

Modern Tools of Molecular Biology

Restriction Enzymes, DNA Vectors,
Molecular Cloning, High Throughput
Sequencing and Protein/DNA Mapping

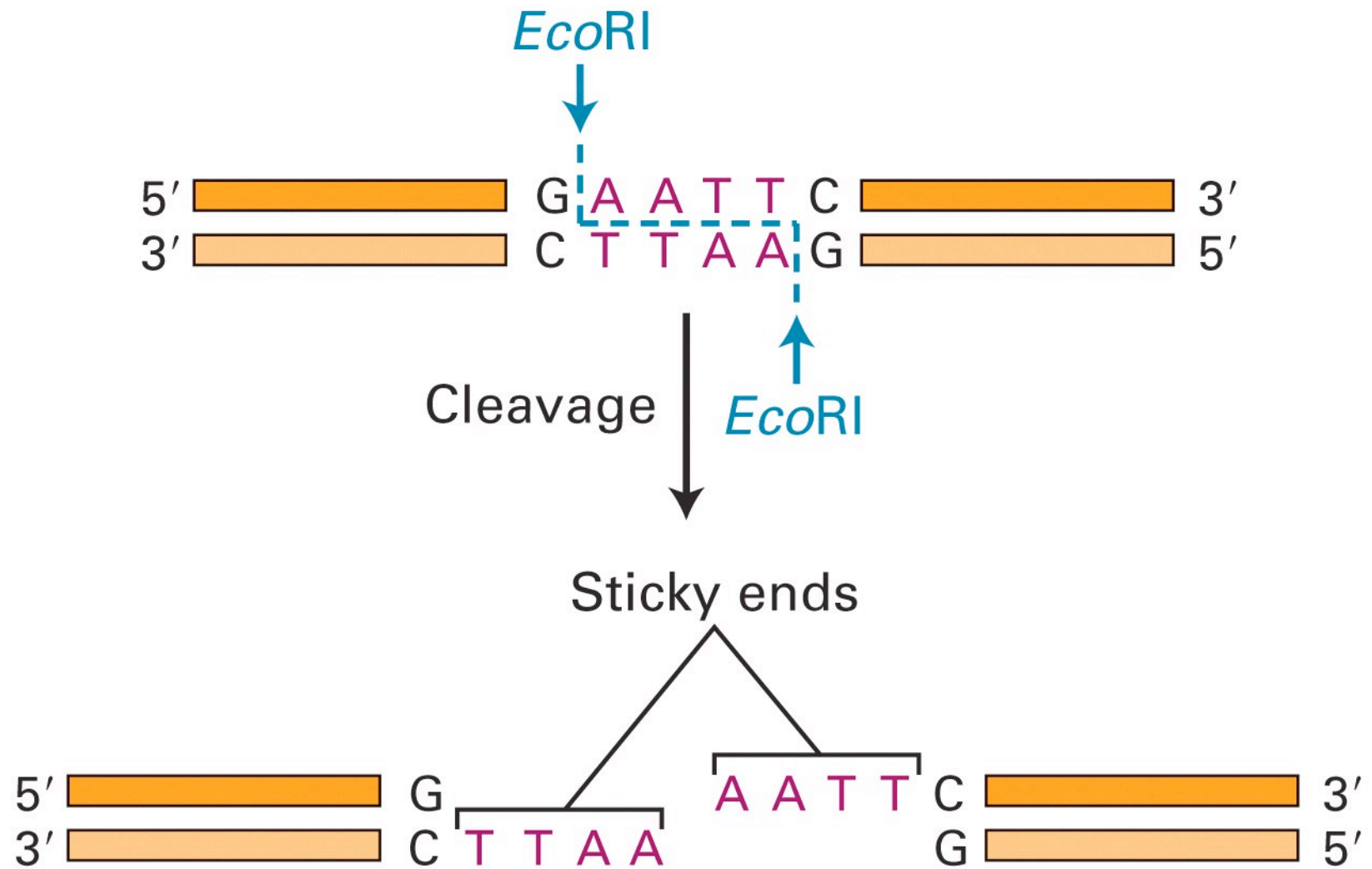
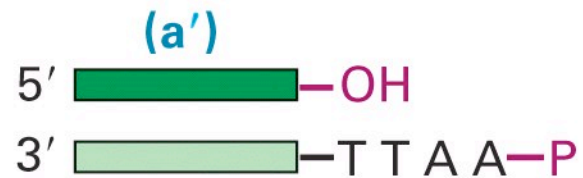


TABLE 9-1 Selected Restriction Enzymes and Their Recognition Sequences

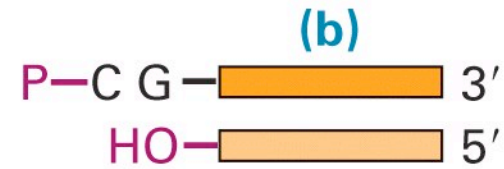
Enzyme	Source Microorganism	Recognition Site*	Ends Produced
<i>Pst</i> I	<i>Providencia stuartii</i>	<pre> ↓ -C-T-G-C-A-G- -G-A-C-G-T-C- ↑ </pre>	Sticky
<i>Sac</i> I	<i>Streptomyces achromogenes</i>	<pre> ↓ -G-A-G-C-T-C- -C-T-C-G-A-G- ↑ </pre>	Sticky
<i>Sal</i> I	<i>Streptomyces albue</i>	<pre> ↓ -G-T-C-G-A-C- -C-A-G-C-T-G- ↑ </pre>	Sticky
<i>Sma</i> I	<i>Serratia marcescens</i>	<pre> ↓ -C-C-C-G-G-G- -G-G-G-C-C-C- ↑ </pre>	Blunt
<i>Sph</i> I	<i>Streptomyces phaeochromogenes</i>	<pre> ↓ -G-C-A-T-G-C- -C-G-T-A-C-G- ↑ </pre>	Sticky
<i>Xba</i> I	<i>Xanthomonas badrii</i>	<pre> ↓ -T-C-T-A-G-A- -A-G-A-T-C-T- ↑ </pre>	Sticky

*These recognition sequences are included in a common polylinker sequence (see Figure 9-12).

