

# Post-Lab Review, Etc

Josh Granek

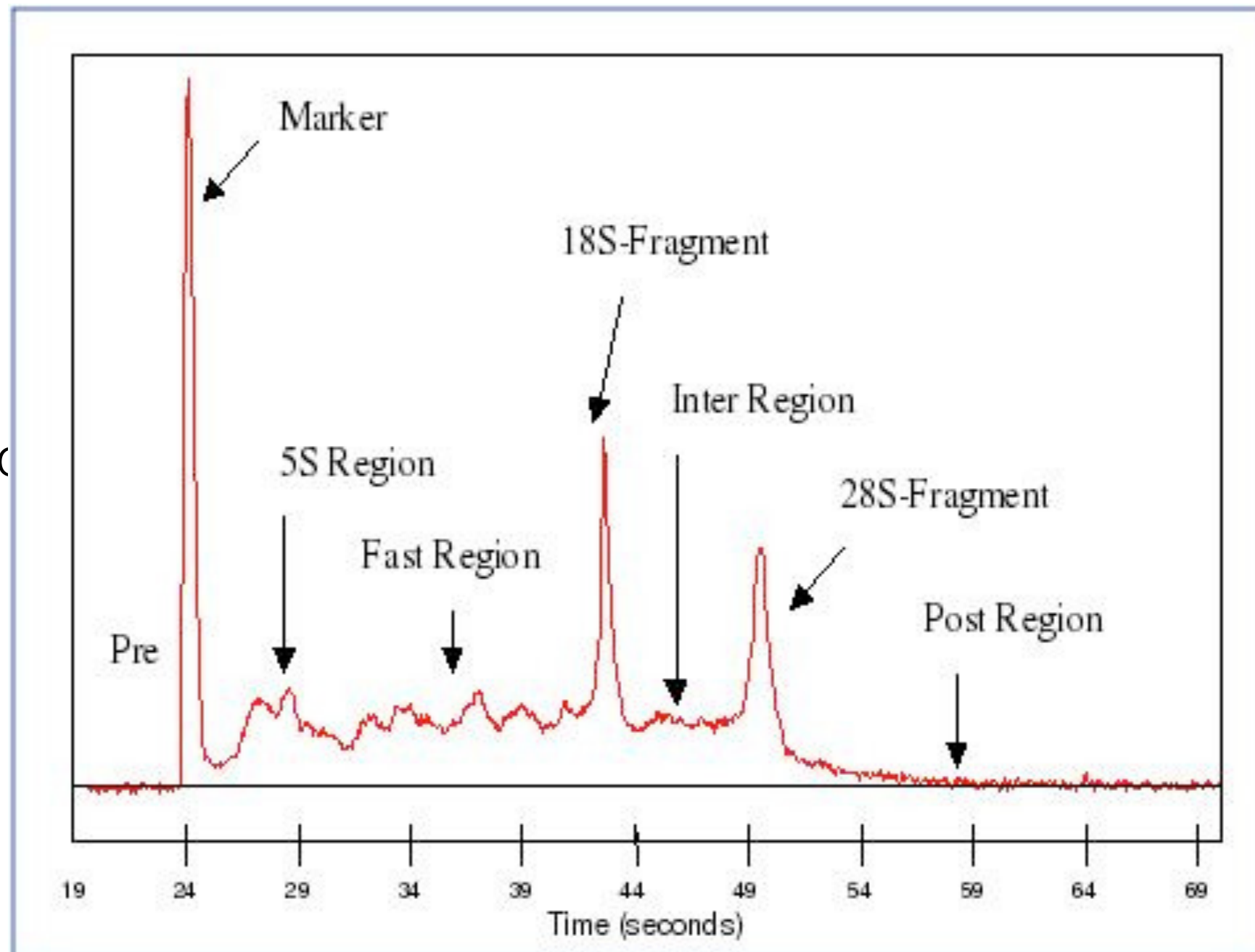
# RNA Quality?

