

# Microbiome Analysis Overview

Josh Granek  
May 26, 2016

# Microsoft Azure

Thanks!!

# Metagenomics

# Metagenomics



**Amplicon**

**Shotgun  
Metagenome**

**Shotgun  
Metatranscriptome**

# Metagenomics

	<b>Information</b>
<b>Amplicon</b>	Who is Present
<b>Shotgun Metagenome</b>	What Genes are Present
<b>Shotgun Metatranscriptome</b>	What is Happening

# Metagenomics

	Information	Analogy
Amplicon	Who is Present	Name
Shotgun Metagenome	What Genes are Present	CV
Shotgun Metatranscriptome	What is Happening	Twitter Feed

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# Metagenomics

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# Metagenomics

	Information	Analogy	Target Size
<b>Amplicon</b>	Who is Present	Name	100bp - 1kb
<b>Shotgun Metagenome</b>	What Genes are Present	CV	100kb - 100Mb
<b>Shotgun Metatranscriptome</b>	What is Happening	Twitter Feed	100kb - 100Mb

# Metagenomics

	Information	Analogy	Target Size	Discovery?
<b>Amplicon</b>	Who is Present	Name	100bp - 1kb	+/-
<b>Shotgun Metagenome</b>	What Genes are Present	CV	100kb - 100Mb	++
<b>Shotgun Metatranscriptome</b>	What is Happening	Twitter Feed	100kb - 100Mb	++

# Metagenomics

	Information	Analogy	Target Size	Discovery?	Cost
<b>Amplicon</b>	Who is Present	Name	100bp - 1kb	+/-	Low
<b>Shotgun Metagenome</b>	What Genes are Present	CV	100kb - 100Mb	++	High
<b>Shotgun Metatranscriptome</b>	What is Happening	Twitter Feed	100kb - 100Mb	++	High

# Metagenomics

	Information	Analogy	Target Size	Discovery?	Cost
<b>Amplicon</b>	Who is Present	Name	100bp - 1kb	+/-	Low
<b>Shotgun Metagenome</b>	What Genes are Present	CV	100kb - 100Mb	++	High
<b>Shotgun Metatranscriptome</b>	What is Happening	Twitter Feed	100kb - 100Mb	++	High

# Amplicon Sequencing

PCR amplify and sequence a marker gene

# Amplicon Sequencing

PCR amplify and sequence a marker gene



Marker Gene

# Amplicon Sequencing

PCR amplify and sequence a marker gene

	Marker Gene
Bacteria	16s rRNA



# Amplicon Sequencing

PCR amplify and sequence a marker gene

	Marker Gene
<b>Bacteria</b>	16s rRNA
<b>Fungi</b>	18s or ITS rRNA

# Amplicon Sequencing

PCR amplify and sequence a marker gene

	Marker Gene
<b>Bacteria</b>	16s rRNA
<b>Fungi</b>	18s or ITS rRNA
<b>Archaea</b>	16s rRNA

# Amplicon Sequencing

PCR amplify and sequence a marker gene

	Marker Gene
<b>Bacteria</b>	16s rRNA
<b>Fungi</b>	18s or ITS rRNA
<b>Archaea</b>	16s rRNA
<b>Protozoa</b>	18s rRNA

# Amplicon Sequencing

PCR amplify and sequence a marker gene

	Marker Gene
<b>Bacteria</b>	16s rRNA
<b>Fungi</b>	18s or ITS rRNA
<b>Archaea</b>	16s rRNA
<b>Protozoa</b>	18s rRNA
<b>Viruses</b>	?????

# Metagenomics

	Information	Analogy	Target Size	Cost	Discovery?
<b>Amplicon</b>	Who is Present	Name	100bp - 1kb	Low	+/-
<b>Shotgun Metagenome</b>	What Genes are Present	CV	100kb - 100Mb	High	++
<b>Shotgun Metatranscriptome</b>	What is Happening	Twitter Feed	100kb - 100Mb	High	++

# Sequencing Details

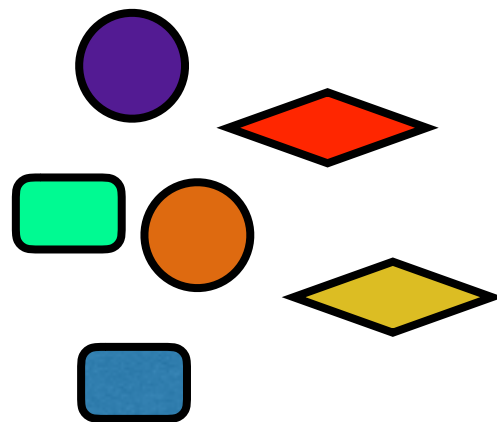
# Amplicon Sequencing

Primers

P1   
P2 

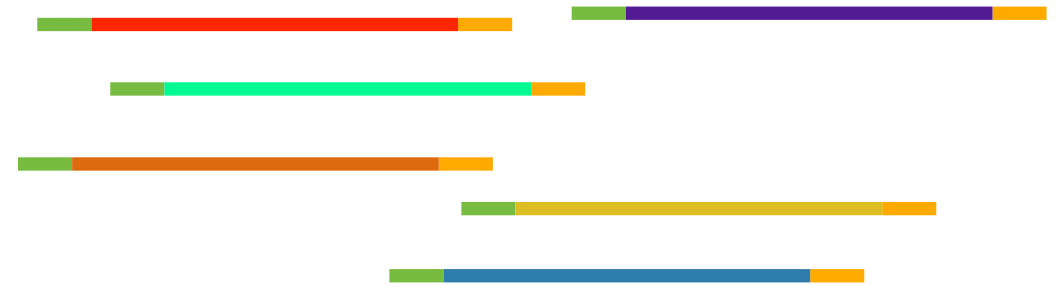
+

Microbes



=

Amplicon Library



# Single-End

TCGAAAAG  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA



# Paired-End

TCGAAAAG  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

# Paired-End

TCGAAAAG  
AGCTTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

AGCTTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA  
GACACACCT

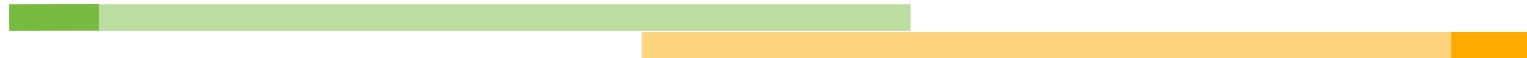
# Read Length

Read  
Length

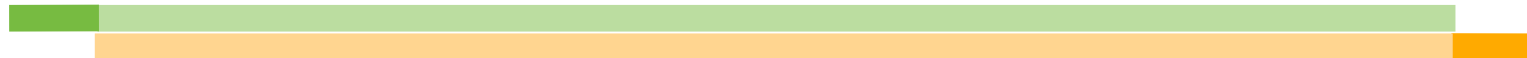
100bp



150bp



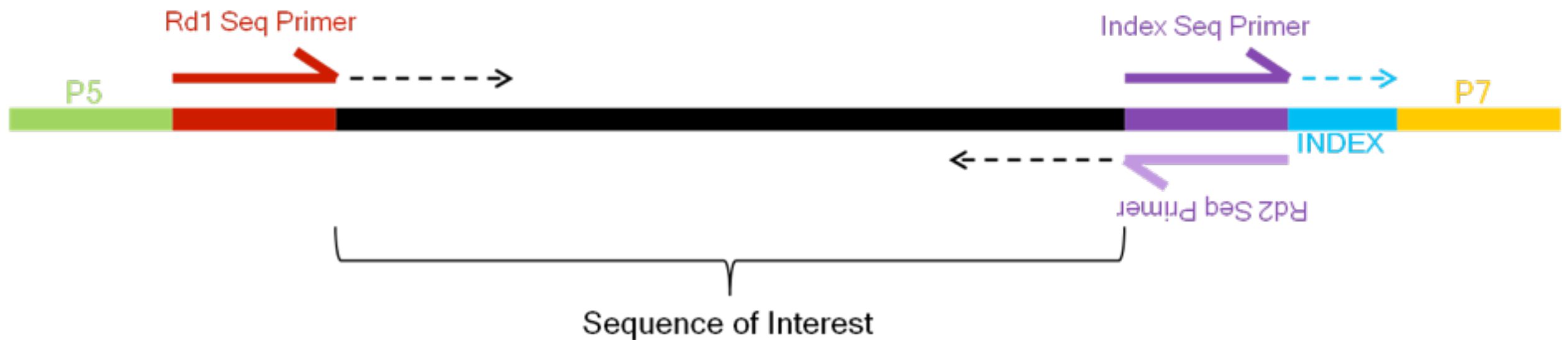
250bp



250bp Amplicon

# Multiplexing (Barcodes)

## STRUCTURE DETAILS



# HiSeq vs. MiSeq

- Same technology! Same libraries!
- Differences:
  - Run-time (MiSeq is faster)
  - Maximum read length (MiSeq is longer)
  - Data yield (HiSeq is higher)
  - Cost (HiSeq is cheaper per base)

