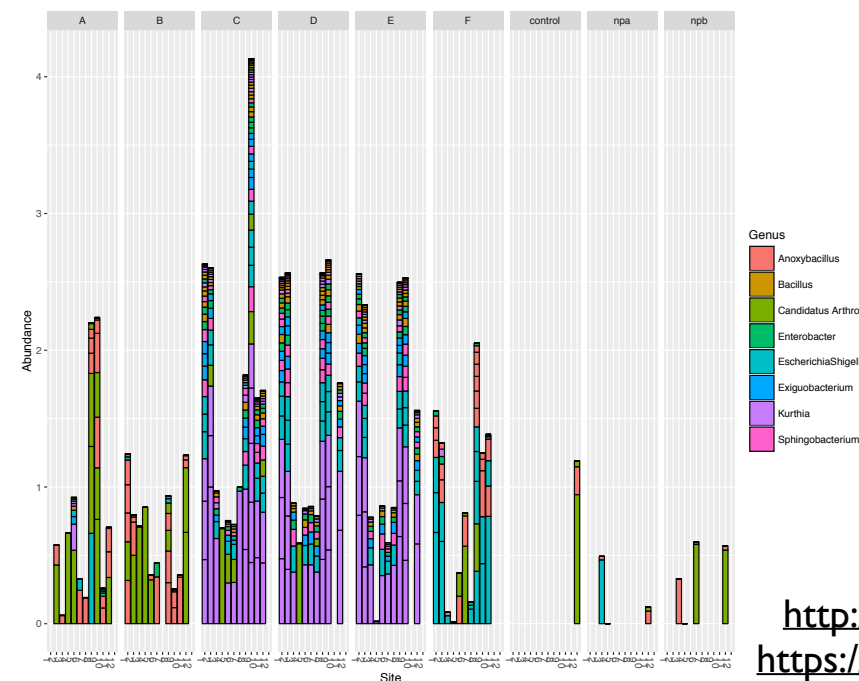
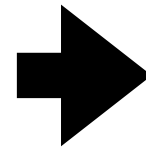
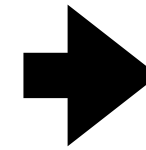
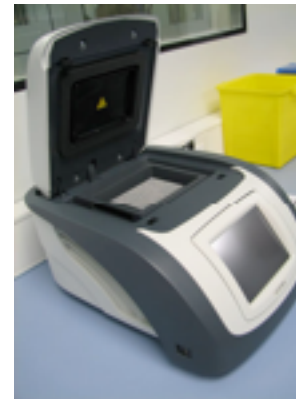
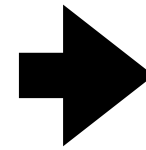
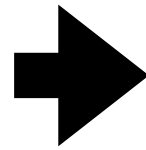
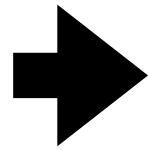


Bring Flow Cells!

# HTS Background and Theory

Josh Granek

# Molecular Biology

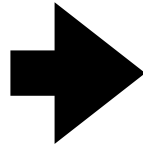


<http://www.geograph.org.uk/photo/2847164>

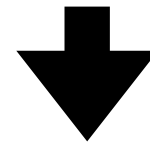
<https://commons.wikimedia.org/wiki/File:Pcr.jpg>

[https://commons.wikimedia.org/wiki/File:Illumina\\_MiSeq\\_sequencer.jpg](https://commons.wikimedia.org/wiki/File:Illumina_MiSeq_sequencer.jpg)

# Bioinformatic Analysis



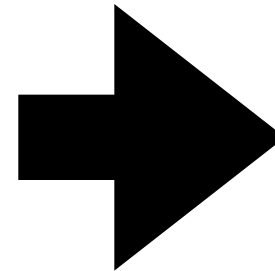
```
@M00698:36:000000000-AFBEL:1:1101:14738:1412 1:N:0:0
TTACGCTAACAGGCGGTAGCCTGGCAGGGTCAGGAAATCAATTAACATCATCGGAAGTGGTGATCTGTTCCATCAAGCGTGCGGCATCGTCAAAACGCCC
+
ABBBABBBBAFFFGGGGGGGGGHGHGGGCG2GF3FFGHHHHHHGGFGHEHHGGGEHHHHAGGHHGHHHFFDHFHHHGEGGGG@F@H?GHH/GBEFGGG
@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0
CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGTGGATAGCTTGTCAAAGCGACGCGCCAGTTCCAGATCCGGCG
+
AAABBFBBBBFFFGGGGGGGGGHGHGGGHHHHHHHGHGHGGGHHHHHHGGGGGGGGGGHHHHHGHFFHHHHHHGHGGGGGGGGHHHHHHHHHHHHGGG
@M00698:36:000000000-AFBEL:1:1101:15928:1413 1:N:0:0
GTAAAGTCCTGAGTGATACCGGCAACTTTTACCCCCAGTCCCACTTTGGAACCGGCAACATATCGGCAAAAGAGCCGTCCTGATTTAAAGCCGTAGGT
+
```



	Sample 1	Sample 2	...	Sample N
Bacteria 1				
Bacteria 2				
...				
Bacteria N				

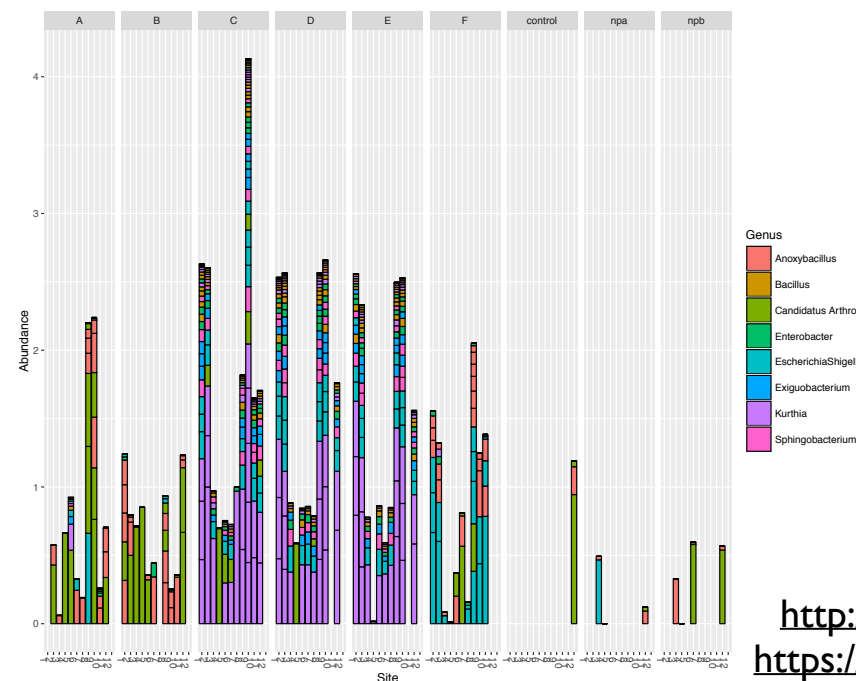
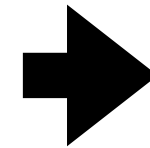
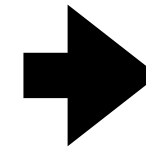
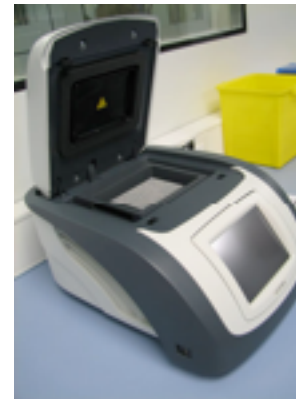
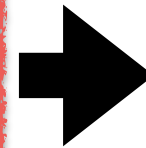
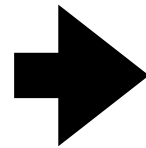
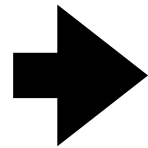
# Statistical Analysis

	Sample 1	Sample 2	...	Sample N
Bacteria 1				
Bacteria 2				
...				
Bacteria N				



1. What is present?
2. How much?
3. Are there differences between treatments, host species, ...?
4. What are the differences?

# Molecular Biology

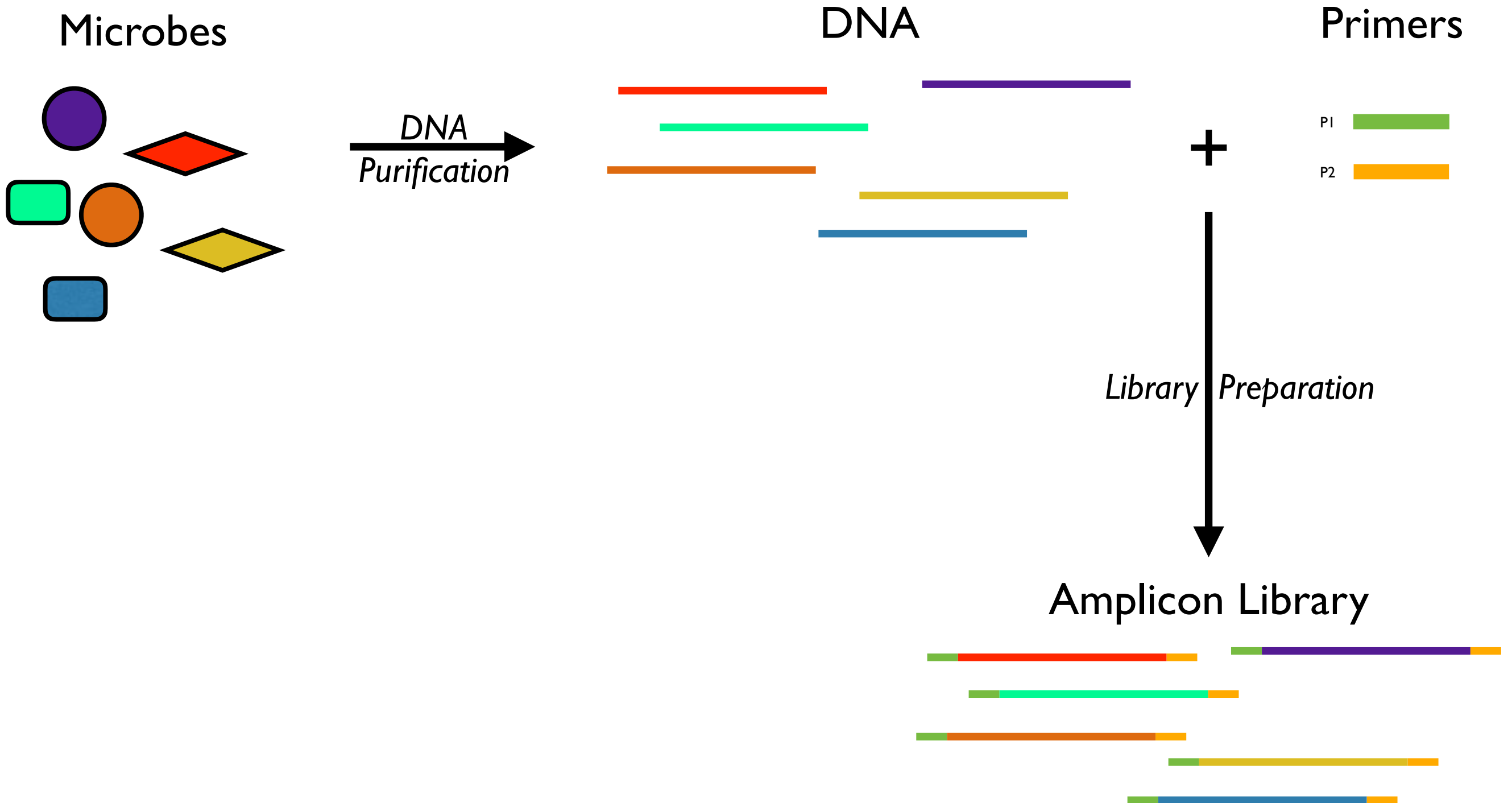


<http://www.geograph.org.uk/photo/2847164>

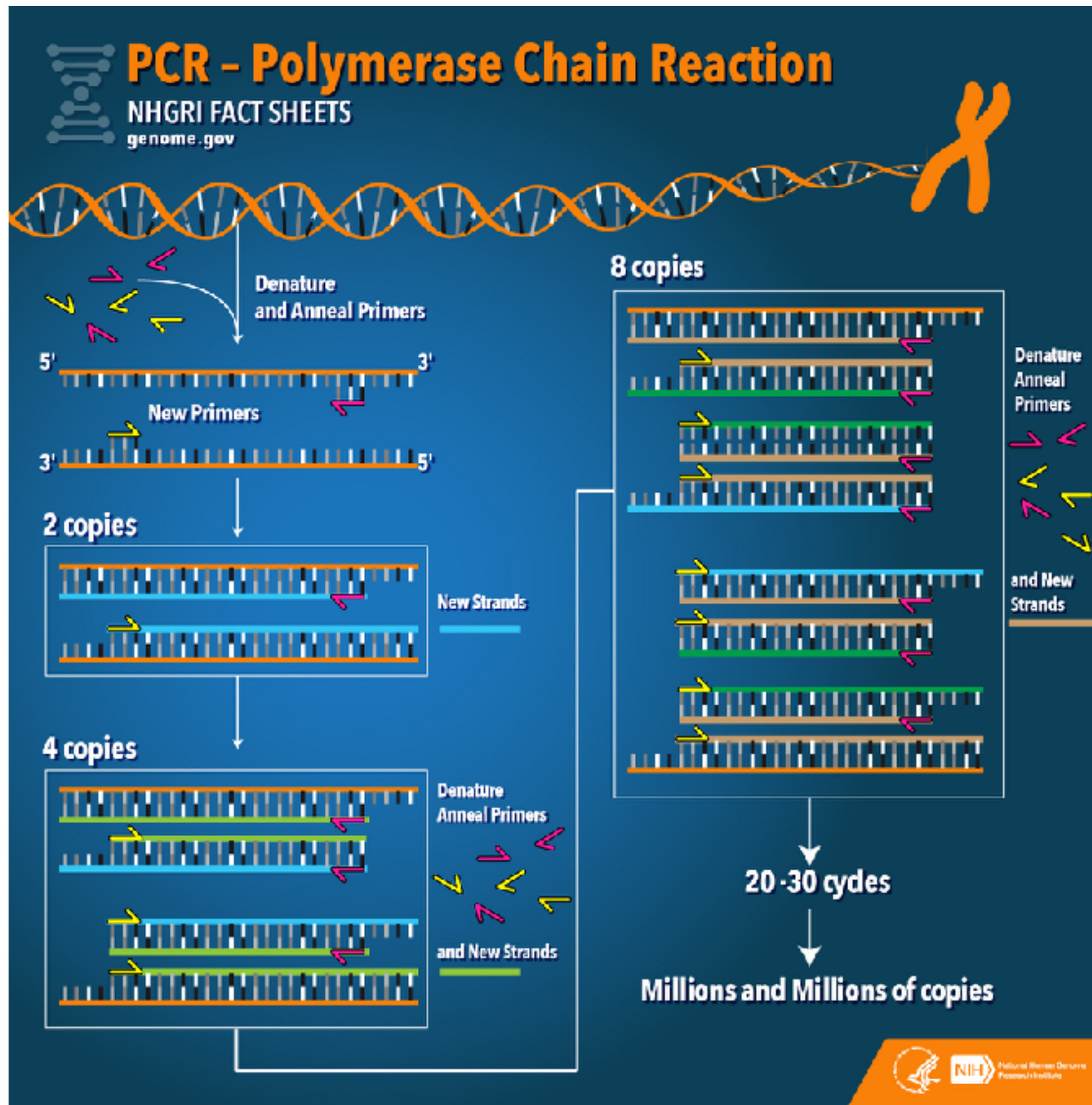
<https://commons.wikimedia.org/wiki/File:Pcr.jpg>