- RIN: RNA Integrity Number

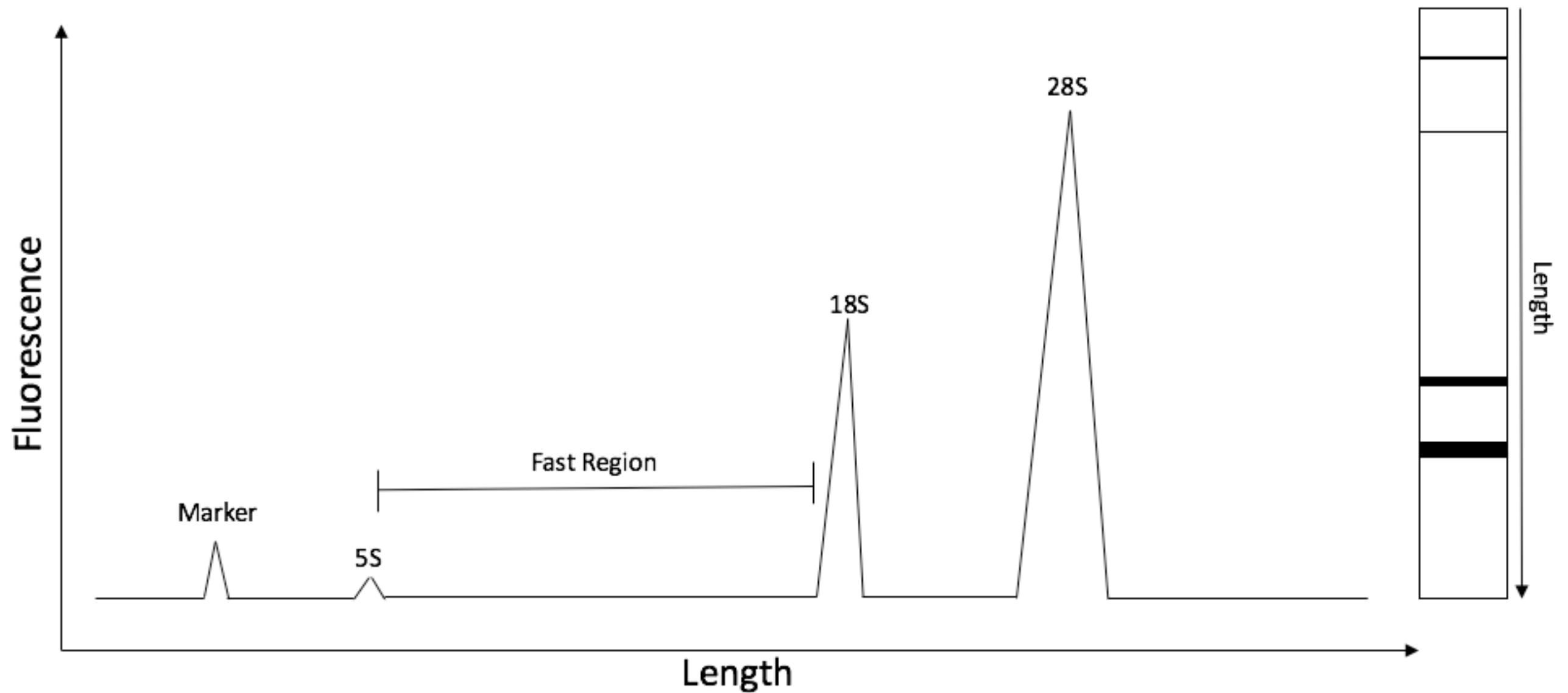


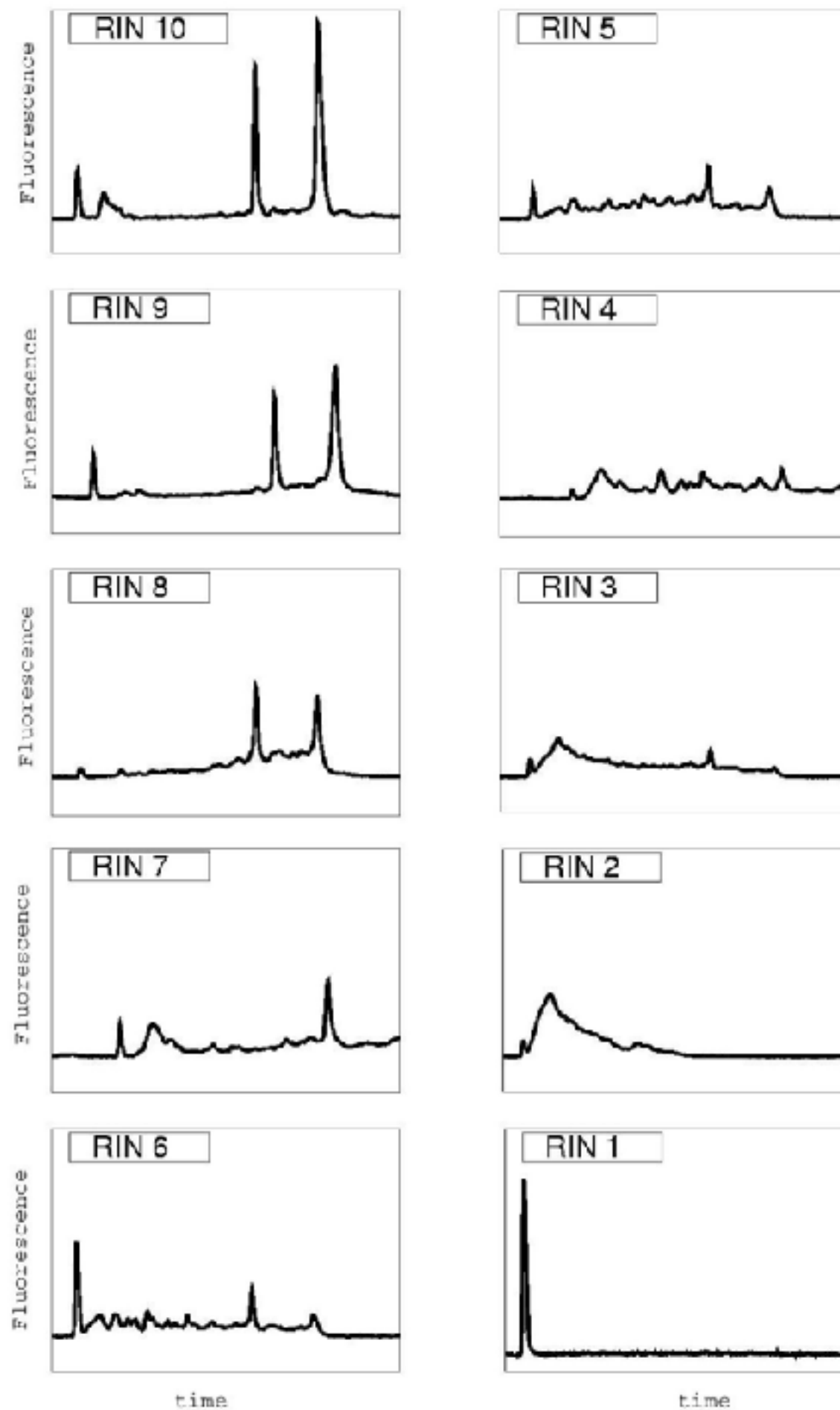
# Ratio of 28S to 18S ribosomal RNA

- Ratio of

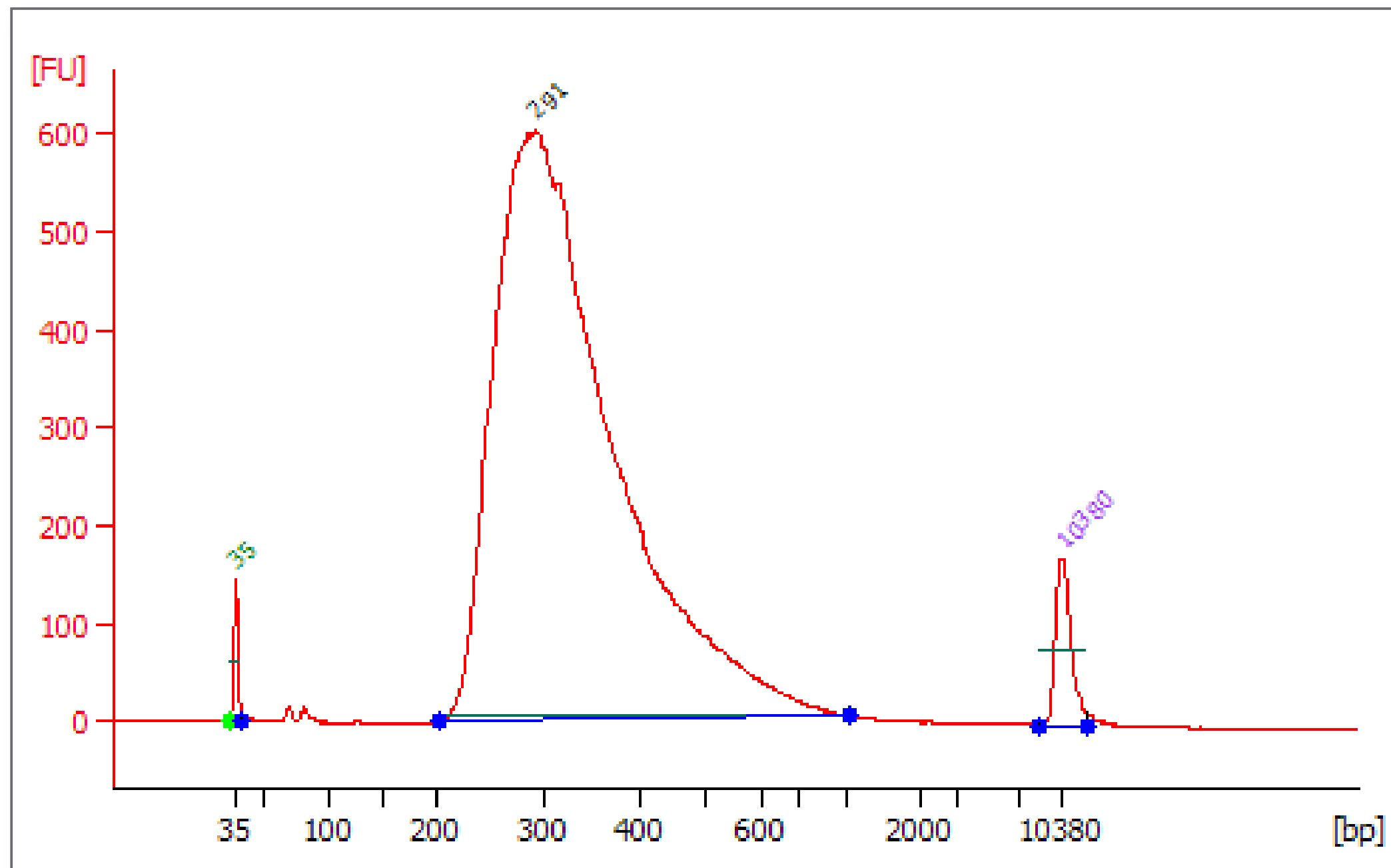


# Electropherogram





# RNA Library Size Distribution



# Assessment of RNA/DNA Quantity and Quality

- Advanced Analytical: Fragment Analyzer
- PerkinElmer: LabChip GX Touch
- Agilent: Bioanalyzer
- Agilent: TapeStation

# Barcode Combinations

- Excitation Frequency
  - Red: A and C
  - Green: G and T
- Need both frequencies in each cycle for image registration