# Illumina Video

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

# FASTQ

- FASTA with Quality
- [https://en.wikipedia.org/wiki/FASTQ\\_format](https://en.wikipedia.org/wiki/FASTQ_format)

# File Formats



# FASTQ: Format

- **FASTA Format**

```
>NC_007779.1 Escherichia coli str. K-12 substr. W3110, complete genome
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTG
GTTACCTGCCGTGAGTAAATTTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGAC
AGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGT
AACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTTTTCGACCAAAGG
TAACGAGGTAACAACCATGCGAGTGTTGAAGTTCGGCGGTACATCAGTGGCAAATGCAGAACGTTTTCTGCGTGTTGCCG
ATATTCTGGAAAGCAATGCCAGGCAGGGGCAGGTGGCCACCGTCCTCTCTGCCCCCGCCAAAATCACCAACCACCTGGTG
GCGATGATTGAAAAAACCATTAGCGGCCAGGATGCTTTACCCAATATCAGCGATGCCGAACGTATTTTTGCCGAACCTTTT
GACGGGACTCGCCGCCGCCAGCCGGGGTTCCCGCTGGCGCAATTGAAAACCTTCGTCGATCAGGAATTTGCCCAAATAA
AACATGTCCTGCATGGCATTAGTTTGTTGGGGCAGTGCCCGGATAGCATCAACGCTGCGCTGATTTGCCGTGGCGAGAAA
```

- **FASTQ Format**

```
@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0
CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG
+
AAABBBFFFFFAGGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHHHHGGGGGGHHHHGGGGGGGGHHHHGHFFHHHHHHGHGGGGGGGGGGHHHHHHHHHHHHGGG
```

# FASTQ: Format

- **FASTA Format**

>NC\_007779.1 Escherichia coli str. K-12 substr. W3110, complete genome

# Header

AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGA ACTG  
GTTACCTGCCGTGAGTAAATTTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGAC  
AGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGT  
AACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTTTTCGACCAAAGG  
TAACGAGGTAACAACCATGCGAGTGTTGAAGTTCGGCGGTACATCAGTGGCAAATGCAGAACGTTTTCTGCGTGTTGCCG  
ATATTCTGGAAAGCAATGCCAGGCAGGGGCAGGTGGCCACCGTCCTCTCTGCCCCCGCCAAAATCACCAACCACCTGGTG  
GCGATGATTGAAAAAACCATTAGCGGCCAGGATGCTTTACCCAATATCAGCGATGCCGAACGTATTTTTGCCGAAC TTTT  
GACGGGACTCGCCGCCGCCAGCCGGGGTTCCCGCTGGCGCAATTGAAAAC TTTTCGTCGATCAGGAATTTGCCCAAATAA  
AACATGTCCTGCATGGCATTAGTTTGTTGGGGCAGTGCCCGGATAGCATCAACGCTGCGCTGATTTGCCGTGGCGAGAAA

- FASTQ Format**

```
@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0
```

CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG  
+  
AAABBBFFFFFGGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHHHHGGGGGGHHHHGGGGGGGGHHHHHHFFHHHHHHGHGGGGGGGGGGHHHHHHHHHHHHGGG

# FASTQ: Format

- **FASTA Format**

>NC\_007779.1 Escherichia coli str. K-12 substr. W3110, complete genome

```
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTG
GTTACCTGCCGTGAGTAAATTTAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGAC
AGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGT
AACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTTTTCGACCAAAGG
TAACGAGGTAACAACCATGCGAGTGTTGAAGTTCGGCGGTACATCAGTGGCAAATGCAGAACGTTTTCTGCGTGTTGCCG
ATATTCTGGAAAGCAATGCCAGGCAGGGGCAGGTGGCCACCGTCCTCTCTGCCCCCGCCAAAATCACCAACCACCTGGTG
GCGATGATTGAAAAAACCATTAGCGGCCAGGATGCTTTACCCAATATCAGCGATGCCGAACGTATTTTTGCCGAACCTTTT
GACGGGACTCGCCGCCGCCAGCCGGGGTTCCCGCTGGCGCAATTGAAAACCTTTCGTCGATCAGGAATTTGCCCAAATAA
AACATGTCCTGCATGGCATTAGTTTGTTGGGGCAGTGCCCGGATAGCATCAACGCTGCGCTGATTTGCCGTGGCGAGAAA
```

Sequence

- **FASTQ Format**

@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0

```
CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG
```

+

```
AAABBFBBBBBFGGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHHHHGGGGGGHHHHGGGGGGGGHHHHGHFFHHHHHHGHGGGGGGGGGGHHHHHHHHHHHHGGG
```

# FASTQ: Format

- **FASTA Format**

```
>NC_007779.1 Escherichia coli str. K-12 substr. W3110, complete genome
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTG
GTTACCTGCCGTGAGTAAATTTAAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGAC
AGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGT
AACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTTTTCGACCAAAGG
TAACGAGGTAACAACCATGCGAGTGTTGAAGTTCGGCGGTACATCAGTGGCAAATGCAGAACGTTTTCTGCGTGTTGCCG
ATATTCTGGAAAGCAATGCCAGGCAGGGGCAGGTGGCCACCGTCCTCTCTGCCCCCGCCAAAATCACCAACCACCTGGTG
GCGATGATTGAAAAAACCATTAGCGGCCAGGATGCTTTACCCAATATCAGCGATGCCGAACGTATTTTTTGCCGAACCTTTT
GACGGGACTCGCCGCCGCCAGCCGGGGTTCCCGCTGGCGCAATTGAAAACCTTTCGTCGATCAGGAATTTGCCCAAATAA
AACATGTCCTGCATGGCATTAGTTTGTGTTGGGGCAGTGCCCGGATAGCATCAACGCTGCGCTGATTTGCCGTGGCGAGAAA
```

- **FASTQ Format**

```
@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0
CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG
+
AAABBBFFFFFGGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHHHHGGGGGGHHHHGGGGGGGGHHHHGHFFHHHHHHGHGGGGGGGGGGHHHHHHHHHHHHGGG
```

**Quality  
Score**

# FASTQ: Format

- **FASTA Format**

>NC\_007779.1 Escherichia coli str. K-12 substr. W3110, complete genome  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGATTAAAAAAAGAGTGTCTGATAGCAGCTTCTGAACTG  
GTTACCTGCCGTGAGTAAATTTAAATTTTATTGACTTAGGTCACTAAATACTTTAACCAATATAGGCATAGCGCACAGAC  
AGATAAAAATTACAGAGTACACAACATCCATGAAACGCATTAGCACCACCATTACCACCACCATCACCATTACCACAGGT  
AACGGTGCGGGCTGACGCGTACAGGAAACACAGAAAAAAGCCCGCACCTGACAGTGCGGGCTTTTTTTTTTCGACCAAAGG  
TAACGAGGTAACAACCATGCGAGTGTTGAAGTTCGGCGGTACATCAGTGGCAAATGCAGAACGTTTTCTGCGTGTTGCCG  
ATATTCTGGAAAGCAATGCCAGGCAGGGGCAGGTGGCCACCGTCCTCTCTGCCCCCGCCAAAATCACCAACCACCTGGTG  
GCGATGATTGAAAAAACCATTAGCGGCCAGGATGCTTTACCCAATATCAGCGATGCCGAACGTATTTTTGCCGAACCTTTT  
GACGGGACTCGCCGCCGCCAGCCGGGGTTCCCGCTGGCGCAATTGAAAACCTTCGTCGATCAGGAATTTGCCCAAATAA  
AACATGTCCTGCATGGCATTAGTTTGTGTTGGGGCAGTGCCCGGATAGCATCAACGCTGCGCTGATTTGCCGTGGCGAGAAA

- **FASTQ Format**

@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0  
CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG  
+  
AAABBBFFFFFAGGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHHHHGGGGGGHHHHGGGGGGGGHHHHGHFFHHHHHHGHGGGGGGGGGGHHHHHHHHHHHHGGG

