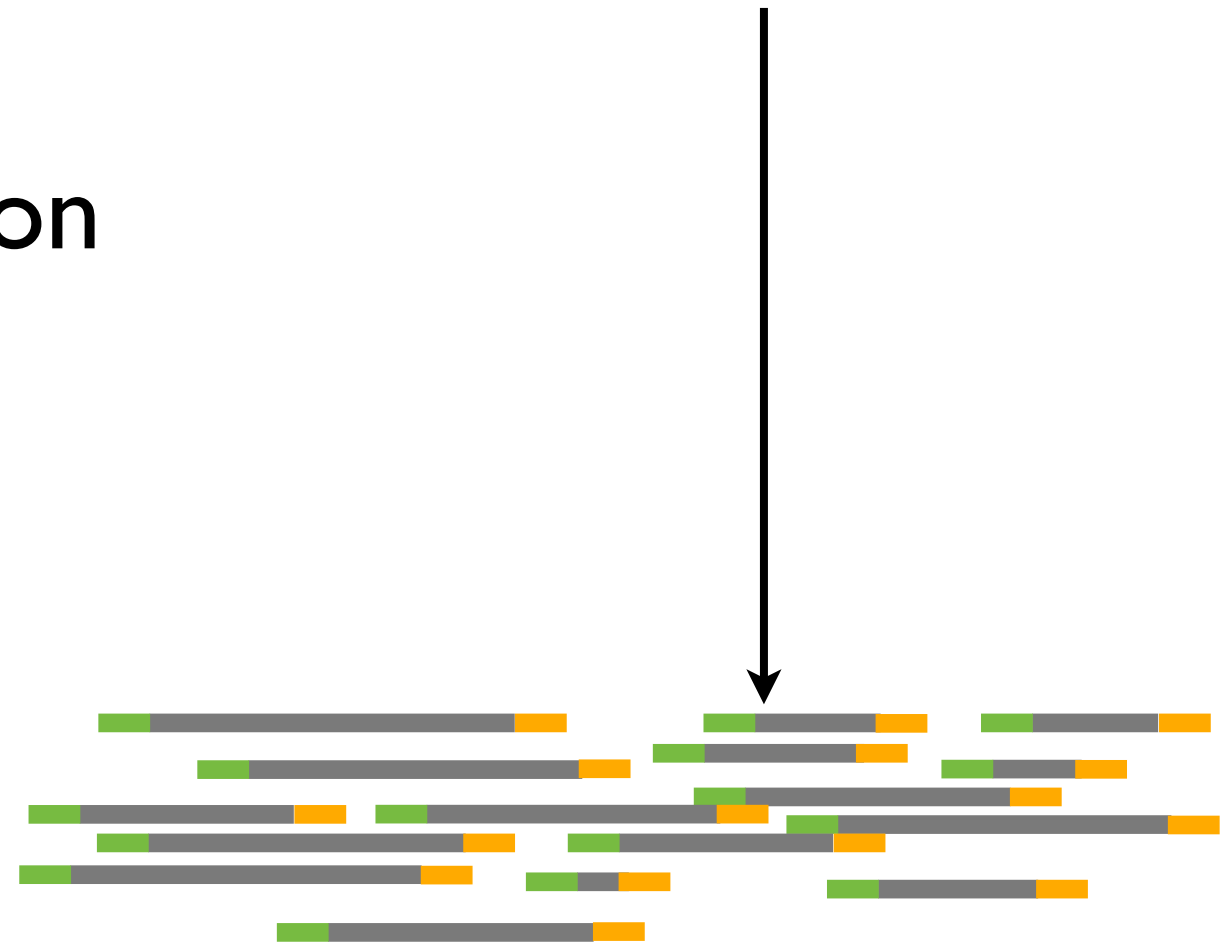
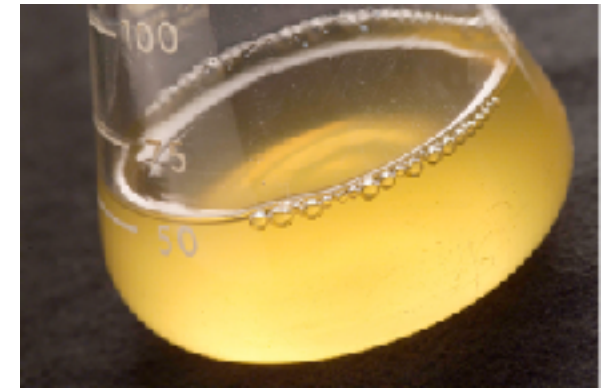


HTS Background and Theory

Josh Granek

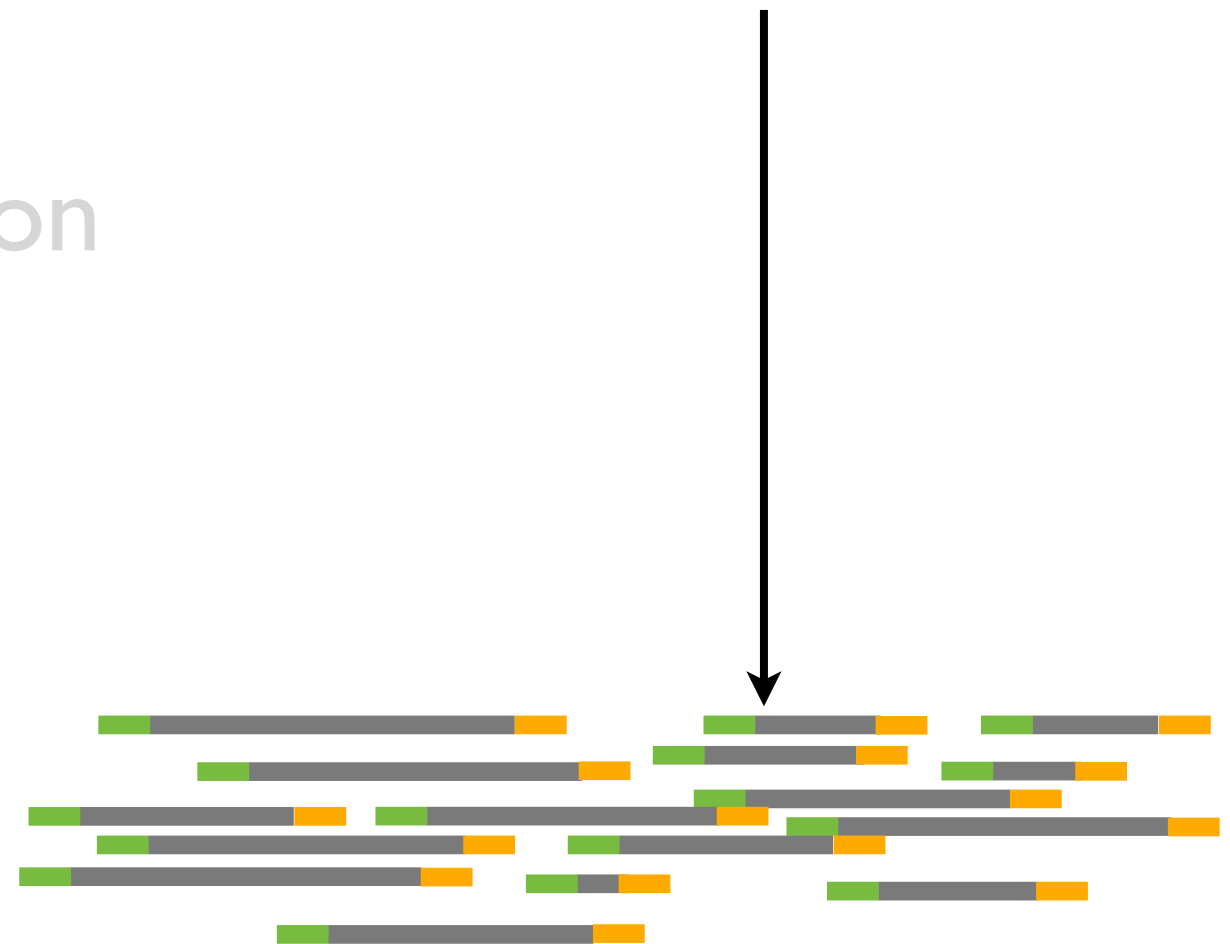
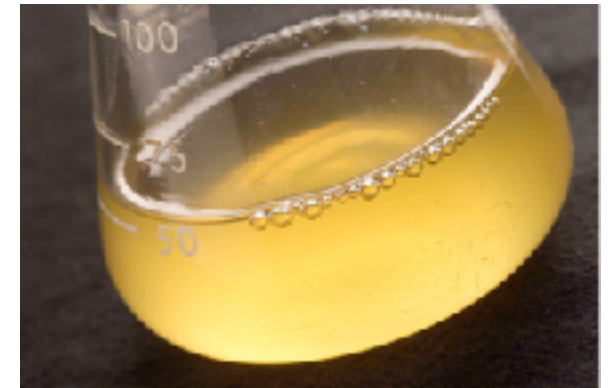
HTS Experiment: Major Components

1. Sample Collection
2. Nucleic Acid Extraction
3. Library Preparation



HTS Experiment: Major Components

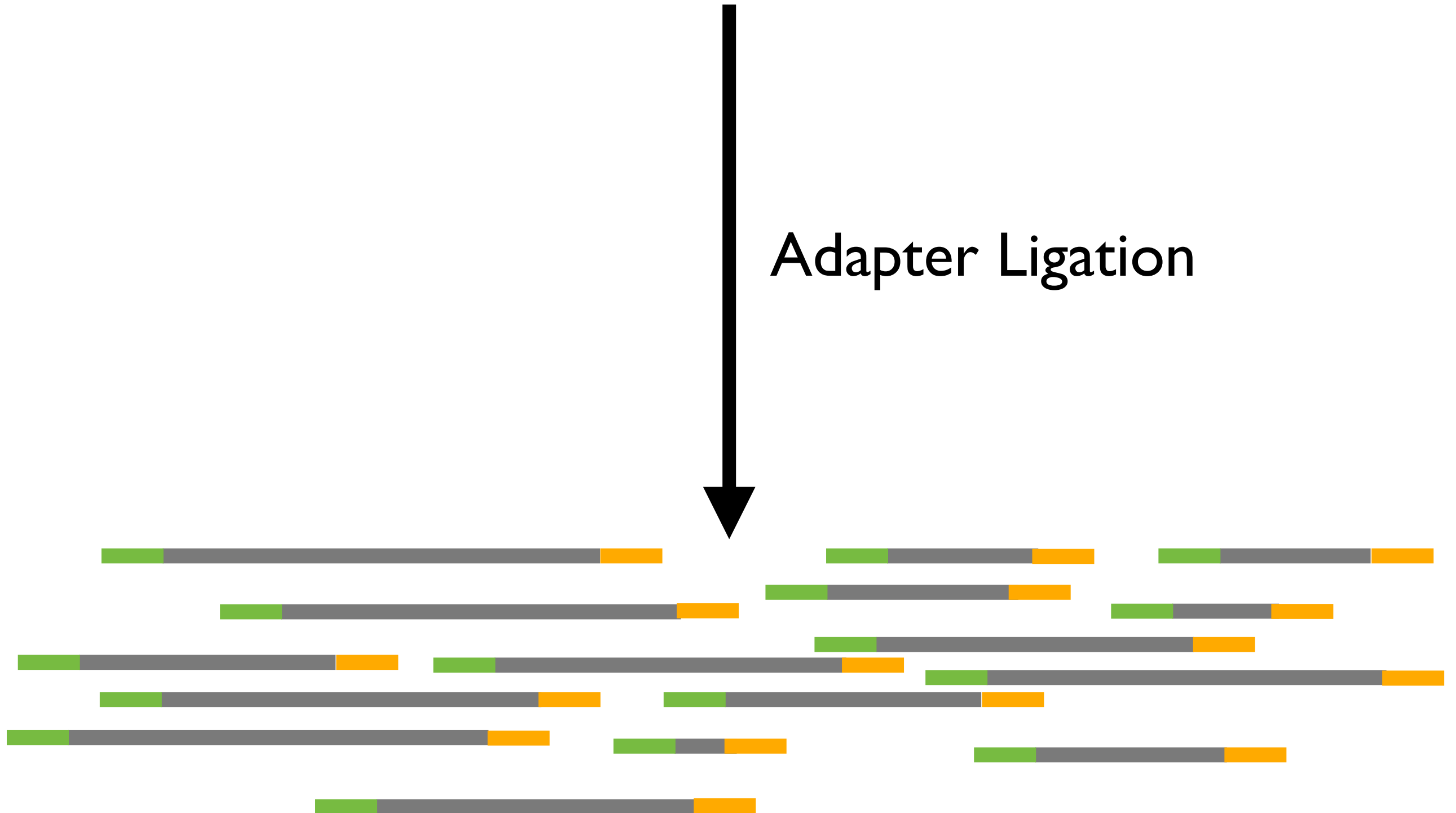
1. Sample Collection
2. Nucleic Acid Extraction
- 3. Library Preparation**



Library Preparation

Purified Nucleic Acid

Adapter Ligation



Sanger Sequencing

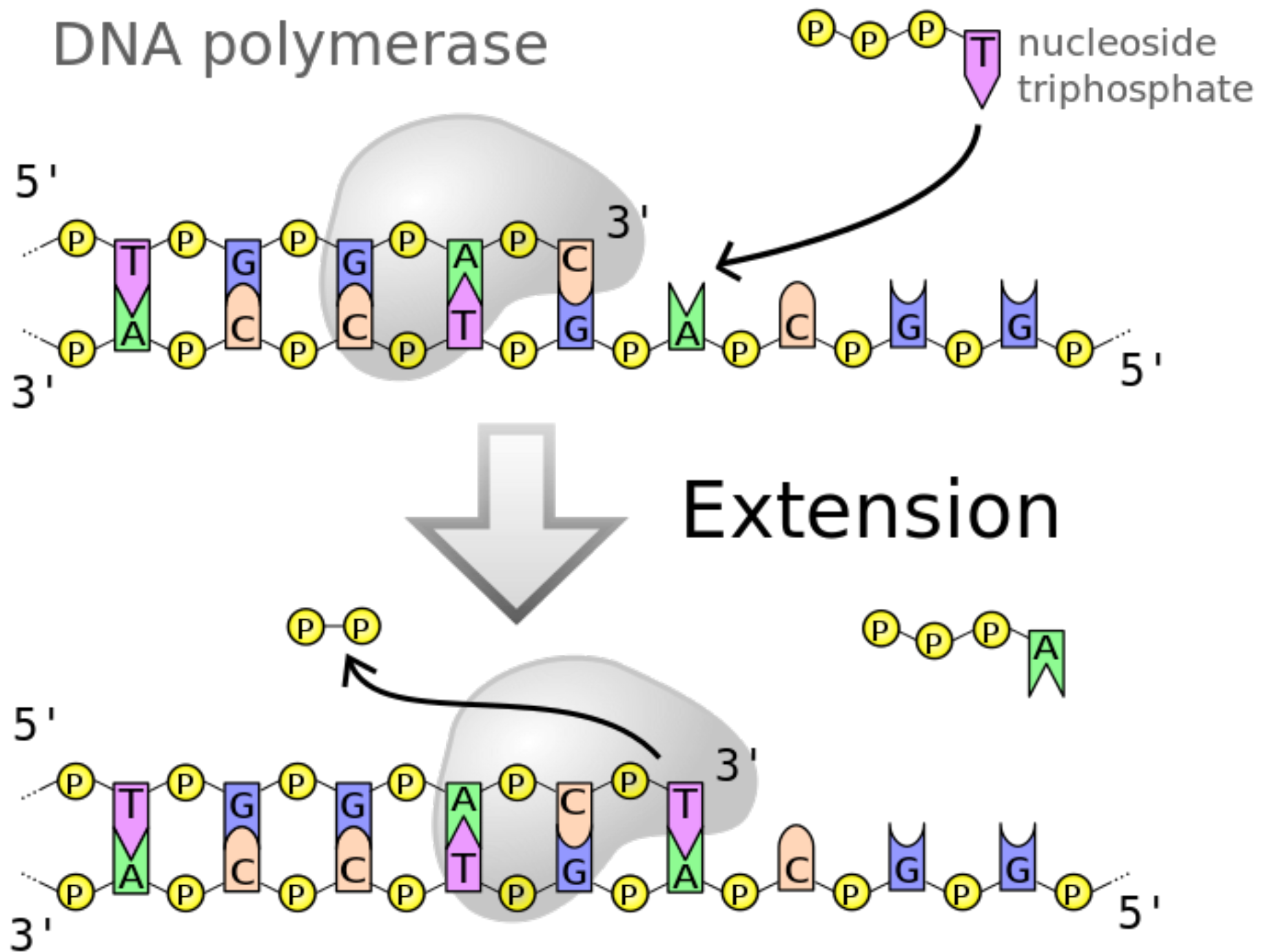
DNA Synthesis

- What are the minimum components for DNA Replication?