# Barcode Combinations

## GOOD

| PRIMER | INDEX SEQUENCE |   |   |   |   |   |   |   | PRIMER | INDEX SEQUENCE |   |   |   |   |   |   |   |
|--------|----------------|---|---|---|---|---|---|---|--------|----------------|---|---|---|---|---|---|---|
| P1-A1  | T              | T | A | C | C | G | A | C | P41-D5 | G              | A | C | G | T | C | A | T |
| P2-A2  | A              | G | T | G | A | C | C | T | P42-D6 | C              | T | T | A | C | A | G | C |
| P3-A3  | T              | C | G | G | A | T | T | C | P43-D7 | T              | C | C | A | T | T | G | C |
| P4-A4  | C              | A | A | G | G | T | A | C | P44-D8 | A              | G | C | G | A | G | A | T |
|        | ✓              | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |        | ✓              | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ | ✓ |

## BAD

| PRIMER  | INDEX SEQUENCE |   |   |   |   |   |   |   | PRIMER  | INDEX SEQUENCE |   |   |   |   |   |   |   |
|---------|----------------|---|---|---|---|---|---|---|---------|----------------|---|---|---|---|---|---|---|
| P9-A9   | C              | G | C | A | A | C | T | A | P56-E8  | T              | A | T | G | G | C | A | C |
| P10-A10 | C              | G | T | A | T | C | T | C | P57-E9  | C              | T | C | G | A | A | C | A |
| P11-A11 | G              | T | A | C | A | C | C | T | P58-E10 | C              | A | A | C | T | C | C | A |
| P12-A12 | C              | G | G | C | A | T | T | A | P59-E11 | G              | T | C | A | T | C | G | T |
|         | ✓              | ✗ | ✓ | ✗ | ✓ | ✓ | ✓ | ✓ |         | ✓              | ✓ | ✓ | ✓ | ✓ | ✗ | ✓ | ✓ |

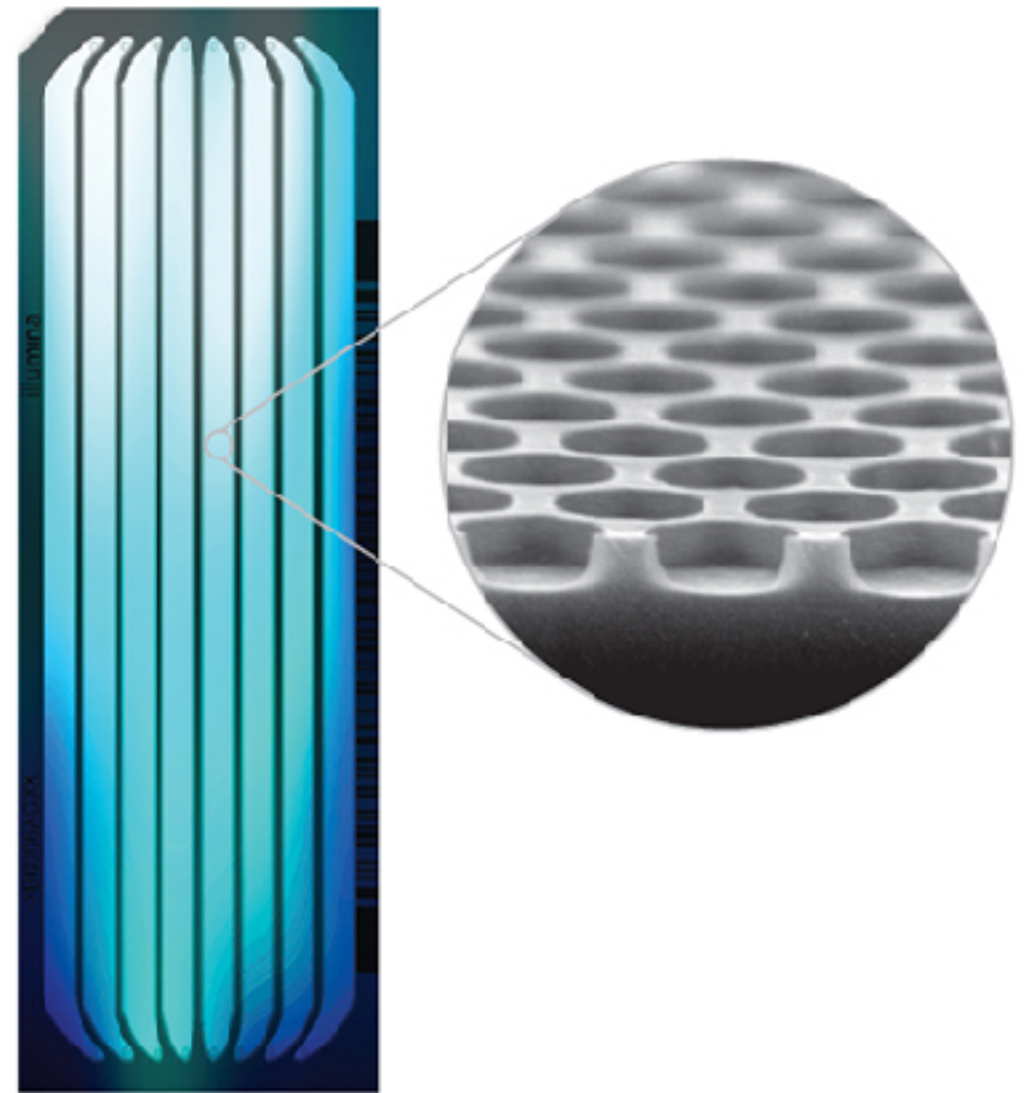
# MiSeq, NextSeq, and More Seqs

|                              | 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 x 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

