

Genomic and cDNA libraries

–Library

- **Contains ≥ 1 copy of all sequences**
 - **Chromosome library**
 - **Genomic library**
 - **cDNA library**

- **Step 1: Obtain DNA to be cloned**
 - **Genomic DNA cut into small pieces**
 - **cDNA prepared from mRNA with reverse transcriptase**
- **Step 2: Insert DNA fragment into vector**
- **Step 3: Insert vector into host**
- **Step 4: Allow host to replicate to high population #**
- **Step 5: Extract DNA**

DNA Libraries

...collections of cloned DNA fragments,

- genomic,
- cDNA (coding sequences).

Genomic Library Construction

- Cloning all fragments of an organisms genome = genomic library
 - Each fragment in a vector transformed into a bacterial cell = Book
 - The collection of all of the clones (thousands) is the genomic library
 - requirement: *random
 - * bigger is better

Genomic Library Construction

DNA fractionating

- DNA shearing
- to ensure that DNA fragments are of size suitable for cloning
 - Digest with enzyme with 4bp recognition site
 - One site every 256bp ($1/4 \times 1/4 \times 1/4 \times 1/4$)
 - Do a partial digestion (not all sites cleaved)
 - Ligate fragments to vector
 - Transform into *E. coli*

Genomic Sequences and Coverage

$$N = \frac{\ln(1 - P)}{\ln(1 - f)}$$

N = number of clones

P = probability of recovering a sequence,

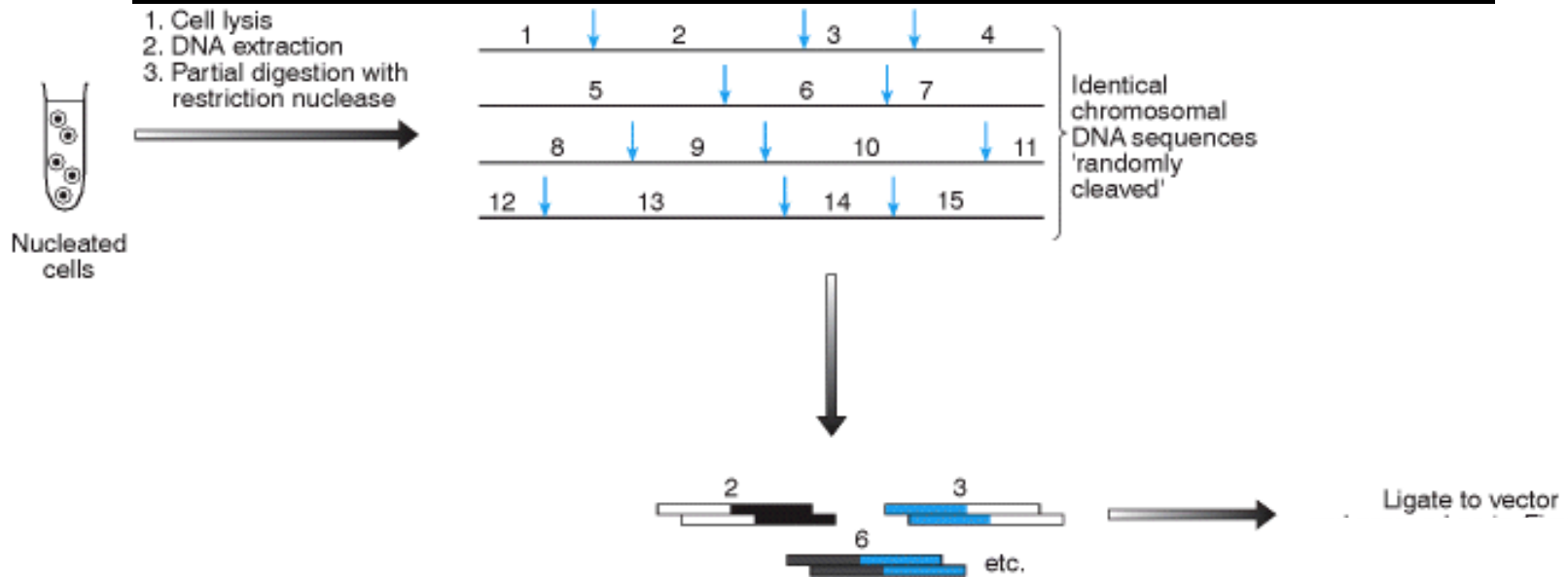
f = fraction of the genome of each clone

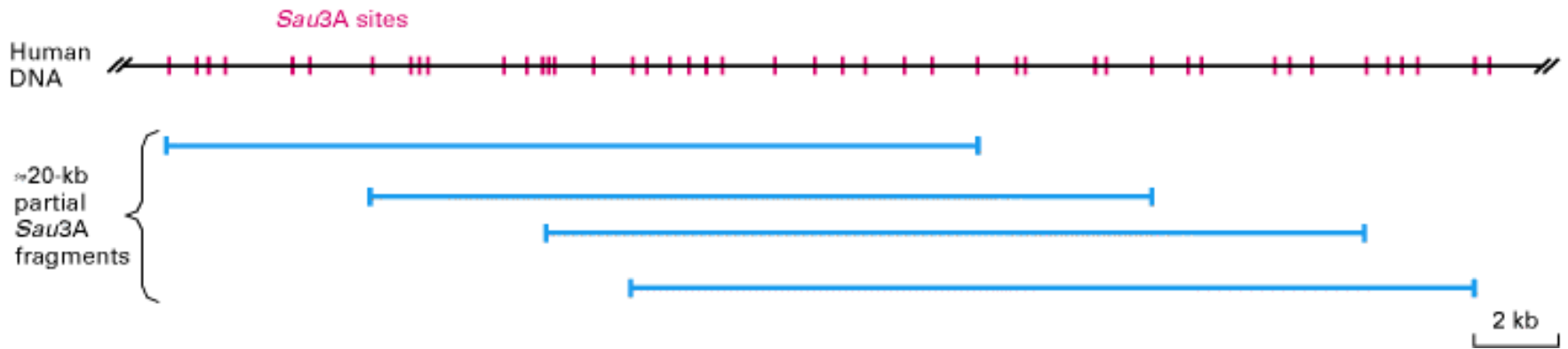
$f = \frac{\text{genome length}}{\text{average length of insert}}$

Probability	Insert lenght	
	15kb	40kb
0.99	860000	320000
0.95	560000	210000
0.9	430000	160000
0.8	300000	115000

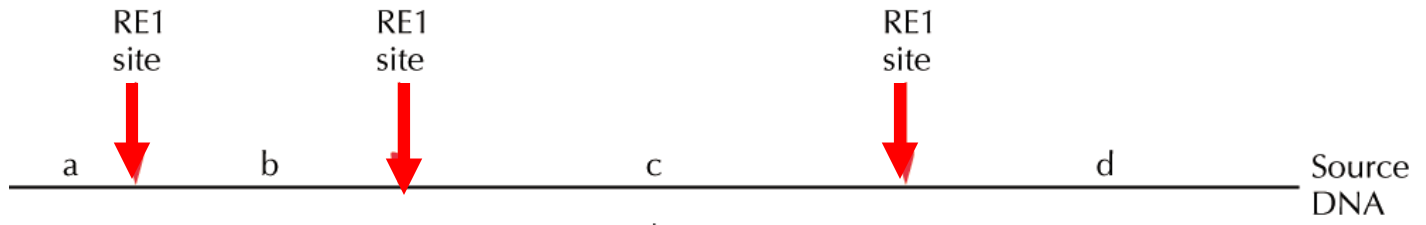
Results for the human genome

Making a genomic DNA library.



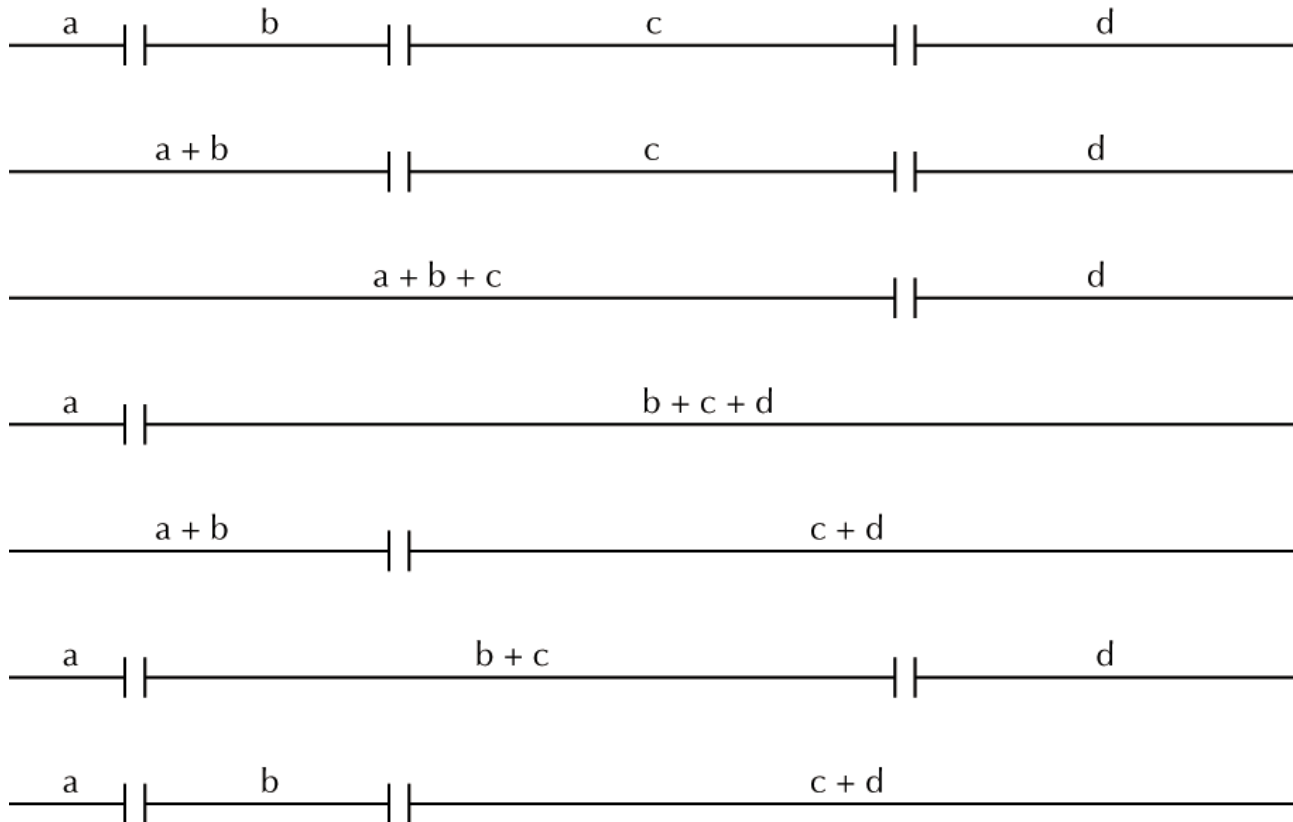


This restriction endonuclease recognizes the 4-bp sequence GATC and produces fragments with single-stranded sticky ends with this sequence on the 5' end of each strand. A hypothetical region of human genomic DNA showing the *Sau3A* recognition sites (red) is shown at the top. Partial digestion of this region of DNA would yield a variety of overlapping fragments (blue) ≈20 kb long. Use of such overlapping fragments increases the probability that all sequences in the genomic DNA will be represented in a λ library.

