Analýza exprese microRNA

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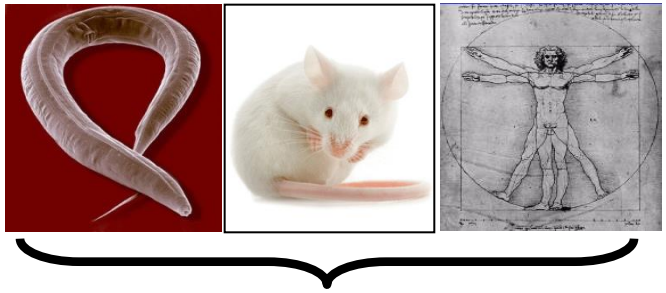
- Nic si nepište…vše bude online

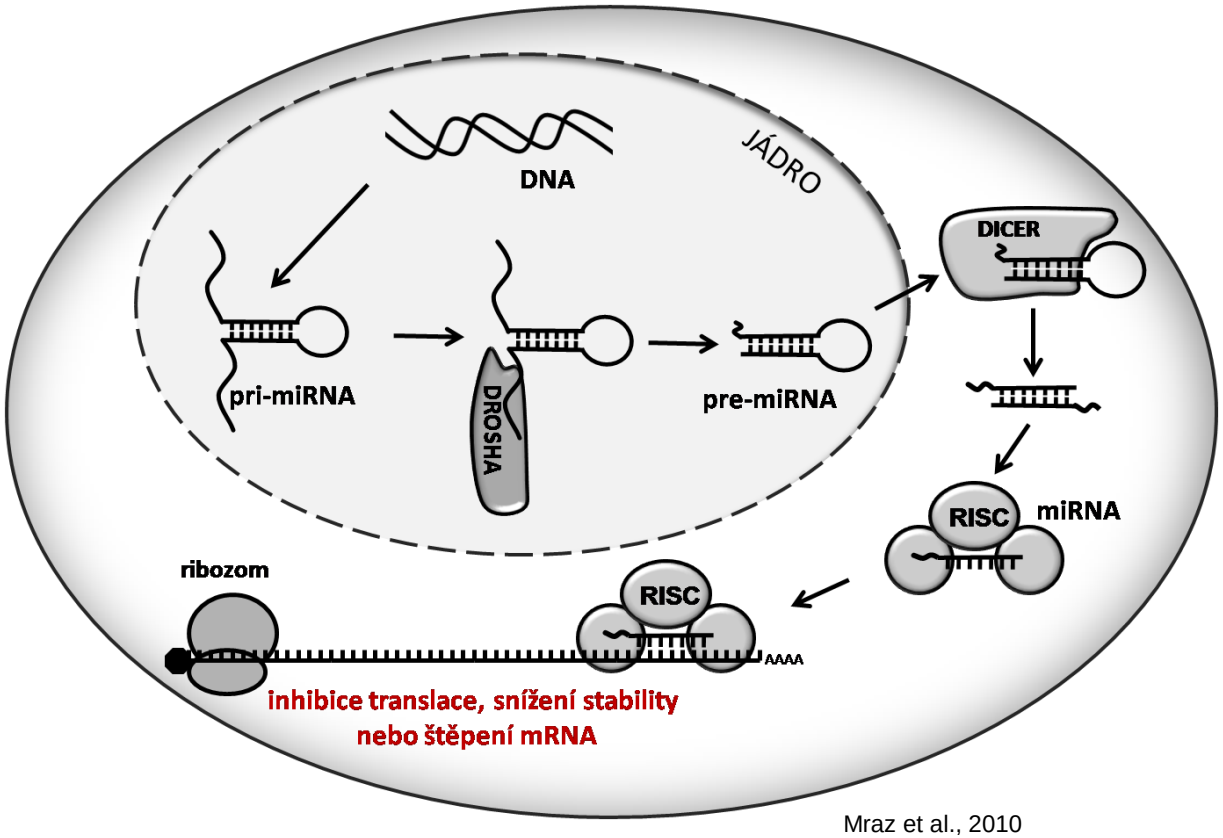
- **Lidské miRNA geny: cca 2000**

microRNA (miRNA)

- krátké RNA molekuly
  ~22 nukleotidů
- komplementární vazba k cílové mRNA
- inhibují translaci a snižují stabilitu mRNA



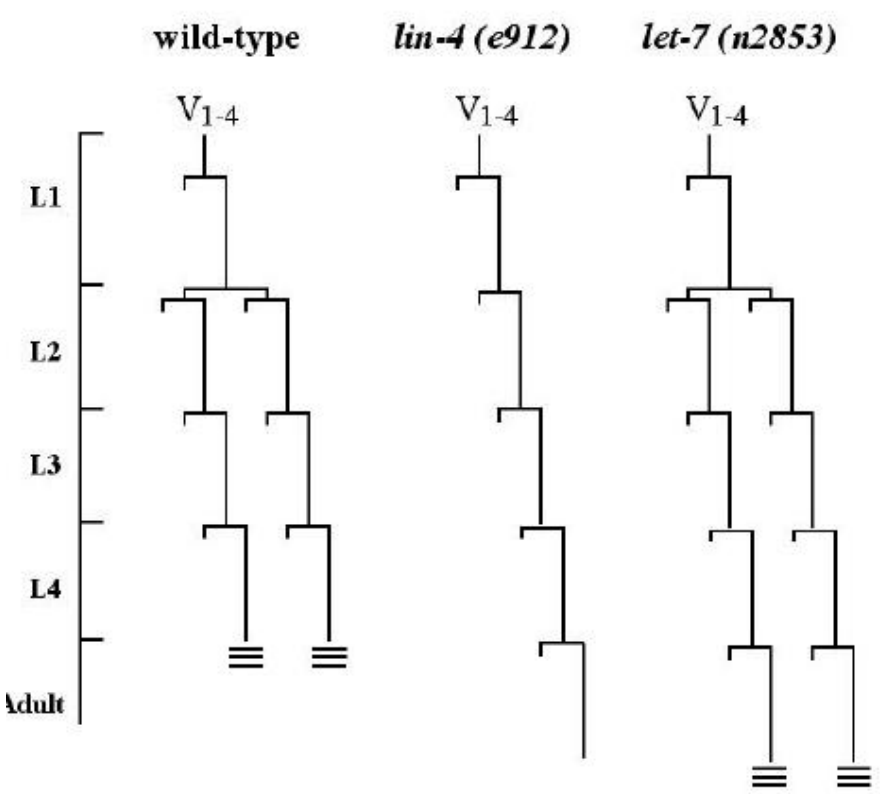
Stovky evolučně konzervovaných microRNA

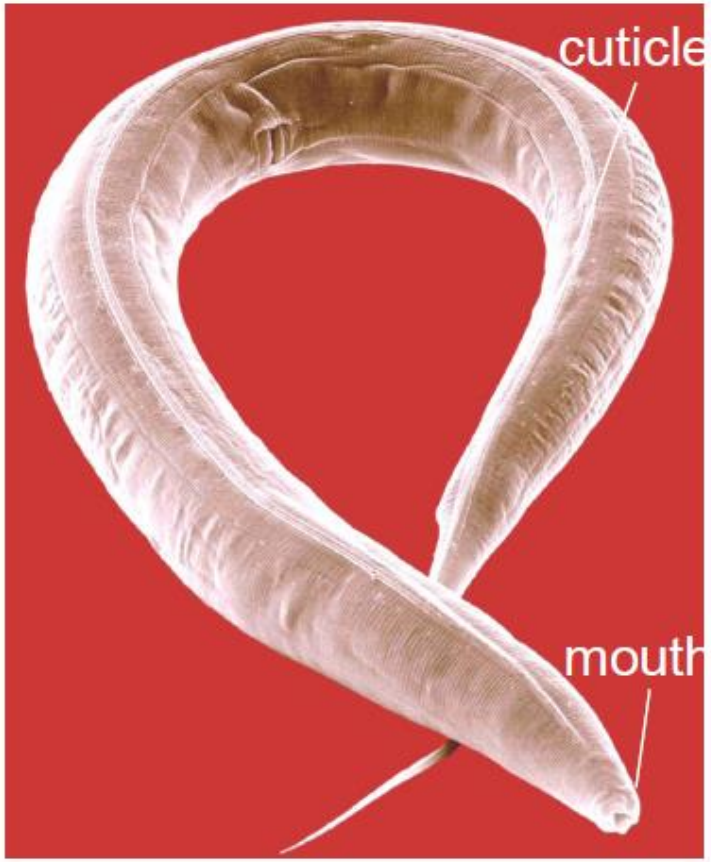


DNA
⇩
mRNA
⇩ ⊣ microRNA
PROTEIN

Mraz et al., 2010

MicroRNAs were discovered by V. Ambros and G. Ruvkun in *C. elegans*

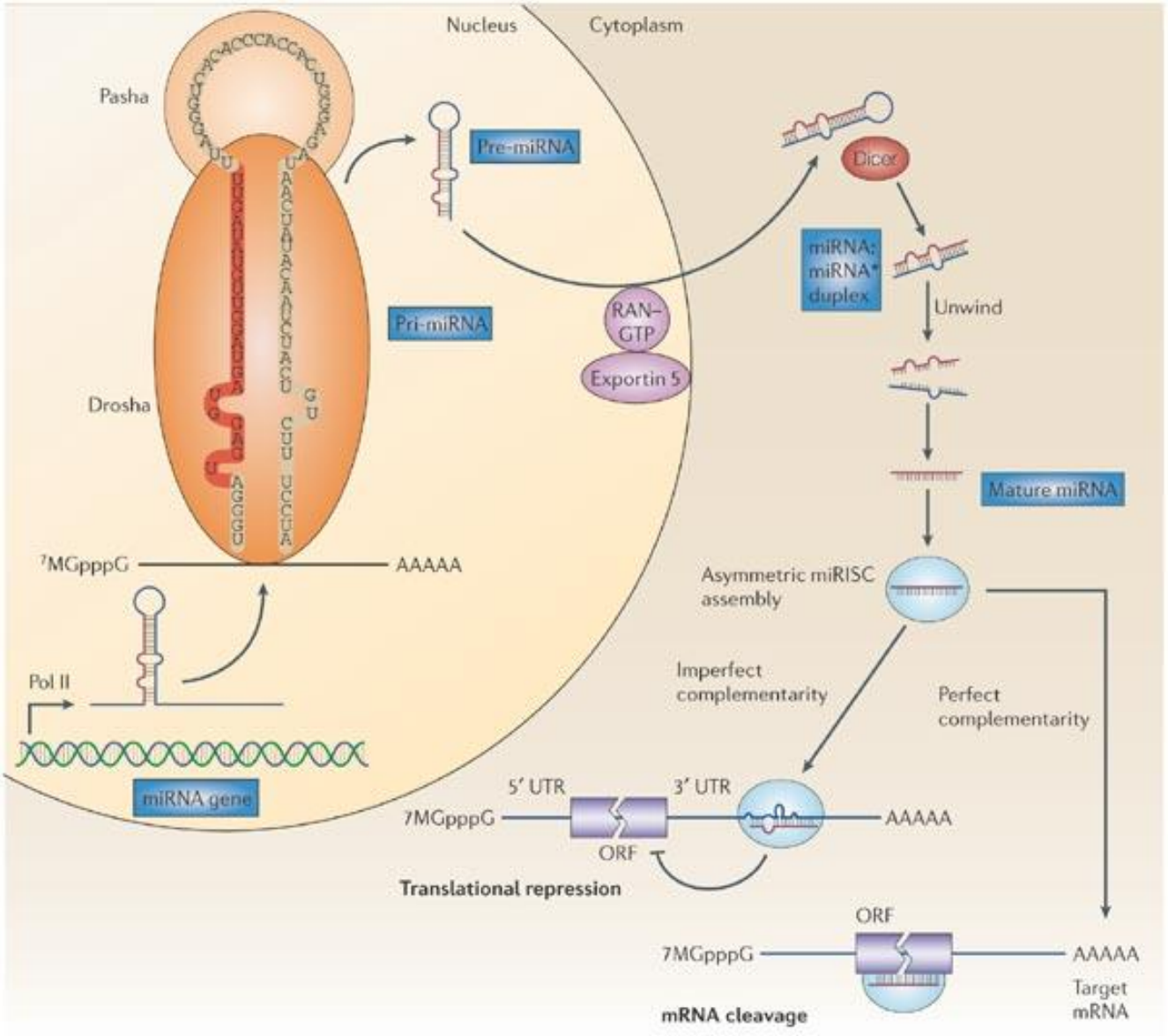




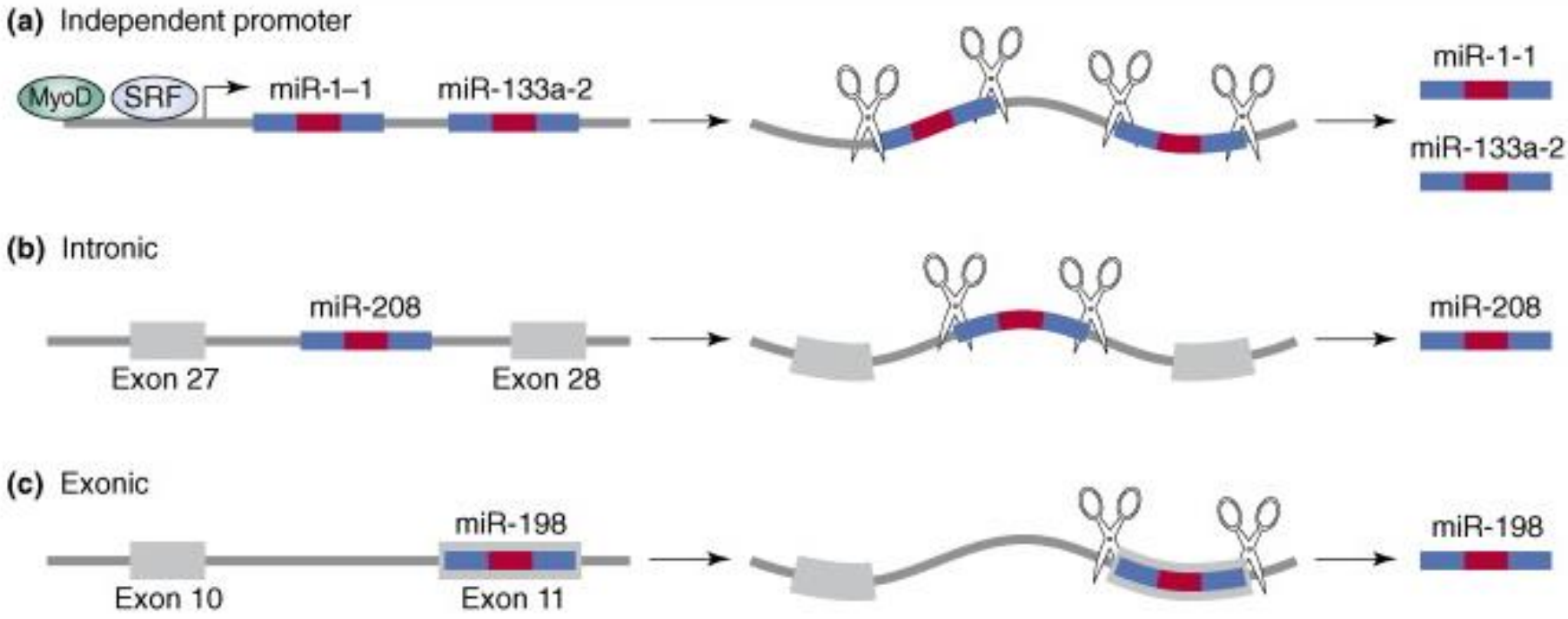
Lee et al. 1993 *Cell*

Reinhart et al. 2000 *Nature*

courtesy of F. Slack



Genomic Organization of miRNA Genes



- Intronic miRNAs often in antisense direction, made from own promoter
- Exonic miRNAs - non-coding (or in alternatively spliced exons)

Zhao Y, Srivastava D, TIBS 32:189,2007

miRBase

http://www.mirbase.org/

miRBase

MANCHESTER 1824

Home | Search | Browse | Genomics | Help | Download | Submit

Search

miRBase has moved to http://www.mirbase.org/ - please update your links.

News - release 14

The miRBase database has moved to a new location at http://www.mirbase.org/, hosted in the Faculty of Life Sciences, University of Manchester. All pre-existing URLs should forward to their new locations. Please update your links, and note the new contact email address (mirbase@manchester.ac.uk).

With release 14, the miRBase sequence database has broken through the 10000 entries barrier!

miRNA count: 10883 entries

Release 14: Sept 2009

Search by miRNA name or keyword

Go | Example

Download published miRNA data

Download page | FTP site

This site is featured in:

NetWatch - *Science* 303:1741 (2004)

Highlights, Web watch - *Nature Reviews Genetics* 5:244 (2004)

miRBase: the microRNA database

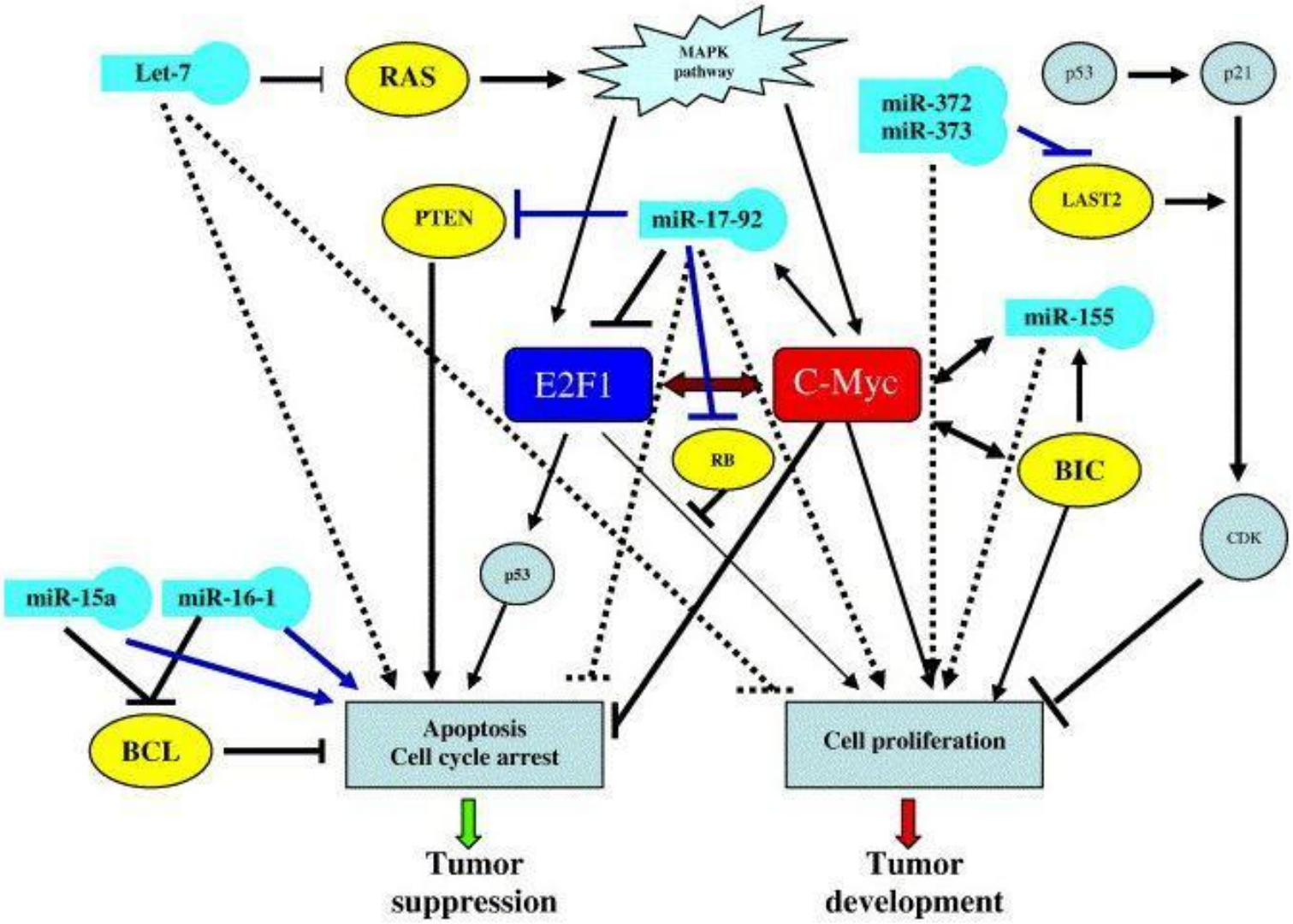
miRBase provides the following services:

- The miRBase database is a searchable database of published miRNA sequences and annotation. Each entry in the miRBase Sequence database represents a predicted hairpin portion of a miRNA transcript (termed mir in the database), with information on the location and sequence of the mature miRNA sequence (termed miR). Both hairpin and mature sequences are available for searching and browsing, and entries can also be retrieved by name, keyword, references and annotation. All sequence and annotation data are also available for download.
- The miRBase Registry provides miRNA gene hunters with unique names for novel miRNA genes prior to publication of results. Visit the help pages for more information about the naming service.
- The miRBase Targets database and pipeline has been rebranded as microCosm, and is now hosted at the EBI. The microCosm resource continues to be maintained by the Enright group. miRBase currently links miRNAs to targets predicted by microCosm, TargetScan and Pictar, and aims to provide a more extensive target prediction aggregation service in the future.

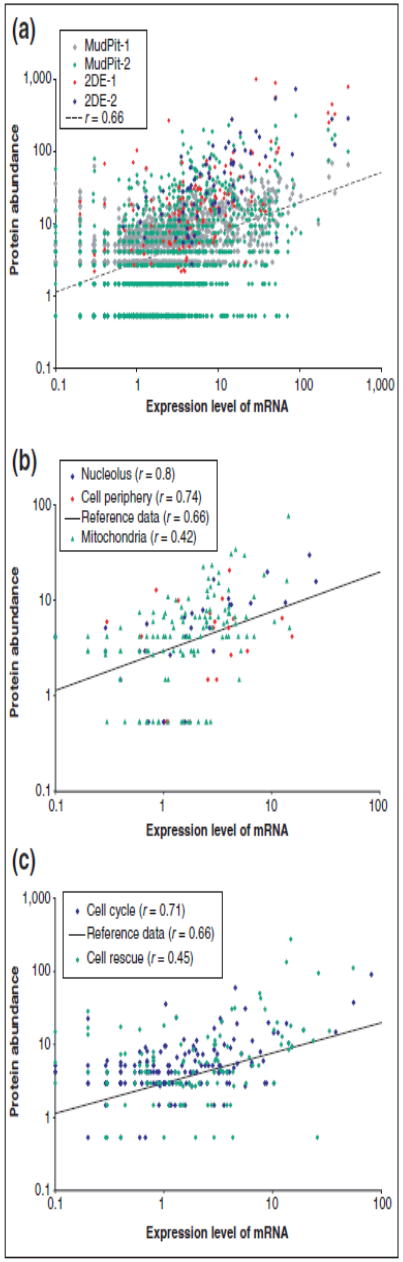
To receive email notification of data updates and feature changes please subscribe to the miRBase announcements mailing list. Any queries about the website or naming service should be directed at mirbase@manchester.ac.uk.

miRBase is hosted and maintained in the Faculty of Life Sciences at the University of Manchester with funding from the BBSRC, and was previously hosted and supported by the Wellcome Trust Sanger Institute.

miRNAs as Oncogenes and Tumor Supressors



Zhang et al Dev Biol. 2007 Feb 1;302(1):1-12



mRNA neznamená, že v buňce bude i protein

Historicky vždy velká neshoda mezi daty z expresních čipů a expresí proteinů (Western Blot)

DNA

⇩

mRNA

⇩ ⊢ **microRNA**

PROTEIN

Specifika analýzy exprese microRNAs:

- velmi malé molekuly – 22nt – specifikum izolace, specifické značení i design sond
- malé zastoupení ve vzorku – separace microRNA
- v lidském genovu cca 2000 genů
- některé mají velmi podobnou sekvenci – rozdíl 1nt
- pre-miR, pri-miR, mature-miR
- málo se ví o jejich funkcích – obtížná interpretace výsledků
- zatím málo zkušeností a standardizace

- ❑Izolace
- ❑NGS
- ❑Real-Time PCR
- ❑Microarrays

1/ Izolace a stabilita microRNA

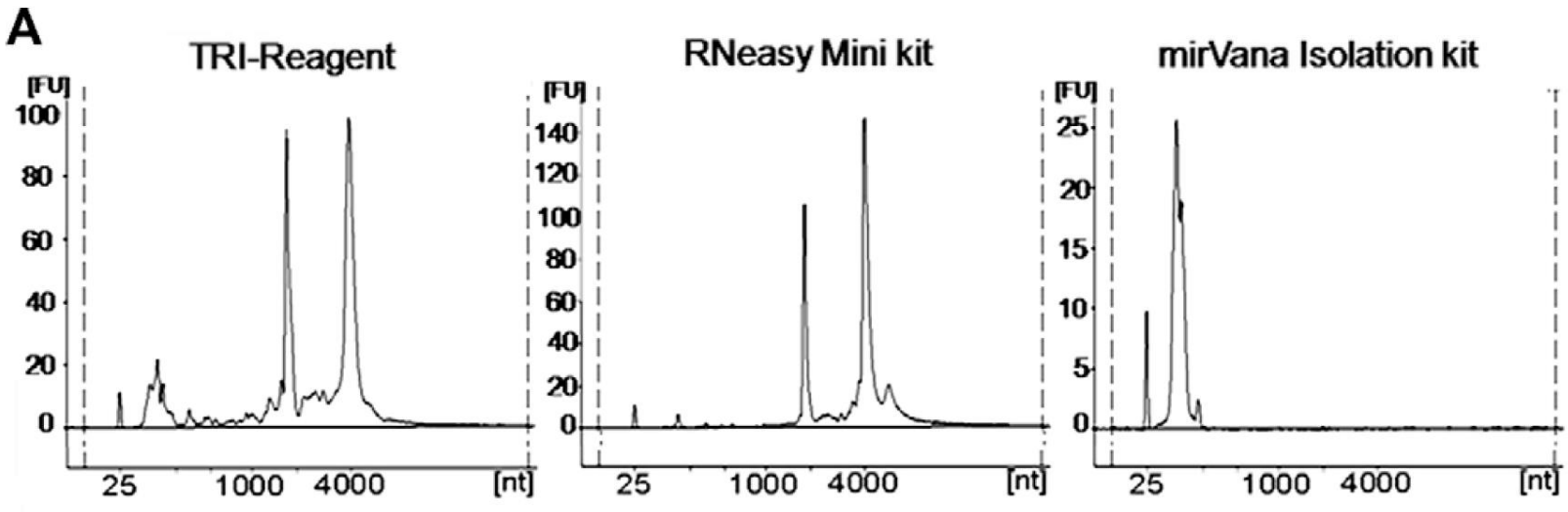
Problémy: velikost 22nt, celkově cca 0,01% z celkové RNA