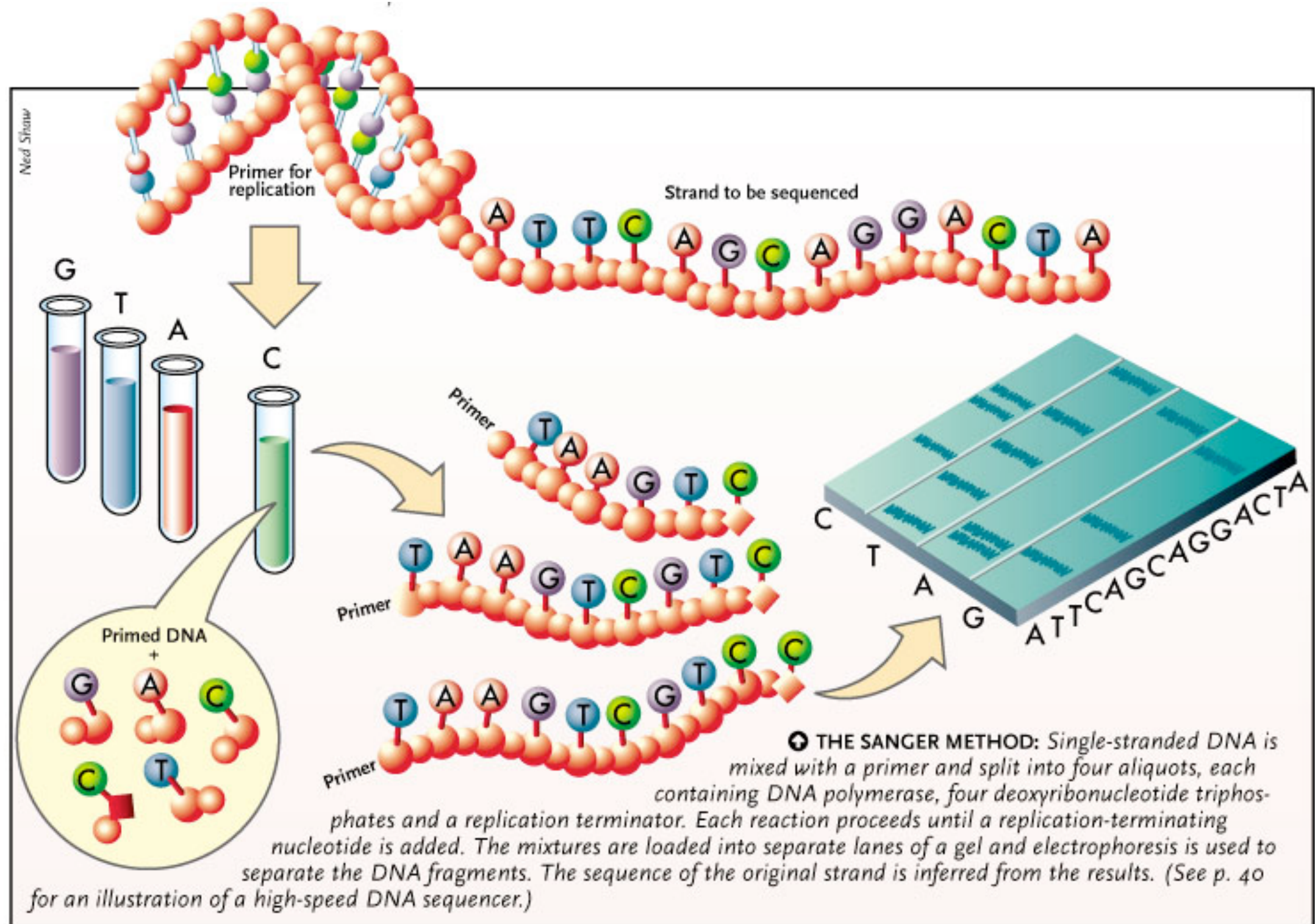
DNA Synthesis

- What are the minimum components for DNA Replication?
 - Template
 - Primer
 - Nucleoside triphosphates
 - DNA Polymerase*

DNA Synthesis



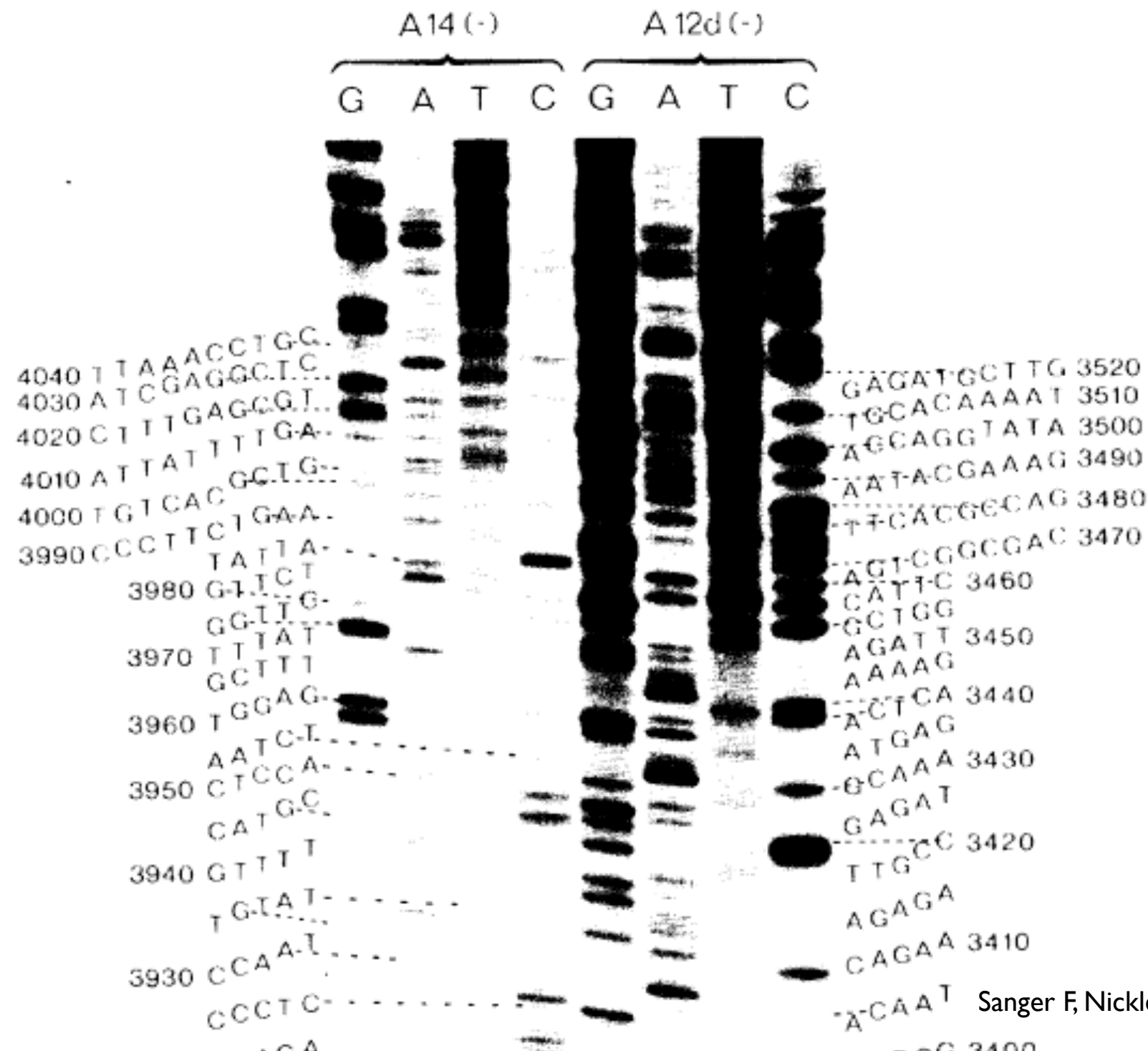
Sanger Sequencing



Sanger Sequencing

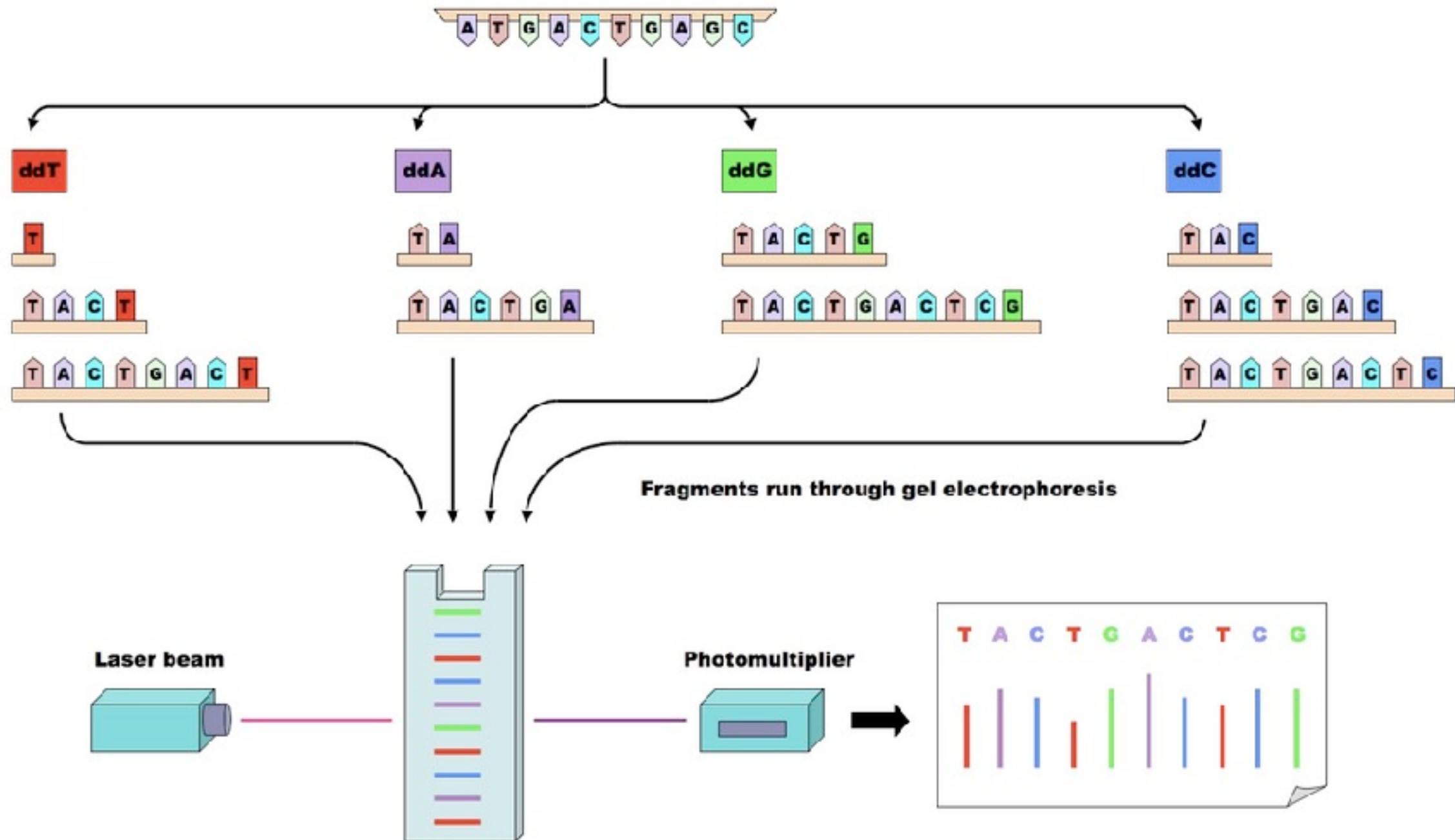
5464 Biochemistry: Sanger *et al.*

Proc. Natl. Acad. Sci. USA 74 (1977)