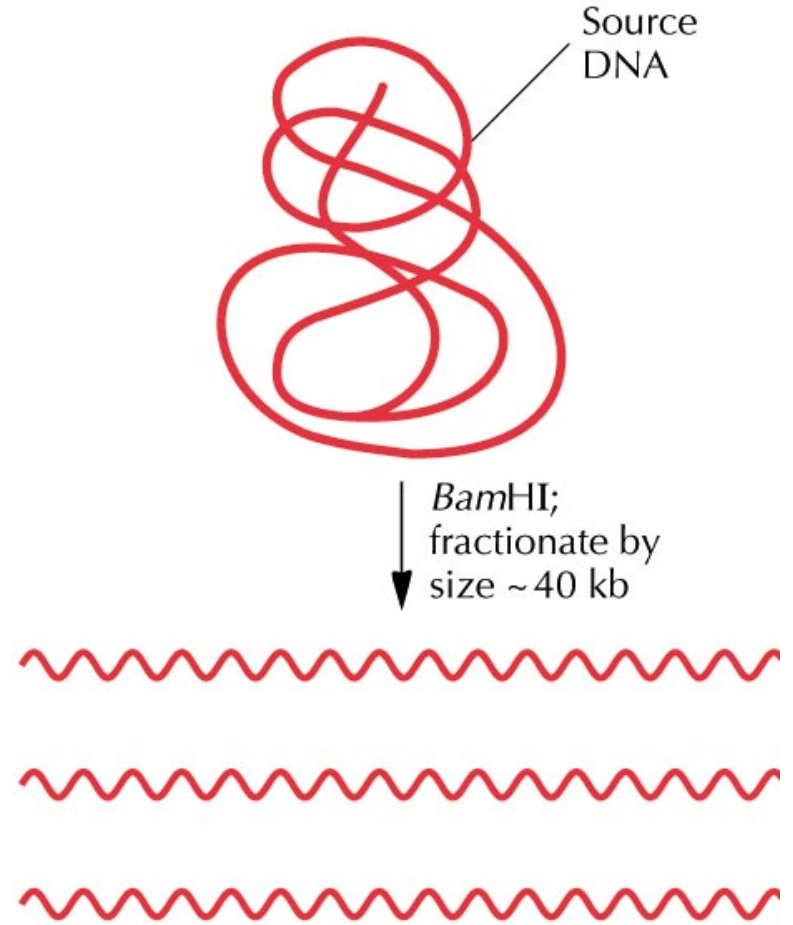
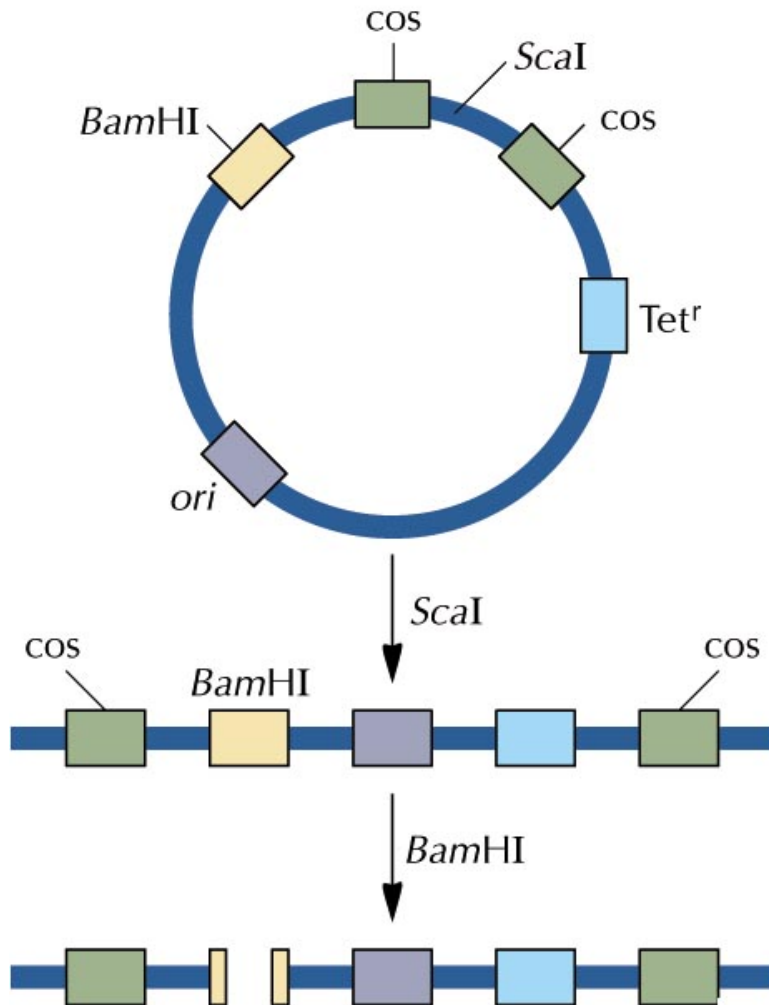


Partial Digest

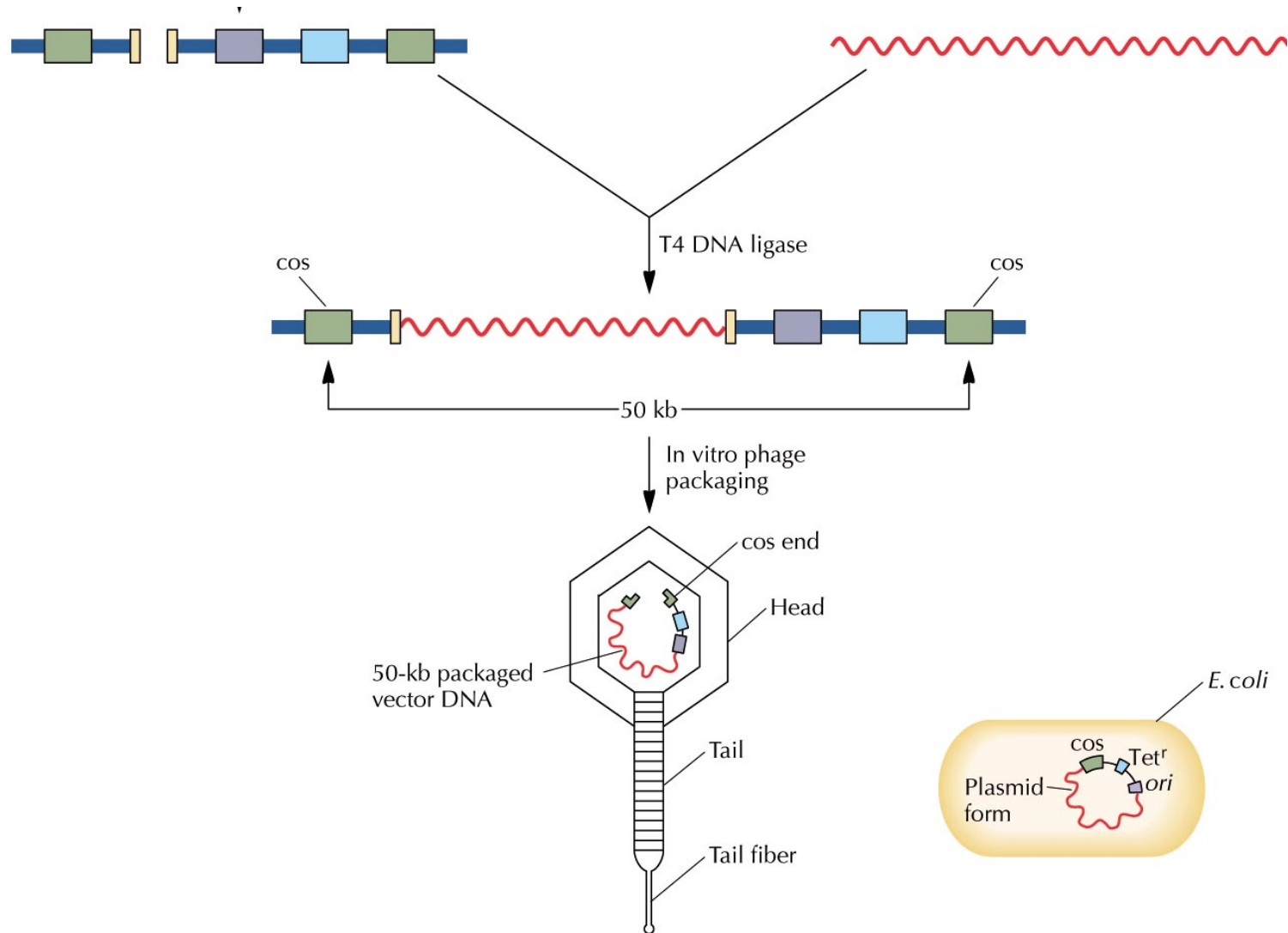
Partial digestion
with a restriction
endonuclease