Izolace:

TRIzol/TriReagent
miRvana (Ambion)
PureLink (Invitrogen)
a další

Obohacení:

PAGE
FlashPAGE Fractionator (Ambion)



Mraz et al., 2009

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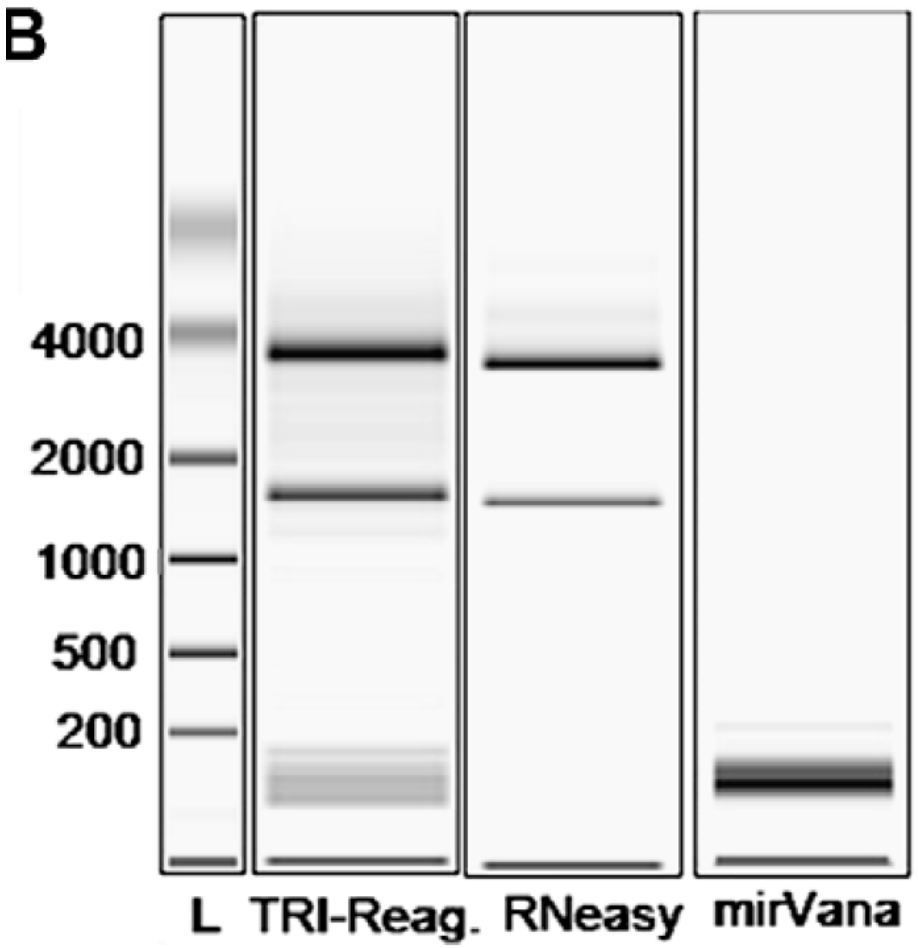
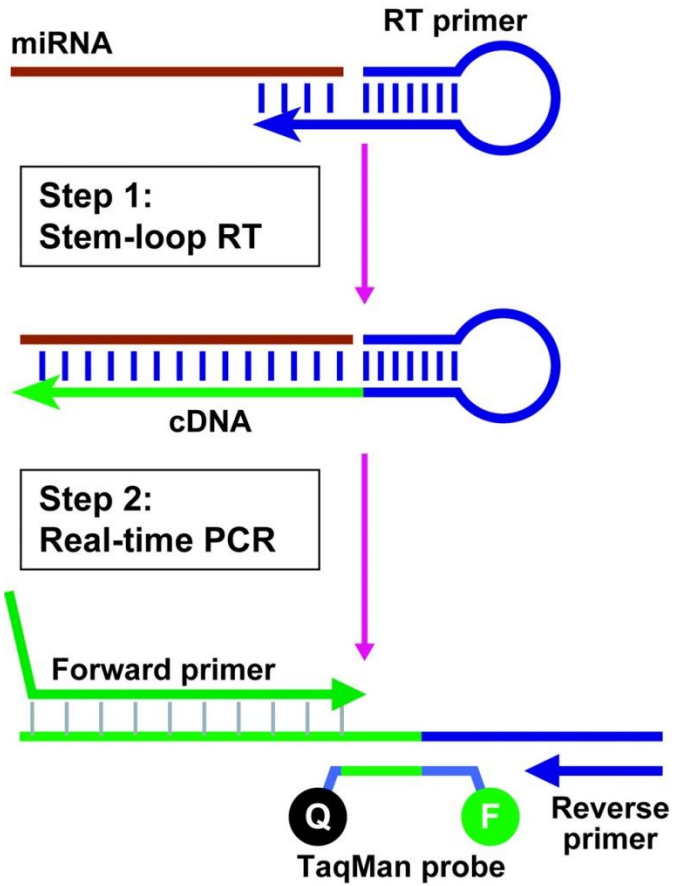


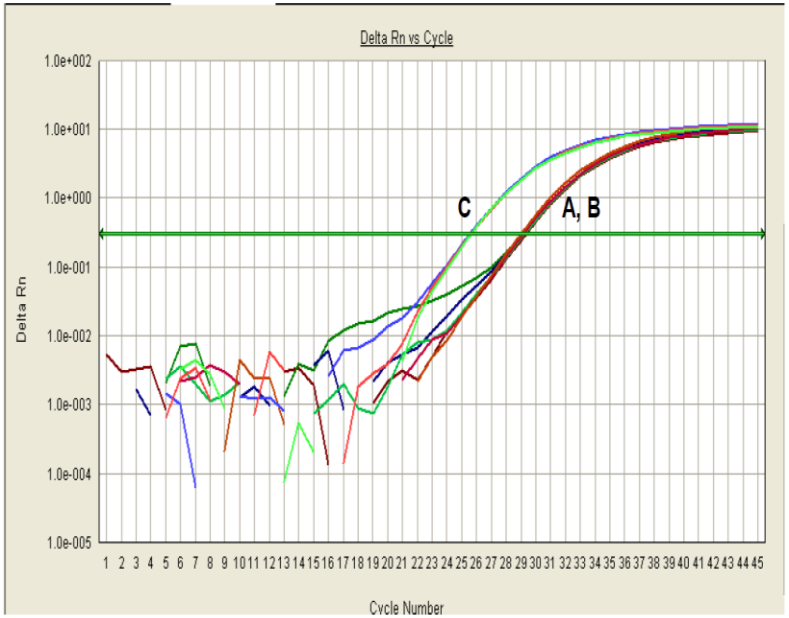
Mraz et al., 2009

RT-PCR

Problems….?

TaqMan-based real-time PCR quantification of mature miRNAs

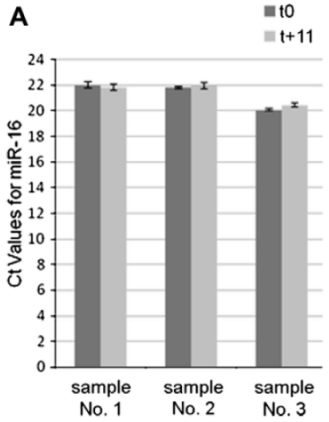




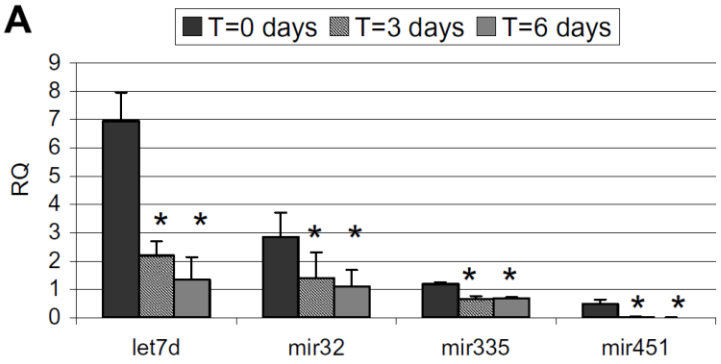
Stabilita microRNA :

Stabilita po izolaci

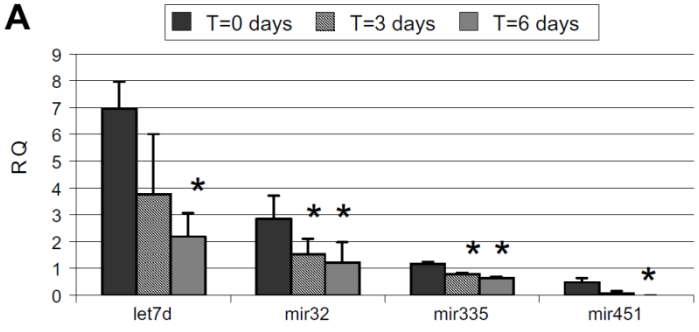
Stabilita v FFPE (formalin-fixed parafin-embedded tissue)



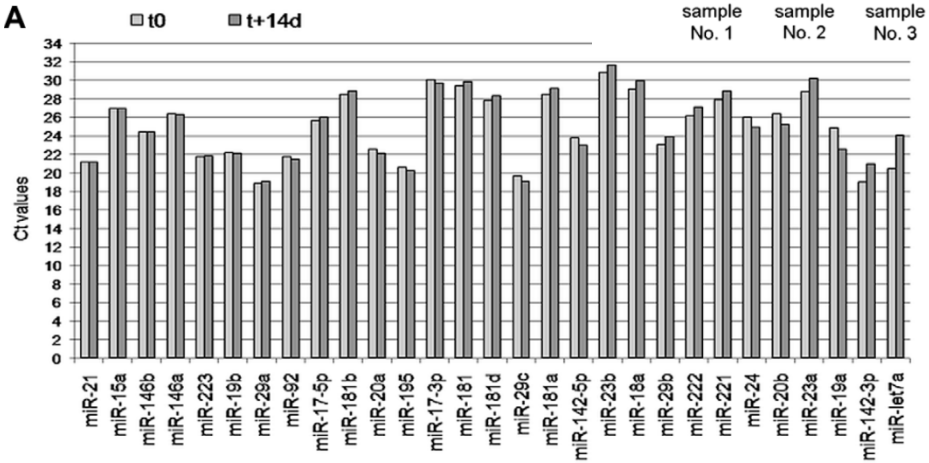
RNA

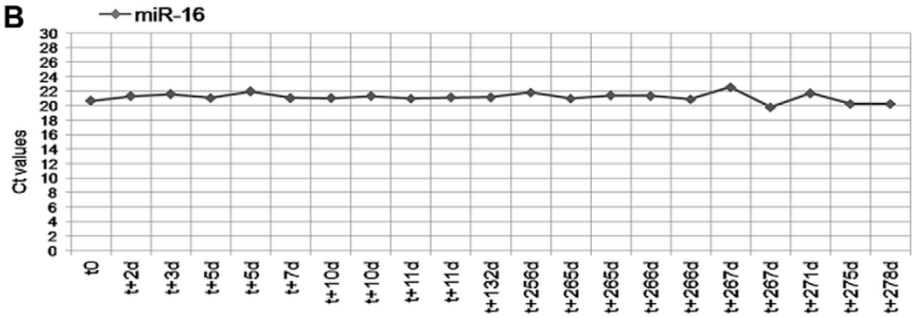


cDNA



Bravo et al., 2007

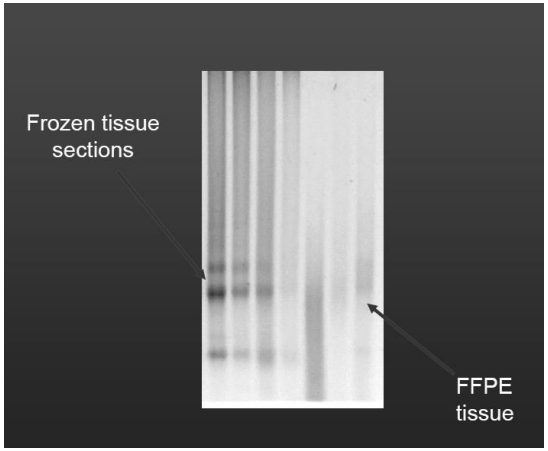


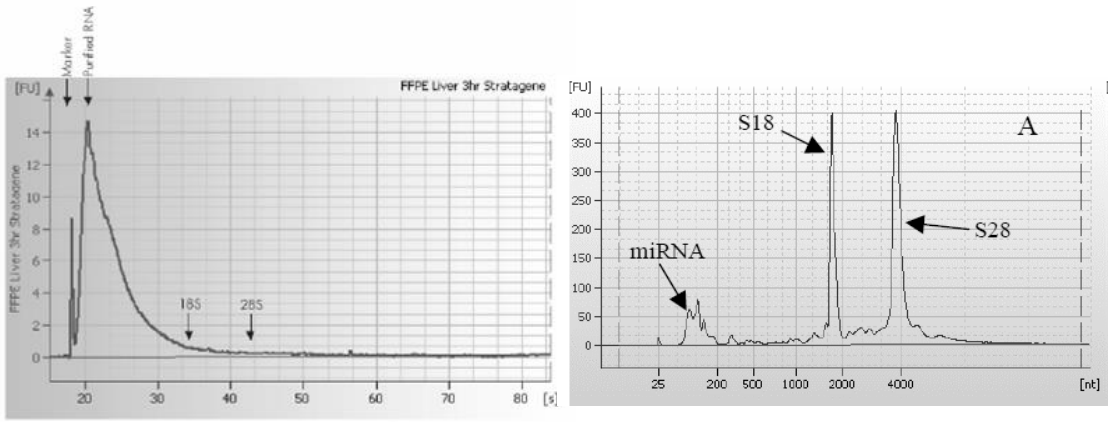


Mraz et al., 2009

Stabilita microRNA :

Stabilita v FFPE (formalin-fixed parafin-embedded tissue)





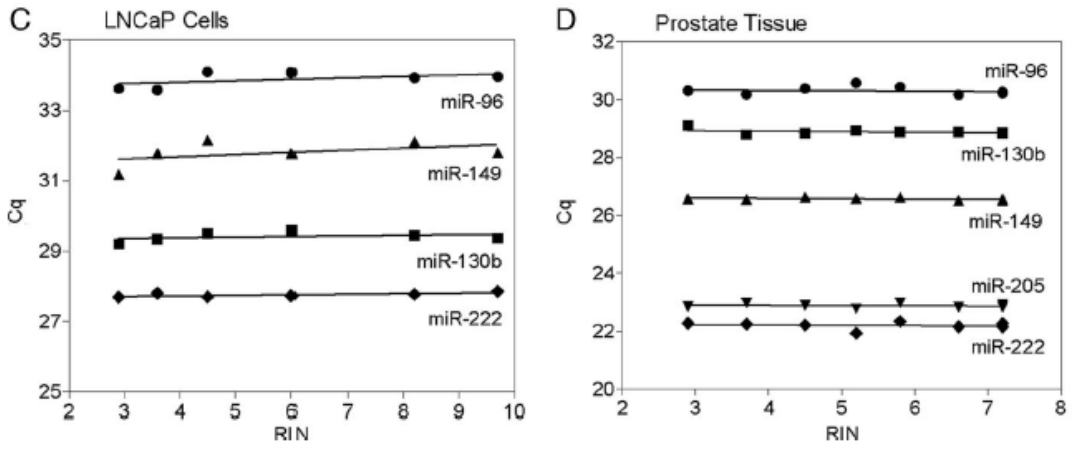


Fig. 2. Influence of RNA integrity on miRNA gene expression.

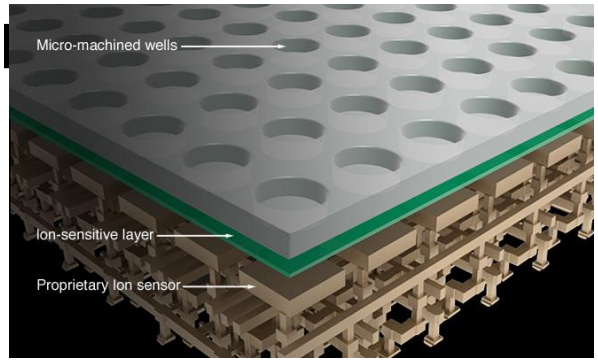
(A), miR-141, miR-155, miR-200c, and miR-210 in RNA samples from ccRCC cell line Caki-2. (B), miR-141, miR-155, miR-200c, and miR-210 in RNA samples from the renal tissue pool. (C), miR-96, miR-130b, miR-149, and miR-222 in RNA samples from PCa cell line LNCaP. (D), miR-96, miR-130b, miR-149, miR-205, and miR-222 in RNA samples from the prostate tissue pool. For further details, including regression line characteristics, 95% CIs of the slopes, and *P* values indicating significant deviations from 0, see Table 5 in the online Data Supplement.

Jung et al., 2010

RNA Seq

Next Generation Sequencing

- Takes advantage of miniaturization to engage in massively parallel analysis
  - Essentially carrying out millions of sequencing reactions simultaneously in each of 10 million tiny wells
- Sophisticated computer analysis of huge amounts of information allows “assembly" of a given sequen



Massive Parallel Seq workflow

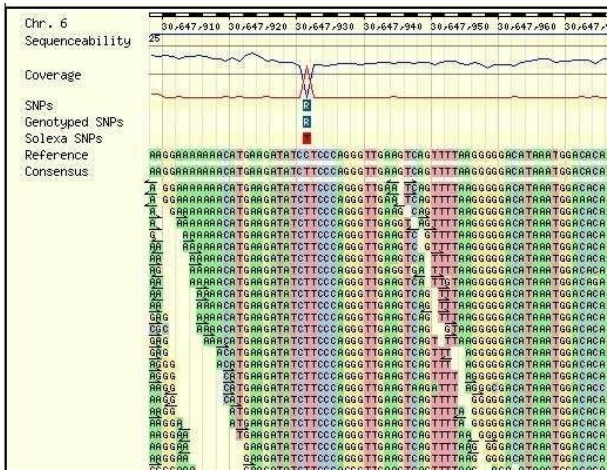
A SAMPLE

1) **Library preparation**

2) **Cluster generation on a flow cell**

3) **Sequencing & imaging**

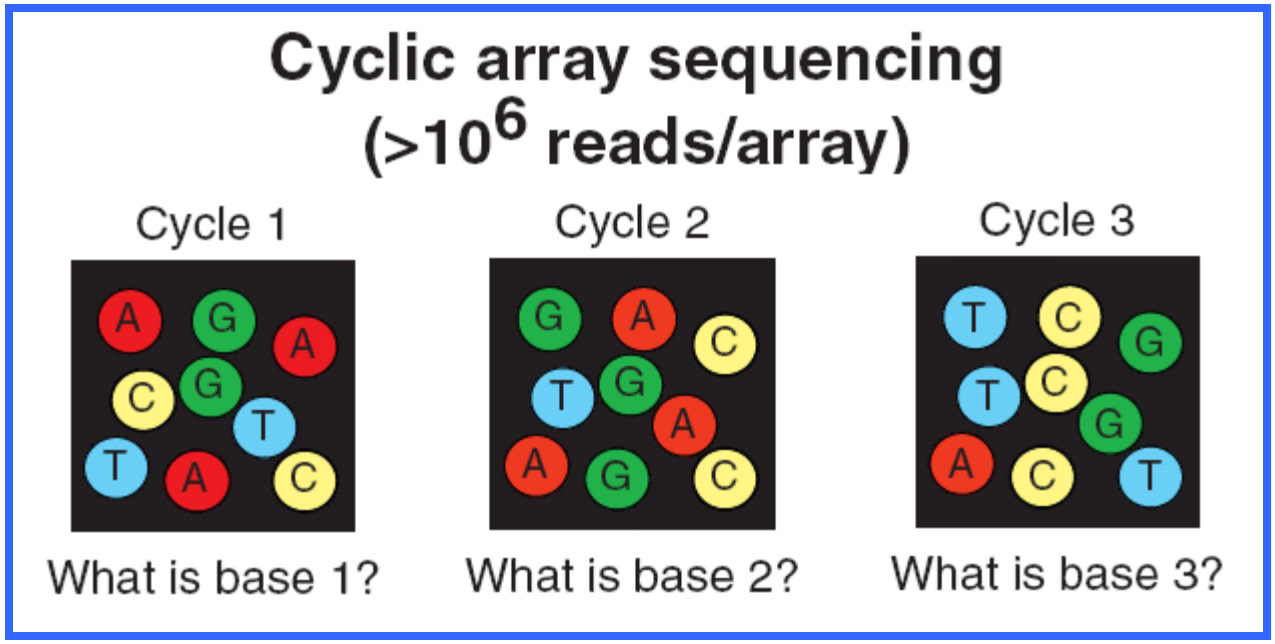
SE, PE reads, 50-250 bases (miseq)



4) **Data processing & analysis**

High Parallelism is Achieved in Polony Sequencing

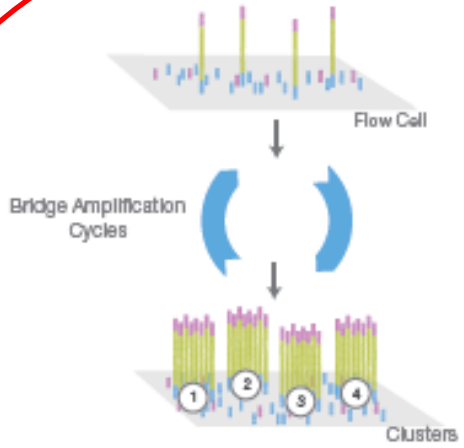
Sanger **Polony**



A. Library Preparation

NGS library is prepared by fragmenting a gDNA sample and ligating specialized adapters to both fragment ends.

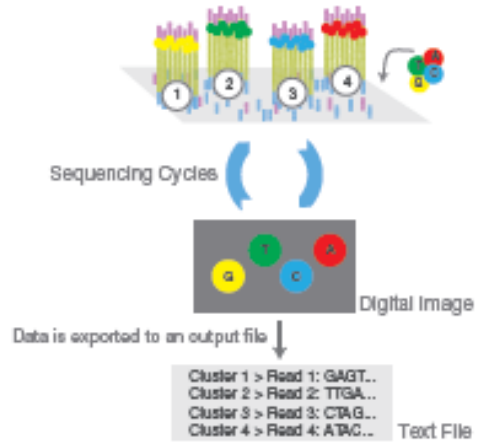
A. Cluster Amplification



Library is loaded into a flow cell and the fragments hybridize to the flow cell surface. Each bound fragment is amplified into a clonal cluster through bridge amplification.

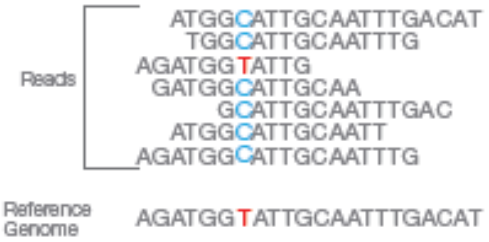
This is the trick

C. Sequencing



Sequencing reagents, including fluorescently labeled nucleotides, are added and the first base is incorporated. The flow cell is imaged and the emission from each cluster is recorded. The emission wavelength and intensity are used to identify the base. This cycle is repeated "n" times to create a read length of "n" bases.

