

# miRNA

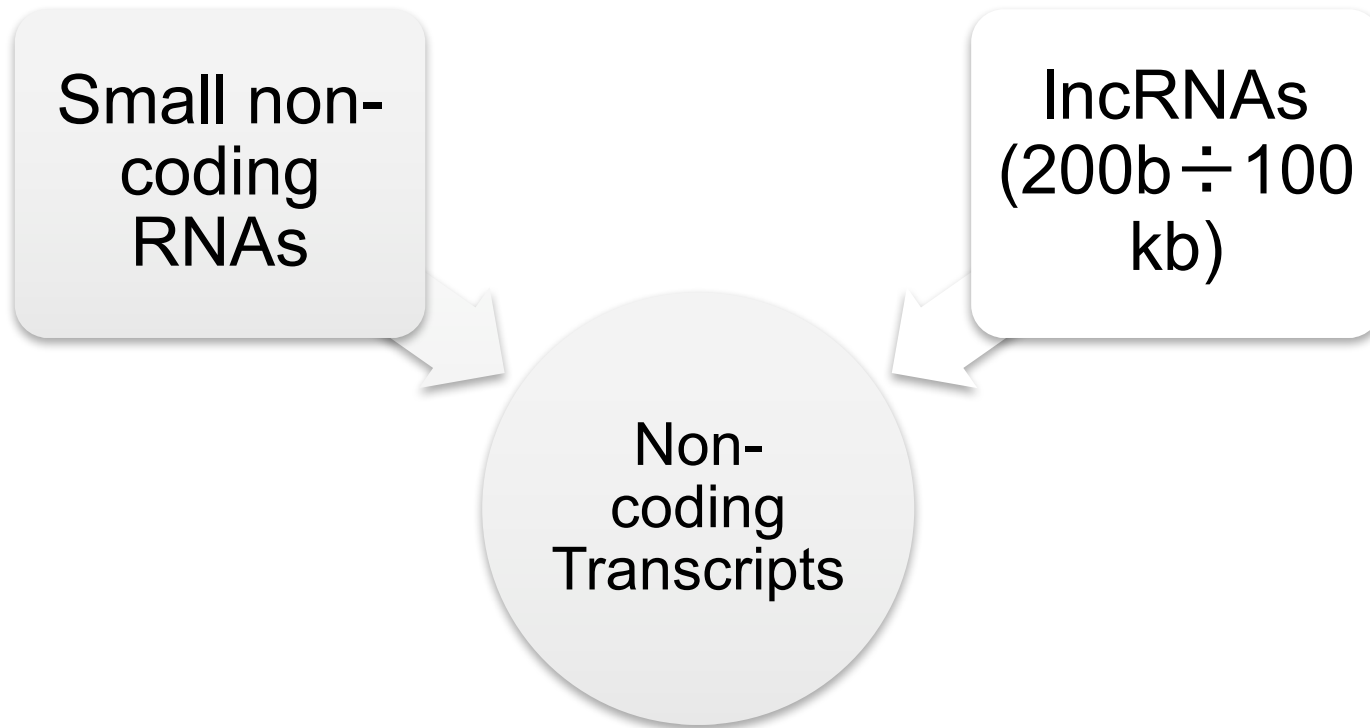
## Perché?

- ✱ Rappresentano uno dei maggiori sistemi regolatori per famiglie di geni nelle cellule eucariotiche.
- ✱ Molti mRNA presentano più siti di legame per miRNA che sono il bersaglio per uno o più miRNA.
- ✱ I miRNA sono coinvolti un vasto campo di processi biologici quali: sviluppo, differenziamento cellulare, proliferazione, apoptosi.....
- ✱ Sono implicati pure nella patogenesi di malattie umane quali: cancro, malattie metaboliche, disordini neurologici, malattie infettive.....

