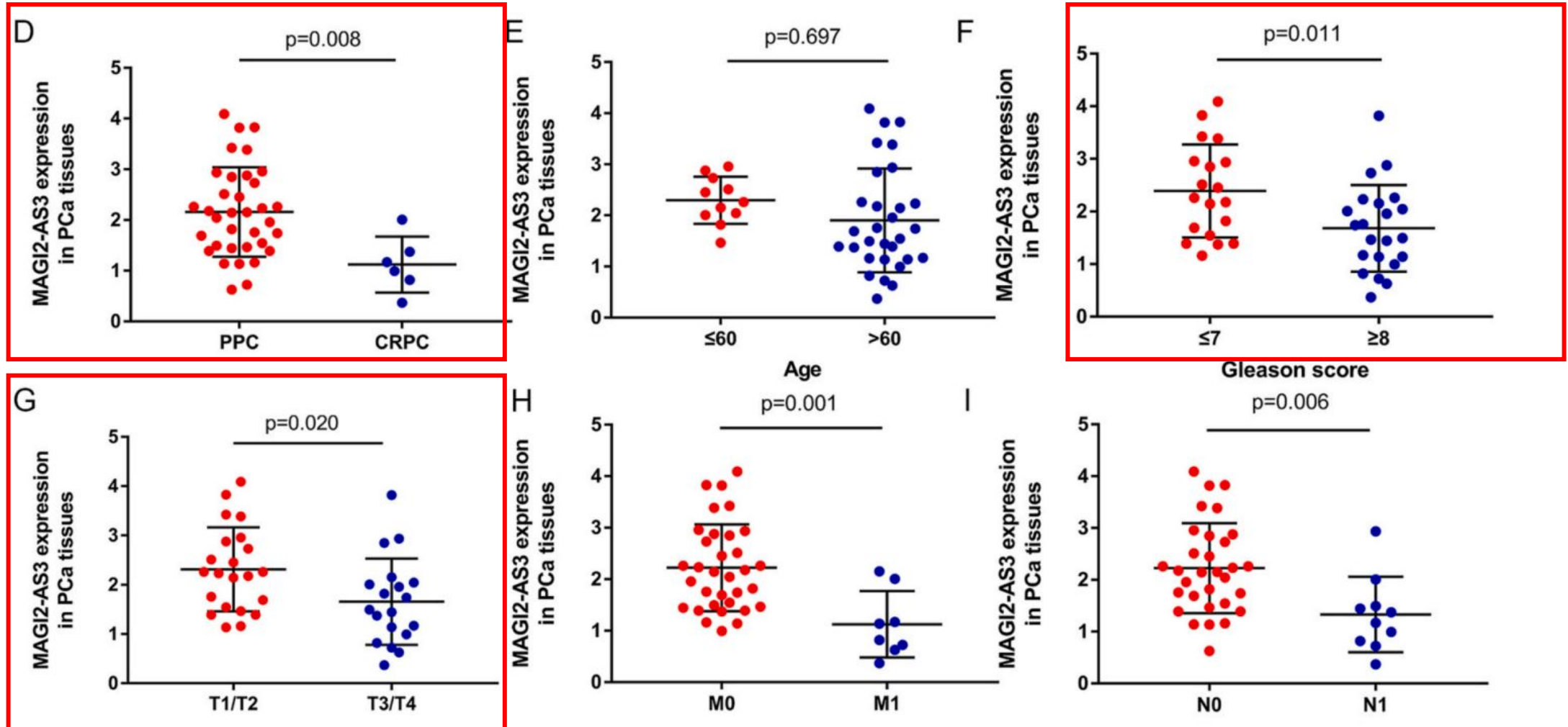
Cells lines: LNCaP, 22RV1, C4-2B, and RWPE-1 cells

Significantly decreased MAGI2-AS3 in CRPC **tissues** compared to primary prostate cancer (PPC) or BPH tissues.(AB).
q-PCR result for MAGI2-AS3 in prostate cell lines (C)



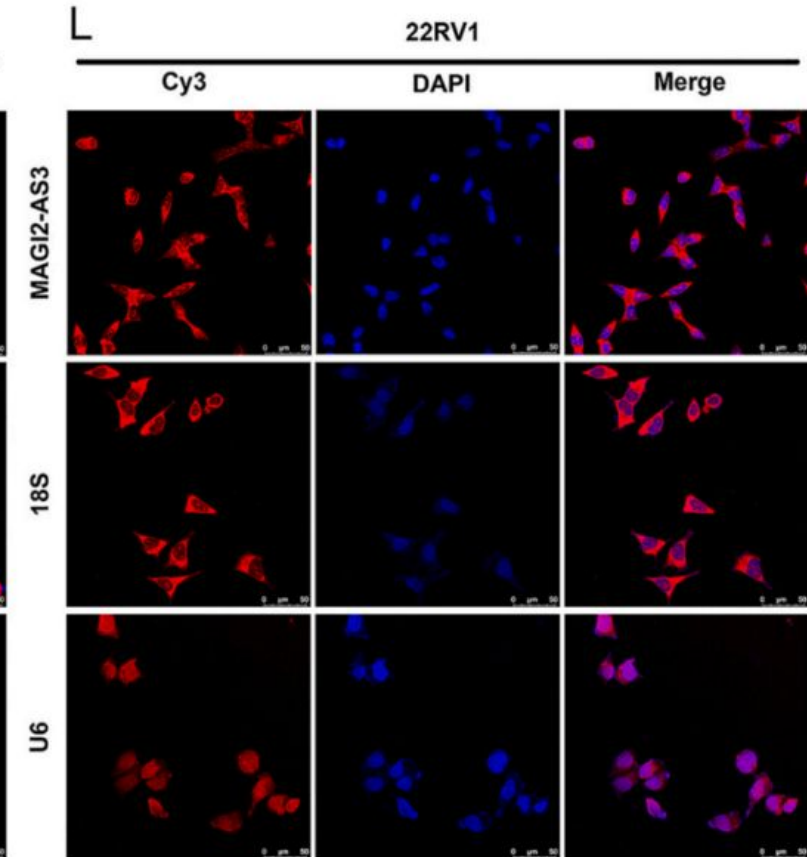
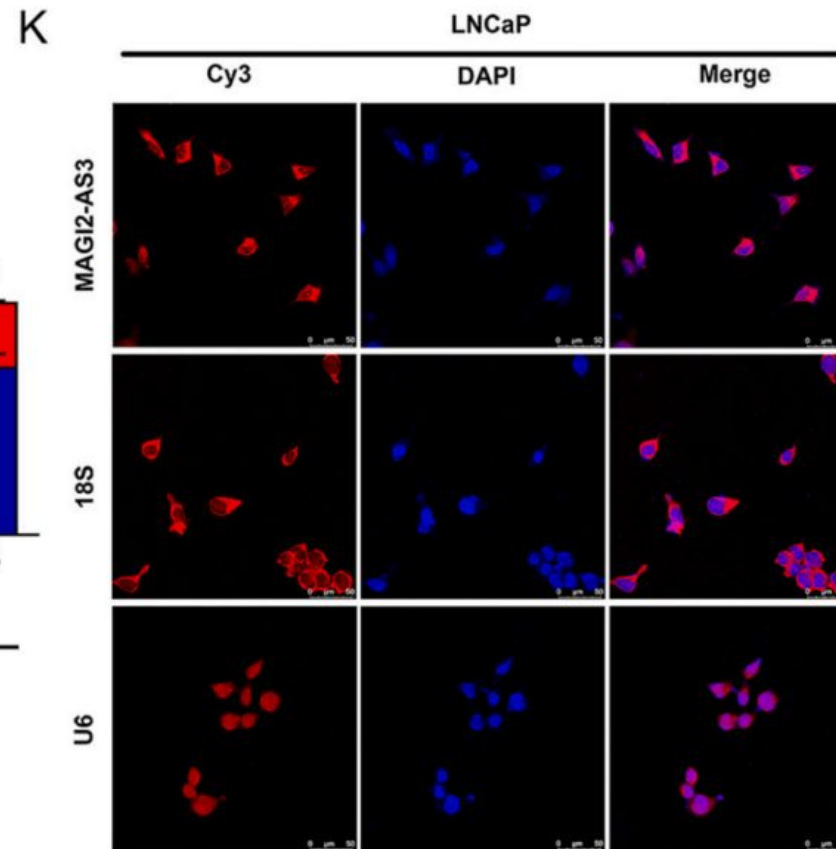
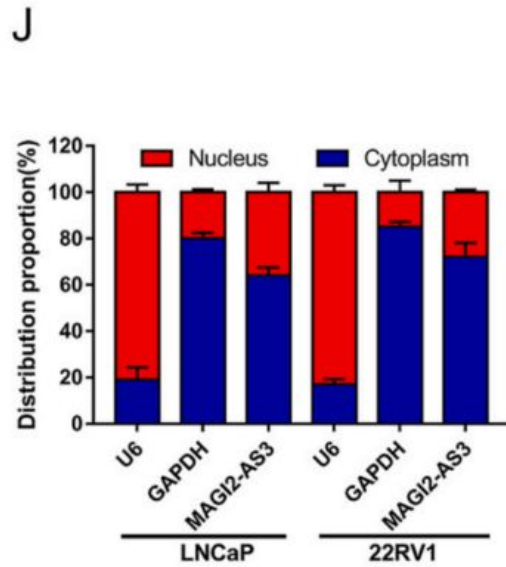
STEP 2: To determine the expression levels of MAGI2-AS3