@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0  
CTGCCAGTTGAACGACGCGCAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG  
+  
AAABBBBBFFFFGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHGHHHGGGGGGHHHGGGGGGHHHGHFFHHHHHHGHGGGGGGGGHHHHHHHHHHHGGG  
@M00698:36:000000000-AFBEL:1:1101:15928:1413 1:N:0:0  
GTAAAGTCCTGAGTGATACCGCACTTTTACCCCCAGTCCCACTTTTGAACCGGCAAACATATCGGCAAAAGAGGCCGTGCCTGATTTAAAGCCGTAGGT  
+  
1>AAAFFFFFFFFGGGGGGGGGCEGGGHHHHHHFHHHHGGGHHHHHHHHGHFA0FEGGGGGHGGHHHHEECEEHFEFH/E/E/>EGGHBHHHDGHHHHC<?E/1  
@M00698:36:000000000-AFBEL:1:1101:15876:1413 1:N:0:0  
CCGGAACAATCGCTGGCAGGCTTTTACGTCCGGTTATAGCGAAGCGGTCTCAATATTATCAGTCCGCTTTGCTGCGGGTGTCGATTGTCCGGCT  
+  
ABCCCCDFFFEGGGGGGGGGGGHHHHHHHHGHGCGGFFHHHHHHGGGHHGCGGGGGHHHHHHHHHHHHHHGGGGGGHHHGGGGGGG<C>HGHGHEHHDGGF  
@M00698:36:000000000-AFBEL:1:1101:15340:1413 1:N:0:0  
CCACTAACAACTAGCCTGATTAAGTTTTAACGCTTCAACCCAGGCAGGGCTTCCACGCGATCTCTTTTGGGTTTGACCTCTCTTGATCCCCGTCCTAAG  
+  
AABABBBBBFCGGGGGGGGGGGFHHGFHHGFHGGGGGHHHGGGGFHGGFGGHHHCFGFFEFCGHHFHHHHGGAFGGFFFFHHHHHHHHHHHGEEGGGHHB  
@M00698:36:000000000-AFBEL:1:1101:16045:1413 1:N:0:0  
GTAGCATTATCAGAGAGTTGCCATTACGCATTGGCTTAACCGCGCGCAGACCATCAACAGTCACTTTGGCGTCAAAGACATTAGGCGTGCAGTATTTTTT  
+  
?ABCCFFFFFFGGGGGGGGGGGGHHHHHHHHGGGHHHHHHHHGGGGGGGGHHHHHHHHHHHHHHHHHHHHGGGGGGHHHHHHHHHHGGGGHHGHHHHHHG  
@M00698:36:000000000-AFBEL:1:1101:17191:1414 1:N:0:0  
TCGGCACCAATATAGGTAACGCATGGTTCACCGTCTTCAGCTACGGCGCGGATTTTGGTCAGGATCGGTGCTACCAATTCATAGGCTTCTTTCTGCCAC  
+  
ABAABBBBFBFFGGGGGGGGGGGGHHHHHHHHGHGHGHHHHHHHGGGGGGGGHGHGGHHHHHHHHGGGGGGHHHHHHHHHHFHGHHHHHHHHHHBFHHG  
@M00698:36:000000000-AFBEL:1:1101:16186:1414 1:N:0:0  
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+  
BCCCCFFCCCCGGGGGGGGGGGGHHHHHHHHHHGGHHHHHHHHHHHHHHHHHHHHGHGHHGGHHHHHHHHGGGGGGGGGGGGHHHHHHGHFFHGGGGG  
@M00698:36:000000000-AFBEL:1:1101:15394:1415 1:N:0:0  
ACTTCTTGAAGTACGTTGCAGGCTGGCACTTCTGCCGTTTCTGATAAGTTGCTTGATTGGTTGGACTTGGTGGCAAGTCTGCCGCTGATAAAGGAAAGG  
+  
@BBCCFFFFFFGGGGGGGGGGGGHHDGHHHHHHHHHGEHGHHHHHHHHHHHHHHHHHHHHHGGHHHHHHHEGGHHGHHHHHHGGGGFHHHHHHHHHH  
@M00698:36:000000000-AFBEL:1:1101:14326:1417 1:N:0:0  
TGGCGCAACTAACAGAACGTCTTGCGTTTTGTTGGCGAAGCCGCTGGTGTTTGTAATTTATTAGTGATCGGCGTAGCGTTACGGGTTTCACCGTAGTTCG  
+  
ABCCCCCCCCFFGGGGGGGGGGGGHHGGGGGHHHHHHGGGGGHGGGGGFGFFHHHHHHHHGHHHHHHHHHHGHGGGGGFAE>EGGGGEGGHHHHGGHGGHHG  
@M00698:36:000000000-AFBEL:1:1101:15479:1417 1:N:0:0  
GCCCCCTCACTCTGACTTTAGTGTGCGCCTTTTGCTGCGCCACGATCTCCTCGACATTTTCCGGCATTGGTTCATACGGCGTTTCTTTGCCGTTGG  
+  
@BCCCCCCFCFGGGGGGGGGGGGHHHHGGGGGHHHHHHHHGGGGGGHHHHHHHHGGGGGGHHHHHHHHGGGGGGHHHHHHGGGGGGGGH  
@M00698:36:000000000-AFBEL:1:1101:16850:1418 1:N:0:0  
CGTTTTCTTCATCGCGCTCTTTGCTGCCTAACAGCGTGCGCCAGCCTGCTTCAGCAAGAAAACGCGCTTTAGCGACAAATTTGCCTTTGGCAATGTCCAGT  
+  
AAACCCFFFFFFGGGGGGGGGGGGHHHHHHHHHHHHGGGGGGGGGGHHHHHHHHHHHHHHHHGGGGGGHGHGGGGGFHHHHHHHHHHHHHHHHHHHHG  
@M00698:36:000000000-AFBEL:1:1101:16255:1418 1:N:0:0  
CCGGCTTGCTGGTTGCAGCCGTTGCTGTACTTGATGTCAGGCGTGCCGGTGCCGTATTTTCAAACGGTGATGCCGGACGCGACTCTACGGGTTTGACATCG  
+  
AAABCCCCFFFGGGGGGGGGGGGGHHHHHHHHHHHHHHGGGGGHGGGGGHGFGHHHHHHHHHHGGGGHGHHHGGGGGGGGGGHHHGGGCGGGHHHHH?  
@M00698:36:000000000-AFBEL:1:1101:17071:1419 1:N:0:0  
CACGCCACCTTTATCCAGTTTGCGGCTTTGCGAAGTGCGAGCCACAGCGGTTTTCTTGCTGGCTATAAGCCATTTCTGAGGCACCTTTACCTACCGCTT  
+  
AABBBBBBFFFFGGGGGGGGGGHGGGGGHHHGGGGFHHGGGGGGHHHHGGGGFGGGHHHHHHHHGHHHHHHHHHHHHHHHGGHGHGHFFHHHHHHGGGG  
@M00698:36:000000000-AFBEL:1:1101:15606:1420 1:N:0:0  
CGGGTTTTTAACTTTCAGCCACGGGCCACCGTCGATCAGTTCACCGCCAAACTCTTCACGCGCCAGCTGGTAGCCCCAGTCTTTAAACGCTCCTTCGGTGA  
+  
BBCDBBCCDCFFGGGGGGGGGGGGGGGGGGGGHGGGGGGHGHHHHHHHGGGGGGHHHHHHHHHHHHGGGGGGHHHHHHHHGGGGHHHHHHHGFGG  
@M00698:36:000000000-AFBEL:1:1101:15945:1421 1:N:0:0  
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+  
?ABABFFFBBBFGEEGGGGGGGGGGGHGHCHGCGGGHGHHHHHHHGGGGHGHHHHHGHGEGDGHHHHHGGG?EB2GGHGHHHGHGHHHHHGHFFHHHHHHGGH  
@M00698:36:000000000-AFBEL:1:1101:16329:1421 1:N:0:0  
GCCCCGACAGCTGTATGCATAGCGATAAATTCAGCAGGCCGGGACGCCGTTCTATTTTGCCCCAGAGTGTCATGTTAGACTTGACGGACATTGTGCAG  
+  
3ABCCCCCCCCFGGGGGGGGGGGHGGHGGHHHHHHHHHHGGGGGGGGGGGGGGGGHHHHHHHHHHGGGHHHHHHHHGHHHHHHHHHHHHHGGGGGGHHHHHHH  
@M00698:36:000000000-AFBEL:1:1101:16260:1423 1:N:0:0