# Patterned Flow Cells

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











# 4-Channel Chemistry








| 4-Channel Chemistry |   |   |   |   |
|---------------------|---|---|---|---|
|                     | <br><b>A</b> | <br><b>G</b> | <br><b>T</b> | <br><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

|         | <br><b>A</b> | <br><b>G</b> | <br><b>T</b> | <br><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

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

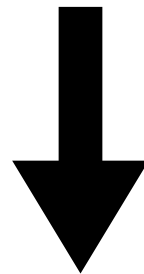
# Uracil DNA glycosylase and DNA lyase

# Uracil DNA glycosylase: What

- Remove Uracil base from DNA

# Uracil DNA glycosylase: What

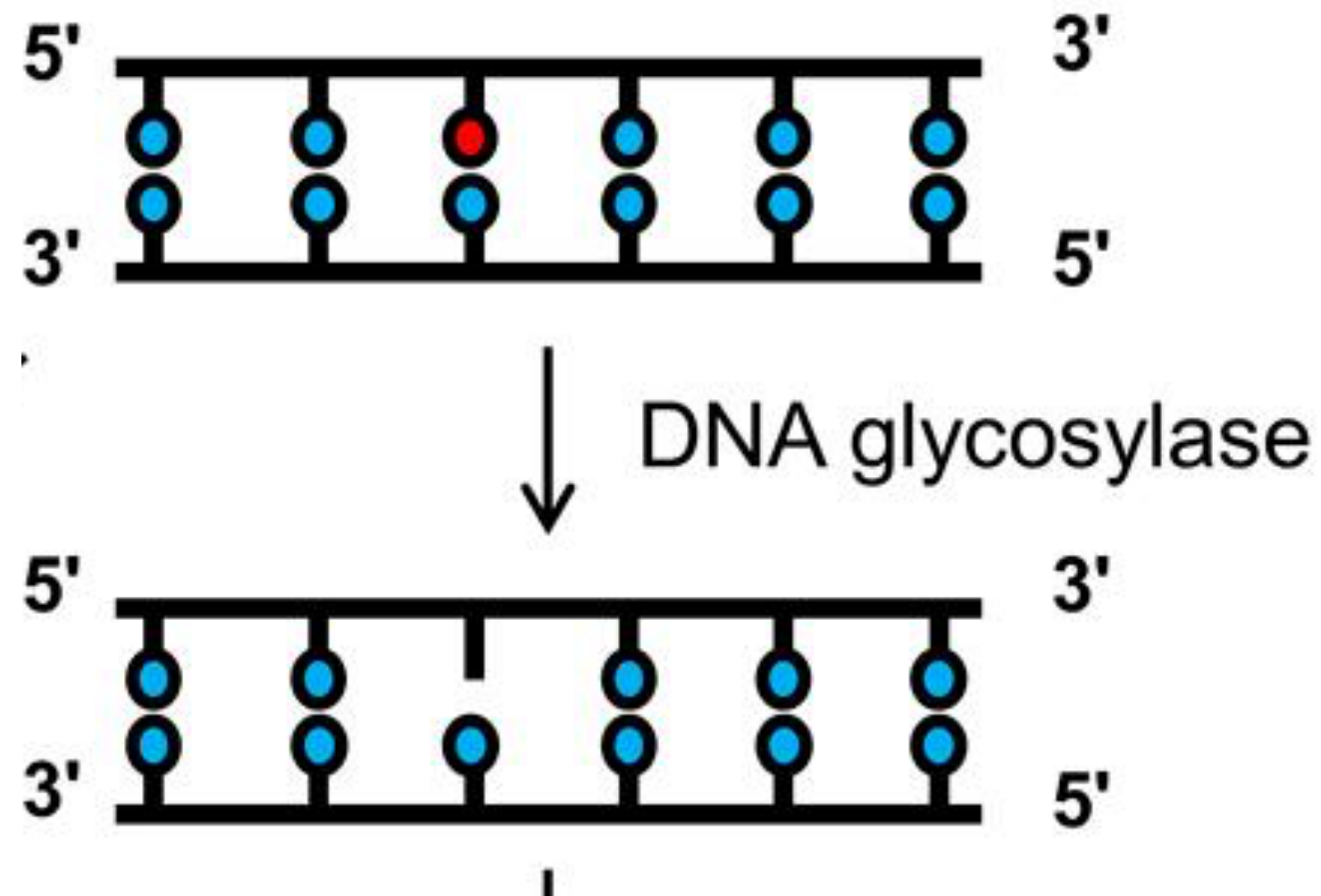
5' –CTGATCUGACTGATG–3'  
3' –GACTAGACTGACTAC–5'



5' –CTGATC–GACTGATG–3'  
3' –GACTAGACTGACTAC–5'



# Uracil DNA glycosylase: What

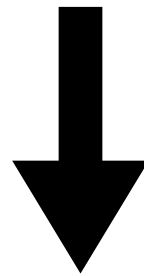


# DNA Lyase: What

- Cleave DNA backbone at abasic site

# DNA Lyase: What

5' -CTGATC-GACTGATG-3'  
3' -GACTAGACTGACTAC-5'