The RT-PCR results confirmed that MAGI2-AS3 levels were negatively associated with PCa progression



STEP 2: To determine the expression levels of MAGI2-AS3

The nuclear and cytoplasmic distribution of MAGI2-AS3



STEP 2: To determine the expression levels of MAGI2-AS3

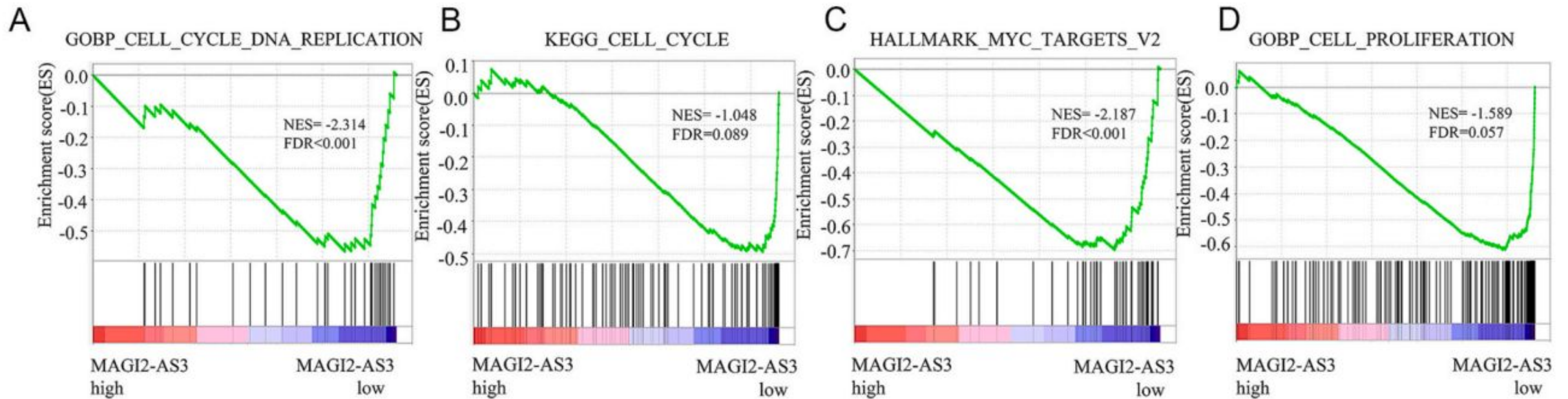
Significantly decreased MAGI2- AS3 in CRPC tissues compared to primary prostate cancer (PPC) or BPH tissues
MAGI2-AS3 levels were negatively associated with PCa progression