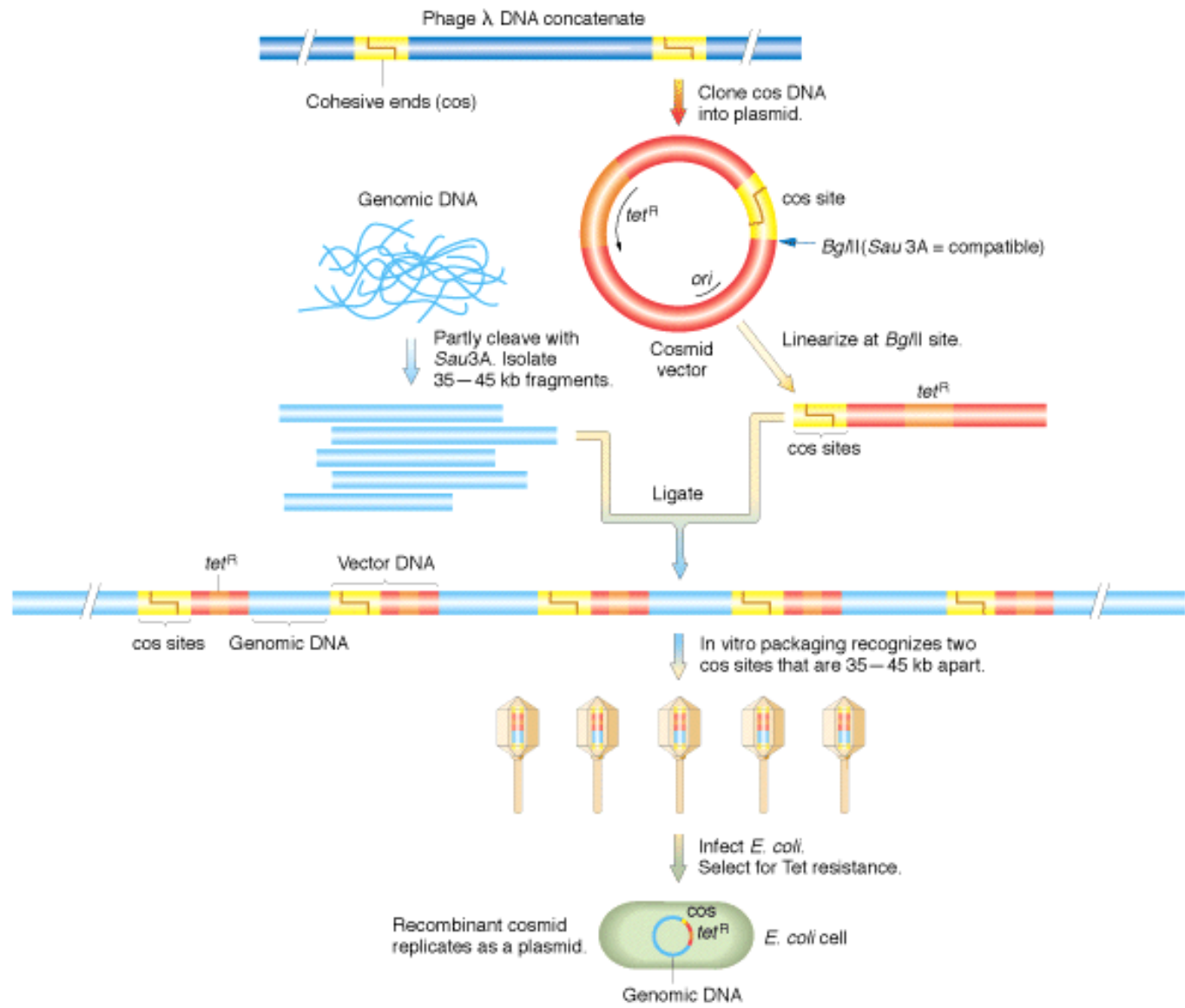


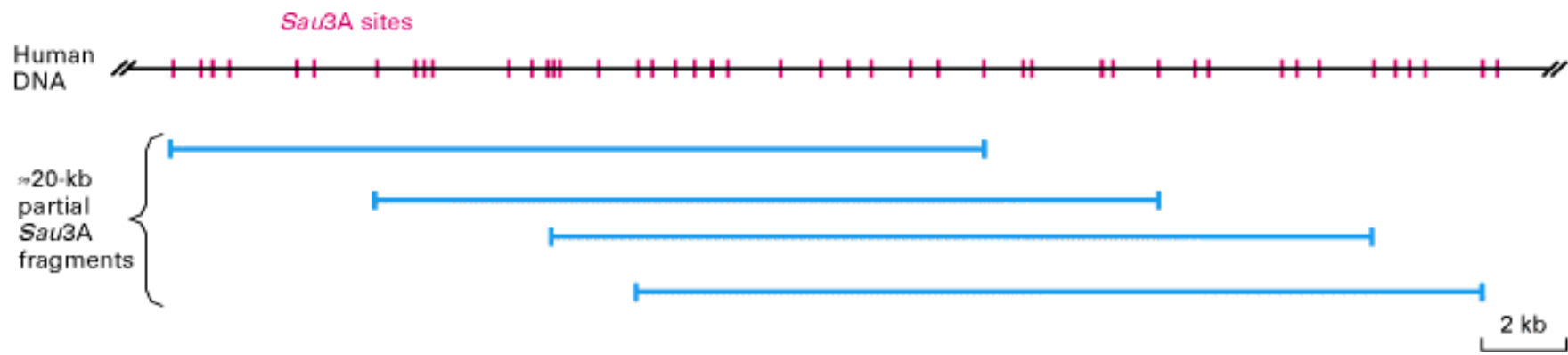
Cosmid Cloning



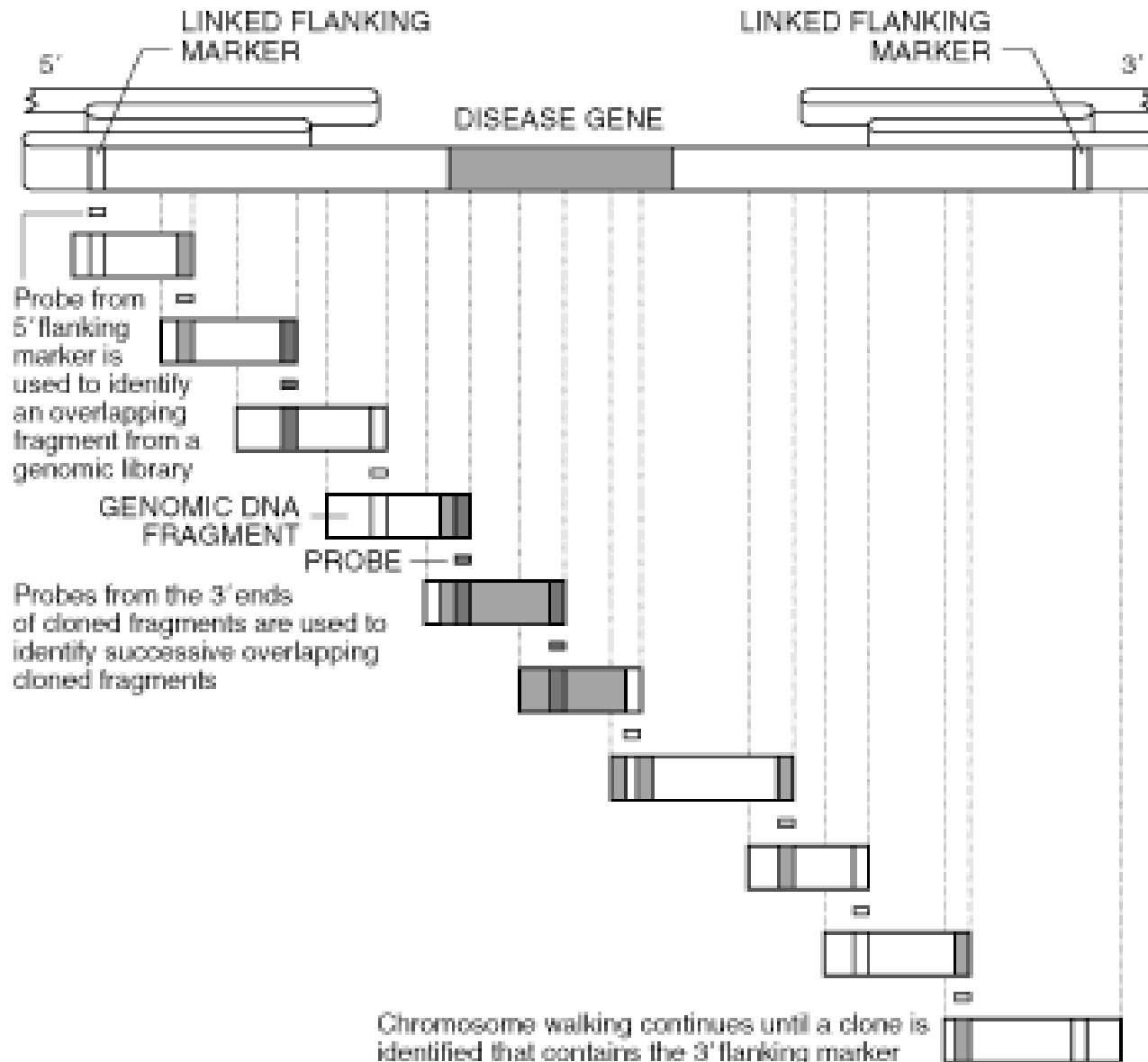
Cloning in Cosmids



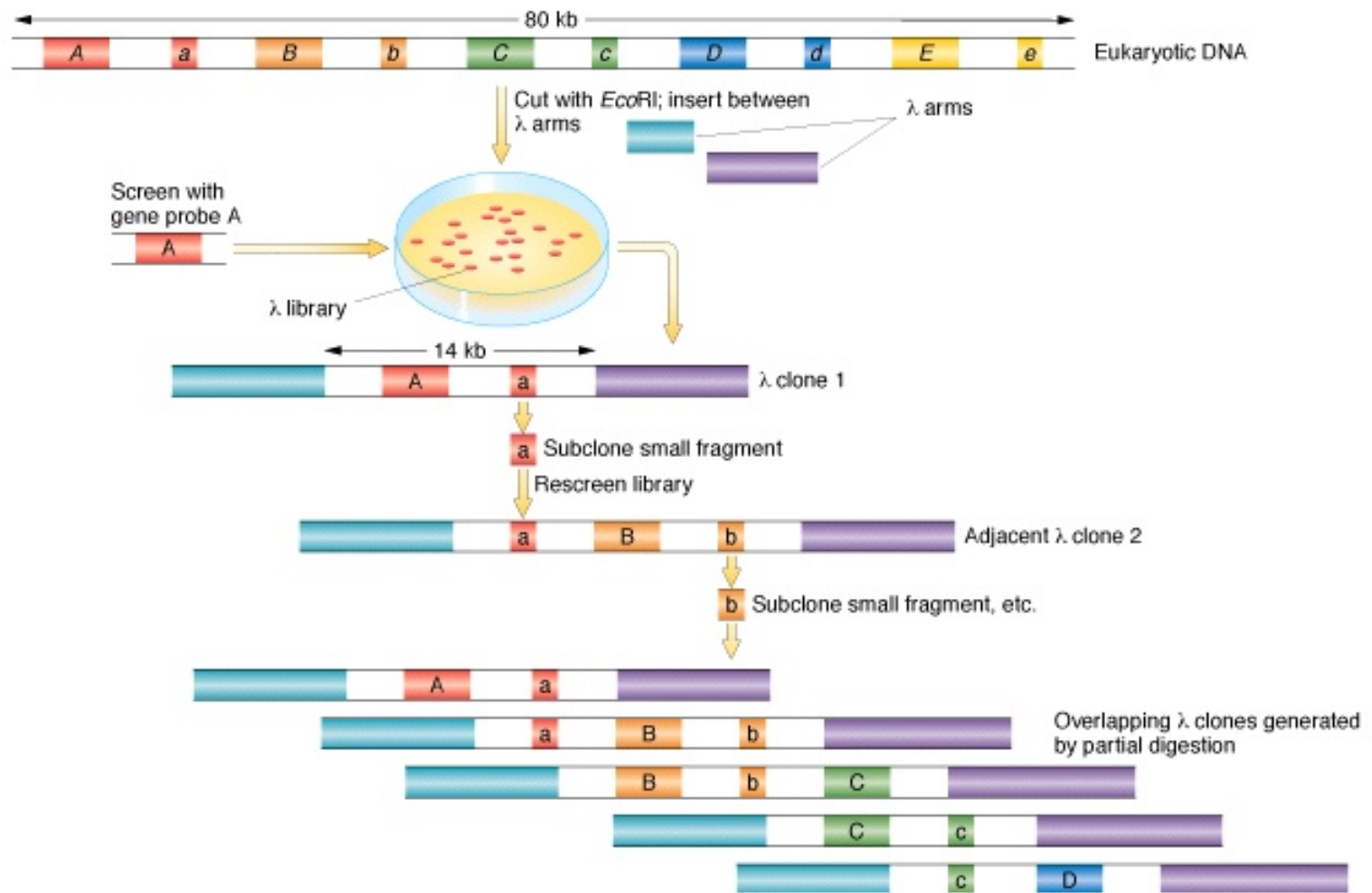




CHROMOSOME WALKING



CHROMOSOME WALKING



Chromosome 'Walking'