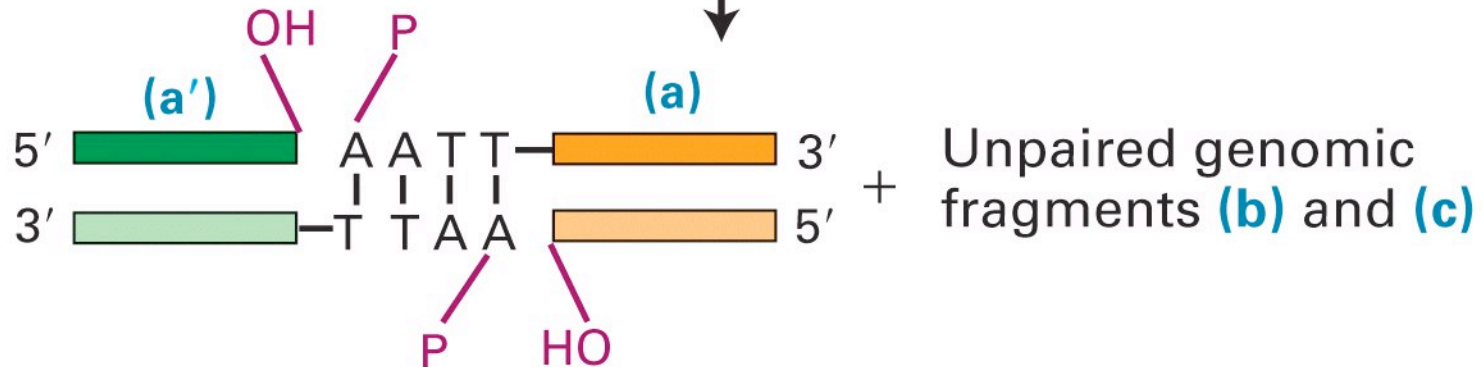
Vector DNA

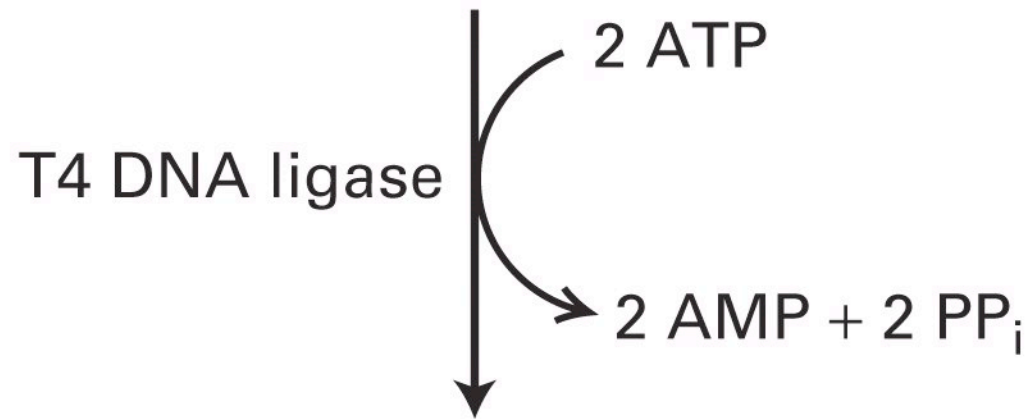
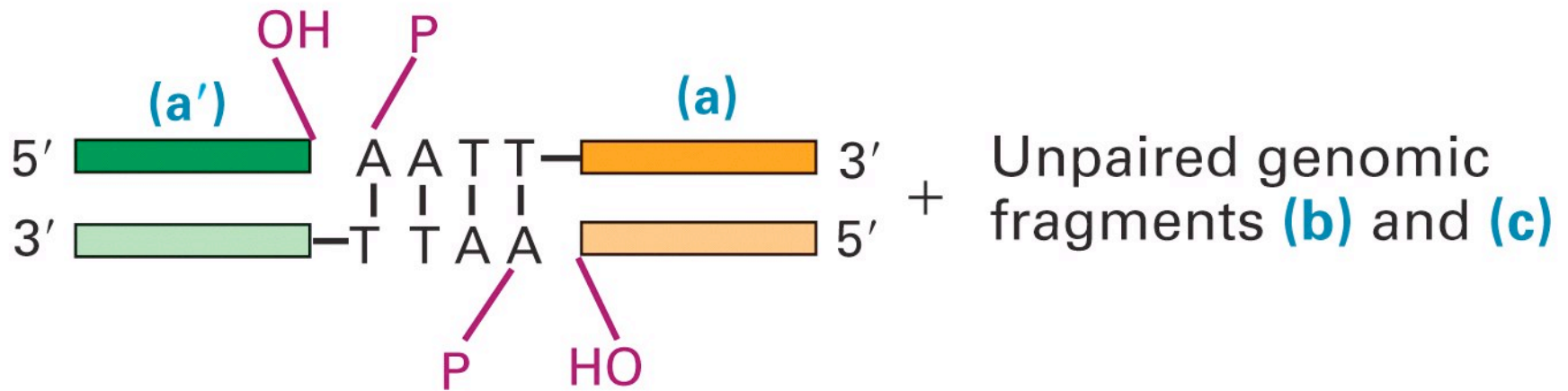