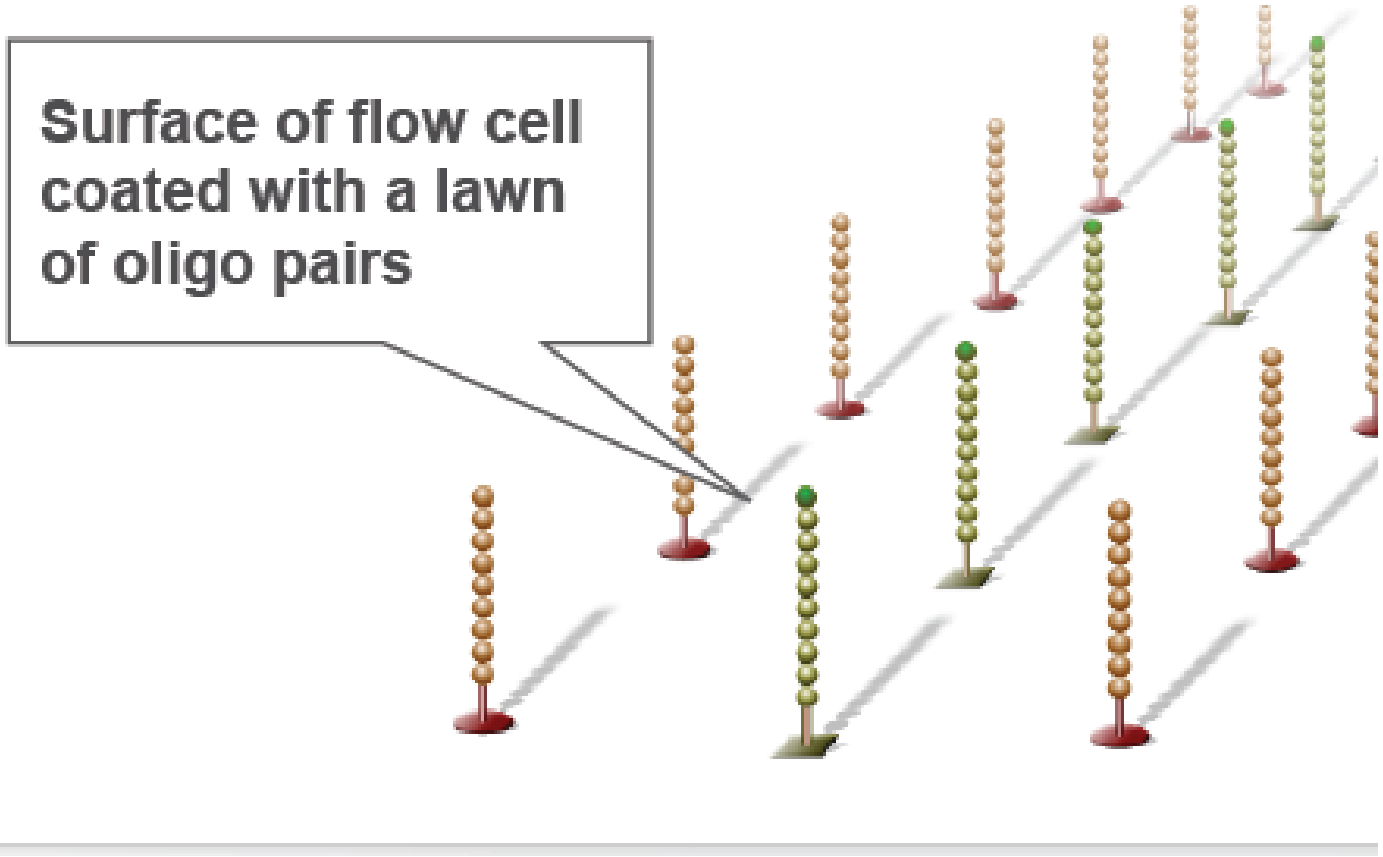
D. Alignment & Data Anaylsis



Reads are aligned to a reference sequence with bioinformatics software. After alignment, differences between the reference genome and the newly sequenced reads can be identified.


E
5'
P5
Index 2
Rd1 SP
DNA Insert
Rd2 SP
Index 1
P7
5'

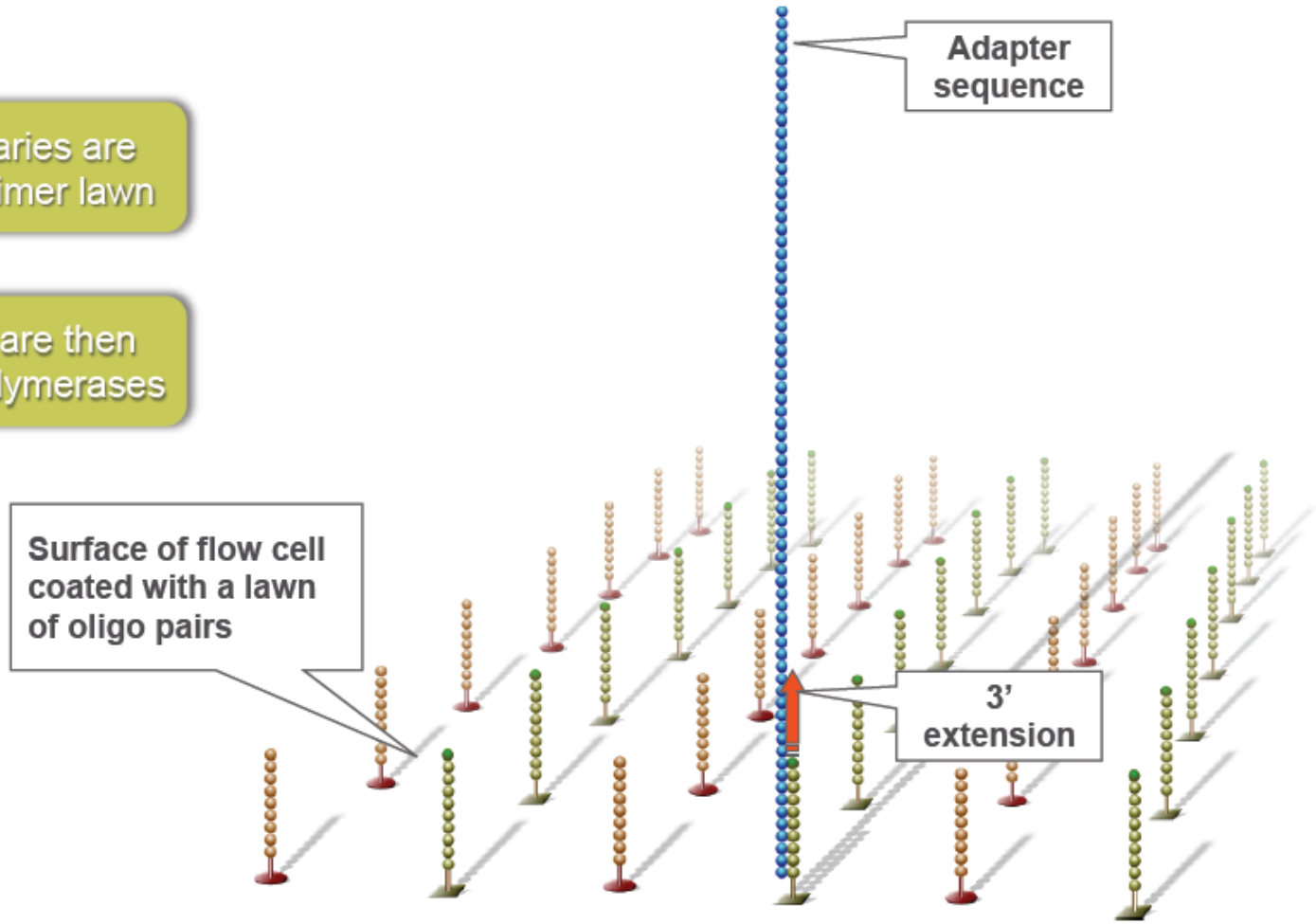
Two PCR primers are attached to the surface of flowcell. One of the primers has a cleavable site



Hybridize Fragment & Extend

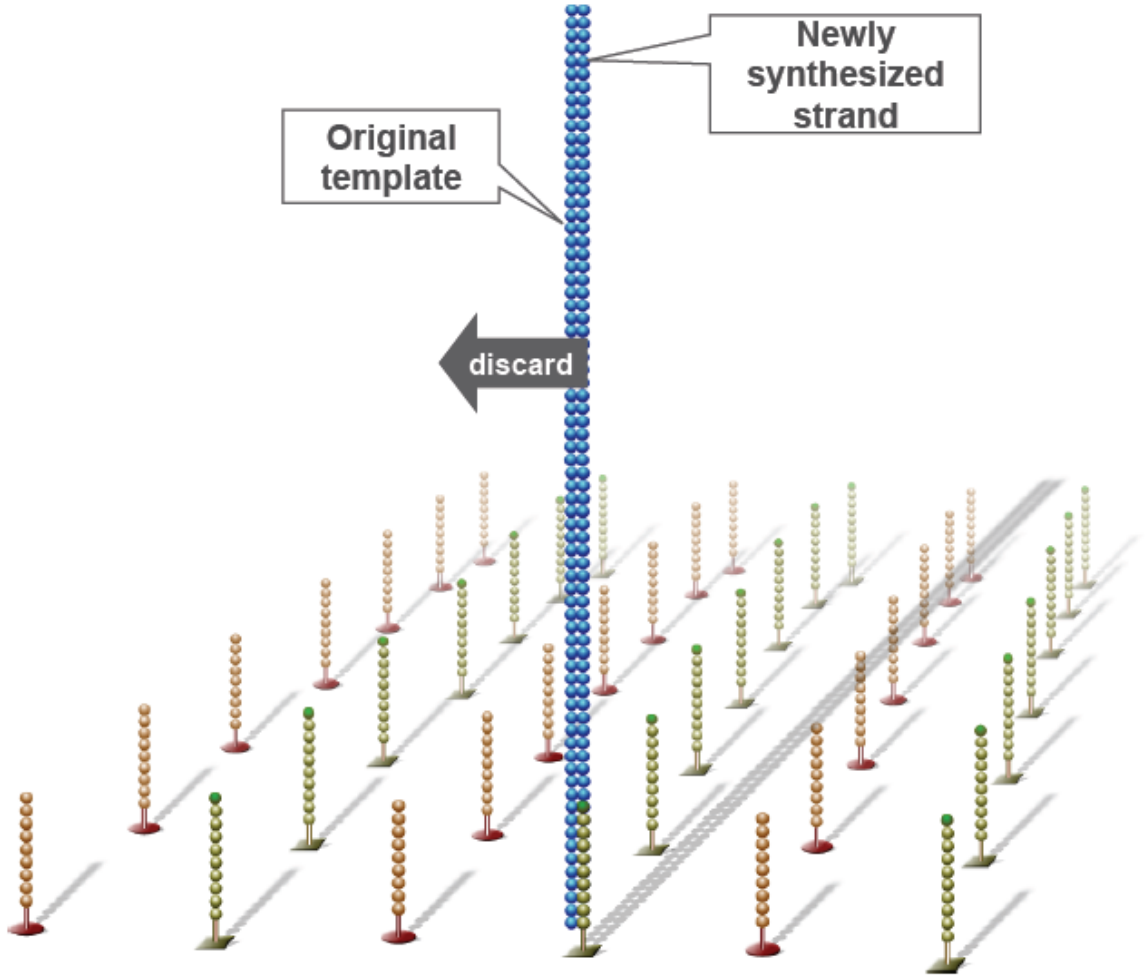
Single DNA libraries are hybridized to primer lawn

Bound libraries are then extended by polymerases

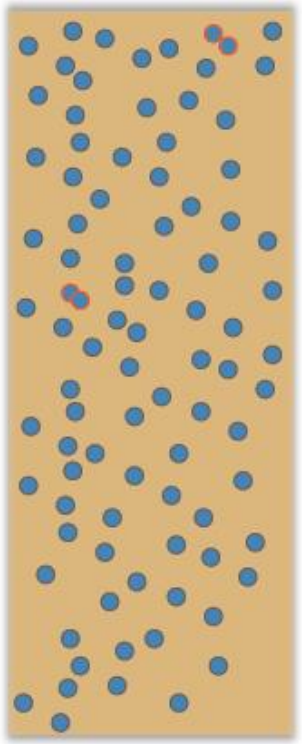


Denature Double-Stranded DNA

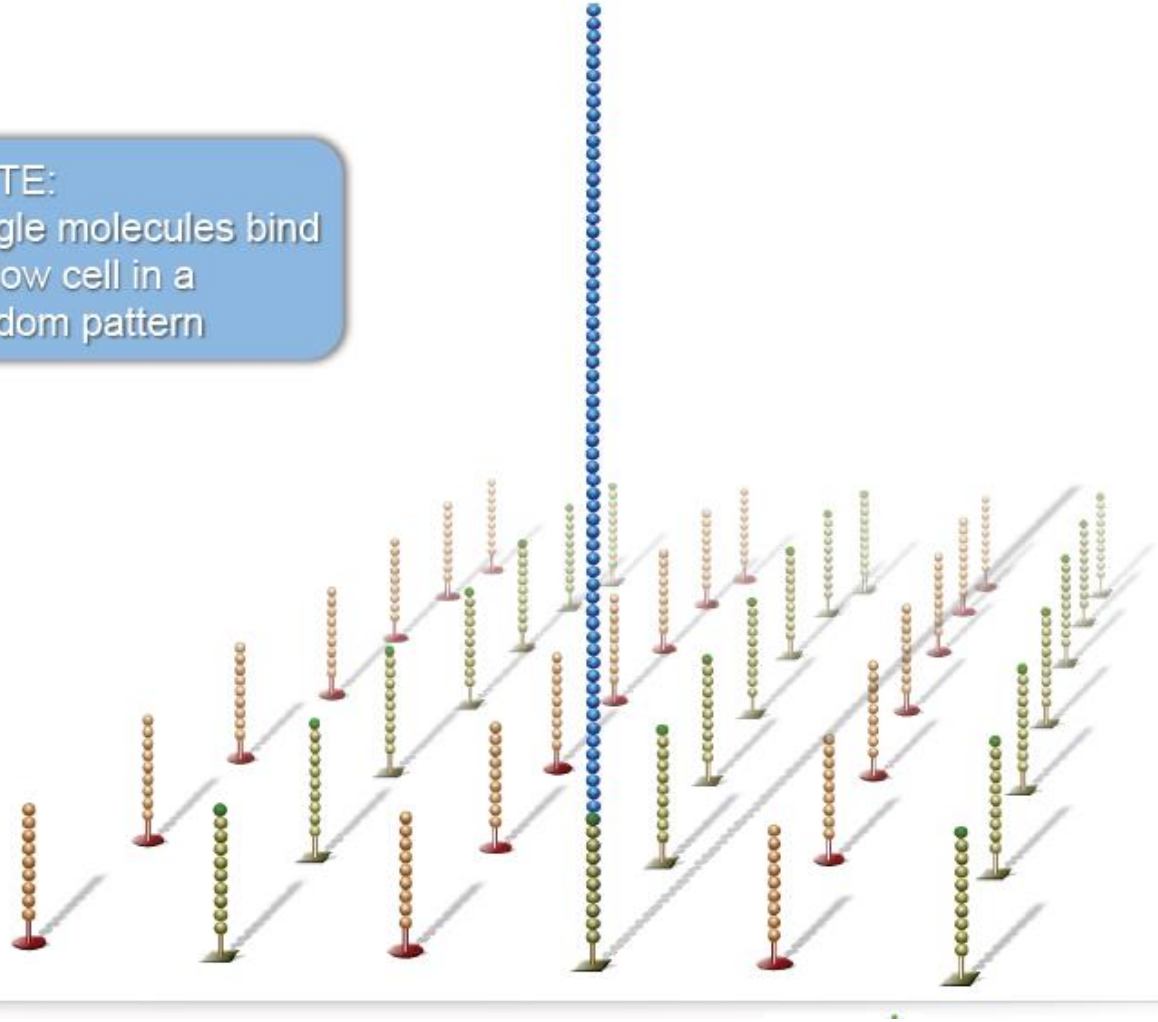
- Double-stranded molecule is denatured
- Original template washed away
- Newly synthesized strand is covalently attached to flow cell surface



Single-Stranded DNA



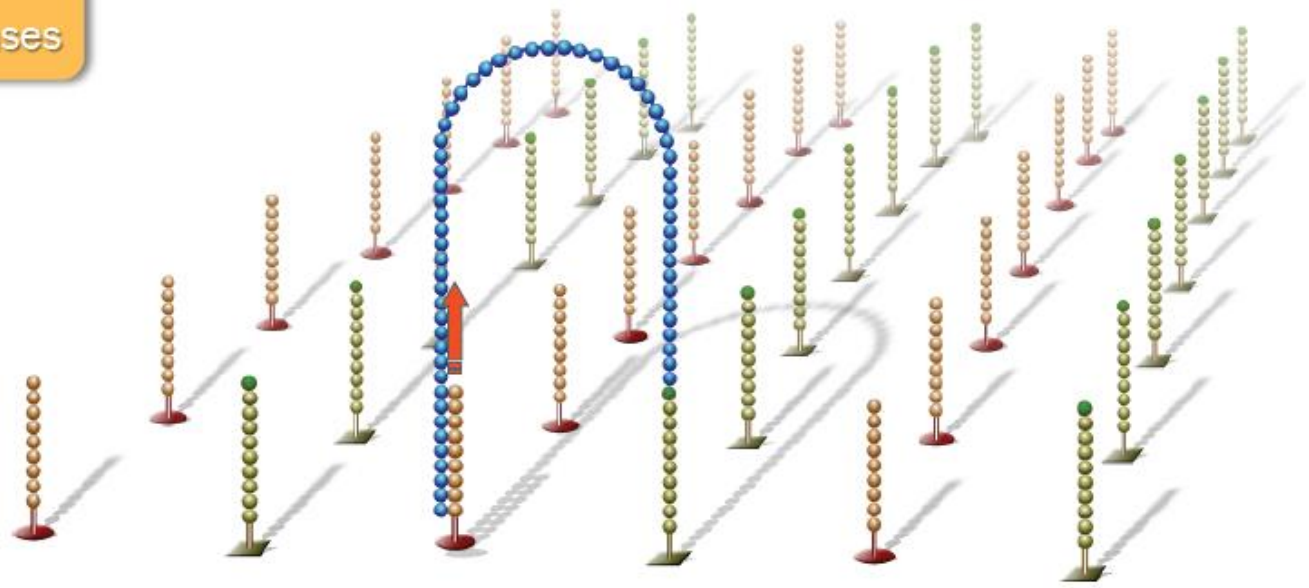
NOTE:
Single molecules bind to flow cell in a random pattern



Bridge Amplification

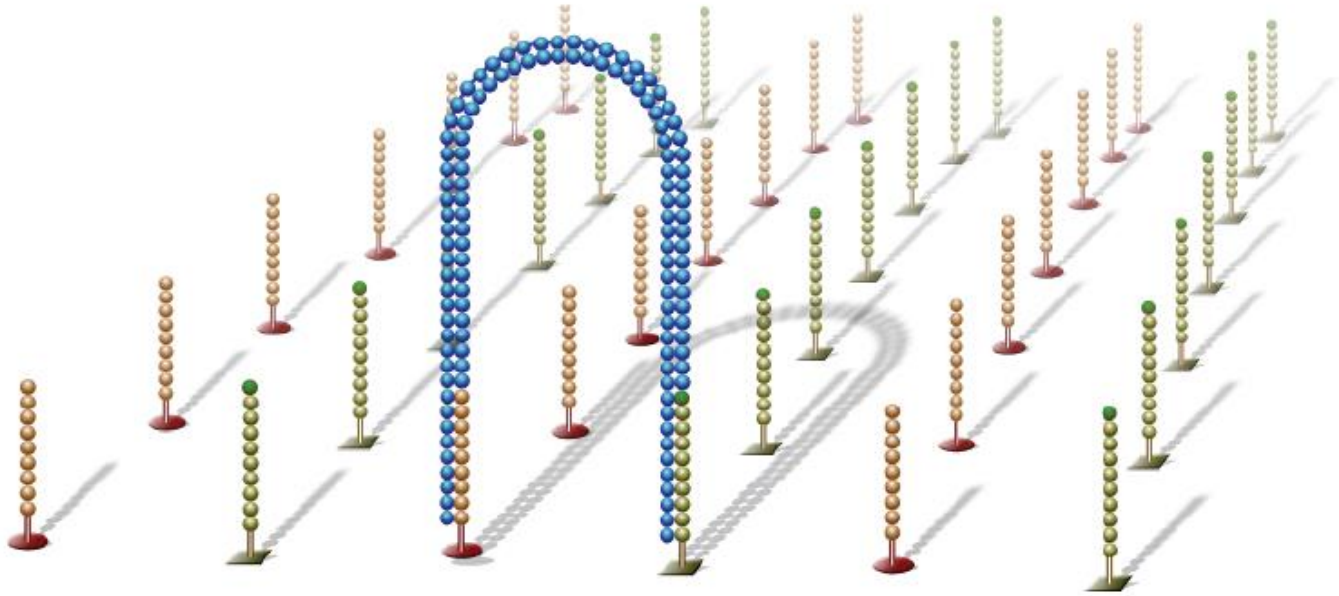
Single-stranded molecule flips over and forms a bridge by hybridizing to adjacent, complementary primer

Hybridized primer is extended by polymerases



Bridge Amplification

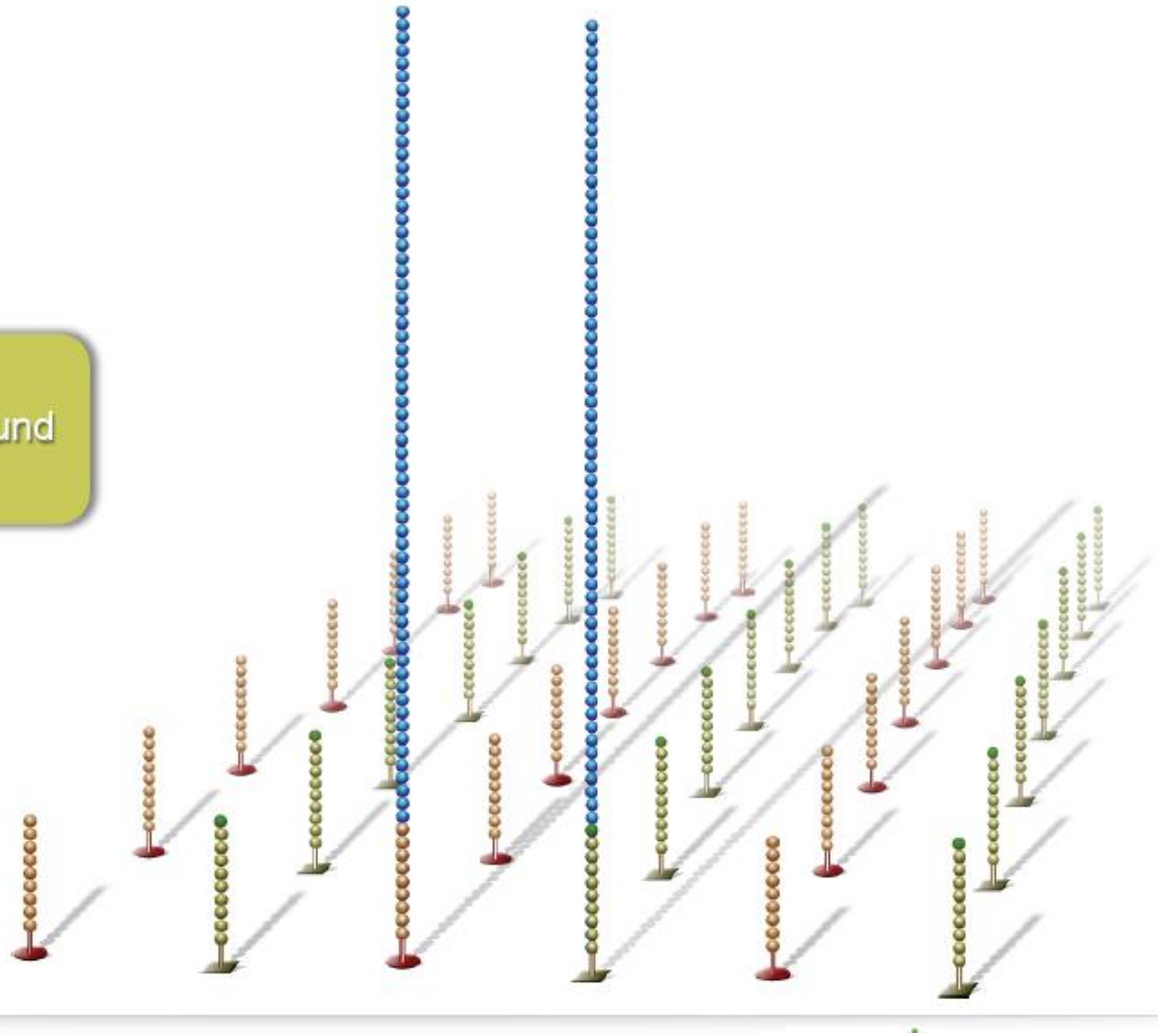
Double-stranded bridge is formed



Denature Double-Stranded Bridge

Double-stranded bridge is denatured

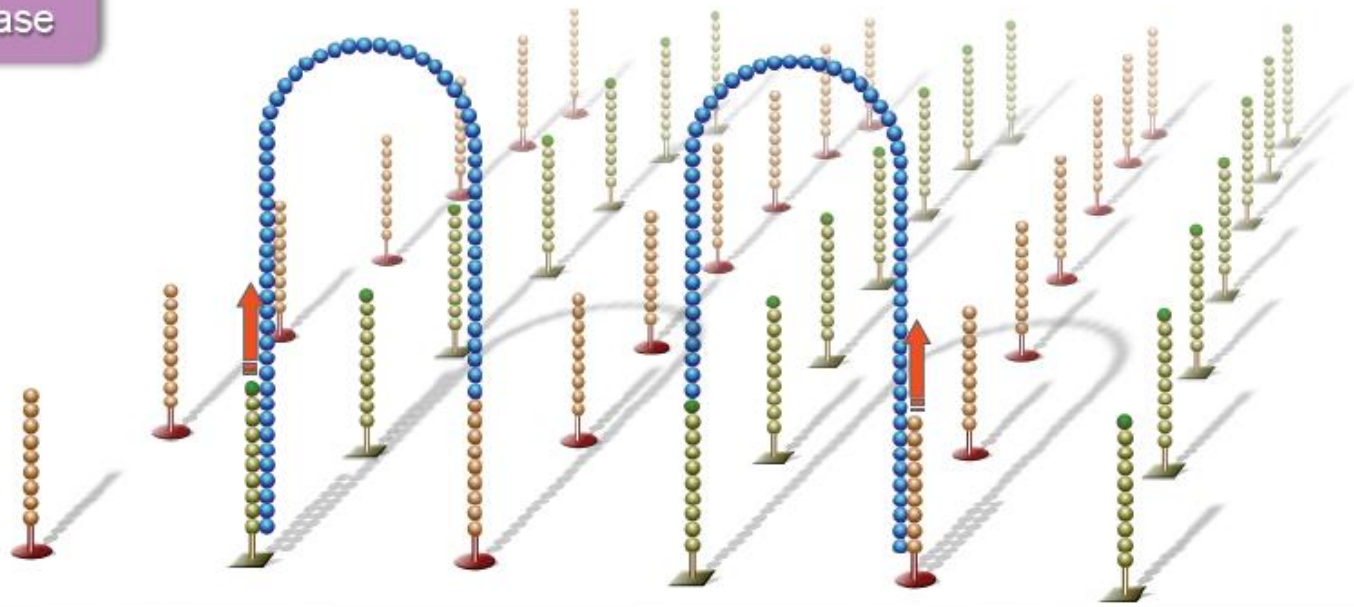
Result:
Two copies of covalently bound single-stranded templates