Genomic



Starting λ clone from genomic library



Isolate DNA fragment from desired end



Re-probe λ genomic library to isolate new clone



Isolate DNA fragment from desired end



Re-probe λ genomic library to isolate new clone



Isolate DNA fragment from desired end



Re-probe λ genomic library to isolate new clone



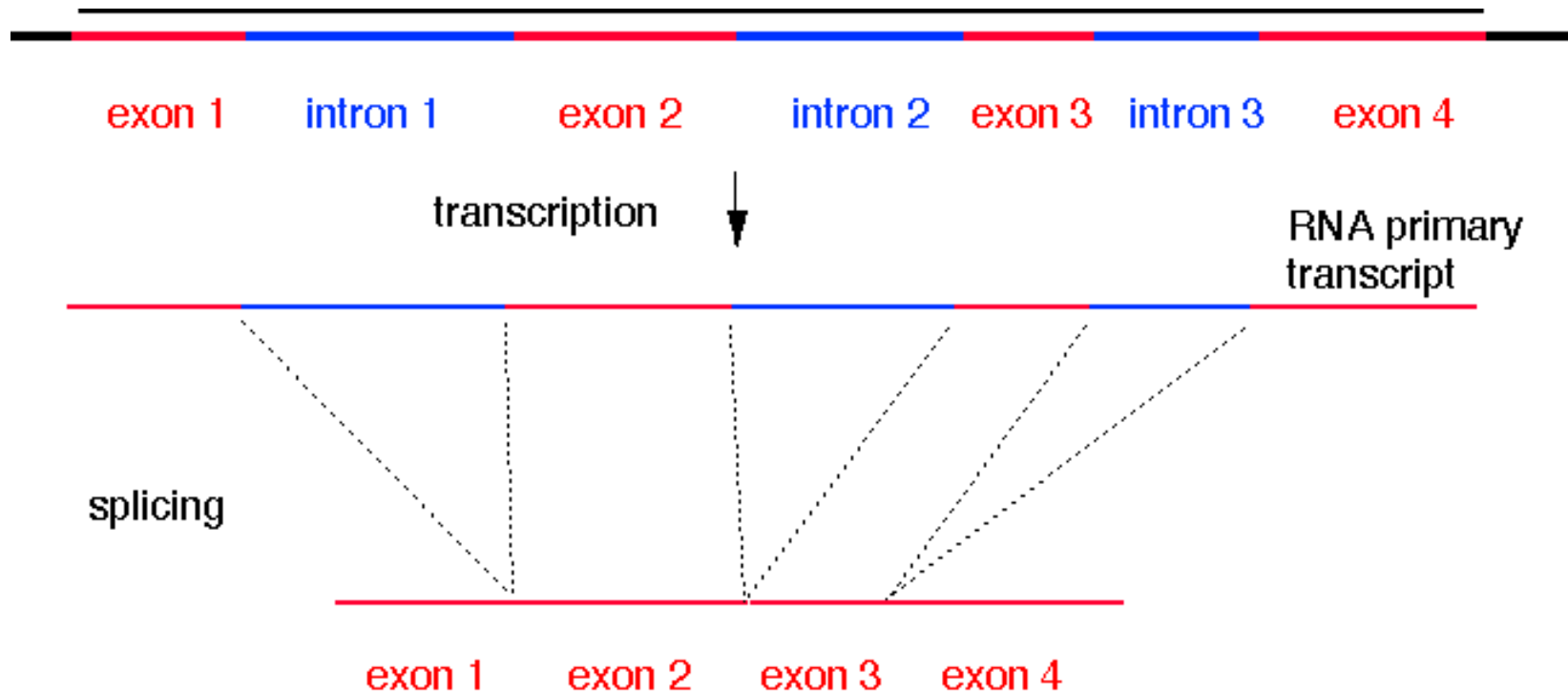
etc., etc.

DNA Libraries

...collections of cloned DNA fragments,

- genomic,
- cDNA (coding sequences).

Cloning eukaryotic genes in prokaryotes require special "tricks" because eukaryotic genes have introns which are removed in the nucleus of eukaryotic cells prior to translation



Introns can account for more than 90% of the length of a eukaryotic gene. It is hard to clone very long DNA segments. In addition, intron-containing eukaryotic genes cannot be expressed in a bacterial host because prokaryotes lack splicing apparatus.

*To overcome these problems, instead of directly cloning a gene, one can clone **cDNA**, a DNA copy of gene mRNA.*

An enzyme, reverse transcriptase, is used to produce cDNA

cDNA

...DNA synthesized from an mRNA template with the enzyme **reverse transcriptase**.

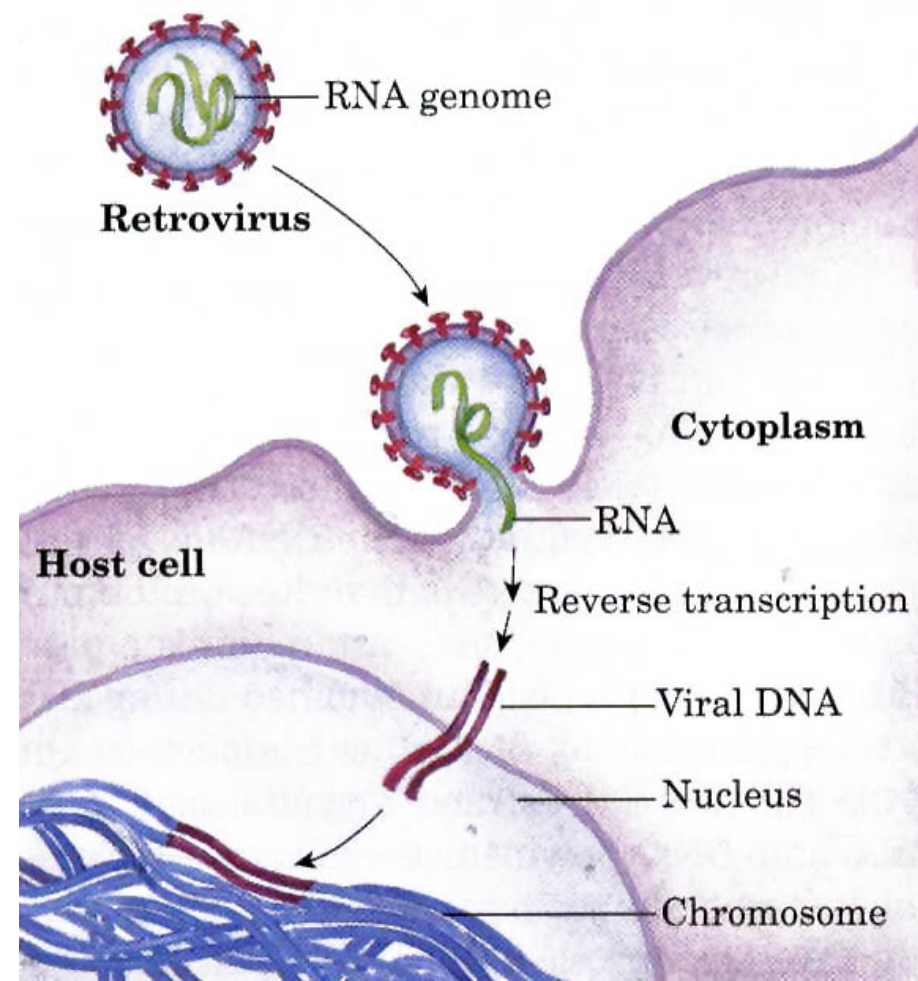
Reverse Transcriptase

1. RNA dependent, DNA synthesis.
2. RNA Degradation.
3. DNA dependent, DNA Synthesis.

Basically two types:

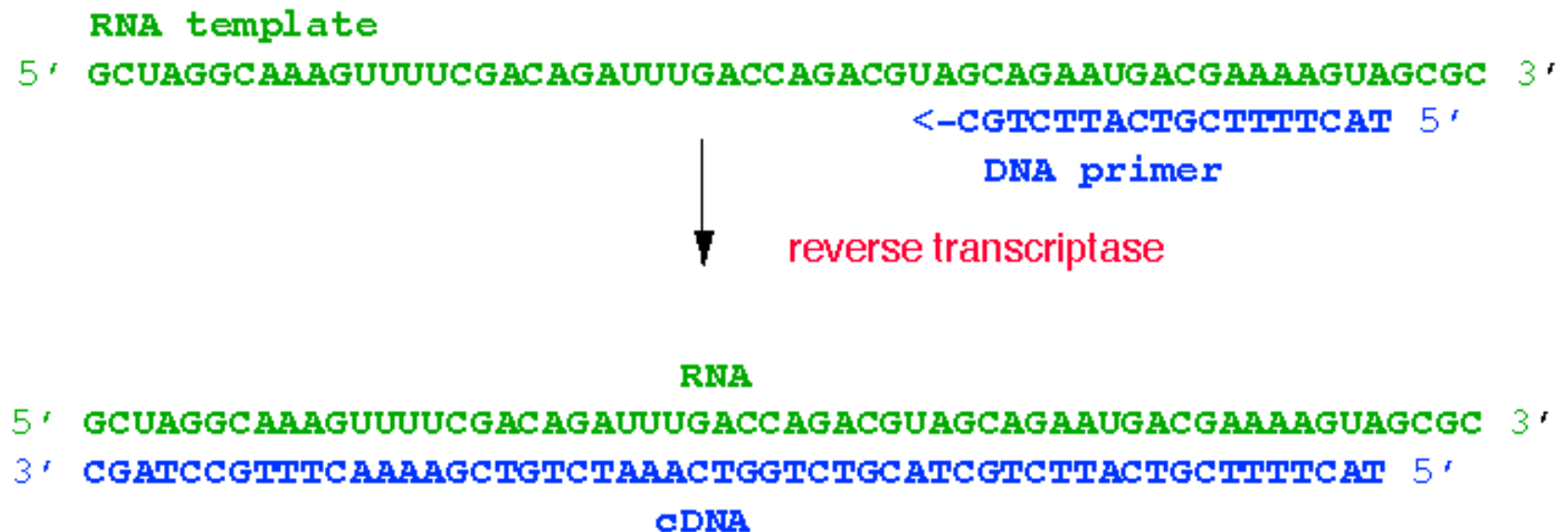
- AMV (avian myeloblastosis)
- MMLV (Moloney Murine Leukemia Virus)

Error Rate: 1 in 20,000 nucleotides.