STEP 3: To determine the function of MAGI2-AS3 in CRPC

GSE200879 dataset: including 129 samples: 116 HNPC, 13 CRPC

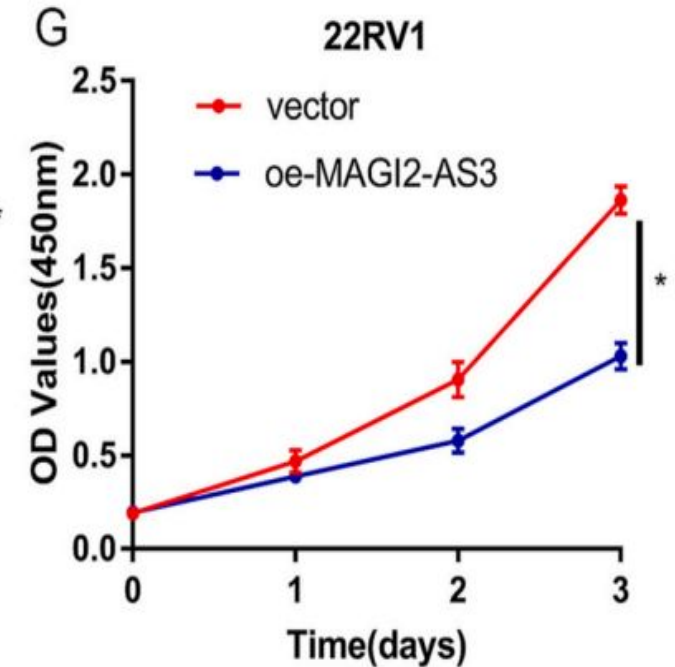
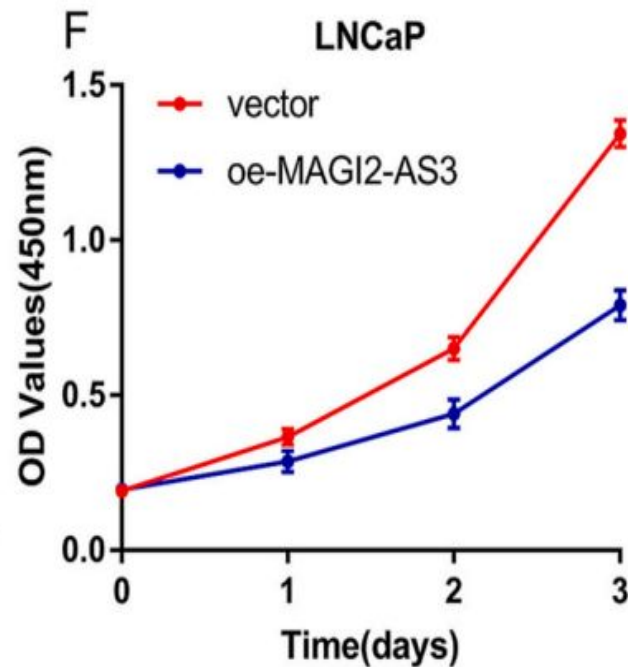
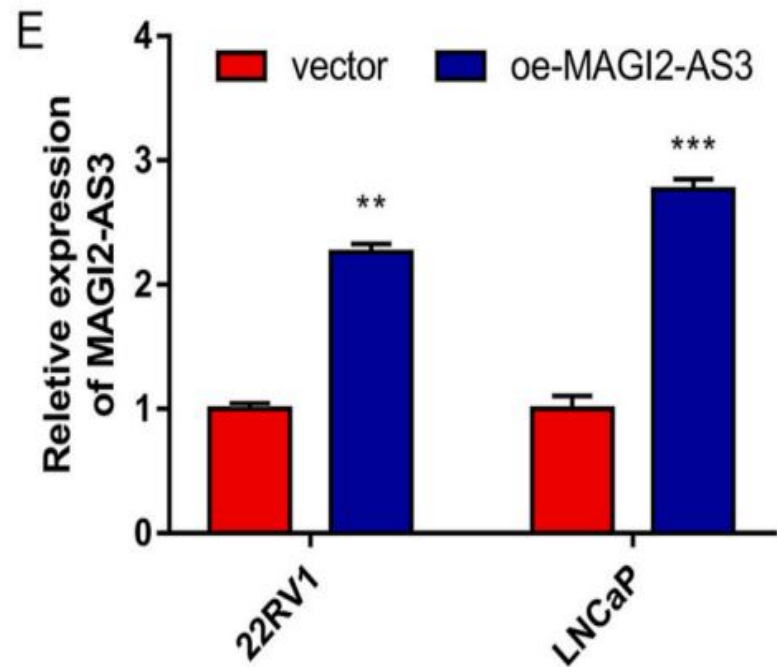
Platform: **Expression profiling by array**

Cell cycle, cell cycle DNA replication, MYC targets, and cell proliferation were found to be enriched in the **low MAGI2-AS3 expression group**.



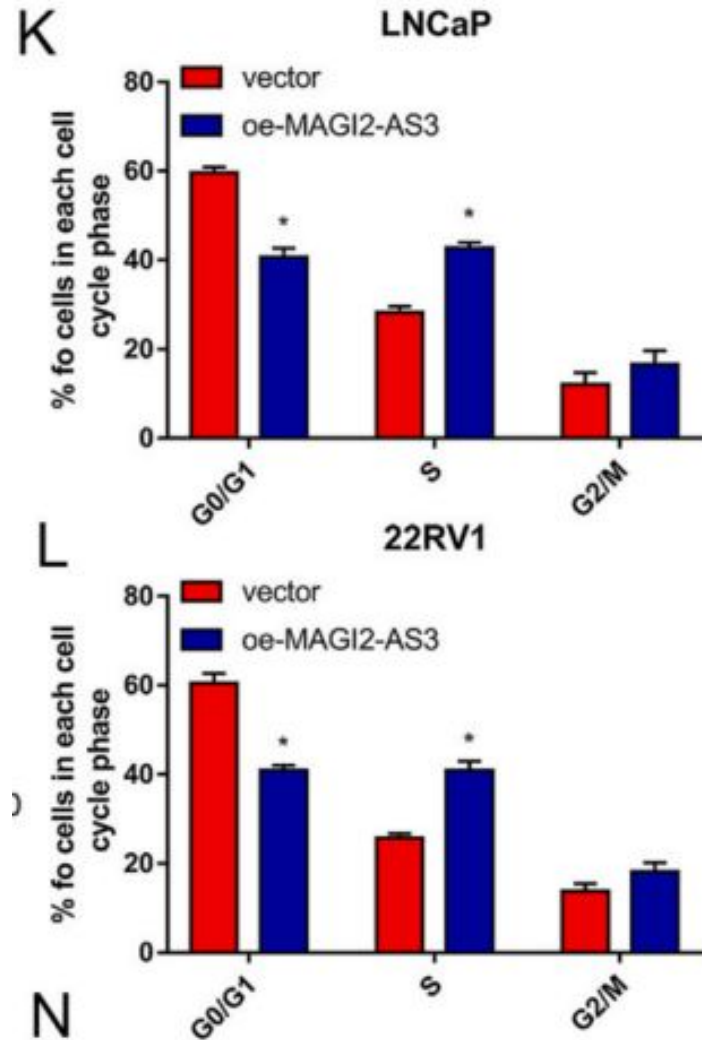
STEP 3: To determine the function of MAGI2-AS3 in CRPC

The full-length cDNA of MAGI2-AS3 (NCBI Reference sequence: NR_038345.1) was synthesized and cloned into the lentiviral vector pcDNA3.1(+) to generate **recombinant lentiviruses overexpressing MAGI2-AS3 (oeMAGI2-AS3)**



STEP 3: To determine the function of MAGI2-AS3 in CRPC

The cell cycle distribution of LNCaP and 22RV1 cells before and after MAGI2-AS3 knockdown or overexpression was detected using flow cytometry. The transition from the G1 phase to the S phase of the cell cycle



- The transition from the G1 phase to the S phase of the cell cycle was significantly blocked after MAGI2-AS3 silencing. In contrast, MAGI2-AS3 overexpression led to the opposite trend.