[https://commons.wikimedia.org/wiki/File:Illumina\\_MiSeq\\_sequencer.jpg](https://commons.wikimedia.org/wiki/File:Illumina_MiSeq_sequencer.jpg)

# Molecular Biology



# PCR





# Sanger Sequencing

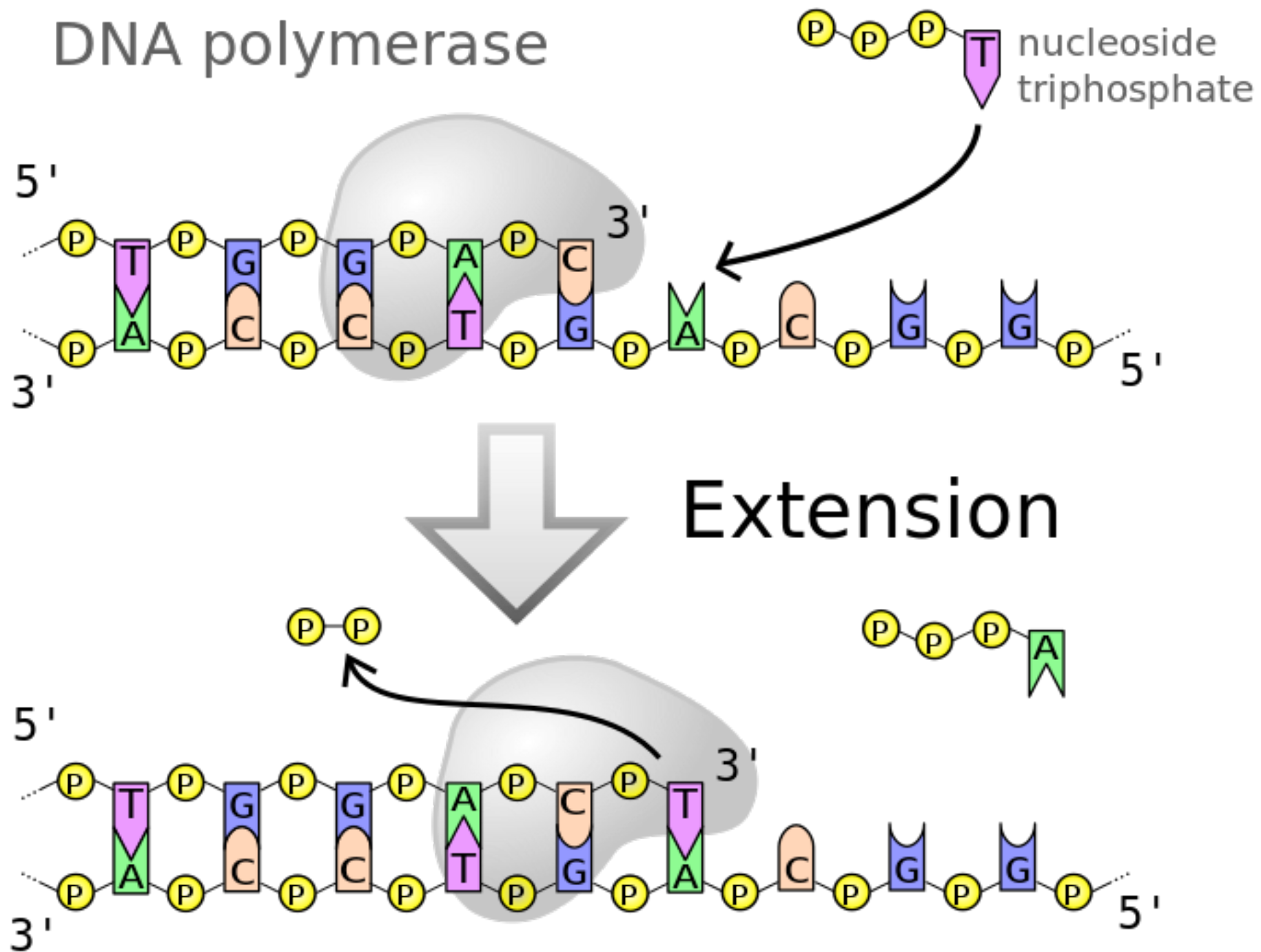
# DNA Synthesis

- What are the minimum components for DNA Replication?

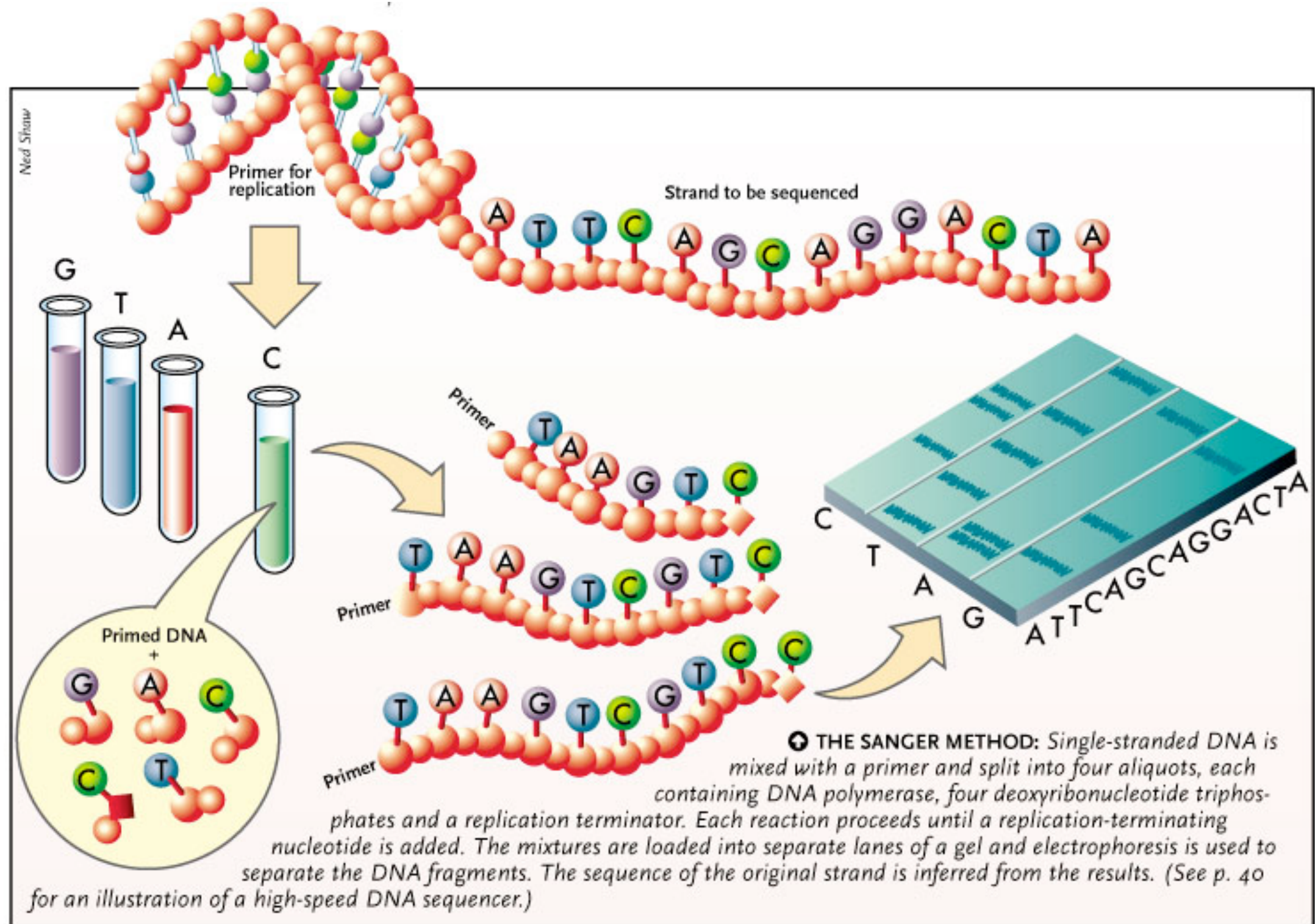
# DNA Synthesis

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

# DNA Synthesis



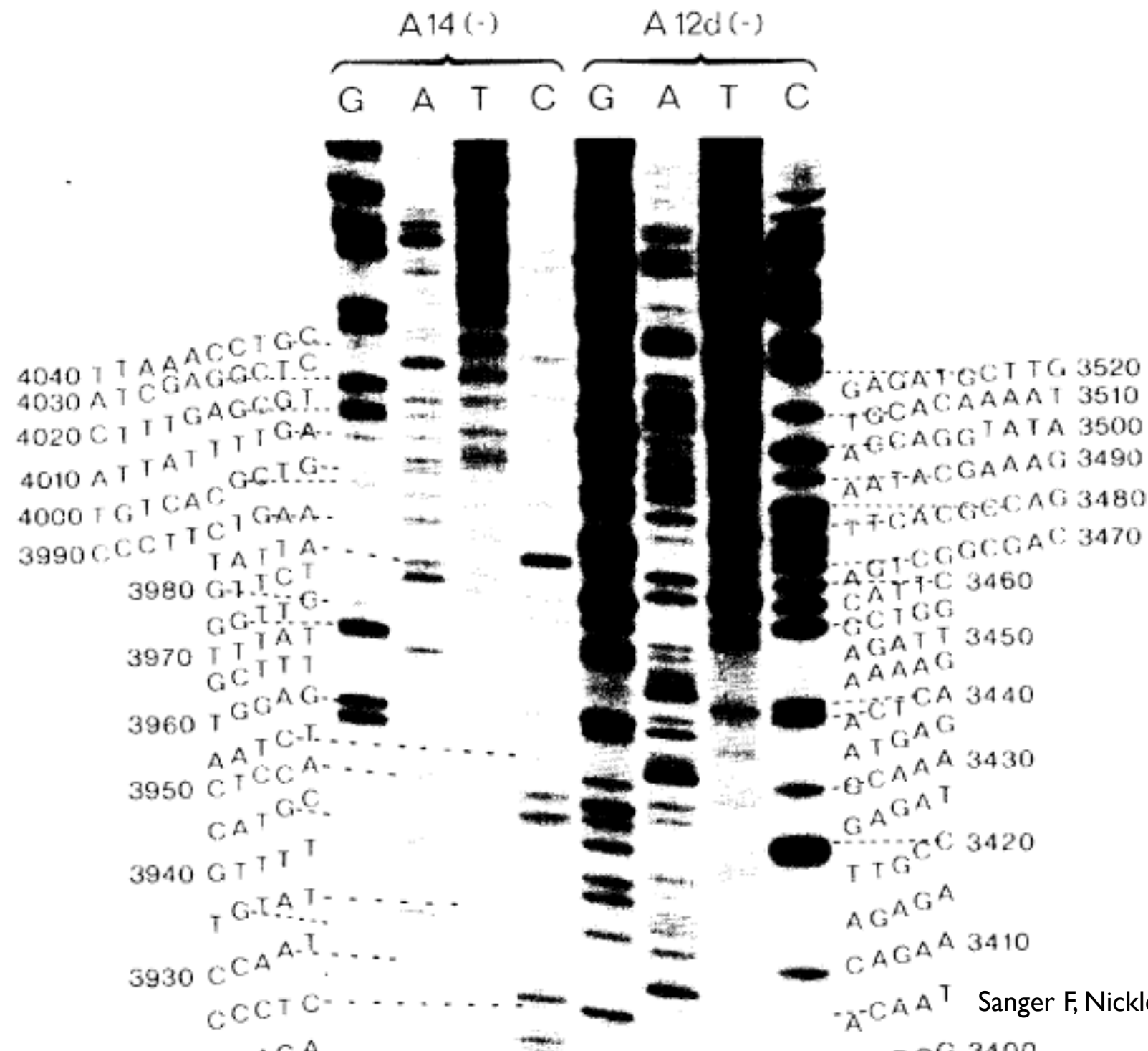
# Sanger Sequencing



# Sanger Sequencing

5464 Biochemistry: Sanger *et al.*

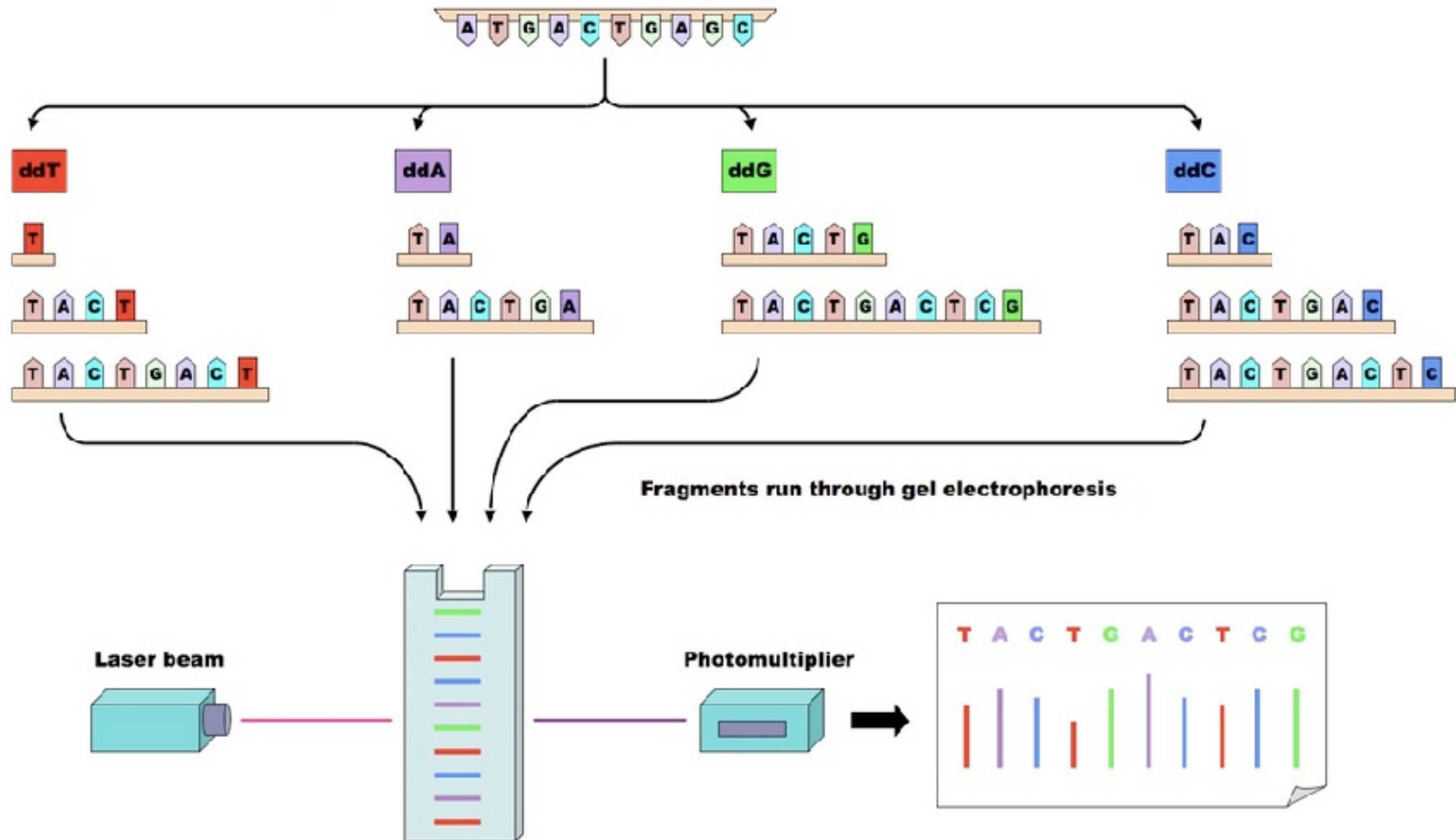
*Proc. Natl. Acad. Sci. USA* 74 (1977)