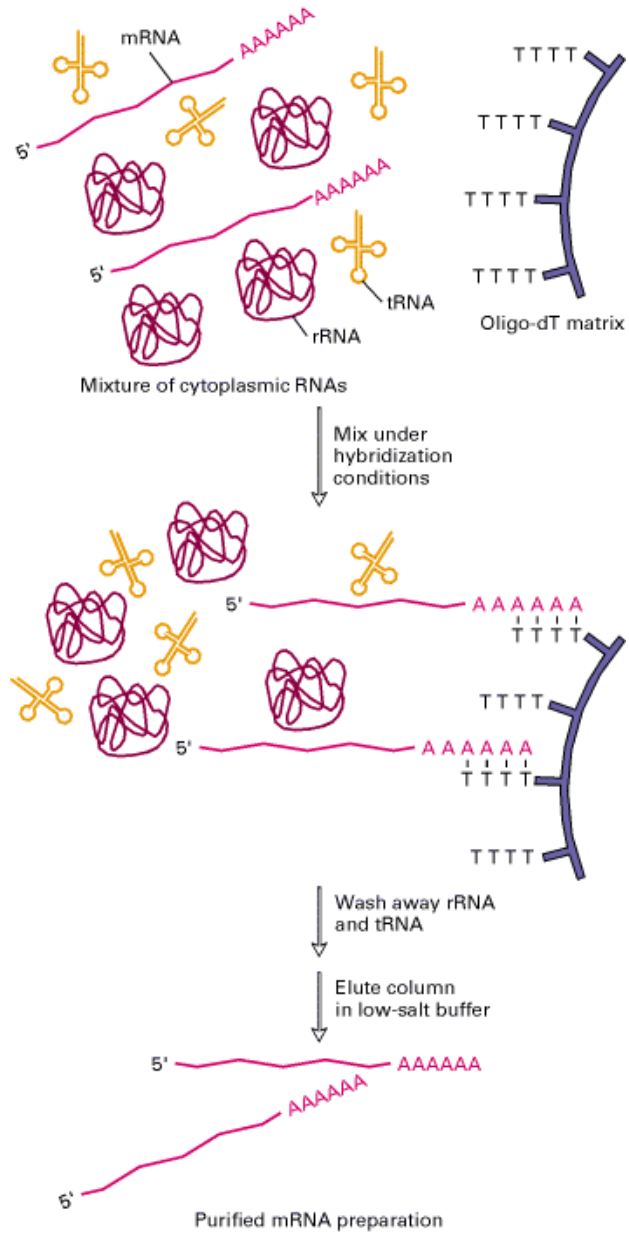


Reverse transcriptase is an RNA-dependent **DNA polymerase**: it synthesizes a complementary DNA strand on the RNA template.

Similar to other DNA-polymerases, reverse transcriptase needs a **PRIMER** to initiate DNA synthesis.

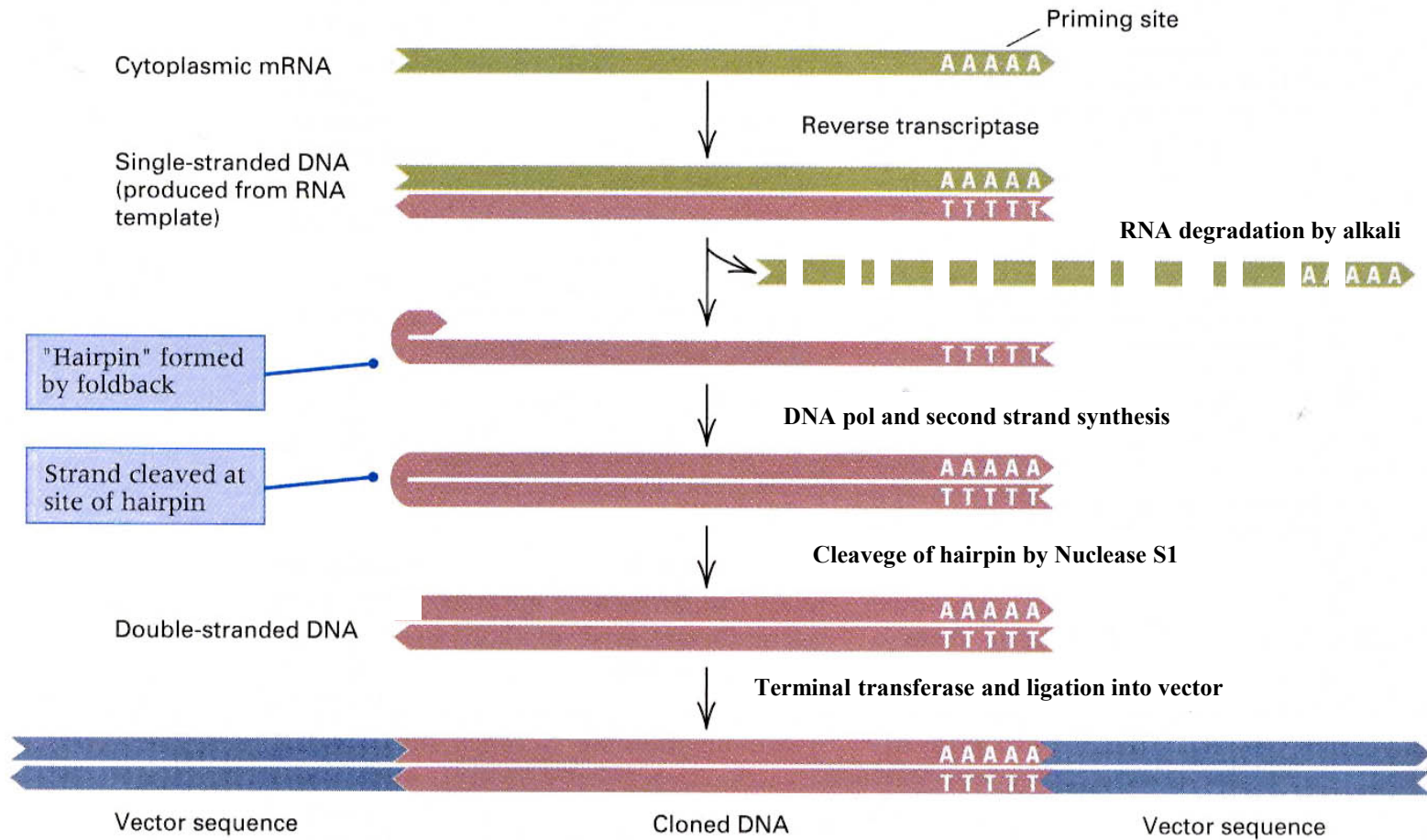


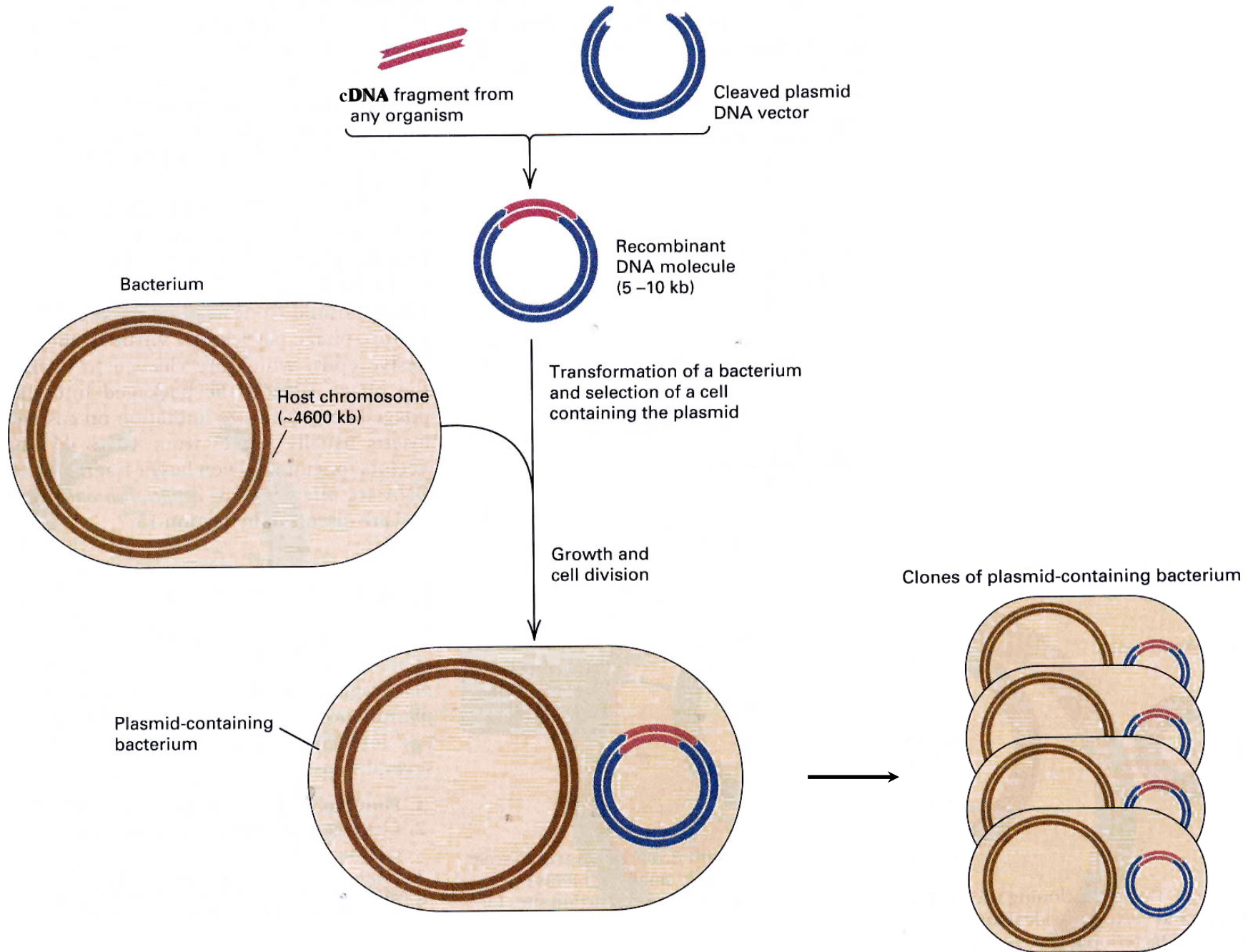
DNA strand synthesized on the RNA template is called **cDNA** (for **c**omplementary **DNA**)



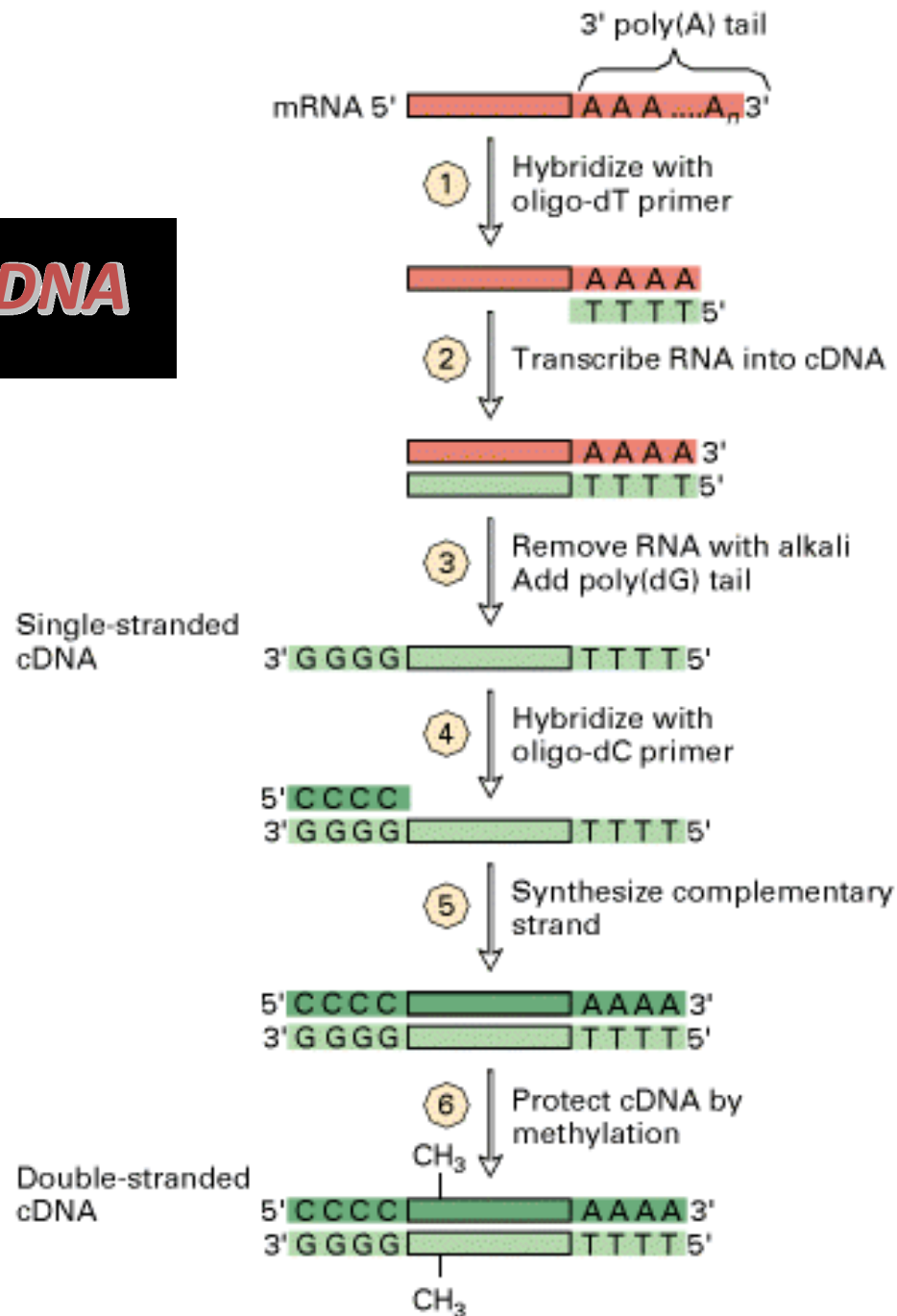
Isolation of mRNA by oligo-dT affinity chromatography.