# FASTQ: Format

# FASTQ: Read Files

## Combined\_R1.fastq.gz

```
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+
ABBBABBBBAFFFGGGGGGGGGHGGHGGGCG2GF3FFGHHHHHHGGFGHEHHGGGEHHHHAGGHHGHHHFFDHFHHHGEGGGG@F@H?GHH/GBEFGGG
@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0
CTGCCAGTTGAACGACGGCGAGCAGTTATAAGCCAGCAGTTTGCCCGGATATTTGCGGTGGATAGCTTGTGCAAAGCGACGCGCCAGTTCCAGATCCGGCG
+
AAABBFFFFFFFFFFGGGGGGGGGGGGHHHHHHHHHGHGHHHHHHHHHHGGGGGGHHHHGGGGGGGGHHHHGHHFFHHHHHHGHGGGGGGGGGGHHHHHHHHHHHHGGG
```

## Combined\_R2.fastq.gz

```
@M00698:36:000000000-AFBEL:1:1101:14738:1412 2:N:0:0
GGAAGATGCGGCGACGGCTGAAATTTCCCGTACCTCGATCTGGCAGTGGATCCATCATCAAAAAACGTTGAGCAATGGCAAACCGGTGACCAAAGCCTTGT
+
ABBABFFFFDBDGC??FFGGGHGHFEG3EAEGGFHAE3GFBGGHGGGHHCFGHFGBGHFHHDFFEGGHFHEFHFFF3BFGF0GFEGGGGGHHA/FGHFHHH
@M00698:36:000000000-AFBEL:1:1101:16483:1412 2:N:0:0
GCTTCTTCCGTACTCATGCGGGCATTGAGCAAGCGATCAGCCGTGGCCTGGCGTATGCGCCATATGCTGACCTGGTCTGGTGTGAAACCTCCACGCCGGAT
+
CCCCCFFFBFFGGGGGGGGCECGHHHHHHHHHHGGHGGGGHGGCGCHHGFHGGGGHHGGGGHHHHHHHHHHHHHHHEHGHHHGHHHHGGGGGGG
```

## Combined\_I1.fastq.gz

```
@M00698:36:000000000-AFBEL:1:1101:14738:1412 1:N:0:0
AGTTCC
+
CCCCDF
@M00698:36:000000000-AFBEL:1:1101:16483:1412 1:N:0:0
CCTGTC
+
A11>>1
```





# Metadata Example

#Example mapping file for the QIIME analysis package. These 9 samples are from a study of the effects of exercise and diet on mouse cardiac physiology (Crawford, et al, PNAS, 2009).

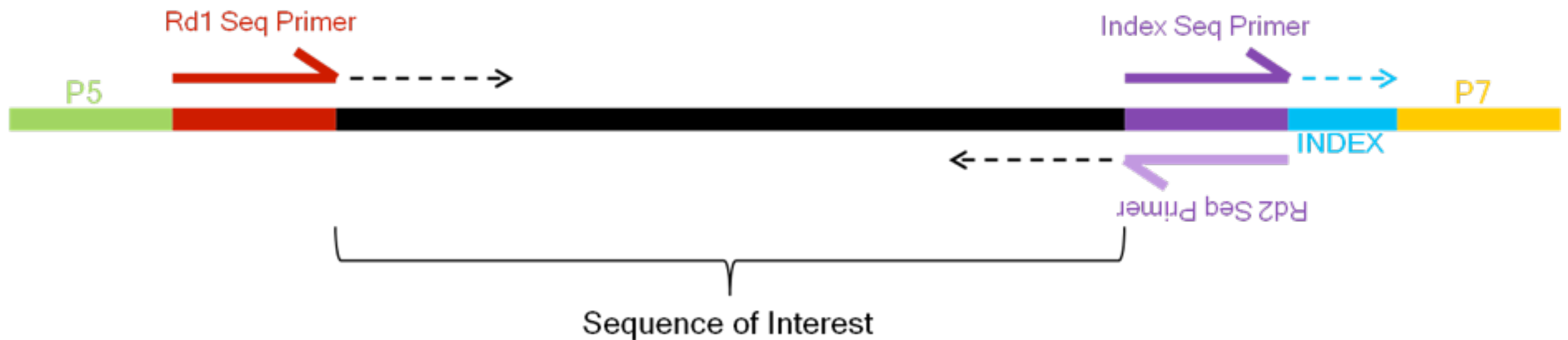
#

#

#SampleID	BarcodeSequence	LinkerPrimerSequence	Treatment	DOB	Description
PC.354	AGCACGAGCCTA	YATGCTGCCTCCCGTAGGAGT	Control	20061218	Control_mouse__I.D._354
PC.355	AGCACGAGCCTA	YATGCTGCCTCCCGTAGGAGT	Control	20061218	Control_mouse__I.D._355
PC.356	ACAGACCACTCA	YATGCTGCCTCCCGTAGGAGT	Control	20061126	Control_mouse__I.D._356
PC.481	ACCAGCGACTAG	YATGCTGCCTCCCGTAGGAGT	Control	20070314	Control_mouse__I.D._481
PC.593	AGCAGCACTTGT	YATGCTGCCTCCCGTAGGAGT	Control	20071210	Control_mouse__I.D._593
PC.607	AACTGTGCGTAC	YATGCTGCCTCCCGTAGGAGT	Fast_2	20071112	Fasting_mouse__I.D._607
PC.634	ACAGAGTCGGCT	YATGCTGCCTCCCGTAGGAGT	Fast	20080116	missing_description
PC.635	ACCGCAGAGTCA	YATGCTGCCTCCCGTAGGAGT	Fast	20080116	Fasting_mouse__I.D._635
PC.636	ACGGTGAGTGTC	YATGCTGCCTCCCGTAGGAGT	Fast	20080116	Fasting_mouse__I.D._636

# Multiplexing (Barcodes)

## STRUCTURE DETAILS



# Metadata Example

#Example mapping file for the QIIME analysis package. These 9 samples are from a study of the effects of exercise and diet on mouse cardiac physiology (Crawford, et al, PNAS, 2009).

#

#

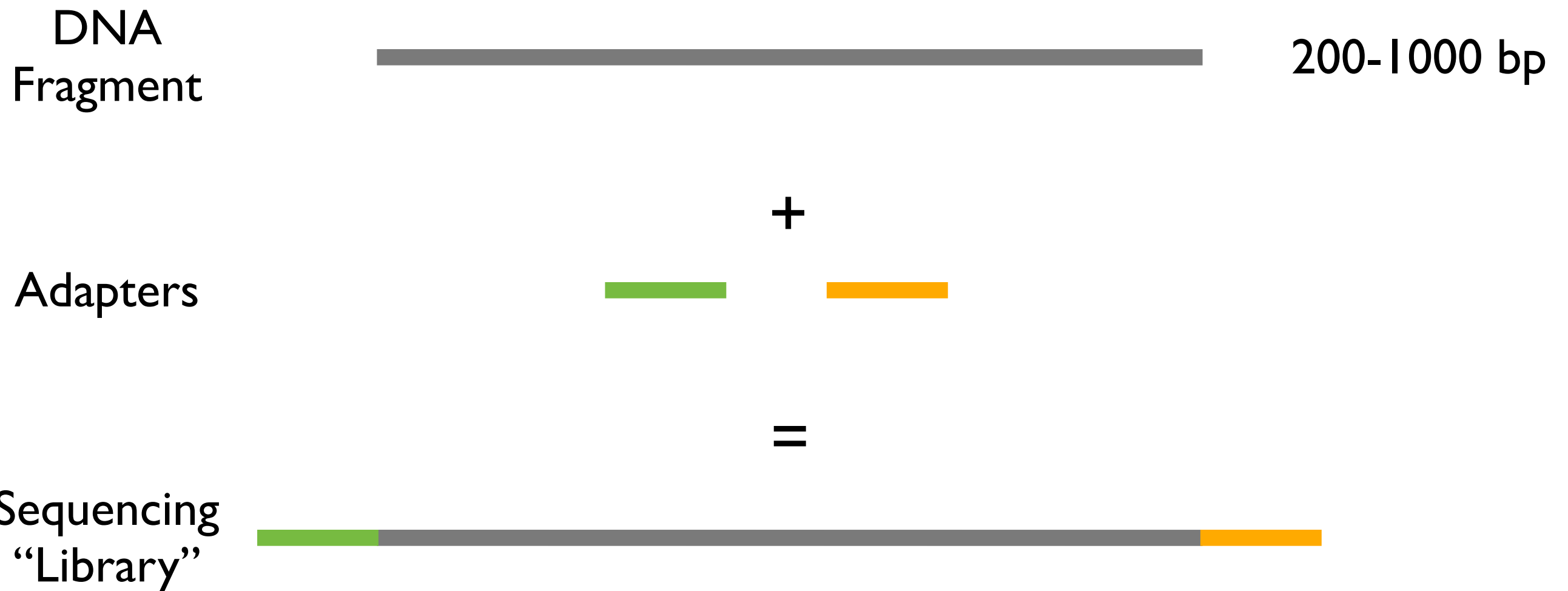
#SampleID	BarcodeSequence	LinkerPrimerSequence	Treatment	DOB	Description
PC.354	AGCACGAGCCTA	YATGCTGCCTCCCGTAGGAGT	Control	20061218	Control_mouse__I.D._354
PC.355	AGCACGAGCCTA	YATGCTGCCTCCCGTAGGAGT	Control	20061218	Control_mouse__I.D._355
PC.356	ACAGACCACTCA	YATGCTGCCTCCCGTAGGAGT	Control	20061126	Control_mouse__I.D._356
PC.481	ACCAGCGACTAG	YATGCTGCCTCCCGTAGGAGT	Control	20070314	Control_mouse__I.D._481
PC.593	AGCAGCACTTGT	YATGCTGCCTCCCGTAGGAGT	Control	20071210	Control_mouse__I.D._593
PC.607	AACTGTGCGTAC	YATGCTGCCTCCCGTAGGAGT	Fast_2	20071112	Fasting_mouse__I.D._607
PC.634	ACAGAGTCGGCT	YATGCTGCCTCCCGTAGGAGT	Fast	20080116	missing_description
PC.635	ACCGCAGAGTCA	YATGCTGCCTCCCGTAGGAGT	Fast	20080116	Fasting_mouse__I.D._635
PC.636	ACGGTGAGTGTC	YATGCTGCCTCCCGTAGGAGT	Fast	20080116	Fasting_mouse__I.D._636