STEP 3: To determine the function of MAGI2-AS3 in CRPC

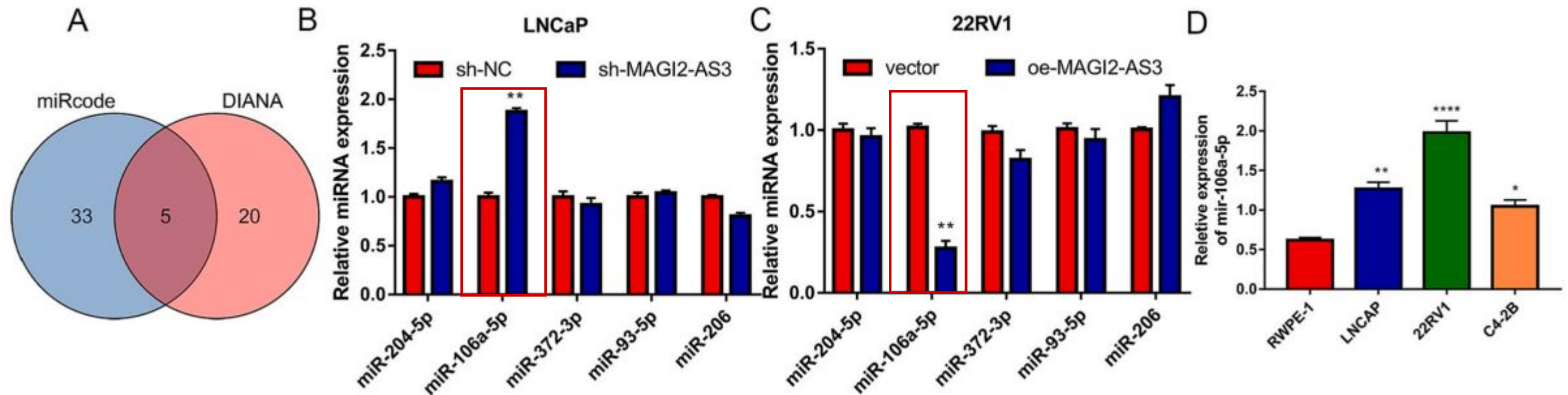
- **MAGI2-AS3 inhibits the proliferation of the PCa cell lines.**

STEP 4: HOW MAGI2-AS3 RESTRAINS PCa PROGRESSION

MAGI2-AS3 is **mainly present in the cytoplasm** of PCa cells, **suggesting a post-transcriptional role** in the malignant biological behavior of tumors.

lncRNA + miRNA → ceRNA

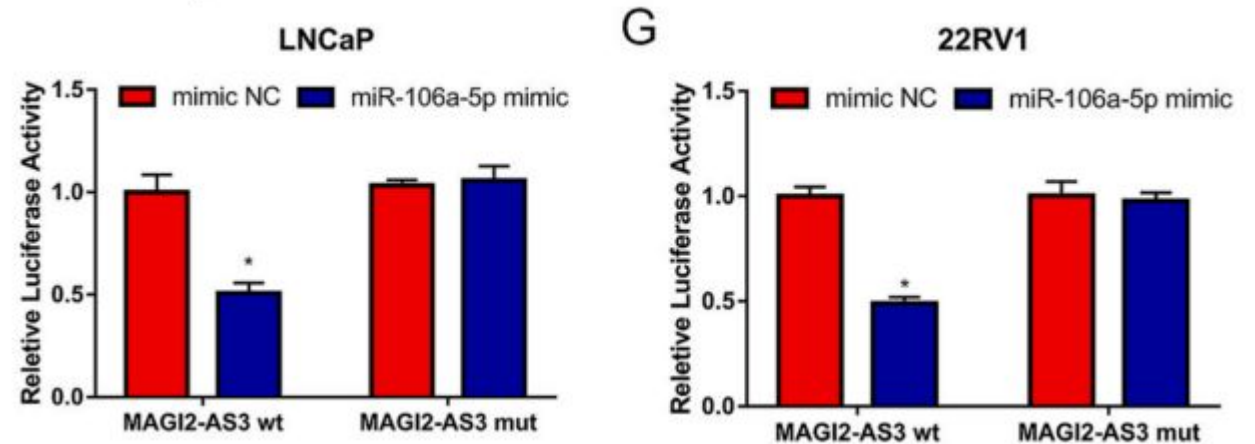
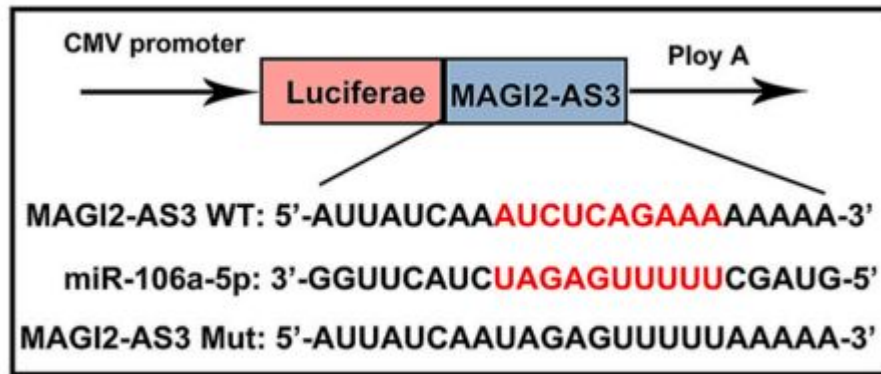
MAGI2-AS3 was overexpressed or knocked down in the PCa cells



miR-106a-5p expression was significantly elevated or decreased in LNCaP and 22RV1 cells.
miR-106a-5p was upregulated in both LNCaP and 22RV1 cells compared to RWPE-1 cells.