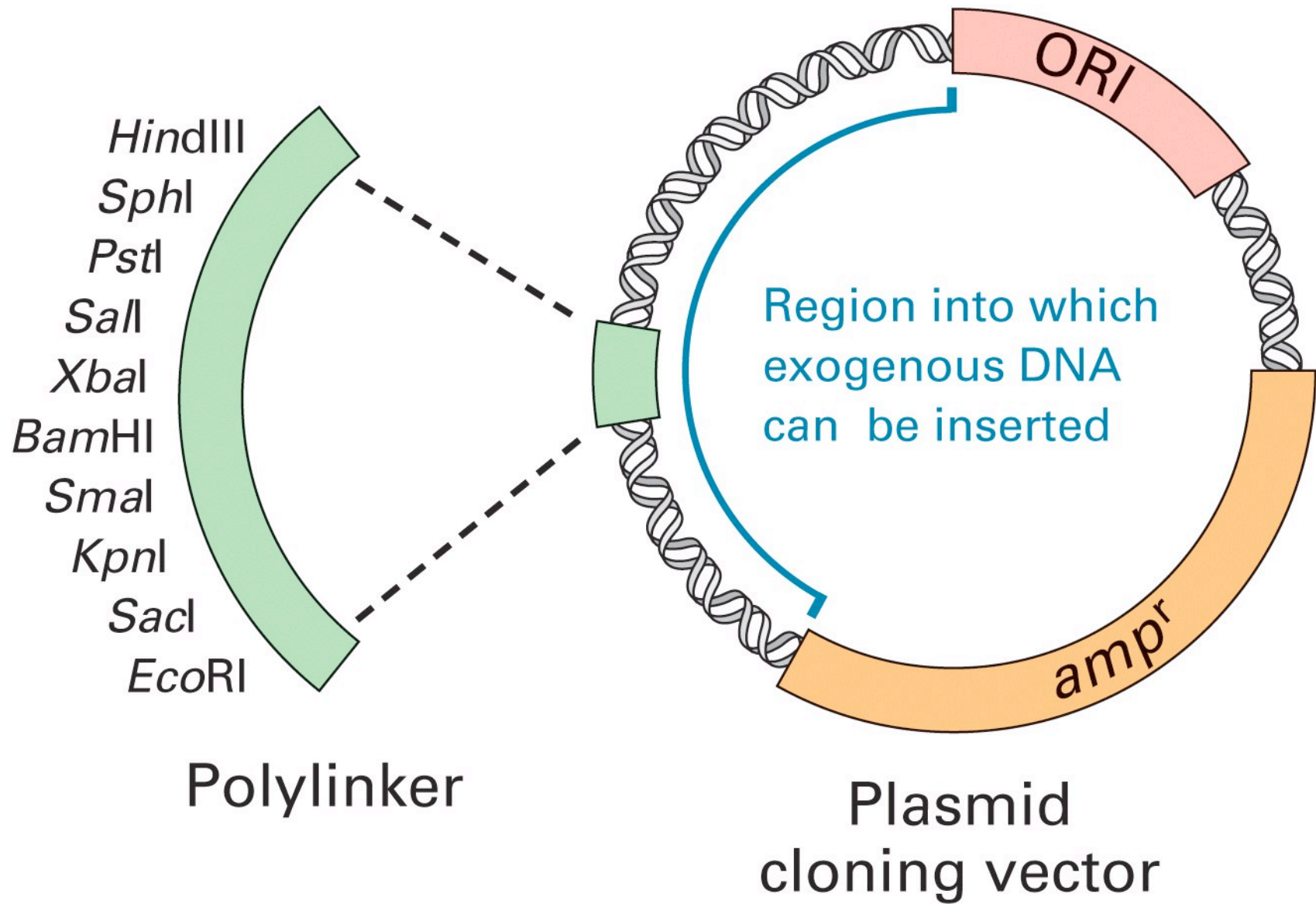
Genomic DNA fragments

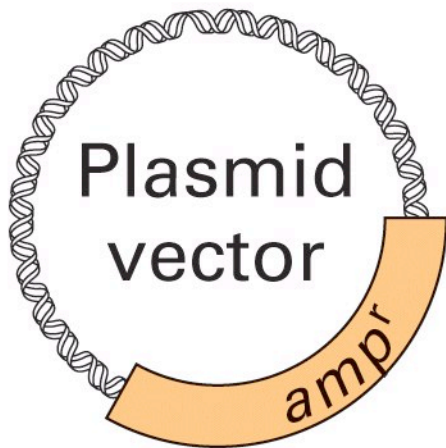


Complementary
ends base-pair

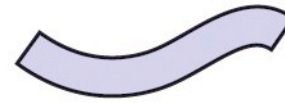








+

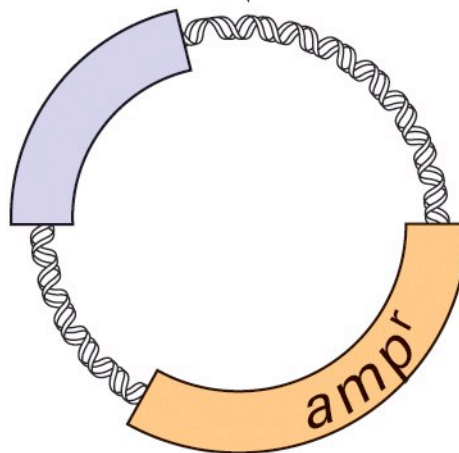


DNA fragment
to be cloned

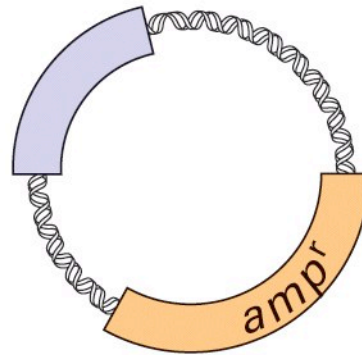


Enzymatically insert
DNA into plasmid vector

Recombinant
plasmid



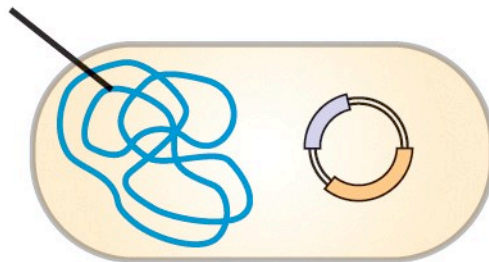
Recombinant
plasmid



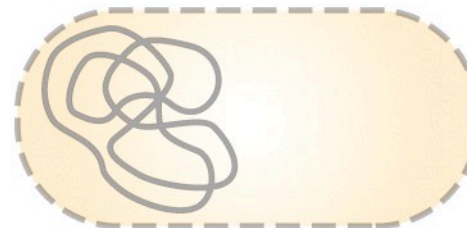
Mix *E. coli* with plasmids
in presence of CaCl_2 ; heat
pulse