# miRNA

## Perché?

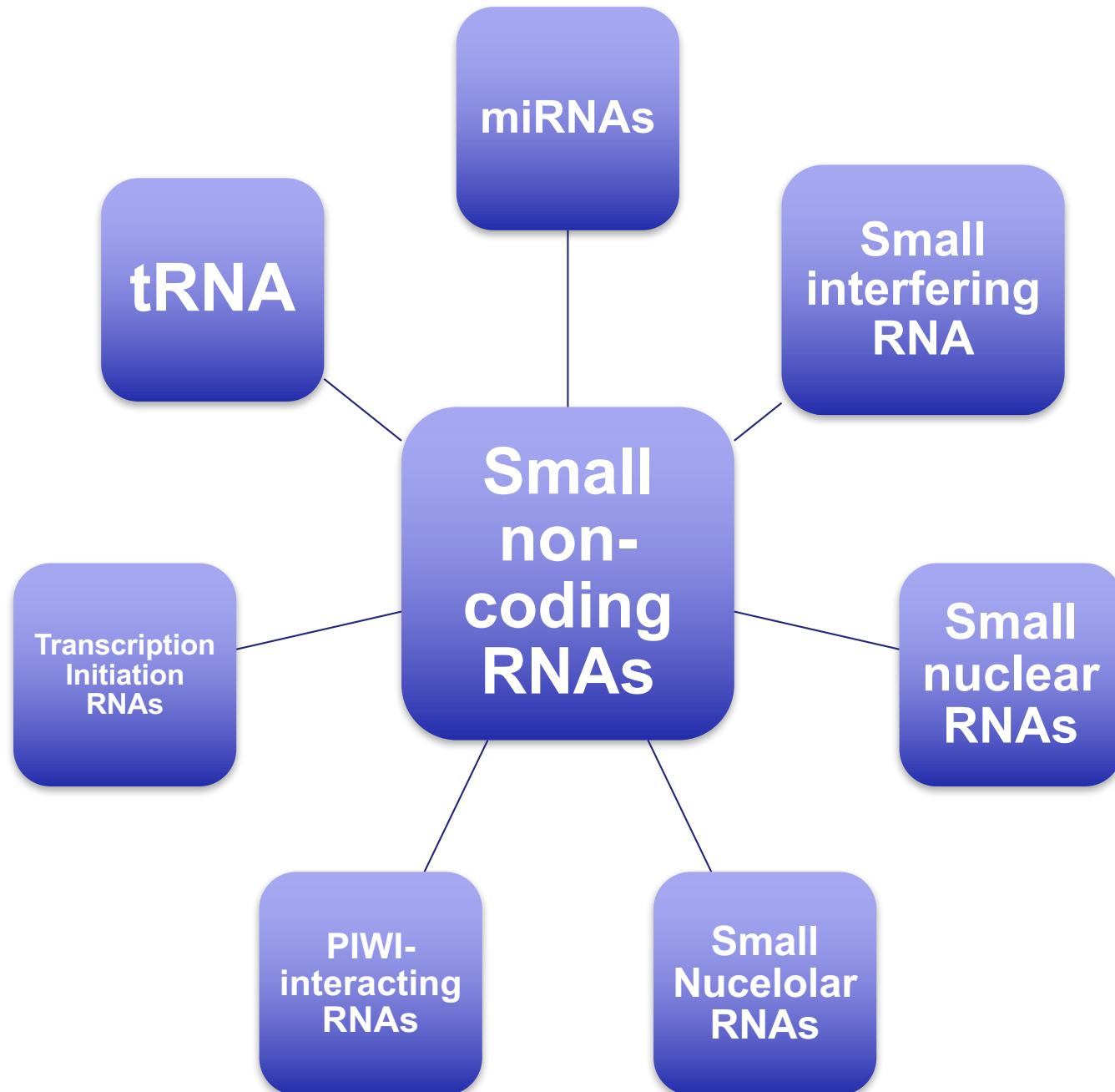
- ✓ La deregolazione dei miRNA nei tumori può coinvolgere delezioni o amplificazioni
- ✓ Il pattern dei miRNA è tessuto specifico
- ✓ Ci possono essere mutazioni nei geni miRNA
- ✓ Molti miRNA sono nello stesso DNA policistronico e vengono processati assieme
- ✓ Ogni miRNA può avere bersagli multipli
- ✓ I miRNA possono funzionare da tumor suppressor o oncogeni dipendentemente dal contesto cellulare.