Bridge Amplification

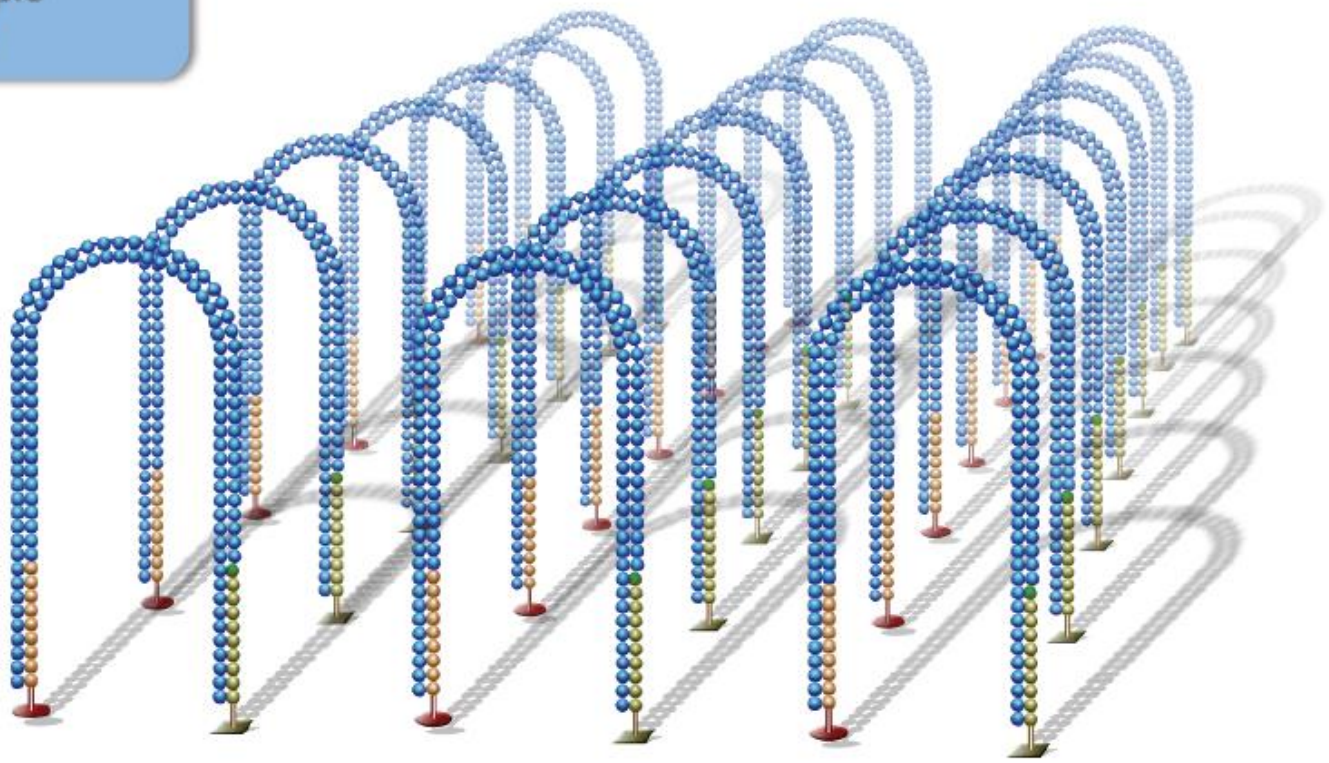
Single-stranded molecules flip over to hybridize to adjacent primers

Hybridized primer is extended by polymerase



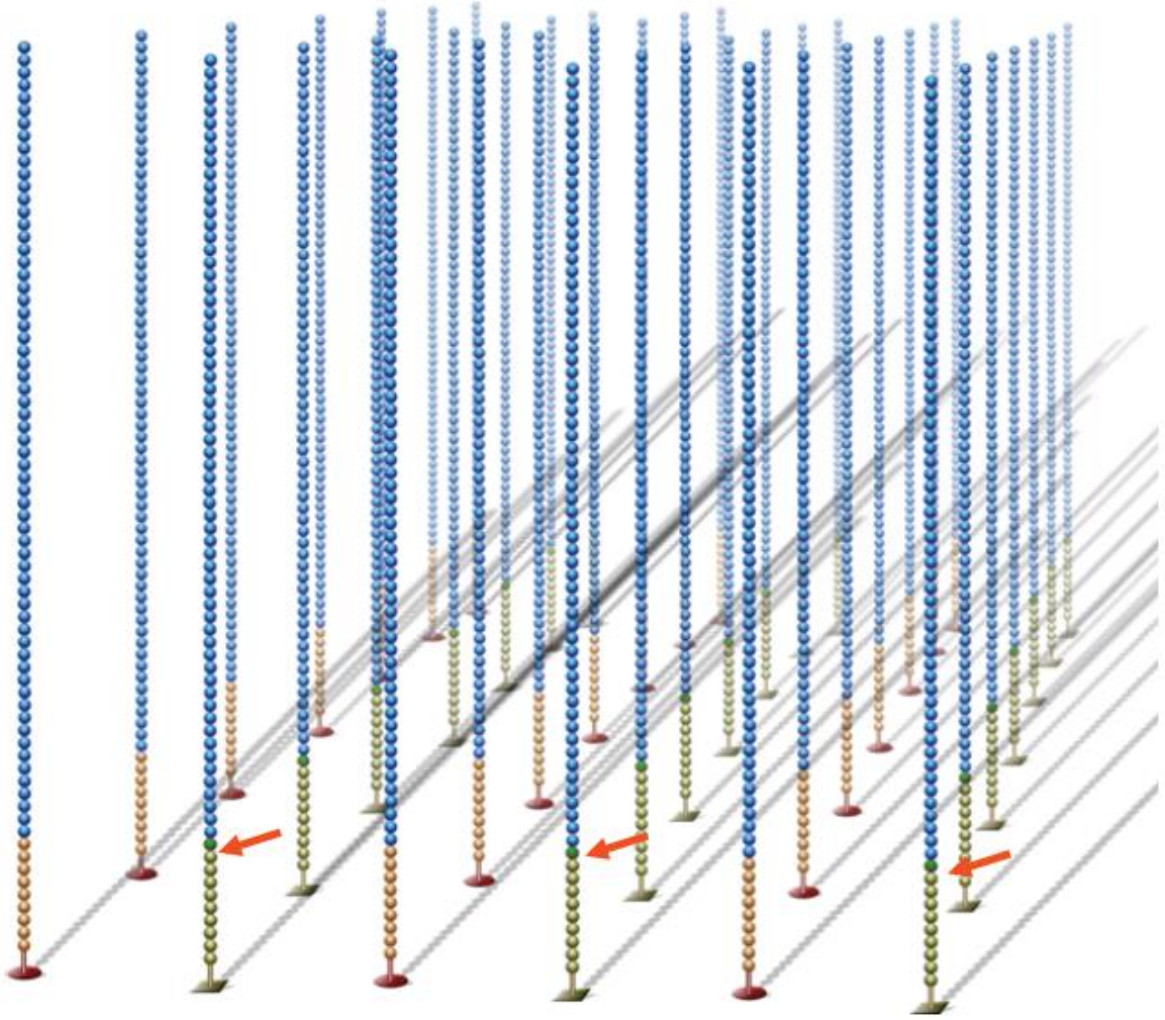
Bridge Amplification

Bridge amplification cycle is repeated until multiple bridges are formed



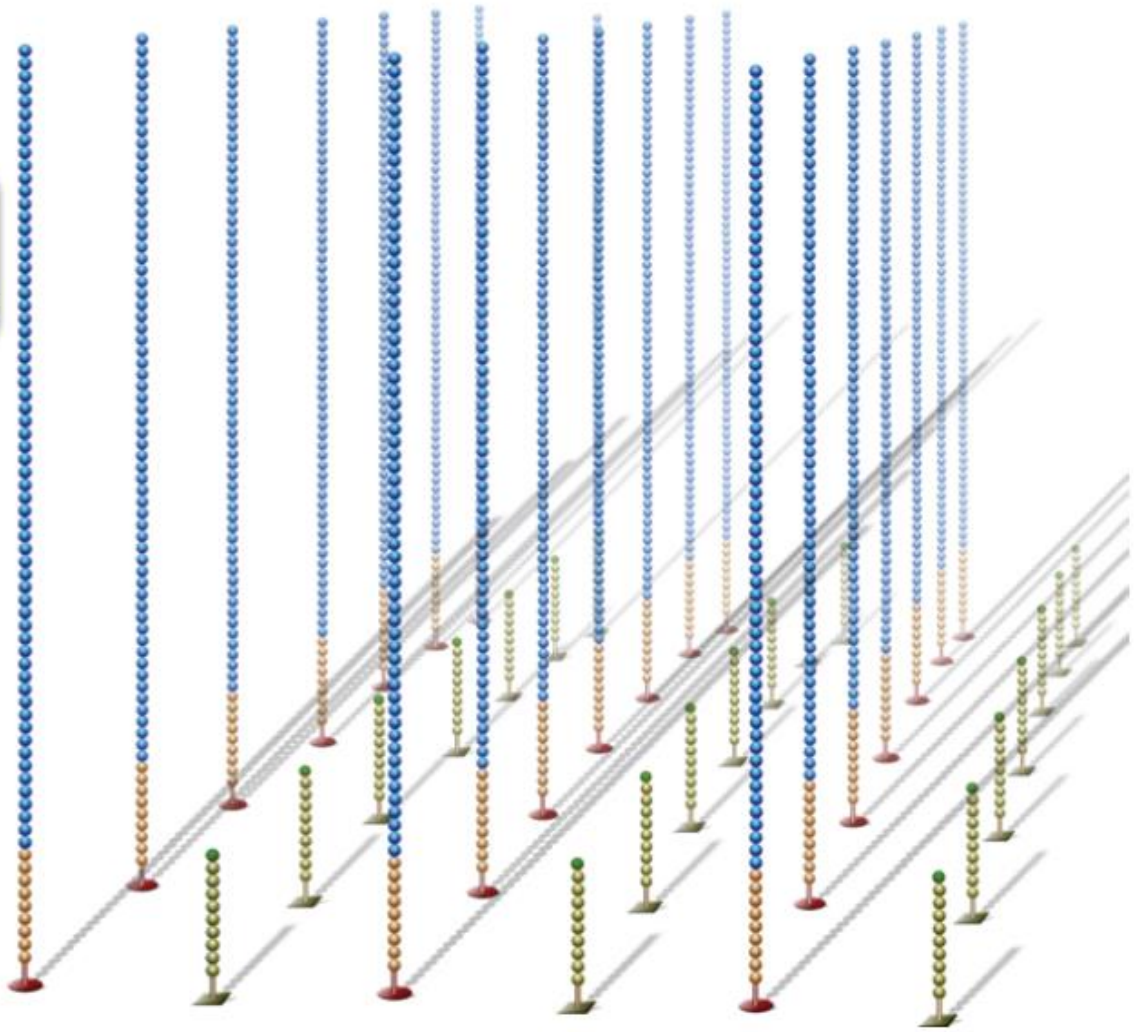
Linearization

dsDNA bridges are denatured



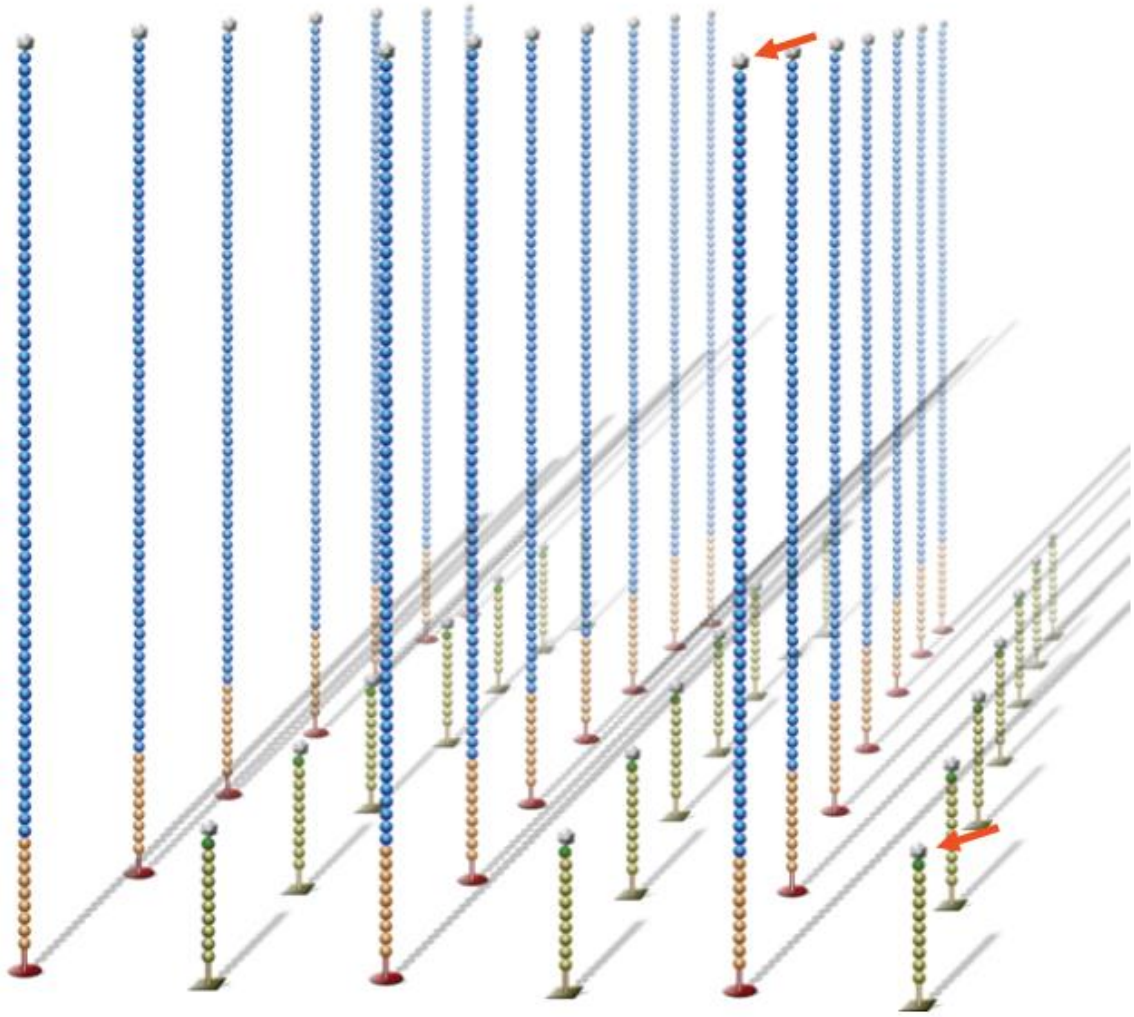
Reverse Strand Cleavage

Reverse strands are cleaved and washed away, leaving a cluster with forward strands only



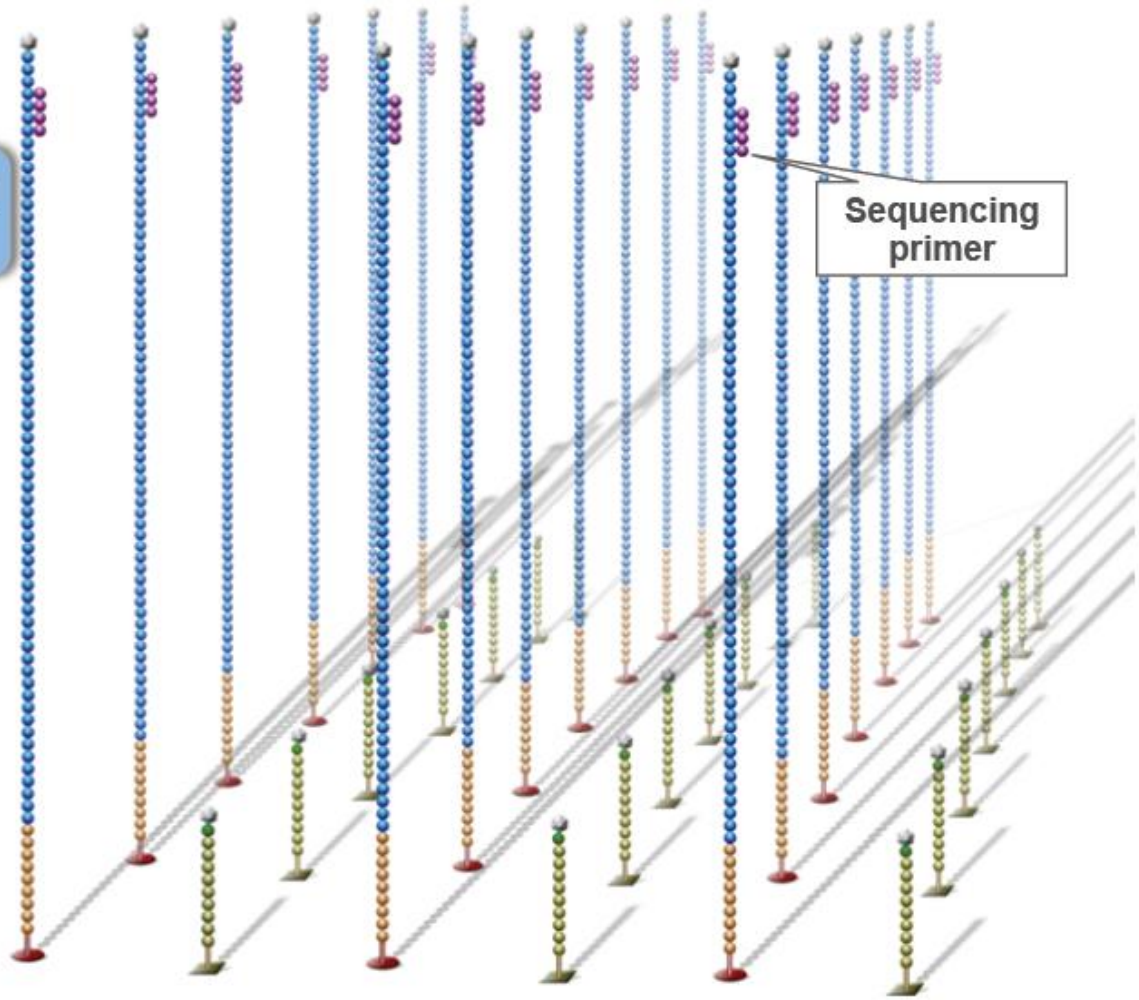
Blocking

Free 3' ends are blocked to prevent unwanted DNA priming

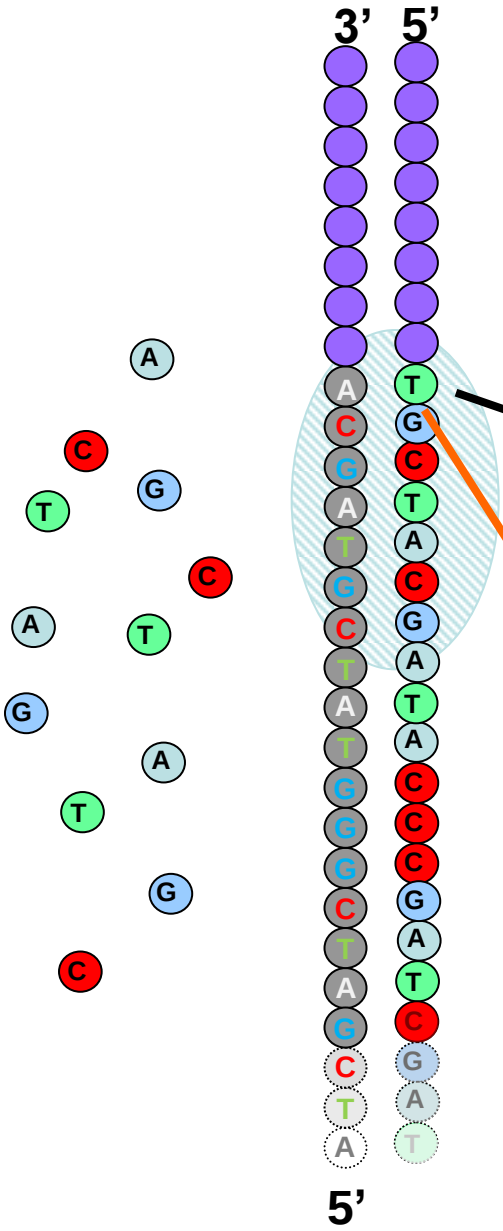


Read 1 Primer Hybridization

Sequencing primer is hybridized to adapter sequence

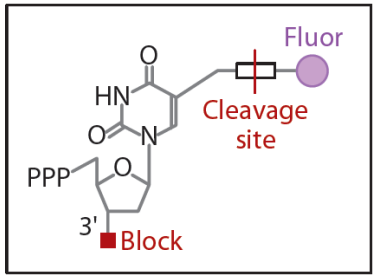


Sequencing by synthesis



Cycle 1: Add sequencing reagents

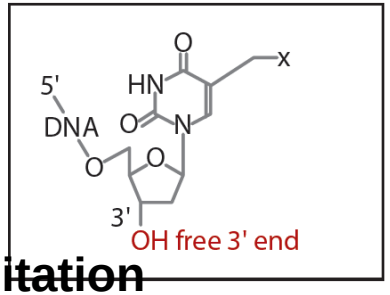
First base incorporated



Emission

Detect signal

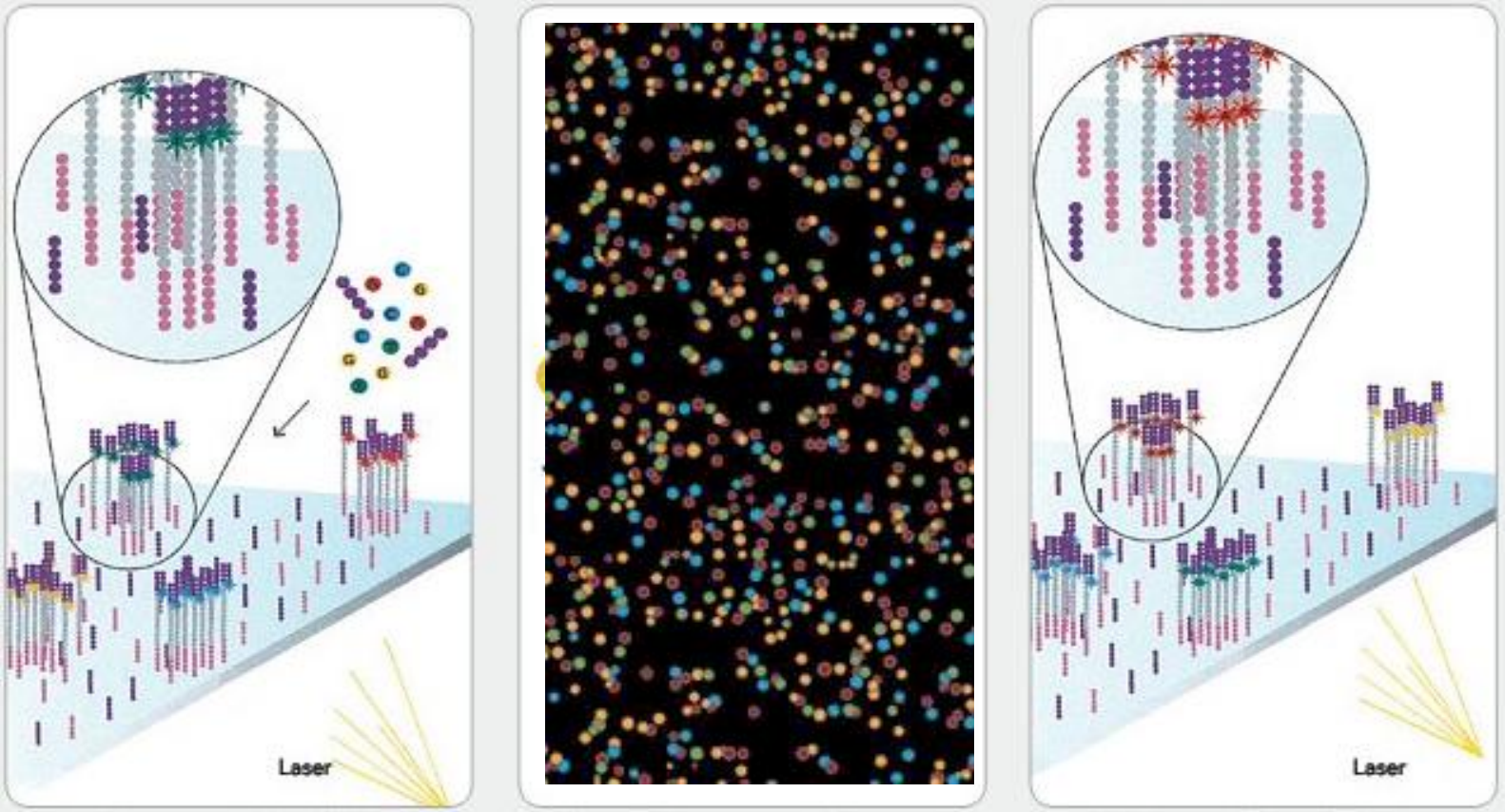
Cleave terminator and dye



Excitation

Cycle 2-n: Add sequencing reagents and repeat

Sequencing by Synthesis - Fluorescently labeled Nucleotides (Illumina)