Culture on nutrient agar
plates containing ampicillin

E. coli
chromosome

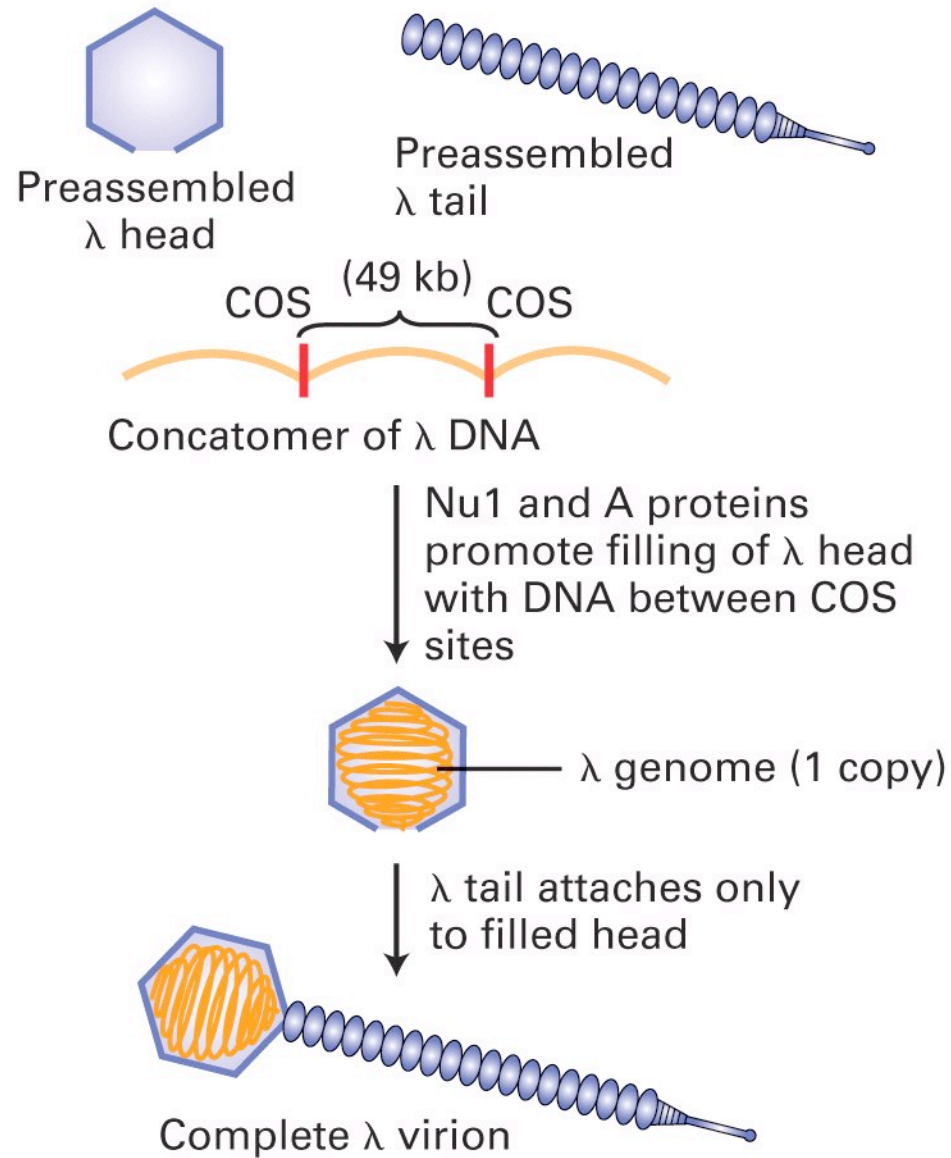


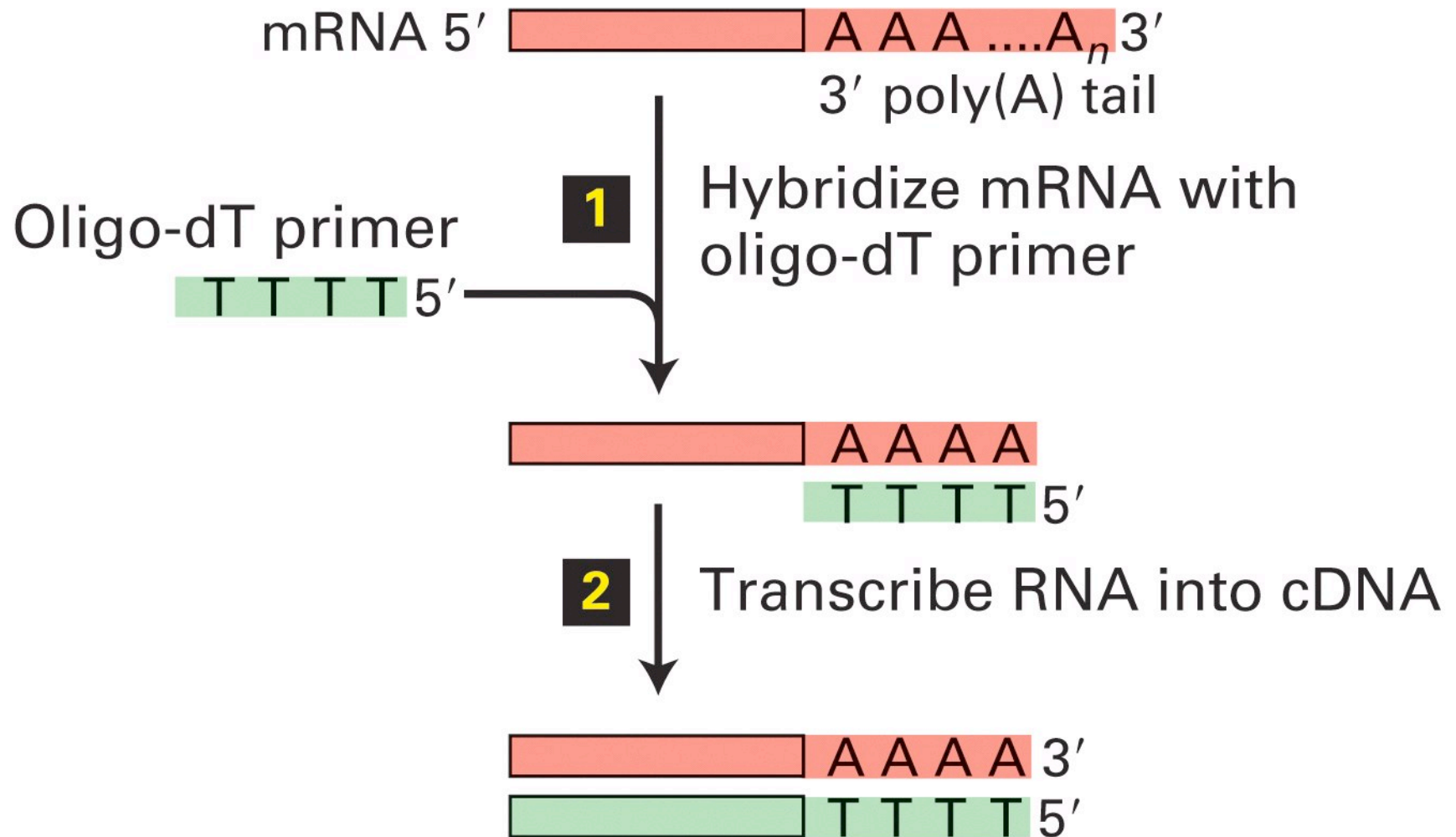
Transformed cell
survives

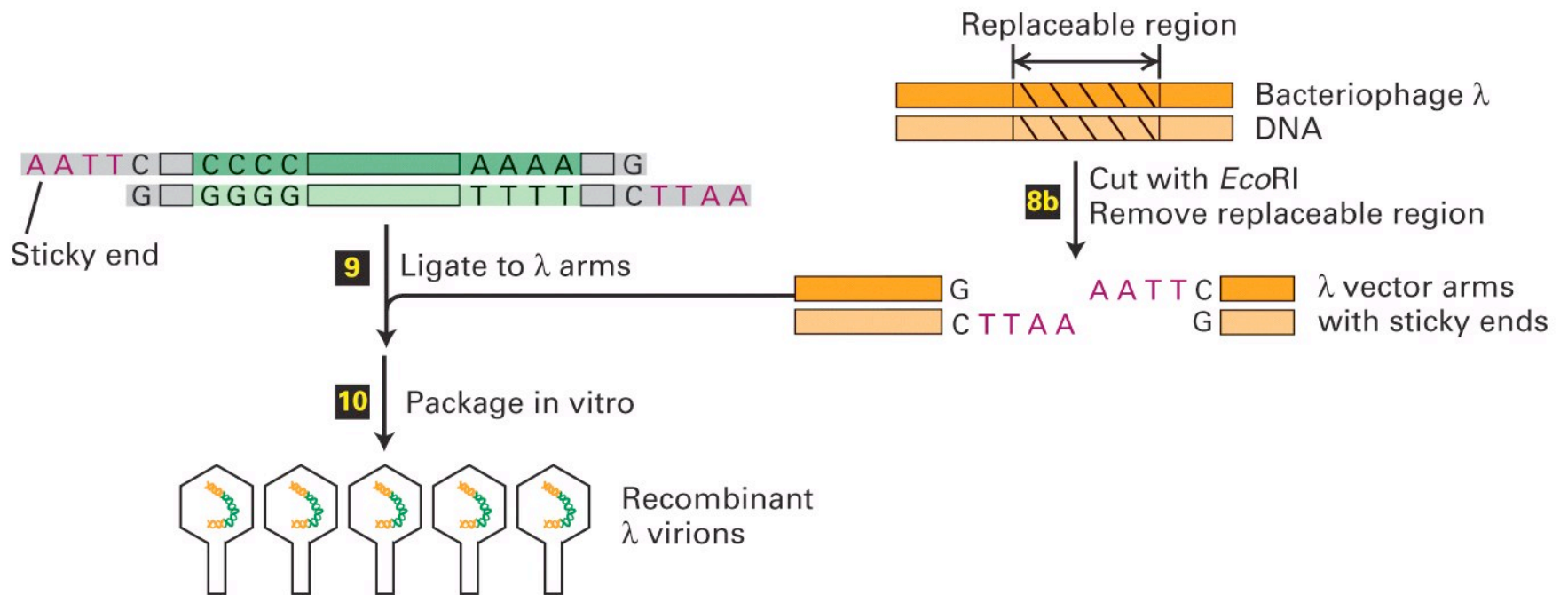


Cells that do not
take up plasmid die