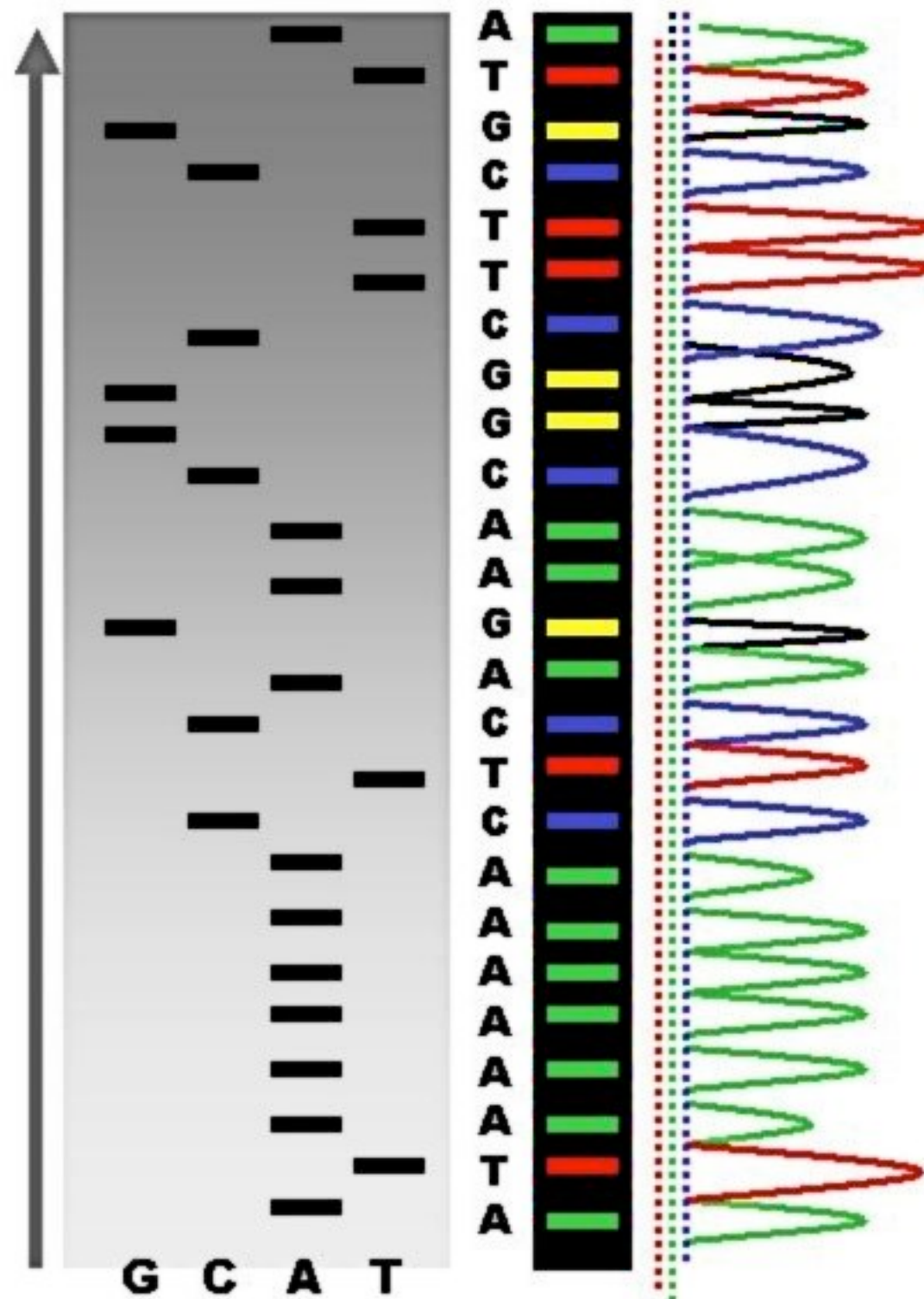
# Dye-terminator

### 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

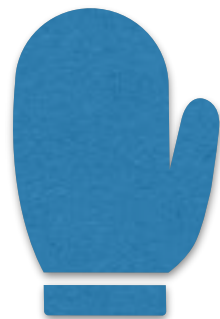
# Sequencing

  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

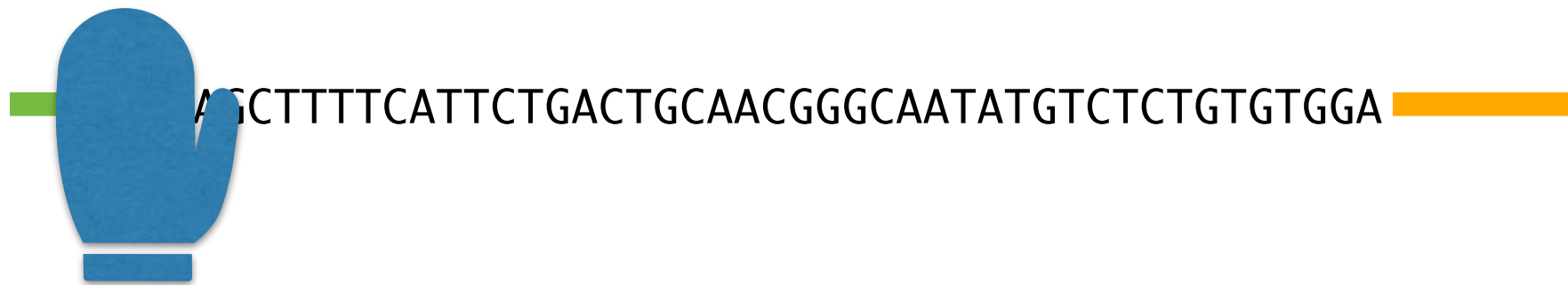
# Sequencing

AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

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

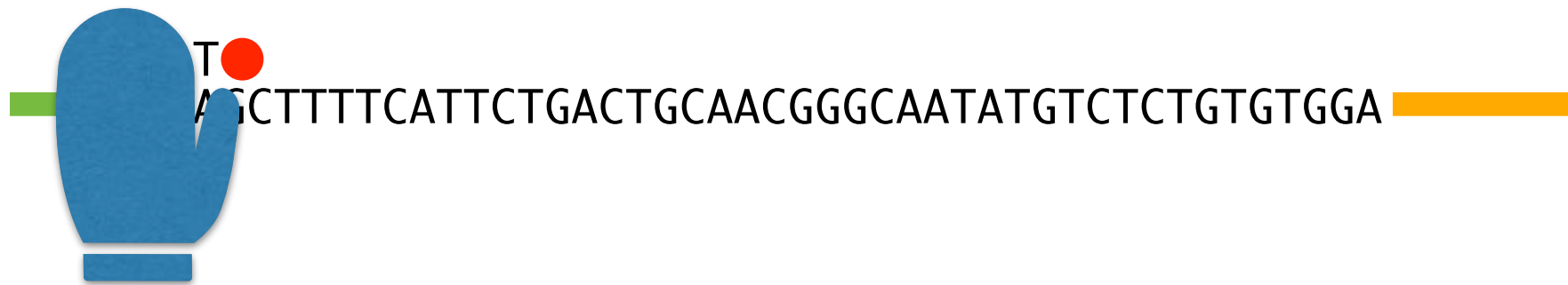


# Sequencing



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 

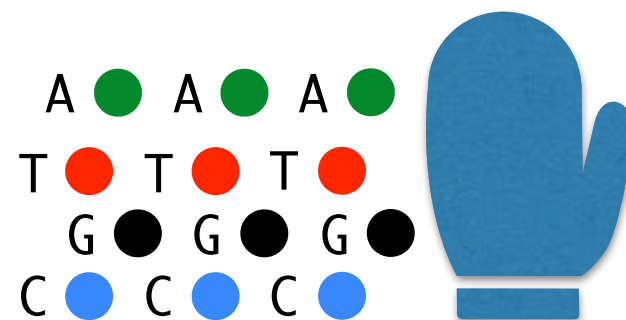


# Sequencing

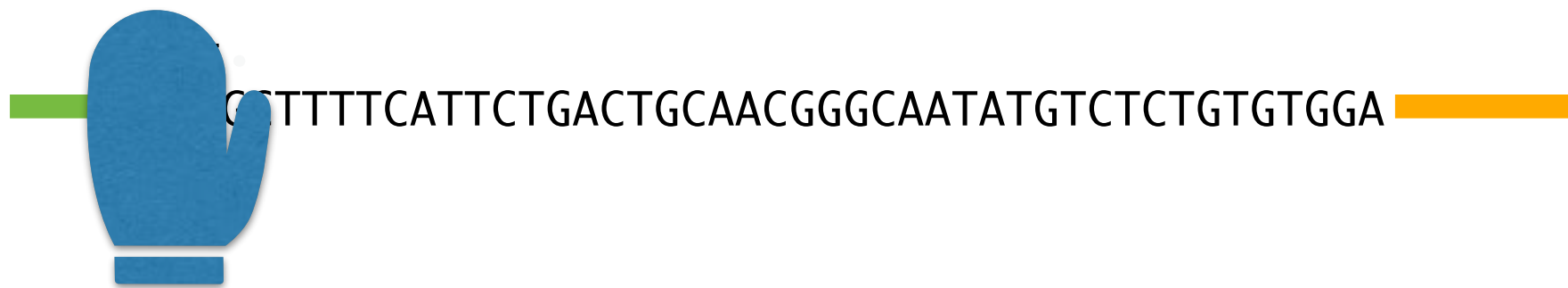
 T   
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

# Sequencing

— T  
— AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA —

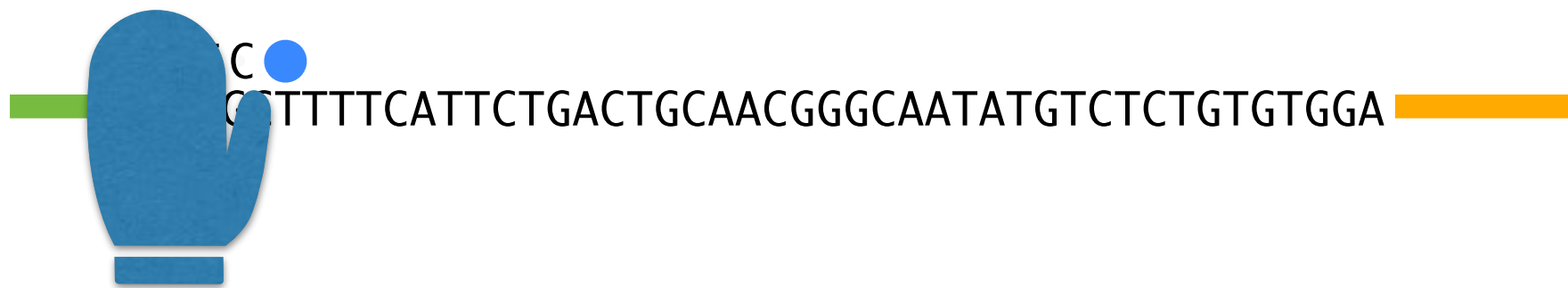


# Sequencing



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

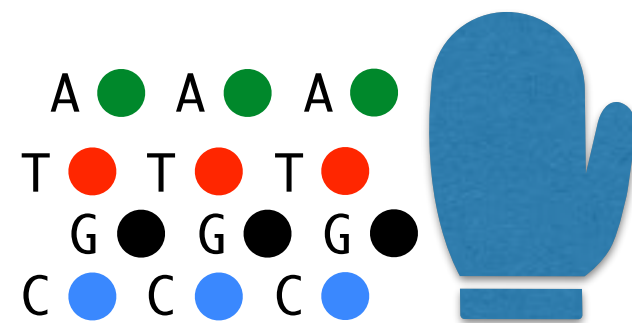
TC ●  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