cDNA Construction *in vitro*

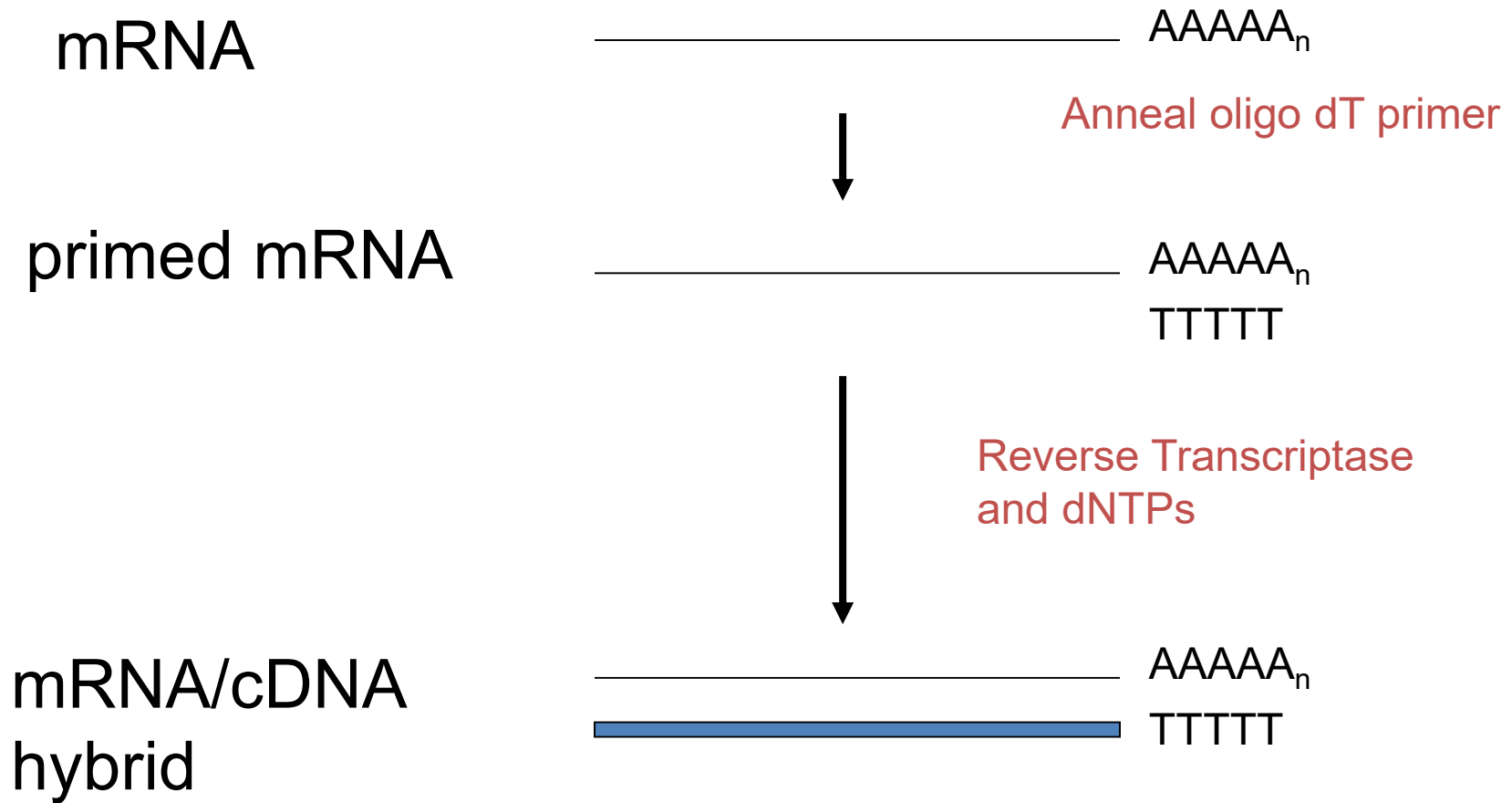




**Strategy to
synthesize
double strand cDNA**



B) cDNA Synthesis



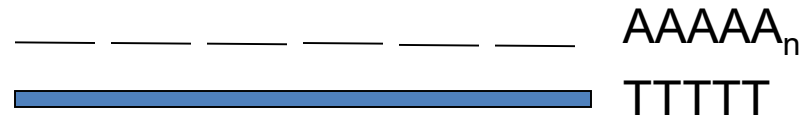
Gubler Hoffman cDNA Synthesis

mRNA/cDNA
hybrid



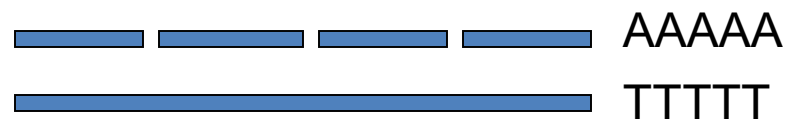
RNase H

nicked RNA



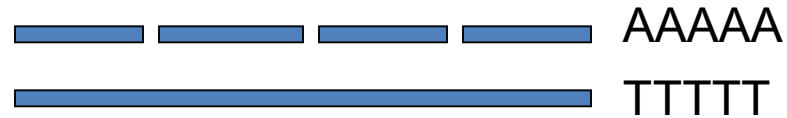
DNA Pol I

nicked RNA used
as primers by Pol



Gubler Hoffman cDNA Synthesis

2nd strand cDNA
in pieces



E. coli DNA
Ligase

ds cDNA



Clone into vector

cDNA Library

cDNA Libraries

...provide a 'snap-shot' of the genes expressed in a particular cell, at a particular time, or under specific condition,

...however, do not provide regulatory sequences.

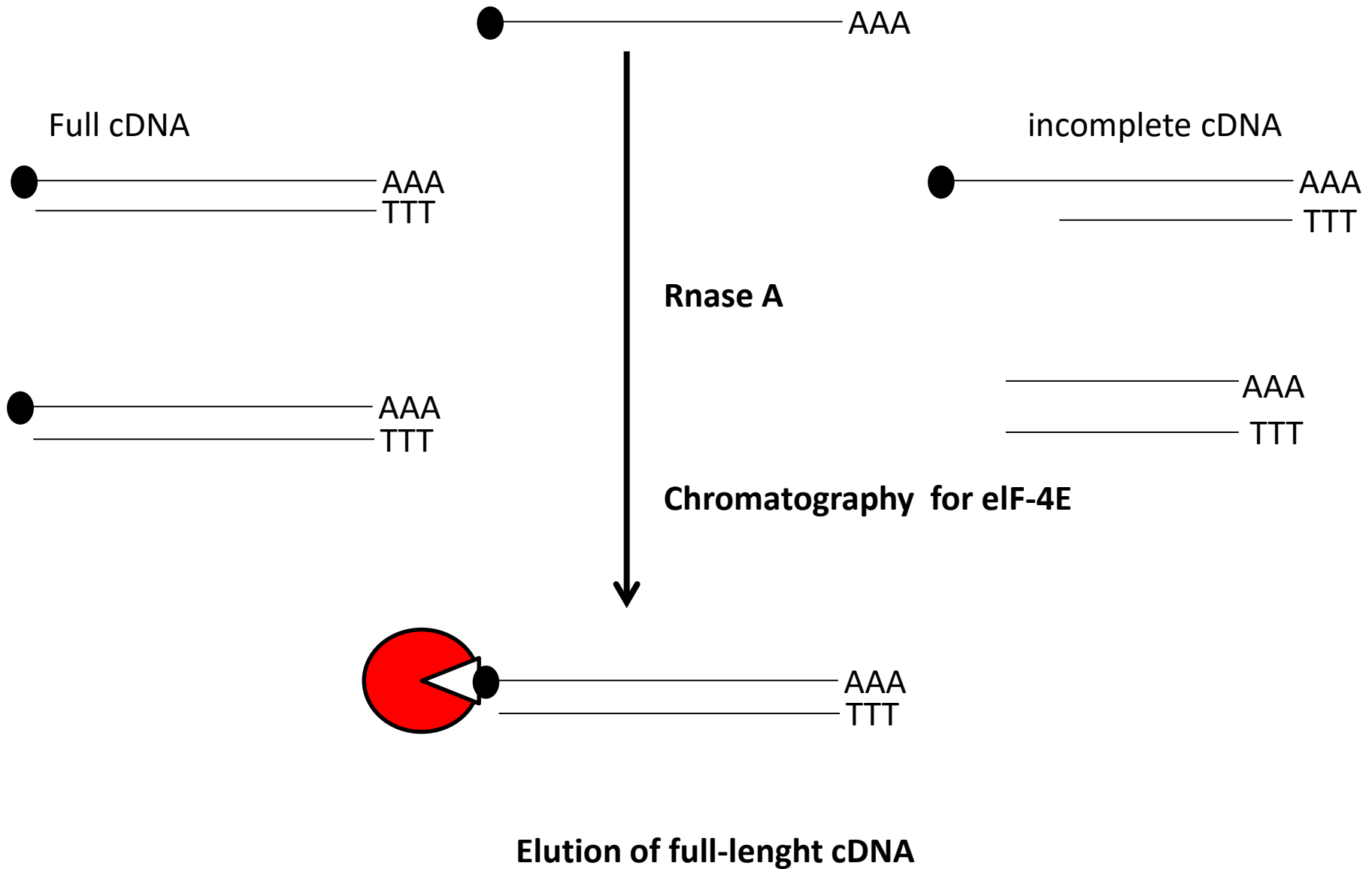
cDNA Libraries Limits:

...using a oligo dT, library has 3'-rich sequences

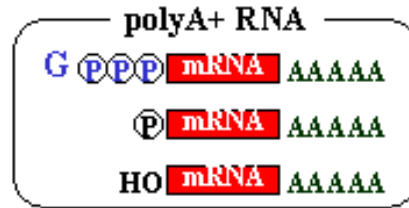
Using random examers it's possible overcome this drawbacks, but the average length of sequences is reduced.