# Illumina Sequencing

From Library to Data

# Library Preparation



# Sequencing

AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

# Sequencing

  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA



# Sequencing

 T   
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

# Sequencing

 T  
 AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA 

# Sequencing

TC ●  
AGCTTTTCATTCTGACTGCAACGGGCAATATGTCTCTGTGTGGA

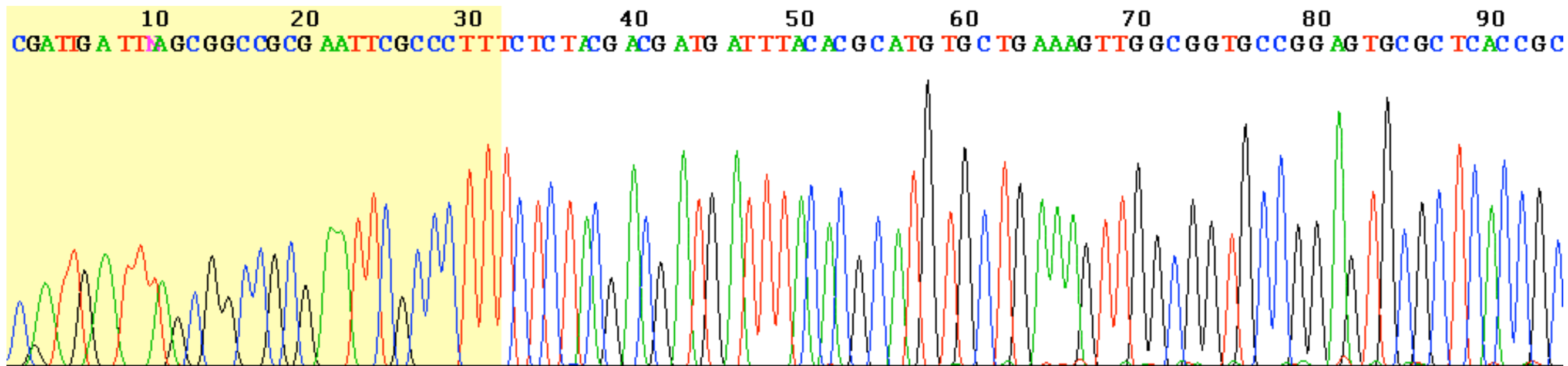
# Sequencing

TC  
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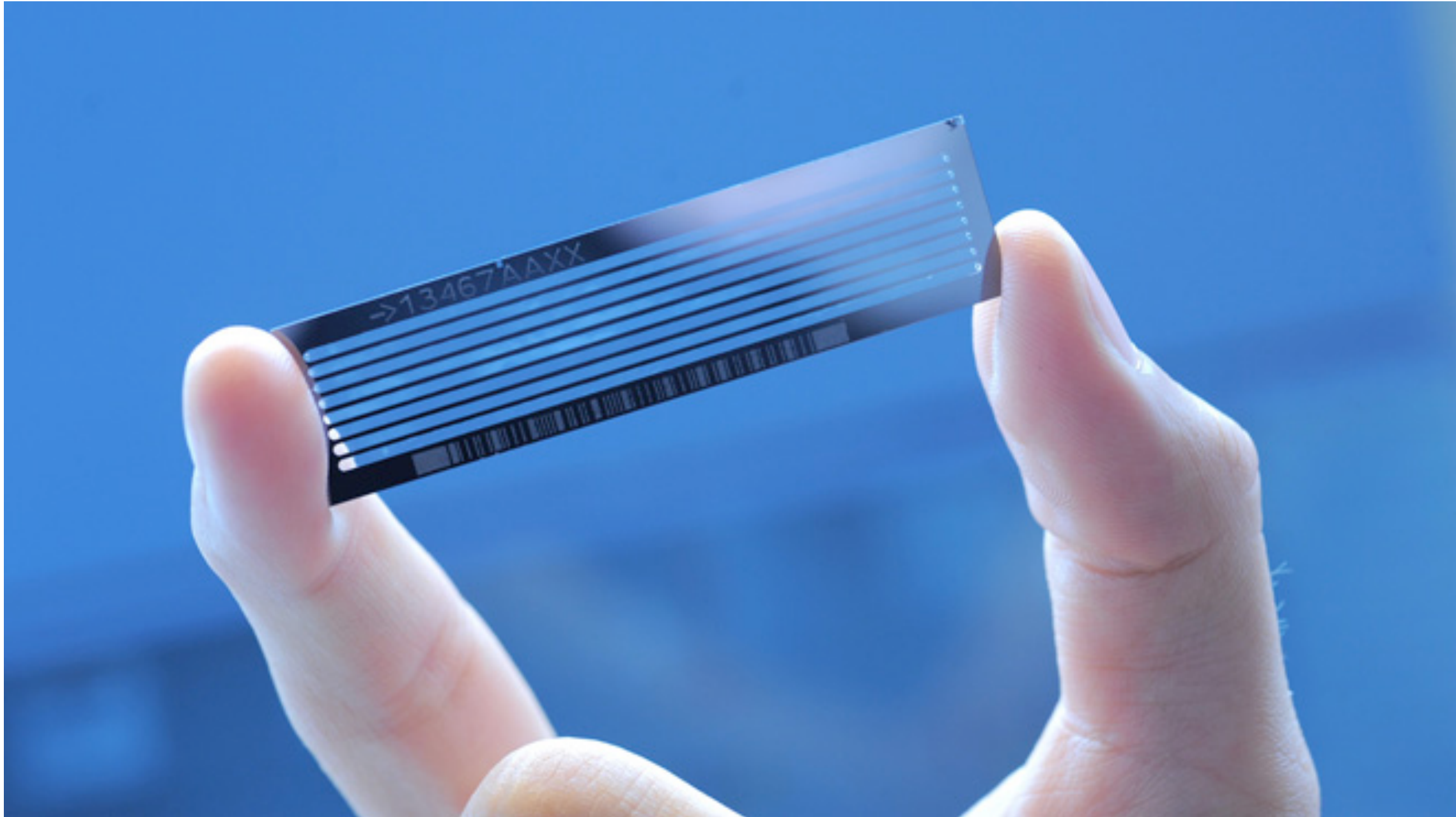
# Sequencing