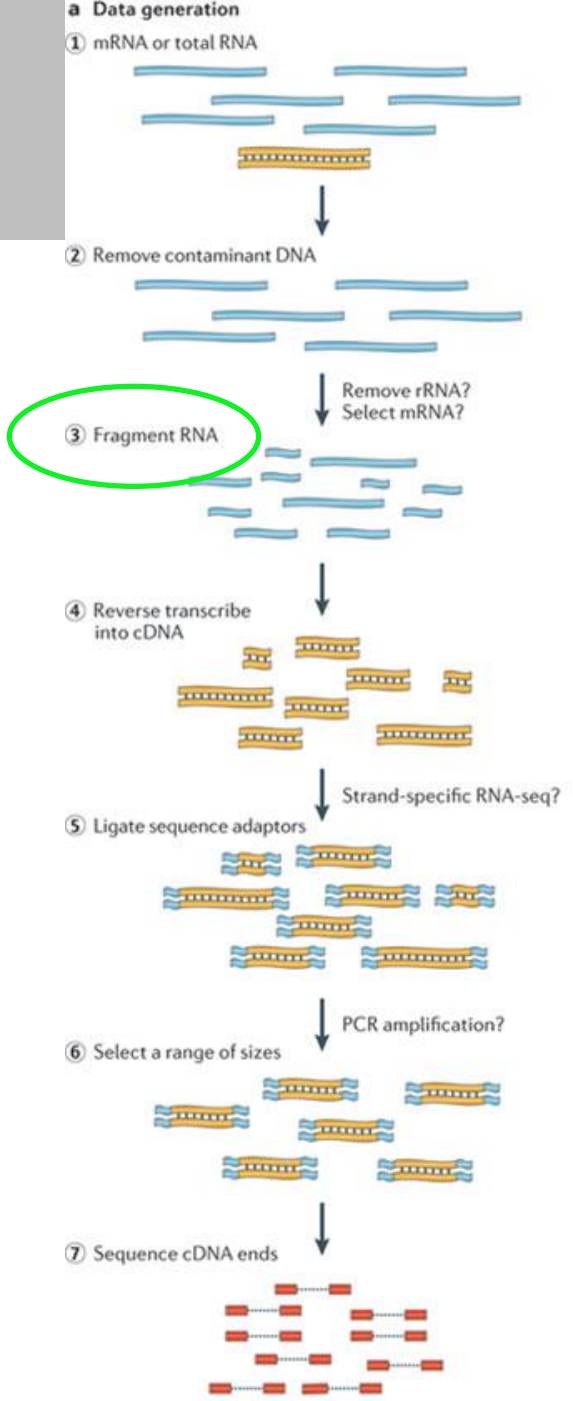
Complementary strand elongation: DNA Polymerase

video

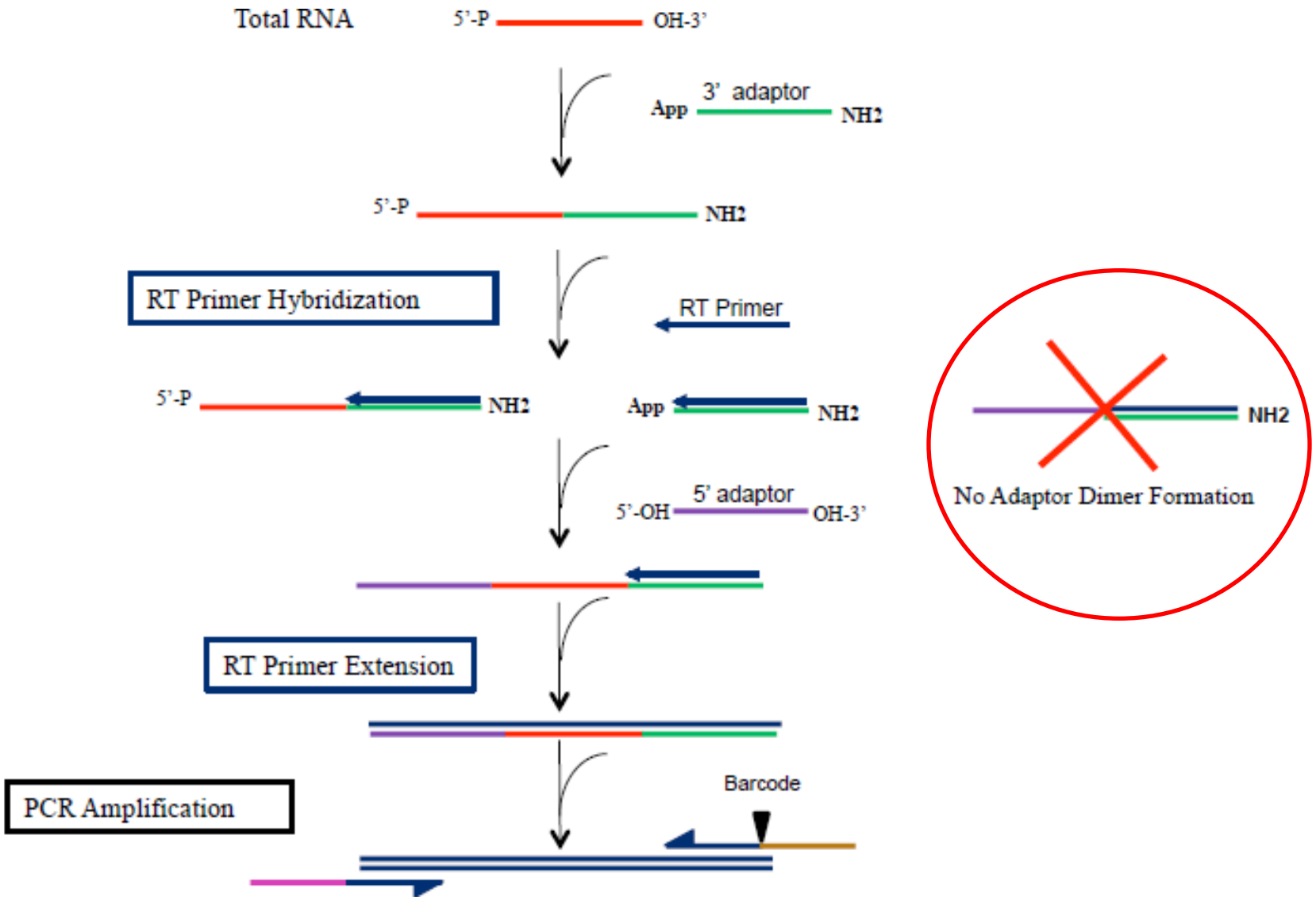
- https://www.youtube.com/watch?v=womKfikWlxM

The general experimental procedure for RNA

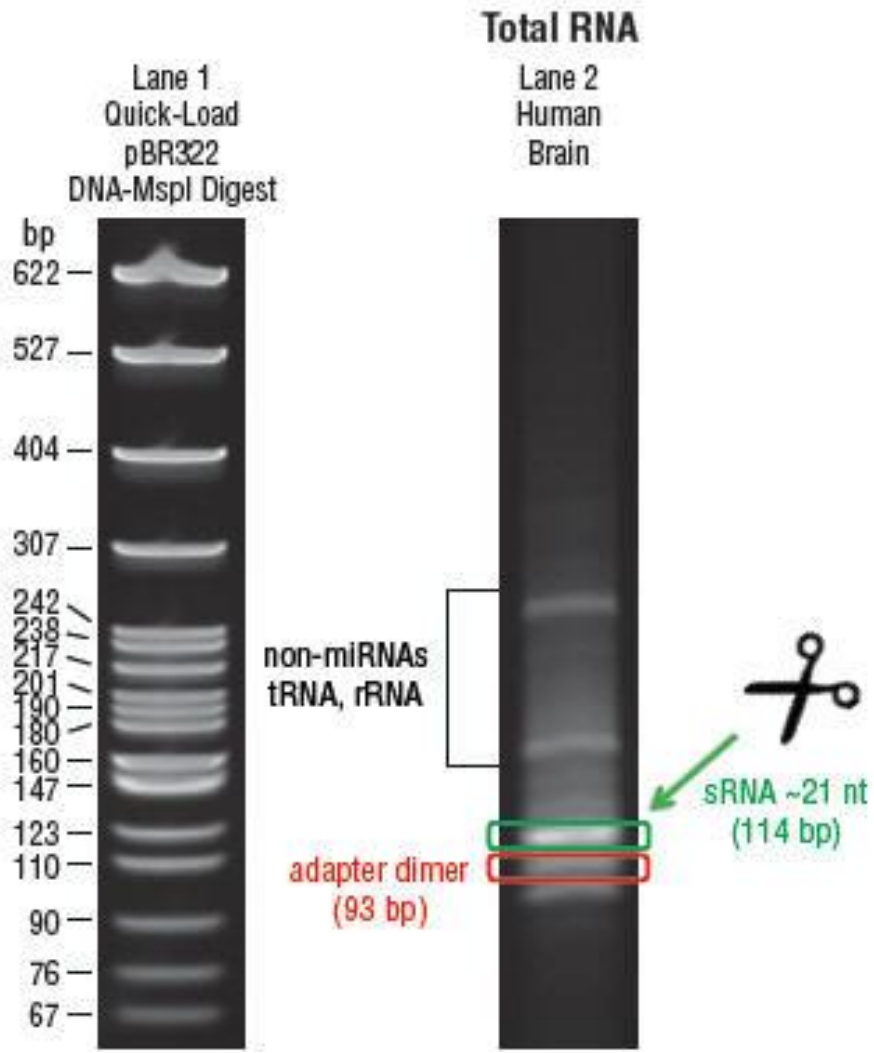
Transcriptom = sum of all RNA (mRNA, rRNA, tRNA and noncoding RNA)

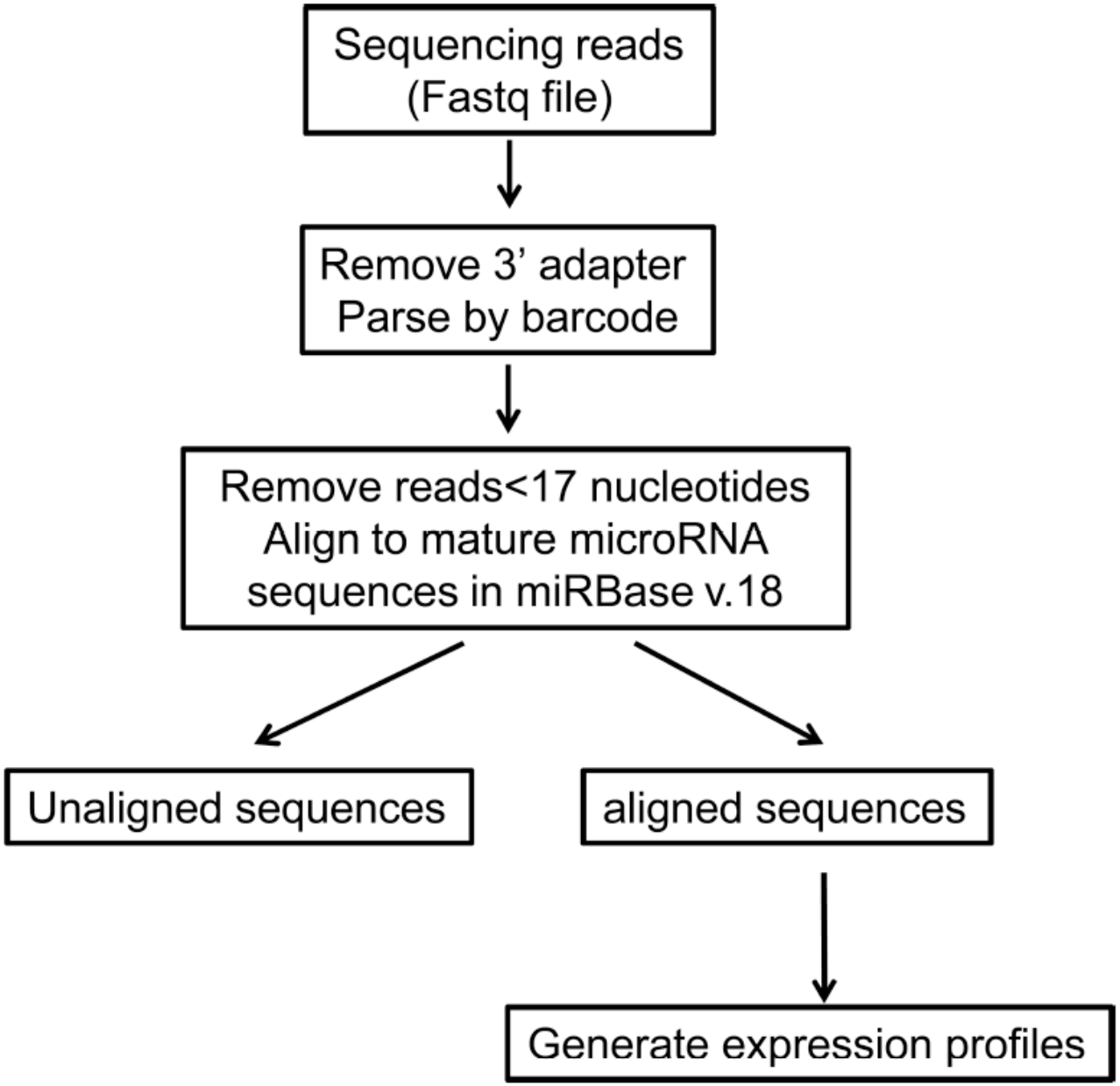


The general experimental procedure for miRNA



The general experimental procedure for miRNA

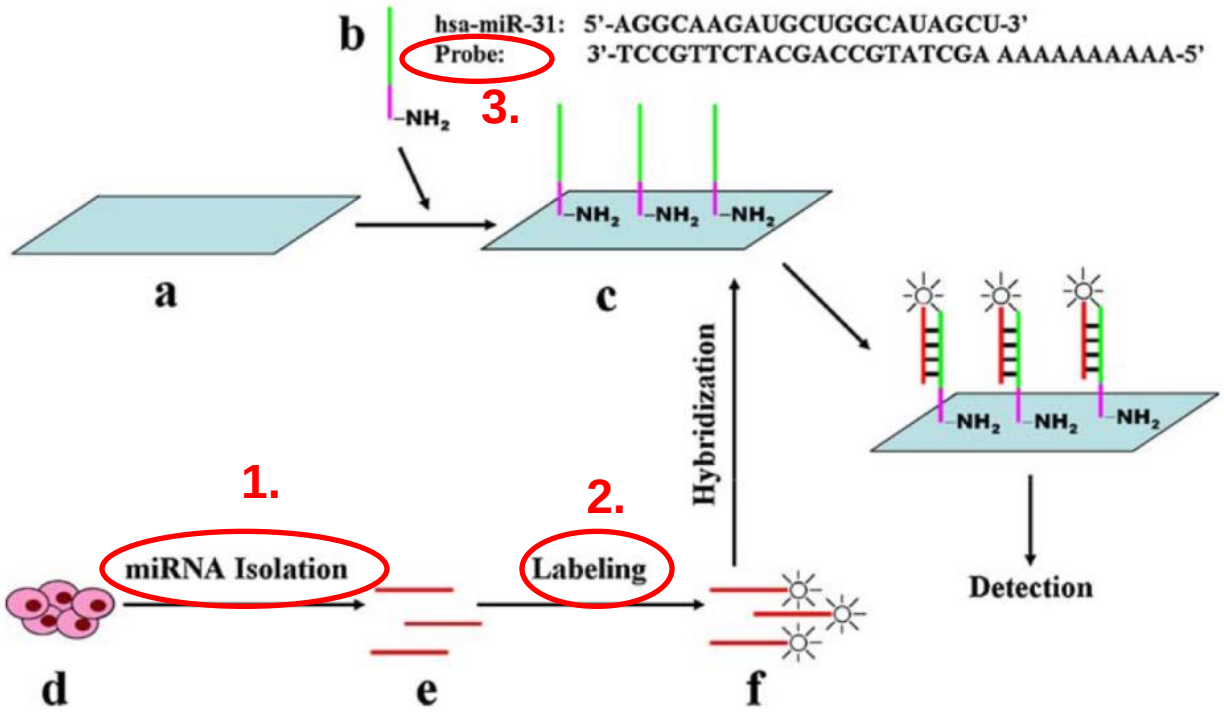



Sequencing reads
(Fastq file)
Remove 3' adapter
Parse by barcode
Remove reads<17 nucleotides
Align to mature microRNA
sequences in miRBase v.18
Unaligned sequences
aligned sequences
Generate expression profiles

MICROARRAYS

Expression microarrays pro microRNAs:

- velmi malé molekuly – 22nt – specifikum izolace, specifické značení i design sond
- malé zastoupení ve vzorku – separace microRNA
- v lidském genovu cca 2000 genů – menší počet sond na čipu
- některé mají velmi podobnou sekvenci – rozdíl 1nt
- pre-miR, pri-miR, mature-miR
- málo se ví o jejich funkcích – obtížná interpretace výsledků
- zatím málo zkušeností a standardizace



Li and Ruan, 2009

3/ Labeling – značení:

- Není možný labeling pomocí značených polyT při reverzní transkripci
- Přímé značení (direct labeling) – většinou nějaká fluorescenční barva
- Nepřímé značení (indirect labeling) – probíhá nějaká reverzní transkripce/PCR

Přímé značení:

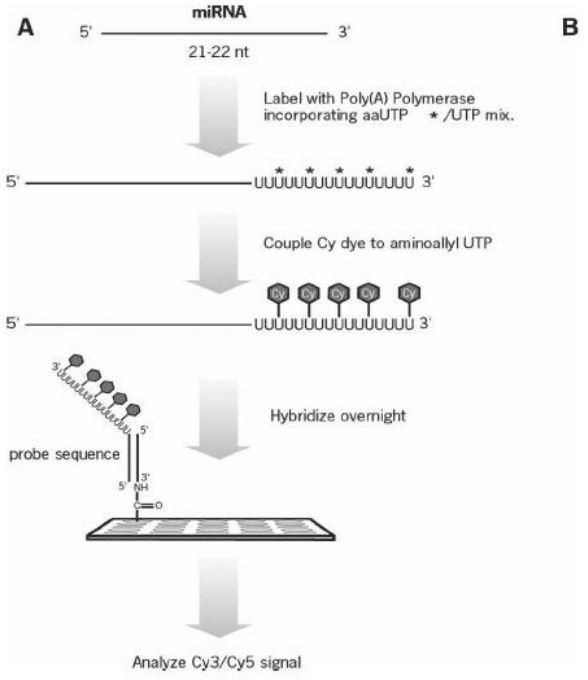
Jednoduché, rychlé a „čím méně kroků tím méně vnesených chyb a variability“

1/ Značení guaninu v microRNA

Flurochromem vážícím se na guanin jsou označeny miRNA (Ulysis Alexa Flour 546/647)
Všechny lidské miRNA obsahují guanin, ale v různém množství
Nemožnost usuzovat na vzájemnou expresi různých miRNA (různý obsah guaninu)
(Babak et al., 2004)

2/ Značení pomocí Poly (A) polymerázy

Můžu se rozhodnout jak dlouhý bude poly(A)
a tím ovlivnit sílu signálu
(Shingara et al., 2005)



4/ značení pomocí T4 ligasy

Krátký značený oligonukleotid
je připojen T4 ligásou k 3‘konci
Výhodou je přednostní vazba
na RNA o velikosti 18-30bp ->total RNA
(Thomson et al., 2004; Castoldi et al., 2007)

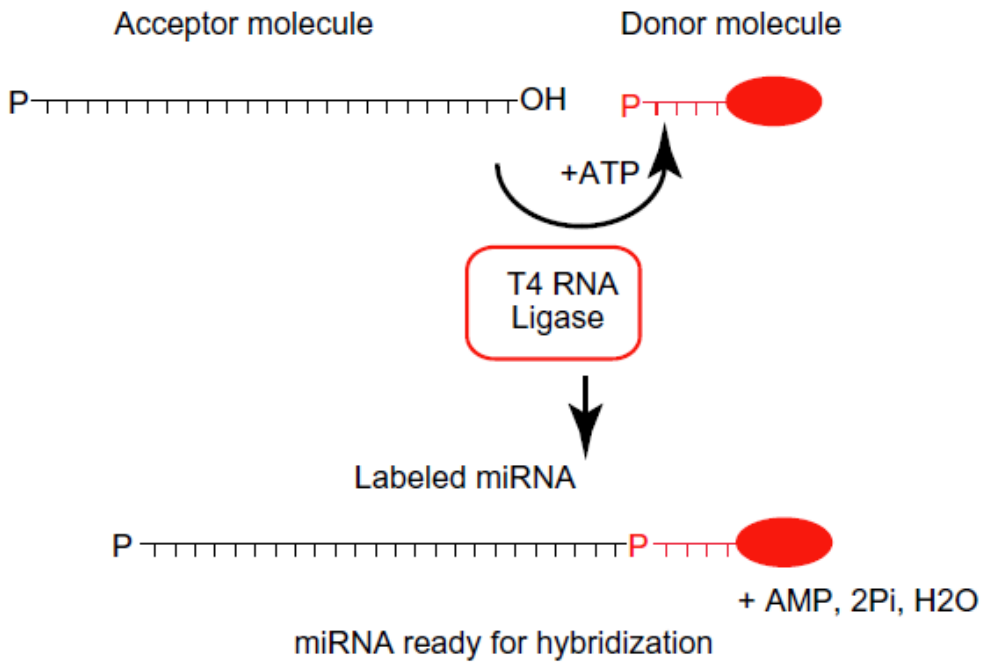


Fig. 2. Schematic representation of the miRNA labeling principle: a short Cy-dye labeled RNA-linker (donor molecule) is ligated to the single-stranded miRNA (acceptor molecule) by T4 RNA ligase in the presence of ATP.