on ampicillin plates

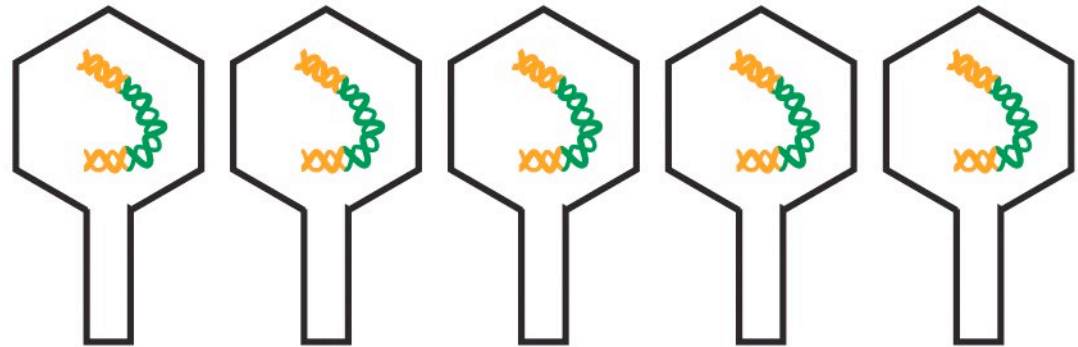
(b) λ Phage assembly







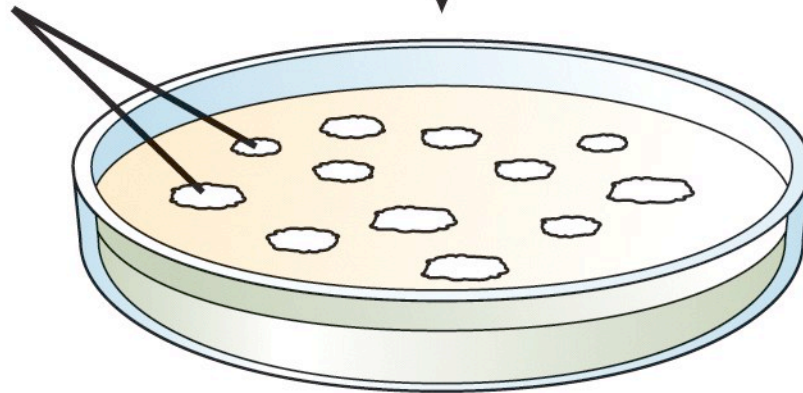
Recombinant
 λ virions

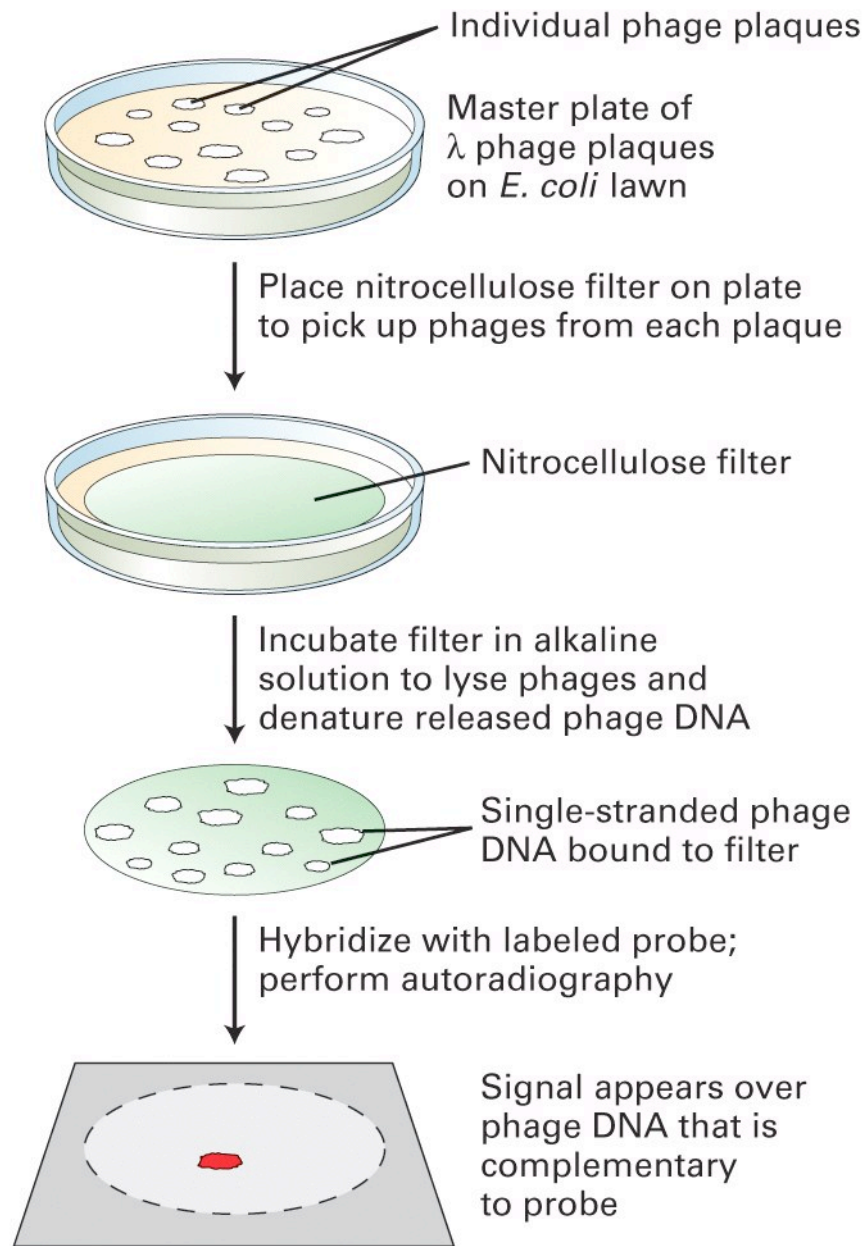


11

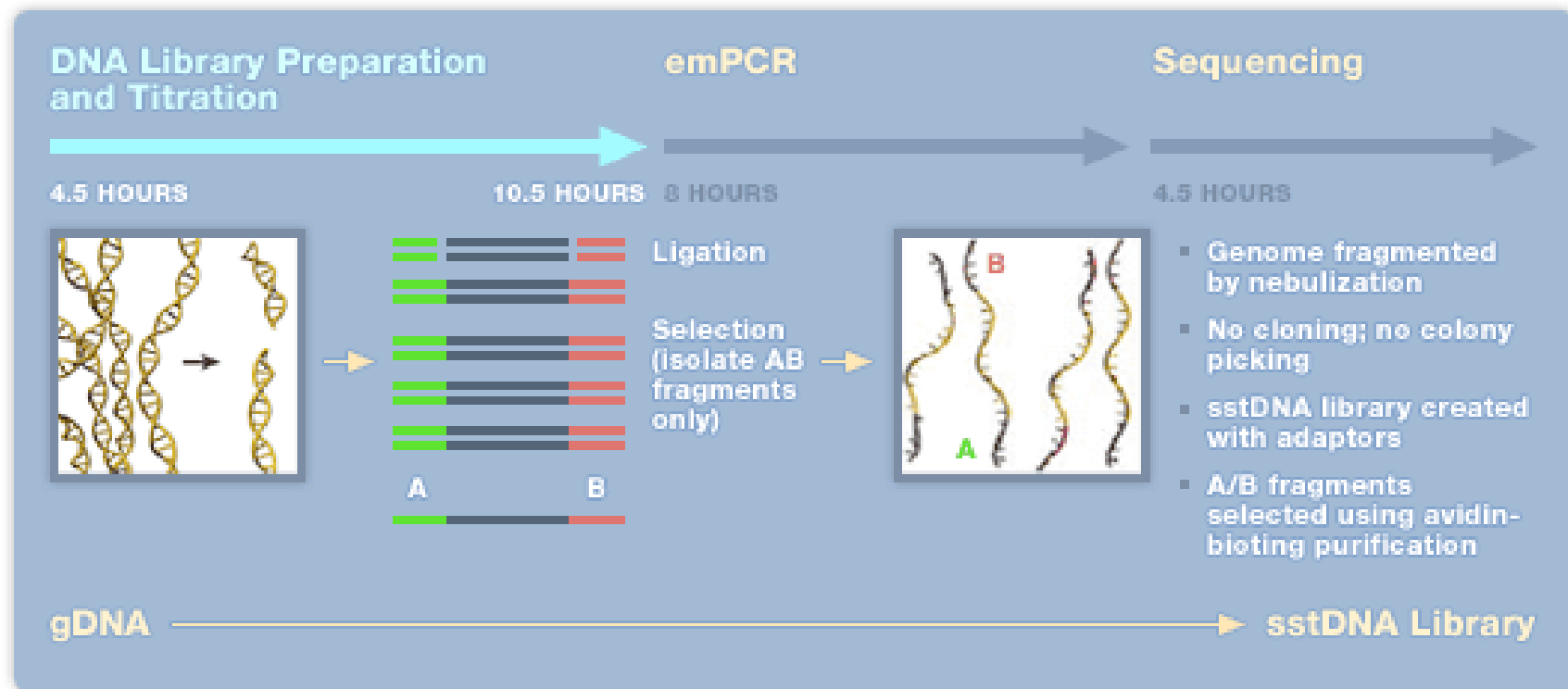
Infect *E. coli*

Individual