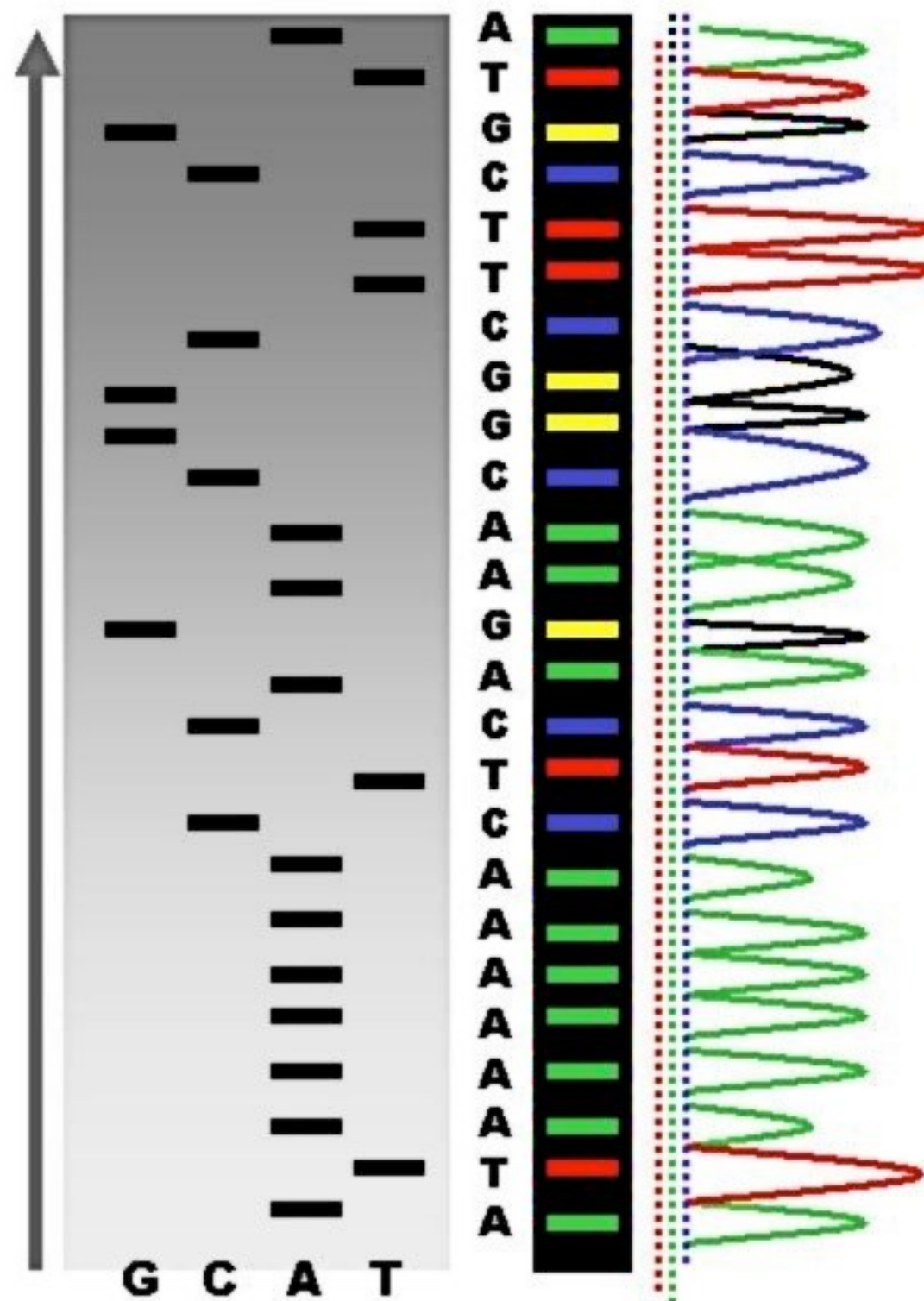
Dye-terminator

PCR in presence of fluorescent, chain-terminating nucleotides



Fluorescent fragments detected by laser and represented on a chromatogram

Radiolabel vs. Dye



High-Throughput Sequencing

Sequencing

AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

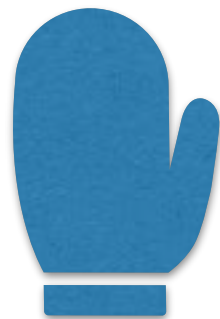
Sequencing


AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

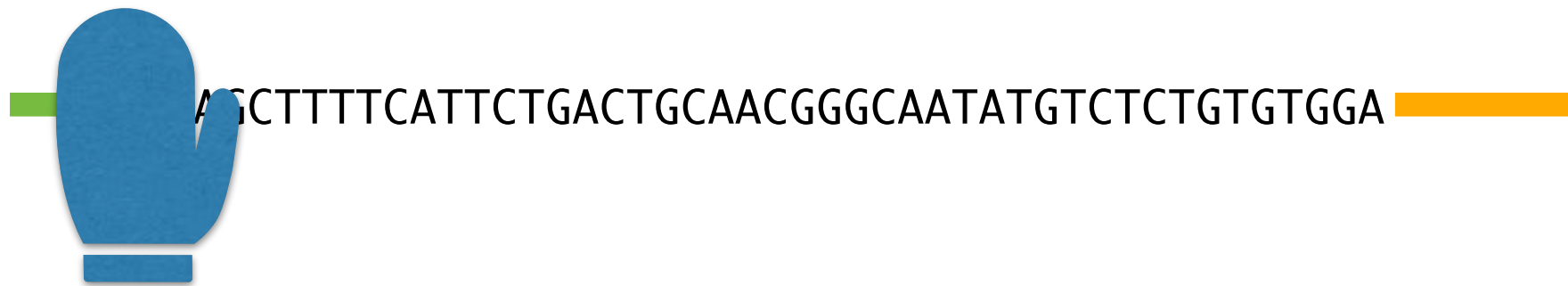
Sequencing

AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

A	●	A	●	A	●
T	●	T	●	T	●
G	●	G	●	G	●
C	●	C	●	C	●

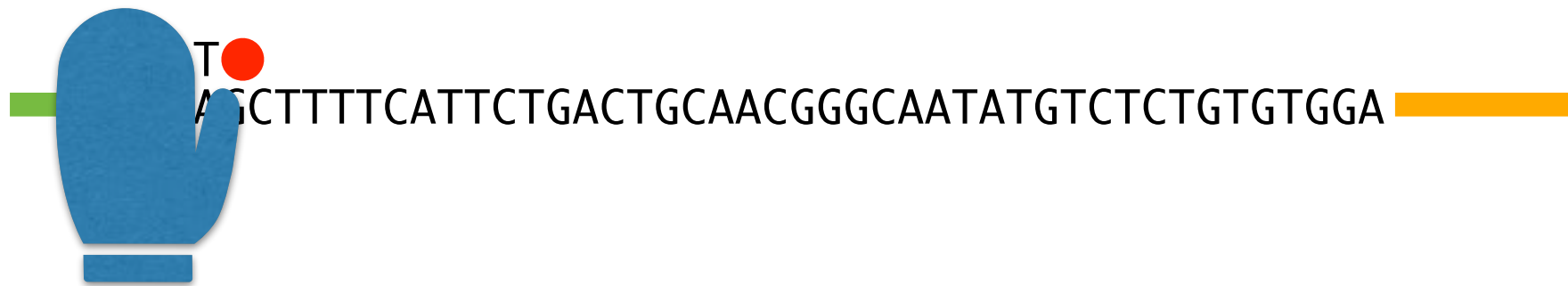


Sequencing



A ● A ● A ●
T ● T ● T ●
G ● G ● G ●
C ● C ● C ●

Sequencing



A ● A ● A ●
T ● T ● T ●
G ● G ● G ●
C ● C ● C ●

Sequencing

 T 
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

Sequencing

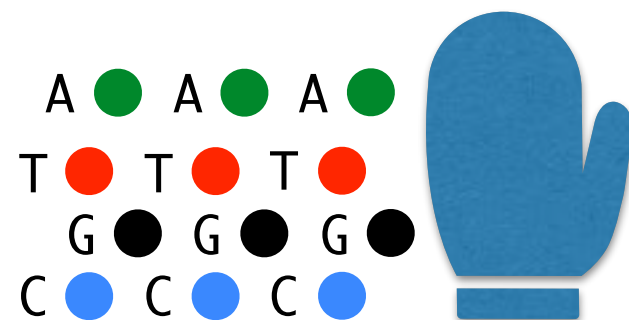
 T 
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

Sequencing

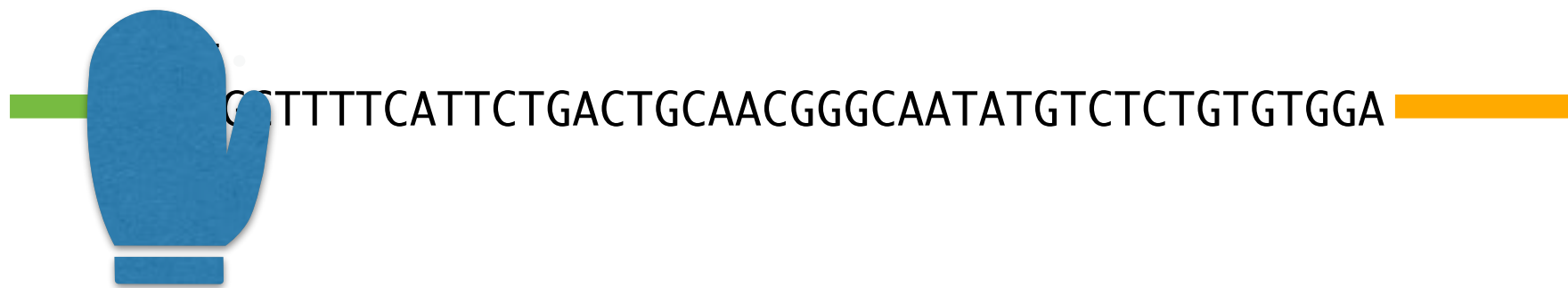
 T 
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

Sequencing

— T
— AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA —

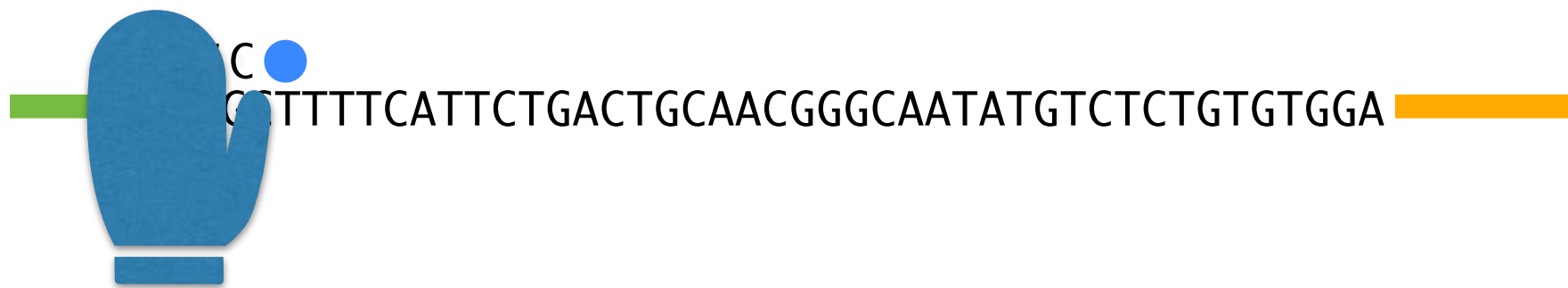


Sequencing



A ● A ● A ●
T ● T ● T ●
G ● G ● G ●
C ● C ● C ●

Sequencing



A ● A ● A ●
T ● T ● T ●
G ● G ● G ●
C ● C ● C ●

Sequencing

TC ●
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

Sequencing

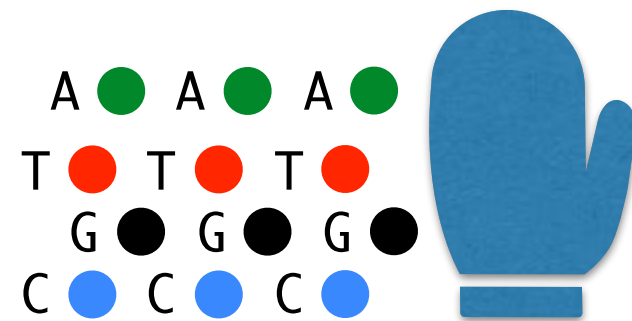
TC ●
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

Sequencing

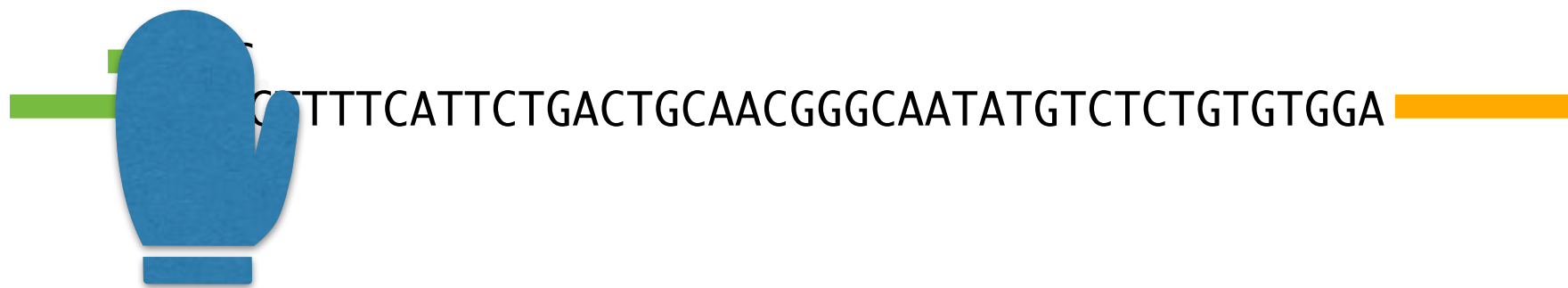
 T C
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