5' -CTGATC GACTGATG-3'  
3' -GACTAGACTGACTAC-5'

# Comparing Technologies

| Method          | Read length             | Accuracy | Reads per run      | Max Output | Cost (\$/Mb) | Pros   | Cons  |
|-----------------|-------------------------|----------|--------------------|------------|--------------|--|---|
| <b>Sanger</b>   | 400-900 bp              | 99.9%    | 1                  | 900 bp     | \$2400       | Longer reads.                                  | Expensive.<br>Low Output                                      |
| <b>Illumina</b> | 600 bp<br>(300bp PE)    | 99.9%    | 20x10 <sup>9</sup> | 6000 Gb    | \$0.01       | High yield<br>per base cost                    | Equipment expense.<br>Short reads                             |
| <b>PacBio</b>   | >10kb ave.<br>>40kb max | 99%      | 5x10 <sup>5</sup>  | 10 Gb      | \$0.08       | Very long reads                                | Homopolymer errors.<br>Moderate Output.<br>Equipment expense. |
| <b>Nanopore</b> | >100 kb N50<br>>1Mb Max | 92%      | 1x10 <sup>6</sup>  | 5 Gb       | \$0.10       | Very long reads<br>Portable<br>Cheap Equipment | Homopolymer errors.<br>Moderate Output.                       |

[https://en.wikipedia.org/wiki/DNA\\_sequencing](https://en.wikipedia.org/wiki/DNA_sequencing)

<https://blog.genohub.com/2017/06/16/pacbio-vs-oxford-nanopore-sequencing/>

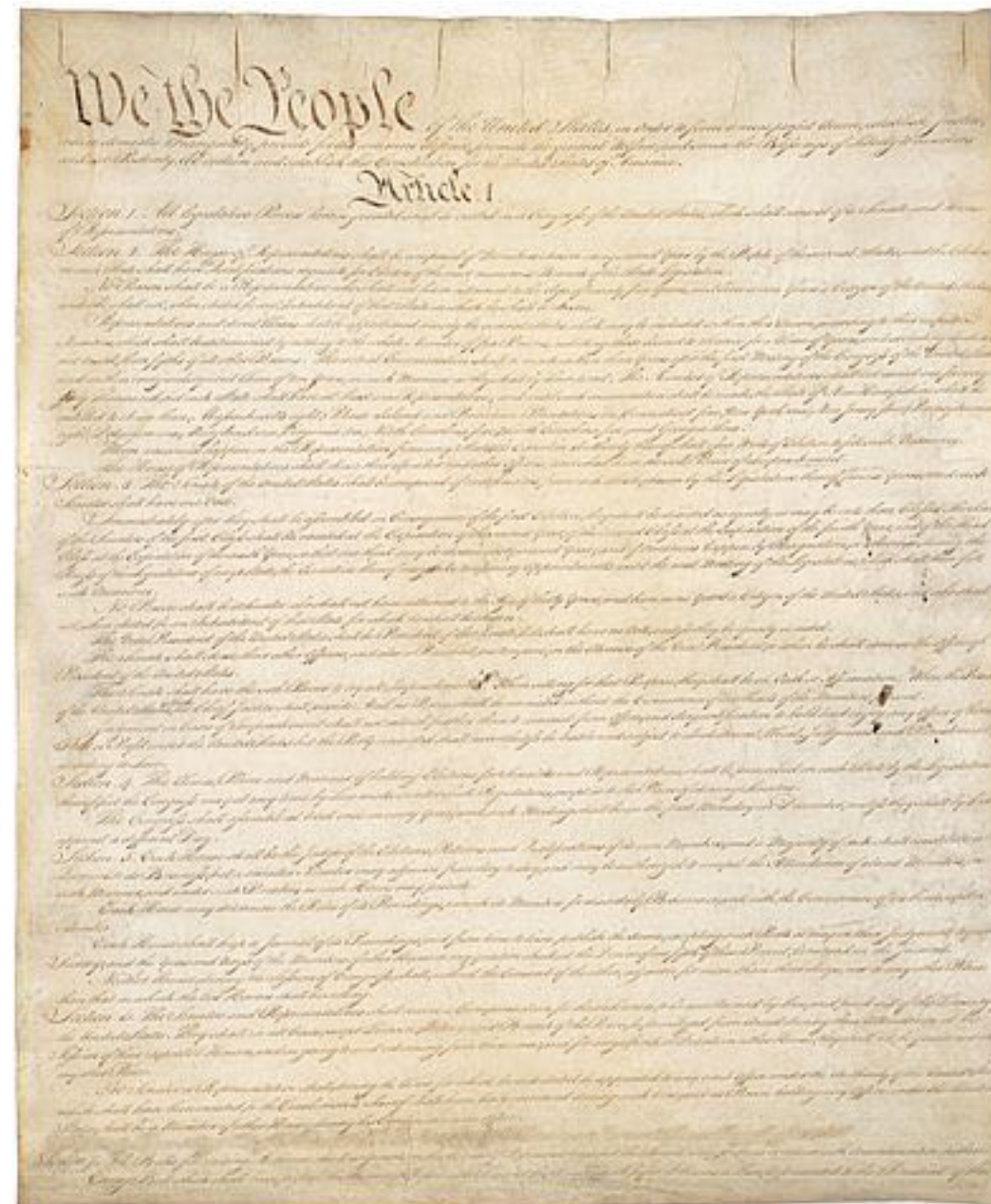
# Why Long Reads?