# Sequencing

 T C  
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

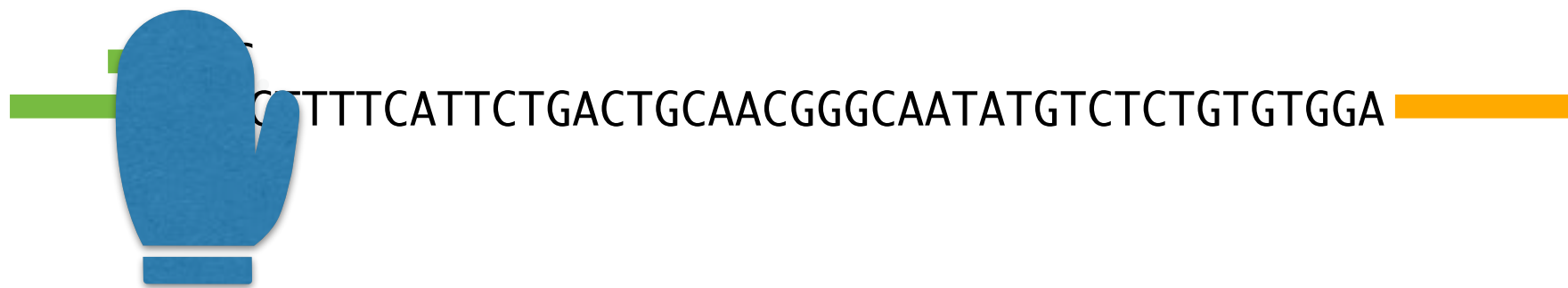
# Sequencing

TC  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA



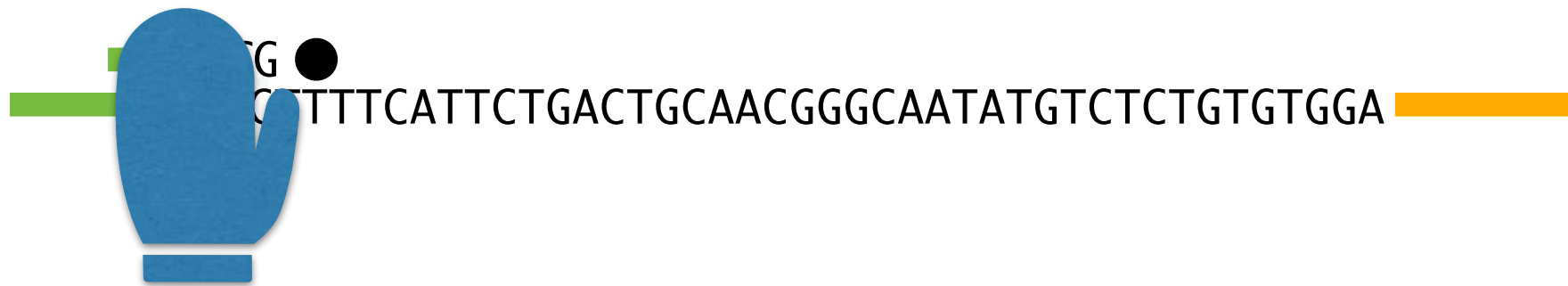


# Sequencing



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	●

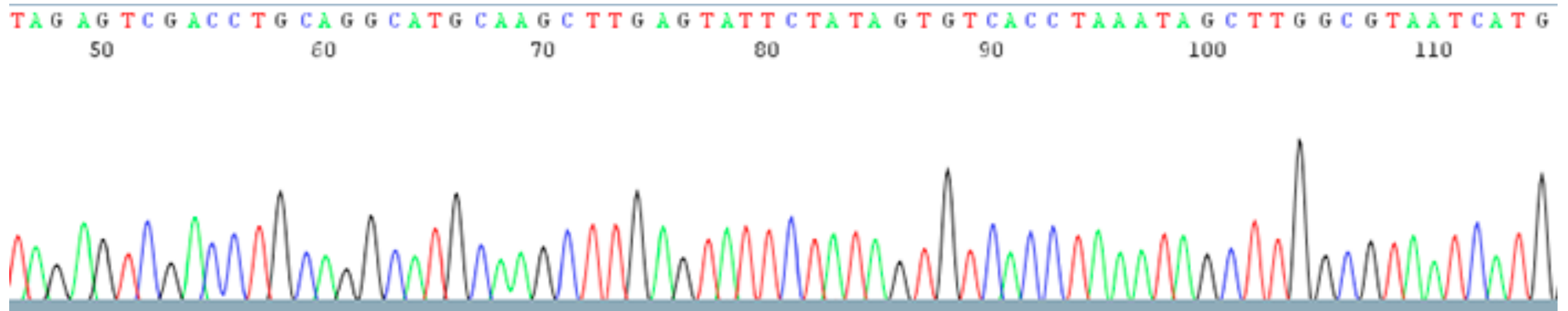
# Sequencing

TCG ●  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

# Sequencing

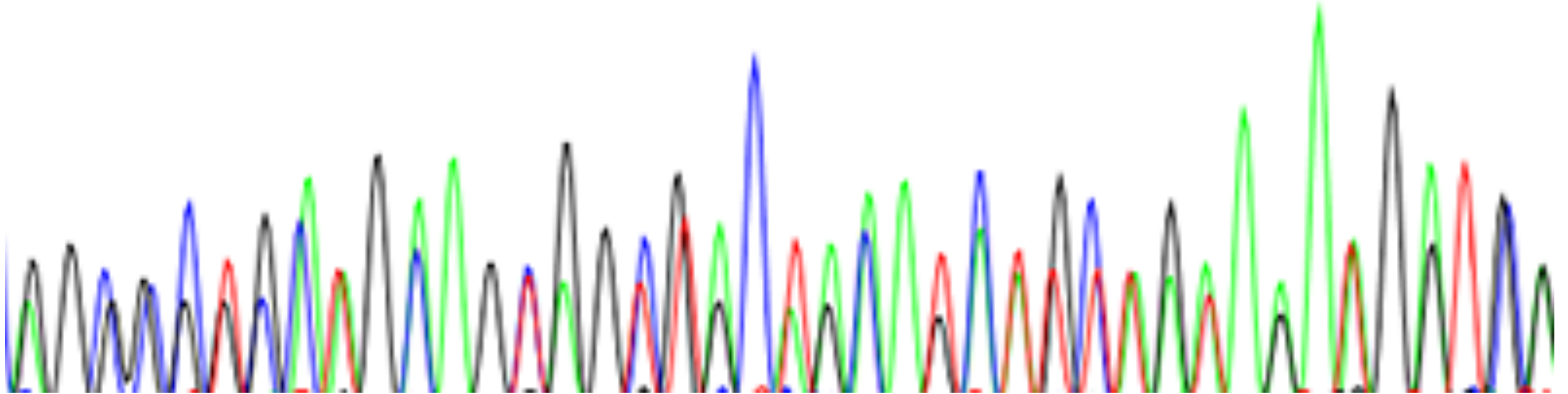
 T C G ●  
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

# 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?

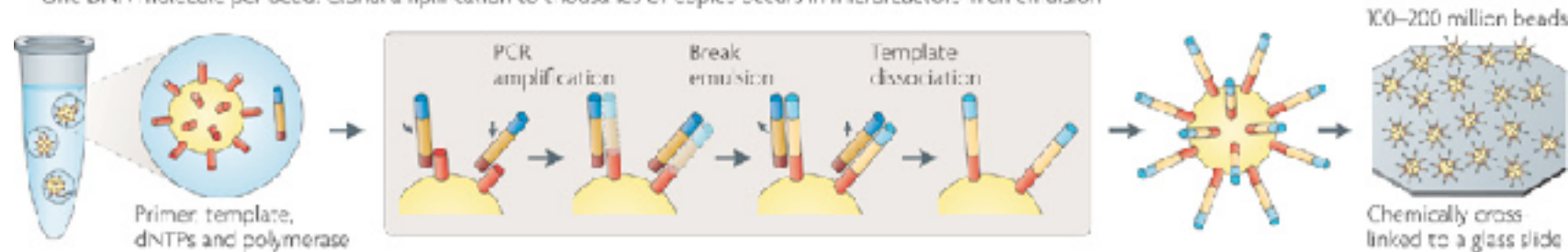
- Separate
- Detect
- Removable Terminator



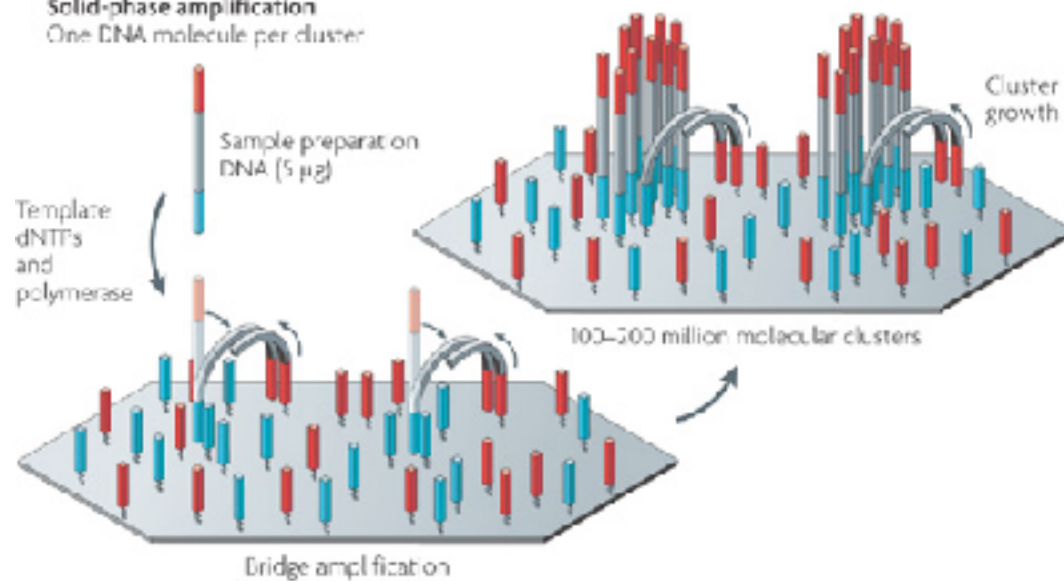
# Template immobilization

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

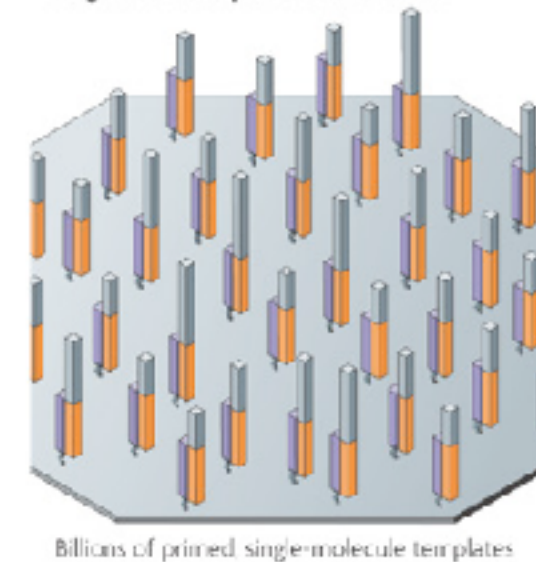
One DNA molecule per bead. Clonal amplification to thousands of copies occurs in microreactors in an emulsion



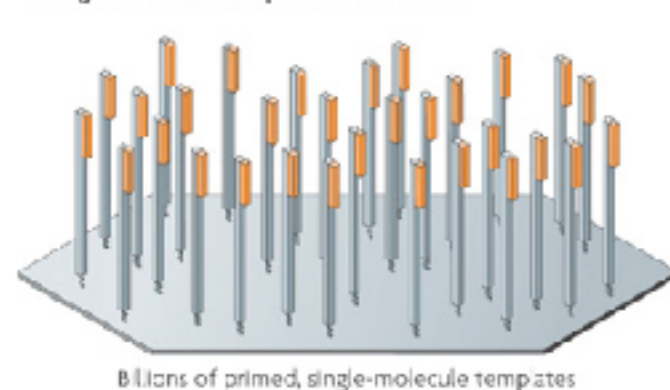
**b Illumina/Solexa  
Solid-phase amplification**  
One DNA molecule per cluster



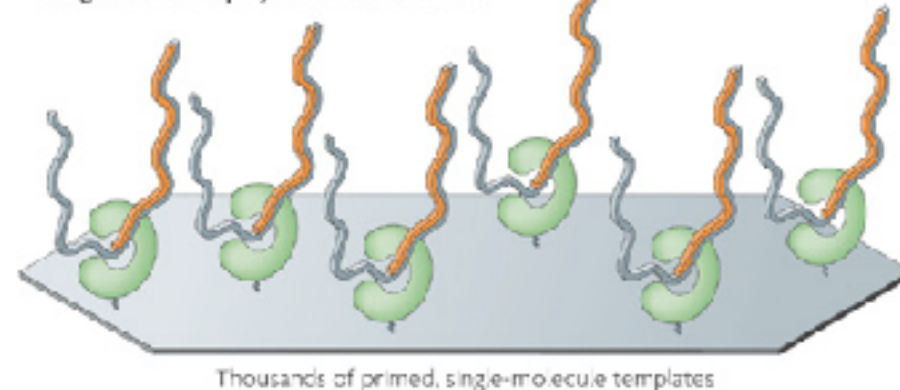
**c Helicos BioSciences: one-pass sequencing  
Single molecule: primer immobilized**



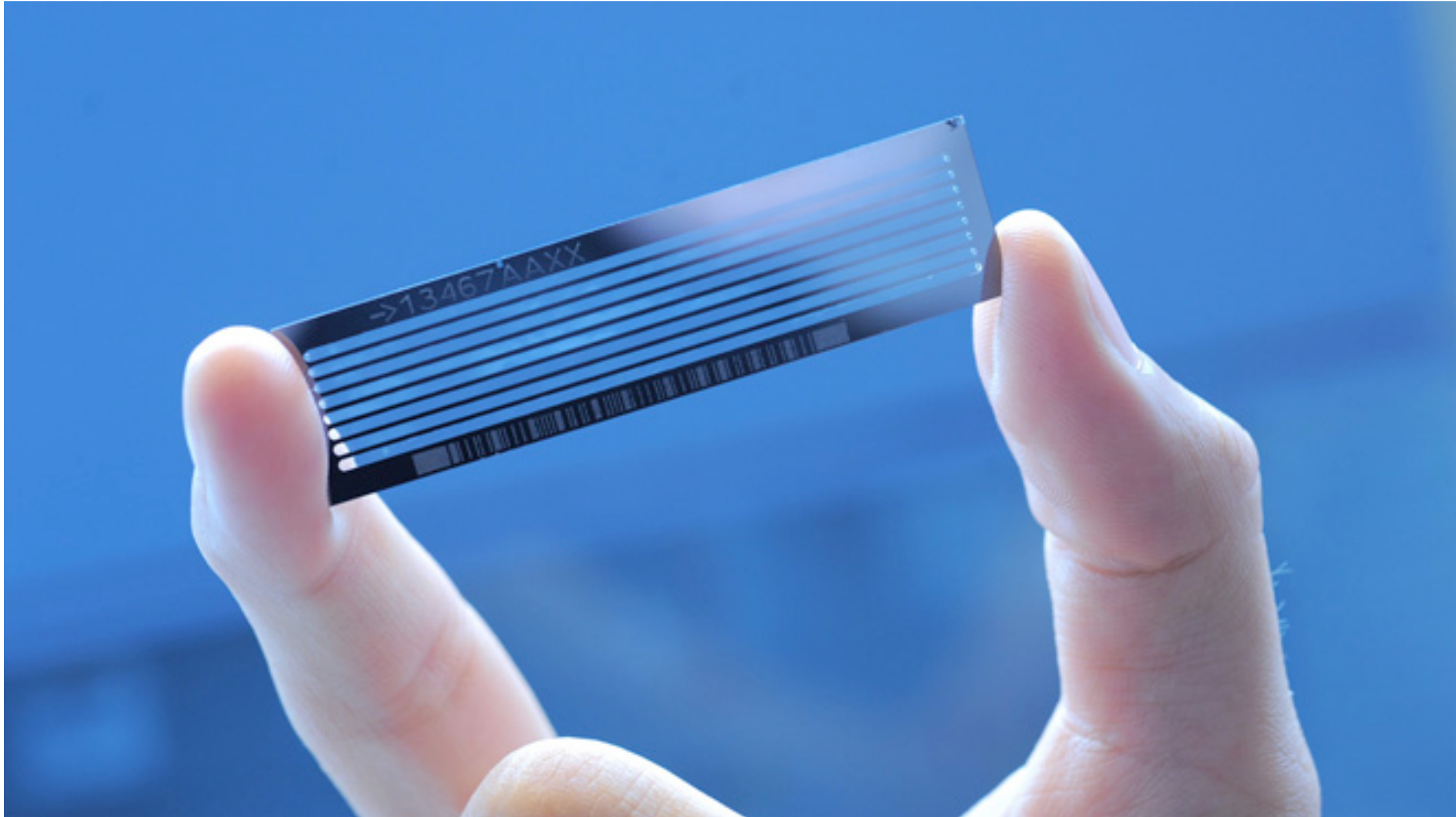
**d Helicos BioSciences: two-pass sequencing  
Single molecule: template immobilized**



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



# A Flow Cell

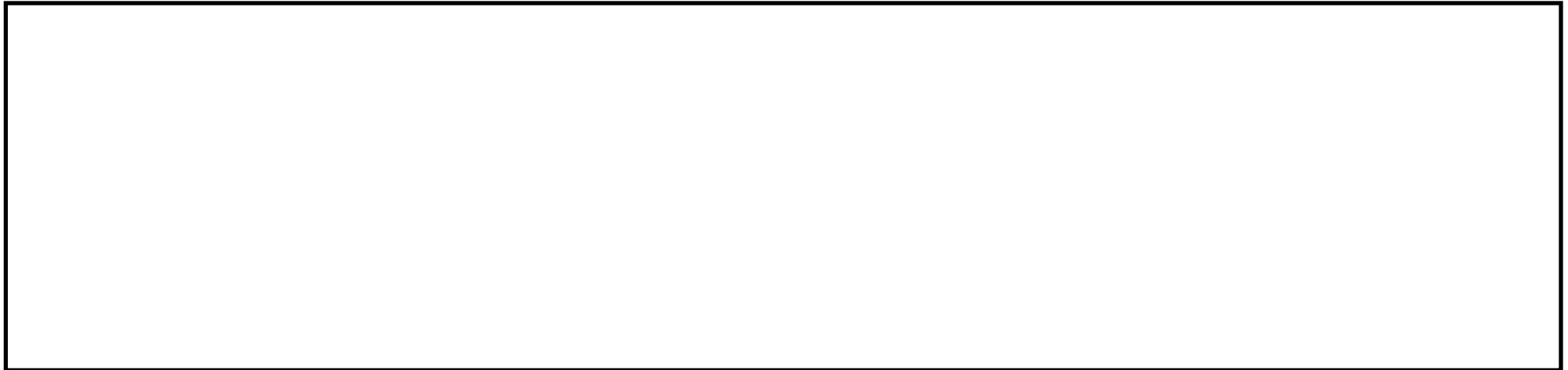


Pass Around Flow  
Cells!!!