Nepřímé značení:

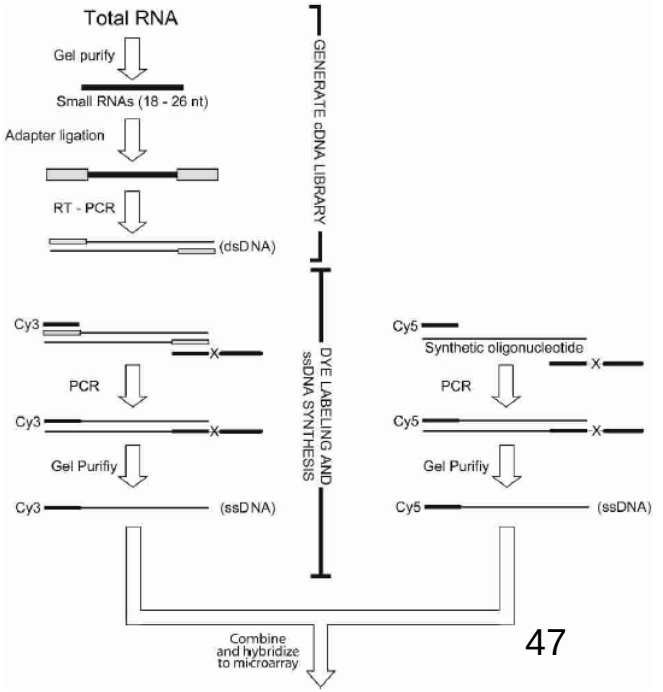
Značen je produkt reverzní transkripce či PCR
Výhody: cDNA je pak stabilní a lze uchovat, Pre-amplifikace a tím snadnější detekce méně exprimovaných miRNA

1/ značení revezního transkriptu miRNA

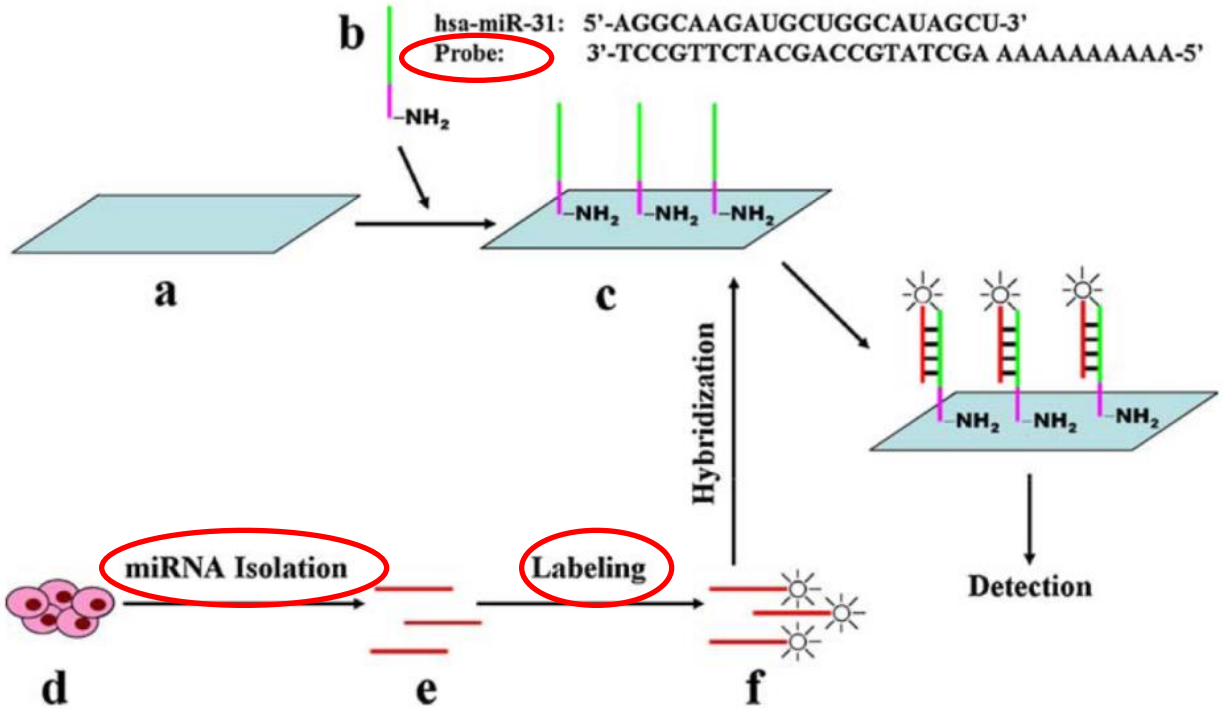
Reverzní transkripce pomocí náhodných 8-merů značených 2 biotiny (3‘-(N)8 – (A)12-biotin-(A)12-biotin-5‘ (Liu et al., 2004)
Reverzní transkripce pomocí náhodných neznačených 7-merů, následně označeny s pomocí terminální transferázy a biotin-dideoxy-UTP (Sun et al., 2004)
Nebezpečí chyb z nespecifické vazby primeru

2/ značení produktu RT-PCR

Výhoda: snadná pre-amplifikace
Dva adaptory
fluorescenčně-značený primer (k adaptoru)
(Miska et al., 2004)
Nevýhoda: antisense strand přiromen při hybridizaci
Rešením je různá délka sense a antisense ->PAGE
(Baskerville, 2005)



3/ Microarrays/ Próby:
Problémy: krátké RNA, malé rozdíly v sekvenci, Tm



Tm – melting temperature určité próby
T – hybridizační teplota

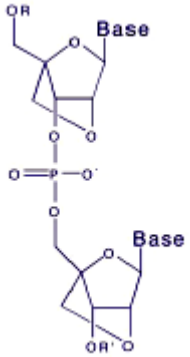
Tm<T .....nižší efektivita vazby miRNA
Tm>T .....vyšší efektivita vazby miRNA

- Je třeba navrhnout próby tak,aby měly všechny podobnou Tm
- To se u „dlouhých“ mRNA řeší vhodným výběrem oblasti genu k němuž bude sonda komplementární nebo délkou sondy
- navíc některé miRNA jsou téměr sekvenčně totožné

```
let-7b : TGAGGTAGTAGGTTGTGTGGTT : 22
let-7e : TGAGGTAGGAGGTTGTATAGT- : 21
let-7d : AGAGGTAGTAGGTTGCATAGT- : 21
let-7a : TGAGGTAGTAGGTTGTATAGTT : 22
let-7f : TGAGGTAGTAGATTGTATAGTT : 22
let-7i : TGAGGTAGTAGTTTGTGCT--- : 19
let-7g : TGAGGTAGTAGTTTGTACAGT- : 21
         tGAGGTAGtAG TTGt   gt
```

ÚPRAVA SÍLY VAZBY NUKLEOTIDŮ

LNA próby (Locked Nucleic Acid)
ribózový kruh je „uzamčen“ methylenovým můstkem mezi atomy 2´-O a 4´-C



Použití LNA pro některé báze v próbě

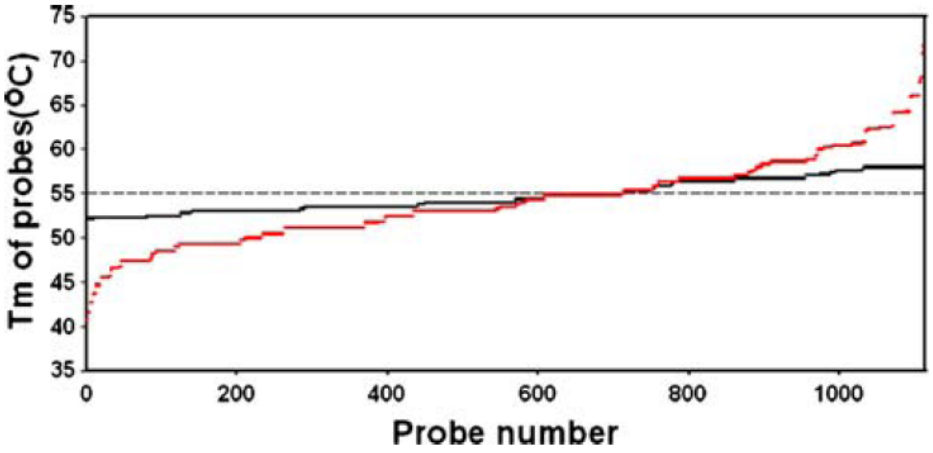


Fig. 2 Tm (melting temperature) distribution for microRNA probes for human, rat and mouse. *Red and black curves* represent the Tm distributions of the raw and normalized probes, respectively

Li and Ruan, 2009

SÍLA VAZBY:
LNA vs DNA próba
Tm až 72^{0}C
(Castoldi et al., 2006)

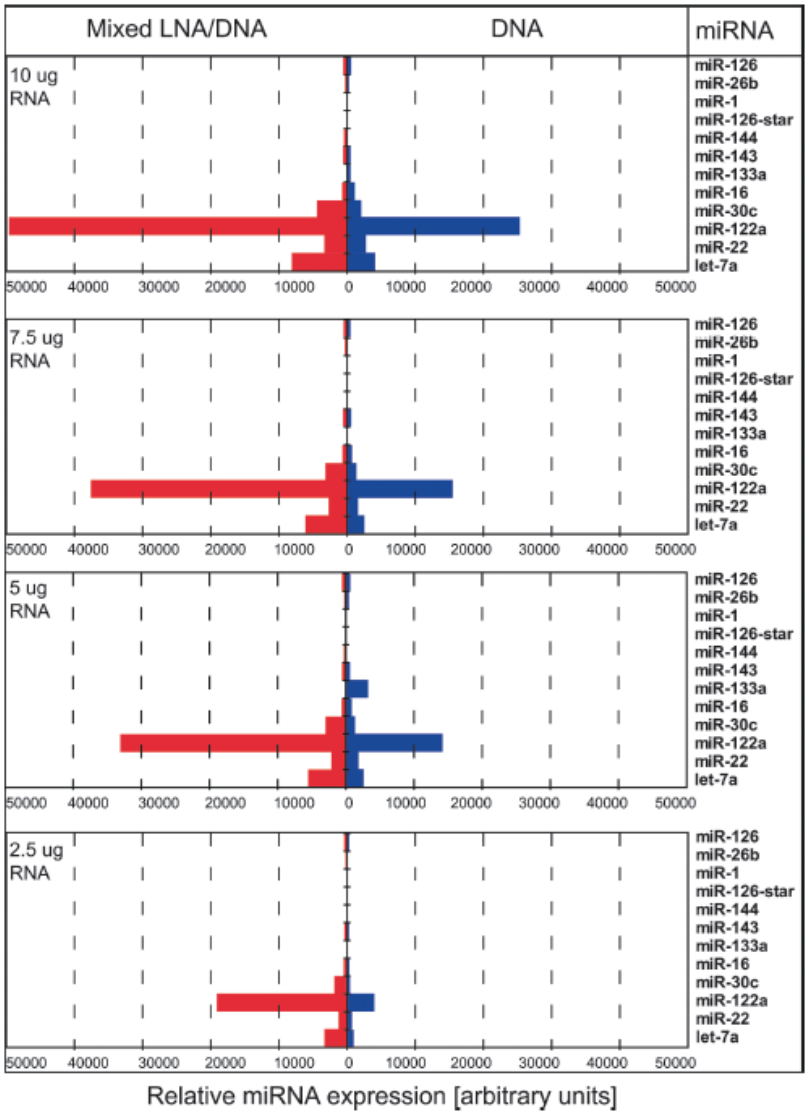
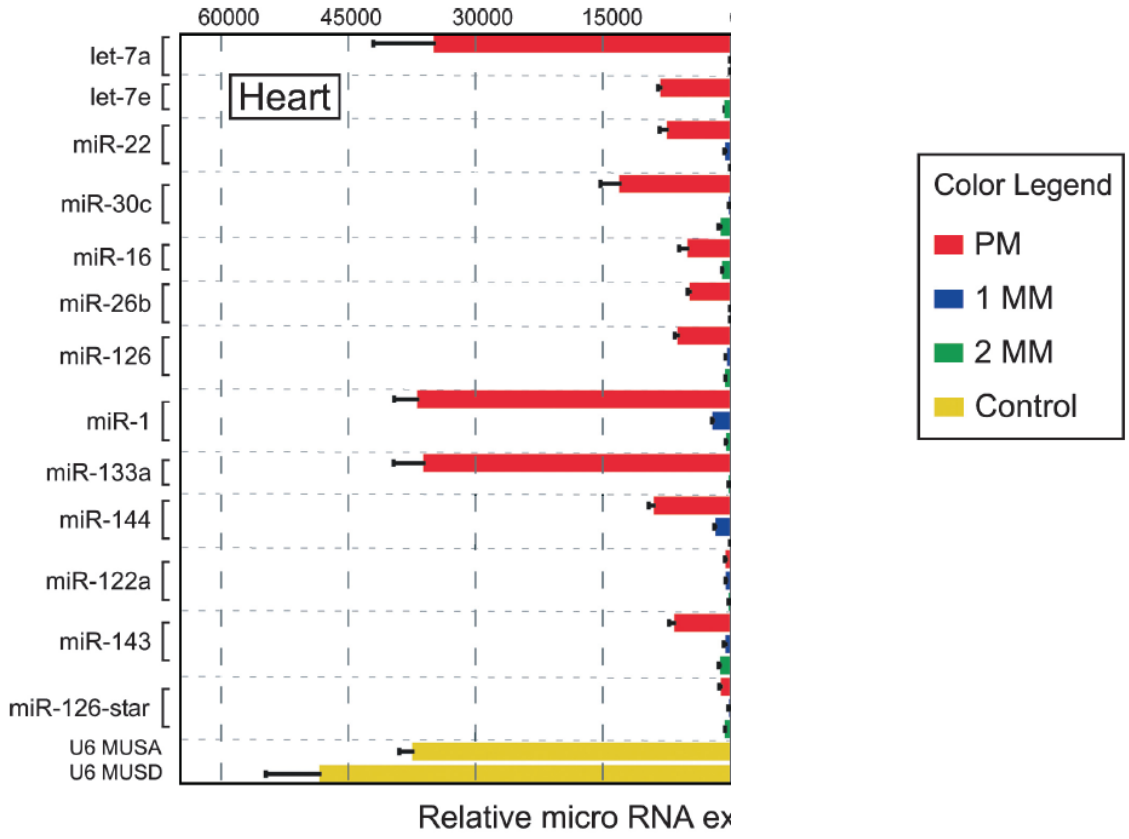


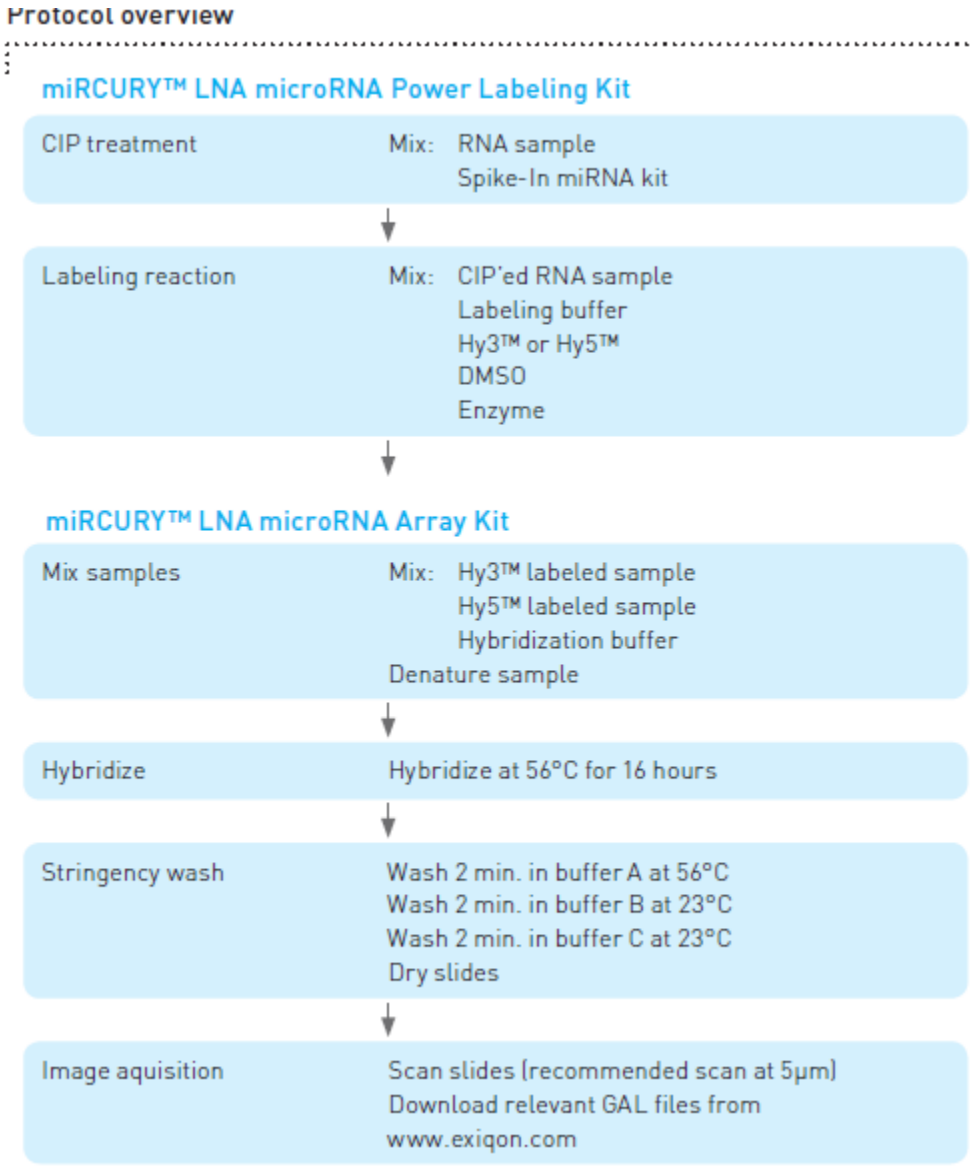
FIGURE 1. Mixed DNA/LNA capture probes display increased sensitivity for miRNA detection. miRNA expression was assessed in murine liver using a test set of LNA-modified (*left*) or unmodified DNA oligonucleotide capture probes (*right*). Decreasing amounts of total RNA were used as input material for miRNA analysis. Data are presented as median intensity (four replicas per miRNA capture probe; a representative experiment is shown).

SPECIFITA VAZBY: LNA vs DNA próba

(Castoldi et al., 2006)

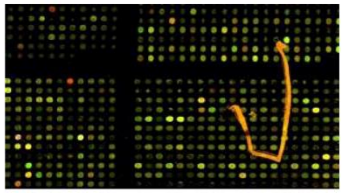


miRCURY LNA Array, Exiqon : 3 dny

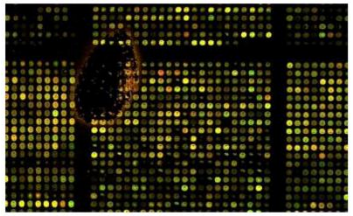


Co se nemusí podařit:

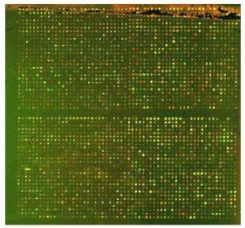
Nekvalitní RNA
Nepodaří se značení
Nepodaří se hybridizace
Nepodaří se promývání
Technická variabilita čipů je větší než ta biologická
Nepodaří se validace dat pomocí RT-PCR, atd



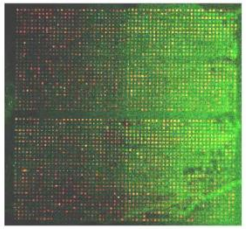
Fiber or scratch?



Bubble



Edge effect



Background haze

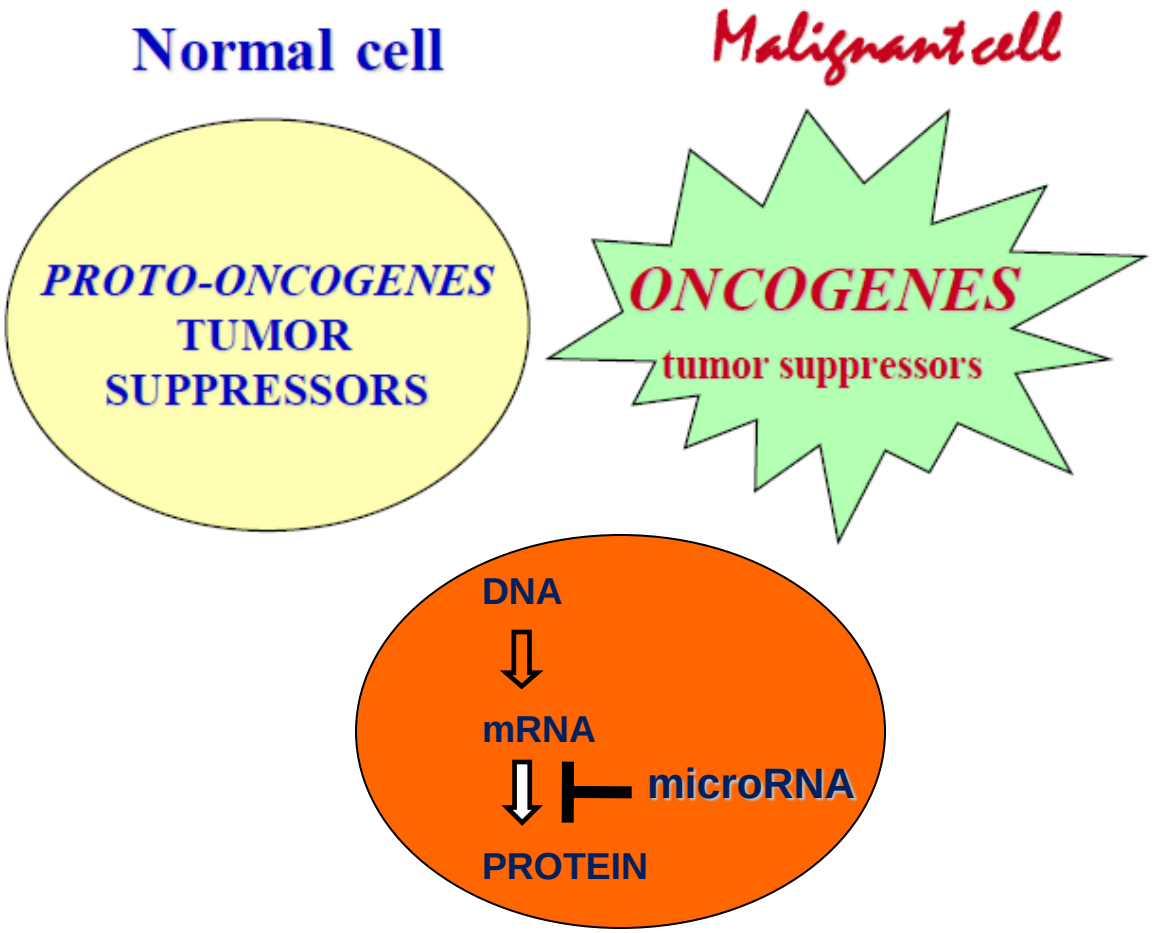
Práce s miRNA čipy je velmi obtížná. Všeobecně nižší míra standardizace. Obtížná interpretace získaných dat z pohledu biologického smyslu např. deregulace několika miRNA (nádor vs. zdravá tkáň apod.)

ODPOČINEK?

Year 2K "Central dogma" of molecular oncology

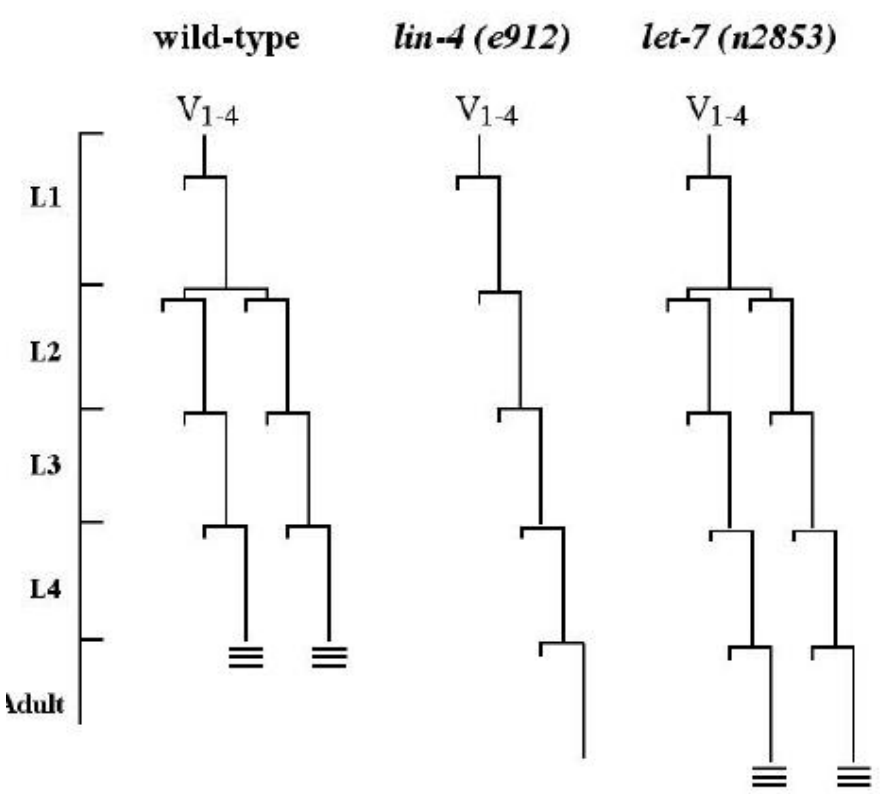
Cancer is the GENETIC DISEASE with the most complex mechanism.