## In numbers

- ✓ 21.000 protein- coding genes
- ✓ 9.000 small RNAs
- ✓ 10.000-32.000 long non-coding RNAs
- ✓ ~ 11.000 pseudogenes

# Small non-coding RNAs-How many?

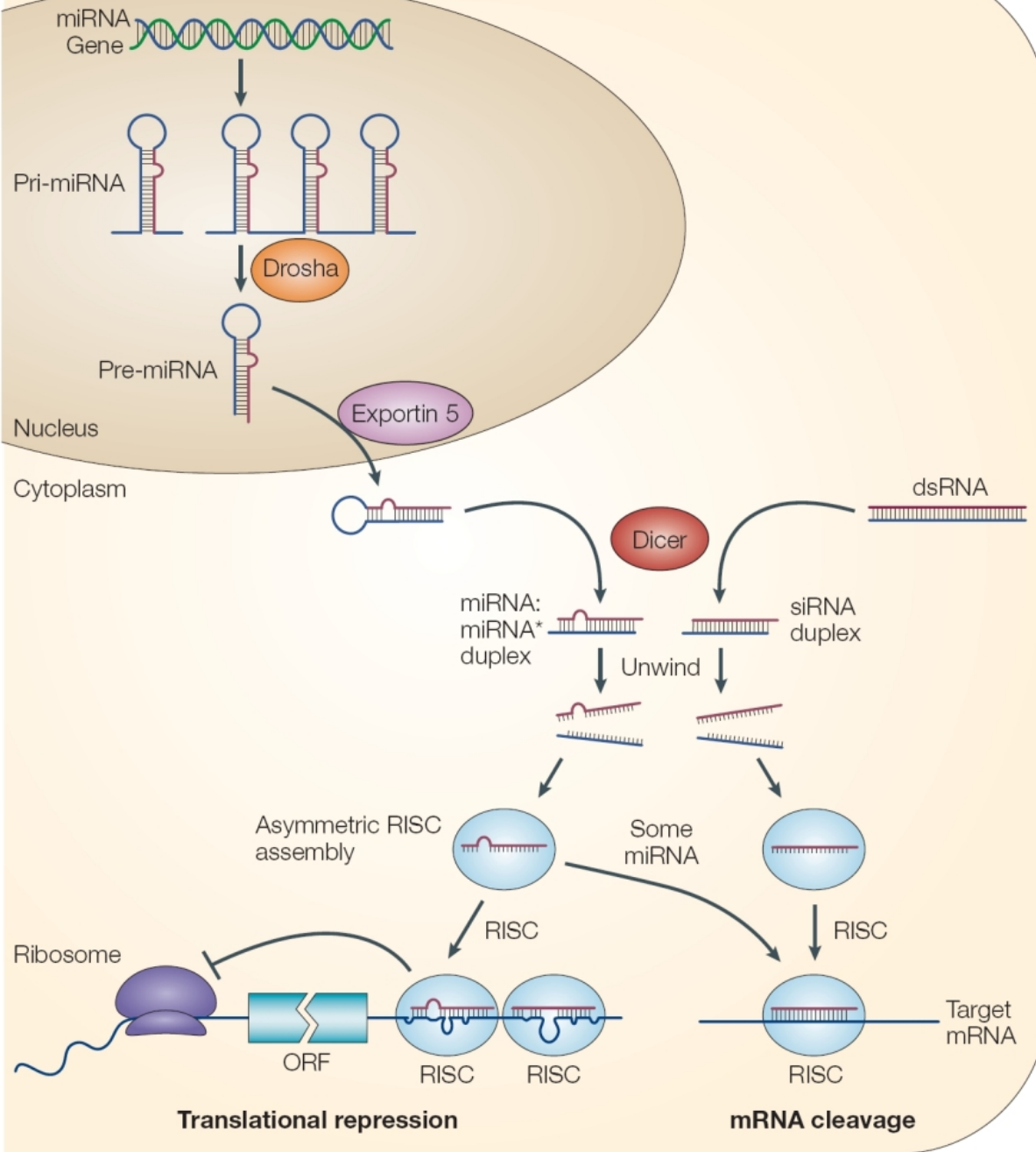


# **RNA-RNA CROSSTALK:**

- 1. New layers of gene regulation***
- 2. Interactions between diverse RNA species***
- 3. There are numerous miRNA-binding sites on a wide variety of RNA transcripts***