...hard to isolate long and full-length transcripts.

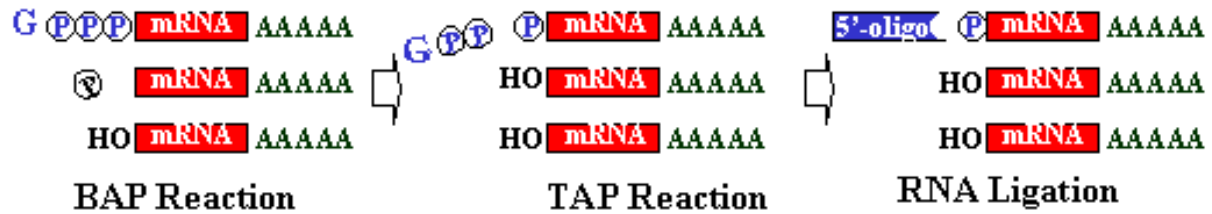
CAPtured method:



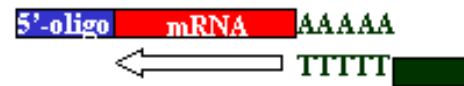
Scheme of Full-Length Library Construction



“Oligo-Capping” Procedure



1st Strand Synthesis



Alkaline Degradation



PCR



*Sfi*I Digestion



Vector Ligation





BAP= Alkaline phosphatase

TAP= acid pyrophosphatase

5' - RACE Rapid Amplification Complementary Ends

mRNA 7-mG  AAAAA-3'

Sintesi primo filamento cDNA \downarrow Trascrittasi inversa + GSP1





7-mG  AAAAA-3'
 GSP1


Aggiunta coda omopolimera al primo filamento cDNA

Trasferasi terminale + dATP

3'-AAAAAAAA  GSP1 5'

Sintesi secondo filamento cDNA \downarrow

 P   GSP1 3'
3'-AAAAAAAA  GSP1 5'

complementarietà al primer  P

I° gruppo di amplificazioni

5'  P   GSP1 3'

3'  GSP1 5'

complementarietà al primer  P(dT)



5'  P   GSP1 3'

3'  P'   GSP1 5'

II° gruppo di amplificazioni

5'  P   GSP1 3'

 GSP2

 P 

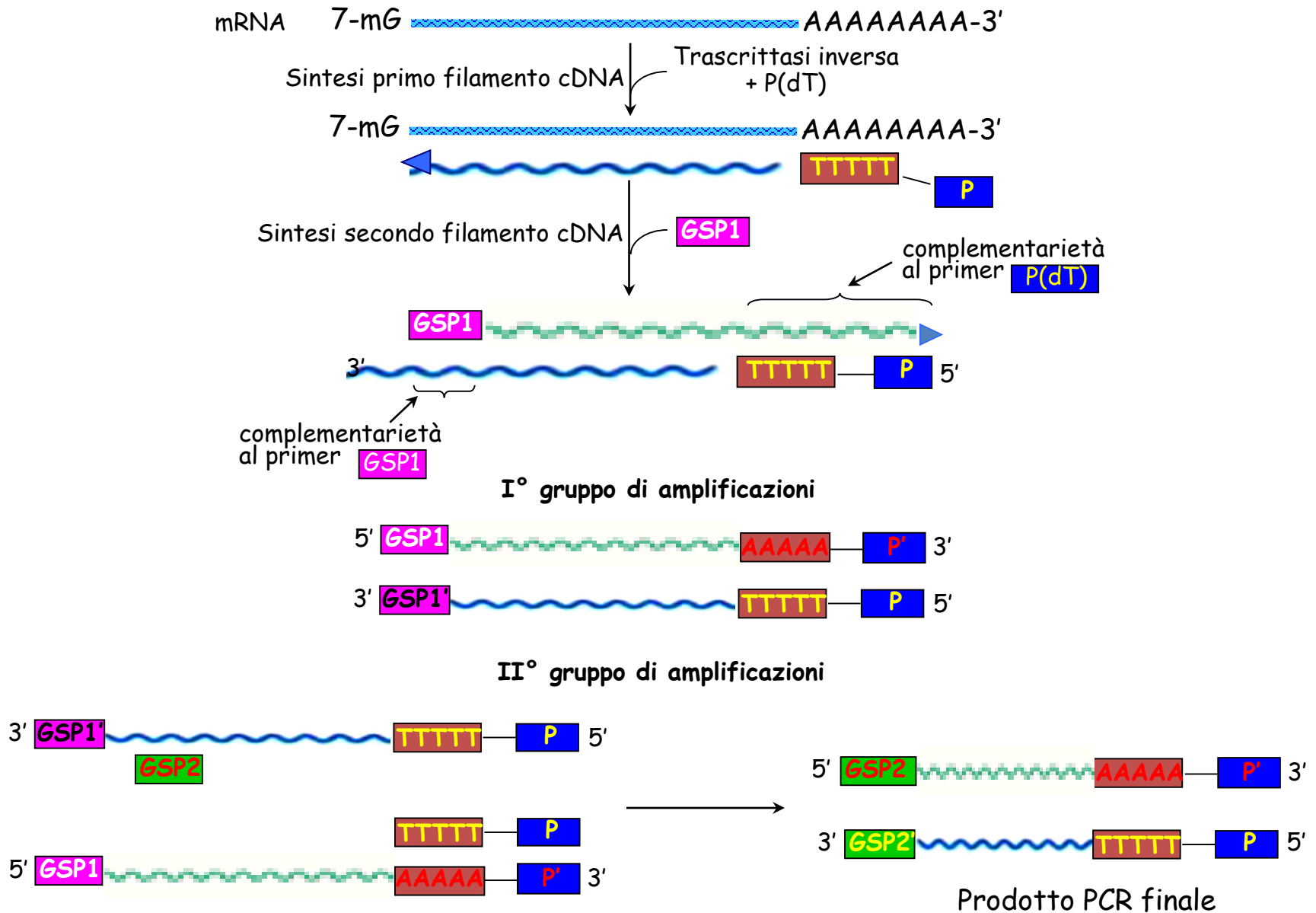
3'  P'   GSP1 5'

5'  P   GSP2 3'

3'  P'   GSP2 5'

Prodotto PCR finale

3' - RACE Rapid Amplification Complementary Ends



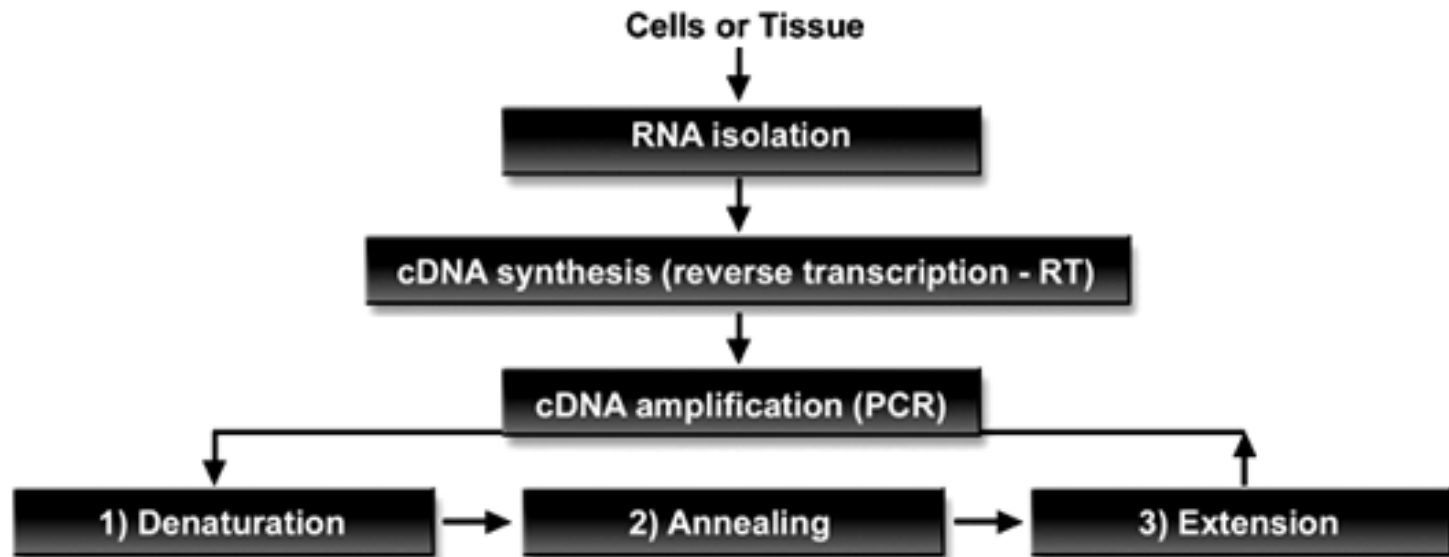
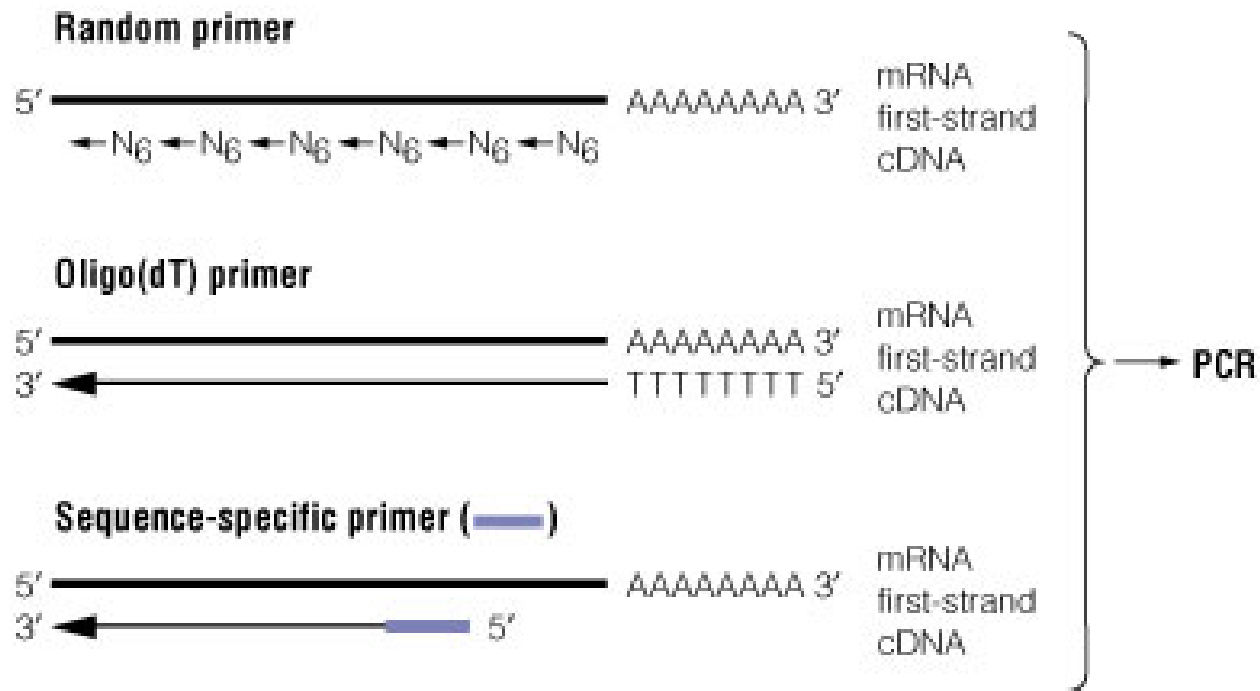


FIGURE 3 - Schematic diagram of RT-PCR showing that RNA isolated from cells or tissue is used as substrate in reverse transcription for synthesis of cDNA that will serve as template for amplification by PCR.