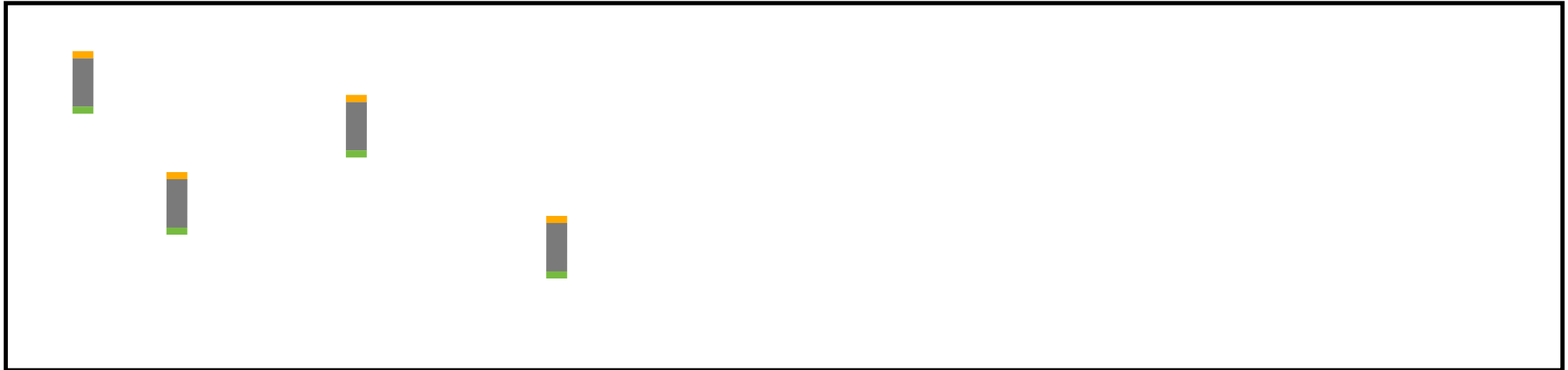
# SBS: Sequencing by Synthesis

An Illumina Story

# A Flow Cell



# Bind Library



# 1st Cycle



# 1st Cycle

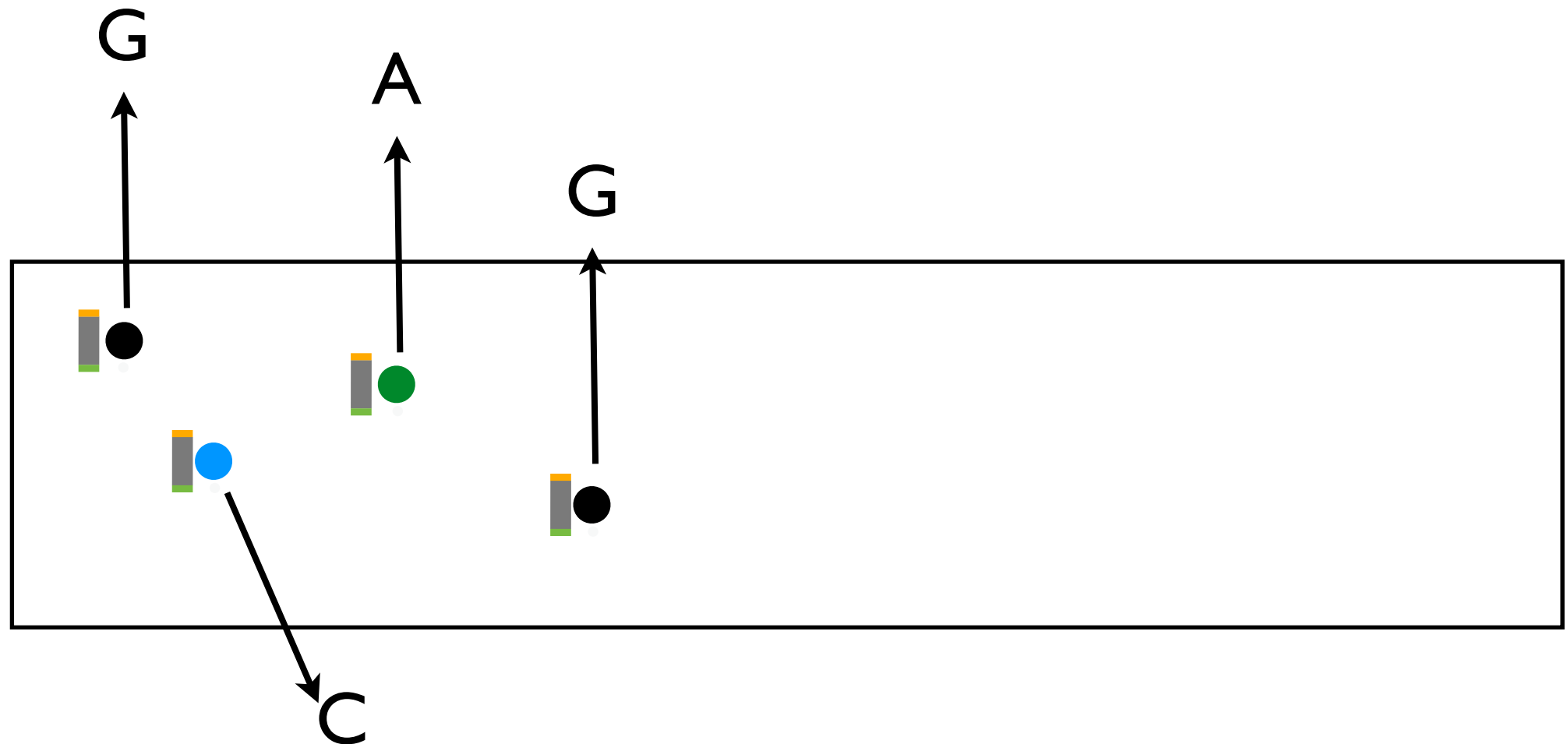




# 1st Cycle



# 1st Cycle



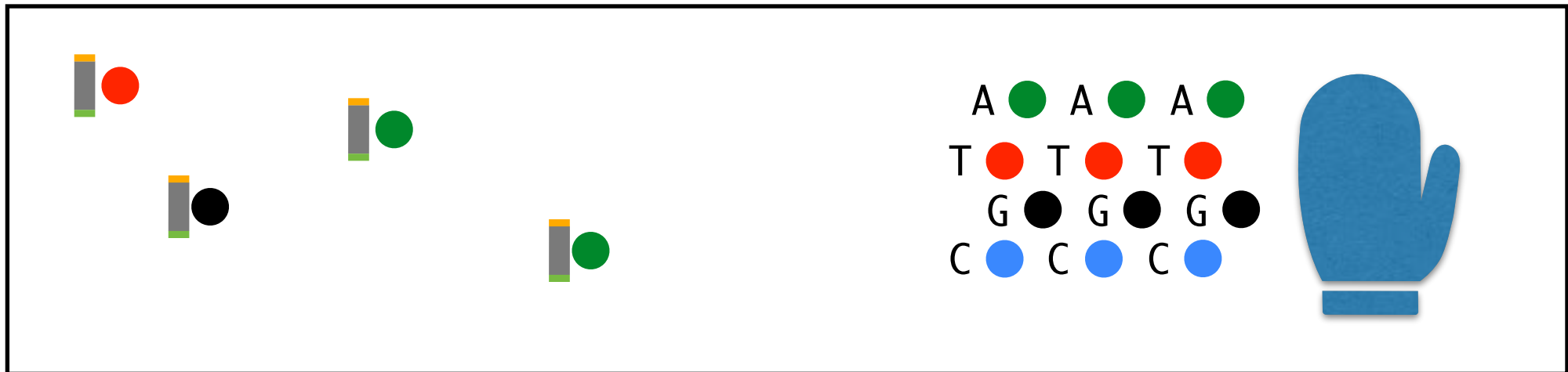
# 2nd Cycle



# 2nd Cycle



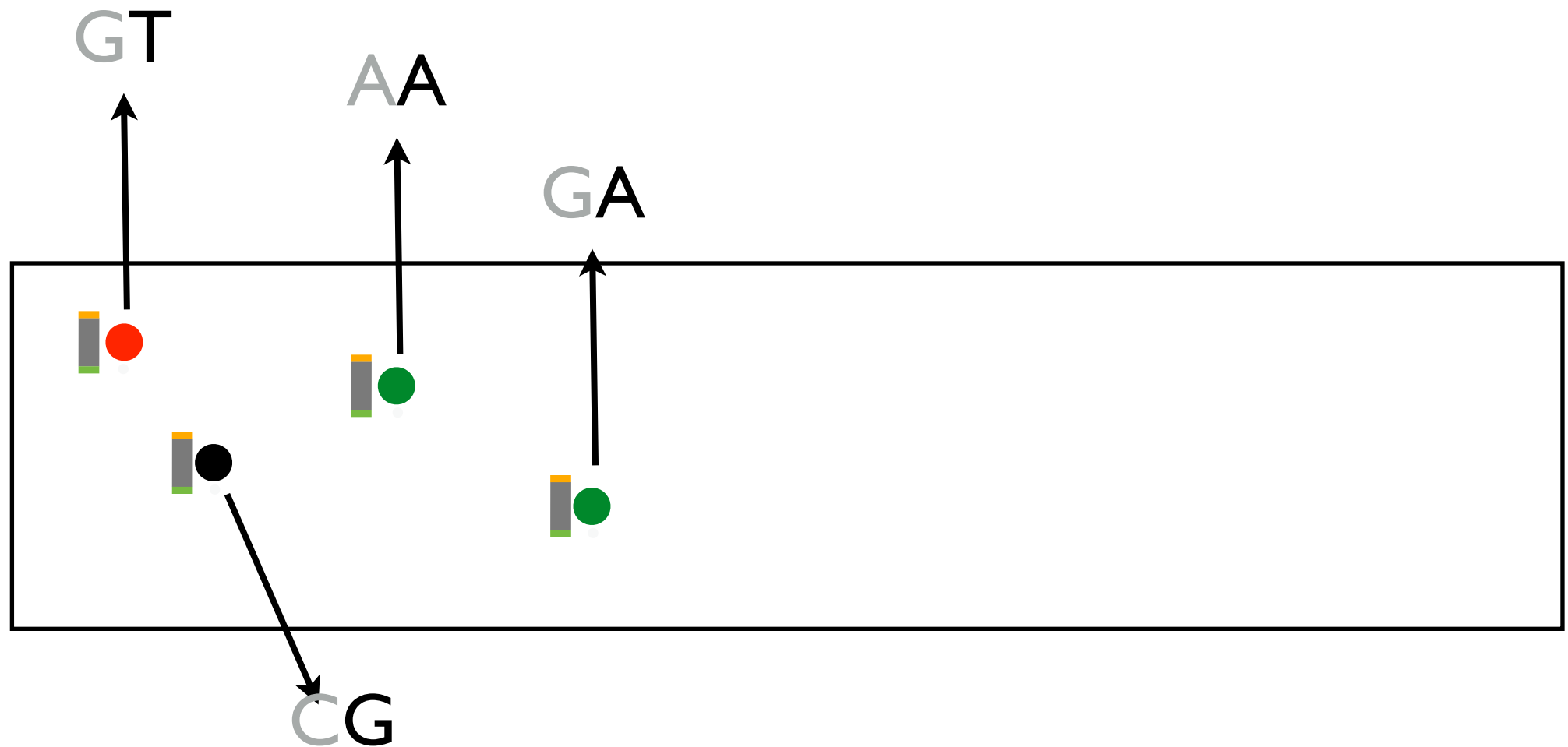
# 2nd Cycle



# 2nd Cycle



# 2nd Cycle

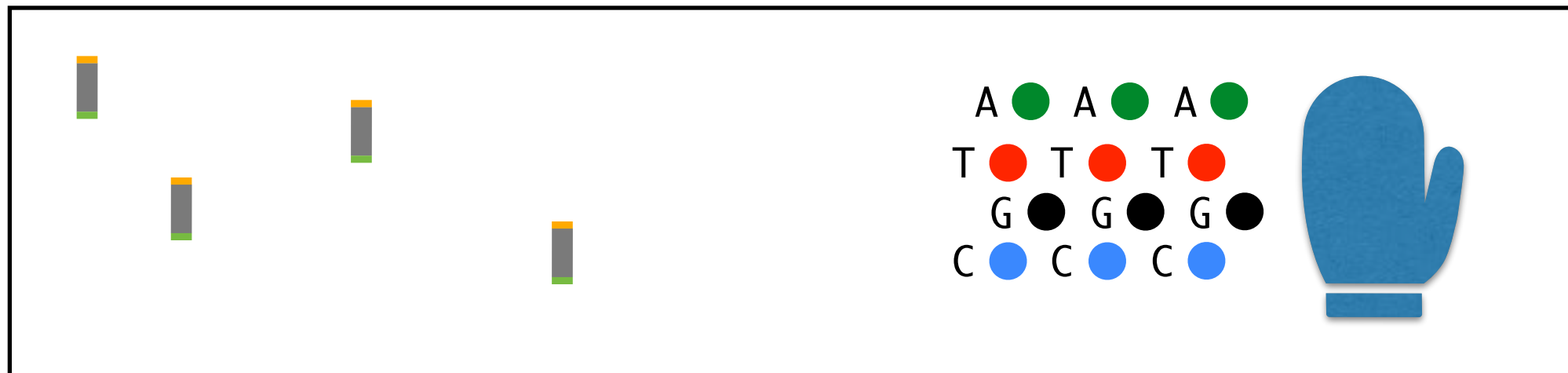


# 3rd Cycle





# 3rd Cycle



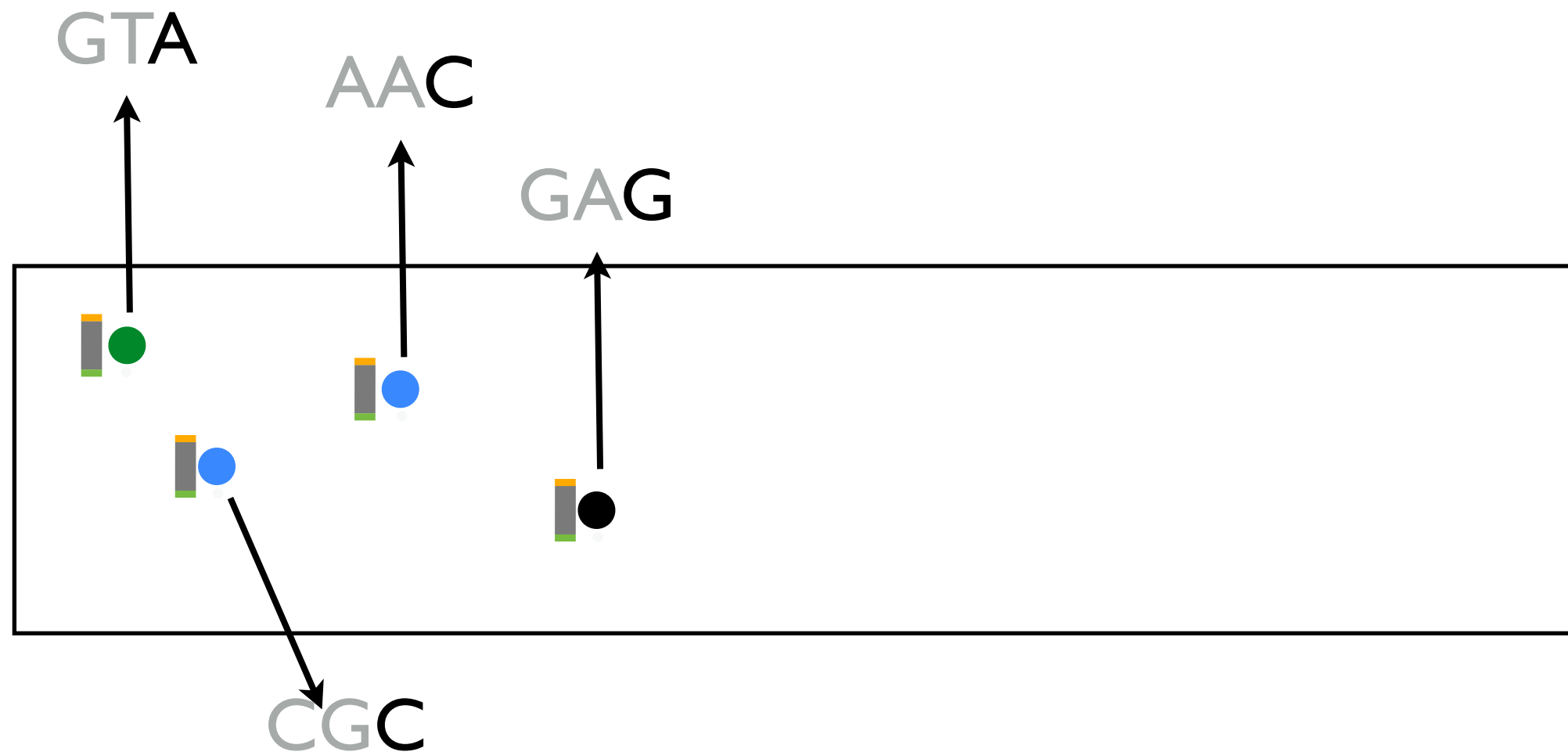
# 3rd Cycle



# 3rd Cycle



# 3rd Cycle

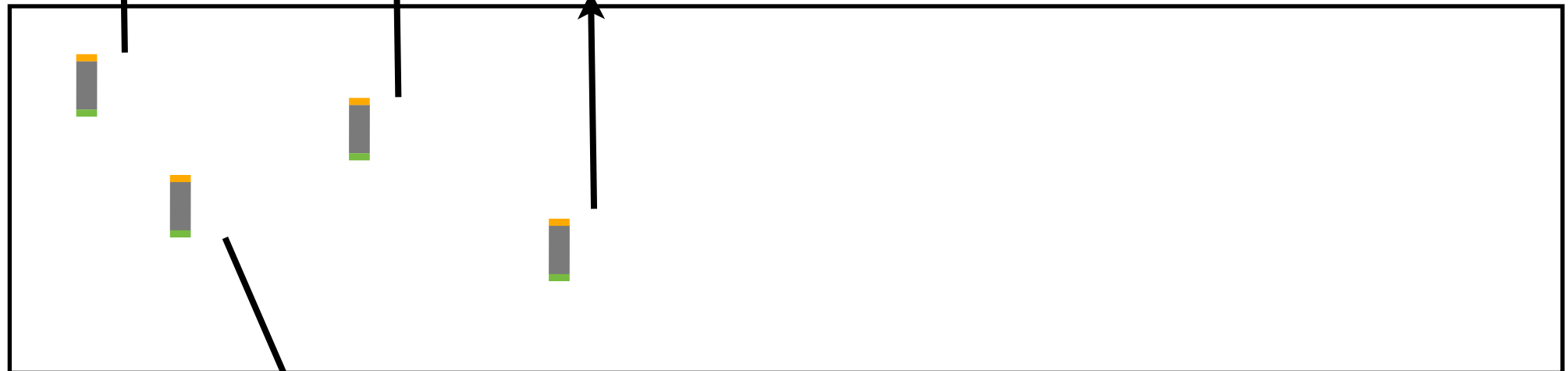