- Structural Variation
  - Large Insertions or Deletions
  - Duplications
  - Translocations
- De Novo Genome Assembly
- Phasing

# Short Reads

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# “Genome” Reference



# Reference Based Mapping

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# Fragmentation

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# Problem Sequences

- Repeats
  - Transposons
  - Centromeres
- Homologs
- Duplications

# De novo “Reference”

ed, under various disguises of Art, through the portraits of every Drinking Age. "You are a little

— *A Tale of Two Cities*



# Single Molecule Technologies

# DNA Sequencing Technologies (Abridged)

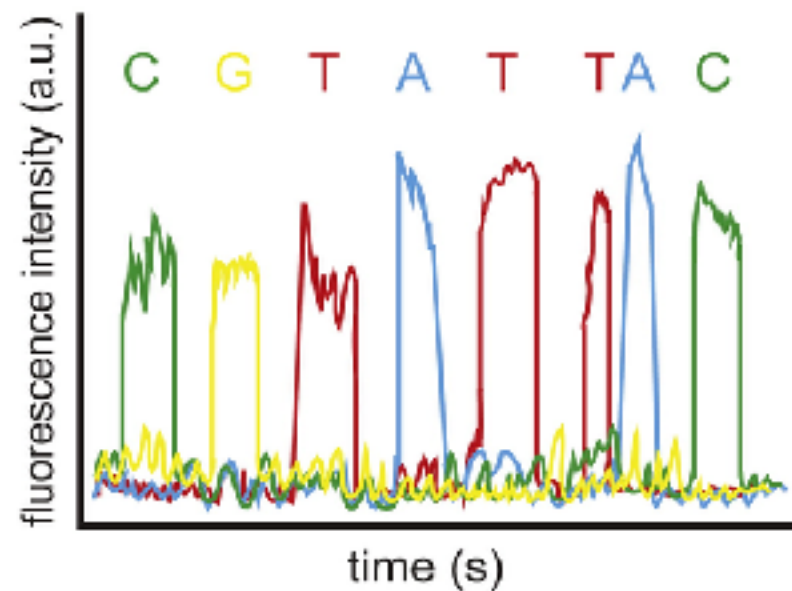
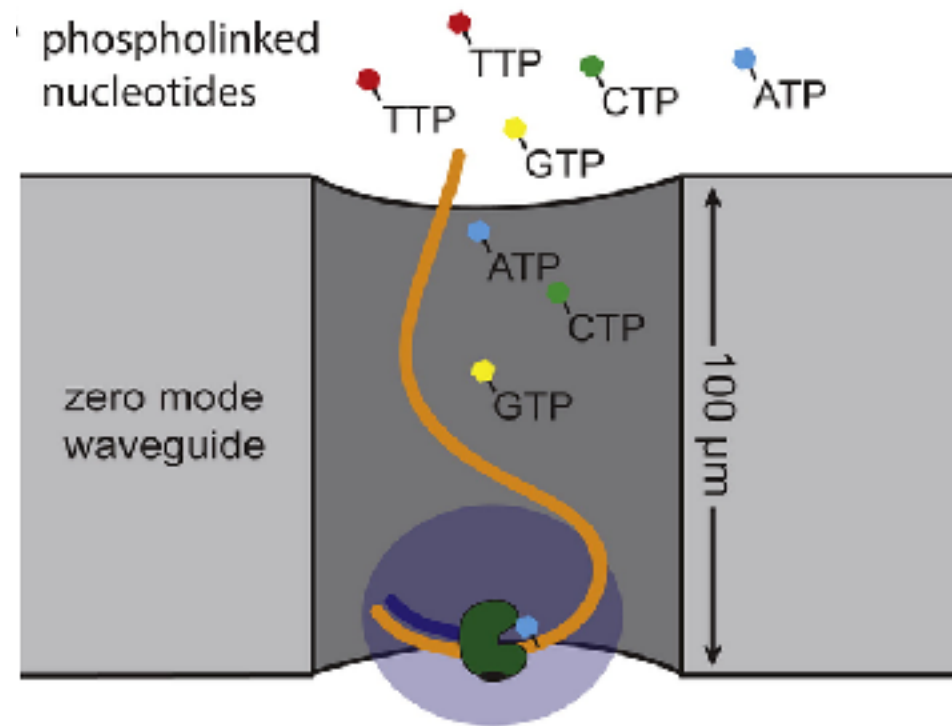
| 1st Generation                | 2nd Generation                               | 3rd Generation                           |
|-------------------------------|--|--|
| Chemical<br>(Maxim-Gilbert)   | Pyrosequencing<br>(454)                      | Single molecule real time<br>(PacBio)    |
| Chain Termination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