STEP 4: HOW MAGI2-AS3 RESTRAINS PCa PROGRESSION

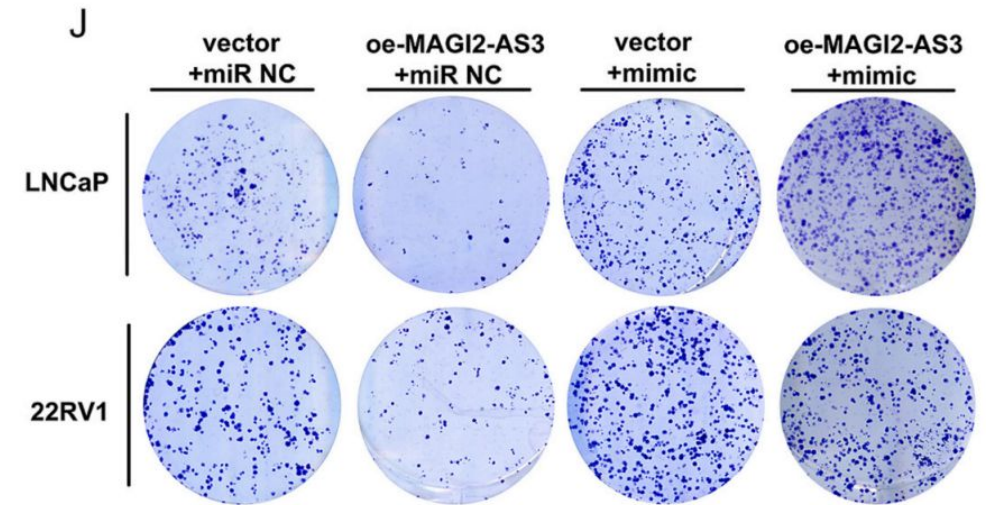
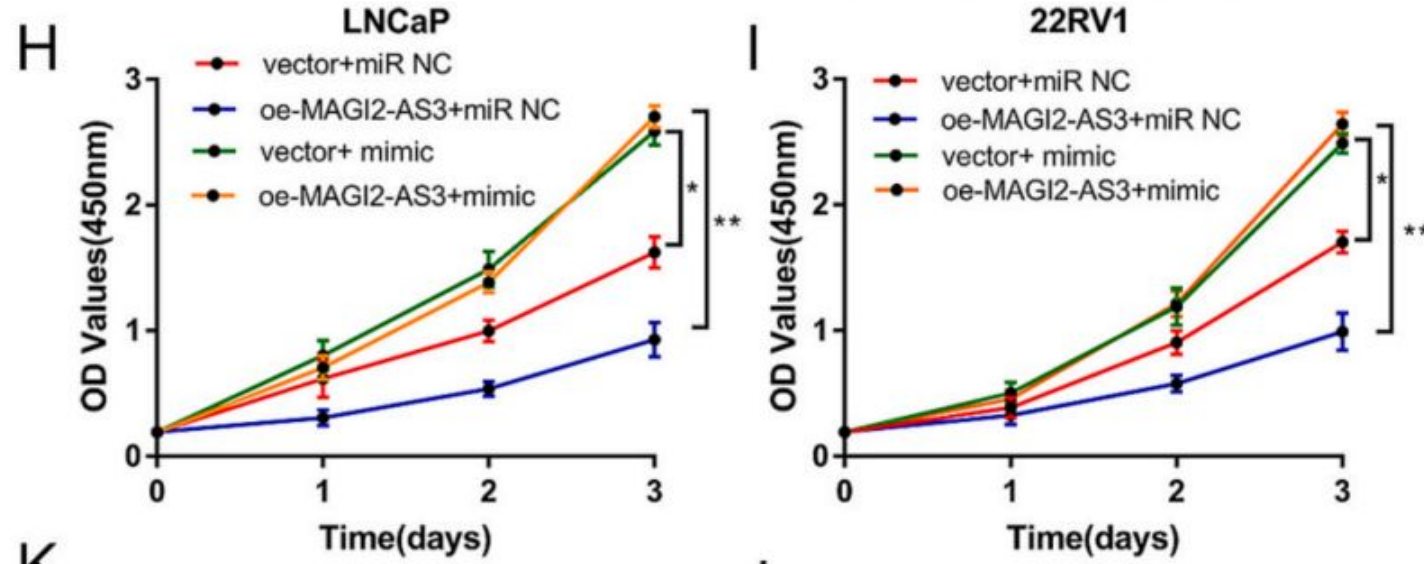
miR-106a-5p mimics **significantly weakened the luciferase activity** of vectors containing **MAGI2-AS3 wt** but **could not decrease** the luciferase activity of the **MAGI2-AS3 mut** vectors.



miR-106a-5p mimics significantly weakened the luciferase activity of vectors containing MAGI2-AS3 wt but could not decrease the luciferase activity of the MAGI2-AS3 mut vectors

STEP 4: HOW MAGI2-AS3 RESTRAINS PCa PROGRESSION

Investigate the biological role of miR-106a-5p

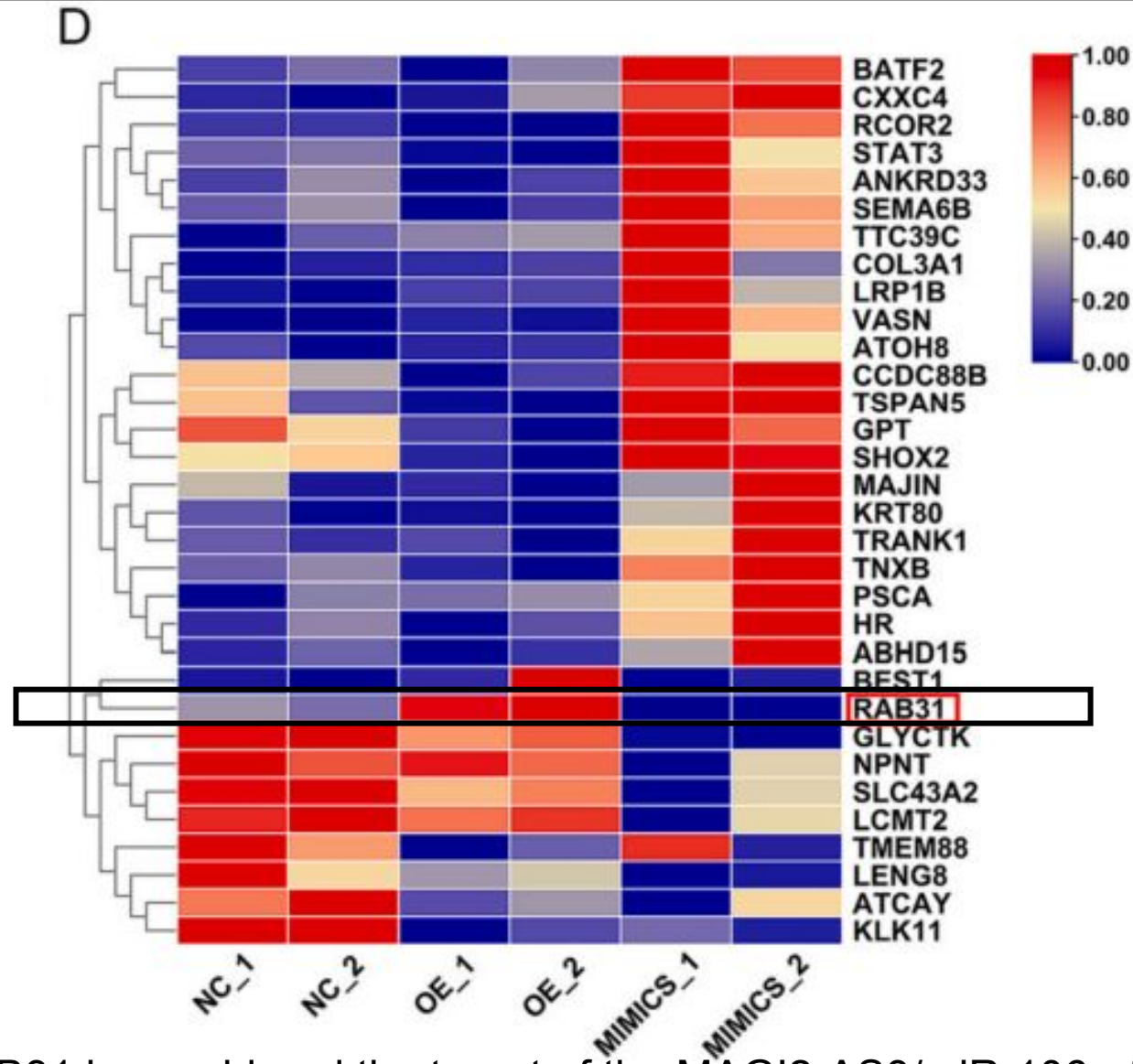


The decreased proliferation ability of cells upon overexpression of MAGI2-AS3 could be rescued by the miR-106a-5p mimic

STEP 4: HOW MAGI2-AS3 RESTRAINS PCa PROGRESSION

Overall, the above experiments demonstrated that MAGI2-AS3 interacts with miR-106a-5p to influence PCa via miR-106a-5p.