 λ clones

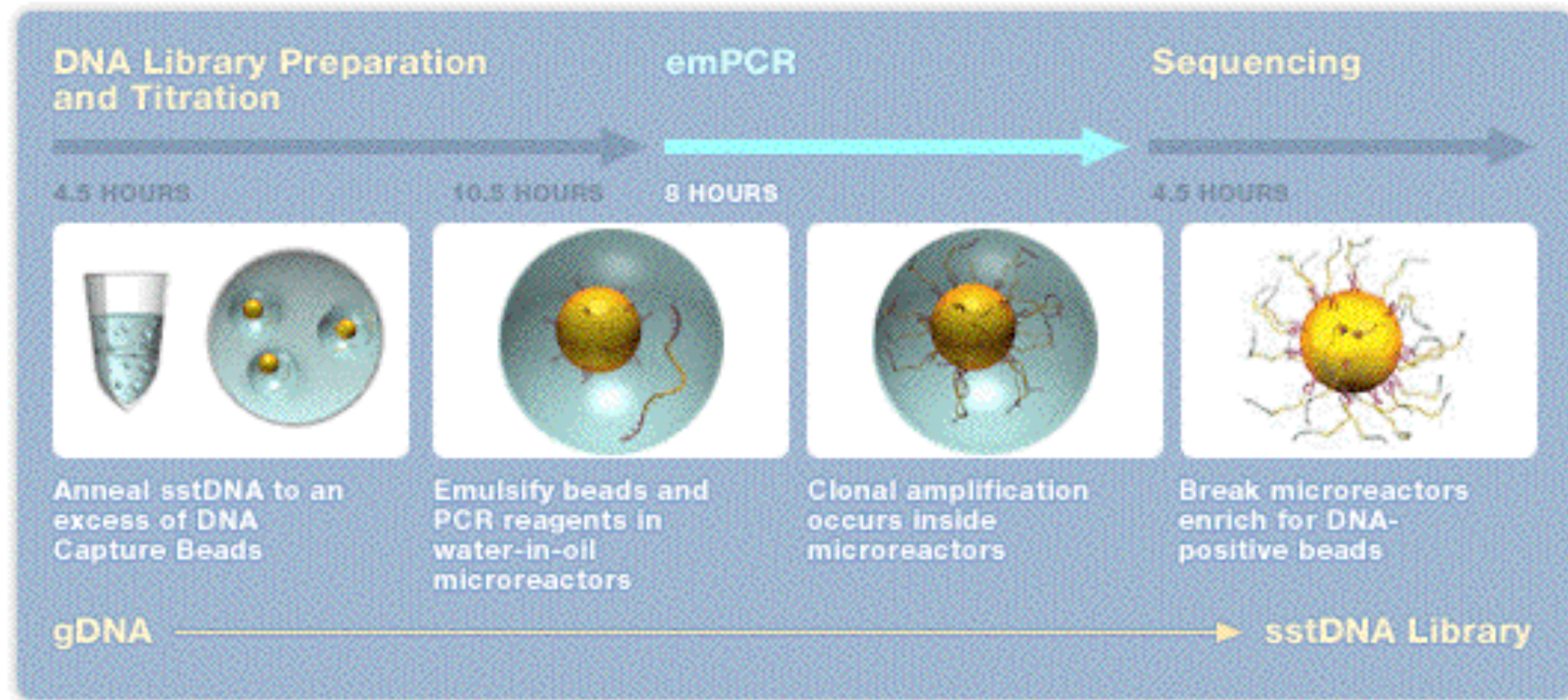




454 : High Through-put DNA Sequencing



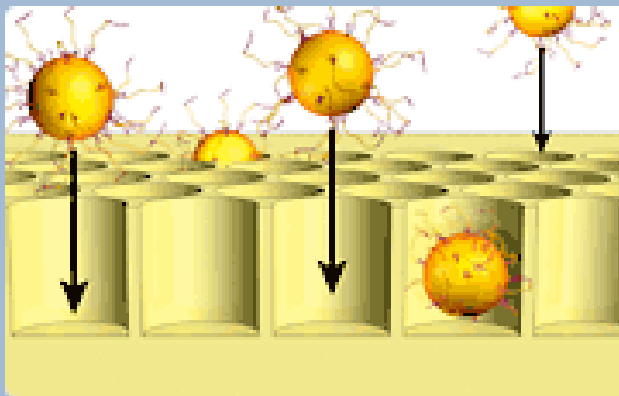
Bead based technology for rapid parallel sequencing



Multi-well Reactions

DNA Library Preparation and Titration