First Strand Synthesis:

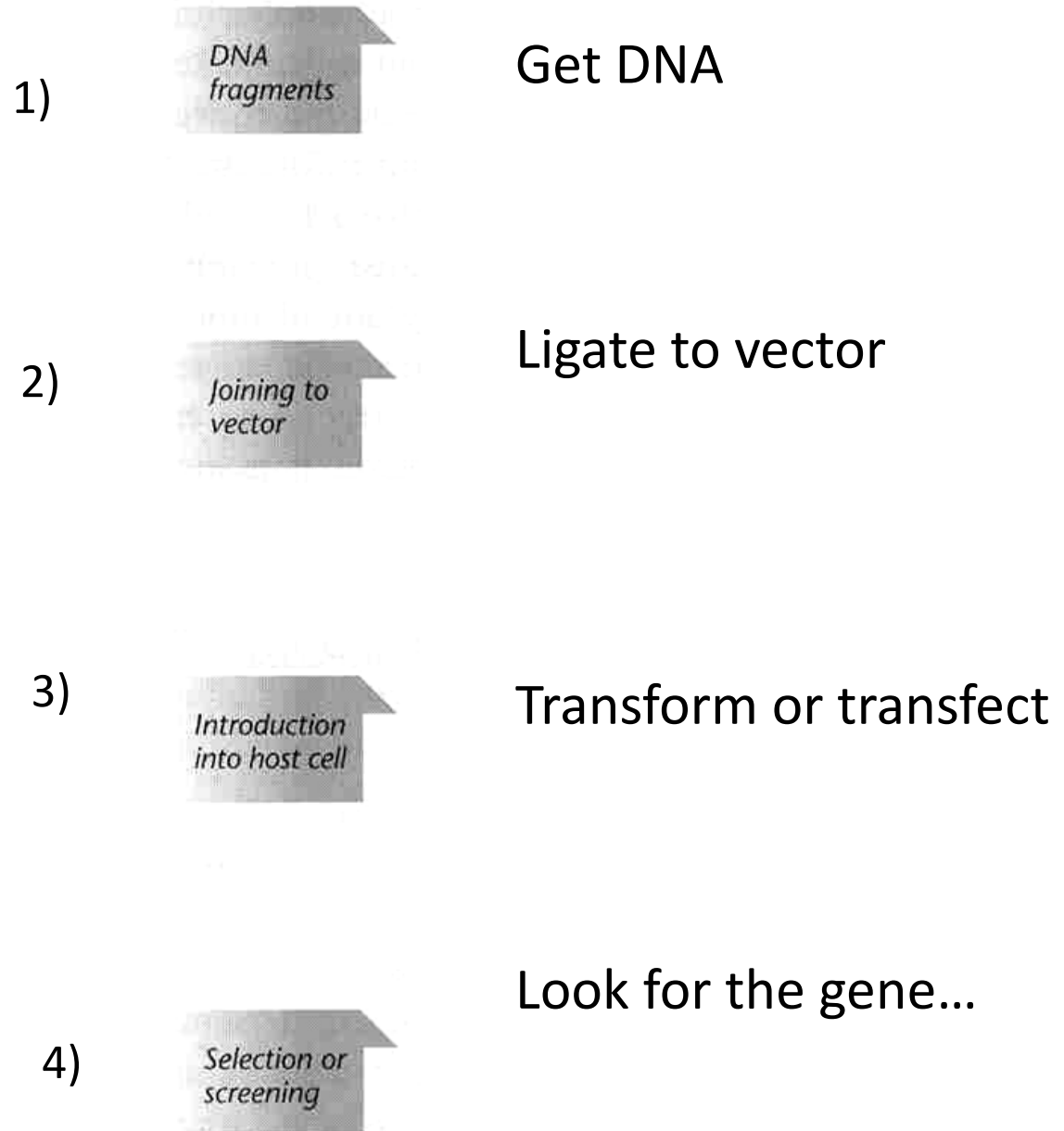


o---- Cloning strategies ----o

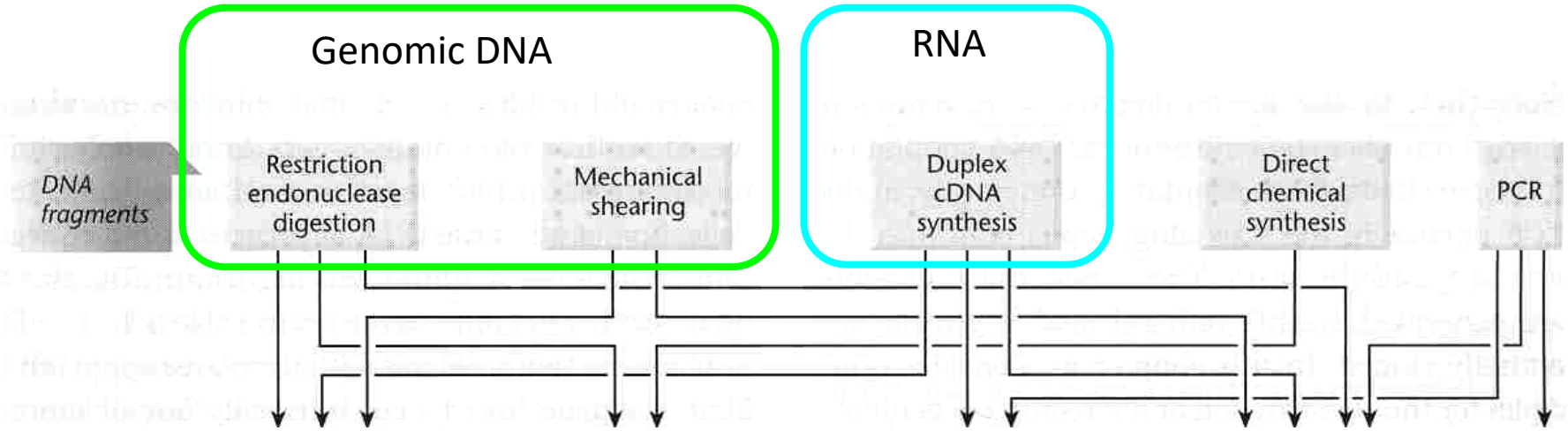
- I. Making DNA “libraries” (from genomic DNA, mRNA “transcriptome”)
- II. Screening to identify a specific clone (the needle in the haystack)
 - by the sequence of the clone
 - by the structure or function of the expressed product of the clone

Course reading: #28
(and 29)

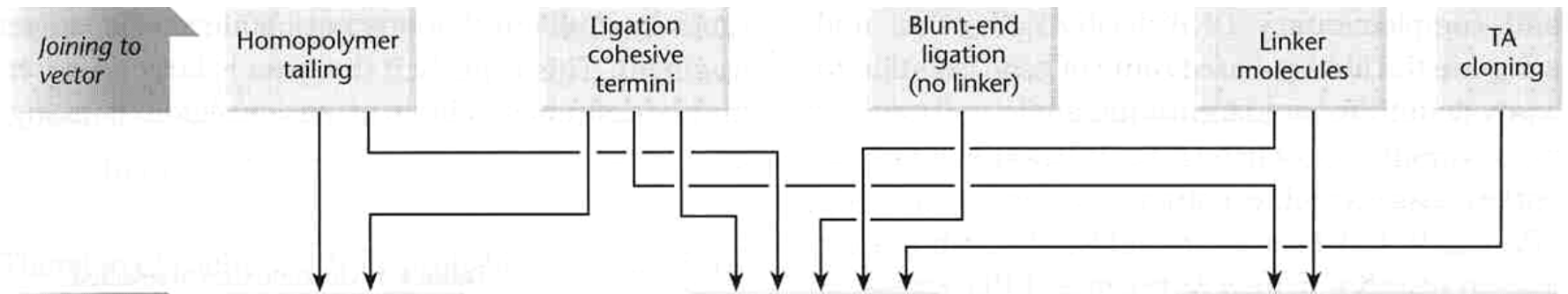
Overview of strategies for cloning genes



1) Get DNA



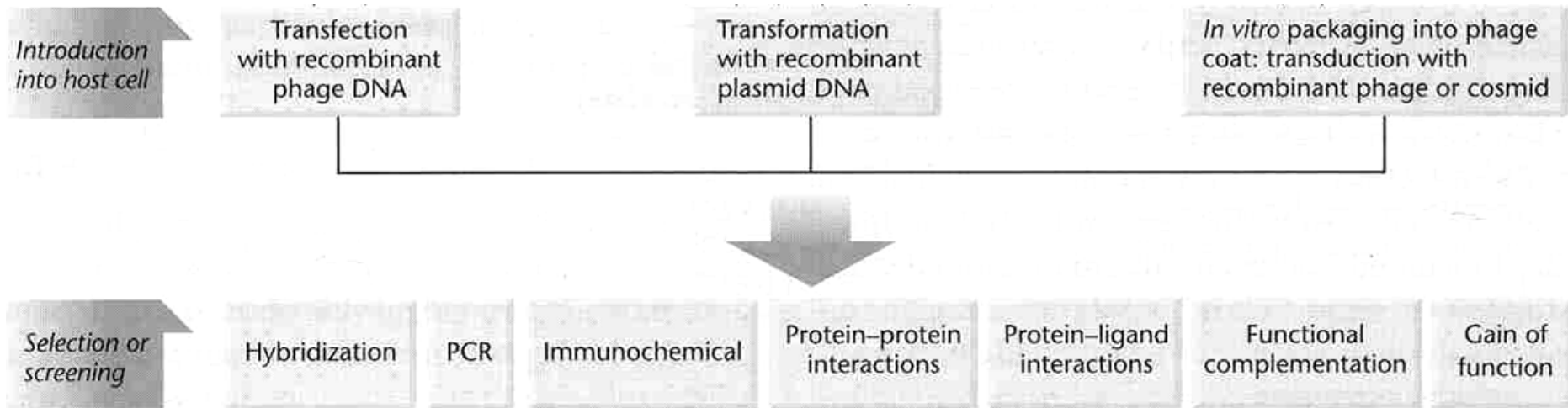
Ligate to vector: how to make this reaction favorable?



This yields a “library”, a representative set of all the pieces of DNA that make up a genome (or all the cDNAs that correspond to the “transcriptome”)

cDNAs from different tissues reflect the different RNA populations that you find in distinct cell types:

Hence “liver” vs. “brain” vs. “heart” cDNA libraries



There are lots of ways to identify a particular gene...

Overview of strategies for cloning genes