# 50th Cycle

GAATTCTAAAACAGTTGCATTCTATAATTACAAAATAATTGAAACACTTC

ACTAATATTATTTAATTAGACACCAACTCGACATTCTGTCTTCGACCTAT

TCCCAGTCATCGCCCAGTAGAATTACCAGGCAATGAACCACGGCCTTTCA

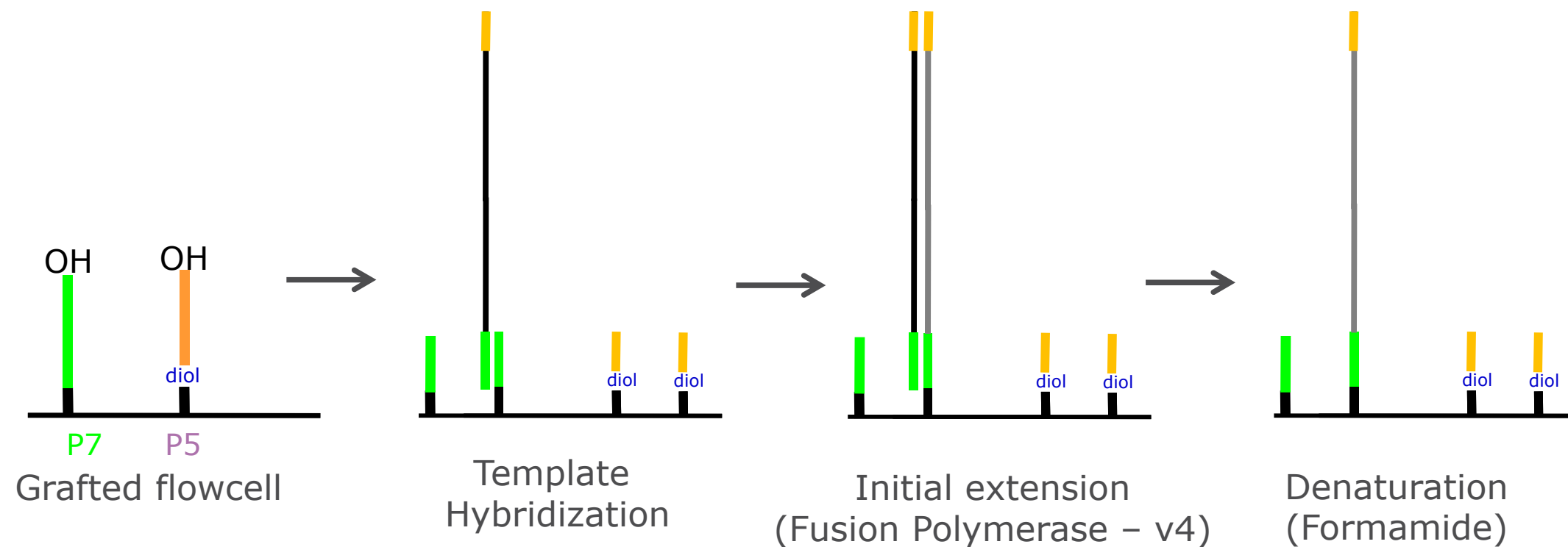


ACAGCATATGGGTTCAC TCCAACAGTGAACCATTCCAAAAGGCCTTGCCT

# Illumina Short Reads

- 50 - 300bp

# Cluster generation – hybridization and amplification



# Hybridization

5' -CTGATCTGACTGATGCGTATGCTAGT-3'

+

3' -GCATAC-5'

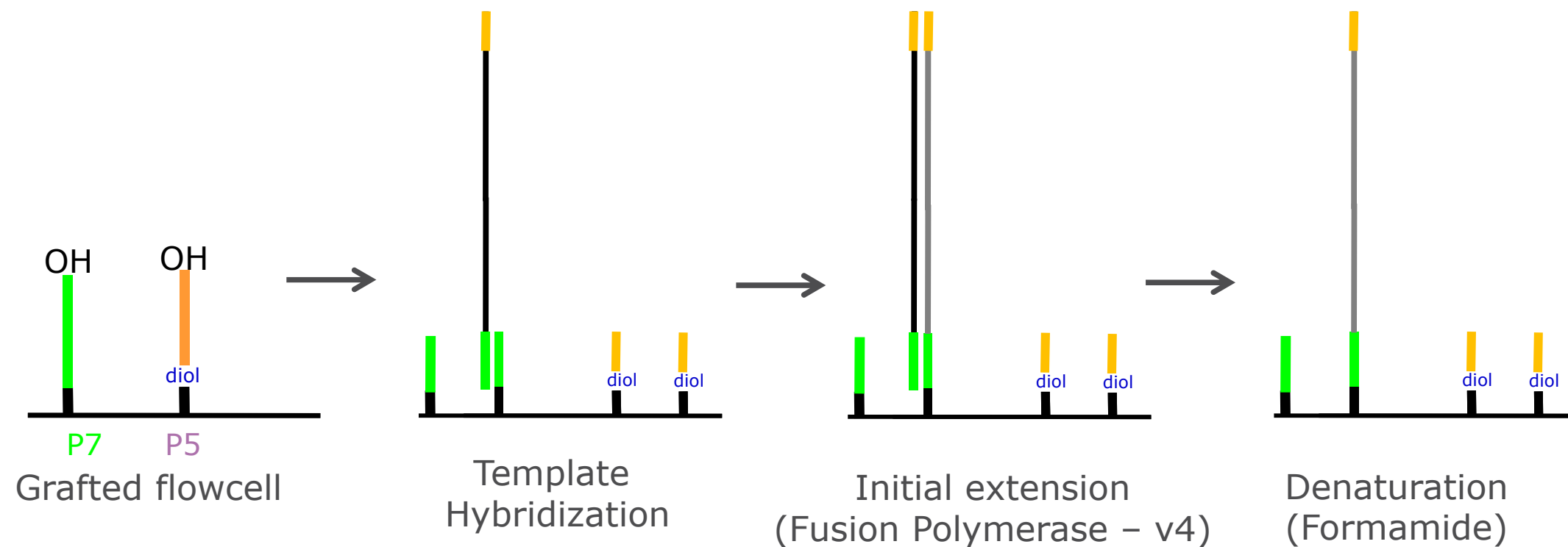
=

5' -CTGATCTGACTGATGCGTATGCTAGT-3'

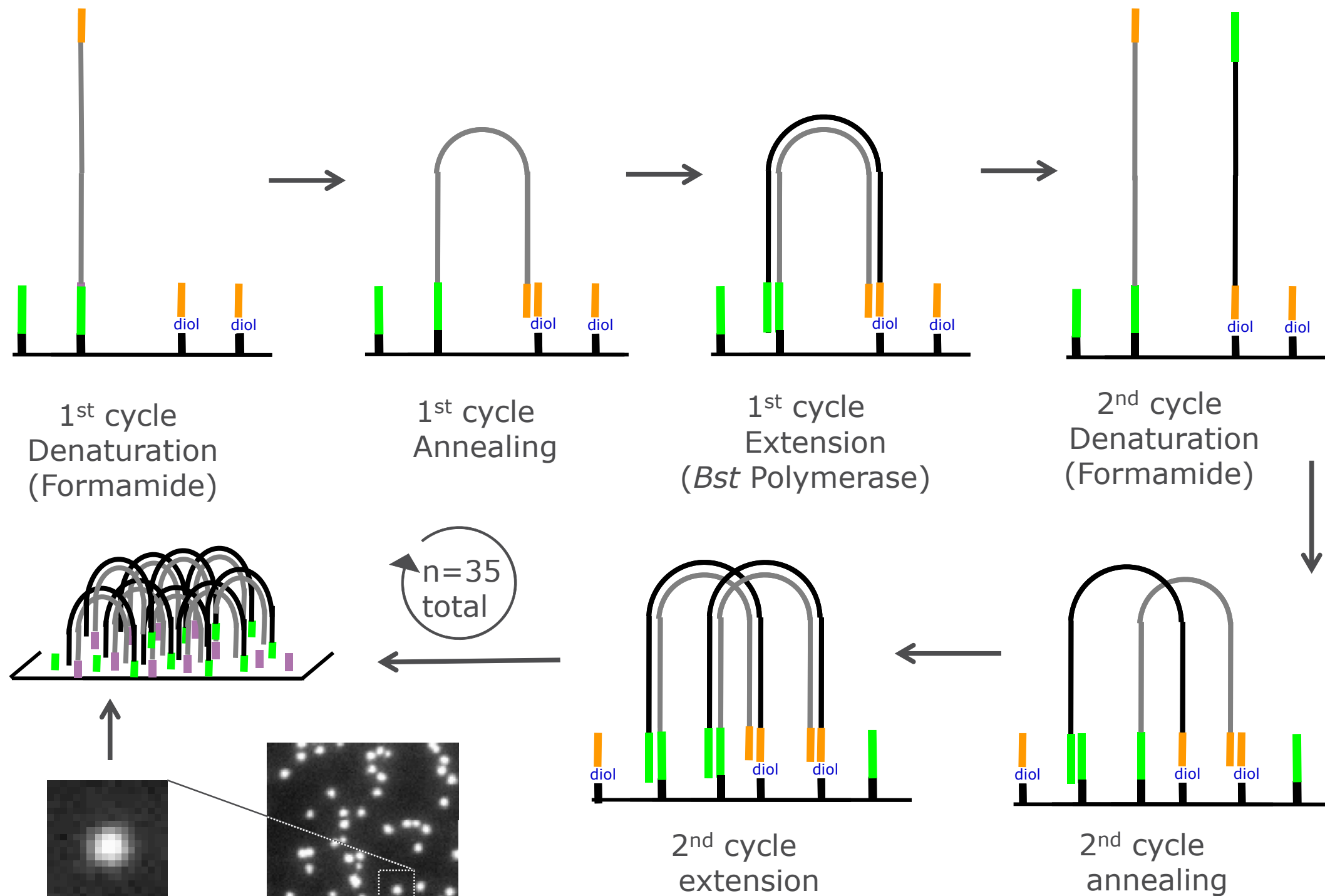
3' -GCATAC-5'