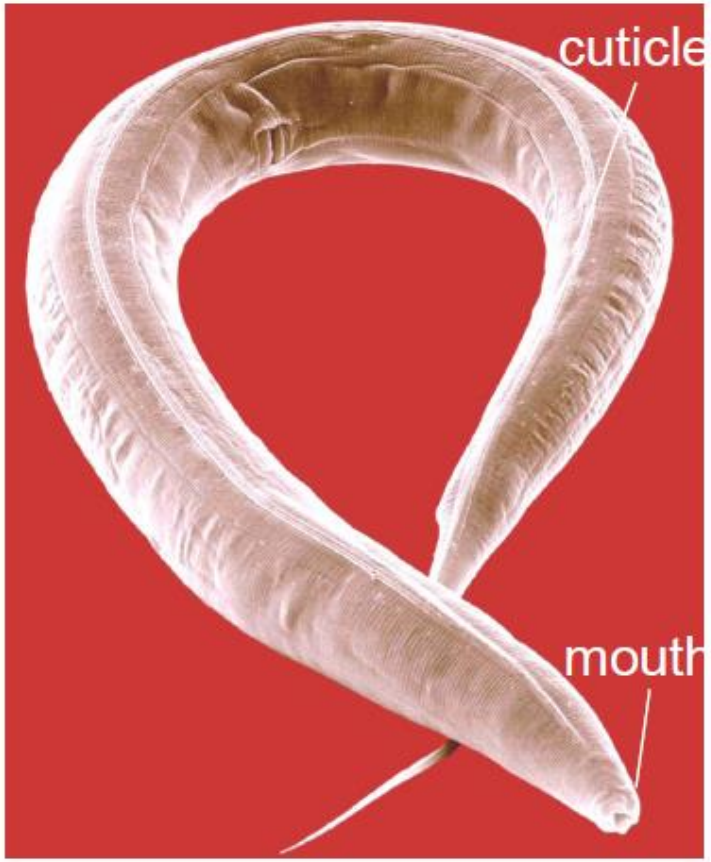
Oncogenes and Tumor-suppressors are the two types of PROTEINS deregulated in cancer cells.



courtesy of G. Calin

MicroRNAs were discovered by V. Ambros and G. Ruvkun in *C. elegans*



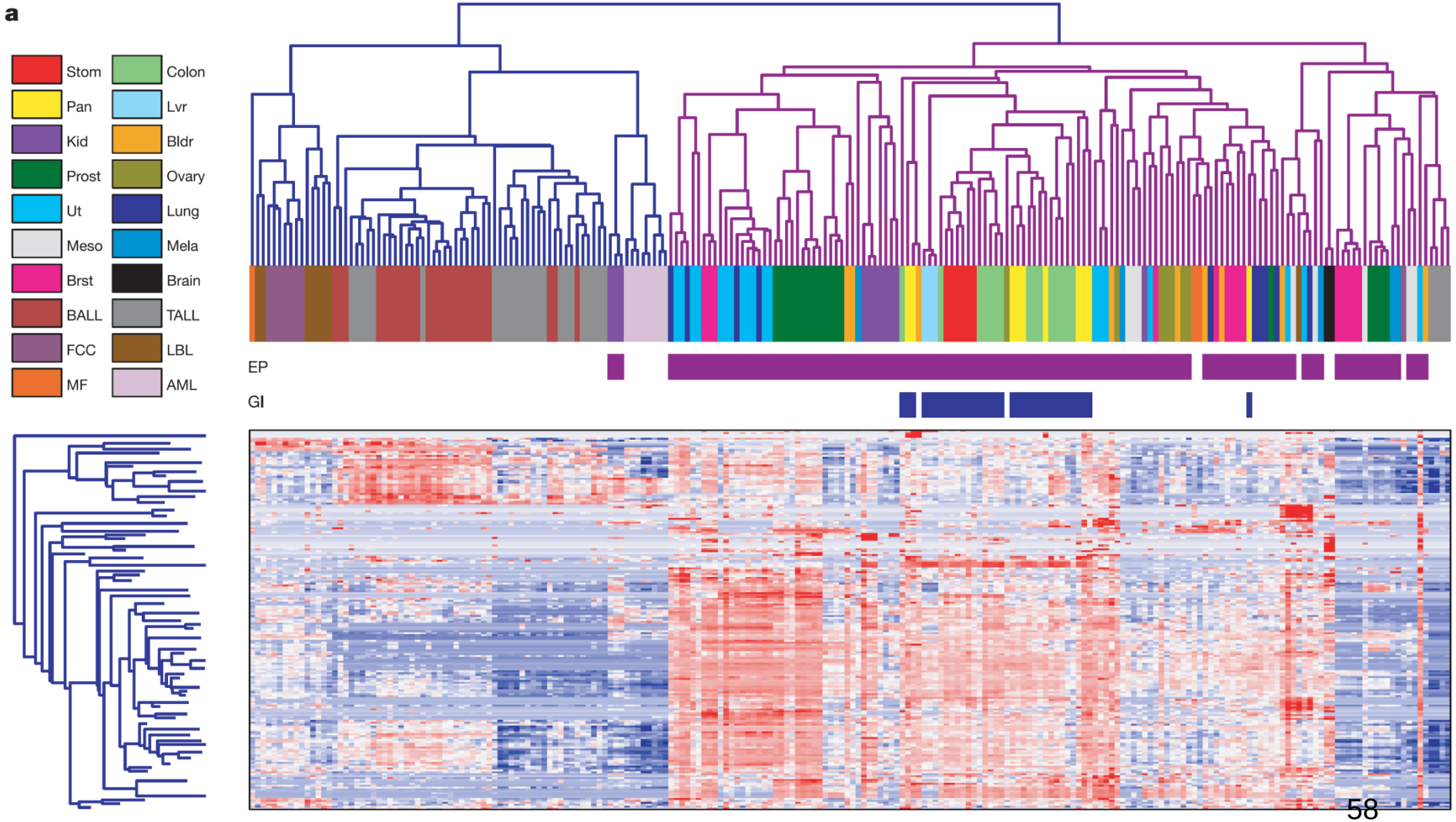


Lee et al. 1993 *Cell*

Reinhart et al. 2000 *Nature*

courtesy of F. Slack

microRNA exprese je schopná rozlišit původ nádoru



Lu et al. Nature 435: 834, 2005

A microRNA expression signature of human solid tumors defines cancer gene targets

Stefano Volinia*†‡, George A. Calin*‡, Chang-Gong Liu*, Stefan Ambs§, Amelia Cimmino*, Fabio Petrocca*, Rosa Visone*, Marilena Iorio*, Claudia Roldo*, Manuela Ferracin¶, Robyn L. Prueitt§, Nozumu Yanaihara§, Giovanni Lanza¶, Aldo Scarpa‖, Andrea Vecchione**, Massimo Negrini¶, Curtis C. Harris§, and Carlo M. Croce*††

*Department of Molecular Virology, Immunology, and Medical Genetics and Cancer Comprehensive Center, Ohio State University, Columbus, OH 43210; §Laboratory of Human Carcinogenesis, Center for Cancer Research, National Cancer Institute, National Institutes of Health, Bethesda, MD 20892; †Telethon Facility–Data Mining for Analysis of DNA Microarrays, Department of Morphology and Embryology, and ¶Department of Experimental and Diagnostic Medicine and Interdepartmental Center for Cancer Research, University of Ferrara, 44100 Ferrara, Italy; ‖Department of Pathology, University of Verona, 37100 Verona, Italy; and **Department of Histopathology, Sant'Andrea Hospital, and University of Rome ''La Sapienza,'' 00185 Rome, Italy

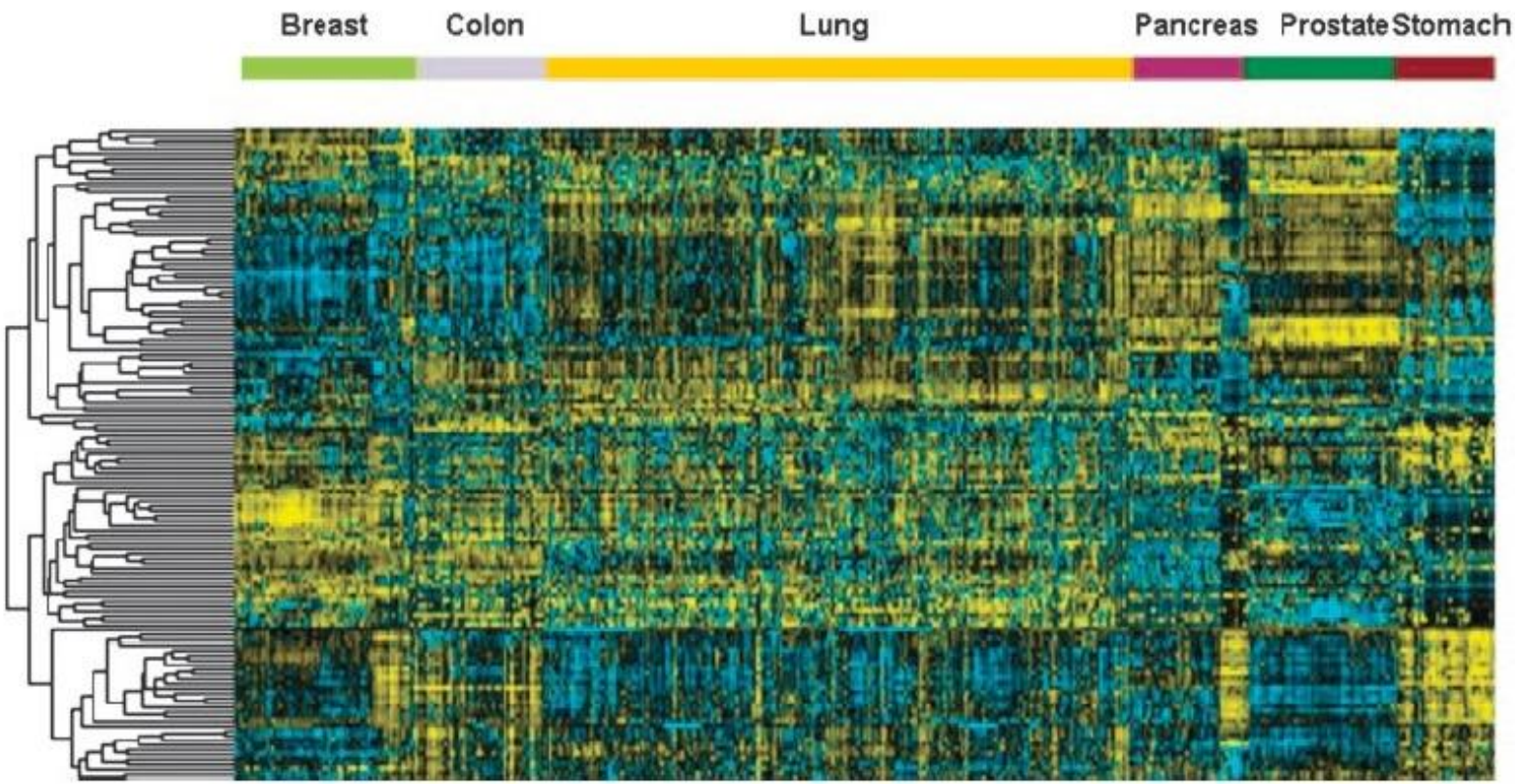
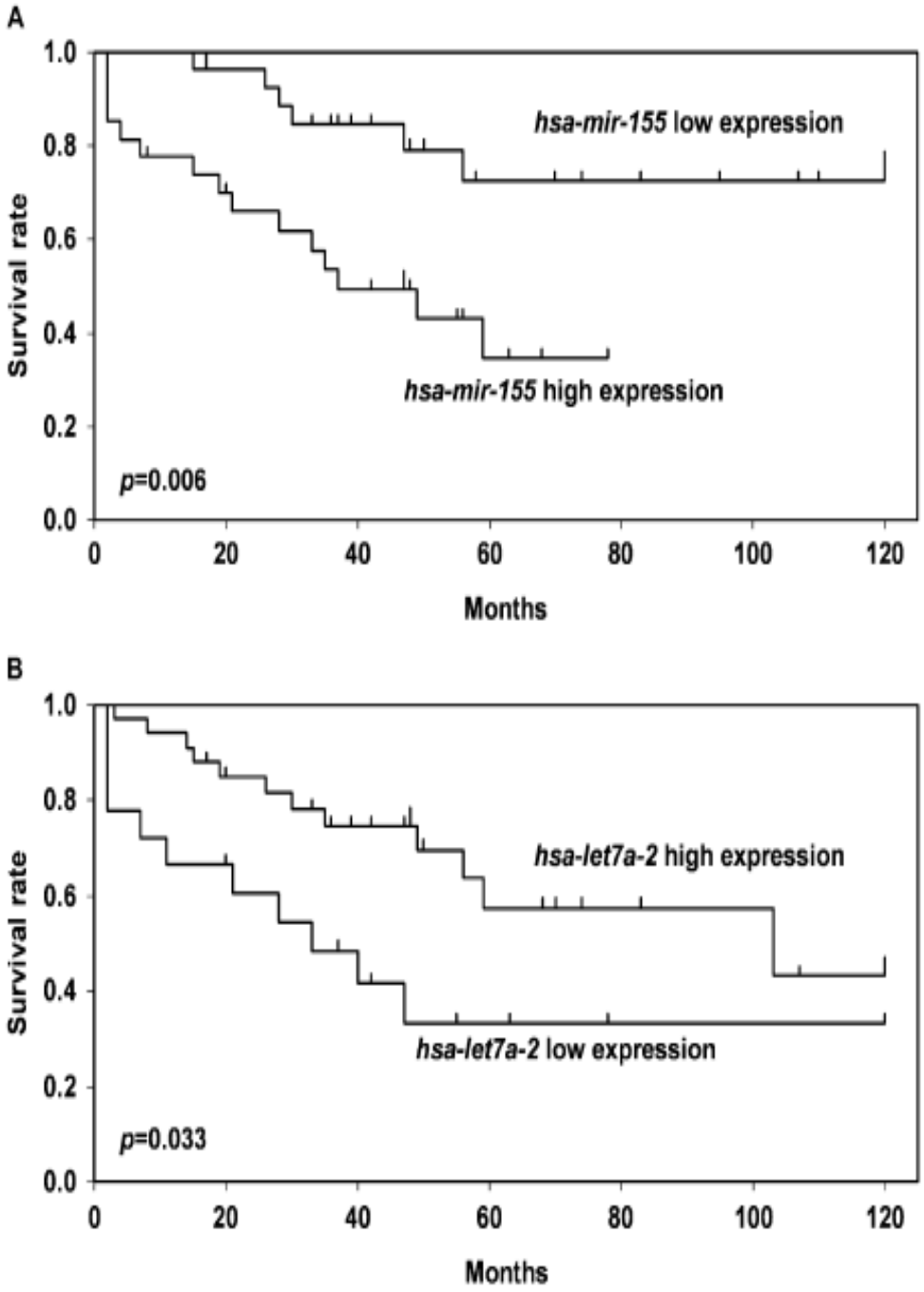


Table 2. The miRNAs shared by the signatures of the six solid cancers

miR	*N*	Tumor type
miR-21	6	Breast, colon, lung, pancreas, prostate, stomach
miR-17-5p	5	Breast, colon, lung, pancreas, prostate
miR-191	5	Colon, lung, pancreas, prostate, stomach
miR-29b-2	4	Breast, colon, pancreas, prostate
miR-223	4	Colon, pancreas, prostate, stomach
miR-128b	3	Colon, lung, pancreas
miR-199a-1	3	Lung, pancreas, prostate
miR-24-1	3	Colon, pancreas, stomach
miR-24-2	3	Colon, pancreas, stomach
miR-146	3	Breast, pancreas, prostate
miR-155	3	Breast, colon, lung
miR-181b-1	3	Breast, pancreas, prostate
miR-20a	3	Colon, pancreas, prostate
miR-107	3	Colon, pancreas, stomach
miR-32	3	Colon, pancreas, prostate
miR-92-2	3	Pancreas, prostate, stomach
miR-214	3	Pancreas, prostate, stomach
miR-30c	3	Colon, pancreas, prostate
miR-25	3	Pancreas, prostate, stomach
miR-221	3	Colon, pancreas, stomach
miR-106a	3	Colon, pancreas, prostate

The list includes 21 commonly up-regulated microRNAs in 3 or more (*N*) types of solid cancers (P value $= 2.5 \times 10^{-3}$).


A
1.0
0.8
0.6
0.4
0.2
0.0
Survival rate
hsa-mir-155 low expression
hsa-mir-155 high expression
p=0.006
0
20
40
60
80
100
120
Months
B
1.0
0.8
0.6
0.4
0.2
0.0
Survival rate
hsa-let7a-2 high expression
hsa-let7a-2 low expression
p=0.033
0
20
40
60
80
100
120
Months

A unique miRNA signature is associated with lung cancer prognosis

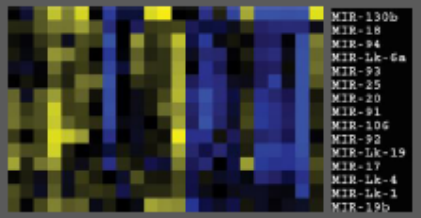
Table 5. Postoperative survival of patients with lung adenocarcinoma in relation to clinicopathological characteristics and miRNA expression analyzed by microarray analysis

Variable	Subset	Hazard ratio (95% confidence interval)	p
Univariate analysis (n = 65)			
Age	age ≥ 67/age < 67	1.41 (0.67–3.06)	0.348
Sex	male/female	1.36 (0.64–2.93)	0.413
Stage	II–IV/I	2.51 (1.29–6.82)	0.010
Smoking history	current/former	1.32 (0.63–2.79)	0.456
hsa-mir-155 (n = 55)	high/low	3.42 (1.42–8.19)	0.006
hsa-let-7a-2 (n = 52)	low/high	2.35 (1.08–6.86)	0.033
Multivariate analysis (n = 55)[a,b]			
Age	age ≥ 67/age < 67	1.92 (0.71–5.17)	0.195
Sex	male/female	1.23 (0.47–3.22)	0.669
Stage	II–IV/I	3.27 (1.31–8.37)	0.013
Smoking history	current/former	1.49 (0.51–4.34)	0.457
hsa-mir-155	high/low	3.03 (1.13–8.14)	0.027

[a]Multivariate analysis, Cox proportional hazard regression model.
[b]*hsa-let-7a-2* low/high was not statistically significant (p = 0.129).

(Yanaihara et al, Cancer Cell, 2006)

A polycistronic cluster of microRNAs are overexpressed in cancer



Proliferation

Angiogenesis

Apoptosis

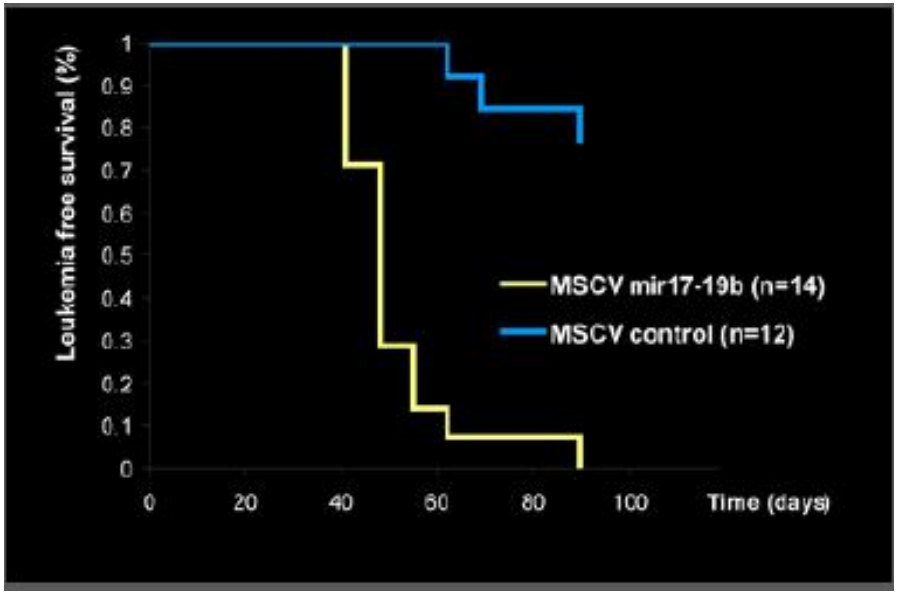
Invasiveness

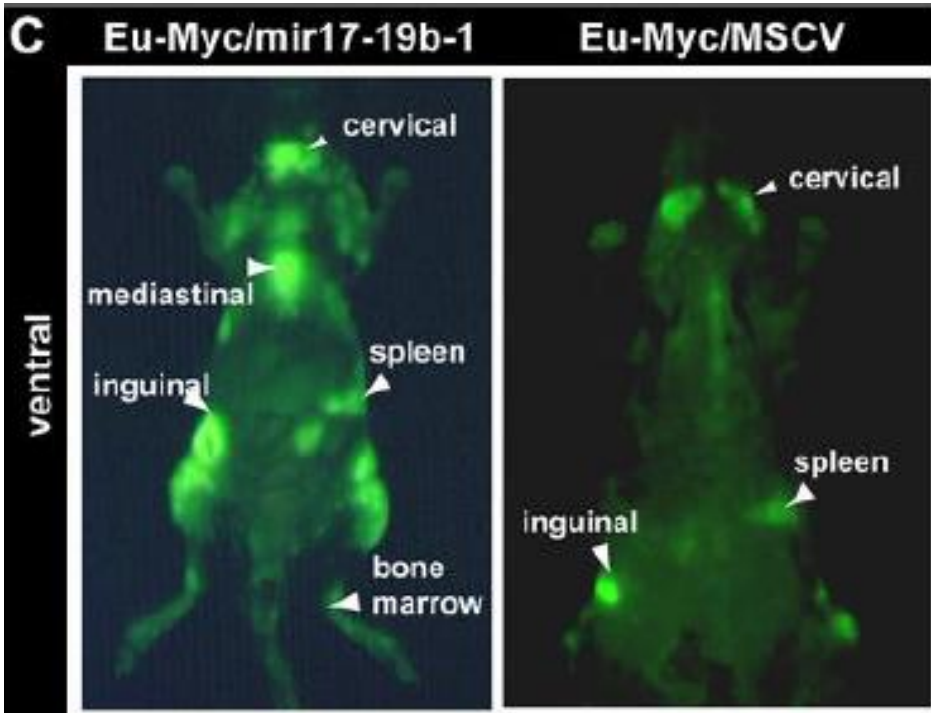
miR-17 miR-18 miR-19a miR-20 miR-19b miR-92

Ch13-ORF25

OncomiR-1 (Oncogenic microRNA-1)

courtesy of S. Hammond



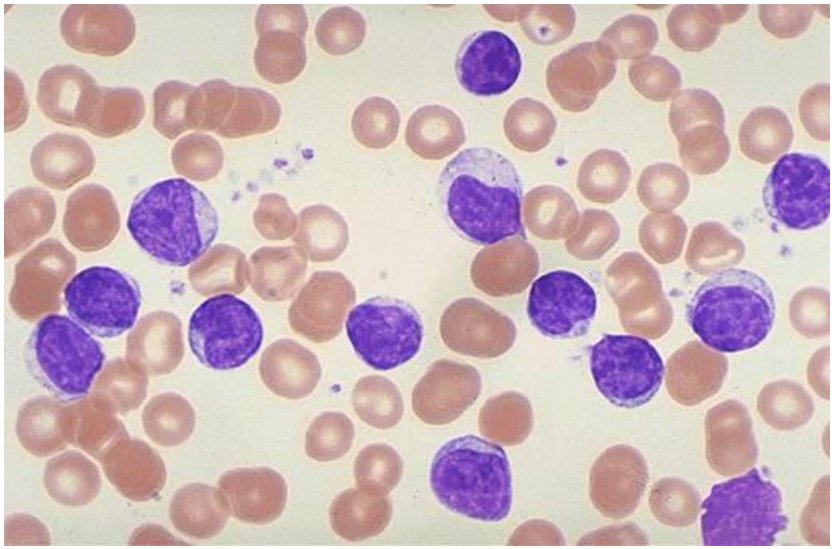


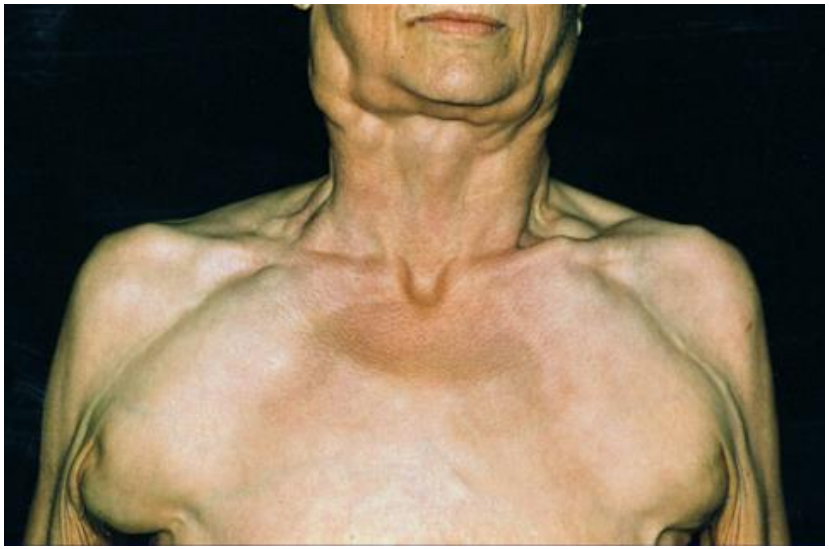
courtesy of S. Hammond

Chronická lymfatické leukémie

- Z maturovaných B lymfocytů
- Nejčastější leukémie dospělých

- Extrémně variabilní prognóza
- Nejčastější aberace del13q14 – obsahuje 2 miRNA (miR-15a, miR-16)

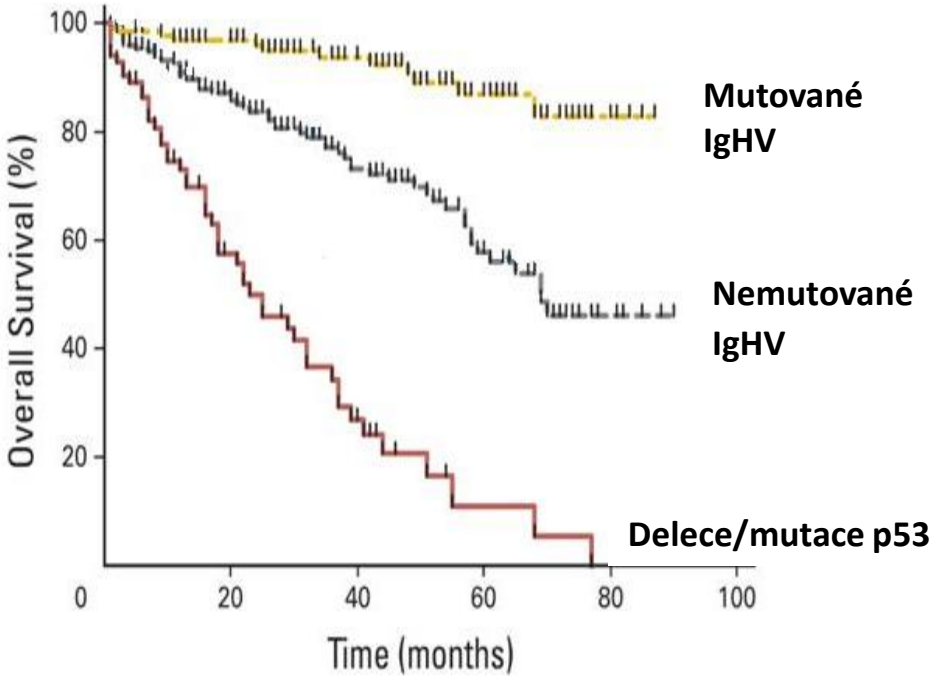




Exprese miRNA asociuje s prognostickými subtypy CLL

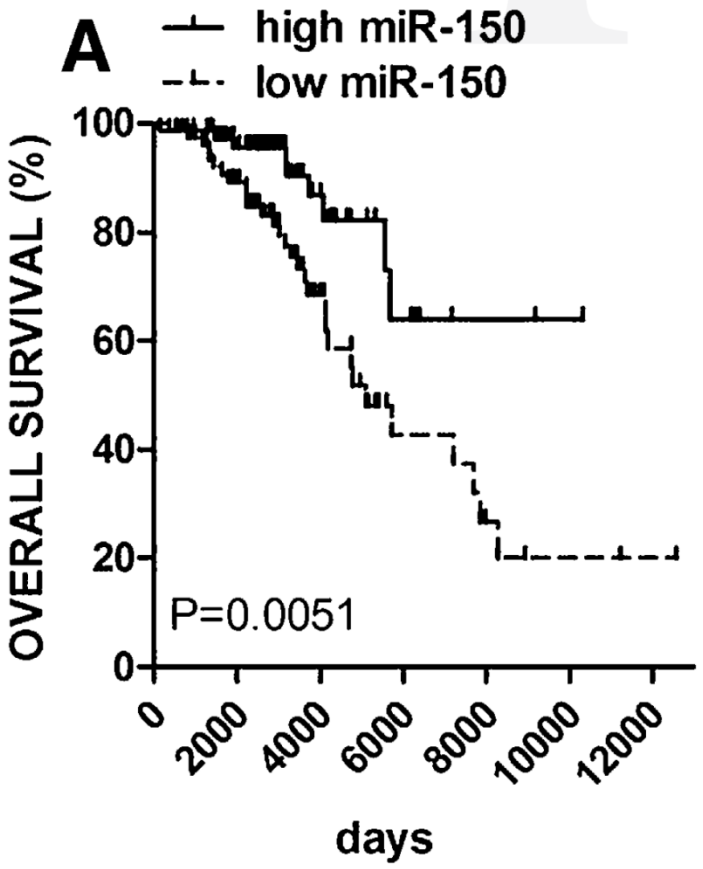
~ 20 miRNAs

Calin et al., 2005
Fulci et al, 2007
Zenz et al., 2009
Stamatopoulos et al., 2009
Mraz et al., 2009a, 2009b, 2012, 2014