 T C G ●  
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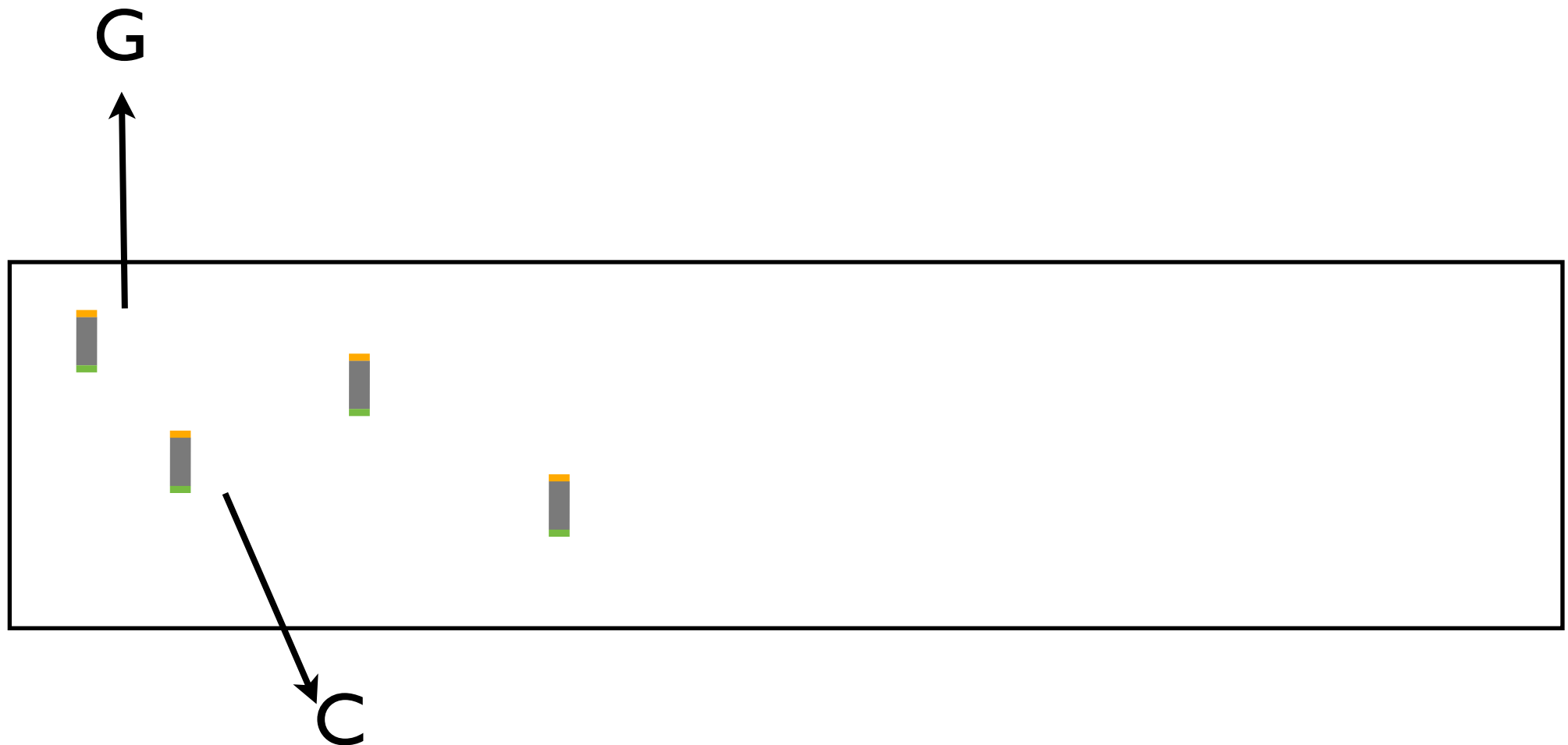
# Dye-terminator Sanger Sequencing