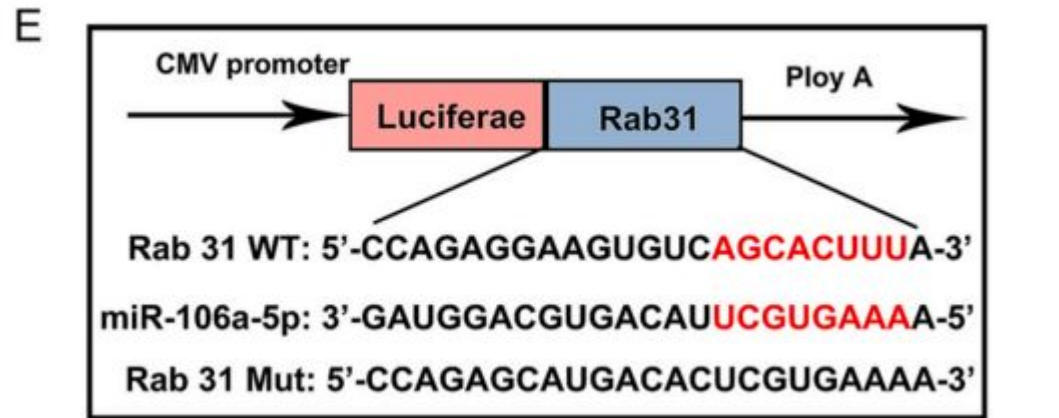
STEP 5: The downstream mechanisms that may be regulated by the MAGI2-AS3/miR-106a-5p axis to inhibit PCa progression



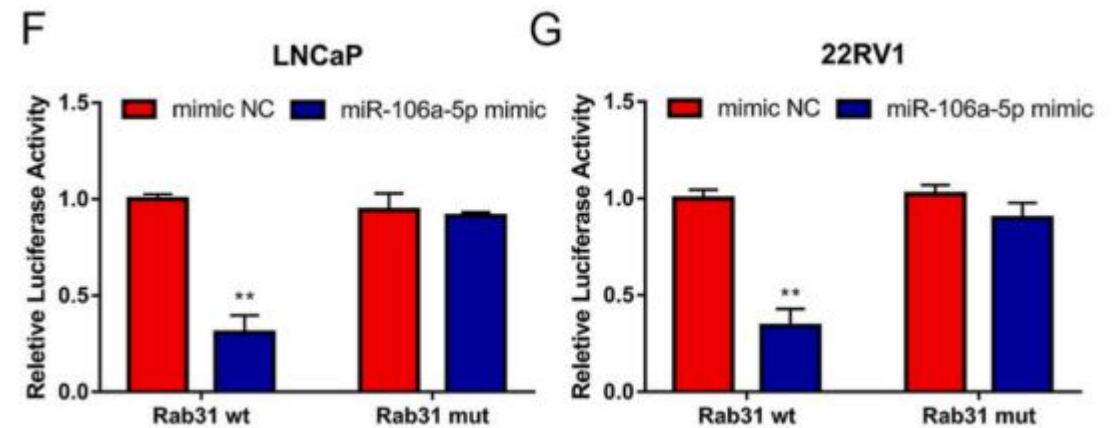
RAB31 is considered the target of the MAGI2-AS3/miR-106a-5p axis

STEP 5: The downstream mechanisms that may be regulated by the MAGI2-AS3/miR-106a-5p axis to inhibit PCa progression

The RAB31 3'UTR fragment, containing the wt or mut binding sites, was inserted into the vector and co-transfected into 22RV1 and LNCaP cells with the miR-106a-5p mimic or miR-NC mimic.



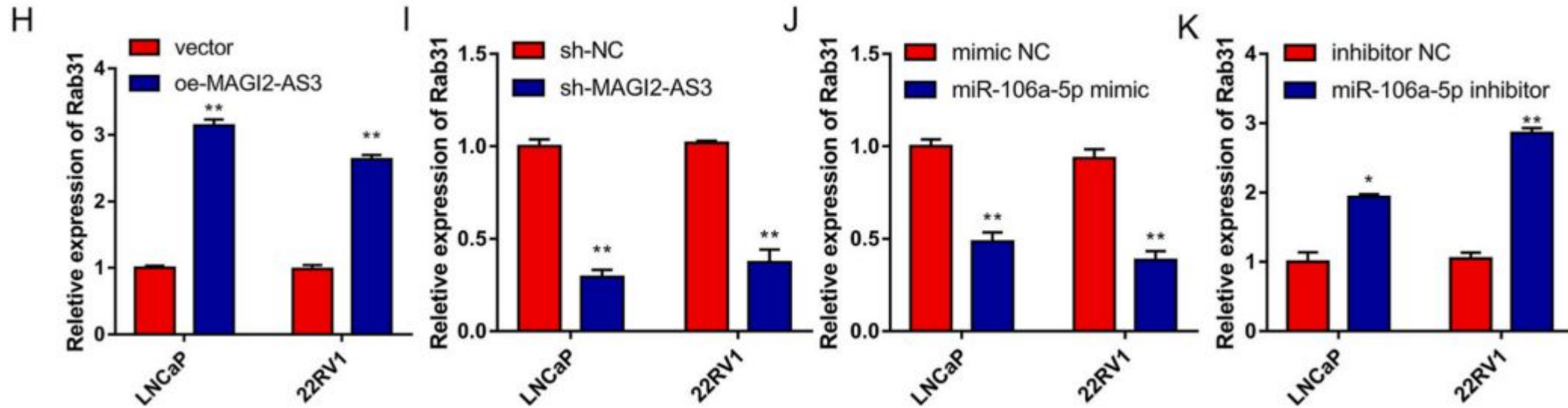
Potential binding sites between miR106a-5p and RAB31



The miR-106a-5p mimic, which contained the RAB31 wt binding site but not the mut-binding site, significantly weakened the luciferase activity

STEP 5: The downstream mechanisms that may be regulated by the MAGI2-AS3/miR-106a-5p axis to inhibit PCa progression

To further confirm that MAGI2-AS3 could regulate RAB31 expression through competitive endogenous binding with miR-106a-5p in PCa. RAB31 WAS expression in LNCaP and 22RV1 cells stably transfected with the miR-106a-5p mimic or inhibitor and MAGI2-AS3 silencing or overexpression vectors.