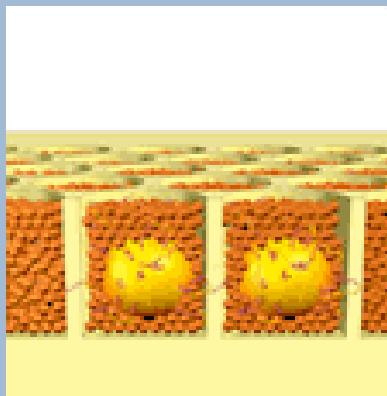
4.5 HOURS



10.5 HOURS

emPCR

8 HOURS



Sequencing

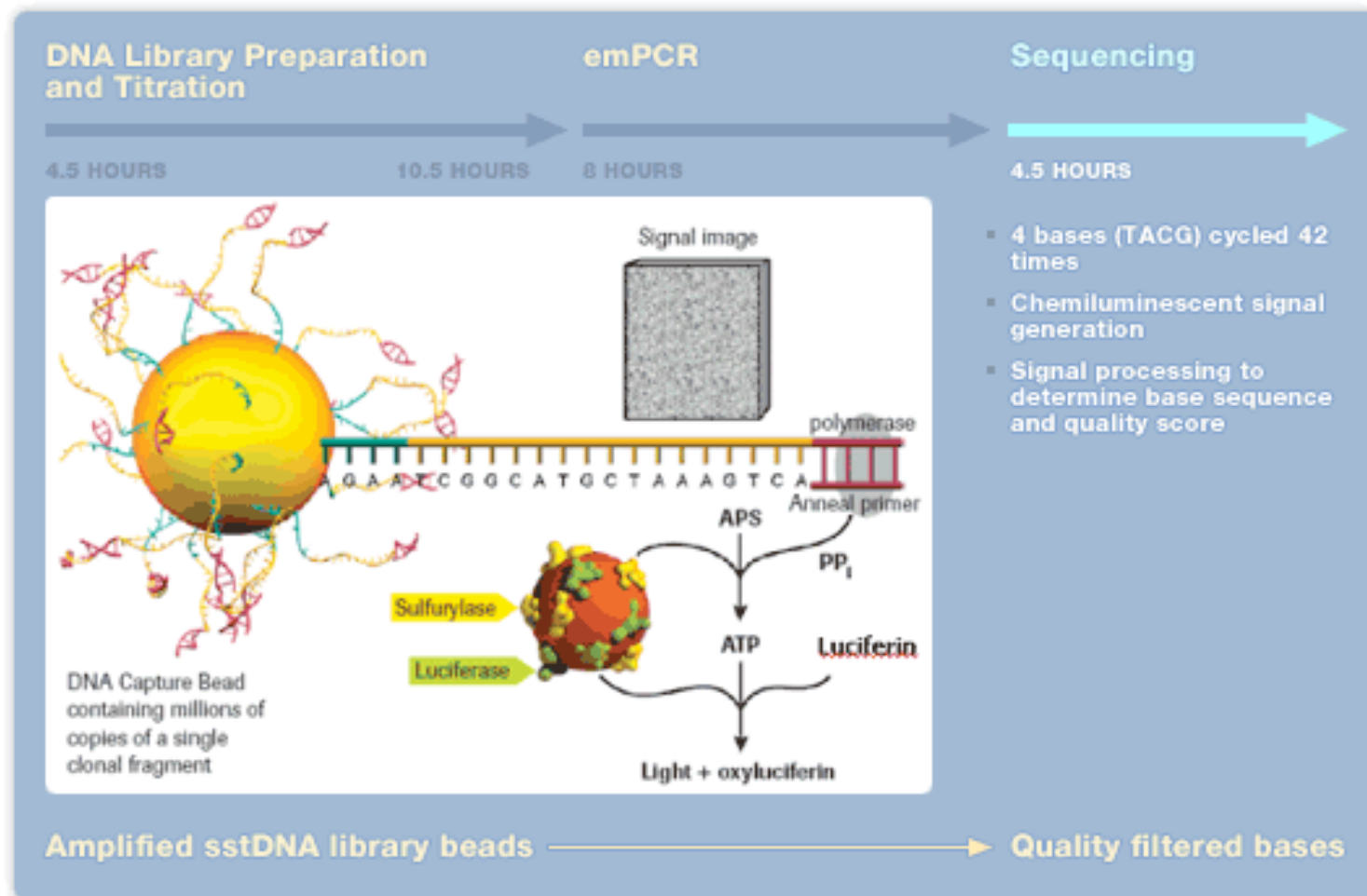
4.5 HOURS

- Well diameter: average of 44µm
- 200,000 reads obtained in parallel
- A single cloned amplified sstDNA bead is deposited per well