## **ceRNA Hypothesis**

- ✓ All RNA transcripts that contain miRNA –binding sites can communicate with and regulate each other by competing endogenous RNAs.**
- ✓ miRNA competition thus extends beyond the non-coding transcriptome and confers an additional non-protein coding function to protein-coding mRNAs .**

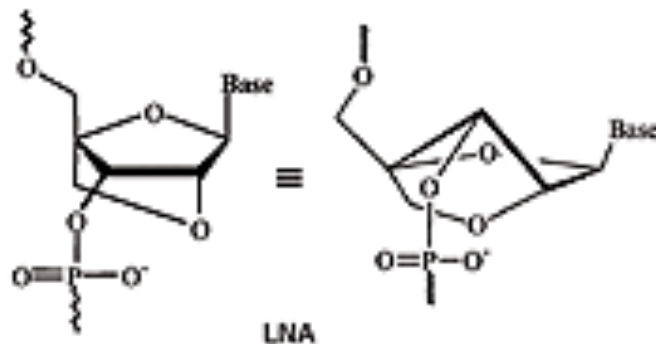


- ✓ Mature miRNA are generally long 21-25 nucleotide
- ✓ Most miRNAs seem to bind to the target 3'UTR
- ✓ Complementarity is imperfect
- ✓ Roles of targeting are not completely understood.

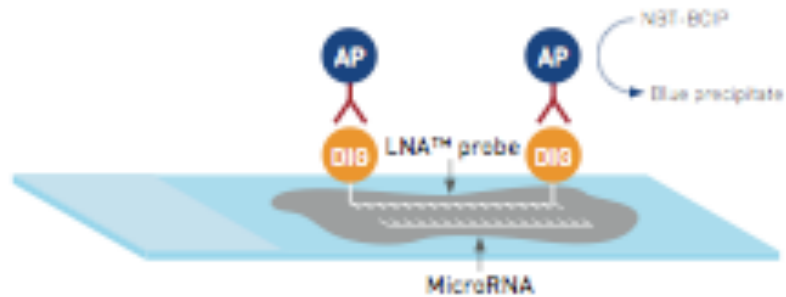
# miRNA

## Come?

- ☺ Le molecole di miRNA sono troppo piccole per analizzarle con una qPCR convenzionale, composta da primer sense, antisense e sonda TaqMan.
- ☺ Ci sono attualmente diversi sistemi disponibili in commercio per analizzarli che spaziano fra la RT-PCR alla ibridazione in situ impiegando sonde LNA.
- ☺ Le basi LNA hanno una modifica alla struttura del ribosio che lega la base alla posizione C3'-endo, favorendo una geometria a doppia elica RNA tipo A.



## Saggio miRCURY LNA



Impiega sonde LNA  
doppiamente marcate con la  
digossigenina

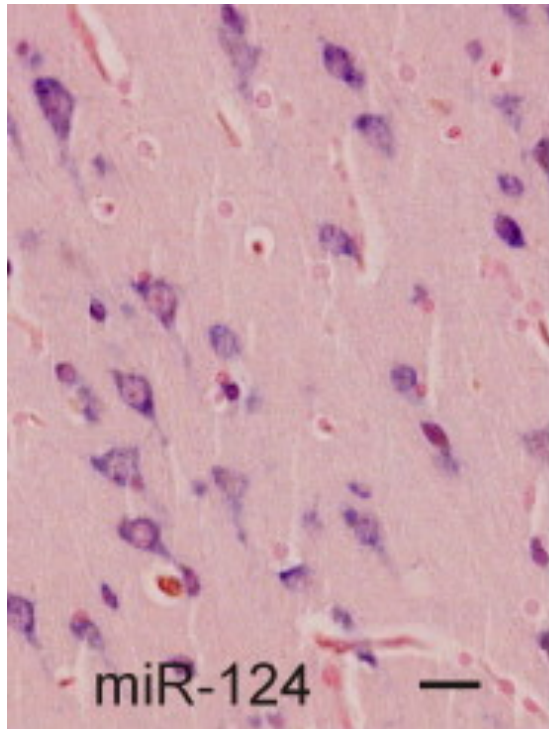
È ottimizzato per i tessuti FFPE e richiede 1 giorno di esecuzione