The RAB31 mRNA level was found to be markedly controlled by MAGI2-AS3 or miR-106a-5p

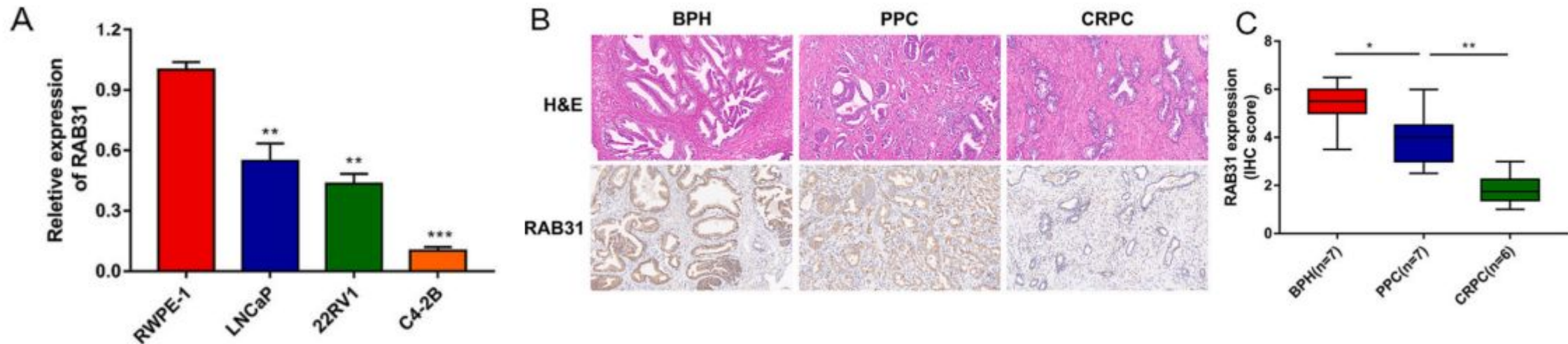
STEP 5: The downstream mechanisms that may be regulated by the MAGI2-AS3/miR-106a-5p axis to inhibit PCa progression

The RAB31 mRNA level was found to be markedly controlled by MAGI2-AS3 or miR-106a-5p. These results indicate that RAB31 is the downstream target gene of MAGI2-AS3.

STEP 6: The downstream mechanisms that may be regulated by the MAGI2-AS3/miR-106a-5p axis to inhibit PCa progression

The **protein expression of RAB31** was identified in a broad spectrum of tumors and **decreased in PCa tissues compared with normal tissues** (two GEO datasets (GSE200879 and GSE3325) and two studies (TCGA-PRAD, SU2C/PCF Dream Team Study).

RAB31 is strongly associated with PCa progression

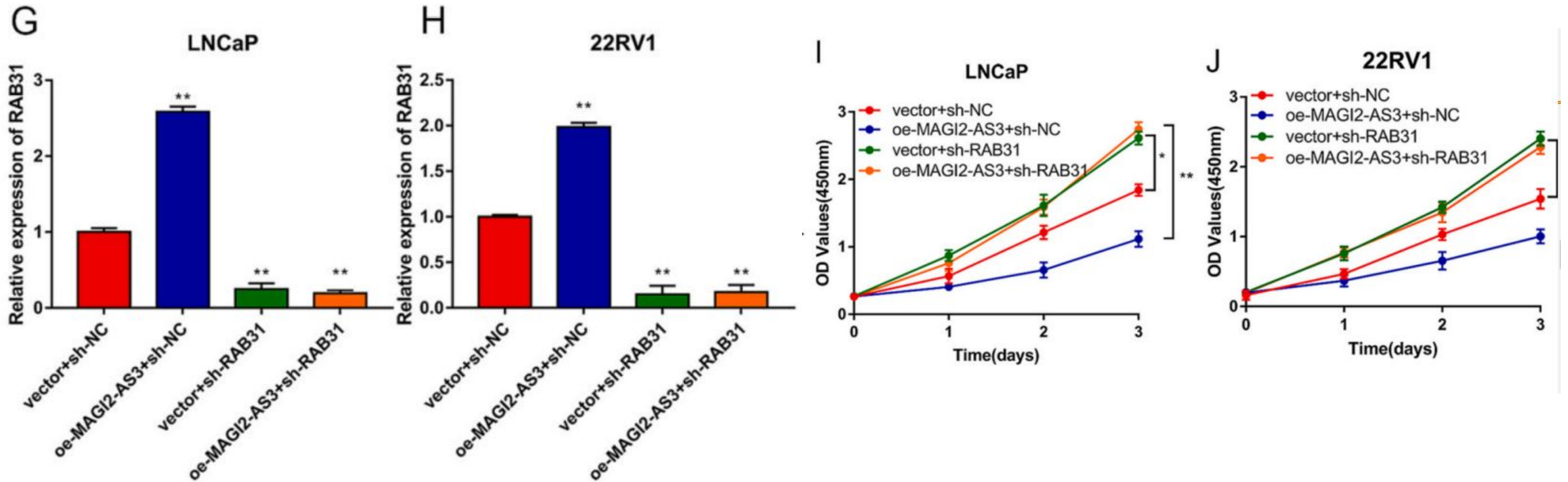


qRT-PCR revealed that RAB31 expression was suppressed in PCa cells

IHC showed that RAB31 was decreased in PCa tissues compared to BPH and more significantly decreased in CRPC samples than in PPC specimens

STEP 6: The downstream mechanisms that may be regulated by the MAGI2-AS3/miR-106a-5p axis to inhibit PCa progression