Amplified sstDNA library beads

Quality filtered bases

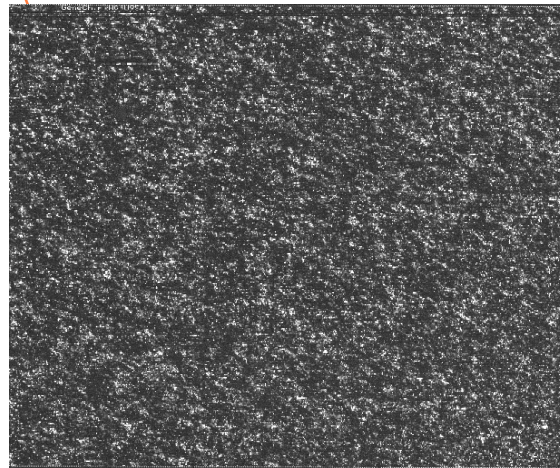
Chemi-luminescent sequencing



Micro Array Technology

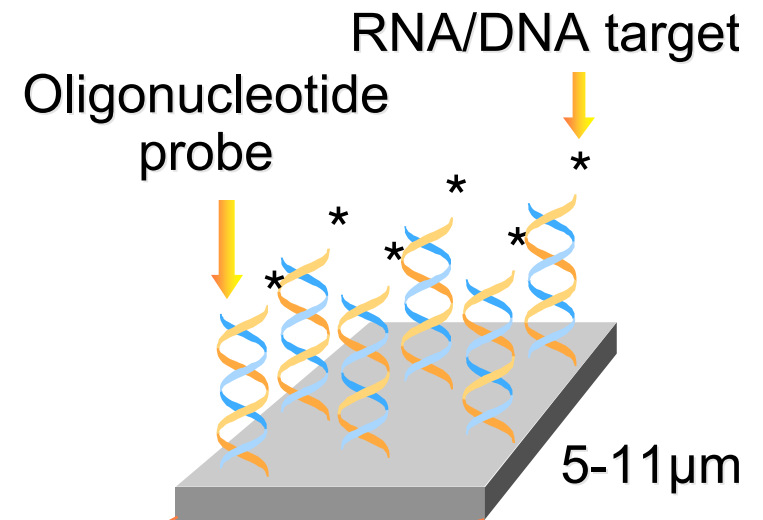


Raw data image with
>6,500,000 different
complementary probes



1.28 cm

Hybridized probe cell




Thousands of copies of a
specific
oligonucleotide probe in
each feature


High Probe Densities Enable New Applications

Feature Size


	18um	11um	8um	5um	1um
Features	500,000	1,300,000	2,600,000	6,500,000	163,000,000



Commercial
expression
arrays



Commercial
genotyping
arrays



Exon, tiling
and 500K
Arrays



Future
development

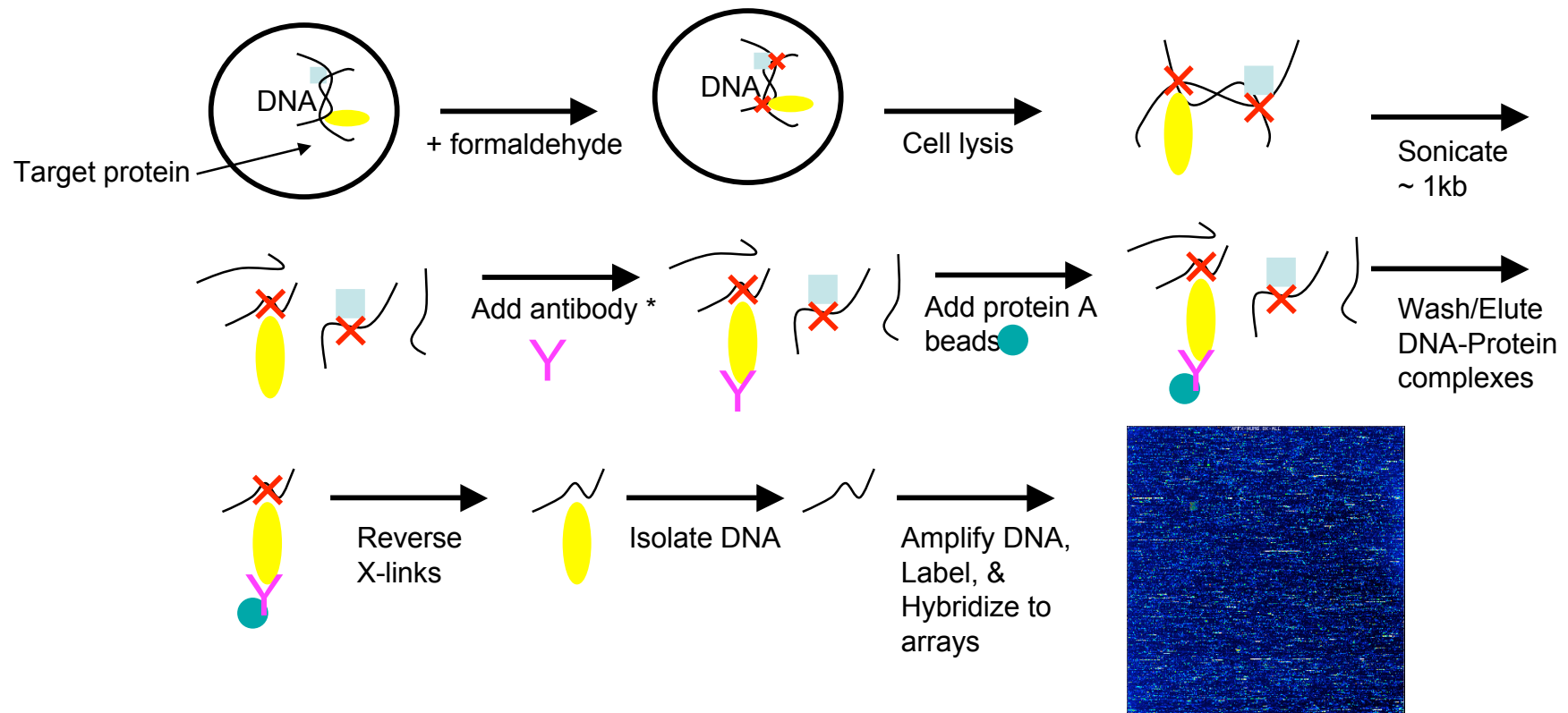
Advances in Genechip technology enable applications requiring high data content

Tiling Array Applications

- Mapping regions of transcription
- ChIP on chip experiments (Chromatin IP)
- Chromosomal origins of replication
- DNA methylation
- Copy number analysis
- SNP discovery

Genome reference arrays for multiple applications

Chromatin Immunoprecipitation



Chromatin IP Assay

- Any nucleotide fraction that can be immunoprecipitated can be interrogated on tiling arrays
- DNA binding proteins
 - Transcription factors
 - Modified histones
 - Structural proteins
- Assay is more complex than typical transcription mapping assay
 - Chromatin-protein immunoprecipitation
 - Purify, amplify and label DNA fragments
- Data analysis more comprehensive than typical transcription assay