**Fasi:**

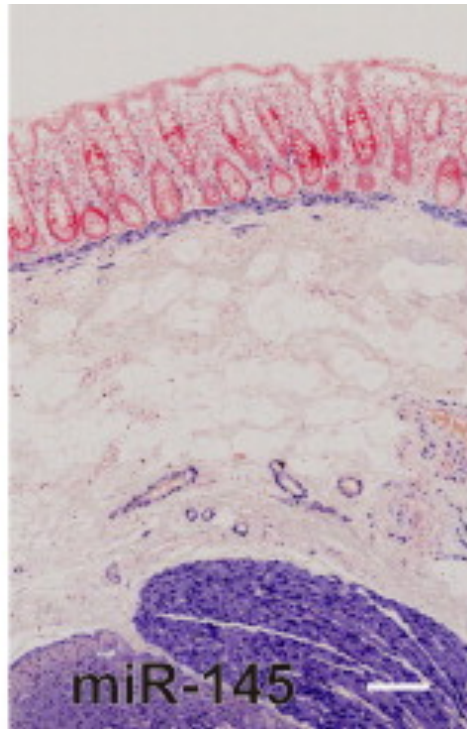
1. Smascheramento dei miRNA con Proteinasi K
2. Ibridazione con le sonde
3. La digossigenina viene riconosciuta da un anticorpo anti-DIG coniugato con la fosfatasi alcalina (AP). AP converte i substrati solubili NBT e BCIP in  $H_2O$  un precipitato insolubile in alcol e  $H_2O$  NBT-BCIP (blu scuro). La controcolorazione consente una miglior risoluzione istologica.



## Saggio miRCURY LNA



Brain



Normal Colon

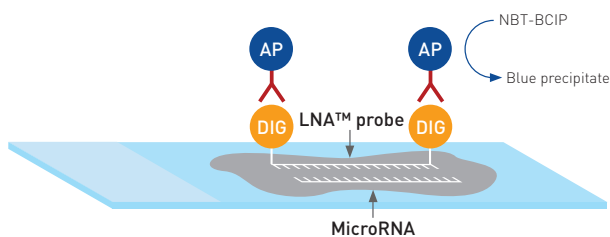


Breast Cancer

[Jørgensen S](#), [Baker A](#), [Møller S](#), [Nielsen BS](#). Robust one-day *in situ* hybridization protocol for detection of microRNAs in paraffin samples using LNA probes. [Methods](#) Volume 52, Issue 4, December 2010, Pages 375-381.