Sequencing

TC
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

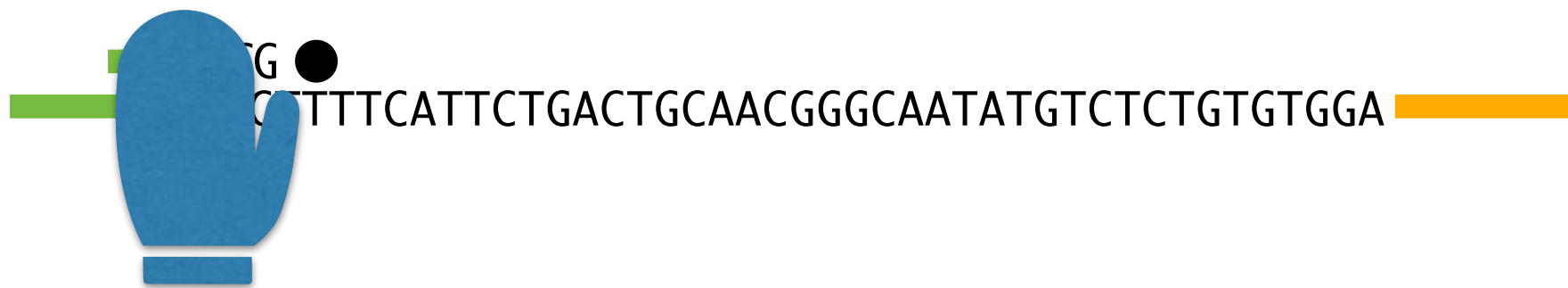


Sequencing



A	●	A	●	A	●
T	●	T	●	T	●
G	●	G	●	G	●
C	●	C	●	C	●

Sequencing



A	●	A	●	A	●
T	●	T	●	T	●
G	●	G	●	G	●
C	●	C	●	C	●

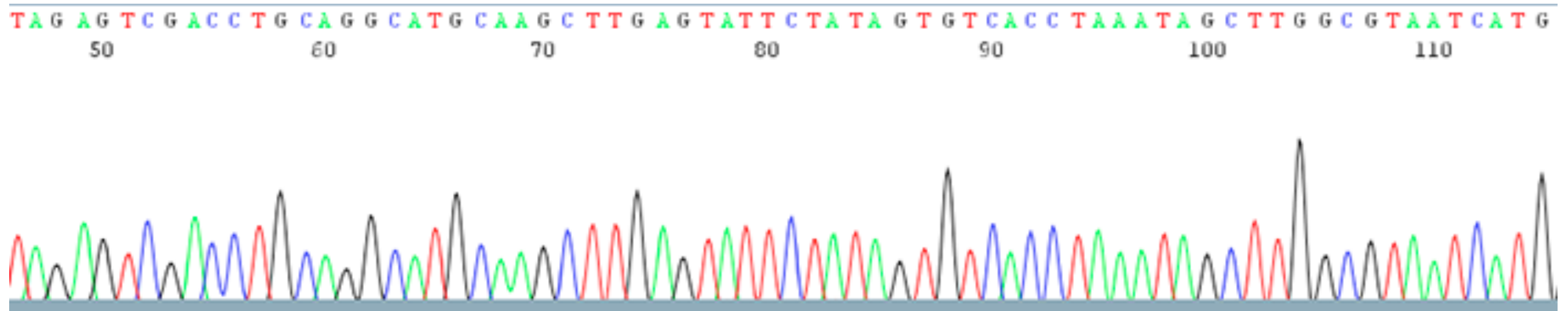
Sequencing

 T C G ●
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

Sequencing

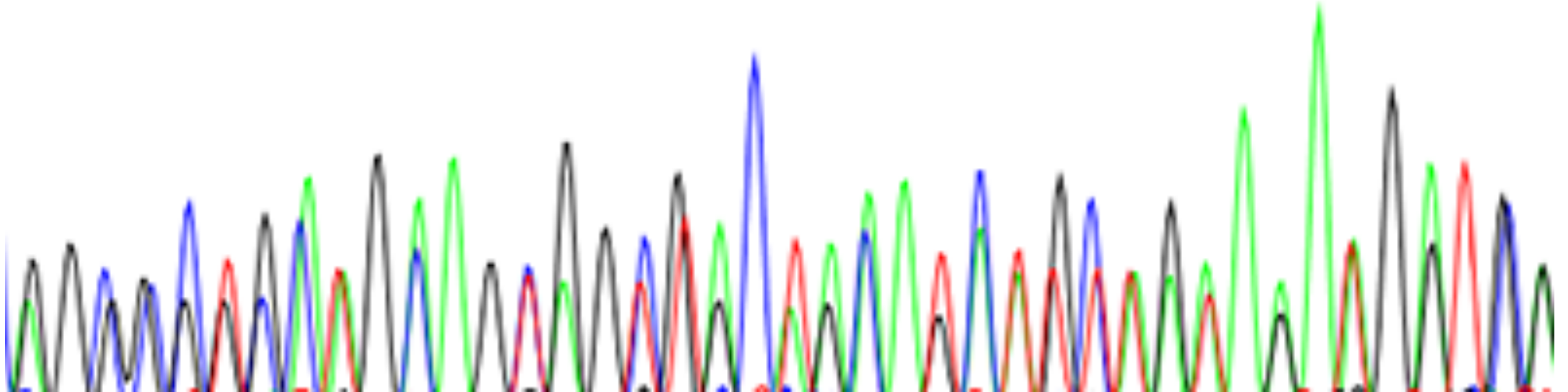
 T C G ●
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

Dye-terminator Sanger Sequencing



Double Sequence

N G N N N N N N G N A G N G N G N C N N N N N C N N C N G N A N A N G N N N N
180 190 200 210



How?

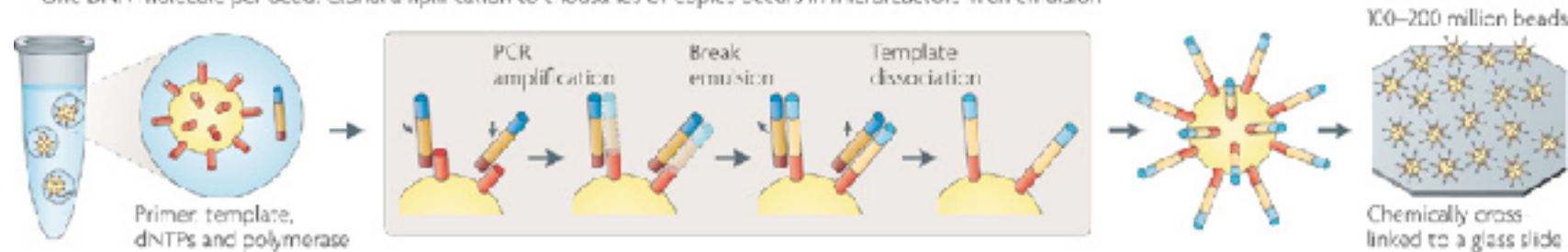
How?

- Separate
- Detect
- Removable Terminator

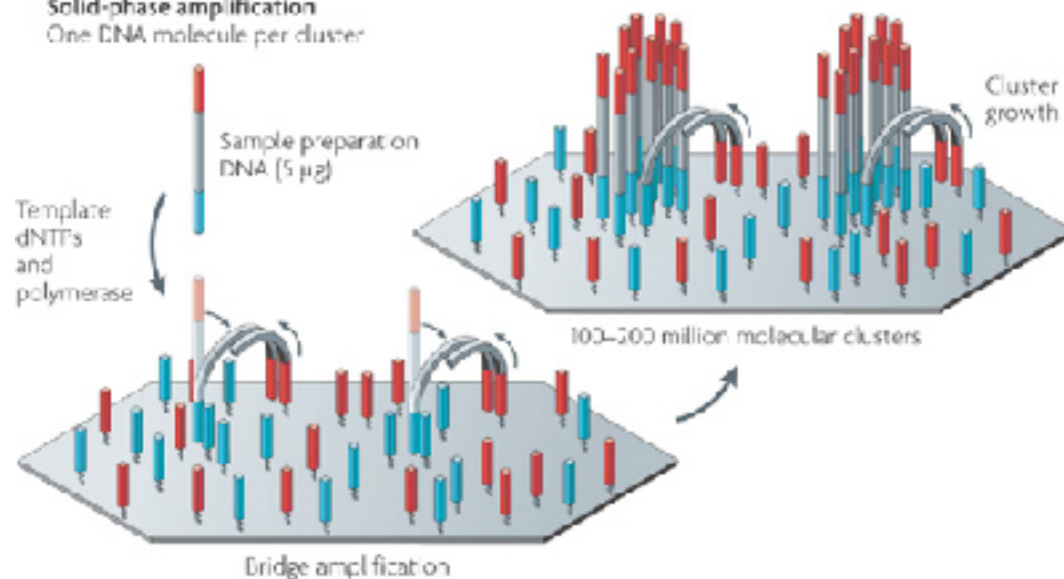
Template immobilization

**a Roche/454, Life/APG, Polonator
Emulsion PCR**

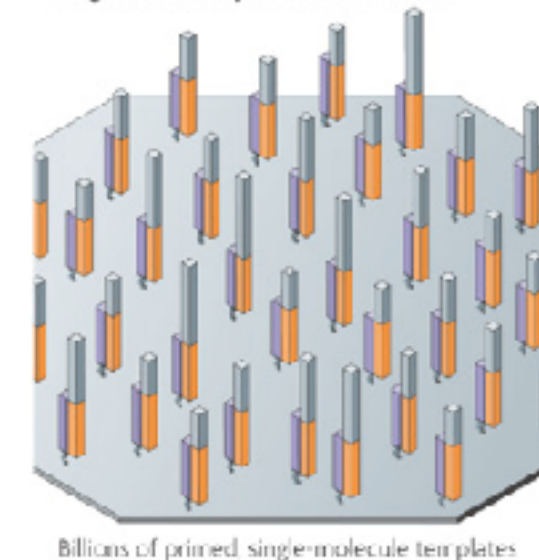
One DNA molecule per bead. Clonal amplification to thousands of copies occurs in microreactors in an emulsion



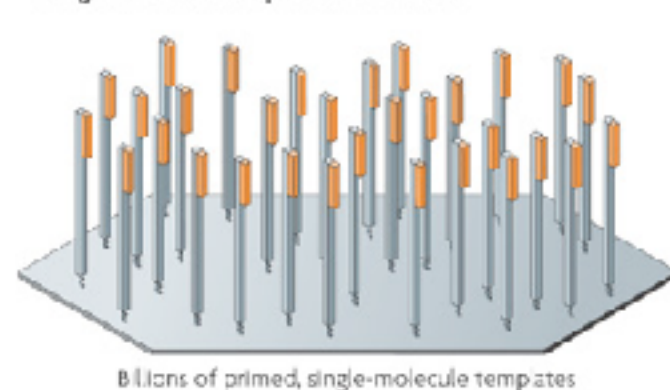
**b Illumina/Solexa
Solid-phase amplification**
One DNA molecule per cluster



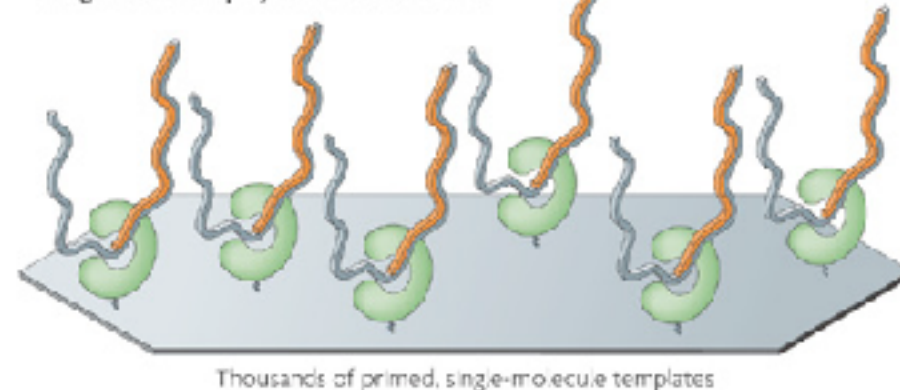
**c Helicos BioSciences: one-pass sequencing
Single molecule: primer immobilized**



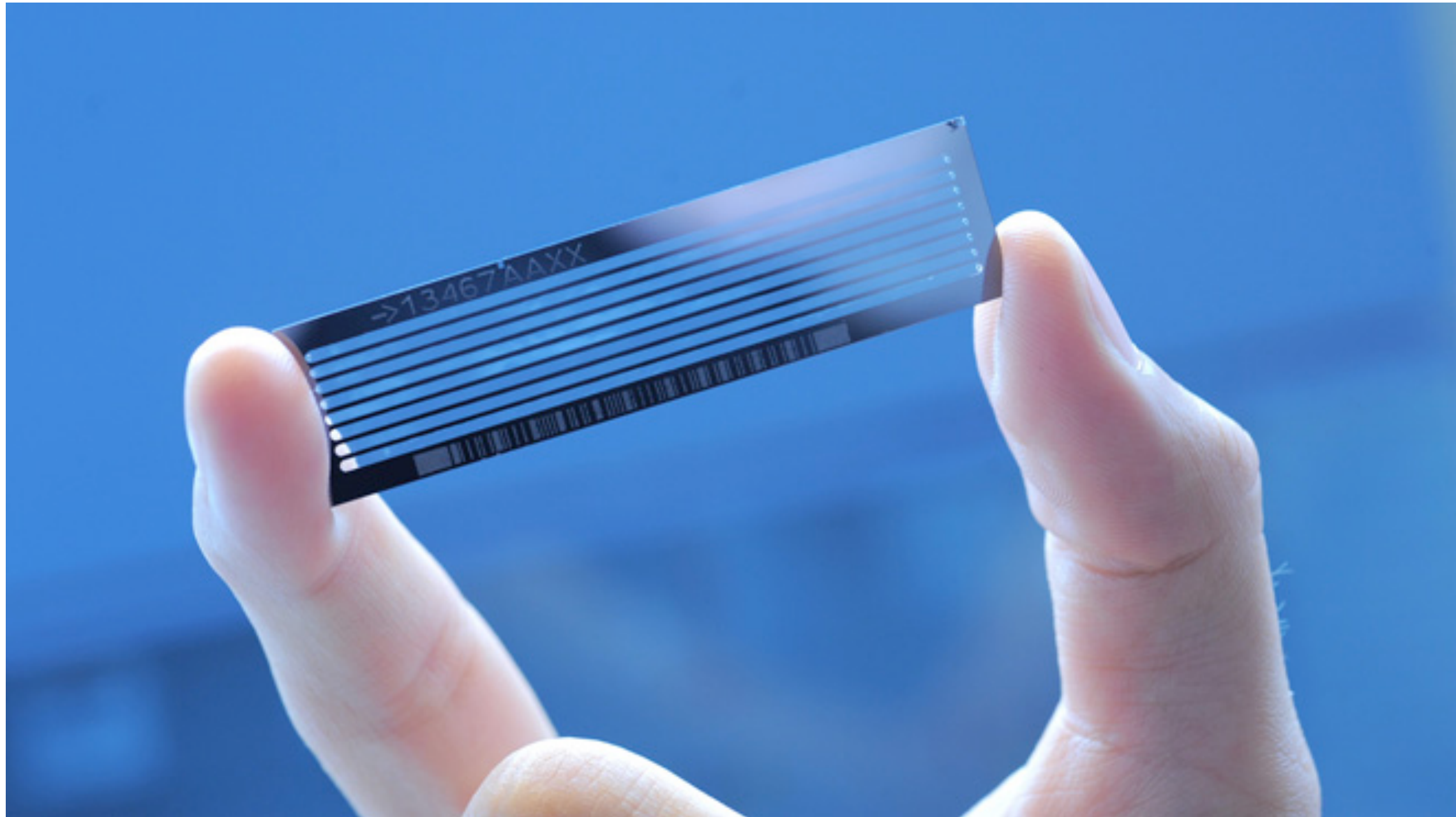
**d Helicos BioSciences: two-pass sequencing
Single molecule: template immobilized**



**e Pacific Biosciences, Life/Visigen, LI-COR Biosciences
Single molecule: polymerase immobilized**



A Flow Cell

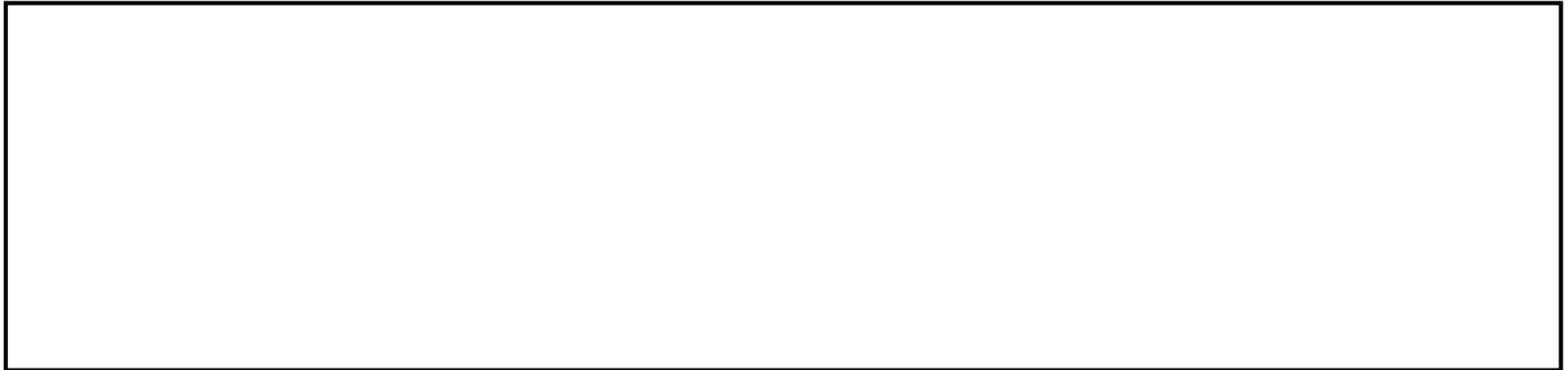


Pass Around Flow
Cells!!!