# Sequencing by Synthesis

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

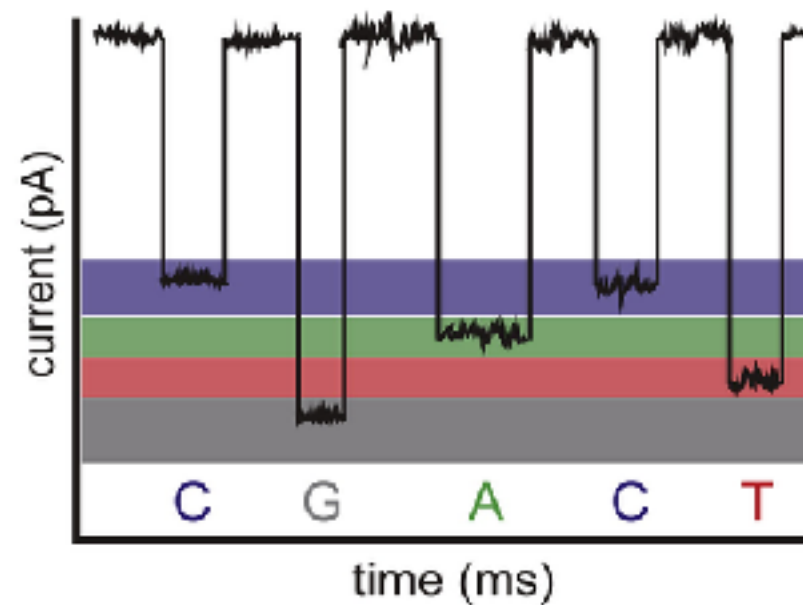
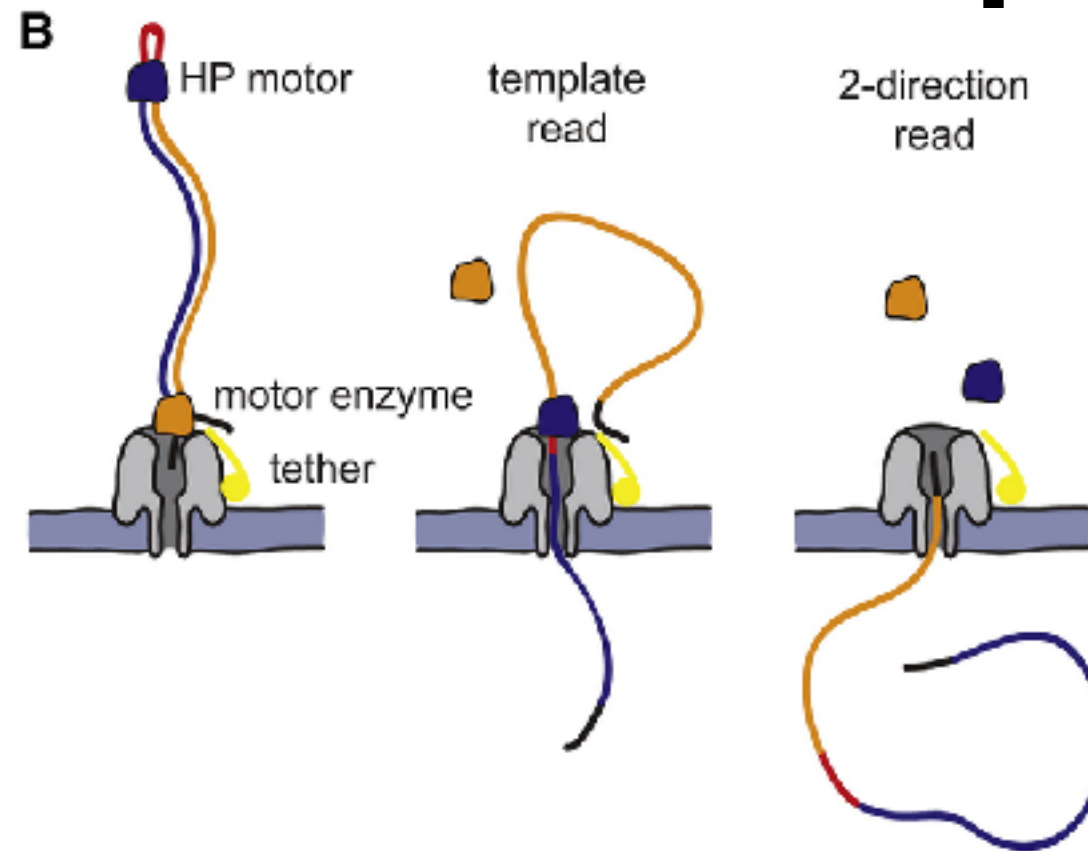
| 1st Generation                | 2nd Generation                               | 3rd Generation                           |
|-------------------------------|--|--|
| Chemical<br>(Maxim-Gilbert)   | Pyrosequencing<br>(454)                      | Single molecule real time<br>(PacBio)    |
| Chain Termination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

# Pacific Biosciences



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

# Oxford Nanopore



# Sequencers



<https://www2.nanoporetech.com/images/product-page/MinION-Banner.jpg>  
<http://www.gatc-biotech.com/en/gatc/sequencing-technologies/pacbio-rs-ii.html>  
<http://www.dnavision.com/illumina.php>



## **DNA-Seq**

1. Purify DNA
2. Fragment
3. Size Select
4. Adapter Ligation

## **RNA-Seq**

1. Purify **RNA**
2. Fragment
3. Size Select
4. **Make DNA From RNA**
5. Adapter Ligation