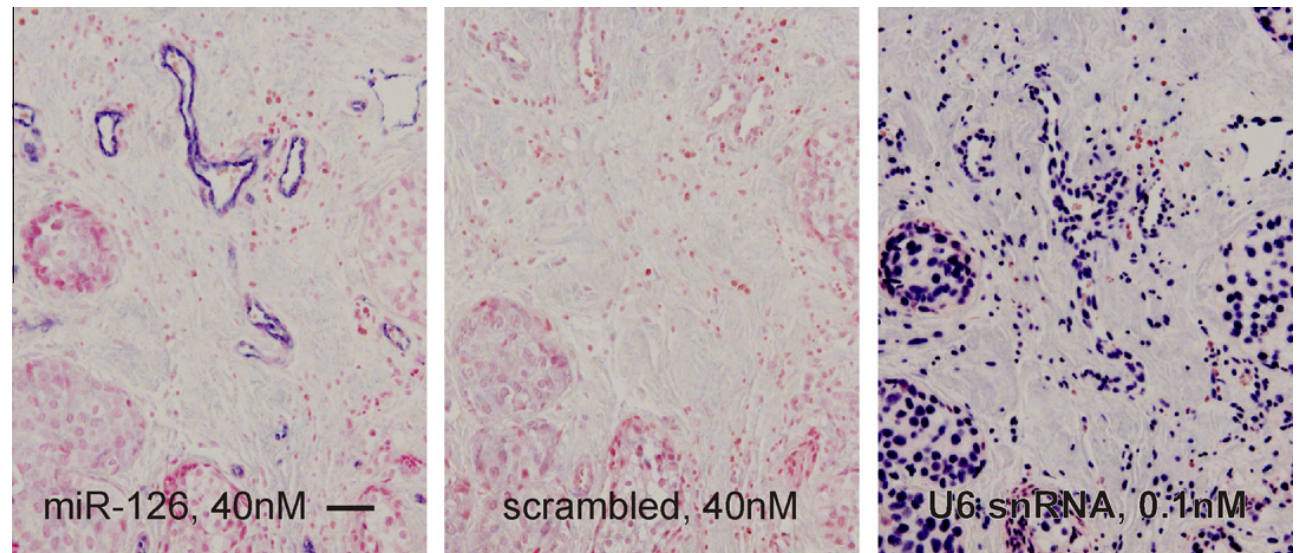
# ISH for mRNA and miR detection

- ✓ Morphology
- ✓ Sensitivity
- ✓ miRs have high degree of similarity between the sequences. Some micro- RNA family members vary by a single nucleotide.
- ✓ Use LNA-enhanced oligonucleotides.
- ✓ The use of LNA™ in probes enables highly sensitive detection and analysis of the short miRNA sequences, but also mRNA.
- ✓ The use of LNA probe allows a better control of T<sub>m</sub> even in AT rich sequences and for short stretches (miR)



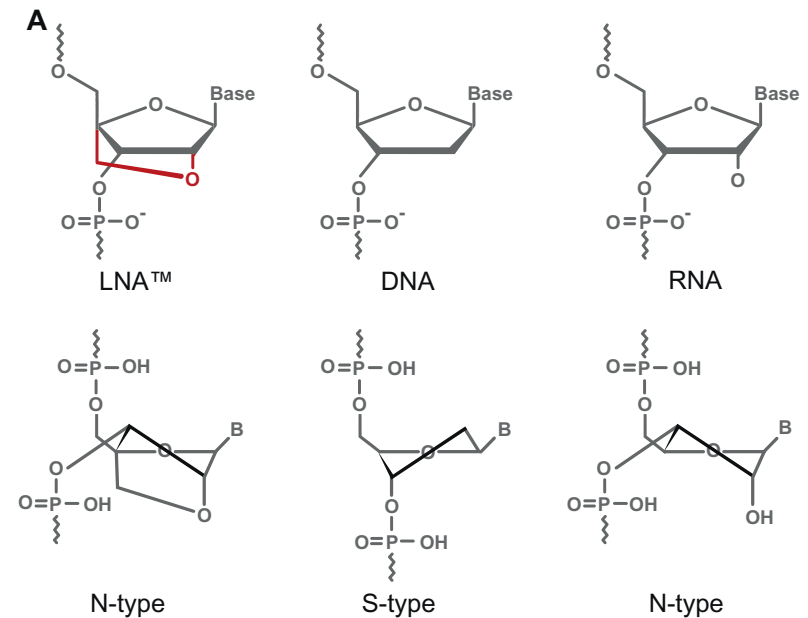
miRCURY LNA™ microRNA ISH  
Exiqon

Methods 52 (2010) 375–381



# Why LNA?

1. High affinity RNA
2. Ribose ring is “locked” in the ideal conformation for Watson–Crick binding.
3. As a result, LNA™ oligonucleotides exhibit thermal stability when hybridized to a complementary DNA or RNA strand.
4. For each incorporated LNA monomer, the melting temperature ( $T_m$ ) of the duplex increases by 2° C–8° C (Figure A-2).
5. LNA oligonucleotides can be made shorter