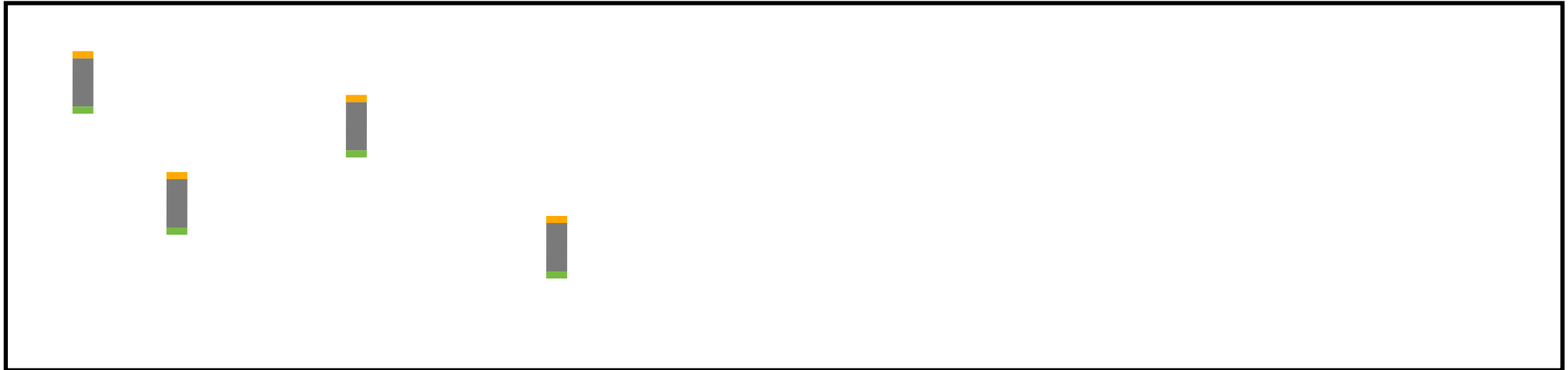
SBS: Sequencing by Synthesis

An Illumina Story

A Flow Cell



Bind Library



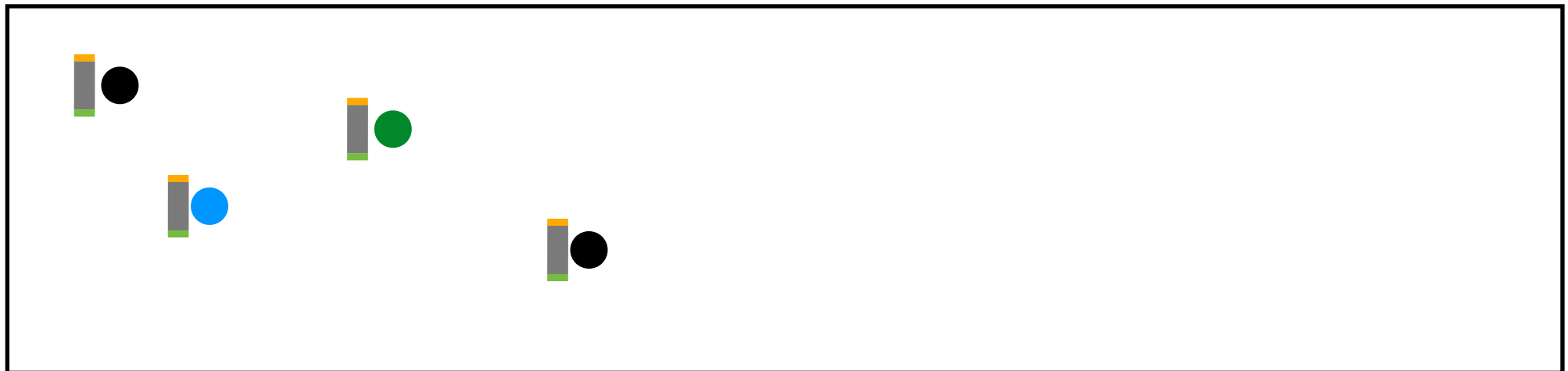
1st Cycle



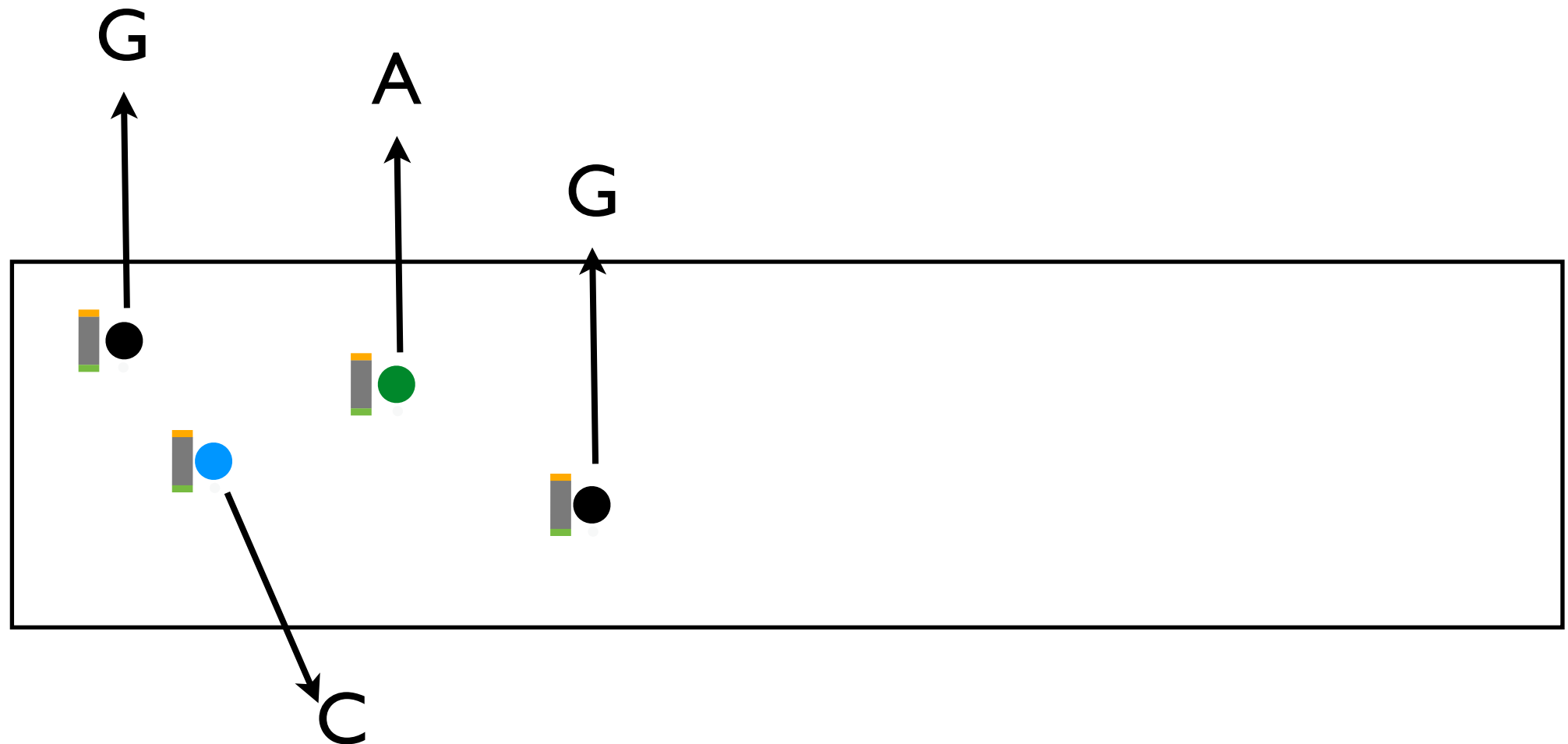
1st Cycle



1st Cycle



1st Cycle



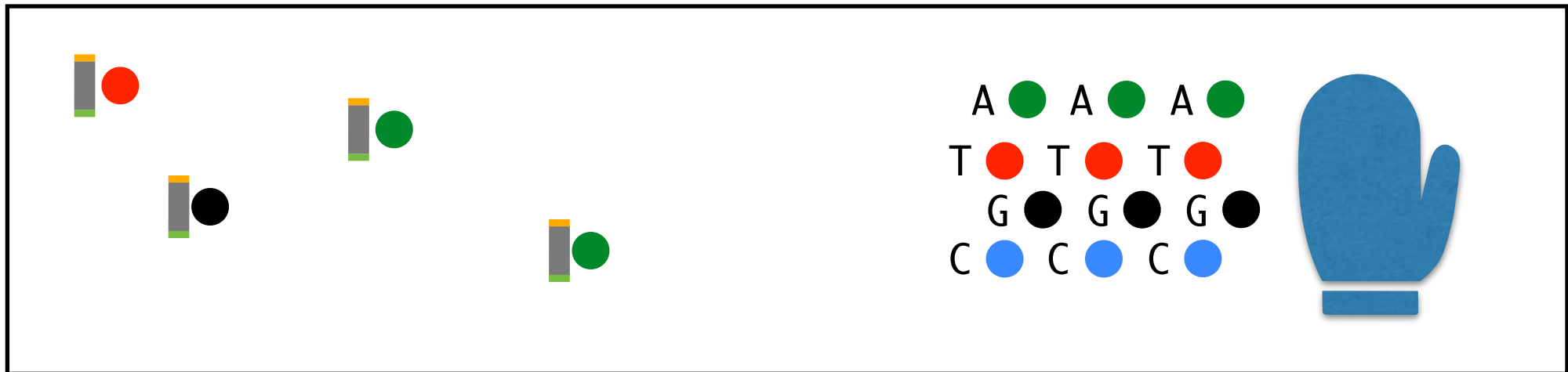
2nd Cycle



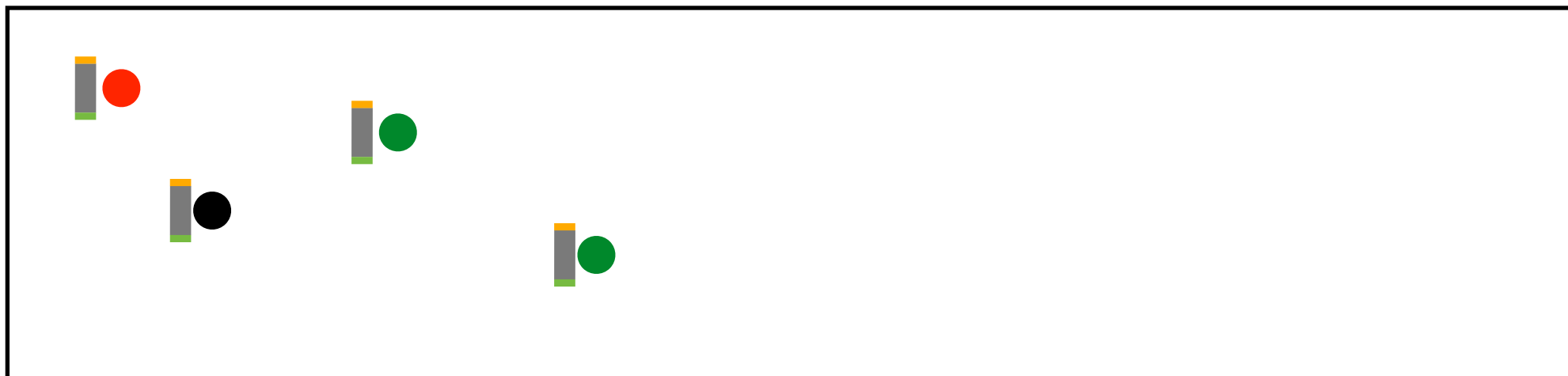
2nd Cycle



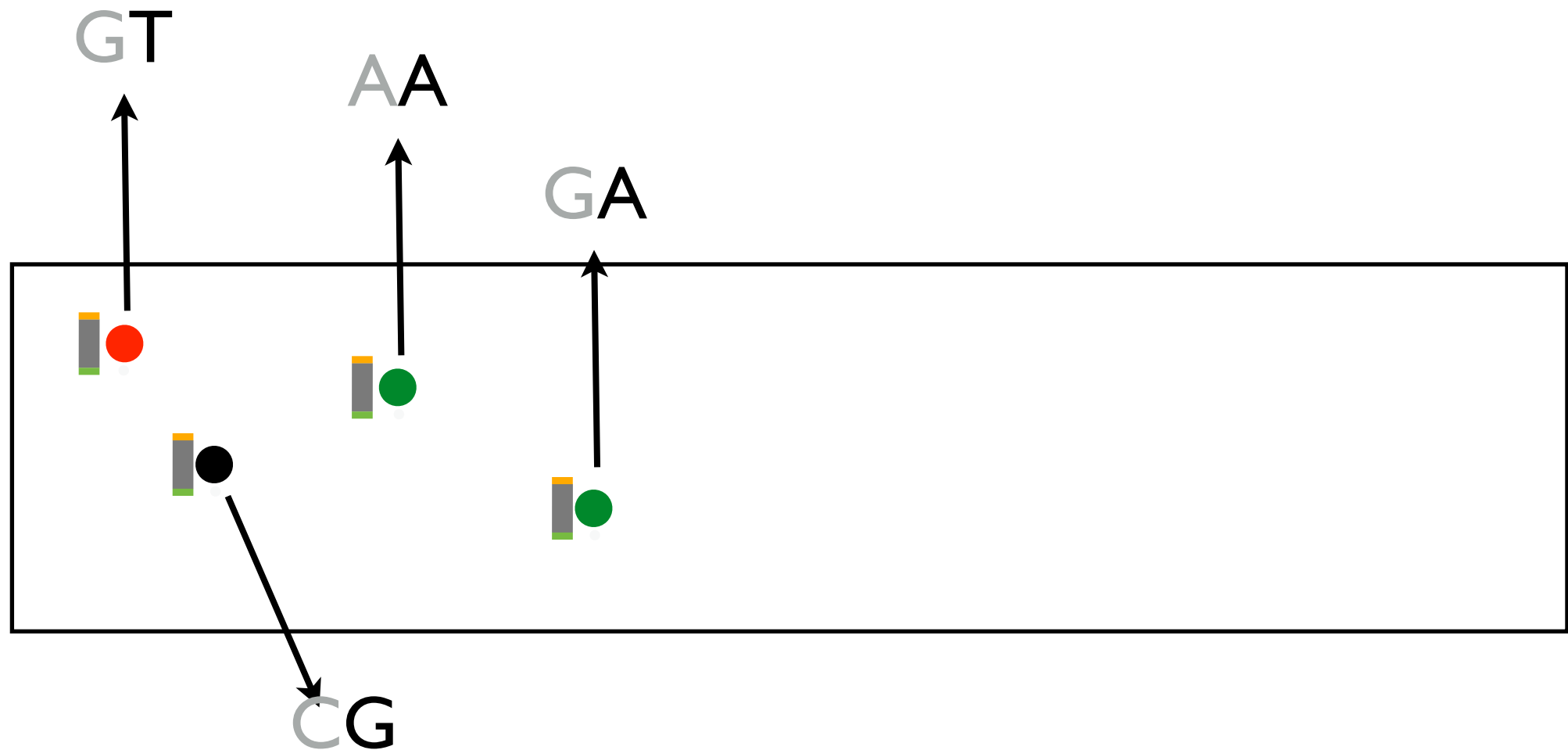
2nd Cycle



2nd Cycle



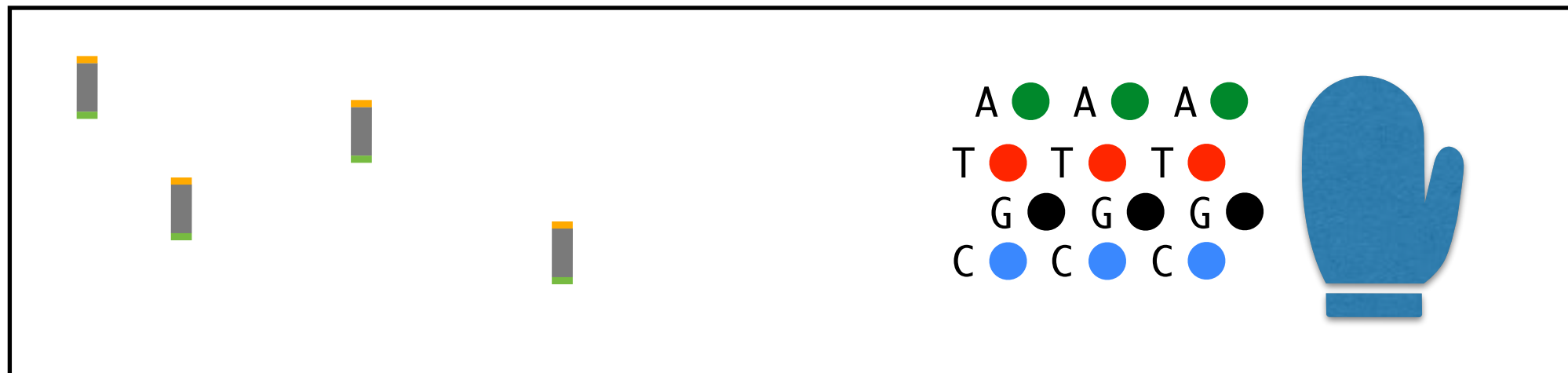
2nd Cycle



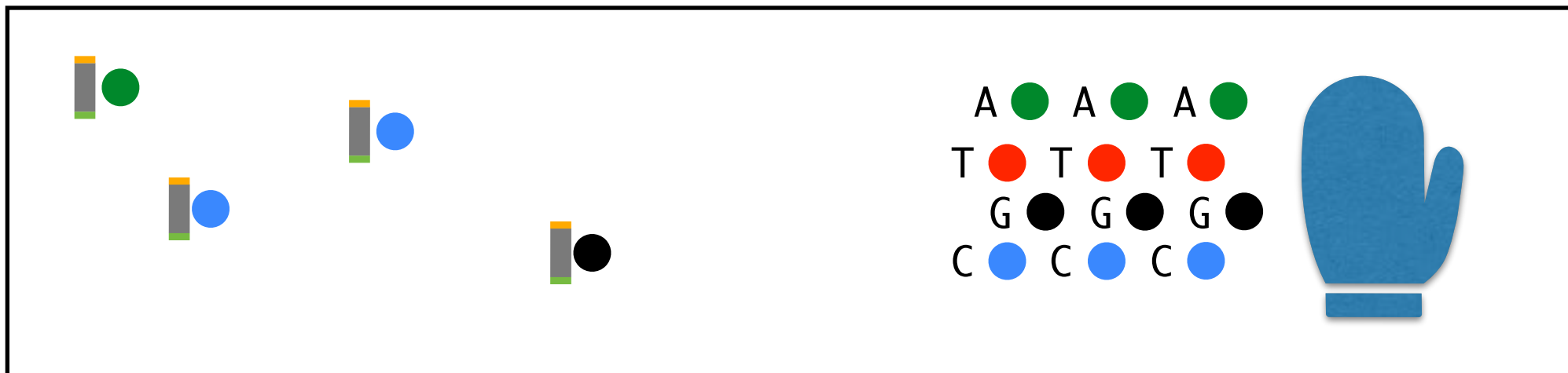
3rd Cycle