# A Flow Cell

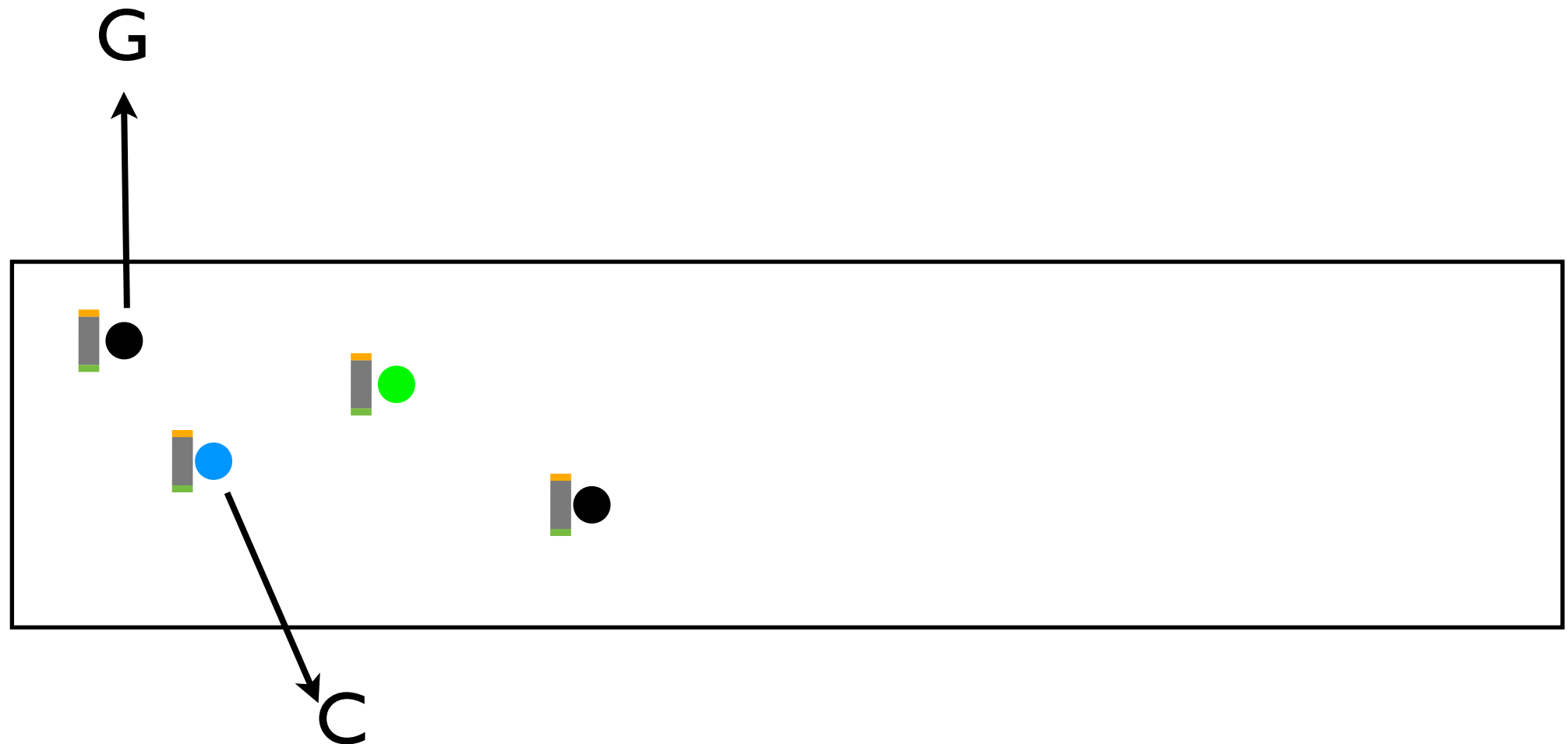


# Parallel Sequencing

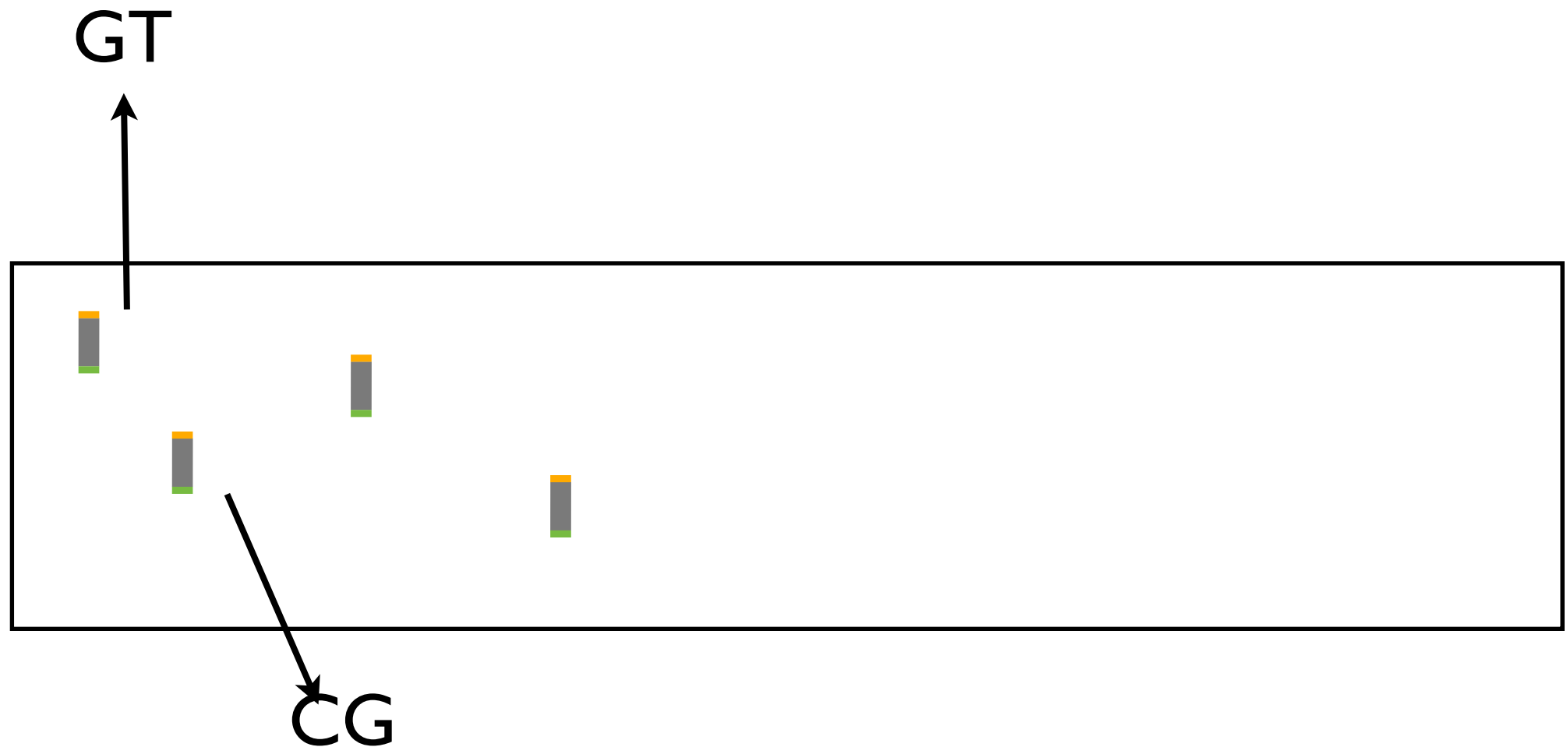




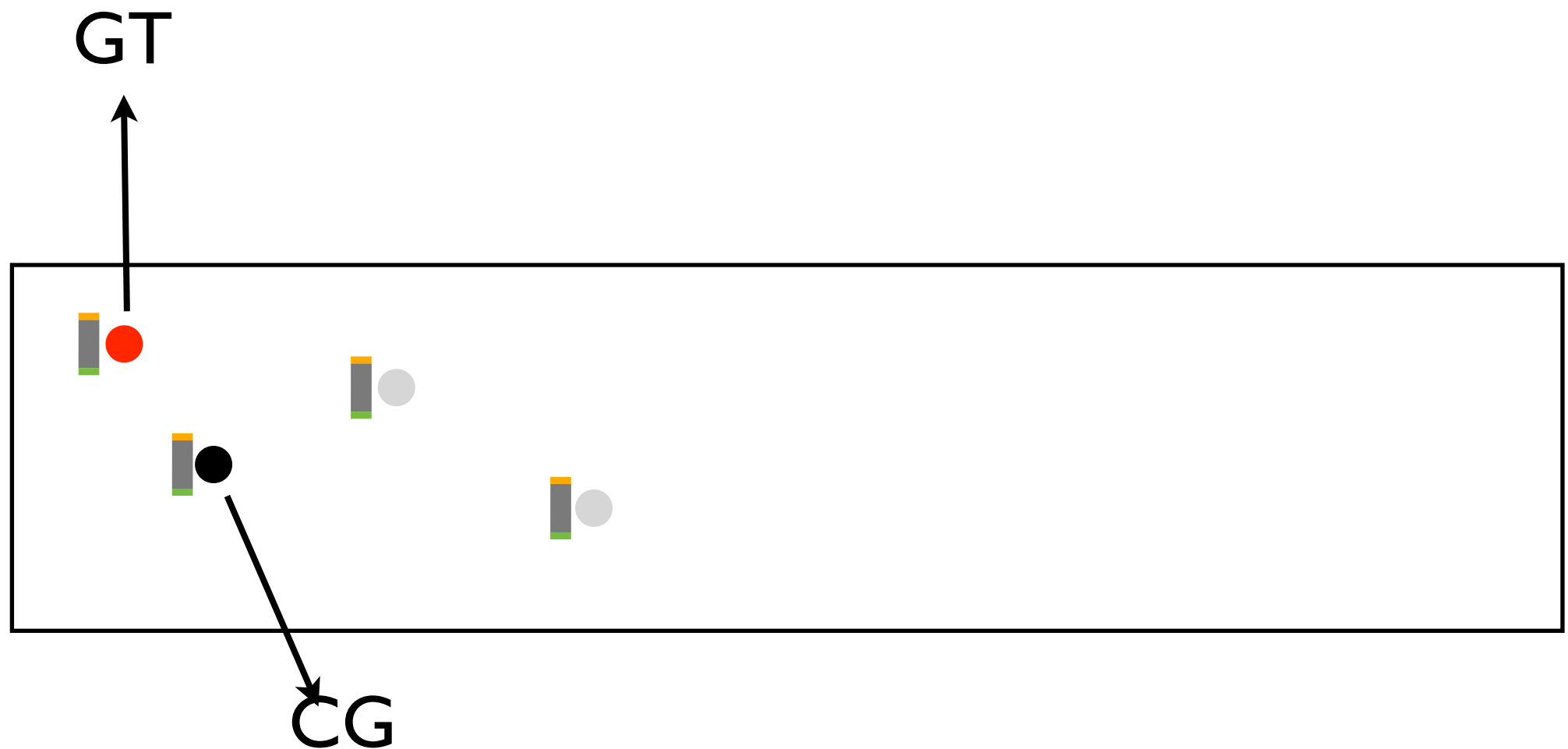
# Parallel Sequencing



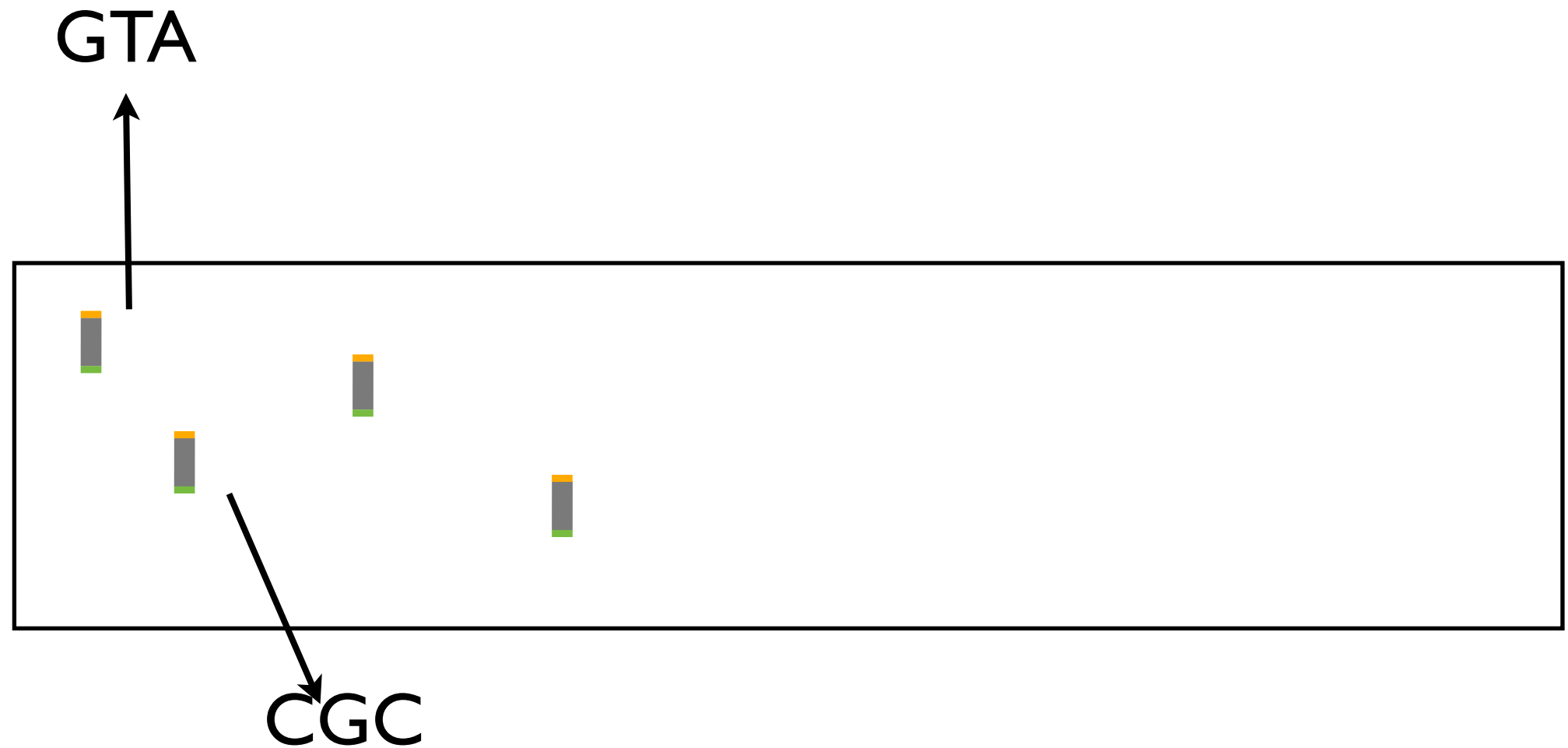