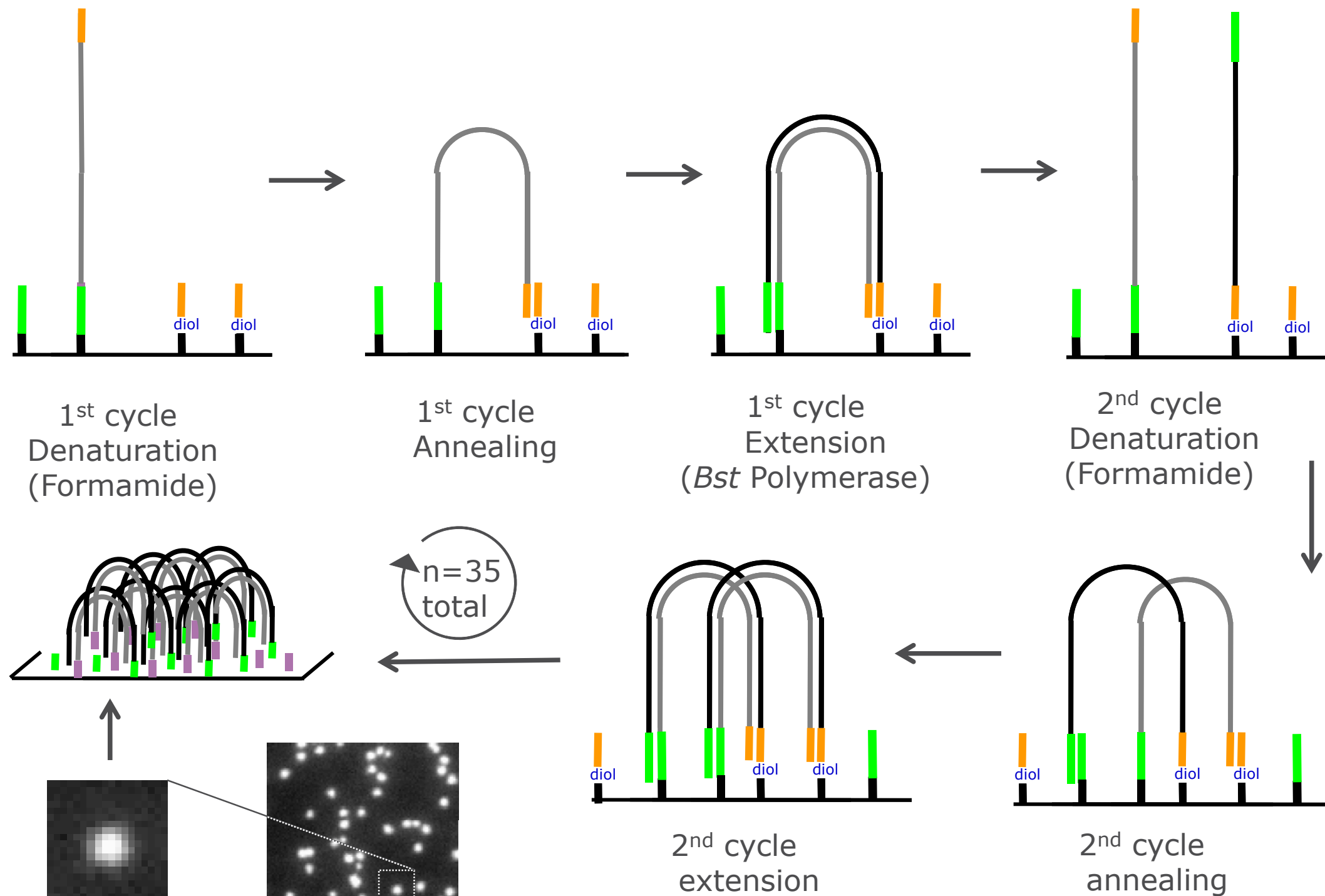
# Cluster generation – hybridization and amplification



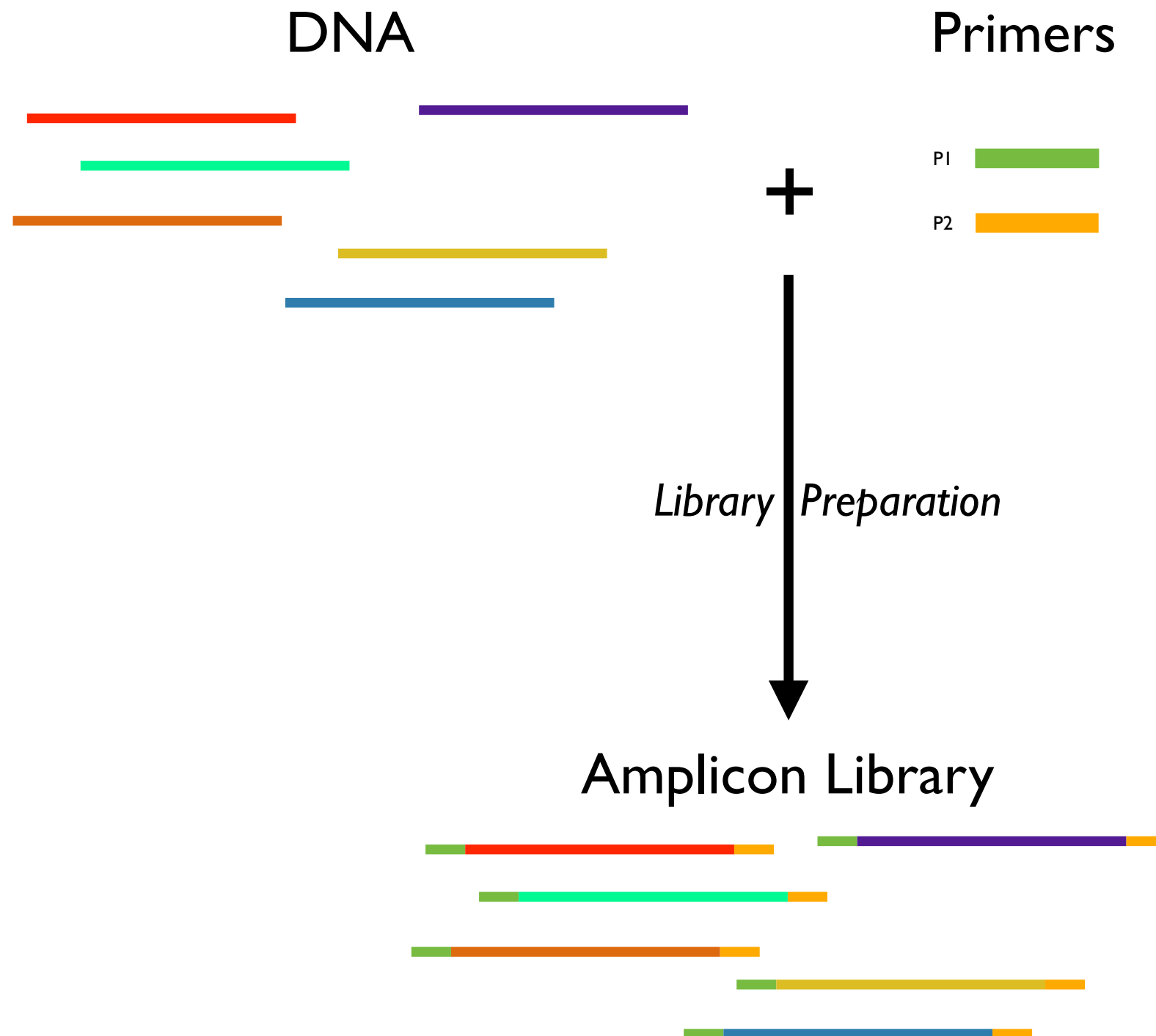
# Cluster generation – hybridization and amplification