3rd Cycle



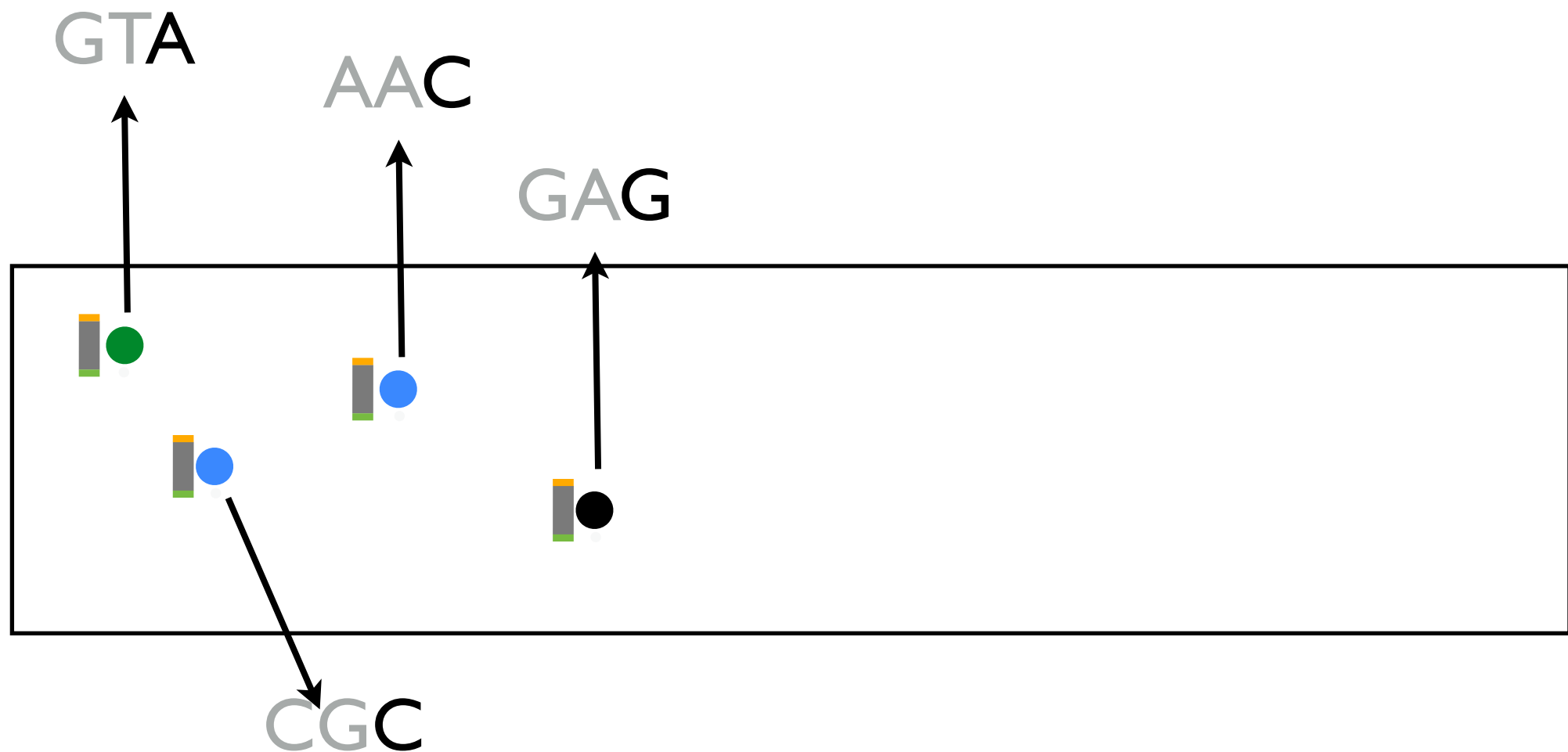
3rd Cycle



3rd Cycle



3rd Cycle

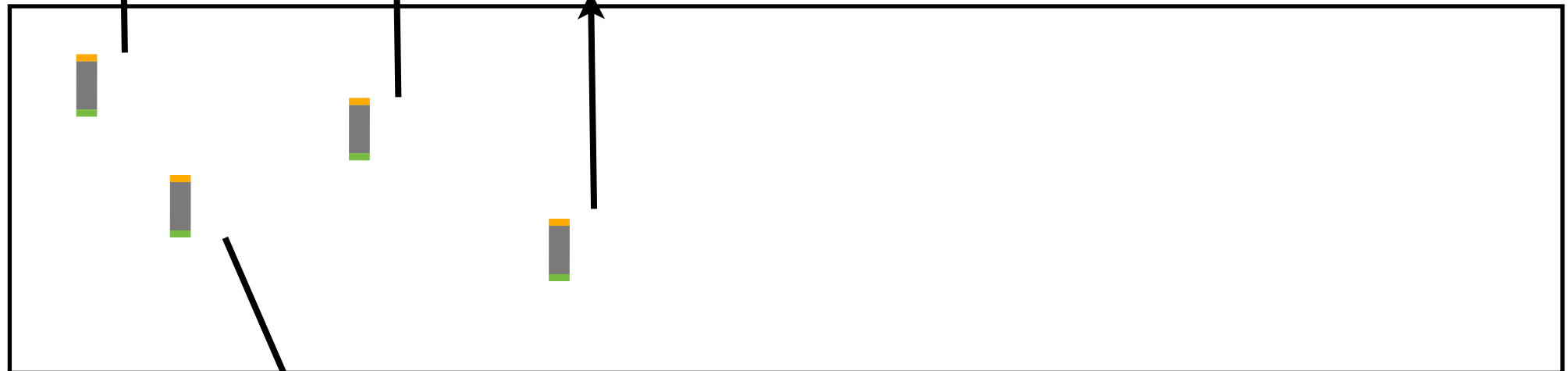


50th Cycle

GAATTCTAAAACAGTTGCATTCTATAATTACAAAATAATTGAAACACTTC

ACTAATATTATTTAATTAGACACCAACTCGACATTCTGTCTTCGACCTAT

TCCCAGTCATCGCCCAGTAGAATTACCAGGCAATGAACCACGGCCTTTCA

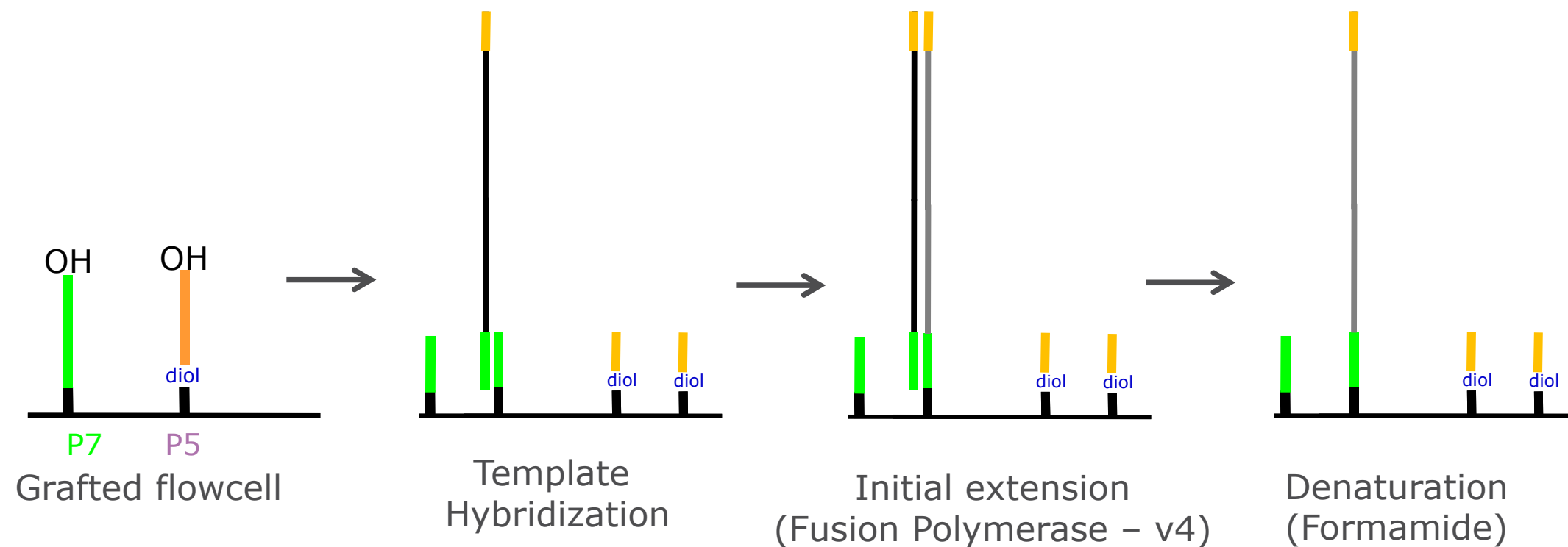


ACAGCATATGGGTTCACCTCCAACAGTGAACCATTCCAAAAGGCCTTGCCT

Illumina Short Reads

- 50 - 300bp

Cluster generation – hybridization and amplification



Hybridization

5' -CTGATCTGACTGATGCGTATGCTAGT-3'