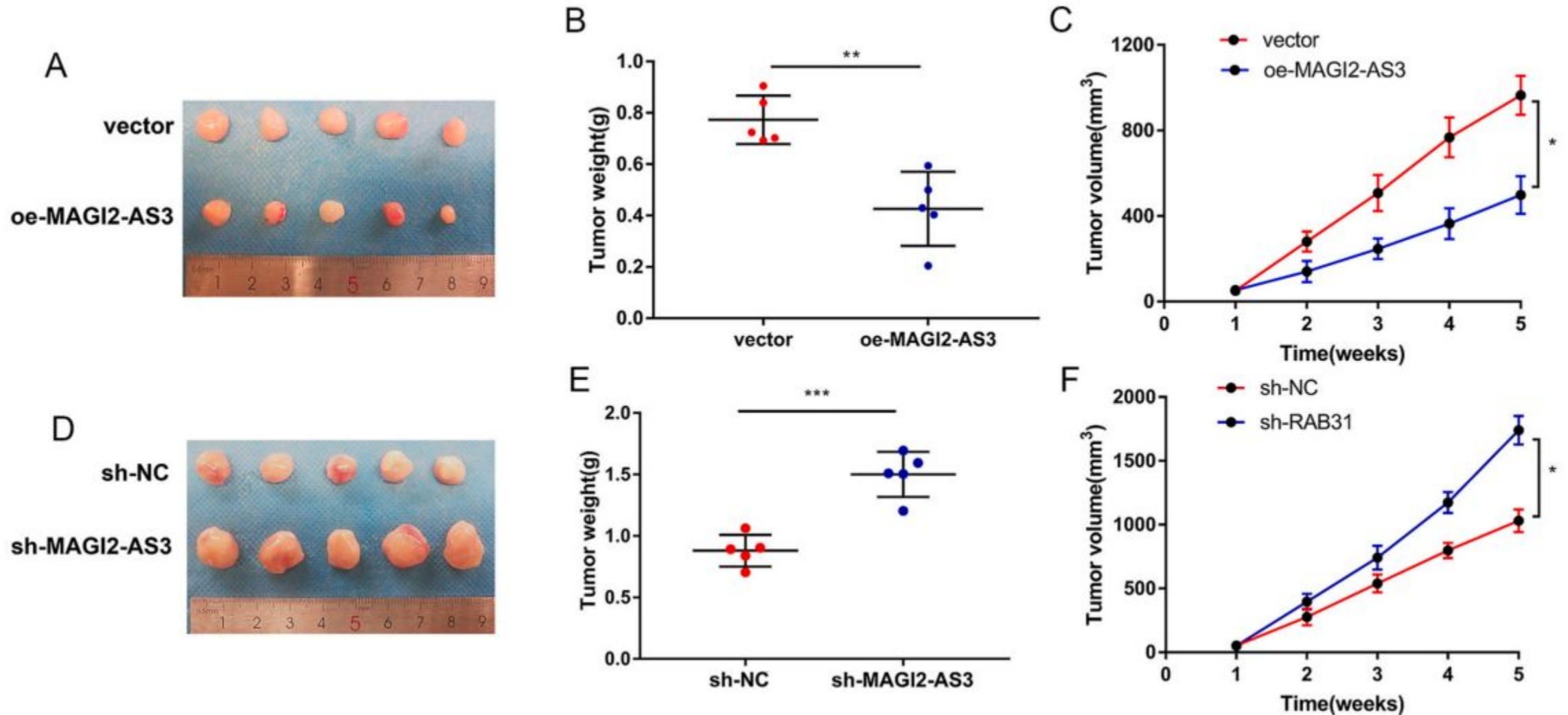
LNCaP and 22RV1 cells stably overexpressing MAGI2-AS3 were transfected with sh-RAB31 vector, and the RAB31 mRNA levels were measured after transfection.



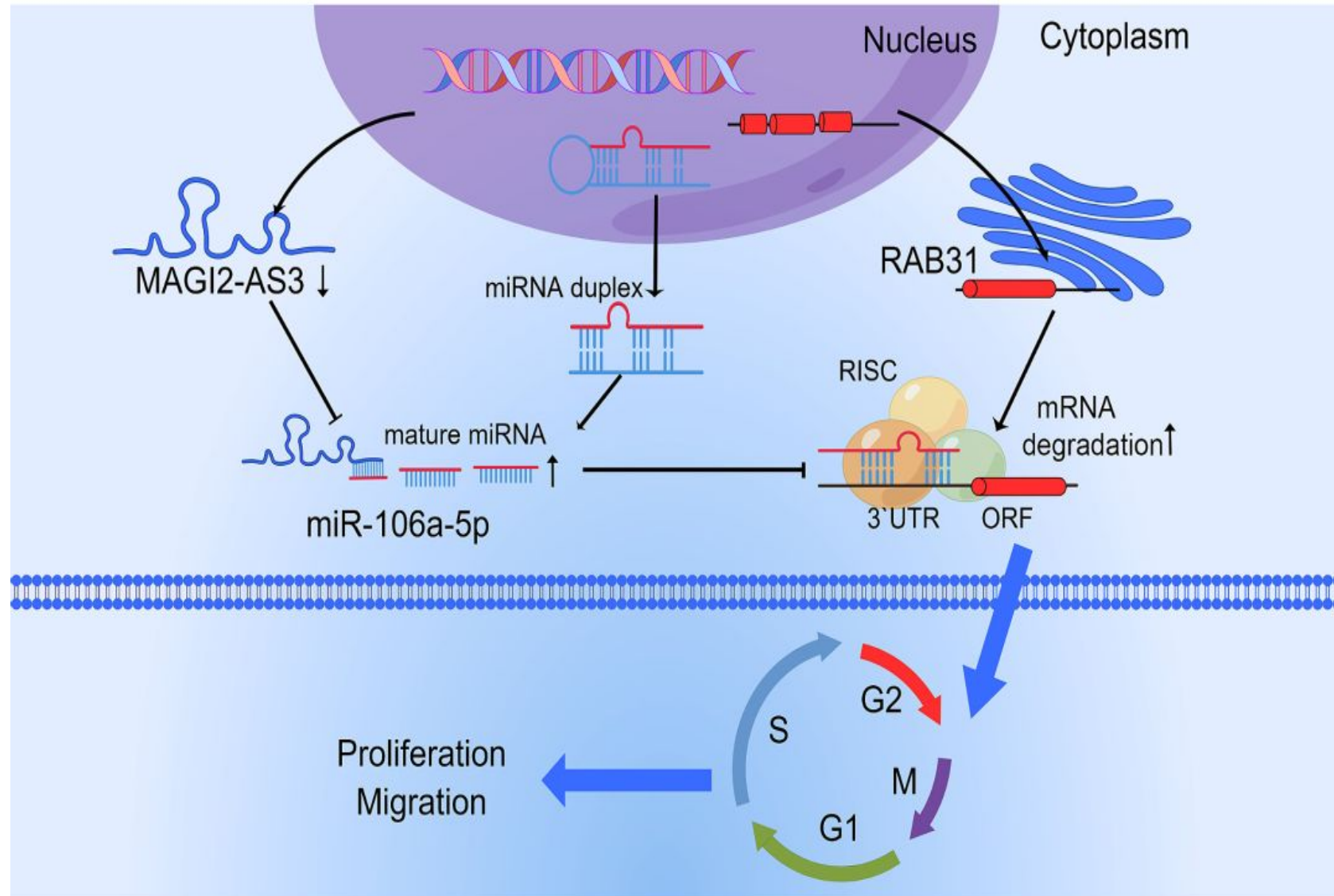
RAB31 knockdown improved the proliferation and migration of PCa cells induced by MAGI2-AS3

STEP 7: MAGI2-AS3 represses PCa progression in vivo

22RV1 cells stably transfected with MAGI2-AS3 or sh-MAGI2-AS3 and NC were implanted subcutaneously into nude mice to establish xenograft tumors.



Schematic representation of the results of this study.



Discussion

- Demonstrate the role of MAGI2-AS3 in the inhibition of CRPC progression.
- MAGI2-AS3 expression could negatively accommodate the migration and proliferation of PCa in vitro and in vivo.
- MAGI2-AS3 was identified to function as a tumor suppressor by interacting with miR-106a-5p to regulate the expression of RAB31 in CRPC.
- MAGI2-AS3 was identified to function as a tumor suppressor by interacting with miR-106a-5p to regulate the expression of RAB31 in CRPC
- mRNA level of RAB31 and found a remarkable association between lower rab31 mRNA level and poorer prognosis in PCa patients.
- GSEA also revealed that decreased RAB31 expression may influence the proliferation and cell cycle signaling pathways of CRPC, including the G2M checkpoint and MYC targets.