# Cluster generation – hybridization and amplification



# Library Preparation



# Why Adapters?

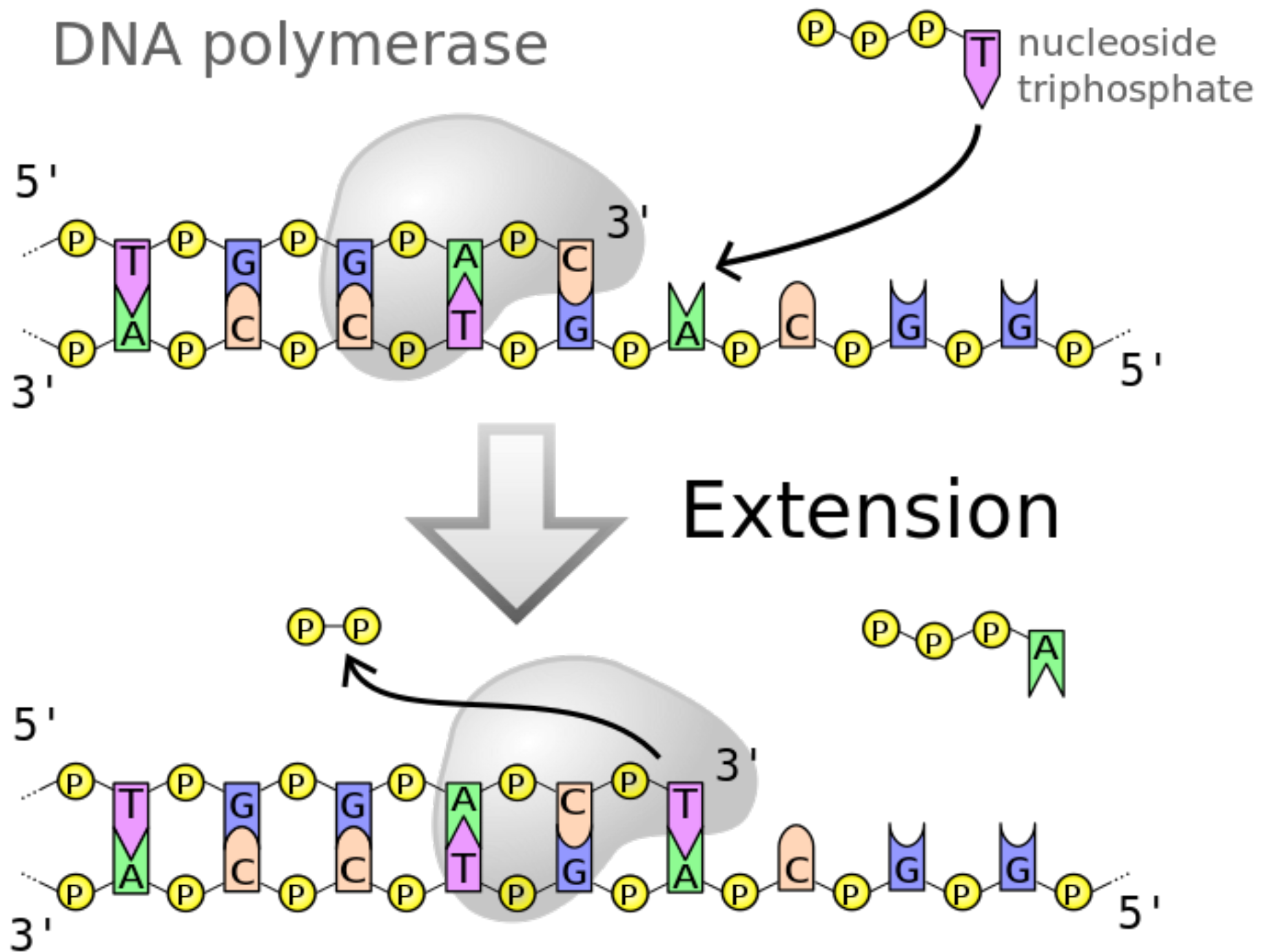
# DNA Synthesis

- 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

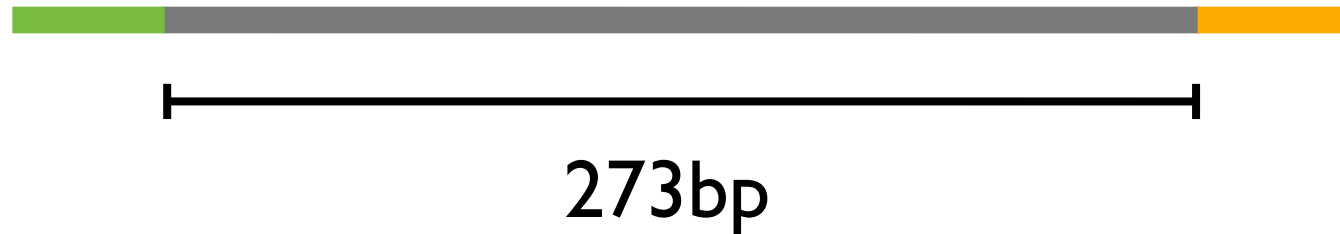
# Read Length

bases

50



100



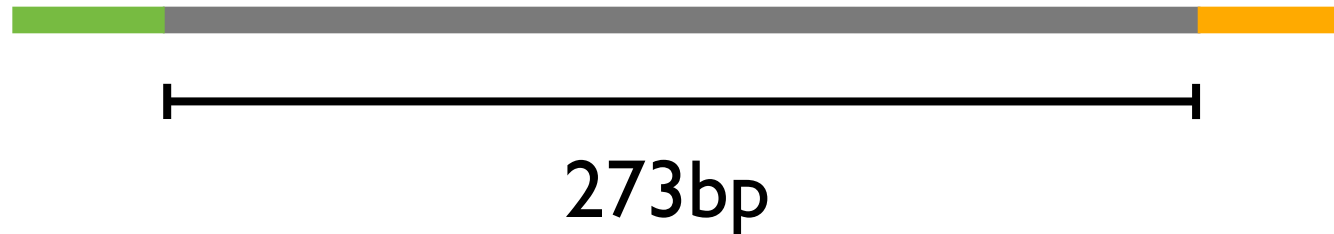
# Read Length

bases

50 →

100 →

150 →



# Read Length

bases

50 →

100 →

150 →

250 →



273bp

# Paired-End

TCGAAAAG  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

# Paired-End

TCGAAAAG  
AGCTTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

AGCTTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA  
GACACACCT



# Read Length

bases

50



273bp

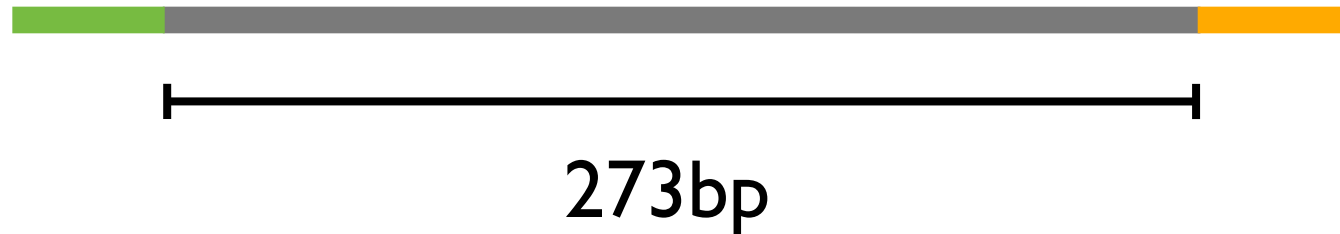
# Read Length

bases

50



100



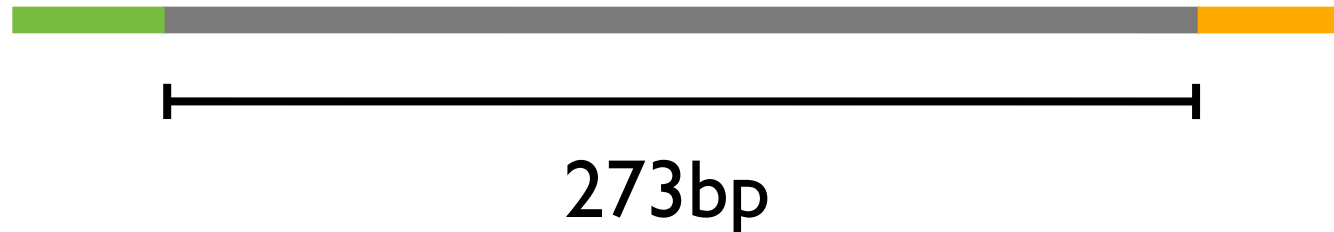
# Read Length

bases

50 →

100 →

150 →



# Read Length

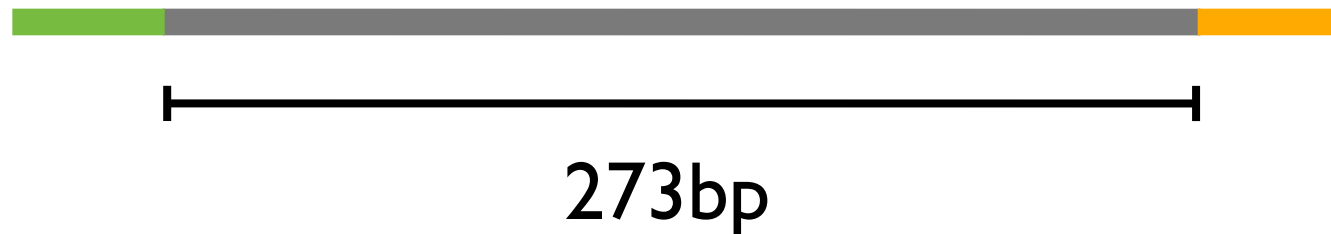
bases

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 →

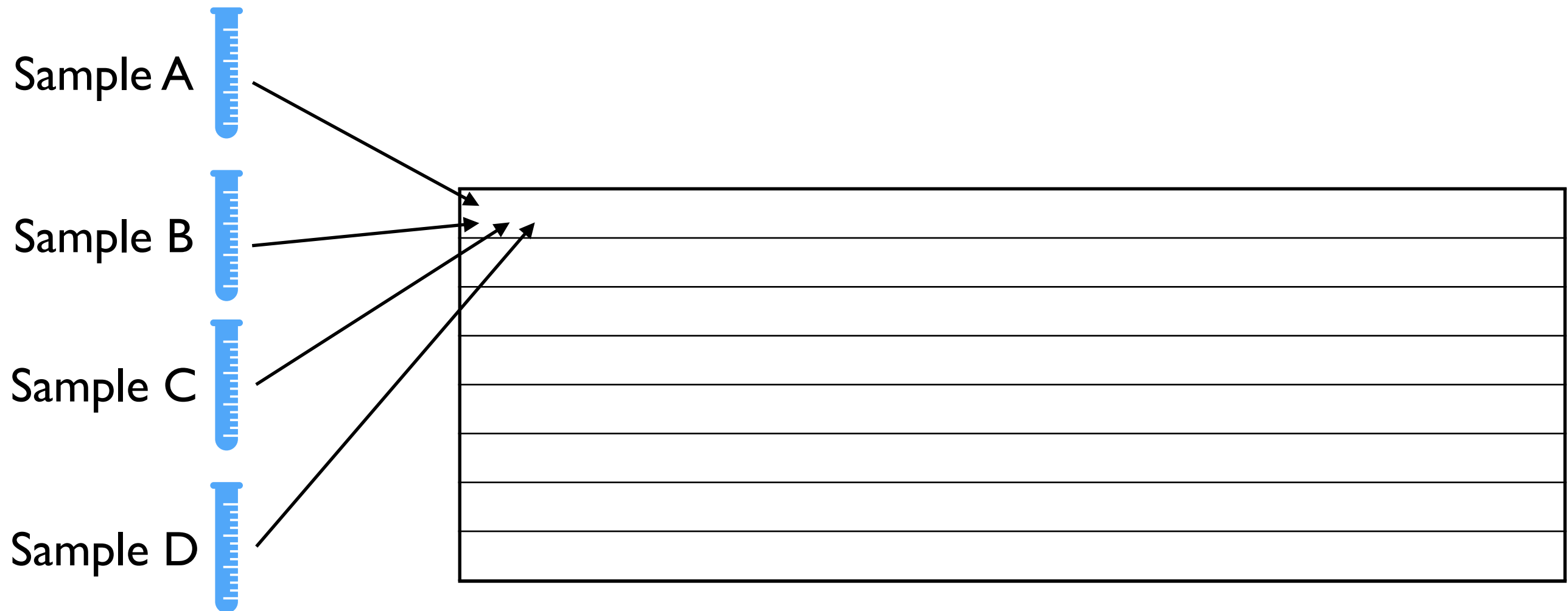


634bp

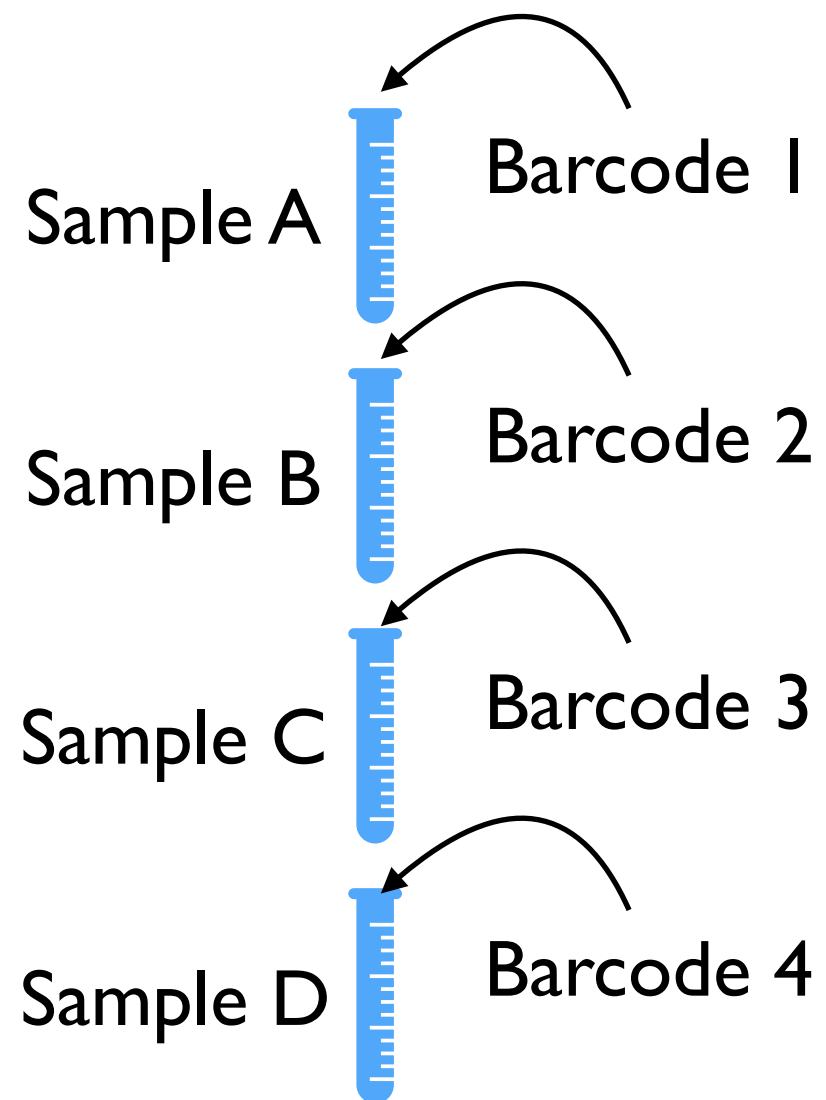


# Barcodes: Why?

Multiplexing: Combine multiple samples in a lane



# Barcodes

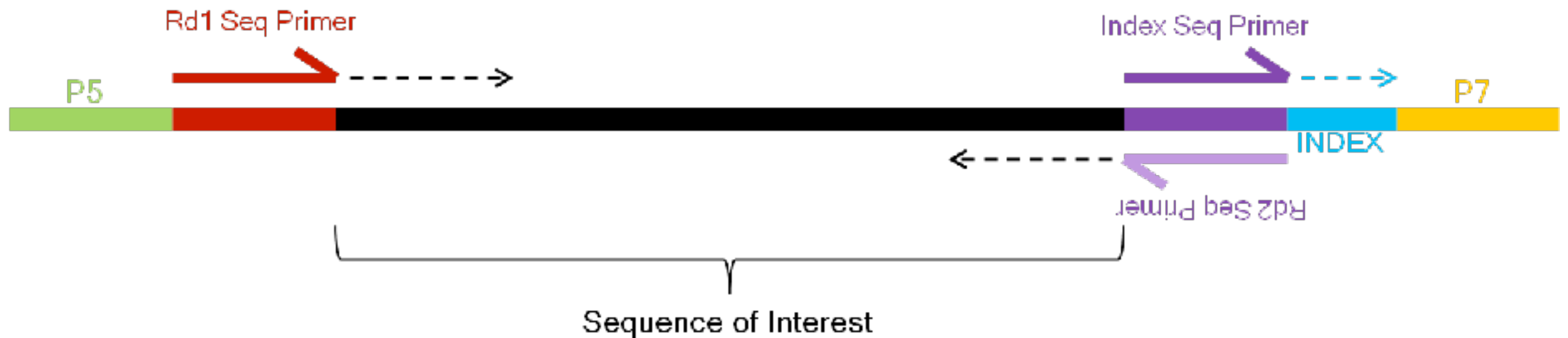


# Barcodes

Sample_Name	I7_Index_ID	index
1_A	P49-E1	AAGACCGT
2_A	P50-E2	TTGCGAGA
3_A	P51-E3	GCAATTCC
4_A	P52-E4	GAATCCGT
5_A	P53-E5	CCGCTTAA
6_A	P54-E6	TACCTGCA
7_B	P55-E7	GTCGATTG
8_B	P56-E8	TATGGCAC
9_B	P57-E9	CTCGAACA
10_B	P58-E10	CAACTCCA

# Multiplexing (Barcodes)

## STRUCTURE DETAILS



# MiSeq, NextSeq, and More Seqs

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

\* Duke Sequencing and Genomic Technologies Shared Resource, July 2018

1st Generation	2nd Generation	3rd Generation
Chemical (Maxim-Gilbert)	Pyrosequencing (454)	Single molecule real time (PacBio)
Chain Termination (Sanger)	Chain Termination (Illumina)	Nanopore sequencing (Oxford Nanopore)
Pyrosequencing	Sequencing by ligation (SOLiD sequencing)	
	Ion semiconductor (Ion Torrent)	

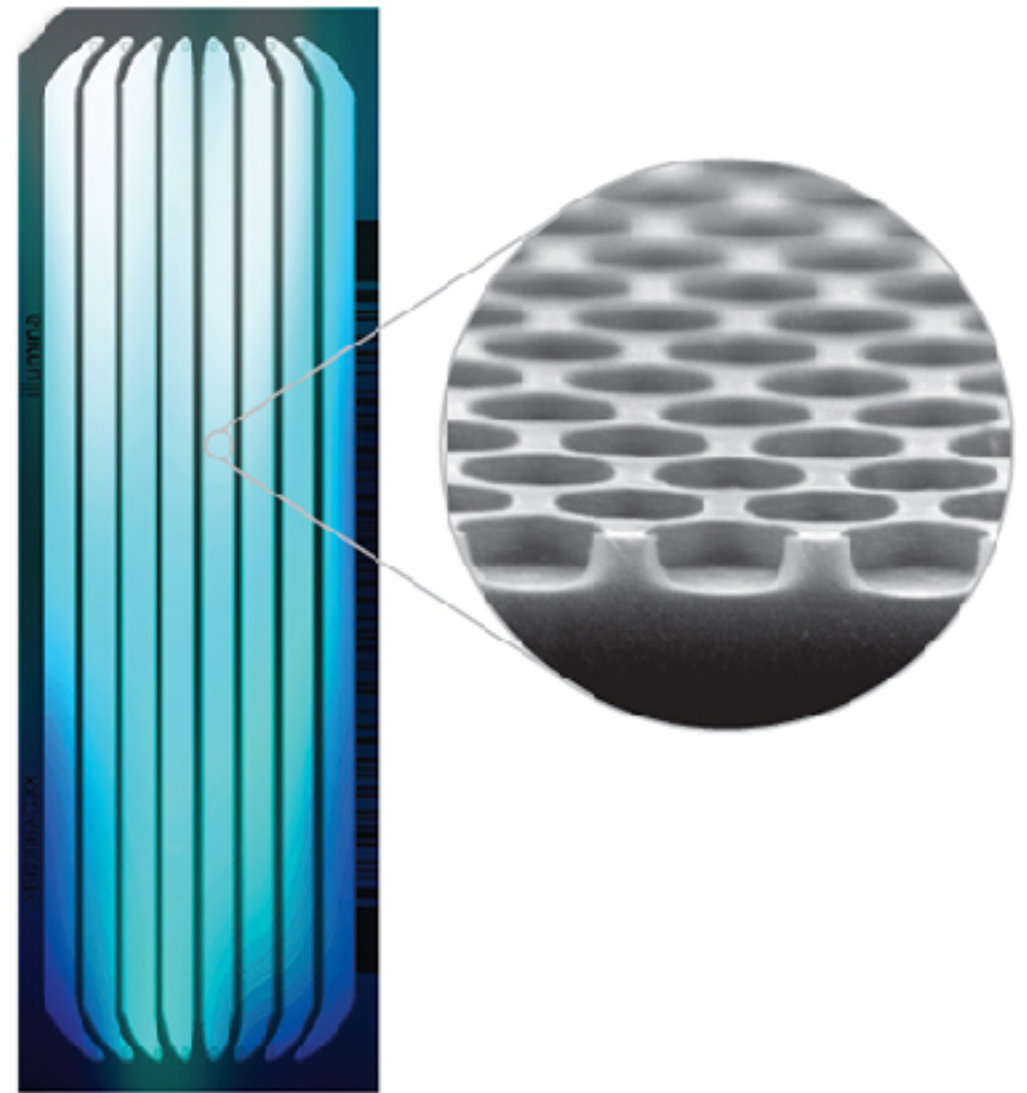


# Illumina Video









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

# Patterned Flow Cells

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











# 4-Channel Chemistry








4-Channel Chemistry				
	 <b>A</b>	 <b>G</b>	 <b>T</b>	 <b>C</b>
Image 1				
Image 2				
Image 3				
Image 4				
Result	<b>A</b>	<b>G</b>	<b>T</b>	<b>C</b>

# 2-Channel Chemistry

## 4-Channel Chemistry

	 <b>A</b>	 <b>G</b>	 <b>T</b>	 <b>C</b>
Image 1				
Image 2				
Image 3				
Image 4				
Result	<b>A</b>	<b>G</b>	<b>T</b>	<b>C</b>

## 2-Channel Chemistry

	 <b>A</b>	<b>G</b>	 <b>T</b>	 <b>C</b>
Image 1				
Image 2				
Result	<b>A</b>	<b>G</b>	<b>T</b>	<b>C</b>