+

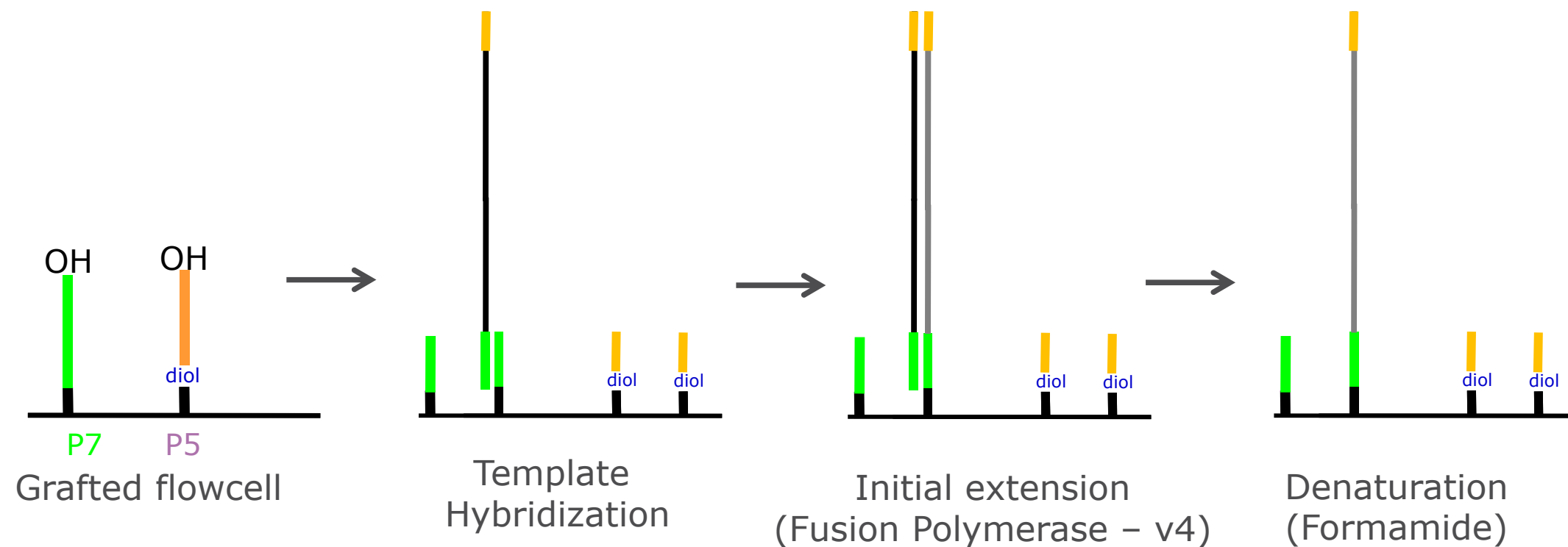
3' -GCATAC-5'

=

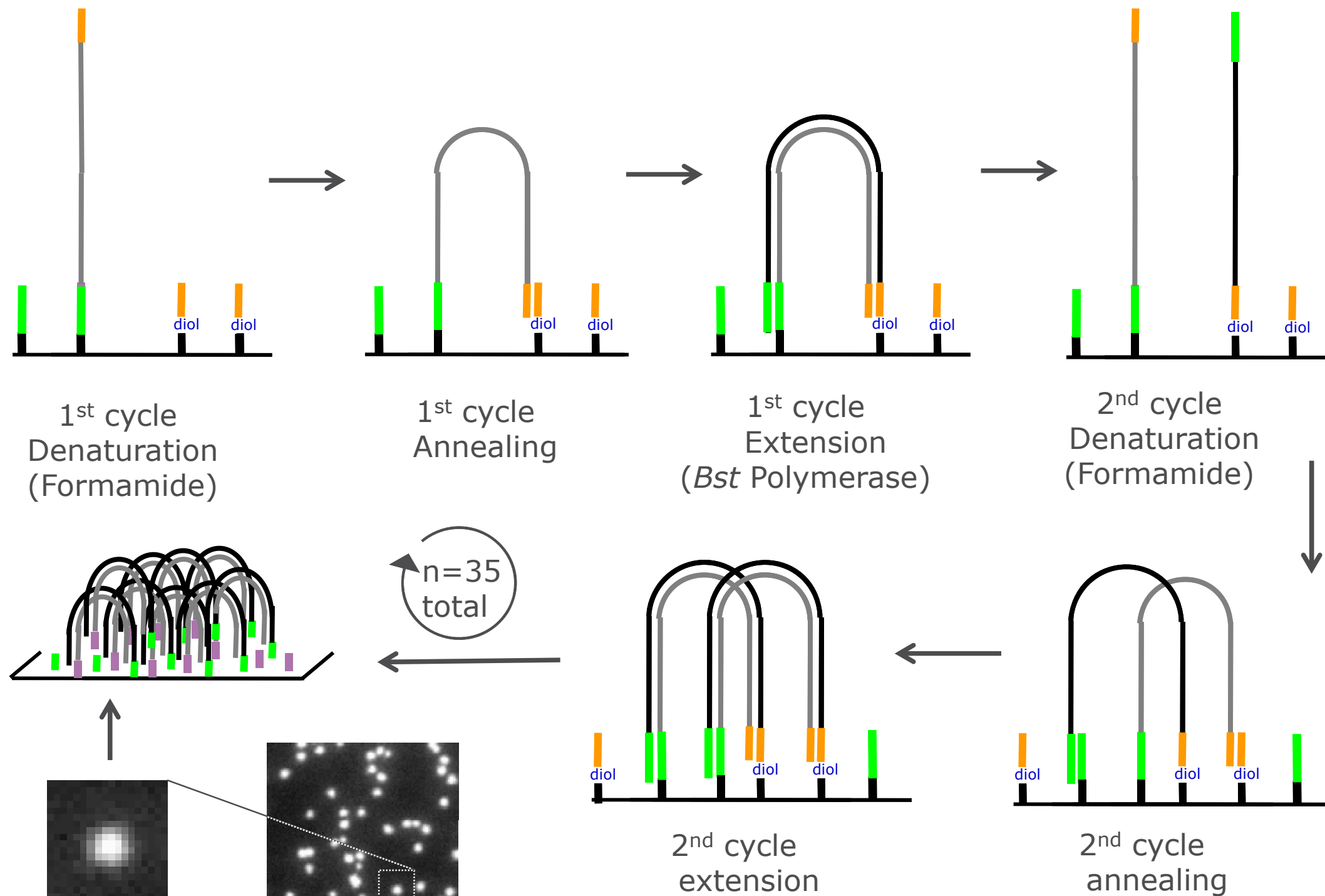
5' -CTGATCTGACTGATGCGTATGCTAGT-3'

3' -GCATAC-5'

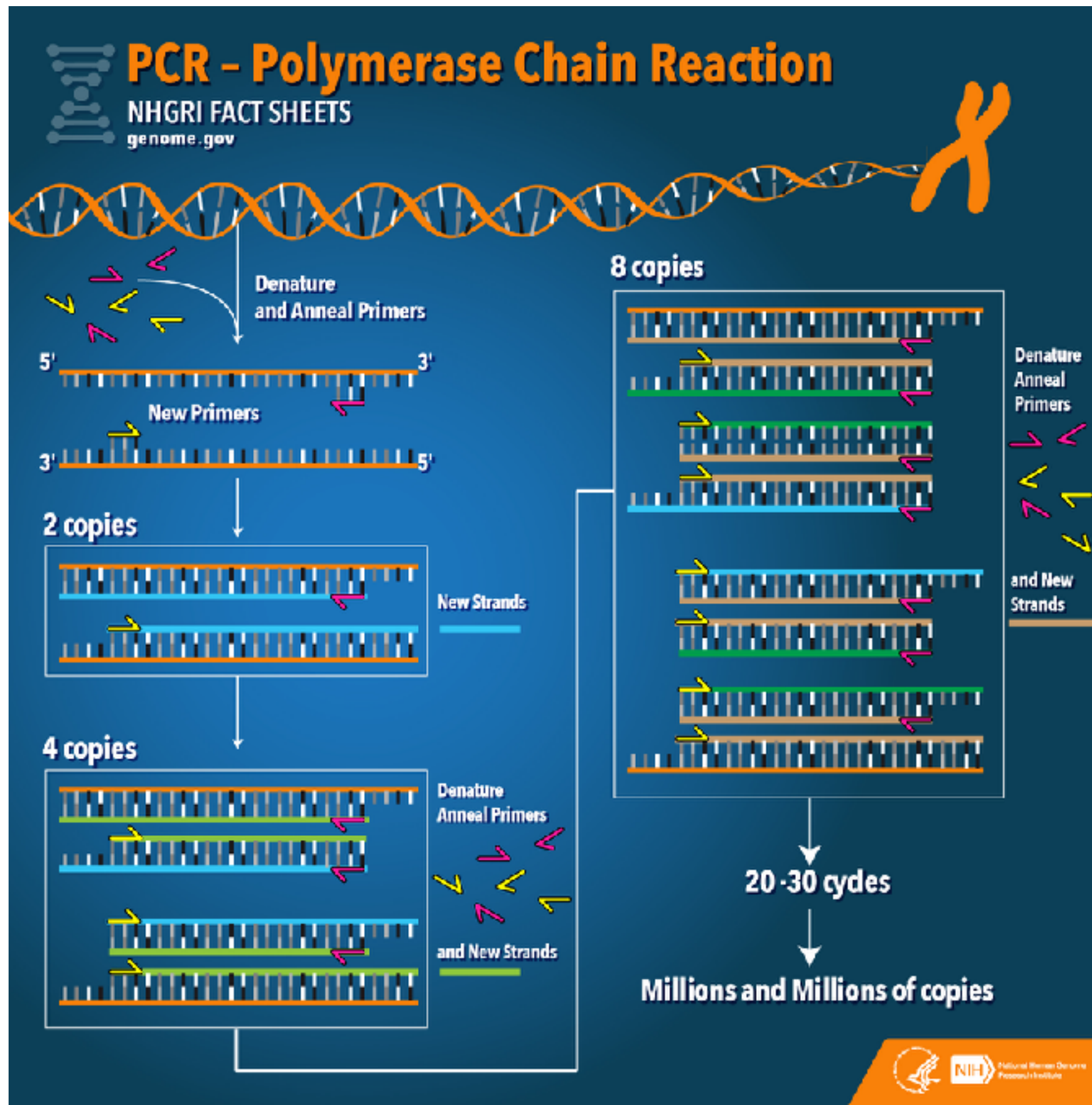
Cluster generation – hybridization and amplification



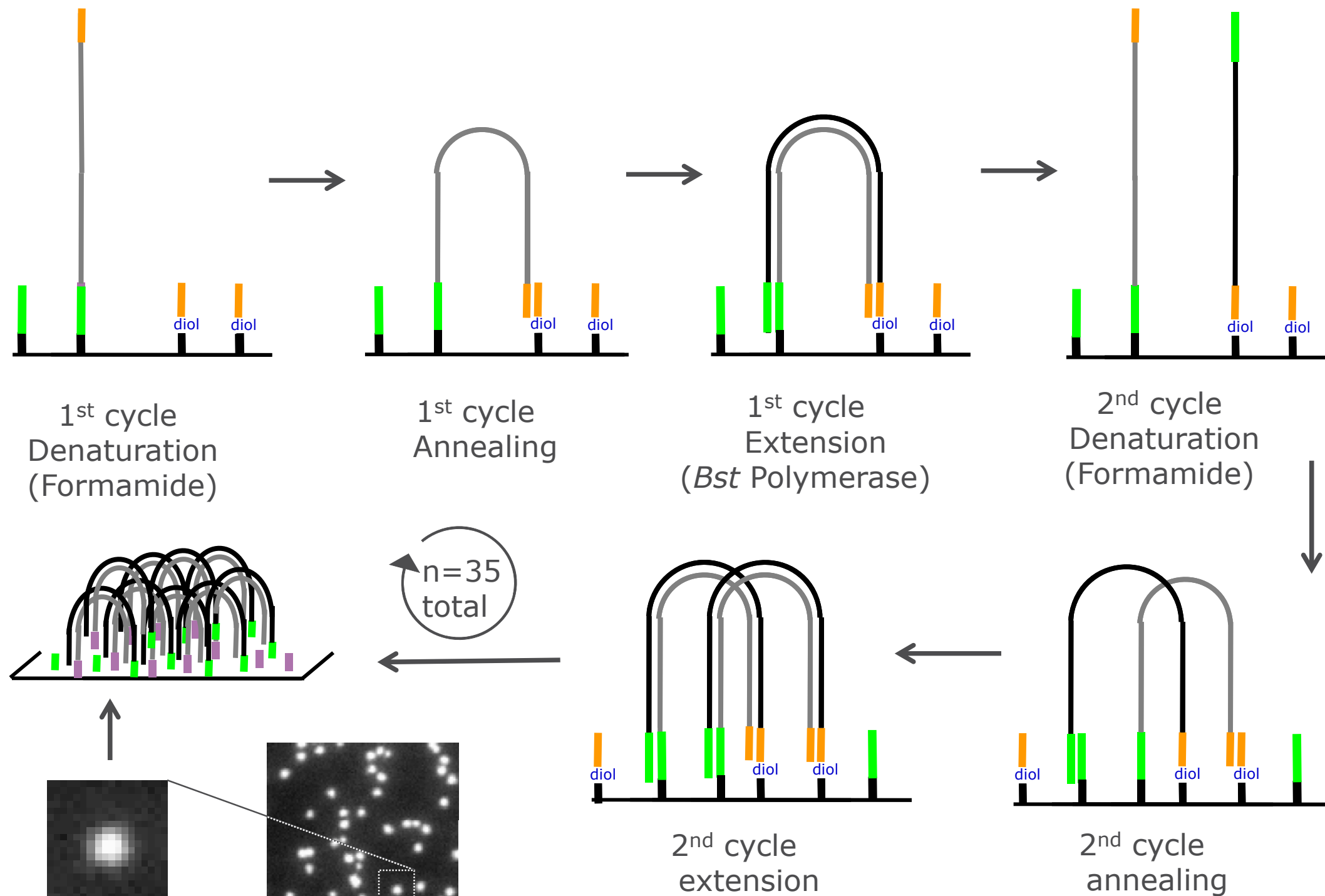
Cluster generation – hybridization and amplification