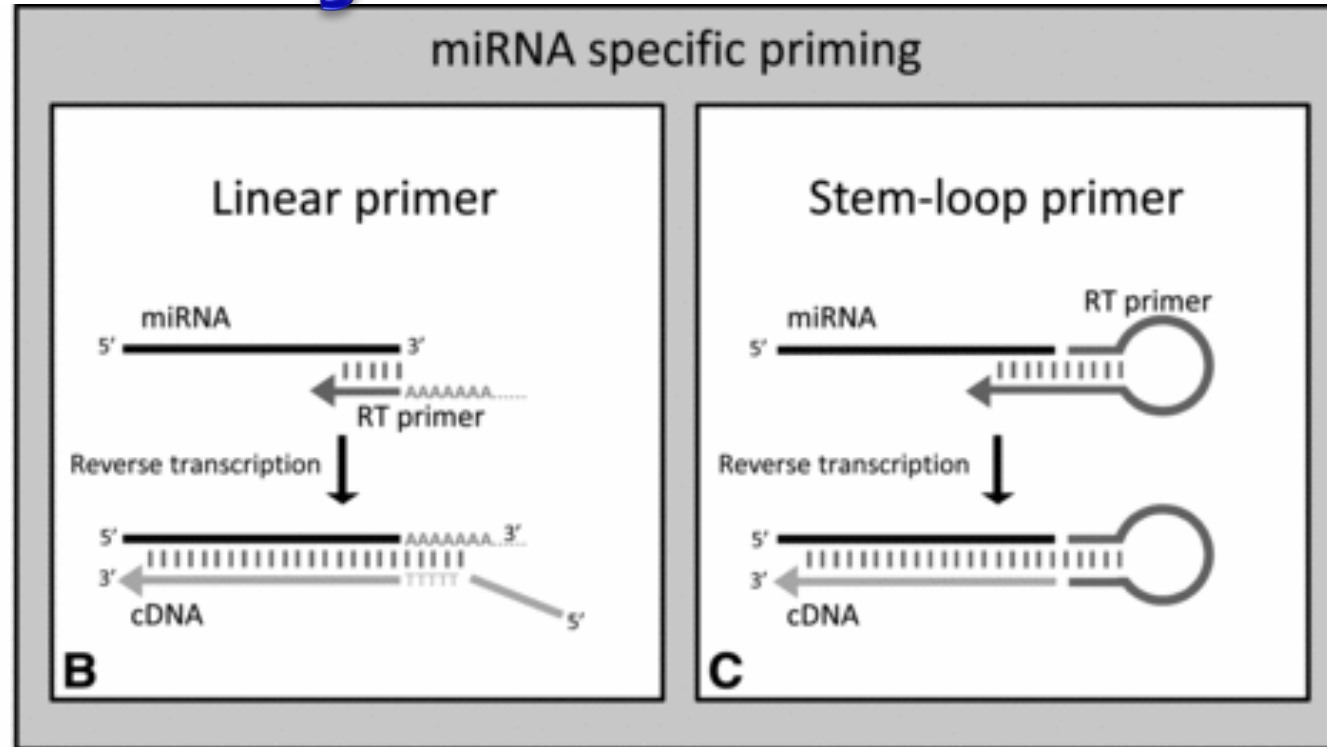
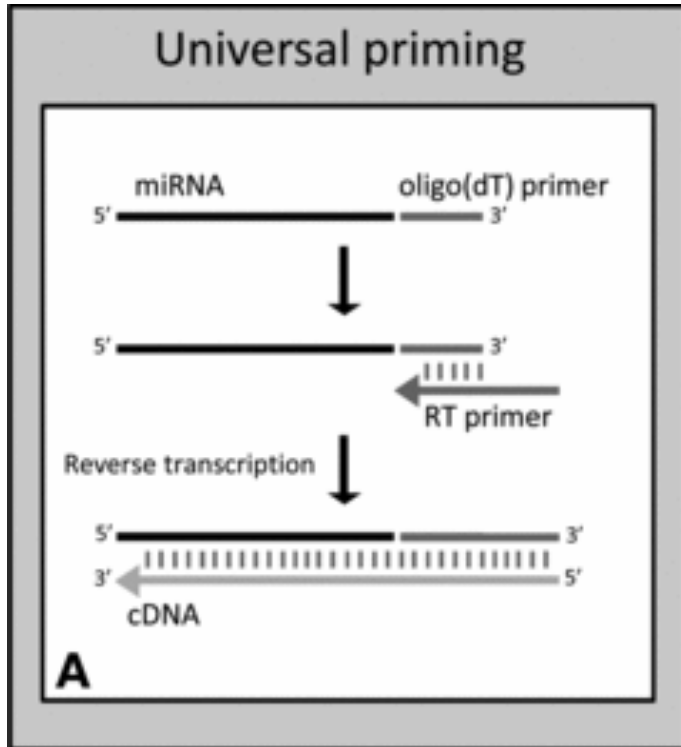
**B**

Probe \ Target	Perfect match 3'-acgaccac-5'	Single mismatch 3'-acg <sup>g</sup> ccac-5'	$\Delta T_m$
DNA 8-mer 5'-tgctggtg-3'	$T_m = 35^\circ \text{C}$	$T_m = 25^\circ \text{C}$	10° C
LNA™ 8-mer 5'-TGCTGGTG-3'	$T_m = 71^\circ \text{C}$	$T_m = 45^\circ \text{C}$	26° C

**Figure A-1** Structure and conformations of nucleotides (A) and the effect of LNA™ on melting temperature of duplexes (B).