Nižší hladiny miR-150 asociují s kratším celkovým přežitím a časem do první léčby

n =168

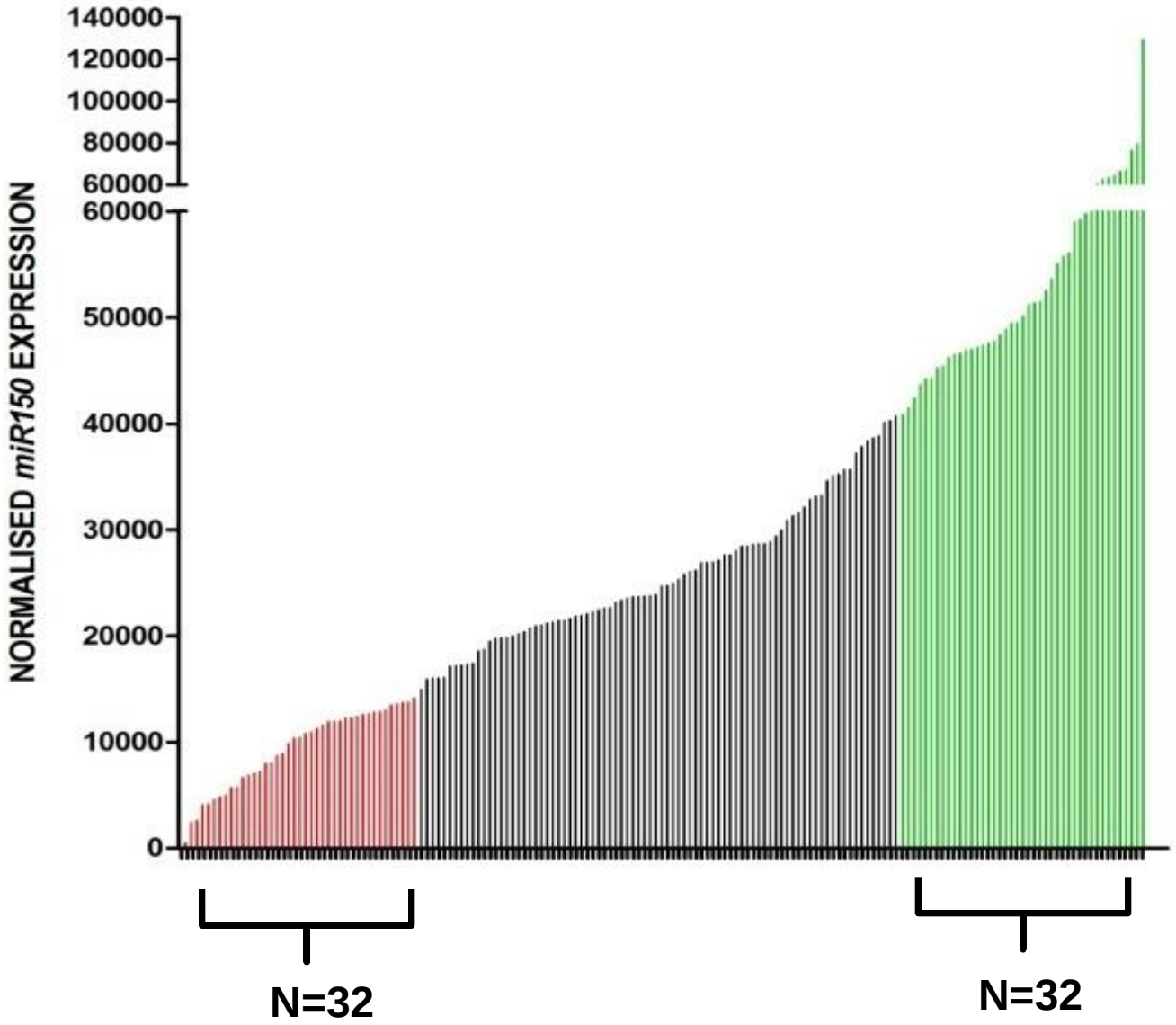


Variable[&]		HR[#]	CI[#]	*P-val*[#]
miR-150 (≤ vs. > median)		**5.6**	2.1-14.9	***0.001***
IGHV (unmut. vs. mut.)		2.8	0.9-9.1	*0.08*
ZAP-70 (pos. vs. neg.)		5.6	1.7-17.9	*0.004*
CD38 (pos. vs. neg.)		1.4	0.7-2.9	*0.37*
Gender (male vs. female)		2.9	1.3-6.5	*0.008*
Rai stage	I vs. 0	4.9	1.4-17	*0.01*
	II vs. 0	6.6	1.7-25.8	*0.01*
	≥III vs. 0	3.6	1-13.1	*0.05*
Age (> vs. ≤ median)		3.0	1.4-6.8	*0.01*

Mraz et al, Blood, 2014

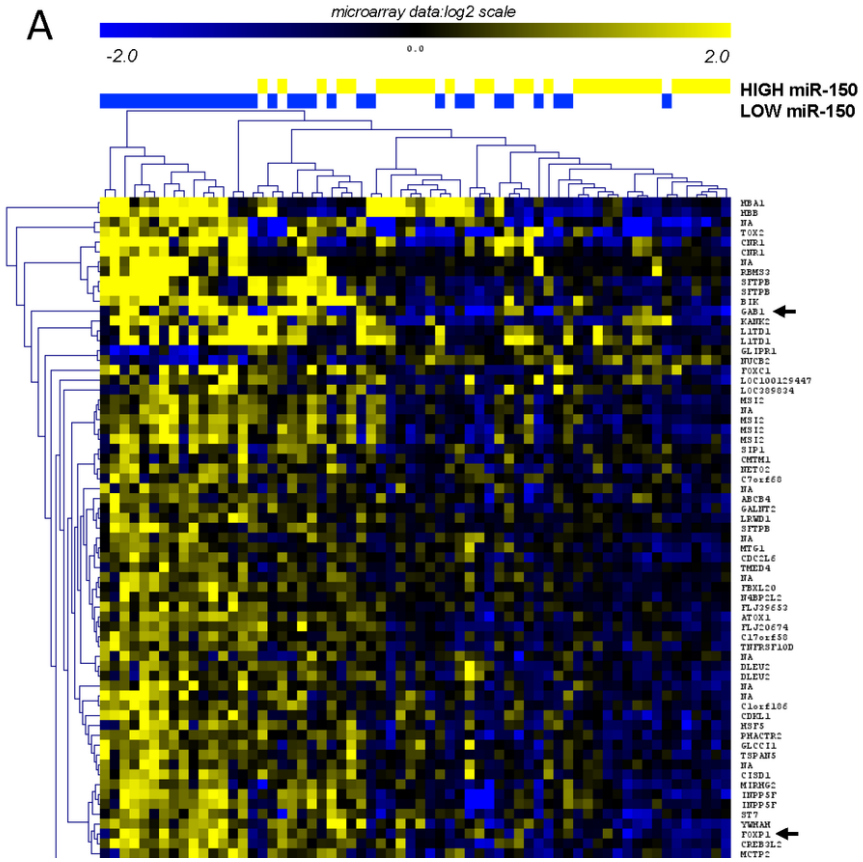
Jak identifikovat cíle miR-150 u CLL?

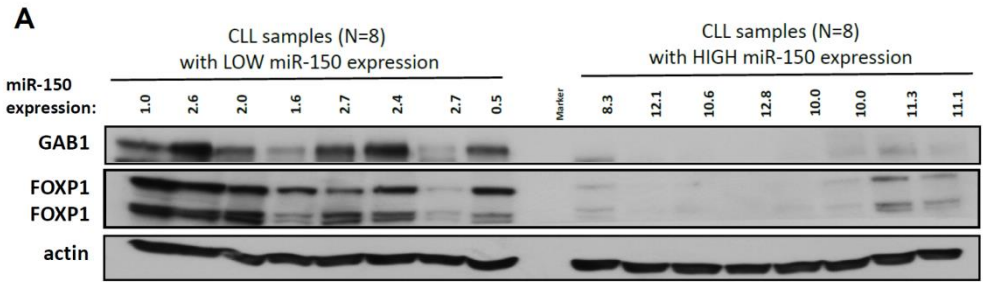
(HG-U133 Plus 2.0, Affymetrix)

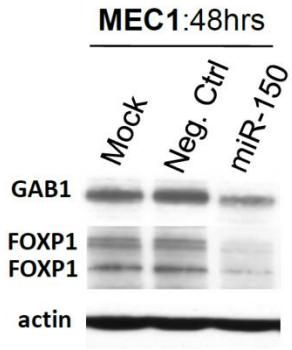


Genové expresní čipy pro CLL s nízkou vs vysokou hladinou miR-150

- 58 rozdílně exprimovaných genů
- 2 geny s evolučně konzervovanými vazebnými místy pro miR-150– **GAB1 a FOXP1**





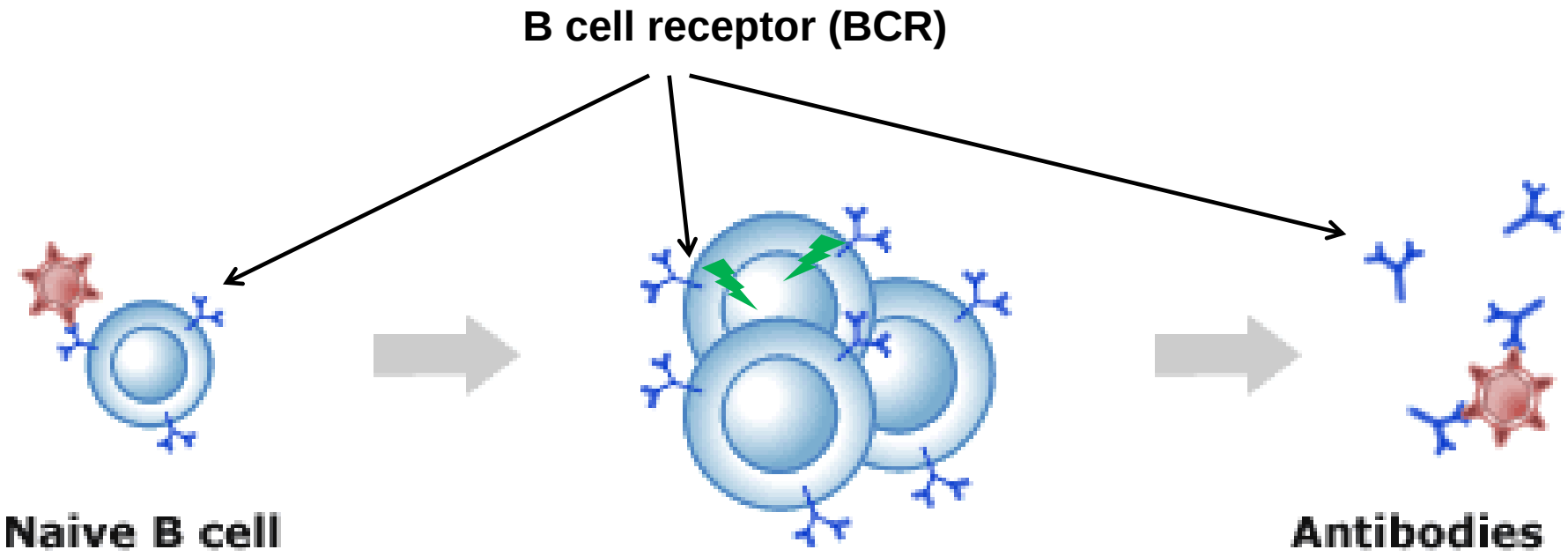


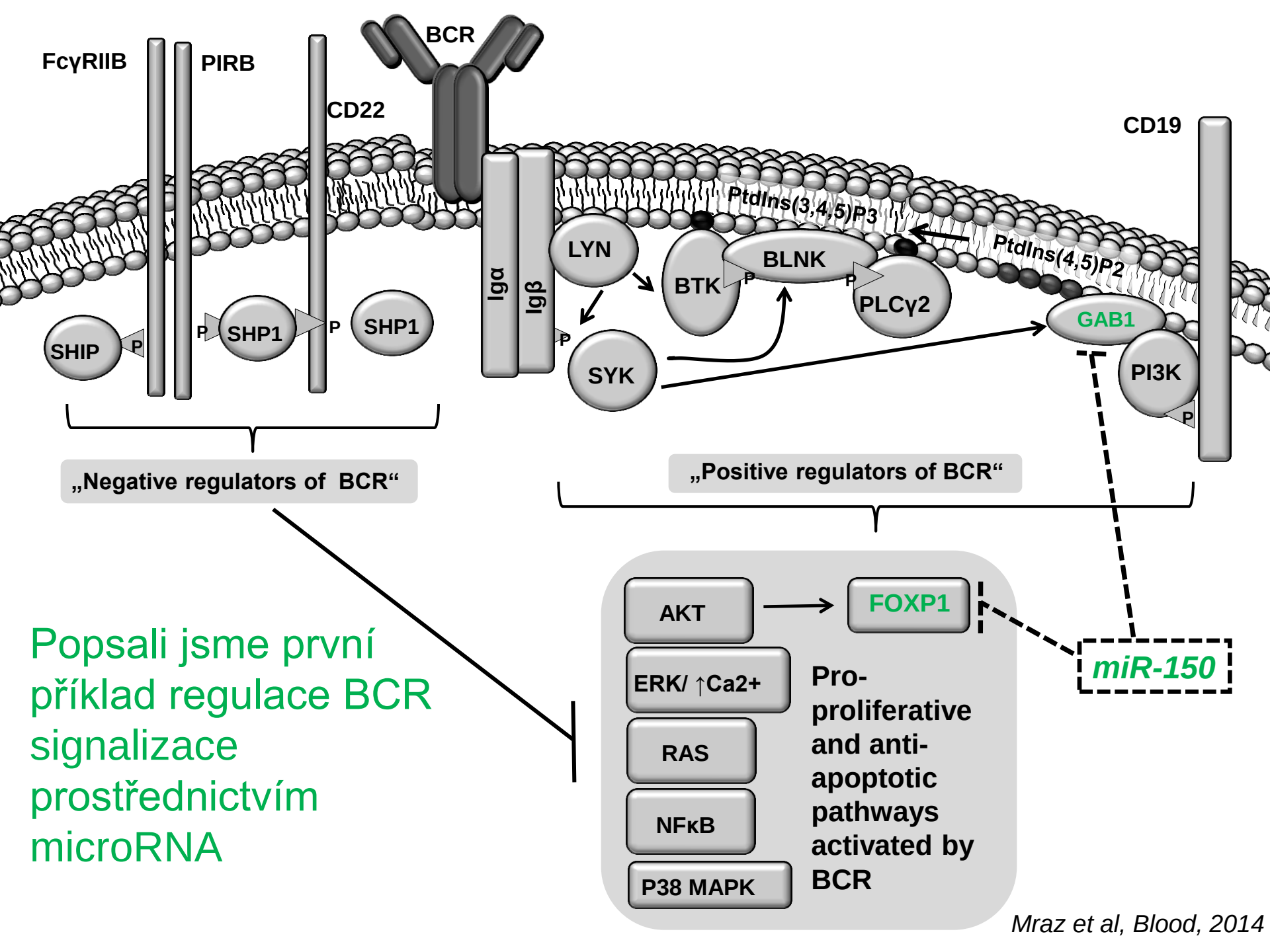
Mraz et al, Blood, 2014

GAB1 je adaptorová molekula, která je nutná k vazbě PI3K na membránu a amplifikaci BCR signalizace (Ingham et al. JBC, 2001).

FOXP1 je transkripční faktor důležitý pro vývoj B lymfocytů a asociovaný s ABC DLBCL a progresí B buněčných lymfomů (Hu et al. Nat Immunol, 2006).

Adaptivní imunity- centrální dráha BCR

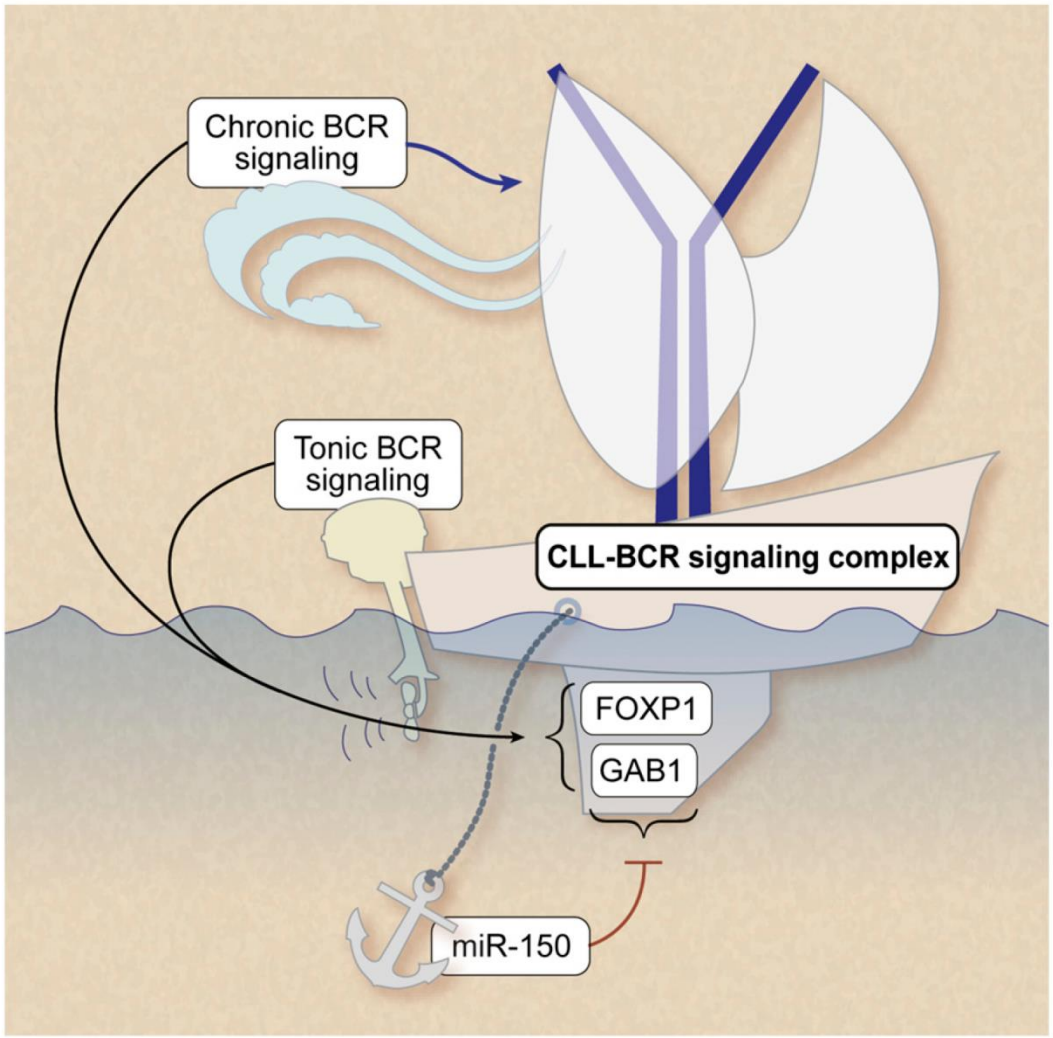




Popsali jsme první příklad regulace BCR signalizace prostřednictvím microRNA

Mraz et al, Blood, 2014

First description of miRNAs role in BCR signalling…not only in CLL



Ligand-independent ("tonic") and ligand-dependent ("chronic") BCR signaling play a pivotal role in CLL survival and growth. MiRNA-150 dampens the threshold for BCR signaling by repressing expression levels of GAB1 and FOXP1. Professional illustration by Debra T. Dartez.

Kater and Eldering, BLOOD, 3 JULY 2014 x VOLUME 124, NUMBER 1

- potentially usefull as **therapeutic targets**

nature Vol 452|17 April 2008|doi:10.1038/nature06783

LETTERS

LNA-mediated microRNA silencing in non-human primates

Joacim Elmén[1]*, Morten Lindow[1]*, Sylvia Schütz[2], Matthew Lawrence[3], Andreas Petri[1], Susanna Obad[1], Marie Lindholm[1], Maj Hedtjärn[1], Henrik Frydenlund Hansen[1], Urs Berger[4], Steven Gullans[3], Phil Kearney[1], Peter Sarnow[2], Ellen Marie Straarup[1] & Sakari Kauppinen[1,5]

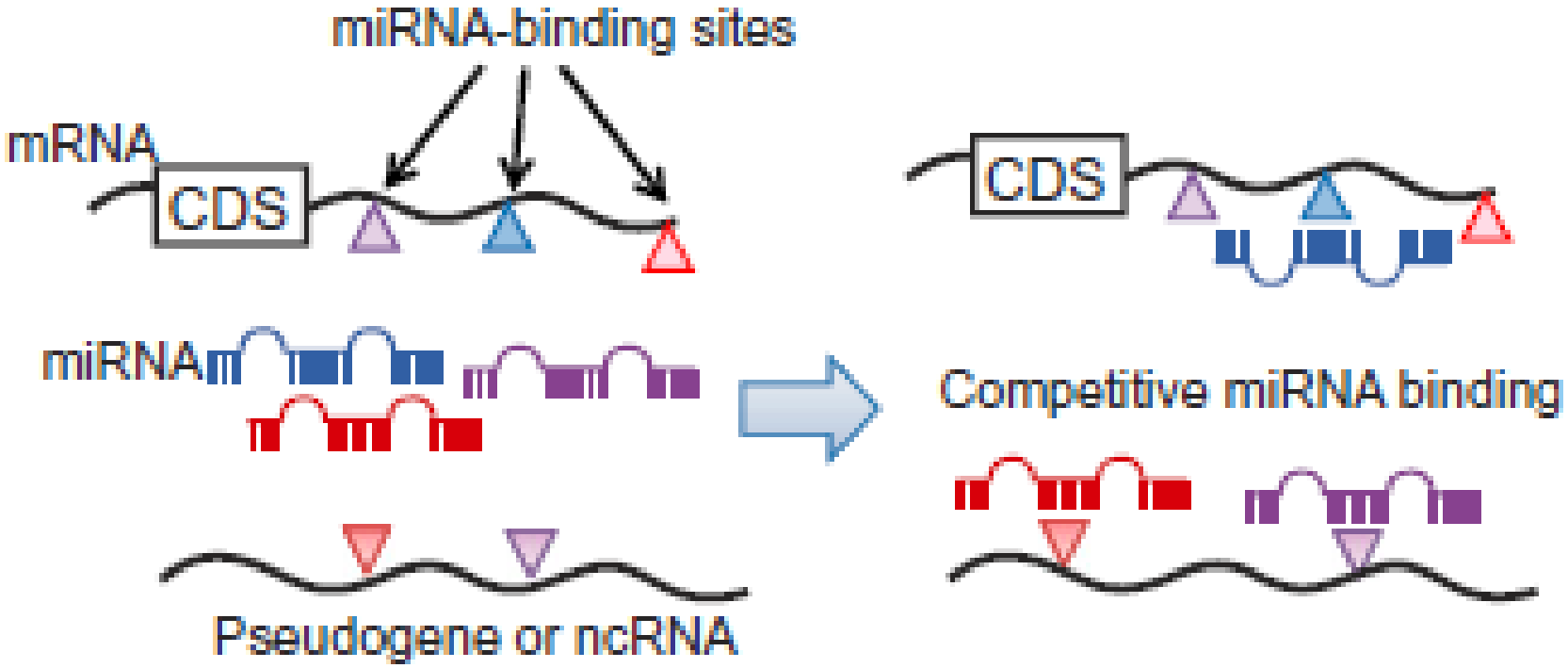
PCR based therapeutics?!

blood 2012 120: 1678-1686
Prepublished online July 13, 2012;
doi:10.1182/blood-2012-02-410647

LNA-mediated anti–miR-155 silencing in low-grade B-cell lymphomas

Yong Zhang, Aldo M. Roccaro, Christopher Rombaoa, Ludmilla Flores, Susanna Obad, Stacey M. Fernandes, Antonio Sacco, Yang Liu, Hai Ngo, Phong Quang, Abdel Kareem Azab, Feda Azab, Patricia Maiso, Michaela Reagan, Jennifer R. Brown, To-Ha Thai, Sakari Kauppinen and Irene M. Ghobrial

miRNA sequestration



Díky za pozornost

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