PCR



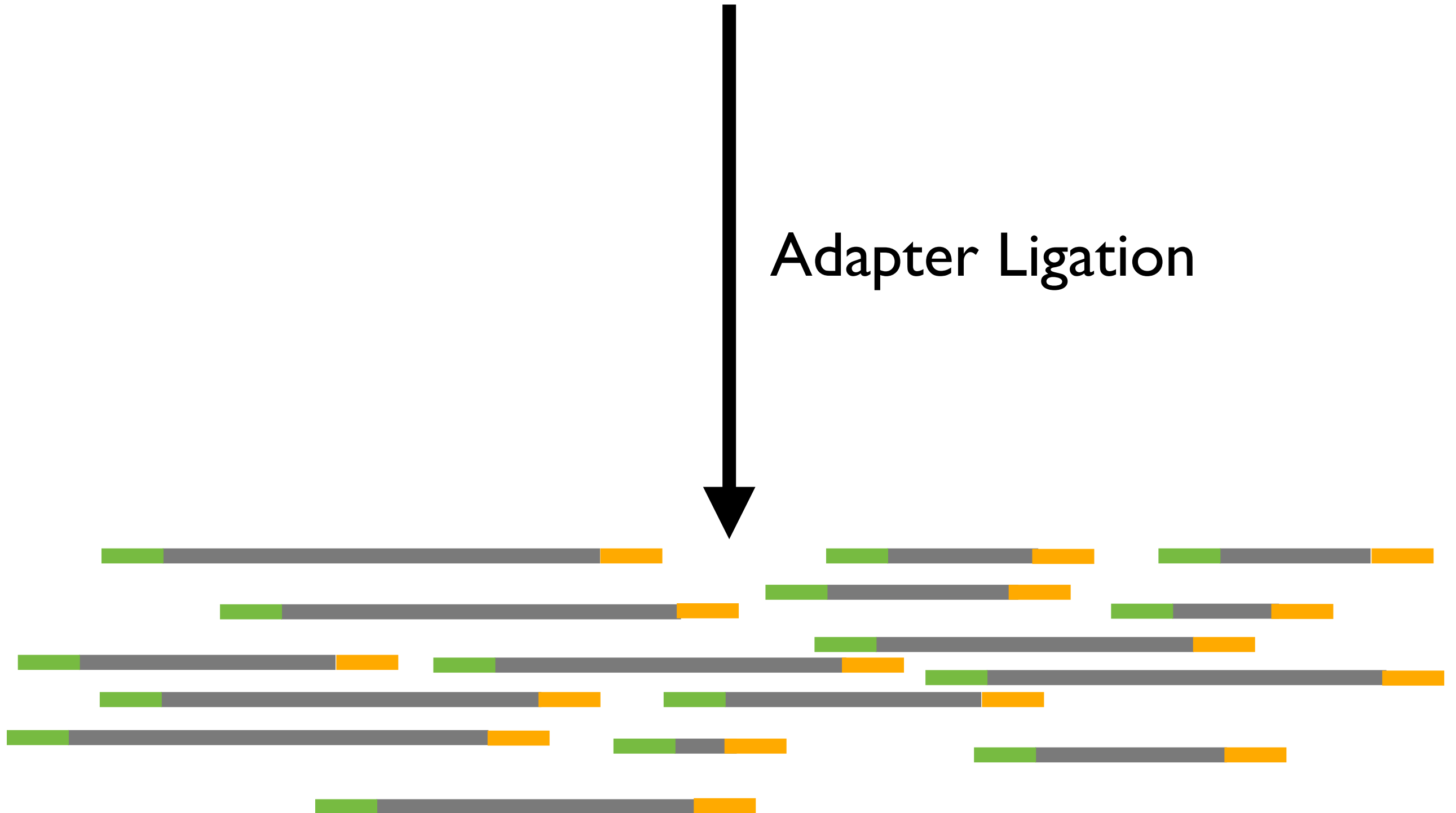
Cluster generation – hybridization and amplification



Library Preparation

Purified Nucleic Acid

Adapter Ligation



Why Adapters?

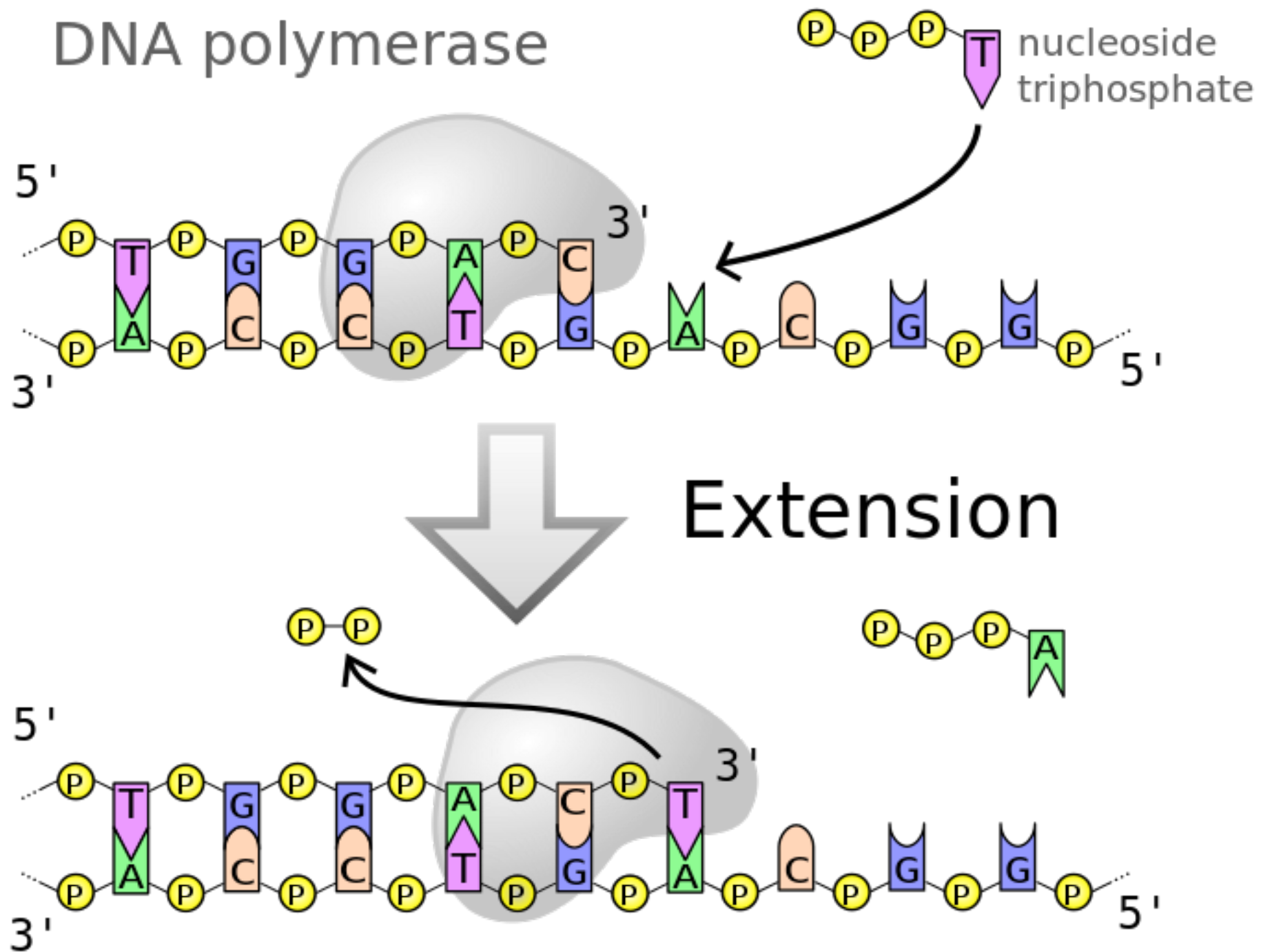
DNA Synthesis

- What are the minimum components for DNA Replication?

DNA Synthesis

- What are the minimum components for DNA Replication?
 - Template
 - Primer
 - Nucleoside triphosphates
 - DNA Polymerase*

DNA Synthesis



Why Adapters?

- Universal Priming Sites
 - Sequencing Primers
 - PCR Primers
- Hybridization to Flow Cell
- (more to come)

Additional Sequencing Details

Read Length

bases

50



273bp

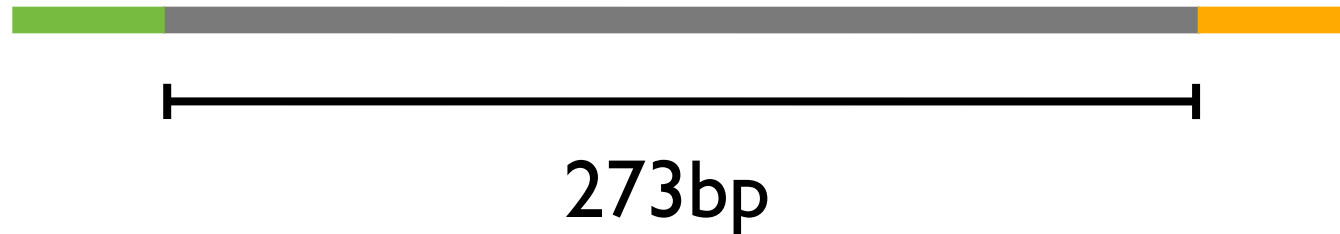
Read Length

bases

50



100



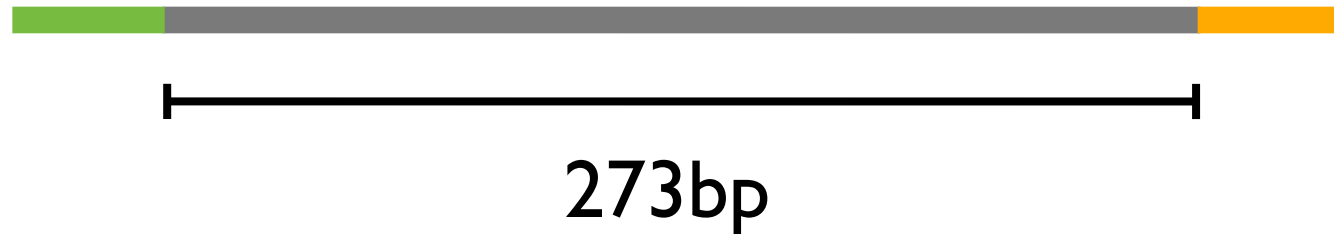
Read Length

bases

50 →

100 →

150 →



Read Length

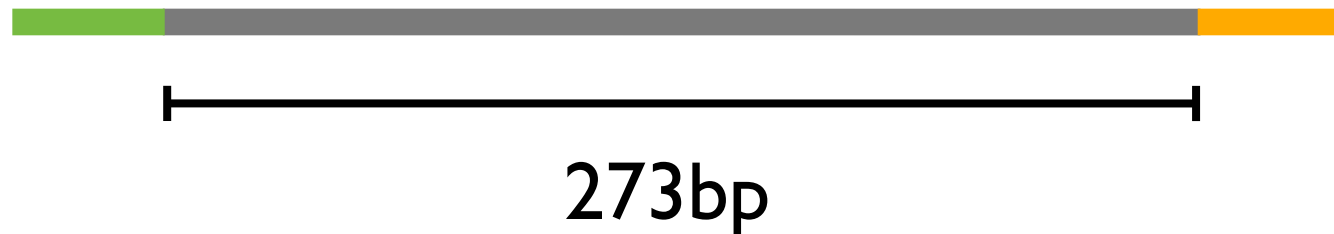
bases

50 →

100 →

150 →

250 →



Paired-End

TCGAAAAG
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

Paired-End

TCGAAAAG
AGCTTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

AGCTTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA
GACACACCT

Read Length

bases

50



273bp

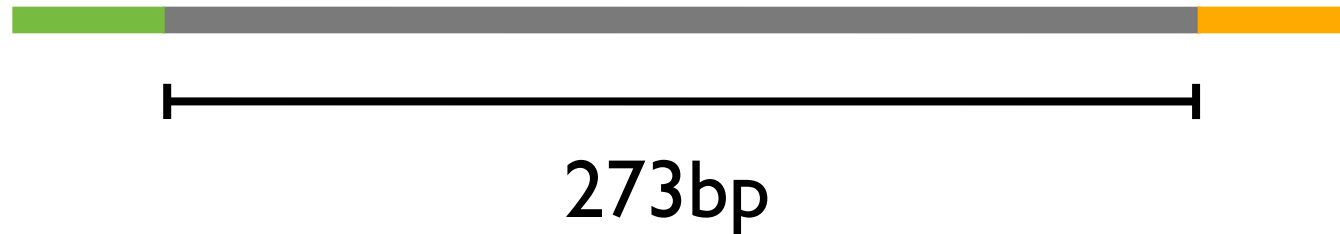
Read Length

bases

50



100



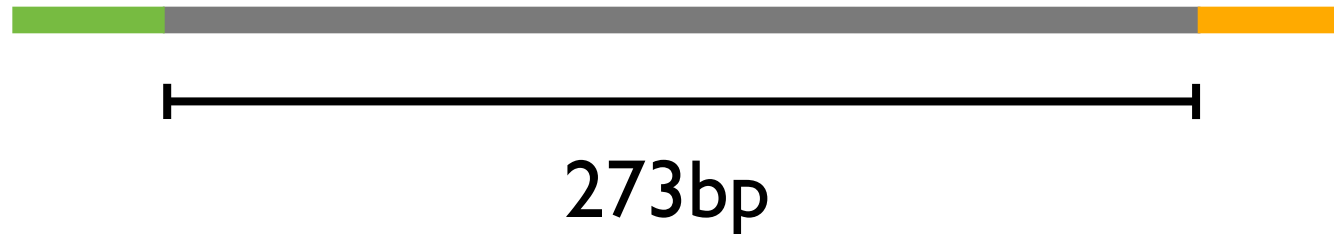
Read Length

bases

50 →

100 →

150 →



Read Length

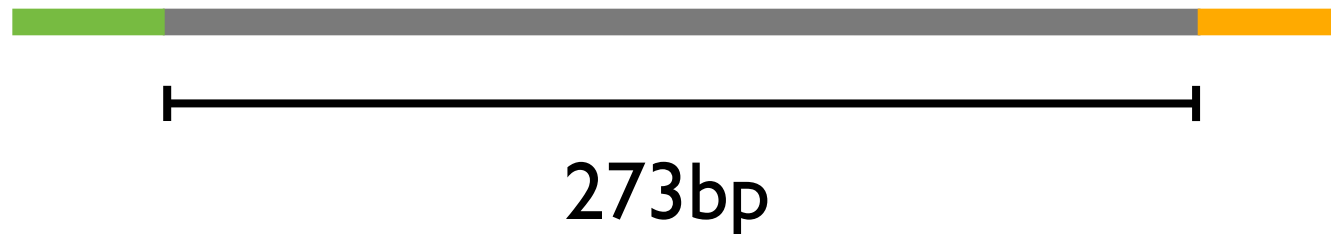
bases

50 →

100 →

150 →

250 →



Read Length

bases



Read Length

bases

50



Read Length

bases

50



100



Read Length

bases

50 →

100 →

150 →



←

←

←

Read Length

bases

50 →

100 →

150 →

250 →



←

←

←

←

Read Length

bases

50 →

100 →

150 →

250 →



634bp

←

←

←

←

MiSeq, NextSeq, and More Seqs

	MiSeq	NextSeq	HiSeq 4000	NovaSeq 6000
Maximum Output	15 Gb	120 Gb	750 Gb	3000 Gb
Maximum Reads per Run	25 million	400 million	2.5 billion	10 billion
Maximum Read Length	2 × 300 bp	2 × 150 bp	2 × 150 bp	2 × 150 bp
Run Time	4-56 hours	15-29 hours	< 1–3.5 days	13-45 hours
Cost*	\$1,787	\$4,695	\$19,206	\$35,538
Cost/Mbp*	\$0.119	\$0.039	\$0.026	\$0.012

* Duke Sequencing and Genomic Technologies Shared Resource, July 2018

Illumina Video

<https://www.youtube.com/watch?v=HMyCqWhwB8E>

Acknowledgements

- NEB
- Illumina

Patterned Flow Cells

- ExAmp
- Machines
 - HiSeq X
 - HiSeq 3000/4000
 - NovaSeq 6000