From: G.J. Nuovo (Eds) *In Situ Molecular Pathology and Co-expression analyses* (2013)

# Variability of RT for miRNA analysis



Journal of Cellular and Molecular Medicine

Volume 16, Issue 4, pages 683-690, 16 APR 2012 DOI: 10.1111/j.1582-4934.2011.01467.x

<http://onlinelibrary.wiley.com/doi/10.1111/j.1582-4934.2011.01467.x/full#f2>

# PCR based miRNA assays

## miRCURY LNA™ Universal RT microRNA PCR

**1** One single cDNA reaction for all microRNAs

First-strand synthesis (RT)

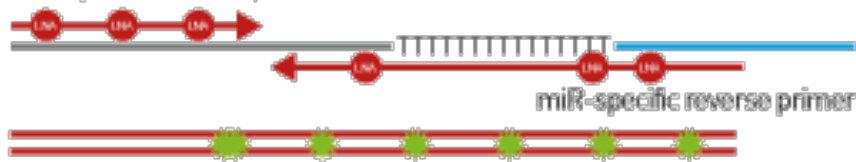
Mature microRNA



**2** Two LNA™-enhanced microRNA-specific qPCR primers

Real-time PCR amplification

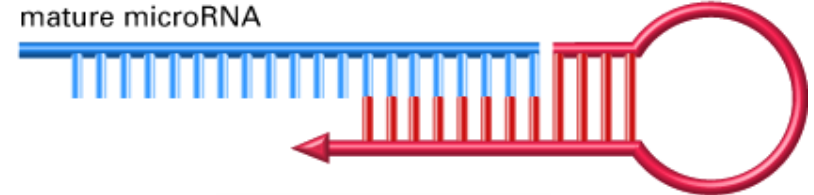
miR-specific forward primer



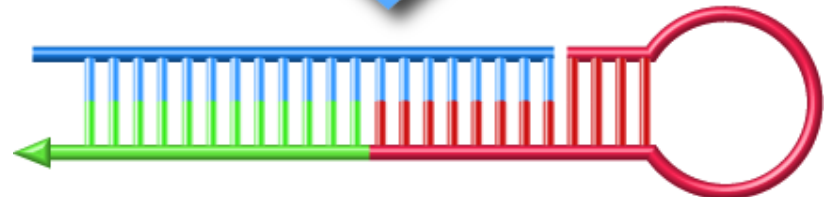
- – LNA™ primers are shorter, so both primers can be specific to the microRNA, enabling single nucleotide discrimination
- **Unrivalled sensitivity** –  $T_m$  normalized LNA™ primers for accurate detection even of AT-rich microRNA from just 1 pg total RNA

## TaqMan Assay

looped RT primer

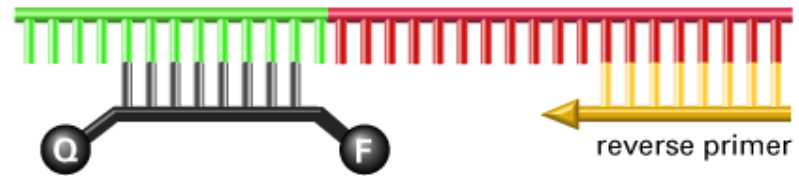
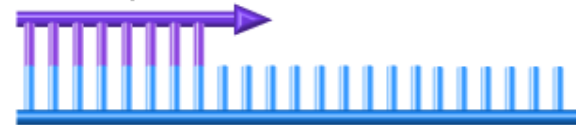


Step 1:  
Stem-loop  
RT



Step 2:  
Real-time  
PCR

forward primer



TaqMan® probe