# Parallel Sequencing



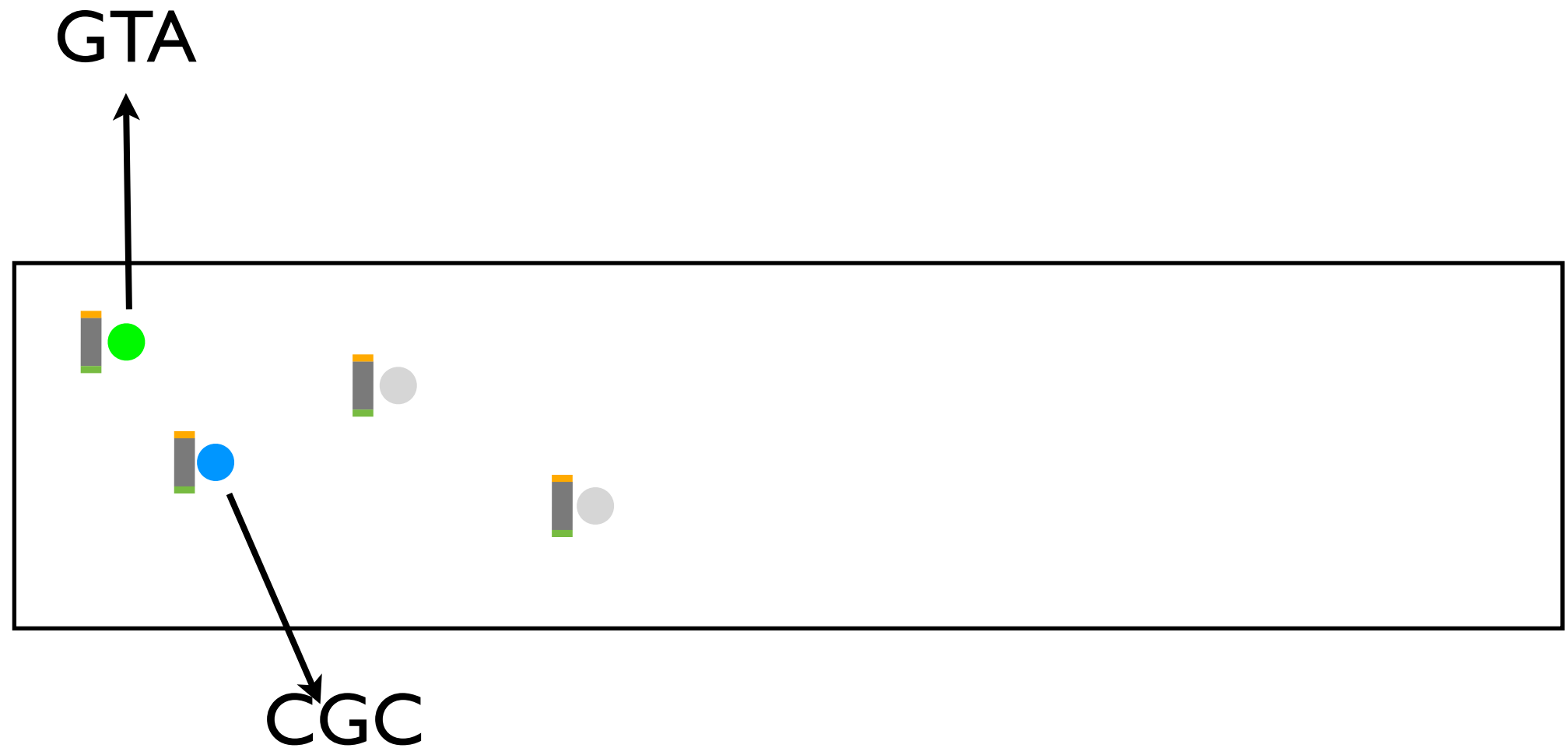
# Parallel Sequencing



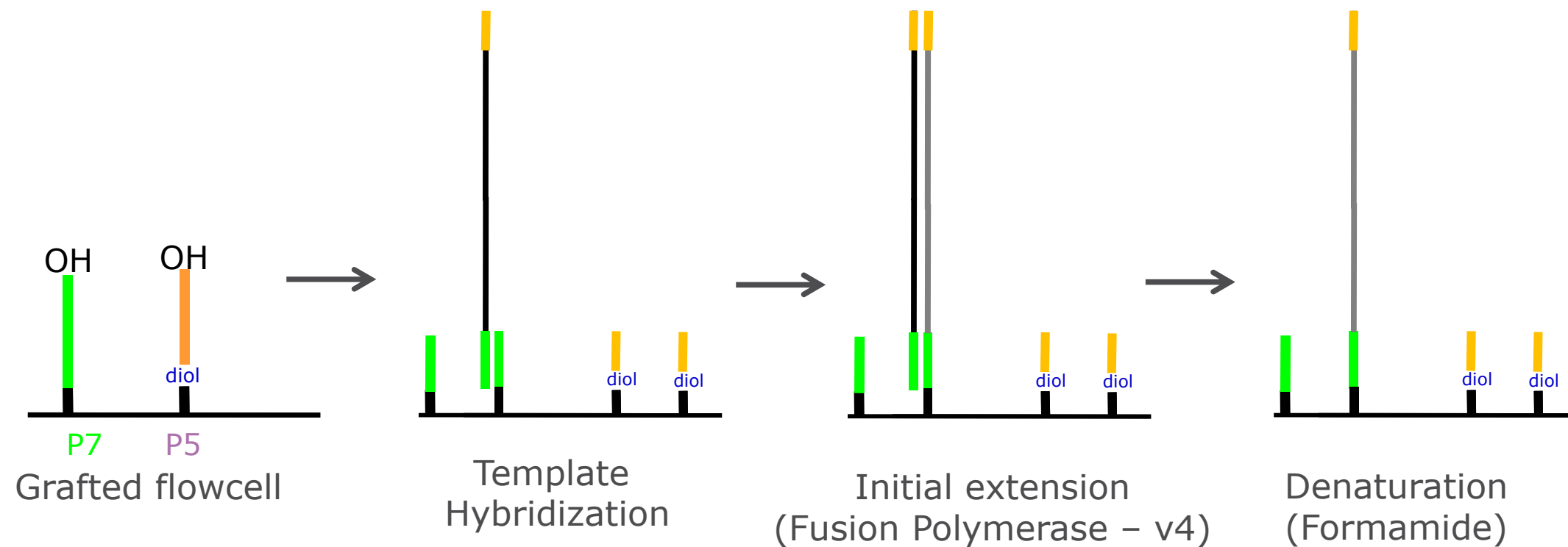
# Parallel Sequencing



# Parallel Sequencing



# Cluster generation – hybridization and amplification



# Cluster generation – hybridization and amplification

